SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO
No. 11-133166- -00000-0000
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Tra. 11 PATENTEIYII Eve: 379 FASENACIONALII
Act. 411 PRESENTACION Folios: 1389

Industria y Comercio

SUPERINTENDENCIA

DELEGATURA DE PROPIEDAD INDUSTRIAL

División de Nuevas Creaciones

SOLICITUD
PATENTE DE INVENCIÓN

21. **EXPEDIENTE No.** _____

54. **TÍTULO** CELULAS ÚTILES PARA ENSAYOS DE ACTIVIDAD DEL SEROTIPO A DE LA TOXINA BOTULINICA BASADOS EN INMUNOENSAYOS.

51. **CLASIFICACIÓN INTERNACIONAL** _____

71. **SOLICITANTE** ALLERGAN, INC

DOMICILIO 2525 Dupont Drive, Irvine, California 92612, E.U.A

74. **APODERADO** JERÓNIMO CASTILLO BONILLA

22. **BOGOTÁ, D.C.,** _____

1615

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO

No. 11-133166- -00000-0000

Fecha: 2011-10-07 16:09:48 Dep: 2020 DIR.NUEVASCR
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FORMULARIO ÙNICO DE SOLICITUD DE PATENTES
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(1) SOLICITUD DE:

[X] Patente de Invención [ ] Patente de Modelo de Utilidad

[ ] Capítulo I [X] Capítulo II

(2) SOLICITANTE

Nombre: ALLERGAN, INC
Dirección: 2525 Dupont Drive, Irvine, California 92612, E.U.A.
Nacionalidad o Domicilio: estadounidense
Lugar de Constitución: Delaware
Teléfono: Fax:
E-mail:

IDENTIFICACION
[ ] C.C. [ ] NIT
[ ] C.E. [ ] Otro
Cual:
Número:

(3) REPRESENTANTE O APODERADO

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Dirección: Calle 93A No. 14-17, Ofc 311 Bogotá, D.C.
Teléfono: 2 363493 Fax: 2 182351
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IDENTIFICACIÓN
[X] C.C. [ ] NIT
[ ] C.E. [ ] Otro
Cúal
Número 79462057 TP 104167

En caso de haber presentado poder general para asuntos que se adelanten ante la Delegatura de Propiedad Industrial, sírvase indicar el numero de radicación (del poder).

(4) INVENTOR (ES)

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(5) PCT (86)

Solicitud Internacional No. PCT/US2010/027242 Fecha Marzo 12, 2010
Publicación internacional No. WO 2010/105234 Fecha Septiembre 16, 2010

(6) Título (54) CELULAS UTILES PARA ENSAYOS DE ACTIVIDAD DEL SEROTIPO A DE LA TOXINA BOTULINICA BASADOS EN INMUNOENSAYOS

(7) Clasificación Internacional (51)

(8) Prioridad

[X] SI [ ] NO

(33)País de Origen	(32) Fecha	(31) Número de Solicitud
US	Marzo 13, 2009	61/160.199

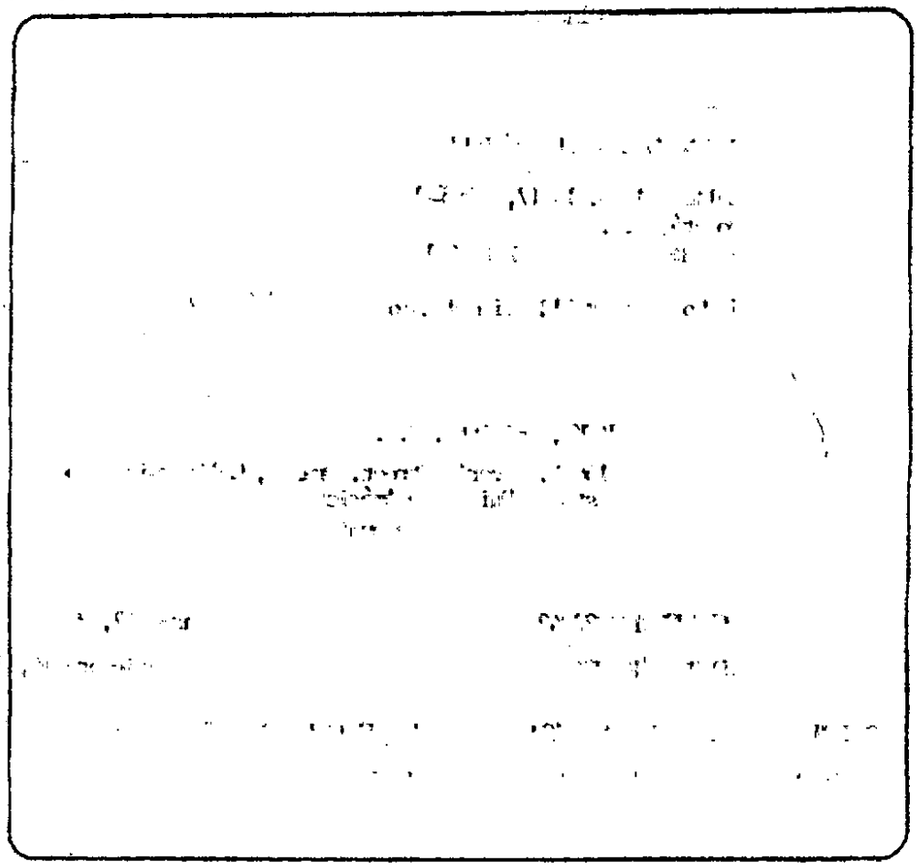
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10 ANEXOS

- [X] Comprobante de pago de la tasa de representación de la solicitud.
- [X] Documento que acredite la existencia y representación legal cuando el solicitante sea persona jurídica.
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- [ ] Otros. **Publicación Internacional**

11 FIGURA CARACTERÍSTICA:



12 Solicito la concesión de la patente.

NOMBRE: **JERONIMO CASTILLO BONILLA**

FIRMA:

C.C. **79462057** T.P. **104167**

Instrucciones para la presentación del os anexos, ver reverso de esta pagina.

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Nacionalidad : estadounidense

3

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ASSOCIATES
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1 Applicant's name	(1)	ALLERGAN, INC.
2 Applicant's address	domiciliado en (2)	domiciled in (2) 2525 Dupont Drive Irvine, CA 92612 USA

nombra al Dr. JERONIMO CASTILLO BONILLA y/o Dra. XIMENA BONILLA PEREIRA, y/o Dr. ALVARO CASTILLO GRAU, Calle 93A N° 14-17 Oficina 311 en Bogotá, Colombia, como sus representantes con poder especial, amplio y suficiente, para recabar de las oficinas y autoridades Colombianas, administrativas, judiciales o de policía, en primera o segunda instancia, la obtención de Patentes de Invención, Registro de Marcas, de Modelos y de Dibujos Industriales, de Nombres Comerciales y Enseñas, Lemas Comerciales y Denominaciones de Origen, lo mismo que traspasos, extensiones, renovaciones, cambios de nombre, registro de licencias de explotación y registro de licencias de uso referentes a tales actuaciones, cancelación de Registros de marca, a cuyo efecto les faculta para dar ante dichas autoridades todos los pasos necesarios al objeto indicado, elevar solicitudes, formular descripciones, enmiendas, protestas, declaraciones, apelaciones y reclamos, solicitar la aplicación de medidas cautelares; solicitar la nulidad de Patentes de Invención, modelos de utilidad, diseños industriales, así como la de registros de marcas ante la autoridad nacional competente; aceptar en nuestro nombre y representación la Cesión de derechos de invención y de patente de invención que se nos haga por cualquier persona, abonar todos los impuestos, cuotas y pagos determinados por la ley, recibir todos los documentos y valores dando el descargo respectivo, llenar cualesquiera otros requisitos, desistir y tomar en fin todas las medidas que creyeren conducentes al resguardo de nuestros intereses y en caso de presentarse oposiciones y/o observaciones para que intervengan como demandantes o como demandados, con todas las demás facultades necesarias, así como iniciar y tramitar procesos jurisdiccionales relativos a competencia desleal. Este poder comprende además las facultades de recibir, desistir, transigir, comprometer, sustituir, revocar sustituciones, conciliar, recibir notificaciones y nombrar apoderados judiciales o extrajudiciales.

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.....
.....

Given and signed in (3).....
Irvine, California
April 12, 2005

4)Applicant's signature

4)Signature (s)

Martin A. Voet
Assistant Secretary

Rosa Mercedes Romero Pinto NOTARIA
Notaría Treinta
DEL CIRCULO DE BOGOTA
23 SEP 2011
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State of California

SECRETARY OF STATE

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5. *At Sacramento, California*
6. *the 21st day of April 2005*
7. *by Deputy Secretary of State, State of California*
8. *No. 236021*
9. *Seal/Stamp:*



10. *Signature*

BRUCE McPHERSON
Secretary of State

BY

NP-24 A (REV. 2-05)

OSP 05 88438

5

CALIFORNIA ALL-PURPOSE ACKNOWLEDGMENT

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County of Orange } ss.

On April 12, 2005 (Date) before me, Tamara J. Hallen, Notary Public (Name and Title of Officer (e.g., "Jane Doe, Notary Public")),

personally appeared Martin A. Voet (Name(s) of Signer(s)),

☑ personally known to me
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to be the person(s) whose name(s) is/~~are~~ subscribed to the within instrument and acknowledged to me that he/~~she/they~~ executed the same in his/~~her/their~~ authorized capacity(~~ies~~), and that by his/~~her/their~~ signature(~~s~~) on the instrument the person(~~s~~), or the entity upon behalf of which the person(s) acted, executed the instrument.

TAMARA J. HALLEN
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Orange County
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I, (name), hereby solemnly and truly declare that I am (post of) for ALLERGAN, INC, domiciled at 2525 Dupont Drive, Irvine, California 92612, United States of America, Corporation organized in accordance with the laws of the State of ~~California~~ Delaware and that I am empowered to grant this declaration.

Signed this 19th day of July, 2006.

ALLERGAN, INC

By: (Signature)
Name

Martin A. Voet, Assistant Secretary

Note: Notarized and Legalized up by Apostille

Rosa Mercedes Romero Pinto
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6. *the 3rd day of August 2006*
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8. *No. 297443*
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23 SEP 2011

10. *Signature*

Secretary of State

BY

NP-24 A (REV. 4-05)

OSP 05 90772

STATE OF CALIFORNIA

County of Orange

I, **TOM DALY**, County Clerk-Recorder in and for said County, having by law a seal do hereby certify that **MARY LOU MC NOWN** whose name is subscribed to the attached certificate of acknowledgement, proof of affidavit, was at the time of taking such acknowledgment, proof or affidavit, a Notary Public IN AND FOR ORANGE COUNTY, duly commissioned and sworn and residing in said County, and was, as such, an officer of said State, duly authorized by the laws thereof to take and certify the same, as well as to take and certify the proof and acknowledgment of deeds and other instruments in writing to be recorded in said State, and that full faith and credit are and ought to be given to his official acts; that the impression of his official seal is not required by law to be filed in the office of the County Clerk-Recorder. I further certify that I am well acquainted with his hand writing and verily believe that the signature to the attached certificate is his genuine signature, and further that the annexed instrument is executed and acknowledged according to the laws of the State of California.

IN WITNESS WHEREOF, I have hereunto set my hand and affixed the seal of said County Clerk-Recorder.

This 25th day of JULY 2006

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State of California
County of ORANGE } ss.

On JULY 19 2006 (Date) before me, MARY LOU MCNOWN, notary public, (Name and Title of Officer (e.g., "Jane Doe, Notary Public"))

personally appeared MARTIN A. VOET (Name(s) of Signer(s))

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to be the person(s) whose name(s) is/are subscribed to the within instrument and acknowledged to me that he/she/they executed the same in his/her/their authorized capacity(ies), and that by his/her/their signature(s) on the instrument the person(s), or the entity upon behalf of which the person(s) acted, executed the instrument.

WITNESS my hand and official seal.

Mary Lou McNown
Signature of Notary Public

MARY LOU MC NOWN
Commission # 1431736
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(71) Applicant *(for all designated States except US)*: ALLERGAN, INC. [US/US]; 2525 Dupont Drive, Irvine, CA 92612 (US).

(72) Inventors; and

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(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PE, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

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Published:

— *with international search report (Art. 21(3))*

— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*

— *with sequence listing part of description (Rule 5.2(a))*

(54) Title: CELLS USEFUL FOR IMMUNO-BASED BOTULINUM TOXIN SEROTYPE A ACTIVITY ASSAYS

(57) Abstract: The present specification discloses clonal cell lines susceptible to BoNT/A intoxication, methods of producing such clonal cell lines, and methods of detecting Botulinum toxin serotype A activity using such clonal cell lines.

WO 2010/105234 A1

Cells Useful for Immuno-Based Botulinum Toxin Serotype A Activity Assays

[01] This patent application claims priority pursuant to 35 U.S.C. § 119(e) to U. S. Provisional Patent Application Serial No. 61/160,199 filed March 13, 2009, which is hereby incorporated by reference in its entirety.

[02] The sequences discosed in the present specification are contained in the Sequence Listing submitted with the present specification which is hereby incorporated by reference in its entirety.

[03] The ability of Clostridial toxins, such as, e.g., Botulinum neurotoxins (BoNTs), BoNT/A, BoNT/B, BoNT/C1, BoNT/D, BoNT/E, BoNT/F and BoNT/G, and Tetanus neurotoxin (TeNT), to inhibit neuronal transmission are being exploited in a wide variety of therapeutic and cosmetic applications, see e.g., William J. Lipham, Cosmetic and Clinical Applications of Botulinum Toxin (Slack, Inc., 2004). Clostridial toxins commercially available as pharmaceutical compositions include, BoNT/A preparations, such as, e.g., BOTOX® (Allergan, Inc., Irvine, CA), DYSPORT®/RELOXIN®, (Ipsen Ltd., Slough, England), PURTOX® (Mentor Corp., Santa Barbara, CA), XEOMIN® (Merz Pharmaceuticals, GmbH., Frankfurt, Germany), NEURONOX® (Medy-Tox, Inc., Ochang-myeon, South Korea), BTX-A (Biogen-tech Ltd., University, Yantai, Shandong, China); and BoNT/B preparations, such as, e.g., MYOBLOC®/NEUROBLOC® (Solstice Neurosciences, Inc., South San Francisco, CA). As an example, BOTOX® is currently approved in one or more countries for the following indications: achalasia, adult spasticity, anal fissure, back pain, blepharospasm, bruxism, cervical dystonia, essential tremor, glabellar lines or hyperkinetic facial lines, headache, hemifacial spasm, hyperactivity of bladder, hyperhidrosis, juvenile cerebral palsy, multiple sclerosis, myoclonic disorders, nasal labial lines, spasmodic dysphonia, strabismus and VII nerve disorder.

[04] At present the mouse LD_{50} bioassay, a lethality test, remains the "gold standard" test used by all pharmaceutical manufacturers to express the potency of their preparations. S. S. Arnon et al., JAMA 285: 1059-1070 (2001). In fact, the units on the pharmaceutical preparations' labels are mouse LD_{50} units and the number of animals needed to produce statistically useful LD_{50} data is large. The advantage of the mouse LD_{50} bioassay is that it measures all the steps necessary for botulinum toxin uptake (*e.g.*, toxin binding to a cell surface receptor, internalization of the toxin-receptor complex, light chain translocation into the cytoplasm, light chain cleavage of substrate), instead of merely determining the activity for only part of this intoxication process, such as, *e.g.*, in vitro assays that only measure light chain enzymatic activity. Unfortunately, the mouse LD_{50} bioassay suffers from many drawbacks including high operational cost due to the large numbers of laboratory animals required, a lack of specificity since all BoNT serotypes will cause the same measurable end-point, and the potential for inaccuracy unless large animal groups are used. In addition, animal rights groups have exerted pressure on regulatory agencies in the United States (FDA/NICEATM/ICCVAM) and Europe (MHRA and EDQM), and on pharmaceutical companies manufacturing botulinum neurotoxin products to reduce animal testing and more importantly replace the mouse LD_{50} bioassay for product release. The regulatory agencies are engaging

pharmaceutical companies to apply the three "Rs" principle to the potency testing of botulinum neurotoxins: Reduce, Refine, Replace. D. Straughan, *Progress in Applying the Three Rs to the Potency Testing of Botulinum Toxin Type A*, Altern. Lab. Anim. 34(3): 305-313 (2006). In recent years, several steps have been already taken to reduce and refine the mouse LD_{50} bioassay in order to standardize the protocol and produce more consistent data using fewer animals per assay.

[05] Thus, a simple, reliable, validated and governmental agency acceptable botulinum toxin activity assay that can evaluate the integrity of all the steps necessary in botulinum toxin uptake would be of significant value because such a non-animal based assay would alleviate the need for animal testing and all the disadvantages, costs and ethical concerns associated with this type of animal-based assay. Companion patent application Ester Fernandez-Salas, et al., *Immuno-Based Botulinum Toxin Serotype A Activity Assays*, U.S. Patent Application Serial No: 12/403,531, provides novel compositions, cells, and methods for assaying the activity of a BoNT/A useful for various industries, such as, *e.g.*, the pharmaceutical and food industries. Such compositions, cells, and methods do not use live animals or tissues taken from live animals, but can evaluate all the steps necessary for neurotoxin action, namely, binding and cellular uptake of toxin, translocation into the cell cytosol, and protease activity.

[06] One of the necessary components for the methods disclosed in U.S. Patent Application Serial No: 12/403,531 is the use of cells from an established cell line that are susceptible to low levels of BoNT/A intoxication because the amount of BoNT/A contained within a commercially-available pharmaceutical composition is very low. For example, approximately 4-5 ng of a BoNT/A complex is contained in the pharmaceutical composition sold as BOTOX®. Thus, there is a need to identify and create established cell lines comprising cells that are susceptible to BoNT/A intoxication when only very low levels of the neurotoxin is present in the sample. The present specification provides novel cells and cell compositions. that are susceptible to BoNT/A intoxication when only very low amounts of BoNT/A is present and thus allow assaying of commercially-available pharmaceutical composition comprising BoNT/A.

BRIEF DESCRIPTION OF THE DRAWINGS

[07] **FIG. 1** shows a schematic of the current paradigm of neurotransmitter release and Clostridial toxin intoxication in a central and peripheral neuron. FIG. 1A shows a schematic for the neurotransmitter release mechanism of a central and peripheral neuron. The release process can be described as comprising two steps: 1) vesicle docking, where the vesicle-bound SNARE protein of a vesicle containing neurotransmitter molecules associates with the membrane-bound SNARE proteins located at the plasma membrane; and 2) neurotransmitter release, where the vesicle fuses with the plasma membrane and the neurotransmitter molecules are exocytosed. FIG. 1B shows a schematic of the intoxication mechanism for tetanus and botulinum toxin activity in a central and peripheral neuron. This intoxication process can be described as comprising four steps: 1) receptor binding, where Clostridial toxin binding to a Clostridial receptor complex and initiates the intoxication process; 2) complex internalization, where after toxin binding, a vesicle containing a toxin/receptor system complex is endocytosed into the cell; 3) light chain

translocation, where multiple events are thought to occur, including changes in the internal pH of the vesicle, formation of a channel pore comprising the H_N domain of Clostridial toxin heavy chain, separation of the Clostridial toxin light chain from the heavy chain, and release of the light chain and 4) enzymatic target modification, where the light chain of Clostridial toxin proteolytically cleaves its target SNARE substrates, such as, *e.g.*, SNAP-25, VAMP or Syntaxin, thereby preventing vesicle docking and neurotransmitter release

[08] **FIG. 2** shows volcano plots of genes that are more than 4-fold ($\log_2(4) = 2$) up or down regulated in BB10 and H1 cell lines as compared to the 2D6 cell line. FIG. 2A shows the genes that are up regulated in the BB10 cell line as compared to the 2D6 cell line. FIG2B shows the genes that are up regulated in the H1 cell line as compared to the 2D6 cell line. FIG2C shows the genes that are up regulated in the BB10 cell line as compared to the parental SiMa cell line (PA). FIG2D shows the genes that are up regulated in the H1 cell line as compared to the parental SiMa cell line (PA). FIG2E shows the genes that are up regulated in the parental SiMa cell line (PA) as compared to the 2D6 cell line. FIG. 2F shows the genes that are down regulated in the BB10 cell line as compared to the 2D6 cell line. FIG2G shows the genes that are down regulated in the H1 cell line as compared to the 2D6 cell line. FIG2H shows the genes that are down regulated in the parental SiMa cell line (PA) as compared to the2D6 cell line. Each dot represents a probe set. The dashed line marks the 95 % confidence interval, $p \leq 0.05$. Most of the genes that are over expressed in BB10 and H1 compared to 2D6 (A and B) are also over or under-expressed in BB10 compared to PA (C), in H1 compared to PA (D), and in PA compared to 2D6 (E), however a number of them are less than 4-fold over-expressed and/or do not pass the 95 % confidence interval.

[09] **FIG. 3** shows normalized BIAcore SPR curves of 7.8 nM of the antibodies 2E2A6, 1D3B8, 3C1A5 and 2C9B10 and commercial MC-6050 and MC-6053. FIG. 3A shows the normalized data for the on-rate of each antibody. FIG. 3B shows the normalized data for the off-rate of each antibody.

DETAILED DESCRIPTION

[010] The present specification provides novel cells and cell compositions that are susceptible to BoNT/A intoxication to allow assaying of BoNT/A and BoNT/A compositions such as, *e.g.*, commercially-available pharmaceutical composition comprising BoNT/A. The cell and cell compositions disclosed in the present specification are useful to conduct methods that can detect picomolar quantities of BoNT/A in a sample, such as the methods disclosed in, *e.g.*, Ester Fernandez-Salas, et al., *Immuno-Based Botulinum Toxin Serotype A Activity Assays*, U.S. Patent Application Serial No: 12/403,531, which is hereby incorporated by reference in its entirety. The cells and cell compositions, and their use in methods of detecting BoNT/A activity reduce the need for animal toxicity studies, yet serve to analyze the multiple steps of BoNT/A intoxication, namely, binding and cellular uptake of toxin, translocation into the cell cytosol, and protease activity. As discussed further below, the novel cells and cell compositions of the present specification can be used in assays that analyze crude and bulk samples as well as highly

purified di-chain toxins and formulated toxin products and further are amenable to automated high throughput assay formats.

[011] Thus, aspects of the present specification provide a cell composition comprising cells from a clonal cell line that are susceptible to BoNT/A intoxication.

[012] Other aspects of the present specification provide a method of detecting BoNT/A activity using the clonal cell lines disclosed in the present specification.

[013] Clostridia toxins produced by *Clostridium botulinum*, *Clostridium tetani*, *Clostridium baratii* and *Clostridium butyricum* are the most widely used in therapeutic and cosmetic treatments of humans and other mammals. Strains of *C. botulinum* produce seven antigenically-distinct serotypes of botulinum toxins (BoNTs), which have been identified by investigating botulism outbreaks in man (BoNT/A, BoNT/B, BoNT/E and BoNT/F), animals (BoNT/C1 and BoNT/D), or isolated from soil (BoNT/G). While all seven botulinum toxin serotypes have similar structure and biological properties, each also displays heterogeneous characteristics, such as, *e.g.*, different pharmacological properties. In contrast, tetanus toxin (TeNT) is produced by a uniform group of *C. tetani*. Two other species of Clostridia, *C. baratii* and *C. butyricum*, also produce toxins similar to BoNT/F and BoNT/E, respectively.

[014] Clostridial toxins are each translated as a single chain polypeptide of approximately 150 kDa that is subsequently cleaved by proteolytic scission within a disulfide loop by a naturally-occurring protease, such as, e.g., an endogenous Clostridial toxin protease or a naturally-occurring protease produced in the environment. This posttranslational processing yields a di-chain molecule comprising an approximately 50 kDa light chain (LC) and an approximately 100 kDa heavy chain (HC) held together by a single disulfide bond and noncovalent interactions. Each mature di-chain molecule comprises three functionally distinct domains: 1) an enzymatic domain located in the LC that includes a metalloprotease region containing a zinc-dependent endopeptidase activity which specifically targets core components of the neurotransmitter release apparatus; 2) a translocation domain contained within the amino-terminal half of the HC (H_N) that facilitates release of the LC from intracellular vesicles into the cytoplasm of the target cell; and 3) a binding domain found within the carboxyl-terminal half of the HC (H_C) that determines the binding activity and binding specificity of the toxin to the receptor complex located at the surface of the target cell.

[015] The binding, translocation and enzymatic activity of these three functional domains are all necessary for toxicity. While all details of this process are not yet precisely known, the overall cellular intoxication mechanism whereby Clostridial toxins enter a neuron and inhibit neurotransmitter release is similar, regardless of serotype or subtype. Although the applicants have no wish to be limited by the following description, the intoxication mechanism can be described as comprising at least four steps: 1) receptor binding, 2) complex internalization, 3) light chain translocation, and 4) enzymatic target modification (FIG. 1). The process is initiated when the H_C binding domain of a Clostridial toxin binds to a

toxin-specific receptor system located on the plasma membrane surface of a target cell. The binding specificity of a receptor complex is thought to be achieved, in part, by specific combinations of gangliosides and protein receptors that appear to distinctly comprise each Clostridial toxin receptor complex. Once bound, the toxin/receptor complexes are internalized by endocytosis and the internalized vesicles are sorted to specific intracellular routes. The translocation step appears to be triggered by the acidification of the vesicle compartment. This process seems to initiate important pH-dependent structural rearrangements that increase hydrophobicity, promote pore formation, and facilitate separation of the heavy and light chains of the toxin. Once separated, the light chain endopeptidase of the toxin is released from the intracellular vesicle into the cytosol where it appears to specifically target core components of the neurotransmitter release apparatus. These core proteins, vesicle-associated membrane protein (VAMP)/synaptobrevin, synaptosomal-associated protein of 25 kDa (SNAP-25) and Syntaxin, are necessary for synaptic vesicle docking and fusion at the nerve terminal and constitute members of the soluble N-ethylmaleimide-sensitive factor-attachment protein-receptor (SNARE) family. BoNT/A and BoNT/E cleave SNAP-25 in the carboxyl terminal region, releasing a nine or twenty six amino acid fragment, respectively, and BoNT/C1 also cleaves SNAP-25 near the carboxyl terminus releasing an eight amino acid fragment. The botulinum serotypes BoNT/B, BoNT/D, BoNT/F and BoNT/G, and tetanus toxin, act on the conserved central portion of VAMP, and release the amino terminal portion of VAMP into the cytosol. BoNT/C1 cleaves syntaxin at a single site near the cytosolic membrane surface. The selective proteolysis of synaptic SNAREs accounts for the block of neurotransmitter release caused by Clostridial toxins in vivo. The SNARE protein targets of Clostridial toxins are common to exocytosis in a variety of non-neuronal types; in these cells, as in neurons, light chain peptidase activity inhibits exocytosis, see, e.g., Yann Humeau et al., *How Botulinum and Tetanus Neurotoxins Block Neurotransmitter Release*, 82(5) Biochimie. 427-446 (2000); Kathryn Turton et al., *Botulinum and Tetanus Neurotoxins: Structure, Function and Therapeutic Utility*, 27(11) Trends Biochem. Sci. 552-558. (2002); Giovanna Lalli et al., *The Journey of Tetanus and Botulinum Neurotoxins in Neurons*, 11(9) Trends Microbiol. 431-437, (2003).

[016] Aspects of the present disclosure comprise, in part, a cell from an established cell line. As used herein, the term "cell" refers to any eukaryotic cell susceptible to BoNT/A intoxication by a BoNT/A or any eukaryotic cell that can uptake a BoNT/A. The term cell encompasses cells from a variety of organisms, such as, *e.g.*, murine, rat, porcine, bovine, equine, primate and human cells; from a variety of cell types such as, *e.g.*, neuronal and non-neuronal; and can be isolated from or part of a heterogeneous cell population, tissue or organism. As used herein, the term "established cell line" is synonymous with "immortal cell line," or "transformed cell line" and refers to a cell culture of cells selected for indefinite propagation from a cell population derived from an organism, tissue, or organ source. By definition, an established cell line excludes a cell culture of primary cells. As used herein, the term "primary cells" are cells harvested directly from fresh tissues or organs and do not have the potential to propagate indefinitely. An established cell line can comprise a heterogeneous population of cells or a uniform population of cells. An established cell line derived from a single cell is referred to as a clonal cell line. An established cell line can be one whose cells endogenously express all component necessary for the

cells to undergo the overall cellular mechanism whereby a BoNT/A proteolytically cleaves a SNAP-25 substrate and encompasses the binding of a BoNT/A to a BoNT/A receptor, the internalization of the neurotoxin/receptor complex, the translocation of the BoNT/A light chain from an intracellular vesicle into the cytoplasm and the proteolytic cleavage of a SNAP-25. Alternatively, an established cell line can be one whose cells have had introduced from an exogenous source at least one component necessary for the cells to undergo the overall cellular mechanism whereby a BoNT/A proteolytically cleaves a SNAP-25 substrate and encompasses the binding of a BoNT/A to a BoNT/A receptor, the internalization of the neurotoxin/receptor complex, the translocation of the BoNT/A light chain from an intracellular vesicle into the cytoplasm and the proteolytic cleavage of a SNAP-25. Also referred to as a genetically-engineered cell line, cells from such an established cell line may, *e.g.*, express an exogenous FGFR2, an exogenous FGFR3, an exogenous SV2, an exogenous SNAP-25, or any combination thereof. As used herein, the term "established clonal cell line" or "clonal cell line" refers to a cell culture of cells selected from a heterogenous population of cell types comprising an established cell line, which can also be referred to as a parental cell line. Thus, as a non-limiting example, the cells from the A6, A7, A9, A10, A11, B5, B10, C5, C11, C12, D7, D11, E11, F10, H1, H3, H8, H10, 1E3, 2B9, 2E4, 3B8, 3D5, 3G10, 4B5, 4C8, 5F3, AC9, AF4, BB3, BB10, BE3, BF8, CC11, CD6, CE6, CG8, CG10, DC4, DD10, DE7, YF5, and H1 1.4 clonal cell lines were selected from the heterogenous population of cell types comprising the SiMa cell line (or parental SiMa cell line) DSMZ ACC 164.

[017] Aspects of the present disclosure comprise, in part, a cell from an established clonal cell line susceptible to BoNT/A intoxication. As used herein, the terms "cell(s) susceptible to BoNT/A intoxication," "cell(s) susceptible to BoNT/A intoxication by a BoNT/A," or "cell(s) from an established clonal cell line susceptible to BoNT/A intoxication by a BoNT/A" refer to cell(s) that can undergo the overall cellular mechanism whereby a BoNT/A proteolytically cleaves a SNAP-25 substrate and encompasses the binding of a BoNT/A to a BoNT/A receptor, the internalization of the neurotoxin/receptor complex, the translocation of the BoNT/A light chain from an intracellular vesicle into the cytoplasm and the proteolytic cleavage of a SNAP-25. By definition, cell(s) susceptible to BoNT/A intoxication must express, or be engineered to express, at least one BoNT/A receptor and at least one SNAP-25 substrate. Non-limiting examples of a cell or cells from an established clonal cell line susceptible to BoNT/A intoxication, include A6, A7, A9, A10, A11, B5, B10, C5, C11, C12, D7, D11, E11, F10, H1, H3, H8, H10, 1E3, 2B9, 2D2, 2D6, 2E4, 3B8, 3D5, 3G10, 4B5, 4C8, 4D3, 5C10, 5F3, AC9, AF4, BB3, BB10, BE3, BF8, CC11, CD6, CE6, CG8, CG10, DC4, DD10, DE7, DF5, YB7, YF5, and H1 1.4 clonal cell lines. As used herein, the terms "cell(s) that can uptake BoNT/A" or "cell(s) comprising an established clonal cell line that can uptake BoNT/A" refer to cells that can undergo the overall cellular mechanism whereby a BoNT/A proteolytically cleaves a SNAP-25 substrate and encompasses the binding of a BoNT/A to a BoNT/A receptor, the internalization of the neurotoxin/receptor complex, the translocation of the BoNT/A light chain from an intracellular vesicle into the cytoplasm and the proteolytic cleavage of a SNAP-25. By definition, cell(s) that can uptake BoNT/A must express, or be engineered to express, at least one BoNT/A receptor and at least one SNAP-25 substrate. Non-limiting examples of a cell or cells from an established clonal cell line that can uptake BoNT/A, include A6, A7, A9, A10, A11, B5, B10, C5, C11, C12, D7, D11, E11, F10, H1,

H3, H8, H10, 1E3, 2B9, 2D2, 2D6, 2E4, 3B8, 3D5, 3G10, 4B5, 4C8, 4D3, 5C10, 5F3, AC9, AF4, BB3, BB10, BE3, BF8, CC11, CD6, CE6, CG8, CC10, DC4, DD10, DE7, DF5, YB7, YF5, and H1 1.4 clonal cell lines. Cell lines comprising cell(s) from an established clonal cell line susceptible to BoNT/A intoxication or cell(s) that can uptake BoNT/A are referred to as a "responder cell line."

[018] Aspects of the present disclosure comprise, in part, cells from an established clonal cell line more susceptible to BoNT/A intoxication. As used herein, the terms "cell(s) more susceptible to BoNT/A intoxication," "cell(s) more susceptible to BoNT/A intoxication by a BoNT/A," or "cell(s) from an established clonal cell line more susceptible to BoNT/A intoxication by a BoNT/A" refer to cell(s) that undergo the overall cellular mechanism whereby a BoNT/A proteolytically cleaves a SNAP-25 substrate to a greater degree as compared to a cell(s) comprising a parental SiMa cell line, such as, *e.g.*, parental SiMa cell line DSMZ ACC 164. Non-limiting examples of a cell or cells from an established clonal cell line more susceptible to BoNT/A intoxication, include a cell or cells from a A10, H1, 2E4, 3B8, 3D5, 5F3, AF4, BB3, BB10, DC4, or H1 1.4 clonal cell lines. As used herein, the terms "cell(s) that uptake BoNT/A more" or "cell(s) comprising an established clonal cell line that uptake BoNT/A more" refer to cells that undergo the overall cellular mechanism whereby a BoNT/A proteolytically cleaves a SNAP-25 substrate to a greater degree as compared to a cell(s) comprising a parental SiMa cell line, such as, *e.g.*, parental SiMa cell line DSMZ ACC 164. Non-limiting examples of a cell or cells from an established clonal cell line that can uptake BoNT/A more, include a cell or cells from a A10, H1, 2E4, 3B8, 3D5, 5F3, AF4, BB3, BB10, DC4, or H1 1.4 clonal cell lines. Cell lines comprising cell(s) from an established clonal cell line more susceptible to BoNT/A intoxication or cell(s) that can uptake BoNT/A more are referred to as a "high responder cell line."

[019] Aspects of the present disclosure comprise, in part, cells from an established clonal cell line less susceptible to BoNT/A intoxication. As used herein, the terms "cell(s) less susceptible to BoNT/A intoxication," "cell(s) less susceptible to BoNT/A intoxication by a BoNT/A," or "cell(s) from an established clonal cell line less susceptible to BoNT/A intoxication by a BoNT/A" refer to cell(s) that undergo the overall cellular mechanism whereby a BoNT/A proteolytically cleaves a SNAP-25 substrate to a lesser degree as compared to a cell(s) comprising a parental SiMa cell line, such as, *e.g.*, parental SiMa cell line DSMZ ACC 164. Non-limiting examples of a cell or cells from an established clonal cell line less susceptible to BoNT/A intoxication, include A7, B10, D11, H10, 2D2, 2D6, 4D3, 5C10, DF5, and YB7 clonal cell lines. As used herein, the terms "cell(s) that uptake BoNT/A less" or "cell(s) comprising an established clonal cell line that uptake BoNT/A less" refer to cells that undergo the overall cellular mechanism whereby a BoNT/A proteolytically cleaves a SNAP-25 substrate to a lesser degree as compared to a cell(s) comprising a parental SiMa cell line, such as, *e.g.*, parental SiMa cell line DSMZ ACC 164. Non-limiting examples of a cell or cells from an established clonal cell line that can uptake BoNT/A less, include A7, B10, D11, H10, 2D2, 2D6, 4D3, 5C10, DF5, and YB7 clonal cell lines. Cell lines comprising cell(s) from an established clonal cell line less susceptible to BoNT/A intoxication or cell(s) that can uptake BoNT/A less are referred to as a "low responder cell line."

[020] Aspects of the present disclosure comprise, in part, a cell from an established clonal cell line not susceptible to BoNT/A intoxication. As used herein, the terms "cell(s) not susceptible to BoNT/A intoxication," "cell(s) not susceptible to BoNT/A intoxication by a BoNT/A," or "cell(s) from an established clonal cell line not susceptible to BoNT/A intoxication by a BoNT/A" refer to cell(s) that cannot undergo the overall cellular mechanism whereby a BoNT/A proteolytically cleaves a SNAP-25 substrate. As used herein, the terms "cell(s) that cannot uptake BoNT/A" or "cell(s) comprising an established clonal cell line that cannot uptake BoNT/A" refer to cells that cannot undergo the overall cellular mechanism whereby a BoNT/A proteolytically cleaves a SNAP-25 substrate. Cell lines comprising cell(s) from an established clonal cell line not susceptible to BoNT/A intoxication or cell(s) that cannot uptake BoNT/A are referred to as a "non-responder cell line."

[021] Thus in an embodiment, cells from an established clonal cell line are susceptible to BoNT/A intoxication. In aspects of this embodiment, cells from an established clonal cell line are susceptible to BoNT/A intoxication by, *e.g.*, about 500 pM or less, about 400 pM or less, about 300 pM or less, about 200 pM or less, or about 100 pM or less of a BoNT/A. In other aspects of this embodiment, cells from an established clonal cell line are susceptible to BoNT/A intoxication by, *e.g.*, about 90 pM or less, about 80 pM or less, about 70 pM or less, about 60 pM or less, about 50 pM or less, about 40 pM or less, about 30 pM or less, about 20 pM or less, or about 10 pM or less of a BoNT/A. In still other aspects, cells from an established clonal cell line are susceptible to BoNT/A intoxication by, *e.g.*, about 9 pM or less, about 8 pM or less, about 7 pM or less, about 6 pM or less, about 5 pM or less, about 4 pM or less, about 3 pM or less, about 2 pM or less, or about 1 pM or less of a BoNT/A. In yet other aspects, cells from an established clonal cell line are susceptible to BoNT/A intoxication by, *e.g.*, about 0.9 pM or less, about 0.8 pM or less, about 0.7 pM or less, about 0.6 pM or less, about 0.5 pM or less, about 0.4 pM or less, about 0.3 pM or less, about 0.2 pM, or about 0.1 pM or less of a BoNT/A. As used herein, the term "about" when qualifying a value of a stated item, number, percentage, or term refers to a range of plus or minus ten percent of the value of the stated item, percentage, parameter, or term.

[022] In another embodiment, cells comprising an established clonal cell line can uptake a BoNT/A. In aspects of this embodiment, cells comprising an established clonal cell line can uptake, *e.g.*, about 500 pM or less, about 400 pM or less, about 300 pM or less, about 200 pM or less, or about 100 pM or less of a BoNT/A. In other aspects of this embodiment, cells comprising an established clonal cell line possess the ability to uptake about 90 pM or less, about 80 pM or less, about 70 pM or less, about 60 pM or less, about 50 pM or less, about 40 pM or less, about 30 pM or less, about 20 pM or less, or about 10 pM or less of a BoNT/A. In still other aspects, cells comprising an established clonal cell line possess the ability to uptake about 9 pM or less, about 8 pM or less, about 7 pM or less, about 6 pM or less, about 5 pM or less, about 4 pM or less, about 3 pM or less, about 2 pM or less, or about 1 pM or less of a BoNT/A. In yet other aspects, cells comprising an established clonal cell line possess the ability to uptake about 0.9 pM or less, about 0.8 pM or less, about 0.7 pM or less, about 0.6 pM or less, about 0.5 pM or less, about 0.4 pM or less, about 0.3 pM or less, about 0.2 pM or less, or about 0.1 pM or less of a BoNT/A. In other aspects, cells comprising an established clonal cell line can uptake BoNT/A from, *e.g.*, about 0.01 pM to

about 100 pM, about 0.01 pM to about 75 pM, about 0.01 pM to about 50 pM, about 0.01 pM to about 25 pM, about 0.01 pM to about 20 pM, about 0.01 pM to about 15 pM, about 0.01 pM to about 10 pM, about 0.01 pM to about 5 pM, about 0.001 pM to about 100 pM, about 0.001 pM to about 75 pM, about 0.001 pM to about 50 pM, about 0.001 pM to about 25 pM, about 0.001 pM to about 20 pM, about 0.001 pM to about 15 pM, about 0.001 pM to about 10 pM, or about 0.001 pM to about 5 pM of BoNT/A.

[023] In another embodiment, cells from an established clonal cell line are not susceptible to BoNT/A intoxication. In aspects of this embodiment, cells from an established clonal cell line are not susceptible to BoNT/A intoxication by, *e.g.*, about 500 pM or less, about 400 pM or less, about 300 pM or less, about 200 pM or less, or about 100 pM or less of a BoNT/A. In other aspects of this embodiment, cells from an established clonal cell line are susceptible to BoNT/A intoxication by, *e.g.*, about 90 pM or less, about 80 pM or less, about 70 pM or less, about 60 pM or less, about 50 pM or less, about 40 pM or less, about 30 pM or less, about 20 pM or less A, or about 10 pM or less of a BoNT/A. In still other aspects, cells from an established clonal cell line are not susceptible to BoNT/A intoxication by, *e.g.*, about 9 pM or less, about 8 pM or less, about 7 pM or less, about 6 pM or less, about 5 pM or less, about 4 pM or less, about 3 pM or less, about 2 pM or less, or about 1 pM or less of a BoNT/A. In yet other aspects, cells from an established clonal cell line are not susceptible to BoNT/A intoxication by, *e.g.*, about 0.9 pM or less, about 0.8 pM or less, about 0.7 pM or less, about 0.6 pM or less, about 0.5 pM or less, about 0.4 pM or less, about 0.3 pM or less, about 0.2 pM, or about 0.1 pM or less of a BoNT/A. In other aspects, cells from an established clonal cell line are not susceptible to BoNT/A intoxication from, *e.g.*, about 0.01 pM to about 100 pM, about 0.01 pM to about 75 pM, about 0.01 pM to about 50 pM, about 0.01 pM to about 25 pM, about 0.01 pM to about 20 pM, about 0.01 pM to about 15 pM, about 0.01 pM to about 10 pM, about 0.01 pM to about 5 pM, about 0.001 pM to about 100 pM, about 0.001 pM to about 75 pM, about 0.001 pM to about 50 pM, about 0.001 pM to about 25 pM, about 0.001 pM to about 20 pM, about 0.001 pM to about 15 pM, about 0.001 pM to about 10 pM, or about 0.001 pM to about 5 pM of BoNT/A.

[024] Aspects of the present disclosure comprise, in part, cells from an established clonal cell line susceptible to BoNT/A intoxication that are more stable than cells from a parental SiMa cell line, such as, *e.g.*, parental SiMa cell line DSMZ ACC 164. As used herein, the term "stable" refers to cells from an established clonal cell line for a particular passage number that exhibit a relative EC_{50}, sensitivity, efficacy, well-defined upper asymptote, and/or a well-defined dose-response curve for BoNT/A activity that is similar to the values for relative EC_{50}, sensitivity, efficacy, well-defined upper asymptote, and/or a well-defined dose-response curve exhibited by cells from a parental SiMa cell line, such as, *e.g.*, parental SiMa cell line DSMZ ACC 164, at the same or similar passage number, where the same assay conditions and the same BoNT/A (or molecule) are used in both assays.

[025] Thus in an embodiment, cells from an established clonal cell line are more stable as compared to a parental SiMa cell line. In an aspect of this embodiment, cells from an established clonal cell line are more stable as compared to the parental SiMa cell line DSMZ ACC 164. In other aspects of this embodiment, cells from an established clonal cell line are more stable for, *e.g.*, at least 5 more passages,

at least 10 more passages, at least 15 more passages, at least 20 more passages, at least 25 more passages, or at least 30 more passages, as compared to a parental SiMa cell line. In yet other aspects of this embodiment, cells from an established clonal cell line are more stable for, *e.g.*, at least 5 more passages, at least 10 more passages, at least 15 more passages, at least 20 more passages, at least 25 more passages, or at least 30 more passages, as compared to a parental SiMa cell line DSMZ ACC 164.

[026] Aspects of the present disclosure comprise, in part, cells from an established clonal cell line susceptible to BoNT/A intoxication that are stable over a plurality of cell passages. As used herein, the term "stable" refers to cells from an established clonal cell line for a particular passage number that exhibit a relative EC_{50}, sensitivity, efficacy, well-defined upper asymptote, and/or a well-defined dose-response curve for BoNT/A activity that is similar to the values for relative EC_{50}, sensitivity, efficacy, well-defined upper asymptote, and/or a well-defined dose-response curve exhibited by cells from the same established clonal cell line, but from a prior passage or passages, where the same assay conditions and the same BoNT/A (or molecule) are used in both assays.

[027] Cells from an established cell line disclosed in the present specification can exhibit consistent sensitivity to BoNT/A activity over a plurality of cell passages. As used herein, the term "sensitivity to BoNT/A activity" refers to the lowest dose that an assay can measure consistently above the signal detected by a non-treatment control or background signal.

[028] Thus, in an embodiment, cells from the established clonal cell line exhibit a sensitivity for BoNT/A activity for any given passages that is *e.g.*, 100 pM or less, about 80 pM or less, about 70 pM or less, about 60 pM or less, about 50 pM or less, about 40 pM or less, about 30 pM or less, about 20 pM or less, about 10 pM or less, about 1 pM or less, about 0.9 pM or less, about 0.8 pM or less, about 0.7 pM or less, about 0.6 pM or less, about 0.5 pM or less, about 0.4 pM or less, about 0.3 pM or less, about 0.2 pM or less, or about 0.1 pM or less of a BoNT/A. In aspects of this embodiment, cells from the established clonal cell line exhibit a sensitivity for BoNT/A activity for any given passages that is, *e.g.*, about 0.01 pM to about 100 pM, about 0.01 pM to about 75 pM, about 0.01 pM to about 50 pM, about 0.01 pM to about 25 pM, about 0.01 pM to about 20 pM, about 0.01 pM to about 15 pM, about 0.01 pM to about 10 pM, about 0.01 pM to about 5 pM, about 0.001 pM to about 100 pM, about 0.001 pM to about 75 pM, about 0.001 pM to about 50 pM, about 0.001 pM to about 25 pM, about 0.001 pM to about 20 pM, about 0.001 pM to about 15 pM, about 0.001 pM to about 10 pM, or about 0.001 pM to about 5 pM of BoNT/A.

[029] In another embodiment, cells from the established clonal cell line exhibit a sensitivity for BoNT/A activity that is about 100 pM or less, about 75 pM or less, about 50 pM or less, about 25 pM or less, less about 20 pM or less, about 15 pM or less, about 10 pM or less, or about 1 pM or less for, *e.g.*, 5 or more cell passages, 10 or more cell passages, 15 or more cell passages, 20 or more cell passages, 25 or more cell passages, 30 or more cell passages, 35 or more cell passages, 40 or more cell passages, 45 or more cell passages, or 50 or more cell passages. In other aspects of this embodiment, cells from the established clonal cell line exhibit a sensitivity for BoNT/A activity that is about 100 pM or less, about 75

pM or less, about 50 pM or less, about 25 pM or less, less about 20 pM or less, about 15 pM or less, about 10 pM or less, or about 1 pM or less for, *e.g.*, about 15 to about 60 passages, about 20 to about 60 passages, about 25 to about 60 passages, about 30 to about 60 passages, about 35 to about 60 passages, about 40 to about 60 passages, about 45 to about 60 passages, about 50 to about 60 passages, about 15 to about 50 passages, about 20 to about 50 passages, about 25 to about 50 passages, about 30 to about 50 passages, about 35 to about 50 passages, about 40 to about 50 passages, about 15 to about 40 passages, about 20 to about 40 passages, about 25 to about 40 passages, or about 30 to about 40 passages.

[030] Cells from an established cell line disclosed in the present specification can exhibit a consistent relative efficacy of BoNT/A uptake, BoNT/A activity, or BoNT/A intoxication over a plurality of cell passages. As used herein, the term "relative efficacy" refers to how well the upper asymptote for the BoNT/A activity detected in the current assay run compares to the upper asymptote for the BoNT/A activity detected in a reference standard, a reference molecule, or a reference passage number used on that assay. As used herein, the term "signal to noise ratio for the upper asymptote" refers to the signal detected in an assay at the upper limit of detection divided by the signal detected by a non-treatment control or background signal. The upper limit of detection is the highest dose that an assay can measure consistently before saturation of the signal occurs.

[031] Thus, in an embodiment, cells from an established cell line disclosed in the present specification can exhibit a well defined upper asymptote over a plurality of cell passages and maintain a signal to noise ratio that is consistent and adequate for the assay. In aspects of this embodiment, cells from an established cell line disclosed in the present specification must have a signal to noise ratio for the upper asymptote for BoNT/A activity of, *e.g.*, at least 3:1, at least 4:1, at least 5:1, at least 6:1, at least 7:1, at least 8:1, at least 9:1, at least 10:1, at least 15:1, at least 20:1, at least 25:1, at least 30:1, at least 35:1, at least 40:1, at least 45:1, at least 50:1, at least 60:1, at least 70:1, at least 80:1, at least 90:1, or at least 100:1, at least 150:1, at least 200:1, at least 250:1, at least 300:1, at least 350:1, at least 400:1, at least 450:1, at least 500:1, at least 550:1, or at least 600:1, over, *e.g.*, 5 or more cell passages, 10 or more cell passages, 15 or more cell passages, 20 or more cell passages, 25 or more cell passages, 30 or more cell passages, 35 or more cell passages, 40 or more cell passages, 45 or more cell passages, or 50 or more cell passages. In other aspects of this embodiment, cells from an established cell line disclosed in the present specification must have a signal to noise ratio for the upper asymptote for BoNT/A activity of, *e.g.*, at least 3:1, at least 4:1, at least 5:1, at least 6:1, at least 7:1, at least 8:1, at least 9:1, at least 10:1, at least 15:1, at least 20:1, at least 25:1, at least 30:1, at least 35:1, at least 40:1, at least 45:1, at least 50:1, at least 60:1, at least 70:1, at least 80:1, at least 90:1, or at least 100:1, at least 150:1, at least 200:1, at least 250:1, at least 300:1, at least 350:1, at least 400:1, at least 450:1, at least 500:1, at least 550:1, or at least 600:1, over, *e.g.*, about 15 to about 60 passages, about 20 to about 60 passages, about 25 to about 60 passages, about 30 to about 60 passages, about 35 to about 60 passages, about 40 to about 60 passages, about 45 to about 60 passages, about 50 to about 60 passages, about 15 to about 50 passages, about 20 to about 50 passages, about 25 to about 50 passages, about 30 to about 50

passages, about 35 to about 50 passages, about 40 to about 50 passages, about 15 to about 40 passages, about 20 to about 40 passages, about 25 to about 40 passages, or about 30 to about 40 passages.

[032] Cells from an established cell line disclosed in the present specification can exhibit a well defined dose-response curve for BoNT/A activity over a plurality of cell passages. As used herein, the term "dose-response curve" refers to the how well the raw data fits the statistical model of choice for that assay. As a non-limiting example, a sigmoidal curve with a four parameter logistics fit is a dose-response curve for an enzymatic activity assay, such as, *e.g.*, a potency assay. As another non-limiting example, a ligand binding with one site saturation fit is a dose-response curve for a ligand/antibody binding assay.

[033] Thus, in an embodiment, cells from an established cell line disclosed in the present specification exhibit a well defined dose-response curve for BoNT/A activity over a plurality of cell passages. In aspects of this embodiment, cells from an established cell line disclosed in the present specification exhibit a well defined dose-response curve for BoNT/A activity over, *e.g.*, 5 or more cell passages, 10 or more cell passages, 15 or more cell passages, 20 or more cell passages, 25 or more cell passages, 30 or more cell passages, 35 or more cell passages, 40 or more cell passages, 45 or more cell passages, or 50 or more cell passages. In other aspects of this embodiment, cells from an established cell line disclosed in the present specification exhibit a well defined dose-response curve for BoNT/A activity over, *e.g.*, about 15 to about 60 passages, about 20 to about 60 passages, about 25 to about 60 passages, about 30 to about 60 passages, about 35 to about 60 passages, about 40 to about 60 passages, about 45 to about 60 passages, about 50 to about 60 passages, about 15 to about 50 passages, about 20 to about 50 passages, about 25 to about 50 passages, about 30 to about 50 passages, about 35 to about 50 passages, about 40 to about 50 passages, about 15 to about 40 passages, about 20 to about 40 passages, about 25 to about 40 passages, or about 30 to about 40 passages.

[034] Cells from an established cell line disclosed in the present specification can exhibit a consistent relative EC_{50} value for BoNT/A activity over a plurality of cell passages. As used herein, the term "relative EC_{50}" or "relative EC_{50} value" refers to an EC_{50} value of BoNT/A activity that is normalized against theEC_{50} calculated for a reference standard, a reference molecule, or a reference passage number used on that assay.

[035] Thus, in an embodiment, cells from an established clonal cell line exhibit a consistent relative EC_{50} for BoNT/A activity over a plurality of cell passages. In aspects of this embodiment, cells from an established clonal cell line exhibit a consistent relative EC_{50} for BoNT/A activity that is, *e.g.*, about ± 10%, about ± 20%, about ± 30%, about ± 40%, about ± 50%, about 60%, about 70%, or about ± 75%, the relative EC_{50} for BoNT/A activity over, *e.g.*, 5 or more cell passages, 10 or more cell passages, 15 or more cell passages, 20 or more cell passages, 25 or more cell passages, 30 or more cell passages, 35 or more cell passages, 40 or more cell passages, 45 or more cell passages, or 50 or more cell passages. In other aspects of this embodiment, cells from an established clonal cell line exhibit a relative EC_{50} for

BoNT/A activity that is, *e.g.*, about ± 10% to about 75%, about ± 10% to about 70%, about ± 10% to about 60%, about ± 10% to about 50%, about ± 10% to about 40%, about ± 10% to about 30%, or about ± 10% to about 20% the relative EC_{50} for BoNT/A activity over, *e.g.*, 5 or more cell passages, 10 or more cell passages, 15 or more cell passages, 20 or more cell passages, 25 or more cell passages, 30 or more cell passages, 35 or more cell passages, 40 or more cell passages, 45 or more cell passages, or 50 or more cell passages

[036] Aspects of the present disclosure comprise, in part, cells from an established clonal cell line susceptible to BoNT/A intoxication that exhibit at least a 1.5-fold difference in gene expression levels of one or more genes listed in Tables 5, 6, 7, or 8 as compared to the expression levels of these genes in cells from the 2D6 cell line. In other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit a difference in gene expression levels of one or more genes listed in Tables 5, 6, 7, or 8 of, *e.g.*, at least a 1.5-fold, at least a 2.0-fold, at least a 2.5-fold, at least a 3.0-fold, at least a 3.5-fold, at least a 4.0-fold, at least a 4.5-fold, at least a 5.0-fold, at least a 5.5-fold, at least a 6.0-fold, at least a 7.0-fold, or at least a 8.0-fold as compared to the expression levels of these genes in cells from the 2D6 cell line. In other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit a difference in gene expression levels of, *e.g.*, 2 or more genes, 3 or more genes, 4 or more genes, 5 or more genes, 6 or more genes, 7 or more genes, 8 or more genes, 9 or more genes, 10 or more genes, 20 or more genes, 30 or more genes, 40 or more genes, 50 or more genes, 60 or more genes, 70 or more genes, 80 or more genes, 90 or more genes, or 100 or more genes listed in Tables 5, 6, 7, or 8 as compared to the expression levels of these genes in cells from the 2D6 cell line. In yet other aspects, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit a difference in gene expression levels of, *e.g.*, about 5 genes to about 100 genes, about 10 genes to about 100 genes, about 15 genes to about 100 genes, about 20 genes to about 100 genes, about 25 genes to about 100 genes, about 5 genes to about 75 genes, about 10 genes to about 75 genes, about 15 genes to about 75 genes, about 20 genes to about 75 genes, about 25 genes to about 75 genes, about 5 genes to about 50 genes, about 10 genes to about 50 genes, about 15 genes to about 50 genes, about 20 genes to about 50 genes, or about 25 genes to about 50 genes listed in Tables 5, 6, 7, or 8 as compared to the expression levels of these genes in cells from the 2D6 cell line. The log ratio in Tables 5, 6, 7, and 8 represent $\log_2$ values where 0.585 is $\log_2(1.5)$ which is a 1.5-fold difference, 1 is $\log_2(2)$ which is a 2-fold difference, 1.584 is $\log_2(3)$ which is a 3-fold difference, 2 is $\log_2(4)$ which is a 4-fold difference, 2.321 is $\log_2(5)$ which is a 5-fold difference, 2.584 is $\log_2(6)$ which is a 6-fold difference, 2.807 is $\log_2(7)$ which is a 7-fold difference, 3 is $\log_2(8)$ which is a 8-fold difference, 3.169 is $\log_2(9)$ which is a 9-fold difference, and 3.321 is $\log_2(10)$ which is a 10-fold difference.

[037] In an embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes listed in Tables 5 or 7 as compared to the expression levels of these genes in cells from the 2D6 cell line. In aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit an increase in gene expression levels of one or more genes listed in Tables 5 or 7 of, *e.g.*, at least a 2.0-fold,

at least a 2.5-fold, at least a 3.0-fold, at least a 3.5-fold, at least a 4.0-fold, at least a 4.5-fold, at least a 5.0-fold, at least a 5.5-fold, at least a 6.0-fold, at least a 7.0-fold, or at least a 8.0-fold as compared to the expression levels of these genes in cells from the 2D6 cell line. In other aspects of this embodiment,cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit an increase in gene expression levels of, *e.g.*, 2 or more genes, 3 or more genes, 4 or more genes, 5 or more genes, 6 or more genes, 7 or more genes, 8 or more genes, 9 or more genes, 10 or more genes, 20 or more genes, 30 or more genes, 40 or more genes, 50 or more genes, 60 or more genes, 70 or more genes, 80 or more genes, 90 or more genes, or 100 or more genes listed in Tables 5 or 7 as compared to the expression levels of these genes in cells from the 2D6 cell line. In yet other aspects, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit an increase in gene expression levels of, *e.g.*, about 5 genes to about 100 genes, about 10 genes to about 100 genes, about 15 genes to about 100 genes, about 20 genes to about 100 genes, about 25 genes to about 100 genes, about 5 genes to about 75 genes, about 10 genes to about 75 genes, about 15 genes to about 75 genes, about 20 genes to about 75 genes, about 25 genes to about 75 genes, about 5 genes to about 50 genes, about 10 genes to about 50 genes, about 15 genes to about 50 genes, about 20 genes to about 50 genes, or about 25 genes to about 50 genes listed in Tables 5 or 7 as compared to the expression levels of these genes in cells from the 2D6 cell line.

[036] In an embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from A2BP1, ACO1, ACOT7, ACOT9, ACTL6A, ACTL6B, ADRBK2, AGPS, AIDA, AKAP13, ALCAM, ALDH7A1, AMOTL1, ANAPC7, ANKRD13A, ANKRD54, ANKS1B, ANLN, ANP32E, ANXA6, APAF1, APBB2, APOO, ARF3, ARHGAP11A, ARHGAP24, ARHGAP24, ARHGAP6, ARHGEF3, ARHGEF6, ARL13B, ARL6, ARL6IP1, ASCL1, ASF1A, ASF1B, ASXL3, ATAD2, ATP6V1A, AURKA, AURKB, BARD1, BASP1, BAX, BCL11A, BCR, BNC2, BOK, BRCA1, BRCA2, BRD4, BRI3BP, BRIP1, BTBD3, BTG3, BUB1, BUB1B, BUB3, BVES, C10ORF58, C10ORF78, C11ORF75, C12ORF48, C12ORF49, C14ORF106, C14ORF143, C15ORF23, C15ORF42, C18ORF54, C1ORF112, C1ORF183, C1ORF43, C1QL1, C20ORF108, C20ORF20, C20ORF7, C20ORF72, C22ORF28, C22ORF29, C22ORF39, C3ORF14, C3ORF70, C4ORF46, C4ORF49, C5ORF32, C6ORF115, C9ORF100, CARHSP1, CBLB, CBWD1, CBX5, CCDC109B, CCDC117, CCDC15, CCDC21, CCDC3, CCDC34, CCDC52, CCDC86, CCDC99, CCNB1, CCNE2, CCNF, CCNYL1, CD24, CD47, CD9, CDC2, CDC25B, CDC42EP4, CDC45L, CDC5L, CDC6, CDCA2, CDCA4, CDCA5, CDCA7, CDCA8, CDH2, CDK2, CDK2AP1, CDK6, CDKAL1, CDKN2C, CDKN2D, CDO1, CDS2, CECR5, CELSR3, CENPF, CENPH), CENPI, CENPJ, CENPK, CENPL, CENPM, CENPN, CENPO, CEP135, CEP152, CEP55, CEP78, CEP97, CHAF1A, CHD6, CHEK1, CHEK2, CHMP4B, CHRNA3, CHRNA7, CHST15, CIT, CKAP2, CKAP2L, CKLF, CKS1B, CLDND1, CLSTN2, CMTM7, CNN3, CNOT4, CNP, CNTN1, CNTN4, COBLL1, COQ3, CPNE4, CPT1A, CPVL, CRISPLD1, CRTAC1, CRYBG3, CRYZ, CSE1L, CSRP2, CSRP2BP, CSTF1, CTDSPL2, CTNNBL1, CTSL2, CUGBP2, CXCR4, CYTSA, DACT1, DAZ1, DBF4B, DBH, DCLRE1B, DCPS, DDAH2, DDT, DEK, DENR, DEPDC1, DEPDC1B, DERA, DGCR14, DGKE, DHX15, DHX35, DIAPH1, DIAPH3, DKFZP434L187, DLEU2, DLGAP5, DLL3, DLX6, DNA2, DNM3, DNMT3B, DOCK10, DOK4, DOK5,

DPF1, DPYD, DPYSL3, DRAM1, DRG1, DSCC1, DSN1, DTL, DTNBP1, DTYMK, DVL2, DYNLT3, DYRK4, E2F1, E2F2, E2F7, E2F8, EAF2, EBF1, ECT2, EFNA5, EFNB2, ELAVL4, ELOVL7, EME1, EMILIN2, EMILIN3, EML1, ENC1, EPB41L5, EPOR, ERCC6L, ESCO2, ESF1, ESPL1, ETS1, ETV1, EXO1, EXOC5, EXOSC6, EXPH5, EZH2, FAM101B, FAM105A, FAM110A, FAM114A1, FAM118A, FAM120C, FAM129B, FAM13A, FAM162B, FAM181B, FAM19A4, FAM19A5, FAM54A, FAM64A, FAM7A3, FAM83D, FANCG, FANCI, FANCI , FANCM, FARP1, FAT1, FBLN1, FRN1, FBP1, FBXO43, FBXO5, FEN1, FGFR2, FH, FIGNL1, FKBP5, FNDC5, FOXD1, FOXN3, FRMD6, FRZB, FSTL1, FZD2, FZD5, FZD8, G2E3, GABBR2, GAP43, GAP43, GAS2L3, GATM, GEMIN4, GFPT2, GFRA1, GFRA2, GGCX, GINS1, GINS3, GJC1, GLDC, GMNN, GNAI1, GNASAS, GNB4, GNG11, GNG12, GNG4, GPAM, GPN3, GPR125, GPR161, GPSM2, GPX3, GRP, GSG2, GSS, GSTCD, GTSE1, GTSF1, GXYLT1, H1F0, H2AFX, HAT1, HAUS6, HDAC8, HEG1, HES6, HGF, HIC2, HMG4L, HMGB1, HMGB2, HMGB3, HMGXB4, HMMR, HOOK3, HPS4, HRH3, HS3ST2, HS6ST2, HSPB11, HTATSF1, IDH2, IFI27L1, IQGAP1, ITGA6, ITGAV, ITGB5, ITPRIP, JARID2, KCNG3, KCNJ8, KCNN1, KCTD12, KDELC2, KHDRBS3, KIAA0101, KIAA0406, KIAA1211, KIAA1524, KIF11, KIF14, KIF16B, KIF18A, KIF23, KIFC1, KLF7, KLHL13, KLHL5, KNTC1, KPNA2, LBH, LGR5, LHFPL2, LIFR, LIG3, LMF2, LMNB1, LOC100127983, LOC100128844, LOC100288551, LOC340109, LOC344595, LOC440288, LOC642597, LOC728052, LPAR1, LRFN2, LRRC1, LSM4, LUM, MAB21L1, MAB21L2, MAGEH1, MAN1A1, MAN2A1, MAOA, MAP3K13, MAPK11, MAPK12, MAPKAPK3, MASTL, MBD2, MCAM, MCM10, MCM3, MCM4, MCM5, MCM6, MCM7, MCM8, MDC1, MDM1, MED20, MEIS1, MEIS2, MELK, MEST, MFAP2, MGAT5B, MINA, MKI67, MKL1, MLF1IP, MMD, MNS1, MPHOSPH9, MPP5, MPPED2, MRC2, MRPL35, MRPL49, MRS2, MSN, MTF2, MTHFD1, MTUS1, MVK, MYBL1, MYBL2, MYD88, MYO1B, MYO6, MYST1, NAAA, NAGA, NANP, NARG1, NASP, NAT11, NAT13, NCAPD3, NCAPG, NCAPG2, NCAPH, NCAPH2, NDN, NEDD1, NEDD9, NEIL3, NELL2, NFIB, NOC4L, NOS1, NR3C1, NRG3, NRM, NRXN1, NSMCE4A, NTAN1, NUCKS1, NUDT1, NUF2, NUP107, NUP37, NUP43, NUP50, NUP93, NUSAP1, NXPH1, NXT2, ODZ3, ODZ4, OIP5, ORC1L, ORC6L, OSBPL3, PAICS, PANK2, PARP3, PASK, PBK, PCDH17, PCDH8, PCGF5, PCNA, PDCL, PDE5A, PDLIM5, PDRG1, PEG3, PELI2, PELO, PEX13, PEX26, PFKFB3, PGAM5, PGM2, PHF19, PHF20, PHF21B, PHF5A, PHLPP1, PHYHIPL, PI4KA, PIP4K2A, PIR, PKMYT1, PLCL2, PLD5, PLEKHF2, PLK2, PLK4, PLS3, PLXNA2, PLXNA4, PLXNB2, PM20D2, POLA1, POLA2, POLE, POLE2, POLQ, POSTN, PPAP2B, PPAT, PPIF, PPIL5, PPM1F, PPP1R13B, PPP1R3C, PPP2R2B, PPP3CB, PRIM1, PRIM2, PRLHR, PRPS1, PRSS12, PSMA7, PSMC3IP, PSMD5, PSMD9, PSRC1, PTER, PTGES2, PTGFRN, PTGR1, PTPRE, PTPRG, PTPRK, PTPRM, PTTG1, PVRL3, PXMP4, PXN, RAB35, RAB3B, RAD18, RAD51, RAD51C, RALY, RAN, RANBP1, RANGAP1, RASEF, RBBP7, RBBP9, RBL1, RBPMS, RBX1, RECQL4, REEP1, RELB, RELL1, REXO2, RFC1, RFC2, RFC3, RFC4, RFC5, RGMA, RGS5, RILPL2, RIMBP2, RMI1, RNASEH2A, RNF182, RNF26, RNF34, RPA1, RPP30, RRM1, RRM2, RRP7A, RSRC1, S1PR3, SALL4, SAP30, SASS6, SBF2, SCD5, SCML1, SCML2, SDC1, SEC23A, SEC61A2, SELM, SEMA6A, SEMA6D, SESN3, SEZ6L, SFI1, SFRP1, SGOL2, SH3D19, SHCBP1, SHMT1, SHOX2, SIM1, SIVA1, SKA1, SKA2, SKA3, SKP2, SLC25A10, SLC26A2, SLC2A4RG, SLC2A8, SLC43A3, SLC44A5, SLC7A2, SLC8A1, SLCO3A1, SLIT3, SLITRK5, SLK, SLMO2, SMC1A, SMC2, SMC4, SMC6, SMO, SMYD5, SNAI2, SNAP29, SNCAIP, SNRPD3, SNX18, SNX5, SORD, SOX4, SPAG6, SPARC, SPATS2L, SPC24, SPC25, SPOCK1, SPSB4, SRGAP1, SRRD,

SRRM4, SSH2, ST8SIA1, ST8SIA2, ST8SIA4, STARD4, STIL, STK17A, STMN3, STOM, STON2, STRA6, SUSD5, SUV39H1, SVIP, SYN2, SYNE2, SYNM, SYT17, SYTL4, TBC1D1, TBX3, TCF19, TCF7L2, TCFL5, TDRKH, TEAD3, TESC, TFDP1, TFDP2, TFPI2, TH1L, THOC4, TIFA, TIMP3, TLE3, TLE4, TMCC3, TMEM107, TMEM132C, TMEM151B, TMEM170B, TMEM178, TMEM194A, TMEM38B, TMEM48, TMEM56, TMEM98, TMPO, TMSB15B, TNFAIP8, TOB2, TOMM34, TPBG, TPTE, TPX2, TRIM29, TRIM36, TRIM68, TRIM9, TRIP13, TROAP, TSH73, TSPAN14, TSPAN4, TSPAN5, TTC28, TTC9, TUBA1B, TUBB, TWIST1, TXNRD1, TYMS, TYRO3, UBE2C, UBE2L3, UBE2V1, UBE3B, UCK1, UCP2, UFD1L, UHRF1, UNC119B, UNG, UQCC, USP1, USP48, UTP18, VAPB, VAV3, VPS29, VSTM2L, WDHD1, WDR51A, WDR53, WDR62, WDR67, WEE1, WEE1, WHSC1, WRAP53, WWC3, XRCC4, XRCC6, ZAK, ZFHX4, ZFP82, ZGPAT, ZNF215, ZNF217, ZNF238, ZNF253, ZNF280B, ZNF367, ZNF43, ZNF443, ZNF503, ZNF521, ZNF560, ZNF608, ZNF626, ZNF681, ZNF71, ZNF823, ZNF85, ZNF92, ZNF93, and/or ZWINT, as compared to the expression levels of these genes in cells from the 2D6 cell line.

[039] In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from A2BP1, ACOT9, ALCAM, ANLN, ARHGAP24, ARHGAP6, ARHGEF3, ARHGEF6, ASCL1, ASF1B, ATAD2, AURKA, AURKB, BARD1, BASP1, BNC2, BRCA2, BRIP1, BTG3, BUB1, BUB1B, BVES, C11ORF75, C12ORF48, C14ORF106, C15ORF42, C18ORF54, C1ORF112, C3ORF70, C4ORF49, CCDC109B, CCDC3, CCNB1, CCNE2, CD9, CDC2, CDC25B, CDC45L, CDC6, CDCA2, CDCA5, CDCA8, CDK2, CDKN2D, CENPF, CENPI, CENPL, CENPN, CEP55, CHEK1, CHEK2, CHRNA7, CIT, CKAP2L, CLSTN2, CNTN1, CNTN4, CPVL, CRYBG3, CSRP2, CTSL2, CUGBP2, CXCR4, DAZ1, DEPDC1, DEPDC1B, DIAPH3, DLGAP5, DNA2, DOK5, DPYD, DPYSL3, DSCC1, DSN1, DTL, DYNLT3, E2F1, E2F2, E2F7, E2F8, ECT2, EFNB2, ELOVL7, EME1, EMILIN2, EMILIN3, EML1, ENC1, ERCC6L, ESCO2, ESPL1, ETV1, EXO1, EXPH5, FAM101B, FAM114A1, FAM54A, FAM64A, FAM7A3, FAM83D, FANCI, FAT1, FBLN1, FBP1, FBXO43, FGFR2, FNDC5, FOXD1, FRMD6, FRZB, FZD5, GAS2L3, GFRA2, GINS1, GINS3, GNAI1, GNB4, GNG11, GNG12, GPSM2, GRP, GTSE1, GTSF1, HGF, HMMR, HS3ST2, ITGA6, ITPRIP, KCNG3, KCTD12, KDELC2, KIAA0101, KIAA1524, KIF11, KIF14, KIF18A, KIF23, KIFC1, LOC340109, LOC642597, LOC728052, LOC728052, LPAR1, LUM, MAB21L1, MAB21L2, MAOA, MCM10, MCM5, MELK, MINA, MKI67, MLF1IP, MPPED2, MRC2, MSN, MYBL1, MYBL2, MYO6, NCAPG, NCAPH, NDN, NEDD9, NEIL3, NR3C1, NRXN1, NUF2, NUSAP1, OIP5, ORC1L, OSBPL3, PBK, PCGF5, PDE5A, PEG3, PELO, PFKFB3, PHLPP1, PLD5, PLK2, PLK4, PLS3, POLA2, POLE2, POLQ, PPAP2B, PPP1R3C, PRLHR, PRSS12, PSRC1, PTGR1, PTPRE, PTPRK, PTPRM, PTTG1, PVRL3, RAD51, RBL1, RBPMS, RELL1, RFC5, RGMA, RGS5, RNF182, RRM2, S1PR3, SGOL2, SHCBP1, SHOX2, SIM1, SKA1, SLC43A3, SLC44A5, SLC7A2, SLITRK5, SMC2, SMC6, SPAG6, SPARC, SPC24, SPC25, ST8SIA4, STK17A, SUSD5, SYN2, SYNM, SYT17, TCF19, TESC, TFDP2, TFPI2, TIMP3, TLE3, TMEM132C, TMEM178, TNFAIP8, TPBG, TPTE, TPX2, TRIM29, TRIM36, TRIM68, TROAP, TWIST1, TYMS, UBE2C, UBE3B, UHRF1, WDHD1, WDR51A, WDR67, WEE1, ZFP82, ZNF367, ZNF521, and/or ZWINT, as compared to the expression levels of these genes in cells from the 2D6 cell line.

[040] In another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from A2BP1, ALCAM, ANLN, ARHGAP24, ARHGAP6, ASCL1, ASF1B, ATAD2, AURKA, AURKB, BARD1, BASP1, BNC2, BRIP1, BUB1, BVES, C11ORF75, C12ORF48, C14ORF106, C18ORF54, C3ORF70, CCDC109B, CCDC3, CD9, CDC2, CDC45L, CDCA2, CDCA8, CDK2, CENPI, CEP55, CHEK2, CHRNA7, CKAP2L, CNTN1, CRYBG3, CUGBP2, CXCR4, DAZ1, DEPDC1, DIAPH3, DLGAP5, DOK5, DPYD, DTL, DYNLT3, E2F1, E2F7, E2F8, EFNB2, ELOVL7, EMILIN2, EML1, ENC1, ESPL1, ETV1, EXO1, EXPH5, FAM54A, FAM64A, FAM7A3, FAM83D, FANCI, FAT1, FBLN1, FBXO43, FGFR2, FZD5, GNAI1, GNB4, GNG11, GNG12, GPSM2, GRP, GTSE1, GTSF1, HGF, HMMR, ITGA6, ITPRIP, KCTD12, KDELC2, KIF11, KIF14, KIF18A, KIF23, KIFC1, LOC340109, LOC728052, LPAR1, LUM, MAB21L1, MAB21L2, MAOA, MCM10, MELK, MINA, MKI67, MSN, MYBL1, NCAPH, NDN, NEDD9, NEIL3, NRXN1, NUF2, NUSAP1, OIP5, ORC1L, OSBPL3, PBK, PCGF5, PEG3, PEG3, PHLPP1, PLD5, PLK2, PLK4, PLS3, POLE2, PPAP2B, PPP1R3C, PRLHR, PRSS12, PTPRE, PTPRK, PTPRM, RBPMS, RELL1, RGS5, RNF182, RRM2, S1PR3, SGOL2, SHCBP1, SHOX2, SIM1, SLC43A3, SLC44A5, SLC7A2, SLITRK5, SMC6, SPAG6, SPARC, SPC24, SPC25, ST8SIA4, STK17A, SYT17, TFPI2, TIMP3, TMEM132C, TMEM178, TPBG, TPTE, TPX2, TRIM36, TWIST1, UBE3B, and/or ZNF367, as compared to the expression levels of these genes in cells from the 2D6 cell line.

[041] In yet another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from A2BP1, ARHGAP24, ARHGAP6, ASCL1, ASF1B, ATAD2, AURKA, BARD1, BASP1, BNC2, BUB1, BVES, C11ORF75, CCDC3, CHEK2, CHRNA7, CKAP2L, CNTN1, CRYBG3, CUGBP2, CUGBP2, CXCR4, DAZ1, DEPDC1, DIAPH3, DLGAP5, DOK5, DPYD, DTL, DYNLT3, E2F8, EFNB2, ELOVL7, ENC1, EXPH5, FAM7A3, FANCI, FAT1, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, GRP, GTSE1, GTSF1, HMMR, ITGA6, ITPRIP, KCTD12, KDELC2, LOC728052, LPAR1, LUM, MAB21L1, MAB21L2, MAOA, MCM10, MELK, MINA, MKI67, MSN, MYBL1, NDN, NEDD9, NRXN1, OSBPL3, PEG3, PLK2, PLS3, PRLHR, PRSS12, PTPRK, PTPRM, RBPMS, RGS5, RNF182, RRM2, SGOL2, SIM1, SLC43A3, SLC44A5, SLC7A2, SMC6, SPAG6, SPARC, STK17A, TFPI2, TIMP3, TMEM132C, TMEM178, and/or TPTE, as compared to the expression levels of these genes in cells from the 2D6 cell line.

[042] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ADAMTS9, ATAD2, C11ORF82, CDC45L, CNTN1, CNTN4, Cyclin A, Cyclin E, E2F1, E2F2, E2F7, ELOVL7, EME1, FGFR, FGFR2, KIAA1524, MELK, MYBL1, MYBL2, NDC80, NDN, ORC1L, PLS3, PRIMA1, RAD54L, RBL1, RBPMS, RRM2, S1PR3, SCLY, SLC1A3, SPC24, SPC25, ST8SIA4, TFDP1, TFP12, TK1, TMEM35, TTK, TWIST1, TYMS, TYK, and/or ZWINT, as compared to the expression levels of these genes in cells from the 2D6 cell line.

[043] In yet another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from AURKB, BIRC5, BRCA1, BRCA2, BRIP1,BUB1B, CD9, DLGAP3, DYNLT3, ENC1, FBLN1, FOXM1, Gβγ, GNAI1, GNG11, GNG12, GPSM2, GUCY1B3, HGF, ITGA6, JNK, KCNJ5, KIF18A, KITLG, MMD, MSN, MYRIP, NEK2, NR3C1, NXPH1, OSBPL3, PKMYT1, PTPRM, RAD51, RAD51AP1, SLC7A2, SLC43A3, SMC6, SNAI2, SNCAIP, SSH2, STK17A, SYNPO2, TOP2A, TPTE, TRAF4, TSPAN, TSPAN4, UBE3, UBE3B, and/or VAV3, as compared to the expression levels of these genes in cells from the 2D6 cell line. In still another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ALCAM, AURKA, CHEK, CIT, CSRP2, E2F, ECT2, EFNB2, ERK, ESPL1, GNAI, GPR161, HMMR, KIF4A, KIF14, KIF15, KIF22, KIF23, KIFC1, LPAR1, MK167, OIP5, PHLPP, PP1/PP2A, PPP1R3C, PRC1, PTTG1, RACGAP, RB, RGS5, SDC2, and/or TPX2, as compared to the expression levels of these genes in cells from the 2D6 cell line.

[044] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ASCL1,HES6, MAPK, NMU, PEG3, PTPRK, PRLHR, PTPRK, SGOL2, SPARC, and/or ZNF217, as compared to the expression levels of these genes in cells from the 2D6 cell line. In yet another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ASF1B, BASP1, CHAF1A, NCAPH, PBK, PRAME, SMC2, UHRF1, and/or VRK1, as compared to the expression levels of these genes in cells from the 2D6 cell line. In still another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from C14ORF106, CEP72, KIF20A, PCNA, PEX13, PFC5, POLQ, SPAG5, SYTL4, TROAP, and/or WDR51A, as compared to the expression levels of these genes in cells from the 2D6 cell line. In a further embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ANLN, ARHGAP24, ASPM, BUB1, CCDC99, CEP55, CKAP2, DRAM, E2F8, PLXNA2, SLC16A10, UBE2C, UBE2S, and/or WDHD1, as compared to the expression levels of these genes in cells from the 2D6 cell line.

[045] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ARHGEF3, CTSL2, DIAPH3, FBP1, KIF2C, KIF11, PFKFB3, and/or PLK4, as compared to the expression levels of these genes in cells from the 2D6 cell line. In yet another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ARHGEF3, CTSL2, DIAPH3, FBP1, KIF2C, KIF11, PFKFB3, and/or PLK4, as compared to the expression levels of these genes in cells from the 2D6 cell line. In still another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected

from FNDC5, HSPC159, MAB21L2, SLITRK5, SYN2, and/or ZNF367, as compared to the expression levels of these genes in cells from the 2D6 cell line. In a further another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from EXO1, KCTD12, MYO6, PHEBL1, SHCBP1, TPBG, and/or TUBB6, as compared to the expression levels of these genes in cells from the 2D6 cell line. In yet another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from BTG3, GABRA5, TR1P10, and/or ZNF521, as compared to the expression levels of these genes in cells from the 2D6 cell line. In still another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from BNC2, DPYD, EMILIN2, PPIL5, and/or TACC3, as compared to the expression levels of these genes in cells from the 2D6 cell line.

[046] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold difference in gene expression levels of one or more genes listed in Tables 14 or 16 as compared to the expression levels levels of these genes in cells from the 2D6 cell line. In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ACOT9, ADAMTS9, ARHGAP24, ARHGEF3, ASCL1, BARD1, BASP1, C3ORF70, C11ORF75, CCDC109B, CD9, CDCA7L, CDK2, CENPL, CLSTN2, CNTN1, CSRP2, CTSL2, CUGBP2, DEPDC1, DIAPH3, DOK5, DPYD, DYNLT3, EMILIN2, ETV1, FAM101B, FBLN1, FGFR2, FNDC5, GNAI1, GNB4, GNG11, GNG12, GPR177, GTSE1, HGF, KITLG, LPAR1, MAB21L2, MAOA, MCM10, MINA, MSN, MYO6, MYRIP, PAG1, PEG3, PLK2, POLA2, PPP1R3C, PRLHR, PRSS12, PTGR1, PTPRK, PVRL3, RAB32, RBPMS, SDC2, SGOL2, SLC43A3, SLC7A2, SMC2, SMC6, SPARC, SPC25, ST8SIA4, TCF7L1, TFPI2, TMEM35, TMEM178, TNFAIP8, TPTE, TRIP10, TWIST1, and/or ZNF521, as compared to the expression levels of these genes in cells from the 2D6 cell line. In another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ADAMTS9, ARHGAP24, ASCL1, BARD1, BASP1, BVES, C11ORF75, CDCA7L, CNTN1, CUGBP2, DOK5, DPYD, DYNLT3, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, GTSE1, GTSF1, ITPRIP, KDELC2, LOC728052, LPAR1, MAB21L2, MAOA, MINA, MSN, PEG3, PLK2, PRLHR, PRSS12, PTPRK, RBPMS, RNF182, SGOL2, SLC43A3, SLC44A5, SLC7A2, SMC6, SPARC, TFPI2, TMEM178, and/or TPTE, as compared to the expression levels of these genes in cells from the 2D6 cell line. In yet another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ADAMTS9, ASCL1, BASP1, DOK5, DPYD, GNB4, GNG11, GTSF1, MAOA, MINA, MSN, PEG3, PLK2, PRSS12, RNF182, SLC44A5, SPARC, TFPI2, and/or TPTE, as compared to the expression levels of these genes in cells from the 2D6 cell line.

[047] In yet another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ADAMTS9, ARHGAP24, ARHGEF3, ASCL1, BARD1, CD9, CDK2, CSRP2, CTSL2, DIAPH3, DOK5, DYNLT3, EMILIN2, ETV1, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, HGF, KITLG, LPAR1, MCM10, MSN, PAG1, PEG3, PLK2, POLA2, PPP1R3C, PTPRK, RAB32, SDC2, SLC43A3, SLC7A2, SMC6, SPARC, SPC25, ST8SIA4, TCF7L1, TFPI2, TMEM35, TNFAIP8, TPTE, TRIP10, and/or TWIST1, as compared to the expression levels of these genes in cells from the 2D6 cell line. In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ADAMTS9, ARHGAP24, ASCL1, BARD1, DOK5, DYNLT3, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, LPAR1, MSN, PEG3, PLK2, PTPRK, SLC43A3, SLC7A2, SMC6, SPARC, TFPI2, and/or TPTE, as compared to the expression levels of these genes in cells from the 2D6 cell line. In another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ADAMTS9, ASCL1, DOK5, GNB4, GNG11, MSN, PEG3, PLK2, SPARC, TFPI2, and/or TPTE, as compared to the expression levels of these genes in cells from the 2D6 cell line.

[048] In still another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ACOT9, BASP1, C11ORF75, CCDC109B, CDCA7L, CLSTN2, CNTN1, CUGBP2, DEPDC1, DPYD, FAM101B, FNDC5, GTSE1, MAOA, MINA, MYO6, MYRIP, PLK2, PRLHR, PVRL3, RBPMS, SGOL2, SMC2, TFP12, TMEM178, and/or ZNF521, as compared to the expression levels of these genes in cells from the 2D6 cell line. In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from BASP1, C11ORF75, CDCA7L, CNTN1, CUGBP2, DPYD, GTSE1, MAOA, MINA, PLK2, PRLHR, RBPMS, SGOL2, TFPI2, and/or TMEM178, as compared to the expression levels of these genes in cells from the 2D6 cell line. In another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from BASP1, DPYD, MAOA, MINA, PLK2, and/or TFPI2, as compared to the expression levels of these genes in cells from the 2D6 cell line.

[049] In a further embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from C3ORF70, MAB21L2, PRSS12, CENPL, GPR177, and/or PTGR1, as compared to the expression levels of these genes in cells from the 2D6 cell line. In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from MAB21L2 and/or PRSS12, as compared to the expression levels of these genes in cells from the 2D6 cell line.

[050] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes listed in Tables 6 or 8 as compared to the expression levels of these genes in cells from a 2D6 cell line. In other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit a decrease in gene expression levels of one or more genes listed in Tables 6 or 8 of, *e.g.*, at least a 1.5-fold, at least a 2.0-fold, at least a 2.5-fold, at least a 3.0-fold, at least a 3.5-fold, at least a 4.0-fold, at least a 4.5-fold, at least a 5.0-fold, at least a 5.5-fold, at least a 6.0-fold, at least a 7.0-fold, or at least a 8.0-fold as compared to the expression levels of these genes in cells from a 2D6 cell line. In other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit a decrease in gene expression levels of, *e.g.*, 2 or more genes, 3 or more genes, 4 or more genes, 5 or more genes, 6 or more genes, 7 or more genes, 8 or more genes, 9 or more genes, 10 or more genes, 20 or more genes, 30 or more genes, 40 or more genes, 50 or more genes, 60 or more genes, 70 or more genes, 80 or more genes, 90 or more genes, or 100 or more genes listed in Tables 6 or 8 as compared to the expression levels of these genes in cells from the 2D6 cell line. In yet other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit an decrease in gene expression levels of, *e.g.*, about 5 genes to about 100 genes, about 10 genes to about 100 genes, about 15 genes to about 100 genes, about 20 genes to about 100 genes, about 25 genes to about 100 genes, about 5 genes to about 75 genes, about 10 genes to about 75 genes, about 15 genes to about 75 genes, about 20 genes to about 75 genes, about 25 genes to about 75 genes, about 5 genes to about 50 genes, about 10 genes to about 50 genes, about 15 genes to about 50 genes, about 20 genes to about 50 genes, or about 25 genes to about 50 genes listed in Tables 6 or 8 as compared to the expression levels of these genes in cells from the 2D6 cell line.

[051] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from AATK, ABCA2, ABCC5, ABCC8, ABR, ABTB1, ACOT1, ACRBP, ACRV1, ACYP2, ADARB1, ADCY1, ADM, AFF1, AGAP4, AGPAT3, AGXT2L2, AHI1, AKAP9, AKIRIN1, AKT2, AMH, ANK2, ANK3, ANKHD1, ANKRD17, ANKRD50, ANKS1A, AQP1, ARF1, ARHGAP1, ARHGAP23, ARL17A, ASAM, ASPHD1, ATP2B3, ATP2B3, ATP6V0A1, ATP8B2, ATP9A, BACE1, BACH2, BLZF1, BPTF, BRUNOL4, BRUNOL5, BRWD1, BRWD2, BTBD18, BTN3A3, BZRAP1, C14ORF159, C15ORF24, C15ORF57, C16ORF52, C17ORF28, C1ORF21, C1ORF21, C1ORF50, C21ORF57, C21ORF59, C21ORF66, C2CD2, C2CD4A, C2ORF60, C2ORF68, C3ORF23, C4ORF41, C5ORF42, C6ORF154, C6ORF52, C7ORF28B, C7ORF54, C9ORF150, C9ORF68, CACNA1D, CALY, CAMK2B, CAMK2N2, CAP2, CAPN2, CARTPT, CBS, CCDC104, CCDC50, CCDC76, CD151, CD163L1, CD302, CDC42EP1, CDH10, CDH12, CDKN1C, CDKN2A, CDS1, CFC1, CHD5, CLCN3, CLDN12, CLIP4, CLMN, CNGA3, CNNM1, CNOT6L, COL6A1, COPA, CPNE8, CRKRS, CRTC1, CRYGS, CSTB, CTSK, CUL4A, CYGB, CYLD, CYP2E1, CYP3A5, CYTL1, D4S234E, DCLK1, DCTD, DEPDC6, DHX36, DIP2A, DIS3, DKFZP547G183, DNAJC22, DTNA, DTWD1, DUSP16, DUSP5, DVL3, EFNB3, EIF3C, ELFN2, ENOSF1, ERAP1, ERBB2, ERBB4, ERMAP, ETFDH, EXOSC6, FADS3, FAM120AOS, FAM150B, FAM165B, FAM184B, FAM30A, FAM46A, FAM66C, FAT4, FBRSL1, FBXW7, FGD5, FGF13, FLJ33630, FNBP1, FOXO6, FUBP3, GAL, GAL,

GLT25D2, GNAS, GOLGA8A, GPR123, GPX7, GRIA2, GRIP2, GRM5, GUCY1A3, H2AFY, HCG 1776018, HCG 2022304, HCN4, HEATR1, HELQ, HERC4, HERPUD2, HEXDC, HGSNAT, HIST1H2AC, HIST1H2AE, HIST1H2BD, HIST1H2BK, HIST1H3I, HIST2H2BE, HIVEP3, HNRNPM, HNRNPR, HPCAL1, HPCAL4, HSPD1, IER3, IL10RB, IL17B, INTU, JMY, KAT2B, KATNB1, KBTBD11, KCNMA1, KCNQ2, KCNS2, KCTD13, KHDC1, KIAA0125, KIAA1370, KIAA1598, KIF1A, KIF5C, KIF5C, KISS1R, KLHDC1, LCORL, LGALS3BP, LOC100130097, LOC100130360, LOC100130522, LOC100272228, LOC284408, LOC399491, LOC401320, LOC641298, LOC642852, LOC90110, LOC94431, LONRF2, LRP2BP, LRRC37A2, LRRFIP1, LTBP3, LYPLAL1, LYRM5, MAP3K5, MAP7, MAP9, MCM3AP, MCM3APAS, MCTP1, MEOX2, METTL3, MFSD4, MGAT4A, MLXIP, MRPL1, MRPS33, MST1, MUC20, MXD1, MZF1, NAMPT, NAP1L3, NBPF1, NBPF10, NCOA7, NCRNA00171, NCRNA00182, NDRG1, NDUFA4L2, NDUFV3, NEBL, NELF, NHEDC2, NHEG1, NIPAL2, NIPAL3, NLRX1, NOL3, NSMAF, NUDT19, NUP153, NUP54, OLFM3, OR7D2, OSBP, PABPC1L, PABPC4, PACRGL, PAM, PAPPA, PAQR6, PARP12, PCBD2, PCNXL2, PDCD6, PDE4C, PDE9A, PDGFRB, PDIA2, PGAP1, PHF17, PHKA1, PHKA2, PHLDA2, PIGH, PION, PKD1, PLA2G4C, PLCB4, PLEKHH1, PLP2, PLRG1, PLXNC1, PNCK, PNMA3, POFUT2, POGK, PPAPDC1A, PPAPDC1B, PPID, PPIE, PPM1K, PPP1R2, PPP2R2C, PPT1, PRKACB, PRPH, PSMB7, PTCD1, PTGER2, PTGS1, PTN, PTPRD, PTPRN, RAB11FIP3, RAB6B, RAF1, RGAG4, RGS11, RGS8, RHBDL1, RHOQ, RHOU, RLF, RNASET2, RNF13, RNF149, RNF165, RNF207, RNF41, RPL37, RSL1D1, RUNDC3A, S100A6, SCMH1, SCN2A, SERP1, SETX, SFRS18, SFXN3, SGK3, SH3BP5, SH3GL2, SH3YL1, SHC2, SHC4, SIGIRR, SIK1, SLC12A7, SLC1A2, SLC1A6, SLC22A17, SLC35F3, SLC38A5, SLCO1A2, SMAGP, SMAP2, SNCA, SOBP, SORCS1, SORL1, SPINT2, SPIRE2, SPOCK2, SRR, ST8SIA3, STAR, STEAP3, STOX2, STX3, SYNJ1, SYT13, SYT5, TAF10, TANC2, TCEA1, THBS2, THSD4, TIMP1, TM2D1, TMEM111, TMEM151A, TMEM184C, TMEM41B, TMEM43, TMEM5, TMEM59L, TMIE, TNFRSF25, TNFRSF25, TOX4, TP53BP1, TPM3, TRA2A, TRIM33, TRIM73, TRIM8, TRIT1, TSR1, TTC17, TTC3, TTC39C, TUSC3, TXLNB, U2AF1, UBE2D3, UBE2G2, UBN2, UBXN6, UCN, UGP2, UNC80, UNQ1887, USP36, USPL1, VN1R1, VPS13C, VPS53, VPS8, WDFY3, WDR27, WDR85, WSB1, YJEFN3, YLPM1, ZDHHC11, ZER1, ZG16B, ZNF275, ZNF440, ZNF573, ZNF641, ZNF662, ZNF785, and/or ZNF814, as compared to the expression levels of these genes in cells from the 2D6 cell line.

[052] In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from ACOT1, ADARB1, ADM, ANK2, AQP1, ASAM, C2CD4A, C3ORF23, CACNA1D, CAMK2B, CAP2, CARTPT, CD163L1, CDC42EP1, CDH10, CDKN1C, CDKN2A, CFC1, CLMN, CPNE8, CYGB, CYP2E1, CYTL1, DNAJC22, DUSP5, ENOSF1, ERAP1, FGF13, FOXO6, GAL, GNAS, GPX7, GRIA2, GRM5, HCG 1776018, HIST1H2AC, HIST1H2BD, HIST1H2BK, HIST2H2BE, IL17B, KIAA0125, KIAA1598, KISS1R, LRP2BP, MEOX2, NCRNA00182, NDRG1, NDUFA4L2, NIPAL2, NUDT19, PDE4C, PHKA2, PHLDA2, PTGER2, RGS11, S100A6, SCN2A, SHC4, SIGIRR, SLC1A2, SLC1A6, SLC35F3, SLC38A5, SORCS1, SYT13, SYT5, THBS2, TIMP1, and/or TMEM111, as compared to the expression levels of these genes in cells from the 2D6 cell line.

[053] In another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from ACOT1, ADARB1, ANK2, AQP1, C3ORF23, CAP2, CARTPT, CD163L1, CDC42EP1, CDKN2A, CFC1, CPNE8, CYGB, CYP2E1, CYTL1, FGF13, FOXO6, GNAS, GRIA2, GRM5, HIST1H2AC, IL17B, KIAA0125, KIAA1598, KISS1R, MEOX2, NDRG1, NDUFA4L2, NIPAL2, PDE4C, PHKA2, RGS11, SCN2A, SLC1A2, SLC35F3, SLC38A5, SYT13, and/or THBS2, as compared to the expression levels of these genes in cells from the 2D6 cell line.

[054] In yet another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from AQP1, CAP2, CARTPT, CD163L1, CDC42EP1, CFC1, CPNE8, CYGB, CYP2E1, CYTL1, FGF13, GNAS, GRIA2, GRM5, HIST1H2AC, IL17B, KIAA0125, MEOX2, NDUFA4L2, PDE4C, PHKA2, RGS11, SLC1A2, SLC35F3, SLC38A5, and/or SYT13, as compared to the expression levels of these genes in cells from the 2D6 cell line.

[055] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from ANXA2, AQP1, ARHGAP9, CDH10, CDKN2A, CHPT1, CNTN2, ERAP1, and/or RGS11, as compared to the expression levels of these genes in cells from the 2D6 cell line. In yet another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from ABCC8, AELIM3, CAP2, IL17B, MEF2A, NEEBL, PHC, S100A6, SLC1A6, SMAD1, SMAD5, SMAD8, SYT13, and/or SYTL1, as compared to the expression levels of these genes in cells from the 2D6 cell line. In still another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from CSTB, GPCR, GRIM5, KISSR, SCN2A, SLC1A2, and/or THBS2, as compared to the expression levels of these genes in cells from the 2D6 cell line.

[056] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from ADARB1, ADM, PTPPH, and/or SLCO1A2, as compared to the expression levels of these genes in cells from the 2D6 cell line. In yet another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from CNGA3, HIST1H3E, and/or PTGS1, as compared to the expression levels of these genes in cells from the 2D6 cell line. In still another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from HIST1H2BD and/or OSCAR as compared to the expression levels of these genes in cells from the 2D6 cell line. In a further embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of

one or more genes selected from CALY as compared to the expression levels of these genes in cells from the 2D6 cell line.

[057] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from COL5A1 and/or MICAL2 as compared to the expression levels of these genes in cells from the 2D6 cell line. In yet another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from OLFML2A and/or SIGIRR as compared to the expression levels of these genes in cells from the 2D6 cell line. In still another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from HPCAL1 and/or LPAR5 as compared to the expression levels of these genes in cells from the 2D6 cell line. In a further embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from ITR1E and/or SORCS1 as compared to the expression levels of these genes in cells from the 2D6 cell line.

[058] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from ANK2, CPNE8, CREB5, IL17B, KIAA0125, LOC100289109, LOC144571, NPAS4, SLC1A2, SORCS1, THBS2, and/or ZNF814, as compared to the expression levels of these genes in cells from the 2D6 cell line.

[059] Aspects of the present disclosure comprise, in part, cells from an established clonal cell line susceptible to BoNT/A intoxication that exhibit at least a 1.5-fold difference in gene expression levels of one or more genes listed in Tables 9, 10, 11, or 12 as compared to the expression levels of these genes in cells from a parental SiMa cell line. In aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold difference in gene expression levels of one or more genes listed in Tables 9, 10, 11, or 12 as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit a difference in gene expression levels of one or more genes listed in Tables 9, 10, 11, or 12 of, *e.g.*, at least a 1.5-fold, at least a 2.0-fold, at least a 2.5-fold, at least a 3.0-fold, at least a 3.5-fold, at least a 4.0-fold, at least a 4.5-fold, at least a 5.0-fold, at least a 5.5-fold, at least a 6.0-fold, at least a 7.0-fold, or at least a 8.0-fold as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In yet other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit a difference in gene expression levels of, *e.g.*, 2 or more genes, 3 or more genes, 4 or more genes, 5 or more genes, 6 or more genes, 7 or more genes, 8 or more genes, 9 or more genes, 10 or more genes, 20 or more genes, 30 or more genes, 40 or more genes, 50 or more genes, 60 or more genes, 70 or more genes, 80 or more genes, 90 or more genes, or 100 or more genes listed in Tables 9,

10, 11, or 12 as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In still other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit a difference in gene expression levels of, *e.g.*, about 5 genes to about 100 genes, about 10 genes to about 100 genes, about 15 genes to about 100 genes, about 20 genes to about 100 genes, about 25 genes to about 100 genes, about 5 genes to about 75 genes, about 10 genes to about 75 genes, about 15 genes to about 75 genes, about 20 genes to about 75 genes, about 25 genes to about 75 genes, about 5 genes to about 50 genes, about 10 genes to about 50 genes, about 15 genes to about 50 genes, about 20 genes to about 50 genes, or about 25 genes to about 50 genes listed in Tables 9, 10, 11, or 12 as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. The log ratio in Tables 9, 10, 11, or 12 represent $\log_2$ values where 0.585 is $\log_2(1.5)$ which is a 1.5-fold difference, 1 is $\log_2(2)$ which is a 2-fold difference, 1.584 is $\log_2(3)$ which is a 3-fold difference, 2 is $\log_2(4)$ which is a 4-fold difference, 2.321 is $\log_2(5)$ which is a 5-fold difference, 2.584 is $\log_2(6)$ which is a 6-fold difference, 2.807 is $\log_2(7)$ which is a 7-fold difference, 3 is $\log_2(8)$ which is a 8-fold difference, 3.169 is $\log_2(9)$ which is a 9-fold difference, and 3.321 is $\log_2(10)$ which is a 10-fold difference.

[060] In an embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold difference in gene expression levels of one or more genes selected from ACOT9, ADAMTS9, ARHGAP24, ARHGEF3, ASCL1, BARD1, BASP1, C3ORF70, C11ORF75, CCDC109B, CD9, CDCA7L, CDK2, CENPL, CLSTN2, CNTN1, CSRP2, CTSL2, CUGBP2, DEPDC1, DIAPH3, DOK5, DPYD, DYNLT3, EMILIN2, ETV1, FAM101B, FBLN1, FGFR2, FNDC5, GNAI1, GNB4, GNG11, GNG12, GPR177, GTSE1, HGF, KITLG, LPAR1, MAB21L2, MAOA, MCM10, MINA, MSN, MYO6, MYRIP, PAG1, PEG3, PLK2, POLA2, PPP1R3C, PRLHR, PRSS12, PTGR1, PTPRK, PVRL3, RAB32, RBPMS, SDC2, SGOL2, SLC43A3, SLC7A2, SMC2, SMC6, SPARC, SPC25, ST8SIA4, TCF7L1, TFPI2, TMEM35, TMEM178, TNFAIP8, TPTE, TRIP10, TWIST1, and/or ZNF521, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold difference in gene expression levels of one or more genes selected from ADAMTS9, ARHGAP24, ASCL1, BARD1, BASP1, BVES, C11ORF75, CDCA7L, CNTN1, CUGBP2, DOK5, DPYD, DYNLT3, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, GTSE1, GTSF1, ITPRIP, KDELC2, LOC728052, LPAR1, MAB21L2, MAOA, MINA, MSN, PEG3, PLK2, PRLHR, PRSS12, PTPRK, RBPMS, RNF182, SGOL2, SLC43A3, SLC44A5, SLC7A2, SMC6, SPARC, TFPI2, TMEM178, and/or TPTE, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In yet another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold difference in gene expression levels of one or more genes selected from ADAMTS9, ASCL1, BASP1, DOK5, DPYD, GNB4, GNG11, GTSF1, MAOA, MINA, MSN, PEG3, PLK2, PRSS12, RNF182, SLC44A5, SPARC, TFPI2, and/or TPTE, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164.

[061] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes listed in Tables 9 or 11 as compared to the expression levels of these genes in cells from a parental SiMa cell line DSMZ ACC 164. In other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit an increase in gene expression levels of one or more genes listed in Tables 9 or 11 of, *e.g.*, at least a 1.5-fold, at least a 2.0-fold, at least a 2.5-fold, at least a 3.0-fold, at least a 3.5-fold, at least a 4.0-fold, at least a 4.5-fold, at least a 5.0-fold, at least a 5.5-fold, at least a 6.0-fold, at least a 7.0-fold, or at least a 8.0-fold as compared to the expression levels of these genes in cells from a parental SiMa cell line DSMZ ACC 164. In other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit an increase in gene expression levels of, *e.g.*, 2 or more genes, 3 or more genes, 4 or more genes, 5 or more genes, 6 or more genes, 7 or more genes, 8 or more genes, 9 or more genes, 10 or more genes, 20 or more genes, 30 or more genes, 40 or more genes, 50 or more genes, 60 or more genes, 70 or more genes, 80 or more genes, 90 or more genes, or 100 or more genes listed in Tables 9 or 11 as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In yet other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit an increase in gene expression levels of, *e.g.*, about 5 genes to about 100 genes, about 10 genes to about 100 genes, about 15 genes to about 100 genes, about 20 genes to about 100 genes, about 25 genes to about 100 genes, about 5 genes to about 75 genes, about 10 genes to about 75 genes, about 15 genes to about 75 genes, about 20 genes to about 75 genes, about 25 genes to about 75 genes, about 5 genes to about 50 genes, about 10 genes to about 50 genes, about 15 genes to about 50 genes, about 20 genes to about 50 genes, or about 25 genes to about 50 genes listed in Tables 9 or 11 as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164.

[062] In an embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from A2BP1, ADRM1, AFF4, AGAP4, ALCAM, ANAPC7, ANKRD13D, ANKRD28, API5, ARF1, ARHGAP6, ARHGEF10, ARHGEF6, ARL17A, ASCL1, ASXL1, ASXL3, ATF7IP, B3GALNT2, BASP1, BLCAP, BNC2, C10ORF58, C12ORF49, C12ORF51, C1ORF43, C20ORF117, C20ORF7, CADM1, CADPS, CALCB, CAPN1, CAPRIN2, CBLB, CBLN2, CBWD1, CCDC150, CCDC3, CD9, CDC25B, CFDP1, CHRNA7, CIAPIN1, CLASP2, CNOT7, CPVL, CRYBG3, CSE1L, CTTNBP2NL, CUGBP2, CXCR4, DACT1, DAZ1, DBH, DCAF8, DENR, DHX35, DKFZP434L187, DLEU2, DLL1, DLL3, DYNC2H1, EAF2, EFNA5, EIF3B, EIF3C, ELOVL7, EML1, EML4, ENC1, EVL, EXOSC6, EXPH5, EZH2, FAM178A, FAM181B, FAM19A4, FAM7A3, FLJ10213, FUBP3, FUS, FZD5, GAP43, GFM1, GFRA2, GGA2, GNAI1, GNAS, GNB4, GNG11, GOLGA4, GPR125, GRM8, GRP, GSPT1, GSS, GSTCD, GULP1, HAUS2, HEG1, HNRNPL, HNRNPM, HOXA7, HOXD4, ID2, IDH3B, IL1A, INSM1, IREB2, ITGA6, ITGB5, KCTD12, KDELC2, KHDRBS3, KIAA0907, KIAA1267, KIF16B, KLC1, KLHL13, LBH, LMO4, LOC100128844, LOC340109, LOC641298, LOC647190, LOC728052, LOC728153, LRPPRC, LRRFIP2, LSM3, LUM, MAB21L1, MAB21L2, MAN2A1, MAOA, MARS, MDN1, MED13L, MED22, MGC24103, MINA, MKLN1, MLEC, MMD, MORF4L2, MPZL1, MSH6, MSI2, MSN, MTMR9, MYO1B, MYO6, N4BP2, NAAA, NDUFS8, NEDD9,

NFIB, NKTR, NLN, NOS1, NR2C1, NUFIP2, NUPL1, OSBPL3, PAPD4, PCBP2, PCDH9, PCGF5, PCNX, PDLIM5, PDZRN3, PELI2, PFKFB3, PCP, PHF20, PLK2, PLXNA2, PLXNA4, PM20D2, POLE, POLQ, PPP2R2A, PPP2R3C, PRDX2, PSMA7, PSME4, PTGFRN, PTK2, PTPN1, PTPRE, PTPRG, QKI, RAB12, RAB35, RAB3GAP2, RAD23B, RAF1, RALGAPA1, RAN, RASEF, RBL1, RDH11, RELL1, REPS1, RGS5, RIMBP2, RNF182, RNF34, RNPEP, ROBO2, RPAIN, RPL35A, RPRD1A, S1PR3, SALL4, SRNO1, SCARB2, SDHA, SEMA6A, SF76I, SF1, SFRS8, SIM1, SIRT2, SKII, SLC20A1, SLC44A5, SLC7A2, SLCO3A1, SLITRK5, SMAD4, SMARCC2, SMC3, SNRPB2, SNRPN, SNX5, SOX2, SPAG6, SPAG9, SPATS2L, SPON1, SR140, SSBP2, ST8SIA1, STMN3, STRA6, SYNCRIP, SYTL3, TAF15, TCF7L2, TDG, TERT, TFPI2, TGFBR1, TH1L, THOC4, TIMP3, TLE3, TMEM132C, TMEM178, TMEM181, TNRC6A, TPBG, TRA2A, TRIM29, TRIM36, TSHZ3, TXNRD1, U2AF1, UBE2O, UBE2V1, UBE2Z, UBXN2A, UCHL1, USP25, USP32, USP34, VPS29, XPO1, XPO7, ZFAND6, ZFHX4, ZFYVE16, ZGPAT, ZNF217, ZNF451, ZNF503, and/or ZNF664, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164.

[063] In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ALCAM, ARHGAP6, ARHGEF6, ASCL1, BNC2, CBLN2, CCDC150, CCDC3, CHRNA7, CRYBG3, CUGBP2, CXCR4, DAZ1, DKFZP434L187, DLL1, EFNA5, ELOVL7, EML1, EML4, ENC1, EXPH5, FAM7A3, FZD5, GFRA2, GNAI1, GNB4, GNG11, GRP, ID2, ITGA6, KCTD12, LOC100128844, LOC340109, LOC728052, LUM, MAB21L1, MAB21L2, MAOA, MGC24103, MSN, NEDD9, NFIB, OSBPL3, PAPD4, PCDH9, PDZRN3, PLK2, POLQ, PTGFRN, PTPRE, PTPRG, RAD23B, RGS5, RNF182, ROBO2, SIM1, SLC20A1, SLC44A5, SLITRK5, SPAG6, SPAG9, SR140, TFPI2, TIMP3, TMEM132C, TPBG, TRIM29, TRIM36, and/or ZFAND6, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164.

[064] In another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ALCAM, ARHGAP6, ARHGEF6, CBLN2, CCDC3, CHRNA7, CRYBG3, CUGBP2, CXCR4, DAZ1, ELOVL7, EML1, EXPH5, FAM7A3, GNB4, GNG11, GRP, ITGA6, KCTD12, LOC340109, LUM, MAB21L1, MAB21L2, MGC24103, PCDH9, PLK2, POLQ, PTPRE, RGS5, RNF182, ROBO2, SIM1, SLC44A5, SLITRK5, SPAG6, TIMP3, and/or TMEM132C, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164.

[065] In yet another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from CBLN2, CCDC3, CHRNA7, CRYBG3, CXCR4, DAZ1, EXPH5, FAM7A3, GNB4, GRP, KCTD12, LUM, MGC24103, PCDH9, PLK2, POLQ, PTPRE, RGS5, ROBO2, SIM1, SLITRK5, TIMP3, and/or TMEM132C, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164.

[066] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes listed in Tables 14 or 16 as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes listed in Tables 14 or 16 as compared to the expression levels of these genes in cells from a parental SiMa cell line DSMZ ACC 164. In other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit an increase in gene expression levels of one or more genes listed in Tables 14 or 16 of, *e.g.*, at least a 1.5-fold, at least a 2.0-fold, at least a 2.5-fold, at least a 3.0-fold, at least a 3.5-fold, at least a 4.0-fold, at least a 4.5-fold, at least a 5.0-fold, at least a 5.5-fold, at least a 6.0-fold, at least a 7.0-fold, or at least a 8.0-fold as compared to the expression levels of these genes in cells from a parental SiMa cell line DSMZ ACC 164. In other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit an increase in gene expression levels of, *e.g.*, 2 or more genes, 3 or more genes, 4 or more genes, 5 or more genes, 6 or more genes, 7 or more genes, 8 or more genes, 9 or more genes, 10 or more genes, 20 or more genes, 30 or more genes, 40 or more genes, 50 or more genes, 60 or more genes, 70 or more genes, 80 or more genes, 90 or more genes, or 100 or more genes listed in Tables 14 or 16 as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In yet other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit an increase in gene expression levels of, *e.g.*, about 5 genes to about 100 genes, about 10 genes to about 100 genes, about 15 genes to about 100 genes, about 20 genes to about 100 genes, about 25 genes to about 100 genes, about 5 genes to about 75 genes, about 10 genes to about 75 genes, about 15 genes to about 75 genes, about 20 genes to about 75 genes, about 25 genes to about 75 genes, about 5 genes to about 50 genes, about 10 genes to about 50 genes, about 15 genes to about 50 genes, about 20 genes to about 50 genes, or about 25 genes to about 50 genes listed in Tables 14 or 16 as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164.

[067] In aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ACOT9, ADAMTS9, ARHGAP24, ARHGEF3, ASCL1, BARD1, BASP1, C3ORF70, C11ORF75, CCDC109B, CD9, CDCA7L, CDK2, CENPL, CLSTN2, CNTN1, CSRP2, CTSL2, CUGBP2, DEPDC1, DIAPH3, DOK5, DPYD, DYNLT3, EMILIN2, ETV1, FAM101B, FBLN1, FGFR2, FNDC3, GNAI1, GNB4, GNG11, GNG12, GPR177, GTSE1, HGF, KITLG, LPAR1, MAB21L2, MAOA, MCM10, MINA, MSN, MYO6, MYRIP, PAG1, PEG3, PLK2, POLA2, PPP1R3C, PRLHR, PRSS12, PTGR1, PTPRK, PVRL3, RAB32, RBPMS, SDC2, SGOL2, SLC43A3, SLC7A2, SMC2, SMC6, SPARC, SPC25, ST8SIA4, TCF7L1, TFPI2, TMEM35, TMEM178, TNFAIP8, TPTE, TRIP10, TWIST1, and/or ZNF521, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected

from ADAMTS9, ARHGAP24, ASCL1, BARD1, BASP1, BVES, C11ORF75, CDCA7L, CNTN1, CUGBP2, DOK5, DPYD, DYNLT3, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, GTSE1, GTSF1, ITPRIP, KDELC2, LOC728052, LPAR1, MAB21L2, MAOA, MINA, MSN, PEG3, PLK2, PRLHR, PRSS12, PTPRK, RBPMS, RNF182, SGOL2, SLC43A3, SLC44A5, SLC7A2, SMC6, SPARC, TFPI2, TMEM178, and/or TPTE, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In yet another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ADAMTS9, ASCL1, BASP1, DOK5, DPYD, GNB4, GNG11, GTSF1, MAOA, MINA, MSN, PEG3, PLK2, PRSS12, RNF182, SLC44A5, SPARC, TFPI2, and/or TPTE, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164.

[068] In yet another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ADAMTS9, ARHGAP24, ARHGEF3, ASCL1, BARD1, CD9, CDK2, CSRP2, CTSL2, DIAPH3, DOK5, DYNLT3, EMILIN2, ETV1, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, HGF, KITLG, LPAR1, MCM10, MSN, PAG1, PEG3, PLK2, POLA2, PPP1R3C, PTPRK, RAB32, SDC2, SLC43A3, SLC7A2, SMC6, SPARC, SPC25, ST8SIA4, TCF7L1, TFPI2, TMEM35, TNFAIP8, TPTE, TRIP10, and/or TWIST1, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ADAMTS9, ARHGAP24, ASCL1, BARD1, DOK5, DYNLT3, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, LPAR1, MSN, PEG3, PLK2, PTPRK, SLC43A3, SLC7A2, SMC6, SPARC, TFPI2, and/or TPTE, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ADAMTS9, ASCL1, DOK5, GNB4, GNG11, MSN, PEG3, PLK2, SPARC, TFPI2, and/or TPTE, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164.

[069] In still another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ACO19, BASP1, C11ORF75, CCDC109B, CDCA7L, CLSTN2, CNTN1, CUGBP2, DEPDC1, DPYD, FAM101B, FNDC5, GTSE1, MAOA, MINA, MYO6, MYRIP, PLK2, PRLHR, PVRL3, RBPMS, SGOL2, SMC2, TFP12, TMEM178, and/or ZNF521, as compared to the expression level of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from BASP1, C11ORF75, CDCA7L, CNTN1, CUGBP2, DPYD, GTSE1, MAOA, MINA, PLK2, PRLHR, RBPMS, SGOL2, TFPI2, and/or TMEM178, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A

intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from BASP1, DPYD, MAOA, MINA, PLK2, and/or TFPI2, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164.

[070] In a further embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from C3ORF70, MAB21L2, PRSS12, CENPL, GPR177, and/or PTGR1, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from MAB21L2 and/or PRSS12, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164.

[071] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes listed in Tables 10 or 12 as compared to the expression levels of these genes in cells from a parental SiMa cell line. In aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes listed in Tables 10 or 12 as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit a decrease in gene expression levels of one or more genes listed in Tables 10 or 12 of, *e.g.*, at least a 1.5-fold, at least a 2.0-fold, at least a 2.5-fold, at least a 3.0-fold, at least a 3.5-fold, at least a 4.0-fold, at least a 4.5-fold, at least a 5.0-fold, at least a 5.5-fold, at least a 6.0-fold, at least a 7.0-fold, or at least a 8.0-fold as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In other aspects cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit a decrease in gene expression levels of, *e.g.*, 2 or more genes, 3 or more genes, 4 or more genes, 5 or more genes, 6 or more genes, 7 or more genes, 8 or more genes, 9 or more genes, 10 or more genes, 20 or more genes, 30 or more genes, 40 or more genes, 50 or more genes, 60 or more genes, 70 or more genes, 80 or more genes, 90 or more genes, or 100 or more genes listed in Tables 10 or 12 as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In yet other aspects cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit an decrease in gene expression levels of, *e.g.*, about 5 genes to about 100 genes, about 10 genes to about 100 genes, about 15 genes to about 100 genes, about 20 genes to about 100 genes, about 25 genes to about 100 genes, about 5 genes to about 75 genes, about 10 genes to about 75 genes, about 15 genes to about 75 genes, about 20 genes to about 75 genes, about 25 genes to about 75 genes, about 5 genes to about 50 genes, about 10 genes to about 50 genes, about 15 genes to about 50 genes, about 20 genes to about 50 genes, or about 25 genes to about 50 genes listed in Tables 10 or 12 as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164.

[072] In an embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from 1-Mar, ABCG1, ABTB1, ACOT1, ACSL1, ACVR1, ACVR2A, ACYP2, ADAMTS1, ADAMTS3, ADAMTSL1, ADARB1, ADCY1, ADD2, ADO, AFF3, AKAP12, ALDH1A2, ALKBH1, ALLC, AMN1, ANKH, ANKRA2, ANKRD50, ANXA5, AP3B2, ARMC10, ARMCX5, ASAM, ASB13, ASPHD1, ATG5, ATL3, ATP2B3, ATP2C1, ATRNL1, B3GALTL, BACE1, BACE2, BBS10, BBS7, BCAP29, BCL2, BCORL1, BRUNOL4, BRUNOL6, BRWD1, BTN3A3, C10ORF10, C10ORF104, C11ORF57, C11ORF70, C14ORF167, C15ORF39, C16ORF52, C17ORF69, C18ORF18, C1GALT1C1, C1ORF21, C1ORF25, C1ORF97, C1RL, , C21ORF57, C2CD2, C2CD4A, C2ORF67, C2ORF68, C3ORF23, C4ORF12, C4ORF39, C4ORF41, C5ORF42, C6ORF120, C9ORF150, CADM2, CAMK2D, CAMK2N1, CAMK2N2, CAP2, CAPN2, CARTPT, CCDC126, CCDC40, CCDC50, CCNY, CD248, CD302, CDC2L6, CDC37L1, CDC42EP3, CDH12, CDKN1C, CDKN2A, CDS1, CFC1, CHMP1B, CLCN3, CLDN12, CLMN, CLN8, CNGA3, CNNM1, CNOT6L, COL27A1, COL5A1, COL6A1, COL6A2, COL6A3, COX18, COX5B, CRYGD, CRYZL1, CTPS2, CTSC, CYB5R2, CYGB, CYLD, CYP2E1, CYP2U1, CYTL1, CYYR1, D4S234E, DAB1, DBT, DCAF10, DCLK1, DCTD, DDAH1, DIRSX, DISP1, DKFZP434I0714, DKK1, DNAJC12, DNAJC24, DNASE1L1, DNER, DOPEY2, DRAM2, DSCAM, DSCR3, DTX3L, DUSP16, DUSP22, ECEL1, ECHDC3, EEF1D, EEF2K, EFEMP2, EFNB3, EMID1, ENOX2, ERAP1, ERBB2, ERBB4, ETFDH, ETS2, EYA1, FAM13C, FAM162B, FAM165B, FAM172A, FAM175A, FAM190A, FAM26F, FAM46A, FAM49A, FAM71E1, FAM76A, FAM85A, FBXL5, FBXW7, FCRLB, FGD5, FGF1, FGF13, FGF19, FGF3, FGF7, FIP1L1, FKTN, FLJ10038, FLJ35220, FLJ35390, FLJ37798, FLJ39051, FOXO6, FSTL1, FUCA2, GAL, GART, GAS5, GDPD5, GLCE, GLI2, GLIS1, GLIS3, GLT25D2, GNA14, GNAS, GPR123, GPX7, GRM5, GTF2H5, GUCY1A3, H2AFJ, HCG 1776018, HDAC4, HEBP2, HELQ, HERPUD2, HHLA3, HIST1H2AC, HIST1H2BD, HIST1H2BK, HIST2H2BE, HMGCLL1, HNRNPR, HPCAL1, HPDL, HPS3, HSBP1L1, HSPA1A, HTATIP2, ICAM2, IFNAR1, IGFBP5, IGFBP7, IGSF5, IL10RB, IL13RA2, IL17D, IL20RA, IL7, IMMP2L, INSR, IRS1, ITGB1BP1, JMY, JRKL, KAT2B, KBTBD11, KCMF1, KCNMA1, KCNQ2, KCNQ5, KCTD18, KDM1A, KDSR, KHDC1, KIAA1109, KIAA1324, KIAA1598, KIAA1804, KIRREL3, KLHDC1, KRCC1, LGALS3, LGALS3BP, LIFR, LINGO1, LIPT1, LMAN2L, LMCD1, LOC100129195, LOC100129884, LOC100130522, LOC100130856, LOC100132167, LOC100216479, LOC100272217, LOC100287039, LOC151146, LOC153682, LOC220930, LOC254128, LOC255167, LOC283588, LOC285286, LOC285550, LOC285878, LOC286052, LOC339290, LOC401321, LOC645513, LOC80154, LOC90246, LOC93622, LOC94431, LPAR3, LPHN2, LRCH2, LRP2BP, LYRM1, LYRM5, MAGI2, MANSC1, MAP3K13, MAP3K5, MAP9, MAPKAP1, MBD5, MBLAC2, MBNL1, MCTP1, MED6, MEGF11, MEOX2, MET, METT5D1, MFSD4, MFSD6, MFSD9, MGAT4A, MORC3, MREG, MRPS18C, MRPS33, MST1, MTMR3, MTUS2, MXRA7, N4BP3, NAP1L3, NCAM1, NCAM2, NCOA7, NCRNA00081, NCRNA00117, NCRNA00171, NDUFA4L2, NDUFV3, NEAT1, NEBL, NEIL2, NETO1, NFATC4, NHEDC2, NIPAL3, NLRX1, NNAT, NOTCH4, NPW, NPY, NR1H3, NR2F1, NT5E, NUDT19, NUDT6, OGFRL1, OLFM3, OMA1, OPRM1, OPTN, P4HTM, PABPC4L, PABPC5, PAK1, PAM, PAPOLG, PAPPA, PBX1, PCDHB10, PCDHB16, PCNX, PCNXL2, PDCD2, PDE4DIP, PDGFRB, PEX12, PEX6, PHKA1, PHLDB3, PIBF1, PID1, PIGH, PIGP, PIK3CB, PIWIL2, PKNOX1, PKNOX2, PLA2G12A, PLCB1, PLEKHA2, PLEKHA3, PLIN2, PLRG1, POLR3GL, POU6F1, PPAPDC1A, PPOX, PPP1R14A, PPP2R5C,

PPP3CA, PRAME, PRKACB, PRMT2, PRPH, PSD3, PSTK, PTGER2, PTGES, PTN, PTP4A3, PTPRD, PTPRN2, PTPRR, QPCT, RAB4A, RAB6B, RAC2, RAI2, RCAN1, RCC1, RDH13, RFPL1S, RG9MTD2, RGAG4, RHBDD1, RHBDF2, RHOU, RNF13, RNF41, RNLS, RPL31, RPL37, RPRD1A, RRN3, RSL1D1, RSPH3, SAP30, SAV1, SCG5, SCN5A, SERTAD4, SGMS1, SH3BGR, SH3GL2, SH3KBP1, SH3YL1, SIAE, SIGIRR, SIK1, SIK3, SIX2, SLC12A7, SLC16A14, SLC22A17, SLC22A5, SLC25A12, SLC25A4, SLC35F3, SLC6A15, SLIT1, SMARCA2, SMEK2, SNAP91, SNCA, SOCS5, SORCS2, SPATA17, SPATA7, SPIN3, SPINT1, SPINT2, SPOCK2, SPRED1, SSPN, ST8SIA3, STAC2, STAR, STEAP3, STOX2, STX12, STXBP5L, SUCLG2, SYNJ1, SYNPR, SYT13, TAF12, TAF1B, TBC1D12, TBC1D15, TCEAL2, TEX264, THAP2, TM2D1, TMCC1, TMEM182, TMEM184C, TMEM196, TMEM45B, TMEM5, TMEM59L, TMEM65, TMIE, TNC, TNFRSF10D, TNFSF4, TOX, TRAPPC9, TRHDE, TRIM61, TRIM69, TSPAN7, TSPAN9, TTC23, TTC39C, TUSC3, TXLNB, UBE2D3, UBE2W, UCN, UNC5A, UTP23, VPS37A, VSTM2A, WASF3, WDFY3, WDTC1, XPR1, XYLT1, ZBTB41, ZC3H12B, ZNF148, ZNF185, ZNF22, ZNF23, ZNF25, ZNF250, ZNF280D, ZNF285A, ZNF295, ZNF346, ZNF528, ZNF585A, ZNF610, ZNF641, ZNF662, ZNF677, and/or ZNF862, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164.

[073] In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from ACOT1, ADARB1, ASAM, BACE2, C11ORF70, C2CD4A, C3ORF23, CADM2, CAP2, CARTPT, CDKN1C, CFC1, CNGA3, COL5A1, CYGB, CYP2E1, CYTL1, DSCAM, ECEL1, ECHDC3, FAM26F, FAM49A, FGF1, FGF13, FGF19, FLJ39051, FUCA2, GAL, GPX7, GRM5, HCG 1776018, HHLA3, HIST1H2AC, HIST1H2BD, HSPA1A, HTATIP2, ICAM2, IGFBP5, IGFBP7, IL13RA2, KCNMA1, KCNQ5, KIAA1598, KRCC1, LMCD1, LOC100216479, LOC254128, LOC339290, LPAR3, MEGF11, MEOX2, NCAM2, NDUFA4L2, NEAT1, NNAT, NPW, NPY, PABPC4L, PAPPA, PID1, PPAPDC1A, PRAME, PRKACB, PTGER2, PTN, PTP4A3, RAC2, SLC35F3, SYT13, TCEAL2, THAP2, TMIE, TNFRSF10D, TRHDE, TXLNB, and/or ZNF662, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164.

[074] In another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from ACOT1, ASAM, BACE2, C11ORF70, C2CD4A, C3ORF23, CADM2, CAP2, CARTPT, CFC1, CNGA3, CYGB, CYP2E1, CYTL1, DSCAM, ECEL1, ECHDC3, FGF1, FGF13, FUCA2, GAL, GPX7, HSPA1A, HTATIP2, ICAM2, IGFBP5, IGFBP7, KIAA1598, KRCC1, LMCD1, LOC100216479, LOC254128, LOC339290, LPAR3, MEOX2, NDUFA4L2, NEAT1, NNAT, NPW, NPY, PAPPA, PID1, PPAPDC1A, PRAME, PTN, SLC35F3, SYT13, TCEAL2, TMIE, TNFRSF10D, TRHDE, and/or ZNF662, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164.

[075] In yet another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes

selected from C11ORF70, CADM2, CAP2, CARTPT, CNGA3, CYGB, CYP2E1, CYTL1, DSCAM, FGF13, FUCA2, CAL, HSPA1A, HTATIP2, ICAM2, IGFBP5, IGFBP7, LMCD1, LOC100216479, MEOX2, NDUFA4L2, NEAT1, NNAT, NPW, PID1, PRAME, SLC35F3, SYT13, TCEAL2, TMIE, TNFRSF10D, and/or ZNF662, as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164.

[076] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes listed in Tables 5 or 7 as compared to the expression levels of these genes in cells from the 2D6 cell line, and at least a 1.5-fold increase in gene expression levels of one or more genes listed in in Tables 9 or 11 as compared to the expression levels of these genes in cells from a parental SiMa cell line. In aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes listed in Tables 5 or 7 as compared to the expression levels of these genes in cells from the 2D6 cell line, and at least a 1.5-fold increase in gene expression levels of one or more genes listed in in Tables 9 or 11 as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit an increase in gene expression levels of one or more genes listed in Tables 5 or 7 of, *e.g.*, at least a 1.5-fold, at least a 2.0-fold, at least a 2.5-fold, at least a 3.0-fold, at least a 3.5-fold, at least a 4.0-fold, at least a 4.5-fold, at least a 5.0-fold, at least a 5.5-fold, at least a 6.0-fold, at least 7.0-fold, or at least 8.0-fold as compared to the expression levels of these genes in cells from the 2D6 cell line, and exhibit an increase in gene expression levels of one or more genes listed in Tables 9 or 11 of, *e.g.*, at least a 1.5-fold, at least a 2.0-fold, at least a 2.5-fold, at least a 3.0-fold, at least a 3.5-fold, at least a 4.0-fold, at least a 4.5-fold, at least a 5.0-fold, at least a 5.5-fold, at least a 6.0-fold, at least 7.0-fold, or at least 8.0-fold as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit an increase in gene expression levels of, *e.g.*, 2 or more genes, 3 or more genes, 4 or more genes, 5 or more genes, 6 or more genes, 7 or more genes, 8 or more genes, 9 or more genes, 10 or more genes, 20 or more genes, 30 or more genes, 40 or more genes, 50 or more genes, 60 or more genes, 70 or more genes, 80 or more genes, 90 or more genes, or 100 or more genes listed in Tables 5 or 7 as compared to the expression levels of these genes in cells from the 2D6 cell line, and listed in Tables 9 or 11 as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In yet other aspects cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit an increase in gene expression levels of, *e.g.*, about 5 genes to about 100 genes, about 10 genes to about 100 genes, about 15 genes to about 100 genes, about 20 genes to about 100 genes, about 25 genes to about 100 genes, about 5 genes to about 75 genes, about 10 genes to about 75 genes, about 15 genes to about 75 genes, about 20 genes to about 75 genes, about 25 genes to about 75 genes, about 5 genes to about 50 genes, about 10 genes to about 50 genes, about 15 genes to about 50 genes, about 20 genes to about 50 genes, or about 25 genes to about 50 genes listed in Tables 5 or 7 as compared to the expression levels of these genes in cells from the 2D6 cell line, and listed in

Tables 9 or 11 as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164.

[077] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from A2BP1, ALCAM, ANAPC7, ARF1, ARHGAP6, ARHGEF6, ARL17A, ASCL1, ASXL3, BASP1, BNC2, C10ORF58, C12ORF49, C1ORF43, C20ORF7, CBLB, CBWD1, CCDC3, CD9, CDC25B, CHRNA7, CPVL, CRYBG3, CSE1L, CUGBP2, CXCR4, DACT1, DAZ1, DBH, DHX35, DKFZP434L187, DLEU2, DLL3, EAF2, EFNA5, EIF3C, ELOVL7, EML1, ENC1, EXOSC6, EXPH5, EZH2, FAM181B, FAM19A4, FAM7A3, FUBP3, FZD5, GAP43, GFRA2, GNAI1, GNB4, GNG11, GPR125, GRP, GSS, ITGA6, ITGA6, ITGB5, KCTD12, KDELC2, KHDRBS3, KIF16B, KLHL13, LBH, LOC100128844, LOC340109, LOC641298, LOC728052, LUM, MAB21L1, MAN2A1, MAOA, MINA, MMD, MSN, MYO1B, MYO6, NAAA, NEDD9, NOS1, OSBPL3, PCGF5, PELI2, PFKFB3, PHF20, PLK2, PLS3, PLXNA2, PLXNA4, PM20D2, POLE, PSMA7, PTGFRN, PTPRE, PTPRG, RAB35, RAF1, RAN, RASEF, RBL1, RELL1, RGS5, RIMBP2, RNF182, RNF34, S1PR3, SALL4, SEMA6A, SEZ6L, SIM1, SLC44A5, SLC7A2, SLCO3A1, SLITRK5, SPAG6, SPATS2L, ST8SIA1, STMN3, STRA6, TCF7L2, TFPI2, TH1L, THOC4, TIMP3, TLE3, TMEM132C, TMEM178, TPBG, TRA2A, TRIM29, TRIM36, TSHZ3, TXNRD1, U2AF1, UBE2V1, VPS29, ZFHX4, ZGPAT, ZNF217, and/or ZNF503, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[078] In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ALCAM, ARHGAP6, ARHGEF6, ASCL1, BNC2, CCDC3, CHRNA7, CRYBG3, CUGBP2, CXCR4, DAZ1, EFNA5, ELOVL7, EML1, ENC1, EXPH5, FAM7A3, FZD5, GFRA2, GNAI1, GNB4, GNG11, GRP, ITGA6, KCTD12, LOC100128844, LOC340109, LOC728052, LUM, MAB21L1, MAB21L2, MAOA, MSN, NEDD9, OSBPL3, PLK2, PTGFRN, PTPRE, RGS5, RNF182, SIM1, SLC44A5, SLITRK5, SPAG6, TFPI2, TIMP3, TMEM132C, TPBG, TRIM29, and/or TRIM36, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[079] In another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ALCAM, ARHGAP6, ARHGEF6, CCDC3, CHRNA7, CRYBG3, CUGBP2, CXCR4, DAZ1, ELOVL7, EML1, EXPH5, FAM7A3, GNB4, GNG11, GRP, ITGA6, KCTD12, LOC340109, LUM, MAB21L1, MAB21L2, PLK2, PTPRE, RGS5, RNF182, SIM1, SLC44A5, SLITRK5, SPAG6, TIMP3, and/or TMEM132C, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[080] In yet another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from CCDC3, CHRNA7, CRYBG3, CXCR4, DAZ1, EXPH5, FAM7A3, GNB4, GRP, KCTD12,

LUM, PLK2, PTPRE, RGS5, SIM1, SLITRK5, TIMP3, and/or TMEM132C, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[081] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from A2BP1, ALCAM, ARF1, ARL17A, ASCL1, BASP1, CD9, CUGBP2, EAF2, EIF3C, FAM181B, FUBP3, GNAI1, GNB4, GNG11, KDELC2, KHDRBS3, KLHL13, LOC641298, LOC728052, MAB21L2, MAOA, MINA, MSN, MYO6, PLK2, PLS3, RAF1, RELL1, RNF182, SEZ6L, SEZ6L, SIM1, SLC44A5, SLC7A2, SLCO3A1, SLITRK5, SPATS2L, TCF7L2, TFPI2, TMEM178, TRA2A, U2AF1, and/or ZNF217, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[082] In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from A2BP1, ALCAM, ARF1, ASCL1, BASP1, CD9, CUGBP2, EIF3C, FUBP3, GNAI1, GNB4, GNG11, KDELC2, KHDRBS3, LOC641298, LOC728052, MAB21L2, MAOA, MINA, MSN, MYO6, PLK2, PLS3, RELL1, RNF182, SIM1, SLC44A5, SLC7A2, SLCO3A1, SLITRK5, TCF7L2, TFPI2, TMEM178, TRA2A, and/or ZNF217, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[083] In another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ASCL1, CUGBP2, GNAI1, GNB4, GNG11, LOC728052, MAB21L2, MAOA, MSN, PLK2, RNF182, SIM1, SLC44A5, SLITRK5, and/or TFPI2, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[084] In yet another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from GNB4, GNG11, PLK2, RNF182, SIM1, SLC44A5, and/or SLITRK5, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[085] In still another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from GNB4, PLK2, SIM1, and/or SLITRK5, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[086] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes listed in Tables 6 or 8 as compared to the expression levels of these genes in cells from the 2D6 cell line, and at

least a 1.5-fold decrease in gene expression levels of one or more genes listed in in Tables 10 or 12 as compared to the expression levels of these genes in cells from a parental SiMa cell line. In aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes listed in Tables 6 or 8 as compared to the expression levels of these genes in cells from the 2D6 cell line, and at least a 1.5-fold decrease in gene expression levels of one or more genes listed in in Tables 10 or 12 as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit a decrease in gene expression levels of one or more genes listed in Tables 6 or 8 of, *e.g.*, at least a 1.5-fold, at least a 2.0-fold, at least a 2.5-fold, at least a 3.0-fold, at least a 3.5-fold, at least a 4.0-fold, at least a 4.5-fold, at least a 5.0-fold, at least a 5.5-fold, at least a 6.0-fold, at least 7.0-fold, or at least 8.0-fold as compared to the expression levels of these genes in cells from the 2D6 cell line, and a decrease in gene expression levels of one or more genes listed in Tables 10 or 12 of, *e.g.*, at least a 1.5-fold, at least a 2.0-fold, at least a 2.5-fold, at least a 3.0-fold, at least a 3.5-fold, at least a 4.0-fold, at least a 4.5-fold, at least a 5.0-fold, at least a 5.5-fold, at least a 6.0-fold, at least 7.0-fold, or at least 8.0-fold as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit a decrease in gene expression levels of, *e.g.*, 2 or more genes, 3 or more genes, 4 or more genes, 5 or more genes, 6 or more genes, 7 or more genes, 8 or more genes, 9 or more genes, 10 or more genes, 20 or more genes, 30 or more genes, 40 or more genes, 50 or more genes, 60 or more genes, 70 or more genes, 80 or more genes, 90 or more genes, or 100 or more genes listed in Tables 6 or 8 as compared to the expression levels of these genes in cells from the 2D6 cell line, and listed in Tables 10 or 12 as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164. In yet other aspects cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit a decrease in gene expression levels of, *e.g.*, about 5 genes to about 100 genes, about 10 genes to about 100 genes, about 15 genes to about 100 genes, about 20 genes to about 100 genes, about 25 genes to about 100 genes, about 5 genes to about 75 genes, about 10 genes to about 75 genes, about 15 genes to about 75 genes, about 20 genes to about 75 genes, about 25 genes to about 75 genes, about 5 genes to about 50 genes, about 10 genes to about 50 genes, about 15 genes to about 50 genes, about 20 genes to about 50 genes, or about 25 genes to about 50 genes listed in Tables 6 or 8 as compared to the expression levels of these genes in cells from the 2D6 cell line, and listed in Tables 10 or 12 as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164.

[087] In an embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from ABTB1, ACOT1, ACYP2, ADARB1, ADCY1, ANKRD50, ASAM, ASPHD1, ATP2B3, BACE1, BRUNOL4, BRWD1, BTN3A3, C16ORF52, C1ORF21, C21ORF57, C2CD2, C2CD4A, C3ORF23, C9ORF150, CAMK2N2, CAP2, CAPN2, CARTPT, CD302, CDH12, CDKN2A, CDS1, CFC1, CLCN3, CLDN12, CLMN, CNGA3, CNNM1, CNOT6L, COL6A1, CYGB, CYLD, CYP2E1, CYTL1, D4S234E, DCLK1, DCTD, DUSP16,

EFNB3, ERAP1, ERBB2, ERBB4, ETFDH, FAM162B, FAM165B, FAM46A, FBXW7, FGD5, FGF13, FOXO6, FSTL1, GAL, GLT25D2, GNAS, GPR123, GPX7, GRM5, GUCY1A3, HCG 1776018, HELQ, HERPUD2, HIST1H2AC, HIST1H2BD, HIST1H2BK, HIST2H2BE, HNRNPR, HPCAL1, IL10RB, JMY, KAT2B, KBTBD11, KCNMA1, KCNQ2, KHDC1, KIAA1598, KLHDC1, LGALS3BP, LIFR, LOC100130522, LOC94431, LRP2BP, LYRM5, MAP3K5, MAP9, MCTP1, MEOX2, MFSD4, MGAT4A, MRPS33, MST1, NAP1L3, NCOA7, NCRNA00171, NDUFA4L2, NDUFV3, NFRI, NHEDC2, NIPAL3, NLRX1, NUDT19, OLFM3, PAM, PAPPA, PCNXL2, PDGFRB, PHKA1, PIGH, PLRG1, PLRG1, PPAPDC1A, PRKACB, PRPH, PTGER2, PTN, PTPRD, RAB6B, RGAG4, RHOU, RNF13, RNF41, RSL1D1, SH3GL2, SH3YL1, SIGIRR, SIK1, SLC12A7, SLC22A17, SLC35F3, SNCA, SPINT2, SPOCK2, ST8SIA3, STAR, STEAP3, STOX2, SYNJ1, SYT13, TM2D1, TMEM184C, TMEM5, TMEM59L, TMIE, TTC39C, TUSC3, TXLNB, UCN, WDFY3, WDFY3, ZNF641, and/or ZNF662, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[088] In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from ACOT1, ADARB1, ASAM, C2CD4A, C3ORF23, CAP2, CARTPT, CFC1, CNGA3, CYGB, CYP2E1, CYTL1, FGF13, GAL, GPX7, GRM5, HCG 1776018, HIST1H2AC, HIST1H2BD, KCNMA1, KIAA1598, MEOX2, NDUFA4L2, PPAPDC1A, PRKACB, PTGER2, PTN, SLC35F3, SYT13, TMIE, TXLNB, and/or ZNF662, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[089] In another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from ACOT1, ASAM, C2CD4A, C3ORF23, CAP2, CARTPT, CFC1, CNGA3, CYGB, CYP2E1, CYTL1, FGF13, GAL, GPX7, KIAA1598, MEOX2, NDUFA4L2, PPAPDC1A, PTN, SLC35F3, SYT13, TMIE, and/or ZNF662, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[090] In yet another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from CAP2, CARTPT, CNGA3, CYGB, CYP2E1, CYTL1, FGF13, GAL, MEOX2, NDUFA4L2, SLC35F3, SYT13, TMIE, and/or ZNF662, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[091] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from CAP2, CDKN2A, CNGA3, FAM162B, FGF13, FOXO6, FSTL1, KCNMA1, KHDC1, LIFR, MCTP1, MEOX2, PPAPDC1A, PTN, SYT13, TMIE, and/or ZNF662, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[092] In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from CAP2, CDKN2A, CNGA3, FGF13, FOXO6, FSTL1, KCNMA1, KHDC1, MCTP1, MEOX2, PPAPDC1A, PTN, SYT13, TMIE, and/or ZNF662, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[093] In another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from CNGA3, FGF13, KCNMA1, MEOX2, PPAPDC1A, PTN, SYT13, TMIE, and/or ZNF662, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[094] In yet another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from CNGA3, FGF13, MEOX2, PPAPDC1A, PTN, SYT13, TMIE, and/or ZNF662, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[095] In still another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold decrease in gene expression levels of one or more genes selected from CNGA3, FGF13, MEOX2, SYT13, TMIE, and/or ZNF662, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[096] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold difference in gene expression levels of one or more genes listed in Tables 14 or 16 as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164. In aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold difference in gene expression levels of one or more genes listed in Tables 14 or 16 as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164. In other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit a difference in gene expression levels of one or more genes listed in Tables 14 or 16 of, *e.g.*, at least a 1.5-fold, at least a 2.0-fold, at least a 2.5-fold, at least a 3.0-fold, at least a 3.5-fold, at least a 4.0-fold, at least a 4.5-fold, at least a 5.0-fold, at least a 5.5-fold, at least a 6.0-fold, at least a 7.0-fold, or at least a 8.0-fold as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164. In other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit an increase in gene expression levels of, *e.g.*, 2 or more genes, 3 or more genes, 4 or more genes, 5 or more genes, 6 or more genes, 7 or more genes, 8 or more genes, 9 or more genes, 10 or more genes, 20 or more genes, 30 or more genes, 40 or more genes, 50 or more genes, 60 or more genes, 70 or more genes, 80 or more genes, 90

or more genes, or 100 or more genes listed in Tables 14 or 16 as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164. In yet other aspects cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit an increase in gene expression levels of, *e.g.*, about 5 genes to about 100 genes, about 10 genes to about 100 genes, about 15 genes to about 100 genes, about 20 genes to about 100 genes, about 25 genes to about 100 genes, about 5 genes to about 75 genes, about 10 genes to about 75 genes, about 15 genes to about 75 genes, about 20 genes to about 75 genes, about 25 genes to about 75 genes, about 5 genes to about 50 genes, about 10 genes to about 50 genes, about 15 genes to about 50 genes, about 20 genes to about 50 genes, or about 25 genes to about 50 genes listed in Tables 14 or 16 as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[097] In an embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold difference in gene expression levels of one or more genes selected from ACOT9, ADAMTS9, ARHGAP24, ARHGEF3, ASCL1, BARD1, BASP1, C3ORF70, C11ORF75, CCDC109B, CD9, CDCA7L, CDK2, CENPL, CLSTN2, CNTN1, CSRP2, CTSL2, CUGBP2, DEPDC1, DIAPH3, DOK5, DPYD, DYNLT3, EMILIN2, ETV1, FAM101B, FBLN1, FGFR2, FNDC5, GNAI1, GNB4, GNG11, GNG12, GPR177, GTSE1, HGF, KITLG, LPAR1, MAB21L2, MAOA, MCM10, MINA, MSN, MYO6, MYRIP, PAG1, PEG3, PLK2, POLA2, PPP1R3C, PRLHR, PRSS12, PTGR1, PTPRK, PVRL3, RAB32, RBPMS, SDC2, SGOL2, SLC43A3, SLC7A2, SMC2, SMC6, SPARC, SPC25, ST8SIA4, TCF7L1, TFPI2, TMEM35, TMEM178, TNFAIP8, TPTE, TRIP10, TWIST1, and/or ZNF521, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164. In another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold difference in gene expression levels of one or more genes selected from ADAMTS9, ARHGAP24, ASCL1, BARD1, BASP1, BVES, C11ORF75, CDCA7L, CNTN1, CUGBP2, DOK5, DPYD, DYNLT3, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, GTSE1, GTSF1, ITPRIP, KDELC2, LOC728052, LPAR1, MAB21L2, MAOA, MINA, MSN, PEG3, PLK2, PRLHR, PRSS12, PTPRK, RBPMS, RNF182, SGOL2, SLC43A3, SLC44A5, SLC7A2, SMC6, SPARC, TFPI2, TMEM178, and/or TPTE, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164. In yet another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold difference in gene expression levels of one or more genes selected from ADAMTS9, ASCL1, BASP1, DOK5, DPYD, GNB4, GNG11, GTSF1, MAOA, MINA, MSN, PEG3, PLK2, PRSS12, RNF182, SLC44A5, SPARC, TFPI2, and/or TPTE, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[098] In another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ADAMTS9, ARHGAP24, ARHGEF3, ASCL1, BARD1, CD9, CDK2, CSRP2, CTSL2, DIAPH3, DOK5, DYNLT3, EMILIN2, ETV1, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, HGF, KITLG,

LPAR1, MCM10, MSN, PAG1, PEG3, PLK2, POLA2, PPP1R3C, PTPRK, RAB32, SDC2, SLC43A3, SLC7A2, SMC6, SPARC, SPC25, ST8SIA4, TCF7L1, TFPI2, TMEM35, TNFAIP8, TPTE, TRIP10, and/or TWIST1, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164. In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ADAMTS9, ARHGAP24, ASCL1, BARD1, DOK5, DYNLT3, FRIN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, LPAR1, MSN, PEG3, PLK2, PTPRK, SLC43A3, SLC7A2, SMC6, SPARC, TFPI2, and/or TPTE, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164. In another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ADAMTS9, ASCL1, DOK5, GNB4, GNG11, MSN, PEG3, PLK2, SPARC, TFPI2, and/or TPTE, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[0099] In yet another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from ACOT9, BASP1, C11ORF75, CCDC109B, CDCA7L, CLSTN2, CNTN1, CUGBP2, DEPDC1, DPYD, FAM101B, FNDC5, GTSE1, MAOA, MINA, MYO6, MYRIP, PLK2, PRLHR, PVRL3, RBPMS, SGOL2, SMC2, TFP12, TMEM178, and/or ZNF521, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164. In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from BASP1, C11ORF75, CDCA7L, CNTN1, CUGBP2, DPYD, GTSE1, MAOA, MINA, PLK2, PRLHR, RBPMS, SGOL2, TFPI2, and/or TMEM178, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164. In another aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from BASP1, DPYD, MAOA, MINA, PLK2, and/or TFPI2, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[0100] In a still another embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from C3ORF70, MAB21L2, PRSS12, CENPL, GPR177, and/or PTGR1, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164. In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit at least a 1.5-fold increase in gene expression levels of one or more genes selected from MAB21L2 and/or PRSS12, as compared to the expression levels of these genes in cells from both the 2D6 cell line and the parental SiMa cell line DSMZ ACC 164.

[0101] Aspects of the present disclosure comprise, in part, cells from an established clonal cell line susceptible to BoNT/A intoxication that exhibit an equivalent or lower EC_{50} for BoNT/A activity relative to the EC_{50} for BoNT/A activity of cells from a parental SiMa cell line. In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit an equivalent or lower EC_{50} for BoNT/A activity relative to the EC_{50} for BoNT/A activity of cells from the parental SiMa cell line DSMZ ACC 164. In an aspect of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit an equivalent EC_{50} for BoNT/A activity relative to the EC_{50} for BoNT/A activity of cells from the parental SiMa cell line DSMZ ACC 164. In aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit a lower EC_{50} for BoNT/A activity of, *e.g.*, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or at least 100% relative to the EC_{50} for BoNT/A activity of cells from the parental SiMa cell line DSMZ ACC 164. In other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit a lower EC_{50} for BoNT/A activity of, *e.g.*, at least 110%, at least 120%, at least 130%, at least 140%, at least 150%, at least 160%, at least 170%, at least 180%, at least 190%, or at least 200% relative to the EC_{50} for BoNT/A activity of cells from the parental SiMa cell line DSMZ ACC 164. In yet other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit a lower EC_{50} for BoNT/A activity of, *e.g.*, at least 225%, at least 250%, at least 275%, at least 300%, at least 325%, at least 350%, at least 375%, at least 400%, at least 425%, at least 450%, at least 475%, or at least 500% relative to the EC_{50} for BoNT/A activity of cells from the parental SiMa cell line DSMZ ACC 164. In still other aspects of this embodiment, cells from an established clonal cell line susceptible to BoNT/A intoxication exhibit an EC_{50} for BoNT/A activity of, *e.g.*, 10 pM or less, 9 pM or less, 8 pM or less, 7 pM or less, 6 pM or less, 5 pM or less, 4 pM or less, 3.0 pM or less, 2.9 pM or less, 2.8 pM or less, 2.7 pM or less, 2.6 pM or less, 2.5 pM or less, 2.4 pM or less, 2.3 pM or less, 2.2 pM or less, 2.1 pM or less, 2.0 pM or less, 1.9 pM or less, 1.8 pM or less, 1.7 pM or less, 1.6 pM or less, 1.5 pM or less, 1.4 pM or less, 1.3 pM or less, 1.2 pM or less, 1.1 pM or less, 1.0 pM or less, 0.9 pM or less, 0.8 pM or less, 0.7 pM or less, 0.6 pM or less, 0.5 pM or less, 0.4 pM or less, 0.3 pM or less, 0.2 pM or less, or 0.1 pM or less.

[0102] Aspects of the present disclosure comprise, in part, a BoNT/A. As used herein, the term "BoNT/A" is synonymous with "botulinum neurotoxin serotype A" or "botulinum neurotoxin type A" and refers to both a naturally-occurring BoNT/A or a non-naturally occurring BoNT/As thereof, and includes BoNT/A complex comprising the about 150 kDa BoNT/A neurotoxin and associated non-toxin associated proteins (NAPs), as well as the about 150 kDa BoNT/A neurotoxin alone. Non-limiting examples of BoNT/A complexes include, *e.g.*, the 900-kDa BoNT/A complex, the 500-kDa BoNT/A complex, the 300-kDa BoNT/A complex. Non-limiting examples of the about 150 kDa BoNT/A neurotoxin include, *e.g.*, SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4.

[0103] As used herein, the term "naturally occurring BoNT/A" refers to any BoNT/A produced by a naturally-occurring process, including, without limitation, BoNT/A isoforms produced from a post-translational modification, an alternatively-spliced transcript, or a spontaneous mutation, and BoNT/A

subtypes, such as, *e.g.*, a BoNT/A1 subtype, BoNT/A2 subtype, BoNT/A3 subtype, BoNT/A4 subtype, and BoNT/A5 subtype. A naturally occurring BoNT/A includes, without limitation, SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, or one that substitutes, deletes or adds, *e.g.*, 1 or more, 2 or more, 3 or more, 4 or more, 5 or more, 6 or more, 7 or more, 8 or more, 9 or more, 10 or more, 20 or more, 30 or more, 40 or more, 50 or more, or 100 amino acids from SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 4. Commercially available pharmaceutical compositions of a naturally-occurring BoNT/A includes, without limitation, BOTOX® (Allergan, Inc., Irvine, CA), DYSPORT®/RELOXIN®, (Ipsen Ltd., Slough, England), PURTOX® (Mentor Corp., Santa Barbara, CA), XEOMIN® (Merz Pharmaceuticals, GmbH., Frankfurt, Germany), NEURONOX® (Medy-Tox, Inc., Ochang-myeon, South Korea), BTX-A.

[0104] As used herein, the term "non-naturally occurring BoNT/A" refers to any BoNT/A whose structure was modified with the aid of human manipulation, including, without limitation, a BoNT/A with an altered amino acid sequence produced by genetic engineering using random mutagenesis or rational design and a BoNT/A produced by in vitro chemical synthesis. Non-limiting examples of non-naturally occurring BoNT/As are described in, *e.g.*, Steward, L.E. et al., *Post-translational Modifications and Clostridial Neurotoxins*, U.S. Patent 7,223,577; Dolly, J.O. et al., *Activatable Clostridial Toxins*, U.S. Patent No. 7,419,676; Steward, L.E. et al., *Clostridial Neurotoxin Compositions and Modified Clostridial Neurotoxins*, US 2004/0220386; Steward, L.E. et al., *Modified Clostridial Toxins With Enhanced Targeting Capabilities For Endogenous Clostridial Toxin Receptor Systems*, U.S. Patent Publication No. 2008/0096248; Steward, L.E. et al., *Modified Clostridial Toxins With Altered Targeting Capabilities For Clostridial Toxin Target Cells*, U.S. Patent Publication No. 2008/0161543; Steward, L.E. et al., *Modified Clostridial Toxins With Enhanced Translocation Capabilities and Altered Targeting Activity For Clostridial Toxin Target Cells*, U.S. Patent Publication No. 2008/0241881, each of which is hereby incorporated by reference in its entirety.

[0105] Thus in an embodiment, the BoNT/A activity being detected is from a naturally occurring BoNT/A. In aspects of this embodiment, the BoNT/A activity being detected is from a BoNT/A isoform or a BoNT/A subtype. In aspects of this embodiment, the BoNT/A activity being detected is from the BoNT/A of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 4. In other aspects of this embodiment, the BoNT/A activity being detected is from a BoNT/A having, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% amino acid identity with SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 4. In other aspects of this embodiment, the BoNT/A activity being detected is from BOTOX®, DYSPORT®/RELOXIN®, PURTOX®, XEOMIN®, NEURONOX®, or BTX-A.

[0106] In another embodiment, the BoNT/A activity being detected is from a non-naturally occurring BoNT/A. In other aspects of this embodiment, the BoNT/A activity being detected is from a non-naturally occurring BoNT/A variant having, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% amino acid identity with SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 4. In other aspects of this embodiment, the BoNT/A activity being detected is from a non-naturally occurring BoNT/A variant having, e.g., 1 or more, 2 or more, 3 or more, 4 or more, 5 or more, 6 or more, 7

or more, 8 or more, 9 or more, 10 or more, 20 or more, 30 or more, 40 or more, 50 or more, or 100 or more non-contiguous amino acid substitutions, deletions, or additions relative to SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 4. In yet other aspects of this embodiment, the BoNT/A activity being detected is from a non-naturally occurring BoNT/A variant having, e.g., 1 or more, 2 or more, 3 or more, 4 or more, 5 or more, 6 or more, 7 or more, 8 or more, 9 or more, 10 or more, 20 or more, 30 or more, 40 or more, 50 or more, or 100 or more contiguous amino acid substitutions, deletions, or additions relative to SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 4.

[0107] Aspects of the present disclosure comprise, in part, a SNAP-25. As used herein, the term "SNAP-25" refers to a naturally-occurring SNAP-25 or a non-naturally occurring SNAP-25 which is preferentially cleaved by a BoNT/A. As used herein, the term "preferentially cleaved" refers to that the cleavage rate of a BoNT/A substrate by a BoNT/A that is at least one order of magnitude higher than the cleavage rate of any other substrate by BoNT/A. In aspects of this embodiment, the cleavage rate of a BoNT/A substrate by a BoNT/A that is at least two orders of magnitude higher, at least three orders of magnitude higher, at least four orders of magnitude higher, or at least five orders of magnitude higher than the cleavage rate of any other substrate by BoNT/A.

[0108] As used herein, the term "naturally occurring SNAP-25" refers to any SNAP-25 produced by a naturally-occurring process, including, without limitation, SNAP-25 isoforms produced from a post-translational modification, an alternatively-spliced transcript, or a spontaneous mutation, and SNAP-25 subtypes. A naturally occurring SNAP-25 includes, without limitation, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, or SEQ ID NO: 24, or one that substitutes, deletes or adds, *e.g.*, 1 or more, 2 or more, 3 or more, 4 or more, 5 or more, 6 or more, 7 or more, 8 or more, 9 or more, 10 or more, 20 or more, 30 or more, 40 or more, 50 or more, or 100 or more amino acids from SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, or SEQ ID NO: 24.

[0109] As used herein, the term "non-naturally occurring SNAP-25" refers to any SNAP-25 whose structure was modified with the aid of human manipulation, including, without limitation, a SNAP-25 produced by genetic engineering using random mutagenesis or rational design and a SNAP-25 produced by in vitro chemical synthesis. Non-limiting examples of non-naturally occurring SNAP-25s are described in, *e.g.*, Steward, L.E. et al., *FRET Protease Assays for Clostridial Toxins*, U.S. Patent 7,332,567; Fernandez-Salas et al., *Lipohilic Dye-based FRET Assays for Clostridial Toxin Activity*, U.S. Patent Publication 2008/0160561, each of which is hereby incorporated by reference in its entirety. A non-naturally occurring SNAP-25 may substitute, delete or add, *e.g.*, 1 or more, 2 or more, 3 or more, 4 or more, 5 or more, 6 or more, 7 or more, 8 or more, 9 or more, 10 or more, 20 or more, 30 or more, 40 or

more, 50 or more, or 100 or more amino acids from SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, or SEQ ID NO: 24.

[0110] This in an embodiment, a SNAP-25 is a naturally occurring SNAP-25. In aspects of this embodiment, the SNAP-25 is a SNAP-25 isoform or a SNAP-25 subtype. In aspects of this embodiment, the naturally occurring SNAP-25 is the naturally occurring SNAP-25 of SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, or SEQ ID NO: 24. In other aspects of this embodiment, the SNAP-25 is a naturally occurring SNAP-25 having, e.g., at least 70% amino acid identity, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% amino acid identity with SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, or SEQ ID NO: 24.

[0111] In another embodiment, a SNAP-25 is a non-naturally occurring SNAP-25. In other aspects of this embodiment, the SNAP-25 is a non-naturally occurring SNAP-25 having, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% amino acid identity with SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, or SEQ ID NO: 24. In other aspects of this embodiment, the SNAP-25 is a non-naturally occurring SNAP-25 having, e.g., 1 or more, 2 or more, 3 or more, 4 or more, 5 or more, 6 or more, 7 or more, 8 or more, 9 or more, 10 or more, 20 or more, 30 or more, 40 or more, 50 or more, or 100 or more non-contiguous amino acid substitutions, deletions, or additions relative to SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, or SEQ ID NO: 24. In yet other aspects of this embodiment, the SNAP-25 is a non-naturally occurring SNAP-25 having, e.g., 1 or more, 2 or more, 3 or more, 4 or more, 5 or more, 6 or more, 7 or more, 8 or more, 9 or more, 10 or more, 20 or more, 30 or more, 40 or more, 50 or more, or 100 or more contiguous amino acid substitutions, deletions, or additions relative to SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, or SEQ ID NO: 24.

[0112] A SNAP-25 can be an endogenous SNAP-25 or an exogenous SNAP-25. As used herein, the term "endogenous SNAP-25" refers to a SNAP-25 naturally present in the cell because it is naturally encoded within the cell's genome, such that the cell inherently expresses the SNAP-25 without the need of an external source of SNAP-25 or an external source of genetic material encoding a SNAP-25. The expression of an endogenous SNAP-25 may be with or without environmental stimulation such as, *e.g.*, cell differentiation. By definition, an endogenous SNAP-25 can only be a naturally-occurring SNAP-25 or variants thereof. For example, the following established cell lines express an endogenous SNAP-25: BE(2)-M17, Kelly, LA1-55n, N1E-115, N4TG3, N18, Neuro-2a, NG108-15, PC12, SH-SY5Y, SiMa, and SK-N-BE(2)-C.

[0113] As used herein, the term "exogenous SNAP-25" refers to a SNAP-25 expressed in a cell through the introduction of an external source of SNAP-25 or an external source of genetic material encoding a SNAP-25 by human manipulation. The expression of an exogenous SNAP-25 may be with or without environmental stimulation such as, *e.g.*, cell differentiation. As a non-limiting example, cells from an established clonal cell line can express an exogenous SNAP-25 by transient or stably transfection of a SNAP-25 coding sequence. As another non-limiting example, cells from an established clonal cell line can express an exogenous SNAP-25 by protein transfection of a SNAP-25. An exogenous SNAP-25 can be a naturally-occurring SNAP-25 or variants thereof, or a non-naturally occurring SNAP-25 or variants thereof.

[0114] Thus in an embodiment, cells from an established clonal cell line express an endogenous SNAP-25. In aspects of this embodiment, the endogenous SNAP-25 expressed by cells from an established clonal cell line is a naturally-occurring SNAP-25. In other aspects of this embodiment, the endogenous SNAP-25 expressed by cells from an established clonal cell line is SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, or SEQ ID NO: 24. In yet other aspects of this embodiment, the endogenous SNAP-25 expressed by cells from an established clonal cell line is a naturally occurring SNAP-25, such as, *e.g.*, a SNAP-25 isoform or a SNAP-25 subtype. In other aspects of this embodiment, the endogenous SNAP-25 expressed by cells from an established clonal cell line is a naturally occurring SNAP-25 having, e.g., at least 70% amino acid identity, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% amino acid identity with SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, or SEQ ID NO: 24.

[0115] In another embodiment, cells from an established clonal cell line are transiently or stably engineered to express an exogenous SNAP-25. In an aspect of this embodiment, cells from an established clonal cell line are transiently or stably engineered to express a naturally-occurring SNAP-25. In other aspects of this embodiment, cells from an established clonal cell line are transiently or stably

engineered to express the naturally-occurring SNAP-25 of SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, or SEQ ID NO: 24. In yet other aspects of this embodiment, cells from an established clonal cell line are transiently or stably engineered to express a naturally occurring SNAP-25, such as, *e.g.*, a SNAP-25 isoform or a SNAP-25 subtype. In still other aspects of this embodiment, cells from an established clonal cell line are transiently or stably engineered to express a naturally occurring SNAP-25 having, e.g., at least 70% amino acid identity, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% amino acid identity with SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, or SEQ ID NO: 24.

[0116] In another aspect of the embodiment, cells from an established clonal cell line are transiently or stably engineered to express a non-naturally occurring SNAP-25. In other aspects of this embodiment, cells from an established clonal cell line are transiently or stably engineered to express a non-naturally occurring SNAP-25 having, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% amino acid identity with SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, or SEQ ID NO: 24. In other aspects of this embodiment, cells from an established clonal cell line are transiently or stably engineered to express a non-naturally occurring SNAP-25 having, e.g., 1 or more, 2 or more, 3 or more, 4 or more, 5 or more, 6 or more, 7 or more, 8 or more, 9 or more, 10 or more, 20 or more, 30 or more, 40 or more, 50 or more, or 100 or more non-contiguous amino acid substitutions, deletions, or additions relative to SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, or SEQ ID NO: 24. In yet other aspects of this embodiment, cells from an established clonal cell line are transiently or stably engineered to express a non-naturally occurring SNAP-25 having, e.g., 1 or more, 2 or more, 3 or more, 4 or more, 5 or more, 6 or more, 7 or more, 8 or more, 9 or more, 10 or more, 20 or more, 30 or more, 40 or more, 50 or more, or 100 or more contiguous amino acid substitutions, deletions, or additions relative to SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, or SEQ ID NO: 24.

[0117] Assays that detect the cleavage of a BoNT/A substrate after exposure to a BoNT/A can be used to assess whether a cell is expressing an endogenous or an exogenous SNAP-25. In these assays, generation of a SNAP-25 cleavage-product would be detected in cells expressing a SNAP-25 after

BoNT/A treatment. Non-limiting examples of specific Western blot analysis, as well as well-characterized reagents, conditions and protocols are readily available from commercial vendors that include, without limitation, Amersham Biosciences, Piscataway, NJ; Bio-Rad Laboratories, Hercules, CA; Pierce Biotechnology, Inc., Rockford, IL; Promega Corporation, Madison, WI, and Stratagene, Inc., La Jolla, CA. It is understood that these and similar assays for SNAP-25 cleavage can be useful in identifying cells expressing an endogenous or an exogenous SNAP-25

[0118] As non-limiting examples, Western blot analysis using an antibody that recognizes BoNT/A SNAP-25-cleaved product or both the cleaved and uncleaved forms of SNAP-25 can be used to assay for uptake of BoNT/A. Examples of α-SNAP-25 antibodies useful for these assays include, without limitation, α-SNAP-25 mouse monoclonal antibody SMI-81 (Sternberger Monoclonals Inc., Lutherville, MD), mouse α-SNAP-25 monoclonal antibody Cl 71.1 (Synaptic Systems, Goettingen, Germany), α-SNAP-25 mouse monoclonal antibody Cl 71.2 (Synaptic Systems, Goettingen, Germany), α-SNAP-25 mouse monoclonal antibody SP12 (Abcam, Cambridge, MA), α-SNAP-25 rabbit polyclonal antiserum (Synaptic Systems, Goettingen, Germany), α-SNAP-25 rabbit polyclonal antiserum (Abcam, Cambridge, MA), and α-SNAP-25 rabbit polyclonal antiserum S9684 (Sigma, St Louis, MO).

[0119] Aspects of the present disclosure comprise, in part, a BoNT/A receptor. As used herein, the term "BoNT/A receptor" refers to either a naturally-occurring BoNT/A receptor or a non-naturally occurring BoNT/A receptor which preferentially interacts with BoNT/A in a manner that elicits a BoNT/A intoxication response. As used herein, the term "preferentially interacts" refers to that the equilibrium dissociation constant (KD) of BoNT/A for a BoNT/A receptor is at least one order of magnitude less than that of BoNT/A for any other receptor. The equilibrium dissociation constant, a specific type of equilibrium constant that measures the propensity of an BoNT/A-BoNT/A receptor complex to separate (dissociate) reversibly into its component molecules, namely the BoNT/A and the BoNT/A receptor complex. The disassociation constant is defined as KD=[L][R]/[C], where [L] equals the molar concentration of BoNT/A, [R] is the molar concentration of a BoNT/A receptor, and [C] is the molar concentration of the BoNT/A-BoNT/A receptor complex, and where all concentrations are of such components when the system is at equilibrium. The smaller the dissociation constant, the more tightly bound the BoNT/A is to its receptor, or the higher the binding affinity between BoNT/A and BoNT/A receptor. In aspects of this embodiment, the disassociation constant of BoNT/A for a BoNT/A receptor is at least two orders of magnitude less, at least three orders of magnitude less, at least four orders of magnitude less, or at least five orders of magnitude less than that of BoNT/A for any other receptor. In other aspects of this embodiment, the binding affinity of a BoNT/A that preferentially interacts with a BoNT/A receptor can have an equilibrium disassociation constant of, *e.g.*, of 500 nM or less, 400 nM or less, 300 nM or less, 200 nM, or less 100 nM or less. In other aspects of this embodiment, the binding affinity of a BoNT/A that preferentially interacts with a BoNT/A receptor can have an equilibrium disassociation constant of, *e.g.*, of 90 nM or less, 80 nM or less, 70 nM or less, 60 nM or less, 50 nM or less, 40 nM or less, 30 nM or less, 20 nM, or less 10 nM or less. As used herein, the term "elicits a BoNT/A intoxication response" refers to the ability

of a BoNT/A receptor to interact with a BoNT/A to form a neurotoxin/receptor complex and the subsequent internalization of that complex into the cell cytoplasm.

[0120] As used herein, the term "naturally occurring BoNT/A receptor" refers to any BoNT/A receptor produced by a naturally-occurring process, including, without limitation, BoNT/A receptor isoforms produced from a post-translational modification, an alternatively-spliced transcript, or a spontaneous mutation, and BoNT/A receptor subtypes. A naturally occurring BoNT/A receptor includes, without limitation, a fibroblast growth factor receptor 2 (FGFR2), a fibroblast growth factor receptor 3 (FGFR3), a synaptic vesicle glycoprotein 2 (SV2), and a complex ganglioside like GT1b, such as those described in Ester Fernandez-Salas, et al., *Botulinum Toxin Screening Assays*, U.S. Patent Publication 2008/0003240; Ester Fernandez-Salas, et al., *Botulinum Toxin Screening Assays*, U.S. Patent Publication 2008/0182799; Min Dong et al., *SV2 is the Protein Receptor for Botulinum Neurotoxin A*, Science (2006); S. Mahrhold et al, *The Synaptic Vesicle Protein 2C Mediates the Uptake of Botulinum Neurotoxin A into Phrenic Nerves*, 580(8) FEBS Lett. 2011-2014 (2006), each of which is hereby incorporated by reference in its entirety. A naturally occurring FGFR2 includes, without limitation, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, and SEQ ID NO: 70, or one that substitutes, deletes or adds, *e.g.*, 1 or more, 2 or more, 3 or more, 4 or more, 5 or more, 6 or more, 7 or more, 8 or more, 9 or more, 10 or more, 20 or more, 30 or more, 40 or more, 50 or more, or 100 or more amino acids from SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, and SEQ ID NO: 70. A naturally occurring FGFR3 includes, without limitation, SEQ ID NO: 25, SEQ ID NO: 26, and SEQ ID NO: 27, or one that substitutes, deletes or adds, *e.g.*, 1 or more, 2 or more, 3 or more, 4 or more, 5 or more, 6 or more, 7 or more, 8 or more, 9 or more, 10 or more, 20 or more, 30 or more, 40 or more, 50 or more, or 100 or more amino acids from SEQ ID NO: 25, SEQ ID NO: 26, and SEQ ID NO: 27. A naturally occurring SV2 includes, without limitation, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, and SEQ ID NO: 31, or one that substitutes, deletes or adds, *e.g.*, 1 or more, 2 or more, 3 or more, 4 or more, 5 or more, 6 or more, 7 or more, 8 or more, 9 or more, 10 or more, 20 or more, 30 or more, 40 or more, 50 or more, or 100 or more amino acids from SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, and SEQ ID NO: 31.

[0121] As used herein, the term "non-naturally occurring BoNT/A receptor variant" refers to any BoNT/A receptor produced with the aid of human manipulation or design, including, without limitation, a BoNT/A receptor produced by genetic engineering using random mutagenesis or rational design and a BoNT/A receptor produced by chemical synthesis. Non-limiting examples of non-naturally occurring BoNT/A variants include, *e.g.*, conservative BoNT/A receptor variants, non-conservative BoNT/A receptor variants, BoNT/A receptor chimeric variants and active BoNT/A receptor fragments.

[0122] As used herein, the term "non-naturally occurring BoNT/A receptor" refers to any BoNT/A receptor whose structure was modified with the aid of human manipulation, including, without limitation, a BoNT/A receptor produced by genetic engineering using random mutagenesis or rational design and a

BoNT/A receptor produced by in vitro chemical synthesis. Non-limiting examples of non-naturally occurring BoNT/A receptors are described in, *e.g.*, Ester Fernandez-Salas, et al., *Botulinum Toxin Screening Assays*, U.S. Patent Publication 2008/0003240; Ester Fernandez-Salas, et al., *Botulinum Toxin Screening Assays*, U.S. Patent Publication 2008/0182799, each of which is hereby incorporated by reference in its entirety. A non-naturally occurring BoNT/A receptor may substitute, delete or add, *e.g.*, 1 or more, 2 or more, 3 or more, 4 or more, 5 or more, 6 or more, 7 or more, 8 or more, 9 or more, 10 or more, 20 or more, 30 or more, 40 or more, 50 or more, or 100 or more amino acids from SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, or SEQ ID NO: 70.

[0123] Thus in an embodiment, a BoNT/A receptor is a naturally occurring BoNT/A receptor such as, *e.g.*, FGFR2, FGFR3 or SV2. In aspects of this embodiment, the BoNT/A receptor is a BoNT/A receptor isoform or a BoNT/A receptor subtype. In aspects of this embodiment, the naturally occurring BoNT/A receptor is the naturally occurring BoNT/A receptor of SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, or SEQ ID NO: 70. In other aspects of this embodiment, the BoNT/A receptor is a naturally occurring BoNT/A receptor having, e.g., at least 70% amino acid identity, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% amino acid identity with SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, or SEQ ID NO: 70.

[0124] In another embodiment, a BoNT/A receptor is a non-naturally occurring BoNT/A receptor, such as, *e.g.*, a genetically-engineered FGFR2, a genetically-engineered FGFR3, or a genetically-engineered SV2. In other aspects of this embodiment, the BoNT/A receptor is a non-naturally occurring BoNT/A receptor having, *e.g.*, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% amino acid identity with SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, or SEQ ID NO: 70. In other aspects of this embodiment, the BoNT/A receptor is a non-naturally occurring BoNT/A receptor having, *e.g.*, 1 or more, 2 or more, 3 or more, 4 or more, 5 or more, 6 or more, 7 or more, 8 or more, 9 or more, 10 or more, 20 or more, 30 or more, 40 or more, 50 or more, or 100 or more non-contiguous amino acid substitutions, deletions, or additions relative to SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, or SEQ ID NO: 70. In yet other aspects of this embodiment, the BoNT/A receptor is a non-naturally occurring BoNT/A receptor having, *e.g.*, 1 or more, 2 or more, 3 or more, 4 or more, 5 or more, 6 or more, 7 or more, 8 or more, 9 or

more, 10 or more, 20 or more, 30 or more, 40 or more, 50 or more, or 100 or more contiguous amino acid substitutions, deletions, or additions relative to SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, or SEQ ID NO: 70.

[0125] A BoNT/A receptor can be an endogenous BoNT/A receptor or an exogenous BoNT/A receptor. As used herein, the term "endogenous BoNT/A receptor" refers to a BoNT/A receptor naturally present in the cell because it is naturally encoded within the cell's genome, such that the cell inherently expresses the BoNT/A receptor without the need an external source of BoNT/A receptor or an external source of genetic material encoding a BoNT/A receptor. Expression of an endogenous BoNT/A receptor may be with or without environmental stimulation such as *e.g.*, cell differentiation or promoter activation. For example, the following established clonal cell lines express at least one endogenous BoNT/A receptor: BE(2)-M17, Kelly, LA1-55n, N1E-115, N4TG3, N18, Neuro-2a, NG108-15, PC12, SH-SY5Y, SiMa, and SK-N-BE(2)-C. An endogenous BoNT/A receptor can only be a naturally-occurring BoNT/A receptor or naturally-occurring variants thereof.

[0126] As used herein, the term "exogenous BoNT/A receptor" refers to a BoNT/A receptor expressed in a cell through the introduction of an external source of BoNT/A receptor or an external source of genetic material encoding a BoNT/A receptor by human manipulation. The expression of an exogenous BoNT/A receptor may be with or without environmental stimulation such as, *e.g.*, cell differentiation or promoter activation. As a non-limiting example, cells from an established clonal cell line can express one or more exogenous BoNT/A receptors by transient or stably transfection of a polynucleotide molecule encoding a BoNT/A receptor, such as, *e.g.*, a FGFR2, a FGFR3, or a SV2. As another non-limiting example, cells from an established clonal cell line can express one or more exogenous BoNT/A receptors by protein transfection of the BoNT/A receptors, such as, *e.g.*, a FGFR2, a FGFR3, or a SV2. An exogenous BoNT/A receptor can be a naturally-occurring BoNT/A receptor or naturally occurring variants thereof, or non-naturally occurring BoNT/A receptor or non-naturally occurring variants thereof.

[0127] Thus in an embodiment, cells from an established clonal cell line express an endogenous BoNT/A receptor. In aspects of this embodiment, the endogenous BoNT/A receptor expressed by cells from an established clonal cell line is a naturally-occurring BoNT/A receptor. In other aspects of this embodiment, the endogenous BoNT/A receptor expressed by cells from an established clonal cell line is SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, or SEQ ID NO: 70. In yet aspects of this embodiment, the endogenous BoNT/A receptor expressed by cells from an established clonal cell line is a naturally occurring BoNT/A receptor, such as, *e.g.*, a BoNT/A receptor isoform or a BoNT/A receptor subtype. In other aspects of this embodiment, the endogenous BoNT/A receptor expressed by cells from an established clonal cell line is a naturally occurring BoNT/A receptor

having, e.g., at least 70% amino acid identity, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% amino acid identity with SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, or SEQ ID NO: 70.

[0128] In another embodiment, cells from an established clonal cell line are transiently or stably engineered to express an exogenous BoNT/A receptor. In an aspect of this embodiment, cells from an established clonal cell line are transiently or stably engineered to express a naturally-occurring BoNT/A receptor. In other aspects of this embodiment, cells from an established clonal cell line are transiently or stably engineered to express the naturally-occurring BoNT/A receptor of SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, or SEQ ID NO: 70. In yet other aspects of this embodiment, cells from an established clonal cell line are transiently or stably engineered to express a naturally occurring BoNT/A receptor, such as, *e.g.*, a BoNT/A receptor isoform or a BoNT/A receptor subtype. In still other aspects of this embodiment, cells from an established clonal cell line are transiently or stably engineered to express a naturally occurring BoNT/A receptor having, e.g., at least 70% amino acid identity, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% amino acid identity with SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, or SEQ ID NO: 70.

[0129] In another aspect of the embodiment, cells from an established clonal cell line are transiently or stably engineered to express a non-naturally occurring BoNT/A receptor. In other aspects of this embodiment, cells from an established clonal cell line are transiently or stably engineered to express a non-naturally occurring BoNT/A receptor having, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% amino acid identity with SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, or SEQ ID NO: 70. In other aspects of this embodiment, cells from an established clonal cell line are transiently or stably engineered to express a non-naturally occurring BoNT/A receptor having, e.g., 1 or more, 2 or more, 3 or more, 4 or more, 5 or more, 6 or more, 7 or more, 8 or more, 9 or more, 10 or more, 20 or more, 30 or more, 40 or more, 50 or more, or 100 or more non-contiguous amino acid substitutions, deletions, or additions relative to SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, or SEQ ID NO: 70. In yet other aspects of this embodiment, cells from an established clonal cell line are transiently or stably engineered

to express a non-naturally occurring BoNT/A receptor having, e.g., 1 or more, 2 or more, 3 or more, 4 or more, 5 or more, 6 or more, 7 or more, 8 or more, 9 or more, 10 or more, 20 or more, 30 or more, 40 or more, 50 or more, or 100 or more contiguous amino acid substitutions, deletions, or additions relative to SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, or SEQ ID NO: 70

[0130] In another embodiment, cells from an established clonal cell line are transiently or stably engineered to express an exogenous FGFR2, an exogenous FGFR3, an exogenous SV2, or any combination thereof. In aspects of this embodiment, cells from an established clonal cell line are transiently or stably engineered to express a naturally-occurring FGFR2, a naturally-occurring FGFR3, a naturally-occurring SV2, or any combination thereof. In yet other aspects of this embodiment, cells from an established clonal cell line are transiently or stably engineered to express a non-naturally-occurring FGFR2, a non-naturally-occurring FGFR3, a non-naturally-occurring SV2, or any combination thereof. In still other aspects of this embodiment, cells from an established clonal cell line are transiently or stably engineered to express either a naturally-occurring FGFR2 or a non-naturally-occurring FGFR2, a naturally-occurring FGFR3 or a non-naturally-occurring FGFR3, a naturally-occurring SV2 or a non-naturally-occurring SV2, or any combination thereof.

[0131] Cells that express one or more endogenous or exogenous BoNT/A receptors can be identified by routine methods including direct and indirect assays for toxin uptake. Assays that determine BoNT/A binding or uptake properties can be used to assess whether a cell is expressing a BoNT/A receptor. Such assays include, without limitation, cross-linking assays using labeled BoNT/A, such as, *e.g.*, [^{125}I] BoNT/A, see, *e.g.*, Noriko Yokosawa et al., *Binding of Clostridium botulinum type C neurotoxin to different neuroblastoma cell lines*, 57(1) Infect. Immun. 272-277 (1989); Noriko Yokosawa et al., *Binding of botulinum type CI, D and E neurotoxins to neuronal cell lines and synaptosomes*, 29(2) Toxicon 261-264 (1991); and Tei-ichi Nishiki et al., *Identification of protein receptor for Clostridium botulinum type B neurotoxin in rat brain synaptosomes*, 269(14) J. Biol. Chem. 10498-10503 (1994). Other non-limiting assays include immunocytochemical assays that detect BoNT/A binding using labeled or unlabeled antibodies, see, e.g., Atsushi Nishikawa et al., *The receptor and transporter for internalization of Clostridium botulinum type C progenitor toxin into HT-29 cells*, 319(2) Biochem. Biophys. Res. Commun. 327-333 (2004) and immunoprecipitation assays, see, *e.g.*, Yukako Fujinaga et al., *Molecular characterization of binding subcomponents of Clostridium botulinum type C progenitor toxin for intestinal epithelial cells and erythrocytes*, 150(Pt 5) Microbiology 1529-1538 (2004), that detect bound toxin using labeled or unlabeled antibodies. Antibodies useful for these assays include, without limitation, antibodies selected against BoNT/A, antibodies selected against a BoNT/A receptor, such as, e.g., FGFR2, FGFR3, or SV2, and/or antibodies selected against a ganglioside, such as, e.g., GD1a, GD1b, GD3, GQ1b, or GT1b. If the antibody is labeled, the binding of the molecule can be detected by various means, including Western blot analysis, direct microscopic observation of the cellular location of the antibody,

measurement of cell or substrate-bound antibody following a wash step, flow cytometry, electrophoresis or capillary electrophoresis, employing techniques well-known to those of skill in the art. If the antibody is unlabeled, one may employ a labeled secondary antibody for indirect detection of the bound molecule, and detection can proceed as for a labeled antibody. It is understood that these and similar assays that determine BoNT/A uptake properties or characteristics can be useful in identifying cells expressing endogenous or exogenous BoNT/A receptors.

[0132] Assays that monitor the release of a molecule after exposure to BoNT/A can also be used to assess whether a cell is expressing one or more endogenous or exogenous BoNT/A receptors. In these assays, inhibition of the molecule's release would occur in cells expressing a BoNT/A receptor after BoNT/A treatment. Well known assays include methods that measure inhibition of radio-labeled catecholamine release from neurons, such as, e.g., [3H] noradrenaline or [3H] dopamine release, see e.g., A Fassio et al., *Evidence for calcium-dependent vesicular transmitter release insensitive to tetanus toxin and botulinum toxin type F*, 90(3) Neuroscience 893-902 (1999); and Sara Stigliani et al., *The sensitivity of catecholamine release to botulinum toxin C1 and E suggests selective targeting of vesicles set into the readily releasable pool*, 85(2) J. Neurochem. 409-421 (2003), or measures catecholamine release using a fluorometric procedure, see, e.g., Anton de Paiva et al., *A role for the interchain disulfide or its participating thiols in the internalization of botulinum neurotoxin A revealed by a toxin derivative that binds to ecto-acceptors and inhibits transmitter release intracellularly*, 268(28) J. Biol. Chem. 20836-20844 (1993); Gary W. Lawrence et al., *Distinct exocytotic responses of intact and permeabilised chromaffin cells after cleavage of the 25-kDa synaptosomal-associated protein (SNAP-25) or synaptobrevin by botulinum toxin A or B*, 236(3) Eur. J. Biochem. 877-886 (1996); and Patrick Foran et al., *Botulinum neurotoxin C1 cleaves both syntaxin and SNAP-25 in intact and permeabilized chromaffin cells: correlation with its blockade of catecholamine release*, 35(8) Biochemistry 2630-2636 (1996). Other non-limiting examples include assays that measure inhibition of hormone release from endocrine cells, such as, e.g., anterior pituitary cells or ovarian cells. It is understood that these and similar assays for molecule release can be useful in identifying cells expressing endogenous or exogenous or BoNT/A receptors.

[0133] Assays that detect the cleavage of a BoNT/A substrate after exposure to a BoNT/A can also be used to assess whether a cell is expressing one or more endogenous or exogenous BoNT/A receptors. In these assays, generation of a BoNT/A substrate cleavage-product, or disappearance of the intact BoNT/A substrate, would be detected in cells expressing a BoNT/A receptor after BoNT/A treatment. Non-limiting examples of specific Western blot analysis, as well as well-characterized reagents, conditions and protocols are readily available from commercial vendors that include, without limitation, Amersham Biosciences, Piscataway, NJ; Bio-Rad Laboratories, Hercules, CA; Pierce Biotechnology, Inc., Rockford, IL; Promega Corporation, Madison, WI, and Stratagene, Inc., La Jolla, CA. It is understood that these and similar assays for BoNT/A substrate cleavage can be useful in identifying cells expressing endogenous or exogenous BoNT/A receptors.

[0134] As non-limiting examples, Western blot analysis using an antibody that recognizes BoNT/A SNAP-25-cleaved product or both the cleaved and uncleaved forms of SNAP-25 can be used to assay for uptake of BoNT/A. Examples of α-SNAP-25 antibodies useful for these assays include, without limitation, SMI-81 α-SNAP-25 mouse monoclonal antibody (Sternberger Monoclonals Inc., Lutherville, MD), CI 71.1 mouse α-SNAP-25 monoclonal antibody (Synaptic Systems, Goettingen, Germany), CI 71.2 α-SNAP-25 mouse monoclonal antibody (Synaptic Systems, Goettingen, Germany), SP12 α-SNAP-25 mouse monoclonal antibody (Abcam, Cambridge, MA), α-SNAP-25 rabbit polyclonal antiserum (Synaptic Systems, Goettingen, Germany), α-SNAP-25 rabbit polyclonal antiserum S9684 (Sigma, St. Louis, MO), and α-SNAP-25 rabbit polyclonal antiserum (Abcam, Cambridge, MA).

[0135] Aspects of the present disclosure provide cells that through genetic manipulation or recombinant engineering are made to express an exogenous SNAP-25 and/or one or more exogenous BoNT/A receptors. Cells useful to express an exogenous SNAP-25 and/or one or more exogenous BoNT/A receptors through genetic manipulation or recombinant engineering include neuronal cells and non-neuronal cells that may or may not express an endogenous SNAP-25 and/or one or more endogenous BoNT/A receptors. It is further understood that such genetically manipulated or recombinantly engineered cells may express an exogenous SNAP-25 and one or more exogenous BoNT/A receptors under control of a constitutive, tissue-specific, cell-specific or inducible promoter element, enhancer element or both. It is understood that any cell is useful as long as the cell can be genetically manipulated or recombinantly engineered to expresses an exogenous SNAP-25 and/or one or more exogenous BoNT/A receptors and is capable of undergoing BoNT/A intoxication.

[0136] Methods useful for introducing into a cell an exogenous polynucleotide molecule encoding a component necessary for the cells to undergo the overall cellular mechanism whereby a BoNT/A proteolytically cleaves a SNAP-25 substrate, such as, *e.g.*, a SNAP-25, a FGFR2, a FGFR3, or a SV2, include, without limitation, chemical-mediated delivery methods, such as, *e.g.*, calcium phosphate-mediated, diethyl-aminoethyl (DEAE) dextran-mediated, lipid-mediated, polyethyleneimine (PEI)-mediated, polylysine-mediated and polybrene-mediated; physical-mediated delivery methods, such as, *e.g.*, biolistic particle delivery, microinjection, protoplast fusion and electroporation; and viral-mediated delivery methods, such as, *e.g.*, retroviral-mediated transfection, *see e.g.*, *Introducing Cloned Genes into Cultured Mammalian Cells*, pp. 16.1-16.62 (Sambrook & Russell, eds., Molecular Cloning A Laboratory Manual, Vol. 3, 3rd ed. 2001); Alessia Colosimo et al., *Transfer and Expression of Foreign Genes in Mammalian Cells*, 29(2) Biotechniques 314-318, 320-322, 324 (2000); Philip Washbourne & A. Kimberley McAllister, *Techniques for Gene Transfer into Neurons*, 12(5) Curr. Opin. Neurobiol. 566-573 (2002); and Current Protocols in Molecular Biology, John Wiley and Sons, pp 9.16.4-9.16.11 (2000), each of which is incorporated by reference in its entirety. One skilled in the art understands that selection of a specific method to introduce a polynucleotide molecule into a cell will depend, in part, on whether the cell will transiently or stably contain a component necessary for the cells to undergo the overall cellular mechanism whereby a BoNT/A proteolytically cleaves a SNAP-25 substrate. Non-limiting examples of polynucleotide molecule encoding a component necessary for the cells to undergo the overall cellular

mechanism whereby a BoNT/A proteolytically cleaves a SNAP-25 substrate as follows: FGFR2 polynucleotide molecule of SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 136, SEQ ID NO: 137, or SEQ ID NO: 138; FGFR3 polynucleotide molecule of SEQ ID NO: 139, SEQ ID NO: 140, or SEQ ID NO: 141; SV2 polynucleotide molecule of SEQ ID NO: 142, SEQ ID NO: 143, or SEQ ID NO: 144; and SNAP-25 polynucleotide molecule of SEQ ID NO: 145, or SEQ ID NO: 146

[0137] Chemical-mediated delivery methods are well-known to a person of ordinary skill in the art and are described in, *e.g.*, Martin Jordan & Florian Worm, *Transfection of Adherent and Suspended Cells by Calcium Phosphate*, 33(2) Methods 136-143 (2004); Chun Zhang et al., *Polyethylenimine Strategies for Plasmid Delivery to Brain-Derived Cells*, 33(2) Methods 144-150 (2004), each of which is hereby incorporated by reference in its entirety. Such chemical-mediated delivery methods can be prepared by standard procedures and are commercially available, see, *e.g.*, CellPhect Transfection Kit (Amersham Biosciences, Piscataway, NJ); Mammalian Transfection Kit, Calcium phosphate and DEAE Dextran, (Stratagene, Inc., La Jolla, CA); Lipofectamine™ Transfection Reagent (Invitrogen, Inc., Carlsbad, CA); ExGen 500 Transfection kit (Fermentas, Inc., Hanover, MD), and SuperFect and Effectene Transfection Kits (Qiagen, Inc., Valencia, CA).

[0138] Physical-mediated delivery methods are well-known to a person of ordinary skill in the art and are described in, *e.g.*, Jeike E. Biewenga et al., *Plasmid-Mediated Gene Transfer in Neurons using the Biolistics Technique*, 71(1) J. Neurosci. Methods. 67-75 (1997); John O'Brien & Sarah C. R. Lummis, *Biolistic and Diolistic Transfection: Using the Gene Gun to Deliver DNA and Lipophilic Dyes into Mammalian Cells*, 33(2) Methods 121-125 (2004); M. Golzio et al., *In Vitro and In Vivo Electric Field-Mediated Permeabilization, Gene Transfer, and Expression*, 33(2) Methods 126-135 (2004); and Oliver Greschet al., *New Non-Viral Method for Gene Transfer into Primary Cells*, 33(2) Methods 151-163 (2004), each of which is hereby incorporated by reference in its entirety.

[0139] Viral-mediated delivery methods are well-known to a person of ordinary skill in the art and are described in, *e.g.*, Chooi M. Lai et al., *Adenovirus and Adeno-Associated Virus Vectors*, 21(12) DNA Cell Biol. 895-913 (2002); Ilya Frolov et al., *Alphavirus-Based Expression Vectors: Strategies and Applications*, 93(21) Proc. Natl. Acad. Sci. U. S. A. 11371-11377 (1996); Roland Wolkowicz et al., *Lentiviral Vectors for the Delivery of DNA into Mammalian Cells*, 246 Methods Mol. Biol. 391-411 (2004); A. Huser & C. Hofmann, *Baculovirus Vectors: Novel Mammalian Cell Gene-Delivery Vehicles and Their Applications*, 3(1) Am. J. Pharmacogenomics 53-63 (2003); Tiziana Tonini et al., *Transient Production of Retroviral- and Lentiviral-Based Vectors for the Transduction of Mammalian Cells*, 285 Methods Mol. Biol. 141-148 (2004); Manfred Gossen & Hermann Bujard, *Tight Control of Gene Expression in Eukaryotic Cells by Tetracycline-Responsive Promoters*, U.S. Patent No. 5,464,758; Hermann Bujard & Manfred Gossen, *Methods for Regulating Gene Expression*, U.S. Patent No. 5,814,618; David S. Hogness, *Polynucleotides Encoding Insect Steroid Hormone Receptor Polypeptides and Cells Transformed With Same*, U.S. Patent No. 5,514,578; David S. Hogness, *Polynucleotide Encoding Insect Ecdysone*

Receptor, U.S. Patent 6,245,531; Elisabetta Vegeto et al., *Progesterone Receptor Having C. Terminal Hormone Binding Domain Truncations*, U.S. Patent No. 5,364,791; Elisabetta Vegeto et al., *Mutated Steroid Hormone Receptors, Methods for Their Use and Molecular Switch for Gene Therapy*, U.S. Patent No. 5,874,534, each of which is hereby incorporated by reference in its entirety. Such viral-mediated delivery methods can be prepared by standard procedures and are commercially available, see, e.g., VIRAPOWER™ Adenoviral Expression System (Invitrogen, Inc., Carlsbad, CA) and VIRAPOWER™ Adenoviral Expression System Instruction Manual 25-0543 version A, Invitrogen, Inc., (Jul. 15, 2002); and ADEASY™ Adenoviral Vector System (Stratagene, Inc., La Jolla, CA) and ADEASY™ Adenoviral Vector System Instruction Manual 064004f, Stratagene, Inc. Furthermore, such viral delivery systems can be prepared by standard methods and are commercially available, see, e.g., BD™ Tet-Off and Tet-On Gene Expression Systems (BD Biosciences-Clonetech, Palo Alto, CA) and BD™ Tet-Off and Tet-On Gene Expression Systems User Manual, PT3001-1, BD Biosciences Clonetech, (Mar. 14, 2003), GeneSwitch™ System (Invitrogen, Inc., Carlsbad, CA) and GENESWITCH™ System A Mifepristone-Regulated Expression System for Mammalian Cells version D, 25-0313, Invitrogen, Inc., (Nov. 4, 2002); VIRAPOWER™ Lentiviral Expression System (Invitrogen, Inc., Carlsbad, CA) and VIRAPOWER™ Lentiviral Expression System Instruction Manual 25-0501 version E, Invitrogen, Inc., (Dec. 8, 2003); and COMPLETE CONTROL® Retroviral Inducible Mammalian Expression System (Stratagene, La Jolla, CA) and COMPLETE CONTROL® Retroviral Inducible Mammalian Expression System Instruction Manual, 064005e.

[0140] As mentioned above, an exogenous component necessary for the cells to undergo the overall cellular mechanism whereby a BoNT/A proteolytically cleaves a SNAP-25 substrate, such as, *e.g.*, a SNAP-25, a FGFR2, a FGFR3, or a SV2 disclosed in the present specification can be introduced into a cell. Any and all methods useful for introducing such an exogenous component with a delivery agent into a cell population can be useful with the proviso that this method introduce the exogenous component disclosed in the present specification in at least 50% of the cells within a given cell population. Thus, aspects of this embodiment can include a cell population in which, e.g., at least 50%, at least 60%, at least 70%, at least 80%, or at least 90% of the given cell population contains an exogenous component necessary for the cells to undergo the overall cellular mechanism whereby a BoNT/A proteolytically cleaves a SNAP-25 substrate, such as, *e.g.*, a SNAP-25, a FGFR2, a FGFR3, or a SV2 disclosed in the present specification. As used herein, the term "delivery agent" refers to any molecule that enables or enhances internalization of a covalently-linked, non-covalently-linked or in any other manner associated with a polypeptide into a cell. Thus, the term "delivery agent" encompasses, without limitation, proteins, peptides, peptidomimetics, small molecules, polynucleotide molecules, liposomes, lipids, viruses, retroviruses and cells that, without limitation, transport a covalently or non-covalently linked molecule to the cell membrane, cell cytoplasm or nucleus. It further is understood that the term "delivery agent" encompasses molecules that are internalized by any mechanism, including delivery agents which function via receptor mediated endocytosis and those which are independent of receptor mediated endocytosis.

[0141] A delivery agent can also be an agent that enables or enhances cellular uptake of a covalently linked component, like FGFR2, FGFR3, SV2, or SNAP-25, such as, e.g., by chemical conjugation or by genetically produced fusion proteins. Methods that covalently link delivery agents and methods of using such agents are described in, e.g., Steven F. Dowdy, *Protein Transduction System and Methods of Use Thereof*, International Publication No WO 00/34308; Gérard Chassaing & Alain Prochiantz, *Peptides which can be Used as Vectors for the Intracellular Addressing of Active Molecules*, U.S. Patent No. 6,080,724; Alan Frankel et al., *Fusion Protein Comprising TAT-derived Transport Moiert*, U.S. Patent No. 5,674,980; Alan Frankel et al., *TAT-derived Transport Polypeptide Conjugates*, U.S. Patent No. 5,747,641; Alan Frankel et al., *TAT-derived Transport Polypeptides and Fusion Proteins*, U.S. Patent No. 5,804,604; Peter F. J. O'Hare et al., *Use of Transport Proteins*, U.S. Patent No. 6,734,167; Yao-Zhong Lin & Jack J. Hawiger, *Method for Importing Biologically Active Molecules into Cells*, U.S. Patent No. 5,807,746; Yao-Zhong Lin & Jack J. Hawiger, *Method for Importing Biologically Active Molecules into Cells*, U.S. Patent No. 6,043,339; Yao-Zhong Lin et al., *Sequence and Method for Genetic Engineering of Proteins with Cell Membrane Translocating Activity*, U.S. Patent No. 6,248,558; Yao-Zhong Lin et al., Sequence and Method for Genetic *Engineering of Proteins with Cell Membrane Translocating Activity*, U.S. Patent No. 6,432,680; Jack J. Hawiger et al., *Method for Importing Biologically Active Molecules into Cells*, U.S. Patent No. 6,495,518; Yao-Zhong Lin et al., *Sequence and Method for Genetic Engineering of Proteins with Cell Membrane Translocating Activity*, U.S. Patent No. 6,780,843; Jonathan B. Rothbard & Paul A Wender, *Method and Composition for Enhancing Transport Across Biological Membranes*, U.S. Patent No. 6,306,993; Jonathan B. Rothbard & Paul A Wender, *Method and Composition for Enhancing Transport Across Biological Membranes*, U.S. Patent No. 6,495,663; and Pamela B. Davis et al., *Fusion Proteins for Protein Delivery*, U.S. Patent No. 6,287,817, each of which is incorporated by reference in its entirety.

[0142] A delivery agent can also be an agent that enables or enhances cellular uptake of a non-covalently associated component, like FGFR2, FGFR3, SV2c, or SNAP-25. Methods that function in the absence of covalent linkage and methods of using such agents are described in, e.g., Gilles Divita et al, *Peptide-Mediated Transfection Agents and Methods of Use*, U.S. Patent No. 6,841,535; Philip L Felgner and Olivier Zelphati, *Intracellular Protein Delivery Compositions and Methods of Use*, U.S. Patent Publication No. 2003/0008813; and Michael Karas, *Intracellular Delivery of Small Molecules, Proteins and Nucleic Acids*, U.S. Patent Publication 2004/0209797, each of which is incorporated by reference in its entirety. Such peptide delivery agents can be prepared and used by standard methods and are commercially available, see, e.g. the CHARIOT™ Reagent (Active Motif, Carlsbad, CA); BIO-PORTER® Reagent (Gene Therapy Systems, Inc., San Diego, CA), BIO TREK™ Protein Delivery Reagent (Stratagene, La Jolla, CA), and PRO-JECT™ Protein Transfection Reagent (Pierce Biotechnology Inc., Rockford, IL).

[0143] Aspects of the present disclosure can also be described as follows:

1. An established clonal cell line comprising a cell susceptible to intoxication by BoNT/A.

2. The established clonal cell line of 1, wherein the clonal cell line is selected from a parental SiMa cell line.

3. The established clonal cell line of 1 or 2, wherein the cell is susceptible to BoNT/A intoxication by about 100 pM or less, by about 50 pM or less, by about 10 pM or less, by about 5 pM or less, by about 1 pM or less, by about 0.5 pM or less, or by about 0.1 pM or less of a BoNT/A.

4. The established clonal cell line of 1 or 2, wherein susceptibility to BoNT/A intoxication is measured before differentiation of the cell.

5. The established clonal cell line of 2, wherein in the undifferentiated state, the cell exhibits at least a 1.5-fold increase in gene expression of one or more genes relative to the expression of the one or more genes in a cell from a 2D6 cell line, the genes being taken from Table 5, or wherein the cell exhibits at least a 1.5-fold decrease in gene expression of one or more genes relative to the expression of the one or more genes in a cell from a 2D6 cell line, the genes being taken from Table 6.

6. The established clonal cell line of 2, wherein in the differentiated state, the cell exhibits at least a 1.5-fold increase in gene expression of one or more genes relative to the expression of the one or more genes in a cell from a 2D6 cell line, the genes being taken from Table 9, or wherein the cell exhibits at least a 1.5-fold decrease in gene expression of one or more genes relative to the expression of the one or more genes in a cell from a 2D6 cell line, the genes being taken from Table 10.

7. The established clonal cell line of 2, wherein in the undifferentiated state, the cell exhibits at least a 1.5-fold increase in gene expression of one or more genes relative to the expression of the one or more genes in a cell from a parental SiMa cell line, the genes being taken from Table 7, or wherein the cell exhibits at least a 1.5-fold decrease in gene expression of one or more genes relative to the expression of the one or more genes in a cell from a parental SiMa cell line, the genes being taken from Table 8.

8. The established clonal cell line of 2, wherein in the differentiated state, the cell exhibits at least a 1.5-fold increase in gene expression of one or more genes relative to the expression of the one or more genes in a cell from a parental SiMa cell line, the genes being taken from Table 11, or wherein the cell exhibits at least a 1.5-fold decrease in gene expression of one or more genes relative to the expression of the one or more genes in a cell from a parental SiMa cell line, the genes being taken from Table 12.

9. The established clonal cell line of 1 or 2, wherein the cell exhibits a sensitivity for BoNT/A activity that is 100 pM or less or about 25 pM for about 5 or more cell passages, 10 or more cell passages, 15 or

more cell passages, 20 or more cell passages, 25 or more cell passages, 30 or more cell passages, 35 or more cell passages, 40 or more cell passages, 45 or more cell passages, 50 or more cell passage, 55 or more cell passage, or 60 or more cell passage.

10. The established clonal cell line of 1 or 2, wherein the cell from an established clonal cell line exhibits a well defined signal to noise ratio for the upper asymptote for BoNT/A activity of at least 3:1, at least 4:1, at least 5:1, at least 6:1, at least 7:1, at least 8:1, at least 9:1, at least 10:1, over, e.g., 5 or more cell passages, 10 or more cell passages, 15 or more cell passages, 20 or more cell passages, 25 or more cell passages, 30 or more cell passages, 35 or more cell passages, 40 or more cell passages, 45 or more cell passages, 50 or more cell passage, 55 or more cell passage, or 60 or more cell passage.

11. An established clonal cell line comprising a cell susceptible to intoxication by BoNT/A produced from a parental SiMa cell line, wherein the cell is susceptible to BoNT/A intoxication by about 100 pM or less, by about 50 pM or less, by about 10 pM or less, by about 5 pM or less, by about 1 pM or less, by about 0.5 pM or less, or by about 0.1 pM or less of a BoNT/A.

12. An established clonal cell line comprising cells susceptible to intoxication by BoNT/A,

wherein the clonal cell line is selected from a parental SiMa cell line; and

wherein the the clonal cell line comprises cells susceptible to BoNT/A intoxication by about 100 pM or less of a BoNT/A.

13. The established clonal cell line of 12, wherein the parental SiMa cell line is the parental SiMa cell line DSMZ ACC 164.

14. The established clonal cell line of 12, wherein the cell exhibits a sensitivity for BoNT/A activity that is 100 pM or less or about 25 pM for about 5 or more cell passages, 10 or more cell passages, 15 or more cell passages, 20 or more cell passages, 25 or more cell passages, 30 or more cell passages, 35 or more cell passages, 40 or more cell passages, 45 or more cell passages, 50 or more cell passage, 55 or more cell passage, or 60 or more cell passage.

15. The established clonal cell line of 12, wherein the cell from an established clonal cell line exhibits a well defined signal to noise ratio for the upper asymptote for BoNT/A activity of at least 3:1, at least 4:1, at least 5:1, at least 6:1, at least 7:1, at least 8:1, at least 9:1, at least 10:1, over, e.g., 5 or more cell passages, 10 or more cell passages, 15 or more cell passages, 20 or more cell passages, 25 or more cell passages, 30 or more cell passages, 35 or more cell passages, 40 or more cell passages, 45 or more cell passages, 50 or more cell passage, 55 or more cell passage, or 60 or more cell passage.

16. The established clonal cell line of 12, wherein susceptibility to BoNT/A intoxication is measured before differentiation of the cell or after differentiation of the cell.

17. An established clonal cell line comprising cells susceptible to intoxication by BoNT/A,

wherein the cells exhibits at least a 1.5-fold difference in gene expression levels of three or more genes as compared to the expression levels of these genes in cells from the 2D6 cell line;

wherein the gene expression levels are selected from th group ADAMTS9, ASCL1, BASP1, DOK5, DPYD, GNB4, GNG11, GTSF1, MAOA, MINA, MSN, PEG3, PLK2, PRSS12, RNF182, SLC44A5, SPARC, TFPI2, and TPTE; and

wherein the the clonal cell line comprises cells susceptible to BoNT/A intoxication by about 100 pM or less of a BoNT/A.

18. The established clonal cell line of 17, wherein the cells exhibits at least a 2.0-fold difference in gene expression levels of one or more genes as compared to the expression levels of these genes in cells from the 2D6 cell line, at least a 3.0-fold difference in gene expression levels of one or more genes as compared to the expression levels of these genes in cells from the 2D6 cell line, or at least a 4.0-fold difference in gene expression levels of one or more genes as compared to the expression levels of these genes in cells from the 2D6 cell line.

19. The established clonal cell line of 17, wherein the gene expression levels are measured before differentiation of the cell or after differentiation of the cell.

20. The established clonal cell line of 17, wherein the cell exhibits a sensitivity for BoNT/A activity that is 100 pM or less or about 25 pM for about 5 or more cell passages, 10 or more cell passages, 15 or more cell passages, 20 or more cell passages, 25 or more cell passages, 30 or more cell passages, 35 or more cell passages, 40 or more cell passages, 45 or more cell passages, 50 or more cell passage, 55 or more cell passage, or 60 or more cell passage.

21. The established clonal cell line of 17, wherein the cell from an established clonal cell line exhibits a well defined signal to noise ratio for the upper asymptote for BoNT/A activity of at least 3:1, at least 4:1, at least 5:1, at least 6:1, at least 7:1, at least 8:1, at least 9:1, at least 10:1, over, *e.g.*, 5 or more cell passages, 10 or more cell passages, 15 or more cell passages, 20 or more cell passages, 25 or more cell passages, 30 or more cell passages, 35 or more cell passages, 40 or more cell passages, 45 or more cell passages, 50 or more cell passage, 55 or more cell passage, or 60 or more cell passage.

EXAMPLES

Example I

Screening for Cell Lines Comprising Cells Susceptible to BoNT/A Intoxication

[0144] The following example illustrates how to identify clonal cells from a parental established cell line that are susceptible to BoNT/A intoxication or have neurotoxin uptake capacity.

1. Isolation of clonal cell lines.

[0145] Companion patent application Ester Fernandez-Salas, et al., *Immuno-Based Botulinum Toxin Serotype A Activity Assays*, U.S. Patent Application Serial No: 12/403,531 identified several established cell lines useful for conducting the disclosed immuno-based methods of detecting BoNT/A activity, including, e.g., LA1-55n (ECACC 06041203), N18 (ECACC 88112301), Neuro-2a (ATCC CCL-131), PC12 (ATCC CRL-1721), SH-SY5Y (ATCC CRL-2266), and SiMa (DSMZ ACC 164). During characterization of the SiMa cell line, it was discovered that the cells comprising this established cell line comprised at least five different cellular phenotypes. To determine whether any one of these phenotypically-distinct cell types was responsible for the susceptibility of this cell line to BoNT/A intoxication, two different limited-dilution screens were conducted to obtain single colony isolates for each phenotypically-distinct cell type.

[0146] In both screens, a suitable density of cells from a SiMa stock were grown in RPMI 1640 medium, having 10% fetal bovine serum, 1% Penicillin-Streptomycin, 2 mM L-Glutamine, contained in a T175 Collagen IV coated flask. After the second passage, the cells were trypsin-treated to produce a cell suspension and the cell concentration was determined. About 4.0 x 10^6 cells from this cell suspension was transferred into a 50 mL tube and the cells were dissociated into single cells by repeated vigorous expulsion through an 18.5 gauge needle using a 10 mL syringe. Cells from this disassociated single-cell suspension were then diluted to a concentration of 0.2 x 10^6 cells/mL by adding 15 mL of fresh growth medium, and 2.5 µL of this dilution was added to 50 mL of fresh growth medium to obtain a concentration of 10 cells/mL. From this final dilution stock, 100 µL of growth medium was added to each well of a 96-well Collagen IV coated plates (final average density of one cell/well), and the cells were grown undisturbed in a 37 °C incubator under 5% carbon dioxide for four weeks. A total of nineteen 96-well plates were setup for analysis. Plates were microscopically examined periodically to assess colony growth. After four weeks, each well was microscopically examined to identify growing colonies, and for each growing colony identified, 100 µL of fresh growth medium was added to each well and the cells were grown undisturbed in a 37 °C incubator under 5% carbon dioxide for two weeks. After two additional weeks of growth, the growing single colonies were trypsin-treated and transferred to a new 96-well plate for continued growth. Once colonies grew to about 1,000 cells, based on visual inspection, the cells were trypsin-treated and each cell-suspension was transferred into a new well from a 24-well Collagen IV-coated plate. The cells were grown in a 37 °C incubator under 5% carbon dioxide with fresh growth

medium being replenished every 2-3 days, if needed. The cells were grown until the culture reached approximately 60% confluence or greater, at which point the cells were trypsin-treated and each cell-suspension was transferred into a 25 cm^2 Collagen IV-coated flask. The cells were grown in a 37 °C incubator under 5% carbon dioxide with fresh growth medium being replenished every 2-3 days, if needed. Once the cells in the flask reached 70-80% confluence, they were frozen and stored in liquid nitrogen until the clonal cell lines were tested to determine their susceptibility to BoNT/A intoxication. Of the 1,824 colony isolates initially setup from both screens, 130 clonal cell lines were selected based on viability and growth criteria and expanded for subsequent screening procedures.

2. Primary screen for BoNT/A intoxication susceptibility of cells from a clonal cell line using a BoNT/A complex.

[0147] One way to determine whether cells from a clonal cell line were susceptible to BoNT/A intoxication was to conduct a primary screen using a CELLTITER-GLO® luminescent cell viability assay (Promega, Madison, WI) for normalizing the cell number in each well and an immuno-based method for determining BoNT/A activity as described in Ester Fernandez-Salas, et al., *Immuno-Based Botulinum Toxin Serotype A Activity Assays*, U.S. Patent Application Serial No: 12/403,531, which is hereby incorporated by reference in its entirety. Two separate 96-well plates were set up, one for the BoNT/A activity assay and the other for the cell viability assay.

[0148] To conduct the BoNT/A activity assay, a lysate was prepared from cells treated with BoNT/A by plating cells from each isolated clonal cell line into a well from a poly-D-lysine 96-well plate (BD Biosciences, Bedford, MA). The wells contained 0.1 mL of a serum-free medium comprising Minimum Essential Medium, 2 mM GlutaMAX™ I with Earle's salts, 1 x B27 supplement, 1 x N2 supplement, 0.1 mM Non-Essential Amino Acids, 10 mM HEPES and 25 µg/mL GT1b (302-011-M005, Alexis Biochemicals, San Diego, CA). These cells were incubated in a 37 °C incubator under 5% carbon dioxide until the cells differentiated, as assessed by standard and routine morphological criteria, such as growth arrest and neurite extension (approximately 3 days). The media from the differentiated cells was aspirated from each well and replaced with fresh media containing 1 nM of a BoNT/A complex. After a 24 hrs incubation, the cells were washed by aspirating the growth media and rinsing each well with 200 µL of 1 x PBS. To harvest the cells, 1 x PBS was aspirated, the cells lysed by adding 30 µl of Lysis Buffer comprising 20 mM Tris-HCl (pH 7,5), 150 mM NaCl, 1 mM EDTA, 1 mM EGTA, 1% Triton X-100 to each well, and the plate incubated on a shaker rotating at 500 rpm for 30 minutes at 4 °C. The plate was centrifuged at 4000 rpm for 20 minutes at 4 °C to pellet cellular debris and the supernatant was transferred to a capture antibody coated 96-well plate to perform the detection step.

[0149] To prepare an α-SNAP-25 capture antibody solution, the α-SNAP-25 mouse monoclonal antibody contained in the ascites from hybridoma cell line 2E2A6 (Example VII) was purified using a standard Protein A purification protocol.

[0150] To prepare an α-SNAP-25 detection antibody solution, α-SNAP-25 rabbit polyclonal antibody S9684 (Sigma, St. Louis, MO) was conjugated to Ruthenium(II)-tris-bipyridine-(4-methysulfonate) NHS ester labeling reagent (Meso Scale Discovery, Gaithersburg, MD) according to the manufacturer's instructions (Meso Scale Discovery, Gaithersburg, MD). The conjugation reaction was performed by adding 30 µL of distilled water reconstituted MSD SULFO-TAG™ stock solution to 200 µL of 2 mg/mL α-SNAP-25 polyclonal antibodies and incubating the reaction at room temperature for 2 hours in the dark. The labeled antibodies were purified using a standard spin column protocol and the protein concentration determined using a standard colorimetric protein assay. The absorbance of the α-SNAP-25 antibody/MSD SULFO-TAG™ conjugate was measured at 455 nm using a spectrophotometer to determine the concentration in moles per liter. The detection antibody solution was stored at 4 °C until needed.

[0151] To prepare an α-SNAP-25 solid phase support comprising an α-SNAP-25 capture antibody, approximately 5 µL of the appropriate α-SNAP-25 monoclonal antibody solution (20 µg/mL in 1 x PBS) is added to each well of a 96-well MSD High Bind plate and the solution is allowed to air dry in a biological safety cabinet for 2-3 hours in order to liquid evaporate the solution. The capture antibody-bound wells were sealed and stored at 4 °C until needed.

[0152] To detect the presence of a cleaved SNAP-25 product by ECL sandwich ELISA, the wells from an α-SNAP-25 solid phase support were then blocked by adding 150 µL of Blocking Buffer comprising 2% Amersham Blocking Reagent (GE Life Sciences, Piscataway, NJ) and 10% goat serum (VWR, West Chester, PA) at room temperature for 2 hours. The Blocking Buffer was aspirated, 25 µL of a lysate from cells treated with BoNT/A was added to each well and the plates were incubated at 4 °C for overnight. Plate wells were washed three times by aspirating the cell lysate and rinsing each well three times with 200 µL 1 x PBS, 0.1% TWEEN-20® (polyoxyethylene (20) sorbitan monolaureate). After washing, 25 µl of 5 µg/mL α-SNAP-25 detection antibody solution comprising 2% Amersham Blocking Reagent in 1 x PBS, 0.1% TWEEN-20® (polyoxyethylene (20) sorbitan monolaureate) was added to each well, sealed, and incubated at room temperature for 1 hour with shaking. After α-SNAP-25 detection antibody incubation, the wells were washed three times with 200 µL 1 x PBS, 0.1% TWEEN-20® (polyoxyethylene (20) sorbitan monolaureate). After washing 150 µL of 1 x Read Buffer (Meso Scale Discovery, Gaithersburg, MD) was added to each well and the plates were read using a SECTOR™ Imager 6000 Image Reader (Meso Scale Discovery, Gaithersburg, MD). The raw data was collected using the ECL imager.

[0153] To conduct the luminescent cell viability assay, cells from each isolated clonal cell line were plated and differentiated as described above. The media from the differentiated cells was aspirated from each well and replaced with 100 µl of the reagent mixture comprising the CELLTITER-GLO® substrate and CELLTITER-GLO® buffer according to the manufacturer's instructions. The plate was then protected from light and mixed for two minutes on an orbital shaker. The solution from the 96-well cell plate with clear bottom was transferred to a white luminometer plate and after 10 minutes incubation was read on the luminometer.

[0154] These results indicated that the cell viability readings ranged from 9,838 to 10,423,188 and BoNT/A activity signals ranged from 84 to 27,242 (Table 1). In addition, a ratio of BoNT/A activity over cell viability was calculated to normalize the data, although there was not always a 1:1 ratio of viability and activity. Seven clonal cell lines exhibited activity/viability ratios of about 0.2×10^{-2} or greater: H1, A7, A11, F10, A9, A10, and C11 (Table 1). Nine clonal cell lines exhibited activity/viability ratios of about 0.125×10^{-2} to about 0.150×10^{-2}: H3, H8, E11, H10, A6, C5, C12, D11, and B5 (Table 1). Two cell lines exhibited activity/viability ratios of about 0.100×10^{-2}: D7 and B10 (Table 1). Based on these activity/viability ratios in conjunction with the cell viability and BoNT/A activity signal measurements, these 18 clonal cell lines were selected for further testing by conducting a secondary screen using a BoNT/A activity assay in order to generate a dose-response curve to BoNT/A.

Table 1. Primary Screen for Clonal Cell Lines Susceptible to BoNT/A Intoxication Using Viability and Activity Signals

Well	Cell Viability Reading (RLU)	BoNT/A Activity Signal (RLU)	Activity/Viability Ratio	Well	Cell Viability Reading (RLU)	BoNT/A Activity Signal (RLU)	Activity/Viability Ratio
A1	2634417	2425	0.092×10^{-2}	A7	10132753	27242	0.269×10^{-2}
B1	731808	198	0.027×10^{-2}	B7	2977371	1642	0.055×10^{-2}
C1	4258160	1641	0.039×10^{-2}	C7	5746577	4878	0.085×10^{-2}
D1	6554606	4885	0.075×10^{-2}	D7	5861338	6044	0.103×10^{-2}
E1	2374483	897	0.038×10^{-2}	E7	2819910	1399	0.050×10^{-2}
F1	2801444	1842	0.066×10^{-2}	F7	23523	84	0.357×10^{-2}
G1	5094510	4579	0.090×10^{-2}	G7	6232344	4031	0.065×10^{-2}
H1	3808699	10861	0.285×10^{-2}	H7	4916756	2759	0.056×10^{-2}
A2	9593106	7090	0.074×10^{-2}	A8	5945833	5611	0.094×10^{-2}
B2	5374966	5673	0.106×10^{-2}	B8	4591002	2128	0.046×10^{-2}
C2	4170158	2972	0.071×10^{-2}	C8	5648241	8758	0.155×10^{-2}
D2	31283	88	0.281×10^{-2}	D8	4207887	3360	0.080×10^{-2}
E2	5706902	3743	0.066×10^{-2}	E8	5804699	3844	0.065×10^{-2}
F2	4884798	4568	0.094×10^{-2}	F8	5585487	4651	0.083×10^{-2}
G2	3552045	2190	0.062×10^{-2}	G8	4758800	4545	0.096×10^{-2}
H2	3743690	3421	0.091×10^{-2}	H8	5439137	8017	0.147×10^{-2}
A3	15372	89	0.579×10^{-2}	A9	10423188	20706	0.199×10^{-2}
B3	5381672	1551	0.029×10^{-2}	B9	6493693	4444	0.068×10^{-2}
C3	4270534	3959	0.093×10^{-2}	C9	5742047	5788	0.101×10^{-2}
D3	48702	97	0.199×10^{-2}	D9	3424405	1848	0.054×10^{-2}
E3	4707349	2671	0.057×10^{-2}	E9	5771943	8064	0.140×10^{-2}
F3	3053132	1539	0.050×10^{-2}	F9	24524	88	0.359×10^{-2}
G3	5518292	4195	0.076×10^{-2}	G9	7291510	6674	0.092×10^{-2}
H3	4156632	6339	0.153×10^{-2}	H9	4169883	6048	0.145×10^{-2}
A4	19793	89	0.450×10^{-2}	A10	9050811	17617	0.195×10^{-2}
B4	6224766	4299	0.069×10^{-2}	B10	5590113	5175	0.093×10^{-2}
C4	3212859	3202	0.100×10^{-2}	C10	2325807	1713	0.074×10^{-2}
D4	4376180	2367	0.054×10^{-2}	D10	2644116	2589	0.098×10^{-2}

E4	3931793	3975	0.101×10^{-2}	E10	4210945	2666	0.063×10^{-2}
F4	1150134	526	0.046×10^{-2}	F10	2032749	6390	0.218×10^{-2}
G4	19023	94	0.494×10^{-2}	G10	3980127	3114	0.078×10^{-2}
H4	3368425	2645	0.079×10^{-2}	H10	4519035	6187	0.137×10^{-2}
A5	8231689	7809	0.095×10^{-2}	A11	9870025	24690	0.250×10^{-2}
B5	5332004	6545	0.123×10^{-2}	B11	4973892	2235	0.045×10^{-2}
C5	3669441	5042	0.138×10^{-2}	C11	3326446	6405	0.193×10^{-2}
D5	2554300	1161	0.045×10^{-2}	D11	5747961	7169	0.125×10^{-2}
E5	3781403	764	0.020×10^{-2}	E11	5831546	8432	0.145×10^{-2}
F5	4608801	3720	0.081×10^{-2}	F11	5291803	4317	0.082×10^{-2}
G5	7105403	7330	0.103×10^{-2}	G11	3499587	2790	0.080×10^{-2}
H5	5585607	7544	0.135×10^{-2}	H11	3225750	4518	0.140×10^{-2}
A6	7698708	10152	0.132×10^{-2}	A12	9838	89	0.905×10^{-2}
B6	4706560	3196	0.068×10^{-2}	B12	3728293	2016	0.054×10^{-2}
C6	5866251	6145	0.105×10^{-2}	C12	4086862	5308	0.130×10^{-2}
D6	2285787	768	0.034×10^{-2}	D12	5044526	3860	0.077×10^{-2}
E6	2471979	1038	0.042×10^{-2}	E12	4787913	2719	0.057×10^{-2}
F6	10958	91	0.830×10^{-2}	F12	5101695	2585	0.051×10^{-2}
G6	19590	91	0.465×10^{-2}	G12	2887390	1622	0.056×10^{-2}
H6	2057687	2564	0.125×10^{-2}	H12	2829307	5105	0.180×10^{-2}

[0155] To conduct BoNT/A activity assay in order to generate a dose-response curve to BoNT/A, cells from each isolated clonal cell line were seeded in a poly-D-lysine 96-well plate and differentiated as described above. Of the top 18 clonal cell lines selected for further testing, only 8 remained viable, the remaining 10 clonal cell lines failed to regrow and were lost. The media from the differentiated cells was aspirated from each well and replaced with fresh media containing either 0 (untreated sample), 0.03 pM, 0.1 pM, 0.3 pM, 0.9 pM, 2.8 pM, 8.3 pM, and 25 pM of a BoNT/A complex. After a 24 hrs treatment, the cells were washed, incubated for an additional two days in serum-free medium without toxin to allow for the cleavage of the SNAP-25 substrate, and harvested as described above. The supernatant was transferred to a capture antibody coated 96-well plate to perform the detection step.

[0156] The α-SNAP-25 capture antibody solution, the α-SNAP-25 detection antibody solution, and the α-SNAP-25 solid phase support were prepared as described above. Detection of the presence of cleaved SNAP-25 product by ECL sandwich ELISA analysis was performed as described above. The raw data obtained from the ECL imager was then transferred to SigmaPlot v. 9.0 and a 4-parameter logistics fit was used to define the dose-response curves. There were no constraints used for the 4-parameter logistic function when plotting the data. Graphical reports were generated using the following analysis: R2 (correlation coefficient), a (Max for data set), b (hillslope), and X0 ± SE (EC_{50} value ± standard error).

[0157] These results indicate that of the 8 clonal cell lines tested, only two were more susceptible to BoNT/A intoxication when compared to cells comprising the parental SiMa cell line (Table 2). For example, cells comprising the parental SiMa cell line exhibited an EC_{50} activity for BoNT/A of 2.20 pM, whereas cells comprising the H1 and A10 cell lines exhibited an EC_{50} activity for BoNT/A of 1.76 pM or

less. Conversely, cells comprising the H10 and D11 cell line exhibited an EC_{50} activity for BoNT/A that was higher than that observed for cells comprising the parental SiMa cell line, but less than 5.0 pM. It should be noted that any clonal cell line exhibiting an EC_{50} activity for BoNT/A that is 5.0 pM or less (100 U/mL or less) is useful for an immuno-based method for determining BoNT/A activity described in Ester Fernandez-Salas, et al., *Immuno-Based Botulinum Toxin Serotype A Activity Assays*, U.S. Patent Application Serial No: 12/403,531

Table 2. Secondary Screen for Clonal Cell Lines Susceptible to BoNT/A Intoxication

Clone	BoNT/A Activity		
	EC_{50} (pM)	$Signal_{MIN}$ (RI U)	$Signal_{MAX}$ (RI U)
SiMa	2.20	123	47,611
H1	0.77	193	125,252
H3	ND	ND	ND
B5	>25.0	115	22,277
C5	ND	ND	ND
A6	ND	ND	ND
A7	5.59	153	100,412
D7	ND	ND	ND
H8	ND	ND	ND
A9	ND	ND	ND
A10	1.76	207	113,029
B10	6.35	147	101,935
F10	>25.0	111	32,663
H10	2.80	171	120,975
A11	ND	ND	ND
C11	ND	ND	ND
D11	4.4	1.84	105,527
E11	ND	ND	ND
C12	ND	ND	ND

ND = Not determined.

3. Primary screen for BoNT/A intoxication susceptibility of cells from a clonal cell line using a formulated BoNT/A pharmaceutical product.

[0158] Another way to determine whether cells from a clonal cell line were susceptibility to BoNT/A intoxication was to conduct a primary screen by generating a dose-response curve to BoNT/A and calculate the EC_{50} value using an immuno-based method for determining BoNT/A activity as described in Ester Fernandez-Salas, et al., *Immuno-Based Botulinum Toxin Serotype A Activity Assays*, U.S. Patent Application Serial No: 12/403,531, which is hereby incorporated by reference in its entirety.

[0159] Initially six of 35 clonal cell line isolates were examined using a full dose response to BoNT/A. To prepare a lysate from cells treated with BoNT/A, cells from six clonal cell line were seeded in a poly-D-lysine 96-well plate and differentiated as described above in Section 2 except that the serum-free medium

comprised 60 µg/mL GT1b. The clonal cell lines used were 3D8, YB8, 1D4, 2D6, 1E11, 2F5. The H1 and H10 clonal cell lines identified above, along with the parental SiMa cell line, were used as references to identify cell lines highly susceptible to BoNT/A intoxication. The media from the differentiated cells was aspirated from each well and replaced with fresh media containing either 0 (untreated sample), 0.98 U/mL, 1.9 U/mL, 3.91 U/mL, 7.81 U/mL, 15.6 U/mL, 31.3 U/mL, 62.5 U/mL, 125 U/mL, 250 U/mL, or 500 U/ml of a formulated BoNT/A pharmaceutical product. After a 24 hrs treatment, the cells were washed, incubated for an additional two days in serum-free medium without toxin to allow for the cleavage of the SNAP-25 substrate. To harvest the cells, 1 x PBS was aspirated, the cells lysed by adding 30 µl of Lysis Buffer comprising 20 mM Tris-HCl (pH 7,5), 150 mM NaCl, 1 mM EDTA, 1 mM EGTA, 1% Triton X-100 to each well, and the plate incubated on a shaker rotating at 500 rpm for 30 minutes at 4 °C. The plate was centrifuged at 4000 rpm for 20 minutes at 4 °C to pellet cellular debris. The protein concentration was determined using standard methods. The supernatant was transferred to a capture antibody coated 96-well plate to perform the detection step of the immuno-based method.

[0160] The α-SNAP-25 capture antibody solution, the α-SNAP-25 detection antibody solution, and the α-SNAP-25 solid phase support were prepared as described above in Section 2. Detection of the presence of SNAP-25 cleavage product by ECL sandwich ELISA analysis was performed, collected data was analyzed and the EC_{50} calculated as described above in Section 2, except that SigmaPlot v. 10 was used.

[0161] These results show that clonal cell line H1 comprises cells that are more susceptible to BoNT/A than the parental SiMa cell line (Table 3). In addition, results indicate that although clonal cell lines H10, 1D4, 1E11, 2D6, 2F5, 3D8, and YB8 all comprise cells that are less susceptible to BoNT/A than the parental SiMa cell line, all have an EC_{50} of BoNT/A activity that is below 30 U/mL (Table 3). It should be noted that any clonal cell line exhibiting an EC_{50} activity for BoNT/A that is 100 U/mL or less (5.0 pM or less) is useful for an immuno-based method for determining BoNT/A activity described in Ester Fernandez-Salas, et al., *Immuno-Based Botulinum Toxin Serotype A Activity Assays*, U.S. Patent Application Serial No: 12/403,531.

Table 3. Primary Screen for Clonal Cell Lines Susceptible to BoNT/A Intoxication

Clone	BoNT/A Activity		
	EC_{50} (U/mL)	$Signal_{MIN}$ (RLU)	$Signal_{MAX}$ (RLU)
SiMa	10.8 ± 1.0	10,519	253,484
H1	10.2 ± 0.6	13,996	276,982
H10	22.2 ± 2.0	5,379	296,168
1D4	22.4 ± 0.8	6,064	239,096
1E11	14.2 ± 1.7	8,698	276,323
2D6	27.3 ± 1.8	3,347	179,454
2F5	15.8 ± 0.9	7,007	265,461
3D8	13.4 ± 0.6	11,658	266,279
YB8	19.7 ± 1.3	8,477	293,559

[0162] This initial primary screen using a dose-response curve with the 10 different BoNT/A concentrations identified three concentrations that were useful for a shortened assay using 3 different BoNT/A concentrations, with one concentration being slightly higher than the lower asymptote (8 U/mL), one concentration near the EC_{50} (25 U/mL), and one concentration representing about 80% of the upper asymptote (80 U/mL). In these subsequent primary screens the remaining 29 clonal cell line isolates were tested as described above except that the cells were treated with either 0 (untreated sample), 8 U/mL, 25 U/mL, or 80 U/mL of a formulated BoNT/A pharmaceutical product. The clonal cell lines tested were 1E3, 2B9, 2D2, 2E4, 3B8, 3D5, 3G10, 4B5, 4C8, 4D3, 5C10, 5F3, AC9, AF4, BB3, BB10, BE3, BF8, CC11, CD6, CE6, CG8, CG10, DC4, DD10, DE7, DF5, YB7, and YF5. In addition, the parental SiMa was used as positive control.

[0163] These results show that clonal cell lines 2E4, 3B8, 3D5, 5F3, AF4, BB3, BB10, and DC4 all comprise cells that are more susceptible to BoNT/A than the parental SiMa cell line (Table 4). In addition, these results indicate that clonal cell lines 1E3, 2B9, 3G10, 4B5, 4C8, AC9, BE3, BF8, CC11, CD6, CE6, CG8, CG10, DD10, DE7, and YF5 all comprise cells that are of similar susceptibility to BoNT/A to that of the parental SiMa cell line (Table 4). Lastly, these results reveal that clonal cell lines 2D2, 4D3, 5C10, DF5, and YB7 all comprise cells that are less susceptible to BoNT/A than the parental SiMa cell line (Table 4).

Table 4. Primary Screen for Clonal Cell Lines Susceptible to BoNT/A Intoxication

Clone	8 U/mL BoNT/A		25 U/mL BoNT/A		80 U/mL BoNT/A	
	Activity Signal (RLU)	Fold Difference	Activity Signal (RLU)	Fold Difference	Activity Signal (RLU)	Fold Difference
SiMa	75811/ 80562*	—	138952/ 175685*	—	173979/ 225768*	—
1E3	71040	0.9	128771	0.9	155107	0.9
2B9	66962	0.9	135006	1.0	166871	1.0
2D2	60224*	0.8	136947*	0.8	199786*	0.9
2E4	103680	1.4	217980	1.6	270463	1.6
3B8	123521	1.6	227367	1.6	249218	1.4
3D5	113532	1.5	201663	1.5	270578	1.6
3G10	83049	1.1	130930	0.9	175540	1.0
4B5	74344	1.0	137604	1.0	177363	1.0
4C8	87047	1.1	144395	1.0	185115	1.1
4D3	38063	0.5	80180	0.6	101724	0.6
5C10	16024*	0.2	49030	0.3	116396*	0.6
5F3	98263*	1.7	182902*	1.4	212275*	1.5
AC9	60016*	1.0	127030*	1.0	180384*	1.4
AF4	115460	1.5	179901	1.3	190867	1.1
BB3	74668	1.3	120966	1.4	170177	1.4
BB10	152748	2.0	232406	1.7	266555	1.5
BE3	100849	1.0	199487	0.9	236415	1.0
BF8	55763*	1.0	111746*	1.0	153074*	1.3
CC11	54421*	1.0	123576*	1.0	155337*	1.2

CD6	74970	1.0	151862	1.1	183377	1.1
CE6	70019	0.9	146202	1.1	208184	1.2
CG8	81790*	1.0	159098*	1.0	189209*	1.3
CG10	69503	0.9	141079	1.0	185801	1.1
DC4	112085	1.5	163319	1.2	169352	1.0
DD10	116325	1.5	205445	1.5	223473	1.3
DE7	60994*	0.9	131237*	0.9	174467*	0.9
DF5	34,165*	0.5	104,696*	0.7	179,314*	0.9
YB7	50433	0.7	103707	0.7	143423	0.8
YF5	65848	0.9	122487	0.9	146263	0.4

* Two separate screens were done. In the first, the signal detected for the SiMa cell line was 75811 RLU and this value was used to determine the fold difference for clonal cell lines tested in this screen (numbers with no asterisk). For the second screen, the signal detected for the SiMa cell line was 80562 RLU and this value was used to determine the fold difference for clonal cell lines tested in this screen (numbers with asterisk).

Example II

Stability Analysis of Clonal Cell Lines

[0164] The following example illustrates how to characterize the stability of cells from an established clonal cell line that are susceptible to BoNT/A intoxication or have neurotoxin uptake capacity.

[0165] During characterization of the SiMa cell line, it was determined that the parental SiMa cell line became unstable in terms of a significant loss of sensitivity to BoNT/A. For example, prior to passage 13, cells comprising the parental SiMa cell line routinely exhibited an EC_{50} for BoNT/A activity that was under 5.0 pM. However, after passages about 14 to about 20 passages, cells comprising the parental SiMa cell exhibited an EC_{50} for BoNT/A activity that was routinely over 20.0 pM. One reason for this dramatic reduction in the EC_{50} value may be because the SiMa cell line is heterogeneous in nature since it comprises at least five different cell types. Over time, one of these cell types could overtake the culture to the exclusion of the other four. If the overtaking cell type was less susceptible to BoNT/A intoxication, or not susceptible at all, then as this cell type became the dominant one in the cell line the EC_{50} for BoNT/A activity in this overtaken SiMa cell line would decrease. Thus, because the established clonal cell lines were derived from only one of these cell types, then it follows that the clonal cell line would exhibit greater stability in terms of maintaining an EC_{50} for BoNT/A activity that was routinely under 5.0 pM.

[0166] To determine whether the cells from the established clonal cell lines showed increased stability relative to the cells comprising the parental SiMa cell line, the EC_{50} for BoNT/A activity was determined for clonal cell lines BB10, H1, H10, and the parental SiMa cell line at different passage numbers using an immuno-based method for determining BoNT/A activity. The media from the differentiated cells was aspirated from each well and replaced with fresh media containing either 0 (untreated sample), 0.98 U/mL, 1.9 U/mL, 3.91 U/mL, 7.81 U/mL, 15.6 U/mL, 31.3 U/mL, 62.5 U/mL, 125 U/mL, 250 U/mL, or 500 U/mL of a formulated BoNT/A pharmaceutical product. After a 24 hrs treatment, the cells were washed, incubated for an additional two days in serum-free medium without toxin to allow for the cleavage of the

SNAP-25 substrate, and harvested as described above. The supernatant was transferred to a capture antibody coated 96-well plate to perform the detection step.

[0167] Similarly, the preparation of the α-SNAP-25 capture antibody solution, α-SNAP-25 detection antibody solution, and the solid phase support comprising an α-SNAP-25 capture antibody were as described in Section 3. Lastly, detection of the presence of SNAP-25 cleavage product by ECL sandwich ELISA was performed, collected data was analyzed, and the EC_{50} calculated as described above in Section 2, except that PLA v. 2 was used for the 4-parameter logistics fit.

[0168] The results from this stability experiments indicated that BB10, H1 and H10 cell lines all exhibited increase stability as compared to the parental SiMa cell line. For example, where cells from the parental SiMa cell line exhibited an EC_{50} for BoNT/A activity that was over 500 U/mL (or 25 pM) after passages about 14 to about 20 passages, cells comprising the BB10, H1 and H10 cell lines all exhibited an EC_{50} for BoNT/A activity that was below 10 U/mL (or 0.5 pM) after passage about 30.

Example III

Gene Expression Profile of Cell Lines Comprising Cells Susceptible to BoNT/A Intoxication

[0169] The following example illustrates how to characterize cells from an established clonal cell line that are susceptible to BoNT/A intoxication or have neurotoxin uptake capacity by gene expression profiling.

[0170] To determine the changes in genome-wide gene transcription levels in cells susceptible to BoNT/A intoxication, gene expression analysis was performed on cells from H1, BB10, 2D6 and the parental SiMa cell line, in both differentiated and undifferentiated states using GENECHIP® U133 Plus 2 microarray technology (Affymetrix, Inc., Santa Clara, CA) according to the manufacturer's instructions, see, *e.g.*, *GENECHIP® Expression Analysis Technical Manual*, 702232, Rev. 2 (2006) which is hereby incorporated by reference in its entirety.

[0171] To prepare differentiated cells for these cell lines, a suitable density of cells from the H1, BB10, 2D6, and SiMa cell lines were seeded in separate T175 tissue culture flasks containing 50 mL of a serum-free medium comprising Enhanced Minimum Essential Medium, 10 mM HEPES, 1 mM sodium pyruvate, 0.1 mM Non-Essential Amino Acids, 1 x B27 supplement, 1 x N2 supplement, and 60 µg/mL GT1b (302-011-M005, Alexis Biochemicals, San Diego, CA). These cells were incubated in a 37 °C incubator under 5% carbon dioxide until the cells differentiated, as assessed by standard and routine morphological criteria, such as growth arrest and neurite extension, and attained 80% confluence (approximately 3 days). The cells were then washed with 50 mL of 1 x PBS, trypsin-treated for 5 min at room temperature, and then 15 mL of growth medium was added to the flask to inactivate the trypsin. The cell suspension was transferred to a 50 mL tube and centrifuge at 200 RCF for 5 min at room temperature to pellet the cells. The cell pellet was washed once in 50 mL of 1 x PBS, centrifuge at 200 RCF for 5 min at room

temperature to pellet the cells, and the supernatant was removed. The cell pellet was quick frozen on dry ice and stored at -80 °C until needed.

[0172] To prepare undifferentiated cells for these cell lines, a suitable density of cells from the H1, BB10, 2D6, and SiMa cell lines were seeded in separate T175 tissue culture flasks containing 50 mL of growth medium comprising RPMI 1640, 10% fetal bovine serum, 10 mM HEPES, 1 mM sodium pyruvate, 0.1 mM Non-Essential Amino Acids, and 60 µg/mL GT1b. These cells were incubated in a 37 °C incubator under 5% carbon dioxide until the cells attained 80% confluence (approximately 3 days). The cells were then processed as described above and the cell pellet was quick frozen on dry ice and stored at -80 °C until needed.

[0173] To prepare total RNA, cells for each cell line were lysed and total RNA isolated and purified using a RNA isolation kit (QIAGEN, Valencia, CA) according to the manufacturer's protocols. DNA was digested using an on-column DNase I procedure (QIAGEN, Valencia, CA). RNA was quantified photospectrometrically at 260 nm and purity assessed by the A260A280 ratio using a spectrophotometer. RNA integrity was assessed using a Bioanalyser 2100 (Agilent Technologies, Inc., Santa Clara, CA). Extracted total RNA aliquots were snap-frozen in liquid nitrogen and stored at -80 °C.

[0174] To prepare cDNA probes for the gene microarray chips, about 1-15 µg was reversed transcribed using a T7-Oligo(dT) promoter primer in the first strand cDNA synthesis reaction. Following RNase H-mediated second strand cDNA synthesis, the double-stranded cDNA was purified and served as a template for subsequent in vitro transcription reaction. The in vitro transcription reaction was carried out in the presence of T7 RNA polymerase and a biotinylated nucleotide analog/ribonucleotide mix for complementary RNA (cRNA) amplification and biotin labeling. The biotinylated cRNA targets were then cleaned up, fragmented, and hybridized to microchip expression arrays for 17 hours at 65 °C according to the manufacturer's instructions, see, *e.g.*, *GENECHIP® Expression Analysis Technical Manual*, 702232, Rev. 2 (2006) which is hereby incorporated by reference in its entirety. To identify substantial treatment-related up- or down-regulated gene expression differences compared to control cell lines, greater than 1.5-fold differences ($\log_2$ 0.58) were considered significant, and only those genes that displayed consistent changes in expression in the triplicate analysis were considered (Tables 5-12).

[0175] Expression profiling for cell lines H1, BB10 and 2D6 analyzed in the undifferentiated state revealed that 1,323 genes were identified as having their expression levels increase by 1.5-fold ($\log_2$ 0.58) or more in the H1 and BB10 cell lines as compared to the gene expression levels obtained from the 2D6 cell line (Table 5). Of these, 686 genes exhibited an increase in expression levels in the H1 and BB10 cell lines by 2-fold ($\log_2$ 1.0) or more as compared to the expression level for these genes determined from the 2D6 cell line; and 231 genes exhibited an increase in expression levels in the H1 and BB10 cell lines by 4-fold ($\log_2$ 2.0) or more as compared to the expression level for these genes determined from the 2D6 cell line. With respect to decreased expression, 1,438 genes were identified as having their expression levels decreased by 1.5-fold ($\log_2$ 0.58) or more in the H1 and BB10 cell lines as

compared to the gene expression levels obtained from the 2D6 cell line (Table 6). Of these, 668 genes exhibited a decrease in expression levels in the H1 and BB10 cell lines by 2-fold (log_2 1.0) or more as compared to the expression level for these genes determined from the 2D6 cell line; and 107 genes exhibited a decrease in expression levels in the H1 and BB10 cell lines by 4-fold (log_2 2.0) or more as compared to the expression level for these genes determined from the 2D6 cell line.

[0176] Expression profiling for cell lines H1, BB10 and 2D6 analyzed in the differentiated state revealed that 2,556 genes were identified as having their expression levels increased by 1.5-fold (log_2 0.58) or more in the H1 and BB10 cell lines as compared to the gene expression levels obtained from the 2D6 cell line (Table 7). Of these, 1,634 genes exhibited an increase in expression levels in the H1 and BB10 cell lines by 2-fold (log_2 1.0) or more as compared to the expression level for these genes determined from the 2D6 cell line; and 696 genes exhibited an increase in expression levels in the H1 and BB10 cell lines by 4-fold (log_2 2.0) or more as compared to the expression level for these genes determined from the 2D6 cell line. With respect to decreased expression, 2,087 genes were identified as having their expression levels decreased by 1.5-fold (log_2 0.58) or more in the H1 and BB10 cell lines as compared to the gene expression levels obtained from the 2D6 cell line (Table 8). Of these, 1,215 genes exhibited a decrease in expression levels in the H1 and BB10 cell lines by 2-fold (log_2 1.0) or more as compared to the expression level for these genes determined from the 2D6 cell line; and 280 genes exhibited a decrease in expression levels in the H1 and BB10 cell lines by 4-fold (log_2 2.0) or more as compared to the expression level for these genes determined from the 2D6 cell line.

[0177] Expression profiling for cell lines H1, BB10 and SiMa analyzed in the undifferentiated state revealed that 1,232 genes were identified as having their expression levels increase by 1.5-fold (log_2 0.58) or more in the H1 and BB10 cell lines as compared to the gene expression levels obtained from the SiMa parental cell line (Table 9). Of these, 764 genes exhibited an increase in expression levels in the H1 and BB10 cell lines by 2-fold (log_2 1.0) or more as compared to the expression level for these genes determined from the SiMa parental cell line; and 228 genes exhibited an increase in expression levels in H1 and BB10 cell lines by 4-fold (log_2 2.0) or more as compared to the expression level for these genes determined from the SiMa parental cell line. With respect to decreased expression, 1,265 genes were identified as having their expression levels decreased by 1.5-fold (log_2 0.58) or more in the H1 and BB10 cell lines as compared to the gene expression levels obtained from the SiMa parental cell line (Table 10). Of these, 648 genes exhibited a decrease in expression levels in the H1 and BB10 cell lines by 2-fold (log_2 1.0) or more as compared to the expression level for these genes determined from the SiMa parental cell line; and 189 genes exhibited a decrease in expression levels in H1 and BB10 cell lines by 4-fold (log_2 2.0) or more as compared to the expression level for these genes determined from the SiMa parental cell line.

[0178] Expression profiling for cell lines H1, BB10 and SiMa analyzed in the differentiated state revealed that 756 genes were identified as having their expression levels increase by 1.5-fold (log_2 0.58) or more in the H1 and BB10 cell lines as compared to the gene expression levels obtained from the SiMa parental

cell line (Table 11). Of these, 472 genes exhibited an increase in expression levels in the H1 and BB10 cell lines by 2-fold (log_2 1.0) or more as compared to the expression level for these genes determined from the SiMa parental cell line; and 150 genes exhibited an increase in expression levels in H1 and BB10 cell lines by 4-fold (log_2 2.0) or more as compared to the expression level for these genes determined from the SiMa parental cell line. With respect to decreased expression, 912 genes were identified as having their expression levels decreased by 1.5-fold (log_2 0.58) or more in the H1 and BB10 cell lines as compared to the gene expression levels obtained from the SiMa parental cell line (Table 12). Of these, 411 genes exhibited a decrease in expression levels in the H1 and BB10 cell lines by 2-fold (log_2 1.0) or more as compared to the expression level for these genes determined from the SiMa parental cell line; and 108 genes exhibited a decrease in expression levels in H1 and BB10 cell lines by 4-fold (log_2 2.0) or more as compared to the expression level for these genes determined from the SiMa parental cell line.

Example IV

Pathway Analysis of Gene Expression Profiles from Clonal Cell Lines

[0179] The following example illustrates how to characterize gene expression profiles from clonal cells from an established clonal cell line that are susceptible to BoNT/A intoxication or have neurotoxin uptake capacity in order to identify biological networks or pathways associated with BoNT/A intoxication.

[0180] An Ingenuity Pathway Analysis (IPA) Core Analysis (Ingenuity Systems Inc., Redwood City, CA) was performed to characterize the RNA expression phenotype of two independently derived BoNT/A very sensitive single clone cell lines, BB10 and H1, compared to a related but much less BoNT/A sensitive single clone cell line, 2D6. The analysis was done to identify the specific gene expression phenotype of a BoNT/A sensitive cell line. The result can also be used to predict and potentially identify proteins that function to enhance BoNT/A uptake.

[0181] An Ingenuity Pathway Analysis (IPA) Core Analysis was performed that identified biologically relevant networks to BoNT/A intoxication based on connectivity among the genes from an IPA library and the genes exhibiting significant changes as determined from the expression profiling discussed above. For this analysis, all genes that exhibited an increased or decrease in expression levels in the H1 and BB10 cell lines by 4-fold (log_2 2.0) or more as compared to the expression level for these genes determined from the 2D6 cell line were used, in conjunction with, selected genes with known or suspected relevance to BoNT/A intoxication, hereafter referred to as the Profile genes. The significance of the association to a given network was measured and ranked by the ratio of the number of Profile genes that mapped to the specific network divided by the total number of genes that map to that network. Fisher's exact test was used to calculate p-scores, which represent the association between the Profile genes and the network, and based on the p-scores the genes from the Profile genes were used to rank the networks. The p-scores were derived from p-values. If there are n genes in the network and f of them are Profile genes, then the p-value is the probability of finding f or more Profile genes in a set of n

genes randomly selected from the Global Molecular Network. Since significant p-values are quite low (e.g., 1×10^{-6}), a p-score was defined as the component of the p-value; p-score = -log10 (p-value). The identified networks were overlaid with differentially expressed genes which had more than 1.5-fold differential expression and a p-value ≤ 0.001 either before or after differentiation.

[0182] Using IPA Core Analysis the differentially expressed Profile genes were connected to 26 Networks. Nineteen of these included 10 or more Profile genes (Table 13). Among these nineteen networks three overall networks groups, named A, B and C were identified (Table 13). Within the networks in these three groups there were overlapping genes and the expression for more than three genes was increased after differentiation. Group A genes include the FGFR2 receptor which has been shown to function in the BoNT/A intoxication process as a receptor for BoNT/A and are as follows: genes exhibiting a 1.5-fold or more decrease in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, ANXA2, AQP1, ARHGAP9, CDH10, CDKN2A, CHPT1, CNTN2, ERAP1, and RGS11; genes exhibiting a 1.5-fold or more increase in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, ADAM1S9, ATAD2, C11ORF82, CDC45L, CNTN1, CNTN4, Cyclin A, Cyclin E, E2F1, E2F2, E2F7, ELOVL7, EME1, FGFR, FGFR2, KIAA1524, MELK, MYBL1, MYBL2, NDC80, NDN, ORC1L, PLS3, PRIMA1, RAD54L, RBL1, RBPMS, RRM2, S1PR3, SCLY, SLCIA3, SPC24, SPC25, ST8SIA4, TFDP1, TFP12, TK1, TMEM35, TTK, TWIST1, TYMS, TYK, and ZWINT.

[0183] Group B genes include the EGFR, a receptor which is regulated by NGF, which has been shown to increase BoNT/A uptake in cell culture experiments and are as follows: genes exhibiting a 1.5-fold or more decrease in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, ABCC8, AELIM3, CAP2, IL17B, MEF2A, NEEBL, PHC, S100A6, SLC1A6, SMAD1, SMAD5, SMAD8, SYT13, and SYTL1; genes exhibiting a 1.5-fold or more increase in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, AURKB, BIRC5, BRCA1, BRCA2, BRIP1,BUB1B, CD9, DLGAP3, DYNLT3, ENC1, FBLN1, FOXM1, Gβγ, GNAI1, GNG11, GNG12, GPSM2, GUCY1B3, HGF, ITGA6, JNK, KCNJ5, KIF18A, KITLG, MMD, MSN, MYRIP, NEK2, NR3C1, NXPH1, OSBPL3, PKMYT1, PTPRM, RAD51, RAD51AP1, SLC7A2, SLC43A3, SMC6, SNAI2, SNCAIP, SSH2, STK17A, SYNPO2, TOP2A, TPTE, TRAF4, TSPAN, TSPAN4, UBE3, UBE3B, and VAV3.

[0184] Group C genes include a number of microtubule motor proteins of the kinesin family that may function in the intracellular trafficking of BoNT/A and are as follows: genes exhibiting a 1.5-fold or more decrease in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, CSTB, GPCR, GRIM5, KISSR, SCN2A, SLC1A2, and THBS2; genes exhibiting a 1.5-fold or more increase in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, ALCAM, AURKA, CHEK, CIT, CSRP2, E2F, ECT2, EFNB2, ERK, ESPL1, GNAI, GPR161, HMMR, KIF4A, KIF14, KIF15, KIF22, KIF23, KIFC1, LPAR1, MK167, OIP5, PHLPP, PP1/PP2A, PPP1R3C, PRC1, PTTG1, RACGAP, RB, RGS5, SDC2, and TPX2.

[0185] The remaining networks identified did not share common genes between any other network. For Network 3, genes exhibiting a 1.5-fold or more decrease in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, ADARB1, ADM, PTPPH, and SLCO1A2; genes exhibiting a 1.5-fold or more increase in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, ASCL1,HES6, MAPK, NMU, PEG3, PTPRK, PRLHR, PTPRK, SGOL2, SPARC, and ZNF217. For Network 6, genes exhibiting a 1.5-fold or more decrease in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, CNGA3, HIST1H3E and PTGS1; genes exhibiting a 1.5-fold or more increase in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, ASF1B, BASP1, CHAF1A, NCAPH, PBK, PRAME, SMC2, UHRF1, and VRK1. For Network 9, genes exhibiting a 1.5-fold or more decrease in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, HIST1H2BD and OSCAR; genes exhibiting a 1.5-fold or more increase in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, C14ORF106, CEP72, KIF20A, PCNA, PEX13, PFC5, POLQ, SPAG5, SYTL4, TROAP, and WDR51A. For Network 12, genes exhibiting a 1.5-fold or more increase in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, ANLN, ARHGAP24, ASPM, BUB1, CCDC99, CEP55, CKAP2, DRAM, E2F8, PLXNA2, SLC16A10, UBE2C, UBE2S, and WDHD1. For Network 13, genes exhibiting a 1.5-fold or more decrease in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, CALY; genes exhibiting a 1.5-fold or more increase in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, ARHGEF3, CTSL2, DIAPH3, FBP1, KIF2C, KIF11, PFKFB3, and PLK4. For Network 14, genes exhibiting a 1.5-fold or more decrease in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, COL5A1 and MICAL2; genes exhibiting a 1.5-fold or more increase in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, FNDC5, HSPC159, MAB21L2, SLITRK5, SYN2, and ZNF367. For Network 15, genes exhibiting a 1.5-fold or more decrease in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, OLFML2A and SIGIRR; genes exhibiting a 1.5-fold or more increase in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, EXO1, KCTD12, MYO6, PHEBL1, SHCBP1, TPBG, and TUBB6. For Network 17, genes exhibiting a 1.5-fold or more decrease in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, HPCAL1 and LPAR5; genes exhibiting a 1.5-fold or more increase in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, BTG3, GABRA5, TR1P10, and ZNF521. For Network 19, genes exhibiting a 1.5-fold or more decrease in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, HTR1E and SORCS1; genes exhibiting a 1.5-fold or more increase in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, BNC2, DPYD, EMILIN2, PPIL5, and TACC3.

Table 13. IPA Core Analysis of Profile Genes

Group	Network	Proteins in Network	pvalue	Profile Gene Number	Expression Undifferentiated State		Expression Differentiated State	
					Decreased	Increased	Decreased	Increased
A	1	ADAMTS9, ATAD2, CDC45L, CDKN2A, CNTN1, CNTN2, Cyclin A, Cyclin E, DIRAS3, E2F1, E2F2, E2F7, FGFR2, HDAC, MYBL1, MYBL2, NDC80, NDN, NFkB, ORC1L, PLS3, RAD54L, RBL1, RRM2, S1PR3, SPC24, SPC25, TFDP1, TFPI2, TK1, TNFRSF10D, TTK, TYMS, TYK, ZWINT	51	30	CDKN2A	ADAMTS9, CNTN1, HDAC, NDN, PLS3, S1PR3,TFPI2	CDKN2A, CNTN2,	ADAMTS9, ATAD2, CDC45L, CNTN1, Cyclin A, Cyclin E, E2F1, E2F2, E2F7, FGFR2, MYBL1, MYBL2, NDC80, NDN, ORC1L, PLS3, RAD54L, RBL1, RRM2, S1PR3, SPC24, SPC25, TFDP1, TFPI2, TK1, TTK, TYMS, TYK, ZWINT
C	2	ALCAM, ANK2, ANK3, AURKA, DOK5, E2F, ERK, ESPL1, GDF15, GFRA2, HMMR, ITGA9, KIF15, KIF22, KISS1R, KPNA, KPNB, LGI1, MAFB, MAP2K1, MAP2K2, MKI67, NRG3, OIP5, PHKA2, PHLPP, POSTN, PP1/PP2A, PP2A, PPP1R3C, PPP2R2B, PPP2R2C, PTTG1, RAF1, RB, SCN2A, TPX2	46	28	ANK2, ANK3, PHKA2, PPP2R2C, SCN2A	ALCAM, DOK5, ERK, GFRA2, PP1/PP2A, PP2A, PPP1R3C, PPP2R2B	KISSR, SCN2A	ALCAM, AURKA, E2F, ERK, ESPL1, HMMR, KIF15, KIF22, MKI67, OIP5, PHLPP, PP1/PP2A, PPP1R3C, PTTG1, RB, TPX2

—	3	ADARB1, ADM, AKAP12, ALP, ASCL1, BHLHB2, CRH, DLL1, FRZB, FSH, GRIA2, GRIP2, hCG, HES6, HTATIP2, IL13RA2, MAPK, NMU, PDGF BB, PDLIM3, PEG3, PLAT, PPFIA4, PRLHR, PTPRH, PTPRK, SGOL2, SLCO1A2, SMAD6, SPARC, STC1, TEAD4, TGFB, VEGF, ZNF217	46	28	ADARB1, GRIP2, SLCO1A2	ASCL1, DLL1, FRZB, MAPK, PEG3, PLAT, PRLHR, SMAD6, SPARC, ZNF217	ADARB1, ADM, PTPPH, SLCO1A2	ASCL1, HES6, MAPK, NMU, PEG3, PRLHR, PTPRK, SGOL2, SPARC, ZNF217
C	4	AKT, ACTN1, ACTN2, ACTN3, ATF5, ATM/ATR, BDKRB2, CHEK1, CHEK2, CIT, CSRP2, CSTB, CTSH, ECT2, EFNB2, ELMO1, GNAI, GABBR2, GPCR, GPR161, GRM5, ICAM2, KIF4A, KIF14, KIF23, KIFC1, LPAR1, MMP, PDGFA PDGFB, PRC1, RAC, RAC2, RACGAP1, RGS5, SDC2, SLC1A2, THBS2	43	27	CSTB, GPCR, GRIM5, SLC1A2	GNAI, GPR161, LPAR1, RGS5	CSTB, GPCR, GRIM5, SLC1A2, THBS2	CIT, CSRP2, ECT2, EFNB2, CHEK, GNAI, GPR161, KIF4A, KIF14, KIF23, KIFC1, LPAR1, PRC1, RACGAP, RGS5, SDC2,
B	5	ABLIM3, F-ACTF, G-ACT, CD9, CXCR4, DTNA, ENC1, FNBP1, Gβγ, GNAI1, GNG11, GNG12, GPSM2, ITG,	38	25	SYT13, S100A6	CD9, CXCR4, ENC1, Gβγ, GNAI1, GNG11, GNG12, ITGA6, JNK, MSN, MYRIP, STK17A	AELIM3, S100A6, SYT13, SYTL1	CD9, ENC1, Gβγ, GNAI1, GNG11, GNG12, GPSM2, ITGA6, JNK, KCNJ4, MSN, MYRIP,

		ITA5, ITGA6, JNK, KCNJ4, MLC, MSN, MYRIP, NOX, NET1, NRXN1, NXPH1, PI3K, RHO, S100A6, STK17A, SYT13, SYTL1, TRAF4, TSPAN, TSPAN3, TSPAN4, VAV3						NXPH1, STK17A, TRAF4, TSPAN, TSPAN4, VAV3
—	6	ADCY, ADCY1, AP1, ASF1B, ATP2B4, BASP1, BCL11B, CAM, CAMK2B, CHAF1A, CNGA3, CYP2E1, DACH1, HIST1H3E, HISH3, HRH3, HSP90, IL1, IL12, INS, INFA, ISG20, KCNN2, LDL, MMP14, NCAPH, PBK, PDGF, PIAS1, PRAME, PTGS1, SEC31A, SMC2, UHRF1, VRK1	36	24	CAMK2B	BASP1, HRH3	CNGA3, HIST1H3E, PTGS1	ASF1B, BASP1, CHAF1A, NCAPH, PBK, PRAME, SMC2, UHRF1, VRK1
B	7	BARD1, BRCA1, BRCA2, BRIP1, BUB1B, CNA, CAP2, CK2, DLGAP5, FAT, GUCY1B3, HSP70, KITLG, MEF2A, NEK2, NFAT, NR3C1, NF1, PHLDA2, PKC(s), RAD51, RAD51AP1, TOP2, SAMD4A, SLC1A6, SMC6, SNAI2, SNCAIP,	32	24	CAP2, CNA, PHLDA2, PKC(s)	NR3C1, SMC6, SNCAIP, TCF7L2	CAP2, MEF2A, PKC(s), SLC1A6	BRCA1, BRCA2, BRIP1, BUB1B, DLGAP3, GUCY1B3, NEK2, KITLG, NR3C1, RAD51, RAD51AP1, SMC6, SNAI2, SNCAIP, UBE3, UBE3B

		STAT5a, STAT5b. TCF7L2, UBE3, UBE3B, UBN, XPO1						
B	8	CBP, AURKB, BIRC5, CACNA1D, CBP/p300, CD3, CREB, CREB5, DBH, EGR1, ERK1, ERK2, FBLN1, FBN1, FOXM1, HGF, INCENP, KCNMA1, LGALS1, MAOA, MEK, NDRG1, NID1, P38 MAPK, PKA, PKMYT1, PRKAC, PRKACB, RAF, RAP1, RAS, RGMA, RSK, SMAD1, SMAD5, SMAD8, SYNPO2, TOP2A	30	21	KCNMA1, NDRG1, RAS	ERK1, ERK2, MAOA, P38 MAPK, RGMA	NDRG1, SMAD1, SMAD5, SMAD8	AURKB, BIRC5, ERK1, ERK2, FBLN1, FOXM1, HGF, MAOA, P38 MAPK, PKMYT1, SYNPO2, TOP2A
—	9	C14ORF106, CDKN1A, CEP72, DHX8, FKBPL, HIST1H2BD, HNF4A, KIF20A, KRT18, MTHFS, OSCAR, PCGF5, PCNA, PELO, PEX13, PFC5, POLD4, POLK, POLL, POLM, POLQ, POLS, R3HDM1, RASL12, RFC5, SLC33A1, SPAG5, STA14, SULT1A1, SULT1C2, SYTL4, TCEAL3, TROAP, VEZT, WDR51A,	19	15	—	PCGF5	HIST1H2BD, OSCAR	C14ORF106, CEP72, KIF20A, PCNA, PEX13, PFC5, POLQ, SPAG5, SYTL4, TROAP, WDR51A

		ZBTB16						
A	10	ARHGAP9, CDH10, CDS1, CDS2, CHPT1, CNTN4, ELOVL7, EME1, FGFR, GAS6, HAND1, IFI202B, ISL1, KIAA1524, KRT74, MIRN31, MUS81, MYF6, MYOD1, NFYB, OTX1, PRIMA1, QKI, RBM9, RBPMS, RORA, SHOX2, SLC39A8, SOX2, SOX15, ST8SIA4, STAT3, TWIST1, VPS39, ZFHX3	18	15	CHPT1	CNTN4, ELOVL7, HAND1, ODS2, SOX2, TWIST1	ARHGAP9, CDH10	CNTN4, ELOVL7, EME1, FGFR, KIAA1524, PRIMA1, RBPMS, ST8SIA4, TWIST1
B	11	ALDH3A2, B3GALT2, BAMBI, CNN2, CTNNAL1, CTNNB1, CTSC, CUGBP2, DYNLT3, IL13, KIF18A, LIN7C, MFI2, MPP5, MRC2, NDST1, PDGF-CC, PHLDA2, PLAU, PPM1J, PPP1CA, PTPN14, PTPRM, SLC16A3, SLC26A2, SLC43A3, SLC7A2, SSH2, STK17A, TAX1BP3, TCF7L1, TGFB1, TPTE, TSPAN8	18	15	PHLDA2	BAMBI, CUGBP2, DYNLT3, SLC7A2, SLC43A3, STK17A, TPTE	—	DYNLT3, KIF18A, PTPRM, SLC7A2, SLC43A3, SSH2, STK17A, TPTE
—	12	AHR, AHRR, ANLN, APH1B, ARHGAP24, ASPM, BUB1, CCDC99,	17	15	HS3ST1	PDZRN3, PVRL3	—	ANLN, ARHGAP24, ASPM, BUB1, CCDC99,

		CEP55, CKAP2, DRAM, E2F8, HS3ST1, JPH1, MIRN124-1, NMT2, PDZRN3, PLXNA2, PMM1, PPP1R13L, PVRL3, RFFL, S100A2, SLC16A10, TP53, UBE2A, UBE2C, UBE2D2, UBE2S, UBE2V1, UBE2V2, UBL3, VPS37C, WDHD1						CEP55, CKAP2, DRAM, E2F8, PLXNA2, SLC16A10, UBE2C, UBE2S, WDHD1
—	13	ARHGEF3, CALY, CSH2, CTSL2, DIAPH3, ECEL1, FBP1, FFAR2, FRAT2, GSK3B, HSD17B4, IL6, IL19, KIF11, KIF2C, KNG1, LARGE, LEFTY2, LGR5, LIF, LPAR3, MPZ, MSLN, ORM2, PFKFB3, PLK4, PMP22, PRPH, PRSS8, PTGER3, SCN7A, SCNN1B, SLC4A11, TAL1	17	14	CALY	ARHGEF3, GSK3B, RMP22	CALY	ARHGEF3, CTSL2, DIAPH3, FBP1, KIF2C, KIF11, PFKFB3, PLK4
—	14	AGT, AGTRAP, Beta ARK, CADPS, CD160, COL5A1, CPNE8, FNDC5, HSPC159, INA, ITGA7, LIMA1, LPP, MAB21L2,	15	13	CPNE3	CADPS, FNDC5, MAB21L2, SLITRK5, ST8SIA2	COL5A1, MICAL2	FNDC5, HSPC159, MAB21L2, SLITRK5, SYN2, ZNF367

		MAPK1, MERTK. MICAL2, MIRN294, MIRN185, MIRN352, NTN1, PLCG1, PLCG2, PTGFR, RASGEF1B, RBM4B, RSU1, SKAP1, SLITRK5, SPRED1, ST8SIA2, SYN2, TGFB3, TNS1, ZNF367						
—	15	ACT1, BAG5, CPVL, EXO1, GIPC1, GJC1, GPR37, HSPA5, HSPA1A, HSPBP1, IkBKB, KCTD12, MAP3K3, MAP3K14, MEKK3/NIK, MIRN30B, MYO6, OLFML2A, PELI3, RHEBL1, RNF126, RPL10A, RPN1, SEC16A, SHC1, SHCBP1, SIGIRR, TJP3, TPBG, TRAF6, TRAF2-TRAF5, TRAF2-TRAF5, TRAF6, TUBB6, TUBB2B	15	13	—	KCTD12, TPBG	OLFML2A, SIGIRR	EXO1, KCTD12, MYO6, PHEBL1, SHCBP1, TPBG, TUBB6
B	16	ABCC8, BACE2, CLASP1, COLEC12, CXCR7, DACT1, ENTPD5, FGD6, FMO1, GSTT1, IL17B, KRT34, KYNU, LAMP3,	15	13	IL17B	DACT1, PCDH8	ABCC8, IL17B, NEEBL	MMD, OSBPL3, SYNPO2

		LMCD1, MIRN101B. MMD, NEBL, NFRKB, OSBPL3, PCDH8, PEMT, RASAL2, SAMD4A, ST3GAL3, SYNGR3, SYNPO2, TNF, TNNC1, TXN2, YWHAG, ZNF267, ZYX						
—	17	ARPP-19, BTG3, CBFA2T2, CBLN1, CNGA2, EBF1, EGF, EGFR, GABA, GABRA5, GABRB3, GABRD, GABRR1, HDAC9, HPCAL1, HTT, IDS, INSL3, LPAR5, OPRL1, PCDH9, PDE10A, PDE11A, PDE1A, PDE1B, PDE2A, PDE4C, PDE6H, PPAP2B, PPP1R1B, ROBO2, SH3D2C1, TRIP10, ZNF521	14	13	HPCAL1	PPAP2B	HPCAL1, LPAR5	BTG3, GABRA5, TRIP10, ZNF521
A	18	ANXA2, AQP1, C11ORF82, CCNI, CDKN2A, DEFB104A, DEFB4, EGLN3, ERAP1, FAM129A, GNAO1, IFNG, IL1B, IL1F7, INCA, LOC729667,	14	12	AQP1, CDKN2A	MINA, PDE5A	ANXA2, CDKN2A, ERAP1, RGS11	C11ORF82, MELK, MINA, PDE5A, SCLY, SLC1A3, TMEM35

		MELK, MINA, MIRN210, MPA2L, MYC, NNAT, PDE5A, RGS11, RNASE7, RT1-B, SCLY, SCUBE1, SLC11A1, SLC14A1, SLC1A3, ST18, TSH, TMEM35, TREM3						
—	19	BIRC8, BNC2, CASP5, CASP10, CASP14, CASP, CBLN2, DEDD2, DNASE1L1, DPYD, DSG3, EIF4E, EMILIN2, HTR1D, HTR1E, HTR1F, HTR3A, IFT57, KHDC1, MIRN20A, MTCH1, NGFR, PLXNA4, PPIL5, RB1, RP11-257K9.7, SEMA6D, SERPINA3K, SORCS1, STK25, SYT5, TACC3, TERT	10	10	—	EMILIN2, PLXNA4	HTR1E, SORCS1	BNC2, DPYD, EMILIN2, PPIL5, TACC3
—	20	EGFL7, GFI1B	2	1	—	—	—	—
—	21	AGRN, PRSS12	2	1	—	—	—	—
—	22	KCNB1, KCNG3	2	1	—	—	—	—
—	23	NUP37, NUP43	2	1	—	—	—	—
—	24	HS6ST1, HS6ST2	2	1	—	—	—	—
—	25	FUCA1, FUCA2	2	1	—	—	—	—
—	26	IQGAP, IQGAP3, MIRN339	2	1	—	—	—	—

Example V

Pathway Analysis of Gene Expression Profiles from Clonal Cell Lines

[0186] The following example illustrates how to characterize gene expression profiles from clonal cells from an established clonal cell line that are susceptible to BoNT/A intoxication or have neurotoxin uptake capacity in order to identify biological networks or pathways associated with BoNT/A intoxication.

[0187] Computer analysis was performed to characterize the RNA expression phenotype of two independently derived single clone cell lines, BB10 and H1, very sensitive to BoNT/A activity and a single clone cell line, 2D6, that was less sensitive BoNT/A activity. The results are useful in identifying clonal cell lines selected from the SiMa parental cell line that are useful to practice the methods disclosed in the present specification.

[0188] To identify the specific gene expression phenotype associated with a BoNT/A sensitive cell line, the data was analyzed using JMP Genomic (SAS Institute Inc., Cary, NC). To perform a JMP Genomics analysis, the RNA expression data was imported to JMP Genomics by creating two SAS files, designated "data" and "Experiment design." A basic expression workflow was performed, including a variance analysis and one-way analysis of variance (one-way ANOVA) to identify differences in mean expression values. The variance analysis was used to identify differences between the cell lines and the differentiation state of each cell line (differentiated or non-differentiated). The expression values of all four cell lines were compared pair wise, independent of differentiation and genes that were ≥ 4-fold over-expressed in the H1 cell line as compared to the 2D6 cell line, in the BB10 cell line as compared to the 2D6 cell line, and in SiMa parental cell line (PA) compared to the 2D6 cell line. The variance analysis treats all factors in the study as random effects, to find out what their contribution is to the proportion of variance explained (total variance = 100%). About half of the variance, 46.9% was assigned to differences among the different cell types, while 26% was assigned to differences before and after differentiation. Only 4.6% of the variance was assigned to differences among differentiated or non-differentiated cells types, meaning that the genes that were differentially expressed after differentiation were similar for all cell types examined, suggesting that the difference in BoNT/A sensitivity among the cell lines is independent of differentiation state. As such, the focus was placed on genes that are different among the different cells types irrespective of differentiation.

[0189] Based on the results from the variance analysis, the expression values of all cell lines were compared pair wise, independent of differentiation (FIG. 2). Only gene probes that were ≥ 4-fold over-expressed in the H1 cell line as compared to the 2D6 cell line, and in the BB10 cell line as compared to the 2D6 cell line are shown. The gene probes were plotted as expression value (Log_2) on the x-axis and p-value ($-log_{10}$(p-value)) on the y-axis. The red dashed line marks the 95% confidence interval. The genes probes that were ≥ 4-fold over-expressed in the H1 cell line as compared to the 2D6 cell line (FIG. 2A), and the BB10 cell line as compared to the 2D6 cell line (FIG. 2B), were also to a large extend among

the genes that were over-expressed in the BB10 cell line as compared to the SiMa parental cell line (PA, FIG. 2C), in the H1 cell line as compared to the SiMa parental cell line (FIG. 2D), and in the SiMa parental cell line as compared to the 2D6 cell line (FIG. 2E). These data suggest that BoNT/A sensitivity was related to a gradual increase in expression of these genes. Based on this finding, the number of gene probes was further narrowed down to 119 by including only gene probes that were also over-expressed in the SiMa parental cell line compared to the 2D6 cell line, rationalizing that gene probes that were differential expressed across one more cell line would be even more likely to be important for BoNT/A sensitivity. As such, the JMP Genomic analysis resulted in the identification of 119 gene probes, designated the JMP probe set.

[0190] The JMP probe set was exported to Ingenuity Pathway Analysis (IPA) Core Analysis (Ingenuity Systems Inc., Redwood City, CA) to further characterize the JMP probe set. Using this analysis, biologically relevant networks to BoNT/A intoxication were identified based on connectivity among the genes from an IPA library and the gene probes contained in the JMP probe set. The significance of the association to a given network was measured and ranked by the ratio of the number of gene probes from the JMP probe set that mapped to the specific network divided by the total number of genes that map to that network. Fisher's exact test was used to calculate p-scores, and based on the p-scores the genes from the JMP probe set were used to rank the networks. The p-scores were derived from p-values. If there are *n* genes in the network and *f* of them are gene probes from the JMP probe set, then the p-value is the probability of finding *f* or more gene probes from the JMP probe set in a set of *n* genes randomly selected from the Global Molecular Network. Since significant p-values are quite low (*e.g.*, 1×10^{-6}), a p-score was defined as the component of the p-value; p-score = -log10 (p-value). The identified networks were overlaid with differentially expressed genes which had more than 1.5-fold differential expression and a p-value ≤ 0.001 either before or after differentiation. Using IPA Core Analysis, 111 of the 119 gene probes from the JMP probe set were mapped to networks. The eight unmapped probes most likely represent either a probe with an outdated nomenclature or one representing a gene without a known gene product. The 111 gene probes corresponded to 79 genes that were greater than 4.0-fold differentially expressed in the H1 and BB10 cell lines when compared to the 2D6 cell line and that were also greater than 4.0-fold differentially expressed in the SiMa parental cell lines when compared to the 2D6 cell line, when the p-value cut off was set to 0.05 (Table 14).

Table 14. Genes Identified using IPA Core Analysis

Gene Name	Gene Symbol	Probe ID. No.	Location	Type	Log Ratio
Achaete-scute complex homolog 1	ASCL1	209985_s_at	Nucleus	Transcription regulator	4.469
Achaete-scute complex homolog 1	ASCL1	209988_s_at	Nucleus	Transcription regulator	2.774
Achaete-scute complex homolog 1	ASCL1	213768_s_at	Nucleus	Transcription regulator	2.955

Acyl-CoA thioesterase 9	ACOT9	221641_s_at	Cytoplasm	Enzyme	2.251
ADAM metallopeptidase with thrombospondin type 1 motif, 9	ADAMTS9	226814_at	Extracellular Space	Peptidase	4.034
Ankyrin 2, neuronal	ANK2	216195_at	Plasma Membrane	Other	-2.673
Ankyrin 2, neuronal	ANK2	232606_at	Plasma Membrane	Other	-2.621
Blood vessel epicardial substance	BVES	228783_at	Plasma Membrane	Other	3.174
Brain abundant, membrane attached signal protein 1	BASP1	202391_at	Plasma Membrane	Other	4.549
BRCA1 associated RING domain 1	BARD1	205345_at	Nucleus	Transcription regulator	3.44
Calsyntenin 2	CLSTN2	219414_at	Plasma Membrane	Transporter	2.024
cAMP responsive element binding protein 5	CREB5	232555_at	Nucleus	Transcription	-2.67
Cathepsin L2	CTSL2	210074_at	Cytoplasm	Peptidase	2.119
CD9 molecule	CD9	201005_at	Plasma Membrane	Other	2.887
Cell division cycle associated 7-like	CDCA7L	225081_s_at	Nucleus	Other	3.737
Centromere protein L	CENPL	1554271_a_at	Unknown	Other	2.582
Chromosome 11 open reading frame 75	C11ORF75	219806_s_at	Unknown	Other	3.914
Chromosome 3 open reading frame 70	C3ORF70	242447_at	Unknown	Other	2.705
Coiled-coil domain containing 109B	CCDC109B	218802_at	Unknown	Other	2.881
Contactin 1	CNTN1	211203_s_at	Plasma Membrane	Enzyme	3.684
Contactin 1	CNTN1	227202_at	Plasma Membrane	Enzyme	3.184
Contactin 1	CNTN1	227209_at	Plasma Membrane	Enzyme	3.188
Copine VIII	CPNE8	228365_at	Unknown	Other	-3.355
Copine VIII	CPNE8	241706_at	Unknown	Other	-2.736
CUG triplet repeat, RNA binding protein 2	CUGBP2	202157_s_at	Nucleus	Other	3.588
Cyclin-dependent kinase 2	CDK2	204252_at	Nucleus	Kinase	2.744
Cysteine and glycine-rich protein 2	CSRP2	207030_s_at	Nucleus	Other	2.487

Cysteine and glycine-rich protein 2	CSRP2	211126_s_at	Nucleus	Other	2.109
DEP domain containing 1	DEPDC1	220295_x_at	Unknown	Other	2.795
Diaphanous homolog 3	DIAPH3	232596_at	Cytoplasm	Enzyme	2.434
Dihydropyrimidine dehydrogenase	DPYD	204646_at	Cytoplasm	Enzyme	4.248
Docking protein 5	DOK5	214844_s_at	Plasma Membrane	Other	4.56
Dynein, light chain, Tctex-type 3	DYNLT3	203303_at	Cytoplasm	Other	3.449
Elastin microfibril interfacer 2	EMILIN2	224374_s_at	Extracellular Space	Other	2.603
Ets variant 1	ETV1	206501_x_at	Nucleus	Transcription regulator	2.578
Ets variant 1	ETV1	217053_x_at	Nucleus	Transcription regulator	2.499
Ets variant 1	ETV1	217061_s_at	Nucleus	Transcription regulator	2.557
Family with sequence similarity 101, member B	FAM101B	226876_at	Unknown	Other	2.399
Fibroblast growth factor receptor 2	FGFR2	203638_s_at	Plasma Membrane	Kinase	2.306
Fibroblast growth factor receptor 2	FGFR2	203639_s_at	Plasma Membrane	Kinase	3.239
Fibroblast growth factor receptor 2	FGFR2	208228_s_at	Plasma Membrane	Kinase	2.151
Fibronectin type III domain containing 5	FNDC5	226096_at	Unknown	Other	2.054
Fibulin 1	FBLN1	201787_at	Extracellular Space	Other	2.801
Fibulin 1	FBLN1	202994_s_at	Extracellular Space	Other	2.378
Fibulin 1	FBLN1	202995_s_at	Extracellular Space	Other	3.733
G protein-coupled receptor 177	GPR177	221958_s_at	Unknown	Other	2.389
G protein-coupled receptor 177	GPR177	228950_s_at	Unknown	Other	2.622
G-2 and S-phase expressed 1	GTSE1	204317_at	Cytoplasm	Other	3.334
Gametocyte specific factor 1	GTSF1	227711_at	Unknown	Other	6.407
Guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	GNAI1	227692_at	Plasma Membrane	Enzyme	3.123
Guanine nucleotide binding protein (G protein), beta polypeptide 4	GNB4	225710_at	Plasma Membrane	Enzyme	6.066

Guanine nucleotide binding protein (G protein), gamma 11	GNG11	204115_at	Plasma Membrane	Enzyme	4.251
Guanine nucleotide binding protein (G protein), gamma 12	GNG12	212294_at	Plasma Membrane	Enzyme	2.315
Guanine nucleotide binding protein (G protein), gamma 12	GNG12	222834_s_at	Plasma Membrane	Enzyme	3.403
Hepatocyte growth factor (hepapoietin A)	HGF	209960_at	Extracellular Space	Growth factor	2.939
Hypothetical protein LOC100289109	LOC100289 109	216189_at	Unknown	Other	-3.256
Hypothetical protein LOC144571	LOC144571	1564139_at	Unknown	Other	-2.394
Inositol 1,4,5-triphosphate receptor interacting protein	ITPRIP	225582_at	Unknown	Other	3.522
Interleukin 17B	IL17B	220273_at	Extracellular Space	Cytokine	-4.735
KDEL (Lys-Asp-Glu-Leu) containing 2	KDELC2	225128_at	Unknown	Other	3.003
KIAA0125	KIAA0125	206478_at	Unknown	Other	-8.436
KIT ligand	KITLG	226534_at	Extracellular Space	Growth factor	2.59
LY6/PLAUR domain containing 6	LYPD6	227764_at	Extracellular Space	Other	2.64
Lysophosphatidic acid receptor 1	LPAR1	204036_at	Plasma Membrane	Receptor	3.151
MAB-21-like 2	MAB21L2	210303_at	Unknown	Other	3.817
Minichromosome maintenance complex component 10	MCM10	223570_at	Nucleus	Other	2.249
Moesin	MSN	200600_at	Plasma Membrane	Other	5.842
Monoamine oxidase A	MAOA	204388_s_at	Cytoplasm	Enzyme	4.029
Monoamine oxidase A	MAOA	204389_at	Cytoplasm	Enzyme	3.355
Monoamine oxidase A	MAOA	212741_at	Cytoplasm	Enzyme	4.157
MYC induced nuclear antigen	MINA	213188_s_at	Nucleus	Other	4.019
MYC induced nuclear antigen	MINA	213189_at	Nucleus	Other	4.636
Myosin VI	MYO6	203216_s_at	Cytoplasm	Other	2.406
Myosin VIIA and Rab interacting protein	MYRIP	214156_at	Cytoplasm	Other	2.805
Neuronal PAS domain protein 4	NPAS4	1554299_at	Nucleus	Transcription regulator	-2.515
Paternally expressed 3	PEG3	209242_at	Nucleus	Kinase	5.896
Paternally expressed 3	PEG3	209243_s_at	Nucleus	Kinase	4.556

Phosphoprotein associated with glycosphingolipid microdomains 1	PAG1	225626_at	Plasma Membrane	Other	2.193
Poliovirus receptor-related 3	PVRL3	213325_at	Plasma Membrane	Other	2.325
Polo-like kinase 2	PLK2	201939_at	Nucleus	Kinase	4.93
Polymerase (DNA directed), alpha 2 (70kD subunit)	POLA2	204441_s_at	Nucleus	Enzyme	2.196
Prolactin releasing hormone receptor	PRLHR	231805_at	Plasma Membrane	Receptor	3.19
Prostaglandin reductase 1	PTGR1	228824_s_at	Cytoplasm	Enzyme	2.398
Prostaglandin reductase 1	PTGR1	231897_at	Cytoplasm	Enzyme	2.33
Protease, serine, 12 (neurotrypsin, motopsin)	PRSS12	205515_at	Extracellular Space	Peptidase	5.146
Protein phosphatase 1, regulatory (inhibitor) subunit 3C	PPP1R3C	204284_at	Cytoplasm	Phosphatase	2.827
Protein tyrosine phosphatase, receptor type, K	PTPRK	203038_at	Plasma Membrane	Phosphatase	3.451
RAB32, member RAS oncogene family	RAB32	204214_s_at	Cytoplasm	Other	2.192
RELT-like 1	RELL1	226430_at	Unknown	Other	2.88
Rho GTPase activating protein 24	ARHGAP24	223422_s_at	Cytoplasm	Other	3.043
Rho guanine nucleotide exchange factor (GEF) 3	ARHGEF3	218501_at	Cytoplasm	Other	2.473
Ring finger protein 182	RNF182	230720_at	Unknown	Other	4.746
RNA binding protein with multiple splicing	RBPMS	209487_at	Unknown	Other	2.329
RNA binding protein with multiple splicing	RBPMS	209488_s_at	Unknown	Other	3.292
Secreted protein, acidic, cysteine-rich (osteonectin)	SPARC	200665_s_at	Extracellular Space	Other	4.919
Secreted protein, acidic, cysteine-rich (osteonectin)	SPARC	212667_at	Extracellular Space	Other	4.58
Shugoshin-like 2	SGOL2	230165_at	Nucleus	Other	3.108
Similar to hCG2031213	LOC728052	1558795_at	Unknown	Other	3.402
Solute carrier family 1 (glial high affinity glutamate transporter), member 2	SLC1A2	225491_at	Plasma Membrane	Transporter	-4.354
Solute carrier family 43, member 3	SLC43A3	210692_s_at	Extracellular Space	Other	3.126
Solute carrier family 43, member 3	SLC43A3	213113_s_at	Extracellular Space	Other	2.804
Solute carrier family 44, member	SLC44A5	1569112_at	Unknown	Other	3.923

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Solute carrier family 44, member 5	SLC44A5	235763_at	Unknown	Other	4.439
Solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	SLC7A2	225516_at	Plasma Membrane	Transporter	3.23
Sortilin-related VPS10 domain containing receptor 1	SORCS1	1556891_at	Plasma Membrane	Transporter	-2.424
SPC25, NDC80 kinetochore complex component, homolog	SPC25	209891_at	Unknown	Other	2.634
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	ST8SiA4	230836_at	Cytoplasm	Enzyme	2.705
Structural maintenance of chromosomes 2	SMC2	204240_s_at	Nucleus	Transporter	2.442
Structural maintenance of chromosomes 6	SMC6	218781_at	Nucleus	Other	3.327
Structural maintenance of chromosomes 6	SMC6	236535_at	Nucleus	Other	3.44
Syndecan 2	SDC2	212154_at	Plasma Membrane	Other	2.367
Syndecan 2	SDC2	212158_at	Plasma Membrane	Other	2.098
Thrombospondin 2	THBS2	203083_at	Extracellular Space	Other	-2.81
Thyroid hormone receptor interactor 10	TRIP10	202734_at	Cytoplasm	Other	2.663
Tissue factor pathway inhibitor 2	TFPI2	209278_s_at	Extracellular Space	Other	4.666
Transcription factor 7-like 1 (T-cell specific, HMG-box)	TCF7L1	221016_s_at	Nucleus	Transcription regulator	2.835
Transmembrane phosphatase with tensin homology	TPTE	220205_at	Plasma Membrane	Phosphatase	6.04
Transmembrane protein 178	TMEM178	229302_at	Unknown	Other	3.194
Transmembrane protein 35	TMEM35	219685_at	Unknown	Other	2.879
Tumor necrosis factor, alpha-induced protein 8	TNFAIP8	210260_s_at	Cytoplasm	Other	2.389
Twist homolog 1	TWIST1	213943_at	Nucleus	Transcription regulator	2.573
Zinc finger protein 521	ZNF521	226676_at	Nucleus	Other	2.382
Zinc finger protein 521	ZNF521	226677_at	Nucleus	Other	2.943
Zinc finger protein 814	ZNF814	1556204_a_at	Unknown	Other	-2.505
The log ratio represent log_2 values where 0.585 is $log_2(1.5)$ which is a 1.5-fold difference, 1 is $log_2(2)$					

which is a 2-fold difference, 1.584 is $\log_2(3)$ which is a 3-fold difference, 2 is $\log_2(4)$ which is a 4-fold difference, 2.321 is $\log_2(5)$ which is a 5-fold difference, 2.584 is $\log_2(6)$ which is a 6-fold difference, 2.807 is $\log_2(7)$ which is a 7-fold difference, 3 is $\log_2(8)$ which is a 8-fold difference, 3.169 is $\log_2(9)$ which is a 9-fold difference, and 3.321 is $\log_2(10)$ which is a 10-fold difference.

[0191] Using IPA Core Analysis, 73 of the 79 genes were mapped to 5 different protein networks (Table 15). Based on overlapping gene mapping, 73 of the 79 genes that were up-regulated could be associated with two major protein network groups, named A and B (Table 15). Networks 1, 2 and 5 belong to Group A, and Networks 3 and 4 belong to Group B. Similarly, all down-regulated genes were all associated with one network, named C (Table 15).

Group A genes include the FGFR2 receptor which has been shown to function in the BoNT/A intoxication process as a receptor for BoNT/A and are as follows: genes exhibiting a 1.5-fold or more increase in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, ADAMTS9, ARHGAP24, ARHGEF3, ASCL1, BARD1, CD9, CDK2, CSRP2, CTSL2, DIAPH3, DOK5, DYNLT3, EMILIN2, ETV1, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, HGF, KITLG, LPAR1, MCM10, MSN, PAG1, PEG3, PLK2, POLA2, PPP1R3C, PTPRK, RAB32, SDC2, SLC43A3, SLC7A2, SMC6, SPARC, SPC25, ST8SIA4, TCF7L1, TFPI2, TMEM35, TNFAIP8, TPTE, TRIP10, and TWIST1.

[0192] Group B genes are as follows: genes exhibiting a 1.5-fold or more increase in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, ACOT9, BASP1, C11ORF75, CCDC109B, CDCA7L, CLSTN2, CNTN1, CUGBP2, DEPDC1, DPYD, FAM101B, FNDC5, GTSE1, MAOA, MINA, MYO6, MYRIP, PLK2, PRLHR, PVRL3, RBPMS, SGOL2, SMC2, TPP12, TMEM178, and ZNF521.

[0193] Group C genes are as follows: genes exhibiting a 1.5-fold or more decrease in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line, ANK2, CPNE8, CREB5, IL17B, KIAA0125, LOC100289109, LOC144571, NPAS4, SLC1A2, SORCS1, THBS2, and/or ZNF814.

[0194] The remaining networks identified did not share common genes between any other network. Individually, however, genes exhibiting a 1.5-fold or more increase in expression levels in the H1 and BB10 cell lines as compared to their expression in cells from the 2D6 cell line were as follows: C3ORF70 (Network 6), MAB21L2 (Network 7), PRSS12 (Network 8), CENPL (Network 9), GPR177 (Network 10), and PTGR1 (Network 11).

Table 15. IPA Core Analysis of Genes

Network	Group	Proteins in Network	pvalue	JMP Gene Number	Expression Profile	
					Increased	Decreased
1	A	ADAMTS9, AKT, ASCL1, CDK2, CSRP2, CTSL2, DOK5, E2F, FBLN1, FSH, GNAI1, GNG11, hCG, HGF, KITLG, LPAR1, MAPK, MCM10, MEK, MSN, NFκB, P38, MAPK, PAG1, PDGF BB, PEG3, PLK2, RAC, RAS, SDC2, SPARC, TFPI2, TGFβ, TNFAIP8, TRIP10, VEGF	48	22	ADAMTS9, ASCL1, CDK2, CSRP2, CTSL2, DOK5, FBLN1, GNAI1, GNG11, HGF, KITLG, LPAR1, MCM10, MSN, PAG1, PEG3, PLK2, SDC2, SPARC, TFPI2, TNFAIP8, TRIP10	—
2	A	CASP3, Caspase 3/7, CCL6, DIAPH3, DYNLT3, EMILIN2, EPM2A, ETV1, EYA2, FAM3B, FASTK, GNAI1, GNB4, GNG10, GNG11, GNG12, GSTM2, HK1, IGFBP3, IL13, PLCE1, POLA2, PPP1R3C, PTPRK, PTPRZ1, RAB32, SLC43A3, SLC7A2, SRC, ST8SIA4, TNF, TPTE, TWIST1	35	17	DIAPH3, DYNLT3, EMILIN2, ETV1, GNAI1, GNB4, GNG11, GNG12, POLA2, PPP1R3C, PTPRK, RAB32, SLC43A3, SLC7A2, ST8SIA4, TPTE, TWIST1	—
3	B	ACOT9, AR, ATXN7, BASP1, CCNE2, CCNK, CLSTN2, CNTN1, CUGBP2, DGKA, FNDC5, GTSE1, IL4, MAOA, MSH2, NOVA1, NF1, PICK1, PLK2, PNRC1, POM121, PRLHR, PTP4A1, PTP4A2, PVRL1, PVRL3, PVRL4, RBPMS, SERPINB5, SMARCA4, SPN, TFP12, TP53, ZNF521	26	14	ACOT9, BASP1, CLSTN2, CNTN1, CUGBP2, FNDC5, GTSE1, MAOA, PLK2, PRLHR, PVRL3, RBPMS, TFP12, ZNF521	—
4	B	ARHGAP17, AXL, C11ORF75, CAPN6, CCDC109B, CDCA7L, DEPDC1, DPYD, EIF4E, FAM101B, GRB2, HNRNPF, HTATIP2, MAOA, MINA, MIR124, MIRLET7A1, MYC, MYO6, MYRIP, NCAPD3, NF2, PPP2R5A, PPP2R5D, PPP2R5E, RPS16, RPS23, SGOL2, SLC25A12, SMC2, SMC4, TMEM178, TUSC2, TXNIP, ZBTB16	24	13	C11ORF75, CCDC109B, CDCA7L, DEPDC1, DPYD, FAM101B, MAOA, MINA, MYO6, MYRIP, SGOL2, SMC2, TMEM178	—
5	A	ARHGAP24, ARHGEF,	17	10	ARHGAP24,	

		ARHGEF3, BARD1, CD9, CD53, CTNNB1, DUSP3, ERK, ERM, FGF9, FGF18, FGF21, FGF23, FGFR2, IL1, IL6, IL17RD, Integrinα6β1, KLB, LEF/TCF, LPAR1, MIRN297-2, PI3K, RAS homolog, RNAPOLII, SLC26A2, SMC6, SPC25, SREBF1, TACC1, TCF7L1, TMEM35, TPT1, WISP1			ARHGEF3, BARD1, CD9, FGFR2, LPAR1, SMC6, SPC25, TCF7L1, TMEM35	
6	—	C3ORF70, MIR31	2	1	C3ORF70	—
7	—	MAB21L2, MIRN294	2	1	MAB21L2	—
8	—	AGPN, PRSS12	2	1	PRSS12	—
9	—	CENPL, MIRN340	2	1	CENPL	—
10	—	GPR177, MIRN324	2	1	GPR177	—
11	—	ADH, PTGR1	2	1	PTGR1	—
12	C	ANK2, ATP2A2, BDNF, CEBPG, CPNE8, CREB5, GRM3, GRM5, IGFBP2, IL17B, ITPR, ITPR1, K+, L1CAM, MIRN330, Neurotrophin, NFE2L1, NGFR, NME1, NPAS4, Pro-Inflammatory Cytokine, PSEN1, SCN2A, SCN3A, SCNN1B, SLC1A2, SLC8A1, SORCS1, SORT1, TGFA, THBS2, TNF, TNFAIP6	22	8	—	ANK2, CPNE8, CREB5, IL17B, KIAA0125, LOC100289109, LOC144571, NPAS4, SLC1A2, SORCS1, THBS2, ZNF814

[0195] Computer analysis was performed as in Example V, except that the list of probes reflects genes that were greater than 1.5-fold differential expressed in the H1 and the BB10 cell lines when compared to both the 2D6 and SiMa parental cell lines. When the p-value cut off was set to 0.05, this analysis identified 439 gene probes that could be classified to 369 genes (Table 16).

Table 16. Genes Identified using IPA Core Analysis

Gene Name	Gene Symbol	Probe ID. No.	Location	Type	Log Ratio
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	PFKFB3	202464_s_at	Cytoplasm	kinase	1.811
achaete-scute complex homolog 1	ASCL1	209985_s_at	Nucleus	transcription regulator	2.429
achaete-scute complex homolog 1	ASCL1	209987_s_at	Nucleus	transcription regulator	2.097
achaete-scute complex homolog 1	ASCL1	209988_s_at	Nucleus	transcription regulator	1.446
achaete-scute complex homolog 1	ASCL1	213768_s_at	Nucleus	transcription regulator	1.578
activated leukocyte cell adhesion molecule	ALCAM	1569362_at	Plasma Membrane	other	2.612

activated leukocyte cell adhesion molecule	ALCAM	201951_at	Plasma Membrane	other	1.774
activated leukocyte cell adhesion molecule	ALCAM	201952_at	Plasma Membrane	other	1.521
acyl-CoA thioesterase 1	ACOT1	202982_s_at	Cytoplasm	enzyme	-2.875
acylphosphatase 2, muscle type	ACYP2	200833_s_at	unknown	enzyme	-1.15
additional sex combs like 3	ASXL3	233536_at	unknown	other	1.572
adenosine deaminase, RNA-specific, B1	ADARB1	203865_s_at	Nucleus	enzyme	-2.474
adenylate cyclase 1	ADCY1	213245_at	Plasma Membrane	enzyme	-1.935
adipocyte-specific adhesion molecule	ASAM	228082_at	Plasma Membrane	other	-2.802
ADP-ribosylation factor 1	ARF1	1565651_at	Cytoplasm	enzyme	1.063
ADP-ribosylation factor-like 17A	ARL17A	243899_at	unknown	other	0.741
anaphase promoting complex subunit 7	ANAPC7	225554_s_at	unknown	other	0.679
ankyrin repeat and BTB (POZ) domain containing 1	ABTB1	229164_s_at	Cytoplasm	translation regulator	-0.656
ankyrin repeat domain 50	ANKRD50	225731_at	unknown	other	-0.654
ankyrin repeat domain 50	ANKRD50	225735_at	unknown	other	-1.114
aspartate beta-hydroxylase domain containing 1	ASPHD1	214993_at	unknown	other	-0.763
ataxin 2-binding protein 1	A2BP1	1553422_s_at	Cytoplasm	other	1.453
ataxin 2-binding protein 1	A2BP1	221217_s_at	Cytoplasm	other	1.497
ATPase, Ca++ transporting, plasma membrane 3	ATP2B3	207026_s_at	Plasma Membrane	transporter	-1.248
ATPase, Ca++ transporting, plasma membrane 3	ATP2B3	242036_x_at	Plasma Membrane	transporter	-1.777
basonuclin 2	BNC2	220272_at	Nucleus	other	2.466
basonuclin 2	BNC2	230722_at	Nucleus	other	1.641
βγcrystallin domain containing 3	CRYBG3	214030_at	unknown	other	4.74
β-site APP-cleaving enzyme 1	BACE1	217904_s_at	Cytoplasm	peptidase	-1.57
brain abundant, membrane attached signal protein 1	BASP1	202391_at	Plasma Membrane	other	1.146
bromodomain and WD repeat domain containing 1	BRWD1	225446_at	Nucleus	transcription regulator	-1.018

bruno-like 4, RNA binding protein	BRUNOL4	238966_at	Nucleus	translation regulator	-0.81
butyrophilin, subfamily 3, member A3	BTN3A3	38241_at	unknown	other	-1.108
C2 calcium-dependent domain containing 2	C2CD2	212875_s_at	unknown	other	-1.27
C2 calcium-dependent domain containing 4A	C2CD4A	241031_at	unknown	other	-2.615
cadherin 12, type 2 (N-cadherin 2)	CDH12	207149_at	Plasma Membrane	other	-1.408
calcium/calmodulin-dependent protein kinase II inhibitor 2	CAMK2N2	230706_s_at	Nucleus	other	-0.692
calmin (calponin-like, transmembrane)	CLMN	213839_at	Cytoplasm	other	-1.911
calpain 2, (m/II) large subunit	CAPN2	208683_at	Cytoplasm	peptidase	-1.429
CAP, adenylate cyclase-associated protein, 2	CAP2	212551_at	Plasma Membrane	other	-1.974
CAP, adenylate cyclase-associated protein, 2	CAP2	212554_at	Plasma Membrane	other	-3.68
carboxypeptidase, vitellogenic-like	CPVL	208146_s_at	unknown	peptidase	1.708
CART prepropeptide	CARTPT	206339_at	Extracellular Space	other	-4.676
Cas-Br-M (murine) ecotropic retroviral transforming sequence b	CBLB	209682_at	Nucleus	other	1.032
CCR4-NOT transcription complex, subunit 6-like	CNOT6L	227119_at	Cytoplasm	other	-0.785
CD302 molecule	CD302	203799_at	Plasma Membrane	receptor	-1.518
CD9 molecule	CD9	201005_at	Plasma Membrane	other	1.415
CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1	CDS1	226185_at	Cytoplasm	enzyme	-1.74
cell division cycle 25 homolog B (S. pombe)	CDC25B	201853_s_at	Nucleus	phosphatase	1.453
chemokine (C-X-C motif) receptor 4	CXCR4	209201_x_at	Plasma Membrane	receptor	4.135
chemokine (C-X-C motif) receptor 4	CXCR4	211919_s_at	Plasma Membrane	receptor	3.957
chemokine (C-X-C motif) receptor 4	CXCR4	217028_at	Plasma Membrane	receptor	3.176

chloride channel 3	CLCN3	201733_at	Plasma Membrane	ion channel	-0.908
chloride channel 3	CLCN3	201734_at	Plasma Membrane	ion channel	-0.987
cholinergic receptor, nicotinic, alpha 7	CHRNA7	210123_s_at	Plasma Membrane	receptor	3.098
chromosome 1 open reading frame 21	C1ORF21	221272_s_at	unknown	other	-0.74
chromosome 1 open reading frame 21	C1ORF21	223127_s_at	unknown	other	-0.748
chromosome 1 open reading frame 43	C1ORF43	1555225_at	unknown	other	1.604
chromosome 10 open reading frame 58	C10ORF58	224435_at	Extracellular Space	other	0.918
chromosome 12 open reading frame 49	C12ORF49	218867_s_at	unknown	other	0.692
chromosome 16 open reading frame 52	C16ORF52	230721_at	unknown	other	-0.87
chromosome 20 open reading frame 7	C20ORF7	227160_s_at	unknown	other	0.624
chromosome 21 open reading frame 57	C21ORF57	227421_at	unknown	other	-1.086
chromosome 21 open reading frame 57	C21ORF57	239208_s_at	unknown	other	-0.657
chromosome 3 open reading frame 23	C3ORF23	1555905_a_at	Cytoplasm	other	-2.797
chromosome 3 open reading frame 23	C3ORF23	1555906_s_at	Cytoplasm	other	-1.502
chromosome 3 open reading frame 23	C3ORF23	241666_at	Cytoplasm	other	-1.017
chromosome 9 open reading frame 150	C9ORF150	227443_at	unknown	other	-1.773
claudin 12	CLDN12	223249_at	Plasma Membrane	other	-0.766
COBW domain containing 1	CBWD1	226193_x_at	unknown	other	0.849
coiled-coil domain containing 3	CCDC3	223316_at	Cytoplasm	other	3.357
collagen, type VI, alpha 1	COL6A1	213428_s_at	Extracellular Space	other	-1.638
cripto, FRL-1, cryptic family 1	CFC1	223753_s_at	Extracellular Space	other	-2.834
cripto, FRL-1, cryptic family 1	CFC1	236724_at	Extracellular Space	other	-1.636

CSE1 chromosome segregation 1-like	CSE1L	210765_at	Nucleus	transporter	1.581
CUG triplet repeat, RNA binding protein 2	CUGBP2	202156_s_at	Nucleus	other	1.318
CUG triplet repeat, RNA binding protein 2	CUGBP2	202157_s_at	Nucleus	other	2.156
CUG triplet repeat, RNA binding protein 2	CUGBP2	202158_s_at	Nucleus	other	2.539
cyclic nucleotide gated channel alpha 3	CNGA3	207261_at	Plasma Membrane	ion channel	-3.182
cyclin M1	CNNM1	220166_at	Plasma Membrane	other	-1.214
cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	CDKN2A	209644_x_at	Nucleus	transcription regulator	-1.277
cylindromatosis (turban tumor syndrome)	CYLD	213295_at	Nucleus	transcription regulator	-0.815
cytochrome P450, family 2, subfamily E, polypeptide 1	CYP2E1	1431_at	Cytoplasm	enzyme	-4.466
cytochrome P450, family 2, subfamily E, polypeptide 1	CYP2E1	209975_at	Cytoplasm	enzyme	-3.946
cytochrome P450, family 2, subfamily E, polypeptide 1	CYP2E1	209976_s_at	Cytoplasm	enzyme	-3.429
cytoglobin	CYGB	1553572_a_at	Cytoplasm	transporter	-4.921
cytokine-like 1	CYTL1	219837_s_at	Extracellular Space	cytokine	-6.33
dapper, antagonist of beta-catenin, homolog 1	DACT1	219179_at	Cytoplasm	other	1.682
dCMP deaminase	DCTD	201572_x_at	unknown	enzyme	-0.649
DEAH (Asp-Glu-Ala-His) box polypeptide 35	DHX35	218579_s_at	unknown	enzyme	0.735
deleted in azoospermia 1	DAZ1	207909_x_at	Nucleus	translation regulator	6.92
deleted in azoospermia 1	DAZ1	207912_s_at	Nucleus	translation regulator	5.558
deleted in azoospermia 1	DAZ1	208281_x_at	Nucleus	translation regulator	5.258
deleted in azoospermia 1	DAZ1	208282_x_at	Nucleus	translation regulator	7.008
deleted in azoospermia 1	DAZ1	216351_x_at	Nucleus	translation regulator	3.596
deleted in azoospermia 1	DAZ1	216922_x_at	Nucleus	translation regulator	5.185

deleted in lymphocytic leukemia 2 (non-protein coding)	DLEU2	216870_x_at	unknown	other	1.233
delta-like 3 (Drosophila)	DLL3	219537_x_at	Extracellular Space	other	0.779
DNA segment on chromosome 4 (unique) 234 expressed sequence	D4S234E	209569_x_at	Cytoplasm	other	-1.247
DNA segment on chromosome 4 (unique) 234 expressed sequence	D4S234E	209570_s_at	Cytoplasm	other	-1.488
DNA segment on chromosome 4 (unique) 234 expressed sequence	D4S234E	213533_at	Cytoplasm	other	-1.507
dopamine beta-hydroxylase (dopamine beta-monooxygenase)	DBH	206450_at	Cytoplasm	enzyme	1.311
doublecortin-like kinase 1	DCLK1	215303_at	Cytoplasm	kinase	-1.62
dual specificity phosphatase 16	DUSP16	224832_at	Nucleus	phosphatase	-0.918
echinoderm microtubule associated protein like 1	EML1	204797_s_at	Cytoplasm	other	2.668
ectodermal-neural cortex (with BTB-like domain)	ENC1	201340_s_at	Nucleus	peptidase	2.445
ectodermal-neural cortex (with BTB-like domain)	ENC1	201341_at	Nucleus	peptidase	1.91
electron-transferring-flavoprotein dehydrogenase	ETFDH	33494_at	Cytoplasm	enzyme	-0.807
ELL associated factor 2	EAF2	219551_at	Nucleus	transcription regulator	0.693
ELOVL family member 7, elongation of long chain fatty acids	ELOVL7	227180_at	unknown	other	2.644
endoplasmic reticulum aminopeptidase 1	ERAP1	214012_at	Extracellular Space	peptidase	-1.885
enhancer of zeste homolog 2	EZH2	203358_s_at	Nucleus	transcription regulator	0.94
ephrin-A5	EFNA5	214036_at	Plasma Membrane	kinase	2.041
ephrin-A5	EFNA5	227955_s_at	Plasma Membrane	kinase	1.84
ephrin-A5	EFNA5	233814_at	Plasma Membrane	kinase	1.805
ephrin-B3	EFNB3	205031_at	Plasma Membrane	kinase	-0.816
eukaryotic translation initiation	EIF3C	236700_at	Cytoplasm	translation	1.378

factor 3, subunit C				regulator	
exophilin 5	EXPH5	214734_at	unknown	other	3.973
exosome component 6	EXOSC6	231916_at	Nucleus	other	1.057
family with sequence similarity 162, member B	FAM162B	228875_at	unknown	other	-0.743
family with sequence similarity 165, member B	FAM165B	228239_at	Plasma Membrane	other	-0.822
family with sequence similarity 181, member B	FAM181B	231430_at	unknown	other	0.794
family with sequence similarity 19 (chemokine (C-C motif)-like), member A4	FAM19A4	242348_at	Extracellular Space	other	1.282
family with sequence similarity 46, member A	FAM46A	224973_at	unknown	other	-1.509
family with sequence similarity 7, member A3	FAM7A3	243356_at	unknown	other	3.495
far upstream element (FUSE) binding protein 3	FUBP3	239193_at	Nucleus	transcription regulator	1.192
F-box and WD repeat domain containing 7	FBXW7	229419_at	Nucleus	transcription regulator	-0.921
fibroblast growth factor 13	FGF13	205110_s_at	Extracellular Space	growth factor	-3.522
follistatin-like 1	FSTL1	208782_at	Extracellular Space	other	-1.275
forkhead box O6	FOXO6	239657_x_at	Nucleus	other	-1.512
frizzled homolog 5	FZD5	221245_s_at	Plasma Membrane	receptor	2.347
FYVE, RhoGEF and PH domain containing 5	FGD5	226985_at	Cytoplasm	other	-1.952
G protein-coupled receptor 123	GPR123	239221_at	Plasma Membrane	receptor	-1.302
G protein-coupled receptor 125	GPR125	210473_s_at	Plasma Membrane	receptor	0.714
galanin prepropeptide	GAL	207466_at	Extracellular Space	other	-1.434
galanin prepropeptide	GAL	214240_at	Extracellular Space	other	-3.128
gastrin-releasing peptide	GRP	206326_at	Extracellular Space	growth factor	4.698
GDNF family receptor alpha 2	GFRA2	205721_at	Plasma Membrane	receptor	1.847
GDNF family receptor alpha 2	GFRA2	205722_s_at	Plasma	receptor	2.265

glutamate receptor, metabotropic 5	GRM5	214217_at	Membrane Plasma Membrane	receptor	-2.231
glutathione peroxidase 7	GPX7	213170_at	Cytoplasm	enzyme	-2.692
glutathione synthetase	GSS	211630_s_at	Cytoplasm	enzyme	0.599
glycosyltransferase 25 domain containing 2	GLT25D2	209883_at	unknown	other	-1.223
GNAS complex locus	GNAS	214157_at	Plasma Membrane	enzyme	-1.794
growth associated protein 43	GAP43	204471_at	Plasma Membrane	other	0.869
growth associated protein 43	GAP43	216963_s_at	Plasma Membrane	other	1.151
guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	GNAI1	209576_at	Plasma Membrane	enzyme	2.225
guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	GNAI1	227692_at	Plasma Membrane	enzyme	2.111
guanine nucleotide binding protein (G protein), beta polypeptide 4	GNB4	225710_at	Plasma Membrane	enzyme	4.695
guanine nucleotide binding protein (G protein), gamma 11	GNG11	204115_at	Plasma Membrane	enzyme	2.587
guanylate cyclase 1, soluble, alpha 3	GUCY1A3	221942_s_at	Cytoplasm	enzyme	-1.522
guanylate cyclase 1, soluble, alpha 3	GUCY1A3	229530_at	Cytoplasm	enzyme	-1.696
helicase, POLQ-like	HELQ	228736_at	Nucleus	enzyme	-1.28
HERPUD family member 2	HERPUD2	236170_x_at	unknown	other	-0.897
heterogeneous nuclear ribonucleoprotein R	HNRNPR	208765_s_at	Nucleus	other	-0.64
hippocalcin-like 1	HPCAL1	205462_s_at	Cytoplasm	other	-1.551
hippocalcin-like 1	HPCAL1	212552_at	Cytoplasm	other	-1.387
histone cluster 1, H2ac	HIST1H2AC	215071_s_at	Nucleus	other	-2.462
histone cluster 1, H2bd	HIST1H2BD	209911_x_at	Nucleus	other	-2.036
histone cluster 1, H2bk	HIST1H2BK	209806_at	Nucleus	other	-1.575
histone cluster 2, H2be	HIST2H2B	202708_s_at	Nucleus	other	-1.735

	E				
hypothetical LOC100130522	LOC100130522	230477_at	unknown	other	-0.928
hypothetical LOC26082	DKFZP434L187	230861_at	unknown	other	0.968
hypothetical protein LOC100128844	LOC100128844	229110_at	unknown	other	2.106
hypothetical protein LOC643401	LOC340109	1557765_at	unknown	other	2.848
integrin, alpha 6	ITGA6	201656_at	Plasma Membrane	other	2.822
integrin, alpha 6	ITGA6	215177_s_at	Plasma Membrane	other	2.024
integrin, beta 5	ITGB5	201125_s_at	Plasma Membrane	other	0.913
interleukin 10 receptor, beta	IL10RB	209575_at	Plasma Membrane	transmembrane receptor	-1.444
junction mediating and regulatory protein, p53 cofactor	JMY	226352_at	Nucleus	transcription regulator	-0.744
K(lysine) acetyltransferase 2B	KAT2B	203845_at	Nucleus	transcription regulator	-0.731
KDEL (Lys-Asp-Glu-Leu) containing 2	KDELC2	225128_at	unknown	other	1.085
kelch domain containing 1	KLHDC1	1552733_at	unknown	other	-0.952
kelch repeat and BTB (POZ) domain containing 11	KBTBD11	204301_at	unknown	other	-0.733
kelch-like 13 (Drosophila)	KLHL13	227875_at	unknown	other	0.902
KH domain containing, RNA binding, signal transduction associated 3	KHDRBS3	209781_s_at	Nucleus	other	1.082
KH homology domain containing 1	KHDC1	230055_at	unknown	other	-1.656
KIAA1598	KIAA1598	221802_s_at	unknown	other	-2.811
kinesin family member 16B	KIF16B	232083_at	Cytoplasm	other	1.688
lectin, galactoside-binding, soluble, 3 binding protein	LGALS3BP	200923_at	Plasma Membrane	transmembrane receptor	-1.417
leukemia inhibitory factor receptor alpha	LIFR	225575_at	Plasma Membrane	transmembrane receptor	-0.941
limb bud and heart development homolog (mouse)	LBH	221011_s_at	Nucleus	transcription regulator	0.788
LRP2 binding protein	LRP2BP	207797_s_at	unknown	other	-1.365

lumican	LUM	201744_s_at	Extracellular Space	other	5.638
LYR motif containing 5	LYRM5	225469_at	unknown	other	-0.93
mab-21-like 1	MAB21L1	206163_at	unknown	other	2.722
mab-21-like 2	MAB21L2	210302_s_at	unknown	other	2.871
mab-21-like 2	MAB21L2	210303_at	unknown	other	2.204
macrophage stimulating 1 (hepatocyte growth factor-like)	MST1	216320_x_at	Extracellular Space	growth factor	-1.012
major facilitator superfamily domain containing 4	MFSD4	229254_at	unknown	other	-1.752
mannosidase, alpha, class 2A, member 1	MAN2A1	226538_at	Cytoplasm	enzyme	0.864
mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	MGAT4A	226039_at	unknown	enzyme	-0.904
mesenchyme homeobox 2	MEOX2	206201_s_at	Nucleus	transcription regulator	-4.213
microtubule associated protein 9	MAP9	220145_at	unknown	other	0.7
microtubule-associated protein 9	MAP9	228423_at	unknown	other	-1.108
microtubule-associated protein 9	MAP9	235550_at	unknown	other	-0.863
mitochondrial ribosomal protein S33	MRPS33	219654_s_at	Cytoplasm	other	-0.600
mitogen-activated protein kinase kinase kinase 5	MAP3K5	203836_s_at	Cytoplasm	kinase	-1.159
moesin	MSN	200600_at	Plasma Membrane	other	2.082
monoamine oxidase A	MAOA	204388_s_at	Cytoplasm	enzyme	2.15
monoamine oxidase A	MAOA	204389_at	Cytoplasm	enzyme	1.88
monoamine oxidase A	MAOA	212741_at	Cytoplasm	enzyme	2.048
monocyte to macrophage differentiation-associated	MMD	244523_at	Plasma Membrane	other	1.045
multiple C2 domains, transmembrane 1	MCTP1	220122_at	unknown	other	-1.597
MYC induced nuclear antigen	MINA	213166_s_at	Nucleus	other	1.391
MYC induced nuclear antigen	MINA	213189_at	Nucleus	other	1.641
myosin IB	MYO1B	212365_at	Cytoplasm	other	0.71
myosin VI	MYO6	203216_s_at	Cytoplasm	other	1.104

myosin VI	MYO6	210480_s_at	Cytoplasm	other	1.41
Na+/H+ exchanger domain containing 2	NHEDC2	1564746_at	Plasma Membrane	other	-1.462
N-acylethanolamine acid amidase	NAAA	214765_s_at	Cytoplasm	enzyme	0.911
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	NDUFA4L2	218484_at	unknown	enzyme	-3.507
NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	NDUFV3	226616_s_at	Cytoplasm	enzyme	-0.875
nebulette	NEBL	203961_at	Cytoplasm	other	-1.359
neural precursor cell expressed, developmentally down-regulated 9	NEDD9	202150_s_at	Nucleus	other	2.41
NIPA-like domain containing 3	NIPAL3	225876_at	unknown	other	-1.203
nitric oxide synthase 1 (neuronal)	NOS1	239132_at	Cytoplasm	enzyme	1.138
nitric oxide synthase 1 (neuronal)	NOS1	240911_at	Cytoplasm	enzyme	1.187
NLR family member X1	NLRX1	219680_at	unknown	other	-1.541
non-protein coding RNA 171	NCRNA00171	215985_at	unknown	other	-0.692
nuclear receptor coactivator 7	NCOA7	225344_at	Nucleus	other	-0.842
nucleosome assembly protein 1-like 3	NAP1L3	204749_at	Nucleus	other	-1.53
nudix (nucleoside diphosphate linked moiety X)-type motif 19	NUDT19	235384_at	Cytoplasm	other	-1.685
olfactomedin 3	OLFM3	1554524_a_at	Cytoplasm	other	-0.927
oxysterol binding protein-like 3	OSBPL3	209626_s_at	Cytoplasm	other	2.083
pecanex-like 2	PCNXL2	1554256_a_at	unknown	other	-0.728
pellino homolog 2	PELI2	219132_at	Cytoplasm	other	0.732
peptidase M20 domain containing 2	PM20D2	225421_at	unknown	other	1.6
peptidylglycine alpha-amidating monooxygenase	PAM	202336_s_at	Plasma Membrane	enzyme	-0.861
peripherin	PRPH	213847_at	Plasma Membrane	other	-1.417
PHD finger protein 20	PHF20	235389_at	Nucleus	other	0.596

phosphatidic acid phosphatase type 2 domain containing 1A	PPAPDC1A	236044_at	unknown	phosphatase	-2.621
phosphatidylinositol glycan anchor biosynthesis, class H	PIGH	209625_at	Cytoplasm	enzyme	-0.597
phosphoinositide-interacting regulator of transient receptor potential channels	HCG 1776018	232887_at	unknown	other	-2.019
phosphorylase kinase, alpha 1 (muscle)	PHKA1	229876_at	Cytoplasm	kinase	-1.2
plastin 3 (T isoform)	PLS3	201215_at	Cytoplasm	other	1.068
platelet-derived growth factor receptor, beta polypeptide	PDGFRB	202273_at	Plasma Membrane	kinase	-1.373
pleiotrophin	PTN	209466_x_at	Extracellular Space	growth factor	-1.426
pleiotrophin	PTN	211737_x_at	Extracellular Space	growth factor	-2.929
pleiotropic regulator 1	PLRG1	225194_at	Nucleus	transcription regulator	-0.701
pleiotropic regulator 1	PLRG1	227246_at	Nucleus	transcription regulator	-1.228
plexin A2	PLXNA2	213030_s_at	Plasma Membrane	other	0.946
plexin A4	PLXNA4	232317_at	Plasma Membrane	receptor	1.368
polo-like kinase 2	PLK2	201939_at	Nucleus	kinase	3.606
polycomb group ring finger 5	PCGF5	227935_s_at	unknown	other	0.791
polymerase (DNA directed), epsilon	POLE	216026_s_at	Nucleus	enzyme	1.053
potassium channel tetramerisation domain containing 12	KCTD12	212188_at	unknown	ion channel	3.396
potassium channel tetramerisation domain containing 12	KCTD12	212192_at	unknown	ion channel	4.806
potassium large conductance calcium-activated channel, subfamily M, alpha member 1	KCNMA1	221584_s_at	Plasma Membrane	ion channel	-2.389
potassium voltage-gated channel, KQT-like subfamily, member 2	KCNQ2	205737_at	Plasma Membrane	ion channel	-1.246
pregnancy-associated plasma protein A, pappalysin 1	PAPPA	201982_s_at	Extracellular Space	peptidase	-1.672
prostaglandin E receptor 2 (subtype EP2), 53kDa	PTGER2	206631_at	Plasma Membrane	receptor	-2.328

prostaglandin F2 receptor negative regulator	PTGFRN	224937_at	Plasma Membrane	other	2.301
proteasome (prosome, macropain) subunit, alpha type, 7	PSMA7	216088_s_at	Cytoplasm	peptidase	0.658
protein kinase, cAMP-dependent, catalytic, beta	PRKACB	235780_at	Cytoplasm	kinase	-2.17
protein tyrosine phosphatase, receptor type, D	PTPRD	214043_at	Plasma Membrane	phosphatase	-1.16
protein tyrosine phosphatase, receptor type, E	PTPRE	221840_at	Plasma Membrane	phosphatase	3.044
protein tyrosine phosphatase, receptor type, G	PTPRG	204944_at	Plasma Membrane	phosphatase	1.237
RAB35, member RAS oncogene family	RAB35	205461_at	Cytoplasm	enzyme	0.737
RAB6B, member RAS oncogene family	RAB6B	225259_at	Cytoplasm	enzyme	-1.229
Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	ARHGEF6	209539_at	Cytoplasm	other	2.719
RAN, member RAS oncogene family	RAN	200750_s_at	Nucleus	enzyme	0.59
RAS and EF-hand domain containing	RASEF	1553986_at	unknown	other	1.393
ras homolog gene family, member U	RHOU	223168_at	Cytoplasm	enzyme	-1.154
regulator of G-protein signaling 5	RGS5	1555725_a_at	Plasma Membrane	other	4.038
regulator of G-protein signaling 5	RGS5	209070_s_at	Plasma Membrane	other	3.729
regulator of G-protein signaling 5	RGS5	209071_s_at	Plasma Membrane	other	3.468
regulator of G-protein signaling 5	RGS5	218353_at	Plasma Membrane	other	3.65
RELT-like 1	RELL1	226430_at	unknown	other	1.214
retinoblastoma-like 1 (p107)	RBL1	1559307_s_at	Nucleus	other	0.959
retrotransposon gag domain containing 4	RGAG4	227823_at	unknown	other	-1.775
Rho GTPase activating protein 6	ARHGAP6	206167_s_at	Cytoplasm	other	2.809
ribosomal L1 domain containing 1	RSL1D1	213750_at	Cytoplasm	other	-0.816
RIMS binding protein 2	RIMBP2	238817_at	Plasma Membrane	other	1.679

ring finger protein 13	RNF13	201780_s_at	Nucleus	other	-0.707
ring finger protein 182	RNF182	230720_at	unknown	other	2.696
ring finger protein 34	RNF34	219035_s_at	Cytoplasm	enzyme	0.85
ring finger protein 41	RNF41	201962_s_at	Cytoplasm	other	-0.591
RNA polymerase I transcription factor homolog pseudogene 1	LOC94431	216908_x_at	unknown	other	-0.674
sal-like 4	SALL4	229661_at	Nucleus	other	1.586
salt-inducible kinase 1	SIK1	208078_s_at	Cytoplasm	kinase	-1.403
seizure related 6 homolog (mouse)-like	SEZ6L	207873_x_at	Plasma Membrane	other	0.866
seizure related 6 homolog (mouse)-like	SEZ6L	211894_x_at	Plasma Membrane	other	0.797
sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	SEMA6A	220454_s_at	Plasma Membrane	other	1.356
serine peptidase inhibitor, Kunitz type, 2	SPINT2	210715_s_at	Extracellular Space	other	-1.889
SH3 domain containing, Ysc84-like 1	SH3YL1	204019_s_at	unknown	other	-0.859
SH3-domain GRB2-like 2	SH3GL2	205751_at	Plasma Membrane	enzyme	-1.605
similar to hCG2031213	LOC728052	1558795_at	unknown	other	2.239
similar to hCG2031213	LOC728052	1558796_a_at	unknown	other	1.887
single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	SIGIRR	52940_at	Plasma Membrane	receptor	-1.42
single-minded homolog 1	SIM1	1556300_s_at	Nucleus	transcription regulator	6.36
single-minded homolog 1	SIM1	206876_at	Nucleus	transcription regulator	5.737
SLIT and NTRK-like family, member 5	SLITRK5	214930_at	unknown	other	4.094
SMG1 homolog, phosphatidylinositol 3-kinase-related kinase pseudogene	LOC641298	244766_at	unknown	other	1.065
solute carrier family 12 (potassium/chloride transporters), member 7	SLC12A7	218066_at	Plasma Membrane	transporter	-1.258
solute carrier family 22, member 17	SLC22A17	218675_at	Plasma Membrane	transporter	-0.724

solute carrier family 35, member F3	SLC35F3	229065_at	unknown	other	-3.048
solute carrier family 44, member 5	SLC44A5	1569112_at	unknown	other	2.738
solute carrier family 44, member 5	SLC44A5	235763_at	unknown	other	1.845
solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	SLC7A2	225516_at	Plasma Membrane	transporter	1.892
solute carrier organic anion transporter family, member 3A1	SLCO3A1	219229_at	Plasma Membrane	transporter	1.622
solute carrier organic anion transporter family, member 3A1	SLCO3A1	227367_at	Plasma Membrane	transporter	1.045
sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	SPOCK2	202524_s_at	Extracellular Space	other	-0.83
sperm associated antigen 6	SPAG6	210032_s_at	Cytoplasm	other	1.687
sperm associated antigen 6	SPAG6	210033_s_at	Cytoplasm	other	2.774
spermatogenesis associated, serine-rich 2-like	SPATS2L	222154_s_at	unknown	other	0.907
sphingosine-1-phosphate receptor 3	S1PR3	228176_at	Plasma Membrane	receptor	1.9
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	ST8SIA1	210073_at	Cytoplasm	enzyme	1.114
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	ST8SIA3	230262_at	Cytoplasm	enzyme	-1.039
stathmin-like 3	STMN3	222557_at	Nucleus	other	0.788
STEAP family member 3	STEAP3	218424_s_at	Cytoplasm	transporter	-1.827
steroidogenic acute regulatory protein	STAR	204548_at	Cytoplasm	transporter	-1.093
stimulated by retinoic acid gene 6 homolog	STRA6	1569334_at	Plasma Membrane	other	1.359
stimulated by retinoic acid gene 6 homolog	STRA6	1569335_a_at	Plasma Membrane	other	1.167
storkhead box 2	STOX2	226822_at	unknown	other	-0.854
synaptojanin 1	SYNJ1	212990_at	Cytoplasm	phosphatase	-0.624
synaptotagmin XIII	SYT13	226086_at	unknown	transporter	-4.754
synuclein, alpha (non A4 component of amyloid precursor)	SNCA	236081_at	Cytoplasm	other	-0.935
taxilin beta	TXLNB	227834_at	Cytoplasm	other	-2.226

teashirt zinc finger homeobox 3	TSHZ3	223392_s_at	Nucleus	transcription regulator	1.472
teashirt zinc finger homeobox 3	TSHZ3	223393_s_at	Nucleus	transcription regulator	0.962
tetratricopeptide repeat domain 39C	TTC39C	238480_at	unknown	other	-0.824
TH1-like	TH1L	220607_x_at	Nucleus	other	1.027
TH1-like	TH1L	225006_x_at	Nucleus	other	0.884
TH1-like	TH1L	225261_x_at	Nucleus	other	0.883
TH1-like	TH1L	225865_x_at	Nucleus	other	0.904
thioredoxin reductase 1	TXNRD1	201266_at	Cytoplasm	enzyme	1.032
THO complex 4	THOC4	226319_s_at	Nucleus	transcription regulator	0.996
TIMP metallopeptidase inhibitor 3	TIMP3	201147_s_at	Extracellular Space	other	5.151
TIMP metallopeptidase inhibitor 3	TIMP3	201148_s_at	Extracellular Space	other	3.637
TIMP metallopeptidase inhibitor 3	TIMP3	201149_s_at	Extracellular Space	other	5.037
TIMP metallopeptidase inhibitor 3	TIMP3	201150_s_at	Extracellular Space	other	4.312
tissue factor pathway inhibitor 2	TFPI2	209277_at	Extracellular Space	other	1.592
tissue factor pathway inhibitor 2	TFPI2	209278_s_at	Extracellular Space	other	2.326
TM2 domain containing 1	TM2D1	213882_at	Plasma Membrane	receptor	-0.769
transcription factor 7-like 2 (T-cell specific, HMG-box)	TCF7L2	212761_at	Nucleus	transcription regulator	1.005
transcription factor 7-like 2 (T-cell specific, HMG-box)	TCF7L2	212762_s_at	Nucleus	transcription regulator	1.224
transcription factor 7-like 2 (T-cell specific, HMG-box)	TCF7L2	216035_x_at	Nucleus	transcription regulator	1.072
transcription factor 7-like 2 (T-cell specific, HMG-box)	TCF7L2	216037_x_at	Nucleus	transcription regulator	0.81
transcription factor 7-like 2 (T-cell specific, HMG-box)	TCF7L2	216511_s_at	Nucleus	transcription regulator	1.003
transducin-like enhancer of split 3	TLE3	212770_at	Nucleus	other	0.976
transformer 2 alpha homolog	TRA2A	213593_s_at	Nucleus	other	1.12
transmembrane inner ear	TMIE	1553601_a_at	unknown	other	-3.334

transmembrane protein 132C	TMEM132C	232313_at	unknown	other	4.02
transmembrane protein 178	TMEM178	229302_at	unknown	other	1.697
transmembrane protein 184C	TMEM184C	219074_at	unknown	other	-0.779
transmembrane protein 5	TMEM5	204808_s_at	Plasma Membrane	other	-1.074
transmembrane protein 59-like	TMEM59L	219005_at	Cytoplasm	other	-0.845
tripartite motif-containing 29	TRIM29	211002_s_at	Cytoplasm	transcription regulator	2.005
tripartite motif-containing 36	TRIM36	219736_at	Cytoplasm	other	2.221
trophoblast glycoprotein	TPBG	203476_at	Plasma Membrane	other	2.158
tumor suppressor candidate 3	TUSC3	232770_at	Extracellular Space	enzyme	-1.407
U2 small nuclear RNA auxiliary factor 1	U2AF1	232141_at	Nucleus	other	0.776
ubiquitin-conjugating enzyme E2 variant 1	UBE2V1	201003_x_at	Nucleus	transcription regulator	0.663
urocortin	UCN	206072_at	Extracellular Space	other	-0.961
vacuolar protein sorting 29 homolog	VPS29	223026_s_at	Cytoplasm	transporter	0.805
v-erb-a erythroblastic leukemia viral oncogene homolog 4	ERBB4	206794_at	Plasma Membrane	kinase	-1.537
v-erb-a erythroblastic leukemia viral oncogene homolog 4	ERBB4	214053_at	Plasma Membrane	kinase	-1.708
v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog	ERBB2	216836_s_at	Plasma Membrane	kinase	-0.698
v-raf-1 murine leukemia viral oncogene homolog 1	RAF1	1557675_at	Cytoplasm	kinase	0.696
WD repeat and FYVE domain containing 3	WDFY3	212602_at	Cytoplasm	enzyme	-0.626
WD repeat and FYVE domain containing 3	WDFY3	212606_at	Cytoplasm	enzyme	-0.785
zinc finger homeobox 4	ZFHX4	219779_at	unknown	other	1.36
zinc finger homeobox 4	ZFHX4	241700_at	unknown	other	1.234
zinc finger protein 217	ZNF217	203739_at	Nucleus	transcription regulator	1.096

zinc finger protein 503	ZNF503	227195_at	Nucleus	other	1.373
zinc finger protein 641	ZNF641	226509_at	unknown	other	-1.427
zinc finger protein 662	ZNF662	228538_at	unknown	other	-3.352
zinc finger, CCCH-type with G patch domain	ZGPAT	221848_at	unknown	other	0.991

[0196] Computer analysis was performed as in Example V, except that the list of probes reflects genes that were greater than 1.5-fold differential expressed in the H1 cell line and the BB10 cell line when compared to both the 2D6 and SiMa parental cell lines, and also a greater than 1.5-fold differential expressed in the SiMa parental cell line when compared to the 2D6 cell line. When the p-value cut off was set to 0.05, this analysis identified 94 gene probes that could be classified to 70 genes (Table 17).

Table 17. Genes Identified using IPA Core Analysis

Gene Name	Gene Symbol	Probe ID. No.	Location	Type	Log Ratio
achaete-scute complex homolog 1	ASCL1	209985_s_at	Nucleus	transcription regulator	2.429
achaete-scute complex homolog 1	ASCL1	209988_s_at	Nucleus	transcription regulator	1.446
achaete-scute complex homolog 1	ASCL1	213768_s_at	Nucleus	transcription regulator	1.578
activated leukocyte cell adhesion molecule	ALCAM	201952_at	Plasma Membrane	other	1.521
ADP-ribosylation factor 1	ARF1	1565651_at	Cytoplasm	enzyme	1.063
ADP-ribosylation factor-like 17A	ARL17A	243899_at	unknown	other	0.741
ataxin 2-binding protein 1	A2BP1	1553422_s_at	Cytoplasm	other	1.453
ataxin 2-binding protein 1	A2BP1	221217_s_at	Cytoplasm	other	1.497
brain abundant, membrane attached signal protein 1	BASP1	202391_at	Plasma Membrane	other	1.146
CAP, adenylate cyclase-associated protein, 2	CAP2	212551_at	Plasma Membrane	other	-1.974
CD9 molecule	CD9	201005_at	Plasma Membrane	other	1.415
CUG triplet repeat, RNA binding protein 2	CUGBP2	202167_s_at	Nucleus	other	2.156
cyclic nucleotide gated channel alpha 3	CNGA3	207261_at	Plasma Membrane	ion channel	-3.182
cyclin-dependent kinase inhibitor 2A (melanoma, p16,	CDKN2A	209644_x_at	Nucleus	transcription regulator	-1.277

inhibits CDK4)					
ELL associated factor 2	EAF2	219551_at	Nucleus	transcription regulator	0.693
eukaryotic translation initiation factor 3, subunit C	EIF3C	236700_at	Cytoplasm	translation regulator	1.378
family with sequence similarity 162, member B	FAM162B	228875_at	unknown	other	-0.743
family with sequence similarity 181, member B	FAM181B	231430_at	unknown	other	0.794
far upstream element (FUSE) binding protein 3	FUBP3	239193_at	Nucleus	transcription regulator	1.192
fibroblast growth factor 13	FGF13	205110_s_at	Extracellular Space	growth factor	-3.522
follistatin-like 1	FSTL1	208782_at	Extracellular Space	other	-1.275
forkhead box O6	FOXO6	239657_x_at	Nucleus	other	-1.512
guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	GNAI1	227692_at	Plasma Membrane	enzyme	2.111
guanine nucleotide binding protein (G protein), beta polypeptide 4	GNB4	225710_at	Plasma Membrane	enzyme	4.695
guanine nucleotide binding protein (G protein), gamma 11	GNG11	204115_at	Plasma Membrane	enzyme	2.587
KDEL (Lys-Asp-Glu-Leu) containing 2	KDELC2	225128_at	unknown	other	1.085
kelch-like 13	KLHL13	227875_at	unknown	other	0.902
KH domain containing, RNA binding, signal transduction associated 3	KHDRBS3	209781_s_at	Nucleus	other	1.082
KH homology domain containing 1	KHDC1	230055_at	unknown	other	-1.656
leukemia inhibitory factor receptor alpha	LIFR	225575_at	Plasma Membrane	transmembrane receptor	-0.941
mab-21-like 2	MAB21L2	210303_at	unknown	other	2.204
mesenchyme homeobox 2	MEOX2	206201_s_at	Nucleus	transcription regulator	-4.213
moesin	MSN	200600_at	Plasma Membrane	other	2.082
monoamine oxidase A	MAOA	204388_s_at	Cytoplasm	enzyme	2.15
monoamine oxidase A	MAOA	204389_at	Cytoplasm	enzyme	1.88

monoamine oxidase A	MAOA	212741_at	Cytoplasm	enzyme	2.048
multiple C2 domains, transmembrane 1	MCTP1	220122_at	unknown	other	-1.597
MYC induced nuclear antigen	MINA	213188_s_at	Nucleus	other	1.391
MYC induced nuclear antigen	MINA	213189_at	Nucleus	other	1.641
myosin VI	MYO6	203216_s_at	Cytoplasm	other	1.104
phosphatidic acid phosphatase type 2 domain containing 1A	PPAPDC1A	236044_at	unknown	phosphatase	-2.621
plastin 3 (T isoform)	PLS3	201215_at	Cytoplasm	other	1.068
pleiotrophin	PTN	209466_x_at	Extracellular Space	growth factor	-1.426
pleiotrophin	PTN	211737_x_at	Extracellular Space	growth factor	-2.929
polo-like kinase 2 (Drosophila)	PLK2	201939_at	Nucleus	kinase	3.606
potassium large conductance calcium-activated channel, subfamily M, alpha member 1	KCNMA1	221584_s_at	Plasma Membrane	ion channel	-2.389
RELT-like 1	RELL1	226430_at	unknown	other	1.214
ring finger protein 182	RNF182	230720_at	unknown	other	2.696
seizure related 6 homolog-like	SEZ6L	207873_x_at	Plasma Membrane	other	0.866
seizure related 6 homolog (mouse)-like	SEZ6L	211894_x_at	Plasma Membrane	other	0.797
similar to hCG2031213	LOC728052	1558795_at	unknown	other	2.239
single-minded homolog 1 (Drosophila)	SIM1	1556300_s_at	Nucleus	transcription regulator	6.36
single-minded homolog 1 (Drosophila)	SIM1	206876_at	Nucleus	transcription regulator	5.737
SLIT and NTRK-like family, member 5	SLITRK5	214930_at	unknown	other	4.094
SMG1 homolog, phosphatidylinositol 3-kinase-related kinase pseudogene	LOC641298	244766_at	unknown	other	1.065
solute carrier family 44, member 5	SLC44A5	1569112_at	unknown	other	2.738
solute carrier family 44, member 5	SLC44A5	235763_at	unknown	other	1.845
solute carrier family 7 (cationic amino acid	SLC7A2	225516_at	Plasma Membrane	transporter	1.892

transporter, y+ system), member 2					
solute carrier organic anion transporter family, member 3A1	SLCO3A1	219229_at	Plasma Membrane	transporter	1.622
spermatogenesis associated, serine-rich 2-like	SPATS2L	222154_s_at	unknown	other	0.907
synaptotagmin XIII	SYT13	226086_at	unknown	transporter	-4.754
tissue factor pathway inhibitor 2	TFPI2	209278_s_at	Extracellular Space	other	2.326
transcription factor 7-like 2 (T-cell specific, HMG-box)	TCF7L2	212761_at	Nucleus	transcription regulator	1.005
transformer 2 alpha homolog	TRA2A	213593_s_at	Nucleus	other	1.12
transmembrane inner ear	TMIE	1553601_a_at	unknown	other	-3.334
transmembrane protein 178	TMEM178	229302_at	unknown	other	1.697
U2 small nuclear RNA auxiliary factor 1	U2AF1	232141_at	Nucleus	other	0.776
v-raf-1 murine leukemia viral oncogene homolog 1	RAF1	1557675_at	Cytoplasm	kinase	0.696
zinc finger protein 217	ZNF217	203739_at	Nucleus	transcription regulator	1.096
zinc finger protein 662	ZNF662	228538_at	unknown	other	-3.352
The log ratio represent $\log_2$ values where 0.585 is $\log_2(1.5)$ which is a 1.5-fold difference, 1 is $\log_2(2)$ which is a 2-fold difference, 1.584 is $\log_2(3)$ which is a 3-fold difference, 2 is $\log_2(4)$ which is a 4-fold difference, 2.321 is $\log_2(5)$ which is a 5-fold difference, 2.584 is $\log_2(6)$ which is a 6-fold difference, 2.807 is $\log_2(7)$ which is a 7-fold difference, 3 is $\log_2(8)$ which is a 8-fold difference, 3.169 is $\log_2(9)$ which is a 9-fold difference, and 3.321 is $\log_2(10)$ which is a 10-fold difference.					

Example VI

Immuno-Based Method to Detect Picomolar Amounts of BoNT/A

[0197] The following example illustrates how to perform immuno-based methods of detecting BoNT/A activity that can detect picomolar amounts of the BoNT/A pharmaceutical product, such as, *e.g.*, BOTOX® DYSPORT®/RELOXIN®, PURTOX®, XEOMIN®, NEURONOX®, or BTX-A.

1. Immuno-based method of detecting BoNT/A using ECL sandwich ELISA.

[0198] To prepare a lysate from cells treated with a BoNT/A, approximately 150,000 cells from an established clonal cell line was plated into the wells of 96-well tissue culture poly-D-lysine plates containing 100 µL of a serum-free medium containing Minimum Essential Medium, 2 mM GlutaMAX™ I with Earle's salts, 1 x B27 supplement, 1 x N2 supplement, 0.1 mM Non-Essential Amino Acids, 10 mM

HEPES and 60 µg/mL GT1b. The cell lines used were BB10, H1, and SiMa. These cells were incubated in a 37 °C incubator under 5% carbon dioxide until the cells differentiated, as assessed by standard and routine morphological criteria, such as growth arrest and neurite extension (approximately 3 days). The media from the differentiated cells was aspirated from each well and replaced with fresh media containing one of the following: 1) SiMa cell line, 0 (untreated), 0.98 U/mL, 1.9 U/mL, 3.91 U/mL, 7.81 U/mL, 15.6 U/mL, 31.3 U/mL, 62.5 U/mL, 125 U/mL, 250 U/mL, or 500 U/mL of a BoNT/A pharmaceutical product reconstituted in a sodium chloride free medium; 2) BB10, 0 (untreated), 0.49 U/mL, 0.98 U/mL, 1.9 U/mL, 3.91 U/mL, 7.81 U/mL, 15.6 U/mL, 31.3 U/mL, 62.5 U/mL, 125 U/mL, 250 U/mL; 3) H1, 0 (untreated), 0.3 U/mL, 1 U/mL, 3 U/mL, 9 U/mL, 28 U/mL, 83 U/mL, and 250 U/mL. Because the BoNT/A pharmaceutical product contains sodium chloride, its addition to the culture medium resulted in a hypertonic media that was detrimental to cell viability. To circumvent the hypertonicity issue, 200 µL of MEM media made without sodium chloride was used to reconstitute the BoNT/A pharmaceutical product giving a final concentration of 25 pM BoNT/A (500 U/mL). The matrix was kept constant for all concentrations along the dose-response curve by adding sodium chloride in the media used to make the dilutions match the amount of excipients present at the highest concentration used (25 pM or 500 U/mL). After a 24 hr treatment, the cells were washed, and incubated for an additional two days without toxin. To harvest the cells, 1 x PBS was aspirated, the cells lysed by adding 75 µL of Lysis Buffer comprising 50 mM HEPES, 150 mM NaCl, 1.5 mM $MgCl_2$, 1 mM EGTA, 1% Triton X-100 to each well, and the plate incubated on a shaker rotating at 500 rpm for 30 minutes at 4 °C. The plate was centrifuged at 4000 rpm for 20 minutes at 4 °C to pellet cellular debris and the supernatant was transferred to a capture antibody coated 96-well plate to perform the detection step.

[0199] To prepare the α-SNAP-25 capture antibody solution, the α-SNAP-25 monoclonal antibody contained in the ascites from hybridoma cell line 2E2A6 (Example VII) was purified using a standard Protein A purification protocol. To prepare the α-SNAP-25 detection antibody solution, α-SNAP-25 rabbit polyclonal antibody S9684 (Sigma, St. Louis, MO) was conjugated to Ruthenium(II)-tris-bipyridine-(4-methysulfonate) NHS ester labeling reagent (Meso Scale Discovery, Gaithersburg, MD) according to the manufacturer's instructions (Meso Scale Discovery, Gaithersburg, MD). The conjugation reaction was performed by adding 30 µL of distilled water reconstituted MSD SULFO-TAG™ stock solution to 200 µL of 2 mg/mL α-SNAP-25 polyclonal antibodies and incubating the reaction at room temperature for 2 hours in the dark. The labeled antibodies were purified using a standard spin column protocol and the protein concentration determined using a standard colorimetric protein assay. The absorbance of the α-SNAP-25 antibody/MSD SULFO-TAG™ conjugate was measured at 455 nm using a spectrophotometer to determine the concentration in moles per liter. The detection antibody solution was stored at 4 °C until needed.

[0200] To prepare the solid phase support comprising the capture antibody that is specific for a SNAP-25 cleaved product, approximately 1 µL of α-SNAP-25 monoclonal antibody 2E2A6 solution (45 µg/mL in 1 x PBS, 750 µg/mL of BSA) was added to each well of a 96-well MSD High Bind plate (Meso Scale

Discovery, Gaithersburg, MD) and the solution is allowed to air dry in a biological safety cabinet for 2-3 hours in order to liquid evaporate the solution, and then the plates were sealed and stored at 4 °C until needed. The dried capture antibody-bound wells were then blocked by adding 150 µL of Blocking Buffer comprising 1 x PBS, 0.05% Tween-20, 2 % ECL Blocking reagent (GE Healthcare-Amersham), and 1 % goat serum (Rockland Immunochemicals, Gilbertsville, PA) at room temperature for 2 hours with rotation at 600 rpm.

[0201] To detect the presence of a SNAP-25 cleavage product by ECL sandwich ELISA analysis, the Blocking Buffer from plates was aspirated, 25 µL of a lysate from cells treated with BoNT/A was added to each well and the plates were incubated at 4 °C for overnight. Plate wells were washed three times by aspirating the cell lysate and rinsing each well three times with 200 µL 1 x PBS, 0.1% TWEEN-20® (polyoxyethylene (20) sorbitan monolaureate). After washing, 25 µl of 5 µg/mL α-SNAP-25 detection antibody solution comprising 2% Amersham Blocking Reagent in 1 x PBS, 0.1% TWEEN-20® (polyoxyethylene (20) sorbitan monolaureate) was added to each well, the plate was sealed, and the sealed plate was incubated at room temperature for 1 hour with shaking. After α-SNAP-25 detection antibody incubation, the wells were washed three times with 250 µL 1 x PBS, 0.1% TWEEN-20® (polyoxyethylene (20) sorbitan monolaureate). After washing 150 µL of 1 x Read Buffer (Meso Scale Discovery, Gaithersburg, MD) was added to each well and the plates were read using a SECTOR™ Imager 6000 Image Reader (Meso Scale Discovery, Gaithersburg, MD). The raw data was then transferred to SigmaPlot v 10.0 and a 4-parameter logistics fit was used to define the dose-response curves. There were no constraints used for the 4-parameter logistic function when plotting the data. Graphical reports were generated using the following analysis: R2 (correlation coefficient), a (Max for data set), b (hillslope), and X0 ± SE (EC_{50} value ± standard error).

[0202] These results indicated that on average the cells comprising the BB10 and H1 clonal cell lines were more susceptible to BoNT/A intoxication as compared to cells comprising the parental SiMa cell line. Cells from a BB10 cell line exhibited an EC_{50} for BoNT/A activity of 7 U/mL, cells from a H1 cell line exhibited an EC_{50} for BoNT/A activity of 8 U/mL, and cells from the parental SiMa cell line exhibited an EC_{50} for BoNT/A activity of 13 U/mL. This method can also be performed in a multiplex fashion as described in Ester Fernandez-Salas, et al., *Immuno-Based Botulinum Toxin Serotype A Activity Assays*, U.S. Patent Application Serial No: 12/403,531, which is hereby incorporated by reference in its entirety.

Example VII

Transfection of BoNT/A receptor DNA into sensitive clonal cell lines further improves sensitivity of the clonal cell line for BoNT/A

[0203] The following example illustrates how to introduce a polynucleotide molecule encoding a BoNT/A receptor into cells from a clonal cell line to further improve susceptibility to BoNT/A intoxication or improve BoNT/A uptake capacity.

[0204] To introduce an exogenous BoNT/A receptor into cells comprising an established clonal cell line, a mammalian expression construct comprising a polynucleotide molecule of SEQ ID NO: 139 encoding the FGFR3 of SEQ ID NO: 25, was transfected into cells from a H1 clonal cell line by a cationic lipid method. A suitable density (about 5 x10^6 cells) of cells from an established clonal cell line are plated in a 100 mm tissue culture dish containing 5 mL of complete culture media and grown in a 37 °C incubator under 5% carbon dioxide until the cells reached a density appropriate for transfection. A 3 mL transfection solution is prepared by adding 1.5 mL of OPTI-MEM® Reduced Serum Medium containing 60 µL of LIPOFECTAMINE® 2000 (Invitrogen, Carlsbad, CA) incubated at room temperature for 5 minutes to 1.5 mL of OPTI-MEM® Reduced Serum Medium containing 24 µg of an expression construct encoding the FGFR3 of SEQ ID NO: 25. This transfection mixture is incubated at room temperature for approximately 30 minutes. The complete media on the cells is replaced with the 3 mL transfection solution and the cells are incubated in a 37 °C incubator under 5% carbon dioxide for approximately 8 hours. Transfection media is replaced with 3 mL of fresh complete culture media and the cells are incubated in a 37 °C incubator under 5% carbon dioxide for approximately 24 hours. Media is replaced with 3 mL of fresh complete culture media containing approximately 1mM G418 (Invitrogen, Carlsbad, CA) for selection of transfected cells. Cells are incubated in a 37 °C incubator under 5% carbon dioxide for approximately 1 week, the old media is replaced with fresh complete culture media containing 0.5 mM G418 and the cells are plated onto one 96-well collagen IV coated plate at a plating density of 0.5 cells per well. Cell growth and viability was monitored by microscopic examination and after about 3 weeks single clones appeared in about 20% of the wells. These clones were grown for an additional 2 weeks and then transferred to duplicate 24-well collagen IV coated plates, one to maintain the clonal cell line and the other to test for BoNT/A susceptibility.

[0205] To determine the susceptibility of the cells comprising the clonal cell lines overexpressing a BoNT/A receptor, a Western blot analysis was done to determine sensitivity and an ECL sandwich ELISA was done to determine an EC_{50} value. A total of eight clones were tested for the FGFR3 stably transfected H1 cells.

[0206] To prepare a cell lysate for the Western blot analysis, cells from the clonal cell line were plated into two wells in a poly-D-lysine coated 96-well plate in serum-free medium containing Minimum Essential Medium, 2 mM GLUTAMAX™ I with Earle's salts, 1 x B27 supplement, 1 x N2 supplement, 0.1 mM Non-Essential Amino Acids, 10 mM HEPES and 25 µg/mL GT1b (Alexis Biochemicals, Lausen, Switzerland). These cells were incubated in a 37 °C incubator under 5% carbon dioxide until the cells differentiated, as assessed by standard and routine morphological criteria, such as growth arrest and neurite extension (approximately 3 days). The media from the differentiated cells was aspirated from each well and replaced with fresh media containing either 0 (untreated), 0.5 nM or 0.25 nM of a BoNT/A complex. After a 6 hr treatment, the cells were washed, and incubated for an additional 18 hr without toxin. After the incubation, the cells were washed by aspirating the growth media and rinsing each well with 200 µl of 1 x

PBS. To harvest the cells, the 1 x PBS was aspirated, the cells were lysed by adding 40 µL of 2 x SDS Loading Buffer and the plate was swirled for an even coating of Loading Buffer. The lysate was transferred to a new 96-well PCR plate (Axygen, Union City, CA) and the plate was heated to 95 °C for 5 min to complete cell lysis and denature proteins.

[0207] To detect for the presence of both uncleaved SNAP-25 substrate and cleaved SNAP-25 products, an aliquot from each harvested sample was analyzed by Western blot. In this analysis, a 12 µL aliquot of the harvested sample was separated by MOPS polyacrylamide gel electrophoresis using NUPAGE® Novex 12% Bis-Tris precast polyacrylamide gels (Invitrogen Inc., Carlsbad, CA) under denaturing, reducing conditions. Separated proteins were transferred from the gel onto nitrocellulose membranes (Bio-Rad Laboratories, Hercules, CA) by Western blotting using a "Transfer +4 cassettes & Cooler" transfer chamber (GE Healthcare, Piscataway, NJ). Membranes were blocked by incubating at room temperature for 1 hr with gentle agitation in a solution containing Tris-Buffered Saline (TBS) (25 mM 2-amino-2-hydroxymethyl-1,3-propanediol hydrochloric acid (Tris-HCl)(pH 7.4), 137 mM sodium chloride, 2.7 mM potassium chloride), 0.1% TWEEN-20® (polyoxyethylene (20) sorbitan monolaureate), 2% Bovine Serum Albumin (BSA), 5% nonfat dry milk. Blocked membranes were incubated at 4 °C for overnight in TBS, 0.1% TWEEN-20® (polyoxyethylene (20) sorbitan monolaureate), 2% BSA, and 5% nonfat dry milk containing a 1:5,000 dilution of α-SNAP-25 rabbit polyclonal antiserum S9684 (Sigma, St. Louis, MO) as the primary antibody. The α-SNAP-25 rabbit polyclonal antibodies can detect both the uncleaved SNAP-25 substrate and the SNAP-25 cleavage product, allowing for the assessment of overall SNAP-25 expression in each cell line and the percent of SNAP-25 cleaved after BoNT/A treatment as a parameter to assess the amount of BoNT/A uptake. Primary antibody probed blots were washed three times for 5 minutes each time in TBS, TWEEN-20® (polyoxyethylene (20) sorbitan monolaureate). Washed membranes were incubated at room temperature for 2 hours in TBS, 0.1% TWEEN-20® (polyoxyethylene (20) sorbitan monolaureate), 2% BSA, and 5% nonfat dry milk containing a 1:10,000 dilution of goat polyclonal anti-rabbit immunoglobulin G, heavy and light chains (IgG, H+L) antibody conjugated to horseradish peroxidase (Invitrogen, Inc., Carlsbad, CA) as a secondary antibody. Secondary antibody-probed blots were washed five times for 5 minutes each time in TBS, 0.1% TWEEN-20® (polyoxyethylene (20) sorbitan monolaureate). Signal detection of the labeled SNAP-25 products were visualized using the ECL Plus™ Western Blot Detection System (GE Healthcare, Amersham Biosciences, Piscataway, NJ) and the membrane was imaged and the percent of cleaved SNAP-25 products quantified with a Typhoon 9410 Variable Mode Imager and Imager Analysis software (GE Healthcare, Amersham Biosciences, Piscataway, NJ). The choice of pixel size (100 to 200 pixels) and PMT voltage settings (350 to 600, normally 400) depended on the individual blot. The volumes of the bands corresponding to either intact and cleaved SNAP-25 product were quantified using Image Quant TL and the total amount of SNAP-25 and the percentage of SNAP-25 cleaved were calculated based on the intensity of these two SNAP-25 bands.

[0208] Clone H1 1.4 had a high percentage of SNAP-25 cleavage and high levels of total SNAP25 and was selected for further testing. The selected clone was first grown on a 10 cm^2 dish and then in T175 flasks to ensure that enough cells were produced for both ECL sandwich ELISA assay and for freezing stocks. Frozen stocks were made with 1 x 10^6 cells and 1 mL of Recovery Cell Culture Freezing Media (GIBCO-Invitrogen, #12648-010 Freezing media).

[0209] To prepare a cell lysate for the ECL sandwich ELISA, approximately 50,000 cells from H1 clonal cell line and from H1 1.4 clonal cell line overexpressing FGFR3 were plated and differentiated as described above. The media from the differentiated cells was aspirated from each well and replaced with fresh media containing either (untreated), 0.27 pM, 0.82 pM, 2.47 pM, 7.4 pM, 22.2 pM, 66.6 pM, or 200 pM of a BoNT/A complex of a BoNT/A complex. After a 6 hr treatment, the cells were washed, and incubated overnight without toxin. After a 24 hr treatment, the cells were washed by aspirating the BoNT/A containing media and rinsing each well with 200 µL of 1 x PBS. Washed cells were harvested by lysing in freshly prepared Triton X-100 Lysis Buffer (150 mM NaCl, 20 mM Tris-HCl (pH 7.5), 1 mM EDTA, 1 mM EGTA, 1% Triton X-100 plus protease inhibitors) at 4°C for 30 minutes with constant agitation. Lysed cells were centrifuged at 4000 rpm for 20 min at 4°C to pellet debris.

[0210] The α-SNAP-25 capture antibody solution, the α-SNAP-25 detection antibody solution, and the solid phase support comprising the capture antibody that is specific for a SNAP-25 cleaved product were prepared as described in Example V. To detect the presence of a cleaved SNAP-25 product by ECL sandwich ELISA, the plates were processed, and the data collected and analyzed, and the EC_{50} calculated as described in Example VI. The EC_{50} for H1 1.4 cells was estimated to about 1.7 pM, compared to an EC_{50} about 8.7 pM for H1 cells indicating that the newly generated H1 1.4 cell line is about 5 times more sensitive than the H1 cell line for BoNT/A uptake (average of two independent experiments with similar results). The maximum signal for both cell lines was identical indicating similar efficacy towards SNAP25 cleavage. The increase in sensitivity is especially prominent at lower concentrations of BoNT/A, where the H1 1.4 cells are many times more sensitive to BoNT/A compared to H1 cells producing a very robust signal over background at the 0.27 pM concentration. Over-expression of FGFR3 was verified in a Western blot using α-FGFR3 antibodies sc-123 (Santa Cruz Biotechnologies, Santa Cruz, CA).

Example VIII

Development of α-SNAP-25 Monoclonal Antibodies that Selectively Bind a SNAP-25 Epitope Having a Free Carboxyl-terminus at the P_1 Residue of the BoNT/A Cleavage Site Scissile Bond

[0211] The following example illustrates how to make α-SNAP-25 monoclonal antibodies that can selectively bind to a SNAP-25 epitope having a carboxyl-terminus at the P_1 residue of the BoNT/A cleavage site scissile bond.

1. Generation of α-SNAP-25 monoclonal antibodies.

[0212] α-SNAP-25 monoclonal antibodies with higher binding affinity for a SNAP-25 cleavage product and/or α-SNAP-25 antibodies with a higher binding specificity for a SNAP-25 cleavage product were developed. In addition, because a permanent, stable and renewable source of α-SNAP-25 antibodies is preferable for an FDA-approved assay, screens to isolate monoclonal antibodies were undertaken. To develop monoclonal α-SNAP-25 antibodies the 13-residue peptide CDSNKTRIDEANQ$_{COOH}$ (SEQ ID NO: 38) was designed as a SNAP-25 antigen having a carboxyl-terminus at the P_1 residue of the BoNT/A cleavage site scissile bond. This peptide comprises a flexible linker region and a N-terminal Cysteine residue for conjugation to KLH and amino acids 186-197 of human SNAP-25 (SEQ ID NO: 5) with a carboxylated C-terminal glutamine (SEQ ID NO: 38). The generation of monoclonal antibodies to well-chosen, unique peptide sequences provides control over epitope specificity, allowing the identification of a particular subpopulation of protein among a pool of closely related isoforms. Blast searches revealed that this peptide has high homology only to SNAP-25 and almost no possible cross-reactivity with other proteins in neuronal cells. The sequence was also carefully scrutinized by utilizing computer algorithms to determine hydropathy index, protein surface probability, regions of flexibility, and favorable secondary structure, followed by proper orientation and presentation of the chosen peptide sequence. The peptide was synthesized and conjugated to Keyhole Limpet Hemocyanin (KLH) to increase immunogenicity. Six Balb/c mice were immunized with this peptide, and after three immunizations in about eight weeks, the mice were bled for testing. The blood was allowed to clot by incubating at 4 °C for 60 minutes. The clotted blood was centrifuged at 10,000x g at 4 °C for 10 minutes to pellet the cellular debris. The resulting serum sample was dispensed into 50 µL aliquots and stored at -20 °C until needed.

[0213] A similar strategy based on other SNAP-25 antigens disclosed in the present specification is used to develop α-SNAP-25 monoclonal antibodies that can selectively bind to a SNAP-25 having a carboxyl-terminus at the P_1 residue of the BoNT/A cleavage site scissile bond. For example, the SNAP-25 antigen of SEQ ID NO: 45 can be conjugated to KLH instead of the SNAP-25 antigen of SEQ ID NO: 38. As another example, the amino acids 186-197 of human SNAP-25 from the SNAP-25 antigen of SEQ ID NO: 38 can be replaced with SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 147, or SEQ ID NO: 148.

2. Screening for the presence of α-SNAP-25 monoclonal antibodies.

[0214] To determine the presence of an α-SNAP-25 monoclonal antibody that can selectively bind to a SNAP-25 antigen having a carboxyl-terminus at the P_1 residue of the BoNT/A cleavage site scissile bond, comparative ELISA and cell-based cleavage assay were performed using the extracted mouse serum. For comparative ELISA, two fusion proteins were constructed: BIRA-HIS TAG®-SNAP-25$_{134-197}$ of SEQ ID NO: 48 and the BIRA-HIS TAG®-SNAP-25$_{134-206}$ of SEQ ID NO: 49. BIRA-HIS TAG®-SNAP-25$_{134-197}$

comprised a naturally-biotinylated 16 amino acid BirA peptide of SEQ ID NO: 50 amino-terminally linked to a SNAP-25 peptide comprising amino acids 134-197 of SEQ ID NO: 5. BIRA-HIS TAG®-SNAP-$25_{134-206}$ comprised a naturally-biotinylated 16 amino acid BirA peptide of SEQ ID NO: 50 amino-terminally linked to a SNAP-25 peptide comprising amino acids 134-206 of SEQ ID NO: 5. These two substrates were suspended in 1 x PBS at a concentration of 10 µg/mL BIRA-HIS TAG®-SNAP-$25_{134-197}$ and the BIRA-HIS TAG®-SNAP-$25_{134-206}$. The BIRA-HIS TAG®-SNAP-$25_{134-197}$ and the BIRA-HIS TAG®-SNAP-$25_{134-206}$ were coated onto separate plates by adding approximately 100 µl of the appropriate Substrate Solution and incubating the plates at room temperature for one hour. Washed plates were incubated at 37 °C for one hour in 0.5% BSA in 1 x TBS containing a 1:10 to 1:100 dilution of an antibody-containing serum derived from one of the six immunized mice (Mouse 1, Mouse 2, Mouse 3, Mouse 4, Mouse 5, and Mouse 6). Primary antibody probed plates were washed four times for 5 minutes each time in 200 µl TBS, 0.1% TWEEN-20® (polyoxyethylene (20) sorbitan monolaureate). Washed plates were incubated at 37 °C for 1 hour in 1 x TBS containing a 1:10,000 dilution of goat polyclonal anti-mouse IgG antibody conjugated to Horseradish peroxidase (Pierce Biotechnology, Rockford, IL) as a secondary antibody. Secondary antibody-probed plates were washed four times in 200 µl TBS, 0.1% TWEEN-20® (polyoxyethylene (20) sorbitan monolaureate). Chromogenic detection of the labeled SNAP-25 products were visualized by chromogenic detection using ImmunoPure TMB substrate kit (Pierce Biotechnology, Rockford, IL). The development of a yellow color in the BIRA-HIS TAG®-SNAP-$25_{134-197}$ coated plates, but not the BIRA-HIS TAG®-SNAP-$25_{134-206}$ coated plates, indicated that the α-SNAP-25 antibody preferentially recognized the SNAP-25_{197} cleavage product. The resulted indicated that of the six mice used for immunization, three mice (Mouse 2, Mouse 3, and Mouse 4) had higher titers and more specificity towards a SNAP-25 antigen having a carboxyl-terminus at the P_1 residue of the BoNT/A cleavage site scissile bond.

[0215] These results were confirmed using an ELISA light chain activity assay. A 96-well Reacti-Bind Streptavidin coated plates (Pierce Biotechnology, Rockford, IL) were prepared by adding approximately 100 µl of the following Substrate Solution: Rows A-C were coated with 100 µL of BIRA-HIS TAG®-SNAP-$25_{134-197}$ at twelve different concentrations; Rows D-H were coated with 100 µL of BIRA-HIS TAG®-SNAP-$25_{134-206}$ at 10 µg/mL. The plates were washed by aspirating the Substrate Solution and rinsing each well three times with 200 µl TBS, 0.1% TWEEN-20® (polyoxyethylene (20) sorbitan monolaureate). Dilutions of BoNT/A were pre-reduced at 37 °C for 20 minutes in BoNT/A Incubation Buffer (50 mM HEPES, pH 7.4, 1% fetal bovine serum, 10 µM $ZnCl_2$, 10 mM dithiothrietol) and 100 µl of the pre-reduced BoNT/A was added to the substrate-coated plates and incubated at 37 °C for 90 minutes. BoNT/A treated plates were washed by aspirating the BoNT/A Incubation Buffer and rinsing each plate three times with 200 µl TBS, 0.1% TWEEN-20® (polyoxyethylene (20) sorbitan monolaureate). Washed plates were incubated at 37 °C for one hour in 0.5% BSA in 1 x TBS containing a 1:10 to 1:100 dilution of the antibody-containing serum being tested. Primary antibody probed plates were washed four times for 5 minutes each time in 200 µl TBS, 0.1% TWEEN-20® (polyoxyethylene (20) sorbitan monolaureate). Washed plates were incubated at 37 °C for 1 hour in 1 x TBS containing a 1:10,000 dilution of goat polyclonal anti-mouse IgG

antibody conjugated to Horseradish peroxidase (Pierce Biotechnology, Rockford, IL) as a secondary antibody. Secondary antibody-probed plates were washed four times in 200 µl TBS, 0.1% TWEEN-20® (polyoxyethylene (20) sorbitan monolaureate). Chromogenic detection of the labeled SNAP-25 products were visualized by chromogenic detection using ImmunoPure TMB substrate kit (Pierce Biotechnology, Rockford, IL). The development of a yellow color, which correlated with the presence of the SNAP-25_{197} cleavage product was detected in BoNT/A treated samples, but not untreated controls, using antibody-containing serum derived from all six immunized mice (Mouse 1, Mouse 2, Mouse 3, Mouse 4, Mouse 5, and Mouse 6). Thus, the comparative ELISA analysis indicated that of the mice used for immunization, three mice (Mouse 2, Mouse 3, and Mouse 4) had higher titers and more specificity towards a SNAP-25 antigen having a carboxyl-terminus at the P_1 residue of the BoNT/A cleavage site scissile bond.

[0216] For cell-based cleavage assay, a suitable density of PC12 cells were plated into 60 mm^2 tissue culture plates containing 3 mL of an appropriate serum medium (Table 1). The cells were grown in a 37 °C incubator under 5% carbon dioxide until cells reached the appropriate density. A 500 µL transfection solution was prepared by adding 250 µL of OPTI-MEM® Reduced Serum Medium containing 15 µL of LIPOFECTAINE® 2000 (Invitrogen Inc., Carlsbad, CA) incubated at room temperature for 5 minutes to 250 µL of OPTI-MEM® Reduced Serum Medium containing 10 µg of a pQBI-25/GFP-BoNT/A-LC expression construct (SEQ ID NO: 51). The pQBI-25/GFP-BoNT/A-LC expression construct comprises a pQBI-25 expression vector (Qbiogene Inc., Carlsbad, CA) whose promoter elements are functionally linked to a polynucleotide encoding the GFP-BoNT/A light chain of SEQ ID NO: 52. This transfection mixture was incubated at room temperature for approximately 20 minutes. The media was replaced with fresh unsupplemented media and the 500 µL transfection solution was added to the cells. The cells were then incubated in a 37 °C incubator under 5% carbon dioxide for approximately 6 to 18 hours. The cells were washed and harvested as described in Example II. To detect for the presence of the cleaved SNAP-25_{197} product, an aliquot from each harvested sample was analyzed by Western blot as described in Example II, except that the primary antibody used was a 1:1,000 dilution of the antibody-containing serum and the secondary antibody used was a 1:20,000 of mouse α-IgG Horseradish Peroxidase (Pierce Biotechnology, Rockford, IL). A single band corresponding to the SNAP-25_{197} cleavage product was detected in BoNT/A treated samples, but not untreated controls, using antibody-containing serum derived from three mice (Mouse 2, Mouse 3, and Mouse 4). Thus, the cell-based cleavage assay indicated that of the mice used for immunization, three mice (Mouse 2, Mouse 3, and Mouse 4) had higher titers and more specificity towards a SNAP-25 antigen having a carboxyl-terminus at the P_1 residue of the BoNT/A cleavage site scissile bond.

3. Production of hybridomas.

[0217] To make hybridomas producing α-SNAP-25 monoclonal antibodies that can selectively bind to a SNAP-25 antigen having a carboxyl-terminus at the P_1 residue of the BoNT/A cleavage site scissile bond, the spleen from Mouse 2 was harvested three days subsequent to a final "booster" immunization and the

spleen cells were fused with myeloma cells P3-X63 Ag8.653 using standard hybridoma protocols. These cells were plated into five 96-well plates and hybrids were selected using HAT medium. Within 8-14 days after fusion, the first screening of the approximately 480 parent clones was carried out using comparative ELISA with the BIRA-HIS TAG®-SNAP-$25_{134-197}$ and the BIRA-HIS TAG®-SNAP-$25_{134-206}$ peptides coated in two separate plates. The comparative ELISA provided a quick screen method to identify hybridomas producing antibodies specific for the cleaved SNAP-25_{197}. The top 18 clones were subjected to further screening using the cell-based cleavage assay described above and immunostaining of LC/A transfected cells. (Table 18).

Table 18. Analysis of Supernatants Containing α-SNAP-25 Monoclonal Antibody

Clone	Comparative ELISA				Cell-Based Assay	
	OD SNAP-25_{197}	OD SNAP-25_{206}	$Ratio_{197/206}$	$Ratio_{206/197}$	SNAP-25_{197}	SNAP-25_{206}
1D3	1.805	0.225	8.02	0.13	+++	–
1F12	0.365	0.093	3.92	0.25	–	–
1G10	0.590	0.137	4.31	0.23	++	–
1H1	0.335	0.121	2.77	0.36	–	–
1H8	0.310	0.302	1.03	0.97	+	–
2C9	0.139	0.274	0.51	1.97	–	–
2E2	0.892	0.036	24.78	0.04	++	–
2E4	0.228	0.069	3.30	0.30	+	–
2F11	1.095	1.781	0.61	1.63	–	–
3C1	1.268	0.053	23.92	0.04	++	–
3C3	0.809	0.052	15.56	0.06	++	–
3E1	0.086	0.155	0.55	1.80	0	–
3E8	2.048	0.053	38.64	0.03	+++	–
3G2	0.053	0.158	0.34	2.98	–	–
4D1	0.106	0.218	0.49	2.06	–	–
4G6	0.061	0.159	0.38	2.61	–	–
5A5	0.251	0.106	2.37	0.42	+	–
5F11	0.243	0.061	3.98	0.25	–	–

[0218] Clones 1D3, 1G10, 2E2, 3C1, 3C3, and 3E8 were further cloned by limiting dilution because the conditioned media produced by these clones comprised α-SNAP-25 antibodies with a preferential binding specificity having a $ratio_{197/206}$ of at least 4:1 for the SNAP-25_{197} cleavage product relative to the SNAP-25_{206} uncleaved substrate and detected the SNAP-25_{197}-cleavage product using the cell-based cleavage assay and the immunostaining of PC12 cells transfected with GFP-LC/A. Similarly clones 2C9, 2F11, 3G2, 4D1 and 4G6 were further cloned by limiting dilution because the conditioned media produced by these clones comprised α-SNAP-25 antibodies with a preferential binding specificity having a $ratio_{206/197}$ of at least 1.5:1 for the SNAP-25_{206} uncleaved substrate relative to the SNAP-25_{197} cleavage product and detected the SNAP-25_{206}-uncleaved substrate using the cell-based cleavage assay. These single-cell derived clones were screened again using comparative ELISA, cell-based cleavage, and immunostaining to confirm their affinity and specificity, and the antibodies were isotyped using standard procedures.

Ascites were produced from clones 1D3B8 (IgM.k), 1G10A12 (IgG3.k), 2C9B10 (IgG3.k), 2E2A6 (IgG3.k), 2F11B6 (IgM.k), 3C1A5 (IgG2a.k), and 3C3E2 (IgG2a.k). Clone 3E8 stopped producing antibodies during the cloning process and could not be further evaluated.

4. Evaluation of binding specificity of α-SNAP-25 monoclonal antibodies.

[0219] To evaluate binding specificity of an α-SNAP-25 monoclonal antibody that can selectively bind to a SNAP-25 antigen having a carboxyl-terminus at the P_1 residue of the BoNT/A cleavage site scissile bond, ascites from clones 1D3B8, 1G10A12, 2C9B10, 2E2A6, 2F11B6, 3C1A5, and 3C3E2 were used to detect SNAP-25 cleavage product using the cell-based activity assay, immunocytochemistry and immunoprecipitation.

[0220] For the cell-based activity assay, binding specificity was determined by analyzing the ability of α-SNAP-25 antibody-containing ascites to detect the uncleaved SNAP-25_{206} substrate and the cleaved SNAP-25_{197} product by Western blot analysis. A suitable density of PC12 cells were plated into 60 mm^2 tissue culture plates containing 3 mL of an appropriate serum medium, grown in a 37 °C incubator under 5% carbon dioxide until an appropriate cell density was reached, and transfected with the either a transfection solution lacking the pQBI-25/GFP-BoNT/A-LC expression construct (untransfected cells) or a transfection solution containing the pQBI-25/GFP-BoNT/A-LC expression construct (transfected cells) as described above. The cells were washed and harvested as described in Example I. To detect for the presence of both the uncleaved SNAP-25_{206} substrate and the cleaved SNAP-25_{197} product, an aliquot from each harvested sample was analyzed by Western blot as described in Example I, except that the primary antibody used was a 1:100 dilution of the α-SNAP-25 monoclonal antibody-containing ascites and the secondary antibody used was a 1:20,000 of α-mouse IgG conjugated to Horseradish Peroxidase (Pierce Biotechnology, Rockford, IL). In addition, three commercially available mouse α-SNAP-25 monoclonal antibodies were tested. SMI-81 (Sternberger Monoclonals Inc., Lutherville, MD), an α-SNAP-25 antibody the manufacturer indicates detects both the uncleaved SNAP-25_{206} substrate and the cleaved SNAP-25_{197} product, was used at a 15,000 dilution according to the manufacturer's recommendations. MC-6050 (Research & Diagnostic Antibodies, Las Vegas, NV), an α-SNAP-25 antibody the manufacturer indicates detects both the uncleaved SNAP-25_{206} substrate and the cleaved SNAP-25_{197} product, was used at a 1:100 dilution according to the manufacturer's recommendations. MC-6053 (Research & Diagnostic Antibodies, Las Vegas, NV), an α-SNAP-25 antibody the manufacturer indicates detects only the cleaved SNAP-25_{197} product, was used at a 1:100 dilution according to the manufacturer's recommendations.

[0221] Table 19 indicates the α-SNAP-25 antibody-containing ascites that detected only the SNAP-25_{197} cleavage product. The cell-based cleavage assay indicated that ascites produced from clones 1D3B8, 2C9B10, 2E2A6, 3C1A5, and 3C3E2 synthesize an α-SNAP-25 monoclonal antibody having high binding specificity for the SNAP-25_{197} cleavage product that allows for the selective recognition of this cleavage

product relative to the SNAP-25_{206} uncleaved substrate. Commercial antibody SMI-81 detected the SNAP-25_{206} uncleaved substrate, but only poorly recognized the SNAP-25_{197} cleavage product (Table 19). Surprisingly, commercial antibody MC-6050 only detected the SNAP-25_{206} uncleaved substrate, and failed to recognize the SNAP-25_{197} cleavage product (Table 19). Even more surprisingly, commercial antibody MC-6050 only detected the SNAP-25_{206} uncleaved substrate, and failed to recognize the SNAP-25_{197} cleavage product, even though the manufacturer advertises that this antibody selectively detects the SNAP-25_{197} cleavage product (Table 19). Thus, this analysis indicates that while 1D3B8, 2C9B10, 2E2A6, 3C1A5, and 3C3E2 exhibit suitable selectivity for the SNAP-25_{197} cleavage product, 1G10A12 and 2F11B6 do not. In addition, commercial antibodies SMI-81, MC-6050 and MC-6053 all are unsuitable for the immuno-based methods disclosed in the present application because all failed to selectivity detect the SNAP-25_{197} cleavage product.

[0222] For immunocytochemistry analysis, binding specificity was determined by analyzing the ability of α-SNAP-25 antibody-containing ascites to detect the uncleaved SNAP-25_{206} substrate and the cleaved SNAP-25_{197} product by immunostaining. *See e.g.*, Ester Fernandez-Salas et al., *Plasma Membrane Localization Signals in the Light Chain of Botulinum Neurotoxin*, Proc. Natl. Acad. Sci., U.S.A. 101(9): 3208-3213 (2004). A suitable density of PC12 cells were plated, grown, and transfected with either a transfection solution lacking the pQBI-25/GFP-BoNT/A-LC expression construct (untransfected cells) or a transfection solution containing the pQBI-25/GFP-BoNT/A-LC expression construct (transfected cells) as described above. The cells were washed in 1 x PBS and fixed in 5 mL of PAF at room temperature for 30 minutes. Fixed cells were washed in phosphate buffered saline, incubated in 5 mL of 0.5% Triton® X-100 (polyethylene glycol octylphenol ether) in 1 x PBS, washed in 1 x PBS, and permeabilized in 5 mL of methanol at -20 °C for six minutes. Permeabilized cells were blocked in 5 mL of 100 mM glycine at room temperature for 30 minutes, washed in 1 x PBS, and blocked in 5 mL of 0.5% BSA in 1 x PBS at room temperature for 30 minutes. Blocked cells were washed in 1 x PBS and incubated at room temperature for two hours in 0.5% BSA in 1 x PBS containing a 1:10 dilution of an ascites from a clonal hybridoma cell line being tested. Primary antibody probed cells were washed three times for 5 minutes each time in 1 x PBS. Washed cells were incubated at room temperature for 2 hours in 1 x PBS containing a 1:200 dilution of goat polyclonal anti-mouse immunoglobulin G, heavy and light chains (IgG, H+L) antibody conjugated to ALEXA® FLUOR 568 (Invitrogen Inc., Carlsbad, CA) as a secondary antibody. Secondary antibody-probed cells were washed three times for 5 minutes each time in 1 x PBS. Washed cells were prepared for microscopic examination by mounting in VECTASHIELD® Mounting Media (Vector Laboratories, Burlingame, CA) and coverslipped. Images of signal detection were obtained with a Leica confocal microscope using appropriate laser settings. Table 19 indicates that the α-SNAP-25 antibody-containing ascites that specifically detected the SNAP-25_{197}-cleavage product. The immunocytochemistry analysis indicated that ascites produced from clones 1D3B8, 2C9B10, 2E2A6, 3C1A5, and 3C3E2 synthesize an α-SNAP-25 monoclonal antibody having high binding specificity for the SNAP-25_{197} cleavage product that allows for the preferential recognition of this cleavage product relative to the SNAP-25_{206} uncleaved substrate.

[0223] For immunoprecipitation analysis, binding specificity was determined by analyzing the ability of Protein A (HiTrap™ Protein A HP Columns, GE Healthcare, Amersham, Piscataway, NJ), purified α-SNAP-25 monoclonal antibodies to precipitate the uncleaved SNAP-25_{206} substrate and the cleaved SNAP-25_{197} product. *See e.g.*, Chapter 8 *Storing and Purifying Antibodies*, pp. 309-311, Harlow & Lane, *supra*, 1998a. A suitable density of PC12 cells were plated, grown, and transfected with either a transfection solution containing a pQBI-25/GFP expression construct (control cells; SEQ ID NO: 53) or a transfection solution containing the pQBI-25/GFP-BoNT/A-LC expression construct (experimental cells) as described above. The pQBI-25/GFP expression construct comprises an expression vector whose promoter elements are functionally linked to a polynucleotide encoding GFP of SEQ ID NO: 54. After an overnight incubation, the cells were washed by aspirating the growth media and rinsing each well with 200 µL 1 x PBS. To harvest the cells, the PBS was aspirated, the cells were lysed by adding an Immunoprecipitation Lysis Buffer comprising 50 mM HEPES, 150 mM NaCl, 1.5 mM $MgCl_2$, 1 mM EGDT, 10% glycerol, 1% Triton® X-100 (polyethylene glycol octylphenol ether) and a 1 x COMPLETE™ Protease inhibitor cocktail (Roche Applied Biosciences, Indianapolis, IN) and incubating at 4 °C for one hour. The lysed cells were centrifuged at 3,000 x *g* at 4 °C for 10 minutes to remove cellular debris and the supernatant transferred to a clean tube and diluted to a protein concentration of approximately 1 mg/mL. Approximately 5 µg of purified monoclonal antibody was added to 0.5 mL of diluted supernatant and incubated at 4 °C for two hours. After primary antibody incubation, approximately 50 µl of immobilized Protein G (Pierce Biotechnology, Rockford, IL) was added to the diluted supernatant and incubated at 4 °C for one hour. The incubated supernatant was washed three times for 30 minutes each time by adding 0.5 mL of Immunoprecipitation Lysis Buffer, centrifuging at 300 x *g* at 4 °C for one minute to pellet the immobilized Protein G, and decanting the supernatant. After washing, the pellet was resuspended in 30 µL of 1 x SDS Loading Buffer and the sample was heated to 95 °C for 5 minutes. To detect for the presence of both the uncleaved SNAP-25_{206} substrate and the cleaved SNAP-25_{197} product, an aliquot from each harvested sample was analyzed by Western blot as described in Example I, except that the primary antibody used was a 1:1,000 dilution of the α-SNAP-25 polyclonal antibody serum (see Example IV) and the secondary antibody used was a 1:20,000 of rabbit α-IgG Horseradish Peroxidase (Pierce Biotechnology, Rockford, IL). Table 19 indicates the α-SNAP-25 antibody-containing ascites that specifically pulled down the SNAP-25_{197}-cleavage product by immunoprecipitation analysis. The immunoprecipitation analysis indicated that ascites produced from clones 2E2A6 and 3C1A5 synthesize an α-SNAP-25 monoclonal antibody having high binding specificity for the SNAP-25_{197} cleavage product that allows for the preferential recognition of this cleavage product relative to the SNAP-25_{206} uncleaved substrate.

Table 19. Analysis of Clone Ascites Containing α-SNAP-25 Monoclonal Antibody

Clone	Cell-Based Assay		Immunocytochemistry		Immunoprecipitation	
	SNAP-25_{197}	SNAP-25_{206}	SNAP-25_{197}	SNAP-25_{206}	SNAP-25_{197}	SNAP-25_{206}
1D3B8	++	–	++	-	Not Tested	Not Tested
1G10A12	++	++	Not Tested	Not Tested	Not Tested	Not Tested

2C9B10	++	–	++	-	Not Tested	Not Tested
2E2A6	++	–	++	-	++	–
2F11B6	+	+	+	+	Not Tested	Not Tested
3C1A5	++	–	++	–	++	–
3C3E2	+	–	Not Tested	Not Tested	Not Tested	Not Tested
MC-6050	–	+	Not Tested	Not Tested	Not Tested	Not Tested
MC-6053	–	+	Not Tested	Not Tested	Not Tested	Not Tested
SMI-81	-/+	++	Not Tested	Not Tested	Not Tested	Not Tested

5. Evaluation of binding affinity of α-SNAP-25 monoclonal antibodies.

[0225] To determine the binding affinity of an α-SNAP-25 monoclonal antibody showing high binding specificity for either the SNAP-25_{197} cleavage product or the SNAP-25_{206} uncleaved substrate, binding affinity assays were performed on a BIACORE 3000 instrument using carboxymethyl dextran (CM5) sensor chips (BIAcore, Inc., Piscataway, NJ). Runs were conducted at 25 °C with HBS-EP buffer comprising 10 mM HEPES (pH 7.4), 150 mM sodium chloride, 3 mM EDTA, 0.005% (v/v) surfactant P20 at a flow rate of 10 µl/min. SNAP-25 peptides comprising amino acids 134-197 of SEQ ID NO: 5 (SNAP-$25_{134-197}$) or amino acids 134-206 of SEQ ID NO: 5 (SNAP-$25_{134-206}$) were covalently attached to the surface of the CM5 sensor chips using standard amine coupling. Briefly, the CM5 chips were activated by a 7 minute injection of a mixture of 0.2 M 1-ethyl-3-(3-dimethylaminopropyl) carbodiimide and 0.05 M N-hydroxysuccimide; the SNAP-25 peptides were then injected in 10 mM sodium acetate (pH 4.0) for 20 min at a flow rate of 10 µL/min; and unreacted succimide esters were blocked by a 7-min injection of 1 M ethanolamine hydrochloride, pH 8.5. The immobilized amount of SNAP-$25_{134-197}$ or SNAP-$25_{134-206}$ on the chip was reflected by a 100-150 increase in response units (about 0.10-0.15 ng/mm^2). Antibody samples comprising either ascites or purified monoclonal antibodies produced from clones 1D3B8, 2C9B10, 2E2A6, 3C1A5, and 3C3E2, as well as, commercially available α-SNAP-25 antibodies were passed over the surface of the CM5 chips allowing an association time of 10 min and a dissociation time of 20 min. The surfaces were regenerated between runs by a 1 minute injection of 10 mM glycine-HCl (pH 2.5) at a flow rate of 15 µL/min. Sensorgram curves were fitted to a 1:1 kinetic binding model with the BIAevaluation 3.0 software.

[0226] The results indicate that both 2E2A6 and 3C1A5 were highly specific for cleaved SNAP-25_{197} product over SNAP-25 uncleaved substrate (Table 20). When compared to the binding affinities of MC-6050 and MC-6053, 1D3B6 had an approximately 10-fold higher equilibrium disassociation constant for the SNAP-25 cleavage product relative to these commercial antibodies (Table 20). Interestingly, 2E2A6 had only a slightly lower equilibrium disassociation constant for the SNAP-25 cleavage product relative to these commercial antibodies (0.405 nM versus 0.497 and 0.508)(Table 20). As neither of these commercial α-SNAP-25 antibodies selectively recognized the SNAP-25 cleavage product (Table 19), an equilibrium disassociation constant lower than about 0.5 nM appears, in part, critical to achieve such selectivity. Similarly, when compared to the binding affinities of MC-6050 and MC-6053, 2E2A6 had an

about at least one-fold slower off rate/dissociation constant (6.74 x 10^{-5} versus 8.82 x 10^{-4} s^{-1} and 1.18 x 10^{-3} s^{-1}) (Table 20). This further suggests that an off rate/dissociation constant lower than about 8.82 x 10^{-4} appears, in part, critical to achieve selective binding for the SNAP-25 cleavage product. This result is consistent with 1D3B8, which had an off rate/dissociation constant of 5.78 x 10^{-5} s^{-1} (Table 20).

Table 20. Analysis of Binding Affinity α-SNAP-25 Monoclonal Antibodies

SPR Parameter	1D3B8		2E2A6	
	$SNAP\text{-}25_{197}$	$SNAP\text{-}25_{206}$[a]	$SNAP\text{-}25_{197}$	$SNAP\text{-}25_{206}$[b]
Ka (M^{-1} s^{-1})	1.06 x 10^{6}	—	1.70 x 10^{6} (1.66 x 10^{5})	— (—)
Kd (s^{-1})	5.78 x 10^{-5}	—	1.53 x 10^{-4} (6.74 x 10^{-5})	— (—)
KD (nM)	0.050	—	0.090 (0.405)	— (—)
SPR Parameter	**3C1A5**		**2C9B10**	
	$SNAP\text{-}25_{197}$	$SNAP\text{-}25_{206}$[c]	$SNAP\text{-}25_{197}$	$SNAP\text{-}25_{206}$[d]
Ka (M^{-1} s^{-1})	2.17 x 10^{5}	—	1.15 x 10^{4}	—
Kd (s^{-1})	2.88 x 10^{-4}	—	3.11 x 10^{-4}	—
KD (nM)	1.33	—	27.1	—
SPR Parameter	**MC-6050**		**MC-6053**	
	$SNAP\text{-}25_{197}$	$SNAP\text{-}25_{206}$	$SNAP\text{-}25_{197}$	$SNAP\text{-}25_{206}$
Ka (M^{-1} s^{-1})	1.78 x 10^{6}	3.06 x 10^{2}	2.32 x 10^{6}	1.06 x 10^{2}
Kd (s^{-1})	8.82 x 10^{-4}	6.07 x 10^{-3}	1.18 x 10^{-3}	2.56 x 10^{-5}
KD (nM)	0.497	19,800	0.508	240

[a] No binding was observed when up to 125 nM of α-SNAP-25 monoclonal antibody 1D3B8 was passed over the surface of the CM5 sensor chip after a 10 minute association time.

[b] No binding was observed when up to 10 μM of α-SNAP-25 monoclonal antibody 2E2A6 was passed over the surface of the CM5 sensor chip after a 10 minute association time.

[c] No binding was observed when up to 100 nM of α-SNAP-25 monoclonal antibody 3C1A5 was passed over the surface of the CM5 sensor chip after a 10 minute association time.

[d] No binding was observed when up to 100 nM of α-SNAP-25 monoclonal antibody 2C9B10 was passed over the surface of the CM5 sensor chip after a 10 minute association time.

[0227] To compare the six different antibodies, the on-rate (ka) and off-rate (kd) for each was normalized using a program from the BIA evaluation 4.1 software. For comparison of the on-rates, the data were first individually trimmed by deleting the re-generation portion and the injection spikes, and then normalized to a 0 to 100 scale. For comparison of the off-rate, the data were normalized to the injection stop/top point. This analysis showed that 2C9B10 had a much slower on-rate than the other antibodies (FIG. 3A), and that MC-6053 has a much faster off-rate (dissociation) that the other antibodies (FIG. 3B). The fast off-rate of MC-6053 indicates that this antibody will not perform well in the methods disclosed in the present specification because this antibody will have difficulty staying bound to the substrate antigen during the washing steps.

6. Sequencing of the epitope from isolated α-SNAP-25 monoclonal antibodies.

[0228] To determine the epitope of an isolated α-SNAP-25 monoclonal antibody that can selectively bind to a SNAP-25 antigen having a carboxyl-terminus at the P_1 residue of the BoNT/A cleavage site scissile bond, the polynucleotide molecule encoding the variable heavy (V_H) and variable light (V_L) chains of the α-SNAP-25 monoclonal antibody produced by hybridomas 1D3B8, 2C9B10, 2E2A6, 3C1A5 and 3C3E2 were sequenced. mRNA was extracted and purified from each hybridoma using standard protocols and reversed transcribed into cDNA using either an oligo dT anti-sense primer or a gene-specific (murine IgG1 CH and kappa CL) anti-sense primer. Specific murine and human constant domain primers were used to amplify the cDNA by PCR after cDNA production to determine the isotype of the antibody. Degenerate V_H and V_L primers were used to amplify the variable domains from the cDNA. For 5'RACE, a homopolymeric dCTP tail was added to the 3' end of the cDNA. The heavy and light chains were then amplified with an oligo dG sense primer and a gene specific (CH/KC) anti-sense primer. PCR products included the sequence of the signal peptide, variable domains and constant domains up to the anti-sense primer. The PCR products were gel purified to remove small fragments, and cloned into a blunt or TA vector for sequencing. Five independent clones for each chain were sequenced and alignments of V_H and VL chains and consensus sequences were determined. Methods used to determine the V_H and V_L amino acid sequences are described in, *e.g.*, Roger A. Sabbadini, et al., *Novel Bioactive Lipid Derivatives and Methods of Making and Using Same*, U.S. Patent Publication 2007/0281320; and Peter Amersdorfer, et al., *Molecular Characterization of Murine Humoral Immune Response to Botulinum Neurotoxin Type A Binding Domain as Assessed by Using Phage Antibody Libraries*, 65(9) Infect. Immun. 3743-3752, each of which is hereby incorporated by reference in its entirety. In addition, commercial services are available to sequence the variable heavy (V_H) and variable light (V_L) chains of an antibody and identify the CDR regions, see, *e.g.*, Fusion Antibodies Ltd., Northern Ireland.

[0229] The polynucleotide sequence comprising the V_H and V_L chains of the α-SNAP-25 monoclonal antibody produced by the hybridomas disclosed in the present specification is as follows: 1D3B8 V_H (SEQ ID NO: 71), 2C9B10 V_H (SEQ ID NO: 73), 2E2A6 V_H (SEQ ID NO: 75), 3C1A5 V_H (SEQ ID NO: 77), 3C3E2 V_H variant 1 (SEQ ID NO: 79), 3C3E2 V_H variant 2 (SEQ ID NO: 81), 3C3E2 V_H variant 3 (SEQ ID NO: 149), 1D3B8 V_L (SEQ ID NO: 83), 2C9B10 V_L (SEQ ID NO: 85), 2E2A6 V_L (SEQ ID NO: 87), 3C1A5 V_L (SEQ ID NO: 89), and 3C3E2 V_L (SEQ ID NO: 91). The amino acid sequence comprising the V_H and V_L chains of the α-SNAP-25 monoclonal antibody produced by the hybridomas disclosed in the present specification is as follows: 1D3B8 V_H (SEQ ID NO: 72), 2C9B10 V_H (SEQ ID NO: 74), 2E2A6 V_H (SEQ ID NO: 76), 3C1A5 V_H (SEQ ID NO: 78), 3C3E2 V_H variant 1 (SEQ ID NO: 80), 3C3E2 V_H variant 2 (SEQ ID NO: 82); 3C3E2 V_H variant 2 (SEQ ID NO: 150), 1D3B8 V_L (SEQ ID NO: 84), 2C9B10 V_L (SEQ ID NO: 86), 2E2A6 V_L (SEQ ID NO: 88), 3C1A5 V_L (SEQ ID NO: 90), and 3C3E2 V_L (SEQ ID NO: 92). The amino acid sequences comprising the V_H and V_L CDR domains of the α-SNAP-25 monoclonal antibody produced by the hybridomas 1D3B8, 2C9B10, 2E2A6, 3C1A5, and 3C3E2 are given in Table 21.

Table 21. CDR Sequences of V_H and V_L domains from α-SNAP-25 Monoclonal Antibodies			
CDR	**Sequence**	**Identified In**	**SEQ ID NO:**
V_H CDR 1	TFTDHSIH	2E2A6 2C9B10 3C1A5	93
V_H CDR 1	TFTNYVIH	3C3E2	94
V_H CDR 1	IFTDHALH	1D3B8	95
V_H CDR 2	YIFPGNGNIEYNDKFKG	2E2A6	96
V_H CDR 2	YLFPGNGNFEYNEKFKG	2C9B10 3C1A5	97
V_H CDR 2	YINPYNDGSKYNEKFKG	3C3E2	98
V_H CDR 2	YIFPGNGNIEYNEKFKG	1D3B8	99
V_H CDR 3	KRMGY	2E2A6 3C1A5	100
V_H CDR 3	KKMDY	2C9B10 1D3B8	101
V_H CDR 3	ARMDY	3C3E2var1	102
V_H CDR 3	ARMGY	3C3E2var2	151
V_H CDR 3	ARHLANTYYYFDY	3C3E2var3	152
V_L CDR 1	RSSQSIVHSNGNTYLE	1D3B8	103
V_L CDR 1	RTTENIYSYFV	2C9B10	104
V_L CDR 1	KSSQSLLYTNGKTYLT	2E2A6	105
V_L CDR 1	KSSQSLLNTNGKTYLT	3C1A5	106
V_L CDR 1	RASQNIGNYLH	3C3E2	107
V_L CDR 2	KVSNRFS	1D3B8	108
V_L CDR 2	NAKSLAE	2C9B10	109
V_L CDR 2	LVSELDS	2E2A6	110
V_L CDR 2	LVSKLDS	3C1A5	111
V_L CDR 2	YASQSIS	3C3E2	112
V_L CDR 3	FQGSHVPPT	1D3B8	113
V_L CDR 3	QHHYGTPYT	2C9B10	114
V_L CDR 3	LQSAHFPFT	2E2A6	115
V_L CDR 3	LQSSHFPFT	3C1A5	116
V_L CDR 3	QQSDTWPLT	3C3E2	117

[0230] Non-limiting examples of amino acid sequences comprising V_H CDR domain variants of the α-SNAP-25 monoclonal antibody produced by the hybridomas disclosed in the present specification include V_H CDR1 variant SEQ ID NO: 118 for 1D3B8; V_H CDR1 variant SEQ ID NO: 119 for 2C9B10, 2E2A6 and 3C1A5 V_H; V_H CDR1 variant SEQ ID NO: 120 for 3C1A5 V_H and 3C3E2 variant 3; V_H CDR2 variant SEQ ID NO: 121 for 1D3B8 and 2E2A6; V_H CDR2 variant SEQ ID NO: 122 for 2C9B10 and 3C1A5 V_H; V_H CDR2 variant SEQ ID NO: 123 for 3C1A5 V_H and 3C3E2 variant 3; V_H CDR3 variant MDY for 1D3B8 and 2C9B10; V_H CDR3 variant MGY for 2E2A6 and 3C1A5 V_H; and V_H CDR3 variant SEQ ID NO: 124 for 3C1A5 V_H and 3C3E2 variant 3. Non-limiting examples of amino acid sequences comprising V_L CDR domain variants of the α-SNAP-25 monoclonal antibody produced by the hybridomas disclosed in the

present specification include V_L CDR1 variant SEQ ID NO: 125 for 1D3B8; V_L CDR1 variant SEQ ID NO: 126 for 2C9B10; V_L CDR1 variant SEQ ID NO: 127 for 2E2A6; V_L CDR1 variant SEQ ID NO: 128 for 3C1A5; V_L CDR1 variant SEQ ID NO: 129 for 3C3E2; V_L CDR2 variant KVS for 1D3B8; V_L CDR2 variant NAK for 2C9B10; V_L CDR2 variant LVS for 2E2A6; V_L CDR2 variant YAT for 3C1A5; and V_L CDR2 variant YAS for 3C3E2.

Example IX

Development of α-SNAP-25 Polyclonal Antibodies that Selectively Bind a SNAP-25 Epitope Having a Free Carboxyl-terminus at the P_1 Residue of the BoNT/A Cleavage Site Scissile Bond

[0231] The following example illustrates how to make α-SNAP-25 polyclonal antibodies that can selectively bind to a SNAP-25 epitope having a carboxyl-terminus at the P_1 residue of the BoNT/A cleavage site scissile bond.

[0232] To develop α-SNAP-25 polyclonal antibodies that bind an epitope comprising a carboxyl-terminus at the P1 residue from the BoNT/A cleavage site scissile bond from a SNAP-25 cleavage product, the 10-residue peptide CGGGRIDEANQ (SEQ ID NO: 46) was designed as a SNAP-25 cleavage product antigen. This peptide comprising a N-terminal Cysteine residue for conjugation to KLH, a G-spacer flexible spacer (GGG) linked to amino acids 191-197 of human SNAP-25 (SEQ ID NO: 5) and has a carboxylated C-terminal glutamine. Blast searches revealed that this peptide has high homology only to SNAP-25 and almost no possible cross-reactivity with other proteins in neuronal cells. The sequence was also carefully scrutinized by utilizing computer algorithms to determine hydropathy index, protein surface probability, regions of flexibility, and favorable secondary structure, followed by proper orientation and presentation of the chosen peptide sequence. The peptide was synthesized and conjugated to Keyhole Limpet Hemocyanin (KLH) to increase immunogenicity. Before the animals were immunized, naïve rabbits were first screened against cell lysates from candidate cell lines in a Western blot in order to identify animals that had no immunoreactivity to the proteins present in the cell lysates. Two pre-screened rabbits were immunized with this peptide, and after three immunizations in about eight weeks, the rabbits were bled for testing. The blood was allowed to clot by incubating at 4 °C for 60 minutes. The clotted blood was centrifuged at 10,000x g at 4 °C for 10 minutes to pellet the cellular debris. The resulting serum sample was dispensed into 50 µL aliquots and stored at -20 °C until needed.

[0233] A similar strategy based on other SNAP-25 antigens disclosed in the present specification is used to develop α-SNAP-25 polyclonal antibodies that bind an epitope comprising a carboxyl-terminus at the P1 residue from the BoNT/A cleavage site scissile bond from a SNAP-25 cleavage product. For example, the SNAP-25 antigen of SEQ ID NO: 47 can be conjugated to KLH instead of the SNAP-25 antigen of SEQ ID NO: 46. As another example, the amino acids 191-197 of human SNAP-25 from the SNAP-25 antigen of SEQ ID NO: 38 can be replaced with SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID

NO: 36, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, or SEQ ID NO: 44.

2. Screening for the presence of α-SNAP-25 polyclonal antibodies.

[0234] To determine the presence of α-SNAP-25 polyclonal antibodies that can selectively bind to a SNAP-25 antigen having a carboxyl-terminus at the P_1 residue of the BoNT/A cleavage site scissile bond, comparative ELISA and cell-based cleavage assays were performed using the extracted rabbit serum as described in Example VIII. The serum from both rabbits contained α-SNAP-25 polyclonal antibodies that can selectively bind to a SNAP-25 antigen having a carboxyl-terminus at the P_1 residue of the BoNT/A cleavage site scissile bond. The α-SNAP-25 rabbit polyclonal antibodies were designated as NTP 22 and NTP 23.

3. Purification of α-SNAP-25 polyclonal antibodies.

[0235] To purify α-SNAP-25 polyclonal antibodies that can selectively bind to a SNAP-25 antigen having a carboxyl-terminus at the P_1 residue of the BoNT/A cleavage site scissile bond, NTP 22 and NTP 23 antibodies from rabbit serum were purified using affinity columns containing the SNAP-25 antigen of SEQ ID NO: 46.

4. Evaluation of binding specificity of α-SNAP-25 polyclonal antibodies.

[0236] To evaluate binding specificity of an α-SNAP-25 polyclonal antibody that can selectively bind to a SNAP-25 antigen having a carboxyl-terminus at the P_1 residue of the BoNT/A cleavage site scissile bond, purified NTP 22 and NTP 23 α-SNAP-25 polyclonal antibodies were used to detect cleavage product using the cell-based activity assay, immunnocytochemistry and immunoprecipitation as described in Example VIII. The cell-based cleavage assay, immunocytochemistry analysis and immunoprecipitation analysis all indicated that NTP 22 and NTP 23 α-SNAP-25 polyclonal antibodies did not cross-react with uncleaved SNAP-25. Thus both NTP 22 and NTP 23 have high binding specificity for the SNAP-25_{197} cleavage product that allows for the preferential recognition of this cleavage product relative to the SNAP-25_{206} uncleaved substrate. Affinity for the antigens can be determined using SPR in the BiAcore as described in Example VIII.

[0237] Unless otherwise indicated, all numbers expressing quantities of ingredients, properties such as molecular weight, reaction conditions, and so forth used in the specification and claims are to be understood as being modified in all instances by the term "about." Accordingly, unless indicated to the contrary, the numerical parameters set forth in the specification and attached claims are approximations that may vary depending upon the desired properties sought to be obtained by the present invention. At the very least, and not as an attempt to limit the application of the doctrine of equivalents to the scope of

the claims, each numerical parameter should at least be construed in light of the number of reported significant digits and by applying ordinary rounding techniques. Notwithstanding that the numerical ranges and parameters setting forth the broad scope of the invention are approximations, the numerical values set forth in the specific examples are reported as precisely as possible. Any numerical value, however, inherently contains certain errors necessarily resulting from the standard deviation found in their respective testing measurements.

[0238] The terms "a," "an," "the" and similar referents used in the context of describing the invention (especially in the context of the following claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context. Recitation of ranges of values herein is merely intended to serve as a shorthand method of referring individually to each separate value falling within the range. Unless otherwise indicated herein, each individual value is incorporated into the specification as if it were individually recited herein. All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., "such as") provided herein is intended merely to better illuminate the invention and does not pose a limitation on the scope of the invention otherwise claimed. No language in the specification should be construed as indicating any non-claimed element essential to the practice of the invention.

[0239] Groupings of alternative elements or embodiments of the invention disclosed herein are not to be construed as limitations. Each group member may be referred to and claimed individually or in any combination with other members of the group or other elements found herein. It is anticipated that one or more members of a group may be included in, or deleted from, a group for reasons of convenience and/or patentability. When any such inclusion or deletion occurs, the specification is deemed to contain the group as modified thus fulfilling the written description of all Markush groups used in the appended claims.

[0240] Certain embodiments of this invention are described herein, including the best mode known to the inventors for carrying out the invention. Of course, variations on these described embodiments will become apparent to those of ordinary skill in the art upon reading the foregoing description. The inventor expects skilled artisans to employ such variations as appropriate, and the inventors intend for the invention to be practiced otherwise than specifically described herein. Accordingly, this invention includes all modifications and equivalents of the subject matter recited in the claims appended hereto as permitted by applicable law. Moreover, any combination of the above-described elements in all possible variations thereof is encompassed by the invention unless otherwise indicated herein or otherwise clearly contradicted by context.

[0241] Specific embodiments disclosed herein may be further limited in the claims using consisting of or consisting essentially of language. When used in the claims, whether as filed or added per amendment,

the transition term "consisting of" excludes any element, step, or ingredient not specified in the claims. The transition term "consisting essentially of" limits the scope of a claim to the specified materials or steps and those that do not materially affect the basic and novel characteristic(s). Embodiments of the invention so claimed are inherently or expressly described and enabled herein.

[0242] Furthermore, numerous references have been made to patents and printed publications throughout this specification. Each of the above-cited references and printed publications are individually incorporated herein by reference in their entirety.

[0243] In closing, it is to be understood that the embodiments of the invention disclosed herein are illustrative of the principles of the present invention. Other modifications that may be employed are within the scope of the invention. Thus, by way of example, but not of limitation, alternative configurations of the present invention may be utilized in accordance with the teachings herein. Accordingly, the present invention is not limited to that precisely as shown and described.

Table 5. Increased Gene Expression in Cell Lines H1 and BB10 vs. Cell Line 2D6 in Undifferentiated State Using Microarray Analysis

Gene Symbol	Probe Set ID	Representative Public ID	RefSeq Transcript ID	Entrez Gene ID	Log2 Ratio	pvalue
PLS3	201215_at	NM_005032	NM_005032	5358	6.56	2.91E-12
H99792	225710_at	H99792	---	---	6.46	1.81E-07
DAZ1	208282_x_at	NM_020363	NM_00100537	1617	6.45	4.63E-04
DAZ3			5	57054		
DAZ2			NM_00100578	57055		
DAZ4			5	57135		
			NM_00100578			
			6			
			NM_004081			
			NM_020363			
			NM_020364			
			NM_020420			
TPTE	220205_at	NM_013315	NM_013315	7179	6.44	3.16E-08
			NM_199259			
			NM_199260			
			NM_199261			
DAZ1	207909_x_at	U21663	NM_00100537	1617	6.20	2.48E-04
DAZ3			5	57054		
DAZ2			NM_00100578	57055		
DAZ4			5	57135		
			NM_00100578			
			6			
			NM_004081			
			NM_020363			
			NM_020364			
			NM_020420			
MSN	200600_at	NM_002444	NM_002444	4478	6.11	2.92E-09
CXCR4	217028_at	AJ224869	NM_00100854	7852	5.95	3.23E-04
			0			
			NM_003467			
NDN	209550_at	U35139	NM_002487	4692	5.81	3.18E-06
FLJ32942	227711_at	BG150433	NM_144594	121355	5.73	8.08E-09
AI197932	229498_at	AI197932	---	---	5.59	3.21E-08
PEG3	209242_at	AL042588	NM_006210	5178	5.58	1.13E-07
TIMP3	201149_s_at	U67195	NM_000362	7078	5.57	3.00E-05
NEDD9	202149_at	AL136139	NM_006403	4739	5.49	3.70E-09
			NM_182966			
TIMP3	201150_s_at	NM_000362	NM_000362	7078	5.40	1.53E-03
PRSS12	205515_at	NM_003619	NM_003619	8492	5.37	1.39E-06
LUM	201744_s_at	NM_002345	NM_002345	4060	5.37	1.04E-06
RGS5	1555725_a_at	AF493929	NM_003617	8490	5.22	2.23E-07
TFPI2	209278_s_at	L27624	NM_006528	7980	5.22	1.95E-05
CXCR4	211919_s_at	AF348491	NM_00100854	7852	5.18	9.56E-04
			0			
			NM_003467			
RGS5	218353_at	NM_025226	NM_003617	8490	5.15	1.82E-07
ASCL1	209985_s_at	BE797438	NM_004316	429	5.09	8.38E-06
KCTD12	212192_at	AI718937	NM_138444	115207	5.04	6.32E-06
SPARC	200665_s_at	NM_003118	NM_003118	6678	4.97	2.45E-06
CXCR4	209201_x_at	L01639	NM_00100854	7852	4.97	9.51E-04
			0			
			NM_003467			

TIMP3	201147_s_at	BF347089	NM_000362	7078	4.95	1.56E-04
DAZ1	207912_s_at	NM_004081	NM_00100537	1617	4.94	1.79E-03
DAZ3			5	57054		
DAZ2			NM_00100578	57055		
DAZ4			5	57135		
			NM_00100578			
			6			
			NM_004081			
			NM_020363			
			NM_020364			
			NM_020420			
MINA	213189_at	BE966695	NM_032778	84864	4.92	1.50E-08
			NM_153182			
CUGBP2	202157_s_at	U69546	NM_006561	10659	4.91	1.20E-06
BF000203	236385_at	BF000203	---	---	4.87	6.43E-06
GRP	206326_at	NM_002091	NM_002091	2922	4.82	1.83E-06
RGS5	209070_s_at	AI183997	NM_003617	8490	4.78	1.01E-07
AI183997	233858_at	AU144918	---	---	4.72	1.79E-05
RNF182	230720_at	AI884906	NM_152737	221687	4.72	4.74E-07
PEG3	209243_s_at	AF208967	NM_006210	5178	4.69	8.13E-06
RAM2	225081_s_at	AK022955	NM_018719	55536	4.52	1.18E-04
)KFZp667G211	214030_at	BE501352	XM_376254	131544	4.52	6.37E-10
RGS5	209071_s_at	AF159570	NM_003617	8490	4.50	1.74E-07
VIP	206577_at	NM_003381	NM_003381	7432	4.44	2.77E-04
			NM_194435			
PRSS12	213802_at	AI810767	NM_003619	8492	4.41	1.46E-03
MGC34032	235763_at	AA001450	NM_152697	204962	4.40	3.84E-08
DAZ1	208281_x_at	NM_020364	NM_00100537	1617	4.39	5.53E-04
DAZ3			5	57054		
DAZ2			NM_00100578	57055		
DAZ4			5	57135		
			NM_00100578			
			6			
			NM_004081			
			NM_020363			
			NM_020364			
			NM_020420			
DAZ1	216922_x_at	AF271088	NM_00100537	1617	4.35	6.79E-04
DAZ3			5	57054		
DAZ2			NM_00100578	57055		
DAZ4			5	57135		
			NM_00100578			
			6			
			NM_004081			
			NM_020363			
			NM_020364			
			NM_020420			
SPARC	212667_at	AL575922	NM_003118	6678	4.30	4.26E-05
MAB21L2	210302_s_at	AF262032	NM_006439	10586	4.28	1.96E-08
CCDC3	223316_at	AL136562	NM_031455	83643	4.21	1.24E-06
SLAC2-B	214734_at	AB014524	NM_015065	23086	4.20	1.64E-03
ARHGAP6	206167_s_at	NM_001174	NM_001174	395	4.19	1.68E-05
			NM_006125			
			NM_013422			
			NM_013423			
			NM_013427			
BASP1	202391_at	NM_006317	NM_006317	10409	4.18	3.67E-08
SIM1	206876_at	AL121948	NM_005068	6492	4.16	4.38E-05

SMC6L1	236535_at	AW069285	NM_024624	79677	4.09	2.41E-07
CUGBP2	202158_s_at	NM_006561	NM_006561	10659	4.09	8.95E-04
FAT	201579_at	NM_005245	NM_005245	2195	4.08	5.01E-03
GNG11	204115_at	NM_004126	NM_004126	2791	4.07	6.53E-04
ITGA6	201656_at	NM_000210	NM_000210	3655	3.98	4.23E-09
ACATE2	221641_s_at	AF241787	NM_012332	23597	3.97	4.71E-05
TCTE1L	203303_at	NM_006520	NM_006520	6990	3.96	2.11E-07
NEDD9	202150_s_at	U64317	NM_006403	4739	3.94	1.90E-06
			NM_182966			
DOK5	214844_s_at	AL050069	NM_018431	55816	3.83	1.64E-05
			NM_177959			
EDG2	204036_at	AW269335	NM_001401	1902	3.82	2.36E-08
			NM_057159			
MAOA	204388_s_at	NM_000240	NM_000240	4128	3.80	8.51E-05
SPAG6	210033_s_at	AF079363	NM_012443	9576	3.78	6.66E-06
			NM_172242			
BF476109	1556300_s_at	BF476109	---	---	3.78	7.77E-06
PTPRK	203038_at	NM_002844	NM_002844	5796	3.75	1.34E-03
GFRA2	205722_s_at	NM_001495	NM_001495	2675	3.74	7.15E-06
PTPRE	221840_at	AA775177	NM_006504	5791	3.72	2.12E-06
			NM_130435			
ADAMTS9	226814_at	AI431730	NM_020249	56999	3.70	9.69E-05
			NM_182920			
			NM_182921			
MINA	213188_s_at	AI823896	NM_032778	84864	3.69	3.36E-05
			NM_153182			
PLK2	201939_at	NM_006622	NM_006622	10769	3.69	1.39E-06
KIAA1754	225582_at	AA425726	NM_033397	85450	3.67	2.03E-04
FN5	219806_s_at	NM_020179	NM_020179	56935	3.65	2.97E-04
SMC6L1	218781_at	NM_024624	NM_024624	79677	3.64	1.72E-08
EML1	204797_s_at	NM_004434	NM_00100870	2009	3.64	6.58E-05
			7			
			NM_004434			
ADAMTS9	1562275_at	AL832835	NM_020249	56999	3.58	1.72E-06
			NM_182920			
			NM_182921			
LOC441157	1558795_at	AL833240	XM_499037	441157	3.56	7.55E-06
MAOA	212741_at	AA923354	NM_000240	4128	3.55	6.62E-04
TRIM29	211002_s_at	AF230389	NM_012101	23650	3.51	2.23E-07
			NM_058193			
MAOA	204389_at	NM_000240	NM_000240	4128	3.50	4.16E-07
MGC34032	1569112_at	AW020413	NM_152697	204962	3.50	9.78E-06
ELOVL7	227180_at	AW138767	XM_371740	79993	3.45	6.72E-04
TFPI2	209277_at	AL574096	NM_006528	7980	3.43	6.92E-06
ASCL1	213768_s_at	AW950513	NM_004316	429	3.36	5.80E-07
CHRNA7	210123_s_at	U62436	NM_000746	1139	3.33	4.22E-06
CHRFAM7A			NM_139320	89832		
			NM_148911			
ASCL1	209987_s_at	BC002341	NM_004316	429	3.33	1.82E-08
FRZB	203697_at	U91903	NM_001463	2487	3.31	1.02E-05
SLC43A3	210692_s_at	BC003163	NM_014096	29015	3.31	7.81E-05
			NM_017611			
			NM_199329			
LOC253012	242601_at	AA600175	NM_198151	253012	3.30	2.75E-04
CD9	201005_at	NM_001769	NM_001769	928	3.26	3.31E-04
SMAD6	207069_s_at	NM_005585	NM_005585	4091	3.26	6.45E-06
PCGF5	226326_at	AI798098	NM_032373	84333	3.26	7.00E-07
MAB21L2	210303_at	AF262032	NM_006439	10586	3.26	6.74E-05

SLC7A2	225516_at	AA876372	NM_00100853 9 NM_003046	6542	3.22	1.59E-06
AL109791	233932_at	AL109791	---	---	3.20	1.60E-03
MGC33926	229302_at	AA058832	NM_152390	130733	3.20	1.16E-03
KCTD12	212188_at	AA551075	NM_138444	115207	3.19	7.60E-05
MAFB	218559_s_at	NM_005461	NM_005461	9935	3.16	7.22E-03
BNC2	220272_at	NM_017637	NM_017637	54796	3.14	3.14E-03
ASCL1	209988_s_at	BC001638	NM_004316	429	3.14	4.77E-08
CBLN2	242301_at	R60224	NM_182511	147381	3.14	3.35E-03
ALCAM	240655_at	BE502785	NM_001627	214	3.13	2.14E-04
AF131795	233139_at	AF131795	---	---	3.12	8.04E-03
AI656180	242447_at	AI656180	---	---	3.12	3.69E-05
LOC402524	242206_at	AW590588	XM_379850	402524	3.10	5.25E-04
EDG3	228176_at	AA534817	NM_005226	1903	3.10	4.81E-04
KDELC2	225128_at	AL548941	NM_153705	143888	3.09	2.21E-04
NEGR1	243357_at	AA115106	NM_173808	257194	3.09	1.42E-05
DACT1	219179_at	NM_016651	NM_016651	51339	3.09	2.14E-04
DAZ1	216351_x_at	AF248483		1617	3.06	4.06E-04
DAZ3			NM_00100537	57054		
DAZ2			5	57055		
DAZ4			NM_00100578 5 NM_00100578 6 NM_004081 NM_020363 NM_020364 NM_020420	57135		
KIAA0527	214954_at	BF977837	XM_171054	26032	3.03	2.02E-04
TPBG	203476_at	NM_006670	NM_006670	7162	3.02	2.88E-05
LGR5	213880_at	AL524520	NM_003667	8549	3.02	2.16E-03
FLJ23091	228950_s_at	AL534095	NM_00100229 2 NM_024911	79971	3.01	2.38E-03
PLXNA4	232317_at	AB046770	XM_039393 XM_379927	57671	2.99	6.60E-07
FLJ20647	218802_at	NM_017918	NM_017918	55013	2.99	7.56E-03
CNTN4	229084_at	R42166	NM_175607 NM_175612 NM_175613	152330	2.96	2.55E-06
RBPMS	209488_s_at	D84109	NM_00100871 0 NM_00100871 1 NM_00100871 2 NM_006867	11030	2.96	5.32E-03
E2F7	228033_at	AI341146	NM_203394	144455	2.94	1.26E-03
TRIM29	202504_at	NM_012101	NM_012101 NM_058193	23650	2.93	6.42E-08
N26620	227503_at	N26620	---	---	2.93	1.14E-04
TIMP3	201148_s_at	AW338933	NM_000362	7078	2.91	1.23E-03
C2orf31	221245_s_at	NM_030804	---	81561	2.91	2.25E-05
)KFZp761O201	232313_at	AL122107	XM_044062	92293	2.91	1.59E-06
BC041965	1560411_at	BC041965	---	---	2.91	8.58E-04
GNAI1	227692_at	AU153866	NM_002069	2770	2.90	2.00E-06
GPR10	231805_at	AL563031	NM_004248	2834	2.90	1.19E-04

LGR5	210393_at	AF062006	NM_003667	8549	2.89	4.97E-05
ENC1	201340_s_at	AF010314	NM_003633	8507	2.89	4.72E-05
LOC51760	205613_at	NM_016524	NM_016524	51760	2.88	9.54E-03
GNG12	222834_s_at	N32508	NM_018841	55970	2.88	1.98E-04
BARD1	205345_at	NM_000465	NM_000465	580	2.87	6.84E-03
A2BP1	1553422_s_at	NM_145892	NM_018723	54715	2.86	4.30E-03
			NM_145891			
			NM_145892			
			NM_145893			
PPP1R3C	204284_at	N26005	NM_005398	5507	2.84	1.93E-05
AF086027	1559697_a_at	AF086027	---	---	2.83	1.45E-03
PMP22	210139_s_at	L03203	NM_000304	5376	2.83	1.89E-04
			NM_153321			
			NM_153322			
GFRA2	205721_at	U97145	NM_001495	2675	2.83	4.80E-04
PFKFB3	202464_s_at	NM_004566	NM_004566	5209	2.82	3.61E-03
BF222929	242346_x_at	BF222929	---	---	2.82	2.87E-04
SLC43A3	213113_s_at	AI630178	NM_014096	29015	2.80	1.02E-06
			NM_017611			
			NM_199329			
PEX5L	1562473_at	BC037943	NM_016559	51555	2.79	1.76E-04
PELO	226731_at	AA156873		53918	2.76	4.84E-03
			NM_015946			
FBN1	202765_s_at	AI264196	NM_000138	2200	2.76	2.17E-03
PLEKHE1	212719_at	AB011178	NM_194449	23239	2.75	5.65E-03
MYRIP	214156_at	AL050090	NM_015460	25924	2.75	2.44E-06
BNC2	235723_at	AA843242	NM_017637	54796	2.74	2.24E-03
CPVL	208146_s_at	NM_031311	NM_019029	54504	2.73	2.87E-03
			NM_031311			
PLXNA4	228104_at	AL117427	XM_039393	57671	2.72	4.31E-04
			XM_379927			
BF940761	229427_at	BF940761	---	---	2.69	4.80E-03
ARHGEF6	209539_at	D25304	NM_004840	9459	2.68	2.81E-04
H17657	241444_at	H17657	---	---	2.67	2.17E-04
GNAI1	209576_at	AL049933	NM_002069	2770	2.65	1.06E-07
LOC441157	1558796_a_at	AL833240	XM_499037	441157	2.65	1.11E-03
CADPS	1568603_at	AI912173	NM_003716	8618	2.64	4.31E-04
			NM_183393			
			NM_183394			
POSTN	210809_s_at	D13665	NM_006475	10631	2.63	1.47E-03
PTPRR	210675_s_at	U77917	NM_002849	5801	2.60	4.53E-03
			NM_130846			
MGC24103	232568_at	AU145658	---	158295	2.59	3.96E-04
STK17A	202693_s_at	AW194730	NM_004760	9263	2.59	1.11E-04
LOC440738	221697_at	AF276659	NM_001004343	440738	2.58	1.85E-03
MYO6	203215_s_at	AA877789	NM_004999	4646	2.56	7.95E-03
CADPS	1568604_a_at	AI912173	NM_003716	8618	2.56	2.70E-07
			NM_183393			
			NM_183394			
NR3C1	211671_s_at	U01351	NM_000176	2908	2.56	2.36E-09
FRZB	203698_s_at	NM_001463	NM_001463	2487	2.56	3.80E-04
FLJ23091	221958_s_at	AA775681	NM_00100229	79971	2.54	5.86E-03
			2			
			NM_024911			
ADAMTS9	1554697_at	AF488803	NM_020249	56999	2.54	1.99E-04
			NM_182920			
			NM_182921			
AW130600	226865_at	AW130600	---	---	2.53	4.86E-04

ST8SIA4	230836_at	AI422986	NM_005668 NM_175052	7903	2.50	7.33E-03
CNTN1	211203_s_at	U07820	NM_001843 NM_175038	1272	2.49	1.34E-04
EMILIN2	224374_s_at	AF270513	NM_032048	84034	2.48	1.13E-04
HGF	210997_at	M77227	NM_000601 NM_001010931 NM_001010932 NM_001010933 NM_001010934	3082	2.46	4.58E-03
AI582818	229053_at	AI582818	---	---	2.44	6.88E-03
LOC253981	226430_at	AI394438	---	253981	2.44	3.85E-03
GNG12	212294_at	BG111761	NM_018841	55970	2.42	1.06E-06
C6orf148	220513_at	NM_030568	NM_030568	80759	2.41	5.89E-03
OSBPL3	209626_s_at	AI202969	NM_015550 NM_145320 NM_145321 NM_145322 NM_145323 NM_145324	26031	2.40	9.56E-04
SEMA6D	233882_s_at	AK022831	NM_020858 NM_024966 NM_153616 NM_153617 NM_153618 NM_153619	80031	2.39	1.02E-03
PCDH8	206935_at	NM_002590	NM_002590 NM_032949	5100	2.37	6.17E-07
MAB21L1	206163_at	NM_005584	NM_005584	4081	2.36	4.98E-03
TSC	218872_at	NM_017899	NM_017899	54997	2.36	1.01E-05
PPP2R2B	213849_s_at	AA974416	NM_004576 NM_181674 NM_181675 NM_181676 NM_181677 NM_181678	5521	2.35	2.05E-06
PDE5A	227088_at	BF221547	NM_001083 NM_033430 NM_033431 NM_033437	8654	2.35	2.27E-04
ZNF521	226676_at	AK021452	NM_015461	25925	2.34	1.55E-03
PVRL3	213325_at	AA129716	NM_015480	25945	2.34	3.70E-06
ENC1	201341_at	NM_003633	NM_003633	8507	2.33	3.06E-05
RGMA	223468_s_at	AL136826	NM_020211	56963	2.33	1.24E-07
ST8SIA2	239537_at	AW589904	NM_006011	8128	2.32	8.94E-07

FGFR2	203639_s_at	M80634	NM_000141 NM_022969 NM_022970 NM_022971 NM_022972 NM_022973 NM_022974 NM_022975 NM_022976 NM_023028 NM_023029 NM_023030 NM_023031	2263	2.29	4.06E-03
BAMBI	203304_at	NM_012342	NM_012342	25805	2.29	2.34E-08
ARHGAP6	1563386_at	AL079282	NM_001174 NM_006125 NM_013422 NM_013423 NM_013427	395	2.27	2.07E-03
PLCL2	213309_at	AL117515	NM_015184	23228	2.27	1.92E-03
A2BP1	221217_s_at	NM_018723	NM_018723 NM_145891 NM_145892 NM_145893	54715	2.26	5.56E-03
LOC340109	1557765_at	BC039509	XM_379322	340109	2.25	2.28E-05
SLC39A8	209267_s_at	AB040120	NM_022154	64116	2.25	4.91E-03
ITGA6	215177_s_at	AV733308	NM_000210	3655	2.23	2.05E-03
CNTN1	227209_at	AI091445	NM_001843 NM_175038	1272	2.23	4.31E-03
EGLN3	219232_s_at	NM_022073	NM_022073	112399	2.23	7.56E-03
ZFHX4	219779_at	NM_024721	NM_024721	79776	2.22	1.39E-03
AF086027	1559696_at	AF086027	---	---	2.21	1.05E-03
AL050204	213929_at	AL050204	---	---	2.20	2.15E-03
TPTE	233879_at	AL137389	NM_013315 NM_199259 NM_199260 NM_199261	7179	2.20	2.76E-03
TMEM35	219685_at	NM_021637	NM_021637	59353	2.20	8.17E-03
MSX2	205555_s_at	D31771	NM_002449	4488	2.20	6.02E-04
GPR51	211679_x_at	AF095784	NM_005458	9568	2.19	5.89E-03
BE856929	239349_at	BE856929	---	---	2.17	2.00E-03
SYN2	210247_at	AW139618	NM_003178 NM_133625	6854	2.15	5.68E-03
COLEC12	221019_s_at	NM_030781	NM_030781 NM_130386	81035	2.15	7.66E-03
TCF7L1	221016_s_at	NM_031283	NM_031283	83439	2.14	1.38E-03
NRXN1	228547_at	BF509242	NM_004801 NM_138735	9378	2.13	8.92E-03
CRH	205630_at	NM_000756	NM_000756	1392	2.13	1.12E-03
GPR161	230369_at	AI743151	NM_007369 NM_153832	23432	2.12	1.61E-04
ZNF217	203739_at	NM_006526	NM_006526	7764	2.12	3.18E-04
NEDD9	233223_at	AK000850	NM_006403 NM_182966	4739	2.11	4.23E-04
RASEF	235144_at	AA826324	NM_152573	158158	2.09	2.92E-03
PLAT	201860_s_at	NM_000930	NM_000930 NM_000931 NM_033011	5327	2.09	6.29E-04

GPR51	209990_s_at	AF056085	NM_005458	9568	2.05	1.33E-05
AL161982	1563494_at	AL161982	---	---	2.05	1.21E-03
SEMA6D	226492_at	AL036088	NM_020858 NM_024966 NM_153616 NM_153617 NM_153618 NM_153619	80031	2.05	1.22E-04
ORF1-FL49	224707_at	AL522667	NM_032412	84418	2.04	2.79E-05
NID	202007_at	BF940043	NM_002508	4811	2.04	2.24E-03
PCGF5	229194_at	AL045882	NM_032373	84333	2.02	2.51E-04
TCF7L2	216035_x_at	AV721430	NM_030756	6934	2.02	2.84E-07
AA156721	201952_at	AA156721	---	---	2.02	1.05E-06
FBN1	202766_s_at	NM_000138	NM_000138	2200	2.02	7.81E-04
DBH	206450_at	NM_000787	NM_000787	1621	2.01	2.59E-03
PTPRR	206084_at	NM_002849	NM_002849 NM_130846	5801	2.01	4.19E-03
CNTN1	227202_at	AW072790	NM_001843 NM_175038	1272	2.00	1.32E-03
ARHGEF3	218501_at	NM_019555	NM_019555	50650	2.00	4.42E-05
SLITRK5	214930_at	AW449813	NM_015567	26050	2.00	7.82E-06
ETV1	206501_x_at	NM_004956	NM_004956	2115	1.99	3.21E-03
SPAG6	210032_s_at	AI651156	NM_012443 NM_172242	9576	1.99	2.72E-04
LCRISP1	223475_at	AF142573	NM_031461	83690	1.99	3.27E-03
FGFR2	211401_s_at	AB030078	NM_000141 NM_022969 NM_022970 NM_022971 NM_022972 NM_022973 NM_022974 NM_022975 NM_022976 NM_023028 NM_023029 NM_023030 NM_023031	2263	1.99	1.83E-04
FLJ30058	238047_at	AA405456	NM_144967	158763	1.99	3.10E-03
BF434771	1568598_at	BF434771	XM_498494	440000	1.98	2.21E-03
TCF7L2	216511_s_at	AJ270770	NM_030756	6934	1.97	7.59E-05
MYO6	203216_s_at	NM_004999	NM_004999	4646	1.96	8.88E-05
ATP2B4	212136_at	AW517686	NM_00100139 6 NM_001684	493	1.96	7.81E-03
RAB32	204214_s_at	NM_006834	NM_006834	10981	1.96	3.53E-03
AI703256	231336_at	AI703256	---	---	1.95	4.67E-04
FLJ40773	1563933_a_at	AK091691	NM_152666	200150	1.95	1.13E-03
LOC92689	213455_at	W87466	NM_138389	92689	1.95	5.71E-04
TCF7L2	212761_at	AI949687	NM_030756	6934	1.94	5.52E-05
TDRD7	213361_at	AW129593	NM_014290	23424	1.93	4.13E-03
GFPT2	205100_at	NM_005110	NM_005110	9945	1.92	3.68E-04

FGFR2	203638_s_at	NM_022969	NM_000141 NM_022969 NM_022970 NM_022971 NM_022972 NM_022973 NM_022974 NM_022975 NM_022976 NM_023028 NM_023029 NM_023030 NM_023031	2263	1.92	3.46E-03
ALCAM	201951_at	BF242905	NM_001627	214	1.91	6.46E-06
ETV1	217053_x_at	X87175	NM_004956	2115	1.91	7.09E-03
NR3C1	201865_x_at	AI432196	NM_000176	2908	1.90	1.19E-05
PDLIM5	203242_s_at	BG054550	NM_001011513 NM_001011514 NM_001011515 NM_001011516 NM_006457	10611	1.89	7.00E-05
ST8SIA2	221285_at	NM_006011	NM_006011	8128	1.89	8.94E-04
TWIST1	213943_at	X99268	NM_000474	7291	1.88	3.85E-04
TLE4	216997_x_at	AL358975	NM_007005	7091	1.88	7.83E-03
GPR161	214104_at	AI703188	NM_007369 NM_153832	23432	1.88	5.85E-03
EDG2	204037_at	BF055366	NM_001401 NM_057159	1902	1.87	9.88E-08
PDLIM5	216804_s_at	AK027217	NM_001011513 NM_001011514 NM_001011515 NM_001011516 NM_006457	10611	1.87	2.39E-05
R39126	230932_at	R39126	---	---	1.87	2.27E-04
AI377043	230722_at	AI377043	---	---	1.87	1.53E-03
W93046	230068_s_at	W93046	---	---	1.86	2.03E-03
DMN	212730_at	AK026420	NM_015286 NM_145728	23336	1.86	2.15E-03
ARHGAP24	223422_s_at	AI743534	NM_031305	83478	1.86	1.60E-03
CCNE2	211814_s_at	AF112857	NM_004702 NM_057735 NM_057749	9134	1.85	5.31E-03
NRXN1	209914_s_at	AW149405	NM_004801 NM_138735	9378	1.84	2.88E-03
ETV1	217061_s_at	AC004857	NM_004956	2115	1.83	4.93E-04
FAM19A5	229459_at	AV723914	NM_015381	25817	1.82	1.07E-06
ITPR1	240052_at	AA648993	NM_002222	3708	1.82	7.08E-04
ZAK	222757_s_at	AB030034	NM_016653 NM_133646	51776	1.81	3.74E-04

FGFR2	208228_s_at	M87771	NM_000141 NM_022969 NM_022970 NM_022971 NM_022972 NM_022973 NM_022974 NM_022975 NM_022976 NM_023028 NM_023029 NM_023030 NM_023031	2263	1.81	1.44E-03
ZNF545	1555793_a_at	AL834267	NM_133466	284406	1.80	4.60E-04
AW024890	229942_at	AW024890	---	---	1.79	6.14E-05
AI733341	240911_at	AI733341	---	---	1.79	7.62E-04
PPAP2B	209355_s_at	AB000889	NM_003713 NM_177414	8613	1.79	4.28E-04
TBX3	222917_s_at	U69556	NM_005996 NM_016569	6926	1.79	9.78E-06
TRIP10	202734_at	NM_004240	NM_004240	9322	1.79	8.00E-03
TCF7L2	212762_s_at	AI375916	NM_030756	6934	1.79	3.86E-07
PELO	214660_at	X68742	NM_015946	53918	1.78	2.39E-03
GPR51	217077_s_at	AF095723	NM_005458	9568	1.78	3.16E-04
FBLN1	202994_s_at	Z95331	NM_001996 NM_006485 NM_006486 NM_006487	2192	1.77	2.59E-03
DOK5	1554863_s_at	BC008992	NM_018431 NM_177959	55816	1.77	3.36E-03
NRXN1	209915_s_at	AB035356	NM_004801 NM_138735	9378	1.76	7.05E-03
FLJ25067	243507_s_at	AV715251	NM_152504	149840	1.76	6.53E-07
DNAPTP6	222154_s_at	AK002064	NM_015535	26010	1.76	4.90E-04
MGC21654	1556429_a_at	BC026969	NM_145647	93594	1.76	6.54E-03
CPNE4	228796_at	BE645967	NM_130808	131034	1.75	4.64E-04
POSTN	1555778_a_at	AY140646	NM_006475	10631	1.75	4.56E-05
ATOH8	228890_at	BF434995	NM_032827	84913	1.75	7.05E-04
ALCAM	1569362_at	BC041127	NM_001627	214	1.75	9.54E-03
HTATSF1	202601_s_at	AI373539	NM_014500	27336	1.75	5.33E-05
MYD88	209124_at	U70451	NM_002468	4615	1.74	3.20E-04
PPAP2B	212230_at	AV725664	NM_003713 NM_177414	8613	1.74	1.11E-05
ZNF253 LOC114977	242919_at	AV683221	NM_021047	114977 56242	1.73	1.13E-03
DCLRE1B	219490_s_at	NM_022836	NM_022836	64858	1.73	3.54E-03
TBX3	229576_s_at	N29712	NM_005996 NM_016569	6926	1.72	6.02E-07
KHDRBS3	230249_at	AI650382	NM_006558	10656	1.72	3.44E-04
FLJ39609	1555980_a_at	CA447406	XM_379692	284598	1.72	9.03E-03
BF110268	238178_at	BF110268	---	---	1.71	1.80E-04
KLF7	238482_at	AL120562	NM_003709	8609	1.71	1.93E-03
ELL2	226099_at	AI924426	NM_012081	22936	1.71	8.96E-04
KHDRBS3	209781_s_at	AF069681	NM_006558	10656	1.71	3.55E-05
TRIM37	1569114_at	BC011742	NM_00100520 7 NM_015294	4591	1.71	3.38E-03

DLL3	222898_s_at	BE350882	NM_016941 NM_203486	10683	1.70	5.19E-07
SNAI2	213139_at	AI572079	NM_003068	6591	1.70	2.74E-03
FAM19A5	229655_at	N66656	NM_015381	25817	1.70	4.35E-05
ZNF560	1553276_at	NM_152476	NM_152476	147741	1.70	2.56E-04
TBX3	219682_s_at	NM_016569	NM_005996 NM_016569	6926	1.69	1.06E-06
C20orf23	232083_at	AB046810	NM_024704	55614	1.69	8.35E-06
AF131796	231916_at	AF131796	---	---	1.69	2.15E-03
NSE1	229546_at	AI378035	NM_145175	151354	1.69	2.85E-08
CXorf34	205238_at	NM_024917	NM_024917	79979	1.68	6.46E-03
CRH	205629_s_at	BC002599	NM_000756	1392	1.68	5.48E-03
NR3C1	216321_s_at	X03348	NM_000176	2908	1.68	5.45E-07
PTGFRN	224937_at	BF311866	NM_020440	5738	1.67	6.89E-04
ARG99	226322_at	BF109231	NM_031920 NM_175861	83857	1.67	4.14E-03
NXN	243503_at	AI632740	NM_022463	64359	1.67	2.57E-04
STK17A	202695_s_at	NM_004760	NM_004760	9263	1.66	2.52E-03
C11orf8	205413_at	NM_001584	NM_001584	744	1.66	1.85E-05
PI15	229947_at	AI088609	NM_015886	51050	1.66	1.62E-04
NXT2	209629_s_at	AF201942	NM_018698	55916	1.65	3.43E-04
CDC25B	201853_s_at	NM_021873	NM_004358 NM_021872 NM_021873 NM_021874 NM_212530	994	1.65	4.80E-05
TPST2	204079_at	NM_003595	NM_00100856 6 NM_003595	8459	1.65	2.97E-04
LOC344595	235606_at	AA417117	XM_298151	344595	1.64	2.58E-05
H22448	242530_at	H22448	---	---	1.64	2.20E-04
BF981643	214720_x_at	BF981643	NM_144710 NM_178584	151011	1.64	1.45E-04
LOC93349	214791_at	AK023116	NM_138402	93349	1.64	9.50E-05
DOK4	209690_s_at	BF591163	NM_018110	55715	1.64	7.06E-06
LZTS1	47550_at	N21184	NM_021020	11178	1.63	3.08E-04
TBX3	225544_at	AI806338	NM_005996 NM_016569	6926	1.63	5.24E-06
FSTL1	208782_at	BC000055	NM_007085	11167	1.63	2.00E-03
EMILIN3	228307_at	AL137580	NM_052846	90187	1.63	2.86E-03
ATP2B4	212135_s_at	AW517686	NM_00100139 6 NM_001684	493	1.63	4.64E-03
AL833029	1559444_at	AL833029	---	---	1.63	2.28E-03
PDLIM5	203243_s_at	NM_006457	NM_00101151 3 NM_00101151 4 NM_00101151 5 NM_00101151 6 NM_006457	10611	1.62	2.91E-05
TBC1D19	220260_at	NM_018317	NM_018317	55296	1.62	6.08E-05
FZD5	206136_at	NM_003468	NM_003468	7855	1.62	1.51E-03
PCDH9	219737_s_at	AI524125	NM_020403 NM_203487	5101	1.62	3.72E-03

PDLIM5	212412_at	AV715767	NM_00101151 3 NM_00101151 4 NM_00101151 5 NM_00101151 6 NM_006457	10611	1.61	7.77E-04
ZNF537	223393_s_at	AL136805	NM_020856	57616	1.61	2.15E-03
AW052186	239942_at	AW052186	---	---	1.61	5.57E-03
GPR51	209991_x_at	AF069755	NM_005458	9568	1.60	1.65E-06
BF509125	232198_at	BF509125	---	---	1.60	4.75E-03
C14orf31	225464_at	N30138	NM_152330	122786	1.60	3.92E-03
PARVA	217890_s_at	NM_018222	NM_018222	55742	1.59	6.06E-03
CBLB	227900_at	AV701750	NM_170662	868	1.59	2.60E-03
EB-1	227441_s_at	AW005572	NM_020140 NM_152788 NM_181670	56899	1.59	2.08E-04
NAGA	1555041_a_at	M29276	NM_000262	4668	1.59	2.23E-06
KIAA1713	233536_at	AI202664	XM_290811	80816	1.59	9.66E-04
HOMER3	215489_x_at	AI871287	NM_004838	9454	1.58	2.88E-04
NFIB	233304_at	AU145782	NM_005596	4781	1.58	6.95E-03
SOX5	238009_at	AI446064	NM_006940 NM_152989 NM_178010	6660	1.58	9.49E-06
TCF7L2	216037_x_at	AA664011	NM_030756	6934	1.57	2.43E-03
LOC152573	229485_x_at	AI735586	XM_496688	152573	1.57	6.34E-05
DCBLD2	213865_at	AI378788	NM_080927	131566	1.57	1.25E-04
NS5ATP13TP2	1558613_at	BC040647	NM_178507	220323	1.56	8.59E-03
SAMHD1	204502_at	NM_015474	NM_015474	25939	1.56	9.98E-05
N50083	229110_at	N50083	---	---	1.56	4.18E-04
LRRN3	209840_s_at	AI221950	NM_018334	54674	1.55	9.99E-07
CADPS	233950_at	AK000873	NM_003716 NM_183393 NM_183394	8618	1.55	1.09E-04
ELL2	226982_at	AI745624	NM_012081	22936	1.55	3.35E-03
HRH3	220447_at	NM_007232	NM_007232	11255	1.54	6.15E-04
LRRN3	209841_s_at	AL442092	NM_018334	54674	1.54	6.25E-07
PLK4	211088_s_at	Z25433	NM_014264	10733	1.53	1.15E-03
NOS1	239132_at	BE299830	NM_000620	4842	1.53	1.65E-03
PLEKHF2	218640_s_at	NM_024613	NM_024613	79666	1.53	1.36E-03
MGC72104	243689_s_at	AI681945	NM_207350	284802	1.52	1.75E-04
NOS1	207309_at	NM_000620	NM_000620	4842	1.52	2.45E-04
C1orf43	1555225_at	BC008306	NM_015449 NM_138740	25912	1.52	2.71E-03
GPR161	206972_s_at	NM_007369	NM_007369 NM_153832	23432	1.52	4.09E-03
ODZ3	219523_s_at	NM_018104	XM_371717	55714	1.51	2.29E-04
DOK4	209691_s_at	BC003541	NM_018110	55715	1.50	1.43E-04
TRIM68	219405_at	NM_018073	NM_018073	55128	1.50	2.70E-05
DPYSL3	201431_s_at	NM_001387	NM_001387	1809	1.50	7.17E-03
RBL1	1559307_s_at	BG387892	NM_002895 NM_183404	5933	1.50	2.27E-03
MYO6	210480_s_at	U90236	NM_004999	4646	1.50	1.85E-05
SYNGR1	210613_s_at	BC000731	NM_004711 NM_145731 NM_145738	9145	1.50	8.09E-03

CDO1	204154_at	NM_001801	NM_001801	1036	1.50	3.73E-04
NXT2	209628_at	AK023289	NM_018698	55916	1.49	1.70E-03
ACO1	207071_s_at	NM_002197	NM_002197	48	1.49	5.20E-03
STOM	201060_x_at	AI537887	NM_004099 NM_198194	2040	1.49	3.02E-04
ZNF503	227195_at	AA603467	NM_032772	84858	1.49	8.67E-07
CBX5	242069_at	BE568225	NM_012117	23468	1.48	3.23E-04
PPAP2B	212226_s_at	AA628586	NM_003713 NM_177414	8613	1.48	2.29E-03
C20orf102	226973_at	AA206763	NM_080607	128434	1.47	1.33E-04
CDKN2C	211792_s_at	U17074	NM_001262 NM_078626	1031	1.47	7.95E-03
PDZRN3	212915_at	AL569804	NM_015009	23024	1.47	5.49E-04
CRYGD	207532_at	NM_006891	NM_006891	1421	1.46	3.28E-03
AW207243	238617_at	AW207243	---	---	1.46	3.92E-09
EIF5A2	235296_at	BG500474	NM_020390	56648	1.46	5.19E-09
ANKRD5	220144_s_at	NM_022096	NM_022096 NM_198798	63926	1.45	8.13E-04
UNQ470	228403_at	AL541276	NM_198573	375704	1.45	3.48E-03
KCNJ8	205303_at	BF514158	NM_004982	3764	1.45	5.86E-05
ID1	208937_s_at	D13889	NM_002165 NM_181353	3397	1.45	1.41E-04
SALL4	229661_at	NM_020436	NM_020436	57167	1.44	2.91E-05
DPYSL3	201430_s_at	W72516	NM_001387	1809	1.44	2.58E-03
MSX2	210319_x_at	D89377	NM_002449	4488	1.44	1.48E-03
FNDC5	226096_at	AI760132	NM_153756	252995	1.44	7.61E-04
ZNF239	206261_at	NM_005674	NM_005674	8187	1.44	6.22E-05
COBLL1	203642_s_at	NM_014900	NM_014900	22837	1.44	6.55E-03
KIAA1524	1553810_a_at	NM_020890	NM_020890	57650	1.44	8.59E-03
AL038824	213676_at	AL038824	XM_496810	441151	1.44	6.78E-04
ARL6	235320_at	AL138043	NM_032146 NM_177976	84100	1.44	4.10E-07
MGC15937	227794_at	BF432254	NM_080661	92292	1.43	3.16E-03
BE671123	235798_at	BE671123	---	---	1.43	4.96E-06
ARL6	223735_at	AL136815	NM_032146 NM_177976	84100	1.43	7.57E-05
LOC221810	221911_at	BE881590	---	221810	1.43	2.72E-03
SEZ6L	207873_x_at	NM_021115	NM_021115	23544	1.42	2.45E-05
DOK4	207747_s_at	NM_018110	NM_018110	55715	1.42	3.44E-05
SLC1A1	206396_at	NM_004170	NM_004170	6505	1.42	4.65E-03
NSE1	225667_s_at	AI601101	NM_145175	151354	1.42	1.15E-03
ARHGAP24	230803_s_at	AI761947	NM_031305	83478	1.42	3.92E-03
C6orf152	242006_at	AI379143	NM_181714	167691	1.42	6.09E-03
LOC132671	229331_at	AI559300	NM_145263	132671	1.41	1.82E-03
TH	208291_s_at	NM_000360	NM_000360 NM_199292 NM_199293	7054	1.40	7.49E-04
RBL1	1555004_a_at	BC032247	NM_002895 NM_183404	5933	1.40	5.16E-03
SFRP1	202037_s_at	NM_003012	NM_003012	6422	1.40	5.74E-05
CTNNA1	1558214_s_at	BG330076	NM_001903	1495	1.40	5.25E-07
CPT1A	210688_s_at	BC000185	NM_001876	1374	1.40	1.43E-03
AI917901	243140_at	AI917901	---	---	1.40	1.50E-04
HES1	203394_s_at	BE973687	NM_005524	3280	1.40	4.39E-06
GALNT7	222587_s_at	BF699855	NM_017423	51809	1.40	1.79E-03
MGC33846	231430_at	AW205640	NM_175885	220382	1.39	1.42E-03
SEZ6L	211894_x_at	AB041736	NM_021115	23544	1.39	9.95E-07
CHML	206079_at	NM_001821	NM_001821	1122	1.39	8.74E-03

EGLN3	222847_s_at	AI378406	NM_022073	112399	1.39	3.90E-03
MDM1	213761_at	AW664850	NM_017440 NM_020128	56890	1.38	1.18E-04
SFRP1	202035_s_at	AI332407	NM_003012	6422	1.38	3.39E-03
CBLN1	205747_at	NM_004352	NM_004352	869	1.38	1.13E-03
PDLIM5	211681_s_at	AF116705	NM_00101151 3 NM_00101151 4 NM_00101151 5 NM_00101151 6 NM_006457	10611	1.38	1.41E-04
NQO1	210519_s_at	BC000906	NM_000903	1728	1.38	4.39E-03
ST8SIA1	210073_at	L32867	NM_003034	6489	1.38	9.29E-04
AL359594	1566867_at	AL359594	---	---	1.38	4.68E-03
DLEU2	216870_x_at	AF264787	NM_006021	8847	1.38	2.48E-04
BF966021	212698_s_at	BF966021	NM_144710 NM_178584	151011	1.37	4.75E-04
C14orf125	226510_at	BF435286	XM_113763 XM_370759	25938	1.37	5.78E-03
TRIM37	1554001_at	BC036012	NM_00100520 7 NM_015294	4591	1.37	1.10E-05
TLE3	228340_at	BE967118	NM_005078	7090	1.36	2.10E-03
SFRP1	202036_s_at	AF017987	NM_003012	6422	1.36	1.13E-03
C5orf13	222344_at	AW972765	NM_004772	9315	1.36	3.74E-03
SLC8A3	1562403_a_at	AK096553	NM_033262 NM_058240 NM_182932 NM_182933 NM_182936 NM_183002	6547	1.36	1.60E-04
FGFR2	208234_x_at	NM_022976	NM_000141 NM_022969 NM_022970 NM_022971 NM_022972 NM_022973 NM_022974 NM_022975 NM_022976 NM_023028 NM_023029 NM_023030 NM_023031	2263	1.36	2.95E-03
DLL3	219537_x_at	NM_016941	NM_016941 NM_203486	10683	1.35	4.38E-05
CUGBP2	202156_s_at	N36839	NM_006561	10659	1.35	2.49E-03
APBB2	213419_at	U62325	NM_173075	323	1.35	5.44E-04
DOCK10	219279_at	NM_017718	NM_014689	55619	1.34	5.78E-05
MAPK12	206106_at	AL022328	NM_002969	6300	1.34	2.33E-06
TLE3	212770_at	AW873621	NM_005078	7090	1.34	8.20E-04
BE670307	227955_s_at	BE670307	---	---	1.34	1.89E-05

HGF	210998_s_at	M77227	NM_000601 NM_001010931 NM_001010932 NM_001010933 NM_001010934	3082	1.34	9.86E-03
FLJ11259	218627_at	NM_018370	NM_018370	55332	1.33	4.22E-03
AI826125	229866_at	AI826125	---	---	1.33	4.02E-04
SEZ6L	240709_at	AW204757	NM_021115	23544	1.33	5.75E-03
RAB27B	228708_at	BF438386	NM_004163	5874	1.33	9.45E-03
MAP3K1	225927_at	AA541479	XM_042066	4214	1.33	1.90E-03
AL040051	225481_at	AL040051	---	---	1.33	5.84E-04
BE967311	226225_at	BE967311	---	---	1.32	2.96E-05
TLE4	204872_at	NM_007005	NM_007005	7091	1.32	4.50E-03
SNCAIP	219511_s_at	NM_005460	NM_005460	9627	1.32	3.58E-04
KIAA0376	212480_at	AB002374	NM_015330	23384	1.32	2.79E-05
LZTS1	219042_at	NM_021020	NM_021020	11178	1.32	3.07E-04
KIAA0318	238817_at	BF063412	NM_015347	23504	1.32	5.00E-04
RNF34	219035_s_at	NM_025126	NM_025126 NM_194271	80196	1.32	1.40E-03
STXBP4	244404_at	AI376134	NM_178509	252983	1.31	3.35E-05
AU144956	232501_at	AU144956	---	---	1.31	6.46E-06
FLJ11127	219694_at	NM_019018	NM_019018	54491	1.31	1.32E-03
MITF	226066_at	AL117653	NM_000248 NM_006722 NM_198158 NM_198159 NM_198177 NM_198178	4286	1.31	1.07E-03
ETS1	224833_at	BE218980	NM_005238	2113	1.31	2.75E-03
NANOS1	228523_at	AW970089	NM_001009553 NM_199461	340719	1.31	1.30E-03
FAM19A5	237094_at	AI953086	NM_015381	25817	1.31	2.32E-07
LBH	221011_s_at	NM_030915	NM_030915	81606	1.31	1.22E-04
PEX26	219180_s_at	AI817074	NM_017929	55670	1.30	3.74E-03
GALNT7	218313_s_at	NM_017423	NM_017423	51809	1.30	1.80E-04
C2orf23	204365_s_at	NM_022912	NM_022912	65055	1.30	5.58E-03
AL049709	216548_x_at	AL049709	---	---	1.30	5.30E-04
MGC34032	1552782_at	AK091400	NM_152697	204962	1.30	1.97E-03
DLL1	224215_s_at	AF196571	NM_005618	28514	1.30	1.62E-04
TMEM20	236219_at	AI452512	NM_153226	159371	1.30	3.29E-03
AW305300	238962_at	AW305300	---	---	1.30	4.31E-04
C20orf23	219570_at	NM_024704	NM_024704	55614	1.29	1.18E-03
DRIM	209725_at	AF072718	NM_014503	27340	1.29	1.99E-03
CBLB	209682_at	U26710	NM_170662	868	1.29	3.69E-03
STRA6	1569335_a_at	BC015881	NM_022369	64220	1.29	9.19E-04
CRTAC1	221204_s_at	NM_018058	NM_018058	55118	1.28	5.56E-04
AF070602	216214_at	AF070602	---	---	1.28	5.02E-03
NAGA	202943_s_at	M38083	NM_000262	4668	1.28	1.26E-03
AK025909	233814_at	AK025909	---	---	1.27	1.16E-04
AI141426	229898_at	AI141426	---	---	1.27	6.87E-05
SLC8A1	241752_at	AA094434	NM_021097	6546	1.27	6.10E-04

INSIG1	201625_s_at	BE300521	NM_005542 NM_198336 NM_198337	3638	1.26	8.33E-03
IQGAP1	210840_s_at	D29640	NM_003870	8826	1.26	2.60E-04
GAP43	204471_at	NM_002045	NM_002045	2596	1.26	5.02E-04
PDLIM5	213684_s_at	BF671400	NM_00101151 3 NM_00101151 4 NM_00101151 5 NM_00101151 6 NM_006457	10611	1.26	9.47E-04
GAP43	216963_s_at	AF279774	NM_002045	2596	1.26	5.66E-03
KLHL5	226001_at	AK002174	NM_00100707 5 NM_199039	51088	1.26	3.67E-04
RGS4	204339_s_at	BC000737	NM_005613	5999	1.25	4.16E-04
AF279774	216967_at	AF279774	---	---	1.25	9.39E-03
PTER	218967_s_at	NM_030664	NM_00100148 4 NM_030664	9317	1.25	1.22E-03
TLE3	212769_at	AI567426	NM_005078	7090	1.25	3.78E-03
TLE3	206472_s_at	NM_005078	NM_005078	7090	1.25	4.37E-03
RGS4	204338_s_at	NM_005613	NM_005613	5999	1.25	3.77E-04
CPT1A	203634_s_at	NM_001876	NM_001876	1374	1.25	1.93E-03
ASAHL	227135_at	AI436803	NM_014435	27163	1.25	9.20E-06
LOC344595	239466_at	AA463827	XM_298151	344595	1.25	4.65E-05
TH1L	225006_x_at	AJ238379	NM_016397 NM_198976	51497	1.24	9.26E-03
SEZ6L	216047_x_at	AL050253	NM_021115	23544	1.24	1.75E-05
NSE1	234331_s_at	AK025063	NM_145175	151354	1.24	1.19E-04
LRRIQ2	219886_at	NM_024548	NM_024548	79598	1.24	1.44E-03
GALNT10	207357_s_at	NM_017540	NM_017540 NM_198321	55568	1.24	2.18E-03
BF815640	238517_at	BF815640	---	---	1.23	4.48E-03
SLC30A9	229500_at	AI609256	NM_006345	10463	1.23	2.32E-03
LOC63929	227910_at	AI635379	NM_022098	63929	1.23	1.48E-04
CSE1L	210765_at	AF053640	NM_001316 NM_177436	1434	1.23	7.45E-03
BCL2L11	1558143_a_at	AK027160	NM_006538 NM_138621 NM_138622 NM_138623 NM_138624 NM_138625 NM_138626 NM_138627 NM_207002 NM_207003	10018	1.23	6.27E-03
TM4SF14	221002_s_at	NM_030927	NM_030927	81619	1.22	4.04E-03
SLIT3	203813_s_at	NM_003062	NM_003062	6586	1.22	1.58E-06
RAPGEF5	204681_s_at	NM_012294	XM_499059	9771	1.22	6.58E-04
ZNF184	213452_at	AI811577	NM_007149	7738	1.22	9.16E-03
PCYT2	209577_at	BC000351	NM_002861	5833	1.22	2.05E-03
WDR51A	234749_s_at	AL117629	NM_015426	25886	1.22	2.87E-03
MAN2A1	226538_at	AV700323	NM_002372	4124	1.21	3.05E-03

TLE4	233575_s_at	AA705845	NM_007005	7091	1.21	2.34E-04
AW665447	230113_at	AW665447	---	---	1.21	3.86E-03
SAP30	204899_s_at	BF247098	NM_003864	8819	1.21	2.33E-03
LOC221810	221910_at	BF131965	---	221810	1.21	8.18E-03
HOMER3	204647_at	NM_004838	NM_004838	9454	1.20	4.61E-03
SLC1A1	213664_at	AW235061	NM_004170	6505	1.20	5.98E-03
C20orf108	224690_at	BG432350	NM_080821	116151	1.20	8.73E-03
ZNF238	207164_s_at	NM_006352	NM_006352 NM_205768	10472	1.20	7.96E-03
PIR	207469_s_at	NM_003662	NM_003662	8544	1.20	1.53E-05
FLRT3	219250_s_at	NM_013281	NM_013281 NM_198391	23767	1.19	7.10E-04
SLIT3	203812_at	AB011538	NM_003062	6586	1.19	1.40E-03
TGIF	203313_s_at	NM_003244	NM_003244 NM_170695 NM_173207 NM_173208 NM_173209 NM_173210 NM_173211 NM_174886	7050	1.19	5.40E-05
CDKN2C	204159_at	NM_001262	NM_001262 NM_078626	1031	1.19	8.59E-05
MTUS1	212095_s_at	BE552421	NM_001001924 NM_001001925 NM_001001927 NM_001001931 NM_020749	57509	1.19	2.48E-04
SCARA3	223842_s_at	AB007830	NM_016240 NM_182826	51435	1.19	3.33E-04
HTATSF1	202602_s_at	NM_014500	NM_014500	27336	1.19	2.42E-05
TRAM2	202369_s_at	NM_012288	NM_012288	9697	1.18	7.27E-03
PTGFRN	224950_at	BF476250	NM_020440	5738	1.18	2.73E-03
DRD2	216938_x_at	S69899	NM_000795 NM_016574	1813	1.18	2.02E-03
TOP3B	215781_s_at	D87012	NM_003935	8940	1.18	2.21E-03
ACY1L2	225421_at	AI654133	NM_001010853	135293	1.18	7.34E-04
BC025350	1569418_at	BC025350	---	---	1.18	1.04E-06
KIAA1706	225630_at	AB051493	NM_030636	80820	1.18	1.55E-04
AW874669	239834_at	AW874669	---	---	1.18	7.57E-04
CPT1A	203633_at	BF001714	NM_001876	1374	1.17	1.23E-03
C2orf23	204364_s_at	BE535746	NM_022912	65055	1.17	2.59E-04
SMO	218629_at	NM_005631	NM_005631	6608	1.17	3.37E-05
RPH3A	205230_at	NM_014954	NM_014954	22895	1.17	6.35E-03
VIL2	208621_s_at	BF663141	NM_003379	7430	1.17	8.04E-04
SEC15L2	225900_at	AW294630	XM_039570	23233	1.17	7.12E-03
MCC	206132_at	NM_002387	NM_002387	4163	1.17	5.91E-04
C20orf108	224693_at	AI133137	NM_080821	116151	1.16	2.04E-05
RFC5	203209_at	BC001866	NM_007370 NM_181578	5985	1.16	9.74E-03
MAPK11	211499_s_at	U92268	NM_002751 NM_138993	5600	1.16	3.08E-04

EB-1	227439_at	AI806510	NM_020140 NM_152788 NM_181670	56899	1.16	9.25E-08
FBXL7	213249_at	AU145127	NM_012304	23194	1.16	5.25E-07
TTC9	213172_at	AW235608	XM_027236	23508	1.16	7.95E-04
SLC40A1	223044_at	AL136944	NM_014585	30061	1.16	6.08E-04
AI452715	229817_at	AI452715	---	---	1.16	3.41E-03
MAN2A1	235103_at	AA029155	NM_002372	4124	1.16	5.37E-04
VIL2	217234_s_at	AF199015	NM_003379	7430	1.16	3.24E-03
SEZ6L	213609_s_at	AB023144	NM_021115	23544	1.15	2.65E-06
TLX2	207410_s_at	NM_016170	NM_001534 NM_016170	3196	1.15	3.55E-05
CGI-96	202937_x_at	AL022316	NM_015703	27341	1.15	2.55E-03
KCNJ8	205304_s_at	NM_004982	NM_004982	3764	1.14	5.54E-03
ZNF537	223392_s_at	BF510588	NM_020856	57616	1.14	9.47E-06
DHX35	234728_s_at	AL023803	NM_021931	60625	1.14	6.62E-06
STRA6	1569334_at	BC015881	NM_022369	64220	1.14	5.40E-03
EAF2	219551_at	NM_018456	NM_018456	55840	1.14	9.77E-04
ITPR1	203710_at	NM_002222	NM_002222	3708	1.14	1.07E-03
LIFR	225575_at	AI680541	NM_002310	3977	1.13	4.19E-06
GJA7	208460_at	NM_005497	NM_005497	10052	1.13	4.63E-03
MBD2	214397_at	AI827820	NM_003927 NM_015832	8932	1.13	1.61E-03
ANKRD13	224810_s_at	AL569476	NM_033121	88455	1.13	2.65E-04
HDAC8	223908_at	AF212246	NM_018486	55869	1.13	1.96E-04
STN2	227461_at	AA632295	NM_033104	85439	1.12	4.18E-03
BE464799	214036_at	BE464799	---	---	1.12	1.37E-04
SOX2	228038_at	AI669815	NM_003106	6657	1.12	1.75E-04
GTF2E1	205930_at	NM_005513	NM_005513	2960	1.12	1.67E-03
H10661	242317_at	H10661	---	---	1.12	3.16E-04
HSZFP36	229732_at	AI417785	XM_375568	55552	1.12	2.16E-03
RBBP9	221440_s_at	NM_006606	NM_006606 NM_153328	10741	1.12	9.04E-04
DNAJB6	209015_s_at	BC002446	NM_005494 NM_058246	10049	1.12	2.51E-03
KNTC1	206316_s_at	NM_014708	NM_014708	9735	1.12	7.31E-03
FUT11	238551_at	BF541967	NM_173540	170384	1.12	1.14E-03
MAP2K6	205698_s_at	NM_002758	NM_002758 NM_031988	5608	1.11	8.00E-03
NRM	225592_at	D81048	NM_007243	11270	1.11	8.62E-03
STMN3	222557_at	AL353715	NM_015894	50861	1.11	1.13E-03
INSIG1	201626_at	BG292233	NM_005542 NM_198336 NM_198337	3638	1.11	1.47E-03
SH3MD2	225589_at	AB040927	NM_020870	57630	1.11	3.78E-04
BCL2L11	225606_at	AI949179	NM_006538 NM_138621 NM_138622 NM_138623 NM_138624 NM_138625 NM_138626 NM_138627 NM_207002 NM_207003	10018	1.11	4.77E-07
TYRO3	211432_s_at	U05682	NM_006293	7301	1.11	7.76E-03

APAF1	204859_s_at	NM_013229	NM_001160 NM_013229 NM_181861 NM_181868 NM_181869	317	1.11	8.54E-03
LRRC1	218816_at	NM_018214	NM_018214 NM_025168	55227	1.11	4.89E-03
DNM3	209839_at	AL136712	NM_015569	26052	1.11	5.67E-06
MAN2A1	205105_at	NM_002372	NM_002372	4124	1.11	6.81E-03
FLJ23322	220707_s_at	NM_024955	NM_024955	80020	1.10	2.15E-03
NDRG2	214279_s_at	W74452	NM_016250 NM_201535 NM_201536 NM_201537 NM_201538 NM_201539 NM_201540 NM_201541	57447	1.10	5.44E-03
SCAM-1	207788_s_at	NM_005775	NM_005775	10174	1.10	9.08E-03
LMO1	206718_at	NM_002315	NM_002315	4004	1.10	5.27E-04
ITPR1	216944_s_at	U23850	NM_002222	3708	1.10	8.15E-03
PCNXL2	39650_s_at	AB007895	NM_014801 NM_024938	80003	1.10	9.56E-05
RBBP9	232751_at	AL121893	NM_006606 NM_153328	10741	1.10	8.94E-04
AP3B1	203142_s_at	NM_003664	NM_003664	8546	1.09	2.19E-03
SNAP29	222597_at	AI346639	NM_004782	9342	1.09	1.46E-04
C20orf161	1553960_at	CA447177	NM_033421 NM_152897	90203	1.09	2.01E-03
LOC283464	232021_at	AI864273	XM_290597	283464	1.09	1.32E-03
AI589594	238694_at	AI589594	---	---	1.09	2.79E-05
SOX2	213721_at	L07335	NM_003106	6657	1.08	7.40E-04
ST3GAL6	210942_s_at	AB022918	NM_006100	10402	1.08	2.47E-04
BG231758	227615_at	BG231758	---	---	1.08	5.95E-08
FLJ33814	225644_at	BF060776	NM_173510	150275	1.08	2.63E-06
TYMS	1554696_s_at	AB077208	NM_001071	7298	1.08	7.83E-03
BOK	223349_s_at	BE614255	NM_032515	666	1.08	3.19E-06
C1QL1	205575_at	NM_006688	NM_006688	10882	1.08	1.06E-04
GMPS	236648_at	AI684467	NM_003875	8833	1.08	6.96E-04
AI733583	243235_at	AI733583	---	---	1.08	6.94E-03
BE066500	239729_at	BE066500	---	---	1.08	8.69E-04
ASAHL	232072_at	AK025371	NM_014435	27163	1.08	3.73E-04
SNX5	229981_at	AA131508	NM_014426 NM_152227	27131	1.08	1.66E-05
CYBA	203028_s_at	NM_000101	NM_000101	1535	1.07	5.76E-04
PTER	222798_at	BF112019	NM_00100148 4 NM_030664	9317	1.07	2.48E-03
LOC440820	226602_s_at	T30183	XM_496519	440820	1.07	2.20E-05
AA214369	238545_at	AA214369	---	---	1.07	3.48E-03
ELAVL4	241424_at	BF111117	NM_021952	1996	1.07	4.96E-03
C6orf189	228875_at	AI540210	---	221303	1.07	1.85E-04
PARG1	203910_at	NM_004815	NM_004815	9411	1.07	1.74E-04
OLFML3	218162_at	NM_020190	NM_020190	56944	1.07	4.22E-03
PI4K2B	222631_at	AI862887	NM_018323	55300	1.07	2.03E-03
PHYHIPL	226623_at	AI829726	NM_032439	84457	1.07	5.85E-05
AA156933	236141_at	AA156933	---	---	1.07	9.86E-04
AI346432	229132_at	AI346432	---	---	1.07	3.94E-04

AI919519	235092_at	AI919519	---	---	1.07	8.75E-03
ELK3	221773_at	AW575374	NM_005230	2004	1.07	2.45E-03
LPPR4	213496_at	AW592563	NM_014839	9890	1.07	1.23E-05
EZH2	203358_s_at	NM_004456	NM_004456	2146	1.06	5.13E-03
			NM_152998			
NS5ATP13TP2	225510_at	BG033561	NM_178507	220323	1.06	1.40E-04
KIAA1102	212325_at	AK027231	NM_014988	22998	1.06	1.82E-09
ZNF505	208119_s_at	NM_031218	NM_00100412	81931	1.06	5.75E-03
			6			
			NM_031218			
C20orf40	231200_at	BG222606	NM_144703	149986	1.06	1.73E-03
SLC8A1	238546_at	BF344961	NM_021097	6546	1.06	6.63E-03
PREX1	224909_s_at	BF308645	NM_020820	57580	1.06	7.16E-03
MAK3	222393_s_at	AU149868	NM_025146	80218	1.06	1.11E-05
TMPO	209753_s_at	BG391171	NM_003276	7112	1.06	3.02E-03
ADORA2A	205013_s_at	NM_000675	NM_000675	135	1.06	9.97E-03
MGC3040	223523_at	BC000568	NM_023943	66000	1.06	7.88E-07
AI700633	212812_at	AI700633	---	---	1.06	8.55E-03
TWSG1	219201_s_at	NM_020648	NM_020648	57045	1.06	9.70E-04
PPP3CB	209817_at	M29550	NM_021132	5532	1.06	2.71E-06
MAP3K13	206249_at	NM_004721	NM_004721	9175	1.06	3.52E-03
SKP2	210567_s_at	BC001441	NM_005983	6502	1.06	8.10E-04
			NM_032637			
SYN2	210315_at	AF077737	NM_003178	6854	1.05	9.08E-03
			NM_133625			
CGI-96	33307_at	AL022316	NM_015703	27341	1.05	7.16E-04
GNG12	1555240_s_at	AF493879	NM_018841	55970	1.05	6.35E-04
CUTL2	213920_at	AB006631	NM_015267	23316	1.04	1.63E-03
FLRT3	222853_at	N71923	NM_013281	23767	1.04	9.61E-07
			NM_198391			
FLJ13842	219877_at	NM_024645	NM_024645	79698	1.04	6.38E-03
ADRBK2	228771_at	AI651212	NM_005160	157	1.04	7.18E-05
SEC61A2	228747_at	AI694646	NM_018144	55176	1.04	4.56E-03
ST3GAL6	213355_at	AI989567	NM_006100	10402	1.04	1.38E-04
BF434228	235850_at	BF434228	---	---	1.04	4.97E-03
PCGF5	227935_s_at	AA522681	NM_032373	84333	1.04	8.11E-04
MYST1	214885_at	AL050395	NM_032188	84148	1.04	5.82E-03
PEX13	1558163_at	BC040953	NM_002618	5194	1.03	3.87E-03
INSIG1	201627_s_at	NM_005542	NM_005542	3638	1.03	2.57E-06
			NM_198336			
			NM_198337			
NELL2	203413_at	NM_006159	NM_006159	4753	1.03	1.75E-03
RND3	212724_at	BG054844	NM_005168	390	1.03	1.50E-03
TFDP2	203588_s_at	BG034328	NM_006286	7029	1.03	9.43E-03
CTNNBL1	221021_s_at	NM_030877	NM_030877	56259	1.03	3.20E-03
CHML	1565951_s_at	AJ293392	NM_001821	1122	1.03	8.52E-03
ITPR1	211323_s_at	L38019	NM_002222	3708	1.02	3.21E-05
DKFZP564O12	202536_at	AK002165	NM_014043	25978	1.02	9.94E-05
CKLF	219161_s_at	NM_016951	NM_016326	51192	1.02	8.63E-03
			NM_016951			
			NM_181640			
			NM_181641			
IQGAP1	213446_s_at	AI679073	NM_003870	8826	1.02	1.01E-03
C11orf8	215692_s_at	BE645386	NM_001584	744	1.02	1.49E-03
AL559474	235918_x_at	AL559474	---	---	1.02	2.13E-03
ADRBK2	204184_s_at	NM_005160	NM_005160	157	1.02	3.30E-04
LOC152185	234995_at	AA668779	NM_144718	152185	1.02	9.02E-04

XRCC4	205071_x_at	AB017445	NM_003401 NM_022406 NM_022550	7518	1.02	3.71E-03
GPR125	210473_s_at	M37712	NM_145290	166647	1.01	1.54E-08
SLCO3A1	219229_at	NM_013272	NM_013272	28232	1.01	7.19E-04
POLE	216026_s_at	AL080203	NM_006231	5426	1.01	8.50E-03
TMOD3	223078_s_at	AF177171	NM_014547	29766	1.01	2.98E-05
SKP2	203626_s_at	NM_005983	NM_005983 NM_032637	6502	1.01	9.59E-08
RBPMS	207836_s_at	NM_006867	NM_00100871 0 NM_00100871 1 NM_00100871 2 NM_006867	11030	1.00	5.05E-03
PHTF2	217097_s_at	AC004990	NM_020432	57157	1.00	4.53E-03
TM4SF14	223314_at	BF025955	NM_030927	81619	1.00	2.72E-03
SDC2	212157_at	BE048514	NM_002998	6383	1.00	6.35E-03
TP53I3	210609_s_at	BC000474	NM_004881 NM_147184	9540	1.00	8.78E-04
AL049385	232297_at	AL049385	---	---	1.00	1.36E-05
MTUS1	212096_s_at	AL096842	NM_00100192 4 NM_00100192 5 NM_00100192 7 NM_00100193 1 NM_020749	57509	1.00	1.43E-04
KLF7	1555420_a_at	BC012919	NM_003709	8609	1.00	1.21E-04
ZNF555	1556187_at	AF052118	NM_152791	148254	0.99	7.62E-03
GPAM	225424_at	AB046780	NM_020918	57678	0.99	5.06E-03
FLJ13273	1554518_at	BC032942	NM_024751	79807	0.99	2.86E-04
SAP30	204900_x_at	NM_003864	NM_003864	8819	0.99	3.10E-03
FBXL10	229855_at	AA779208	NM_00100536 6 NM_032590	84678	0.99	1.80E-03
NEUROD4	221318_at	NM_021191	NM_021191	58158	0.99	2.89E-03
FLJ12649	219626_at	NM_024597	XM_291344	79649	0.99	9.37E-05
TMPO	209754_s_at	AF113682	NM_003276	7112	0.99	6.52E-03
RASL11B	219142_at	NM_023940	NM_023940	65997	0.99	4.29E-03
ASAHL	214765_s_at	AK024677	NM_014435	27163	0.98	1.03E-05
ZNF238	212774_at	AJ223321	NM_006352 NM_205768	10472	0.98	6.70E-05
ITPR2	202662_s_at	NM_002223	NM_002223	3709	0.98	8.48E-03
SEZ6L	231650_s_at	BE672217	NM_021115	23544	0.98	1.12E-04
C10orf47	229801_at	AI640157	NM_153256	254427	0.98	7.31E-03
SNAG1	226683_at	AU146771	NM_052870	112574	0.98	1.70E-04
FGF11	227271_at	AU151265	NM_004112	2256	0.98	9.49E-03
DDT	202929_s_at	NM_001355	NM_001355	1652	0.98	3.16E-04
KLHL5	233866_at	AK001836	NM_00100707 5 NM_199039	51088	0.97	7.05E-03
PVRL3	241970_at	C14898	NM_015480	25945	0.97	5.02E-03
SEMA5A	205405_at	NM_003966	NM_003966	9037	0.97	2.27E-03
RFC1	209085_x_at	L14922	NM_002913	5981	0.97	6.24E-03

TRIM36	219736_at	NM_018700	NM_018700	55521	0.97	4.06E-03
FLJ23322	231846_at	AK026975	NM_024955	80020	0.97	3.27E-03
IMP-1	223689_at	AF198254	NM_006546	10642	0.97	1.78E-04
MDFI	205375_at	NM_005586	NM_005586	4188	0.97	7.23E-03
BE878277	212829_at	BE878277	---	---	0.97	1.51E-04
FLJ14451	227430_at	AI969773	NM_032786	84872	0.97	8.15E-03
NARG1	226998_at	AL556909	NM_057175	80155	0.96	1.89E-06
TMEM38B	222736_s_at	BC000049	NM_018112	55151	0.96	3.02E-05
LAMP2	203041_s_at	J04183	NM_002294 NM_013995	3920	0.96	1.13E-04
FANCL	218397_at	NM_018062	NM_018062	55120	0.96	3.05E-03
APOBEC3G	204205_at	NM_021822	NM_021822	60489	0.96	7.76E-03
NM_024853	220533_at	NM_024853	---	---	0.96	3.50E-03
UNG	202330_s_at	NM_003362	NM_003362 NM_080911	7374	0.96	2.31E-03
ACTL6A	202666_s_at	NM_004301	NM_004301 NM_177989 NM_178042	86	0.96	1.28E-03
N71074	238078_at	N71074	---	---	0.96	7.93E-04
FLJ40432	228810_at	AW135279	NM_152523	151195	0.96	4.18E-06
KIAA1102	212327_at	AK026815	NM_014988	22998	0.96	1.66E-05
C12orf2	225946_at	BG484552	NM_007211	11228	0.96	4.33E-06
FLJ11539	219791_s_at	NM_024748	XM_496724	79804	0.96	4.56E-04
MNS1	219703_at	NM_018365	NM_018365	55329	0.96	6.11E-04
SLC8A1	235518_at	AI741439	NM_021097	6546	0.95	4.16E-03
PSMD9	209334_s_at	BC002383	NM_002813	5715	0.95	5.08E-06
ACY1L2	225431_x_at	BE779764	NM_001010853	135293	0.95	7.73E-04
SOD2	215223_s_at	W46388	NM_000636	6648	0.95	3.07E-03
PPP1R3D	204554_at	AL109928	NM_006242	5509	0.95	2.56E-03
BF056892	229024_at	BF056892	---	---	0.95	1.67E-04
CHD6	225031_at	AL031667	NM_032221	84181	0.95	4.37E-05
MGC7036	227983_at	AI810244	NM_145058	196383	0.95	2.13E-04
CCBE1	243805_at	BG035826	NM_133459	147372	0.95	1.68E-03
AL110237	232959_at	AL110237	---	---	0.95	9.01E-04
LOC134111	226612_at	H17038	XM_059689	134111	0.94	3.88E-03
ELAVL4	234904_x_at	S73887	NM_021952	1996	0.94	1.21E-04
PANK2	238856_s_at	BG108346	NM_024960 NM_153637 NM_153638 NM_153639 NM_153640 NM_153641	80025	0.94	3.01E-05
CBX5	230752_at	AI638063	NM_012117	23468	0.94	6.48E-04
NDUFA6	202000_at	BC002772	NM_002490	4700	0.94	5.54E-04
HSPC117	200042_at	NM_014306	NM_014306	51493	0.94	6.59E-07
TLE4	235765_at	AI742932	NM_007005	7091	0.94	9.75E-04
SDC4	202071_at	NM_002999	NM_002999	6385	0.94	8.24E-05
CD47	211075_s_at	Z25521	NM_001777 NM_198793	961	0.94	1.46E-03
EGFR	224999_at	BE878463	NM_005228 NM_201282 NM_201283 NM_201284	1956	0.93	4.74E-03
TLX2	211049_at	BC006356	NM_001534 NM_016170	3196	0.93	6.56E-04
VIL2	208622_s_at	AA670344	NM_003379	7430	0.93	3.33E-03
JPH1	1553533_at	NM_020647	NM_020647	56704	0.93	2.57E-03
TEAD3	209454_s_at	AF142482	NM_003214	7005	0.93	5.72E-03

FKBP5	204560_at	NM_004117	NM_004117	2289	0.93	2.37E-03
SEC61A2	219499_at	NM_018144	NM_018144	55176	0.93	9.99E-03
PGM2	225366_at	AI652855	NM_018290	55276	0.93	6.09E-04
P4HA1	207543_s_at	NM_000917	NM_000917	5033	0.93	2.61E-04
SEC23A	204344_s_at	NM_006364	NM_006364	10484	0.93	3.24E-03
KIAA1102	212328_at	AB029025	NM_014988	22998	0.93	1.29E-05
RANBP1	202483_s_at	NM_002882	NM_002882	5902	0.93	7.82E-03
STARD4	226390_at	AA628398	NM_139164	134429	0.93	1.59E-04
B4GALT6	206232_s_at	NM_004775	NM_004775	9331	0.93	2.63E-03
AHI1	220842_at	NM_017651	NM_017651	54806	0.92	6.04E-03
MCM4	212142_at	AI936566	NM_005914	4173	0.92	7.62E-04
			NM_182746			
CHD6	225026_at	BF572029	NM_032221	84181	0.92	3.17E-03
HMGB2	208808_s_at	BC000903	NM_002129	3148	0.92	7.83E-03
DNMT3B	220668_s_at	NM_006892	NM_006892	1789	0.92	2.56E-03
			NM_175848			
			NM_175849			
			NM_175850			
AI095542	235759_at	AI095542	---	---	0.92	4.36E-03
SLC25A1	210010_s_at	U25147	NM_005984	6576	0.92	2.10E-03
ELAVL4	238073_at	R55745	NM_021952	1996	0.92	1.01E-03
BG149337	229814_at	BG149337	---	---	0.92	2.56E-03
R43103	243642_x_at	R43103	---	---	0.92	3.67E-03
NEDD1	1552417_a_at	NM_152905	NM_152905	121441	0.91	2.33E-03
MTUS1	212093_s_at	AI695017	NM_00100192	57509	0.91	4.60E-04
			4			
			NM_00100192			
			5			
			NM_00100192			
			7			
			NM_00100193			
			1			
			NM_020749			
ALG10	1552306_at	BC033730	NM_032834	84920	0.91	7.39E-04
ELAVL4	206051_at	NM_021952	NM_021952	1996	0.91	1.99E-03
MLF1	204783_at	AI911434	NM_022443	4291	0.91	1.31E-04
SLC2A8	218985_at	NM_014580	NM_014580	29988	0.91	6.78E-03
ITPR2	202660_at	AA834576	NM_002223	3709	0.91	9.15E-03
CISH	223377_x_at	AF035947	NM_013324	1154	0.91	4.28E-03
			NM_145071			
C3orf4	1554149_at	BC013610	NM_019895	56650	0.91	2.11E-05
LOC134111	226618_at	AW572911	XM_059689	134111	0.91	5.63E-04
BE857972	243781_at	BE857972	---	---	0.91	1.20E-03
Cep70	224150_s_at	AF289495	NM_024491	80321	0.91	4.27E-03
PP2447	232706_s_at	AW009248	NM_025204	80305	0.90	4.10E-03
RGS4	204337_at	AL514445	NM_005613	5999	0.90	1.42E-03
KLF7	204334_at	AA488672	NM_003709	8609	0.90	9.17E-04
SLCO3A1	227367_at	AW976431	NM_013272	28232	0.90	4.34E-03
FZD2	210220_at	L37882	NM_001466	2535	0.90	2.77E-04
SESTD1	226763_at	AW409611	NM_178123	91404	0.90	9.00E-04
DHX35	218579_s_at	NM_021931	NM_021931	60625	0.90	2.42E-05
PDLIM1	208690_s_at	BC000915	NM_020992	9124	0.90	6.24E-04
BICD1	1554020_at	BC010091	NM_00100339	636	0.90	3.41E-06
			8			
			NM_001714			
PXMP2	219076_s_at	NM_018663	NM_018663	5827	0.90	6.61E-03
SPOCK	202363_at	AF231124	NM_004598	6695	0.90	5.89E-03
AA581439	244650_at	AA581439	---	---	0.89	5.83E-03

BC003667	222487_s_at	BC003667	---	---	0.89	8.10E-03
NFYB	218128_at	AU151875	NM_006166	4801	0.89	2.19E-03
SYNJ2	212828_at	AA191573	NM_003898	8871	0.89	6.92E-03
ITGB5	201124_at	AL048423	NM_002213	3693	0.89	4.74E-03
SLC39A8	219869_s_at	NM_022154	NM_022154	64116	0.89	1.30E-03
AI333006	240432_x_at	AI333006	---	---	0.89	2.24E-03
BRD4	202103_at	AI991631	NM_014299	23476	0.89	3.39E-03
			NM_058243			
MCM8	233560_x_at	AA370141	NM_032485	84515	0.89	2.33E-03
			NM_182802			
PKIA	226864_at	BF245954	NM_006823	5569	0.89	4.86E-04
			NM_181839			
FAM43A	227410_at	AW264102	NM_153690	131583	0.89	4.81E-03
ZMYM1	220206_at	NM_024772	NM_024772	79830	0.89	5.27E-03
SLK	206875_s_at	NM_014720	NM_014720	9748	0.89	9.22E-06
EPB41L5	225855_at	AB046768	NM_020909	57669	0.89	8.39E-04
RAD18	223417_at	AF169796	NM_020165	56852	0.89	2.04E-04
MEIS2	207480_s_at	NM_020149	NM_002399	4212	0.89	4.23E-04
			NM_020149			
			NM_170674			
			NM_170675			
			NM_170676			
			NM_170677			
			NM_172315			
			NM_172316			
NFYA	204107_at	BF445142	NM_002505	4800	0.88	3.28E-06
			NM_021705			
SREBF2	201248_s_at	NM_004599	NM_004599	6721	0.88	4.75E-03
FLJ31842	237515_at	AA054642	NM_152487	148534	0.88	8.21E-04
ZFD25	205739_x_at	NM_016220	---	51427	0.88	8.79E-03
DLEU2	215629_s_at	AA905286	NM_006021	8847	0.88	6.43E-04
ZNF85	206572_x_at	NM_003429	NM_003429	7639	0.88	6.85E-06
PCDH17	228863_at	N69091	NM_014459	27253	0.88	6.70E-03
PTPRG	204944_at	NM_002841	NM_002841	5793	0.88	3.65E-03
AL833487	1562245_a_at	AL833487	---	---	0.88	8.59E-03
PCDH17	205656_at	NM_014459	NM_014459	27253	0.88	6.19E-03
ANAPC7	225554_s_at	AA131793	NM_016238	51434	0.88	8.37E-04
BE504215	228563_at	BE504215	---	---	0.88	1.17E-03
MLLT3	204917_s_at	AV756536	NM_004529	4300	0.88	5.47E-03
CD47	213857_s_at	BG230614	NM_001777	961	0.88	3.54E-04
			NM_198793			
PTK7	1555324_at	BC046109	NM_002821	5754	0.87	3.45E-03
			NM_152880			
			NM_152881			
			NM_152882			
			NM_152883			
EP300	1562921_at	BC040700	NM_001429	2033	0.87	3.55E-03
VPS29	223026_s_at	AF201946	NM_016226	51699	0.87	9.51E-03
			NM_057180			
EBF	227646_at	BG435302	NM_024007	1879	0.87	6.32E-04
GPC6	223730_at	AF111178	NM_005708	10082	0.87	7.72E-03
PHF5A	225309_at	AL008582	NM_032758	84844	0.87	1.93E-03
FLJ31842	234980_at	AI004375	NM_152487	148534	0.87	3.12E-04
AW953794	230968_at	AW953794	---	---	0.87	3.09E-03
AI888657	244189_at	AI888657	---	---	0.87	1.23E-03
FLJ21415	218867_s_at	NM_024738	NM_024738	79794	0.87	2.65E-03
MAK3	217745_s_at	NM_025146	NM_025146	80218	0.87	5.22E-04
SEC23A	212887_at	AI753659	NM_006364	10484	0.86	6.69E-03

PAX5	221969_at	BF510692	NM_016734	5079	0.86	4.37E-03
UNC84B	212144_at	AL021707	NM_015374	25777	0.86	9.44E-03
PRIM2A	205628_at	NM_000947	NM_000947	5558	0.86	1.80E-03
ISL1	206104_at	NM_002202	NM_002202	3670	0.86	2.89E-03
NAGA	202944_at	NM_000262	NM_000262	4668	0.86	1.12E-04
SCD4	224901_at	AL571375	NM_024906	79966	0.86	2.89E-04
PHYH	203335_at	NM_006214	NM_006214	5264	0.86	3.64E-05
HMGCS1	205822_s_at	NM_002130	NM_002130	3157	0.86	5.71E-04
3ALNAC4S-6S'	203066_at	NM_014863	NM_015892	51363	0.86	1.55E-04
DKFZp762A217	235775_at	AI765006	NM_152588	160335	0.86	2.87E-03
ADRBK2	204183_s_at	AI478542	NM_005160	157	0.85	7.45E-05
BC002942	31837_at	U62317	NM_033200	91289	0.85	2.32E-03
KIAA1853	236151_at	BF315452	NM_194286	84530	0.85	8.93E-03
C10orf58	228155_at	BF512388	NM_032333	84293	0.85	4.55E-08
KIAA0286	212619_at	AW205215	NM_015257	23306	0.85	2.40E-03
AU146017	234082_at	AU146017	---	---	0.85	5.56E-03
GPR85	219898_at	NM_018970	NM_018970	54329	0.85	2.12E-03
KIAA1145	235146_at	N51717	NM_020698	57458	0.85	4.62E-05
CSTF1	202190_at	NM_001324	NM_001324	1477	0.85	2.75E-03
BF510533	228107_at	BF510533	---	---	0.85	7.13E-04
PANK2	218809_at	NM_024960	NM_024960 NM_153637 NM_153638 NM_153639 NM_153640 NM_153641	80025	0.85	5.93E-04
DHX37	223364_s_at	BC004463	NM_032656	57647	0.85	1.99E-03
HMGB3	203744_at	NM_005342	NM_005342	3149	0.85	6.52E-03
BNIP3	201848_s_at	U15174	NM_004052	664	0.85	1.65E-03
LOC284244	214162_at	AF070541	---	284244	0.85	2.94E-03
SV2C	216086_at	AB028977	XM_043493	22987	0.85	3.24E-03
MTP18	223172_s_at	AF060924	NM_00100370 4 NM_016498	51537	0.85	6.41E-03
SNAP29	218327_s_at	NM_004782	NM_004782	9342	0.85	4.67E-03
NFYA	204109_s_at	NM_002505	NM_002505 NM_021705	4800	0.85	4.40E-03
FLJ37858	227354_at	BF589359	NM_001007548	441357	0.84	6.04E-03
R58282	238557_at	R58282	---	---	0.84	5.38E-03
CDH2	203441_s_at	NM_001792	NM_001792	1000	0.84	1.55E-03
C20orf45	217851_s_at	NM_016045	NM_016045	51012	0.84	1.50E-03
MYO1B	212364_at	BF432550	NM_012223	4430	0.84	1.02E-03
PAICS	201014_s_at	NM_006452	NM_006452	10606	0.84	4.23E-04
ZNF505	215758_x_at	AC007204	NM_00100412 6 NM_031218	81931	0.84	1.32E-04
SEMA6A	215028_at	AB002438	NM_020796	57556	0.84	1.21E-04
SLIT2	209897_s_at	AF055585	NM_004787	9353	0.84	3.51E-03
CELSR3	40020_at	AB011536	NM_001407	1951	0.84	1.82E-06
DIRAS2	219619_at	NM_017594	NM_017594	54769	0.84	9.62E-03
TOB2	222243_s_at	AB051450	NM_016272	10766	0.84	3.84E-03
HAND1	220138_at	NM_004821	NM_004821	9421	0.84	8.36E-04
RAD18	224200_s_at	AB035274	NM_020165	56852	0.83	3.81E-03
LRIG3	226908_at	AI627704	NM_153377	121227	0.83	9.44E-03
AI150000	226671_at	AI150000	---	---	0.83	7.72E-04
EIF5A2	235289_at	AV747725	NM_020390	56648	0.83	2.77E-03
CDK2AP1	201938_at	NM_004642	NM_004642	8099	0.83	8.12E-03
MLF1	204784_s_at	NM_022443	NM_022443	4291	0.83	2.50E-03

MPP5	219321_at	NM_022474	NM_022474	64398	0.83	1.84E-03
TXNRD1	201266_at	NM_003330	NM_003330 NM_182729 NM_182742 NM_182743	7296	0.83	6.73E-05
C10orf58	224435_at	BC005871	NM_032333	84293	0.82	5.15E-06
EVE1	225162_at	BG285417	NM_001009555	152503	0.82	5.43E-03
RALY	201271_s_at	NM_016732	NM_007367 NM_016732	22913	0.82	1.71E-03
SEC10L1	228418_at	BF509391	NM_006544	10640	0.82	6.79E-06
MFAP2	203417_at	NM_017459	NM_002403 NM_017459	4237	0.82	9.64E-05
MYO1B	212365_at	BF215996	NM_012223	4430	0.82	2.49E-04
ACAA1	214274_s_at	AI860341	NM_001607	30	0.82	5.44E-03
KIAA0701	1554292_a_at	BC014891	NM_001006947 NM_015054	23074	0.81	5.60E-03
AK022598	232662_x_at	AK022598	---	---	0.81	5.55E-03
PLXNA2	213030_s_at	AI688418	NM_025179	5362	0.81	6.66E-03
BE501881	227565_at	BE501881	---	---	0.81	2.21E-03
BF447112	236192_at	BF447112	---	---	0.81	2.02E-03
LOC85028	228990_at	AI339426	XM_378848	85028	0.81	4.87E-04
BF511170	227332_at	BF511170	---	---	0.81	3.67E-03
KLF3	219657_s_at	NM_016531	NM_016531	51274	0.81	3.64E-03
GRIA1	209793_at	AL567302	NM_000827	2890	0.81	3.68E-03
SUHW2	229360_at	N22886	NM_080764	140883	0.81	8.50E-03
LOC401022	242042_s_at	AA406052	---	401022	0.81	5.97E-04
C3orf4	208925_at	AF161522	NM_019895	56650	0.81	1.42E-08
MRPL40	203152_at	NM_003776	NM_003776	64976	0.81	6.67E-03
PVT1	1558290_a_at	BG200951	XM_372058	441378	0.81	2.88E-03
LOC441378			XM_499128	5820		
KELCHL	221837_at	BG325646	NM_032775	84861	0.81	3.12E-04
CELSR3	205165_at	NM_001407	NM_001407	1951	0.81	1.43E-04
RAB35	205461_at	NM_006861	NM_006861	11021	0.81	6.64E-03
MGC70857	226710_at	AI199072	NM_001001795	414919	0.81	3.76E-05
AA446953	241749_at	AA446953	XM_294592	347273	0.81	2.10E-04
PSMD5	203447_at	AU157008	NM_005047	5711	0.80	8.55E-04
NUP50	222583_s_at	AF116624	NM_007172 NM_153645 NM_153684	10762	0.80	2.54E-04
ARL6IP6	225707_at	AL581082	NM_152522	151188	0.80	4.86E-03
H1F0	208886_at	BC000145	NM_005318	3005	0.80	2.95E-04
RQCD1	1554080_at	BC007102	NM_005444	9125	0.80	5.80E-03
MVK	215649_s_at	AF217536	NM_000431	4598	0.80	4.39E-04
CDC5L	209055_s_at	AW268817	NM_001253	988	0.80	9.38E-03
LGR4	218326_s_at	NM_018490	NM_018490	55366	0.80	1.35E-04
C19orf32	226597_at	AI348159	NM_138393	92840	0.80	6.56E-03
HPS4	218402_s_at	NM_022081	NM_022081 NM_152840 NM_152841 NM_152842 NM_152843	89781	0.80	8.60E-04
MGC18216	243358_at	BF347362	---	145815	0.79	8.83E-03
ZNF43	222136_x_at	AK022905	NM_003423	7594	0.79	1.19E-06
DRG1	236537_at	AI760332	NM_004147	4733	0.79	9.05E-03
SLC2A4RG	218494_s_at	NM_020062	NM_020062	56731	0.79	1.26E-04
CHRNA3	211772_x_at	BC006114	NM_000743	1136	0.79	5.89E-03

UBE2L3	200683_s_at	BE964689	NM_003347 NM_198157	7332	0.79	2.55E-04
NUP43	238474_at	BF978064	NM_024647 NM_198887	348995	0.79	6.09E-03
EML5	1568777_at	BM677635	NM_183387	161436	0.79	2.74E-03
N24703	238637_at	N24703	---	---	0.79	1.03E-03
CHRNA3	211587_x_at	M37981	NM_000743	1136	0.79	2.09E-03
ZNF20	213916_at	AU154474	NM_021143	7568	0.79	2.24E-03
VAMP1	213326_at	AU150319	NM_014231 NM_016830 NM_199245	6843	0.79	2.99E-03
TMEM38B	222735_at	AW452608	NM_018112	55151	0.79	1.36E-05
MAPKAPK3	202788_at	NM_004635	NM_004635	7867	0.79	7.86E-03
GNB4	223488_s_at	BC000873	NM_021629	59345	0.79	5.46E-03
EPOR	209962_at	M34986	NM_000121	2057	0.78	2.19E-04
C6orf115	223361_at	AF116682	XM_371848	58527	0.78	1.07E-03
AK057923	1556364_at	AK057923	XM_498935	440960	0.78	4.56E-03
PGM2	225367_at	BF512139	NM_018290	55276	0.78	3.75E-04
CECR5	218592_s_at	NM_017829	NM_017829 NM_033070	27440	0.78	4.74E-03
CHRNA3	210221_at	BC000513	NM_000743	1136	0.78	2.56E-05
STMN3	218207_s_at	NM_015894	NM_015894	50861	0.78	8.10E-04
UCP2	208997_s_at	U82819	NM_003355	7351	0.78	3.02E-04
SFRS8	202773_s_at	AI023864	NM_004592 NM_152235	6433	0.78	4.72E-03
FIGNL1	1552921_a_at	NM_022116	NM_022116	63979	0.78	5.97E-03
MEST	202016_at	NM_002402	NM_002402 NM_177524 NM_177525	4232	0.78	9.96E-03
C20orf45	222441_x_at	BF032213	NM_016045	51012	0.78	2.01E-05
PLCXD2	235230_at	AW170015	NM_153268	257068	0.78	7.04E-03
UCK1	223142_s_at	AF237290	NM_031432	83549	0.78	3.34E-05
SNAP29	239084_at	BE896490	NM_004782	9342	0.78	7.09E-03
SNRPD3	202567_at	NM_004175	NM_004175	6634	0.78	8.05E-03
GABPB2	204618_s_at	NM_005254	NM_002041 NM_005254 NM_016654 NM_016655 NM_181427	2553	0.78	4.11E-04
RNF10	208632_at	AL578551	NM_014868	9921	0.77	7.94E-04
RFC1	208021_s_at	NM_002913	NM_002913	5981	0.77	9.34E-03
PAPPA	240295_at	AL045014	NM_002581	5069	0.77	2.94E-03
TM4SF9	225387_at	AA059445	NM_005723	10098	0.77	1.49E-03
PDCL	204448_s_at	AF031463	NM_005388	5082	0.77	8.07E-03
GNAZ	204993_at	NM_002073	NM_002073	2781	0.77	3.40E-03
STK39	202786_at	NM_013233	NM_013233	27347	0.77	5.82E-03
UBE2L3	200684_s_at	AI819709	NM_003347 NM_198157	7332	0.77	4.66E-06
BZRP	202096_s_at	NM_000714	NM_000714 NM_007311	706	0.77	2.65E-03
ELK3	206127_at	NM_005230	NM_005230	2004	0.77	2.08E-03
ZDHHC13	219296_at	NM_019028	NM_00100148 3 NM_019028	54503	0.77	9.19E-04
TIMP2	231579_s_at	BE968786	NM_003255	7077	0.77	2.80E-03
C8orf13	226614_s_at	BE856336	NM_053279	83648	0.77	3.12E-03

BAX	208478_s_at	NM_004324	NM_004324 NM_138761 NM_138762 NM_138763 NM_138764 NM_138765	581	0.77	5.20E-03
TCF8	239952_at	AI743662	NM_030751	6935	0.77	2.84E-04
LOC128977	227086_at	AA194312	NM_173793	128977	0.77	3.39E-03
PAICS	201013_s_at	AA902652	NM_006452	10606	0.76	3.48E-03
AKAP8	203848_at	AL050160	NM_005858	10270	0.76	6.90E-05
TWSG1	225406_at	AA195009	NM_020648	57045	0.76	1.41E-03
PDK1	206686_at	NM_002610	NM_002610	5163	0.76	4.33E-04
TIMP2	224560_at	BF107565	NM_003255	7077	0.76	7.63E-03
CDS2	212862_at	AL568982	NM_003818	8760	0.76	2.78E-05
384D8-2	205086_s_at	NM_014551	NM_014551 NM_152299	29781	0.76	4.69E-04
DTNBP1	223445_at	AF061734	NM_032122 NM_183040 NM_183041	84062	0.76	9.22E-04
BG492376	1557961_s_at	BG492376	---	---	0.76	3.56E-03
ARL6IP6	225711_at	AA654338	NM_152522	151188	0.76	8.52E-03
LRP10	201412_at	NM_014045	NM_014045	26020	0.75	8.53E-03
G22P1	200792_at	NM_001469	NM_001469	2547	0.75	1.40E-05
SDCBP	200958_s_at	NM_005625	NM_001007067 NM_001007068 NM_001007069 NM_001007070 NM_005625	6386	0.75	8.95E-04
PELI2	219132_at	NM_021255	NM_021255	57161	0.75	4.32E-04
NFYB	218129_s_at	NM_006166	NM_006166	4801	0.75	6.84E-03
BTBD3	202946_s_at	NM_014962	NM_014962 NM_181443	22903	0.75	2.02E-04
CSE1L	201111_at	AF053641	NM_001316 NM_177436	1434	0.75	9.19E-03
CAMKK1	223460_at	AL136576	NM_032294 NM_172206 NM_172207	84254	0.75	6.46E-03
TFDP2	244043_at	AI049624	NM_006286	7029	0.75	1.03E-03
AU154030	242141_at	AU154030	---	---	0.75	6.48E-03
C20orf20	218586_at	NM_018270	NM_018270	55257	0.75	4.07E-04
PPAT	209434_s_at	U00238	NM_002703	5471	0.75	4.18E-04
FH	203032_s_at	AI363836	NM_000143	2271	0.75	3.75E-04
USP28	231837_at	AB040948	NM_020886	57646	0.75	4.33E-04
COVA1	32042_at	S72904	NM_006375 NM_182314	10495	0.75	1.36E-03
KIAA1432	226221_at	AL138104	XM_039698	57589	0.75	1.64E-03
ZNF43	206695_x_at	NM_003423	NM_003423	7594	0.75	2.70E-03
MICAL-L1	55081_at	W46406	NM_033386	85377	0.75	4.38E-03
HPRP8BP	215905_s_at	AL157420	NM_004814	9410	0.74	1.02E-04
MAC30	214283_at	AU150186	NM_014573	27346	0.74	8.38E-06
C10orf78	238794_at	N23586	NM_001002759 NM_145247	119392	0.74	7.02E-03
Cep70	219036_at	NM_024491	NM_024491	80321	0.74	1.04E-03

CDKAL1	214877_at	BE794663	NM_017774	54901	0.74	7.46E-04
CUGBP2	227178_at	AI652861	NM_006561	10659	0.74	1.87E-03
SQLE	213562_s_at	BF979497	NM_003129	6713	0.74	1.93E-03
RABL3	226089_at	AI742028	NM_173825	285282	0.74	2.21E-03
TRAM2	202368_s_at	AI986461	NM_012288	9697	0.74	4.19E-03
CD47	227259_at	BF439618	NM_001777	961	0.74	6.22E-03
			NM_198793			
T87730	242500_at	T87730	---	---	0.74	5.92E-05
DGCR2	214198_s_at	AU150824	NM_005137	9993	0.74	5.08E-05
GIT2	209876_at	AF124491	NM_014776	9815	0.74	1.42E-03
			NM_057169			
			NM_057170			
			NM_139201			
MKKS	222530_s_at	AF275813	NM_018848	8195	0.74	8.92E-03
			NM_170784			
NFKBIE	203927_at	NM_004556	NM_004556	4794	0.73	7.87E-03
PTCH	209815_at	BG054916	NM_000264	5727	0.73	4.15E-07
SORT1	212807_s_at	BF447105	NM_002959	6272	0.73	6.06E-04
SKP2	203625_x_at	BG105365	NM_005983	6502	0.73	2.38E-03
			NM_032637			
B3GNT1	219326_s_at	NM_006577	NM_006577	10678	0.73	3.66E-03
			NM_033252			
TST	209605_at	D87292	NM_003312	7263	0.73	3.44E-03
RQCD1	1553510_s_at	NM_005444	NM_005444	9125	0.73	7.31E-03
LOC440928	235147_at	R56118	XM_498917	440928	0.73	8.09E-05
EPB41L5	220977_x_at	NM_020909	NM_020909	57669	0.73	9.69E-03
B4GALT6	206233_at	AF097159	NM_004775	9331	0.73	3.61E-04
MTHFD1	202309_at	NM_005956	NM_005956	4522	0.73	5.58E-03
SUHW2	230789_at	AI015954	NM_080764	140883	0.73	4.75E-03
TCF4	228837_at	BE857360	NM_003199	6925	0.73	1.23E-05
C20orf22	224742_at	BF570412	NM_015600	26090	0.73	5.04E-04
EIF4ENIF1	218626_at	NM_019843	NM_019843	56478	0.73	3.09E-06
ZNF141	206931_at	NM_003441	NM_003441	7700	0.73	1.09E-03
ZNF278	209494_s_at	AI807017	NM_014323	23598	0.73	1.80E-03
			NM_032050			
			NM_032051			
			NM_032052			
RNF26	224947_at	AL559247	NM_032015	79102	0.73	9.69E-04
GNG4	1555765_a_at	AF493872	NM_004485	2786	0.73	2.53E-03
BCR	202315_s_at	NM_004327	NM_004327	613	0.72	5.57E-03
			NM_021574			
FPGT	205140_at	NM_003838	NM_003838	8790	0.72	4.20E-05
FLJ13273	235387_at	AA740875	NM_024751	79807	0.72	2.00E-06
PRIM2A	215708_s_at	AL121975	NM_000947	5558	0.72	3.15E-03
TOMM22	217960_s_at	NM_020243	NM_020243	56993	0.72	3.02E-03
CDH2	203440_at	M34064	NM_001792	1000	0.72	1.27E-04
DENR	234915_s_at	BC000925	NM_003677	8562	0.72	5.52E-06
KIAA1280	219520_s_at	NM_018458	NM_015691	55841	0.72	1.98E-03
CDC5L	209056_s_at	NM_001253	NM_001253	988	0.72	5.21E-03
MYH9	211926_s_at	AI827941	NM_002473	4627	0.72	5.89E-03
SLC25A13	203775_at	NM_014251	NM_014251	10165	0.72	5.47E-03
SEMA6A	220454_s_at	NM_020796	NM_020796	57556	0.72	5.20E-04
SOX2	213722_at	AW007161	NM_003106	6657	0.72	3.52E-04
RP2	205191_at	NM_006915	NM_006915	6102	0.72	1.30E-03
AI291804	242856_at	AI291804	---	---	0.72	6.53E-03
SLC26A2	224963_at	AK025078	NM_000112	1836	0.72	3.23E-03
GRIA1	211520_s_at	M64752	NM_000827	2890	0.71	6.86E-04
SCD	211162_x_at	AF116616	NM_005063	6319	0.71	8.56E-03

TM4SF6	209109_s_at	U84895	NM_003270	7105	0.71	1.07E-04
CYB5-M	201634_s_at	NM_030579	NM_030579	80777	0.71	8.39E-03
AW025579	213429_at	AW025579	---	---	0.71	1.53E-04
CDW92	224595_at	AK022549	NM_022109 NM_080546	23446	0.71	4.42E-03
KIAA1853	230010_at	AA608629	NM_194286	84530	0.71	1.11E-03
GCLM	203925_at	NM_002061	NM_002061	2730	0.71	2.48E-03
TLK2	228627_at	AL041560	NM_006852	11011	0.71	1.99E-03
RNF144	204040_at	NM_014746	NM_014746	9781	0.71	3.67E-03
PAXIP1L	212825_at	AI357401	NM_007349	22976	0.71	7.70E-03
PHOX2B	207009_at	NM_003924	NM_003924	8929	0.71	1.10E-05
FAM19A2	241399_at	AI142028	NM_178539	338811	0.71	3.12E-03
RSN	210716_s_at	M97501	NM_002956 NM_198240	6249	0.71	1.47E-03
RB1	203132_at	NM_000321	NM_000321	5925	0.71	9.52E-03
AA603344	235964_x_at	AA603344	---	---	0.71	5.50E-03
ZNF278	211392_s_at	AF242522	NM_014323 NM_032050 NM_032051 NM_032052	23598	0.71	9.10E-03
DEK	200934_at	NM_003472	NM_003472	7913	0.71	7.14E-03
GPC6	227059_at	AI651255	NM_005708	10082	0.71	1.48E-03
KBTBD4	223765_s_at	AF151086	NM_016506 NM_018095	55709	0.71	2.77E-04
AA521504	235952_at	AA521504	---	---	0.71	7.68E-03
LOC163404	231397_at	AF131783	XM_375754	163404	0.71	9.06E-03
CHRNB4	207516_at	NM_000750	NM_000750	1143	0.70	2.92E-04
UBE2L3	200676_s_at	NM_003347	NM_003347 NM_198157	7332	0.70	3.80E-07
MAGEH1	218573_at	NM_014061	NM_014061	28986	0.70	8.04E-07
PKM2	201251_at	NM_002654	NM_002654 NM_182470 NM_182471	5315	0.70	5.34E-03
DVL2	57532_at	AW016304	NM_004422	1856	0.70	2.07E-03
AMMECR1	1553219_a_at	NM_015365	NM_015365	9949	0.70	2.11E-03
SLA/LP	235516_at	AI038867	NM_016955 NM_153825	51091	0.70	3.09E-03
PEPD	202108_at	NM_000285	NM_000285	5184	0.70	7.53E-04
LDHA	200650_s_at	NM_005566	NM_005566	3939	0.70	3.92E-03
MVK	204056_s_at	NM_000431	NM_000431	4598	0.70	3.92E-03
RAB22A	218360_at	NM_020673	NM_020673	57403	0.70	2.55E-03
MAP3K7IP1	203901_at	NM_006116	NM_006116 NM_153497	10454	0.70	4.29E-03
HMGCR	202540_s_at	NM_000859	NM_000859	3156	0.70	6.44E-04
AGPS	225113_at	BF688144	NM_003659	8540	0.70	1.13E-03
ZNF305	240181_at	AI939511	NM_014724	9753	0.70	2.45E-03
SATB2	213435_at	AB028957	NM_015265	23314	0.70	6.66E-03
HPS4	54037_at	AL041451	NM_022081 NM_152840 NM_152841 NM_152842 NM_152843	89781	0.70	1.86E-05
B4GALT4	210540_s_at	BC004523	NM_003778 NM_212543	8702	0.70	4.75E-03
ZNF555	1556188_a_at	AF052118	NM_152791	148254	0.70	9.31E-03
NEDD1	234984_at	AA236927	NM_152905	121441	0.70	9.72E-03
KIAA1648	213058_at	AL033538	---	284900	0.70	4.59E-03

MITF	207233_s_at	NM_000248	NM_000248 NM_006722 NM_198158 NM_198159 NM_198177 NM_198178	4286	0.69	9.18E-03
TM4SF9	225388_at	AI928507	NM_005723	10098	0.69	1.96E-05
GGA2	214190_x_at	AI799984	NM_015044 NM_138640	23062	0.69	5.04E-04
FLJ10199	218815_s_at	NM_018022	NM_018022	55092	0.69	5.48E-03
SAMHD1	234987_at	AV715309	NM_015474	25939	0.69	8.34E-03
IDH3B	210418_s_at	AF023265	NM_006899 NM_174855 NM_174856	3420	0.69	9.34E-05
BNIP3	201849_at	NM_004052	NM_004052	664	0.69	3.88E-03
CANP	1557129_a_at	AA960844	NM_198947	374393	0.69	8.06E-03
GNG4	205184_at	NM_004485	NM_004485	2786	0.69	4.91E-03
G3BP	201514_s_at	NM_005754	NM_005754 NM_198395	10146	0.69	7.45E-05
B3GNT1	222870_s_at	AF288208	NM_006577 NM_033252	10678	0.69	3.54E-03
CENTB2	212476_at	D26069	NM_012287	23527	0.69	1.34E-03
LBR	201795_at	NM_002296	NM_002296 NM_194442	3930	0.69	3.92E-04
EB-1	227440_at	AW005572	NM_020140 NM_152788 NM_181670	56899	0.69	8.38E-06
LANCL1	202019_s_at	AI935255	NM_006055	10314	0.69	4.49E-03
AI857788	227126_at	AI857788	---	---	0.69	9.75E-03
GPC1	202756_s_at	NM_002081	NM_002081	2817	0.69	1.42E-05
RBM14	204178_s_at	NM_006328	NM_006328	10432	0.69	2.67E-03
CRKL	212180_at	AK000311	NM_005207	1399	0.68	3.46E-07
SMC1L1	201589_at	D80000	NM_006306	8243	0.68	1.70E-03
NFIB	213032_at	AI186739	NM_005596	4781	0.68	4.95E-03
RBM14	1555639_a_at	AF315633	NM_006328	10432	0.68	5.28E-04
IDH3B	210014_x_at	AF023266	NM_006899 NM_174855 NM_174856	3420	0.68	2.88E-04
SC4MOL	209146_at	AV704962	NM_006745	6307	0.68	1.06E-05
SLC25A15	222705_s_at	BC002702	NM_014252	10166	0.68	5.67E-05
ESD	228162_at	AA193515	NM_001984	2098	0.68	7.72E-03
PPAT	209433_s_at	AI457120	NM_002703	5471	0.68	1.12E-03
ROD1	224618_at	BF059136	NM_005156	9991	0.68	6.34E-03
ATP7A	205197_s_at	BE567813	NM_000052	538	0.68	6.71E-03
AK022438	233508_at	AK022438	---	---	0.68	3.52E-03
BG337831	238065_at	BG337831	---	---	0.68	8.60E-03
CDS2	212864_at	Y16521	NM_003818	8760	0.68	1.15E-04
MGC34646	224996_at	N30209	NM_173519	157807	0.68	1.11E-04
RECK	205407_at	NM_021111	NM_021111	8434	0.67	8.99E-03
MCAM	211042_x_at	BC006329	NM_006500	4162	0.67	2.11E-04
LOC128977	1553974_at	BC030758	NM_173793	128977	0.67	2.13E-04
SNX5	222417_s_at	AF121855	NM_014426 NM_152227	27131	0.67	7.63E-04
C20orf22	228123_s_at	AW303865	NM_015600	26090	0.67	2.89E-04
PHF20	235389_at	BG168139	NM_016436	51230	0.67	9.09E-03
NM_014838	204799_at	NM_014838	---	---	0.67	1.84E-04
Cep70	1554489_a_at	BC016050	NM_024491	80321	0.67	5.84E-03
GCAT	205164_at	NM_014291	NM_014291	23464	0.67	9.67E-03

MGC20255	225257_at	AA534536	NM_052848	90324	0.67	2.25E-04
KIAA1715	225717_at	AI814587	NM_030650	80856	0.67	2.65E-03
SH3MD1	224817_at	W93554	NM_014631	9644	0.67	3.37E-04
NFYA	204108_at	AL031778	NM_002505 NM_021705	4800	0.67	6.22E-03
MGC10854	223456_s_at	BC004285	NM_032300	84260	0.67	2.49E-03
DNAJC13	212467_at	AB014578	NM_173823	23317	0.67	4.58E-05
SEMA6A	223449_at	AF225425	NM_020796	57556	0.67	7.98E-03
BC017932	1569283_at	BC017932	XM_495940	440122	0.67	1.88E-03
CDW92	224596_at	AI634866	NM_022109 NM_080546	23446	0.67	6.95E-03
HMGCS1	221750_at	BG035985	NM_002130	3157	0.67	5.27E-04
IDH3B	201509_at	NM_006899	NM_006899 NM_174855 NM_174856	3420	0.66	3.23E-04
CECR6	224393_s_at	AF307451	NM_031890	27439	0.66	3.23E-05
IPO11	222659_at	AK001696	NM_016338	51194	0.66	3.34E-03
ACTL6B	206013_s_at	NM_016188	NM_016188	51412	0.66	5.47E-03
D15Wsu75e	212527_at	BF057059	XM_039495	27351	0.66	1.32E-04
AL134573	228208_x_at	AL134573	---	---	0.66	1.64E-03
MLLT3	204918_s_at	NM_004529	NM_004529	4300	0.66	8.51E-03
GGA2	208913_at	AA868560	NM_015044 NM_138640	23062	0.66	2.22E-03
ROD1	224617_at	AI735576	NM_005156	9991	0.66	3.70E-03
SNN	218032_at	AF070673	NM_003498	8303	0.66	5.14E-03
CD47	213055_at	BF693956	NM_001777 NM_198793	961	0.66	2.63E-03
ENO1	217294_s_at	U88968	NM_001428	2023	0.66	2.43E-04
SESN3	235150_at	AW376955	NM_144665	143686	0.66	7.70E-04
CRY1	209674_at	D83702	NM_004075	1407	0.66	2.50E-03
NM_018243	201308_s_at	NM_018243	NM_018243	55752	0.66	3.72E-03
CBX5	241875_at	AA204654	NM_012117	23468	0.66	1.75E-03
ZFYVE16	203651_at	NM_014733	NM_014733	9765	0.66	1.76E-05
NRF1	204652_s_at	NM_005011	NM_005011	4899	0.66	2.20E-03
GALNT2	217788_s_at	NM_004481	NM_004481	2590	0.66	6.79E-06
SNX5	217792_at	NM_014426	NM_014426 NM_152227	27131	0.66	1.46E-03
ALK	208212_s_at	NM_004304	NM_004304	238	0.65	2.47E-03
WDR44	219297_at	NM_019045	NM_019045	54521	0.65	3.28E-04
ELMOD2	1553928_at	NM_153702	NM_153702	255520	0.65	1.79E-04
VAPB	202550_s_at	NM_004738	NM_004738	9217	0.65	3.71E-05
LOC129285	1553955_at	AY134855	NM_152994	129285	0.65	3.87E-03
MPHOSPH9	206205_at	NM_022782	NM_022782	10198	0.65	7.66E-05
SCML2	206147_x_at	NM_006089	NM_006089	10389	0.65	1.04E-03
HS6ST2	230030_at	AI767756	NM_147174 NM_147175	90161	0.65	3.43E-03
NUP43	219007_at	NM_024647	NM_024647 NM_198887	348995	0.65	6.58E-03
R12027	241836_x_at	R12027	---	---	0.65	6.67E-03
H16725	239138_at	H16725	---	---	0.65	7.65E-03
AGPS	205401_at	NM_003659	NM_003659	8540	0.65	1.27E-03
DKFZP564M082	204218_at	NM_014042	NM_014042	25906	0.65	2.63E-03
MCART1	214126_at	N39314	NM_033412	92014	0.65	6.73E-04
NUP50	218295_s_at	NM_007172	NM_007172 NM_153645 NM_153684	10762	0.65	4.08E-04
PDK1	226452_at	AU146532	NM_002610	5163	0.65	7.55E-03
GPR125	1555122_at	BC026009	NM_145290	166647	0.65	1.16E-03

KIAA0692	212200_at	AK025933	---	23141	0.65	3.35E-04
ZADH1	230774_at	BE465894	NM_152444	145482	0.65	1.11E-03
CD24	209772_s_at	X69397	NM_013230	934	0.65	3.11E-04
KIAA1715	225718_at	AL133768	NM_030650	80856	0.65	2.15E-03
MANEA	222805_at	AI587307	NM_024641	79694	0.65	3.26E-04
C10orf86	219067_s_at	NM_017615	NM_017615	54780	0.65	6.76E-03
AL524175	225479_at	AL524175	---	---	0.64	4.37E-05
MICAL-L1	221779_at	BC001090	NM_033386	85377	0.64	1.27E-03
AI708256	229342_at	AI708256	---	---	0.64	1.31E-05
G3BP	201503_at	BG500067	NM_005754 NM_198395	10146	0.64	3.53E-03
PLCXD1	222795_s_at	BE675241	NM_018390	55344	0.64	2.51E-03
CD47	226016_at	AL118798	NM_001777 NM_198793	961	0.64	1.22E-07
RAB8B	219210_s_at	NM_016530	NM_016530	51762	0.64	2.35E-04
RNF150	227657_at	AA722069	NM_020724	57484	0.64	5.51E-03
TEX261	212083_at	BG170659	NM_144582	113419	0.64	6.37E-03
BE893995	234983_at	BE893995	---	---	0.64	1.28E-03
MGC3731	222057_at	AW002578	NM_024313	79159	0.64	8.73E-03
LOC284801	225762_x_at	AL531683	XM_378973	284801	0.64	3.26E-03
SLC25A17	211754_s_at	BC005957	NM_006358	10478	0.64	9.76E-04
KIAA0692	212201_at	AW274877	---	23141	0.64	2.57E-03
PCDHB2	231725_at	NM_018936	NM_018936	56133	0.64	1.47E-03
ATP1A1	220948_s_at	NM_000701	NM_000701 NM_00100158 6	476	0.64	2.01E-03
CHKB	204193_at	NM_005198	NM_005198 NM_152253	1120	0.64	3.36E-03
MPHOSPH9	215731_s_at	X98258	NM_022782	10198	0.64	3.26E-03
KIAA0877	1560916_a_at	BI461155	XM_371891 XM_374422	23333	0.64	1.49E-03
MAC30	212279_at	BE779865	NM_014573	27346	0.64	1.07E-03
RPA1	201529_s_at	NM_002945	NM_002945	6117	0.64	4.43E-03
HADHSC	211569_s_at	AF001903	NM_005327	3033	0.64	4.68E-03
HNRPC	227110_at	AA126793	NM_004500 NM_031314	3183	0.64	8.86E-04
C2orf12	225269_s_at	BE384529	---	192137	0.64	5.65E-05
GSK3B	209945_s_at	BC000251	NM_002093	2932	0.64	8.48E-04
RCN3	61734_at	AI797684	NM_020650	57333	0.64	1.45E-03
MANEA	219003_s_at	NM_024641	NM_024641	79694	0.63	1.47E-04
LOC339448	238010_at	BF970340	NM_207356	339448	0.63	6.74E-03
U1SNRNPBP	205300_s_at	NM_022717	NM_007020 NM_022717 NM_180699 NM_180703	11066	0.63	7.93E-03
AB014540	209307_at	AB014540	---	---	0.63	5.07E-03
MKL1	212748_at	AB037859	NM_020831	57591	0.63	9.09E-04
NBS1	217299_s_at	AK001017	NM_002485	4683	0.63	5.38E-03
ACSL3	201662_s_at	D89053	NM_004457 NM_203372	2181	0.63	3.55E-04
GALNT2	223991_s_at	AF130059	NM_004481	2590	0.63	9.09E-04
FBXL10	226215_s_at	AI989996	NM_00100536 6 NM_032590	84678	0.63	6.47E-03
C1orf48	230592_at	BE501789	NM_015471	25936	0.63	6.21E-03
FSCN1	210933_s_at	BC004908	NM_003088	6624	0.63	7.38E-03
ALMS1	214221_at	AI825212	NM_015120	7840	0.63	6.34E-03
MGC3040	223524_s_at	BC000568	NM_023943	66000	0.63	8.05E-03

WDR5	223308_s_at	AL521101	NM_017588 NM_052821	11091	0.63	1.08E-03
RBMS1	203748_x_at	NM_016839	NM_002897 NM_016836 NM_016839	5937	0.63	4.92E-04
ACTR6	218395_at	NM_022496	NM_022496	64431	0.63	1.97E-06
TOMM22	222474_s_at	AB041906	NM_020243	56993	0.63	2.85E-03
LOC129138	231847_at	Z97630	NM_138797	129138	0.63	1.02E-04
LOC338799	226369_at	AW138760	---	338799	0.63	3.36E-03
SLC2A4RG	222650_s_at	BE898559	NM_020062	56731	0.63	7.06E-04
SCOC	224786_at	AL133580	NM_032547	60592	0.63	1.37E-05
MGC3731	219324_at	NM_024313	NM_024313	79159	0.62	1.54E-03
C10orf6	203481_at	AI655902	NM_018121	55719	0.62	2.18E-04
NUP133	233421_s_at	AU146738	NM_018230	55746	0.62	7.97E-03
CSRP2BP	228543_at	AA780252	NM_020536 NM_177926	57325	0.62	6.49E-04
HSPC129	1555106_a_at	BC035744	NM_016396	51496	0.62	1.80E-03
MGC5139	202365_at	BC004815	---	84747	0.62	1.02E-04
HIC2	212964_at	AI912206	NM_015094	23119	0.62	1.32E-04
FCHO2	228220_at	AI627666	NM_138782	115548	0.62	4.50E-03
CDK5RAP1	218315_s_at	NM_016408	NM_016082 NM_016408	51654	0.62	7.08E-05
FH	214170_x_at	AA669797	NM_000143	2271	0.62	9.05E-03
ENTPD6	201704_at	NM_001247	NM_001247	955	0.62	1.44E-03
NUP50	213682_at	AL036344	NM_007172 NM_153645 NM_153684	10762	0.62	2.73E-03
SNX5	229980_s_at	AA131508	NM_014426 NM_152227	27131	0.62	1.66E-04
B4GALT6	235333_at	BG503479	NM_004775	9331	0.62	4.18E-03
LOC150383	227590_at	BE501980	NM_00100891 7 NM_207327	150383	0.62	1.10E-03
SYNGR1	213854_at	BF511590	NM_004711 NM_145731 NM_145738	9145	0.62	3.40E-03
DZIP3	207231_at	NM_014648	NM_014648	9666	0.62	5.60E-05
CSRP2BP	228544_s_at	AA780252	NM_020536 NM_177926	57325	0.62	8.59E-03
SCC-112	212138_at	AK021757	NM_015200	23244	0.62	2.22E-06
TEAD1	224955_at	AI590088	NM_021961	7003	0.62	1.84E-03
DYRK4	212954_at	AF263541	NM_003845	8798	0.62	2.89E-04
RAPH1	243012_at	BF196252	NM_025252 NM_203365 NM_213589	65059	0.62	5.72E-03
SC5DL	211423_s_at	D85181	NM_006918	6309	0.61	1.75E-03
BUB3	201457_x_at	AF081496	NM_00100779 3 NM_004725	9184	0.61	5.81E-03
TMEM38B	218772_x_at	NM_018112	NM_018112	55151	0.61	1.91E-03
TPARL	218095_s_at	NM_018475	NM_018475	55858	0.61	1.44E-03
HRPT2	235196_at	AA447464	NM_024529	79577	0.61	2.37E-03
KIAA0406	212898_at	AB007866	NM_014657	9675	0.61	1.44E-03
FBXO30	226541_at	AI808182	NM_032145	84085	0.61	1.59E-03
EPOR	209963_s_at	M34986	NM_000121	2057	0.61	8.17E-03
AP3B1	203141_s_at	AW058575	NM_003664	8546	0.61	1.23E-04
FLJ33008	228954_at	AW452620	NM_152449	145748	0.61	3.98E-04
FLJ21908	1557984_s_at	BI464019	NM_024604	79657	0.61	1.58E-03

ALS2CR2	223266_at	AB038950	NM_018571	55437	0.61	6.51E-05
RPP30	203436_at	NM_006413	NM_006413	10556	0.61	4.85E-03
LOC388272	226608_at	AW157311	NM_001001436	388272	0.61	7.08E-03
AI421677	242964_at	AI421677	---	---	0.61	2.28E-04
HSDL1	223248_at	AK025626	NM_031463	83693	0.61	3.31E-04
GLT25D1	222644_s_at	AI924150	NM_024656	79709	0.61	3.50E-03
CBX5	209715_at	L07515	NM_012117	23468	0.61	7.77E-03
SCOC	223341_s_at	AF330205	NM_032547	60592	0.61	7.55E-03
FLJ22531	204922_at	NM_024650	NM_024650	79703	0.61	4.70E-03
TMOD3	220800_s_at	NM_014547	NM_014547	29766	0.61	1.32E-03
ZFP161	209724_s_at	AL534416	NM_003409	7541	0.61	7.01E-05
AL563613	226532_at	AL563613	---	---	0.61	3.89E-03
SESN3	242899_at	N78412	NM_144665	143686	0.61	2.87E-03
PGM2	223738_s_at	AL136705	NM_018290	55276	0.61	9.76E-05
ORC4L	203352_at	NM_002552	NM_002552	5000	0.60	3.05E-03
			NM_181741			
			NM_181742			
PANK3	218433_at	NM_024594	NM_024594	79646	0.60	9.11E-03
MGC13170	224468_s_at	BC006151	NM_199249	84798	0.60	2.79E-04
			NM_199250			
HABP4	209818_s_at	AF241831	NM_014282	22927	0.60	5.02E-04
RBMS1	225265_at	AI580100	NM_002897	5937	0.60	1.37E-03
			NM_016836			
			NM_016839			
SESN3	225123_at	BE883841	NM_144665	143686	0.60	3.28E-05
RG9MTD1	223267_at	AF226052	NM_017819	54931	0.60	4.25E-05
SEMA6A	225660_at	W92748	NM_020796	57556	0.60	3.33E-03
PPM1F	37384_at	D86995	NM_014634	9647	0.60	9.35E-04
BMP2K	219546_at	NM_017593	NM_017593	55589	0.60	7.82E-04
			NM_198892			
SCD	211708_s_at	BC005807	NM_005063	6319	0.60	3.69E-03
LOC286505	226421_at	AA707320	---	286505	0.60	6.02E-03
TOMM70A	201512_s_at	BC003633	NM_014820	9868	0.60	8.65E-03
ANXA11	206200_s_at	NM_001157	NM_001157	311	0.60	1.86E-03
			NM_145868			
			NM_145869			
AW971254	222369_at	AW971254	---	---	0.60	7.78E-04
AI754928	226347_at	AI754928	---	---	0.60	4.04E-03
NHLRC2	235356_at	AW297204	NM_198514	374354	0.60	4.48E-03
HDAC1	201209_at	NM_004964	NM_004964	3065	0.60	2.74E-05
MGC14141	225568_at	BE728983	NM_032928	85014	0.60	4.04E-04
NIT2	218557_at	NM_020202	NM_020202	56954	0.59	8.84E-03
SREBF2	201247_at	BE513151	NM_004599	6721	0.59	7.04E-03
MKKS	218138_at	NM_018848	NM_018848	8195	0.59	1.60E-04
			NM_170784			
EPIM	213434_at	H95263	NM_001980	2054	0.59	3.73E-03
			NM_194356			
NDRG3	221082_s_at	NM_022477	NM_022477	57446	0.59	7.59E-04
			NM_032013			
TIGD7	224365_s_at	AF251050	NM_033208	91151	0.59	8.93E-03
R68654	236971_at	R68654	---	---	0.59	5.73E-03
BE675101	236384_at	BE675101	---	---	0.59	2.31E-04
MAC30	212281_s_at	BF038366	NM_014573	27346	0.59	1.68E-04
FLJ12806	220199_s_at	NM_022831	NM_022831	64853	0.59	2.17E-05
ASF1A	203427_at	NM_014034	NM_014034	25842	0.59	1.25E-04
CTCF	202521_at	NM_006565	NM_006565	10664	0.59	4.94E-05
PSCD3	225147_at	AL521959	NM_004227	9265	0.59	9.96E-03

IQSEC3	213834_at	AB029033	XM_370667 XM_495902	440073	0.59	2.90E-04
MPHOSPH9	221965_at	AI990326	NM_022782	10198	0.58	9.17E-03
DNCI2	236698_at	AI823600	NM_001378	1781	0.58	1.70E-03
ZNRF3	226360_at	AK022809	XM_290972	84133	0.58	2.94E-03
OSBPL11	222586_s_at	AI884890	NM_022776	114885	0.58	2.49E-03
NIPSNAP3A	224436_s_at	BC005935	NM_015469	25934	0.58	3.38E-03
NBS1	202906_s_at	AF049895	NM_002485	4683	0.58	4.86E-03
MGC3162	218860_at	NM_024078	NM_024078	79050	0.58	3.07E-04
FLJ13149	219016_at	NM_021826	NM_021826	60493	0.58	8.95E-03
DIAPH1	213514_s_at	AU158818	NM_005219	1729	0.58	7.31E-03
IGSF4	209031_at	AL519710	NM_014333	23705	0.58	2.03E-03
ATP6V1A	201971_s_at	NM_001690	NM_001690	523	0.58	4.36E-04
FLJ25952	225365_at	BG249221	NM_153251	253832	0.58	2.88E-03

Table 6. Decreased Gene Expression in Cell Lines H1 and BB10 vs. Cell Line 2D6 in Undifferentiated State Using Microarray Analysis

Gene Symbol	Probe Set ID	Representative Public ID	RefSeq Transcript ID	Entrez Gene ID	Log2 Ratio	pvalue
KIAA0125	206478_at	NM_014792	NM_014792	9834	-7.57	6.75E-06
CART	206339_at	NM_004291	NM_004291	9607	-6.35	6.05E-07
CPNE8	228365_at	AI765180	NM_153634	144402	-5.76	5.62E-09
MEOX2	206201_s_at	NM_005924	NM_005924	4223	-5.64	6.26E-06
CYTL1	219837_s_at	NM_018659	NM_018659	54360	-5.64	1.55E-10
CYGB	226632_at	AL513673	NM_134268	114757	-5.63	1.66E-03
FGF13	205110_s_at	NM_004114	NM_004114 NM_033642	2258	-5.18	1.42E-06
CPNE8	241706_at	AA431782	NM_153634	144402	-4.70	2.99E-10
CYGB	1553572_a_at	NM_134268	NM_134268	114757	-4.40	5.68E-05
BC036254	1557443_s_at	BC036254	---	---	-4.26	3.10E-05
SLC1A2	225491_at	AL157452	NM_004171	6506	-4.14	7.08E-13
CAP2	212554_at	N90755	NM_006366	10486	-4.08	3.14E-07
AL353759	215071_s_at	AL353759	---	---	-3.91	1.82E-05
GNAS	217057_s_at	AF107846	NM_000516 NM_016592 NM_080425 NM_080426	2778	-3.79	5.67E-04
CFC1	223753_s_at	AF312769	NM_032545	55997	-3.75	5.58E-06
GRM5	214217_at	D60132	NM_000842	2915	-3.73	3.90E-09
CYP2E1	1431_at	J02843	NM_000773	1571	-3.66	1.03E-03
LOC56901	218484_at	NM_020142	NM_020142	56901	-3.66	1.04E-04
PAPPA	224942_at	BG434272	NM_002581	5069	-3.64	2.15E-04
AQP1	209047_at	AL518391	NM_000385 NM_198098	358	-3.61	1.21E-05
BG325630	234973_at	BG325630	---	---	-3.57	9.05E-04
CDKN2A	209644_x_at	U38945	NM_000077 NM_058195 NM_058197	1029	-3.30	4.00E-06
CYP2E1	209975_at	AF182276	NM_000773	1571	-3.28	1.91E-03
BF432956	229057_at	BF432956	---	---	-3.21	2.21E-06
ANK3	237839_at	BF433975	NM_001149 NM_020987	288	-3.19	4.55E-03
AU144437	232887_at	AU144437	---	---	-3.17	9.97E-06
LOC158572	243017_at	AA032156	XM_379705	158572	-3.12	5.87E-07
SAMD4	212845_at	AB028976	NM_015589	23034	-3.12	2.46E-03
M160	223655_at	AF264014	NM_174941	283316	-3.12	3.65E-05
SYT13	226086_at	AB037848	NM_020826	57586	-3.11	1.85E-05
AI093492	237435_at	AI093492	---	---	-3.03	2.14E-03
CYP2E1	209976_s_at	AF182276	NM_000773	1571	-3.01	9.74E-04
N39597	1555993_at	N39597	---	---	-2.99	1.61E-04
ASAM	226834_at	BG112263	NM_024769	79827	-2.98	6.28E-03
KIAA1598	221802_s_at	AU157109	NM_018330	57698	-2.94	8.29E-05
CDC42EP1	204693_at	NM_007061	NM_007061 NM_152243	11135	-2.90	4.19E-03
N92599	241421_at	N92599	---	---	-2.86	2.63E-05
GDF15	221577_x_at	AF003934	NM_004864	9518	-2.84	2.08E-03
AI341823	239657_x_at	AI341823	---	---	-2.82	2.19E-05
AW665665	237187_at	AW665665	---	---	-2.78	1.83E-03
SLC35F3	229065_at	BF968270	NM_173508	148641	-2.76	7.38E-06
AA151917	230503_at	AA151917	---	---	-2.73	3.30E-05
PAPPA	201982_s_at	NM_002581	NM_002581	5069	-2.70	2.76E-06

IL17B	220273_at	NM_014443	NM_014443	27190	-2.67	2.02E-04
KIAA0125	220377_at	NM_014151		9834	-2.65	1.07E-05
			NM_014792			
ANK2	232606_at	AK021894	NM_001148	287	-2.65	4.00E-08
			NM_020977			
AK021495	215571_at	AK021495	---	---	-2.65	9.41E-04
ANK3	239726_at	AI743588	NM_001149	288	-2.64	4.93E-04
			NM_020987			
ANK2	1561895_at	BC030740	NM_001148	287	-2.63	1.24E-04
			NM_020977			
PAPPA	224940_s_at	BF107618	NM_002581	5069	-2.63	4.08E-04
PAPPA	228128_x_at	AI110886	NM_002581	5069	-2.60	6.58E-04
AW274468	242299_at	AW274468	---	---	-2.54	9.96E-08
GRIA2	205358_at	NM_000826	NM_000826	2891	-2.54	3.09E-03
PAPPA	201981_at	AA148534	NM_002581	5069	-2.51	2.17E-04
ANK2	216195_at	AF131823	NM_001148	287	-2.51	1.40E-06
			NM_020977			
PAPPA	224941_at	BF107618	NM_002581	5069	-2.50	1.61E-03
LOC283404	1558195_at	BG204230	---	283404	-2.49	1.03E-07
GRIP2	216481_at	AF052177	XM_042936	80852	-2.44	1.03E-04
BF000047	235736_at	BF000047	---	---	-2.43	2.70E-05
FGF1	1552721_a_at	NM_033136	NM_000800	2246	-2.43	2.69E-04
			NM_033136			
			NM_033137			
GRIA2	236538_at	BE219628	NM_000826	2891	-2.40	8.42E-04
BM977131	1557478_at	BM977131	---	---	-2.38	9.09E-05
BHLHB2	201170_s_at	NM_003670	NM_003670	8553	-2.37	5.35E-03
CAP2	212551_at	NM_006366	NM_006366	10486	-2.36	1.47E-03
PTN	211737_x_at	BC005916	NM_002825	5764	-2.35	1.99E-06
AI051127	231478_at	AI051127	---	---	-2.34	3.52E-03
PHLDA2	209803_s_at	AF001294	NM_003311	7262	-2.32	1.79E-05
RGS11	206107_at	NM_003834	NM_003834	8786	-2.31	1.17E-03
			NM_183337			
EGR1	201694_s_at	NM_001964	NM_001964	1958	-2.30	5.17E-03
DKK1	204602_at	NM_012242	NM_012242	22943	-2.29	9.68E-04
ZAP128	202982_s_at	NM_006821	NM_006821	10965	-2.29	2.38E-03
AK096401	1556204_a_at	AK096401	XM_375664	400721	-2.28	4.02E-05
AI459194	227404_s_at	AI459194	---	---	-2.28	8.03E-03
)KFZp313N062	1555905_a_at	AI147556	NM_173826	285343	-2.26	6.00E-04
LOC51315	222585_x_at	BE326678	NM_016618	51315	-2.26	7.70E-05
HIST2H2BE	202708_s_at	NM_003528	NM_003528	8349	-2.25	5.90E-05
BC035768	1559987_at	BC035768	---	---	-2.24	2.82E-04
ERBB4	206794_at	NM_005235	NM_005235	2066	-2.24	7.92E-04
IL7	206693_at	NM_000880	NM_000880	3574	-2.20	1.47E-04
AA601031	228919_at	AA601031	---	---	-2.18	1.30E-03
HS3ST1	205466_s_at	NM_005114	NM_005114	9957	-2.18	6.77E-04
ANK3	215314_at	AU146646	NM_001149	288	-2.18	3.85E-04
			NM_020987			
LOC144571	1564139_at	AK056852	---	144571	-2.17	1.36E-03
ENOSF1	213645_at	AF305057	NM_017512	55556	-2.16	1.79E-06
RASGEF1B	230233_at	BF110534	NM_152545	153020	-2.16	7.76E-03
CREB5	205931_s_at	NM_004904	NM_004904	9586	-2.15	5.67E-03
			NM_182898			
			NM_182899			
CG018	213375_s_at	N80918	NM_052818	90634	-2.14	7.06E-03
GAL	214240_at	AL556409	NM_015973	51083	-2.12	7.95E-03
ANK2	202921_s_at	NM_001148	NM_001148	287	-2.11	3.33E-05
			NM_020977			

CAMK2B	209956_s_at	U23460	NM_001220 NM_172078 NM_172079 NM_172080 NM_172081 NM_172082 NM_172083 NM_172084	816	-2.10	8.15E-06
PHKA2	1560358_at	BC038597	NM_000292	5256	-2.08	2.64E-05
CACNA1D	210108_at	BE550599	NM_000720	776	-2.08	2.44E-03
AW954199	239331_at	AW954199	---	---	-2.08	1.68E-07
LOC150759	221973_at	AI983904	XM_498456 XM_499585	150759	-2.05	4.18E-04
ADCY1	235049_at	AA021120	NM_021116	107	-2.05	1.26E-03
AI435590	237193_s_at	AI435590	---	---	-2.02	9.66E-04
AQP1	207542_s_at	NM_000385	NM_000385 NM_198098	358	-2.02	1.79E-03
BE219849	240180_at	BE219849	---	---	-2.00	1.75E-03
BF111884	230491_at	BF111884	---	---	-2.00	8.24E-07
KIAA0251	1558430_at	R08650	NM_015027	23042	-2.00	5.90E-03
AI810266	235456_at	AI810266	---	---	-2.00	2.25E-07
PPP3CA	1562467_at	AK097085	NM_000944	5530	-1.97	1.35E-03
SYNPR	230303_at	H11380	NM_144642	132204	-1.96	6.12E-03
ADCY1	213245_at	AL120173	NM_021116	107	-1.96	8.54E-05
BCAR3	239908_at	AA496799	NM_003567	8412	-1.96	2.42E-03
BC025319	1568974_at	BC025319	---	---	-1.95	6.55E-05
DDEF1	1557685_at	AK054840	NM_018482	50807	-1.94	5.02E-04
NEURL	230767_at	BF448300	NM_004210	9148	-1.94	4.29E-04
STAR	204548_at	NM_000349	NM_000349 NM_001007243	6770	-1.93	5.97E-05
NAG8	210109_at	AF191492	NM_014411	27099	-1.92	7.56E-03
LOC55831	215250_at	AU147317	NM_018447	55831	-1.92	4.21E-04
AI927692	228528_at	AI927692	---	---	-1.91	1.93E-03
BC041941	1559597_at	BC041941	---	---	-1.90	9.44E-04
CLDN10	1556687_a_at	BE465772	NM_006984 NM_182848	9071	-1.90	2.11E-03
AI800713	235122_at	AI800713	---	---	-1.88	8.12E-04
ADARB1	203865_s_at	NM_015833	NM_001112 NM_015833 NM_015834	104	-1.87	6.53E-04
LOC92162	229452_at	AL544576	NM_203411	92162	-1.86	1.23E-03
AL049252	216527_at	AL049252	---	---	-1.85	4.62E-05
ARC	210090_at	AF193421	NM_015193	23237	-1.85	1.06E-04
FYN	1559101_at	AK090692	NM_002037 NM_153047 NM_153048	2534	-1.85	6.72E-04
AAK1	214956_at	AF090101	NM_014911	22848	-1.85	2.35E-03
FARP1	227996_at	BF725250	NM_001001715 NM_005766	10160	-1.85	2.09E-03
PTGER2	206631_at	NM_000956	NM_000956	5732	-1.84	5.50E-04
LOC360030	232744_x_at	BG485129	---	360030	-1.84	1.99E-03
TCEAL2	211276_at	AF063606	NM_080390	140597	-1.84	4.69E-04
SIGIRR	218921_at	NM_021805	NM_021805	59307	-1.83	2.45E-03
RAB7	239405_at	AI022632	NM_004637	7879	-1.83	1.40E-04

CAMK2B	210404_x_at	AF078803	NM_001220 NM_172078 NM_172079 NM_172080 NM_172081 NM_172082 NM_172083 NM_172084	816	-1.82	2.11E-06
ERBB4	214053_at	AW772192	NM_005235	2066	-1.82	9.63E-05
FLJ13955	227001_at	AI096706	NM_024759	79815	-1.81	1.39E-03
AI697701	243666_at	AI697701	---	---	-1.81	1.63E-04
AK024567	234597_at	AK024567	---	---	-1.81	4.51E-07
RHOQ	1559582_at	BC033251	NM_012249	23433	-1.81	2.02E-03
ATP2B3	207026_s_at	NM_021949	NM_00100134 4 NM_021949	492	-1.81	3.94E-03
BF055351	231205_at	BF055351	---	---	-1.79	3.90E-03
ACYP2	206833_s_at	NM_001108	NM_138448	98	-1.79	1.40E-04
CAMK2B	211483_x_at	AF081924	NM_001220 NM_172078 NM_172079 NM_172080 NM_172081 NM_172082 NM_172083 NM_172084	816	-1.78	7.39E-06
DUSP5	209457_at	U16996	NM_004419	1847	-1.77	7.59E-04
NLF1	241031_at	BE218239	NM_207322	145741	-1.77	1.06E-06
DTNA	240125_at	AI697494	NM_001390 NM_001391 NM_001392 NM_032975 NM_032978 NM_032979 NM_032980 NM_032981	1837	-1.77	2.09E-03
FLJ12671	233728_at	AU148213	NM_030980	81875	-1.77	1.42E-03
TM4SF2	234245_at	AL162055	NM_004615	7102	-1.76	3.16E-03
MGC13040	224463_s_at	BC006128	NM_032930	85016	-1.76	9.67E-03
IGFBP5	211959_at	AW007532	NM_000599	3488	-1.76	5.39E-03
COL9A2	213622_at	AI733465	NM_001852	1298	-1.76	2.66E-03
AB088847	1555547_at	AB088847	---	---	-1.76	4.05E-06
UGCGL2	1558467_a_at	BE156619	NM_020121	55757	-1.75	2.63E-03
GPX7	213170_at	AA406605	NM_015696	2882	-1.75	1.66E-03
RLF	241438_at	AI742686	NM_012421	6018	-1.75	3.53E-03
DUSP16	1558739_at	R30807	NM_030640	80824	-1.74	1.87E-04
SORCS1	1556891_at	BE328250	NM_052918	114815	-1.74	2.33E-03
ANK2	202920_at	BF726212	NM_001148 NM_020977	287	-1.73	1.72E-04
AL119491	244292_at	AL119491	---	---	-1.73	2.74E-03
ATP2B3	242036_x_at	H09073	NM_00100134 4 NM_021949	492	-1.72	2.83E-03
DRD1IP	219896_at	NM_015722	NM_015722	50632	-1.72	4.50E-04

KCNQ2	205737_at	NM_004518	NM_004518 NM_172106 NM_172107 NM_172108 NM_172109	3785	-1.72	4.02E-06
LOC51315	233329_s_at	AK025986	NM_016618	51315	-1.71	4.22E-05
PNCK	229411_at	AI986390	NM_198452	139728	-1.71	9.68E-05
AA007336	237586_at	AA007336	---	---	-1.71	5.37E-04
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C9orf3	232783_at	AI147867	NM_032823	84909	-1.70	4.59E-03
RGAG4	227823_at	BE348679	XM_291322	340526	-1.70	6.60E-05
AK098781	1560814_a_at	AK098781	---	---	-1.69	7.73E-04
ERBB4	233498_at	AK024204	NM_005235	2066	-1.69	1.49E-03
C9orf10	241242_at	BE503118	NM_014612	23196	-1.68	1.66E-03
BF342356	238934_at	BF342356	---	---	-1.67	6.33E-06
IER3	201631_s_at	NM_003897	NM_003897 NM_052815	8870	-1.67	2.10E-06
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SNX27	244349_at	AI807658	NM_030918	81609	-1.66	4.72E-04
ACSL4	1559663_at	AF090916	NM_004458 NM_022977	2182	-1.66	4.29E-04
AA705933	239866_at	AA705933	---	---	-1.66	1.19E-04
PRR3	244204_at	W87300	NM_025263	80742	-1.66	4.53E-03
TMP21	239851_at	AW629289	NM_006827	10972	-1.66	5.43E-03
DDHD1	231165_at	BE857355	NM_030637	80821	-1.65	5.85E-07
BRD4	232551_at	AA521443	NM_014299 NM_058243	23476	-1.65	1.19E-03
LRRC5	234148_at	AK025238	NM_018103	55144	-1.65	6.30E-04
BE674309	230913_at	BE674309	---	---	-1.64	9.40E-04
AI052447	236796_at	AI052447	---	---	-1.64	1.69E-05
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AGPAT3	223182_s_at	AI337300	NM_020132	56894	-1.62	7.22E-06
C9orf150	216769_x_at	AK025180	NM_203403	286343	-1.62	6.30E-03
LOC286411	1557133_at	AV753446	---	286411	-1.62	1.50E-03
HNRPD	213359_at	W74620	NM_00100381 0 NM_002138 NM_031369 NM_031370	3184	-1.61	9.97E-03
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CRYGS	223643_at	AI762135	NM_017541	1427	-1.58	2.85E-05
BACH2	221234_s_at	NM_021813	NM_021813	60468	-1.58	2.32E-05
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CDH12	207149_at	L33477	NM_004061	1010	-1.58	7.69E-03
AB062488	1555014_x_at	AB062488	---	---	-1.58	1.71E-03
RHOU	223168_at	AL096776	NM_021205	58480	-1.57	2.07E-07

C21orf66	239407_at	AI793248	NM_013329 NM_016631 NM_058191 NM_145328	94104	-1.57	4.80E-03
ENOSF1	204143_s_at	NM_017512	NM_017512	55556	-1.56	4.33E-04
BE894882	235681_at	BE894882	---	---	-1.55	4.33E-05
AW606588	239008_at	AW606588	---	---	-1.54	5.81E-03
SYTL1	227134_at	AI341537	NM_032872	84958	-1.54	6.41E-03
AK025360	216173_at	AK025360	---	---	-1.54	2.23E-04
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LGALS3BP	200923_at	NM_005567	NM_005567	3959	-1.54	5.18E-09
AI768374	228661_s_at	AI768374	---	---	-1.54	1.48E-03
AA639707	243837_x_at	AA639707	---	---	-1.54	3.39E-03
AI821995	240201_at	AI821995	---	---	-1.54	1.51E-04
PHGDHL1	241932_at	AI073803	NM_177967	337867	-1.53	2.06E-03
LOC51315	218303_x_at	NM_016618	NM_016618	51315	-1.53	2.32E-05
C10orf10	209183_s_at	AL136653	NM_007021	11067	-1.52	3.47E-03
AI817960	239649_at	AI817960	---	---	-1.52	9.05E-05
CTBP2	215377_at	AK024129	NM_001329 NM_022802	1488	-1.52	3.37E-04
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ARHGAP20	228368_at	AI936560	NM_020809	57569	-1.51	1.86E-03
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NDRG1	200632_s_at	NM_006096	NM_006096	10397	-1.51	1.79E-04
SLICK	234103_at	AU145191	NM_198503	343450	-1.51	8.70E-03
PROM1	204304_s_at	NM_006017	NM_006017	8842	-1.51	1.53E-04
THADA	233692_at	AK024928	NM_022065 NM_198554	63892	-1.51	8.55E-05
FBXL13	243057_at	AI923673	NM_145032	222235	-1.50	2.27E-03
LOC54103	222150_s_at	AK026747	XM_379881 XM_499340	54103	-1.50	3.51E-04
BE552011	230208_at	BE552011	---	---	-1.50	4.21E-03
MGC45477	1554250_s_at	BC033812	---	387277	-1.50	3.37E-04
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PRSS11	201185_at	NM_002775	NM_002775	5654	-1.48	7.56E-04
PTPRH	208300_at	NM_002842	NM_002842	5794	-1.48	2.27E-03
C9orf150	227443_at	AI972386	NM_203403	286343	-1.48	1.85E-03
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LOC133308	229491_at	BF433180	NM_178833	133308	-1.47	2.89E-03
KIAA1276	233823_at	AB033102	XM_039169	27146	-1.46	3.60E-04
GNRHR	1568661_at	BC039430	NM_000406	2798	-1.46	8.63E-03
RAB6B	221792_at	AW118072	NM_016577	51560	-1.46	2.71E-03
FLJ12666	215029_at	AL117451	NM_024595	79647	-1.45	1.46E-04
LOC23117	238342_at	BF677084	XM_290670	23117	-1.45	1.20E-05
BG430958	1559455_at	BG430958	---	---	-1.44	7.89E-04
C6orf148	237347_at	AL039379	NM_030568	80759	-1.44	3.82E-04
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NDFIP2	1568807_a_at	AI301081	NM_019080	54602	-1.43	4.05E-06
SFRS1	239384_at	R18746	NM_006924	6426	-1.43	8.25E-03

STMN2	203001_s_at	NM_007029	NM_007029	11075	-1.43	6.36E-03
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TPD52	239862_at	W89022	NM_005079	7163	-1.42	1.59E-04
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CEBPD	203973_s_at	NM_005195	NM_005195	1052	-1.42	2.21E-03
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HIAT1	242374_at	AA747563	NM_033055	64645	-1.41	1.51E-03
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ABR	214671_s_at	L19704	NM_001092 NM_021962	29	-1.40	1.63E-04
BE219187	237594_at	BE219187	---	---	-1.40	1.72E-03
HLCS	207833_s_at	NM_000411	NM_000411	3141	-1.39	7.33E-03
NFYC	1558782_a_at	BG390627	NM_014223	4802	-1.39	2.59E-03
SNF1LK	208078_s_at	NM_030751	NM_173354	150094	-1.39	3.83E-03
C9orf150	233112_at	AW301393	NM_203403	286343	-1.39	1.07E-03
SCFD1	243525_at	AA808051	NM_016106 NM_182835	23256	-1.39	5.74E-04
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BC037911	1568981_at	BC037911	---	---	-1.38	1.58E-05
RHOU	223169_s_at	AB051826	NM_021205	58480	-1.38	6.23E-03
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TRIM32	1557315_a_at	AL134420	NM_012210	22954	-1.37	2.53E-03
AI394334	232696_at	AI394334	---	---	-1.37	2.28E-03
BIRC6	242068_at	AA608834	NM_016252	57448	-1.37	7.28E-03
ETFA	239830_at	AW850555	NM_000126	2108	-1.37	4.23E-04
PDGFRB	202273_at	NM_002609	NM_002609	5159	-1.37	1.64E-04
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KIAA1904	1559072_a_at	BC032083	NM_052906	114794	-1.34	4.03E-03
ACSL4	1557418_at	W95007	NM_004458	2182	-1.34	4.22E-04
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MAP2K5	244298_at	AA702999	NM_002757	5607	-1.34	3.13E-05
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GAL	207466_at	NM_015973	NM_015973	51083	-1.33	8.78E-03
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PCTK3	214797_s_at	BC000281	NM_002596	5129	-1.33	9.10E-04
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RAC2	207419_s_at	NM_002872	NM_002872	5880	-1.33	4.07E-03
STMN2	203000_at	BF967657	NM_007029	11075	-1.32	8.36E-03
D4S234E	209569_x_at	NM_014392	NM_014392	27065	-1.32	1.21E-06
AV709727	225996_at	AV709727	---	---	-1.32	2.28E-03
C19orf4	219005_at	NM_012109	NM_012109	25789	-1.32	6.30E-06
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AI973085	239765_at	AI973085	---	---	-1.32	9.72E-03
DJ462O23.2	225876_at	T84558	NM_020448	57185	-1.31	3.81E-03
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DDEF1	238193_at	W87434	NM_018482	50807	-1.31	6.32E-04
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FYN	243006_at	BG222258	NM_002037	2534	-1.31	1.31E-04
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GART	236969_at	AI961651	NM_000819	2618	-1.30	9.66E-06
			NM_175085			
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C6orf198	227834_at	AL589605	XM_371849	167838	-1.30	9.19E-03
DTNA	210736_x_at	U46746	NM_001390	1837	-1.30	5.47E-03
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SERP1	235475_at	AI580135	NM_014445	27230	-1.30	1.39E-03
C21orf25	212875_s_at	AP001745	NM_199050	25966	-1.30	5.16E-05
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BM989131	1558075_at	BM989131	---	---	-1.30	1.86E-04
ENOSF1	204142_at	NM_017512	NM_017512	55556	-1.30	6.73E-04
AW014345	236229_at	AW014345	---	---	-1.29	1.23E-05
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BE672499	230962_at	BE672499	---	---	-1.28	1.31E-05
FLJ20753	229918_at	AB046860	XM_371082	55036	-1.28	1.20E-05
SIGIRR	52940_at	AA085764	NM_021805	59307	-1.28	3.70E-04
S100A6	217728_at	NM_014624	NM_014624	6277	-1.28	5.27E-04
UCN	206072_at	NM_003353	NM_003353	7349	-1.28	1.49E-03
INSL3	214572_s_at	NM_005543	NM_005543	3640	-1.28	3.79E-03
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LOC440457	206088_at	NM_014834	XM_496239	440457	-1.28	1.40E-03
LONP	221833_at	AI971258	NM_031490	83752	-1.27	6.14E-03
LOC158301	239193_at	BF060981	---	158301	-1.27	2.55E-04
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ST7L	216123_x_at	AK024158	NM_017744 NM_138727 NM_138728 NM_138729 NM_198327 NM_198328	54879	-1.27	1.64E-04
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CDKN1C	213182_x_at	R78668	NM_000076	1028	-1.26	1.79E-03
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ICAM2	213620_s_at	AA126728	NM_000873	3384	-1.26	5.57E-03
KIAA0256	216278_at	AL109705	NM_014701	9728	-1.26	1.61E-03
BF432875	235782_at	BF432875	XM_497668	388620	-1.26	4.13E-04
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CTBP2	233315_at	AK024947	NM_001329 NM_022802	1488	-1.19	1.31E-03
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P15RS	231502_at	BF591615	NM_018170	55197	-1.06	4.06E-03
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TRIM33	214815_at	AU136587	NM_015906 NM_033020	51592	-1.05	9.87E-04
WDR42A	233637_at	AU146915	NM_015726	50717	-1.05	1.13E-03
AA757630	236724_at	AA757630	---	---	-1.05	7.93E-03
NM_014152	220694_at	NM_014152	---	---	-1.05	4.06E-04
AW665538	244532_x_at	AW665538	XM_496692	441014	-1.05	2.86E-03
MYST4	215597_x_at	AU143799	NM_012330	23522	-1.05	4.35E-04
CAPZA1	238407_at	AI792880	NM_006135	829	-1.05	2.34E-07
KIAA1276	235288_at	AI627532	XM_039169	27146	-1.05	5.52E-05
CNNM1	220166_at	NM_020348	NM_020348	26507	-1.05	2.70E-05
RPH3AL	221614_s_at	BC005153	NM_006987	9501	-1.04	8.30E-04
MGC13098	60815_at	AA601208	XM_379817 XM_499280	84820	-1.04	3.22E-05
AI003508	244114_x_at	AI003508	XM_496690	401131	-1.04	2.52E-03
RAC2	213603_s_at	BE138888	NM_002872	5880	-1.04	2.21E-03
PLXNC1	206471_s_at	NM_005761	NM_005761	10154	-1.04	5.22E-03
C19orf30	223913_s_at	AB058892	NM_174947	284424	-1.04	1.45E-03
BF002625	229530_at	BF002625	---	---	-1.04	2.72E-03
ATP6V0A1	1559375_s_at	AV739195	NM_005177	535	-1.04	7.96E-03
BACE1	224335_s_at	AB050436	NM_012104 NM_138971 NM_138972 NM_138973	23621	-1.04	1.07E-03
MGC9850	224857_s_at	BE378670	NM_152705	219404	-1.04	1.09E-03
BC035958	1569540_at	BC035958	---	---	-1.04	3.88E-03
FLJ32130	1554770_x_at	BC040642	NM_152458	146540	-1.04	1.31E-05
GFRA3	229936_at	AA694259	NM_001496	2676	-1.04	1.40E-03
FKBP11	228308_at	AI452444	NM_016594	51303	-1.04	8.54E-03
AL137290	233724_at	AL137290	---	---	-1.04	4.79E-04
FRAS1	226145_s_at	AL157471	NM_020875 NM_025074 NM_032863 NM_206841	80144	-1.04	3.23E-04
AU145394	215370_at	AU145394	XM_496203	440423	-1.04	3.51E-06
BRUNOL6	227775_at	BE467313	NM_052840	60677	-1.04	1.58E-03
METAP2	240769_at	AI733395	NM_006838	10988	-1.04	8.99E-03
NDP52	238560_at	AI684710	NM_005831	10241	-1.04	2.82E-07
AW150065	217653_x_at	AW150065	---	---	-1.04	2.30E-04

C21orf57	227421_at	BF026326	NM_00100611 4 NM_058181	54059	-1.04	4.05E-06
CDKL3	1561190_at	AF087989	NM_016508	51265	-1.03	1.48E-04
CLN8	219341_at	NM_018941	NM_018941	2055	-1.03	2.97E-03
CACNA1B	235781_at	AA448208	NM_000718	774	-1.03	6.51E-04
CPEB4	242384_at	AI452469	NM_030627	80315	-1.03	8.14E-03
BCAN	223632_s_at	AI739071	NM_021948 NM_198427	63827	-1.03	2.54E-03
KIAA0746	212314_at	AB018289	NM_015187	23231	-1.03	5.88E-05
PGAP1	233479_at	AU148008	NM_024989	80055	-1.03	2.96E-03
C1orf50	219406_at	NM_024097	NM_024097	79078	-1.03	7.42E-04
AF130084	1569538_at	AF130084	---	---	-1.03	5.41E-03
PCF11	239926_at	AI675753	NM_015885	51585	-1.03	2.46E-03
FNBP1	230086_at	AA937109	NM_015033	23048	-1.03	1.57E-04
AW117322	239415_at	AW117322	XM_374094	389237	-1.03	5.77E-03
BC033530	1560209_at	BC033530	---	---	-1.03	9.56E-05
AA888777	242740_at	AA888777	---	---	-1.03	1.32E-04
SFRS1	226419_s_at	AA046439	NM_006924	6426	-1.03	8.12E-03
HNRPD	229434_at	AA865357	NM_00100381 0 NM_002138 NM_031369 NM_031370	3184	-1.03	1.17E-04
LOC222070	51774_s_at	AW014299	---	222070	-1.03	7.32E-05
PHKA1	229876_at	BE503584	NM_002637	5255	-1.02	1.73E-05
NPY	206001_at	NM_000905	NM_000905	4852	-1.02	5.51E-03
CD302	203799_at	NM_014880	NM_014880	9936	-1.02	5.85E-04
UBE3A	1560741_at	AL832250	NM_000462 NM_130838 NM_130839	7337	-1.02	1.28E-03
AI582773	214373_at	AI582773	XM_498956	440996	-1.02	5.09E-03
C21orf66	240105_at	AI021902	NM_013329 NM_016631 NM_058191 NM_145328	94104	-1.02	3.11E-04
ICA1	204002_s_at	NM_022307	NM_004968 NM_022307 NM_022308	3382	-1.02	8.76E-05
CAPN2	208683_at	M23254	NM_001748	824	-1.02	7.34E-04
CYLD	213295_at	AA555096	NM_015247	1540	-1.02	8.54E-04
AK021477	232710_at	AK021477	---	---	-1.02	9.52E-03
AV658469	244699_at	AV658469	---	---	-1.02	6.27E-04
GUCY1A3	221942_s_at	AI719730	NM_000856	2982	-1.02	1.00E-03
FLJ10287	232489_at	AK001149	NM_019083	54482	-1.02	1.54E-03
PAQR6	219236_at	NM_024897	NM_024897 NM_198406	79957	-1.02	6.43E-04
PELI1	232304_at	AK026714	NM_020651	57162	-1.01	4.26E-04
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SORL1	203509_at	NM_003105	NM_003105	6653	-1.01	7.27E-03
PPIE	210502_s_at	AF042386	NM_006112 NM_203456 NM_203457	10450	-1.01	7.51E-03
FNBP1	239453_at	AA262084	NM_015033	23048	-1.01	1.33E-05
C9orf126	233246_at	AI523450	NM_173690	286205	-1.01	4.78E-03
FAM13A1	232628_at	AI740629	NM_014883	10144	-1.01	2.51E-03

DDX31	236210_at	AW628575	NM_022779 NM_138620	64794	-1.01	3.89E-03
CRABP2	202575_at	NM_001878	NM_001878	1382	-1.01	3.16E-03
KIAA0746	212311_at	AA522514	NM_015187	23231	-1.01	2.25E-03
PDE4C	206791_s_at	BF511742	NM_000923	5143	-1.01	1.92E-03
BE669703	229541_at	BE669703	---	---	-1.01	8.81E-05
MLL	212079_s_at	AA715041	NM_005933	4297	-1.01	8.80E-04
ZDHHC11	221646_s_at	AF267859	NM_024786	79844	-1.01	2.90E-04
BC038589	1569311_at	BC038589	---	---	-1.01	9.76E-04
C21orf66	1555125_at	BC030539	NM_013329 NM_016631 NM_058191 NM_145328	94104	-1.00	1.94E-03
AK024879	216751_at	AK024879	---	---	-1.00	8.95E-06
EFNB3	205031_at	NM_001406	NM_001406	1949	-1.00	1.02E-03
AW188311	243281_at	AW188311	---	---	-1.00	1.13E-03
N95363	213183_s_at	N95363	---	---	-1.00	2.68E-05
RAB6IP2	232565_at	AK025052	NM_015064 NM_178037 NM_178038 NM_178039 NM_178040	23085	-1.00	3.56E-03
RASA4 FLJ21767	208534_s_at	NM_006989	NM_006989 XM_376602 XM_379820	10156 401331	-1.00	1.13E-03
DCTD	210137_s_at	BC001286	NM_001921	1635	-1.00	2.80E-03
EIF3S9	236274_at	AW129967	NM_003751 NM_182712	8662	-1.00	7.13E-04
PTP4A3	206574_s_at	NM_007079	NM_007079 NM_032611	11156	-1.00	8.68E-03
ARIH1	1558710_at	BI791845	NM_005744	25820	-1.00	2.71E-03
BF507816	240517_at	BF507816	---	---	-1.00	3.52E-04
C10orf42	243335_at	BE764796	NM_138357	90550	-0.99	5.78E-03
LNK	203320_at	NM_005475	NM_005475	10019	-0.99	9.93E-05
OPTN	202073_at	AV757675	NM_00100821 1 NM_00100821 2 NM_00100821 3 NM_021980	10133	-0.99	1.43E-03
AK022461	232472_at	AK022461	---	---	-0.99	8.48E-04
GRK4	241989_at	AW269179	NM_00100405 6 NM_00100405 7 NM_005307 NM_182982	2868	-0.99	1.24E-04
LOC200030 LOC400781 AG1	242191_at	AI701905	NM_183372 XM_371384 XM_378897 XM_496394	200030 400781 440673	-0.99	5.68E-07
RAB3-GAP150	240234_at	AI216539	NM_012414	25782	-0.99	3.46E-03
DHX57	239311_at	AI367034	NM_144995 NM_145646 NM_198963	90957	-0.99	3.00E-03
LRRN5	216167_at	AK024867	NM_006338 NM_201630	10446	-0.99	3.96E-03

GART	230097_at	AI207338	NM_000819 NM_175085	2618	-0.99	1.29E-03
KIAA2024	1566166_at	AL833423	NM_172070	130507	-0.99	2.85E-03
MLL3	244010_at	AI057455	NM_021230 NM_170606	58508	-0.99	1.91E-03
GSDML	215659_at	AK025174	NM_018530	55876	-0.99	4.78E-03
DSCAM	237268_at	BE503065	NM_001389 NM_206887	1826	-0.99	1.16E-03
AK057701	1558515_at	AK057701	---	---	-0.99	6.69E-03
MGC11332	213393_at	AI767210	NM_032718	84804	-0.99	7.13E-04
ISYNA1	222240_s_at	AL137749	NM_016368	51477	-0.99	2.38E-04
CLTC	220855_at	NM_014127	NM_004859	1213	-0.99	7.98E-03
COL6A2	209156_s_at	AY029208	NM_001849 NM_058174 NM_058175	1292	-0.98	2.04E-03
SUV420H1	242646_at	AA702946	NM_016028 NM_017635	51111	-0.98	1.65E-04
KIAA1223	225735_at	AL110131	XM_048747	57182	-0.98	5.36E-05
DNAJC12	218976_at	NM_021800	NM_021800 NM_201262	56521	-0.98	1.57E-06
RHBDL1	207383_s_at	NM_003961	NM_003961	9028	-0.98	6.79E-03
UBE2E1	236062_at	AI742722	NM_003341 NM_182666	7324	-0.98	5.85E-03
HEL308	228736_at	AW084661	NM_133636	113510	-0.98	1.68E-03
H28915	244359_s_at	H28915	XM_496692	441014	-0.98	5.93E-03
BRUNOL5	232416_at	AL390161	NM_021938	60680	-0.98	4.62E-03
RNF12	242121_at	AW973232	NM_016120 NM_183353	51132	-0.98	6.21E-03
SFRS15	222310_at	AA648521	NM_020706	57466	-0.98	2.65E-04
ACSL4	1557419_a_at	W95007	NM_004458 NM_022977	2182	-0.98	4.91E-03
SPOCK2	202524_s_at	NM_014767	NM_014767	9806	-0.98	6.88E-05
KIAA0999	242920_at	AW590838	NM_025164	23387	-0.97	3.05E-03
KCNK10	220727_at	NM_021161	NM_021161 NM_138317 NM_138318	54207	-0.97	9.90E-03
AATK	205986_at	NM_004920	---	9625	-0.97	2.81E-05
SERTAD4	230660_at	AU146709	NM_019605	56256	-0.97	5.49E-03
CDC2L5	242693_at	AW664859	NM_003718 NM_031267	8621	-0.97	6.26E-03
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SMG1	244766_at	BG180003	NM_014006	23049	-0.97	2.50E-03
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LOC440345			XM_496125	440345		
DNAJB5	212817_at	AK023253	NM_012266	25822	-0.97	1.18E-03
HIST3H2A	221582_at	BC001193	NM_033445	92815	-0.97	2.09E-03
SORL1	212560_at	AV728268	NM_003105	6653	-0.97	4.84E-03
BBP	213882_at	AA012917	NM_032027	83941	-0.97	7.60E-03
UGCGL2	218801_at	NM_020121	NM_020121	55757	-0.96	1.53E-03
TLE1	228284_at	BE302305	NM_005077	7088	-0.96	2.82E-06
CRYZL1	1552347_at	NM_145311	NM_005111 NM_145311 NM_145858	9946	-0.96	8.59E-03
KIAA1223	225731_at	BF196876	XM_048747	57182	-0.96	1.92E-04
CTNND1	238884_at	AW195351	NM_001331	1500	-0.96	7.20E-03
FLJ10980	225327_at	AB037791	NM_019600	56204	-0.96	4.11E-04
LOC255783	227325_at	AW172584	---	255783	-0.96	6.35E-03
SLICK	244455_at	AI732637	NM_198503	343450	-0.96	5.42E-04

MCM3AP	212269_s_at	AJ010089	NM_003906	8888	-0.96	2.03E-05
EMR3	1561042_at	AF086249	NM_032571	84658	-0.96	1.76E-03
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OCIAD2	225314_at	BG291649	NM_152398	132299	-0.96	6.40E-05
BACE1	222463_s_at	AF190725	NM_012104	23621	-0.96	5.33E-04
			NM_138971			
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			NM_138973			
DNAJC12	223721_s_at	AF176013	NM_021800	56521	-0.95	9.38E-05
			NM_201262			
CCNJ	1557830_at	AW063658	NM_019084	54619	-0.95	1.55E-03
KLF12	243089_at	AA551114	NM_007249	11278	-0.95	3.83E-03
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RSL1D1	212019_at	AK025446	NM_015659	26156	-0.95	2.34E-04
AK022004	233003_at	AK022004	---	---	-0.95	3.09E-03
FTO	215385_at	AK022473	XM_051200	79068	-0.95	4.76E-03
AKAP10	236007_at	AU147278	NM_007202	11216	-0.95	8.23E-04
PDXK	202671_s_at	NM_003681	NM_003681	8566	-0.95	3.67E-06
TRIT1	218617_at	NM_017646	NM_017646	54802	-0.95	3.17E-07
MYT1L	210016_at	BF223003	NM_015025	23040	-0.95	8.33E-05
AA573901	227783_at	AA573901	---	---	-0.95	5.00E-04
AA804267	243185_at	AA804267	---	---	-0.95	9.14E-03
AW593330	237064_x_at	AW593330	---	---	-0.95	2.04E-03
HERC1	237632_at	AA765387	NM_003922	8925	-0.95	3.34E-04
INPP1	202794_at	NM_002194	NM_002194	3628	-0.95	1.43E-04
LOC169834	230876_at	AI827906	XM_095965	169834	-0.95	1.26E-04
C21orf5	205248_at	NM_005128	NM_005128	9980	-0.95	3.75E-04
FBXW7	222729_at	BE551877	NM_018315	55294	-0.95	4.83E-05
			NM_033632			
NFASC	214799_at	AI821777	NM_00100538	23114	-0.95	1.20E-03
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			NM_00100538			
			8			
			NM_00100538			
			9			
			NM_015090			
LOC90639	235533_at	AW021673	---	90639	-0.95	6.72E-03
BRUNOL5	230497_at	BE503640	NM_021938	60680	-0.95	1.48E-06
CHPT1	1559739_at	AK025141	NM_020244	56994	-0.95	1.25E-05
APOC1	204416_x_at	NM_001645	NM_001645	341	-0.95	8.52E-03
TPD52	228818_at	BF110792	NM_005079	7163	-0.94	2.91E-03
HBXAP	215786_at	AK022170	NM_016578	51773	-0.94	8.66E-03
ATXN1	203232_s_at	NM_000332	NM_000332	6310	-0.94	1.93E-03
PDXK	218019_s_at	NM_021941	NM_003681	8566	-0.94	1.93E-04
FBXW7	218751_s_at	NM_018315	NM_018315	55294	-0.94	8.91E-05
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ANKRD11	228866_at	BF514864	NM_013275	29123	-0.94	9.50E-03
LOC149297	1558113_at	BM545032	XM_097622	149297	-0.94	3.48E-03
FLJ20758	228512_at	AW138833	NM_017952	55037	-0.94	8.02E-05
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PDE4DIP	244511_at	AV700591	NM_00100281	9659	-0.94	2.74E-03
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MGC9850	224874_at	N32181	NM_152705	219404	-0.94	2.65E-04
DUSP8	206374_at	NM_004420	NM_004420	1850	-0.94	1.10E-05
LOC400729	243021_at	AI344101	XM_378824	400729	-0.94	5.94E-03
LOC440745			XM_498840	440745		
AI939586	237930_at	AI939586	---	---	-0.94	6.80E-03
PHF17	225820_at	AV646599	NM_024900	79960	-0.94	5.13E-03
			NM_199320			
LOC222070	58900_at	AW025284	---	222070	-0.93	6.09E-04
APOE	203381_s_at	N33009	NM_000041	348	-0.93	7.96E-03
AF086134	1561754_at	AF086134	XM_498989	441057	-0.93	4.00E-03
AMH	206516_at	NM_000479	NM_000479	268	-0.93	3.43E-04
SYT15	1560879_a_at	AI971263	NM_031912	83849	-0.93	1.08E-03
			NM_181519			
KCNJ12	207110_at	NM_021012	NM_021012	3768	-0.93	5.28E-03
ARHGEF4	205109_s_at	NM_015320	NM_015320	50649	-0.93	2.32E-03
			NM_032995			
PPM1B	232580_x_at	AL117553	NM_002706	5495	-0.93	7.12E-04
			NM_177968			
			NM_177969			
ZNF587	60794_f_at	AI400621	NM_032828	84914	-0.93	6.69E-06
HIPK2	224016_at	AF111850	NM_022740	28996	-0.93	8.37E-03
LOC133926	235628_x_at	BG025030	---	133926	-0.93	4.71E-03
AI681025	230220_at	AI681025	---	---	-0.93	2.78E-04
LOC64744	225282_at	AL137764	NM_022733	64744	-0.92	4.81E-05
ICA1	214191_at	W67992	NM_004968	3382	-0.92	2.91E-04
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SFRS15	222311_s_at	AA648521	NM_020706	57466	-0.92	6.79E-03
RNF111	241413_at	W80457	NM_017610	54778	-0.92	5.97E-04
KATNB1	203162_s_at	NM_005886	NM_005886	10300	-0.92	3.97E-04
PPM1K	235061_at	AV706522	NM_152542	152926	-0.92	2.02E-03
PHC3	233431_x_at	AU148142	NM_024947	80012	-0.92	1.61E-03
TJP1	244476_at	R39769	NM_003257	7082	-0.91	9.46E-04
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ZDHHC11	232417_x_at	AU150300	NM_024786	79844	-0.91	3.90E-03
AKAP9	215483_at	AK000270	NM_005751	10142	-0.91	3.78E-03
			NM_147166			
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PLRG1	227246_at	BF438014	NM_002669	5356	-0.91	4.23E-03
AL390216	234317_s_at	AL390216	---	---	-0.91	9.52E-03
METAP2	244185_at	AA921841	NM_006838	10988	-0.91	3.64E-04
PER1	36829_at	AF022991	NM_002616	5187	-0.91	3.45E-03
FLJ44796	230757_at	AA195276	NM_001001704	401209	-0.91	3.23E-03
R3HDM	240503_at	AW274946	NM_015361	23518	-0.91	3.05E-03
NME5	206197_at	NM_003551	NM_003551	8382	-0.91	1.53E-04
MGC5566	220449_at	NM_024049	---	79015	-0.90	2.88E-03
MGC13098	222208_s_at	W07700	XM_379817	84820	-0.90	1.93E-05
			XM_499280			
W90010	238271_x_at	W90010	---	---	-0.90	3.98E-03
DCTD	201572_x_at	NM_001921	NM_001921	1635	-0.90	3.11E-03
MGC42174	244304_at	AW129650	NM_152383	129563	-0.90	8.32E-03

DJ328E19.C1. 1	214693_x_at	BE732345	NM_015383 NM_173638	200030 25832	-0.90	2.29E-04
LOC200030			NM_183372	284565		
MGC8902			XM_371384	401967		
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AG1			XM_496406			
AA714835	1556646_at	AA714835	---	---	-0.90	8.70E-04
PPID	204186_s_at	AI014573	NM_005038	5481	-0.90	1.20E-03
ST18	206135_at	NM_014682	NM_014682	9705	-0.90	1.28E-03
ZNF275	225382_at	U82670	XM_372267	10838	-0.90	3.80E-03
W80446	231013_at	W80446	---	---	-0.90	2.17E-03
AI200555	228275_at	AI200555	---	---	-0.90	1.34E-05
CXorf43	1553646_at	NM_144657	NM_144657	139324	-0.90	5.46E-04
PAPD4	222282_at	AV761453	NM_173797	167153	-0.90	7.86E-03
AI015847	1568838_at	AI015847	---	---	-0.90	3.96E-03
CTGLF1	1565620_at	BG621044	NM_133446	119016	-0.90	3.42E-03
KIAA1838	241152_at	BE466903	NM_032448	84498	-0.90	1.43E-03
SLC22A17	218675_at	NM_020372	NM_016609 NM_020372	51310	-0.89	2.14E-04
FLJ21159	220145_at	NM_024826	NM_024826	79884	-0.89	6.77E-03
TRIP12	244659_at	AL120025	NM_004238	9320	-0.89	1.07E-03
FAM46A	224973_at	AL078599	NM_017633	55603	-0.89	5.88E-03
PPP2R2C	228010_at	AI669212	NM_020416 NM_181876	5522	-0.89	1.10E-03
MAST4	210958_s_at	BC003646	XM_291141	23227	-0.89	1.00E-03
KIDINS220	1557246_at	AA992480	NM_020738	57498	-0.89	4.66E-03
NOB1P	223018_at	BC000050	NM_014062	28987	-0.89	6.87E-03
AI469960	230653_at	AI469960	---	---	-0.89	4.89E-03
HCG8	215985_at	X92110	---	80869	-0.89	5.08E-03
BRUNOL4	238966_at	AA678985	NM_020180	56853	-0.89	1.12E-05
C21orf51	228239_at	AA148789	NM_058182	54065	-0.89	8.47E-04
MST1	216320_x_at	U37055	NM_020998	4485	-0.89	7.59E-03
DVL3	201908_at	NM_004423	NM_004423	1857	-0.89	2.80E-03
NR2F1	209506_s_at	BC004154	NM_005654	7025	-0.89	2.53E-05
STK19	243719_at	AI973206	NM_004197 NM_032454	8859	-0.89	3.23E-03
KLF9	203543_s_at	NM_001206	NM_001206	687	-0.89	1.00E-03
AA830545	235730_at	AA830545	---	---	-0.89	1.23E-03
AI949265	229156_s_at	AI949265	XM_499089	441301	-0.89	2.40E-04
SHANK2	213307_at	AF131790	NM_012309 NM_133266	22941	-0.88	1.79E-04
AI802997	235211_at	AI802997	---	---	-0.88	8.15E-06
GPR123	239221_at	AI884909	NM_032422	84435	-0.88	8.91E-04
ABCA2	212772_s_at	AL162060	NM_001606 NM_212533	20	-0.88	4.48E-04
AL049377	1562684_at	AL049377	---	---	-0.88	5.29E-05
SAT2	225272_at	AA128261	NM_133491	112483	-0.88	1.49E-03
ERMAP	219905_at	NM_018538	NM_018538	114625	-0.88	1.01E-03
C20orf103	219463_at	NM_012261	NM_012261	24141	-0.88	2.58E-03
CDS1	226185_at	AK026697	NM_001263	1040	-0.88	1.82E-04
AI459283	231220_at	AI459283	---	---	-0.88	1.08E-03
)KFZp313N062	226688_at	AW003508	NM_173826	285343	-0.88	1.19E-03
AW235215	238913_at	AW235215	---	---	-0.87	7.73E-03
SLC27A2	205768_s_at	NM_003645	NM_003645	11001	-0.87	3.01E-03
AA975422	242829_x_at	AA975422	---	---	-0.87	5.23E-03
DEPDC6	218858_at	NM_022783	NM_022783	64798	-0.87	7.47E-04

CDC2L5	210965_x_at	BC001274	NM_003718 NM_031267	8621	-0.87	1.03E-03
AHSA2	212980_at	AL050376	NM_152392	130872	-0.87	8.94E-03
AK056212	1557215_at	AK056212	---	---	-0.87	4.38E-04
BF114733	236703_at	BF114733	---	---	-0.87	8.70E-03
AW628665	235555_at	AW628665	---	---	-0.87	4.04E-04
FXR1	229519_at	H48840	NM_005087	8087	-0.86	7.99E-03
AF5Q31	232865_at	N59653	NM_014423	27125	-0.86	2.34E-03
TAF15	241885_at	BF431050	NM_003487 NM_139215	8148	-0.86	2.03E-03
NM_001048	213921_at	NM_001048	---	---	-0.86	1.92E-03
PFAAP5	214753_at	AW084068	NM_014887	10443	-0.86	1.88E-03
FRMD4A	1560031_at	R19413	NM_018027	55691	-0.86	1.21E-04
NELF	221214_s_at	NM_015537	NM_015537	26012	-0.86	5.19E-05
MGC11332	213403_at	BF223370	NM_032718	84804	-0.86	5.38E-03
ETV3	1552423_at	NM_005240	NM_005240	2117	-0.86	4.99E-04
TMF1	242243_at	AI767435	NM_007114	7110	-0.86	4.40E-03
PIAS2	244633_at	AA404996	NM_004671 NM_173206	9063	-0.86	6.85E-03
SLC19A1	229489_at	AI681043	NM_003056 NM_194255	6573	-0.86	4.96E-03
ECE2	230706_s_at	AI084921	NM_014693	9718	-0.86	7.23E-04
HNRPM	238610_s_at	AI906424	NM_005968 NM_031203	4670	-0.86	2.13E-03
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HNRPM	233605_x_at	AK022050	NM_005968 NM_031203	4670	-0.86	3.84E-05
FBXO15	231472_at	BE464323	NM_152676	201456	-0.86	5.46E-03
UBE2B	239163_at	AW364833	NM_003337	7320	-0.86	1.91E-03
BE467787	243835_at	BE467787	---	---	-0.86	3.40E-04
SORCS1	228194_s_at	AI675836	NM_052918	114815	-0.86	7.48E-05
ZDHHC11	1552283_s_at	NM_024786	NM_024786	79844	-0.86	1.80E-04
DEADC1	227213_at	AA706895	NM_182503	134637	-0.85	7.30E-04
RRAGC	218088_s_at	NM_022157	NM_022157	64121	-0.85	7.96E-03
UBE3C	242673_at	AA931284	NM_014671	9690	-0.85	2.73E-03
MGC13098	224517_at	BC006435	XM_379817 XM_499280	84820	-0.85	2.71E-05
FLJ23825	1555866_a_at	BM980844	NM_173620	284004	-0.85	2.22E-03
SLC16A1	1560579_s_at	BC023568	NM_003051	6566	-0.85	6.33E-04
RSNL2	226425_at	AU144247	NM_024692	79745	-0.85	1.24E-03
LOC283922	228688_at	AA843726	XM_208908	283922	-0.85	3.51E-04
GOLGIN-67	213650_at	AW006438	NM_015003 NM_181076 NM_181077	23015	-0.85	2.66E-03
FLJ37953	241825_at	AI265967	NM_152382	129450	-0.85	1.32E-03
AV700050	228835_at	AV700050	---	---	-0.85	2.40E-03
KIAA1915	1569706_at	BC017579	XM_055481	114803	-0.85	6.38E-03
CEPT1	1561884_at	AL833102	NM_00100779 4 NM_006090	10390	-0.85	1.37E-03
BF510762	230262_at	BF510762	---	---	-0.85	2.02E-06
TAGLN2	210978_s_at	BC002616	NM_003564	8407	-0.84	3.57E-03
DUSP6	208893_s_at	BC005047	NM_001946 NM_022652	1848	-0.84	1.45E-04
AI811800	241846_at	AI811800	---	---	-0.84	3.44E-03
AA167167	243684_at	AA167167	---	---	-0.84	3.92E-03
CNOT6L	227119_at	BF103856	NM_144571	246175	-0.84	2.79E-07
ARIH1	242431_at	AI656728	NM_005744	25820	-0.84	2.27E-03

BC037935	1569539_at	BC037935	---	---	-0.84	6.55E-04
DUSP6	208891_at	BC003143	NM_001946	1848	-0.84	3.81E-03
			NM_022652			
C15orf28	220710_at	NM_024970	---	80035	-0.84	9.94E-03
AA935515	242790_at	AA935515	---	---	-0.84	1.15E-03
MSI2	243010_at	BE000929	NM_138962	124540	-0.84	1.62E-03
			NM_170721			
CXorf45	205583_s_at	NM_024810	NM_024810	79868	-0.84	2.89E-03
PMS2L5	242201_at	AI418253	NM_174930	5383	-0.84	7.25E-04
AW000942	240230_s_at	AW000942	---	---	-0.84	6.90E-03
C9orf94	229585_at	AI803088	NM_152702	206938	-0.84	1.26E-03
FLJ20719	230712_at	AI634549	XM_373827	55672	-0.84	5.27E-03
GA17	215190_at	AV717062	NM_006360	10480	-0.84	6.82E-03
CD200	209582_s_at	H23979	NM_00100419	4345	-0.84	7.62E-03
			6			
			NM_00100419			
			7			
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AA928506	213750_at	AA928506	---	---	-0.84	2.15E-04
AHI1	221569_at	AL136797	NM_017651	54806	-0.84	2.48E-05
RPIP8	213439_x_at	AI197870	NM_006695	10900	-0.84	1.33E-06
AI929792	236081_at	AI929792	---	---	-0.84	3.07E-04
CTNNB1	242558_at	AW362945	NM_001904	1499	-0.84	1.09E-04
ELOVL5	1566079_at	AL833001	NM_021814	60481	-0.83	1.76E-03
WDR11	229694_at	BF062828	NM_018117	55717	-0.83	2.23E-03
MAN2A2	219999_at	NM_018621	NM_006122	4122	-0.83	4.36E-03
AA825721	242228_at	AA825721	---	---	-0.83	8.71E-04
RAB12	238714_at	AA504249	XM_113967	201475	-0.83	4.32E-04
KCNMA1	221584_s_at	U11058	NM_002247	3778	-0.83	7.71E-04
BE467087	231075_x_at	BE467087	---	---	-0.83	4.80E-03
FGD5	226985_at	AW269340	NM_152536	152273	-0.83	5.34E-03
ProSAPiP1	204447_at	NM_014731	NM_014731	9762	-0.83	1.67E-04
ZNF539	1559449_a_at	BF679633	NM_203282	399655	-0.83	2.80E-04
NKX6-1	221366_at	NM_006168	NM_006168	4825	-0.83	7.76E-03
FLJ22624	236560_at	BE218020	NM_024808	79866	-0.83	7.40E-03
MGC72104	234949_at	AL117574	NM_207350	284802	-0.83	1.91E-03
GRIK2	1563754_at	AJ252246	NM_021956	2898	-0.83	6.46E-03
			NM_175768			
AI018235	240314_at	AI018235	---	---	-0.82	3.87E-03
ZNF518	242343_x_at	H57111	NM_014803	9849	-0.82	6.06E-03
FNBP4	235101_at	AV683244	NM_015308	23360	-0.82	3.49E-03
C21orf86	226995_at	AV705934	NM_153454	257103	-0.82	2.10E-03
AW148862	235217_at	AW148862	XM_380136	402582	-0.82	8.18E-03
AL559202	226458_at	AL559202	---	---	-0.82	5.40E-05
JMJD2C	214861_at	AI341811	NM_015061	23081	-0.82	2.97E-03
AOF2	212348_s_at	AB011173	NM_00100099	23028	-0.82	1.77E-05
			9			
			NM_015013			
TTC3	208663_s_at	AI652848	NM_00100189	7267	-0.82	7.37E-05
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BE327722	239840_at	BE327722	---	---	-0.82	1.21E-06
AK021474	215892_at	AK021474	---	---	-0.82	9.46E-05
BF344235	242202_at	BF344235	XM_379855	402530	-0.82	5.35E-04
YLPM1	1557065_at	AA927802	XM_085151	56252	-0.82	8.82E-03
CaMKIINalpha	228302_x_at	AW162846	NM_018584	55450	-0.81	1.09E-03
AKT2	236664_at	AA448167	NM_001626	208	-0.81	3.20E-03

PRKCD	202545_at	NM_006254	NM_006254 NM_212539	5580	-0.81	2.09E-04
CYLD	39582_at	AL050166	NM_015247	1540	-0.81	1.26E-03
EIF4G1	208624_s_at	BE966878	NM_004953 NM_182917 NM_198241 NM_198242 NM_198244	1981	-0.81	7.60E-04
ACVR2	244332_at	AW974077	NM_001616	92	-0.81	1.17E-06
AI150690	228466_at	AI150690	---	---	-0.81	4.49E-04
AV700891	222303_at	AV700891	---	---	-0.81	1.60E-03
C20orf13	233719_s_at	AL121754	NM_017714	55617	-0.81	6.92E-04
SMURF2	230099_at	AI139993	NM_022739	64750	-0.81	2.36E-03
SHC2	213464_at	AV705938	XM_375550	25759	-0.81	4.62E-06
AW167298	228116_at	AW167298	XM_210856	283029	-0.80	5.41E-03
GPR56	206582_s_at	NM_005682	NM_005682 NM_201524 NM_201525	9289	-0.80	4.72E-03
ATXN7	209964_s_at	AF032105	NM_000333	6314	-0.80	2.95E-03
AK000995	215349_at	AK000995	---	---	-0.80	4.02E-03
AW086077	232800_at	AW086077	---	---	-0.80	1.60E-03
SLC37A1	218928_s_at	NM_018964	NM_018964	54020	-0.80	5.55E-03
PCNXL2	229202_at	AI768826	NM_014801 NM_024938	80003	-0.80	2.18E-04
SCMH1	221216_s_at	NM_012236	NM_012236	22955	-0.80	5.20E-06
FLJ31951	236322_at	AA830854	NM_144726	153830	-0.80	5.68E-03
CXXC5	233955_x_at	AK001782	NM_016463	51523	-0.80	9.43E-05
KIAA0220	231989_s_at	AC003007	---	283846	-0.80	5.47E-04
POLR3C	239383_at	AW023610	NM_006468	10623	-0.79	4.37E-03
SLC9A3R2	209830_s_at	AF035771	NM_004785	9351	-0.79	1.09E-04
CACNA1D	207998_s_at	NM_000720	NM_000720	776	-0.79	2.71E-03
AI417268	225028_at	AI417268	---	---	-0.79	5.37E-03
CTSB	213274_s_at	AA020826	NM_001908 NM_147780 NM_147781 NM_147782 NM_147783	1508	-0.79	2.12E-04
C9orf85	1557805_at	AF085969	NM_182505 NM_198394	138241	-0.79	4.15E-06
TNRC15	1560133_at	BC012484	NM_015575	26058	-0.79	1.04E-04
ARSD	225280_x_at	N51673	NM_001669 NM_009589	414	-0.79	8.39E-03
KLHDC1	1552733_at	NM_172193	NM_172193	122773	-0.79	8.55E-05
PRO0478	220696_at	NM_014129	---	29048	-0.79	7.62E-04
RAB40B	204547_at	NM_006822	NM_006822	10966	-0.79	3.04E-04
ETFDH	33494_at	S69232	NM_004453	2110	-0.79	1.02E-03
TGFBR1	236561_at	AV700621	NM_004612	7046	-0.79	6.33E-03
GPR18	233554_at	AF339764	NM_005292	2841	-0.79	2.72E-04
U2AF1	231904_at	AU122448	NM_006758	7307	-0.79	1.73E-03
DKFZP434I071	231954_at	AL137273	---	54553	-0.79	1.34E-03
YAP	244803_at	AI335191	NM_018253 NM_139118 NM_139119 NM_139120 NM_139121	55249	-0.79	7.84E-05
LOC23117	238341_at	BF677084	XM_290670	23117	-0.79	1.63E-03
CLASP2	212308_at	AL137636	NM_015097	23122	-0.78	1.67E-03
C18orf17	238480_at	AI871745	NM_153211	125488	-0.78	8.79E-04

LOC51066	206741_at	NM_015931	NM_015931	51066	-0.78	3.65E-05
S100A13	202598_at	NM_005979	XM_371380	6284	-0.78	4.04E-03
FLJ39653	1553145_at	BC010030	NM_152684	202020	-0.78	4.89E-03
ANP32A	235954_at	AA972597	NM_006305	8125	-0.78	9.06E-03
TAF15	227884_at	AW296067	NM_003487 NM_139215	8148	-0.78	1.80E-03
HNRPR	208765_s_at	NM_005826	NM_005826	10236	-0.78	8.21E-05
AF194537	224549_x_at	AF194537	---	---	-0.78	6.16E-03
AF5Q31	1555436_a_at	BC025700	NM_014423	27125	-0.78	9.74E-05
MGC47869	229888_at	AA861435	NM_175874	144608	-0.78	5.64E-03
MEG3	235077_at	BF956762	XR_000277	55384	-0.78	2.12E-03
DKFZp547A023	214731_at	AB037854	NM_018704	55917	-0.78	1.66E-03
AI820796	217704_x_at	AI820796	---	---	-0.78	1.61E-04
CCNB1IP1	217988_at	NM_021178	NM_021178 NM_182849 NM_182851 NM_182852	57820	-0.77	9.59E-03
WDFY1	1562955_at	BC028181	NM_020830	57590	-0.77	2.91E-03
GPLD1	238752_at	AA780295	NM_001503 NM_177483	2822	-0.77	2.12E-04
CTSB	213275_x_at	W47179	NM_001908 NM_147780 NM_147781 NM_147782 NM_147783	1508	-0.77	2.40E-03
PLA2G4B	222256_s_at	AK000550	NM_005090	8681	-0.77	2.03E-03
BE856980	230961_at	BE856980	---	---	-0.77	2.41E-03
ABTB1	229164_s_at	AI337369	NM_032548 NM_172027 NM_172028	80325	-0.77	2.25E-03
AI702720	242309_at	AI702720	---	---	-0.77	2.84E-03
MGC4707	238161_at	AA813859	NM_001003676 NM_001003677 NM_001003678 NM_024113	79096	-0.77	2.25E-03
CD200	209583_s_at	AF063591	NM_001004196 NM_001004197 NM_005944	4345	-0.77	1.43E-03
GTF3C3	1555439_at	AF465407	NM_012086	9330	-0.77	3.57E-05
PTPRD	214043_at	BF062299	NM_002839 NM_130391 NM_130392 NM_130393	5789	-0.77	6.45E-05
MLR1	235970_at	AI807408	NM_153686	254251	-0.77	1.70E-03
AI305170	235747_at	AI305170	---	---	-0.77	8.11E-04
PLXNC1	213241_at	AF035307	NM_005761	10154	-0.77	8.27E-03
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LRCH3	1559490_at	AL832278	NM_032773	84859	-0.77	7.53E-03
BC035170	1561079_at	BC035170	---	---	-0.77	3.38E-03
BC029480	1554447_at	BC029480	---	---	-0.77	1.93E-03
AI598222	235679_at	AI598222	---	---	-0.77	4.88E-04
SH3KBP1	223082_at	AF230904	NM_031892	30011	-0.77	9.30E-05
TNFSF13B	223502_s_at	AF134715	NM_006573	10673	-0.77	2.15E-06

AP3B2	205678_at	NM_004644	NM_004644	8120	-0.76	1.23E-04
MDS009	236649_at	AA907927	NM_020234	56986	-0.76	6.41E-04
CLIPR-59	212358_at	AL117468	NM_015526	25999	-0.76	2.11E-03
EDG4	206723_s_at	AF011466	NM_004720	9170	-0.76	2.87E-04
RNASET2	217984_at	NM_003730	NM_003730	8635	-0.76	7.52E-03
AI979338	229364_at	AI979338	---	---	-0.76	5.81E-03
KIAA1545	225704_at	AA527531	XM_495939	57666	-0.76	8.16E-03
MGC29898	235259_at	AA398590	NM_145048	133015	-0.76	3.12E-03
SIDT2	56256_at	AA150165	NM_015996	51092	-0.76	8.92E-03
MGC20741	232826_at	AU144129	NM_018561	25862	-0.76	2.64E-03
WBSCR19	232964_at	AL137266	NM_175064	285955	-0.76	3.56E-03
ACTR2	234210_x_at	AK025051	NM_00100538 6 NM_005722	10097	-0.76	2.63E-03
LOC92249	212957_s_at	AU154785	XM_499179	92249	-0.76	1.06E-03
JAK1	234193_at	AK025218	NM_002227	3716	-0.76	5.21E-03
PRH1	243389_at	AW663570	NM_006250	5554	-0.76	3.39E-03
AI523613	222358_x_at	AI523613	---	---	-0.76	4.89E-06
HSPA12A	214434_at	AB007877	XM_048898	259217	-0.76	6.62E-03
PIK3R2	1568629_s_at	BC033311	NM_005027	5296	-0.76	4.17E-03
MEG3	212732_at	AI950273	XR_000277	55384	-0.76	2.60E-03
AI743452	237031_at	AI743452	---	---	-0.76	8.51E-03
PVT1	222087_at	AW451806	XM_372058	5820	-0.76	1.17E-04
HNRPD	235999_at	AA863112	NM_00100381 0 NM_002138 NM_031369 NM_031370	3184	-0.75	2.35E-03
BG253162	242585_at	BG253162	---	---	-0.75	7.96E-04
LOC401320	238540_at	AA933883	XM_379482 XM_380098	401320	-0.75	9.69E-03
AK024681	231972_at	AK024681	---	---	-0.75	5.89E-05
FLJ14167	232289_at	BF237871	---	92080	-0.75	9.36E-03
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TMEM25	226647_at	AL562445	NM_032780	84866	-0.75	1.43E-03
BC003629	210230_at	BC003629	---	---	-0.75	7.07E-03
DUSP6	208892_s_at	BC003143	NM_001946 NM_022652	1848	-0.75	5.05E-03
H63	1552719_at	NM_138423	NM_138423 NM_177974	113201	-0.75	2.02E-03
CXorf45	205584_at	NM_024810	NM_024810	79868	-0.75	2.96E-03
BG396868	1559957_a_at	BG396868	---	---	-0.75	1.66E-04
CLDN12	223249_at	AL136770	NM_012129	9069	-0.75	3.65E-04
UBE2G2	209042_s_at	BC001738	NM_003343 NM_182688	7327	-0.75	1.16E-05
BTN3A1	209770_at	U90552	NM_007048 NM_194441	11119	-0.75	8.21E-03
MRPL1	223154_at	AF212225	NM_020236	65008	-0.75	1.63E-03
SYNJ1	207594_s_at	NM_003895	NM_003895 NM_203446	8867	-0.75	9.53E-03
SORBS1	218087_s_at	NM_015385	NM_006434 NM_015385	10580	-0.75	9.17E-03
PORCN	219483_s_at	NM_022825	NM_022825 NM_203473 NM_203474 NM_203475 NM_203476	64840	-0.75	3.19E-05
ZRANB3	244092_at	AI670931	NM_032143	84083	-0.75	9.19E-03

MRPS30	231207_at	AW263539	NM_016640	10884	-0.75	6.93E-04
FLJ12666	217893_s_at	NM_024595	NM_024595	79647	-0.74	3.79E-03
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H2AFY	226840_at	AW291297	NM_004893	9555	-0.74	2.05E-04
			NM_138609			
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MCAM	209087_x_at	AF089868	NM_006500	4162	-0.74	6.99E-03
SH3YL1	204019_s_at	NM_015677	NM_015677	26751	-0.74	1.21E-03
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LOC400099	230136_at	AI573252	XM_378399	400099	-0.74	3.10E-03
ASB13	239610_at	BF509210	NM_024701	79754	-0.74	1.28E-03
POU6F1	216330_s_at	L14482	NM_002702	5463	-0.74	2.20E-03
SH2D3C	1552667_a_at	NM_005489	NM_005489	10044	-0.74	7.58E-03
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JAM2	219213_at	NM_021219	NM_021219	58494	-0.74	3.58E-05
AW665096	214188_at	AW665096	---	---	-0.74	2.49E-03
RIOK3	215588_x_at	AK024958	NM_003831	8780	-0.73	2.49E-04
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AI963605	230269_at	AI963605	---	---	-0.73	8.73E-04
BE217923	228686_at	BE217923	---	---	-0.73	1.71E-03
C6orf111	226412_at	N66397	NM_032870	25957	-0.73	9.78E-03
BG109865	222459_at	BG109865	---	---	-0.73	1.83E-03
SP3	232529_at	AU144413	NM_003111	6670	-0.73	2.50E-03
RAB18	229398_at	AI769954	NM_021252	22931	-0.73	3.78E-03
KIAA1324	243349_at	AI672868	NM_020775	57535	-0.73	8.70E-03
CTSB	227961_at	AA130998	NM_001908	1508	-0.73	7.63E-04
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AV733292	225444_at	AV733292	---	---	-0.73	1.88E-04
H73101	1556984_at	H73101	---	---	-0.73	1.17E-03
MGAT4A	219797_at	NM_012214	NM_012214	11320	-0.73	2.44E-03
EPOR	396_f_at	X97671	NM_000121	2057	-0.73	4.18E-03
LOC401394	231406_at	AW205664	XM_379512	401394	-0.73	2.54E-04
GPR153	221902_at	AL567940	NM_207370	387509	-0.73	2.83E-03
KIAA0241	1563452_at	AL833560	NM_015060	23080	-0.73	5.29E-04
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SMA4	214850_at	X75940	NM_021652	11039	-0.73	1.38E-03
ADFP	209122_at	BC005127	NM_001122	123	-0.73	5.72E-04
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LOC283174	229734_at	BF507379	NM_001001873	283174	-0.73	1.27E-04
IGBP1	242337_at	AI347128	NM_001551	3476	-0.73	3.64E-03
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PEX6	204545_at	NM_000287	NM_000287	5190	-0.73	9.95E-03
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GPR56	212070_at	AL554008	NM_005682 NM_201524 NM_201525	9289	-0.72	1.51E-03
AMOTL2	203002_at	NM_016201	NM_016201	51421	-0.72	5.43E-04
LOC440360	236838_at	H11609	XM_498641	440360	-0.72	5.58E-03
MYEF2	222153_at	AK023133	NM_016132	50804	-0.72	2.99E-03
T82487	241759_at	T82487	---	---	-0.72	2.18E-03
CSTB	201201_at	NM_000100	NM_000100	1476	-0.72	9.61E-04
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DUSP8	238594_x_at	AI864441	NM_004420	1850	-0.72	6.31E-03
LUZP1	1558173_a_at	AK093016	NM_033631	7798	-0.72	3.02E-04
BRUNOL4	223654_s_at	BC004167	NM_020180	56853	-0.72	3.06E-04
RGS8	234297_at	AL359941	NM_033345	85397	-0.72	8.24E-03
AI950023	244433_at	AI950023	---	---	-0.72	5.91E-03
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PDE8B	243590_at	AA860184	NM_003719	8622	-0.72	9.18E-03
ARHGAP1	241419_at	AA709154	NM_004308	392	-0.72	4.95E-03
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DNASE1L1	203912_s_at	NM_006730	NM_001009932 NM_001009933 NM_001009934 NM_006730	1774	-0.72	1.52E-03
ANKRD17	225852_at	BE463523	NM_032217 NM_198889	26057	-0.72	7.58E-06
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FBXW7	229419_at	BF222826	NM_018315 NM_033632	55294	-0.72	5.69E-04
ABCG1	204567_s_at	NM_004915	NM_004915 NM_016818 NM_207174 NM_207627 NM_207628 NM_207629 NM_207630	9619	-0.72	3.49E-04
TRA2A	213593_s_at	AW978896	NM_013293	29896	-0.72	4.15E-03
APC	215310_at	AF038181	NM_000038	324	-0.72	3.73E-03
CXXC5	222996_s_at	BC002490	NM_016463	51523	-0.71	8.07E-04
CSNK1A1	235464_at	AA010757	NM_001892	1452	-0.71	6.52E-04
USP7	230967_s_at	BF433061	NM_003470	7874	-0.71	1.69E-03
TAS2R14	235762_at	AI458566	NM_023922	50840	-0.71	1.07E-03
HNRPR	208766_s_at	BC001449	NM_005826	10236	-0.71	5.99E-04
CAPN1	232012_at	AV691296	NM_005186	823	-0.71	4.07E-03
AI825987	235889_at	AI825987	---	---	-0.71	1.70E-03
FLJ23867	226706_at	BE301252	---	200058	-0.71	5.23E-03
IGF2	202410_x_at	NM_000612	NM_000612	3481	-0.71	2.47E-03
AI887898	228423_at	AI887898	XM_374094	389237	-0.71	2.25E-03
MGC14801	224443_at	BC005997	NM_032705	84791	-0.71	1.76E-03
C1orf50	62212_at	W37846	NM_024097	79078	-0.71	1.18E-03
RLF	204243_at	NM_012421	NM_012421	6018	-0.71	2.22E-04
AW268719	236798_at	AW268719	---	---	-0.71	1.17E-04
AL080112	216858_x_at	AL080112	---	---	-0.71	6.17E-04
AI022648	242972_at	AI022648	---	---	-0.71	3.82E-04

AW072078	230959_at	AW072078	XM_496690	401131	-0.71	2.04E-05
PHKA1	205450_at	NM_002637	NM_002637	5255	-0.71	2.60E-05
AA694209	229066_at	AA694209	---	---	-0.71	1.09E-04
MAP1LC3B	208786_s_at	AF183417	NM_022818	81631	-0.71	4.58E-03
PABPC4	201064_s_at	NM_003819	NM_003819	8761	-0.71	2.02E-04
IGF2	210881_s_at	M17863	NM_000612	3481	-0.70	3.36E-03
C5orf16	1564031_a_at	AK054889	NM_173828	285613	-0.70	3.27E-03
UBXD1	223012_at	AF272894	NM_025241	80700	-0.70	2.81E-03
ANKRD28	229307_at	N32051	NM_015199	23243	-0.70	5.01E-03
UNQ1912	226752_at	AI816071	NM_198507	345757	-0.70	3.53E-03
ARHGAP1	202117_at	BG468434	NM_004308	392	-0.70	2.81E-03
C21orf59	218123_at	NM_017835	NM_017835	56683	-0.70	6.33E-07
			NM_021254			
MONDOA	225157_at	AW245631	NM_014938	22877	-0.70	1.12E-04
NM_024900	218517_at	NM_024900	---	---	-0.70	8.22E-04
C6orf133	215558_at	AK001118	NM_015255	23304	-0.70	6.83E-03
TRIM14	203147_s_at	BE962483	NM_014788	9830	-0.70	7.70E-03
			NM_033219			
			NM_033220			
			NM_033221			
NM_018678	220494_s_at	NM_018678	---	---	-0.70	1.04E-03
LOC144766	243986_at	BE409452	XM_378419	144766	-0.70	1.05E-03
PPP3CA	202429_s_at	AL353950	NM_000944	5530	-0.70	5.44E-04
RNF41	201962_s_at	NM_005785	NM_005785	10193	-0.70	4.15E-04
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RPL35A	215208_x_at	AK021571	NM_000996	6165	-0.70	5.45E-03
CLSTN3	204375_at	NM_014718	NM_014718	9746	-0.70	4.42E-04
PTK2	241387_at	AW276701	NM_005607	5747	-0.70	5.63E-04
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SYNJ1	212990_at	AB020717	NM_003895	8867	-0.69	1.15E-06
			NM_203446			
KIAA1276	227504_s_at	N64630	XM_039169	27146	-0.69	7.28E-06
MLR1	240592_at	AI939336	NM_153686	254251	-0.69	3.41E-04
LMNA	1554600_s_at	BC033088	NM_005572	4000	-0.69	9.76E-03
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ZNF207	1556035_s_at	AI201248	NM_003457	7756	-0.69	3.42E-03
TM4SF2	202242_at	NM_004615	NM_004615	7102	-0.69	2.98E-03
AGRN	212285_s_at	AW008051	NM_198576	375790	-0.69	4.04E-03
AF116695	224254_x_at	AF116695	---	---	-0.69	4.32E-03
FLJ20758	228020_at	BG055431	NM_017952	55037	-0.69	3.97E-05
MYLIP	223130_s_at	AF212221	NM_013262	29116	-0.69	8.41E-03
PTPRD	213362_at	N73931	NM_002839	5789	-0.69	4.67E-03
			NM_130391			
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			NM_130393			
UNC5A	236448_at	R37358	XM_030300	90249	-0.69	1.44E-05
USP36	224979_s_at	AU154368	NM_025090	57602	-0.69	1.61E-03
RBPMS2	228802_at	BE348466	XM_496072	348093	-0.69	1.05E-03
SENP2	222523_at	BE622841	NM_021627	59343	-0.69	4.48E-03
ATXN1	203231_s_at	AW235612	NM_000332	6310	-0.69	9.97E-03
AA630955	242133_s_at	AA630955	---	---	-0.69	1.82E-03
LOC285458	242577_at	BF109197	---	285458	-0.69	9.98E-03
ZNF573	217627_at	BE515346	NM_152360	126231	-0.69	5.61E-03
APC	216933_x_at	S67788	NM_000038	324	-0.69	1.03E-03

WDFY3	212598_at	BE348236	NM_014991 NM_178583 NM_178585	23001	-0.69	1.37E-05
FNBP1	244286_at	AI017983	NM_015033	23048	-0.69	3.21E-03
DSCR3	203635_at	NM_006052	NM_006052	10311	-0.68	1.64E-05
MONDOA	202519_at	NM_014938	NM_014938	22877	-0.68	3.72E-04
AI859990	244197_x_at	AI859990	---	---	-0.68	1.47E-03
C7orf19	1558426_x_at	BC016797	NM_032831	80228	-0.68	6.95E-04
MGC20419	225642_at	AL581536	NM_138417	112970	-0.68	5.44E-03
KIAA1644	221901_at	BF516072	XM_376018	85352	-0.68	3.43E-03
AI146751	242565_x_at	AI146751	---	---	-0.68	1.09E-03
PHF17	225816_at	AW138134	NM_024900 NM_199320	79960	-0.68	8.15E-04
NFASC	213438_at	AA995925	NM_001005387 NM_001005388 NM_001005389 NM_015090	23114	-0.68	1.25E-03
AI332346	225445_at	AI332346	---	---	-0.68	4.20E-03
PEX6	238672_at	AW953952	NM_000287	5190	-0.68	1.21E-05
PALM2-AKAP2	226694_at	BG540494	NM_007203 NM_147150	445815	-0.68	3.43E-04
AI821721	241223_x_at	AI821721	---	---	-0.68	5.48E-04
BF197705	230401_at	BF197705	---	---	-0.68	7.84E-03
BG527339	226457_at	BG527339	---	---	-0.68	2.91E-04
LOC146174	230721_at	BF436957	NM_173501	146174	-0.68	1.72E-03
C1orf21	223127_s_at	AW003850	NM_030806	81563	-0.68	6.33E-04
FBXO31	222352_at	BE465371	NM_024735	79791	-0.68	1.00E-04
TAF15	227891_s_at	AU144462	NM_003487 NM_139215	8148	-0.68	9.77E-03
ZNF207	231848_x_at	AW192569	NM_003457	7756	-0.68	1.45E-03
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ATP11A	1556055_at	U90905	NM_015205 NM_032189	23250	-0.68	4.26E-03
TIM14	225358_at	AI003794	NM_145261 NM_201259 NM_201260 NM_201261	131118	-0.68	2.38E-03
COL5A1	212489_at	AI983428	NM_000093	1289	-0.68	8.47E-03
MGC35274	226748_at	AI674731	NM_153374	256586	-0.68	1.32E-05
ST7L	238512_at	BF961733	NM_017744 NM_138727 NM_138728 NM_138729 NM_198327 NM_198328	54879	-0.67	2.66E-03
HUMPPA	213230_at	AI422335	NM_014603	30850	-0.67	7.14E-03
Cep164	204251_s_at	NM_014956	NM_014956	22897	-0.67	5.51E-03
C14orf159	218298_s_at	NM_024952	NM_024952	80017	-0.67	2.50E-03
MCTP1	235740_at	BG250585	NM_001002796 NM_024717	79772	-0.67	3.10E-03
ZNF451	215012_at	AU144775	NM_015555	26036	-0.67	3.81E-03

MAPT	225379_at	AA199717	NM_005910 NM_016834 NM_016835 NM_016841	4137	-0.67	6.84E-04
SMURF2	241900_at	AW195928	NM_022739	64750	-0.67	7.08E-03
FOXP1	235444_at	AI417897	NM_032682	27086	-0.67	5.32E-04
ZBED3	228402_at	AI679868	NM_032367	84327	-0.67	3.66E-03
ABCC8	210246_s_at	AF087138	NM_000352	6833	-0.67	5.10E-03
FLJ11016	219754_at	NM_018301	NM_018301	55285	-0.67	4.87E-03
AI344332	227227_at	AI344332	XM_373737	388397	-0.67	6.03E-05
HIS1	202814_s_at	AW193511	NM_006460	10614	-0.67	5.23E-04
LOC401394	217529_at	BE547674	XM_379512	401394	-0.67	1.35E-04
TMEM34	219074_at	NM_018241	NM_018241	55751	-0.67	2.81E-03
PPID	204185_x_at	NM_005038	NM_005038	5481	-0.67	2.92E-03
SFRS2IP	232597_x_at	AK025132	NM_004719	9169	-0.67	3.06E-03
SLC35E1	227518_at	AW051365	NM_024881	79939	-0.67	7.53E-03
C14orf118	229514_at	AB032978	NM_017926 NM_017972	55668	-0.67	8.14E-04
KIAA0913	212359_s_at	W89120	NM_015037	23053	-0.67	7.72E-03
C9orf85	238912_x_at	AA824363	NM_182505 NM_198394	138241	-0.67	1.86E-03
CaMKIINalpha	218309_at	NM_018584	NM_018584	55450	-0.67	1.94E-07
TAF1	227205_at	AW575233	NM_004606 NM_138923	6872	-0.67	3.47E-03
LOC144363	225469_at	AA015609	NM_00100166C	144363	-0.66	4.42E-03
TNKS	233152_x_at	AL049979	NM_003747	8658	-0.66	2.23E-03
C1orf52	228135_at	AA738437	NM_198077	148423	-0.66	3.10E-03
BG502771	226397_s_at	BG502771	---	---	-0.66	6.19E-05
ELMO1	204513_s_at	NM_014800	NM_014800 NM_130442	9844	-0.66	6.47E-03
AI627803	236194_at	AI627803	---	---	-0.66	2.79E-03
AA604601	1570566_at	AA604601	---	---	-0.66	1.29E-04
RAMP1	204916_at	NM_005855	NM_005855	10267	-0.66	2.24E-06
AL137655	231886_at	AL137655	XM_373814	388572	-0.66	1.31E-04
PCDHB16	232099_at	AB046841		57717	-0.66	4.23E-03
KIAA0804	209553_at	BC001001	NM_020957 NM_00100992 1 NM_015303	23355	-0.66	2.61E-03
N63920	226179_at	N63920	---	---	-0.66	3.55E-04
MCPH1	219592_at	NM_024596	NM_024596	79648	-0.66	3.60E-03
MLLT6	224784_at	BG024886	NM_005937	4302	-0.66	6.68E-04
ARRDC1	226405_s_at	AK001822	NM_152285	92714	-0.66	2.73E-03
RAB11FIP4	224482_s_at	BC006240	NM_032932	84440	-0.66	3.11E-03
EFNA1	202023_at	NM_004428	NM_004428 NM_182685	1942	-0.66	2.72E-03
C18orf17	1552307_a_at	NM_153211	NM_153211	125488	-0.66	6.53E-03
MBTD1	207115_x_at	NM_017643	NM_017643	54799	-0.66	6.47E-03
ALG3	207396_s_at	NM_005787	NM_00100694 0 NM_00100694 1 NM_00100694 2 NM_005787	10195	-0.66	8.88E-04
IFNAR1	225661_at	AA811138	NM_000629	3454	-0.66	2.66E-03
FER1L4	222245_s_at	AF218012	---	80307	-0.66	3.17E-03
DDX50	1568815_a_at	AA903184	NM_024045	79009	-0.66	4.02E-03

ELK1	210376_x_at	M25269	NM_005229	2002	-0.66	8.45E-03
FBXO31	224162_s_at	BC002985	NM_024735	79791	-0.66	3.15E-03
RNF13	201779_s_at	AF070558	NM_007282 NM_183381 NM_183382 NM_183383 NM_183384	11342	-0.66	1.55E-03
LOC440345	238449_at	BG534511	XM_496125	440345	-0.66	1.28E-03
CXXC5	224516_s_at	BC006428	NM_016463	51523	-0.66	1.05E-05
MKNK2	223199_at	AA404592	NM_017572 NM_199054	2872	-0.66	2.26E-03
NFYC	202215_s_at	NM_014223	NM_014223	4802	-0.66	4.41E-04
RAB12	236019_at	AI076335	XM_113967	201475	-0.66	1.77E-03
ETFDH	205530_at	NM_004453	NM_004453	2110	-0.66	1.11E-03
LOC153364	230298_at	AI692906	NM_203406	153364	-0.66	1.11E-04
ELMO3	219411_at	NM_024712	NM_024712	79767	-0.66	2.82E-03
SERTAD4	229674_at	AL035414	NM_019605	56256	-0.66	3.57E-04
GPRASP1	204793_at	NM_014710	NM_014710	9737	-0.65	1.35E-03
SMAD4	1565703_at	AL832789	NM_005359	4089	-0.65	4.45E-03
ATP9A	216129_at	AL117659	XM_030577	10079	-0.65	3.73E-03
MGC21688	232806_s_at	AU158601	NM_144635	131408	-0.65	3.23E-03
LOC90410	210312_s_at	BC002640	NM_174887	90410	-0.65	1.34E-04
BE348430	230235_at	BE348430	---	---	-0.65	1.62E-04
UBE2G2	1557053_s_at	BC035653	NM_003343 NM_182688	7327	-0.65	1.15E-03
TRA2A	229574_at	AI268231	NM_013293	29896	-0.65	1.49E-03
MGC42174	238602_at	AL036541	NM_152383	129563	-0.65	9.27E-03
QSCN6	201482_at	NM_002826	NM_00100412 8 NM_002826	5768	-0.65	6.49E-03
C15orf24	217898_at	NM_020154	NM_020154	56851	-0.65	6.93E-03
SLCO1A2	211480_s_at	AF085224	NM_005075 NM_021094 NM_134431	6579	-0.65	3.46E-04
ATP2C1	230387_at	AL038450	NM_00100148 5 NM_00100148 6 NM_00100148 7 NM_014382	27032	-0.65	6.34E-03
AF5Q31	232864_s_at	N59653	NM_014423	27125	-0.65	1.51E-03
AL049975	234020_x_at	AL049975	---	---	-0.64	1.81E-03
AI634543	242208_at	AI634543	---	---	-0.64	1.23E-03
AI695743	244534_at	AI695743	---	---	-0.64	9.29E-03
CCNDBP1	223084_s_at	AF246144	NM_012142 NM_037370	23582	-0.64	1.19E-03
ZBED3	235109_at	AI887983	NM_032367	84327	-0.64	4.83E-03
BACE1	222462_s_at	AI653425	NM_012104 NM_138971 NM_138972 NM_138973	23621	-0.64	2.24E-05
SERTAD4	235337_at	AI276403	NM_019605	56256	-0.64	9.08E-04
ZNF596	240324_at	H50654	NM_173539	169270	-0.64	6.01E-04
AA845825	217534_at	AA845825	---	---	-0.64	1.19E-03
BE551142	241091_at	BE551142	XM_497668	388620	-0.64	2.87E-03
KIAA1181	224576_at	AK000752	NM_020462	57222	-0.64	9.10E-03
JMJD1C	221763_at	AI694023	NM_004241	221037	-0.64	1.29E-04

PPP2R5B	635_s_at	L42374	NM_006244	5526	-0.64	7.89E-04
FLJ31438	228316_at	AA905470	NM_152385	130162	-0.64	3.25E-05
AI524240	238863_x_at	AI524240	---	---	-0.64	3.04E-05
DJ971N18.2	240094_at	AL042660	NM_021156	56255	-0.64	7.59E-03
TTC3	208661_s_at	AW510696	NM_00100189 4 NM_003316	7267	-0.64	1.95E-04
JMJD3	41386_i_at	AB002344	XM_043272	23135	-0.64	6.66E-03
SEC6L1	228847_at	W69265	NM_007277	11336	-0.64	8.93E-03
C21orf106	227199_at	AW027812	NM_015151 NM_206889 NM_206890 NM_206891	23181	-0.64	1.63E-03
KIAA1919	242851_at	BE964989	NM_153369	91749	-0.64	1.22E-03
AI683552	217679_x_at	AI683552	---	---	-0.64	3.76E-03
ICA1	207949_s_at	NM_004968	NM_004968 NM_022307 NM_022308	3382	-0.64	3.58E-06
AI885665	238360_s_at	AI885665	---	---	-0.64	3.47E-04
AW511239	229765_at	AW511239	---	---	-0.64	7.38E-03
BI496583	1557675_at	BI496583	---	---	-0.63	3.19E-03
LOC253982	214993_at	AF070642	NM_181718 NM_198907	253982	-0.63	1.41E-04
ASB13	218862_at	NM_024701	NM_024701	79754	-0.63	2.48E-03
C18orf23	230143_at	BF433220	NM_152470	147341	-0.63	3.83E-03
WDFY3	212602_at	AI806395	NM_014991 NM_178583 NM_178585	23001	-0.63	3.16E-04
TMEM5	204808_s_at	NM_014254	NM_014254	10329	-0.63	4.54E-05
SPTBN1	200671_s_at	N92501	NM_003128 NM_178313	6711	-0.63	4.18E-04
AI216567	236754_at	AI216567	---	---	-0.63	2.90E-03
PTPRN2	203030_s_at	AF007555	NM_002847 NM_130842 NM_130843	5799	-0.63	7.43E-03
M17S2	1568857_a_at	BC012591	NM_005899 NM_031858 NM_031862	4077	-0.63	6.88E-03
C6orf170	1553726_s_at	NM_152730	NM_152730	221322	-0.63	2.53E-04
SON	201085_s_at	AA664291	NM_003103 NM_032195 NM_058183 NM_138925 NM_138926 NM_138927	6651	-0.63	2.20E-03
AA102332	240172_at	AA102332	---	---	-0.63	6.39E-03
MGC15416	225861_at	AW001250	NM_032371 NM_138418	84331	-0.63	4.24E-04
AK024602	222207_x_at	AK024602	---	---	-0.63	1.29E-03
AW945538	239208_s_at	AW945538	---	---	-0.63	2.53E-03
AI140364	221740_x_at	AI140364	XM_373737	388397	-0.63	1.10E-04
ARHGEF7	1562271_x_at	AL831814	NM_003899 NM_145735	8874	-0.63	5.76E-03
AG1	215434_x_at	AV684285	XM_371384 XM_496394	440673	-0.63	1.46E-03
BZRAP1	205839_s_at	NM_004758	NM_004758	9256	-0.63	3.66E-03
C14orf149	227699_at	BF511003	NM_144581	112849	-0.63	5.42E-03
U2AF1	232141_at	AU144161	NM_006758	7307	-0.63	2.12E-03

CAMK2B	213276_at	T15766	NM_001220 NM_172078 NM_172079 NM_172080 NM_172081 NM_172082 NM_172083 NM_172084	816	-0.63	7.05E-03
NRD1	229422_at	AA448346	NM_002525	4898	-0.63	5.72E-03
C10orf18	244165_at	AI809511	XM_374765	54906	-0.62	9.92E-03
TMPIT	234084_x_at	AU147104	NM_031925	83862	-0.62	7.32E-04
AI334297	225961_at	AI334297	---	---	-0.62	9.96E-03
MAPT	203929_s_at	AI056359	NM_005910 NM_016834 NM_016835 NM_016841	4137	-0.62	6.17E-04
XRN1	242995_at	AW976347	NM_019001	54464	-0.62	5.64E-03
NFIC	226377_at	AI093722	NM_005597 NM_205843	4782	-0.62	1.82E-03
FBXO9	212991_at	AL137520	NM_012347 NM_033480 NM_033481	26268	-0.62	1.09E-05
OSBPL6	223805_at	AF323728	NM_032523 NM_145739	114880	-0.62	1.05E-04
NRD1	242235_x_at	AW978721	NM_002525	4898	-0.62	6.13E-04
ATXN7L1	227732_at	AB033044	---	57485	-0.62	5.06E-03
PDPK1	32029_at	AC005591	NM_002613 NM_031268	5170	-0.62	8.86E-03
BF110411	221878_at	BF110411	XM_371506	388969	-0.62	4.02E-03
SNX1	1559154_at	AK098001	NM_003099 NM_148955 NM_152826	6642	-0.62	2.16E-03
LOC282965	230108_at	BF433475	---	282965	-0.62	7.42E-03
AA045233	224686_x_at	AA045233	XM_373737	388397	-0.62	1.42E-04
TIMM9	218316_at	NM_012460	NM_012460	26520	-0.62	9.93E-03
PTPRN2	203029_s_at	NM_002847	NM_002847 NM_130842 NM_130843	5799	-0.62	1.78E-04
MGC52110	226039_at	AW006441	NM_001008215	493753	-0.62	2.08E-04
SCN5A	207413_s_at	NM_000335	NM_000335 NM_198056	6331	-0.62	2.09E-03
ATF7	244473_at	R37637	NM_006856	11016	-0.62	6.77E-04
AL162054	1559420_x_at	AL162054	---	---	-0.62	2.91E-03
INHA	1569409_x_at	BC037812	NM_002191	3623	-0.62	9.67E-03
CTTN	214782_at	AU155105	NM_005231 NM_138565	2017	-0.62	3.85E-03
FLJ20758	228590_at	AA045257	NM_017952	55037	-0.62	1.29E-06
DTX3	221835_at	N92708	NM_178502	196403	-0.61	6.82E-03
AFG3L2	232919_at	AU147380	NM_006796	10939	-0.61	7.83E-03
NR2F1	209505_at	AI951185	NM_005654	7025	-0.61	1.18E-04
MYLIP	228098_s_at	AW292746	NM_013262	29116	-0.61	9.86E-05
FLJ00312	221971_x_at	BE672818	XM_374801	399761	-0.61	2.00E-05
STAT3	235680_at	AI914925	NM_003150 NM_139276 NM_213662	6774	-0.61	7.44E-04
PALM2-AKAP2	202759_s_at	BE879367	NM_007203 NM_147150	445815	-0.61	1.06E-05
AI692645	230206_at	AI692645	---	---	-0.61	7.26E-04

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PPP3CA	202457_s_at	AA911231	NM_000944	5530	-0.61	1.76E-04
POM121	212178_s_at	AK022555	NM_172020	340318	-0.61	6.29E-04
LOC340318			XM_290401	9883		
			XM_379877			
AK024255	232569_at	AK024255	---	---	-0.61	5.98E-03
TRIM8	223132_s_at	AF220034	NM_030912	81603	-0.61	5.53E-05
PDLIM4	211564_s_at	BC003096	NM_003687	8572	-0.61	4.83E-04
SHFM3	221519_at	AF281859	NM_022039	6468	-0.61	8.52E-06
RIC3	220282_at	NM_024557	NM_024557	79608	-0.61	3.26E-03
AK024881	234723_x_at	AK024881	---	---	-0.61	7.62E-03
ZKFZP434H132	204494_s_at	AW516789	NM_015492	56905	-0.61	1.22E-04
SMA3	206565_x_at	NM_006780	NM_006780	10571	-0.61	8.06E-03
C21orf108	212996_s_at	AI803485	---	9875	-0.61	8.23E-04
MAP1LC3B	208785_s_at	BE893893	NM_022818	81631	-0.61	2.42E-03
PRKCZ	202178_at	NM_002744	NM_002744	5590	-0.61	2.33E-03
BICD1	214806_at	U90030	NM_00100339	636	-0.61	1.56E-03
			8			
			NM_001714			
MAP3K12	205447_s_at	BE222201	NM_006301	7786	-0.61	3.86E-03
PSIP1	232363_at	AK024516	NM_021144	11168	-0.61	2.71E-03
			NM_033222			
HPCAL1	205462_s_at	NM_002149	NM_002149	3241	-0.61	1.40E-05
			NM_134421			
PALM2-AKAP2	202760_s_at	NM_007203	NM_007203	445815	-0.61	4.74E-03
			NM_147150			
LOC282997	222307_at	AI695595	---	282997	-0.61	8.47E-03
BF339133	213296_at	BF339133	---	---	-0.60	3.76E-03
AI791303	238890_at	AI791303	---	---	-0.60	2.71E-03
KIAA1881	207730_x_at	NM_017932	XM_375558	114782	-0.60	1.50E-03
AL355532	213845_at	AL355532	---	---	-0.60	1.88E-04
ELOVL5	214153_at	BE467941	NM_021814	60481	-0.60	2.39E-03
FLJ38991	227442_at	BG283902	NM_173827	285521	-0.60	9.08E-05
C3orf6	226713_at	AI247881	NM_174908	152137	-0.60	6.70E-03
			NM_178335			
FNTA	230808_at	AA833870	NM_002027	2339	-0.60	3.58E-03
MGC54289	225228_at	AI474054	NM_178454	128338	-0.60	6.20E-03
KIAA1536	209002_s_at	BC003177	NM_020898	57658	-0.60	9.44E-03
CDK5R1	204995_at	AL567411	NM_003885	8851	-0.60	4.65E-04
SFXN3	1559993_at	AK091504	NM_030971	81855	-0.60	4.27E-03
AU157441	226511_at	AU157441	---	---	-0.60	3.90E-03
FLJ23861	231252_at	AI680874	NM_152519	151050	-0.60	5.09E-03
BE219067	243641_at	BE219067	---	---	-0.60	2.03E-06
BC042959	1556194_a_at	BC042959	---	---	-0.60	5.58E-03
PFAAP5	221899_at	AI809961	NM_014887	10443	-0.60	8.51E-03
PPP2R2C	223573_s_at	AW166283	NM_020416	5522	-0.60	4.24E-03
			NM_181876			
CLASP2	212309_at	AV725315	NM_015097	23122	-0.60	3.17E-04
INSR	226450_at	AV703054	NM_000208	3643	-0.60	8.36E-06
USP34	207365_x_at	NM_014709	NM_014709	9736	-0.60	8.70E-03
RUNX1	236114_at	AI798118	NM_00100189	861	-0.59	5.87E-03
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			NM_001754			
VPS13C	218396_at	NM_017684	NM_017684	54832	-0.59	6.96E-03
KPNA1	202057_at	BC002374	NM_002264	3836	-0.59	3.30E-04
RPS6KL1	223534_s_at	BC004540	NM_031464	83694	-0.59	6.25E-04
CNNM3	240339_at	AA829860	NM_017623	26505	-0.59	2.25E-03
			NM_199078			
AK022428	234731_at	AK022428	---	---	-0.59	3.34E-04

NT5C3	223298_s_at	AF312735	NM_016489	51251	-0.59	8.53E-04
JMJD3	213146_at	AA521267	XM_043272	23135	-0.59	7.42E-03
NM_018289	219794_at	NM_018289	---	---	-0.59	4.18E-07
FCMD	205283_at	NM_006731	NM_006731	2218	-0.59	4.33E-03
C18orf17	1570552_at	AF363068	NM_153211	125488	-0.59	2.11E-03
FLJ23451	1569601_at	BF106979	NM_024766	79823	-0.59	1.13E-03
BF514509	239050_s_at	BF514509	---	---	-0.59	1.54E-03
LOC442647	229157_at	AI949265	XM_499544	442647	-0.59	2.37E-03
SLC24A5	228792_at	AU145100	NM_205850	283652	-0.59	1.36E-03
AI796076	243339_at	AI796076	---	---	-0.59	2.87E-03
BE857570	235677_at	BE857570	---	---	-0.59	2.57E-03
RALGDS	209051_s_at	AF295773	NM_006266	5900	-0.59	8.43E-03
SND1	242506_at	AI138785	NM_014390	27044	-0.59	1.79E-03
BM914560	1558220_at	BM914560	XM_496669	440993	-0.58	6.65E-03
SEZ6L2	218720_x_at	NM_012410	NM_012410 NM_201575	26470	-0.58	3.65E-03
AW294192	228040_at	AW294192	---	---	-0.58	3.57E-04
PCNT2	233387_s_at	AK024009	NM_006031	5116	-0.58	5.43E-03
CHST5	219182_at	NM_024533	NM_012126 NM_024533	23563	-0.58	9.75E-03
MGC15416	1553715_s_at	NM_032371	NM_032371 NM_138418	84331	-0.58	4.55E-03
ABAT	209460_at	AF237813	NM_000663 NM_020686	18	-0.58	5.91E-03
C9orf112	225586_at	BF222775	NM_138778	92715	-0.58	3.08E-03
DSCR3	217309_s_at	AJ001867	NM_006052	10311	-0.58	6.91E-03
IER2	202081_at	NM_004907	NM_004907	9592	-0.58	6.30E-03
MGC4796	223852_s_at	BC005169	NM_032017	83931	-0.58	7.87E-03
CD151	204306_s_at	NM_004357	NM_004357 NM_139030	977	-0.58	1.98E-03
MACF1	208633_s_at	W61052	NM_012090 NM_033044	23499	-0.58	1.19E-03
MGC16279	65585_at	AA527515	NM_032916	85002	-0.58	2.75E-03
ZBTB4	225629_s_at	AI669498	NM_020899	57659	-0.58	4.70E-05
GRIPAP1	1557562_at	AI984118	NM_020137 NM_207672	56850	-0.58	3.18E-03
AU145662	233399_x_at	AU145662	XM_499131	441383	-0.58	1.90E-03
SYNGAP1	230297_x_at	AW002361	NM_006772	8831	-0.58	5.57E-03
MGC15407	224968_at	AL518311	NM_080667	112942	-0.58	3.50E-03

Table 7. Increased Gene Expression in Cell Lines H1 and BB10 vs. Cell Line 2D6 in Differentiated State Using Microarray Analysis

Gene Symbol	Probe Set ID	Representative Public ID	RefSeq Transcript ID	Entrez Gene	Log2 Ratio	pvalue
PLS3	201215_at	NM_005032	NM_005032	5358	6.46	2.18E-11
PEG3	209242_at	AL042588	NM_006210	5178	6.29	4.38E-07
FLJ32942	227711_at	BG150433	NM_144594	121355	6.29	3.26E-08
MSN	200600_at	NM_002444	NM_002444	4478	6.24	7.65E-10
)KFZp667G211	214030_at	BE501352	XM_376254	131544	6.06	3.72E-05
MCM10	220651_s_at	NM_018518	NM_018518 NM_182751	55388	5.94	2.90E-06
TPTE	220205_at	NM_013315	NM_013315 NM_199259 NM_199260 NM_199261	7179	5.89	2.90E-07
DLG7	203764_at	NM_014750	NM_014750	9787	5.79	1.58E-05
PLK2	201939_at	NM_006622	NM_006622	10769	5.72	1.74E-08
HMMR	209709_s_at	U29343	NM_012484 NM_012485	3161	5.64	2.12E-07
BUB1	209642_at	AF043294	NM_004336	699	5.53	9.46E-06
RGS5	1555725_a_at	AF493929	NM_003617	8490	5.49	1.14E-04
NDN	209550_at	U35139	NM_002487	4692	5.42	1.66E-05
FLJ34013	225710_at	H99792	---	---	5.39	6.18E-08
FAT	201579_at	NM_005245	NM_005245	2195	5.36	1.20E-03
RGS5	218353_at	NM_025226	NM_003617	8490	5.29	4.83E-04
KCTD12	212192_at	AI718937	NM_138444	115207	5.28	1.26E-06
TFPI2	209278_s_at	L27624	NM_006528	7980	5.28	1.22E-05
AI813331	229097_at	AI813331	---	---	5.23	3.44E-07
GNG11	204115_at	NM_004126	NM_004126	2791	5.21	7.49E-06
AI197932	229498_at	AI197932	---	---	5.17	1.33E-07
RGS5	209070_s_at	AI183997	NM_003617	8490	5.14	3.20E-04
MKI67	212021_s_at	AU132185	NM_002417	4288	5.04	2.78E-05
PRSS12	205515_at	NM_003619	NM_003619	8492	5.01	3.19E-07
MCM10	222962_s_at	AB042719	NM_018518 NM_182751	55388	5.01	2.63E-07
BIRC5	210334_x_at	AB028869	NM_001168	332	5.00	5.51E-05
RAMP	222680_s_at	AK001261	NM_016448	51514	5.00	2.74E-05
ASF1B	218115_at	NM_018154	NM_018154	55723	4.97	3.08E-05
MKI67	212023_s_at	AU147044	NM_002417	4288	4.97	7.09E-06
MKI67	212020_s_at	AU152107	NM_002417	4288	4.97	3.98E-07
ATAD2	218782_s_at	NM_014109	NM_014109	29028	4.96	7.16E-07
BIRC5	202094_at	AA648913	NM_001168	332	4.96	3.70E-05
FLJ40629	229610_at	AW088063	NM_152515	150468	4.96	2.93E-05
EXO1	204603_at	NM_003686	NM_003686 NM_006027 NM_130398	9156	4.90	1.18E-05
DEPDC1	222958_s_at	AK000490	NM_017779	55635	4.89	2.51E-07
RGS5	209071_s_at	AF159570	NM_003617	8490	4.87	1.25E-04
RRM2	209773_s_at	BC001886	NM_001034	6241	4.86	4.36E-05
KIF14	236641_at	AW183154	XM_375825	9928	4.86	1.11E-05
OIP5	213599_at	BE045993	NM_007280	11339	4.85	5.98E-08
C10orf3	218542_at	NM_018131	NM_018131	55165	4.85	4.79E-06
BRRN1	212949_at	D38553	NM_015341	23397	4.85	2.87E-06
FLJ10719	223785_at	BC004277	NM_018193	55215	4.84	6.89E-06

CHEK2	210416_s_at	BC004207	NM_00100573 5 NM_007194 NM_145862	11200	4.81	1.17E-03
N31731	230165_at	N31731	---	---	4.80	2.02E-07
BRIP1	235609_at	BF056791	NM_032043	83990	4.80	3.95E-05
MELK	204825_at	NM_014791	NM_014791	9833	4.80	2.52E-04
KIF20A	218755_at	NM_005733	NM_005733	10112	4.71	2.34E-05
SPARC	200665_s_at	NM_003118	NM_003118	6678	4.71	6.23E-06
BUB1	215509_s_at	AL137654	NM_004336	699	4.69	2.73E-06
BASP1	202391_at	NM_006317	NM_006317	10409	4.68	5.50E-07
SULT1C2	1553321_a_at	NM_006588	NM_006588	27233	4.66	9.28E-06
GTSE1	204317_at	BF305380	NM_016426	51512	4.64	2.33E-08
DAZ1 DAZ3 DAZ2 DAZ4	208282_x_at	NM_020363	NM_00100537 5 NM_00100578 5 NM_00100578 6 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	4.64	4.44E-03
CDC45L	204126_s_at	NM_003504	NM_003504	8318	4.62	2.60E-04
PRSS12	213802_at	AI810767	NM_003619	8492	4.61	1.09E-05
BRIP1	221703_at	AF360549	NM_032043	83990	4.60	7.21E-06
RNF182	230720_at	AI884906	NM_152737	221687	4.59	1.15E-07
SLC1A3	202800_at	NM_004172	NM_004172	6507	4.55	1.78E-06
DAZ1 DAZ3 DAZ2 DAZ4	207912_s_at	NM_004081	NM_00100537 5 NM_00100578 5 NM_00100578 6 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	4.55	1.51E-03
GTSE1	204315_s_at	AI340239	NM_016426	51512	4.54	9.21E-06
NEIL3	219502_at	NM_018248	NM_018248	55247	4.54	8.88E-06
SPARC	212667_at	AL575922	NM_003118	6678	4.53	5.72E-05
FN5	219806_s_at	NM_020179	NM_020179	56935	4.53	2.58E-05
CENPA	204962_s_at	NM_001809	NM_001809	1058	4.53	1.46E-06
MYBL1	213906_at	AW592266	XM_034274	4603	4.52	2.33E-05
MAOA	212741_at	AA923354	NM_000240	4128	4.52	9.33E-07
HMMR	207165_at	NM_012485	NM_012484 NM_012485	3161	4.51	5.91E-06
ZNF367	229551_x_at	N62196	NM_153695	195828	4.50	2.65E-05
NMU	206023_at	NM_006681	NM_006681	10874	4.50	1.75E-04
CDCA8	221520_s_at	BC001651	NM_018101	55143	4.49	1.67E-06
FLJ10156	221591_s_at	BC005004	NM_019013	54478	4.48	1.61E-06
SHCBP1	219493_at	NM_024745	NM_024745	79801	4.47	1.26E-05
DIAPH3	232596_at	AL354829	NM_030932	81624	4.46	1.53E-06

DAZ1	207909_x_at	U21663	NM_00100537	1617	4.46	3.63E-03
DAZ3			5	57054		
DAZ2			NM_00100578	57055		
DAZ4			5	57135		
			NM_00100578			
			6			
			NM_004081			
			NM_020363			
			NM_020364			
			NM_020420			
FOXM1	202580_x_at	NM_021953	NM_021953	2305	4.44	1.30E-04
			NM_202002			
			NM_202003			
MAB21L2	210302_s_at	AF262032	NM_006439	10586	4.43	9.15E-04
KIF18A	221258_s_at	NM_031217	NM_031217	81930	4.42	2.20E-07
STK6	204092_s_at	NM_003600	NM_003600	6790	4.41	1.58E-06
			NM_198433			
			NM_198434			
			NM_198435			
			NM_198436			
			NM_198437			
ANLN	1552619_a_at	NM_018685	NM_018685	54443	4.41	6.79E-05
MINA	213188_s_at	AI823896	NM_032778	84864	4.41	1.40E-04
			NM_153182			
CENPE	205046_at	NM_001813	NM_001813	1062	4.40	5.00E-07
FLJ20641	227928_at	AI224977	NM_017915	55010	4.40	5.48E-07
CDC2	203214_x_at	NM_001786	NM_001786	983	4.37	1.70E-06
			NM_033379			
KIF4A	218355_at	NM_012310	NM_012310	24137	4.36	5.88E-08
CDCA2	226661_at	T90295	NM_152562	157313	4.34	2.67E-07
BRCA1	211851_x_at	AF005068	NM_007294	672	4.34	1.52E-05
			NM_007295			
			NM_007296			
			NM_007297			
			NM_007298			
			NM_007299			
			NM_007300			
			NM_007301			
			NM_007302			
			NM_007303			
			NM_007304			
			NM_007305			
			NM_007306			
DEPDC1	235545_at	AI810054	NM_017779	55635	4.32	1.48E-07
MINA	213189_at	BE966695	NM_032778	84864	4.31	1.18E-06
			NM_153182			
CDKN3	209714_s_at	AF213033	NM_005192	1033	4.31	8.89E-05
PLK4	204887_s_at	NM_014264	NM_014264	10733	4.29	1.64E-04
RRM2	201890_at	BE966236	NM_001034	6241	4.28	5.37E-05
RAD51	205024_s_at	NM_002875	NM_002875	5888	4.27	1.40E-05
			NM_133487			
AURKB	209464_at	AB011446	NM_004217	9212	4.27	2.23E-05
TTK	204822_at	NM_003318	NM_003318	7272	4.27	7.61E-06
POLE2	205909_at	NM_002692	NM_002692	5427	4.27	9.18E-04

OSBPL3	209627_s_at	AY008372	NM_015550 NM_145320 NM_145321 NM_145322 NM_145323 NM_145324	26031	4.26	1.75E-05
PEG3	209243_s_at	AF208967	NM_006210	5178	4.26	3.95E-05
KIF11	204444_at	NM_004523	NM_004523	3832	4.25	4.91E-04
Spc24	235572_at	AI469788	NM_182513	147841	4.25	7.74E-09
FGFR2	203639_s_at	M80634	NM_000141 NM_022969 NM_022970 NM_022971 NM_022972 NM_022973 NM_022974 NM_022975 NM_022976 NM_023028 NM_023029 NM_023030 NM_023031	2263	4.24	9.58E-06
CDCA1	223381_at	AF326731	NM_031423 NM_145697	83540	4.22	1.90E-05
ANLN	222608_s_at	AK023208	NM_018685	54443	4.22	2.01E-04
MAB21L1	206163_at	NM_005584	NM_005584	4081	4.21	2.65E-05
CDC6	203967_at	U77949	NM_001254	990	4.20	1.21E-03
ESPL1	38158_at	D79987	NM_012291	9700	4.17	1.15E-06
MCM5	201755_at	NM_006739	NM_006739	4174	4.16	4.33E-04
MGC57827	225834_at	AL135396	NM_207418	389835	4.16	6.28E-06
STK6	208079_s_at	NM_003158	NM_003600 NM_198433 NM_198434 NM_198435 NM_198436 NM_198437	6790	4.16	1.80E-05
SLD5	211767_at	BC005995	NM_032336	84296	4.16	3.72E-03
RAMP	218585_s_at	NM_016448	NM_016448	51514	4.16	1.38E-04
KNTC2	204162_at	NM_006101	NM_006101	10403	4.14	1.03E-06
DEPDC1	220295_x_at	NM_017779	NM_017779	55635	4.14	6.26E-07
KNSL7	219306_at	NM_020242	NM_020242	56992	4.14	7.68E-06
CDCA2	236957_at	AI248206	NM_152562	157313	4.13	1.53E-05
MLF1IP	229305_at	AA460299	NM_024629	79682	4.13	2.13E-06
CDC2	210559_s_at	D86357	NM_001786 NM_033379	983	4.11	3.40E-06
CDKN3	1555758_a_at	AF213040	NM_005192	1033	4.10	5.09E-07
ATAD2	222740_at	AI925583	NM_014109	29028	4.10	1.44E-05
FAM54A	228069_at	AL138828	NM_138419	113115	4.10	8.67E-07
CDK2	204252_at	M68520	NM_001798 NM_052827	1017	4.10	1.46E-06
AI377043	230722_at	AI377043	---	---	4.10	2.84E-08
CDC25C	205167_s_at	NM_001790	NM_001790 NM_022809	995	4.09	1.38E-05
GTSE1	204318_s_at	NM_016426	NM_016426	51512	4.08	6.60E-06
UHRF1	225655_at	AK025578	NM_013282	29128	4.08	5.58E-05
FLJ23311	219990_at	NM_024680	NM_024680	79733	4.08	1.87E-05
PBK	219148_at	NM_018492	NM_018492	55872	4.08	2.74E-06
MGC34032	235763_at	AA001450	NM_152697	204962	4.07	4.96E-06

Spc25	209891_at	AF225416	NM_020675	57405	4.07	2.08E-04
ASPM	219918_s_at	NM_018123	NM_018136	259266	4.06	1.74E-06
IQGAP3	229538_s_at	AW271106	NM_178229	128239	4.04	3.66E-05
UBE3B	213822_s_at	BE856776	NM_130466	89910	4.03	1.32E-06
			NM_183414			
			NM_183415			
SMC2L1	204240_s_at	NM_006444	NM_006444	10592	4.02	1.45E-04
SYNPO2	225720_at	AW009747	NM_133477	171024	4.02	2.27E-04
FBLN1	202995_s_at	NM_006486	NM_001996	2192	4.01	1.34E-06
			NM_006485			
			NM_006486			
			NM_006487			
ITGA6	201656_at	NM_000210	NM_000210	3655	4.00	1.10E-06
CDC6	203968_s_at	NM_001254	NM_001254	990	4.00	3.34E-04
TK1	1554408_a_at	BC007986	NM_003258	7083	4.00	4.33E-07
FLJ25416	228281_at	BF343258	NM_145018	220042	3.99	1.36E-06
ORC1L	205085_at	NM_004153	NM_004153	4998	3.98	1.89E-05
CNTN1	211203_s_at	U07820	NM_001843	1272	3.97	1.43E-05
			NM_175038			
NUSAP1	218039_at	NM_016359	NM_016359	51203	3.97	2.83E-06
			NM_018454			
KIF23	204709_s_at	NM_004856	NM_004856	9493	3.96	7.58E-05
			NM_138555			
FBLN1	201787_at	NM_001996	NM_001996	2192	3.96	1.15E-04
			NM_006485			
			NM_006486			
			NM_006487			
RAD54L	204558_at	NM_003579	NM_003579	8438	3.95	6.59E-06
CENPF	209172_s_at	U30872	NM_016343	1063	3.95	2.98E-08
FGL1	205305_at	NM_004467	NM_004467	2267	3.94	2.35E-05
			NM_147203			
			NM_201552			
			NM_201553			
ARHGAP24	223422_s_at	AI743534	NM_031305	83478	3.94	2.71E-05
DKFZp564A232	1556300_s_at	BF476109	---	---	3.93	1.17E-03
DEPDC1	232278_s_at	AJ278112	NM_017779	55635	3.93	3.60E-05
GRP	206326_at	NM_002091	NM_002091	2922	3.92	5.54E-05
MAOA	204388_s_at	NM_000240	NM_000240	4128	3.92	3.38E-07
POLQ	219510_at	NM_006596	NM_006596	10721	3.91	8.49E-06
			NM_199420			
DKFZp762E131	218726_at	NM_018410	NM_018410	55355	3.91	7.86E-06
GTSE1	215942_s_at	BF973178	NM_016426	51512	3.90	9.11E-06
TPX2	210052_s_at	AF098158	NM_012112	22974	3.90	3.85E-06
LOC440738	221697_at	AF276659	NM_001004343	440738	3.90	2.27E-03
LOC340109	1557765_at	BC039509	XM_379322	340109	3.89	2.74E-05
NUSAP1	219978_s_at	NM_018454	NM_016359	51203	3.89	3.26E-06
			NM_018454			
LOC253981	226430_at	AI394438	---	253981	3.88	6.06E-07
ESPL1	204817_at	NM_012291	NM_012291	9700	3.85	7.34E-05
KIFC1	209680_s_at	BC000712	XM_371813	3833	3.83	1.36E-06
KCTD12	212188_at	AA551075	NM_138444	115207	3.82	1.05E-05
KIF14	206364_at	NM_014875	XM_375825	9928	3.82	6.29E-07
SGOL2	235425_at	AW965339	NM_152524	151246	3.81	3.04E-05
KIAA0186	206102_at	NM_021067	XM_375911	9837	3.81	4.00E-06
C20orf129	225687_at	BC001068	NM_030919	81610	3.80	4.60E-05
DNA2L	213647_at	D42046	XM_166103	1763	3.79	4.96E-07
CCDC3	223316_at	AL136562	NM_031455	83643	3.78	9.60E-05
CIT	212801_at	AI861788	NM_007174	11113	3.78	9.25E-05

BUB1B	203755_at	NM_001211	NM_001211	701	3.78	6.66E-07
CDCA3	221436_s_at	NM_031299	NM_031299	83461	3.77	1.69E-04
MCM10	223570_at	AL136840	NM_018518 NM_182751	55388	3.76	8.71E-06
C18orf24	217640_x_at	BF038461	NM_145060	220134	3.76	7.58E-05
EMILIN2	224374_s_at	AF270513	NM_032048	84034	3.75	2.71E-05
C18orf54	229442_at	BF059556	NM_173529	162681	3.75	4.74E-08
MAB21L2	210303_at	AF262032	NM_006439	10586	3.73	4.97E-07
BNC2	238478_at	H97386	NM_017637	54796	3.73	6.40E-07
AI926924	239253_at	AI926924	---	---	3.73	3.76E-04
CDC2	203213_at	AL524035	NM_001786 NM_033379	983	3.73	5.41E-06
Pfs2	221521_s_at	BC003186	NM_016095	51659	3.73	2.20E-05
MGC34032	1569112_at	AW020413	NM_152697	204962	3.72	5.15E-06
NEK2	204641_at	NM_002497	NM_002497	4751	3.71	2.52E-05
MGC45871	226876_at	AI961778	NM_182705	359845	3.71	6.58E-06
DPYD	204646_at	NM_000110	NM_000110	1806	3.70	1.06E-04
BIRC5	202095_s_at	NM_001168	NM_001168	332	3.70	1.51E-06
ELOVL7	227180_at	AW138767	XM_371740	79993	3.69	9.47E-05
BF000203	236385_at	BF000203	---	---	3.69	1.75E-05
STK17A	202693_s_at	AW194730	NM_004760	9263	3.68	3.33E-04
CHEK1	205394_at	NM_001274	NM_001274	1111	3.67	2.79E-04
FLJ13912	45633_at	AI421812	NM_022770	64785	3.67	3.76E-06
FLJ10719	213008_at	BG403615	NM_018193	55215	3.67	4.86E-06
CENPF	207828_s_at	NM_005196	NM_016343	1063	3.65	1.58E-06
E2F2	228361_at	AL561296	NM_004091	1870	3.65	2.93E-06
NEGR1	243357_at	AA115106	NM_173808	257194	3.65	1.29E-06
CENPA	210821_x_at	BC002703	NM_001809	1058	3.65	7.15E-06
MGC40179	242560_at	AA579890	NM_173472	115795	3.64	1.89E-04
SPAG6	210033_s_at	AF079363	NM_012443 NM_172242	9576	3.64	3.09E-03
SLAC2-B	214734_at	AB014524	NM_015065	23086	3.64	3.42E-04
ASCL1	209985_s_at	BE797438	NM_004316	429	3.63	3.48E-04
ZNF521	226677_at	AF141339	NM_015461	25925	3.62	6.14E-07
NEK2	211080_s_at	Z25425	NM_002497	4751	3.62	4.42E-05
TK1	202338_at	NM_003258	NM_003258	7083	3.62	1.03E-05
CCNB1	214710_s_at	BE407516	NM_031966	891	3.62	5.65E-07
TCF7L1	221016_s_at	NM_031283	NM_031283	83439	3.61	1.36E-03
MYBL2	201710_at	NM_002466	NM_002466	4605	3.60	5.06E-05
BRCA2	208368_s_at	NM_000059	NM_000059	675	3.60	1.84E-05
TOP2A	201292_at	AL561834	NM_001067	7153	3.60	4.23E-06
CCNE2	205034_at	NM_004702	NM_004702 NM_057735 NM_057749	9134	3.60	1.96E-05
AI937080	244033_at	AI937080	---	---	3.59	1.30E-04
MKI67	212022_s_at	BF001806	NM_002417	4288	3.59	3.34E-05
dJ383J4.3	1554271_a_at	BC019022	NM_033319	91687	3.57	3.09E-05
SMC6L1	236535_at	AW069285	NM_024624	79677	3.56	3.19E-05
ECT2	219787_s_at	NM_018098	NM_018098	1894	3.56	7.41E-08
CDCA3	223307_at	BC002551	NM_031299	83461	3.56	9.80E-05
CDCA5	224753_at	BE614410	NM_080668	113130	3.56	1.86E-05
TRIP10	202734_at	NM_004240	NM_004240	9322	3.55	1.98E-05
C14orf106	226630_at	BF062175	NM_018353	55320	3.55	5.62E-07
TMEM35	219685_at	NM_021637	NM_021637	59353	3.55	9.24E-05
POLA2	204441_s_at	NM_002689	NM_002689	23649	3.54	5.49E-06
FLJ13912	218719_s_at	NM_022770	NM_022770	64785	3.52	1.92E-06

PDE5A	227088_at	BF221547	NM_001083 NM_033430 NM_033431 NM_033437	8654	3.52	7.25E-04
SIM1	206876_at	AL121948	NM_005068	6492	3.52	9.26E-04
WDR51A	226355_at	AW001089	NM_015426	25886	3.52	2.74E-05
TFPI2	209277_at	AL574096	NM_006528	7980	3.51	1.33E-04
CUGBP2	202158_s_at	NM_006561	NM_006561	10659	3.51	3.91E-03
ATAD2	235266_at	AI139629	NM_014109	29028	3.49	5.52E-05
DOK5	1554863_s_at	BC008992	NM_018431 NM_177959	55816	3.49	1.51E-03
ATAD2	228401_at	AI656807	NM_014109	29028	3.49	2.96E-06
WDHD1	204728_s_at	NM_007086	NM_00100839 6 NM_007086	11169	3.48	1.11E-05
BC002493	223274_at	BC002493	---	---	3.47	3.08E-05
BARD1	205345_at	NM_000465	NM_000465	580	3.46	1.90E-03
MGC45866	230021_at	AI638593	NM_152259	90381	3.46	1.66E-05
Cep152	239413_at	AI130715	NM_014985	22995	3.46	2.08E-07
)KFZp761O201	232313_at	AL122107	XM_044062	92293	3.46	1.14E-04
TOP2A	201291_s_at	AU159942	NM_001067	7153	3.45	8.58E-06
TRAF4	202871_at	NM_004295	NM_004295 NM_145751	9618	3.44	2.74E-06
RBPMS	209488_s_at	D84109	NM_00100871 0 NM_00100871 1 NM_00100871 2 NM_006867	11030	3.44	6.92E-04
CNTN1	227202_at	AW072790	NM_001843 NM_175038	1272	3.44	1.89E-06
DCC1	219000_s_at	NM_024094	NM_024094	79075	3.43	2.54E-04
KIF2C	211519_s_at	AY026505	NM_006845	11004	3.42	9.85E-05
SLC43A3	210692_s_at	BC003163	NM_014096 NM_017611 NM_199329	29015	3.41	1.35E-04
KIAA0101	202503_s_at	NM_014736	NM_014736	9768	3.40	1.33E-05
FBP1	209696_at	D26054	NM_000507	2203	3.40	3.15E-04
AA224205	238075_at	AA224205	---	---	3.39	1.33E-05
ADAMTS9	226814_at	AI431730	NM_020249 NM_182920 NM_182921	56999	3.38	2.69E-06
FLJ10706	220840_s_at	NM_018186	NM_018186	55732	3.38	4.66E-05
HCAP-G	218662_s_at	NM_022346	NM_022346	64151	3.37	3.87E-06
SLC7A2	225516_at	AA876372	NM_00100853 9 NM_003046	6542	3.37	1.80E-08
BF477980	242775_at	BF477980	---	---	3.36	1.18E-04
UBE2C	202954_at	NM_007019	NM_007019 NM_181799 NM_181800 NM_181801 NM_181802 NM_181803	11065	3.36	1.60E-06
CSRP2	207030_s_at	NM_001321	NM_001321	1466	3.35	9.35E-07

PRC1	218009_s_at	NM_003981	NM_003981 NM_199413 NM_199414	9055	3.35	2.53E-06
GNG12	222834_s_at	N32508	NM_018841	55970	3.34	4.89E-06
AB040957	231855_at	AB040957	---	---	3.34	2.91E-07
DAZ1 DAZ3 DAZ2 DAZ4	208281_x_at	NM_020364	NM_00100537 5 NM_00100578 5 NM_00100578 6 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	3.34	4.52E-03
MCM5	216237_s_at	AA807529	NM_006739	4174	3.34	1.01E-04
CCNA2	203418_at	NM_001237	NM_001237	890	3.34	2.17E-04
FLJ20105	219650_at	NM_017669	NM_00100995 4 NM_017669	54821	3.34	1.12E-05
BF108778	235363_at	BF108778	---	---	3.33	1.13E-04
BM039	222118_at	AK023669	NM_018455	55839	3.33	1.47E-07
SDC2	212154_at	AI380298	NM_002998	6383	3.33	5.56E-04
LOC440928	235147_at	R56118	XM_498917	440928	3.33	1.32E-03
LOC146909	222039_at	AA292789	XM_085634	146909	3.31	2.57E-05
RAD51AP1	204146_at	BE966146	NM_006479	10635	3.31	4.07E-06
SMC6L1	218781_at	NM_024624	NM_024624	79677	3.30	2.52E-08
ZWINT	204026_s_at	NM_007057	NM_00100541 3 NM_00100541 4 NM_007057 NM_032997	11130	3.29	7.56E-06
KIAA1754	225582_at	AA425726	NM_033397	85450	3.29	3.22E-06
CCNB1	228729_at	N90191	NM_031966	891	3.29	3.59E-06
PRAME	204086_at	NM_006115	NM_006115 NM_206953 NM_206954 NM_206955 NM_206956	23532	3.28	3.84E-04
BRCA1	204531_s_at	NM_007295	NM_007294 NM_007295 NM_007296 NM_007297 NM_007298 NM_007299 NM_007300 NM_007301 NM_007302 NM_007303 NM_007304 NM_007305 NM_007306	672	3.28	2.73E-04
CNTN1	227209_at	AI091445	NM_001843 NM_175038	1272	3.27	3.23E-05
SLC43A3	213113_s_at	AI630178	NM_014096 NM_017611 NM_199329	29015	3.27	1.59E-06

TIMP3	201147_s_at	BF347089	NM_000362	7078	3.27	2.90E-04
LTB4DH	231897_at	AL135787	NM_012212	22949	3.27	4.25E-05
FLJ22624	219544_at	NM_024808	NM_024808	79866	3.27	4.96E-04
GNAI1	227692_at	AU153866	NM_002069	2770	3.26	1.36E-05
BC035780	1560258_a_at	BC035780	---	---	3.26	1.57E-07
CCNB2	202705_at	NM_004701	NM_004701	9133	3.24	2.06E-06
PTTG1	203554_x_at	NM_004219	NM_004219	9232	3.24	8.78E-06
LOC157570	235588_at	AA740849	XM_088331	157570	3.23	2.41E-04
BG391951	236852_at	BG391951	---	---	3.22	1.77E-04
MLF1IP	218883_s_at	NM_024629	NM_024629	79682	3.21	1.31E-05
MGC24665	226456_at	AW138157	NM_152308	116028	3.21	6.88E-05
GNAI1	209576_at	AL049933	NM_002069	2770	3.21	1.53E-06
PLK4	204886_at	AL043646	NM_014264	10733	3.20	2.80E-04
GPSM2	205240_at	NM_013296	NM_013296	29899	3.20	9.04E-07
TROAP	204649_at	NM_005480	NM_005480	10024	3.19	2.23E-05
SYNPO2	227662_at	AA541622	NM_133477	171024	3.19	1.95E-03
C14orf106	206500_s_at	NM_018353	NM_018353	55320	3.19	5.08E-04
HCAP-G	218663_at	NM_022346	NM_022346	64151	3.19	1.36E-04
FLJ10719	213007_at	W74442	NM_018193	55215	3.18	1.31E-05
LTB4DH	228824_s_at	BE566894	NM_012212	22949	3.17	2.71E-05
TRIM36	219736_at	NM_018700	NM_018700	55521	3.17	4.38E-05
HGF	209960_at	X16323	NM_000601	3082	3.17	6.34E-04
			NM_00101093 1 NM_00101093 2 NM_00101093 3 NM_00101093 4			
CHAF1A	203976_s_at	NM_005483	NM_005483	10036	3.17	3.20E-04
AK022040	233445_at	AK022040	---	---	3.17	1.50E-06
AA938184	236312_at	AA938184	---	---	3.17	1.06E-04
CTSL2	210074_at	AF070448	NM_001333	1515	3.17	5.51E-04
FKSG14	222848_at	BC005400	NM_022145	64105	3.16	3.35E-06
EME1	234465_at	AK021607	NM_152463	146956	3.16	8.50E-06
TCTE1L	203303_at	NM_006520	NM_006520	6990	3.15	2.23E-04
SBLF	213413_at	BG434174	NM_006873	11037	3.15	3.72E-03
MCM6	201930_at	NM_005915	NM_005915	4175	3.15	3.87E-06
LOC402524	242206_at	AW590588	XM_379850	402524	3.14	1.94E-07
INCENP	242787_at	AI924134	NM_020238	3619	3.14	7.83E-06
LTB4DH	228825_at	BE566894	NM_012212	22949	3.12	1.25E-04
FNDC5	226096_at	AI760132	NM_153756	252995	3.12	3.00E-04
P2RY5	218589_at	NM_005767	NM_005767	10161	3.12	2.25E-03
GABRA5	206456_at	NM_000810	NM_000810	2558	3.11	3.01E-04
E2F1	204947_at	NM_005225	NM_005225	1869	3.11	1.27E-05
E2F7	228033_at	AI341146	NM_203394	144455	3.11	9.10E-05
EDG2	204036_at	AW269335	NM_001401 NM_057159	1902	3.11	9.74E-05
RFC5	203210_s_at	NM_007370	NM_007370 NM_181578	5985	3.09	2.74E-05
BNC2	220272_at	NM_017637	NM_017637	54796	3.09	7.83E-06
DEPDC1B	226980_at	AK001166	NM_018369	55789	3.09	1.82E-06
PPAP2B	209355_s_at	AB000889	NM_003713	8613	3.09	1.33E-03
RBL1	1555004_a_at	BC032247	NM_177414 NM_002895 NM_183404	5933	3.09	1.25E-05
LOC132671	229331_at	AI559300	NM_145263	132671	3.09	2.77E-04

AI656180	242447_at	AI656180	---	---	3.09	6.33E-05
KCNG3	1552897_a_at	NM_133329	NM_133329 NM_172344	170850	3.09	1.62E-04
EFNB2	202668_at	BF001670	NM_004093	1948	3.08	7.07E-04
TACC3	218308_at	NM_006342	NM_006342	10460	3.07	1.21E-05
SHOX2	210135_s_at	AF022654	NM_003030 NM_006884	6474	3.07	2.01E-03
TYMS	1554696_s_at	AB077208	NM_001071	7298	3.07	2.09E-06
CDK2	211804_s_at	AB012305	NM_001798 NM_052827	1017	3.06	3.25E-06
MGC33887	213644_at	AI979276	NM_145036	201134	3.06	7.13E-03
BVES	228783_at	AA993518	NM_007073 NM_147147	11149	3.06	3.06E-04
C20orf172	219512_at	NM_024918	NM_024918	79980	3.05	1.03E-05
OSBPL3	209626_s_at	AI202969	NM_015550 NM_145320 NM_145321 NM_145322 NM_145323 NM_145324	26031	3.05	2.81E-04
CXCR4	211919_s_at	AF348491	NM_00100854 0 NM_003467	7852	3.05	2.72E-03
GAS2L3	235709_at	H37811	NM_174942	283431	3.04	8.83E-03
CENPJ	220885_s_at	NM_018451	NM_018451	55835	3.04	5.23E-04
TIMP3	201149_s_at	U67195	NM_000362	7078	3.03	3.76E-05
AW271106	229490_s_at	AW271106	---	---	3.03	3.24E-06
SPAG5	203145_at	NM_006461	NM_006461	10615	3.03	2.06E-06
CXCR4	217028_at	AJ224869	NM_00100854 0 NM_003467	7852	3.03	8.98E-04
PRIMA1	230087_at	AI823645	NM_178004 NM_178013	145270	3.02	1.47E-05
DDA3	201896_s_at	BC001425	NM_00100529 0 NM_032636	84722	3.02	5.61E-06
DAZ1 DAZ3 DAZ2 DAZ4	216922_x_at	AF271088	NM_00100537 5 NM_00100578 5 NM_00100578 6 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	3.02	8.33E-03
MYRIP	214156_at	AL050090	NM_015460	25924	3.02	2.47E-05
KITLG	226534_at	AI446414	NM_000899 NM_003994	4254	3.01	4.26E-04
GAS2L3	238756_at	AI860012	NM_174942	283431	3.00	7.34E-05
NRXN1	228547_at	BF509242	NM_004801 NM_138735	9378	3.00	1.59E-03
ORC6L	219105_x_at	NM_014321	NM_014321	23594	3.00	2.00E-07
CHEK1	205393_s_at	NM_001274	NM_001274	1111	2.99	6.29E-05
FLJ20641	220060_s_at	NM_017915	NM_017915	55010	2.98	3.74E-07
SLITRK5	214930_at	AW449813	NM_015567	26050	2.98	2.02E-05
BNC2	233036_at	AU146418	NM_017637	54796	2.98	6.17E-03

SYNPO2	225895_at	AI634580	NM_133477	171024	2.98	8.59E-04
UCP2	208998_at	U94592	NM_003355	7351	2.97	3.77E-05
ETV1	217061_s_at	AC004857	NM_004956	2115	2.96	6.17E-07
MNS1	219703_at	NM_018365	NM_018365	55329	2.96	3.49E-04
MGC11266	226118_at	BE326728	NM_024322	79172	2.95	4.33E-06
AW075105	228868_x_at	AW075105	---	---	2.95	2.52E-05
LOC91431	228859_at	BF056790	NM_138698	91431	2.95	1.95E-05
OSAP	223734_at	AF329088	NM_032623	84709	2.95	4.92E-04
ARHGAP11A	204492_at	NM_014783	NM_014783 NM_199357	9824	2.95	3.64E-08
C6orf173	226936_at	BG492359	---	---	2.95	2.93E-07
HSPA2	211538_s_at	U56725	NM_021979	3306	2.95	2.25E-03
MYO6	203216_s_at	NM_004999	NM_004999	4646	2.94	2.66E-07
MAOA	204389_at	NM_000240	NM_000240	4128	2.94	4.60E-06
ZNF521	226676_at	AK021452	NM_015461	25925	2.94	8.51E-04
ASPM	232238_at	AK001380	NM_018136	259266	2.94	4.78E-04
ENC1	201340_s_at	AF010314	NM_003633	8507	2.94	2.73E-05
KDELC2	225128_at	AL548941	NM_153705	143888	2.94	4.64E-05
SYNPO2	225894_at	AL589603	NM_133477	171024	2.93	8.98E-05
ENC1	201341_at	NM_003633	NM_003633	8507	2.93	2.30E-05
LOC441157	1558796_a_at	AL833240	XM_499037	441157	2.93	2.03E-03
SDC2	212158_at	AL577322	NM_002998	6383	2.92	7.40E-07
TROAP	1568596_a_at	AI199355	NM_005480	10024	2.92	8.12E-06
LOC253012	242601_at	AA600175	NM_198151	253012	2.92	1.02E-03
MGC24103	232568_at	AU145658	---	158295	2.91	1.01E-02
TFDP1	242939_at	AI950069	NM_007111	7027	2.91	4.17E-05
LOC441157	1558795_at	AL833240	XM_499037	441157	2.90	7.52E-07
C22orf18	218741_at	NM_024053	NM_00100287 6 NM_024053	79019	2.90	2.43E-05
TYMS	202589_at	NM_001071	NM_001071	7298	2.89	1.61E-06
CXCR4	209201_x_at	L01639	NM_00100854 0 NM_003467	7852	2.88	5.99E-03
MGC45871	226905_at	BG036514	NM_182705	359845	2.88	3.75E-04
KNTC1	206316_s_at	NM_014708	NM_014708	9735	2.87	5.79E-05
PCNA	201202_at	NM_002592	NM_002592 NM_182649	5111	2.87	8.09E-06
NEUROD4	221318_at	NM_021191	NM_021191	58158	2.86	1.12E-04
AF15Q14	1552680_a_at	NM_020380	NM_020380 NM_144508 NM_170589	57082	2.85	1.73E-04
AA699443	241838_at	AA699443	---	---	2.85	9.18E-05
CCNE1	213523_at	AI671049	NM_001238 NM_057182	898	2.85	3.52E-04
ST8SIA4	230836_at	AI422986	NM_005668 NM_175052	7903	2.85	4.72E-06
MGC33926	229302_at	AA058832	NM_152390	130733	2.84	2.64E-05
DDB2	203409_at	NM_000107	NM_000107	1643	2.84	2.16E-03
TWIST1	213943_at	X99268	NM_000474	7291	2.83	1.05E-05
DHRS6	218285_s_at	NM_020139	NM_020139	56898	2.82	4.65E-05
DHFR	202533_s_at	BC003584	NM_000791	1719	2.82	4.52E-05
FLJ11029	228273_at	BG165011	NM_018304	55771	2.82	6.55E-07
RNASEH2A	203022_at	NM_006397	NM_006397	10535	2.82	9.96E-07
DCLRE1B	222889_at	AI703304	NM_022836	64858	2.81	7.59E-05
C13orf3	227165_at	AI829603	NM_145061	221150	2.81	9.72E-05

RBPMS	209487_at	D84109	NM_001008710 NM_001008711 NM_001008712 NM_006867	11030	2.81	2.78E-06
ETV1	217053_x_at	X87175	NM_004956	2115	2.80	4.43E-07
CHRNA7	210123_s_at	U62436	NM_000746	1139	2.80	1.15E-04
CHRFAM7A			NM_139320 NM_148911	89832		
MARLIN1	238600_at	AW157571	NM_144720	152789	2.80	1.18E-03
PLCL2	213309_at	AL117515	NM_015184	23228	2.80	1.93E-04
Cep152	238535_at	AW955956	NM_014985	22995	2.79	8.14E-06
RAB32	204214_s_at	NM_006834	NM_006834	10981	2.79	1.16E-03
MAD2L1	1554768_a_at	AF394735	NM_002358	4085	2.79	3.08E-06
ITGA6	215177_s_at	AV733308	NM_000210	3655	2.79	2.99E-04
ENDOG	204824_at	NM_004435	NM_004435	2021	2.78	3.20E-04
TFDP2	203588_s_at	BG034328	NM_006286	7029	2.78	7.51E-05
BTG3	1556213_a_at	BC028229	NM_006806	10950	2.78	5.93E-04
KIF2C	209408_at	U63743	NM_006845	11004	2.77	6.84E-05
CD9	201005_at	NM_001769	NM_001769	928	2.77	9.74E-06
TMPO	209754_s_at	AF113682	NM_003276	7112	2.77	9.71E-06
CDC25B	201853_s_at	NM_021873	NM_004358 NM_021872 NM_021873 NM_021874 NM_212530	994	2.77	2.17E-06
TMPO	209753_s_at	BG391171	NM_003276	7112	2.76	7.36E-06
AURKB	239219_at	N55457	NM_004217	9212	2.76	3.82E-04
TIFA	226117_at	AA195074	NM_052864	92610	2.75	2.55E-05
CDCA7	224428_s_at	AY029179	NM_031942 NM_145810	83879	2.75	2.27E-06
CDT1	209832_s_at	AF321125	NM_030928	81620	2.75	4.06E-04
HS3ST2	219697_at	NM_006043	NM_006043	9956	2.75	9.91E-05
C18orf54	244324_at	BG283921	NM_173529	162681	2.75	1.19E-05
PTPRM	1555579_s_at	BC029442	NM_002845	5797	2.74	5.55E-05
PLK1	202240_at	NM_005030	NM_005030	5347	2.74	4.99E-06
FBLN1	202994_s_at	Z95331	NM_001996 NM_006485 NM_006486 NM_006487	2192	2.74	5.20E-04
RAD54B	219494_at	NM_012415	NM_012415 NM_134434	25788	2.74	3.14E-04
C14orf31	225464_at	N30138	NM_152330	122786	2.74	6.69E-06
EDG3	228176_at	AA534817	NM_005226	1903	2.73	2.38E-04
UBL3	243072_at	AI733828	NM_007106	5412	2.72	2.94E-04
ASCL1	213768_s_at	AW950513	NM_004316	429	2.71	5.62E-05
RHEBL1	1570253_a_at	BC014155	NM_144593	121268	2.70	1.21E-05
FLJ40773	1563933_a_at	AK091691	NM_152666	200150	2.70	3.08E-04
ALCAM	240655_at	BE502785	NM_001627	214	2.70	9.75E-04
BRCA2	214727_at	X95152	NM_000059	675	2.70	4.89E-03
SCAP1	1560861_at	BG210619	NM_003726	8631	2.70	9.27E-05
CCNA2	213226_at	AI346350	NM_001237	890	2.69	3.29E-05
PKMYT1	204267_x_at	NM_004203	NM_004203 NM_182687	9088	2.69	2.26E-05
VRK1	203856_at	NM_003384	NM_003384	7443	2.69	6.68E-06
ARHGEF3	218501_at	NM_019555	NM_019555	50650	2.69	2.18E-04

ASPM	239002_at	AA748494	NM_018136	259266	2.69	7.18E-03
H17657	241444_at	H17657	---	---	2.69	3.92E-04
TNFAIP8	210260_s_at	BC005352	NM_014350	25816	2.68	5.03E-05
Cep72	219531_at	NM_018140	NM_018140	55722	2.68	5.02E-05
FGFR2	203638_s_at	NM_022969	NM_000141 NM_022969 NM_022970 NM_022971 NM_022972 NM_022973 NM_022974 NM_022975 NM_022976 NM_023028 NM_023029 NM_023030 NM_023031	2263	2.68	4.60E-05
CSRP2	211126_s_at	U46006	NM_001321	1466	2.68	6.18E-07
FAM49A	208092_s_at	NM_030797	NM_030797	81553	2.68	1.51E-03
CHAF1A	214426_x_at	BF062223	NM_005483	10036	2.67	2.14E-07
LOC387816	241360_at	BG413368	XM_370664	387816	2.67	1.92E-05
MTB	219588_s_at	NM_017760	NM_017760	54892	2.67	4.22E-05
EML1	204797_s_at	NM_004434	NM_00100870 7 NM_004434	2009	2.67	3.68E-03
MAD2L1	203362_s_at	NM_002358	NM_002358	4085	2.67	1.55E-06
RBL1	205296_at	AL365505	NM_002895 NM_183404	5933	2.66	2.73E-05
SYNPO2	225721_at	AI658662	NM_133477	171024	2.66	4.01E-04
SYNE2	202761_s_at	NM_015180	NM_015180 NM_182910 NM_182912 NM_182913 NM_182914	23224	2.66	1.44E-06
RASSF2	203185_at	NM_014737	NM_014737 NM_170773 NM_170774	9770	2.65	1.34E-04
AI001880	242723_at	AI001880	---	---	2.65	9.66E-04
PTPRK	203038_at	NM_002844	NM_002844	5796	2.65	5.22E-06
ETV1	206501_x_at	NM_004956	NM_004956	2115	2.65	2.26E-07
WDHD1	216228_s_at	AK001538	NM_00100839 6 NM_007086	11169	2.64	9.95E-04
ZNF505	1569241_a_at	BC020837	NM_00100412 6 NM_031218	81931	2.64	6.40E-03
SESN3	235683_at	BF685808	NM_144665	143686	2.63	1.07E-03
BLM	205733_at	NM_000057	NM_000057	641	2.63	3.91E-03
MYO6	210480_s_at	U90236	NM_004999	4646	2.62	1.11E-06
SIL	205339_at	NM_003035	NM_003035	6491	2.61	1.15E-04
CENPH	231772_x_at	AL572471	NM_022909	64946	2.60	1.04E-05
GUCY1B3	211555_s_at	AF020340	NM_000857	2983	2.60	8.17E-05
MLF1IP	229304_s_at	AA460299	NM_024629	79682	2.60	9.56E-06
ASCL1	209987_s_at	BC002341	NM_004316	429	2.60	2.04E-04
BF111626	228559_at	BF111626	---	---	2.60	2.36E-05
GAJ	223700_at	AY028916	NM_032117	84057	2.60	2.48E-05
LOC494143	235117_at	AI191897	NM_00100870[illegible]	494143	2.59	9.30E-04
BG252802	229641_at	BG252802	---	---	2.58	2.53E-05

AA406603	230002_at	AA406603	---	---	2.58	3.50E-06
AW024890	229942_at	AW024890	---	---	2.58	9.80E-04
GPR10	231805_at	AL563031	NM_004248	2834	2.58	2.33E-04
Cep152	215170_s_at	AB020719	NM_014985	22995	2.58	6.05E-06
EB-1	227441_s_at	AW005572	NM_020140	56899	2.57	1.57E-03
			NM_152788			
			NM_181670			
TLE3	206472_s_at	NM_005078	NM_005078	7090	2.57	3.99E-04
WEE1	215711_s_at	AJ277546	NM_003390	7465	2.56	8.25E-05
BM039	219555_s_at	NM_018455	NM_018455	55839	2.56	9.17E-08
TMSNB	205347_s_at	NM_021992	NM_021992	11013	2.56	1.86E-04
KIAA1524	1553810_a_at	NM_020890	NM_020890	57650	2.55	1.25E-06
ACATE2	221641_s_at	AF241787	NM_012332	23597	2.54	6.19E-04
AF15Q14	228323_at	BF248364	NM_020380	57082	2.54	2.09E-04
			NM_144508			
			NM_170589			
CDC7	204510_at	NM_003503	NM_003503	8317	2.54	7.24E-04
PTPRM	203329_at	NM_002845	NM_002845	5797	2.53	3.83E-04
PLEKHE1	212719_at	AB011178	NM_194449	23239	2.52	1.61E-05
MYO6	203215_s_at	AA877789	NM_004999	4646	2.51	2.63E-04
AL035461	231827_at	AL035461	---	---	2.51	3.24E-04
BF509125	232198_at	BF509125	---	---	2.51	3.41E-03
TIMP3	201150_s_at	NM_000362	NM_000362	7078	2.51	1.89E-05
NRXN1	209915_s_at	AB035356	NM_004801	9378	2.51	9.30E-04
			NM_138735			
LOC221810	221911_at	BE881590	---	221810	2.51	4.94E-06
SLC16A10	222939_s_at	N30257	NM_018593	117247	2.51	2.79E-04
PPAP2B	212230_at	AV725664	NM_003713	8613	2.50	1.17E-04
			NM_177414			
C14orf143	214264_s_at	AI656610	NM_145231	90141	2.50	1.62E-05
FLJ11259	218627_at	NM_018370	NM_018370	55332	2.50	3.56E-04
FAM46C	226811_at	AL046017	NM_017709	54855	2.50	6.18E-03
CLSTN2	219414_at	NM_022131	NM_022131	64084	2.50	2.54E-04
OVOS	228245_s_at	AW594320	XM_495907	408186	2.49	1.90E-04
LOC440080			XM_495909	440080		
MCM8	224320_s_at	BC005170	NM_032485	84515	2.49	1.61E-05
			NM_182802			
ARG99	226322_at	BF109231	NM_031920	83857	2.49	6.26E-04
			NM_175861			
SUV39H1	218619_s_at	NM_003173	NM_003173	6839	2.49	1.39E-03
BG109249	1558750_a_at	BG109249	---	---	2.48	6.02E-05
CKAP2	218252_at	NM_018204	NM_018204	26586	2.48	9.73E-07
MGC17791	227420_at	BF338045	NM_152362	126282	2.48	2.52E-04
AK025909	233814_at	AK025909	---	---	2.48	3.30E-04
MGC20533	226308_at	AA099118	NM_00101169	93323	2.48	8.23E-06
			9			
			NM_033417			
GATM	216733_s_at	X86401	NM_001482	2628	2.48	4.09E-04
TPBG	203476_at	NM_006670	NM_006670	7162	2.47	4.81E-05
PTER	222798_at	BF112019	NM_00100148	9317	2.47	8.26E-04
			4			
			NM_030664			

FGFR2	208228_s_at	M87771	NM_000141 NM_022969 NM_022970 NM_022971 NM_022972 NM_022973 NM_022974 NM_022975 NM_022976 NM_023028 NM_023029 NM_023030 NM_023031	2263	2.47	2.00E-05
SMC4L1	201663_s_at	NM_005496	NM_001002799 NM_001002800 NM_005496	10051	2.47	1.52E-06
AW963185	241700_at	AW963185	---	---	2.46	2.26E-04
RFC3	204128_s_at	NM_002915	NM_002915 NM_181558	5983	2.46	3.05E-05
GLDC	204836_at	NM_000170	NM_000170	2731	2.46	4.48E-04
BF432331	242519_at	BF432331	---	---	2.46	1.67E-04
AW151660	239744_at	AW151660	---	---	2.46	4.79E-05
HRH3	220447_at	NM_007232	NM_007232	11255	2.46	1.62E-03
VAV3	218807_at	NM_006113	NM_006113	10451	2.46	6.79E-08
MCM6	238977_at	R54683	NM_005915	4175	2.45	1.80E-04
KIF22	202183_s_at	NM_007317	NM_007317	3835	2.44	1.23E-04
HSPC150	223229_at	AB032931	NM_014176	29089	2.44	1.16E-05
QKI	212636_at	AL031781	NM_006775 NM_206853 NM_206854 NM_206855	9444	2.43	4.26E-03
MGC21654	1556429_a_at	BC026969	NM_145647	93594	2.43	3.09E-06
ASCL1	209988_s_at	BC001638	NM_004316	429	2.43	1.00E-04
FLJ37034	229622_at	H16258	---	151176	2.42	4.51E-03
FSHPRH1	207590_s_at	NM_006733	NM_006733	2491	2.42	3.10E-03
PPP1R3C	204284_at	N26005	NM_005398	5507	2.42	2.95E-04
MASTL	228468_at	BF108964	NM_032844	84930	2.42	1.20E-05
DPYSL3	201430_s_at	W72516	NM_001387	1809	2.41	3.61E-06
AW052186	239942_at	AW052186	---	---	2.41	9.52E-03
RAM2	225081_s_at	AK022955	NM_018719	55536	2.40	3.44E-03
PCSK1	205825_at	NM_000439	NM_000439	5122	2.40	1.58E-03
TMPO	203432_at	AW272611	NM_003276	7112	2.40	5.20E-05
CUGBP2	202157_s_at	U69546	NM_006561	10659	2.40	6.84E-03
C19orf14	215218_s_at	AC004144	NM_173636	284403	2.38	1.41E-03
TRIM68	219405_at	NM_018073	NM_018073	55128	2.38	3.90E-03
TEX15	221448_s_at	NM_031271	NM_031271	56154	2.38	6.78E-03
AU156421	233413_at	AU156421	---	---	2.37	1.88E-03
CDKN2D	210240_s_at	U20498	NM_001800 NM_079421	1032	2.36	8.95E-04
PTGFRN	224937_at	BF311866	NM_020440	5738	2.36	4.21E-05
DERA	218102_at	NM_015954	NM_015954	51071	2.36	4.21E-04
VAV3	218806_s_at	AF118887	NM_006113	10451	2.35	2.50E-04
RASEF	1553986_at	BC023566	NM_152573	158158	2.34	4.65E-04
TNFSF13B	223502_s_at	AF134715	NM_006573	10673	2.34	3.38E-03
STN2	235852_at	BE379761	NM_033104	85439	2.34	2.91E-03
SLC4A11	223748_at	AF336127	NM_032034	83959	2.34	7.89E-03

C20orf72	225890_at	AI678096	NM_052865	92667	2.33	7.53E-05
CPVL	208146_s_at	NM_031311	NM_019029 NM_031311	54504	2.33	1.12E-03
HMGB2	208808_s_at	BC000903	NM_002129	3148	2.33	5.57E-07
FLJ13215	220466_at	NM_025004	NM_025004	80071	2.32	1.61E-04
PLK4	211088_s_at	Z25433	NM_014264	10733	2.31	1.24E-05
MRC2	37408_at	AB014609	NM_006039	9902	2.31	4.86E-03
ZNF488	229901_at	AI056483	NM_153034	118738	2.31	3.12E-03
TM4SF7	209264_s_at	AF054841	NM_003271	7106	2.31	1.36E-04
CCNF	204827_s_at	U17105	NM_001761	899	2.31	1.47E-04
RECQL4	1553015_a_at	NM_004260	NM_004260	9401	2.31	2.02E-04
CDR2	209501_at	AL582414	NM_001802	1039	2.31	1.41E-05
HGF	210997_at	M77227	NM_000601 NM_001010931 NM_001010932 NM_001010933 NM_001010934	3082	2.30	3.55E-03
WHSC1	209052_s_at	BF111870	NM_007331 NM_014919 NM_133330 NM_133331 NM_133332 NM_133333 NM_133334 NM_133335 NM_133336	7468	2.30	2.39E-03
CDCA7	230060_at	AI277642	NM_031942 NM_145810	83879	2.30	9.28E-03
SNAI2	213139_at	AI572079	NM_003068	6591	2.30	9.13E-04
NM_004260	213520_at	NM_004260	---	---	2.30	1.47E-04
DIRAS3	215506_s_at	AK021882	NM_004675	9077	2.30	2.88E-03
FLJ32363	229886_at	AA502768	NM_198566	375444	2.30	4.42E-04
KCNJ4	208359_s_at	NM_004981	NM_004981 NM_152868	3761	2.30	6.70E-04
PLCXD2	235230_at	AW170015	NM_153268	257068	2.29	2.14E-03
3ALNAC4S-6S'	203066_at	NM_014863	NM_015892	51363	2.29	8.81E-05
TREX2	207891_s_at	NM_017518	---	11219	2.29	6.18E-05
DHFR	202534_x_at	NM_000791	NM_000791	1719	2.29	3.70E-05
dJ383J4.3	232065_x_at	N29457	NM_033319	91687	2.29	1.75E-05
ITGA9	227297_at	AI479176	NM_002207	3680	2.29	1.72E-03
NUP43	238474_at	BF978064	NM_024647 NM_198887	348995	2.28	1.07E-03
SSB4	229929_at	AL563476	NM_080862	92369	2.28	5.85E-04
GNG12	212294_at	BG111761	NM_018841	55970	2.28	2.93E-05
POLD1	203422_at	NM_002691	NM_002691	5424	2.27	8.87E-04
SHMT1	209980_s_at	L23928	NM_004169 NM_148918	6470	2.27	6.54E-05
DMN	212730_at	AK026420	NM_015286 NM_145728	23336	2.27	9.70E-05
EB-1	227439_at	AI806510	NM_020140 NM_152788 NM_181670	56899	2.27	3.41E-05
SGOL1	231938_at	AK024292	NM_138484	151648	2.26	2.13E-07

ARG99	226931_at	AU151239	NM_031920 NM_175861	83857	2.26	3.38E-04
U79256	37577_at	U79256	---	---	2.26	3.97E-05
HS6ST2	1552766_at	NM_147174	NM_147174 NM_147175	90161	2.26	2.22E-04
AW305300	238962_at	AW305300	---	---	2.25	3.89E-05
CCNF	204826_at	NM_001761	NM_001761	899	2.25	6.97E-06
CNAP1	201774_s_at	AK022511	NM_014865	9918	2.25	6.86E-05
AA019836	241733_at	AA019836	---	---	2.25	3.30E-04
SPAG6	210032_s_at	AI651156	NM_012443 NM_172242	9576	2.24	1.37E-03
PEX13	1558163_at	BC040953	NM_002618	5194	2.24	3.22E-04
AW953794	230968_at	AW953794	---	---	2.24	1.52E-03
TBPIP	213951_s_at	BE964655	NM_013290 NM_016556	29893	2.24	3.20E-05
SESN3	235150_at	AW376955	NM_144665	143686	2.24	4.11E-05
JPH1	229139_at	AI202201	NM_020647	56704	2.24	3.22E-03
CTSH	202295_s_at	NM_004390	NM_004390 NM_148979	1512	2.24	4.20E-03
NRG3	229233_at	H05240	NM_001010848	10718	2.24	1.44E-03
DPYSL3	201431_s_at	NM_001387	NM_001387	1809	2.23	2.10E-06
RACGAP1	222077_s_at	AU153848	NM_013277	29127	2.23	3.69E-06
BF222929	242346_x_at	BF222929	---	---	2.23	1.34E-03
FBXO5	218875_s_at	NM_012177	NM_012177	26271	2.23	3.85E-05
LOC143381	227550_at	AW242720	---	143381	2.23	7.49E-03
KIAA0056	212789_at	AI796581	NM_015261	23310	2.22	1.47E-05
GSG2	223759_s_at	AB039834	NM_031965	83903	2.22	7.72E-05
ZNF537	223392_s_at	BF510588	NM_020856	57616	2.22	4.48E-06
ADAMTS9	1554697_at	AF488803	NM_020249 NM_182920 NM_182921	56999	2.21	5.03E-04
CHAF1A	203975_s_at	BF000239	NM_005483	10036	2.21	6.39E-04
TEAD4	41037_at	U63824	NM_003213 NM_201441 NM_201443	7004	2.21	6.00E-03
PTER	218967_s_at	NM_030664	NM_001001484 NM_030664	9317	2.21	8.86E-03
ARHGAP20	228368_at	AI936560	NM_020809	57569	2.20	2.69E-04
GMNN	218350_s_at	NM_015895	NM_015895	51053	2.20	1.84E-05
RAD18	224200_s_at	AB035274	NM_020165	56852	2.20	8.40E-08
CCNE2	211814_s_at	AF112857	NM_004702 NM_057735 NM_057749	9134	2.20	8.82E-03
RAD18	223417_at	AF169796	NM_020165	56852	2.19	2.68E-06
HGF	210755_at	U46010	NM_000601 NM_001010931 NM_001010932 NM_001010933 NM_001010934	3082	2.19	4.99E-03
ALCAM	1569362_at	BC041127	NM_001627	214	2.19	3.28E-04
RFC3	204127_at	BC000149	NM_002915 NM_181558	5983	2.19	1.51E-04
KIF22	216969_s_at	AC002301	NM_007317	3835	2.18	7.12E-04

SALL4	229661_at	NM_020436	NM_020436	57167	2.18	3.50E-03
BNC2	235723_at	AA843242	NM_017637	54796	2.18	6.54E-03
VMP	239293_at	R38624	NM_080723	140767	2.18	7.44E-03
AU154486	213253_at	AU154486	---	---	2.18	1.78E-04
EBF	229487_at	W73890	NM_024007	1879	2.17	1.69E-03
CDC25A	204696_s_at	NM_001789	NM_001789 NM_201567	993	2.17	7.52E-04
FLJ23091	221958_s_at	AA775681	NM_00100229 2 NM_024911	79971	2.17	1.84E-06
MGC33846	231430_at	AW205640	NM_175885	220382	2.17	4.57E-05
BG028209	230521_at	BG028209	---	---	2.17	1.18E-04
FLJ20920	218844_at	NM_025149	NM_025149	80221	2.16	2.85E-04
AF131796	231916_at	AF131796	---	---	2.16	7.81E-05
RFC5	203209_at	BC001866	NM_007370	5985	2.16	3.16E-06
ATP2B4	212136_at	AW517686	NM_181578 NM_00100139 6 NM_001684	493	2.16	8.96E-03
AI653240	240247_at	AI653240	XM_496059	440261	2.16	3.06E-03
SNCAIP	219511_s_at	NM_005460	NM_005460	9627	2.15	6.77E-04
DHFR	48808_at	AI144299	NM_000791	1719	2.14	6.65E-05
KCNN2	220116_at	NM_021614	NM_021614 NM_170775	3781	2.14	8.09E-03
AI144156	238670_at	AI144156	---	---	2.14	4.87E-06
C15orf20	228252_at	AF108138	NM_025049	80119	2.14	6.49E-04
AA287223	238748_at	AA287223	---	---	2.13	7.76E-04
CKS1B	201897_s_at	NM_001826	NM_001826	1163	2.13	2.30E-06
RHEBL1	1553713_a_at	NM_144593	NM_144593	121268	2.13	1.90E-05
PVRL3	213325_at	AA129716	NM_015480	25945	2.13	3.03E-03
H2AFX	212525_s_at	AA760862	NM_002105	3014	2.13	2.86E-04
XRCC4	205071_x_at	AB017445	NM_003401 NM_022406 NM_022550	7518	2.13	6.87E-07
STK17A	202695_s_at	NM_004760	NM_004760	9263	2.12	4.96E-04
MCM2	202107_s_at	NM_004526	NM_004526	4171	2.12	7.65E-06
DHFR	202532_s_at	BC000192	NM_000791	1719	2.12	1.71E-04
INCENP	219769_at	NM_020238	NM_020238	3619	2.12	7.09E-03
CBLN1	205747_at	NM_004352	NM_004352	869	2.11	1.51E-03
ZNF545	1555793_a_at	AL834267	NM_133466	284406	2.11	5.39E-07
GGH	203560_at	NM_003878	NM_003878	8836	2.10	7.91E-06
FLJ23091	228950_s_at	AL534095	NM_00100229 2 NM_024911	79971	2.10	5.48E-05
TLE3	212769_at	AI567426	NM_005078	7090	2.09	4.14E-03
BE464799	214036_at	BE464799	---	---	2.09	9.39E-04
ANP32E	208103_s_at	NM_030920	NM_030920	81611	2.09	1.57E-05
NXPH1	232377_at	N62902	NM_152745	30010	2.08	8.71E-05
CDC25A	1555772_a_at	AY137580	NM_001789 NM_201567	993	2.08	1.17E-03
PPAP2B	212226_s_at	AA628586	NM_003713 NM_177414	8613	2.08	2.24E-03
FABP6	210445_at	U19869	NM_001445	2172	2.08	2.58E-03
T96523	237469_at	T96523	---	---	2.08	5.67E-03
KIAA0286	212621_at	AB006624	NM_015257	23306	2.08	1.03E-05
DTYMK	203270_at	NM_012145	NM_012145	1841	2.08	4.74E-05
NRM	225592_at	D81048	NM_007243	11270	2.08	4.53E-05
FLJ25067	243507_s_at	AV715251	NM_152504	149840	2.08	2.73E-04

ZNF215	220214_at	NM_013250	NM_013250	7762	2.08	6.34E-05
SEMA6A	220454_s_at	NM_020796	NM_020796	57556	2.07	4.90E-04
SEMA6A	223449_at	AF225425	NM_020796	57556	2.07	1.30E-03
PPIL5	235113_at	AA742244	NM_152329	122769	2.07	2.13E-05
			NM_203466			
			NM_203467			
SMC4L1	201664_at	AL136877	NM_001002799	10051	2.06	2.53E-06
			NM_001002800			
			NM_005496			
MPHOSPH1	205235_s_at	NM_016195	NM_016195	9585	2.06	3.99E-06
SKP2	210567_s_at	BC001441	NM_005983	6502	2.06	9.75E-05
			NM_032637			
ZNF537	223393_s_at	AL136805	NM_020856	57616	2.06	1.76E-04
PLEKHK1	230469_at	AW665138	NM_145307	219790	2.06	6.70E-04
ALCAM	201951_at	BF242905	NM_001627	214	2.06	1.36E-03
AI733341	240911_at	AI733341	---	---	2.06	4.21E-04
C14orf94	218383_at	NM_017815	NM_017815	54930	2.05	4.04E-05
HES6	226446_at	AW249678	NM_018645	55502	2.05	1.20E-04
EAF2	219551_at	NM_018456	NM_018456	55840	2.05	1.74E-04
GJA7	208460_at	NM_005497	NM_005497	10052	2.05	2.33E-03
PHF21B	1560091_a_at	AK092243	NM_138415	112885	2.04	6.65E-04
SEMA6A	225660_at	W92748	NM_020796	57556	2.04	7.90E-04
BF593263	228018_at	BF593263	---	---	2.03	4.92E-03
FLJ20647	218802_at	NM_017918	NM_017918	55013	2.03	1.70E-03
C20orf58	228017_s_at	BF593263	NM_152864	128414	2.03	1.08E-04
NET1	201830_s_at	NM_005863	NM_005863	10276	2.03	1.27E-03
FNDC5	226097_at	AI686488	NM_153756	252995	2.03	1.40E-03
HSDL2	209513_s_at	BC004331	NM_032303	84263	2.03	3.49E-05
NRXN1	209914_s_at	AW149405	NM_004801	9378	2.02	6.83E-03
			NM_138735			
CXorf34	205238_at	NM_024917	NM_024917	79979	2.02	5.46E-03
SYTL4	227703_s_at	AL391688	NM_080737	94121	2.02	3.25E-04
FGFR2	211401_s_at	AB030078	NM_000141	2263	2.01	3.92E-04
			NM_022969			
			NM_022970			
			NM_022971			
			NM_022972			
			NM_022973			
			NM_022974			
			NM_022975			
			NM_022976			
			NM_023028			
			NM_023029			
			NM_023030			
			NM_023031			
LOC440288	239792_at	N75594	XM_496075	440288	2.01	5.78E-04
TEX15	232760_at	AL133653	NM_031271	56154	2.00	9.86E-04
C6orf189	228875_at	AI540210	---	221303	2.00	1.16E-05
NSE1	229546_at	AI378035	NM_145175	151354	2.00	2.29E-04
KLHL13	227875_at	AB037730	NM_033495	90293	2.00	3.06E-06
ARHGAP24	230803_s_at	AI761947	NM_031305	83478	2.00	2.48E-04
RFC4	204023_at	NM_002916	NM_002916	5984	1.99	1.39E-05
			NM_181573			
TFDP2	203589_s_at	NM_006286	NM_006286	7029	1.99	1.73E-06
THBS4	204776_at	NM_003248	NM_003248	7060	1.99	4.42E-03
EMILIN3	228307_at	AL137580	NM_052846	90187	1.99	6.67E-03

SESN3	242906_at	BE787063	NM_144665	143686	1.99	2.42E-04
TLE4	216997_x_at	AL358975	NM_007005	7091	1.99	1.02E-02
MYH11	227249_at	AI857685	NM_002474	4629	1.99	3.80E-04
SMTN	209427_at	AF064238	NM_022844 NM_006932 NM_134269 NM_134270	6525	1.99	3.97E-03
FLJ11127	219694_at	NM_019018	NM_019018	54491	1.99	1.47E-03
AA156721	201952_at	AA156721	---	---	1.98	1.86E-04
LOC338773	227300_at	AL521682	NM_181724	338773	1.98	1.37E-03
SDC1	201286_at	Z48199	NM_00100694 6 NM_002997	6382	1.98	1.62E-04
LYN	202625_at	AI356412	NM_002350	4067	1.98	1.63E-05
TLE3	212770_at	AW873621	NM_005078	7090	1.98	1.14E-04
LOX	204298_s_at	NM_002317	NM_002317	4015	1.96	7.97E-04
KIAA0286	212619_at	AW205215	NM_015257	23306	1.96	2.89E-06
LHFPL2	212658_at	N66633	NM_005779	10184	1.96	3.29E-05
C11orf8	205413_at	NM_001584	NM_001584	744	1.96	1.73E-06
Cep70	1554489_a_at	BC016050	NM_024491	80321	1.96	2.05E-06
GPR155	231166_at	AI733474	NM_152529	151556	1.96	8.30E-05
POLA	204835_at	NM_016937	NM_016937	5422	1.96	2.08E-04
ZAK	225665_at	AI129320	NM_016653 NM_133646	51776	1.96	2.36E-06
)KFZP564K196	223170_at	AF132000	NM_015544	26022	1.96	2.12E-05
TPST2	204079_at	NM_003595	NM_00100856 6 NM_003595	8459	1.95	1.43E-03
TRIP	205598_at	NM_005879	NM_005879	10293	1.95	1.00E-05
TPTE	233879_at	AL137389	NM_013315 NM_199259 NM_199260 NM_199261	7179	1.94	3.31E-03
FLJ10408	220535_at	NM_018088	NM_018088	55138	1.94	9.00E-03
DNAPTP6	222154_s_at	AK002064	NM_015535	26010	1.94	2.39E-07
DKFZp434P055	232398_at	AK001064	NM_173466	91531	1.93	5.72E-03
FBXO5	234863_x_at	AK026197	NM_012177	26271	1.93	2.02E-05
STRA6	1569335_a_at	BC015881	NM_022369	64220	1.93	3.41E-04
PASK	213534_s_at	D50925	NM_015148	23178	1.93	6.33E-04
DRF1	238508_at	BG026951	NM_025104 NM_145663	80174	1.93	4.54E-04
R71596	229580_at	R71596	---	---	1.93	8.51E-03
TTF2	204407_at	AF080255	NM_003594	8458	1.93	3.06E-03
KIAA0635	206003_at	NM_014645	NM_025009	9662	1.93	1.09E-05
OLFML3	218162_at	NM_020190	NM_020190	56944	1.93	7.36E-03
GPSM2	221922_at	AW195581	NM_013296	29899	1.92	1.45E-05
AW022607	226806_s_at	AW022607	---	---	1.92	6.78E-03
OPN3	219032_x_at	NM_014322	NM_014322	23596	1.92	2.34E-03
DTYMK	1553983_at	AF258562	NM_012145	1841	1.92	1.06E-04
NY-REN-41	226287_at	AI458313	NM_080654	91057	1.92	1.77E-04
RGMA	223468_s_at	AL136826	NM_020211	56963	1.91	2.31E-03
EBF	232204_at	AF208502	NM_024007	1879	1.91	4.36E-05
C9orf140	225777_at	AW250904	NM_178448	89958	1.91	8.55E-05
HPCA	205454_at	BC001777	NM_002143	3208	1.91	2.09E-04
RFC2	1053_at	M87338	NM_002914 NM_181471	5982	1.91	2.20E-06
GUCY1B3	203817_at	W93728	NM_000857	2983	1.91	1.10E-03
SEZ6L	207873_x_at	NM_021115	NM_021115	23544	1.90	4.82E-07

CUGBP2	202156_s_at	N36839	NM_006561	10659	1.90	8.07E-04
AF15Q14	1552682_a_at	NM_144508	NM_020380 NM_144508 NM_170589	57082	1.90	2.18E-04
CENPJ	223513_at	AF139625	NM_018451	55835	1.90	1.64E-05
SEZ6L	211894_x_at	AB041736	NM_021115	23544	1.90	1.44E-05
SDC1	201287_s_at	NM_002997	NM_001006946 NM_002997	6382	1.90	6.29E-05
PLAUR	210845_s_at	U08839	NM_001005376 NM_001005377 NM_002659	5329	1.90	5.08E-03
CBLN2	242301_at	R60224	NM_182511	147381	1.90	4.25E-03
DCLRE1B	219490_s_at	NM_022836	NM_022836	64858	1.89	2.44E-04
ZFHX4	219779_at	NM_024721	NM_024721	79776	1.89	6.77E-05
CYBA	203028_s_at	NM_000101	NM_000101	1535	1.89	3.82E-05
DOCK10	219279_at	NM_017718	NM_014689	55619	1.88	9.11E-04
MCM3	201555_at	NM_002388	NM_002388	4172	1.88	1.06E-05
ECT2	234992_x_at	BG170335	NM_018098	1894	1.87	2.46E-04
ADA	204639_at	NM_000022	NM_000022	100	1.87	8.91E-04
SOX4	213668_s_at	AI989477	NM_003107	6659	1.87	2.08E-04
STN2	227461_at	AA632295	NM_033104	85439	1.87	6.01E-04
HS6ST2	230030_at	AI767756	NM_147174 NM_147175	90161	1.87	6.20E-07
NAGA	1555041_a_at	M29276	NM_000262	4668	1.87	2.11E-04
GCHFR	204867_at	NM_005258	NM_005258	2644	1.86	8.27E-03
KIAA1596	234733_s_at	AK001672	XM_048128	57697	1.86	9.32E-05
RFC2	203696_s_at	NM_002914	NM_002914 NM_181471	5982	1.86	8.69E-06
HUNK	1555935_s_at	T58129	NM_014586	30811	1.86	2.81E-04
PEX13	1558164_s_at	BC040953	NM_002618	5194	1.85	9.05E-05
DTYMK	1553984_s_at	AF258562	NM_012145	1841	1.85	4.47E-04
TCF3	209151_x_at	AA768906	NM_003200	6929	1.85	2.01E-04
LOC91614	228293_at	AJ245600	NM_139160	91614	1.85	4.22E-03
CDCA4	218399_s_at	NM_017955	NM_017955 NM_145701	55038	1.84	3.08E-04
Cep152	215882_at	AK025247	NM_014985	22995	1.84	1.38E-03
TIMELESS	203046_s_at	NM_003920	NM_003920	8914	1.84	2.25E-04
ZNF505	208119_s_at	NM_031218	NM_001004126 NM_031218	81931	1.84	1.87E-04
SESN3	242899_at	N78412	NM_144665	143686	1.84	2.44E-03
FLJ14146	218546_at	NM_024709	NM_024709	79762	1.83	4.55E-04
PHF19	225533_at	AL117477	NM_001009936 NM_015651	26147	1.83	6.38E-04
C19orf32	226597_at	AI348159	NM_138393	92840	1.83	5.57E-05
SATB2	213435_at	AB028957	NM_015265	23314	1.83	9.07E-03
PASK	216945_x_at	U79240	NM_015148	23178	1.83	1.22E-03
MSH5	210410_s_at	AF034759	NM_002441 NM_025259 NM_172165 NM_172166	4439	1.83	2.29E-04
CBLB	227900_at	AV701750	NM_170662	868	1.82	5.23E-03
AI984541	235434_at	AI984541	---	---	1.82	1.15E-03
NEDD1	1552417_a_at	NM_152905	NM_152905	121441	1.82	2.63E-03

KDELR3	204017_at	NM_006855	NM_006855 NM_016657	11015	1.82	4.53E-03
TYMS	228989_at	AW291159	NM_001071	7298	1.82	3.40E-03
PCNXL2	39650_s_at	AB007895	NM_014801 NM_024938	80003	1.82	9.16E-05
HS6ST2	1552767_a_at	NM_147174	NM_147174 NM_147175	90161	1.82	8.21E-07
KIF23	244427_at	AW192521	NM_004856 NM_138555	9493	1.81	8.25E-03
EBF	227646_at	BG435302	NM_024007	1879	1.81	2.17E-05
BE466145	227041_at	BE466145	---	---	1.81	5.47E-05
KCNJ8	205303_at	BF514158	NM_004982	3764	1.81	1.32E-06
TRIP13	204033_at	NM_004237	NM_004237	9319	1.80	1.65E-04
SMAD3	218284_at	NM_015400	NM_005902	4088	1.80	2.69E-03
AI582818	229053_at	AI582818	---	---	1.80	1.03E-03
TBC1D1	212350_at	AB029031	NM_015173	23216	1.80	1.24E-04
FEN1	204768_s_at	NM_004111	NM_004111	2237	1.79	7.12E-05
HELLS	223556_at	AF155827	NM_018063	3070	1.79	4.87E-04
SFI1	36545_s_at	AB011114	NM_00100746 7 NM_014775	9814	1.78	8.13E-03
WASPIP	202664_at	AW058622	NM_003387	7456	1.78	6.38E-03
RASEF	235144_at	AA826324	NM_152573	158158	1.78	9.50E-04
NOS1	239132_at	BE299830	NM_000620	4842	1.78	9.36E-04
DNMT3B	220668_s_at	NM_006892	NM_006892 NM_175848 NM_175849 NM_175850	1789	1.78	3.32E-05
H10545	242137_at	H10545	---	---	1.77	7.47E-04
PKP4	214874_at	AL050364	NM_00100547 6 NM_003628	8502	1.76	7.22E-04
T86830	227835_at	T86830	XM_374317	389831	1.76	2.76E-03
HSDL2	209512_at	BC004331	NM_032303	84263	1.76	1.97E-03
AI146450	228073_at	AI146450	---	---	1.76	4.60E-06
BC041029	1569025_s_at	BC041029	XM_371697	389211	1.76	4.47E-06
AMOTL1	225459_at	AU157155	NM_130847	154810	1.76	8.01E-05
C2orf31	221245_s_at	NM_030804	---	81561	1.75	5.43E-05
STK3	204068_at	NM_006281	NM_006281	6788	1.75	3.93E-05
FAM19A4	242348_at	AA757457	NM_00100552 7 NM_182522	151647	1.75	6.22E-07
CHTF18	226569_s_at	AK024476	NM_022092	63922	1.75	5.44E-06
SOX4	201417_at	AL136179	NM_003107	6659	1.75	6.42E-05
RRM1	201476_s_at	AI692974	NM_001033	6240	1.74	5.08E-04
AV717623	212738_at	AV717623	---	---	1.74	2.87E-04
FGD4	227948_at	AI949549	NM_139241	121512	1.74	3.49E-04
NTRK2	221796_at	AA707199	NM_00100709 7 NM_006180	4915	1.74	2.14E-04
SOX4	201416_at	BG528420	NM_003107	6659	1.73	5.20E-04
SESN3	225123_at	BE883841	NM_144665	143686	1.73	4.70E-04
C6orf139	219294_at	NM_018132	NM_018132	55166	1.73	3.59E-05
SRGAP1	233888_s_at	AK023899	NM_020762	57522	1.73	7.93E-04
CDK6	235287_at	AW192700	NM_001259	1021	1.73	2.32E-03
TNFAIP8	208296_x_at	NM_014350	NM_014350	25816	1.73	9.57E-04
TUBG1	201714_at	NM_001070	NM_001070	7283	1.73	1.25E-04
LOC221810	221910_at	BF131965	---	221810	1.73	1.75E-04

AI220427	230696_at	AI220427	---	---	1.73	4.25E-03
AI685824	244565_at	AI685824	XM_370580	387716	1.73	2.27E-04
AL566034	224944_at	AL566034	---	---	1.72	1.01E-05
WEE1	212533_at	X62048	NM_003390	7465	1.72	1.55E-05
RRM1	201477_s_at	NM_001033	NM_001033	6240	1.72	1.46E-04
EZH2	203358_s_at	NM_004456	NM_004456 NM_152998	2146	1.72	4.30E-06
WHSC1	222777_s_at	AI770166	NM_007331 NM_014919 NM_133330 NM_133331 NM_133332 NM_133333 NM_133334 NM_133335 NM_133336	7468	1.72	4.09E-04
H2AFX	205436_s_at	NM_002105	NM_002105	3014	1.72	4.53E-05
)KFZP434L011	227818_at	AL133609	NM_022778	64793	1.72	2.15E-04
C9orf100	230522_s_at	BG028209	NM_032818	84904	1.72	3.63E-04
ANKRD9	230972_at	AW194999	NM_152326	122416	1.71	5.46E-06
ACTA2	200974_at	NM_001613	NM_001613	59	1.71	1.89E-03
GALNT10	212256_at	BE906572	NM_017540 NM_198321	55568	1.71	2.83E-03
AI826125	229866_at	AI826125	---	---	1.71	1.06E-03
LRRC20	218550_s_at	NM_018205	NM_018205 NM_018239 NM_207119	55222	1.70	6.18E-03
C6orf213	1562443_at	AK095527	NM_001010852	134829	1.70	2.22E-07
EDG2	204037_at	BF055366	NM_001401 NM_057159	1902	1.69	2.85E-03
DLL3	222898_s_at	BE350882	NM_016941 NM_203486	10683	1.69	3.90E-05
TBPIP	205956_x_at	NM_013290	NM_013290 NM_016556	29893	1.69	8.09E-05
GFRA2	205721_at	U97145	NM_001495	2675	1.69	3.03E-03
AI140305	228849_at	AI140305	---	---	1.69	5.44E-03
MBD2	214397_at	AI827820	NM_003927 NM_015832	8932	1.68	7.38E-05
POLE	216026_s_at	AL080203	NM_006231	5426	1.68	1.73E-04
TIMP3	201148_s_at	AW338933	NM_000362	7078	1.68	3.70E-06
RBMS3	206767_at	NM_014483	NM_00100379 2 NM_00100379 3 NM_014483	27303	1.68	5.38E-04
BE670307	227955_s_at	BE670307	---	---	1.68	3.67E-04
LAMA4	202202_s_at	NM_002290	NM_002290	3910	1.68	8.97E-03
NUDT1	204766_s_at	NM_002452	NM_002452 NM_198948 NM_198949 NM_198950 NM_198952 NM_198953 NM_198954	4521	1.68	4.44E-03
LOC81691	208107_s_at	NM_030941	NM_030941	81691	1.68	6.55E-05
PKP4	201927_s_at	BG292559	NM_00100547 6 NM_003628	8502	1.68	8.23E-03

AI919519	235092_at	AI919519	---	---	1.68	4.50E-04
KPNA2	211762_s_at	BC005978	NM_002266	3838	1.67	1.78E-06
ZNF519	1568873_at	BC010705	NM_145287	162655	1.67	8.56E-03
PELO	226731_at	AA156873	NM_015946	53918	1.67	5.20E-03
HIRIP3	204504_s_at	NM_003609	NM_003609	8479	1.67	1.47E-05
RAD54B	235846_at	AI208616	NM_012415 NM_134434	25788	1.67	2.55E-03
)KFZP761M151	225355_at	AK026748	---	54492	1.67	5.04E-03
SYN2	210247_at	AW139618	NM_003178 NM_133625	6854	1.67	7.92E-04
SNAG1	226683_at	AU146771	NM_052870	112574	1.67	1.69E-04
CDC25A	204695_at	AI343459	NM_001789 NM_201567	993	1.66	4.73E-04
MEST	202016_at	NM_002402	NM_002402 NM_177524 NM_177525	4232	1.66	1.55E-04
HPSE	222881_at	AF155510	NM_006665	10855	1.66	3.24E-04
AI673553	203061_s_at	AI673553	---	---	1.66	1.97E-05
SANG	232881_at	AI500353	---	149775	1.66	2.02E-04
HGF	210998_s_at	M77227	NM_000601 NM_00101093 1 NM_00101093 2 NM_00101093 3 NM_00101093 4	3082	1.66	6.82E-03
SCD4	224901_at	AL571375	NM_024906	79966	1.66	1.68E-03
RDH10	226021_at	AW150720	NM_172037	157506	1.66	1.99E-03
SYNPO2	232119_at	BF984227	NM_133477	171024	1.66	5.45E-03
LSM4	202737_s_at	NM_012321	NM_012321	25804	1.65	5.27E-05
BE857972	243781_at	BE857972	---	---	1.65	7.56E-04
NET1	201829_at	AW263232	NM_005863	10276	1.65	7.05E-05
LYN	210754_s_at	M79321	NM_002350	4067	1.65	3.45E-05
DACH1	228915_at	AI650353	NM_004392 NM_080759 NM_080760	1602	1.65	6.68E-03
LIG1	202726_at	NM_000234	NM_000234	3978	1.65	3.00E-04
LYN	202626_s_at	NM_002350	NM_002350	4067	1.64	1.87E-05
ST8SIA2	221285_at	NM_006011	NM_006011	8128	1.64	2.88E-03
FLJ23322	233250_x_at	AL022313	NM_024955	80020	1.64	1.54E-04
GNG12	1555240_s_at	AF493879	NM_018841	55970	1.64	9.06E-05
BC025350	1569418_at	BC025350	---	---	1.63	1.39E-03
EVE1	225162_at	BG285417	NM_001009555	152503	1.63	1.62E-03
SCML1	222747_s_at	BF001786	NM_006746	6322	1.63	2.63E-04
C20orf100	228737_at	AA211909	NM_032883	84969	1.63	9.04E-04
LMNB1	203276_at	NM_005573	NM_005573	4001	1.63	1.56E-04
TNFSF13B	223501_at	AW151360	NM_006573	10673	1.63	2.45E-03
ZAK	225662_at	H28667	NM_016653 NM_133646	51776	1.63	2.26E-05
N36085	227221_at	N36085	---	---	1.63	2.85E-04
SOX4	201418_s_at	NM_003107	NM_003107	6659	1.62	4.87E-04
LOC342892	244640_at	AW440392	XM_292740	342892	1.62	9.38E-05
MCM4	222037_at	AI859865	NM_005914 NM_182746	4173	1.62	4.15E-03

RAD51C	206066_s_at	NM_002876	NM_002876 NM_058216 NM_058217	5889	1.62	2.63E-04
SORT1	212807_s_at	BF447105	NM_002959	6272	1.62	7.88E-04
AV687517	228498_at	AV687517	---	---	1.62	4.00E-03
FLJ44635	227618_at	AI250910	NM_207422	392490	1.62	4.08E-03
HMG2L1	212597_s_at	AL079310	NM_00100368 1 NM_005487 NM_014250	10042	1.62	1.26E-04
PLXNA2	213030_s_at	AI688418	NM_025179	5362	1.62	1.87E-04
ST8SIA2	239537_at	AW589904	NM_006011	8128	1.61	3.33E-06
SCML1	218793_s_at	NM_006746	NM_006746	6322	1.61	6.46E-07
KIAA1754L	240037_at	R37132	NM_00100894 9 NM_178495	150771	1.61	8.33E-03
COBLL1	203642_s_at	NM_014900	NM_014900	22837	1.61	1.06E-03
N26620	227503_at	N26620	---	---	1.61	1.67E-03
RPA3	209507_at	BC005264	NM_002947	6119	1.61	2.30E-04
RODH	205700_at	NM_003725	NM_003725	8630	1.61	9.72E-03
CARHSP1	224910_at	AL575747	NM_014316	23589	1.61	7.34E-03
AL049709	216548_x_at	AL049709	---	---	1.61	2.85E-04
POLD3	212836_at	D26018	NM_006591	10714	1.61	3.76E-04
BZRP	202096_s_at	NM_000714	NM_000714 NM_007311	706	1.61	7.10E-03
LOC286044	222662_at	W60806	---	286044	1.60	2.19E-04
MICAL3	229474_at	BF055090	XM_032996 XM_032997	57553	1.60	4.74E-03
C1QL1	205575_at	NM_006688	NM_006688	10882	1.60	1.17E-03
EGFR	224999_at	BE878463	NM_005228 NM_201282 NM_201283 NM_201284	1956	1.60	1.02E-02
AL040051	225481_at	AL040051	---	---	1.60	1.85E-03
GLRX	209276_s_at	AF162769	NM_002064	2745	1.59	8.29E-03
CDC25C	217010_s_at	AF277724	NM_001790 NM_022809	995	1.59	8.33E-03
DNM3	209839_at	AL136712	NM_015569	26052	1.59	3.88E-04
LOC81691	215215_s_at	AC004381	NM_030941	81691	1.59	1.47E-05
SCD4	224018_s_at	BC004936	NM_024906	79966	1.59	5.27E-04
PAG	225626_at	AK000680	NM_018440	55824	1.59	7.40E-03
SLC8A1	235518_at	AI741439	NM_021097	6546	1.58	5.49E-04
W93046	230068_s_at	W93046	---	---	1.58	3.19E-03
Cep70	224150_s_at	AF289495	NM_024491	80321	1.58	1.32E-03
DACH1	205471_s_at	AW772082	NM_004392 NM_080759 NM_080760	1602	1.58	3.93E-03
FLJ12484	219361_s_at	NM_022767	NM_022767	64782	1.58	3.84E-04
IMP-1	223689_at	AF198254	NM_006546	10642	1.57	2.37E-03
AI697657	229128_s_at	AI697657	---	---	1.57	1.62E-05
LOC90139	227307_at	AL565381	NM_130783	90139	1.57	2.80E-03
SEZ6L	216047_x_at	AL050253	NM_021115	23544	1.57	1.21E-04
CENPC1	204739_at	NM_001812	NM_001812	1060	1.57	4.21E-04
CKS2	204170_s_at	NM_001827	NM_001827	1164	1.57	6.57E-04
LOC92689	213455_at	W87466	NM_138389	92689	1.57	6.69E-04
ROR1	211057_at	BC006374	NM_005012	4919	1.57	9.11E-04

PHF19	227211_at	BE544837	NM_00100993 6 NM_015651	26147	1.56	3.54E-04
PHF21B	1562309_s_at	AK092243	NM_138415	112885	1.56	5.12E-05
USP48	229812_at	BE645018	NM_032236	84196	1.56	4.62E-03
LOC221362	213248_at	AL577024	---	221362	1.56	9.52E-06
CRYZ	202950_at	NM_001889	NM_001889	1429	1.56	3.29E-04
GATM	203178_at	NM_001482	NM_001482	2628	1.56	1.90E-05
NM_014641	203062_s_at	NM_014641	---	---	1.55	5.41E-05
FLJ38964	235699_at	H19232	NM_173527	161253	1.55	4.09E-03
SPA17	205406_s_at	NM_017425	NM_017425	53340	1.55	1.75E-03
NRP1	212298_at	BE620457	NM_003873	8829	1.55	7.51E-03
NXN	243503_at	AI632740	NM_022463	64359	1.55	1.68E-04
TCFL5	235694_at	N49233	NM_006602	10732	1.55	7.24E-05
UNG	202330_s_at	NM_003362	NM_003362 NM_080911	7374	1.54	5.21E-06
TREX2	213334_x_at	BE676218	---	11219	1.54	6.50E-04
WHSC1	209053_s_at	BE793789	NM_007331 NM_014919 NM_133330 NM_133331 NM_133332 NM_133333 NM_133334 NM_133335 NM_133336	7468	1.54	1.93E-04
ITGB3BP	205176_s_at	NM_014288	NM_014288	23421	1.54	1.06E-04
LSM4	202736_s_at	AA112507	NM_012321	25804	1.54	8.14E-05
MPP5	226092_at	BF115203	NM_022474	64398	1.54	7.77E-03
MGC21654	214061_at	AI017564	NM_145647	93594	1.54	4.22E-04
C9orf76	218979_at	NM_024945	NM_024945	80010	1.54	2.48E-04
KLF7	238482_at	AL120562	NM_003709	8609	1.54	5.35E-03
LZTS1	47550_at	N21184	NM_021020	11178	1.54	9.06E-03
SLC8A1	238546_at	BF344961	NM_021097	6546	1.54	1.55E-03
FGD4	242445_at	AA296351	NM_139241	121512	1.54	9.73E-03
ZNF217	203739_at	NM_006526	NM_006526	7764	1.54	4.11E-06
TM4SF14	221002_s_at	NM_030927	NM_030927	81619	1.54	1.44E-03
NAGA	202943_s_at	M38083	NM_000262	4668	1.53	1.02E-03
RAI14	202052_s_at	NM_015577	NM_015577	26064	1.53	4.59E-04
PARD6G	227204_at	AI817448	NM_032510	84552	1.53	7.67E-04
MMD	203414_at	NM_012329	NM_012329	23531	1.53	7.58E-05
C15orf23	225300_at	BF792864	NM_033286	90417	1.53	6.24E-04
ACO1	207071_s_at	NM_002197	NM_002197	48	1.53	6.67E-03
FLJ10514	218365_s_at	AI765051	NM_018122	55157	1.53	2.72E-03
RAB3B	227123_at	AU156710	NM_002867	5865	1.52	1.25E-03
TCFL5	204849_at	NM_006602	NM_006602	10732	1.52	8.79E-04
GEMIN4	205527_s_at	NM_015487	NM_015721	50628	1.52	2.20E-03
CBLB	209682_at	U26710	NM_170662	868	1.52	9.18E-07
HMG2L1	212596_s_at	AJ010070	NM_00100368 1 NM_005487 NM_014250	10042	1.52	1.65E-04
CARHSP1	218384_at	NM_014316	NM_014316	23589	1.52	1.20E-03
PTPRR	210675_s_at	U77917	NM_002849 NM_130846	5801	1.51	6.84E-03
ZNF85	1554445_at	BC008688	NM_003429	7639	1.51	8.78E-03
C20orf58	230668_at	AI758937	NM_152864	128414	1.51	2.35E-04
AK098258	1564175_at	AK098258	---	---	1.51	4.42E-03

ADPN	220675_s_at	NM_025225	NM_025225	80339	1.51	6.52E-04
RANBP1	202483_s_at	NM_002882	NM_002882	5902	1.51	9.75E-06
CDK6	224851_at	AW274756	NM_001259	1021	1.51	3.51E-04
GPR161	206972_s_at	NM_007369	NM_007369 NM_153832	23432	1.51	3.61E-05
MCFP	205716_at	NM_018843	NM_018843	55972	1.51	5.29E-03
RTN4IP1	224509_s_at	BC006399	NM_032730	84816	1.51	1.29E-03
RANGAP1	212125_at	NM_002883	NM_002883	5905	1.50	4.37E-04
BF057492	221871_s_at	BF057492	---	---	1.50	2.08E-03
MMD	244523_at	AW104453	NM_012329	23531	1.50	4.38E-05
PHF19	227212_s_at	BE544837	NM_00100993 6 NM_015651	26147	1.50	4.91E-05
HMGB3	203744_at	NM_005342	NM_005342	3149	1.50	1.38E-06
RODH	37512_at	U89281	NM_003725	8630	1.50	6.29E-03
AW665447	230113_at	AW665447	---	---	1.50	8.13E-03
RANGAP1	1553535_a_at	NM_002883	NM_002883	5905	1.50	6.68E-05
PRIM1	205053_at	NM_000946	NM_000946	5557	1.49	7.62E-05
FEN1	204767_s_at	BC000323	NM_004111	2237	1.49	2.41E-04
MAN1A1	208116_s_at	NM_005907	NM_005907	4121	1.49	2.54E-03
SLC1A1	213664_at	AW235061	NM_004170	6505	1.49	1.97E-04
LOC283027	1562527_at	AF519622	---	283027	1.49	6.56E-03
BUB3	201457_x_at	AF081496	NM_00100779 3 NM_004725	9184	1.49	1.77E-05
GPR161	230369_at	AI743151	NM_007369 NM_153832	23432	1.49	2.32E-04
TRIM59	235476_at	AW182459	NM_173084	286827	1.49	9.48E-03
TLE4	204872_at	NM_007005	NM_007005	7091	1.48	3.51E-05
LOC401022	242042_s_at	AA406052	---	401022	1.48	1.50E-03
ZAK	238613_at	AI475164	NM_016653 NM_133646	51776	1.48	7.42E-03
DHRS10	228713_s_at	AI742586	NM_016246	51171	1.48	3.31E-03
FLJ10747	222673_x_at	AI582192	NM_018202	159090	1.48	4.86E-05
LOC159090			NM_145284	55219		
MGC13186	223272_s_at	BC005102	NM_032324	84284	1.47	5.80E-03
FLJ11535	220798_x_at	NM_024888	NM_024888	79948	1.47	8.54E-03
C9orf81	228774_at	AW268594	XM_095991	84131	1.47	2.00E-04
DHX35	234728_s_at	AL023803	NM_021931	60625	1.47	9.46E-04
EPOR	209962_at	M34986	NM_000121	2057	1.47	4.25E-03
DUT	208955_at	AB049113	NM_001948	1854	1.47	1.77E-03
KHDRBS3	209781_s_at	AF069681	NM_006558	10656	1.47	5.70E-06
AA218973	237245_at	AA218973	XM_372330	390009	1.47	2.67E-03
PVT1	1558290_a_at	BG200951	XM_372058	441378	1.47	4.77E-04
LOC441378			XM_499128	5820		
MCM7	210983_s_at	AF279900	NM_005916 NM_182776	4176	1.47	5.48E-05
POLR3K	218866_s_at	NM_016310	NM_016310	51728	1.47	2.20E-03
LOC159090	225361_x_at	AI348001	NM_145284	159090	1.47	4.60E-05
CNP	208912_s_at	BC001362	NM_033133	1267	1.47	7.89E-04
LOC201725	235088_at	AI276663	NM_001008393	201725	1.46	1.25E-03
CHRNA3	211772_x_at	BC006114	NM_000743	1136	1.46	8.95E-04
LOC126295	1554628_at	BC028974	NM_173480	126295	1.46	8.70E-03
FARP1	201911_s_at	NM_005766	NM_00100171 5 NM_005766	10160	1.46	7.82E-05
PAX5	221969_at	BF510692	NM_016734	5079	1.46	8.27E-04
HTR2B	206638_at	NM_000867	NM_000867	3357	1.46	5.49E-03

SLC25A10	218275_at	NM_012140	NM_012140	1468	1.46	6.48E-03
HELLS	242890_at	AI650364	NM_018063	3070	1.46	2.08E-03
CCBE1	243805_at	BG035826	NM_133459	147372	1.46	3.38E-03
BE877357	228314_at	BE877357	---	---	1.46	3.26E-03
MAK3	222393_s_at	AU149868	NM_025146	80218	1.46	4.59E-03
BE222344	226034_at	BE222344	---	---	1.46	5.03E-04
FLJ10375	243230_at	AA918375	NM_018075	55129	1.46	6.10E-03
BRI3BP	231810_at	BG106919	NM_080626	140707	1.46	5.53E-04
LCRISP1	223475_at	AF142573	NM_031461	83690	1.46	8.87E-04
ARHGAP6	206167_s_at	NM_001174	NM_001174	395	1.45	6.89E-03
			NM_006125			
			NM_013422			
			NM_013423			
			NM_013427			
TLX3	208495_at	NM_021025	NM_021025	30012	1.45	3.06E-04
H2AFV	202487_s_at	NM_012412	NM_012412	94239	1.45	4.29E-03
			NM_138635			
			NM_201436			
			NM_201516			
			NM_201517			
BIRC5	1555826_at	BQ021146	NM_001168	332	1.45	3.48E-03
AI357639	225716_at	AI357639	---	---	1.44	3.04E-04
ARMC7	229906_at	BF194773	NM_024585	79637	1.44	2.42E-03
OSBPL10	219073_s_at	NM_017784	NM_017784	114884	1.44	1.05E-03
TUBB4	212664_at	AL567012	NM_006087	10382	1.44	2.03E-03
LRRIQ2	219886_at	NM_024548	NM_024548	79598	1.44	8.76E-04
CUGBP2	1557422_at	R49146	NM_006561	10659	1.44	7.78E-03
SRGAP2	213329_at	AA742261	XM_059095	23380	1.44	1.39E-03
NUP93	202188_at	NM_014669	NM_014669	9688	1.44	2.68E-06
LOC440288	238511_at	BF982733	XM_496075	440288	1.44	3.83E-04
AI346432	229132_at	AI346432	---	---	1.44	3.77E-04
HSZFP36	229732_at	AI417785	XM_375568	55552	1.43	1.60E-04
DLG2	206253_at	NM_001364	NM_001364	1740	1.43	7.70E-04
PTX3	206157_at	NM_002852	NM_002852	5806	1.43	3.96E-04
FIGNL1	1552921_a_at	NM_022116	NM_022116	63979	1.43	3.50E-04
CHML	206079_at	NM_001821	NM_001821	1122	1.43	7.71E-03
AI889959	227350_at	AI889959	---	---	1.43	3.94E-04
TLE4	233575_s_at	AA705845	NM_007005	7091	1.43	5.78E-04
LOC388272	226608_at	AW157311	NM_001001436	388272	1.43	2.91E-03
MGC2603	220011_at	NM_024037	NM_024037	79000	1.43	1.24E-04
KIAA1853	230010_at	AA608629	NM_194286	84530	1.43	8.35E-04
LOC51760	205613_at	NM_016524	NM_016524	51760	1.42	1.17E-03
CSE1L	210766_s_at	AF053640	NM_001316	1434	1.42	1.06E-05
			NM_177436			
FAD158	223533_at	AL136919	NM_032270	84230	1.42	2.21E-04
FAM54A	234944_s_at	AL138828	NM_138419	113115	1.42	4.74E-03
UNC84B	212144_at	AL021707	NM_015374	25777	1.42	1.88E-03
BICD1	1554020_at	BC010091	NM_001003398	636	1.42	9.68E-03
			NM_001714			
GNG2	1555766_a_at	AF493870	NM_053064	54331	1.42	1.16E-06
WDR51A	234749_s_at	AL117629	NM_015426	25886	1.42	5.03E-03
EME1	234464_s_at	AK021607	NM_152463	146956	1.42	1.54E-05
TNFRSF19L	227060_at	AW571669	NM_032871	84957	1.42	3.79E-03
			NM_152222			
TSC	218872_at	NM_017899	NM_017899	54997	1.42	3.16E-03
LOC201725	238015_at	BE620598	NM_001008393	201725	1.42	7.24E-05
FAM33A	225686_at	BE048371	NM_182620	348235	1.42	9.89E-05

GTF2E1	205930_at	NM_005513	NM_005513	2960	1.42	2.50E-04
TYRO3	211432_s_at	U05682	NM_006293	7301	1.42	1.33E-03
GFPT2	205100_at	NM_005110	NM_005110	9945	1.42	1.08E-03
SNX10	218404_at	NM_013322	NM_013322	29887	1.41	4.80E-04
BU077901	1557214_at	BU077901	---	---	1.41	2.12E-04
KPNA2	201088_at	NM_002266	NM_002266	3838	1.41	1.16E-05
LZTS1	219042_at	NM_021020	NM_021020	11178	1.41	5.78E-03
NOS1	207309_at	NM_000620	NM_000620	4842	1.41	5.32E-04
CGI-96	33307_at	AL022316	NM_015703	27341	1.41	4.76E-04
WDR34	224715_at	BG338983	NM_052844	89891	1.40	1.09E-03
RAB3B	205924_at	BC005035	NM_002867	5865	1.40	2.80E-03
GCH1	204224_s_at	NM_000161	NM_000161	2643	1.40	2.84E-03
C14orf145	1557755_at	AW028337	XM_496002	145508	1.40	1.22E-03
PDLIM5	203242_s_at	BG054550	NM_001011513 NM_001011514 NM_001011515 NM_001011516 NM_006457	10611	1.40	6.09E-03
MPP5	219321_at	NM_022474	NM_022474	64398	1.40	2.21E-05
CDO1	204154_at	NM_001801	NM_001801	1036	1.40	3.42E-05
CHAF1B	204775_at	NM_005441	NM_005441	8208	1.40	9.66E-04
RECQL	210568_s_at	BC001052	NM_002907 NM_032941	5965	1.40	3.54E-03
MAPK12	206106_at	AL022328	NM_002969	6300	1.40	1.10E-06
PTTG3	208511_at	NM_021000	---	26255	1.39	1.10E-03
HAT1	203136_at	NM_003642	NM_003642	8520	1.39	2.54E-05
MYD88	209124_at	U70451	NM_002468	4615	1.39	2.89E-03
NUDT15	219347_at	NM_018283	NM_018283	55270	1.39	1.29E-04
PCDH9	219737_s_at	AI524125	NM_020403 NM_203487	5101	1.39	7.01E-03
182-FIP	243119_at	AA810156	NM_020772	57532	1.39	2.92E-04
MCM4	212141_at	AA604621	NM_005914 NM_182746	4173	1.39	3.82E-03
RAB23	229504_at	AI810826	NM_016277 NM_183227	51715	1.39	1.82E-05
C9orf88	223019_at	BC001979	NM_022833	64855	1.39	2.37E-03
DLX6	242940_x_at	AA040332	XM_376652 XM_379892	1750	1.39	2.34E-06
FLJ13909	219556_at	NM_025108	NM_025108	80178	1.39	5.95E-04
CDKN2C	204159_at	NM_001262	NM_001262 NM_078626	1031	1.39	5.88E-04
MEIS1	1559477_s_at	AL832770	NM_002398	4211	1.39	3.54E-04
STRA6	1569334_at	BC015881	NM_022369	64220	1.39	6.72E-03
AW069181	223519_at	AW069181	---	---	1.39	9.35E-04
SEZ6L	213609_s_at	AB023144	NM_021115	23544	1.38	5.40E-04
FKBP14	235311_at	BG110260	NM_017946	55033	1.38	1.16E-04
BG231758	227615_at	BG231758	---	---	1.38	1.85E-04
GEMIN4	217099_s_at	AF258545	NM_015721	50628	1.38	2.18E-03
H2AFV	227085_at	AI823792	NM_012412 NM_138635 NM_201436 NM_201516 NM_201517	94239	1.38	1.65E-04
KLF10	202393_s_at	NM_005655	NM_005655	7071	1.38	4.37E-03

MRE11A	205395_s_at	NM_005590	NM_005590 NM_005591	4361	1.38	9.90E-04
FDXR	207813_s_at	NM_004110	NM_004110 NM_024417	2232	1.38	6.17E-04
GNG4	205184_at	NM_004485	NM_004485	2786	1.38	2.86E-05
MYOHD1	219320_at	NM_025109	NM_025109	80179	1.38	6.52E-04
CTL2	224609_at	AI264216	NM_020428	57153	1.37	2.31E-03
FLJ13273	235387_at	AA740875	NM_024751	79807	1.37	1.76E-05
EDA2R	221399_at	NM_021783	NM_021783	60401	1.37	4.37E-03
MGC10744	238590_x_at	BF981428	NM_032354	84314	1.37	6.04E-03
ACYP1	205260_s_at	NM_001107	NM_183065 NM_001107 NM_203488	97	1.37	7.99E-03
MGC12197	1555501_s_at	BC010357	NM_016625	51319	1.37	1.22E-03
MGC13186	226813_at	AA883980	NM_032324	84284	1.37	9.86E-04
MRE11A	242456_at	AA931565	NM_005590 NM_005591	4361	1.37	6.99E-03
BCR	202315_s_at	NM_004327	NM_004327 NM_021574	613	1.36	1.69E-04
CHRNA3	211587_x_at	M37981	NM_000743	1136	1.36	8.91E-04
GPR161	235961_at	BF248385	NM_007369 NM_153832	23432	1.36	5.62E-05
DUSP4	204015_s_at	BC002671	NM_001394 NM_057158	1846	1.36	6.68E-04
GNG4	1555765_a_at	AF493872	NM_004485	2786	1.36	8.13E-05
FLJ11712	219056_at	NM_024570	NM_024570	79621	1.36	2.93E-03
BUB3	209974_s_at	AF047473	NM_00100779 3 NM_004725	9184	1.36	2.12E-06
LOC93081	213346_at	BE748563	NM_138779	93081	1.36	2.01E-05
UNQ470	228403_at	AL541276	NM_198573	375704	1.36	9.85E-03
FLJ20364	221685_s_at	AF269167	NM_017785	54908	1.36	4.22E-05
LOC283454	242715_at	AA331548	---	283454	1.36	8.25E-04
LOC388272	242555_at	AW578854	NM_001001436	388272	1.35	7.50E-03
SELM	226051_at	BF973568	NM_080430	140606	1.35	1.09E-04
PAQR4	212858_at	AL520675	NM_152341	124222	1.35	3.60E-05
C20orf7	222894_x_at	AI640582	NM_024120	79133	1.35	1.37E-04
PKP4	201929_s_at	NM_003628	NM_199052 NM_00100547 6 NM_003628	8502	1.35	6.66E-05
CBX5	242069_at	BE568225	NM_012117	23468	1.35	1.98E-03
CPNE4	228796_at	BE645967	NM_130808	131034	1.35	4.28E-03
CSE1L	201112_s_at	NM_001316	NM_001316 NM_177436	1434	1.35	2.61E-06
TBC1D1	227945_at	BE882538	NM_015173	23216	1.34	4.34E-03
B4GALT1	201883_s_at	D29805	NM_001497	2683	1.34	1.44E-03
TAF5	1553528_a_at	NM_139052	NM_006951	6877	1.34	9.10E-04
CEP1	205642_at	NM_007018	NM_007018	11064	1.34	3.35E-04
STOM	201061_s_at	M81635	NM_004099 NM_198194	2040	1.34	1.41E-04
C6orf182	1554019_s_at	BC033448	NM_173830	285753	1.34	1.74E-05
LOC284465	229382_at	AW149270	---	284465	1.34	3.05E-03
C20orf108	224690_at	BG432350	NM_080821	116151	1.34	1.10E-03
TDRD7	213361_at	AW129593	NM_014290	23424	1.34	5.01E-03
CDK6	224847_at	AW051349	NM_001259	1021	1.33	2.41E-04
C20orf102	226973_at	AA206763	NM_080607	128434	1.33	2.65E-03
TMPO	227578_at	H28597	NM_003276	7112	1.33	1.51E-03

TUBB6	209191_at	BC002654	NM_032525	84617	1.33	1.57E-04
ANP32E	221505_at	AW612574	NM_030920	81611	1.33	1.41E-05
FLJ20516	219258_at	NM_017858	NM_017858	54962	1.33	1.05E-03
DC13	218447_at	NM_020188	NM_020188	56942	1.33	3.60E-03
CKLF	219161_s_at	NM_016951	NM_016326	51192	1.33	6.08E-05
			NM_016951			
			NM_181640			
			NM_181641			
DLL3	219537_x_at	NM_016941	NM_016941	10683	1.33	1.14E-05
			NM_203486			
DOCK4	205003_at	NM_014705	NM_014705	9732	1.33	1.67E-03
UBAP2L	201377_at	NM_014847	NM_014847	9898	1.33	1.35E-05
FLJ10036	218349_s_at	NM_017975	NM_017975	55055	1.33	1.50E-03
SERPING1	200986_at	NM_000062	NM_000062	710	1.33	3.17E-03
SCML2	206147_x_at	NM_006089	NM_006089	10389	1.33	2.97E-05
BE877775	1568955_at	BE877775	---	---	1.33	1.57E-05
LOC440820	226602_s_at	T30183	XM_496519	440820	1.33	3.16E-05
FKBP5	224856_at	W86302	NM_004117	2289	1.33	1.42E-03
PPM1D	230330_at	AI312083	NM_003620	8493	1.33	4.50E-04
)KFZp313A243:	226278_at	AI150224	---	258010	1.32	1.69E-04
MAN1A1	221760_at	BG287153	NM_005907	4121	1.32	1.75E-05
RFWD3	218564_at	BC002574	---	55159	1.32	4.99E-04
C10orf78	238794_at	N23586	NM_00100275	119392	1.32	9.64E-05
			9			
			NM_145247			
NEGR1	229461_x_at	AI123532	NM_173808	257194	1.32	1.20E-03
DCK	203302_at	NM_000788	NM_000788	1633	1.32	3.62E-05
K-ALPHA-1	211072_x_at	BC006481	NM_006082	10376	1.32	6.06E-06
AI092265	228088_at	AI092265	---	---	1.32	9.95E-04
UCHL5	220083_x_at	NM_016017	NM_015984	51377	1.32	2.96E-04
TRIM37	1554001_at	BC036012	NM_00100520	4591	1.32	8.08E-04
			7			
			NM_015294			
MGC39900	214051_at	BF677486	NM_194324	286527	1.32	7.28E-03
NFYB	218129_s_at	NM_006166	NM_006166	4801	1.32	5.07E-03
FAS	204781_s_at	NM_000043	NM_000043	355	1.32	1.70E-03
			NM_152871			
			NM_152872			
			NM_152873			
			NM_152874			
			NM_152875			
			NM_152876			
			NM_152877			
C2orf23	204364_s_at	BE535746	NM_022912	65055	1.31	8.43E-05
YPEL1	228296_at	AW450686	NM_013313	29799	1.31	7.66E-03
TRAF4	211899_s_at	AF082185	NM_004295	9618	1.31	4.10E-03
			NM_145751			
GLS	203158_s_at	AF097493	NM_014905	2744	1.31	9.13E-04
FARP1	201910_at	BF213279	NM_00100171	10160	1.31	6.05E-04
			5			
			NM_005766			
C9orf40	222781_s_at	BF590861	NM_017998	55071	1.31	1.00E-02
ADCY3	235441_at	BF217471	NM_004036	109	1.31	9.61E-03
ZNF253	242919_at	AV683221	NM_021047	114977	1.31	1.27E-03
LOC114977				56242		
NASP	201970_s_at	NM_002482	NM_002482	4678	1.31	8.90E-05
			NM_152298			
			NM_172164			

ACTL6A	202666_s_at	NM_004301	NM_004301 NM_177989 NM_178042	86	1.30	1.03E-07
HOXD3	206601_s_at	BC005124	NM_006898	3232	1.30	3.02E-04
SORD	201563_at	L29008	NM_003104	6652	1.30	6.16E-05
COQ3	223515_s_at	AL136726	NM_017421	51805	1.30	1.20E-05
SKP2	203626_s_at	NM_005983	NM_005983 NM_032637	6502	1.30	9.20E-03
CDK6	224848_at	AA922068	NM_001259	1021	1.30	3.32E-03
BOK	223349_s_at	BE614255	NM_032515	666	1.30	4.78E-06
PCDH17	205656_at	NM_014459	NM_014459	27253	1.30	1.41E-03
BCAS4	220588_at	NM_017843	NM_001010974 NM_017843 NM_198799	55653	1.30	3.33E-04
TDP1	219715_s_at	NM_018319	NM_001008744 NM_018319	55775	1.30	5.37E-05
LOC283683 LOC339003	217520_x_at	BG396614	XM_290660	283683 339003	1.30	9.14E-03
C6orf152	242006_at	AI379143	NM_181714	167691	1.30	2.64E-03
AA824298	222606_at	AA824298	---	---	1.30	2.38E-03
PRPS1	208447_s_at	NM_002764	NM_002764	5631	1.30	1.12E-04
AA401256	230537_at	AA401256	---	---	1.30	2.49E-03
SUV39H2	1554572_a_at	BC029360	NM_024670	79723	1.29	2.41E-05
LOC284244	214162_at	AF070541	---	284244	1.29	9.39E-03
WDR53	227814_at	AA789329	NM_182627	348793	1.29	5.37E-06
CPT1A	210688_s_at	BC000185	NM_001876	1374	1.29	5.31E-03
RFC1	208021_s_at	NM_002913	NM_002913	5981	1.29	1.61E-06
MGC10812	223469_at	BC004942	---	83542	1.29	3.11E-04
CSE1L	201111_at	AF053641	NM_001316 NM_177436	1434	1.29	1.01E-03
PPFIBP2	212841_s_at	AI692180	NM_003621	8495	1.29	4.46E-04
CHRNA3	210221_at	BC000513	NM_000743	1136	1.29	6.31E-03
RBL1	1559307_s_at	BG387892	NM_002895 NM_183404	5933	1.29	5.93E-05
ZNF43	206695_x_at	NM_003423	NM_003423	7594	1.28	2.30E-04
TM4SF7	209263_x_at	BC000389	NM_003271	7106	1.28	2.01E-04
PDLIM5	216804_s_at	AK027217	NM_001011513 NM_001011514 NM_001011515 NM_001011516 NM_006457	10611	1.28	1.45E-03
KCNJ8	205304_s_at	NM_004982	NM_004982	3764	1.28	8.99E-05
NLN	225943_at	BF222737	NM_020726	57486	1.28	6.53E-03
ORF1-FL49	224707_at	AL522667	NM_032412	84418	1.28	6.23E-05
AL833487	1562244_at	AL833487	---	---	1.28	1.81E-04
EB-1	227440_at	AW005572	NM_020140 NM_152788 NM_181670	56899	1.28	2.28E-03
MEIS1	204069_at	NM_002398	NM_002398	4211	1.28	3.15E-04
SESTD1	226763_at	AW409611	NM_178123	91404	1.27	1.35E-03
GNG2	224964_s_at	AK026424	NM_053064	54331	1.27	1.89E-05
DPF1	231599_x_at	AI939563	NM_004647	8193	1.27	1.45E-03

STMN1	200783_s_at	NM_005563	NM_005563 NM_203399 NM_203401	3925	1.27	5.04E-04
AF279774	216967_at	AF279774	---	---	1.27	8.55E-03
DUSP4	204014_at	NM_001394	NM_001394 NM_057158	1846	1.27	1.77E-04
MCM4	222036_s_at	AI859865	NM_005914 NM_182746	4173	1.27	2.04E-03
C6orf151	1553274_a_at	NM_152551	NM_152551	154007	1.27	8.31E-03
RRM2B	223342_at	AB036063	NM_015713	50484	1.27	4.55E-04
TDRKH	223530_at	AF227192	NM_006862	11022	1.27	1.02E-06
PRIM2A	215708_s_at	AL121975	NM_000947	5558	1.26	1.78E-03
GPR161	214104_at	AI703188	NM_007369 NM_153832	23432	1.26	1.74E-05
NR3C1	211671_s_at	U01351	NM_000176	2908	1.26	1.39E-04
TCF7L2	212761_at	AI949687	NM_030756	6934	1.26	8.24E-03
HECA	218603_at	NM_016217	NM_016217	51696	1.26	8.85E-03
KREMEN1	227250_at	BF221745	NM_032045 NM_153379	83999	1.26	3.46E-04
RBMS3	241789_at	AW338699	NM_001003792 NM_001003793 NM_014483	27303	1.26	7.52E-03
PLAUR	211924_s_at	AY029180	NM_001005376 NM_001005377 NM_002659	5329	1.26	2.35E-03
FLJ25059	229025_s_at	AW008627	NM_144981	196294	1.26	2.34E-03
FKBP5	204560_at	NM_004117	NM_004117	2289	1.26	5.66E-03
HOMER3	215489_x_at	AI871287	NM_004838	9454	1.26	3.85E-03
ZNF503	227195_at	AA603467	NM_032772	84858	1.26	6.66E-04
AL833634	1562699_at	AL833634	---	---	1.26	8.19E-05
BAX	211833_s_at	U19599	NM_004324 NM_138761 NM_138762 NM_138763 NM_138764 NM_138765	581	1.25	6.21E-04
SUHW2	229360_at	N22886	NM_080764	140883	1.25	5.46E-04
CNTN4	229084_at	R42166	NM_175607 NM_175612 NM_175613	152330	1.25	9.69E-04
ZNF184	213452_at	AI811577	NM_007149	7738	1.25	4.11E-05
MPP1	202974_at	NM_002436	NM_002436	4354	1.25	1.81E-03
LOC93349	214791_at	AK023116	NM_138402	93349	1.25	5.56E-06
TOP3B	215781_s_at	D87012	NM_003935	8940	1.25	1.49E-03
RTTN	227072_at	BG167480	NM_173630	25914	1.25	8.89E-06
ASK	204244_s_at	NM_006716	NM_006716	10926	1.25	3.89E-05
FANCG	203564_at	NM_004629	NM_004629	2189	1.25	1.29E-04
WIG1	1555609_a_at	AF355465	NM_022470 NM_152240	64393	1.25	2.45E-03
RFC1	209085_x_at	L14922	NM_002913	5981	1.24	3.75E-07
TRIM59	227801_at	N90779	NM_173084	286827	1.24	3.52E-03
KIAA1522	224746_at	AB040955	XM_036299	57648	1.24	8.59E-03
SLC17A6	220551_at	NM_020346	NM_020346	57084	1.24	4.19E-04
PFKFB3	202464_s_at	NM_004566	NM_004566	5209	1.24	4.76E-04

BF110268	238178_at	BF110268	---	---	1.24	1.57E-03
TCF3	209152_s_at	AI655986	NM_003200	6929	1.24	2.72E-03
AMOTL1	225450_at	AI433831	NM_130847	154810	1.24	5.65E-06
TUBA2	210527_x_at	L11645	NM_006001 NM_079836	7278	1.24	3.79E-05
AB033091	225295_at	AB033091	---	---	1.23	8.34E-06
Cep70	219036_at	NM_024491	NM_024491	80321	1.23	6.01E-03
RTN4IP1	1555679_a_at	AF439711	NM_032730	84816	1.23	3.15E-03
HTATSF1	202601_s_at	AI373539	NM_014500	27336	1.23	1.15E-03
CA773938	1558517_s_at	CA773938	---	---	1.23	7.86E-04
RAB27A	210951_x_at	AF125393	NM_004580 NM_183234 NM_183235 NM_183236	5873	1.23	4.76E-03
TLE3	228340_at	BE967118	NM_005078	7090	1.23	4.90E-03
AI452715	229817_at	AI452715	---	---	1.23	3.71E-03
AK022598	232662_x_at	AK022598	---	---	1.22	2.67E-03
RNF26	224947_at	AL559247	NM_032015	79102	1.22	2.05E-04
C2orf23	204365_s_at	NM_022912	NM_022912	65055	1.22	9.80E-05
KIAA0574	213997_at	AB011146	---	23359	1.22	4.46E-03
K-ALPHA-1	213646_x_at	BE300252	NM_006082	10376	1.22	1.24E-05
SKP2	203625_x_at	BG105365	NM_005983 NM_032637	6502	1.22	4.38E-06
ZNF443	205928_at	NM_005815	NM_005815	10224	1.22	2.72E-03
MAPKAPK3	202788_at	NM_004635	NM_004635	7867	1.22	1.73E-04
RUSC1	206949_s_at	NM_014328	NM_014328	23623	1.22	4.02E-04
FIGNL1	222843_at	AK023411	NM_022116	63979	1.22	1.26E-04
SENP1	1552812_a_at	NM_014554	NM_014554	29843	1.22	2.44E-03
AW874669	239834_at	AW874669	---	---	1.22	1.90E-04
USP1	202413_s_at	NM_003368	NM_003368	7398	1.22	3.61E-04
KIAA0318	238817_at	BF063412	NM_015347	23504	1.22	1.61E-03
MGC5576	201764_at	NM_024056	NM_024056	79022	1.22	1.26E-03
MGC34032	1552782_at	AK091400	NM_152697	204962	1.21	2.92E-03
septin 6	213666_at	AK026589	NM_015129 NM_145799 NM_145800 NM_145802	23157	1.21	5.69E-03
AI143124	212832_s_at	AI143124	---	---	1.21	2.67E-04
SLC2A4RG	218494_s_at	NM_020062	NM_020062	56731	1.21	6.93E-04
ZNF423	214761_at	AW149417	NM_015069	23090	1.21	8.23E-03
CSRP2BP	228543_at	AA780252	NM_020536 NM_177926	57325	1.21	9.19E-06
MTUS1	212095_s_at	BE552421	NM_001001924 NM_001001925 NM_001001927 NM_001001931 NM_020749	57509	1.21	2.45E-04
BF056092	242629_at	BF056092	---	---	1.21	6.11E-03
HPSE	219403_s_at	NM_006665	NM_006665	10855	1.21	1.02E-02
BF445001	238212_at	BF445001	---	---	1.21	2.00E-03
SRGAP2	1568957_x_at	BE877775	XM_059095	23380	1.21	1.43E-04
CDKN1A	202284_s_at	NM_000389	NM_000389 NM_078467	1026	1.21	1.36E-03

RAD51C	209849_s_at	AF029669	NM_002876 NM_058216 NM_058217	5889	1.21	2.70E-03
GTPBP1	219357_at	NM_014027	NM_004286	9567	1.20	7.29E-04
SLC25A1	210010_s_at	U25147	NM_005984	6576	1.20	5.15E-04
KIAA1713	233536_at	AI202664	XM_290811	80816	1.20	2.85E-03
APAF1	204859_s_at	NM_013229	NM_001160 NM_013229 NM_181861 NM_181868 NM_181869	317	1.20	5.73E-05
WHSC1	222778_s_at	AW024870	NM_007331 NM_014919 NM_133330 NM_133331 NM_133332 NM_133333 NM_133334 NM_133335 NM_133336	7468	1.20	4.19E-05
T87730	242500_at	T87730	---	---	1.20	1.38E-03
EHD4	209536_s_at	AF320070	NM_139265	30844	1.20	5.84E-03
WIG1	219628_at	NM_022470	NM_022470 NM_152240	64393	1.20	8.50E-04
BF977829	229067_at	BF977829	---	---	1.20	3.26E-04
NUP62	202153_s_at	NM_016553	NM_012346 NM_016553 NM_153718 NM_153719	23636	1.20	3.85E-04
N50083	229110_at	N50083	---	---	1.20	1.89E-03
ARL6	223735_at	AL136815	NM_032146 NM_177976	84100	1.20	5.56E-03
MGC2574	203119_at	NM_024098	NM_024098	79080	1.19	1.54E-04
FLJ10407	218073_s_at	NM_018087	NM_018087	55706	1.19	1.01E-02
)KFZp313A243	230006_s_at	AI742358	---	258010	1.19	1.25E-04
C20orf7	227160_s_at	AW102828	NM_024120 NM_199052	79133	1.19	8.46E-04
MVK	215649_s_at	AF217536	NM_000431	4598	1.19	4.73E-03
PPP1R3D	204554_at	AL109928	NM_006242	5509	1.19	9.07E-04
MGC14560	218461_at	NM_016301	NM_016301	51184	1.19	2.49E-06
AC007277	216508_x_at	AC007277	---	---	1.19	1.79E-05
EPHA2	203499_at	NM_004431	NM_004431	1969	1.19	7.06E-04
UBE2L3	200684_s_at	AI819709	NM_003347 NM_198157	7332	1.19	4.60E-07
NFS1	218455_at	NM_021100	NM_021100 NM_181679	9054	1.19	2.24E-03
RELB	205205_at	NM_006509	NM_006509	5971	1.19	8.97E-03
GAS2L1	31874_at	Y07846	NM_006478 NM_152236 NM_152237	10634	1.19	1.72E-03
FLJ33814	225644_at	BF060776	NM_173510	150275	1.19	2.07E-05
K-ALPHA-1	211058_x_at	BC006379	NM_006082	10376	1.18	1.05E-05
NUP62	207740_s_at	NM_012346	NM_012346 NM_016553 NM_153718 NM_153719	23636	1.18	1.26E-04
K-ALPHA-1	201090_x_at	NM_006082	NM_006082	10376	1.18	1.13E-05
NLN	225944_at	AW006938	NM_020726	57486	1.18	5.24E-03

ALS2CR4	1553956_at	BG194770	NM_152388	65062	1.18	8.49E-04
FZD2	210220_at	L37882	NM_001466	2535	1.18	2.21E-05
RET	205879_x_at	BC004257	NM_020630 NM_020975	5979	1.18	2.08E-04
FLJ23322	231846_at	AK026975	NM_024955	80020	1.18	2.79E-04
BE878277	212829_at	BE878277	---	---	1.18	6.73E-04
ZNF286	239898_x_at	AI498484	NM_020652	57335	1.18	2.96E-03
HIVEP2	243254_at	T08739	NM_006734	3097	1.18	6.77E-04
SUCLG2	215772_x_at	AL050226	NM_003848	8801	1.18	3.77E-04
ARF4L	203586_s_at	NM_001661	NM_001661	379	1.18	3.10E-03
DDX11	213378_s_at	AI983033	NM_004399 NM_030653 NM_030655	1663	1.18	6.41E-03
PLEKHF2	218640_s_at	NM_024613	NM_024613	79666	1.18	2.90E-03
MCM7	208795_s_at	D55716	NM_005916 NM_182776	4176	1.18	2.26E-04
CDK6	207143_at	NM_001259	NM_001259	1021	1.18	4.14E-04
BAX	208478_s_at	NM_004324	NM_004324 NM_138761 NM_138762 NM_138763 NM_138764 NM_138765	581	1.17	5.30E-04
FLJ23322	220707_s_at	NM_024955	NM_024955	80020	1.17	2.10E-03
LOC139886	228654_at	AU145277	XM_066946	139886	1.17	1.82E-06
TANC	225308_s_at	AB051515	NM_033394	85461	1.17	1.16E-03
FBXO22	225736_at	BE966247	NM_012170 NM_147188	26263	1.17	3.53E-05
BE504215	228563_at	BE504215	---	---	1.17	2.17E-04
FAM43A	227410_at	AW264102	NM_153690	131583	1.17	2.24E-04
PXN	201087_at	NM_002859	NM_002859	5829	1.17	5.53E-04
BCLP	225536_at	AL545105	NM_033504	113452	1.16	9.28E-03
C1orf43	1555225_at	BC008306	NM_015449 NM_138740	25912	1.16	4.74E-04
CABYR	219928_s_at	NM_012189	NM_012189 NM_138643 NM_138644 NM_153768 NM_153769 NM_153770	26256	1.16	4.76E-04
SEZ6L	231650_s_at	BE672217	NM_021115	23544	1.16	9.63E-04
USP1	202412_s_at	AW499935	NM_003368	7398	1.16	9.85E-04
C21orf45	228597_at	AW151538	NM_018944	54069	1.16	9.08E-04
PDLIM5	203243_s_at	NM_006457	NM_00101151 3 NM_00101151 4 NM_00101151 5 NM_00101151 6 NM_006457	10611	1.16	3.70E-05
LGR4	218326_s_at	NM_018490	NM_018490	55366	1.16	1.79E-03
LOC284307	235773_at	AW029293	NM_00101087	284307	1.16	2.08E-03
ZCCHC4	220473_s_at	NM_014150	XM_376310	29063	1.16	2.21E-04
H10661	242317_at	H10661	---	---	1.16	4.34E-03
MFGE8	210605_s_at	BC003610	NM_005928	4240	1.16	5.08E-03
CDC5L	209055_s_at	AW268817	NM_001253	988	1.16	2.21E-06

ARL6IP	211935_at	D31885	NM_015161	23204	1.16	1.46E-04
NAGA	202944_at	NM_000262	NM_000262	4668	1.16	4.02E-05
RAB23	220955_x_at	NM_016277	NM_016277 NM_183227	51715	1.16	5.82E-04
KCNN1	206231_at	NM_002248	NM_002248	3780	1.16	4.89E-04
ch-TOG	1555278_a_at	BC035554	NM_00100893 8 NM_014756	9793	1.16	1.57E-04
MPHOSPH9	206205_at	NM_022782	NM_022782	10198	1.16	5.99E-04
AI141426	229898_at	AI141426	---	---	1.16	4.31E-04
POU2F1	206789_s_at	NM_002697	NM_002697	5451	1.15	5.40E-03
DKFZP434L187	230861_at	AA889613	XM_496054	26082	1.15	5.85E-05
C14orf160	224460_s_at	BC006117	NM_024884	79944	1.15	3.17E-03
PPM1D	204566_at	NM_003620	NM_003620	8493	1.15	1.21E-04
KIAA1853	236151_at	BF315452	NM_194286	84530	1.15	1.89E-03
GLS	203159_at	NM_014905	NM_014905	2744	1.15	4.23E-03
FLJ31842	234980_at	AI004375	NM_152487	148534	1.15	5.24E-03
FLJ20512	219219_at	NM_017854	NM_017854	54958	1.15	2.66E-03
C13orf7	219303_at	NM_024546	NM_024546	79596	1.15	1.92E-07
ADPN	233030_at	AK025665	NM_025225	80339	1.14	4.14E-03
FANCL	218397_at	NM_018062	NM_018062	55120	1.14	1.80E-04
MAK3	217745_s_at	NM_025146	NM_025146	80218	1.14	3.70E-06
H05254	244170_at	H05254	---	---	1.14	1.12E-03
FAM14B	230172_at	AL039706	NM_145249 NM_206949	122509	1.14	5.19E-03
NR3C1	216321_s_at	X03348	NM_000176	2908	1.14	4.77E-03
FH	203032_s_at	AI363836	NM_000143	2271	1.14	1.19E-03
SIVA	203489_at	NM_006427	NM_006427 NM_021709	10572	1.14	1.23E-04
C10orf58	224435_at	BC005871	NM_032333	84293	1.14	2.67E-05
MCAM	211042_x_at	BC006329	NM_006500	4162	1.14	2.97E-06
LOC144997	227289_at	AU119437	---	144997	1.14	8.41E-04
SAFB2	32099_at	D50928	NM_014649	9667	1.14	1.08E-03
MTUS1	212093_s_at	AI695017	NM_00100192 4 NM_00100192 5 NM_00100192 7 NM_00100193 1 NM_020749	57509	1.14	1.51E-04
SORD	201562_s_at	NM_003104	NM_003104	6652	1.14	8.56E-04
HMGB1	200679_x_at	BE311760	NM_002128	3146	1.14	4.89E-05
TUBB	212320_at	BC001002	NM_178014	203068	1.14	1.69E-04
CDC42EP4	218062_x_at	NM_012121	NM_012121	23580	1.13	4.75E-04
PACSIN1	227053_at	N47315	NM_020804	29993	1.13	8.60E-03
KIAA1712	228334_x_at	AI633734	NM_030633	80817	1.13	1.79E-03
CDK2AP1	201938_at	NM_004642	NM_004642	8099	1.13	4.73E-05
AI650582	226475_at	AI650582	---	---	1.13	9.58E-03
ZNF626	1552643_at	NM_145297	NM_145297	199777	1.13	4.93E-04
MAPKAPK3	202787_s_at	U43784	NM_004635	7867	1.13	2.06E-03
BTG3	205548_s_at	NM_006806	NM_006806	10950	1.13	3.73E-03
UBE2S	202779_s_at	NM_014501	NM_014501	27338	1.13	1.67E-04
TP53INP1	225912_at	AW341649	NM_033285	94241	1.13	6.83E-03
Cep192	218827_s_at	NM_018069	NM_018069 NM_032142	55125	1.13	3.17E-04
SUHW2	230789_at	AI015954	NM_080764	140883	1.13	1.79E-05

LOC128977	1553974_at	BC030758	NM_173793	128977	1.12	4.40E-04
CDH2	203441_s_at	NM_001792	NM_001792	1000	1.12	5.79E-03
ST8SIA1	210073_at	L32867	NM_003034	6489	1.12	1.10E-03
PTP4A1	200733_s_at	U48296	NM_003463	7803	1.12	2.69E-03
RNF34	219035_s_at	NM_025126	NM_025126	80196	1.12	2.20E-04
			NM_194271			
DDX11	208159_x_at	NM_004399	NM_004399	1663	1.12	2.66E-03
			NM_030653			
			NM_030655			
PTGES2	218083_at	NM_025072	NM_025072	80142	1.12	5.25E-05
			NM_198938			
			NM_198939			
			NM_198940			
PCCB	212694_s_at	NM_000532	NM_000532	5096	1.12	1.29E-03
ETV4	211603_s_at	U35622	NM_001986	2118	1.12	1.80E-03
MGC7036	227983_at	AI810244	NM_145058	196383	1.12	1.70E-05
GAP43	204471_at	NM_002045	NM_002045	2596	1.12	2.85E-05
DATF1	222595_s_at	AL578222	NM_022105	11083	1.12	9.82E-04
			NM_080796			
			NM_080797			
C1orf41	215691_x_at	AV702994	NM_016126	51668	1.11	6.15E-03
CHES1	218031_s_at	NM_018589	NM_005197	1112	1.11	3.51E-04
LOC89944	213713_s_at	R48779	NM_138342	89944	1.11	4.60E-03
AI807356	227349_at	AI807356	---	---	1.11	7.01E-03
RANGAP1	212127_at	BE379408	NM_002883	5905	1.11	1.65E-03
CHRNA5	206533_at	NM_000745	NM_000745	1138	1.11	2.14E-03
RNF138	239143_x_at	AW291944	NM_016271	51444	1.11	1.74E-04
			NM_198128			
LOC440145	225578_at	AI885466	XM_495961	440145	1.11	2.53E-04
FGF1	1552721_a_at	NM_033136	NM_000800	2246	1.11	1.39E-03
			NM_033136			
			NM_033137			
AL533234	225725_at	AL533234	---	---	1.11	7.91E-04
TM7SF3	222477_s_at	BC005176	NM_016551	51768	1.11	5.89E-04
FLJ90430	229533_x_at	AI963028	NM_178558	340252	1.11	7.02E-03
RPS27L	218007_s_at	NM_015920	NM_015920	51065	1.11	3.68E-03
CRTAC1	221204_s_at	NM_018058	NM_018058	55118	1.11	1.69E-03
SKD3	221845_s_at	AI655698	NM_030813	81570	1.11	1.33E-04
ZNF85	206572_x_at	NM_003429	NM_003429	7639	1.11	3.31E-03
XRCC3	216299_s_at	AK022829	NM_005432	7517	1.11	7.35E-05
AKAP13	222024_s_at	AK022014	NM_006738	11214	1.11	5.22E-03
			NM_007200			
			NM_144767			
C9orf81	1557985_s_at	AA248753	XM_095991	84131	1.11	6.85E-04
PDCL	204448_s_at	AF031463	NM_005388	5082	1.10	4.06E-03
RAPH1	243012_at	BF196252	NM_025252	65059	1.10	2.75E-03
			NM_203365			
			NM_213589			
DEK	200934_at	NM_003472	NM_003472	7913	1.10	5.01E-06
PPIF	201490_s_at	NM_005729	NM_005729	10105	1.10	3.89E-06
PTP4A1	200730_s_at	BF576710	NM_003463	7803	1.10	4.25E-03
AI888657	244189_at	AI888657	---	---	1.10	1.81E-05
TCF7L2	216037_x_at	AA664011	NM_030756	6934	1.10	1.01E-02
SNX5	222417_s_at	AF121855	NM_014426	27131	1.10	2.71E-03
			NM_152227			
SSH2	226080_at	BE676214	NM_033389	85464	1.10	4.02E-04
BE671123	235798_at	BE671123	---	---	1.10	2.84E-05
MSH6	211450_s_at	D89646	NM_000179	2956	1.10	4.87E-04

PDZRN3	212915_at	AL569804	NM_015009	23024	1.10	4.32E-03
PPP3CB	209817_at	M29550	NM_021132	5532	1.10	4.16E-04
FAM29A	218602_s_at	NM_017645	NM_017645	54801	1.09	1.73E-04
MINA	1554774_at	AB083191	NM_032778 NM_153182	84864	1.09	7.48E-03
SRGAP1	1569269_s_at	BM912471	NM_020762	57522	1.09	8.29E-03
LOC152185	234995_at	AA668779	NM_144718	152185	1.09	2.38E-04
LOC63929	227910_at	AI635379	NM_022098	63929	1.09	2.09E-03
ITPR2	202662_s_at	NM_002223	NM_002223	3709	1.09	4.74E-03
PCDH17	228863_at	N69091	NM_014459	27253	1.09	2.79E-04
ELAVL1	201727_s_at	NM_001419	NM_001419	1994	1.09	1.03E-02
PKP4	201928_at	AA194254	NM_00100547 6 NM_003628	8502	1.09	5.68E-05
MTUS1	212096_s_at	AL096842	NM_00100192 4 NM_00100192 5 NM_00100192 7 NM_00100193 1 NM_020749	57509	1.09	8.18E-06
SPOCK	202363_at	AF231124	NM_004598	6695	1.09	4.27E-04
DIAPH1	209190_s_at	AF051782	NM_005219	1729	1.09	3.00E-03
CKLFSF7	226017_at	AI708432	NM_138410 NM_181472	112616	1.09	7.48E-04
CORO6	1552301_a_at	NM_032854	NM_032854	84940	1.09	3.51E-03
C18orf9	219311_at	NM_024899	NM_024899	79959	1.09	7.95E-04
PDGFD	219304_s_at	NM_025208	NM_025208 NM_033135	80310	1.09	1.44E-03
UBE2L3	200676_s_at	NM_003347	NM_003347 NM_198157	7332	1.09	3.98E-06
SLA/LP	227982_at	AI806592	NM_016955 NM_153825	51091	1.08	6.59E-03
HOMER3	204647_at	NM_004838	NM_004838	9454	1.08	1.80E-04
SNRPD3	202567_at	NM_004175	NM_004175	6634	1.08	1.90E-05
3'HEXO	226416_at	AL137679	NM_153332	90459	1.08	3.50E-03
LMNB2	216952_s_at	M94363	NM_032737	84823	1.08	2.28E-04
CBX5	209715_at	L07515	NM_012117	23468	1.08	2.29E-03
ASF1A	203428_s_at	AB028628	NM_014034	25842	1.08	4.83E-05
UBE2L3	200682_s_at	BG531983	NM_003347 NM_198157	7332	1.08	7.87E-06
PDLIM5	212412_at	AV715767	NM_00101151 3 NM_00101151 4 NM_00101151 5 NM_00101151 6 NM_006457	10611	1.08	2.29E-03
PLEKHG3	212823_s_at	AI738980	NM_015549	26030	1.08	9.61E-03
ASXL1	244519_at	AI829840	NM_015338	171023	1.08	1.17E-03
HIST1H4C	205967_at	NM_003542	NM_003542	8364	1.08	4.91E-03
UBE2L3	200683_s_at	BE964689	NM_003347 NM_198157	7332	1.07	1.25E-06
DPYSL5	222797_at	BF508726	NM_020134	56896	1.07	7.59E-04

ZFP36L2	201368_at	U07802	NM_006887	678	1.07	1.86E-04
PUSL1	228733_at	AU154793	NM_153339	126789	1.07	3.30E-03
AA973128	242294_at	AA973128	---	---	1.07	3.63E-03
SAP30	204899_s_at	BF247098	NM_003864	8819	1.07	7.88E-05
ETV4	1554576_a_at	BC007242	NM_001986	2118	1.07	2.79E-03
RARA	203749_s_at	AI806984	NM_000964	5914	1.07	3.55E-03
TUBB	211714_x_at	BC005838	NM_178014	203068	1.07	3.33E-04
STARD4	226390_at	AA628398	NM_139164	134429	1.07	1.71E-05
TUBA6	211750_x_at	BC005946	NM_032704	84790	1.07	1.66E-05
CKLFSF8	235099_at	AW080832	NM_178868	152189	1.07	5.68E-03
THOC3	224623_at	BE614567	NM_032361	84321	1.07	3.08E-05
PRPS1	209440_at	BC001605	NM_002764	5631	1.07	2.15E-05
PRPS2	203401_at	NM_002765	NM_002765	5634	1.07	2.40E-03
CRY1	209674_at	D83702	NM_004075	1407	1.06	3.45E-03
DKFZP547N043	223511_at	AL512744	NM_00101098 4 NM_032018	83932	1.06	1.17E-03
FSTL1	208782_at	BC000055	NM_007085	11167	1.06	2.60E-03
NDRG2	214279_s_at	W74452	NM_016250 NM_201535 NM_201536 NM_201537 NM_201538 NM_201539 NM_201540 NM_201541	57447	1.06	7.80E-03
FLJ13273	1554518_at	BC032942	NM_024751	79807	1.06	4.36E-05
EPB41L1	212336_at	AA912711	NM_012156 NM_177996	2036	1.06	6.75E-05
FAM55C	243011_at	BF317081	NM_145037	91775	1.06	9.28E-03
TCF3	213730_x_at	BE962186	NM_003200	6929	1.06	4.18E-04
PLXNB2	208890_s_at	BC004542	XM_371474	23654	1.06	2.15E-04
BE218067	243662_at	BE218067	---	---	1.06	6.88E-03
PDRG1	225075_at	AL031658	NM_030815	81572	1.06	4.96E-03
BTG3	213134_x_at	AI765445	NM_006806	10950	1.06	2.21E-03
CDC42EP4	214721_x_at	AL162074	NM_012121	23580	1.06	6.10E-04
LOC96610	1569013_s_at	BC033148	NM_080926	96610	1.06	2.71E-03
BF510533	228107_at	BF510533	---	---	1.06	2.14E-03
TFDP1	204147_s_at	NM_007111	NM_007111	7027	1.06	2.66E-03
AI092770	230466_s_at	AI092770	---	---	1.06	1.88E-03
SFRP1	202037_s_at	NM_003012	NM_003012	6422	1.06	2.39E-04
FBXO22	225734_at	AW294765	NM_012170 NM_147188	26263	1.06	1.77E-05
TUBB	209026_x_at	AF141349	NM_178014	203068	1.06	6.65E-04
ELK3	221773_at	AW575374	NM_005230	2004	1.05	1.33E-05
APG4C	228190_at	BF197009	NM_032852 NM_178221	84938	1.05	3.09E-03
BCL11A	210347_s_at	AF080216	NM_018014 NM_022893 NM_138553 NM_138559	53335	1.05	4.33E-03
MFAP2	203417_at	NM_017459	NM_002403 NM_017459	4237	1.05	2.57E-04
C20orf108	224693_at	AI133137	NM_080821	116151	1.05	1.58E-03
CD24	209772_s_at	X69397	NM_013230	934	1.05	1.98E-04

FAS	204780_s_at	AA164751	NM_000043 NM_152871 NM_152872 NM_152873 NM_152874 NM_152875 NM_152876 NM_152877	355	1.05	3.67E-04
GGCX	214005_at	BE326952	NM_000821	2677	1.05	6.80E-03
SESN3	235684_s_at	BF685808	NM_144665	143686	1.05	8.56E-03
ANAPC7	225554_s_at	AA131793	NM_016238	51434	1.05	3.09E-06
INA	230859_at	BF111276	NM_032727	9118	1.05	1.36E-03
FKBP7	223667_at	AF092137	NM_016105 NM_181342	51661	1.05	1.99E-03
ESRRG	207981_s_at	NM_001438	NM_001438 NM_206594 NM_206595	2104	1.05	6.81E-03
RET	215771_x_at	X15786	NM_020630 NM_020975	5979	1.05	9.85E-04
CTNNAL1	202468_s_at	NM_003798	NM_003798	8727	1.05	1.23E-03
SMC1L1	201589_at	D80000	NM_006306	8243	1.05	3.76E-05
NFYB	218128_at	AU151875	NM_006166	4801	1.04	1.55E-04
NFYB	218127_at	AI804118	NM_006166	4801	1.04	2.59E-03
EPOR	209963_s_at	M34986	NM_000121	2057	1.04	9.69E-04
MGC10854	223455_at	BG493862	NM_032300	84260	1.04	2.09E-03
TCF3	210776_x_at	M31222	NM_003200	6929	1.04	6.32E-05
ELAVL4	238073_at	R55745	NM_021952	1996	1.04	6.02E-07
N66584	230593_at	N66584	---	---	1.04	1.67E-03
MGC13204	225836_s_at	AL528840	NM_031465	83695	1.04	4.81E-04
NUCKS	222424_s_at	BC000805	NM_022731	64710	1.04	1.65E-03
FBXO22	225737_s_at	BE966247	NM_012170 NM_147188	26263	1.04	2.33E-04
CXorf40	228809_at	AW006998	NM_178124	91966	1.04	6.72E-03
NEFL	221805_at	AL537457	NM_006158	4747	1.04	3.74E-03
MTHFD1	202309_at	NM_005956	NM_005956	4522	1.04	1.63E-04
SRD5A1	210959_s_at	AF113128	NM_001047	6715	1.04	3.17E-03
NASP	201969_at	AW003362	NM_002482 NM_152298 NM_172164	4678	1.04	8.40E-03
Septin 10	212698_s_at	BF966021	NM_144710 NM_178584	151011	1.04	4.13E-03
PLCXD1	218951_s_at	NM_018390	NM_018390	55344	1.04	2.13E-03
CD24	208650_s_at	BG327863	NM_013230	934	1.04	5.35E-03
ZNF92	235170_at	T52999	NM_007139 NM_152626	168374	1.04	1.71E-05
CENPF	207331_at	NM_016343	NM_016343	1063	1.03	3.14E-04
AA766126	244385_at	AA766126	---	---	1.03	2.59E-04
TENS1	217853_at	NM_022748	NM_022748	64759	1.03	1.28E-03
AL559474	235918_x_at	AL559474	---	---	1.03	7.29E-04
FLJ10407	234672_s_at	AL354612	NM_018087	55706	1.03	4.74E-05
SET8	220200_s_at	NM_020382	NM_020382	387893	1.03	5.39E-04
FLJ21125	226204_at	AI832193	NM_024627	79680	1.03	7.12E-03
PANK2	218809_at	NM_024960	NM_024960 NM_153637 NM_153638 NM_153639 NM_153640 NM_153641	80025	1.03	5.90E-06

TAF5	210053_at	AW138827	NM_006951	6877	1.03	3.76E-04
AI806853	225601_at	AI806853	---	---	1.03	2.08E-05
MMP11	203878_s_at	NM_005940	NM_005940	4320	1.03	2.69E-03
TUBA6	209251_x_at	BC004949	NM_032704	84790	1.03	2.38E-05
BCL2L11	225606_at	AI949179	NM_006538 NM_138621 NM_138622 NM_138623 NM_138624 NM_138625 NM_138626 NM_138627 NM_207002 NM_207003	10018	1.03	1.11E-04
ZGPAT	221848_at	AL121845	NM_032527 NM_181484 NM_181485	84619	1.03	4.13E-04
C14orf106	241816_at	AW103300	NM_018353	55320	1.03	2.05E-03
BCL3	204908_s_at	NM_005178	NM_005178	602	1.03	7.14E-04
CBFA2T2	209145_s_at	AF068266	NM_005093 NM_175864	9139	1.03	4.72E-03
MCFP	227012_at	AI823986	NM_018843	55972	1.03	1.94E-06
THAP10	219596_at	NM_020147	NM_020147	56906	1.03	7.28E-04
AW511319	227167_s_at	AW511319	---	---	1.03	6.48E-04
C2orf7	223312_at	BC005069	NM_032319	84279	1.03	8.00E-05
TTC9	213172_at	AW235608	XM_027236	23508	1.03	5.24E-03
DOT1L	231297_at	AI479899	NM_032482	84444	1.03	7.59E-03
TM7SF3	226478_at	BF540749	NM_016551	51768	1.02	1.16E-03
NFIA	224976_at	R37335	NM_005595	4774	1.02	4.91E-03
MGC72104	243689_s_at	AI681945	NM_207350	284802	1.02	6.29E-03
DGCR14	204383_at	NM_022719	NM_022719	8220	1.02	2.13E-03
TUBB2	208977_x_at	BC004188	NM_006088	10383	1.02	1.96E-05
ZNF505	215758_x_at	AC007204	NM_00100412 6 NM_031218	81931	1.02	1.93E-03
C6orf115	223361_at	AF116682	XM_371848	58527	1.02	3.11E-04
RAB3C	242328_at	BG055348	NM_138453	115827	1.02	5.07E-03
CECR5	218592_s_at	NM_017829	NM_017829 NM_033070	27440	1.02	1.72E-05
PSMD5	203447_at	AU157008	NM_005047	5711	1.02	3.28E-06
PHF6	225501_at	AK027039	NM_032335 NM_032458	84295	1.02	3.94E-05
CSRP2BP	228544_s_at	AA780252	NM_020536 NM_177926	57325	1.02	3.08E-03
M96	209704_at	AL523380	NM_007358	22823	1.01	2.10E-04
PELI2	219132_at	NM_021255	NM_021255	57161	1.01	2.52E-05
RPA1	201529_s_at	NM_002945	NM_002945	6117	1.01	1.36E-04
TCF3	213811_x_at	AW062341	NM_003200	6929	1.01	2.33E-03
C6orf151	226263_at	AA630674	NM_152551	154007	1.01	1.66E-03
C6orf4	215411_s_at	AL008730	NM_147200 NM_147686	10758	1.01	1.04E-02
DUSP6	208893_s_at	BC005047	NM_001946 NM_022652	1848	1.01	4.12E-03
PEG10	212094_at	AL582836	XM_496907 XM_499343	23089	1.01	4.74E-03
CTNNBL1	221021_s_at	NM_030877	NM_030877	56259	1.01	1.87E-05
MPHOSPH9	237158_s_at	AW449069	NM_022782	10198	1.01	8.39E-04
SCLY	221575_at	BC000586	NM_016510	51540	1.01	5.24E-04

NUP50	222583_s_at	AF116624	NM_007172 NM_153645 NM_153684	10762	1.01	9.47E-04
GSTO2	227163_at	AL162742	NM_183239	119391	1.01	9.87E-03
C20orf44	222470_s_at	AA033998	NM_018244 NM_199487 NM_199513	55245	1.01	9.65E-05
N56956	227254_at	N56956	---	---	1.01	6.12E-03
BAGE4 BAGE2	1555408_at	AF218570	NM_181704 NM_182482	85317 85319	1.01	6.41E-03
ARL2L1	228201_at	BE858032	NM_144996 NM_182896	200894	1.01	2.30E-03
TCF7L2	212762_s_at	AI375916	NM_030756	6934	1.01	2.14E-03
C21orf45	219004_s_at	NM_018944	NM_018944	54069	1.01	1.32E-03
C10orf58	228155_at	BF512388	NM_032333	84293	1.00	1.86E-05
LYK5	52169_at	AI302185	NM_001003786 NM_001003787 NM_001003788 NM_153335	92335	1.00	6.85E-04
PGF	209652_s_at	BC001422	NM_002632	5228	1.00	5.14E-03
FLJ14627	221908_at	AL120375	NM_032814	84900	1.00	7.78E-04
NUP37	218622_at	NM_024057	NM_024057	79023	1.00	2.06E-03
SYT3	223901_at	AL136594	NM_032298	84258	1.00	6.98E-05
NARG1	222837_s_at	AF327722	NM_057175	80155	1.00	1.83E-03
RNF144	204040_at	NM_014746	NM_014746	9781	1.00	1.07E-06
MRPL35	222775_s_at	AK026220	NM_016622 NM_145644	51318	1.00	1.64E-03
ROR1	205805_s_at	NM_005012	NM_005012	4919	1.00	3.27E-03
POP1	213449_at	D31765	NM_015029	10940	1.00	7.21E-03
ABTB2	213497_at	AL050374	NM_145804	25841	1.00	2.06E-03
ASCC3	212815_at	AA156961	NM_006828	10973	1.00	4.84E-03
HDGF	216484_x_at	L24521	NM_004494	3068	1.00	1.89E-03
DUSP6	208892_s_at	BC003143	NM_001946 NM_022652	1848	1.00	2.56E-03
DCPS	218774_at	NM_014026	NM_014026	28960	1.00	6.63E-03
AKIP	228800_x_at	BE463815	NM_017900	54998	1.00	1.79E-03
C6orf60	220150_s_at	NM_024581	NM_024581	79632	1.00	2.46E-03
NXT2	209629_s_at	AF201942	NM_018698	55916	1.00	6.17E-03
SEC61A2	219499_at	NM_018144	NM_018144	55176	1.00	1.35E-05
AI095542	235759_at	AI095542	---	---	1.00	3.08E-04
RPA1	201528_at	BG398414	NM_002945	6117	1.00	7.67E-06
FLJ14627	221909_at	AW299700	NM_032814	84900	1.00	1.91E-03
BE967311	226225_at	BE967311	---	---	0.99	6.96E-05
KIAA0841	213054_at	AA845355	XM_049237	23354	0.99	5.40E-05
GNG2	224965_at	AU118419	NM_053064	54331	0.99	5.01E-05
ZNF238	207164_s_at	NM_006352	NM_006352 NM_205768	10472	0.99	3.24E-03
PSMD9	209334_s_at	BC002383	NM_002813	5715	0.99	2.73E-04
SNX5	217792_at	NM_014426	NM_014426 NM_152227	27131	0.99	1.19E-05
PHLDA3	218634_at	NM_012396	NM_012396	23612	0.99	4.00E-04
ITGA2B	206494_s_at	NM_000419	NM_000419	3674	0.99	8.82E-03
SOX2	213722_at	AW007161	NM_003106	6657	0.99	7.14E-03
RALY	201271_s_at	NM_016732	NM_007367 NM_016732	22913	0.99	1.03E-05

PCNT1	218014_at	NM_024844	NM_024844	79902	0.99	2.81E-03
LOC400506	213237_at	AI652058	XM_375305	400506	0.99	8.09E-04
SLC6A15	240419_at	N25883	NM_018057 NM_182767	55117	0.99	6.25E-03
CBFA2T2	209144_s_at	AI810484	NM_005093 NM_175864	9139	0.99	5.43E-03
ASMTL	36554_at	Y15521	NM_004192	8623	0.99	2.79E-04
NARG1	226998_at	AL556909	NM_057175	80155	0.99	2.85E-05
KLHL5	226001_at	AK002174	NM_00100707 5 NM_199039	51088	0.99	5.50E-04
MGC59937	1569144_a_at	BC018787	NM_199001	375791	0.98	9.69E-03
NEDD4L	212445_s_at	AI357376	NM_015277	23327	0.98	3.46E-03
COVA1	32042_at	S72904	NM_006375 NM_182314	10495	0.98	1.78E-04
SWAP70	209306_s_at	AI139569	NM_015055	23075	0.98	1.45E-03
EPLIN	217892_s_at	NM_016357	NM_016357	51474	0.98	1.73E-03
TEF	225840_at	AA779795	NM_003216	7008	0.98	3.69E-03
KIAA0391	202713_s_at	AA129755	XM_375074	9692	0.98	7.23E-05
TXNRD1	201266_at	NM_003330	NM_003330 NM_182729 NM_182742 NM_182743	7296	0.98	7.52E-04
AI220627	213608_s_at	AI220627	XM_377713	402055	0.98	1.61E-04
SLC25A17	211754_s_at	BC005957	NM_006358	10478	0.98	1.22E-03
DDX11	208149_x_at	NM_030653	NM_004399 NM_030653 NM_030655	1663	0.98	2.49E-03
CD24	266_s_at	L33930	NM_013230	934	0.98	9.60E-04
SNAP29	218327_s_at	NM_004782	NM_004782	9342	0.98	4.38E-04
DDEFL1	219103_at	NM_017707	NM_017707	55616	0.98	8.35E-03
MTAP	211363_s_at	AF109294	NM_002451	4507	0.98	8.59E-03
H2AFJ	225245_x_at	BG386566	NM_018267 NM_177925	55766	0.98	9.29E-03
W91876	230240_at	W91876	---	---	0.98	6.38E-03
FLJ38973	227973_at	BF130937	NM_153689	205327	0.97	4.61E-03
ARL6	235320_at	AL138043	NM_032146 NM_177976	84100	0.97	9.35E-03
WWOX	219077_s_at	NM_016373	NM_016373 NM_018560 NM_130788 NM_130790 NM_130791 NM_130792 NM_130844	51741	0.97	2.03E-03
XTP3TPA	218069_at	NM_024096	NM_024096	79077	0.97	1.83E-04
NAPB	225111_s_at	AK022817	NM_022080	63908	0.97	1.32E-05
MRVI1	226047_at	N66571	NM_006069 NM_130385	10335	0.97	6.11E-03
H93038	241574_s_at	H93038	---	---	0.97	4.24E-03
AI700633	212812_at	AI700633	---	---	0.97	4.71E-04
DDAH2	215537_x_at	AJ012008	NM_013974	23564	0.97	4.32E-03
HSPC159	219998_at	NM_014181	NM_014181	29094	0.97	7.46E-04
GRK6	202849_x_at	NM_002082	NM_00100410 5 NM_00100410 6 NM_002082	2870	0.97	5.10E-03

ZNF219	219314_s_at	NM_016423	NM_016423	51222	0.97	2.40E-03
KLF3	219657_s_at	NM_016531	NM_016531	51274	0.97	2.90E-03
K03460	216323_x_at	K03460	---	---	0.96	1.11E-03
IER5	218611_at	NM_016545	NM_016545	51278	0.96	1.63E-03
BC040884	1560156_at	BC040884	---	---	0.96	8.01E-03
PROS1	207808_s_at	NM_000313	NM_000313	5627	0.96	4.30E-03
ALDH1B1	209645_s_at	NM_000692	NM_000692	219	0.96	5.95E-03
PEG10	212092_at	BE858180	XM_496907	23089	0.96	1.83E-03
GRK6	211543_s_at	AF040752	XM_499343 NM_001004105 NM_001004106 NM_002082	2870	0.96	4.44E-04
RPP30	203436_at	NM_006413	NM_006413	10556	0.96	4.98E-04
AD-003	223369_at	BC001396	NM_014064	28989	0.96	5.09E-03
BG026236	230166_at	BG026236	---	---	0.96	6.20E-03
KIAA2002	225913_at	AK025943	XM_370878	79834	0.96	8.75E-03
CD24	208651_x_at	M58664	NM_013230	934	0.96	1.62E-03
TCF3	209153_s_at	M31523	NM_003200	6929	0.96	1.74E-04
NMT1	201157_s_at	AF020500	NM_021079	4836	0.96	7.38E-03
SURB7	209363_s_at	U46837	NM_004264	9412	0.96	1.98E-04
PHYHIPL	226623_at	AI829726	NM_032439	84457	0.96	4.52E-06
HSPC117	200042_at	NM_014306	NM_014306	51493	0.96	2.37E-05
ALDH7A1	208950_s_at	BC002515	NM_001182	501	0.96	1.54E-05
TFDP2	226157_at	AI569747	NM_006286	7029	0.95	1.73E-03
SURB7	209362_at	AI688580	NM_004264	9412	0.95	3.64E-04
BC003636	222756_s_at	BC003636	---	---	0.95	1.07E-04
SCLY	59705_at	AA911739	NM_016510	51540	0.95	8.43E-04
MGC15634	242923_at	AW027457	---	84841	0.95	9.36E-03
KIBRA	216074_x_at	AK001727	NM_015238	23286	0.95	6.38E-03
CASP8AP2	222201_s_at	AB037736	NM_012115	9994	0.95	4.11E-04
AARS	201000_at	NM_001605	NM_001605	16	0.95	1.89E-03
LOC148203	229700_at	BE966267	---	148203	0.95	3.12E-04
CBLL1	220018_at	NM_024814	NM_024814	79872	0.95	1.63E-03
MRPL35	225255_at	AA810707	NM_016622 NM_145644	51318	0.95	4.17E-03
FAM29A	233655_s_at	AK022964	NM_017645	54801	0.95	1.14E-05
DKFZP566E144	223989_s_at	BC003502	NM_015523	25996	0.95	1.35E-04
PHF20	235389_at	BG168139	NM_016436	51230	0.95	7.86E-06
C20orf23	219570_at	NM_024704	NM_024704	55614	0.95	7.76E-04
MRS2L	228542_at	AI631209	NM_020662	57380	0.95	5.03E-04
GPX3	201348_at	NM_002084	NM_002084	2878	0.95	6.41E-03
PRIM2A	205628_at	NM_000947	NM_000947	5558	0.95	1.53E-04
PPAT	209433_s_at	AI457120	NM_002703	5471	0.95	1.28E-06
SLC9A3R1	201349_at	NM_004252	NM_004252	9368	0.95	3.16E-04
SNX5	229980_s_at	AA131508	NM_014426 NM_152227	27131	0.95	2.51E-04
C9orf122	1557014_a_at	BC041970	XM_379636	158228	0.95	9.32E-03
ETV6	235056_at	AV722693	NM_001987	2120	0.95	1.50E-03
ROD1	224617_at	AI735576	NM_005156	9991	0.95	5.78E-04
PPP2R5D	202513_s_at	NM_006245	NM_006245 NM_180976 NM_180977	5528	0.95	5.76E-03
AI392908	230352_at	AI392908	---	---	0.95	5.22E-03
PPAT	209434_s_at	U00238	NM_002703	5471	0.95	1.94E-06
HSPC129	1555106_a_at	BC035744	NM_016396	51496	0.94	1.87E-04
KIAA1333	223256_at	AW007694	NM_017769	55632	0.94	1.83E-05

GAP43	216963_s_at	AF279774	NM_002045	2596	0.94	8.23E-05
C6orf155	226810_at	BE500942	NM_024882	79940	0.94	3.25E-04
FKBP7	224002_s_at	AF100751	NM_016105	51661	0.94	7.01E-04
			NM_181342			
NIT2	218557_at	NM_020202	NM_020202	56954	0.94	8.71E-04
NTAN1	213061_s_at	AA643304	NM_173474	123803	0.94	3.59E-03
FBXL13	243057_at	AI923673	NM_145032	222235	0.94	1.12E-03
SURF5	206593_s_at	NM_006752	NM_006752	6837	0.94	1.04E-03
			NM_133640			
			NM_181491			
ASMTL	209394_at	BC002508	NM_004192	8623	0.94	7.15E-04
PXMP4	219428_s_at	BF057649	NM_007238	11264	0.94	1.03E-03
			NM_183397			
IGF1R	203627_at	AI830698	NM_000875	3480	0.94	5.54E-04
HN1	217755_at	NM_016185	NM_00100203	51155	0.94	1.06E-03
			2			
			NM_00100203			
			3			
			NM_016185			
AL833487	1562245_a_at	AL833487	---	---	0.94	2.02E-03
LIG3	204123_at	NM_013975	NM_002311	3980	0.93	1.64E-05
			NM_013975			
CSTF1	202190_at	NM_001324	NM_001324	1477	0.93	1.15E-03
KIAA0406	212898_at	AB007866	NM_014657	9675	0.93	4.37E-05
LIG3	207348_s_at	NM_002311	NM_002311	3980	0.93	5.83E-05
			NM_013975			
MAML3	242794_at	AI569476	NM_018717	55534	0.93	5.09E-03
SRD5A1	211056_s_at	BC006373	NM_001047	6715	0.93	1.03E-02
ELAVL4	206051_at	NM_021952	NM_021952	1996	0.93	8.90E-05
XRCC4	210813_s_at	BC005259	NM_003401	7518	0.93	5.17E-03
			NM_022406			
			NM_022550			
ALDH7A1	208951_at	BC002515	NM_001182	501	0.93	4.00E-06
SLCO3A1	227367_at	AW976431	NM_013272	28232	0.93	4.38E-03
OGFRL1	219582_at	NM_024576	NM_024576	79627	0.93	1.65E-04
CDH2	203440_at	M34064	NM_001792	1000	0.93	9.39E-06
FLJ31842	237515_at	AA054642	NM_152487	148534	0.93	6.73E-04
LOC283464	226868_at	BF977231	XM_290597	283464	0.93	1.55E-04
DNMT1	201697_s_at	NM_001379	NM_001379	1786	0.93	1.35E-04
H2AFZ	200853_at	NM_002106	NM_002106	3015	0.93	1.62E-06
GAS2L1	209729_at	BC001782	NM_006478	10634	0.93	6.61E-03
			NM_152236			
			NM_152237			
IDH2	210046_s_at	U52144	NM_002168	3418	0.93	2.00E-04
LOC51337	218500_at	NM_016647	NM_016647	51337	0.93	2.50E-03
)KFZp313A243:	230005_at	AI742358	---	258010	0.93	1.41E-03
CKLF	223451_s_at	AF096895	NM_016326	51192	0.93	7.64E-03
			NM_016951			
			NM_181640			
			NM_181641			
APEX2	204408_at	NM_014481	NM_014481	27301	0.92	5.63E-04
UBOX5	215544_s_at	AL121891	NM_014948	22888	0.92	5.63E-03
			NM_199415			
TMEM38B	222735_at	AW452608	NM_018112	55151	0.92	1.79E-03
GPX2	202831_at	NM_002083	NM_002083	2877	0.92	9.43E-04
MPHOSPH9	215731_s_at	X98258	NM_022782	10198	0.92	1.91E-04
HABP4	232341_x_at	AK025144	NM_014282	22927	0.92	1.03E-02

C20orf161	1553960_at	CA447177	NM_033421 NM_152897	90203	0.92	8.23E-03
FKBP5	224840_at	AI753747	NM_004117	2289	0.92	1.63E-03
MGC3162	218860_at	NM_024078	NM_024078	79050	0.92	6.27E-05
DKFZp313A243	230285_at	BF447829	---	258010	0.92	4.30E-03
AA669799	36553_at	AA669799	---	---	0.92	2.04E-04
N93774	229671_s_at	N93774	---	---	0.92	3.48E-03
AW971254	222369_at	AW971254	---	---	0.92	3.06E-03
BF516305	230728_at	BF516305	---	---	0.92	9.61E-04
ALDH1A2	207016_s_at	AB015228	NM_003888 NM_170696 NM_170697	8854	0.92	7.68E-03
ZNF600	242463_x_at	AI620827	NM_198457	162966	0.92	6.82E-03
BUB3	201458_s_at	NM_004725	NM_00100779 3 NM_004725	9184	0.92	3.29E-04
FZD8	227405_s_at	AW340311	NM_031866	8325	0.92	7.53E-04
RAD1	228535_at	AI796010	NM_002853 NM_133282 NM_133377	5810	0.92	3.58E-04
GCAT	205164_at	NM_014291	NM_014291	23464	0.92	4.73E-03
DKFZp761A07	231895_at	AA501453	NM_194292	163786	0.92	1.89E-04
BE464337	229512_at	BE464337	---	---	0.92	2.81E-03
AI670824	238887_at	AI670824	---	---	0.91	4.22E-03
USP49	212872_s_at	AK023092	NM_004275	9477	0.91	1.13E-04
HTATSF1	202602_s_at	NM_014500	NM_014500	27336	0.91	3.64E-05
MAML3	228508_at	AI828006	NM_018717	55534	0.91	2.27E-04
UCHL5	219960_s_at	NM_015984	NM_015984	51377	0.91	1.62E-03
MKKS	222530_s_at	AF275813	NM_018848 NM_170784	8195	0.91	1.32E-04
C18orf9	52285_f_at	AW002970	NM_024899	79959	0.91	2.78E-06
ADRBK2	204183_s_at	AI478542	NM_005160	157	0.91	5.18E-03
LOC90313	225605_at	AL540867	NM_138349	90313	0.91	5.20E-03
FANCE	220255_at	NM_021922	NM_021922	2178	0.91	1.82E-03
SH3BGRL2	225354_s_at	AL035700	NM_031469	83699	0.91	3.32E-04
YEATS4	218911_at	NM_006530	NM_006530	8089	0.91	7.53E-05
FKBP14	219390_at	NM_017946	NM_017946	55033	0.91	3.85E-06
KIAA1712	231850_x_at	AB051499	NM_030633	80817	0.91	6.64E-03
C10orf78	236027_at	N23587	NM_00100275 9 NM_145247	119392	0.91	4.28E-03
BG261385	225906_at	BG261385	XM_499448	442703	0.91	2.60E-03
LOC339903	228721_at	AA225165	XM_291063	339903	0.91	2.86E-03
KIBRA	213085_s_at	AB020676	NM_015238	23286	0.91	5.30E-05
KIAA1333	223255_at	AA642341	NM_017769	55632	0.91	1.02E-03
H2AFJ	224301_x_at	BC003602	NM_018267 NM_177925	55766	0.91	8.07E-03
HRASLS	219984_s_at	NM_020386	NM_020386	57110	0.91	1.08E-03
TUBA3 K-ALPHA-1	212639_x_at	AL581768	NM_006009 NM_006082	10376 7846	0.91	2.50E-05
TOMM34	201870_at	NM_006809	NM_006809	10953	0.91	6.55E-05
RFX5	202964_s_at	NM_000449	NM_000449	5993	0.91	7.31E-04
AK1	202587_s_at	BC001116	NM_000476	203	0.91	7.38E-03
KATNA1	205526_s_at	NM_007044	NM_007044	11104	0.91	2.54E-03
PAICS	201014_s_at	NM_006452	NM_006452	10606	0.91	3.31E-03
KIAA1576	226415_at	AA156723	NM_020927	57687	0.90	4.18E-03
CHML	1565951_s_at	AJ293392	NM_001821	1122	0.90	1.84E-04
SLC2A8	218985_at	NM_014580	NM_014580	29988	0.90	1.85E-04

DKFZp779O175	238952_x_at	BF439163	XM_375606	374899	0.90	1.98E-03
FLJ43505	221477_s_at	BF575213	NM_207468	400823	0.90	2.64E-05
HTLF	226711_at	BF590117	NM_002158	3344	0.90	2.44E-05
FLJ10385	44563_at	AI858000	NM_018081	55135	0.90	1.42E-05
FLJ16517	229349_at	AL039884	NM_001004317	389421	0.90	7.06E-04
SIX5	229009_at	AA527770	NM_175875	147912	0.90	7.46E-03
STMN3	222557_at	AL353715	NM_015894	50861	0.90	3.11E-03
PPP2R5D	211159_s_at	AB000635	NM_006245	5528	0.90	3.08E-03
			NM_180976			
			NM_180977			
AI701857	243359_at	AI701857	---	---	0.90	7.55E-04
PHYH	203335_at	NM_006214	NM_006214	5264	0.90	1.50E-03
UFD1L	209103_s_at	BC001049	NM_005659	7353	0.90	7.15E-04
RAD1	204460_s_at	AF074717	NM_002853	5810	0.90	1.59E-03
			NM_133282			
			NM_133377			
MPHOSPH9	221965_at	AI990326	NM_022782	10198	0.90	5.47E-04
MLF1	204783_at	AI911434	NM_022443	4291	0.90	1.40E-03
THOC4	226319_s_at	AF047002	NM_005782	10189	0.90	3.55E-05
TM4SF15	218693_at	NM_012339	NM_012339	23555	0.90	1.06E-03
MSH6	202911_at	NM_000179	NM_000179	2956	0.90	8.89E-05
ANXA6	200982_s_at	NM_001155	NM_001155	309	0.90	2.34E-06
			NM_004033			
RAB23	223463_at	AF161486	NM_016277	51715	0.90	1.40E-03
			NM_183227			
PCTK1	207239_s_at	NM_006201	NM_006201	5127	0.90	2.68E-03
			NM_033018			
ZNF238	212774_at	AJ223321	NM_006352	10472	0.90	9.30E-04
			NM_205768			
HIP1R	209558_s_at	AB013384	NM_003959	9026	0.90	2.26E-04
UBAP2L	201378_s_at	NM_014847	NM_014847	9898	0.90	3.17E-04
FLJ32745	235644_at	BF213953	NM_144978	165055	0.90	2.95E-03
GGCX	214006_s_at	BE326952	NM_000821	2677	0.89	1.19E-03
HIP1	226364_at	AU145049	NM_005338	3092	0.89	1.85E-04
BG496998	225684_at	BG496998	---	---	0.89	7.38E-05
PIGX	1563111_a_at	AK000529	NM_017861	54965	0.89	1.57E-03
RAN	200750_s_at	AF054183	NM_006325	5901	0.89	7.04E-07
LOC128977	227086_at	AA194312	NM_173793	128977	0.89	7.56E-04
PRIM2A	1554885_a_at	BC017833	NM_000947	5558	0.89	1.97E-03
ACY1L2	225421_at	AI654133	NM_001010853	135293	0.89	1.02E-04
FLJ39582	239015_at	BE675073	XM_498459	439931	0.89	4.23E-03
			XM_499589			
CDK5RAP2	233540_s_at	AK025867	NM_00101164	55755	0.89	1.44E-03
			9			
			NM_018249			
HIP1	205425_at	NM_005338	NM_005338	3092	0.89	3.21E-04
RNF157	226433_at	BF056204	NM_052916	114804	0.89	4.40E-04
AL832468	1560116_a_at	AL832468	---	---	0.89	1.66E-04
CDC5L	209056_s_at	NM_001253	NM_001253	988	0.89	2.06E-05
C20orf17	235616_at	AI694059	NM_173485	128553	0.89	7.79E-03
STAU2	204226_at	NM_014393	NM_014393	27067	0.89	4.24E-05
TUBB2	213726_x_at	AA515698	NM_006088	10383	0.89	1.59E-04
TMEPAI	222449_at	AL035541	NM_020182	56937	0.89	8.38E-03
			NM_199169			
			NM_199170			
			NM_199171			
KIAA1958	239033_at	AI640482	NM_133465	158405	0.89	2.35E-04
TEAD3	209454_s_at	AF142482	NM_003214	7005	0.89	3.41E-03

KIAA1211	227231_at	AI991996	XM_044178	57482	0.88	1.97E-03
TMEFF1	205122_at	BF439316	NM_003692	8577	0.88	6.32E-03
SLC16A10	219915_s_at	NM_018593	NM_018593	117247	0.88	7.05E-04
ACPL2	226925_at	AW069729	NM_152282	92370	0.88	5.44E-07
C1orf41	203960_s_at	NM_016126	NM_016126	51668	0.88	6.92E-03
VPS29	223026_s_at	AF201946	NM_016226 NM_057180	51699	0.88	3.36E-04
FRAT2	209864_at	AB045118	NM_012083	23401	0.88	9.56E-03
IGSF4	209031_at	AL519710	NM_014333	23705	0.88	1.80E-03
PARP2	215773_x_at	AJ236912	NM_005484	10038	0.88	1.31E-03
SLCO3A1	219229_at	NM_013272	NM_013272	28232	0.88	8.63E-04
RNPC1	212430_at	AL109955	NM_017495 NM_183425	55544	0.88	4.48E-03
STAMBP	202811_at	NM_006463	NM_006463 NM_201647 NM_213622	10617	0.88	3.92E-04
RPS6KA1	203379_at	NM_002953	NM_00100666 5 NM_002953	6195	0.88	2.48E-03
BUB3	201456_s_at	AU160695	NM_00100779 3 NM_004725	9184	0.88	1.21E-04
LOC375295	228564_at	AI569804	XM_374020	375295	0.88	2.04E-03
KCNQ2	210508_s_at	D82346	NM_004518 NM_172106 NM_172107 NM_172108 NM_172109	3785	0.88	1.23E-04
EIF4E	201437_s_at	NM_001968	NM_001968	1977	0.88	2.52E-03
AGPS	225113_at	BF688144	NM_003659	8540	0.88	2.42E-03
BRD4	202103_at	AI991631	NM_014299 NM_058243	23476	0.88	2.06E-03
TOX	204529_s_at	AI961231	NM_014729	9760	0.88	4.56E-03
AI032121	227422_at	AI032121	---	---	0.88	5.07E-04
RAB3IP	223471_at	BC002556	NM_022456 NM_175623 NM_175624 NM_175625 NM_175626 NM_175627	117177	0.87	1.10E-03
DDT	202929_s_at	NM_001355	NM_001355	1652	0.87	4.60E-04
C10orf77	219745_at	NM_024789	NM_024789	79847	0.87	9.14E-03
NUCKS	224582_s_at	H09085	NM_022731	64710	0.87	2.99E-05
FBN1	202766_s_at	NM_000138	NM_000138	2200	0.87	9.90E-03
AA287457	226943_at	AA287457	---	---	0.87	2.30E-03
C10orf86	219067_s_at	NM_017615	NM_017615	54780	0.87	6.15E-05
MAGE:3604678	1555875_at	BU733713	---	---	0.87	7.23E-03
HSPA4L	205543_at	NM_014278	NM_014278	22824	0.87	7.62E-04
PLS1	205190_at	NM_002670	NM_002670	5357	0.87	7.93E-03
AW299815	241815_at	AW299815	---	---	0.87	5.59E-03
MRPL42	222466_s_at	AL136659	NM_014050 NM_172177 NM_172178	28977	0.87	3.61E-06

LYK5	221554_at	AF308302	NM_00100378 6 NM_00100378 7 NM_00100378 8 NM_153335	92335	0.87	5.17E-03
C6orf61	219673_at	NM_017696	---	54844	0.87	2.34E-04
NR3C1	201865_x_at	AI432196	NM_000176	2908	0.87	1.11E-03
KIAA1280	219520_s_at	NM_018458	NM_015691	55841	0.87	6.75E-05
HMG20B	209113_s_at	AF288679	NM_006339	10362	0.87	8.93E-05
KIAA1211	227230_s_at	BE855799	XM_044178	57482	0.87	4.76E-04
GAS6	202177_at	NM_000820	NM_000820	2621	0.87	1.87E-03
AKAP13	221718_s_at	M90360	NM_006738 NM_007200 NM_144767	11214	0.87	4.55E-04
H2AFZ	213911_s_at	BF718636	NM_002106	3015	0.87	6.81E-06
NYREN18	1569030_s_at	BC034716	NM_016118	51667	0.87	1.77E-03
C20orf20	218586_at	NM_018270	NM_018270	55257	0.86	1.58E-04
PAICS	201013_s_at	AA902652	NM_006452	10606	0.86	5.07E-04
HPS4	218402_s_at	NM_022081	NM_022081 NM_152840 NM_152841 NM_152842 NM_152843	89781	0.86	9.72E-04
GSS	211630_s_at	L42531	NM_000178	2937	0.86	3.22E-04
AL136980	222603_at	AL136980	---	---	0.86	1.97E-03
septin 11	201307_at	AL534972	NM_018243	55752	0.86	6.58E-05
PDLIM7	214266_s_at	AW206786	NM_005451 NM_203352 NM_203353 NM_213636	9260	0.86	8.67E-04
HIP1	205426_s_at	U79734	NM_005338	3092	0.86	1.59E-03
BF447112	236192_at	BF447112	---	---	0.86	6.78E-04
AW161909	232697_at	AW161909	---	---	0.86	1.71E-04
SEC61A2	228747_at	AI694646	NM_018144	55176	0.86	3.38E-04
PXMP2	219076_s_at	NM_018663	NM_018663	5827	0.86	2.72E-03
AU145336	233446_at	AU145336	---	---	0.86	2.61E-03
SIVA	210792_x_at	AF033111	NM_006427 NM_021709	10572	0.86	5.84E-04
NDUFA6	202000_at	BC002772	NM_002490	4700	0.86	2.77E-03
HMGB1	200680_x_at	NM_002128	NM_002128	3146	0.85	7.80E-05
septin 8	209000_s_at	BC001329	XM_034872	23176	0.85	1.12E-03
EIF2B3	218488_at	NM_020365	NM_020365	8891	0.85	2.51E-06
DCX	204851_s_at	AF040254	NM_000555 NM_178151 NM_178152 NM_178153	1641	0.85	1.15E-03
TBC1D16	1554701_a_at	BC028290	NM_019020	125058	0.85	2.39E-03
CARD10	210026_s_at	AY028896	NM_014550	29775	0.85	2.51E-03
VAV2	205536_at	NM_003371	NM_003371	7410	0.85	2.59E-03
NES	218678_at	NM_024609	NM_006617	10763	0.85	8.46E-03
DRD2	216938_x_at	S69899	NM_000795 NM_016574	1813	0.85	7.98E-03
PARP2	214086_s_at	AK001980	NM_005484	10038	0.85	2.66E-03
MGC13204	225837_at	AL577977	NM_031465	83695	0.85	1.56E-03
SLC29A1	201802_at	NM_004955	NM_004955	2030	0.85	4.79E-03

DONSON	221677_s_at	AF232674	NM_017613 NM_145794 NM_145795	29980	0.85	3.72E-03
SLC37A4	217289_s_at	AF097831	NM_001467	2542	0.85	2.49E-03
HAND1	220138_at	NM_004821	NM_004821	9421	0.85	7.06E-03
ZGPAT	57539_at	AA535065	NM_032527 NM_181484 NM_181485	84619	0.85	3.82E-04
CGI-96	202937_x_at	AL022316	NM_015703	27341	0.85	4.33E-04
NUP107	218768_at	NM_020401	NM_020401	57122	0.84	7.62E-05
AL133101	228007_at	AL133101	---	---	0.84	1.62E-04
CALM3	200622_x_at	AV685208	NM_005184	808	0.84	4.45E-03
AW450360	222072_at	AW450360	---	---	0.84	4.39E-03
BTBD3	202946_s_at	NM_014962	NM_014962 NM_181443	22903	0.84	7.63E-04
RBBP8	203344_s_at	NM_002894	NM_002894 NM_203291 NM_203292	5932	0.84	2.62E-04
FH	203033_x_at	NM_000143	NM_000143	2271	0.84	2.23E-06
VAV2	226063_at	AA481141	NM_003371	7410	0.84	1.78E-04
MRPL49	201717_at	NM_004927	NM_004927	740	0.84	3.26E-03
TUBA3	209118_s_at	AF141347	NM_006009	7846	0.84	7.92E-05
CD24	216379_x_at	AK000168	NM_013230	934	0.84	4.53E-05
FLJ21415	218867_s_at	NM_024738	NM_024738	79794	0.84	3.59E-03
AA004210	229835_s_at	AA004210	---	---	0.84	1.26E-04
PIGX	1552291_at	NM_017861	NM_017861	54965	0.84	2.94E-03
L3MBTL2	1555815_a_at	AL136564	NM_00100368 9 NM_031488	83746	0.84	6.19E-03
SEC23A	212887_at	AI753659	NM_006364	10484	0.84	2.12E-03
AI589594	238694_at	AI589594	---	---	0.84	6.20E-04
C20orf45	222441_x_at	BF032213	NM_016045	51012	0.84	3.50E-03
C8orf20	218777_at	NM_025232	NM_025232	80346	0.84	8.62E-04
PREX1	224925_at	AL445192	NM_020820	57580	0.84	4.97E-03
RPA2	201756_at	NM_002946	NM_002946	6118	0.84	2.53E-03
RECQL	212918_at	AI962943	NM_002907 NM_032941	5965	0.83	5.17E-03
HOXD4	205522_at	NM_014621	NM_014621	3233	0.83	4.47E-03
AU144918	233858_at	AU144918	---	---	0.83	9.47E-03
DATF1	218325_s_at	NM_022105	NM_022105 NM_080796 NM_080797	11083	0.83	3.04E-03
EED	209572_s_at	AF080227	NM_003797 NM_152991	8726	0.83	6.60E-06
RIMS4	227644_at	AL049000	NM_182970	140730	0.83	1.04E-03
CHML	226350_at	AU155565	NM_001821	1122	0.83	1.58E-03
RAD21	200607_s_at	BG289967	NM_006265	5885	0.83	1.96E-03
ZNF555	1556188_a_at	AF052118	NM_152791	148254	0.83	3.68E-04
FSCN1	210933_s_at	BC004908	NM_003088	6624	0.83	1.24E-03
KIAA1467	213234_at	AB040900	XM_370682	57613	0.83	4.71E-03
DDX54	224433_s_at	BC005848	NM_024072	79039	0.83	4.90E-03
TERT	207199_at	NM_003219	NM_003219 NM_198253 NM_198254 NM_198255	7015	0.83	3.88E-03
HRASLS	219983_at	NM_020386	NM_020386	57110	0.83	7.17E-03

BACH	215728_s_at	AL031848	NM_007274 NM_181862 NM_181863 NM_181864 NM_181865 NM_181866	11332	0.83	3.84E-06
MSH5	221406_s_at	NM_025259	NM_002441 NM_025259 NM_172165 NM_172166	4439	0.83	9.50E-03
FLJ22955	221224_s_at	NM_024819	NM_024819	79877	0.83	2.19E-03
ATF7IP	218987_at	NM_018179	NM_018179	55729	0.83	8.71E-04
FLJ20508	218712_at	NM_017850	NM_017850	54955	0.82	1.46E-03
PHF5A	225309_at	AL008582	NM_032758	84844	0.82	1.72E-04
C20orf27	50314_i_at	AI761506	NM_017874	54976	0.82	7.41E-04
SET8	225094_at	AL578116	NM_020382	387893	0.82	8.35E-04
KCNS3	205968_at	NM_002252	NM_002252	3790	0.82	9.42E-03
CHES1	222494_at	AW051527	NM_005197	1112	0.82	1.04E-02
RCBTB1	218352_at	NM_018191	NM_018191	55213	0.82	8.95E-05
NM_024601	220033_at	NM_024601	---	---	0.82	1.30E-03
HCN3	228741_s_at	AA569959	NM_020897	57657	0.82	2.94E-03
ATP6V1A	201971_s_at	NM_001690	NM_001690	523	0.82	1.36E-03
RNF26	224338_s_at	AB055622	NM_032015	79102	0.82	2.45E-03
BC042916	1559111_a_at	BC042916	---	---	0.82	8.94E-03
PINX1	223907_s_at	AF205718	NM_017884	54984	0.82	1.62E-04
AW771952	242434_at	AW771952	---	---	0.82	2.95E-03
HNRPAB	201277_s_at	NM_004499	NM_004499 NM_031266	3182	0.82	1.19E-04
FH	214170_x_at	AA669797	NM_000143	2271	0.82	3.99E-05
LOC283852	238554_at	BE501733	---	283852	0.82	5.07E-03
ZNF79	214138_at	AA284829	NM_007135	7633	0.82	2.28E-04
C22orf19	209418_s_at	BC003615	NM_001002877 NM_001002878 NM_001002879 NM_003678	8563	0.82	2.69E-04
RAD21	200608_s_at	NM_006265	NM_006265	5885	0.82	1.40E-03
H1F0	208886_at	BC000145	NM_005318	3005	0.82	3.44E-03
MAPKAPK5	212871_at	NM_003668	NM_003668 NM_139078	8550	0.82	5.71E-04
PPP1R13B	216347_s_at	AK023188	NM_015316	23368	0.82	4.23E-04
ZNF278	211392_s_at	AF242522	NM_014323 NM_032050 NM_032051 NM_032052	23598	0.81	1.59E-03
ENC2	210307_s_at	AL136796	NM_022480	64410	0.81	6.42E-03
DACH1	1562342_at	AL713717	NM_004392 NM_080759 NM_080760	1602	0.81	4.53E-03
ADRBK2	204184_s_at	NM_005160	NM_005160	157	0.81	3.83E-04
JUP	201015_s_at	NM_021991	NM_002230 NM_021991	3728	0.81	5.55E-03
KIAA1333	223258_s_at	BC000973	NM_017769	55632	0.81	2.69E-03
ETAA16	219216_at	NM_019002	NM_019002	54465	0.81	1.33E-03
LOC387882	225105_at	BF969397	NM_207376	387882	0.81	9.88E-04
KIAA1648	213058_at	AL033538	---	284900	0.81	3.45E-03

DYRK4	212954_at	AF263541	NM_003845	8798	0.81	3.72E-03
LOC200008	229605_at	AI150848	NM_201546	200008	0.81	6.35E-06
GPX3	214091_s_at	AW149846	NM_002084	2878	0.81	1.38E-03
LRP10	201412_at	NM_014045	NM_014045	26020	0.81	4.50E-03
LOC55954	218752_at	NM_019103	NM_00100369 2 NM_019103	55954	0.81	9.27E-03
FLJ23441	219217_at	NM_024678	NM_024678	79731	0.81	5.14E-06
TH1L	220607_x_at	NM_016397	NM_016397 NM_198976	51497	0.81	1.63E-03
AD-003	223368_s_at	BC001396	NM_014064	28989	0.81	2.11E-03
HIP2	202347_s_at	AB022435	NM_005339	3093	0.80	1.48E-04
MGAT5B	238445_x_at	AI609043	NM_144677 NM_198955	146664	0.80	6.85E-04
EPOR	37986_at	M60459	NM_000121	2057	0.80	5.63E-03
HIC2	212966_at	AL043112	NM_015094	23119	0.80	3.15E-05
GJA7	228776_at	AA430014	NM_005497	10052	0.80	4.03E-05
DNAJC9	213088_s_at	BE551340	NM_015190	23234	0.80	2.60E-03
HMGN2	208668_x_at	BC003689	NM_005517	3151	0.80	1.11E-03
MRPL42	217919_s_at	BE782148	NM_014050 NM_172177 NM_172178	28977	0.80	2.11E-03
HSPC129	223270_at	AF161543	NM_016396	51496	0.80	1.61E-05
HNRPA2B1	205292_s_at	NM_002137	NM_002137 NM_031243	3181	0.80	3.05E-04
ANXA4	201301_s_at	BC000182	NM_001153	307	0.80	8.27E-03
SOX13	38918_at	AF083105	NM_005686	9580	0.80	3.55E-03
ACTR1A	200721_s_at	NM_005736	NM_005736	10121	0.80	2.85E-03
MEIS2	207480_s_at	NM_020149	NM_002399 NM_020149 NM_170674 NM_170675 NM_170676 NM_170677 NM_172315 NM_172316	4212	0.80	4.47E-04
APG3L	221492_s_at	AF202092	NM_022488	64422	0.80	1.43E-03
CDYL	203099_s_at	AF081258	NM_004824 NM_170751 NM_170752	9425	0.80	3.28E-03
ODZ3	219523_s_at	NM_018104	XM_371717	55714	0.80	1.87E-03
VAPB	202550_s_at	NM_004738	NM_004738	9217	0.80	8.33E-06
SAP30	204900_x_at	NM_003864	NM_003864	8819	0.80	1.56E-05
HOXD1	205975_s_at	NM_024501	NM_024501	3231	0.80	1.08E-03
FLJ10385	220258_s_at	NM_018081	NM_018081	55135	0.80	1.71E-03
LRRC1	218816_at	NM_018214	NM_018214 NM_025168	55227	0.80	5.23E-03
CD24	209771_x_at	AA761181	NM_013230	934	0.80	5.76E-04
SLC29A1	201801_s_at	AF079117	NM_004955	2030	0.80	7.75E-04
C10orf86	211376_s_at	BC005212	NM_017615	54780	0.80	2.32E-05
GNAZ	204993_at	NM_002073	NM_002073	2781	0.80	8.65E-05
C15orf25	229208_at	AK022939	NM_018097	55142	0.80	8.67E-03
CPT1A	203633_at	BF001714	NM_001876	1374	0.80	1.57E-03
LOC150383	227590_at	BE501980	NM_00100891 7 NM_207327	150383	0.80	1.76E-05
MGC18216	225330_at	AL044092	---	145815	0.80	7.91E-04

384D8-2	205086_s_at	NM_014551	NM_014551 NM_152299	29781	0.80	8.25E-05
USP28	231837_at	AB040948	NM_020886	57646	0.80	4.10E-04
G22P1	200792_at	NM_001469	NM_001469	2547	0.79	1.57E-06
TIMM50	224913_s_at	AA877820	NM_001001563	92609	0.79	1.54E-06
OSRF	219421_at	NM_012382	NM_012382	23548	0.79	1.38E-03
TIAF1	202039_at	NM_004740	NM_004740	399687	0.79	7.17E-03
MYO18A			NM_078471 NM_203318	9220		
SNN	218032_at	AF070673	NM_003498	8303	0.79	3.27E-05
HPS4	54037_at	AL041451	NM_022081 NM_152840 NM_152841 NM_152842 NM_152843	89781	0.79	3.31E-05
AI339606	222852_at	AI339606	---	---	0.79	3.52E-03
CNN3	201445_at	NM_001839	NM_001839	1266	0.79	2.38E-05
C16orf34	212115_at	AK023154	NM_144570	90861	0.79	1.93E-04
)KFZP564K082	208091_s_at	NM_030796	NM_030796	81552	0.79	4.71E-04
LETM2	1557415_s_at	AI023774	NM_144652	137994	0.79	1.29E-03
AW665227	229713_at	AW665227	---	---	0.79	2.47E-05
C14orf130	218108_at	NM_018108	NM_018108 NM_175748	55148	0.79	4.99E-03
NEDD1	234984_at	AA236927	NM_152905	121441	0.79	3.11E-04
LOC57168	227015_at	Z99714	NM_020437	57168	0.79	4.74E-06
ZNF267	219540_at	AU150728	NM_003414	10308	0.79	1.98E-03
HIC2	212964_at	AI912206	NM_015094	23119	0.79	6.64E-06
BG150301	230271_at	BG150301	---	---	0.79	9.81E-03
NM_014838	204799_at	NM_014838	---	---	0.79	1.18E-03
FLJ14827	221777_at	BE966197	NM_032848	84934	0.79	2.97E-05
NP	201695_s_at	NM_000270	NM_000270	4860	0.78	8.55E-03
BACH	208002_s_at	NM_007274	NM_007274 NM_181862 NM_181863 NM_181864 NM_181865 NM_181866	11332	0.78	1.62E-04
GPR155	244509_at	AW449728	NM_152529	151556	0.78	8.05E-03
EIF2S1	201144_s_at	NM_004094	NM_004094	1965	0.78	4.48E-06
CLEC11A	205131_x_at	NM_002975	NM_002975	6320	0.78	3.57E-03
BCL11A	219497_s_at	NM_022893	NM_018014 NM_022893 NM_138553 NM_138559	53335	0.78	8.37E-05
MRPL2	229884_s_at	AA187325	NM_015950	51069	0.78	6.69E-04
PRKAB2	1558027_s_at	AL552001	NM_005399	5565	0.78	1.67E-03
DTX1	227336_at	AW576405	NM_004416	1840	0.78	1.19E-03
M96	203347_s_at	NM_007358	NM_007358	22823	0.78	8.86E-03
ACN9	218981_at	NM_020186	NM_020186	57001	0.78	1.05E-03
IMP-1	227377_at	AK022784	NM_006546	10642	0.78	2.10E-04
DVL2	57532_at	AW016304	NM_004422	1856	0.78	1.49E-04
DKFZp547A023	239525_at	AI733041	NM_018704	55917	0.78	2.26E-04
LOC91431	1565935_at	AF075091	NM_138698	91431	0.78	1.72E-03
H1FX	204805_s_at	NM_006026	NM_006026	8971	0.78	2.36E-03
RNPEP	208270_s_at	NM_020216	NM_020216	6051	0.78	1.53E-03
LOC400960	227969_at	AI627636	XM_379102	400960	0.78	1.32E-04
PXMP4	224210_s_at	BC001147	NM_007238 NM_183397	11264	0.78	7.76E-03

MAP3K7IP1	203901_at	NM_006116	NM_006116 NM_153497	10454	0.78	2.33E-04
LSM2	209449_at	AF196468	NM_021177	57819	0.78	2.81E-03
ODF2	225617_at	AL138382	NM_002540 NM_153437	4957	0.78	1.50E-03
JARID2	203297_s_at	BG029530	NM_004973	3720	0.77	5.30E-03
C20orf27	218081_at	NM_017874	NM_017874	54976	0.77	1.93E-04
FLJ35779	227267_at	AI953478	NM_152408	134359	0.77	5.87E-03
FLJ38973	238974_at	N47077	NM_153689	205327	0.77	3.60E-03
LOC202181	232309_at	Y13871	---	202181	0.77	9.94E-04
DDX54	219111_s_at	NM_024072	NM_024072	79039	0.77	5.24E-03
NELL2	203413_at	NM_006159	NM_006159	4753	0.77	1.82E-04
AZI1	214742_at	AB029041	NM_00100981 1 NM_014984	22994	0.77	4.54E-04
C13orf6	235348_at	AA404347	NM_032859	84945	0.77	6.35E-07
MKL1	212748_at	AB037859	NM_020831	57591	0.77	1.75E-04
MLF1	204784_s_at	NM_022443	NM_022443	4291	0.77	4.84E-03
RPP25	219143_s_at	NM_017793	NM_017793	54913	0.77	2.33E-03
MRPL39	218558_s_at	NM_017446	NM_017446 NM_080794	54148	0.77	1.79E-03
MR-1	225298_at	AA074597	NM_015488 NM_022572	25953	0.77	9.47E-03
SCOC	223341_s_at	AF330205	NM_032547	60592	0.77	5.34E-06
GAMT	1552474_a_at	NM_138924	NM_000156 NM_138924	2593	0.77	8.68E-04
MGC61550	228791_at	BF434655	NM_182616	348110	0.77	5.38E-04
MGC4172	218756_s_at	NM_024308	NM_024308	79154	0.76	8.18E-04
IKIP	227295_at	AW182575	NM_153687 NM_201612 NM_201613 NM_201614	121457	0.76	1.09E-04
BCL11A	219498_s_at	NM_018014	NM_018014 NM_022893 NM_138553 NM_138559	53335	0.76	6.17E-05
LOC115098	225454_at	AW248770	NM_138442	115098	0.76	2.43E-03
NM_016534	219817_at	NM_016534	---	---	0.76	1.74E-03
H15087	238186_at	H15087	---	---	0.76	4.91E-03
D15Wsu75e	212527_at	BF057059	XM_039495	27351	0.76	5.47E-03
TMEM19	229126_at	AI597651	NM_018279	55266	0.76	9.91E-03
TCF3	215260_s_at	X52078	NM_003200	6929	0.76	3.41E-03
PEX19	201706_s_at	BC000496	NM_002857	5824	0.76	6.90E-07
HSPC132	218403_at	NM_016399	NM_016399	51499	0.76	1.21E-03
TMEM33	222642_s_at	BC000948	NM_018126	55161	0.76	1.16E-03
LOC58489	225436_at	AI339710	XM_051862	58489	0.76	6.79E-04
RAB3D	225001_at	AI744658	NM_004283	9545	0.76	1.35E-04
CBWD1 CBWD2 LOC220869 DC36	226193_x_at	AV709992	NM_018491 NM_172003 NM_201453	150472 220869 389760 55871	0.76	7.42E-06
C7orf31	229146_at	AA778688	NM_138811	136895	0.76	4.75E-04
ZNF569	1569366_a_at	BC038737	NM_152484	148266	0.76	2.84E-03
TOB2	222243_s_at	AB051450	NM_016272	10766	0.76	1.66E-04
BF978778	226832_at	BF978778	XM_374070	389188	0.75	2.91E-03
SULF2	233555_s_at	AL034418	NM_018837 NM_198596	55959	0.75	2.13E-03
D50683	208944_at	D50683	---	---	0.75	8.75E-04

TMEFF1	205123_s_at	NM_003692	NM_003692	8577	0.75	5.76E-04
CSNK2A1	206075_s_at	NM_001895	NM_001895 NM_177559 NM_177560	1457	0.75	8.62E-03
MYO1B	212364_at	BF432550	NM_012223	4430	0.75	1.60E-05
TBL1XR1	222634_s_at	AF314544	NM_024665	79718	0.75	8.23E-03
C20orf6	222765_x_at	AL161659	NM_016649	51575	0.75	2.08E-03
TRA16	226839_at	N25631	NM_176880	126382	0.75	4.39E-03
TH1L	225006_x_at	AJ238379	NM_016397 NM_198976	51497	0.75	3.15E-03
LANCL1	202019_s_at	AI935255	NM_006055	10314	0.75	3.29E-04
ZFYVE21	219929_s_at	NM_024071	NM_024071	79038	0.75	5.24E-04
BF697865	235018_at	BF697865	---	---	0.75	3.31E-05
RECQL	212917_x_at	AI814728	NM_002907 NM_032941	5965	0.75	1.03E-03
GPR158	232195_at	R41459	NM_020752	57512	0.75	9.00E-03
TH1L	225865_x_at	AJ238374	NM_016397 NM_198976	51497	0.75	5.42E-03
AW025579	213429_at	AW025579	---	---	0.75	2.61E-03
NDUFA3	218563_at	NM_004542	NM_004542	4696	0.75	1.05E-03
AI857788	227126_at	AI857788	---	---	0.75	3.17E-04
TRIM32	203846_at	BC003154	NM_012210	22954	0.75	9.18E-04
LZIC	226087_at	BG180887	NM_032368	84328	0.75	5.95E-03
CBX1	201518_at	NM_006807	NM_006807	10951	0.75	3.35E-03
TUB	228882_at	AL042088	NM_003320 NM_177972	7275	0.75	1.66E-03
EPOR	215054_at	H16758	NM_000121	2057	0.74	2.51E-03
PDXP	223290_at	BC000320	NM_020315	57026	0.74	3.77E-04
GSS	201415_at	NM_000178	NM_000178	2937	0.74	8.16E-04
SEC10L1	228418_at	BF509391	NM_006544	10640	0.74	1.01E-02
DNAJC9	213092_x_at	AW241779	NM_015190	23234	0.74	4.38E-03
SULF2	224724_at	AL133001	NM_018837 NM_198596	55959	0.74	7.10E-04
KIAA0082	212380_at	D43949	NM_015050	23070	0.74	9.43E-03
NM_003349	201003_x_at	NM_003349	---	---	0.74	2.17E-03
HH114	232506_s_at	AK026504	NM_032499	84529	0.74	2.32E-03
MAP3K13	211083_s_at	Z25428	NM_004721	9175	0.74	1.51E-03
SRR	222844_s_at	AF169974	NM_021947	63826	0.74	1.66E-03
SIP1	205063_at	NM_003616	NM_00100918 2 NM_00100918 3 NM_003616	8487	0.74	5.42E-03
SMPD3	219695_at	NM_024703	NM_018667	55512	0.74	8.85E-03
ARL6IP6	225707_at	AL581082	NM_152522	151188	0.74	3.27E-03
LOC90525	228922_at	AI760446	NM_138356	90525	0.74	8.81E-03
PARP2	204752_x_at	NM_005484	NM_005484	10038	0.74	8.00E-03
EPB41L5	225855_at	AB046768	NM_020909	57669	0.74	2.98E-04
BG492376	1557961_s_at	BG492376	---	---	0.74	8.26E-03
KLF3	225140_at	BF438116	NM_016531	51274	0.74	1.89E-03
R12027	241836_x_at	R12027	---	---	0.74	1.13E-03
MCM8	233560_x_at	AA370141	NM_032485 NM_182802	84515	0.74	7.31E-03
TFR2	210215_at	AF067864	NM_003227	7036	0.74	3.11E-04
EIF4E	201435_s_at	AW268640	NM_001968	1977	0.74	4.34E-05
AK001164	232752_at	AK001164	---	---	0.74	3.62E-03
FLJ21839	218480_at	NM_021831	NM_021831	60509	0.73	2.20E-04
DUT	209932_s_at	U90223	NM_001948	1854	0.73	1.26E-03

RBBP7	201092_at	NM_002893	NM_002893	5931	0.73	2.45E-03
SCOC	224786_at	AL133580	NM_032547	60592	0.73	1.16E-06
ELF2	210361_s_at	AF256223	NM_006874 NM_201999	1998	0.73	1.61E-04
BF315093	227617_at	BF315093	NM_001010866	199953	0.73	3.23E-03
C6orf125	224448_s_at	BC006007	NM_032340	84300	0.73	1.18E-03
AK025512	225514_at	AK025512	---	---	0.73	2.88E-03
TTLL4	203702_s_at	AL043927	NM_014640	9654	0.73	1.86E-03
PHOX2B	207009_at	NM_003924	NM_003924	8929	0.73	6.98E-04
PAK4	33814_at	AF005046	NM_005884	10298	0.73	6.87E-03
TTC8	226120_at	AW293939	NM_144596 NM_198309 NM_198310	123016	0.73	8.67E-04
SSBP3	217991_x_at	NM_018070	NM_001009955 NM_018070 NM_145716	23648	0.73	2.77E-03
PPIF	201489_at	BC005020	NM_005729	10105	0.73	5.19E-05
LOC155435	226732_at	AI823400	NM_001008408	155435	0.73	8.92E-03
RAD1	210216_x_at	AF084513	NM_002853 NM_133282 NM_133377	5810	0.73	1.61E-04
PDE7A	223358_s_at	AW269834	NM_002603 NM_002604	5150	0.73	1.04E-03
LOC284611	226568_at	AI478747	NM_001010883	284611	0.73	4.22E-03
MPHOSPH9	1558369_at	BC036600	NM_022782	10198	0.73	9.01E-03
AHCY	200903_s_at	NM_000687	NM_000687	191	0.73	6.38E-04
KIAA1393	221952_x_at	AB037814	NM_020810	57570	0.73	1.27E-03
WDR50	203721_s_at	NM_016001	NM_016001	51096	0.73	2.41E-06
NRF1	204651_at	AW003022	NM_005011	4899	0.72	2.06E-05
ATP6V1A	201972_at	AF113129	NM_001690	523	0.72	6.11E-06
ATP6V1C1	202872_at	AW024925	NM_001007254 NM_001695	528	0.72	5.21E-03
AP3M1	222517_at	AU152391	NM_012095 NM_207012	26985	0.72	8.61E-04
HIP1R	38340_at	AB014555	NM_003959	9026	0.72	9.01E-03
CDKAL1	214877_at	BE794663	NM_017774	54901	0.72	2.66E-07
C10orf119	222464_s_at	BC004183	NM_024834	79892	0.72	2.58E-04
QRSL1	218949_s_at	NM_018292	NM_018292	55278	0.72	1.91E-04
HSPC129	223271_s_at	AF161543	NM_016396	51496	0.72	1.33E-04
MTAP	204956_at	NM_002451	NM_002451	4507	0.72	9.35E-03
TNFRSF10B	210405_x_at	AF153687	NM_003842 NM_147187	8795	0.72	1.20E-05
NDUFS1	203039_s_at	NM_005006	NM_005006	4719	0.72	3.56E-06
SRPK1	202199_s_at	AW082913	NM_003137	6732	0.71	2.30E-04
B4GALT4	210540_s_at	BC004523	NM_003778 NM_212543	8702	0.71	3.68E-03
RBM9	213901_x_at	AW149379	NM_014309	23543	0.71	8.10E-03
DENR	234915_s_at	BC000925	NM_003677	8562	0.71	1.01E-02
CPOX	204172_at	NM_000097	NM_000097	1371	0.71	4.66E-04
HSPC121	217777_s_at	NM_016395	NM_016395	51495	0.71	2.24E-04
RFX5	202963_at	AW027312	NM_000449	5993	0.71	6.50E-03
SHD1	205449_at	NM_013299	NM_013299	29901	0.71	7.97E-03
ARF3	200734_s_at	BG341906	NM_001659	377	0.71	3.13E-05

ING1	208415_x_at	NM_005537	NM_005537 NM_198217 NM_198218 NM_198219	3621	0.71	1.86E-05
TH1L	225261_x_at	AJ238376	NM_016397 NM_198976	51497	0.71	2.65E-03
VCL	200931_s_at	NM_014000	NM_003373 NM_014000	7414	0.71	4.61E-03
ZNF545	235176_at	AA927918	NM_133466	284406	0.71	8.64E-03
UBOX5	204598_at	NM_014948	NM_014948 NM_199415	22888	0.71	5.08E-03
ELAVL1	201726_at	BC003376	NM_001419	1994	0.71	7.04E-03
ITGB5	201125_s_at	NM_002213	NM_002213	3693	0.71	2.15E-03
NUP205	212247_at	AW008531	NM_015135	23165	0.71	5.94E-04
SLC17A5	221041_s_at	NM_012434	NM_012434	26503	0.71	9.98E-03
AI939588	241156_at	AI939588	---	---	0.71	3.21E-03
SCRIB	212556_at	AI469403	NM_015356 NM_182706	23513	0.71	7.66E-03
SOCS4	226178_at	BF446961	NM_080867 NM_199421	122809	0.71	1.73E-04
C6orf211	218195_at	NM_024573	NM_024573	79624	0.71	6.55E-03
PSMA7	216088_s_at	AL078633	NM_002792 NM_152255	5688	0.71	2.39E-04
AKR1B1	201272_at	NM_001628	NM_001628	231	0.71	4.69E-04
HMG20B	210719_s_at	BC002552	NM_006339	10362	0.71	5.46E-03
DZIP3	213186_at	BG502305	NM_014648	9666	0.71	5.65E-03
MFI2	223723_at	BC001875	NM_005929 NM_033316	4241	0.71	2.36E-03
PPP1CC	200726_at	NM_002710	NM_002710	5501	0.71	1.35E-03
AL521247	225046_at	AL521247	XM_374317	389831	0.71	3.82E-03
KIAA0841	213053_at	AW189966	XM_049237	23354	0.71	9.24E-03
PDE7A	224046_s_at	U67932	NM_002603 NM_002604	5150	0.71	5.94E-03
FBXO30	226541_at	AI808182	NM_032145	84085	0.71	1.04E-02
SRC	213324_at	AK024281	NM_005417 NM_198291	6714	0.70	5.83E-05
LOC57168	227014_at	BE550881	NM_020437	57168	0.70	3.95E-04
CIB2	205008_s_at	NM_006383	NM_006383	10518	0.70	1.68E-03
GPAM	225420_at	AV699379	NM_020918	57678	0.70	5.07E-03
KLF7	1555420_a_at	BC012919	NM_003709	8609	0.70	6.45E-03
AA833830	230896_at	AA833830	---	---	0.70	7.62E-04
BTBD14A	243431_at	BF000597	NM_144653	138151	0.70	2.99E-03
MAPK11	211499_s_at	U92268	NM_002751 NM_138993	5600	0.70	9.93E-03
FSCN1	201564_s_at	NM_003088	NM_003088	6624	0.70	2.66E-03
PLAGL2	202924_s_at	AL562280	NM_002657	5326	0.70	3.13E-04
USP39	217829_s_at	NM_006590	NM_006590	10713	0.70	6.69E-04
ABHD10	222697_s_at	AI521709	NM_018394	55347	0.70	3.65E-04
C20orf142	233061_at	AL117382	XM_371399	128486	0.70	8.68E-03
GPR51	209990_s_at	AF056085	NM_005458	9568	0.70	1.26E-03
CELSR3	205165_at	NM_001407	NM_001407	1951	0.70	1.21E-03
SSBP2	210829_s_at	AF077048	NM_012446	23635	0.70	7.97E-04
POT1	204353_s_at	BC002923	NM_015450	25913	0.70	1.78E-04
B4GALT6	206233_at	AF097159	NM_004775	9331	0.70	1.09E-03

MARF (C3HC4)	210075_at	AF151074	NM_001005415 NM_001005416 NM_016496	51257	0.70	7.91E-03
MGC4825	221620_s_at	AF061264	NM_024122	79135	0.70	9.49E-03
CBLL1	227187_at	AI824009	NM_024814	79872	0.70	2.62E-03
RAB11A	200864_s_at	NM_004663	NM_004663	8766	0.70	7.58E-03
SLBP	206052_s_at	NM_006527	NM_006527	7884	0.70	1.28E-03
TBX3	229576_s_at	N29712	NM_005996 NM_016569	6926	0.70	1.56E-03
RNF10	207801_s_at	NM_014868	NM_014868	9921	0.69	2.04E-03
KIAA0153	1552257_a_at	NM_015140	NM_015140	23170	0.69	9.62E-04
THOC4	226320_at	AF047002	NM_005782	10189	0.69	2.92E-03
SDHA	201093_x_at	NM_004168	NM_004168	6389	0.69	1.14E-05
FKBPL	219187_at	NM_022110	NM_022110	63943	0.69	5.41E-03
EXOSC3	223489_x_at	AW015573	NM_001002269 NM_016042	51010	0.69	2.58E-04
COCH	1554242_a_at	BC007230	NM_004086	1690	0.69	4.57E-03
C16orf34	212109_at	AI590869	NM_144570	90861	0.69	1.30E-04
CITED1	207144_s_at	NM_004143	NM_004143	4435	0.69	6.40E-03
ZDHHC3	218077_s_at	BE542551	NM_016598	51304	0.69	1.09E-03
AW611729	228744_at	AW611729	---	---	0.69	1.38E-03
MBD4	209580_s_at	AF114784	NM_003925	8930	0.69	1.50E-04
CKLF	221058_s_at	NM_016326	NM_016326 NM_016951 NM_181640 NM_181641	51192	0.69	6.66E-03
PPM1F	37384_at	D86995	NM_014634	9647	0.69	9.40E-05
CSTF1	32723_at	L02547	NM_001324	1477	0.69	7.49E-04
KIAA1333	223257_at	AI823905	NM_017769	55632	0.69	1.45E-04
SHB	1557458_s_at	BU685917	NM_003028	6461	0.69	1.46E-03
AA608749	228095_at	AA608749	---	---	0.69	8.96E-03
MPST	203524_s_at	NM_021126	NM_021126	4357	0.69	4.69E-04
METRN	232269_x_at	BE965311	NM_024042	79006	0.69	7.29E-03
NUP43	219007_at	NM_024647	NM_024647 NM_198887	348995	0.69	8.85E-05
TTYH2	223741_s_at	BC004233	NM_032646 NM_052869	94015	0.69	9.46E-03
C20orf178	225119_at	AW299290	NM_176812	128866	0.69	9.97E-06
GTF3A	215091_s_at	BE542815	NM_002097	2971	0.69	1.55E-04
NIPSNAP1	201708_s_at	AW083371	NM_003634	8508	0.69	1.45E-03
C20orf44	217935_s_at	NM_018244	NM_018244 NM_199487 NM_199513	55245	0.68	2.08E-03
PNRC2	222406_s_at	AV738970	NM_017761	55629	0.68	5.58E-05
IGFBP2	202718_at	NM_000597	NM_000597	3485	0.68	8.62E-03
PDE6D	204091_at	NM_002601	NM_002601	5147	0.68	3.97E-04
KIAA0376	212480_at	AB002374	NM_015330	23384	0.68	1.42E-03
PLAGL2	202925_s_at	NM_002657	NM_002657	5326	0.68	1.26E-03
C6orf18	42361_g_at	AI588986	NM_019052	54535	0.68	4.87E-04
C16orf5	223960_s_at	AF195661	NM_013399	29965	0.68	1.19E-03
ZDHHC22	229875_at	AI363193	NM_174976	283576	0.68	8.32E-03
RetSat	1566472_s_at	AK098125	NM_017750	54884	0.68	8.62E-03
CD47	213857_s_at	BG230614	NM_001777 NM_198793	961	0.68	1.35E-04
ADRBK2	228771_at	AI651212	NM_005160	157	0.68	4.73E-04

KCTD9	218823_s_at	NM_017634	NM_017634	54793	0.68	1.27E-03
H49805	239911_at	H49805	---	---	0.68	6.32E-03
ZA20D3	221613_s_at	AL136598	NM_019006	54469	0.68	2.84E-04
KELCHL	221837_at	BG325646	NM_032775	84861	0.68	4.31E-03
HMOX2	218120_s_at	D21243	NM_002134	3163	0.68	2.33E-04
C22orf13	223039_at	BC004144	NM_031444	83606	0.68	2.45E-03
ZNF71	226514_at	W55975	NM_021216	58491	0.68	1.83E-03
MGC12466	223898_at	BC005360	NM_033213	93474	0.68	6.20E-03
HMGB1	224731_at	BF673940	NM_002128	3146	0.68	1.63E-03
TBC1D7	223461_at	AF151073	NM_016495	51256	0.68	8.95E-04
PDCL	204449_at	NM_005388	NM_005388	5082	0.68	1.36E-03
RAD1	235253_at	AI742925	NM_002853	5810	0.68	2.51E-03
			NM_133282			
			NM_133377			
CKB	200884_at	NM_001823	NM_001823	1152	0.68	3.63E-05
SRrp35	239295_at	AA889416	NM_080743	135295	0.68	5.74E-03
SARA2	218254_s_at	NM_016103	NM_016103	51128	0.68	7.27E-06
CBX2	226473_at	BE514414	---	876	0.68	2.77E-04
BLCAP	201032_at	NM_006698	NM_006698	10904	0.68	1.40E-04
MGC5139	202365_at	BC004815	---	84747	0.68	1.18E-03
HIBADH	224812_at	AL577446	NM_152740	11112	0.68	4.29E-05
MOBK1B	201298_s_at	BC003398	NM_018221	55233	0.68	1.42E-05
NIPSNAP1	201709_s_at	NM_003634	NM_003634	8508	0.67	3.88E-03
CSNK2A1	212072_s_at	AL049761	NM_001895	1457	0.67	4.08E-03
			NM_177559			
			NM_177560			
DUT	208956_x_at	U62891	NM_001948	1854	0.67	2.02E-03
HOOK3	224359_s_at	AF241830	NM_032410	84376	0.67	9.68E-04
CSTF3	229665_at	AI653037	NM_001326	1479	0.67	9.91E-03
RUVBL1	201614_s_at	NM_003707	NM_003707	8607	0.67	3.37E-03
PNRC2	217779_s_at	NM_017761	NM_017761	55629	0.67	1.36E-03
KIAA1893	227975_at	AW963386	NM_052899	114787	0.67	8.58E-03
KIAA1949	224927_at	BG251556	---	170954	0.67	8.52E-03
PSMB2	200039_s_at	NM_002794	NM_002794	5690	0.67	2.36E-04
RCOR2	236030_at	BF528119	NM_173587	283248	0.67	3.41E-03
AL157484	221861_at	AL157484	---	---	0.67	8.93E-03
RBX1	218117_at	NM_014248	NM_014248	9978	0.67	4.54E-03
SIPA1	204164_at	NM_006747	NM_006747	6494	0.67	5.05E-03
			NM_153253			
DHRS8	217989_at	NM_016245	NM_016245	51170	0.67	3.77E-03
FBXO45	225100_at	BF590021	XM_117294	200933	0.67	5.60E-03
C19orf25	226378_s_at	AI554705	NM_152482	148223	0.67	2.15E-03
E2F3	203693_s_at	NM_001949	NM_001949	1871	0.67	9.86E-04
SERAC1	232183_at	AA128978	NM_032861	84947	0.67	2.83E-05
LOC129138	231847_at	Z97630	NM_138797	129138	0.67	4.79E-04
AL524175	225479_at	AL524175	---	---	0.67	3.32E-04
CCDC5	225297_at	AV715391	NM_138443	115106	0.67	1.96E-04
KIAA1166	225784_s_at	AU150745	NM_018684	55906	0.67	4.05E-03
SH3BP4	222258_s_at	AF015043	NM_014521	23677	0.67	8.34E-05
YTHDF1	221741_s_at	AL096828	NM_017798	54915	0.66	8.07E-04
DKFZP566E144	218194_at	NM_015523	NM_015523	25996	0.66	9.77E-05
HADHSC	201035_s_at	BC000306	NM_005327	3033	0.66	2.93E-03
GALNT4	231832_at	AI890347	NM_003774	8693	0.66	6.21E-03
FLJ90709	243709_at	BG054799	NM_173514	153129	0.66	1.04E-02
SMARCB1	212167_s_at	AK021419	NM_00100746	6598	0.66	3.27E-05
			8			
			NM_003073			
NDUFC1	203478_at	NM_002494	NM_002494	4717	0.66	4.38E-03

ATP1A1	220948_s_at	NM_000701	NM_000701 NM_00100158 6	476	0.66	9.29E-05
KIAA0265	209256_s_at	AF277177	NM_014997	23008	0.66	5.63E-03
KIAA0153	216251_s_at	BF965437	NM_015140	23170	0.66	1.12E-04
CCNG1	208796_s_at	BC000196	NM_004060 NM_199246	900	0.66	7.05E-03
DT1P1A10	213079_at	AA223871	NM_058163	90121	0.66	1.80E-03
FLJ32065	223443_s_at	BC003669	NM_153032	201283	0.66	8.33E-04
CORO1C	222409_at	AL162070	NM_014325	23603	0.66	6.46E-05
GGA2	208914_at	BE646414	NM_015044 NM_138640	23062	0.66	1.84E-03
SNRPB	208821_at	J04564	NM_003091 NM_198216	6628	0.66	8.27E-05
NUCKS	224581_s_at	AI707721	NM_022731	64710	0.66	5.13E-06
FLJ40432	228810_at	AW135279	NM_152523	151195	0.66	7.36E-05
G6PC3	221759_at	AL583123	NM_138387	92579	0.66	9.07E-04
CAMTA1	225692_at	AV756867	NM_015215	23261	0.66	1.84E-03
CBX5	212126_at	BG391282	NM_012117	23468	0.66	2.40E-03
LIMK2	202193_at	NM_005569	NM_005569 NM_016733	3985	0.66	8.69E-03
MRPL40	203152_at	NM_003776	NM_003776	64976	0.66	7.24E-03
CBR4	244052_at	AI469277	NM_032783	84869	0.66	1.00E-03
NKIRAS1	225930_at	AI970120	NM_020345	28512	0.65	3.27E-04
ASH2L	209517_s_at	AB020982	NM_004674	9070	0.65	4.47E-04
KRAS	204009_s_at	W80678	NM_004985 NM_033360	3845	0.65	2.50E-04
KELCHL	221838_at	N38751	NM_032775	84861	0.65	6.67E-04
MRPL35	218890_x_at	NM_016622	NM_016622 NM_145644	51318	0.65	6.17E-03
NUDT3	221579_s_at	AF062530	NM_006703	11165	0.65	6.42E-03
MAGEH1	218573_at	NM_014061	NM_014061	28986	0.65	1.12E-04
CCNK	225824_at	AA528091	NM_003858	317762	0.65	1.32E-04
C14orf65				8812		
CPE	201117_s_at	NM_001873	NM_001873	1363	0.65	5.66E-03
GAMT	205354_at	NM_000156	NM_000156 NM_138924	2593	0.65	1.31E-03
KIAA1423	225127_at	BF217531	XM_376550	57583	0.65	2.39E-03
EXOSC3	227916_x_at	AA747303	NM_00100226 9 NM_016042	51010	0.65	9.83E-03
RNF166	227726_at	BF057084	NM_178841	115992	0.65	8.38E-04
SFI1	213431_x_at	AB011114	NM_00100746 7 NM_014775	9814	0.65	6.82E-03
FLJ14721	226487_at	BE551088	NM_032829	84915	0.65	9.93E-04
FLJ21908	1557984_s_at	BI464019	NM_024604	79657	0.65	4.41E-03
TNFRSF10B	209294_x_at	BC001281	NM_003842 NM_147187	8795	0.65	9.89E-05
FLJ14827	44065_at	AI937468	NM_032848	84934	0.65	1.53E-04
TMEM33	218465_at	NM_018126	NM_018126	55161	0.65	1.81E-03
PDHA1	1555864_s_at	AW057819	NM_000284	5160	0.65	2.47E-04

SDCBP	200958_s_at	NM_005625	NM_001007067 NM_001007068 NM_001007069 NM_001007070 NM_005625	6386	0.65	5.40E-03
TM4SF9	225387_at	AA059445	NM_005723	10098	0.65	2.21E-04
SARA2	1554482_a_at	BC002847	NM_016103	51128	0.65	1.82E-04
BE138575	214020_x_at	BE138575	---	---	0.65	1.59E-05
LOC440885	239624_at	AA725362	XM_498906	440885	0.65	3.36E-04
MGC4308	224523_s_at	BC006475	NM_032359	84319	0.65	5.54E-03
SSBP2	203787_at	NM_012446	NM_012446	23635	0.65	3.43E-03
ELMOD2	1553928_at	NM_153702	NM_153702	255520	0.65	3.72E-03
KIAA1043	215146_s_at	AB028966	---	23331	0.64	5.53E-04
BC015774	1569973_at	BC015774	XM_496867	441220	0.64	7.67E-03
FLJ14166	219227_at	NM_024565	NM_024565	79616	0.64	4.93E-03
BRMS1L	224484_s_at	BC006250	NM_032352	84312	0.64	1.03E-02
SIP1	211115_x_at	AB037703	NM_001009182 NM_001009183 NM_003616	8487	0.64	4.84E-05
RGS19	204336_s_at	NM_005873	NM_005873	10287	0.64	2.62E-03
HEMK1	52159_at	W93807	NM_016173	51409	0.64	4.05E-03
BCCIP	218264_at	NM_016567	NM_016567 NM_078468 NM_078469	56647	0.64	2.33E-04
RPL5 LOC388650	213689_x_at	AL137958	NM_000969 NM_001006605	388650 6125	0.64	1.28E-03
CYCS	208905_at	BC005299	NM_018947	54205	0.64	6.99E-07
ARF3	211622_s_at	M33384	NM_001659	377	0.64	1.47E-04
C19orf14	1553125_x_at	NM_173636	NM_173636	284403	0.64	9.52E-03
MGC10433	205740_s_at	NM_024321	NM_024321	79171	0.64	3.28E-04
PRKDC	208694_at	U47077	NM_006904	5591	0.64	8.30E-03
SCDR10	1569905_at	BC018336	NM_198533 NM_198704 NM_198705 NM_198706 NM_198707 NM_198708	374875	0.64	8.71E-03
TGIF2	216262_s_at	AL050318	NM_021809	60436	0.64	1.37E-05
LOC90268	229268_at	AA723152	NM_138348	90268	0.64	3.05E-04
PARP1	208644_at	M32721	NM_001618	142	0.64	6.21E-05
RGMB LOC285705	227339_at	BE206621	NM_173670	285704 285705	0.64	2.63E-04
ZNF250	213858_at	BE350026	NM_021061	58500	0.64	6.68E-03
ACTR1A	200720_s_at	AL532041	NM_005736	10121	0.64	3.97E-03
FBXL10	229855_at	AA779208	NM_001005366 NM_032590	84678	0.64	5.29E-03
PIPPIN	209981_at	AL023553	NM_014460	27254	0.64	8.32E-03
C22orf16	224932_at	AI814909	NM_213720	400916	0.64	5.31E-03

DTNBP1	223445_at	AF061734	NM_032122 NM_183040 NM_183041	84062	0.63	1.32E-03
GRWD1	221549_at	AF337808	NM_031485	83743	0.63	8.09E-03
LARS2	34764_at	D21851	NM_015340	23395	0.63	1.98E-03
PPP5C	201979_s_at	NM_006247	NM_006247	5536	0.63	5.76E-05
AW051899	242602_x_at	AW051899	---	---	0.63	2.62E-03
FLJ21125	219560_at	NM_024627	NM_024627	79680	0.63	9.02E-03
MRPS28	219819_s_at	NM_014018	NM_014018	28957	0.63	1.73E-03
SENP1	226619_at	AW665440	NM_014554	29843	0.63	3.06E-03
CENTD2	34206_at	AB018325	NM_015242 NM_139181	116985	0.63	2.69E-04
TPM1	206117_at	NM_000366	NM_000366	7168	0.63	1.78E-03
RAP1GDS1	209444_at	BC001851	NM_021159	5910	0.63	2.24E-04
CELSR3	40020_at	AB011536	NM_001407	1951	0.63	6.88E-04
PPM1F	203063_at	NM_014634	NM_014634	9647	0.63	3.60E-05
HMGB1	214938_x_at	AF283771	NM_002128	3146	0.63	4.46E-04
AW294869	225227_at	AW294369	---	---	0.63	1.30E-03
AI417537	227739_at	AI417537	XM_372169	389822	0.63	9.49E-03
GTF3A	201338_x_at	NM_002097	NM_002097	2971	0.63	4.05E-04
EXOSC3	223490_s_at	AF281132	NM_00100226 9 NM_016042	51010	0.63	4.03E-05
HSPA14	219212_at	NM_016299	NM_016299	51182	0.63	2.58E-05
DHX15	201386_s_at	AF279891	NM_001358	1665	0.63	2.26E-05
CDK5RAP2	220935_s_at	NM_018249	NM_00101164 9 NM_018249	55755	0.62	1.12E-03
CBX5	231862_at	AK023520	NM_012117	23468	0.62	8.64E-03
AW024563	225712_at	AW024563	---	---	0.62	2.41E-03
NME4	212739_s_at	AL523860	NM_005009	4833	0.62	4.02E-04
EEF2K	225545_at	BF001312	NM_013302	29904	0.62	1.58E-06
ECHDC1	219974_x_at	NM_018479	NM_018479	55862	0.62	1.24E-03
SORT1	224818_at	BE622952	NM_002959	6272	0.62	6.15E-03
FKBP7	231130_at	AA683602	NM_016105 NM_181342	51661	0.62	6.59E-03
PPP4R2	225519_at	AA203408	NM_174907	151987	0.62	1.07E-03
JAG1	216268_s_at	U77914	NM_000214	182	0.62	3.91E-03
OSBPL1A	241693_at	BF243603	NM_018030 NM_080597 NM_133268	114876	0.62	3.59E-03
AP1B1	205423_at	NM_001127	NM_001127 NM_145730	162	0.62	5.15E-06
SNRPB	213175_s_at	AL049650	NM_003091 NM_198216	6628	0.62	1.16E-05
MYH9	211926_s_at	AI827941	NM_002473	4627	0.62	7.82E-06
BICD2	213154_s_at	AI934125	NM_00100380 0 NM_015250	23299	0.62	6.85E-03
SNX11	220140_s_at	NM_013323	NM_013323 NM_152244	29916	0.62	6.32E-03
ZNF354A	205427_at	NM_005649	NM_005649	6940	0.62	9.78E-03

ANK1	205390_s_at	NM_000037	NM_000037 NM_020475 NM_020476 NM_020477 NM_020478 NM_020479 NM_020480 NM_020481	286	0.62	1.01E-02
SNRPG	205644_s_at	NM_003096	NM_003096	6637	0.62	1.58E-03
15E1.2	214711_at	BE568184	NM_176818	283459	0.62	9.53E-03
PPOX	204788_s_at	NM_000309	NM_000309	5498	0.62	5.07E-03
GTF2F2	209595_at	BC001771	NM_004128	2963	0.62	6.89E-04
RAC3	206103_at	NM_005052	NM_005052	5881	0.62	8.05E-04
IRAK1BP1	213074_at	BG545769	NM_001010844	134728	0.62	1.38E-03
M96	203345_s_at	AI566096	NM_007358	22823	0.62	1.24E-03
CHPPR	203208_s_at	NM_014637	NM_014637	9650	0.62	5.77E-03
CBFB	206788_s_at	AF294326	NM_001755 NM_022845	865	0.62	3.44E-03
HIVEP2	212641_at	AL023584	NM_006734	3097	0.62	2.38E-03
FDPS	201275_at	NM_002004	NM_002004	2224	0.62	1.13E-03
SCC-112	213983_s_at	AW991219	NM_015200	23244	0.62	4.84E-03
NCOR2	207760_s_at	NM_006312	NM_006312	9612	0.62	2.28E-03
CIAPIN1	208424_s_at	NM_020313	NM_020313	57019	0.62	2.19E-05
STAT1	JMISGF3A/M97	HUMISGF3A/M97	NM_007315 NM_139266	6772	0.62	9.80E-04
EIF5B	201027_s_at	NM_015904	NM_015904	9669	0.62	3.52E-04
FBXO45	225099_at	AA126446	XM_117294	200933	0.62	4.20E-03
COPS6	213504_at	W63732	NM_006833	10980	0.62	7.94E-03
ACO2	200793_s_at	NM_001098	NM_001098	50	0.61	1.19E-03
HADHSC	211569_s_at	AF001903	NM_005327	3033	0.61	1.58E-03
M6PRBP1	202122_s_at	NM_005817	NM_005817	10226	0.61	5.73E-03
GPR51	211679_x_at	AF095784	NM_005458	9568	0.61	2.47E-03
LOC63929	226501_at	BE966628	NM_022098	63929	0.61	5.18E-04
FLJ20331	218577_at	NM_017768	NM_017768	55631	0.61	7.70E-03
AI125670	231431_s_at	AI125670	XM_373626	388114	0.61	5.65E-04
RENT1	211168_s_at	D86988	NM_002911	5976	0.61	5.90E-03
COX7B	202110_at	NM_001866	NM_001866	1349	0.61	1.87E-03
RBMS1	209868_s_at	D28482	NM_002897 NM_016836 NM_016839	5937	0.61	1.58E-05
NAP1L4	1560339_s_at	AK095320	NM_005969	4676	0.61	7.56E-03
DTNBP1	223446_s_at	AF061734	NM_032122 NM_183040 NM_183041	84062	0.61	1.14E-03
SUHW3	235520_at	AA805654	NM_017666	55609	0.61	7.60E-03
RAD1	204461_x_at	NM_002853	NM_002853 NM_133282 NM_133377	5810	0.61	8.03E-03
NAP1L4	201414_s_at	NM_005969	NM_005969	4676	0.61	8.91E-03
DBN1	202806_at	NM_004395	NM_004395 NM_080881	1627	0.61	6.46E-03
LSM3	202209_at	NM_014463	NM_014463	27258	0.61	3.78E-04
ITGAV	202351_at	AI093579	NM_002210	3685	0.61	1.45E-03
PDCD8	205512_s_at	NM_004208	NM_004208 NM_145812 NM_145813	9131	0.61	3.22E-03
GLT28D1	219015_s_at	NM_018466	NM_018466	55849	0.61	1.02E-02
)KFZp586M181	224776_at	BF513102	NM_178819	137964	0.61	3.28E-04

ZNF305	206507_at	NM_014724	NM_014724	9753	0.61	6.84E-03
MRPL37	222993_at	AF325707	NM_016491	51253	0.61	3.36E-03
MYO1B	212365_at	BF215996	NM_012223	4430	0.61	4.15E-06
XRCC5	208642_s_at	AA205834	NM_021141	7520	0.61	1.58E-05
AK096932	1564220_a_at	AK096932	---	---	0.60	2.76E-03
MGC50372	1558097_at	W21283	NM_173566	253143	0.60	1.75E-03
UBE2R2	226954_at	BE221883	NM_017811	54926	0.60	1.57E-04
LOC283484	1556940_at	AW665184	---	283484	0.60	6.08E-03
C20orf77	225024_at	AL117521	NM_021215	58490	0.60	4.10E-05
FLJ10350	217943_s_at	NM_018067	NM_018067	55700	0.60	2.33E-03
LOC84661	224129_s_at	AF226998	NM_032574	84661	0.60	6.46E-03
SMYD5	209516_at	U50383	NM_006062	10322	0.60	2.51E-04
H2AFJ	220936_s_at	NM_018267	NM_018267	55766	0.60	2.36E-03
			NM_177925			
XPNPEP1	208453_s_at	NM_006523	NM_020383	7511	0.60	2.47E-03
APG7L	218673_s_at	NM_006395	NM_006395	10533	0.60	7.62E-03
RASGRP1	205590_at	NM_005739	NM_005739	10125	0.60	8.56E-03
KIAA1333	223254_s_at	AA887053	NM_017769	55632	0.60	1.03E-02
C6orf79	220094_s_at	NM_022102	NM_022102	63933	0.60	1.45E-03
PHACTR3	227949_at	AL357503	NM_080672	116154	0.60	5.45E-04
			NM_183244			
			NM_183246			
CSPG6	209259_s_at	AF020043	NM_005445	9126	0.60	4.65E-03
C6orf108	204238_s_at	NM_006443	NM_006443	10591	0.60	6.02E-03
			NM_199184			
MGC15606	215968_at	AF055018	NM_145037	91775	0.60	6.84E-04
MGC13017	235006_at	AL571598	NM_080656	91368	0.60	6.97E-03
PA2G4	208676_s_at	U87954	NM_006191	5036	0.60	2.40E-03
MRPL2	218887_at	NM_015950	NM_015950	51069	0.60	4.44E-04
FUSIP1	206095_s_at	NM_006625	NM_006625	10772	0.60	6.03E-03
			NM_054016			
NUP98	203194_s_at	AA527238	NM_005387	4928	0.60	2.00E-03
			NM_016320			
			NM_139131			
			NM_139132			
G6PC3	44654_at	AI669655	NM_138387	92579	0.60	2.87E-03
BCR	217223_s_at	U07000	NM_004327	613	0.60	3.32E-03
			NM_021574			
AP3S2	202399_s_at	NM_005829	NM_005829	10239	0.59	2.43E-03
ZNF589	219968_at	NM_016089	NM_016089	51385	0.59	2.39E-03
AHCYL1	200850_s_at	NM_006621	NM_006621	10768	0.59	5.75E-04
SIN3A	225135_at	AI433017	NM_015477	25942	0.59	4.14E-03
CHCHD3	217972_at	NM_017812	NM_017812	54927	0.59	2.72E-03
SSBP3	223635_s_at	BC003605	NM_00100995	23648	0.59	1.16E-03
			5			
			NM_018070			
			NM_145716			
AI127452	228443_s_at	AI127452	---	---	0.59	2.59E-03
LOC113174	225614_at	AI815207	NM_138421	113174	0.59	4.60E-04
C20orf24	224376_s_at	AF274948	NM_018840	55969	0.59	1.49E-04
			NM_199483			
			NM_199484			
			NM_199485			
PITPNB	202522_at	AL031591	NM_012399	23760	0.59	1.72E-04
RPE	216574_s_at	J04742	NM_006916	6120	0.59	1.51E-03
			NM_199229			
AF061733	223477_s_at	AF061733	---	---	0.59	4.14E-03
ECHDC1	223088_x_at	BC003549	NM_018479	55862	0.59	2.67E-05

MRPL30	223996_s_at	AF151083	NM_016503 NM_145212 NM_145213	51263	0.59	5.32E-04
CNOT4	203291_at	NM_013316	NM_00100822 5 NM_013316	4850	0.59	1.86E-04
MGC32020	214816_x_at	BC003535	NM_152266	91442	0.59	1.21E-03
SLC4A7	209884_s_at	AF047033	NM_003615	9497	0.59	8.63E-03
ATXN10	208833_s_at	AF119662	NM_013236	25814	0.59	1.71E-06
POP7	209482_at	BC001430	NM_005837	10248	0.59	4.07E-04
LRRFIP1	223492_s_at	BC004958	NM_004735	9208	0.59	2.17E-03
HIG1	221896_s_at	BE739519	NM_014056	25994	0.58	3.91E-03
PBX3	204082_at	NM_006195	NM_006195	5090	0.58	7.63E-03
LZTR1	203412_at	NM_006767	NM_006767	8216	0.58	7.27E-03
SFI1	215699_x_at	AL096768	NM_00100746 7 NM_014775	9814	0.58	6.00E-03
TOP3B	213660_s_at	AA581879	NM_003935	8940	0.58	3.68E-03
PSMD12	202352_s_at	AI446530	NM_002816 NM_174871	5718	0.58	1.19E-03
RAB7L1	218700_s_at	BC002585	NM_003929	8934	0.58	7.31E-03
NM_016402	217946_s_at	NM_016402	---	---	0.58	3.60E-04
SIP1	211114_x_at	AB037702	NM_00100918 2 NM_00100918 3 NM_003616	8487	0.58	5.55E-03
COPS8	214260_at	AI079287	NM_006710 NM_198189	10920	0.58	9.44E-03
ZNF141	206931_at	NM_003441	NM_003441	7700	0.58	8.62E-05
LANCL1	202020_s_at	NM_006055	NM_006055	10314	0.58	6.88E-03
PXK	225796_at	AI684747	NM_017771	54899	0.58	6.08E-04
AMACR	209424_s_at	AI796120	NM_014324 NM_203382	23600	0.58	8.99E-03
RPE	225040_s_at	AV699857	NM_006916 NM_199229	6120	0.58	5.46E-04
GSPT1	215438_x_at	BE906054	NM_002094	2935	0.58	1.02E-02
ASXL1	212234_at	AL034550	NM_015338	171023	0.58	1.46E-03
EIF4ENIF1	218626_at	NM_019843	NM_019843	56478	0.58	1.12E-04
RIT1	239843_at	AI655057	NM_006912	6016	0.58	2.20E-03
TP53RK	225402_at	BG339450	NM_033550	112858	0.58	1.38E-04
MAT2B	217993_s_at	NM_013283	NM_013283 NM_182796	27430	0.58	2.85E-03
TMCC3	226489_at	BG177562	NM_020698	57458	0.58	3.41E-03
POLRMT	203782_s_at	NM_005035	NM_005035	5442	0.58	2.34E-03
BG109230	228567_at	BG109230	---	---	0.58	2.93E-04
RBMS1	203748_x_at	NM_016839	NM_002897 NM_016836 NM_016839	5937	0.58	1.17E-05
LOC96610	226802_s_at	W87523	NM_080926	96610	0.58	8.19E-03

Table 8. Decreased Gene Expression in Cell Lines H1 and BB10 vs. Cell Line 2D6 in Differentiated State Using Microarray Analysis

Gene Symbol	Probe Set ID	Representative Public ID	RefSeq Transcript ID	Entrez Gene	Log2 Ratio	pvalue
CYTL1	219837_s_at	NM_018659	NM_018659	54360	-6.87	8.62E-11
IL17B	220273_at	NM_014443	NM_014443	27190	-6.24	3.55E-08
KIAA0125	206478_at	NM_014792	NM_014792	9834	-5.76	4.88E-04
OLFML2A	213075_at	AL050002	NM_182487	169611	-5.40	4.32E-12
GNAS	217057_s_at	AF107846	NM_000516 NM_016592 NM_080425 NM_080426	2778	-5.37	6.02E-03
THBS2	203083_at	NM_003247	NM_003247	7058	-5.31	9.79E-08
CAP2	212554_at	N90755	NM_006366	10486	-5.29	4.85E-06
CYGB	226632_at	AL513673	NM_134268	114757	-5.15	2.38E-03
MEOX2	206201_s_at	NM_005924	NM_005924	4223	-4.96	9.77E-08
AI051127	231478_at	AI051127	---	---	-4.84	1.89E-03
CRH	205630_at	NM_000756	NM_000756	1392	-4.78	2.26E-03
NXF	1554299_at	AB049469	NM_178864	266743	-4.75	3.31E-05
SLC1A2	225491_at	AL157452	NM_004171	6506	-4.71	1.26E-09
FGF13	205110_s_at	NM_004114	NM_004114 NM_033642	2258	-4.65	6.61E-06
MICAL2	212473_s_at	BE965029	NM_014632	9645	-4.59	1.59E-05
CART	206339_at	NM_004291	NM_004291	9607	-4.59	4.64E-03
ADM	202912_at	NM_001124	NM_001124	133	-4.47	5.16E-07
OSCAR	1554503_a_at	BC035023	NM_130771 NM_133168 NM_133169 NM_206817 NM_206818	126014	-4.38	3.92E-04
HTR1E	207404_s_at	NM_000865	NM_000865	3354	-4.24	8.64E-04
BF681305	1561817_at	BF681305	---	---	-4.22	5.84E-04
EGFL7	218825_at	NM_016215	NM_016215 NM_201446	51162	-4.16	3.07E-05
SLC1A6	1554593_s_at	BC028721	NM_005071	6511	-4.16	8.15E-04
GPR54	242517_at	AI819198	NM_032551	84634	-4.15	1.40E-04
BC036254	1557443_s_at	BC036254	---	---	-4.14	5.46E-06
NDRG1	200632_s_at	NM_006096	NM_006096	10397	-4.10	8.60E-05
LOC56901	218484_at	NM_020142	NM_020142	56901	-4.10	1.79E-03
STX3A	209238_at	BE966922	NM_004177	6809	-4.02	4.71E-04
AQP1	209047_at	AL518391	NM_000385 NM_198098	358	-4.02	1.49E-03
AA530995	213832_at	AA530995	---	---	-4.00	2.31E-03
AL353759	215071_s_at	AL353759	---	---	-3.90	1.96E-05
ARHGAP9	224451_x_at	BC006107	NM_032496	64333	-3.89	8.61E-04
CAP2	212551_at	NM_006366	NM_006366	10486	-3.86	4.69E-07
LOC158572	243017_at	AA032156	XM_379705	158572	-3.85	1.09E-04
PDE4C	211818_s_at	U88712	NM_000923	5143	-3.78	3.71E-03
RaLP	230538_at	AI027957	NM_203349	399694	-3.67	1.39E-05
PTGS1	215813_s_at	S36219	NM_000962 NM_080591	5742	-3.65	1.09E-08
CYGB	1553572_a_at	NM_134268	NM_134268	114757	-3.65	2.42E-06

ANXA2	201590_x_at	NM_004039	NM_001002857 NM_001002858 NM_004039	302	-3.65	1.12E-05
NEBL	203961_at	AL157398	NM_006393 NM_213569	10529	-3.63	1.91E-05
ANXA2	210427_x_at	BC001388	NM_001002857 NM_001002858 NM_004039	302	-3.61	1.06E-05
BE219849	240180_at	BE219849	---	---	-3.60	1.29E-05
AU157716	227051_at	AU157716	---	---	-3.56	1.17E-07
RaLP	235238_at	BF676462	NM_203349	399694	-3.55	6.19E-07
RGS11	206107_at	NM_003834	NM_003834 NM_183337	8786	-3.53	1.56E-06
AI743780	229385_s_at	AI743780	---	---	-3.53	5.61E-08
CRH	205629_s_at	BC002599	NM_000756	1392	-3.52	2.27E-03
MGC4677	225799_at	BF209337	NM_052871	112597	-3.49	6.17E-05
AW954199	239331_at	AW954199	---	---	-3.49	1.64E-05
PTGS1	205128_x_at	NM_000962	NM_000962 NM_080591	5742	-3.48	3.62E-08
BF449053	238018_at	BF449053	---	---	-3.48	3.99E-07
CDC42EP1	204693_at	NM_007061	NM_007061 NM_152243	11135	-3.46	1.15E-04
CDH10	220115_s_at	NM_006727	NM_006727	1008	-3.43	5.86E-06
AI341823	239657_x_at	AI341823	---	---	-3.42	9.66E-07
HPCAL1	1560154_a_at	AK026500	NM_002149 NM_134421	3241	-3.40	3.33E-08
LOC283454	229552_at	AI698128	---	283454	-3.38	1.29E-03
ABLIM3	205730_s_at	NM_014945	NM_014945	22885	-3.34	4.32E-05
AI885066	239845_at	AI885066	---	---	-3.32	1.56E-05
AI810266	235456_at	AI810266	---	---	-3.31	6.67E-04
HIST1H3E	236278_at	AV705309	NM_003532	8353	-3.26	1.95E-05
SLC35F3	229065_at	BF968270	NM_173508	148641	-3.24	3.97E-06
BHLHB2	201170_s_at	NM_003670	NM_003670	8553	-3.22	2.22E-03
NEBL	203962_s_at	NM_006393	NM_006393 NM_213569	10529	-3.21	3.48E-05
ANXA2	213503_x_at	BE908217	NM_001002857 NM_001002858 NM_004039	302	-3.19	2.51E-07
PHKA2	1560358_at	BC038597	NM_000292	5256	-3.18	3.38E-03
GRM5	214217_at	D60132	NM_000842	2915	-3.18	2.84E-04
AL512727	215014_at	AL512727	---	---	-3.18	8.51E-04
STC1	204595_s_at	AI300520	NM_003155	6781	-3.16	9.00E-03
BG325630	234973_at	BG325630	---	---	-3.15	2.18E-03
SYTL1	227134_at	AI341537	NM_032872	84958	-3.14	1.02E-05
BC002465	216189_at	BC002465	---	---	-3.11	3.46E-03
C1orf24	217967_s_at	AF288391	NM_022083 NM_052966	116496	-3.11	5.38E-03
PDE4C	206791_s_at	BF511742	NM_000923	5143	-3.08	2.33E-03
HIST1H2BD	209911_x_at	BC002842	NM_021063 NM_138720	3017	-3.08	9.52E-06
SYT5	206161_s_at	AI659957	NM_003180	6861	-3.06	3.57E-03
LAMP3	205569_at	NM_014398	NM_014398	27074	-3.06	8.91E-03

ADARB1	203865_s_at	NM_015833	NM_001112 NM_015833 NM_015834	104	-3.06	2.79E-04
CYP2E1	1431_at	J02843	NM_000773	1571	-3.05	1.50E-03
LOC150759	221973_at	AI983904	XM_498456 XM_499585	150759	-3.03	2.56E-03
SORCS1	1556891_at	BE328250	NM_052918	114815	-3.03	3.14E-05
CREB5	232555_at	AI689210	NM_004904 NM_182898 NM_182899	9586	-3.03	1.60E-03
ISG20	204698_at	NM_002201	NM_002201	3669	-3.00	1.76E-03
AA417078	238619_at	AA417078	---	---	-2.99	5.87E-05
AW274468	242299_at	AW274468	---	---	-2.98	2.44E-05
PTPRH	208300_at	NM_002842	NM_002842	5794	-2.97	3.46E-04
BHLHB2	201169_s_at	BG326045	NM_003670	8553	-2.96	1.38E-03
AW270105	229413_s_at	AW270105	---	---	-2.92	9.07E-04
LOC390916	235384_at	AW963217	XM_372723	390916	-2.90	9.52E-08
SLCO1A2	211480_s_at	AF085224	NM_005075 NM_021094 NM_134431	6579	-2.88	2.29E-05
HIST1H2BK	209806_at	BC000893	NM_080593	85236	-2.88	3.64E-05
SYT5	206162_x_at	NM_003180	NM_003180	6861	-2.86	6.38E-04
KFZp761O011	207797_s_at	NM_018409	NM_018409	55805	-2.86	2.54E-05
CDKN1C	219534_x_at	NM_000076	NM_000076	1028	-2.86	3.17E-04
SCHIP1	1566772_at	AL832567	NM_014575	29970	-2.85	7.20E-03
CDKN1C	213182_x_at	R78668	NM_000076	1028	-2.85	3.87E-04
FLJ13955	227001_at	AI096706	NM_024759	79815	-2.82	9.16E-04
SYT13	226086_at	AB037848	NM_020826	57586	-2.80	7.99E-04
M160	223655_at	AF264014	NM_174941	283316	-2.79	3.27E-04
CDKN2A	209644_x_at	U38945	NM_000077 NM_058195 NM_058197	1029	-2.78	1.33E-06
AA954997	243436_at	AA954997	---	---	-2.77	1.59E-05
HIST2H2BE	202708_s_at	NM_003528	NM_003528	8349	-2.75	8.53E-04
GTF2IRD2	1557289_s_at	BU617476	NM_173537	84163	-2.75	3.68E-05
AI079543	236949_at	AI079543	XM_498613	440283	-2.75	7.55E-03
LONP	221833_at	AI971258	NM_031490	83752	-2.75	1.32E-03
AI681941	237663_at	AI681941	---	---	-2.74	1.15E-04
BE894882	235681_at	BE894882	---	---	-2.73	3.37E-06
GRIA2	205358_at	NM_000826	NM_000826	2891	-2.73	7.10E-03
MYO15B	219173_at	NM_024957	XR_000222	80022	-2.73	4.36E-05
BC042953	1561242_at	BC042953	---	---	-2.70	6.39E-03
GRIA2	236538_at	BE219628	NM_000826	2891	-2.69	3.27E-03
MYO15B	59375_at	AI825877	XR_000222	80022	-2.68	1.90E-06
AI927692	228528_at	AI927692	---	---	-2.67	6.22E-06
BC021677	1559631_at	BC021677	---	---	-2.67	4.72E-04
AA088430	242556_at	AA088430	---	---	-2.65	5.20E-07
AI769477	236875_at	AI769477	---	---	-2.65	2.18E-08
HSPA5	230031_at	AW052044	NM_005347	3309	-2.64	7.69E-03
HRK	206865_at	U76376	NM_003806	8739	-2.64	6.03E-03
BE671060	235901_at	BE671060	---	---	-2.63	9.58E-04
PLA2G4C	1554810_at	BC017956	NM_003706	8605	-2.63	4.54E-05
CYP2E1	209976_s_at	AF182276	NM_000773	1571	-2.63	4.37E-03
CDKN1C	213348_at	N33167	NM_000076	1028	-2.62	4.09E-04
ARHGAP9	232543_x_at	BE675685	NM_032496	64333	-2.62	7.93E-05
AI798680	227943_at	AI798680	---	---	-2.62	1.59E-05
BG430958	1559455_at	BG430958	---	---	-2.59	1.73E-06

PPP2R2C	1562290_at	AL157448	NM_020416 NM_181876	5522	-2.59	4.74E-04
ANK2	216195_at	AF131823	NM_001148 NM_020977	287	-2.59	2.14E-03
CYP2E1	209975_at	AF182276	NM_000773	1571	-2.58	3.47E-03
BG231712	230408_at	BG231712	---	---	-2.58	3.02E-03
ACRBP	223717_s_at	AB051833	NM_032489	84519	-2.58	1.02E-04
AU145981	232439_at	AU145981	---	---	-2.57	3.24E-05
SIK2	233648_at	AK026914	NM_015191	23235	-2.55	1.93E-03
ANK2	1561895_at	BC030740	NM_001148 NM_020977	287	-2.55	9.50E-04
RHOB	1553962_s_at	BI668074	NM_004040	388	-2.54	1.06E-03
BC040652	1559528_at	BC040652	---	---	-2.53	1.20E-03
CDKN1C	216894_x_at	D64137	NM_000076	1028	-2.52	2.77E-04
AQP1	207542_s_at	NM_000385	NM_000385 NM_198098	358	-2.52	6.49E-03
)KFZP434N181	232257_s_at	AK022645	NM_032137	84077	-2.51	6.77E-03
CTBP1	243180_at	AW452392	NM_001328	1487	-2.51	1.14E-05
KIAA0500	213839_at	AW028110	---	57237	-2.51	5.06E-05
AW606588	239008_at	AW606588	---	---	-2.50	5.69E-04
AA903473	235666_at	AA903473	---	---	-2.50	1.43E-03
)KFZp313N062	1555905_a_at	AI147556	NM_173826	285343	-2.49	1.95E-04
VEGF	211527_x_at	M27281	NM_003376	7422	-2.49	1.00E-03
FAM46A	224973_at	AL078599	NM_017633	55603	-2.48	2.76E-05
ZNF395	223216_x_at	BC001237	NM_018660	157574	-2.48	7.42E-04
FBXO16			NM_172366	55893		
XPO1	230729_at	AI860764	NM_003400	7514	-2.48	1.68E-05
C20orf119	231838_at	AK026760	---	80336	-2.47	1.43E-06
ANK2	232606_at	AK021894	NM_001148 NM_020977	287	-2.46	1.49E-04
AV702101	238595_at	AV702101	---	---	-2.46	3.03E-04
AW364675	239066_at	AW364675	---	---	-2.45	3.80E-06
FAM46A	221766_s_at	AW246673	NM_017633	55603	-2.45	2.44E-06
AK096401	1556204_a_at	AK096401	XM_375664	400721	-2.44	7.27E-04
ZNF395	221123_x_at	NM_018660	NM_018660	55893	-2.44	8.86E-04
PTGER2	206631_at	NM_000956	NM_000956	5732	-2.43	2.99E-05
FLJ31295	226509_at	AV700302	NM_152320	121274	-2.43	2.75E-05
MEF2A	239571_at	AI123399	NM_005587	4205	-2.42	5.57E-04
AW298171	244346_at	AW298171	---	---	-2.41	1.16E-05
FLJ30594	235836_at	N51413	---	150622	-2.41	3.87E-03
AW205919	229830_at	AW205919	---	---	-2.40	1.33E-04
BE671519	242236_at	BE671519	---	---	-2.39	2.68E-03
SIGIRR	218921_at	NM_021805	NM_021805	59307	-2.39	3.99E-05
AW665665	237187_at	AW665665	---	---	-2.39	6.09E-04
GPR92	230252_at	AW183080	NM_020400	57121	-2.39	1.54E-05
MGC13040	224463_s_at	BC006128	NM_032930	85016	-2.39	2.97E-03
ANKS1	212747_at	AI990523	NM_015245	23294	-2.38	1.37E-03
ABCC8	210246_s_at	AF087138	NM_000352	6833	-2.38	2.60E-04
RHOB	212099_at	AI263909	NM_004040	388	-2.38	7.05E-04
SMOC2	223235_s_at	AB014737	NM_022138	64094	-2.37	1.05E-03
CENTG2	1559491_at	AL390180	NM_014914	116987	-2.36	1.41E-03
ARTS-1	214012_at	BE551138	NM_016442	51752	-2.36	4.64E-05
TM4SF8	232632_at	AU145719	NM_005724 NM_198902	10099	-2.36	2.15E-04
U66046	215057_at	U66046	---	---	-2.36	2.03E-04
KIAA0251	1558430_at	R08650	NM_015027	23042	-2.35	5.89E-03
TIMP1	201666_at	NM_003254	NM_003254	7076	-2.35	1.13E-05
AK024567	234597_at	AK024567	---	---	-2.34	1.59E-04

PPFIA4	214978_s_at	AK023365	NM_015053	8497	-2.34	1.46E-03
BCL11B	233302_at	AU146285	NM_022898 NM_138576	64919	-2.34	1.59E-04
C21orf4	228001_at	N51405	NM_006134	757	-2.34	7.50E-05
ATF5	204999_s_at	BC005174	NM_012068	22809	-2.34	1.08E-03
COL7A1	217312_s_at	L23982	NM_000094	1294	-2.33	2.40E-05
AL049252	216527_at	AL049252	---	---	-2.33	1.19E-03
VGCNL1	228608_at	N49852	NM_052867	259232	-2.32	3.07E-06
OLFM1	205591_at	NM_006334	NM_006334 NM_014279 NM_058199	10439	-2.32	9.85E-03
ZNF395 FBXO16	232693_s_at	AK021850	NM_018660 NM_172366	157574 55893	-2.32	2.21E-03
CNTN2	230045_at	BF740264	NM_005076	6900	-2.31	5.97E-04
ZNF395	239619_at	BF431867	NM_018660	55893	-2.31	2.70E-03
RASGEF1B	230233_at	BF110534	NM_152545	153020	-2.31	2.05E-03
AGPAT3	223182_s_at	AI337300	NM_020132	56894	-2.31	6.95E-03
ZNF395	236474_at	AI797677	NM_018660	55893	-2.30	6.29E-03
MPP5	242779_at	N36400	NM_022474	64398	-2.30	3.44E-08
AL512728	216813_at	AL512728	---	---	-2.30	1.89E-03
PLEKHH1	225727_at	AB033026	NM_020715	57475	-2.29	1.26E-06
PLEKHH1	225726_s_at	AB033026	NM_020715	57475	-2.29	3.43E-07
AI123416	227591_at	AI123416	---	---	-2.29	2.47E-04
ANK2	202921_s_at	NM_001148	NM_001148 NM_020977	287	-2.29	7.41E-03
CKMT1	1561155_at	W76548	NM_020990	1159	-2.28	6.30E-03
CFC1	223753_s_at	AF312769	NM_032545	55997	-2.27	1.79E-03
BF111884	230491_at	BF111884	---	---	-2.27	8.21E-06
SEC31L1	1556416_s_at	AF086242	NM_014933 NM_016211	22872	-2.27	7.06E-05
SCN2A2	206381_at	NM_021007	NM_021007	6326	-2.26	6.33E-06
PLEKHA5	237483_at	AI990790	NM_019012	54477	-2.25	8.37E-03
EDG7	231192_at	AW274018	NM_012152	23566	-2.24	1.41E-03
DTNA	240125_at	AI697494	NM_001390 NM_001391 NM_001392 NM_032975 NM_032978 NM_032979 NM_032980 NM_032981	1837	-2.23	6.58E-03
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AI394334	232696_at	AI394334	---	---	-2.22	2.96E-03
UCN	206072_at	NM_003353	NM_003353	7349	-2.22	5.09E-07
DRD1IP	219896_at	NM_015722	NM_015722	50632	-2.22	1.17E-04
AA412686	244608_at	AA412686	---	---	-2.21	3.65E-03
TSAP6	218424_s_at	NM_018234	NM_00100841 0 NM_018234 NM_182915	55240	-2.21	8.31E-05
LOC201158	1560776_at	AU121725	NM_145301	201158	-2.21	7.37E-04
LAF4	244696_at	AI033582	NM_002285	3899	-2.21	6.82E-03
S100A6	217728_at	NM_014624	NM_014624	6277	-2.20	8.83E-05
BACH2	236307_at	AA085906	NM_021813	60468	-2.20	2.30E-03
KIAA1102	241459_at	AI494113	NM_014988	22998	-2.20	4.06E-03
COL5A1	212488_at	N30339	NM_000093	1289	-2.20	4.18E-06
ENOSF1	213645_at	AF305057	NM_017512	55556	-2.19	2.12E-04
LOC158863	232179_at	AL110203	---	158863	-2.19	1.08E-05

ECEL1	219914_at	NM_004826	NM_004826	9427	-2.19	1.99E-03
C21orf4	222907_x_at	BC000569	NM_006134	757	-2.18	3.97E-04
SMYD2	233713_at	AK022181	NM_020197	56950	-2.18	6.04E-04
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C21orf4	225182_at	AL355685	NM_006134	757	-2.17	1.19E-03
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N95363	213183_s_at	N95363	---	---	-2.17	3.77E-04
ARHGAP9	226906_s_at	AL548053	NM_032496	64333	-2.17	9.12E-04
ZNF395	222536_s_at	N36098	NM_018660	55893	-2.16	4.88E-03
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AU146864	232659_at	AU146864	---	---	-2.16	2.93E-04
SERPINE1	202628_s_at	NM_000602	NM_000602	5054	-2.14	2.61E-05
TYRP1	242893_at	AW195492	NM_000550	7306	-2.14	1.35E-03
SLC33A1	1559232_a_at	BC029450	NM_004733	9197	-2.14	4.34E-03
AI695695	242051_at	AI695695	---	---	-2.13	1.12E-03
HRK	206864_s_at	NM_003806	NM_003806	8739	-2.12	4.70E-03
RLF	241438_at	AI742686	NM_012421	6018	-2.12	4.81E-03
CUL3	237376_at	BF115815	NM_003590	8452	-2.11	9.56E-06
BG704082	1556216_s_at	BG704082	---	---	-2.11	1.16E-03
AI968130	240327_at	AI968130	NM_015129 NM_145799 NM_145800 NM_145802	23157	-2.11	3.06E-04
CNGA3	207261_at	NM_001298	NM_001298	1261	-2.11	6.85E-04
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N73550	244112_x_at	N73550	---	---	-2.10	2.68E-03
BF110426	243237_at	BF110426	XM_114222	200373	-2.10	4.35E-04
BM977131	1557478_at	BM977131	---	---	-2.10	2.99E-03
AV685992	241376_at	AV685992	---	---	-2.09	4.64E-03
PAN3	239393_at	AW510927	NM_175854	255967	-2.08	1.36E-04
VEGF	210513_s_at	AF091352	NM_003376	7422	-2.08	7.20E-03
BDKRB2	205870_at	NM_000623	NM_000623	624	-2.08	2.97E-03
ZNF395	218149_s_at	NM_017606	NM_018660	55893	-2.07	6.79E-04
DEPDC6	218858_at	NM_022783	NM_022783	64798	-2.06	5.34E-04
EVER1	214958_s_at	AK021738	NM_007267	11322	-2.06	2.91E-03
LUC7L2	242024_at	T90999	NM_016019	51631	-2.06	2.82E-03
KIAA0804	1559500_at	BC036005	NM_00100992 1 NM_015303	23355	-2.06	1.55E-05
FOXP4	229763_at	BE504097	NM_032204	116113	-2.05	6.69E-05
ASCC2			NM_138457	84164		
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AA452540	232411_at	AA452540	---	---	-2.04	3.30E-03
FNBP1	230389_at	BE046511	NM_015033	23048	-2.04	1.05E-03
AU144437	232887_at	AU144437	---	---	-2.04	2.07E-03
IDS	1569315_s_at	BC032484	NM_000202 NM_006123	3423	-2.03	1.16E-03
CSTB	236449_at	AI885390	NM_000100	1476	-2.03	8.87E-05
IGF2	210881_s_at	M17863	NM_000612	3481	-2.03	1.78E-04
LOC51315	222585_x_at	BE326678	NM_016618	51315	-2.03	7.77E-03
TRIM66	213748_at	AW271713	XM_084529	9866	-2.02	8.91E-03
AA705933	239866_at	AA705933	---	---	-2.02	3.47E-04
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LOC402617	241353_s_at	AW471181	XM_380151	402617	-2.02	4.90E-04
SERPINE1	202627_s_at	AL574210	NM_000602	5054	-2.01	9.89E-06
SND1	228271_at	AW001186	NM_014390	27044	-2.01	5.63E-03
MIG-6	224657_at	AL034417	NM_018948	54206	-2.01	2.57E-04

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SMYD2	212921_at	AF070592	NM_020197	56950	-2.01	1.62E-06
S100A4	203186_s_at	NM_002961	NM_002961 NM_019554	6275	-2.01	6.07E-04
HIST2H2AA	214290_s_at	AI313324	NM_003516	8337	-2.01	7.64E-04
LOC360030	236404_at	AW197320	---	360030	-2.01	7.91E-03
AL119491	244292_at	AL119491	---	---	-2.00	8.84E-03
FNBP1	230086_at	AA937109	NM_015033	23048	-2.00	6.01E-03
LGALS3	208949_s_at	BC001120	NM_002306	3958	-1.99	1.10E-03
GALIG			NM_194327	81625		
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AA278901	244055_at	AA278901	---	---	-1.99	1.31E-04
NSMAF	232148_at	BF056507	NM_003580	8439	-1.98	6.51E-03
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FLJ21657	1557828_a_at	BE675061	NM_022483	64417	-1.98	5.30E-03
EVER1	230526_at	BF515959	NM_007267	11322	-1.98	5.20E-08
SLITRK3	206732_at	NM_014926	NM_014926	22865	-1.97	7.66E-05
AW973410	244310_at	AW973410	XM_498613	440283	-1.97	3.35E-03
ZC3HDC1	218543_s_at	NM_022750	NM_022750	64761	-1.97	2.63E-03
GPR18	244791_at	AA835936	NM_005292	2841	-1.97	1.52E-03
LOC283666	226682_at	AW006185	---	283666	-1.96	1.61E-04
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PKD2	240370_at	AI432451	NM_000297	5311	-1.96	3.38E-04
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AI758408	227235_at	AI758408	---	---	-1.96	1.28E-03
R63578	242818_x_at	R63578	---	---	-1.95	2.36E-03
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PNMA3	223621_at	AL136878	NM_013364	29944	-1.95	4.80E-07
LOC286411	1557133_at	AV753446	---	286411	-1.94	4.84E-04
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AI817960	239649_at	AI817960	---	---	-1.93	8.93E-03
FLJ10359	232414_at	AA827672	XM_375853	55127	-1.92	2.24E-04
C16orf45	239971_at	AI298297	NM_033201	89927	-1.92	5.46E-03
MGC29875	220251_at	NM_024998	NM_014388	27042	-1.92	3.38E-03
FLJ10159	1563906_at	AK090879	---	55084	-1.92	4.66E-03
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FAT4	219427_at	NM_024582	NM_024582	79633	-1.92	5.03E-03
MGC45477	1554250_s_at	BC033812	---	387277	-1.92	2.59E-03
ARMCX4	1552327_at	NM_152583	NM_152583	158947	-1.91	9.32E-07
IGF2	202410_x_at	NM_000612	NM_000612	3481	-1.91	1.38E-04
PRR3	244204_at	W87300	NM_025263	80742	-1.91	2.49E-03
FLJ20152	218510_x_at	AI816291	NM_019000	54463	-1.90	5.85E-04
PCBD2	240846_at	BF223271	NM_032151	84105	-1.90	3.18E-05
C6orf198	227834_at	AL589605	XM_371849	167838	-1.90	5.03E-03
MTX3	237681_at	AA699464	NM_001010891	345778	-1.89	3.91E-03
BF514509	239049_at	BF514509	---	---	-1.89	9.85E-04
C6orf148	237347_at	AL039379	NM_030568	80759	-1.89	9.86E-05
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C6orf154	235935_at	AI539370	XM_168060	221424	-1.88	2.76E-04
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BF433341	235977_at	BF433341	---	---	-1.88	2.48E-05
TMP21	239851_at	AW629289	NM_006827	10972	-1.88	5.43E-04
GFM1	232295_at	AK000780	NM_024996	85476	-1.88	3.27E-03
AAK1	214956_at	AF090101	NM_014911	22848	-1.87	3.23E-03
LOC283439	238636_at	BG430061	---	283439	-1.87	2.24E-03

FTHFSDC1	240552_at	AA811452	NM_015440	25902	-1.87	1.82E-03
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PAPPA	240295_at	AL045014	NM_002581	5069	-1.87	7.85E-05
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LOC253982	238142_at	AW029203	NM_181718	253982	-1.86	8.13E-03
			NM_198907			
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AK023394	232107_at	AK023394	---	---	-1.86	4.70E-05
VPS13C	235023_at	AA828371	NM_017684	54832	-1.85	5.51E-03
RHBDL1	207383_s_at	NM_003961	NM_003961	9028	-1.85	1.70E-04
C21orf4	219600_s_at	NM_006134	NM_006134	757	-1.85	1.43E-03
TPM3	238079_at	AV713323	NM_152263	7170	-1.85	1.29E-03
			NM_153649			
BACE2	217867_x_at	NM_012105	NM_012105	25825	-1.85	1.57E-03
			NM_138991			
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VEGF	212171_x_at	H95344	NM_003376	7422	-1.84	1.68E-03
ID2	213931_at	AI819238	NM_002166	3398	-1.84	3.39E-03
LOC51315	218303_x_at	NM_016618	NM_016618	51315	-1.84	5.97E-03
TMIE	1553601_a_at	NM_147196	NM_147196	259236	-1.83	8.89E-04
TM4SF2	234245_at	AL162055	NM_004615	7102	-1.83	7.61E-03
FADS3	216080_s_at	AC004770	NM_021727	3995	-1.83	1.05E-04
SNF1LK	208078_s_at	NM_030751	NM_173354	150094	-1.83	2.37E-03
FGD5	226985_at	AW269340	NM_152536	152273	-1.83	1.69E-03
ATP2B3	207026_s_at	NM_021949	NM_00100134	492	-1.83	1.63E-04
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			NM_021949			
LOC51315	233329_s_at	AK025986	NM_016618	51315	-1.83	5.27E-03
FLJ00310	1569664_at	BC035915	XM_496691	375010	-1.82	5.02E-04
FNBP1	244286_at	AI017983	NM_015033	23048	-1.82	1.10E-03
ASAM	228082_at	BF056275	NM_024769	79827	-1.82	4.85E-03
VN1R1	221412_at	NM_020633	NM_020633	57191	-1.82	4.74E-05
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FLJ23754	1553248_at	NM_152675	NM_152675	201252	-1.81	6.36E-03
HSD17B1	205829_at	NM_000413	NM_000413	3292	-1.81	5.39E-05
ZNF407	233239_at	AK024882	NM_017757	55628	-1.81	4.86E-03
ARTS-1	209788_s_at	AF183569	NM_016442	51752	-1.81	5.75E-03
GBE1	203282_at	NM_000158	NM_000158	2632	-1.81	2.17E-03
LONP	221834_at	AV700132	NM_031490	83752	-1.81	7.26E-03
SFXN3	217226_s_at	M95929	NM_030971	81855	-1.80	4.81E-04
AK021973	234098_at	AK021973	---	---	-1.80	1.25E-03
AA682539	235575_at	AA682539	---	---	-1.80	5.79E-03
AI950023	244433_at	AI950023	---	---	-1.80	3.52E-03
C13orf22	1562238_at	AL832776	NM_005800	10208	-1.80	5.58E-04
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AW172407	240908_at	AW172407	XM_373053	391733	-1.79	1.54E-03
ARG2	203946_s_at	U75667	NM_001172	384	-1.79	8.38E-05
AI582773	214373_at	AI582773	XM_498956	440996	-1.79	6.73E-03
C1orf21	221272_s_at	NM_030806	NM_030806	81563	-1.79	1.58E-06
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AI732874	241314_at	AI732874	---	---	-1.79	6.26E-03
AI521273	241702_at	AI521273	---	---	-1.79	2.16E-03
SFXN3	220974_x_at	NM_030971	NM_030971	81855	-1.78	5.28E-05
AA394039	229720_at	AA394039	---	---	-1.78	3.12E-04
AI765607	244631_at	AI765607	XM_374318	389834	-1.78	7.00E-03
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BF000047	235736_at	BF000047	---	---	-1.78	2.66E-03

PPP1R7	1559054_a_at	BC027905	NM_002712	5510	-1.78	8.88E-04
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MLLT2	237006_at	AA703523	NM_005935	4299	-1.77	1.07E-03
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LOC360030	1565804_at	AK025161	---	360030	-1.77	7.53E-03
PAQR6	219236_at	NM_024897	NM_024897	79957	-1.77	1.41E-03
KIAA2024	1566166_at	AL833423	NM_198406 NM_172070	130507	-1.77	1.09E-03
FLJ20152	218532_s_at	NM_019000	NM_019000	54463	-1.77	2.47E-03
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AI150690	228466_at	AI150690	---	---	-1.76	1.91E-03
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FLJ11267	220216_at	NM_019607	NM_019607	56260	-1.76	2.56E-03
CPEB1	219578_s_at	NM_030594	NM_030594	64506	-1.76	3.75E-03
NIT1	202891_at	NM_005600	NM_005600	4817	-1.76	4.55E-04
ZDHHC11	221646_s_at	AF267859	NM_024786	79844	-1.76	1.39E-04
LASS5	1556783_a_at	AF088003	NM_147190	91012	-1.76	4.78E-03
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HIST1H3E	214616_at	NM_003532	NM_003532	8353	-1.75	2.78E-05
PHLDA2	209803_s_at	AF001294	NM_003311	7262	-1.75	1.03E-03
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ABI1	238563_at	AV762916	NM_005470	10006	-1.74	2.03E-03
RAB11FIP3	1563104_at	BC009036	NM_014700	9727	-1.74	2.52E-03
C6orf52	236504_x_at	BE670432	XM_371798	347744	-1.74	5.49E-03
AV658469	244699_at	AV658469	---	---	-1.74	6.93E-07
PLXNC1	206470_at	NM_005761	NM_005761	10154	-1.74	1.25E-03
NTNG2	233072_at	AI348745	NM_032536	84628	-1.74	2.30E-03
AMH	206516_at	NM_000479	NM_000479	268	-1.73	4.35E-04
AI814750	1565692_at	AI814750	---	---	-1.73	7.35E-03
NAG8	210109_at	AF191492	NM_014411	27099	-1.73	8.58E-04
PLXNC1	206471_s_at	NM_005761	NM_005761	10154	-1.73	1.82E-03
LOC283861	1554520_at	BC009880	---	283861	-1.73	1.36E-03
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APOC1	204416_x_at	NM_001645	NM_001645	341	-1.72	7.65E-05
ADCY1	213245_at	AL120173	NM_021116	107	-1.71	4.24E-03
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B3GNT5	225612_s_at	BE672260	NM_032047	84002	-1.71	9.32E-03
ANK2	202920_at	BF726212	NM_001148	287	-1.71	6.21E-03
TTC3	1569472_s_at	BC026260	NM_020977 NM_00100189 4	7267	-1.71	1.33E-03
HSPD1	241716_at	BF965447	NM_003316 NM_002156	3329	-1.71	1.25E-04
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BC015455	1569724_at	BC015455	---	---	-1.71	1.78E-04
RGS16	209324_s_at	BF304996	NM_002928	6004	-1.71	4.44E-03
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PDIP	206691_s_at	NM_006849	NM_006849	64714	-1.71	2.28E-08
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BF434212	237942_at	BF434212	---	---	-1.71	2.50E-03
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LOC256273	229466_at	AU144187	---	256273	-1.70	7.69E-03
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MYO15B	227743_at	AI671062	XR_000222	80022	-1.70	5.37E-03
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CAMK2B	209956_s_at	U23460	NM_001220 NM_172078 NM_172079 NM_172080 NM_172081 NM_172082 NM_172083 NM_172084	816	-1.69	2.99E-03
SCFD1	233229_at	AU147042	NM_016106 NM_182835	23256	-1.69	1.27E-04
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VEGF	210512_s_at	AF022375	NM_003376	7422	-1.69	7.38E-04
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GOPC	236862_at	AA279958	NM_020399	57120	-1.68	4.91E-05
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TUSC3	232770_at	AK026149	NM_006765 NM_178234	7991	-1.67	3.31E-04
FBXW7	222729_at	BE551877	NM_018315 NM_033632	55294	-1.67	6.18E-06
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ST7L	216123_x_at	AK024158	NM_017744 NM_138727 NM_138728 NM_138729 NM_198327 NM_198328	54879	-1.67	2.23E-03
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FARSLB	223036_at	D84430	NM_005687	10056	-1.66	2.56E-03
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PRKACB	235780_at	BE622723	NM_002731 NM_182948 NM_207578	5567	-1.66	3.63E-04
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SLCO1A2	207308_at	NM_021094	NM_005075 NM_021094 NM_134431	6579	-1.65	5.88E-03
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RORA	1562529_s_at	BC040965	NM_002943 NM_134260 NM_134261 NM_134262	6095	-1.65	6.52E-04
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ERBB4	206794_at	NM_005235	NM_005235	2066	-1.64	1.93E-05
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CDKN2A	207039_at	NM_000077	NM_000077 NM_058195 NM_058197	1029	-1.62	4.13E-03
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AHI1	221569_at	AL136797	NM_017651	54806	-1.61	1.18E-03
PLXNC1	213241_at	AF035307	NM_005761	10154	-1.61	1.31E-03
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C9orf41	1564690_at	BC022435	NM_152420	138199	-1.60	3.52E-05
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LGALS3BP	200923_at	NM_005567	NM_005567	3959	-1.60	1.65E-06
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CENTG2	233225_at	AK000798	NM_014914	116987	-1.59	6.55E-03
CLCN3	240237_at	H23230	NM_001829 NM_173872	1182	-1.59	6.03E-03
WASL	216094_at	AK025323	NM_003941	8976	-1.59	7.27E-03
CDK3	229468_at	AI885421	NM_001258	1018	-1.59	7.50E-06
PRKWNK1	216022_at	AL049278	NM_018979	65125	-1.59	2.19E-03
CALR	214315_x_at	AI348935	NM_004343	811	-1.59	3.10E-03
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AA166617	230198_at	AA166617	---	---	-1.58	3.03E-03
TP53BP1	1569098_s_at	BU508386	NM_005657	7158	-1.58	5.76E-04
C21orf66	240105_at	AI021902	NM_013329 NM_016631 NM_058191 NM_145328	94104	-1.58	4.09E-03
BC014200	1570061_at	BC014200	---	---	-1.58	7.06E-05
KIAA1045	213636_at	AB028968	XM_048592	23349	-1.57	2.94E-03
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DDHD1	231165_at	BE857355	NM_030637	80821	-1.57	1.47E-03
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LSS	211018_at	D63807	NM_00100143 8 NM_002340	4047	-1.57	2.49E-03
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FLJ32954	235349_at	AI261321	NM_144713	151393	-1.57	7.97E-05
ISG20	33304_at	U88964	NM_002201	3669	-1.56	1.82E-03
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AL122039	234260_at	AL122039	---	---	-1.56	3.46E-03
ARSD	225280_x_at	N51673	NM_001669 NM_009589	414	-1.56	3.54E-03
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LOC91526	228471_at	AA744636	NM_153697	91526	-1.56	1.49E-03
PKD1	216949_s_at	L39891	NM_000296 NM_00100994 4	5310	-1.56	4.32E-05
FLJ12666	215029_at	AL117451	NM_024595	79647	-1.56	2.57E-03
BF512871	240174_at	BF512871	XM_373962	388903	-1.55	2.49E-04
MGC13098	222208_s_at	W07700	XM_379817 XM_499280	84820	-1.55	3.85E-03
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ENOSF1	204143_s_at	NM_017512	NM_017512	55556	-1.55	5.87E-03
ARG2	203945_at	NM_001172	NM_001172	384	-1.55	3.00E-03
AA583038	238498_at	AA583038	---	---	-1.55	5.09E-04
BG548427	235547_at	BG548427	---	---	-1.55	1.16E-03
LOC338620	230930_at	AI435839	---	338620	-1.55	3.00E-03
LOC286208	1560089_at	AL833509	XM_379668	286208	-1.54	2.16E-03
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T77543	237530_at	T77543	---	---	-1.54	9.66E-04
MLSTD1	1557224_at	BM682057	NM_018099	55711	-1.54	4.35E-03
SIGIRR	52940_at	AA085764	NM_021805	59307	-1.54	4.74E-03
T91323	241093_at	T91323	NM_015129 NM_145799 NM_145800 NM_145802	23157	-1.54	8.22E-03
GRM8	1556800_a_at	BC041397	NM_000845	2918	-1.54	5.54E-05
ILK	235906_at	BE962235	NM_004517	3611	-1.54	5.88E-04
LOC284408	1558809_s_at	AK094324	---	284408	-1.53	2.05E-03
PTPN23	1569104_a_at	BE646227	NM_015466	25930	-1.53	9.23E-04
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CALR	212953_x_at	BE251303	NM_004343	811	-1.53	1.01E-03
HIST1H2BN	239041_at	AV747226	NM_003520	8341	-1.53	9.40E-03
KLF6	211610_at	U51869	NM_00100849 0 NM_001300	1316	-1.53	7.45E-04
TTC17	232323_s_at	AK026217	NM_018259	55761	-1.53	2.27E-05
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AK024879	216751_at	AK024879	---	---	-1.53	7.76E-03
WDFY3	238660_at	AI732512	NM_014991 NM_178583 NM_178585	23001	-1.53	4.22E-05
FLJ20719	230712_at	AI634549	XM_373827	55672	-1.52	3.20E-03
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BE503598	1557658_at	BE503598	---	---	-1.52	5.96E-04
LOC440078	1570397_x_at	BC034777	XM_498534	440078	-1.52	1.46E-03
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EVER1	204328_at	NM_007267	NM_007267	11322	-1.51	7.60E-03
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AW665096	214188_at	AW665096	---	---	-1.51	1.36E-03
LTBP3	219922_s_at	NM_021070	NM_021070	4054	-1.51	8.21E-06

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PGAP1	220576_at	NM_024989	NM_024989	80055	-1.51	4.78E-04
ACTN4	232058_at	AU158358	NM_004924	81	-1.51	6.69E-03
FGD5	226984_at	H09596	NM_152536	152273	-1.50	8.21E-03
HPCAL4	219671_at	AL136591	NM_016257	51440	-1.50	7.58E-05
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HPCAL1	205462_s_at	NM_002149	NM_002149 NM_134421	3241	-1.50	9.84E-04
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LOC400729	243021_at	AI344101	XM_378824	400729	-1.48	9.58E-03
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AU146999	215986_at	AU146999	---	---	-1.48	7.62E-05
MAP3K5	203837_at	NM_005923	NM_005923	4217	-1.48	5.81E-04
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CDK3	207188_at	NM_001258	NM_001258	1018	-1.48	1.93E-05
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PRKACB	202741_at	AA130247	NM_002731 NM_182948 NM_207578	5567	-1.47	3.58E-03
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THRAP2	216109_at	AK025348	NM_015335	23389	-1.47	2.04E-04
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BF347758	240222_at	BF347758	---	---	-1.47	2.67E-04

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MYO9A	242512_at	AI382029	NM_006901	4649	-1.47	5.15E-03
AKNA	225701_at	AK024431	NM_030767	80709	-1.47	5.81E-03
GPM6B	240286_at	AL041745	NM_001001994 NM_001001995 NM_001001996 NM_005278	2824	-1.46	1.79E-03
STK4	223746_at	BC005231	NM_006282	6789	-1.46	1.31E-04
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KIN	236887_at	AA768850	NM_012311	22944	-1.46	5.23E-03
PCNXL2	229202_at	AI768826	NM_014801 NM_024938	80003	-1.46	6.03E-04
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C2orf17	222129_at	AK026155	NM_024293	79137	-1.46	1.21E-03
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AGPAT3	223184_s_at	BC004219	NM_020132	56894	-1.46	2.96E-03
ACYP2	206833_s_at	NM_001108	NM_138448	98	-1.46	1.16E-04
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BRUNOL5	232416_at	AL390161	NM_021938	60680	-1.36	9.03E-03
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LOC200030 LOC400781 AG1	242191_at	AI701905	NM_183372 XM_371384 XM_378897 XM_496394	200030 400781 440673	-1.34	1.70E-03
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SYVN1	225090_at	AA844682	NM_032431 NM_172230	84447	-1.32	5.82E-03
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THRAP2	239561_at	AA780679	NM_015335	23389	-1.32	1.91E-03
PCDHB16	232099_at	AB046841	NM_020957	57717	-1.32	2.25E-03
GPR123	239221_at	AI884909	NM_032422	84435	-1.31	2.84E-03
C1orf21	223127_s_at	AW003850	NM_030806	81563	-1.31	8.71E-04
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BU680365	1562497_at	BU680365	---	---	-1.31	9.25E-03
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MYNN	1566108_at	AK056483	NM_018657	55892	-1.31	3.79E-03
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TTC17	224849_at	AK023161	NM_018259	55761	-1.31	2.03E-04
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AKAP12	241679_at	AI672553	NM_005100 NM_144497	9590	-1.30	1.14E-03
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PTBP2	236962_at	AA521018	NM_021190	58155	-1.30	3.82E-03
C7orf28B	215024_at	AK000993	NM_198097	221960	-1.29	6.75E-04
EFHC1	225656_at	AI564473	NM_018100	114327	-1.29	8.52E-03
KIAA1970	1568858_at	BC013247	NM_133451	124454	-1.29	1.47E-05
CAMK2B	211483_x_at	AF081924	NM_001220 NM_172078 NM_172079 NM_172080 NM_172081 NM_172082 NM_172083 NM_172084	816	-1.29	6.21E-03
LOC142678	226644_at	BE222279	NM_080875	142678	-1.29	4.59E-04
IGBP1	242337_at	AI347128	NM_001551	3476	-1.29	4.53E-03
MAP7	202890_at	AW242297	NM_003980	9053	-1.29	9.83E-04
AK3	230630_at	AI566130	NM_00100535 3 NM_013410 NM_203464	205	-1.29	3.77E-03
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CD302	203799_at	NM_014880	NM_014880	9936	-1.29	1.51E-04
VPS13C	218396_at	NM_017684	NM_017684	54832	-1.29	1.69E-04
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DUSP16	224336_s_at	AB052156	NM_030640	80824	-1.27	3.94E-03
BACE2	222446_s_at	AF178532	NM_012105 NM_138991 NM_138992	25825	-1.27	4.30E-04
PUM2	216121_at	AL080106	NM_015317	23369	-1.27	1.02E-05
AVEN	219366_at	NM_020371	NM_020371	57099	-1.27	5.67E-03
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TAPBP	208829_at	AF029750	NM_003190 NM_172208 NM_172209	6892	-1.26	8.92E-06
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HERC4	225989_at	AB046813	NM_015601	26091	-1.26	1.35E-04
PTGS1	238669_at	BE613133	NM_000962 NM_080591	5742	-1.26	7.68E-05
GTPBP2	221050_s_at	NM_019096	NM_019096	54676	-1.26	5.82E-03
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C6orf111	230375_at	AI936531	NM_032870	25957	-1.26	1.30E-03
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AW104619	229754_at	AW104619	---	---	-1.26	3.59E-03
DISC1	244642_at	AI761381	NM_018662	27185	-1.26	7.13E-03
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EVC	219432_at	NM_014556	NM_014556 NM_153717	2121	-1.25	3.41E-03
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ZFYVE16	240859_at	N20928	NM_014733	9765	-1.25	8.54E-03
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AK025360	216173_at	AK025360	---	---	-1.25	7.46E-03

LOC440157	1558139_at	BE730158	XM_495969	440157	-1.25	8.53E-03
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W18186	239842_x_at	W18186	---	---	-1.25	3.42E-04
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PER2	205251_at	NM_022817	NM_003894	8864	-1.25	4.90E-03
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CHD5	213965_s_at	AL035406	NM_015557	26038	-1.24	1.51E-04
C17orf27	1569078_at	AF318359	NM_020914	57674	-1.24	4.95E-03
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T79942	228465_at	T79942	---	---	-1.23	1.38E-03
RPIP8	206196_s_at	NM_006695	NM_006695	10900	-1.23	2.25E-03
SFRS12	243361_at	N51597	NM_139168	140890	-1.23	4.89E-03
FBXW7	229419_at	BF222826	NM_018315	55294	-1.23	3.99E-04
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GRIK2	1563754_at	AJ252246	NM_021956	2898	-1.23	1.60E-03
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PIK3C2A	241905_at	AA579047	NM_002645	5286	-1.22	8.81E-03
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DHX36	1559039_at	AK096808	NM_020865	170506	-1.22	5.13E-03
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ADAM8	205180_s_at	NM_001109	NM_001109	101	-1.22	7.63E-03
FGF7	230918_at	BE856598	NM_002009	2252	-1.22	1.18E-03
C21orf25	212875_s_at	AP001745	NM_199050	25966	-1.22	1.75E-03

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BF061976	243499_at	BF061976	---	---	-1.22	3.63E-03
RLF	204243_at	NM_012421	NM_012421	6018	-1.21	3.24E-05
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BE467577	228251_at	BE467577	---	---	-1.21	2.37E-03
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PR47	1560526_at	BQ880034	---	266671	-1.21	4.02E-03
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OLFM3	1554526_at	BC022531	NM_058170	118427	-1.21	1.84E-04
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U00954	232180_at	U00954	---	---	-1.21	4.24E-05
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EXOC7	214802_at	AK022397	NM_015219	23265	-1.21	8.35E-03
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FNBP1	212288_at	AB011126	NM_015033	23048	-1.20	9.04E-06
TTC11	244082_at	BF507959	NM_016068	51024	-1.20	7.10E-03
ABR	214671_s_at	L19704	NM_001092 NM_021962	29	-1.20	5.25E-03
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TRIM50C	1554182_at	BC033871	NM_198853	378108	-1.19	6.94E-05
ADAMTS1	222162_s_at	AK023795	NM_006988	9510	-1.19	1.75E-03
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AI435590	237192_at	AI435590	---	---	-1.19	7.36E-04
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AA639707	243837_x_at	AA639707	---	---	-1.18	1.88E-04
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AA888777	242740_at	AA888777	---	---	-1.18	1.23E-03
BMPR2	238393_at	AL047534	NM_001204 NM_033346	659	-1.18	5.95E-03
BACH2	1556451_at	AL833645	NM_021813	60468	-1.18	2.17E-04
CRELD1	203368_at	NM_015513	NM_015513	78987	-1.18	3.92E-03

RPL37	224766_at	AW008221	NM_000997	6167	-1.18	6.73E-06
CSTB	201201_at	NM_000100	NM_000100	1476	-1.18	2.39E-06
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C9orf111	228383_at	AK024443	NM_152286	375775	-1.18	4.27E-03
PLRG1	227246_at	BF438014	NM_002669	5356	-1.18	8.04E-04
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C9orf68	220218_at	NM_017985	NM_017985	55064	-1.16	4.90E-03
C21orf66	1555125_at	BC030539	NM_013329	94104	-1.16	3.17E-05
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GAD2	243265_at	AW444497	NM_000818	2572	-1.16	1.34E-04
ABTB1	226442_at	H06267	NM_032548	80325	-1.16	2.47E-05
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CAPN2	208683_at	M23254	NM_001748	824	-1.16	3.02E-04
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PERLD1	55616_at	AI703342	NM_033419	93210	-1.16	4.41E-03
DTNA	227084_at	AW339310	NM_001390 NM_001391 NM_001392 NM_032975 NM_032978 NM_032979 NM_032980 NM_032981	1837	-1.16	3.40E-03
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ZDHHC11	232417_x_at	AU150300	NM_024786	79844	-1.15	1.16E-03
AK3	204348_s_at	NM_013410	NM_001005353 NM_013410 NM_203464	205	-1.15	4.21E-03
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SIRT5	221010_s_at	NM_031244	NM_012241 NM_031244	23408	-1.11	4.63E-03
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ARSD	223695_s_at	BC003660	NM_001669 NM_009589	414	-1.11	8.01E-03
LOC284361	224727_at	AL045545	NM_175063 NM_206538	284361	-1.11	1.48E-03
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ZNF596	232641_at	AC004908	NM_173539	169270	-1.11	3.61E-03
GOLGIN-67	210424_s_at	AF163441	NM_015003 NM_181076 NM_181077	23015	-1.10	3.73E-04
JMY	226352_at	BF447037	NM_152405	133746	-1.10	1.15E-05
APXL2	239435_x_at	AA588854	NM_133456	134549	-1.10	2.97E-03
BC004287	223366_at	BC004287	---	---	-1.10	3.09E-03
NM_025120	220728_at	NM_025120	---	---	-1.10	4.73E-03
BF510762	230262_at	BF510762	---	---	-1.10	2.62E-04
AI741900	239140_at	AI741900	---	---	-1.10	7.72E-05
INADL	223681_s_at	AB044807	NM_005799 NM_170605 NM_176877 NM_176878	10207	-1.10	3.79E-04
PCDHB14	231726_at	NM_018934	NM_018934	56122	-1.10	7.91E-03
AI435590	237193_s_at	AI435590	---	---	-1.10	9.64E-03
NPIP	204538_x_at	NM_006985	NM_006985	9284	-1.10	2.65E-04
SR140	236696_at	BE464843	XM_031553	23350	-1.09	5.65E-03
CCNL2	221427_s_at	NM_030937	NM_030937	81669	-1.09	1.71E-03
GFRA3	214479_at	NM_001496	NM_001496	2676	-1.09	9.83E-03
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UBXD1	220757_s_at	NM_025241	NM_025241	80700	-1.09	1.00E-03
C20orf103	219463_at	NM_012261	NM_012261	24141	-1.09	5.61E-03
HERC1	240703_s_at	AW591969	NM_003922	8925	-1.09	1.25E-03
FLJ25952	243786_at	AA454190	NM_153251	253832	-1.09	1.88E-03
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UBE2D3	230171_at	AW662789	NM_003340 NM_181886 NM_181887 NM_181888 NM_181889 NM_181890 NM_181891 NM_181892 NM_181893	7323	-1.08	3.01E-03

PRKCSH	200707_at	NM_002743	NM_00100132 9 NM_002743	5589	-1.08	1.56E-03
BRUNOL5	230497_at	BE503640	NM_021938	60680	-1.08	1.26E-03
FLJ35390	1558123_at	AK092709	---	255031	-1.08	6.65E-03
IPO9	225728_at	AI659533	NM_018085	55705	-1.08	2.88E-03
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LOC399491	215921_at	AC002544	---	399491	-1.08	2.25E-04
SMU1	228180_at	AA805653	NM_018225	55234	-1.08	3.97E-03
AKT2	236664_at	AA448167	NM_001626	208	-1.08	1.96E-03
JAK1	234193_at	AK025218	NM_002227	3716	-1.08	2.70E-03
INADL	214705_at	AJ001306	NM_005799 NM_170605 NM_176877 NM_176878	10207	-1.08	9.90E-04
C9orf10OS	1558761_a_at	AK093641	NM_198841	158293	-1.08	2.09E-05
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PLA2G4B	219095_at	NM_005090	NM_005090	8681	-1.07	7.70E-05
AF131844	222184_at	AF131844	---	---	-1.07	1.01E-03
AI939452	240892_at	AI939452	---	---	-1.07	2.32E-03
ANKHD1	229457_at	AU148042	NM_017747 NM_017978 NM_024668	54882	-1.07	1.15E-03
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AA033699	229111_at	AA033699	---	---	-1.07	9.78E-03
GOLGIN-67	208798_x_at	AF204231	NM_015003 NM_181076 NM_181077	23015	-1.07	8.11E-04
SYNE1	209447_at	AF043290	NM_015293 NM_033071 NM_133650 NM_182961	23345	-1.07	2.21E-03
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MAP7	215471_s_at	AJ242502	NM_003980	9053	-1.07	7.77E-04
BC025319	1568974_at	BC025319	---	---	-1.06	9.12E-03
DJ328E19.C1.1 LOC200030 MGC8902 LOC401967 AG1	214693_x_at	BE732345	NM_015383 NM_173638 NM_183372 XM_371384 XM_496394 XM_496406	200030 25832 284565 401967 440673	-1.06	3.98E-04
PIGF	239258_at	BE551407	NM_002643 NM_173074	5281	-1.06	3.15E-04
NPIP LOC339047 LOC440341	214870_x_at	AC002045	NM_006985 XM_290671 XM_352159	339047 440341 9284	-1.06	2.19E-04
KIF5C	203129_s_at	BF059313	XM_377774	3800	-1.06	2.07E-03
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AK3	204347_at	AI653169	NM_00100292	205	-1.06	8.16E-03
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BACE1	217904_s_at	NM_012104	NM_012104	23621	-1.06	1.51E-04
			NM_138971			
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WDFY3	212598_at	BE348236	NM_014991	23001	-1.06	4.22E-03
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CLCN3	201735_s_at	NM_001829	NM_001829	1182	-1.06	2.95E-03
			NM_173872			
PHACTR1	213638_at	AW054711	NM_030948	221692	-1.06	8.09E-03
PPIE	229375_at	AL526713	NM_006112	10450	-1.06	2.02E-06
			NM_203456			
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C10orf57	218174_s_at	NM_025125	NM_025125	80195	-1.06	8.98E-04
PEX6	238672_at	AW953952	NM_000287	5190	-1.06	6.15E-04
BDH	211715_s_at	BC005844	NM_004051	622	-1.06	4.14E-04
			NM_203314			
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BF110411	221878_at	BF110411	XM_371506	388969	-1.05	8.17E-03
R93413	236590_at	R93413	---	---	-1.05	6.60E-04
FLJ36674	244698_at	AW297656	NM_173622	284040	-1.05	4.58E-03
AA729232	241359_at	AA729232	---	---	-1.05	9.24E-03
FLJ21159	235550_at	AV751613	NM_024826	79884	-1.05	4.53E-03
SMPD1	209420_s_at	M59916	NM_000543	6609	-1.05	8.56E-04
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KCNMA1	221584_s_at	U11058	NM_002247	3778	-1.05	7.34E-05
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PAM	202336_s_at	NM_000919	NM_000919	5066	-1.05	1.27E-03
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DCTD	201571_s_at	AI656493	NM_001921	1635	-1.05	9.35E-05
ZNF573	217627_at	BE515346	NM_152360	126231	-1.05	5.34E-04
WDR19	232163_at	AI982884	NM_025132	57728	-1.05	4.32E-04
ETFDH	33494_at	S69232	NM_004453	2110	-1.05	1.51E-03
RRAGC	222514_at	AK023373	NM_022157	64121	-1.05	7.18E-03
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BTG3	215425_at	AL049332	NM_006806	10950	-1.04	5.78E-04
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RRAGC	218088_s_at	NM_022157	NM_022157	64121	-1.04	8.27E-04
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			NM_138576			
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NSUN6	242239_at	AW970888	NM_182543	221078	-1.04	8.03E-03
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AA910371	212952_at	AA910371	---	---	-1.04	3.15E-03
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PPT1	200975_at	NM_000310	NM_000310	5538	-1.04	2.75E-05
TTC3	208663_s_at	AI652848	NM_00100189 4 NM_003316	7267	-1.04	9.53E-06
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FTH1	214211_at	AA083483	NM_002032	2495	-1.03	2.78E-03
SERF2	226692_at	AI092931	NM_005770	10169	-1.03	3.64E-03
MTCP1	239236_at	BE465277	NM_014221	4515	-1.03	2.24E-03
PDCD2	228420_at	AW590850	NM_002598 NM_144781	5134	-1.03	8.82E-03
SPOCK2	202524_s_at	NM_014767	NM_014767	9806	-1.03	2.19E-06
CYLD	221905_at	BF516433	NM_015247	1540	-1.03	1.43E-04
IREB2	1563130_a_at	AL109710	NM_004136	3658	-1.03	3.66E-03
HRMT1L1	221564_at	AL570294	NM_001535 NM_206962	3275	-1.03	1.20E-06
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LOC339047	214682_at	AK023376	XM_290671	339047	-1.02	4.06E-03
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LOC144363	225469_at	AA015609	NM_00100166(	144363	-1.02	6.55E-04
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C3orf6	228693_at	AI681307	NM_174908 NM_178335	152137	-1.02	2.49E-03
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UBXD1	223012_at	AF272894	NM_025241	80700	-1.02	3.65E-04
HERC4	225988_at	AI819938	NM_015601	26091	-1.02	2.15E-03
MYO5A	227761_at	AW235548	NM_000259	4644	-1.02	8.53E-03
LTBP3	227308_x_at	AW515704	NM_021070	4054	-1.02	6.79E-07
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RHOU	223169_s_at	AB051826	NM_021205	58480	-1.02	9.28E-03
SH3BGR	204979_s_at	NM_007341	NM_00100171 3 NM_007341	6450	-1.02	1.78E-03
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SPG3A	223340_at	AF131801	NM_015915 NM_181598	51062	-1.02	7.49E-03
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PHKA1	229876_at	BE503584	NM_002637	5255	-1.01	4.38E-04
STX6	244041_at	AI884934	NM_005819	10228	-1.01	8.65E-03
FLJ23518	233400_at	AU158247	NM_024725	79780	-1.01	3.50E-03
PPIE	210502_s_at	AF042386	NM_006112 NM_203456 NM_203457	10450	-1.01	4.24E-03
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OPTN	202073_at	AV757675	NM_00100821 1 NM_00100821 2 NM_00100821 3 NM_021980	10133	-1.01	2.57E-05
Cep164	1558953_s_at	BC000602	NM_014956	22897	-1.01	1.37E-03
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AK000970	215512_at	AK000970	NM_005885	10299	-1.00	2.13E-03
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PIGH	209625_at	BC004100	NM_004569	5283	-1.00	6.00E-07
MEIS3	1569402_at	BC014430	NM_00100981 3 NM_020160	56917	-1.00	8.61E-03
DDX52	1570415_at	BC012557	NM_007010 NM_152300	11056	-1.00	1.89E-03
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ANXA2			NM_000141	10160		
BIRC4			NM_000144	10197		
APP			NM_000202	10198		
ATM			NM_000227	10206		
ATOX1			NM_000230	10207		
ATP1B3			NM_000294	1021		
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BMPR2			NM_000382	10513		
BRCA1			NM_000441	10524		
C11orf3			NM_000484	10606		
C21orf4			NM_000527	10609		
CACNB2			NM_000554	10611		
CCM1				10712		
CD47				10730		
CDK6				10801		
CHKA				10806		
CHRNB1				10848		
AP3S1				10921		
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CP				11019		
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ITSN1	216472_at	AF003737	NM_00100113 2 NM_003024	6453	-1.00	2.41E-03
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KIAA1345	234936_s_at	AK023876	XM_106386	57545	-0.99	1.60E-03
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LRRFIP1	201861_s_at	BF965566	NM_004735	9208	-0.99	7.92E-06
RAD50	238656_at	AA877043	NM_005732 NM_133482	10111	-0.99	8.65E-03
LOC338758	238893_at	AI377324	---	338758	-0.99	2.11E-03
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Lrp2bp	227337_at	AA886870	NM_181726	353322	-0.99	6.37E-04
SMURF2	227489_at	BE962027	NM_022739	64750	-0.99	4.11E-04
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TMEM41B	212623_at	AU153138	---	23027	-0.99	8.63E-03
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MYO9B	242742_at	AI863135	NM_004145	4650	-0.99	3.16E-03
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HK2	202934_at	AI761561	NM_000189	3099	-0.99	4.09E-03
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MAP1LC3B	208786_s_at	AF183417	NM_022818	81631	-0.99	3.39E-03
AKAP12	227530_at	BF511276	NM_005100 NM_144497	9590	-0.99	7.30E-03
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C1orf50	219406_at	NM_024097	NM_024097	79078	-0.98	2.14E-04
RPL13	1565759_at	BG396520	NM_000977 NM_033251	6137	-0.98	2.65E-04
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AF086554	1558504_at	AF086554	XM_373889	440721	-0.98	2.45E-03
FLJ11196	218651_s_at	NM_018357	NM_018357 NM_197958	55323	-0.98	1.86E-03
C17orf28	225981_at	AW139549	NM_030630	283987	-0.98	3.41E-04
SFXN3	1559993_at	AK091504	NM_030971	81855	-0.98	4.54E-03
C6orf111	226412_at	N66397	NM_032870	25957	-0.98	1.98E-03
RPL13	229590_at	AI369389	NM_000977 NM_033251	6137	-0.98	1.00E-03
LOC133308	1564746_at	BC009732	NM_178833	133308	-0.98	1.21E-04
AK027185	232102_at	AK027185	---	---	-0.98	1.28E-04
AW290940	226773_at	AW290940	---	---	-0.98	1.34E-04
AB040946	222564_at	AB040946	---	---	-0.98	1.34E-03
ILVBL	202993_at	NM_006844	NM_006844 NM_176826	10994	-0.97	1.11E-03
NPR2	204310_s_at	NM_003995	NM_000907 NM_003995	4882	-0.97	1.05E-03

PAM	212958_x_at	AI022882	NM_000919 NM_138766 NM_138821 NM_138822	5066	-0.97	2.87E-03
F11066	242973_at	F11066	---	---	-0.97	5.82E-03
SPIN3	1554099_a_at	BC032490	NM_001010862	169981	-0.97	4.95E-05
AA167167	243684_at	AA167167	---	---	-0.97	1.78E-03
LANCL2	218219_s_at	NM_018697	NM_018697	55915	-0.97	9.88E-03
AFFX-BioB-3	AFFX-BioB-3_a	AFFX-BioB-3	---	---	-0.97	1.52E-04
AHI1	220841_s_at	NM_017651	NM_017651	54806	-0.97	4.15E-04
AI675308	1569154_a_at	AI675308	---	---	-0.97	2.61E-03
AI339837	241741_at	AI339837	---	---	-0.97	9.92E-03
HNLF	238525_at	BF987157	NM_182547	222068	-0.97	3.73E-05
NM_024658	218305_at	NM_024658	---	---	-0.97	8.21E-03
FLJ30294	238867_at	AI298041	NM_144632	130827	-0.97	9.74E-03
FBXO9	1559096_x_at	AK095307	NM_012347 NM_033480 NM_033481	26268	-0.97	6.38E-05
PLP2	201136_at	NM_002668	NM_002668	5355	-0.97	1.29E-04
ZNF542	229187_at	AI026708	NM_194319	147947	-0.97	7.05E-03
TTLL3	210129_s_at	AF078842	NM_015644	26140	-0.97	6.31E-03
D4S234E	213533_at	M98528	NM_014392	27065	-0.97	1.57E-04
SHC2	213464_at	AV705938	XM_375550	25759	-0.97	4.07E-06
GCC1	243306_s_at	BE276093	NM_024523	79571	-0.97	2.70E-07
TSGA2	230093_at	AI683428	NM_080860	89765	-0.97	4.32E-03
HDLBP	222916_s_at	AF116718	NM_005336 NM_203346	3069	-0.97	5.58E-03
C9orf91	221865_at	BF969986	NM_153045	203197	-0.96	6.15E-03
CYorf15B	223646_s_at	AF332225	NM_032576	84663	-0.96	4.37E-03
LTB4R	236172_at	AW206817	NM_181657	1241	-0.96	5.00E-03
MGC11332	213403_at	BF223370	NM_032718	84804	-0.96	5.81E-03
SPIRE2	227706_at	AI215798	NM_032451	84501	-0.96	7.98E-05
AU146901	233264_at	AU146901	---	---	-0.96	1.84E-03
BG000693	1559932_at	BG000693	---	---	-0.96	1.63E-04
FLJ20758	228512_at	AW138833	NM_017952	55037	-0.96	1.99E-03
UNC5D	231325_at	AI802048	NM_080872	137970	-0.96	4.13E-05
THRAP2	242911_at	AW999644	NM_015335	23389	-0.96	5.60E-03
CLDN15	219640_at	NM_014343	NM_014343 NM_138429	24146	-0.96	1.04E-03
DUSP16	1558740_s_at	R30807	NM_030640	80824	-0.96	9.85E-03
TMEM1	209412_at	U61500	NM_00100172 3 NM_003274	7109	-0.96	5.34E-03
DDX26	222239_s_at	AL117626	NM_012141	26512	-0.95	1.60E-03
LOC388526	235322_at	BF038869	XM_371157	388526	-0.95	1.09E-04
OS-9	215399_s_at	AI683900	NM_006812	10956	-0.95	7.81E-03
PRKCSH	214080_x_at	AI815793	NM_00100132 9 NM_002743	5589	-0.95	2.14E-04
BF976290	238768_at	BF976290	XM_371506	388969	-0.95	9.91E-04
FLJ14107	207287_at	NM_025026	NM_025026	80094	-0.95	1.43E-05
ARHGAP23	226638_at	AV701292	XM_290799	57636	-0.95	3.20E-04
AI252004	242696_at	AI252004	---	---	-0.95	2.67E-03
TGFB1I1	209651_at	BC001830	NM_015927	7041	-0.95	7.45E-03
AI598222	235679_at	AI598222	---	---	-0.95	1.26E-03
AA131302	236032_at	AA131302	---	---	-0.95	5.35E-04
AI929792	236081_at	AI929792	---	---	-0.95	6.74E-05
N45312	228159_at	N45312	---	---	-0.95	5.76E-04

MONDOA	202519_at	NM_014938	NM_014938	22877	-0.95	6.48E-04
PLCB4	203895_at	AL535113	NM_000933 NM_182797	5332	-0.95	8.09E-05
RNF149	225414_at	AL558987	NM_173647	284996	-0.95	9.45E-03
DNASE1	1557189_at	AW468509	NM_005223	1773	-0.95	4.38E-04
OS-9	200714_x_at	NM_006812	NM_006812	10956	-0.95	4.30E-03
CCNL2	222999_s_at	AF251294	NM_030937	81669	-0.95	5.76E-03
NPD014	209006_s_at	AF247168	NM_020317 NM_207035	57035	-0.95	1.08E-03
LOC154822	243261_at	BF530486	---	154822	-0.94	6.74E-03
TARSL2	227611_at	AA442856	NM_152334	123283	-0.94	4.59E-03
AA827805	241364_at	AA827805	---	---	-0.94	9.38E-03
KRT18	201596_x_at	NM_000224	NM_000224 NM_199187	3875	-0.94	2.40E-03
CYLD	213295_at	AA555096	NM_015247	1540	-0.94	2.37E-04
BC011119	1569723_a_at	BC011119	---	---	-0.94	7.41E-03
PHF17	225820_at	AV646599	NM_024900 NM_199320	79960	-0.94	3.79E-03
C10orf104	229145_at	AA541762	NM_173473	119504	-0.94	1.46E-03
BF062399	240141_at	BF062399	---	---	-0.94	1.03E-03
LOC286437	239762_at	AI080505	---	286437	-0.94	1.26E-04
AA714835	1556646_at	AA714835	---	---	-0.94	6.42E-04
MGC3222	233480_at	AK026869	NM_024334	79188	-0.94	1.32E-03
NEDD4	213012_at	D42055	NM_006154 NM_198400	4734	-0.94	3.31E-03
MGC26979	232023_at	AL575584	NM_153704	91147	-0.94	2.50E-03
BE669703	229541_at	BE669703	---	---	-0.94	5.09E-04
AW665287	243725_at	AW665287	---	---	-0.94	8.33E-04
SPG7	202104_s_at	NM_003119	NM_003119 NM_199367	6687	-0.94	4.93E-03
FFX-r2-Ec-bioB-5	X-r2-Ec-bioB-5	AFFX-r2-Ec-bioB-5	---	---	-0.94	1.31E-04
AG1	212854_x_at	AB051480	XM_371384 XM_496394	440673	-0.94	2.84E-03
BF478154	242620_at	BF478154	---	---	-0.94	2.31E-03
PPM1K	235061_at	AV706522	NM_152542	152926	-0.94	2.87E-04
MDS010	218587_s_at	NM_020231	NM_020231 NM_152305	56983	-0.94	7.79E-03
RNF13	201779_s_at	AF070558	NM_007282 NM_183381 NM_183382 NM_183383 NM_183384	11342	-0.93	1.21E-06
ATP8B2	226771_at	AB032963	NM_001005855 NM_020452	57198	-0.93	1.31E-06
DCTD	210137_s_at	BC001286	NM_001921	1635	-0.93	4.45E-04
LOC286260	232420_x_at	AA706480	---	286260	-0.93	3.00E-04
IDS	217432_s_at	AF179281	NM_000202 NM_006123	3423	-0.93	1.24E-03
ANKRD10	223251_s_at	BC001727	NM_017664	55608	-0.93	6.05E-05
AK098354	1555824_a_at	AK098354	---	---	-0.93	2.66E-04
DOCK9	212538_at	AL576253	NM_015296	23348	-0.93	3.70E-03
DRE1	206551_x_at	NM_017644	NM_017644	54800	-0.93	7.84E-04
SNF1LK2	213221_s_at	AB018324	NM_015191	23235	-0.93	7.54E-03
KIAA1546	227624_at	AB046766	XM_042301	57667	-0.93	7.15E-03
AI417992	240513_at	AI417992	---	---	-0.93	7.71E-03
U2AF1	231904_at	AU122448	NM_006758	7307	-0.92	7.45E-04
KIAA0492	215109_at	R02172	XM_378914	57238	-0.92	3.40E-03

LOC158563	226273_at	AA218974	---	158563	-0.92	1.79E-04
AF130054	211452_x_at	AF130054	---	---	-0.92	4.58E-03
NCOA7	225344_at	AL035689	NM_181782	135112	-0.92	1.11E-03
LOC284356	1555842_at	BM978026	---	284356	-0.92	8.07E-03
EXOSC3	242590_at	BE464643	NM_00100226 9 NM_016042	51010	-0.92	4.59E-03
MALAT1	224558_s_at	AI446756	---	378938	-0.92	8.89E-03
C20orf44	229672_at	AA707125	NM_018244 NM_199487 NM_199513	55245	-0.92	1.02E-03
N64760	212622_at	N64760	---	---	-0.92	3.14E-04
HRMT1L1	202098_s_at	NM_001535	NM_001535 NM_206962	3275	-0.92	5.36E-05
NEU1	208926_at	U84246	NM_000434	4758	-0.92	6.42E-03
AF131777	215504_x_at	AF131777	---	---	-0.92	7.86E-03
PS1TP4	226381_at	AW450329	---	414327	-0.92	9.25E-03
C3orf6	235051_at	BF696931	NM_174908 NM_178335	152137	-0.92	9.12E-03
MAP1LC3B	208785_s_at	BE893893	NM_022818	81631	-0.91	1.87E-03
NM_024900	218517_at	NM_024900	---	---	-0.91	8.37E-03
P4HA2	202733_at	NM_004199	NM_004199	8974	-0.91	4.34E-03
MBTD1	207115_x_at	NM_017643	NM_017643	54799	-0.91	1.43E-03
BF476403	230218_at	BF476403	---	---	-0.91	2.19E-03
AL080160	217446_x_at	AL080160	---	---	-0.91	1.65E-03
C19orf4	219005_at	NM_012109	NM_012109	25789	-0.91	5.96E-04
LOC399491	214035_x_at	AA308853	---	399491	-0.91	6.27E-04
CHPT1	1559739_at	AK025141	NM_020244	56994	-0.91	6.26E-03
U2AF1L1	206512_at	NM_005083	---	7310	-0.91	8.01E-03
C20orf44	244795_at	AV693986	NM_018244 NM_199487 NM_199513	55245	-0.91	4.26E-04
LOC339047	221501_x_at	AF229069	XM_290671	339047	-0.91	2.33E-04
FLJ35093	235125_x_at	AI078279	NM_198549	374986	-0.91	2.80E-03
SLC22A17	218675_at	NM_020372	NM_016609 NM_020372	51310	-0.91	2.67E-06
EIF4A1	214805_at	U79273	NM_001416	1973	-0.91	7.74E-03
Cep164	204251_s_at	NM_014956	NM_014956	22897	-0.91	4.21E-03
AK2	212172_at	AW277253	NM_001625 NM_013411 NM_172199	204	-0.91	1.68E-04
NFKB1	209239_at	M55643	NM_003998	4790	-0.91	2.66E-03
AL833666	1566854_at	AL833666	---	---	-0.91	3.74E-03
BE857570	235677_at	BE857570	---	---	-0.91	6.67E-04
KIAA1276	227504_s_at	N64630	XM_039169	27146	-0.91	9.00E-05
KIAA0590	204792_s_at	NM_014714	NM_014714	9742	-0.91	2.73E-03
AV733292	225444_at	AV733292	---	---	-0.91	9.09E-04
BF057855	236829_at	BF057855	---	---	-0.91	4.03E-03
BC020820	1562962_at	BC020820	---	---	-0.91	1.89E-04
FFX-r2-Ec-bioB	X-r2-Ec-bioB-3	AFFX-r2-Ec-bioB-3	---	---	-0.91	4.89E-04
AF086478	1558948_a_at	AF086478	---	---	-0.91	5.21E-03
PHF20L1	222133_s_at	AK022280	NM_016018 NM_024878 NM_032205 NM_198513	51105	-0.90	9.98E-03
HERC4	208055_s_at	NM_015601	NM_015601	26091	-0.90	1.92E-03
R42552	239718_at	R42552	---	---	-0.90	1.67E-03

FBXO9	1559094_at	AK095307	NM_012347 NM_033480 NM_033481	26268	-0.90	1.55E-04
OSBP	1563051_at	BC017975	NM_002556	5007	-0.90	8.83E-03
GPR27	227769_at	AI703476	NM_018971	2850	-0.90	3.33E-03
C21orf33	202217_at	NM_004649	NM_004649 NM_198155	8209	-0.90	2.00E-03
RGS8	234297_at	AL359941	NM_033345	85397	-0.90	4.04E-03
AFFX-BioB-M	AFFX-BioB-M_a	AFFX-BioB-M	---	---	-0.90	9.42E-05
POLR3E	233458_at	AB040885	NM_018119	55718	-0.90	1.75E-03
DKFZp761B107	226139_at	BE670598	NM_173463	91050	-0.90	4.14E-03
AA923289	236666_s_at	AA923289	XM_372416	390205	-0.90	1.19E-03
BE247450	244443_at	BE247450	XM_498623	440309	-0.90	3.66E-03
SEMA4B	234725_s_at	AK026133	NM_020210 NM_198925	10509	-0.90	1.81E-03
WDFY3	212606_at	AL536319	NM_014991 NM_178583 NM_178585	23001	-0.90	3.35E-04
NM_018336	205955_at	NM_018336	---	---	-0.90	5.74E-04
SELS	223209_s_at	AF328864	NM_018445 NM_203472	55829	-0.90	2.33E-03
CDH20	243657_at	AW593060	NM_031891	28316	-0.90	7.78E-03
KIAA1223	225735_at	AL110131	XM_048747	57182	-0.90	7.05E-04
BE502826	231550_at	BE502826	---	---	-0.90	5.25E-03
DDX26	218819_at	NM_012141	NM_012141	26512	-0.90	1.74E-03
FLJ32731	218017_s_at	NM_025070	XM_372038	138050	-0.90	3.84E-07
FLJ32499	1552711_a_at	NM_144607	NM_144607	124637	-0.90	6.17E-05
AFFX-BioB-5	AFFX-BioB-5_a	AFFX-BioB-5	---	---	-0.89	2.50E-05
TMEM17	1557137_at	AA084725	NM_198276	200728	-0.89	9.22E-04
R26456	243135_x_at	R26456	---	---	-0.89	2.43E-03
FFX-r2-Ec-bioC	X-r2-Ec-bioC-3	AFFX-r2-Ec-bioC-:	---	---	-0.89	1.35E-04
RAB5A	215956_at	AK022065	NM_004162	5868	-0.89	3.52E-03
FX-r2-Ec-bioB-	X-r2-Ec-bioB-M	AFFX-r2-Ec-bioB-M	---	---	-0.89	3.74E-05
NXPH4	221967_at	AI933199	NM_007224	11247	-0.89	1.39E-05
PERLD1	221811_at	BF033007	NM_033419	93210	-0.89	3.44E-04
WDR21	214758_at	AL080157	NM_015604 NM_181340 NM_181341	26094	-0.89	2.29E-04
MDS009	236649_at	AA907927	NM_020234	56986	-0.89	1.30E-03
DISP1	228184_at	AK023679	NM_032890	84976	-0.89	6.47E-05
HIST1H2BH	208546_x_at	NM_003524	NM_003524	8345	-0.89	5.00E-03
MLR1	240592_at	AI939336	NM_153686	254251	-0.89	2.34E-03
AF088033	1556228_a_at	AF088033	---	---	-0.89	7.95E-05
FLJ10815	228951_at	AI631572	NM_018231	55238	-0.89	1.85E-03
UTP14A	221514_at	BC001149	NM_006649	10813	-0.89	9.63E-03
BBP	213882_at	AA012917	NM_032027	83941	-0.89	3.54E-05
NCSTN	208759_at	AF240468	NM_015331	23385	-0.89	6.91E-06
LOC283922	228688_at	AA843726	XM_208908	283922	-0.88	3.60E-03
Cep164	204250_s_at	AI655714	NM_014956	22897	-0.88	2.74E-03
ZFYVE26	213073_at	AB002319	NM_015346	23503	-0.88	1.02E-03
AI525856	239016_at	AI525856	---	---	-0.88	4.67E-05
IREB2	1555476_at	BC017880	NM_004136	3658	-0.88	1.40E-03
W80462	242194_at	W80462	---	---	-0.88	2.61E-03
C13orf21	228044_at	AI420319	NM_001010897	387923	-0.88	1.82E-03
WTAP	1560274_at	BF679507	NM_004906 NM_152857 NM_152858	9589	-0.88	2.07E-04
MGC4278	220352_x_at	NM_024305	---	79151	-0.88	6.74E-03

PHF17	225816_at	AW138134	NM_024900 NM_199320	79960	-0.88	3.82E-03
LOC401551	243900_at	AI190548	XM_376909	401551	-0.88	6.97E-03
FLJ35630	229603_at	AA971753	NM_152618	166379	-0.88	2.21E-03
KIAA1008	218362_s_at	NM_014953	NM_014953	22894	-0.88	7.57E-04
SON	201085_s_at	AA664291	NM_003103 NM_032195 NM_058183 NM_138925 NM_138926 NM_138927	6651	-0.88	5.49E-03
AK021474	215892_at	AK021474	---	---	-0.88	5.75E-03
DCTD	201572_x_at	NM_001921	NM_001921	1635	-0.88	1.87E-04
H73101	1556984_at	H73101	---	---	-0.87	3.73E-03
USP34	230148_at	AI831431	NM_014709	9736	-0.87	8.65E-03
Ufc1	217797_at	NM_016406	NM_016406	51506	-0.87	7.99E-05
BE044193	229384_at	BE044193	---	---	-0.87	8.85E-03
VMP1	224917_at	BF674052	NM_030938	81671	-0.87	8.73E-03
KIAA0711	204301_at	NM_014867	NM_014867	9920	-0.87	4.26E-05
C21orf66	218515_at	NM_016631	NM_013329 NM_016631 NM_058191 NM_145328	94104	-0.87	2.26E-04
D4S234E	209569_x_at	NM_014392	NM_014392	27065	-0.87	6.40E-03
TJP2	202085_at	NM_004817	NM_004817 NM_201629	9414	-0.87	5.83E-04
MAN1A2	217282_at	AK001970	NM_006699	10905	-0.87	5.09E-03
C15orf17	224798_s_at	AI079857	NM_020447	57184	-0.87	5.80E-03
SLC20A2	231818_x_at	AK023965	NM_006749	6575	-0.87	8.22E-03
C14orf103	222840_at	H96715	NM_018036	55102	-0.87	2.43E-03
AFFX-BioC-3	AFFX-BioC-3_a	AFFX-BioC-3	---	---	-0.87	3.17E-05
MGLL	211026_s_at	BC006230	NM_00100379 4 NM_007283	11343	-0.87	3.12E-03
FZD6	203987_at	NM_003506	NM_003506	8323	-0.87	9.59E-03
AFFX-BioC-5	AFFX-BioC-5_a	AFFX-BioC-5	---	---	-0.87	1.11E-04
ENPP2	210839_s_at	D45421	NM_006209	5168	-0.87	1.49E-04
DKFZP564D166	231799_at	AK021886	XM_371074	26115	-0.87	1.88E-04
ANKRD20A LOC440841	1569608_x_at	BC016022	NM_032250 XM_496541	440841 84210	-0.87	2.10E-03
AW341304	237332_at	AW341304	---	---	-0.87	1.73E-03
USP36	224979_s_at	AU154368	NM_025090	57602	-0.87	8.89E-04
FLJ10980	225327_at	AB037791	NM_019600	56204	-0.87	3.59E-05
AI768374	228661_s_at	AI768374	---	---	-0.87	3.95E-04
CANX	200068_s_at	M94859	NM_001746	821	-0.87	7.71E-03
MED6	207078_at	NM_005466	NM_005466	10001	-0.87	9.36E-03
C3orf6	226713_at	AI247881	NM_174908 NM_178335	152137	-0.87	4.87E-03
DJ328E19.C1.1 LOC200030 MGC8902 AG1	201104_x_at	NM_015383	NM_015383 NM_173638 NM_183372 XM_371384 XM_496394	200030 25832 284565 440673	-0.87	9.45E-04
CARD14	240392_at	BF752351	NM_024110 NM_052819	79092	-0.87	6.29E-03
FKBP2	203391_at	NM_004470	NM_004470 NM_057092	2286	-0.86	6.91E-03
CBS	212816_s_at	BE613178	NM_000071	875	-0.86	6.44E-03

AI695743	244534_at	AI695743	---	---	-0.86	1.23E-04
NGLY1	220742_s_at	NM_018297	NM_018297	55768	-0.86	4.72E-04
H19	224997_x_at	AL575306	---	283120	-0.86	2.98E-03
DYRK1B	204954_s_at	NM_004714	NM_004714 NM_006483 NM_006484	9149	-0.86	6.27E-03
IDS	202439_s_at	NM_000202	NM_000202 NM_006123	3423	-0.86	1.14E-03
LOC284267	228453_at	AW004076	---	284267	-0.86	6.01E-03
JUN	201466_s_at	NM_002228	NM_002228	3725	-0.86	6.35E-03
TRAP1	228929_at	AI341246	NM_016292	10131	-0.86	7.28E-03
TSC1	209390_at	AF013168	NM_000368 NM_00100856 7	7248	-0.86	1.82E-03
MLR1	235970_at	AI807408	NM_153686	254251	-0.86	7.89E-04
AI086530	217604_at	AI086530	---	---	-0.86	1.82E-03
DVL3	201908_at	NM_004423	NM_004423	1857	-0.86	2.67E-04
HIST1H3D	214522_x_at	NM_021065	NM_003530	8351	-0.86	4.36E-05
-HUMRGE/M101	UMRGE/M100	K-HUMRGE/M100	---	---	-0.86	2.30E-03
TPP1	200742_s_at	BG231932	NM_000391	1200	-0.86	7.91E-03
TTC3	208664_s_at	AU131711	NM_00100189 4 NM_003316	7267	-0.86	7.07E-03
RFPL2	207227_x_at	NM_006605	NM_006605	10739	-0.86	3.03E-03
D4S234E	209570_s_at	BC001745	NM_014392	27065	-0.86	1.12E-04
LOC146174	230721_at	BF436957	NM_173501	146174	-0.86	5.19E-04
C9orf68	1554708_s_at	BC034293	NM_017985	55064	-0.86	1.35E-03
R3HDM	240503_at	AW274946	NM_015361	23518	-0.86	6.04E-03
SNCA	204467_s_at	NM_000345	NM_000345 NM_007308	6622	-0.85	9.17E-05
AK094546	1556205_at	AK094546	---	---	-0.85	6.76E-04
KIAA1450	225924_at	AI478634	---	57600	-0.85	6.97E-03
SKP1A	200719_at	BE964043	NM_006930 NM_170679	6500	-0.85	3.06E-03
PGK1	228483_s_at	BE856250	NM_000291	5230	-0.85	2.17E-03
LOC200030	229447_x_at	N32025	NM_183372	200030	-0.85	8.99E-04
PRKCA	1560074_at	AL119889	NM_002737	5578	-0.85	1.54E-03
AI332346	225445_at	AI332346	---	---	-0.85	1.78E-03
COG1	231813_s_at	AV746580	NM_018714	9382	-0.85	1.02E-03
FLJ20203	219846_at	NM_025174	NM_032292	54856	-0.85	1.98E-03
GALNS	206335_at	NM_000512	NM_000512	2588	-0.85	9.33E-03
CASP9	203984_s_at	U60521	NM_001229 NM_032996	842	-0.85	1.05E-03
AU147777	232145_at	AU147777	XM_371506	388969	-0.85	7.96E-03
MGC52110	226039_at	AW006441	NM_00100821	493753	-0.85	9.51E-06
MACF1	208634_s_at	AB029290	NM_012090 NM_033044	23499	-0.85	2.09E-03
FLJ41603	227717_at	BF939317	NM_00100166	389337	-0.84	5.48E-03
FLJ12716	233558_s_at	AK023390	NM_021942 NM_199053	60684	-0.84	1.27E-03
BE676062	231249_at	BE676062	---	---	-0.84	2.18E-03
KIAA0415	209913_x_at	AB007875	XM_166527 XM_379771 XM_499251 XM_499396	9907	-0.84	3.69E-03
PCAF	203845_at	AV727449	NM_003884	8850	-0.84	4.85E-03
MONDOA	211789_s_at	AF312918	NM_014938	22877	-0.84	4.65E-03
C6orf70	227656_at	AW968493	XM_376556	55780	-0.84	1.48E-03

PTPN21	226380_at	N21442	NM_007039	11099	-0.84	1.06E-03
PNMT	206793_at	NM_002686	NM_002686	5409	-0.84	2.71E-03
ALG5	218203_at	NM_013338	NM_013338	29880	-0.84	8.89E-03
LOC90110	226842_at	AV694039	---	90110	-0.84	5.28E-03
CYLD	39582_at	AL050166	NM_015247	1540	-0.84	4.04E-03
LOC150271	228658_at	R54042	---	150271	-0.84	6.95E-03
FER1L4	222245_s_at	AF218012	---	80307	-0.84	5.44E-05
MECT1	213091_at	AB014516	NM_015321	23373	-0.84	2.37E-04
			NM_025021			
AL359605	227318_at	AL359605	---	---	-0.84	4.99E-06
SH3GL2	205751_at	NM_003026	NM_003026	6456	-0.84	3.31E-04
MUC1	213693_s_at	AI610869	NM_002456	4582	-0.84	6.09E-04
			NM_182741			
RSHL2	223713_at	AF353618	NM_031924	83861	-0.84	3.80E-03
MRPS33	218654_s_at	NM_016071	NM_016071	51650	-0.83	2.36E-03
			NM_053035			
FBLP-1	1554795_a_at	BC019895	NM_017556	54751	-0.83	5.75E-03
XPOT	227117_at	AW242820	NM_007235	11260	-0.83	5.63E-03
ACRV1	206776_x_at	NM_001612	NM_001612	56	-0.83	7.51E-03
			NM_020069			
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AI334297	225961_at	AI334297	---	---	-0.83	5.29E-04
TMEM34	219074_at	NM_018241	NM_018241	55751	-0.83	1.81E-03
AI494500	241448_at	AI494500	---	---	-0.83	9.31E-04
LOC440160	239010_at	AI744280	XM_498571	440160	-0.83	6.65E-03
PPID	204186_s_at	AI014573	NM_005038	5481	-0.83	2.63E-04
PAK3	236277_at	H23551	NM_002578	5063	-0.83	1.34E-04
NPM1	221923_s_at	AA191576	NM_002520	4869	-0.83	5.74E-03
			NM_199185			
ProSAPiP1	204447_at	NM_014731	NM_014731	9762	-0.83	4.47E-04
NSMAF	232149_s_at	BF056507	NM_003580	8439	-0.83	6.67E-03
MGC21881	1555874_x_at	BC019880	NM_203448	389741	-0.83	1.97E-03
FLJ37953	241825_at	AI265967	NM_152382	129450	-0.83	2.38E-03
INPP5A	203006_at	NM_005539	NM_005539	3632	-0.83	5.00E-04
SLC25A16	210686_x_at	BC001407	NM_152707	8034	-0.83	2.87E-03
CBS	1553972_a_at	BC007257	NM_000071	875	-0.83	5.27E-03
KIAA0804	209553_at	BC001001	NM_00100992	23355	-0.83	9.90E-04
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AW945538	239208_s_at	AW945538	---	---	-0.83	3.44E-04
AK021583	232931_at	AK021583	---	---	-0.82	4.13E-03
BDP1	224227_s_at	AF298152	NM_018429	55814	-0.82	4.88E-03
SPG7	214494_s_at	NM_005200	NM_003119	6687	-0.82	9.51E-03
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ZNF599	1558390_at	BC033354	NM_00100724	148103	-0.82	1.18E-03
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			NM_00100724			
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FFX-r2-Ec-bioC	X-r2-Ec-bioC-5	AFFX-r2-Ec-bioC-5	---	---	-0.82	2.81E-04
KIAA0690	1559127_x_at	BC042908	NM_015179	23223	-0.82	1.09E-04
KIAA1546	1569385_s_at	BC019007	XM_042301	57667	-0.82	3.51E-04

SSR4	201004_at	NM_006280	NM_006280	6748	-0.82	1.83E-03
TRIT1	218617_at	NM_017646	NM_017646	54802	-0.82	5.10E-05
MAPK10	204813_at	NM_002753	NM_002753 NM_138980 NM_138981 NM_138982	5602	-0.82	2.98E-03
CGI-119	219206_x_at	NM_016056	NM_016056	51643	-0.82	3.02E-03
GPRASP1	204793_at	NM_014710	NM_014710	9737	-0.82	2.03E-04
ARHGAP1	241419_at	AA709154	NM_004308	392	-0.82	2.43E-03
KIAA0934	212504_at	N31807	NM_014974	22982	-0.82	2.71E-04
LOC51619	240014_at	AI821720	NM_015983	51619	-0.82	7.64E-03
MEF2A	212535_at	AA142929	NM_005587	4205	-0.81	8.41E-04
AI859463	242111_at	AI859463	---	---	-0.81	3.79E-03
KLF15	231015_at	AW014734	NM_014079	28999	-0.81	3.05E-03
MGC8902	213612_x_at	AI800419	NM_173638	284565	-0.81	1.93E-03
AG1			XM_371384 XM_496394	440673		
FLJ10038	205511_at	NM_017976	---	55056	-0.81	1.24E-03
PCDHA2	210572_at	BC003126	NM_018905 NM_031495 NM_031496	56146	-0.81	3.16E-04
EYA1	214608_s_at	AJ000098	NM_000503 NM_172058 NM_172059 NM_172060	2138	-0.81	3.74E-03
CENTG1	229917_at	BE551002	NM_014770	116986	-0.81	1.70E-03
PLRG1	225194_at	NM_002669	NM_002669	5356	-0.81	2.39E-03
DUSP16	236511_at	AI798976	NM_030640	80824	-0.81	8.12E-03
LRRFIP1	201862_s_at	NM_004735	NM_004735	9208	-0.81	2.88E-04
AI393706	238944_at	AI393706	---	---	-0.81	3.70E-03
TNIP1	207196_s_at	NM_006058	NM_006058	10318	-0.81	3.18E-03
SYNCRIP	236146_at	BF593158	NM_006372	10492	-0.81	3.42E-03
TAS2R5	231757_at	NM_018980	NM_018980	54429	-0.81	1.10E-03
PABPC4	201064_s_at	NM_003819	NM_003819	8761	-0.81	1.63E-03
AW367380	236408_at	AW367380	---	---	-0.81	6.92E-03
C21orf127	234676_s_at	AK021678	NM_013240 NM_182749	29104	-0.81	6.83E-03
NM_018678	220494_s_at	NM_018678	---	---	-0.81	9.98E-03
AF5Q31	232864_s_at	N59653	NM_014423	27125	-0.81	5.40E-03
LTB4R	216388_s_at	U33448	NM_181657	1241	-0.80	3.43E-03
ENPP2	209392_at	L35594	NM_006209	5168	-0.80	1.95E-05
SMURF2	205596_s_at	AY014180	NM_022739	64750	-0.80	2.21E-04
STS	243858_at	AA699970	NM_000351	412	-0.80	1.20E-03
KLHDC1	1552733_at	NM_172193	NM_172193	122773	-0.80	1.05E-03
ASTN2	215407_s_at	AK024064	NM_014010 NM_198186 NM_198187 NM_198188	23245	-0.80	2.08E-03
BQ008117	1556659_at	BQ008117	---	---	-0.80	5.03E-03
FLJ10534	239042_at	AI282511	NM_018128	55720	-0.80	2.54E-03
RABL5	218785_s_at	NM_022777	NM_022777	64792	-0.80	2.32E-03
RNASET2	217983_s_at	NM_003730	NM_003730	8635	-0.80	7.39E-04
BTBD14B	215587_x_at	AK023891	NM_052876	112939	-0.80	3.30E-03
FALZ	232909_s_at	AU146870	NM_004459 NM_182641	2186	-0.80	7.77E-03
NEUGRIN	228541_x_at	AI049608	NM_016645	51335	-0.80	2.24E-03
UNC5B	213100_at	AA127885	NM_170744	219699	-0.80	6.29E-03

LOC439987	229609_at	BF224281	XM_495841	439987	-0.80	7.79E-04
LOC439993			XM_498488	439993		
RPIP8	213439_x_at	AI197870	NM_006695	10900	-0.80	3.47E-05
LOC285949	1563781_at	AK096687	---	285949	-0.80	3.61E-03
FLJ22313	236170_x_at	AI377423	NM_022373	64224	-0.80	5.62E-04
AQP3	39248_at	N74607	NM_004925	360	-0.80	4.75E-03
FALZ	209271_at	AB032251	NM_004459	2186	-0.80	9.58E-03
			NM_182641			
LOC440118	FX-M27830_M	AFFX-M27830_M	XM_498554	440118	-0.80	9.04E-04
ARF1	232175_at	AI972094	NM_001658	375	-0.80	1.30E-04
ERBB2	216836_s_at	X03363	NM_00100586	2064	-0.80	1.70E-04
			2			
			NM_004448			
LOC440823	227168_at	BF475488	XM_498878	440823	-0.80	8.41E-03
DUSP8	206374_at	NM_004420	NM_004420	1850	-0.80	9.45E-04
ARHGAP1	202117_at	BG468434	NM_004308	392	-0.79	5.77E-04
CYLD	221903_s_at	BE046443	NM_015247	1540	-0.79	4.50E-05
AFFX-BioDn-5	FFX-BioDn-5_a	AFFX-BioDn-5	---	---	-0.79	2.95E-05
CARS	202402_s_at	NM_001751	NM_001751	833	-0.79	7.28E-03
			NM_139273			
ASTN2	209693_at	AF116574	NM_014010	23245	-0.79	9.79E-04
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AK025546	232161_x_at	AK025546	---	---	-0.79	4.20E-03
PTPRD	214043_at	BF062299	NM_002839	5789	-0.79	8.45E-03
			NM_130391			
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			NM_130393			
ATP6V0A1	212383_at	AL096733	NM_005177	535	-0.79	9.12E-04
AIG1	223136_at	AF151861	NM_016108	51390	-0.79	8.00E-03
ANXA7	242027_at	AI732079	NM_001156	310	-0.79	8.52E-04
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HDLBP	225012_at	BE378479	NM_005336	3069	-0.79	4.04E-04
			NM_203346			
C10orf51	231196_x_at	AI333226	---	387644	-0.79	1.33E-05
WASL	227010_at	BF438330	NM_003941	8976	-0.79	1.01E-03
RSNL2	226425_at	AU144247	NM_024692	79745	-0.79	4.96E-05
ATP9A	216129_at	AL117659	XM_030577	10079	-0.79	2.42E-04
AA888098	244426_at	AA888098	---	---	-0.79	7.13E-04
DYM	220774_at	NM_017653	NM_017653	54808	-0.79	1.83E-03
C2orf17	221983_at	AL040896	NM_024293	79137	-0.79	6.51E-03
MGC4618	223462_at	BC005158	NM_032326	84286	-0.78	2.33E-03
RSL1D1	212019_at	AK025446	NM_015659	26156	-0.78	3.44E-03
LOC200030	201103_x_at	BE299495	NM_173638	200030	-0.78	1.09E-03
MGC8902			NM_183372	284565		
AG1			XM_371384	440673		
			XM_496394			
WDR13	222138_s_at	AF158978	NM_017883	64743	-0.78	1.22E-03
SERP1	200971_s_at	NM_014445	NM_014445	27230	-0.78	1.90E-03
KIAA1049	213311_s_at	BF000251	NM_014972	22980	-0.78	2.49E-03
BG502771	226397_s_at	BG502771	---	---	-0.78	2.83E-03
AI652868	225811_at	AI652868	---	---	-0.78	5.96E-03
AL559202	226458_at	AL559202	---	---	-0.78	8.12E-03
R15431	236440_at	R15431	---	---	-0.78	1.66E-05
SLC43A1	204394_at	NM_003627	NM_003627	8501	-0.78	3.44E-03
C18orf17	238480_at	AI871745	NM_153211	125488	-0.78	7.85E-04
C11orf31	228331_at	AA526939	NM_170746	280636	-0.78	1.80E-03

SLC9A3	226125_at	BF346665	NM_004174	6550	-0.78	1.02E-03
EPC2	225838_at	AK002010	NM_015630	26122	-0.78	1.65E-04
KIAA0934	212503_s_at	N22859	NM_014974	22982	-0.78	2.51E-04
EFHC1	231026_at	AW451135	NM_018100	114327	-0.78	9.28E-03
AA883831	244042_x_at	AA883831	---	---	-0.78	9.44E-03
NIN	225921_at	AL359571	NM_016350 NM_020921 NM_182944 NM_182945 NM_182946	51199	-0.78	1.33E-04
AW502656	240800_x_at	AW502656	---	---	-0.77	2.82E-05
SMYD2	212922_s_at	AI809870	NM_020197	56950	-0.77	4.17E-03
NDUFV3	226616_s_at	NM_021075	NM_001001503 NM_021075	4731	-0.77	3.48E-03
LSS	202245_at	AW084510	NM_001001438 NM_002340	4047	-0.77	1.95E-04
TTC3	208662_s_at	AI885338	NM_001001894 NM_003316	7267	-0.77	1.75E-04
IL10RB	209575_at	BC001903	NM_000628	3588	-0.77	1.78E-05
PLTP	202075_s_at	NM_006227	NM_006227 NM_182676	5360	-0.77	6.25E-03
ANKRD17	225852_at	BE463523	NM_032217 NM_198889	26057	-0.77	1.79E-05
LOC283981	232463_at	T77995	---	283981	-0.77	9.63E-03
AI146751	242565_x_at	AI146751	---	---	-0.77	1.83E-03
GDF1	206397_x_at	NM_001492	NM_001492	10715	-0.77	1.04E-04
LASS1			NM_021267 NM_198207	2657		
FLJ10276	218004_at	NM_018045	NM_018045	55108	-0.77	1.60E-03
BF223556	229376_at	BF223556	---	---	-0.77	3.00E-03
KIAA1109	212779_at	AB029032	XM_371706	84162	-0.77	8.29E-04
AI983303	237877_at	AI983303	---	---	-0.77	2.54E-05
JMJD2A	203204_s_at	BC002558	NM_014663	9682	-0.77	5.29E-03
RBM8A	217856_at	AF182415	NM_005105	9939	-0.77	1.77E-03
FLJ12716	218179_s_at	NM_021942	NM_021942 NM_199053	60684	-0.77	4.05E-04
CGI-119	222845_x_at	AF161526	NM_016056	51643	-0.77	4.64E-05
BI520422	1559467_at	BI520422	---	---	-0.77	6.79E-03
AA134418	232150_at	AA134418	---	---	-0.77	3.88E-03
ZNF323	222016_s_at	AW086021	NM_030899 NM_145909	64288	-0.77	3.58E-03
GLG1	214730_s_at	AK025457	NM_012201	2734	-0.77	8.94E-05
AK024602	222207_x_at	AK024602	---	---	-0.76	4.03E-03
BE964222	226589_at	BE964222	---	---	-0.76	2.53E-04
GNAS	228173_at	AA810695	NM_000516 NM_016592 NM_080425 NM_080426	2778	-0.76	5.49E-03
MONDOA	225157_at	AW245631	NM_014938	22877	-0.76	3.06E-04
KIAA2010	215607_x_at	AU144530	NM_017936 NM_032560	55671	-0.76	3.17E-03

DJ328E19.C1.1	226740_x_at	BF740216	NM_015383 NM_173638	200030 25832	-0.76	1.09E-03
LOC200030			NM_183372	284565		
MGC8902			XM_371384	439928		
LOC439928			XM_496394	440673		
AG1			XM_498427			
LEAP-2	1552362_a_at	NM_052971	NM_052971	116842	-0.76	5.61E-03
BRUNOL4	238966_at	AA678985	NM_020180	56853	-0.76	8.60E-03
AA827878	223577_x_at	AA827878	---	---	-0.76	5.84E-03
CDKL1	244670_at	AI767697	NM_004196	8814	-0.76	4.97E-03
NALP1	218380_at	NM_021730	NM_014922 NM_033004 NM_033006 NM_033007	22861	-0.76	2.51E-03
MAN1B1	65884_at	AA631254	NM_016219	11253	-0.76	3.92E-04
GOSR2	235041_at	AW005457	NM_004287 NM_054022	9570	-0.76	9.63E-04
BI496583	1557675_at	BI496583	---	---	-0.76	7.35E-03
AA194266	238728_at	AA194266	---	---	-0.76	2.48E-03
EFEMP2	209356_x_at	AB030655	NM_016938	30008	-0.76	5.52E-03
NM_018705	220572_at	NM_018705	---	---	-0.76	3.25E-03
MGC2747	224712_x_at	AI656658	NM_024104	79086	-0.76	2.38E-04
PIK3R1	212239_at	AI680192	NM_181504 NM_181523 NM_181524	5295	-0.76	7.57E-03
RAB11B	34478_at	X79780	NM_004218	9230	-0.76	5.20E-04
FLJ23867	226706_at	BE301252	---	200058	-0.76	2.32E-03
NELF	221214_s_at	NM_015537	NM_015537	26012	-0.76	9.78E-05
MAP2K7	216206_x_at	BC005365	NM_145185	5609	-0.75	1.08E-03
FLJ43806	213752_at	BF111846	NM_201628	399563	-0.75	3.92E-03
CHMP1.5	218177_at	AA293502	NM_020412	57132	-0.75	3.04E-04
KNDC1	230359_at	N45097	NM_033404 NM_152643	85442	-0.75	6.69E-04
HNRPU	236244_at	AI458297	NM_004501 NM_031844	3192	-0.75	7.10E-03
C1orf50	62212_at	W37846	NM_024097	79078	-0.75	7.56E-04
KIAA0913	212359_s_at	W89120	NM_015037	23053	-0.75	2.87E-05
PPP2CA	215628_x_at	AL049285	NM_002715	5515	-0.75	2.81E-04
C6orf160	225155_at	BG339050	XM_499041	441164	-0.75	3.83E-03
CD151	204306_s_at	NM_004357	NM_004357 NM_139030	977	-0.75	1.69E-06
HLCS	209399_at	D87328	NM_000411	3141	-0.75	2.42E-04
AA017536	242270_at	AA017536	---	---	-0.75	2.11E-05
FLJ43663	215330_at	AL049991	XM_379520 XM_380146	378805	-0.75	1.78E-05
MRRF	225126_at	BF438352	NM_138777 NM_199176 NM_199177	92399	-0.75	5.23E-03
WNK1	211992_at	AI445745	NM_018979	65125	-0.75	3.85E-03
AI870959	244877_at	AI870959	---	---	-0.75	1.78E-03
LOC94431	216908_x_at	AF001549	NM_145237	94431	-0.75	2.16E-03
BG527339	226457_at	BG527339	---	---	-0.75	3.79E-03
AA928506	213750_at	AA928506	---	---	-0.74	4.38E-04
GP1BB	206655_s_at	NM_000407	NM_000407	2812	-0.74	4.60E-04
AA629075	236653_at	AA629075	---	---	-0.74	1.35E-04
TTC3	208661_s_at	AW510696	NM_00100189 4 NM_003316	7267	-0.74	1.79E-05

TNRC6C	227149_at	AB046802	NM_018996	57690	-0.74	5.66E-03
POFUT2	209578_s_at	BC000626	NM_015227 NM_133634 NM_133635	23275	-0.74	1.92E-03
CLDN12	223249_at	AL136770	NM_012129	9069	-0.74	2.31E-03
PICALM	239102_s_at	AW293296	NM_00100866 0 NM_007166	8301	-0.74	3.04E-03
SKIV2L	203727_at	NM_006929	NM_006929	6499	-0.74	4.08E-04
LOC125150	228719_at	BE645222	---	125150	-0.74	7.64E-03
AA026666	235611_at	AA026666	---	---	-0.74	3.78E-03
KIAA0323	212356_at	AB002321	NM_015299	23351	-0.74	1.24E-03
BC031035	1569503_at	BC031035	---	---	-0.74	1.39E-05
UNC5B	226899_at	AK022859	NM_170744	219699	-0.74	6.84E-03
KCNRG	239098_at	W68737	NM_173605 NM_199464	283518	-0.74	5.28E-03
DPCD	226009_at	AI129328	NM_015448	25911	-0.74	8.18E-03
LEPREL2	204854_at	NM_014262	NM_014262	10536	-0.74	3.69E-03
AW341225	1556690_s_at	AW341225	---	---	-0.74	1.25E-06
DPP7	224814_at	NM_013379	NM_013379	29952	-0.74	2.41E-04
GAS5	224841_x_at	BF316352	---	60674	-0.74	1.39E-03
TRIM8	223132_s_at	AF220034	NM_030912	81603	-0.73	1.24E-05
BF056548	232140_at	BF056548	XM_499148	441443	-0.73	8.09E-03
PPT2	208469_s_at	NM_030652	NM_005155	80864	-0.73	3.43E-03
EGFL8			NM_030652 NM_138717 NM_138934	9374		
SH3YL1	204019_s_at	NM_015677	NM_015677	26751	-0.73	4.63E-04
EXOSC6	227696_at	AI701408	NM_058219	118460	-0.73	1.43E-03
SNIP	232547_at	BF062187	NM_025248	80725	-0.73	8.20E-06
AL833564	1563638_at	AL833564	---	---	-0.73	4.87E-05
MACF1	208633_s_at	W61052	NM_012090 NM_033044	23499	-0.73	9.23E-04
CIB1	201953_at	NM_006384	NM_006384	10519	-0.73	5.74E-04
RAMP1	204916_at	NM_005855	NM_005855	10267	-0.73	1.63E-03
AA694209	229066_at	AA694209	---	---	-0.73	9.44E-03
NOTCH4	205247_at	AI743713	NM_004557	4855	-0.73	5.43E-03
BF000009	243952_at	BF000009	---	---	-0.73	9.42E-03
NR2F1	209506_s_at	BC004154	NM_005654	7025	-0.73	4.54E-03
LOC92154	1555894_s_at	AA829283	NM_138383	92154	-0.73	9.70E-03
C9orf94	229585_at	AI803088	NM_152702	206938	-0.73	2.44E-03
MAN1A2	217922_at	AL157902	NM_006699	10905	-0.73	1.21E-03
CGI-119	223892_s_at	AF182414	NM_016056	51643	-0.73	1.67E-03
STAF65(gamma	201836_s_at	AU154740	NM_014860	9913	-0.73	6.03E-03
PLXNA3	203623_at	AI675453	NM_017514	55558	-0.73	4.76E-04
SPATA11	223318_s_at	BC004393	NM_032306	84266	-0.73	9.26E-03
BE674055	236109_at	BE674055	---	---	-0.73	8.42E-03
KIAA2026	228446_at	BF062203	XM_088551	158358	-0.73	2.23E-03
CLN3	210859_x_at	AF077973	NM_000086	1201	-0.72	4.13E-03
AW129145	238992_at	AW129145	---	---	-0.72	3.88E-03
LOC201158	1552377_s_at	NM_145301	NM_145301	201158	-0.72	2.76E-03
FLJ31265	228341_at	AI809108	NM_152395	131870	-0.72	1.87E-03
BF111169	230820_at	BF111169	---	---	-0.72	1.14E-04
D8S2298E	215983_s_at	D83768	NM_005671	7993	-0.72	6.50E-03
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PCDHA9	224212_s_at	AF169689	NM_014005	56134	-0.72	5.55E-04
PCDHAC2			NM_018898	56135		
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PCDHA4			NM_018908	56145		
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PCDHA2			NM_018910	56147		
PCDHA1			NM_018911	9752		
			NM_031410			
			NM_031411			
			NM_031495			
RBM5	201394_s_at	U23946	NM_005778	10181	-0.72	2.11E-03
AFFX-BioDn-3	AFFX-BioDn-3_a	AFFX-BioDn-3	---	---	-0.72	1.31E-04
WBSCR16	1554409_at	BC040695	NM_030798	81554	-0.72	5.09E-04
			NM_148842			
SYNJ1	212990_at	AB020717	NM_003895	8867	-0.72	6.07E-05
			NM_203446			
C19orf2	222266_at	BF796940	NM_003796	8725	-0.72	1.36E-03
			NM_134447			
RAPGEF2	203097_s_at	NM_014247	XM_376350	9693	-0.72	7.01E-03
PQBP1	207769_s_at	NM_005710	NM_005710	10084	-0.72	2.58E-03
			NM_144494			
			NM_144495			
LOC162967	1555790_a_at	BC036301	NM_152681	162967	-0.72	3.31E-03
FLJ38482				201931		
EGFL4	214778_at	AB011541	NM_001410	1954	-0.72	3.38E-05
FLJ21148	219751_at	NM_024860	NM_024860	79918	-0.72	3.93E-04
KIAA0773	205368_at	NM_014690	NM_014690	9715	-0.72	3.08E-03
FBLP-1	1555480_a_at	AF459643	NM_017556	54751	-0.71	6.08E-03
PCDHA3	211870_s_at	AF152481	NM_018906	56145	-0.71	8.36E-04
			NM_031497			
ULK3	225067_at	AL117482	NM_015518	25989	-0.71	5.76E-04
ALS4	201965_s_at	NM_015046	NM_015046	23064	-0.71	1.86E-03
RASEF	243862_at	AW205358	NM_152573	158158	-0.71	2.57E-03
C16orf45	212736_at	BE299456	NM_033201	89927	-0.71	9.07E-06
PAK7	213990_s_at	BF056517	NM_020341	57144	-0.71	5.12E-03
			NM_177990			
SF3B3	200688_at	D13642	NM_012426	23450	-0.71	6.09E-04
BRSK1	1552504_a_at	NM_032430	NM_032430	84446	-0.71	8.13E-04
C14orf103	226684_at	AI217906	NM_018036	55102	-0.71	3.88E-03
SLC35E1	229410_at	AI659219	NM_024881	79939	-0.71	9.27E-04
NFYC	202215_s_at	NM_014223	NM_014223	4802	-0.71	1.98E-03
MRPL53	225523_at	AV726817	NM_053050	116540	-0.71	8.44E-04
C5orf14	220495_s_at	NM_024715	NM_024715	79770	-0.71	8.19E-03
RUFY1	218243_at	NM_025158	NM_025158	80230	-0.71	4.37E-04
C11orf11	214128_at	AB014559	NM_006133	747	-0.71	6.28E-03
ZNF404	239043_at	AA084273	XM_292765	342908	-0.71	6.01E-03
TTC3	208073_x_at	NM_003316	NM_00100189	7267	-0.71	3.39E-04
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			NM_003316			
RNASET2	217984_at	NM_003730	NM_003730	8635	-0.71	8.81E-04

AI200555	228275_at	AI200555	---	---	-0.71	1.65E-03
NM_021031	220452_x_at	NM_021031	---	---	-0.71	1.15E-03
MGC16169	240269_at	BF590274	NM_033115	93627	-0.71	5.80E-03
BF590958	226243_at	BF590958	XM_372919	391356	-0.71	5.37E-05
RNF139	209510_at	AF064801	NM_007218	11236	-0.71	5.26E-04
CNOT4	210203_at	R64001	NM_00100822 5 NM_013316	4850	-0.71	8.35E-05
MCM3APAS	220459_at	NM_018118	---	114044	-0.70	3.02E-03
MGC42090	236705_at	AA017245	NM_152774	256130	-0.70	8.57E-03
KIAA2026	238490_at	BG109896	XM_088551	158358	-0.70	5.75E-03
SLC35E1	235035_at	BF342223	NM_024881	79939	-0.70	2.86E-03
KIAA0690	1559126_at	BC042908	NM_015179	23223	-0.70	2.78E-04
TIM14	225359_at	BF666961	NM_145261 NM_201259 NM_201260 NM_201261	131118	-0.70	5.32E-04
PHKA1	205450_at	NM_002637	NM_002637	5255	-0.70	2.40E-03
RNF13	201780_s_at	NM_007282	NM_007282 NM_183381 NM_183382 NM_183383 NM_183384	11342	-0.70	6.65E-03
CLASP2	212309_at	AV725315	NM_015097	23122	-0.70	9.41E-03
VPS11	203292_s_at	NM_021729	NM_021729	55823	-0.70	2.21E-03
AI791187	241724_x_at	AI791187	---	---	-0.70	4.52E-03
DCTN4	233490_at	AI985890	NM_016221	51164	-0.70	4.12E-03
LASS5	224951_at	BE348305	NM_147190	91012	-0.70	5.49E-04
SLC35E1	227518_at	AW051365	NM_024881	79939	-0.70	4.70E-03
SPPL3	224638_at	AI338356	NM_139015	121665	-0.70	2.98E-03
C11orf1	231530_s_at	BG150085	NM_022761	64776	-0.70	2.09E-04
RNF103	202636_at	NM_005667	NM_005667	7844	-0.69	5.99E-04
LOC134218	230893_at	AI223870	NM_194283	134218	-0.69	5.69E-03
C21orf59	218123_at	NM_017835	NM_017835 NM_021254	56683	-0.69	2.83E-04
C19orf12	227704_at	N21279	NM_031448	83636	-0.69	4.72E-03
ZF	213584_s_at	AI432137	NM_021212	58487	-0.69	2.28E-04
MGC4796	223852_s_at	BC005169	NM_032017	83931	-0.69	5.00E-03
C9orf112	225586_at	BF222775	NM_138778	92715	-0.69	2.74E-06
AK023354	222252_x_at	AK023354	---	---	-0.69	9.83E-04
AW873330	225674_at	AW873330	---	---	-0.69	9.10E-04
INSR	213792_s_at	AA485908	NM_000208	3643	-0.69	6.19E-03
C6orf111	212179_at	AW157501	NM_032870	25957	-0.69	2.41E-03
AY094612	1566887_x_at	AY094612	XM_499198	441699	-0.69	9.34E-03
ZNF275	225383_at	BF793625	XM_372267	10838	-0.68	4.76E-03
AA811371	238098_at	AA811371	---	---	-0.68	6.60E-03
RABGAP1L	203020_at	NM_014857	NM_014857	9910	-0.68	1.28E-04
ARHGEF2	235595_at	AW299534	NM_004723	9181	-0.68	2.77E-03
C6orf52	239417_x_at	AW103116	XM_371798	347744	-0.68	7.21E-05
DCL-1	232371_at	AU155401	NM_014880	9936	-0.68	4.13E-03
PPID	204185_x_at	NM_005038	NM_005038	5481	-0.68	1.13E-03
TP53	201746_at	NM_000546	NM_000546	7157	-0.68	6.97E-03
DHRSX	225503_at	AL547782	NM_145177	207063	-0.68	8.56E-05
ATF6	226941_at	BF439325	NM_007348	22926	-0.68	1.77E-03
PIK3R1	212240_s_at	AI679268	NM_181504 NM_181523 NM_181524	5295	-0.68	2.27E-03
FFX-r2-Ec-bioD-X-r2-Ec-bioD-5		AFFX-r2-Ec-bioD-5	---	---	-0.68	7.51E-04

CCNL1	220046_s_at	NM_020307	NM_020307	57018	-0.68	5.67E-04
BC017431	1570087_at	BC017431	---	---	-0.68	5.92E-03
P29	202553_s_at	NM_015484	NM_015484 NM_207170	25949	-0.68	7.53E-03
KIAA0256	212451_at	N52532	NM_014701	9728	-0.68	2.25E-03
PPP3CA	202425_x_at	NM_000944	NM_000944	5530	-0.68	4.15E-03
QTRT1	221270_s_at	NM_031209	NM_031209	81890	-0.68	7.11E-04
C21orf2	203994_s_at	U84569	NM_004928	755	-0.67	4.72E-06
KCNAB1	210471_s_at	U33428	NM_003471 NM_172159 NM_172160	7881	-0.67	3.93E-03
ASB6	222524_s_at	AF151697	NM_017873 NM_177999	140459	-0.67	1.52E-04
BF438106	228045_at	BF438106	---	---	-0.67	9.75E-03
NFYC	211797_s_at	U62296	NM_014223	4802	-0.67	5.31E-04
AI344253	238412_at	AI344253	---	---	-0.67	1.27E-03
ZNF551	211721_s_at	BC005868	NM_138347	90233	-0.67	3.58E-03
TETRAN	209215_at	L11669	NM_001120	10227	-0.67	2.16E-05
C9orf60	202452_at	AI991574	NM_006336	10444	-0.67	7.13E-04
IGF2AS	220561_at	NM_016412	NM_016412	51214	-0.67	8.13E-03
ERO1L	225750_at	BE966748	NM_014584	30001	-0.67	2.29E-06
MGC16028	226196_s_at	AW827281	NM_052873	112752	-0.67	6.84E-03
KIF1A	225482_at	AL533416	NM_004321	547	-0.67	2.15E-03
CAMTA1	213268_at	Z98884	NM_015215	23261	-0.67	4.84E-03
MAPT	203930_s_at	NM_016835	NM_005910 NM_016834 NM_016835 NM_016841	4137	-0.67	2.43E-03
MGC8721	200847_s_at	NM_016127	NM_016127	51669	-0.67	2.91E-03
LOC158563	226274_at	AK025562	---	158563	-0.67	3.76E-04
MAN1B1	218636_s_at	NM_016219	NM_016219	11253	-0.67	1.77E-05
SFRS7	213649_at	AA524053	NM_006276	6432	-0.67	7.31E-05
AK024117	234969_s_at	AK024117	---	---	-0.67	8.03E-04
AF336878	211454_x_at	AF336878	---	---	-0.67	4.04E-03
SPTBN1	212071_s_at	BE968833	NM_003128 NM_178313	6711	-0.67	1.01E-04
PCBD1	203557_s_at	NM_000281	NM_000281 NM_001001939	5092	-0.67	1.83E-04
CNOT6L	227119_at	BF103856	NM_144571	246175	-0.67	7.28E-04
SLC19A1	229489_at	AI681043	NM_003056 NM_194255	6573	-0.67	1.83E-03
C11orf1	222785_x_at	AJ250229	NM_022761	64776	-0.67	1.97E-04
ACOX1	227962_at	BF435852	NM_004035 NM_007292	51	-0.67	9.83E-03
VGLL4	214004_s_at	AI806207	NM_014667	9686	-0.67	1.59E-04
FBXL6	219189_at	NM_024555	NM_012162 NM_024555	26233	-0.67	5.47E-04
EIF3S9	242550_at	AA628539	NM_003751 NM_182712	8662	-0.67	2.25E-03
CYHR1	223421_at	BC005073	NM_032687	50626	-0.67	2.86E-03
PQBP1	214527_s_at	AB041836	NM_005710 NM_144494 NM_144495	10084	-0.67	7.86E-03
AA813998	235837_at	AA813998	---	---	-0.67	9.41E-03
MYST4	211874_s_at	AF119230	NM_012330	23522	-0.66	1.12E-03
CXXC5	233955_x_at	AK001782	NM_016463	51523	-0.66	8.92E-03
LOC54499	208715_at	BF002031	NM_019026	54499	-0.66	3.49E-04

LOC286437	229531_at	AW182938	---	286437	-0.66	9.60E-03
LOC283970	221992_at	AI925734	XM_498469	283970	-0.66	7.97E-05
PPT2	209826_at	AF020544	NM_005155	9374	-0.66	6.89E-03
			NM_138717			
			NM_138934			
GPR85	234303_s_at	AL161959	NM_018970	54329	-0.66	2.74E-03
KIAA0350	242728_at	AA705118	NM_015226	23274	-0.66	8.55E-03
C18orf23	230143_at	BF433220	NM_152470	147341	-0.66	6.22E-03
LOC493856	226689_at	AI749451	NM_001008388	493856	-0.66	3.86E-04
L1CAM	204584_at	AI653981	NM_000425	3897	-0.66	3.46E-03
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FLNA	214752_x_at	AI625550	NM_001456	2316	-0.66	5.06E-03
CSNK1G1	220640_at	NM_022048	NM_001011664	53944	-0.66	7.24E-03
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C19orf24	221587_s_at	BC000890	NM_017914	55009	-0.66	1.58E-03
KIF5C	203130_s_at	NM_004522	XM_377774	3800	-0.66	3.64E-03
CNOT4	210867_at	AF180475	NM_001008225	4850	-0.66	2.10E-03
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ZNF502	229532_at	AI056364	NM_033210	91392	-0.66	4.74E-03
PCDHA9	210674_s_at	AF152308	NM_014005	56134	-0.66	1.36E-03
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INPP5B	213804_at	AI039084	NM_005540	3633	-0.66	6.73E-03
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MLL2	227528_s_at	AI394529	NM_003482	8085	-0.66	1.08E-03
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BE549909	228172_at	BE549909	---	---	-0.66	4.49E-03
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AA491228	242176_at	AA491228	---	---	-0.66	3.24E-03
USP16	222616_s_at	AI806796	NM_001001992	10600	-0.66	3.36E-03
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FLJ10824	212370_x_at	AL080183	NM_001005751	387680	-0.66	2.44E-04
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MAPRE3	203841_x_at	BG222594	NM_012326	22924	-0.66	1.69E-04
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TMEM43	222418_s_at	AA115485	NM_024334	79188	-0.65	6.70E-03
SCMH1	221216_s_at	NM_012236	NM_012236	22955	-0.65	1.81E-06
NSMAF	203269_at	NM_003580	NM_003580	8439	-0.65	4.56E-03
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BSCL2	208906_at	BC004911	NM_032667	26580	-0.65	1.19E-03
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YWHAZ	214848_at	U79277	NM_003406	7534	-0.65	2.64E-04
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MANSC1	220945_x_at	NM_018050	NM_018050	54682	-0.65	8.05E-04
SELT	225561_at	BF692332	NM_016275	51714	-0.65	1.05E-03
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PSENEN	218302_at	NM_018468	NM_172341	55851	-0.65	3.74E-03
LEMD3	218604_at	NM_014319	NM_014319	23592	-0.65	8.61E-05
KIAA0368	212427_at	AB002366	XM_036708	23392	-0.65	3.72E-04
CTSB	213275_x_at	W47179	NM_001908	1508	-0.65	8.91E-03
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USP32	244871_s_at	AW268357	NM_032582	84669	-0.65	2.06E-03
GAS5	224741_x_at	BG329175	---	60674	-0.65	2.74E-03
ATP13A1	218052_s_at	NM_020410	NM_020410	57130	-0.65	1.62E-03
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MBD3	222183_x_at	AL390153	NM_003926	283579	-0.64	1.72E-03
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CD248	219025_at	NM_020404	NM_020404	57124	-0.64	8.85E-04
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AI631833	227396_at	AI631833	---	---	-0.64	8.39E-03
MICAL2	212472_at	BE965029	NM_014632	9645	-0.64	2.60E-04
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RBM8A	213852_at	BG289199	NM_005105	9939	-0.64	9.90E-03
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TRIM8	221012_s_at	NM_030912	NM_030912	81603	-0.64	3.17E-04
C1orf27	222720_x_at	W72877	NM_017847	54953	-0.64	2.02E-04
TPP1	214196_s_at	AA602532	NM_000391	1200	-0.64	2.31E-03
PMS2L2	215412_x_at	AB017007	NM_002679	5380	-0.64	9.44E-03
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C15orf24	217898_at	NM_020154	NM_020154	56851	-0.64	1.32E-03

SELT	217811_at	NM_016275	NM_016275	51714	-0.64	1.82E-04
URB	225242_s_at	AW303375	NM_199511 NM_199512	151887	-0.64	6.81E-03
EFHC1	219833_s_at	NM_018100	NM_018100	114327	-0.64	1.22E-03
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C14orf43	225980_at	AV740879	NM_194278	91748	-0.64	1.54E-03
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STARD7	236484_at	AW850611	NM_020151 NM_139267	56910	-0.63	1.49E-04
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TTC3	210645_s_at	D83077	NM_001001894 NM_003316	7267	-0.63	2.39E-03
SCN3B	204722_at	AW007335	NM_018400	55800	-0.63	5.01E-05
ATF6	217550_at	AA576497	NM_007348	22926	-0.63	5.13E-03
OFD1	203569_s_at	NM_003611	NM_003611	8481	-0.63	4.46E-04
ITPK1	210740_s_at	AF279372	NM_014216	3705	-0.63	7.31E-04
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BEX2	224367_at	AF251053	NM_032621	84707	-0.63	5.01E-03
KIAA1387	226230_at	AA541716	NM_020463	57223	-0.63	8.30E-03
DND1	222070_at	AW090043	NM_194249	373863	-0.63	9.36E-03
MLL2	227527_at	AI394529	NM_003482	8085	-0.63	6.88E-03
C5orf14	227873_at	BE547587	NM_024715	79770	-0.63	3.10E-03
TMED4	224680_at	AL539253	NM_182547	222068	-0.63	6.32E-04
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MAP3K12	205448_s_at	NM_006301	NM_006301	7786	-0.63	1.84E-03
KIAA0276	243691_at	AA150455	NM_015115	23142	-0.63	1.60E-03
AV736334	237561_x_at	AV736334	---	---	-0.63	5.35E-03
LOC148189	235191_at	BE780373	---	148189	-0.63	7.40E-03
FBXL2	214436_at	AF176518	NM_012157	25827	-0.63	6.41E-03
HT036	223769_x_at	AF284750	NM_031207	81888	-0.63	1.42E-04
MLX	217910_x_at	NM_013383	NM_170607 NM_198204 NM_198205	6945	-0.62	8.02E-03
C5orf5	218518_at	NM_016603	NM_016603	51306	-0.62	3.54E-03
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KCNF1	210263_at	AF029780	NM_002236	3754	-0.62	7.86E-03
LKAP	202386_s_at	NM_019081	NM_014647 NM_019081	9665	-0.62	2.93E-05
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ZNF266	214686_at	AA868898	NM_006631 NM_198058	10781	-0.62	3.90E-03
MAGI-3	226770_at	AI692181	NM_020965 NM_152900	260425	-0.62	8.14E-04
HNRPR	208765_s_at	NM_005826	NM_005826	10236	-0.62	1.26E-03
TSTA3	36936_at	U58766	NM_003313	7264	-0.62	6.42E-03
AK001513	233642_s_at	AK001513	---	---	-0.62	2.84E-04
OGT	212307_s_at	BF001665	NM_003605 NM_181672 NM_181673	8473	-0.62	2.58E-03
POMT2	225560_at	AK023804	NM_013382	29954	-0.62	4.78E-03
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BBS7	235007_at	AI683802	NM_018190 NM_176824	55212	-0.61	9.30E-03
EIF2C4	227930_at	AI669957	NM_017629	192670	-0.61	7.32E-03
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AI140364	221740_x_at	AI140364	XM_373737	388397	-0.61	5.62E-03
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TGDS	237346_at	AA976208	NM_014305	23483	-0.61	7.82E-03
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WDR9	225446_at	AI638279	NM_001007246 NM_018963 NM_033656	54014	-0.61	6.06E-03
LOC157697	227016_at	AA767385	NM_207332	157697	-0.61	8.34E-03
SLC35E1	79005_at	AA504646	NM_024881	79939	-0.61	2.09E-03
RFX1	226786_at	BF507952	NM_002918	5989	-0.61	1.11E-03
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TSPYL2	218012_at	NM_022117	NM_022117	64061	-0.61	4.00E-03
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MKLN1	243959_at	N35099	NM_013255	4289	-0.60	8.87E-04
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CACNB1	210185_at	AB054985	NM_000723 NM_199247 NM_199248	782	-0.60	3.90E-04
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C21orf127	220311_at	NM_013240	NM_013240 NM_182749	29104	-0.60	3.00E-03
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HEL308	1554342_s_at	BC011863	NM_133636	113510	-0.60	9.43E-03
ET	221192_x_at	NM_024311	NM_024311	79157	-0.60	2.02E-03

SNRPB2	1561965_at	BE466925	NM_003092 NM_198220	6629	-0.60	2.74E-03
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RASA2	230669_at	W38444	NM_006506	5922	-0.59	4.05E-03
GRIK5	214966_at	S40369	NM_002088	2901	-0.59	4.00E-03
PARP6	234710_s_at	AK021790	NM_020213 NM_020214	56965	-0.59	2.29E-04
DXYS155E	203624_at	NM_005088	NM_005088	8227	-0.59	9.05E-03
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KATNB1	203163_at	NM_005886	NM_005886	10300	-0.59	1.72E-03
C12orf10	218220_at	NM_021640	NM_021640	60314	-0.59	4.83E-03
SCN3B	204723_at	AB032984	NM_018400	55800	-0.59	5.81E-04
IL17D	227401_at	BE856748	NM_138284	53342	-0.59	5.23E-04
TUSC3	209228_x_at	U42349	NM_006765 NM_178234	7991	-0.59	8.59E-05
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SFRS5	203380_x_at	NM_006925	NM_006925	6430	-0.59	3.73E-03
MRX85	225867_at	BE741869	NM_138440	114990	-0.59	2.02E-03
SBF2	226169_at	AW276572	NM_030962	81846	-0.59	9.95E-04
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LOC493856	226686_at	AI188518	NM_001008388	493856	-0.59	3.94E-03
LAMB2	216264_s_at	X79683	NM_002292	3913	-0.59	5.67E-03
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TLOC1	208942_s_at	BE866511	NM_003262	7095	-0.59	2.74E-03
VPS24	222436_s_at	AF219226	NM_00100575 3 NM_016079	51652	-0.59	9.34E-04
ECE2	230706_s_at	AI084921	NM_014693	9718	-0.59	5.56E-04
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FLNA	200859_x_at	NM_001456	NM_001456	2316	-0.59	6.02E-03
TIGD1	1553099_at	NM_145702	NM_145702	200765	-0.59	5.58E-03
HUMPPA	213230_at	AI422335	NM_014603	30850	-0.59	2.36E-04
NUDT13	214136_at	W80642	NM_015901	25961	-0.58	8.37E-03
NMT2	215069_at	AK025065	NM_004808	9397	-0.58	5.28E-03
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NPD014	209007_s_at	AF267856	NM_020317 NM_207035	57035	-0.58	6.29E-03
DGKD	208072_s_at	NM_003648	NM_003648 NM_152879	8527	-0.58	5.37E-04
FLJ10824 LOC387680	212929_s_at	W68158	NM_00100575 1 XM_290482	387680 55747	-0.58	9.32E-03
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PCNXL2	1554256_a_at	BC008300	NM_014801 NM_024938	80003	-0.58	9.20E-03
MGC54289	225228_at	AI474054	NM_178454	128338	-0.58	2.51E-04
FBXL14	213145_at	BF001666	NM_152441	144699	-0.58	2.17E-03
TFG	239385_at	AI150613	NM_00100756 5 NM_006070	10342	-0.58	1.31E-03
MACF1	215222_x_at	AK023406	NM_012090 NM_033044	23499	-0.58	6.16E-03
AW268719	236798_at	AW268719	---	---	-0.58	1.80E-04
BRUNOL6	227775_at	BE467313	NM_052840	60677	-0.58	7.34E-03

CLN3	209275_s_at	AF015593	NM_000086	1201	-0.58	5.20E-04
CKLFSF3	224733_at	AL574900	NM_144601 NM_181553 NM_181554 NM_181555	123920	-0.58	6.40E-04
DSCR1	208370_s_at	NM_004414	NM_004414 NM_203417 NM_203418	1827	-0.58	2.94E-03
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IDS	212221_x_at	AV703259	NM_000202 NM_006123	3423	-0.58	7.55E-06
ZNF295	225539_at	AP001745	NM_020727	49854	-0.58	4.67E-03
AW292996	236330_at	AW292996	---	---	-0.58	3.90E-03
LOC253982	214993_at	AF070642	NM_181718 NM_198907	253982	-0.58	6.71E-04
USP24	212388_at	AB028980	XM_371254	23358	-0.58	1.07E-03
AW237752	229699_at	AW237752	---	---	-0.58	7.54E-03
UNQ1912	226752_at	AI816071	NM_198507	345757	-0.58	1.56E-03
PHC1	225958_at	AI554106	NM_004426	1911	-0.58	2.64E-03
PAN3	225563_at	AI970788	NM_175854	255967	-0.58	1.42E-04

Table 9. Increased Gene Expression in Cell Lines H1 and BB10 vs. SiMa Cell Line in Undifferentiated State Using Microarray Analysis

Gene Symbol	Probe Set ID	Representative Public ID	RefSeq Transcript ID	Entrez Gene ID	Log2 Ratio	pvalue
DAZ1 DAZ3 DAZ2 DAZ4	208282_x_at	NM_020363	NM_00100537 5 NM_00100578 5 NM_00100578 6 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	6.15	6.22E-05
BF476109	1556300_s_at	BF476109	---	---	6.07	4.58E-08
DAZ1 DAZ3 DAZ2 DAZ4	207909_x_at	U21663	NM_00100537 5 NM_00100578 5 NM_00100578 6 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	6.03	3.64E-05
TIMP3	201147_s_at	BF347089	NM_000362	7078	5.78	9.00E-07
LUM	201744_s_at	NM_002345	NM_002345	4060	5.28	9.11E-07
SIM1	206876_at	AL121948	NM_005068	6492	5.13	3.40E-06
TIMP3	201149_s_at	U67195	NM_000362	7078	5.09	4.07E-05
CXCR4	209201_x_at	L01639	NM_00100854 0 NM_003467	7852	4.91	1.18E-03
GRP	206326_at	NM_002091	NM_002091	2922	4.77	1.84E-06
MGC24103	232568_at	AU145658	---	158295	4.71	1.34E-05
CXCR4	211919_s_at	AF348491	NM_00100854 0 NM_003467	7852	4.65	1.78E-03
KCTD12	212192_at	AI718937	NM_138444	115207	4.61	1.59E-05
DAZ1 DAZ3 DAZ2 DAZ4	207912_s_at	NM_004081	NM_00100537 5 NM_00100578 5 NM_00100578 6 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	4.39	5.11E-04

DAZ1 DAZ3 DAZ2 DAZ4	216922_x_at	AF271088	NM_00100537 5 NM_00100578 5 NM_00100578 6 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	4.30	4.72E-04
DAZ1 DAZ3 DAZ2 DAZ4	208281_x_at	NM_020364	NM_00100537 5 NM_00100578 5 NM_00100578 6 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	4.30	3.22E-04
PTPRE	221840_at	AA775177	NM_006504 NM_130435	5791	4.28	4.00E-07
AF086027	1559697_a_at	AF086027	---	---	4.28	1.11E-04
BNC2	233036_at	AU146418	NM_017637	54796	4.20	2.05E-04
H99792	225710_at	H99792	---	---	4.20	1.70E-06
)KFZp667G211	214030_at	BE501352	XM_376254	131544	4.19	1.81E-09
AL049260	216518_at	AL049260	---	---	4.16	8.81E-04
AU144918	233858_at	AU144918	---	---	4.15	1.87E-05
GPC6	233090_at	AU144140	NM_005708	10082	4.08	1.76E-03
TIMP3	201150_s_at	NM_000362	NM_000362	7078	4.04	7.75E-05
ALCAM	240655_at	BE502785	NM_001627	214	3.98	1.71E-04
SSBP2	1557813_at	BF724621	NM_012446	23635	3.98	1.18E-03
C1orf1	233306_at	AK021509	---	711	3.97	8.32E-06
ARHGAP6	206167_s_at	NM_001174	NM_001174 NM_006125 NM_013422 NM_013423 NM_013427	395	3.91	9.85E-05
TFPI2	209278_s_at	L27624	NM_006528	7980	3.87	1.53E-06
AL049337	215768_at	AL049337	---	---	3.87	3.23E-03
FLJ39639	243547_at	BE176531	XM_370932	283876	3.83	3.19E-04
KIAA1944	236377_at	AW166133	NM_133448	121256	3.80	2.79E-03
AF086027	1559696_at	AF086027	---	---	3.77	3.26E-05
VIP	206577_at	NM_003381	NM_003381 NM_194435	7432	3.72	1.05E-03
CCDC3	223316_at	AL136562	NM_031455	83643	3.72	8.39E-06
POLQ	207746_at	NM_014125	NM_006596 NM_199420	10721	3.54	1.20E-04
SLAC2-B	214734_at	AB014524	NM_015065	23086	3.53	2.59E-03
GPC6	232453_at	AF339813	NM_005708	10082	3.52	8.95E-04
MBNL1	241681_at	AW296451	NM_021038 NM_207292 NM_207293 NM_207294 NM_207295 NM_207296 NM_207297	4154	3.50	2.40E-03

EML4	233940_at	AK022801	NM_019063	27436	3.49	4.67E-03
AW974642	1558410_s_at	AW974642	XM_499534	442612	3.49	1.47E-03
RGS5	1555725_a_at	AF493929	NM_003617	8490	3.47	3.83E-03
TIMP3	201148_s_at	AW338933	NM_000362	7078	3.46	9.21E-03
AI939547	243004_at	AI939547	---	---	3.45	6.37E-03
SLITRK5	214930_at	AW449813	NM_015567	26050	3.42	1.80E-05
GFRA2	205722_s_at	NM_001495	NM_001495	2675	3.38	1.70E-03
RGS5	209070_s_at	AI183997	NM_003617	8490	3.32	3.17E-03
EML1	204797_s_at	NM_004434	NM_00100870	2009	3.29	2.09E-04
			7			
			NM_004434			
FBXL7	241457_at	AI821935	NM_012304	23194	3.27	1.14E-03
PLK2	201939_at	NM_006622	NM_006622	10769	3.27	1.65E-06
NEGR1	243357_at	AA115106	NM_173808	257194	3.26	2.19E-06
ELOVL7	227180_at	AW138767	XM_371740	79993	3.26	3.23E-03
SPAG6	210033_s_at	AF079363	NM_012443	9576	3.23	3.60E-05
			NM_172242			
FLJ39660	1553459_at	NM_173646	NM_173646	284992	3.22	5.48E-03
NEDD9	202150_s_at	U64317	NM_006403	4739	3.22	1.70E-04
			NM_182966			
PDZRN3	233442_at	AU147500	NM_015009	23024	3.21	2.82E-05
TRIM29	211002_s_at	AF230389	NM_012101	23650	3.18	3.79E-05
			NM_058193			
PCDH9	219737_s_at	AI524125	NM_020403	5101	3.13	7.67E-06
			NM_203487			
FAT	201579_at	NM_005245	NM_005245	2195	3.11	4.81E-03
NEDD9	202149_at	AL136139	NM_006403	4739	3.08	2.64E-04
			NM_182966			
ITGA6	201656_at	NM_000210	NM_000210	3655	3.07	8.91E-05
DAZ1	216351_x_at	AF248483	NM_00100537	1617	3.06	3.84E-04
DAZ3			5	57054		
DAZ2			NM_00100578	57055		
DAZ4			5	57135		
			NM_00100578			
			6			
			NM_004081			
			NM_020363			
			NM_020364			
			NM_020420			
FLJ37266	1566948_at	AL831894	NM_175892	283225	3.06	3.09E-03
EFNA5	1559360_at	AL833045	NM_001962	1946	3.03	1.65E-05
RPL10A	242188_at	AI743332	NM_007104	4736	3.03	2.49E-03
BE466926	217671_at	BE466926	---	---	3.02	9.00E-03
PTPRG	1569323_at	BU853579	NM_002841	5793	3.01	1.51E-05
CUGBP2	202158_s_at	NM_006561	NM_006561	10659	3.01	8.47E-05
TULP4	232372_at	AL157491	NM_00100746	56995	3.01	6.44E-03
			6			
			NM_020245			
BC043430	1558714_at	BC043430	---	---	2.99	6.39E-03
LOC340109	1557765_at	BC039509	XM_379322	340109	2.99	6.58E-05
)KFZp761O201	232313_at	AL122107	XM_044062	92293	2.98	3.82E-05
RGS5	218353_at	NM_025226	NM_003617	8490	2.96	3.43E-03
CHRNA7	210123_s_at	U62436	NM_000746	1139	2.96	5.22E-06
CHRFAM7A			NM_139320	89832		
			NM_148911			
LOC440265	1569476_at	BC033224	XM_378506	440265	2.90	2.51E-03
ARHGEF6	209539_at	D25304	NM_004840	9459	2.90	7.95E-05
AL049277	234839_at	AL049277	---	---	2.89	4.82E-03

KIAA0265	238000_at	BF195340	NM_014997	23008	2.85	2.90E-04
DACT1	219179_at	NM_016651	NM_016651	51339	2.85	4.31E-04
KCTD12	212188_at	AA551075	NM_138444	115207	2.84	1.79E-04
RGS5	209071_s_at	AF159570	NM_003617	8490	2.84	3.29E-03
AL832561	1561689_at	AL832561	---	---	2.84	3.60E-05
AA872187	230332_at	AA872187	---	---	2.82	1.50E-03
BG542611	1556277_a_at	BG542611	---	---	2.81	2.09E-03
PIAS2	244633_at	AA404996	NM_004671	9063	2.80	3.93E-05
			NM_173206			
AI630830	243150_at	AI630830	---	---	2.79	2.12E-03
UCHL1	1555834_at	AW974143	NM_004181	7345	2.77	3.11E-03
TRIO	235705_at	BF676361	NM_007118	7204	2.76	4.51E-04
AK022040	233445_at	AK022040	---	---	2.76	7.74E-04
CBLN2	242301_at	R60224	NM_182511	147381	2.76	3.83E-03
MID1	242671_at	BF055144	NM_000381	4281	2.74	4.62E-04
			NM_033290			
			NM_033291			
BC041991	1561690_at	BC041991	---	---	2.73	2.25E-03
EML4	232587_at	AI208611	NM_019063	27436	2.72	8.16E-03
TRIM29	202504_at	NM_012101	NM_012101	23650	2.70	1.08E-03
			NM_058193			
AW139261	243934_at	AW139261	---	---	2.69	5.92E-03
ROBO2	226709_at	BE858548	XM_031246	6092	2.69	1.07E-04
MEF2A	239571_at	AI123399	NM_005587	4205	2.68	1.53E-04
KIAA1128	240499_at	AA482221	NM_018999	54462	2.68	8.42E-03
KLF7	239809_at	BF197708	NM_003709	8609	2.65	5.01E-03
CALCA	217561_at	BF447272	NM_001741	796	2.62	2.08E-03
LOC51760	205613_at	NM_016524	NM_016524	51760	2.61	5.89E-03
EDD	232264_at	AK022204	NM_015902	51366	2.61	7.50E-04
LOC440161	243241_at	AW341473	XM_498572	440161	2.61	2.72E-04
SCHIP1	1566772_at	AL832567	NM_014575	29970	2.61	1.17E-03
TFPI2	209277_at	AL574096	NM_006528	7980	2.61	6.75E-04
EML4	1556732_at	BC039354	NM_019063	27436	2.59	2.34E-03
AA808231	242025_at	AA808231	---	---	2.59	1.52E-04
CUGBP2	202157_s_at	U69546	NM_006561	10659	2.59	6.58E-06
PAPD4	222282_at	AV761453	NM_173797	167153	2.57	4.37E-03
MGC14161	240502_at	AW015920	NM_032892	84978	2.55	2.58E-03
UBE3A	1560741_at	AL832250		7337	2.54	5.57E-03
			NM_000462			
			NM_130838			
			NM_130839			
LRRC5	234148_at	AK025238	NM_018103	55144	2.54	8.12E-04
PEX5L	1562473_at	BC037943	NM_016559	51555	2.54	7.14E-04
IMP-2	218847_at	NM_006548	NM_00100722	10644	2.54	9.50E-05
			5			
			NM_006548			
C2orf31	221245_s_at	NM_030804	---	81561	2.51	8.63E-05
AK024882	233228_at	AK024882	---	---	2.50	4.73E-04
TAS2R45	234042_at	AF264628	NM_176886	259291	2.50	4.78E-04
KIAA1102	241459_at	AI494113	NM_014988	22998	2.48	4.62E-05
BC041965	1560411_at	BC041965	---	---	2.47	7.60E-03
USP31	239348_at	AI285970	NM_020718	57478	2.47	5.27E-03
AU144294	215574_at	AU144294	---	---	2.47	3.25E-03
RNF152	233180_at	AU147152	NM_173557	220441	2.46	7.81E-03
LOC440738	221697_at	AF276659	NM_001004343	440738	2.45	2.37E-03
KATNAL1	243828_at	AA758906	NM_032116	84056	2.44	1.32E-03
MGC39558	1562391_at	AK091497	NM_152490	148789	2.44	7.21E-03
GNG11	204115_at	NM_004126	NM_004126	2791	2.43	1.79E-04

AI076172	236355_s_at	AI076172	XM_495841	439993	2.42	3.12E-03
ITPR1	240052_at	AA648993	NM_002222	3708	2.42	1.52E-04
IARS	239794_at	AI356405	NM_002161 NM_013417	3376	2.42	2.89E-04
PLXNA4	232317_at	AB046770	XM_039393 XM_379927	57671	2.41	8.26E-05
AURKB	239219_at	N55457	NM_004217	9212	2.41	5.13E-04
FBXL7	233276_at	AU146390	NM_012304	23194	2.41	3.40E-04
CDH2	237305_at	AW450381	NM_001792	1000	2.40	2.95E-03
SPRY4	1566968_at	AK024556	NM_030964	81848	2.40	1.67E-05
SYT4	223529_at	AB037763	NM_020783	6860	2.40	4.26E-04
PPP4R2	1560926_at	AF085924	NM_174907	151987	2.38	6.45E-03
BE674460	237849_at	BE674460	---	---	2.38	7.15E-04
AK024956	232726_at	AK024956	---	---	2.37	2.24E-03
PITPNB	242074_at	AA833902	NM_012399	23760	2.37	2.45E-04
KIAA0485	214295_at	AW129056	---	57235	2.36	6.51E-04
BF000203	236385_at	BF000203	---	---	2.33	1.55E-03
BNC2	220272_at	NM_017637	NM_017637	54796	2.33	3.96E-04
SDFR1	242865_at	AI332638	NM_012428 NM_017455	27020	2.31	1.45E-04
DTNA	1557803_at	AF086074	NM_001390 NM_001391 NM_001392 NM_032975 NM_032978 NM_032979 NM_032980 NM_032981	1837	2.31	3.61E-04
NRCAM	233401_at	BF723605	NM_005010	4897	2.31	1.07E-03
FOXO3A	1569477_at	BC025999	NM_001455 NM_201559	2309	2.31	5.92E-03
MSN	200600_at	NM_002444	NM_002444	4478	2.30	1.14E-05
AL832142	1561195_at	AL832142	---	---	2.30	2.10E-03
EDG3	228176_at	AA534817	NM_005226	1903	2.29	2.67E-03
ASCL1	209985_s_at	BE797438	NM_004316	429	2.28	9.42E-05
LOC146174	233832_at	AK021824	NM_173501	146174	2.27	3.37E-04
PLXNA4	228104_at	AL117427	XM_039393 XM_379927	57671	2.26	7.59E-04
KIDINS220	1557246_at	AA992480	NM_020738	57498	2.26	5.87E-03
GFRA2	205721_at	U97145	NM_001495	2675	2.25	3.08E-03
LOC440092	1570571_at	BC035168	XM_498540	440092	2.25	3.18E-05
ROBO2	226766_at	AB046788	XM_031246	6092	2.25	3.58E-05
GAB2	1566959_at	AL049273	NM_012296 NM_080491	9846	2.24	9.27E-03
ARHGAP6	1563386_at	AL079282	NM_001174 NM_006125 NM_013422 NM_013423 NM_013427	395	2.24	2.24E-03
PCNX	215175_at	AB023212	NM_014982	22990	2.24	3.95E-03
C10orf18	216211_at	AL049233	XM_374765	54906	2.23	1.64E-03
AI678013	240165_at	AI678013	---	---	2.22	1.17E-03
AI653240	240247_at	AI653240	XM_496059	440261	2.21	1.90E-04
GFM1	232295_at	AK000780	NM_024996	85476	2.20	4.88E-03
AF116659	210717_at	AF116659	---	---	2.20	2.72E-03
NM_018611	220666_at	NM_018611	---	---	2.20	3.83E-03
PFKFB3	202464_s_at	NM_004566	NM_004566	5209	2.20	1.42E-03
AI671885	230494_at	AI671885	XM_379123	400999	2.20	4.83E-04

TPBG	203476_at	NM_006670	NM_006670	7162	2.20	1.21E-07
ITGA6	215177_s_at	AV733308	NM_000210	3655	2.19	2.48E-03
AW008791	240315_at	AW008791	XM_294019	345930	2.19	7.20E-03
C10orf18	244165_at	AI809511	XM_374765	54906	2.18	1.55E-03
FLJ21148	231005_at	T91195	NM_024860	79918	2.18	3.18E-04
DEFB32	243311_at	BE044548	NM_207469	400830	2.18	1.71E-03
THRAP2	232307_at	AK021554	NM_015335	23389	2.18	7.79E-04
BF057073	231310_at	BF057073	---	---	2.16	3.16E-05
CFDP1	210701_at	D85939	NM_006324	10428	2.16	1.15E-03
SYNE2	242774_at	AI684761	NM_015180	23224	2.16	3.57E-03
			NM_182910			
			NM_182912			
			NM_182913			
			NM_182914			
RNF182	230720_at	AI884906	NM_152737	221687	2.15	1.49E-04
PAPD4	242144_at	AW104325	NM_173797	167153	2.15	8.28E-03
DKFZp761D221	241872_at	AI149963	NM_032291	84251	2.15	7.56E-03
NFIB	230791_at	AU146924	NM_005596	4781	2.14	1.39E-03
PTGFRN	224937_at	BF311866	NM_020440	5738	2.14	1.95E-03
FOXO3A	242320_at	AI435586	NM_001455	2309	2.13	1.69E-03
			NM_201559			
SSBP2	1557814_a_at	BF724621	NM_012446	23635	2.13	6.51E-03
KLF12	243089_at	AA551114	NM_007249	11278	2.13	1.78E-03
			NM_016285			
EXT1	232174_at	AA480392	NM_000127	2131	2.13	2.01E-04
MGC4504	219270_at	NM_024111	NM_024111	79094	2.13	2.30E-03
TTL	244078_at	AI438957	NM_153712	150465	2.12	1.97E-04
ODZ3	233291_at	AU145618	XM_371717	55714	2.11	2.81E-04
MSI2	239232_at	AA521410	NM_138962	124540	2.11	7.13E-04
			NM_170721			
ZNF403	233937_at	AK024883	NM_024835	79893	2.11	2.80E-04
FRZB	203698_s_at	NM_001463	NM_001463	2487	2.10	6.12E-03
ATP1B4	243737_at	AI082610	NM_012069	23439	2.10	3.38E-03
AI077566	243994_at	AI077566	---	---	2.09	3.50E-03
GATA4	243692_at	AW181962	NM_002052	2626	2.09	2.75E-03
ID2	213931_at	AI819238	NM_002166	3398	2.09	3.49E-04
N21631	231329_at	N21631	---	---	2.08	3.60E-03
GNAI1	209576_at	AL049933	NM_002069	2770	2.08	4.56E-05
ZNF292	236435_at	BE219036	XM_048070	23036	2.08	7.00E-03
NEDD9	233223_at	AK000850	NM_006403	4739	2.07	4.93E-04
			NM_182966			
UBE2E3	232528_at	AI338705	NM_006357	10477	2.06	7.31E-03
			NM_182678			
PAN3	239393_at	AW510927	NM_175854	255967	2.05	4.66E-03
SMARCC1	239238_at	AI208857	NM_003074	6599	2.04	7.80E-04
MTMR2	231057_at	AU144266	NM_016156	8898	2.04	8.90E-05
			NM_201278			
			NM_201281			
MGC33926	229302_at	AA058832	NM_152390	130733	2.04	4.33E-05
DREV1	230395_at	AI536637	NM_016025	51108	2.04	3.23E-03
AF238870	215811_at	AF238870	---	---	2.04	1.97E-03
DMXL2	215761_at	AK000156	NM_015263	23312	2.04	2.78E-04
MAOA	204388_s_at	NM_000240	NM_000240	4128	2.04	7.48E-04

OSBPL3	209626_s_at	AI202969	NM_015550 NM_145320 NM_145321 NM_145322 NM_145323 NM_145324	26031	2.04	1.76E-03
AL161982	1563494_at	AL161982	---	---	2.03	1.29E-03
SALL4	229661_at	NM_020436	NM_020436	57167	2.03	2.39E-03
DJ971N18.2	240094_at	AL042660	NM_021156	56255	2.03	1.10E-03
GOLPH4	233877_at	AK000777	NM_014498	27333	2.02	1.37E-03
MSX2	205555_s_at	D31771	NM_002449	4488	2.02	2.73E-03
SR140	236696_at	BE464843	XM_031553	23350	2.02	1.40E-03
PSCD3	243752_s_at	AI870144	NM_004227	9265	2.02	5.25E-05
JMJD2C	239285_at	AI341227	NM_015061	23081	2.02	1.02E-03
THRAP2	238883_at	AW975051	NM_015335	23389	2.01	3.31E-03
BF508839	239907_at	BF508839	---	---	2.01	1.50E-03
VRK1	241737_x_at	T89693	NM_003384	7443	2.01	4.67E-05
AA417878	243463_s_at	AA417878	---	---	2.01	4.39E-03
RAP1GDS1	237856_at	AI052055	NM_021159	5910	1.99	6.70E-03
BF724206	244457_at	BF724206	---	---	1.99	5.28E-03
MAOA	212741_at	AA923354	NM_000240	4128	1.98	7.12E-04
TPTE	233879_at	AL137389	NM_013315 NM_199259 NM_199260 NM_199261	7179	1.97	6.72E-03
SPAG6	210032_s_at	AI651156	NM_012443 NM_172242	9576	1.97	2.71E-04
VDP	222316_at	AW973253	NM_003715	8615	1.97	8.98E-03
FLJ35740	244297_at	AI806762	NM_147195	253650	1.97	7.86E-03
SPPL3	1554565_x_at	BC011943	NM_139015	121665	1.96	5.95E-04
BC028185	1569609_at	BC028185	XM_496328	440546	1.96	4.09E-05
MYH10	237491_at	AA700633	NM_005964	4628	1.96	3.02E-03
TMP21	238886_at	BF056141	NM_006827	10972	1.96	1.48E-03
TFCP2	242859_at	BE156563	NM_005653	7024	1.95	8.85E-03
BE856929	239349_at	BE856929	---	---	1.95	4.12E-03
LOC151878	222372_at	AW971248	---	151878	1.95	1.02E-03
SEC15L2	1569202_x_at	BF847120	XM_039570	23233	1.94	2.05E-05
SCFD1	243525_at	AA808051	NM_016106 NM_182835	23256	1.94	1.42E-03
RTN4	243031_at	N90377	NM_007008 NM_020532 NM_153828 NM_207520 NM_207521	57142	1.94	3.06E-03
TRA1	239451_at	AI684643	NM_003299	7184	1.93	2.01E-03
CSE1L	210765_at	AF053640	NM_001316 NM_177436	1434	1.93	2.75E-04
ATXN2	238589_s_at	AW601184	NM_002973	6311	1.93	1.04E-03
GNAI1	227692_at	AU153866	NM_002069	2770	1.93	7.06E-05
TCF12	235925_at	AW057520	NM_003205 NM_207036 NM_207037 NM_207038 NM_207040	6938	1.93	2.43E-03
LASS5	238299_at	AW005866	NM_147190	91012	1.93	1.53E-04
AA766886	239171_at	AA766886	---	---	1.92	7.67E-03
KIAA1102	1569208_a_at	BC020895	NM_014988	22998	1.92	1.80E-03
SARS	237689_at	BF111108	NM_006513	6301	1.92	5.62E-03

VTI1A	233323_at	AK024973	NM_145206	143187	1.91	6.85E-04
B4GALT5	1559391_s_at	AI084451	NM_004776	9334	1.91	9.95E-03
AA804267	243185_at	AA804267	---	---	1.91	1.67E-03
MGC34032	1569112_at	AW020413	NM_152697	204962	1.90	1.85E-03
AL050204	213929_at	AL050204	---	---	1.90	5.32E-03
FLJ31951	236322_at	AA830854	NM_144726	153830	1.89	9.55E-03
ASCL1	209987_s_at	BC002341	NM_004316	429	1.89	1.70E-06
LOC441157	1558795_at	AL833240	XM_499037	441157	1.89	7.22E-05
NOL7	242143_at	BE674964	NM_016167	51406	1.89	1.62E-03
XPO1	235927_at	BE350122	NM_003400	7514	1.88	1.14E-04
FOXP1	240666_at	AI732568	NM_032682	27086	1.88	6.71E-03
CD9	201005_at	NM_001769	NM_001769	928	1.87	3.75E-03
TNKS	238108_at	AI401627	NM_003747	8658	1.87	8.80E-03
NID	202007_at	BF940043	NM_002508	4811	1.87	3.81E-03
MARS	213672_at	AA621558	NM_004990	4141	1.86	2.54E-04
C20orf23	232083_at	AB046810	NM_024704	55614	1.86	1.17E-04
KIAA1713	233536_at	AI202664	XM_290811	80816	1.86	3.15E-05
U80755	243820_at	U80755	---	---	1.85	8.97E-05
AA700817	241997_at	AA700817	---	---	1.85	4.70E-03
UBE2E1	215577_at	AU146791	NM_003341 NM_182666	7324	1.85	2.95E-03
AP2B1	233800_at	AA805082	NM_001282	163	1.84	4.55E-05
AGTPBP1	242008_at	BE350312	NM_015239	23287	1.83	9.60E-03
RPL4	1562440_at	BC026249	NM_000968	6124	1.83	1.24E-03
LOC441157	1558796_a_at	AL833240	XM_499037	441157	1.83	3.63E-06
EIF3S8	236700_at	AI377875	NM_003752	8663	1.82	1.24E-07
ZDHHC2	243528_at	AW014108	NM_016353	51201	1.82	8.62E-05
WSB1	227501_at	AI377135	NM_015626 NM_134264 NM_134265	26118	1.82	2.98E-03
PTPN12	244356_at	AL079909	NM_002835	5782	1.81	5.18E-03
RB1CC1	237626_at	AI801666	NM_014781	9821	1.81	2.19E-03
PCTK2	243993_at	AA436887	NM_002595	5128	1.80	9.68E-03
PIP5K1A	235646_at	BF515595	NM_003557	8394	1.80	5.13E-03
AU146318	232355_at	AU146318	---	---	1.80	7.55E-03
N59650	244265_at	N59650	---	---	1.80	8.30E-03
YARS	238760_at	AW452122	NM_003680	8565	1.80	4.51E-03
RNF159	241956_at	AI521883	NM_032373	84333	1.80	5.20E-05
AI820961	240331_at	AI820961	---	---	1.79	7.22E-03
FLJ30058	238047_at	AA405456	NM_144967	158763	1.79	5.67E-03
GULP1	223837_at	BC001103	NM_016315	51454	1.79	6.85E-04
CGI-26	230892_at	AI912194	NM_015954	51071	1.79	1.73E-03
LRCH3	1559490_at	AL832278	NM_032773	84859	1.79	6.87E-03
HIRA	240451_at	AA004844	NM_003325	7290	1.79	2.21E-05
SRPK2	239811_at	BF954306	NM_182691 NM_182692	6733	1.78	5.28E-03
C9orf33	217130_at	AF072164	---	90477	1.78	1.23E-04
AI916641	242471_at	AI916641	---	---	1.78	4.35E-04
SCC-112	241798_at	AI339930	NM_015200	23244	1.78	1.62E-03
SLC33A1	1559232_a_at	BC029450	NM_004733	9197	1.78	1.37E-04
ATRX	236778_at	AA826176	NM_000489 NM_138270 NM_138271	546	1.78	2.50E-03
ZFYVE16	1554638_at	BC032227	NM_014733	9765	1.78	1.30E-03
FLJ13089	236816_at	BF110370	NM_024953	80018	1.78	9.12E-03
SLC7A2	225516_at	AA876372	NM_00100853 9 NM_003046	6542	1.78	2.48E-06

DBH	206450_at	NM_000787	NM_000787	1621	1.77	5.25E-04
H15073	236685_at	H15073	---	---	1.77	1.63E-04
R45137	238304_at	R45137	---	---	1.77	4.97E-03
FBXW8	237317_at	AW136338	NM_012174	26259	1.76	4.78E-03
			NM_153348			
MLL3	244010_at	AI057455	NM_021230	58508	1.76	5.04E-05
			NM_170606			
SLC37A3	1569666_s_at	BC035773	NM_032295	84255	1.76	1.21E-05
			NM_207113			
CNOT2	222313_at	AW972359	NM_014515	4848	1.76	1.85E-04
NS5ATP13TP2	1558613_at	BC040647	NM_178507	220323	1.75	7.91E-04
MBNL1	1556657_at	AA744622	NM_021038	4154	1.74	1.02E-04
			NM_207292			
			NM_207293			
			NM_207294			
			NM_207295			
			NM_207296			
			NM_207297			
AU152272	1556650_at	AU152272	---	---	1.74	2.69E-03
AI372879	237134_at	AI372879	---	---	1.73	1.97E-03
N23846	1557804_at	N23846	---	---	1.72	6.11E-03
C10orf47	229801_at	AI640157	NM_153256	254427	1.72	6.95E-03
W72466	231467_at	W72466	---	---	1.72	2.85E-05
MAPRE2	1564733_at	BC013931	NM_014268	10982	1.72	1.15E-03
R38403	240425_x_at	R38403	---	---	1.72	2.69E-03
AF090944	233995_at	AF090944	---	---	1.72	3.50E-04
RANBP17	234137_s_at	AK022022	NM_022897	64901	1.71	3.68E-03
OAZIN	240231_at	AI742383	NM_015878	51582	1.71	1.34E-07
			NM_148174			
L3MBTL	242637_at	C14069	NM_015478	26013	1.71	6.68E-03
			NM_032107			
AB062477	1555303_at	AB062477	---	---	1.71	6.75E-03
AA682539	235575_at	AA682539	---	---	1.70	8.28E-03
AL353942	216147_at	AL353942	NM_018243	55752	1.70	3.06E-04
VPS26	243316_x_at	AA004710	NM_004896	9559	1.70	1.14E-04
LAF4	243967_at	AI424899	NM_002285	3899	1.70	8.24E-03
SEZ6L	240709_at	AW204757	NM_021115	23544	1.70	9.27E-04
AVO3	237330_at	AA603494	XM_380173	253260	1.70	6.44E-04
TPARL	1560622_at	AK000203	NM_018475	55858	1.69	1.26E-03
PDLIM5	213684_s_at	BF671400	NM_001011513	10611	1.69	6.08E-03
			NM_001011514			
			NM_001011515			
			NM_001011516			
			NM_006457			
SOS2	233369_at	AU146027	NM_006939	6655	1.69	9.57E-03
IREB2	1563130_a_at	AL109710	NM_004136	3658	1.68	7.14E-06
MPZL1	210210_at	AF181660	NM_003953	9019	1.68	5.09E-05
			NM_024569			
AW206536	243470_at	AW206536	---	---	1.68	4.56E-03
TOP1	239404_at	BF840360	NM_003286	7150	1.67	5.17E-04
AA936428	244674_at	AA936428	---	---	1.67	1.91E-03
PUM2	235138_at	AA565051	NM_015317	23369	1.67	8.24E-04
MINA	213189_at	BE966695	NM_032778	84864	1.67	9.49E-05
			NM_153182			

LOC152185	239091_at	AA497043	NM_144718	152185	1.67	4.23E-04
SEC31L1	1556416_s_at	AF086242	NM_014933 NM_016211	22872	1.67	6.36E-04
MAOA	204389_at	NM_000240	NM_000240	4128	1.66	2.78E-04
ALCAM	1569362_at	BC041127	NM_001627	214	1.66	8.23E-03
KRT18	201596_x_at	NM_000224	NM_000224 NM_199187	3875	1.66	1.32E-03
N73550	244112_x_at	N73550	---	---	1.66	5.23E-03
MKLN1	1560145_at	BQ942131	NM_013255	4289	1.65	4.78E-03
ARHGAP5	242110_at	AV735587	NM_001173	394	1.65	8.85E-03
GPI	232002_at	AW843302	NM_000175	2821	1.65	6.38E-04
STAU	1569527_at	BC017275	NM_004602 NM_017452 NM_017453 NM_017454	6780	1.65	2.32E-04
BF512254	242695_at	BF512254	---	---	1.65	2.52E-03
EIF4ENIF1	242983_at	AI806626	NM_019843	56478	1.65	4.13E-03
AU144781	233300_at	AU144781	---	---	1.65	2.25E-03
DKFZp547A023	214731_at	AB037854	NM_018704	55917	1.65	8.41E-03
LBH	221011_s_at	NM_030915	NM_030915	81606	1.64	3.86E-05
KIAA0217	241965_at	BF589232	NM_015155	23185	1.64	3.53E-04
MED31	243319_at	AI274981	NM_016060	51003	1.64	2.26E-04
DLEU2	1556821_x_at	H48516	NM_006021	8847	1.64	8.43E-03
AA195014	243769_at	AA195014	---	---	1.63	9.11E-03
N50083	229110_at	N50083	---	---	1.63	1.73E-03
N46436	1556568_a_at	N46436	---	---	1.63	4.33E-04
RAPGEF5	204680_s_at	AI263837	XM_499059	9771	1.62	1.84E-03
AW003140	227576_at	AW003140	---	---	1.62	5.17E-03
AL119001	233440_at	AL119001	---	---	1.62	5.61E-03
CPSF6	238651_at	BF512491	NM_007007	11052	1.62	4.97E-03
RBM5	230742_at	AA742596	NM_005778	10181	1.62	6.51E-03
CADPS	233950_at	AK000873	NM_003716 NM_183393 NM_183394	8618	1.62	3.44E-04
SPON1	209437_s_at	AB051390	NM_006108	10418	1.62	1.60E-03
SCFD1	241775_at	AW298119	NM_016106 NM_182835	23256	1.61	2.89E-03
CDC14A	210742_at	AF064103	NM_003672 NM_033312 NM_033313	8556	1.61	4.92E-03
FZD5	206136_at	NM_003468	NM_003468	7855	1.61	1.56E-03
ZNF451	215012_at	AU144775	NM_015555	26036	1.61	9.28E-03
PCGF5	226326_at	AI798098	NM_032373	84333	1.61	2.79E-05
PTGFRN	224950_at	BF476250	NM_020440	5738	1.61	8.83E-03
TSC	218872_at	NM_017899	NM_017899	54997	1.61	5.32E-04
GRM8	216255_s_at	AC000099	NM_000845	2918	1.60	3.03E-05
MGC47869	243056_at	AI301111	NM_175874	144608	1.60	1.26E-03
DNAPTP6	244597_at	AA701247	NM_015535	26010	1.60	2.38E-03
BC028606	1555485_s_at	BC028606	---	---	1.60	5.40E-03
ARID1B	1558822_at	AF147412	NM_017519 NM_020732 NM_175863	57492	1.60	2.93E-03
BF841212	232096_x_at	BF841212	---	---	1.60	1.12E-03
AU144005	232797_at	AU144005	---	---	1.60	2.27E-03
LOC158160	244075_at	BF224218	NM_182829	158160	1.60	3.37E-03
MYO6	210480_s_at	U90236	NM_004999	4646	1.59	6.83E-04
MBNL2	236699_at	AL566294	NM_144778 NM_207304	10150	1.59	3.46E-03

BI868311	1565651_at	BI868311	---	---	1.59	4.00E-03
LETMD1	242424_at	AA345855	NM_015416	25875	1.59	5.03E-04
N75937	240072_at	N75937	---	---	1.59	6.26E-03
H04482	243287_s_at	H04482	---	---	1.59	3.04E-03
NFIB	233304_at	AU145782	NM_005596	4781	1.59	6.80E-03
PPP3R1	1565811_at	BC033945	NM_000945	5534	1.59	6.08E-05
DLEU2	216870_x_at	AF264787	NM_006021	8847	1.59	2.46E-04
COBRA1	1556434_at	BQ777552	NM_015456	25920	1.59	2.75E-04
C6orf60	1558523_at	AJ420563	NM_024581	79632	1.58	6.89E-03
MAK3	231199_at	AA701676	NM_025146	80218	1.58	3.34E-03
KIAA0485	242824_at	AW191647	---	57235	1.57	3.46E-05
CTBP2	233315_at	AK024947	NM_001329 NM_022802	1488	1.57	2.17E-05
AA935659	240321_at	AA935659	---	---	1.57	9.78E-03
TAF15	227884_at	AW296067	NM_003487 NM_139215	8148	1.56	6.85E-03
KIF5C	1557089_at	CA449408	XM_377774	3800	1.56	2.83E-04
KIAA0143	232356_at	AW003230	NM_015137	23167	1.56	7.00E-03
CPVL	208146_s_at	NM_031311	NM_019029 NM_031311	54504	1.56	4.48E-03
DMXL1	241472_at	N74444	NM_005509	1657	1.55	8.84E-04
SNX5	229981_at	AA131508	NM_014426 NM_152227	27131	1.55	1.33E-05
ALCAM	201951_at	BF242905	NM_001627	214	1.55	2.09E-06
ANKRD11	228866_at	BF514864	NM_013275	29123	1.55	2.95E-04
ID2	201565_s_at	NM_002166	NM_002166	3398	1.55	9.49E-04
PFAAP5	214753_at	AW084068	NM_014887	10443	1.55	8.30E-04
KIAA0318	238817_at	BF063412	NM_015347	23504	1.55	8.89E-05
SR140	236431_at	AI674977	XM_031553	23350	1.54	8.08E-03
API5	229692_at	AW135003	NM_006595	8539	1.54	1.07E-03
AA516469	236375_at	AA516469	---	---	1.54	6.79E-03
NUPL1	241425_at	AA769986	NM_001008564 NM_001008565 NM_014089	9818	1.54	4.72E-05
AI791138	242968_at	AI791138	---	---	1.54	8.93E-03
JAK1	234193_at	AK025218	NM_002227	3716	1.54	3.33E-04
AW052186	239942_at	AW052186	---	---	1.53	6.32E-03
KIF23	244427_at	AW192521	NM_004856 NM_138555	9493	1.53	7.98E-03
AI800470	242836_at	AI800470	---	---	1.53	5.90E-04
BF509125	232198_at	BF509125	---	---	1.52	1.16E-04
SPON1	209436_at	AB018305	NM_006108	10418	1.52	2.06E-04
DLEU2	1556820_a_at	H48516	NM_006021	8847	1.52	1.57E-03
AK025105	232476_at	AK025105	---	---	1.52	2.32E-03
AA228366	236251_at	AA228366	---	---	1.52	4.86E-03
H37807	241060_x_at	H37807	---	---	1.52	4.23E-03
BNC2	238478_at	H97386	NM_017637	54796	1.52	2.14E-05
CADPS	1568604_a_at	AI912173	NM_003716 NM_183393 NM_183394	8618	1.51	7.84E-07
SCARB2	215754_at	AU148040	NM_005506	950	1.51	1.21E-03

MBNL1	238558_at	AI445833	NM_021038 NM_207292 NM_207293 NM_207294 NM_207295 NM_207296 NM_207297	4154	1.51	1.09E-03
BC003528	210920_x_at	BC003528	---	---	1.51	2.78E-03
GPR18	233554_at	AF339764	NM_005292	2841	1.51	8.61E-03
UBE3B	213822_s_at	BE856776	NM_130466 NM_183414 NM_183415	89910	1.51	8.72E-03
WWOX	1556595_at	BQ025203	NM_016373 NM_018560 NM_130788 NM_130790 NM_130791 NM_130792 NM_130844	51741	1.51	1.78E-03
AI740589	243515_at	AI740589	---	---	1.51	4.92E-04
N26620	227503_at	N26620	---	---	1.51	2.93E-03
C18965	242853_at	C18965	XM_379243	401106	1.51	5.39E-03
CPNE4	239990_at	AI821426	NM_130808	131034	1.50	1.95E-03
FBXL11	215191_at	AW836210	NM_012308	22992	1.50	3.06E-03
CHD1L	238070_at	AA573217	NM_004284	9557	1.50	8.83E-03
JARID2	232835_at	AA533080	NM_004973	3720	1.50	3.50E-04
MIB1	240446_at	AI798164	NM_020774	57534	1.50	4.01E-04
Z39232	1560924_at	Z39232	---	---	1.49	6.88E-04
PLEKHE1	212719_at	AB011178	NM_194449	23239	1.49	2.28E-04
UBE1C	1556339_a_at	BM353142	NM_003968 NM_198195 NM_198197	9039	1.49	7.82E-04
NM_030892	220969_s_at	NM_030892	---	---	1.49	4.83E-04
TBX3	219682_s_at	NM_016569	NM_005996 NM_016569	6926	1.48	2.65E-03
PHGDHL1	241932_at	AI073803	NM_177967	337867	1.48	5.92E-03
LOC158301	239193_at	BF060981	---	158301	1.48	1.36E-03
FLJ10579	230843_at	AA482037	NM_018145	55177	1.48	6.04E-04
RPL10A	234224_at	AL137541	NM_007104	4736	1.48	5.43E-03
C10orf119	242167_at	AA703310	NM_024834	79892	1.48	9.08E-06
CORO6	1552301_a_at	NM_032854	NM_032854	84940	1.48	5.48E-03
MGC15912	239635_at	BF510708	NM_032886	84972	1.47	4.46E-03
DTNB	233727_at	AL157472	NM_021907 NM_033147 NM_033148 NM_183360 NM_183361	1838	1.47	4.45E-03
FLJ22955	232447_at	AU147405	NM_024819	79877	1.46	3.56E-03
LOC151194	236607_at	AI921882	NM_145280	151194	1.46	8.35E-04
BC035170	1561079_at	BC035170	---	---	1.46	5.42E-03
XPO7	240168_at	AA679589	NM_015024	23039	1.46	3.12E-03
EZH2	215006_at	AK023816	NM_004456 NM_152998	2146	1.46	2.64E-03
LTB4DH	228825_at	BE566894	NM_012212	22949	1.46	1.02E-03
BBX	1557240_a_at	BU689085	NM_020235	56987	1.46	5.33E-03
ARIH2	1559121_s_at	AI767566	NM_006321	10425	1.46	8.11E-04
ANKRD28	229307_at	N32051	NM_015199	23243	1.45	2.51E-03

LRRFIP2	232704_s_at	AK025207	NM_006309 NM_017724	9209	1.45	2.05E-03
PHLDA1	218000_s_at	NM_007350	NM_007350	22822	1.45	5.61E-03
AF070602	216214_at	AF070602	---	---	1.44	3.75E-03
C6orf133	215558_at	AK001118	NM_015255	23304	1.44	1.76E-04
AW083060	243274_x_at	AW083060	---	---	1.44	6.61E-03
ATOH8	228890_at	BF434995	NM_032827	84913	1.43	9.99E-03
CHC1L	230292_at	AA868809	NM_001268	1102	1.43	2.15E-03
SMG1	244766_at	BG180003	NM_014006	23049	1.43	1.93E-03
KIAA0220 LOC440345			NM_015092 XM_496125	283846 440345		
T98846	239654_at	T98846	---	---	1.43	7.51E-05
ZA20D3	222186_at	AL109684	NM_019006	54469	1.43	2.35E-03
SMC5L1	1562948_at	BC035661	NM_015110	23137	1.43	7.05E-03
SMC4L1	237246_at	AI797163	NM_001002799 NM_001002800 NM_005496	10051	1.43	7.94E-03
SLD5	1554356_at	BC027454	NM_032336	84296	1.43	1.24E-03
AW451426	244480_at	AW451426	---	---	1.42	1.53E-04
ZSWIM6	1560199_x_at	AU120130	XM_035299	57688	1.42	2.96E-04
H06497	243211_at	H06497	---	---	1.42	1.88E-03
ENC1	201340_s_at	AF010314	NM_003633	8507	1.42	8.83E-03
AW963544	238580_at	AW963544	---	---	1.42	1.14E-04
IGSF4	232793_at	AL359567	NM_014333	23705	1.42	6.90E-04
AK022100	233406_at	AK022100	---	---	1.41	8.65E-03
CENTB2	240759_at	AW593931	NM_012287	23527	1.41	8.75E-04
PTPRK	203038_at	NM_002844	NM_002844	5796	1.41	2.80E-04
LOC286109	243304_at	AI733824	---	286109	1.41	8.07E-03
ASCL1	213768_s_at	AW950513	NM_004316	429	1.40	2.65E-05
AW293174	244290_at	AW293174	XM_499534	442612	1.40	2.89E-05
MGC15937	227794_at	BF432254	NM_080661	92292	1.40	2.78E-03
PTK2	1559529_at	BC043202	NM_005607 NM_153831	5747	1.40	3.63E-03
MAN2A1	205105_at	NM_002372	NM_002372	4124	1.39	3.32E-04
CBLB	233614_at	AU145361	NM_170662	868	1.39	9.21E-04
KIAA0998	215898_at	AK021879	NM_015072	23093	1.39	5.01E-03
PMAIP1	204285_s_at	AI857639	NM_021127	5366	1.39	3.88E-06
FNBP1L	242310_at	AA665058	NM_017737	54874	1.38	4.27E-03
AI755057	233055_at	AI755057	---	---	1.38	1.05E-03
RAB3-GAP150	240234_at	AI216539	NM_012414	25782	1.38	7.73E-03
ACSL4	1557418_at	W95007	NM_004458 NM_022977	2182	1.38	5.61E-04
FAM13A1	232628_at	AI740629	NM_014883	10144	1.37	4.61E-03
FLJ23451	1569601_at	BF106979	NM_024766	79823	1.37	4.24E-05
ZNF217	203739_at	NM_006526	NM_006526	7764	1.37	5.73E-03
BF197705	230401_at	BF197705	---	---	1.37	9.92E-04
HEG	212822_at	AA121502	XM_087386	57493	1.37	2.43E-04
MGC15523	1563226_at	BC020925	NM_138570	124565	1.37	7.40E-03
AA156721	201952_at	AA156721	---	---	1.37	1.55E-04
AL110237	232959_at	AL110237	---	---	1.37	7.09E-03
PSME4	237180_at	T97717	NM_014614	23198	1.37	1.78E-03
IGSF4	244345_at	AI627453	NM_014333	23705	1.36	7.17E-03
MRPS25	244019_at	T89845	NM_022497	64432	1.36	2.01E-03
BF801735	238712_at	BF801735	---	---	1.36	2.63E-03
SPRY4	221489_s_at	W48843	NM_030964	81848	1.35	7.35E-04
SCN7A	239984_at	AI333640	NM_002976	6332	1.35	8.33E-04

HIVEP2	243254_at	T08739	NM_006734	3097	1.35	5.09E-03
PTPN11	241930_x_at	AA223204	NM_002834	5781	1.35	9.28E-04
AW235215	238913_at	AW235215	---	---	1.35	9.92E-03
C10orf6	1553909_x_at	NM_144592	NM_018121	55719	1.35	2.80E-04
ZFHX4	219779_at	NM_024721	NM_024721	79776	1.35	1.82E-05
MEST	202016_at	NM_002402	NM_002402 NM_177524 NM_177525	4232	1.34	2.65E-04
TRIO	231403_at	N21108	NM_007118	7204	1.34	9.69E-03
UBE3C	242673_at	AA931284	NM_014671	9690	1.34	3.34E-04
PPP2R2A	236492_at	AI934447	NM_002717	5520	1.34	4.98E-03
HIAT1	230868_at	BF433103	NM_033055	64645	1.34	7.24E-04
LOC440971	1556744_a_at	AI732587	XM_496651	440971	1.33	3.92E-03
CUGBP2	202156_s_at	N36839	NM_006561	10659	1.33	2.42E-03
CNTN4	229084_at	R42166	NM_175607 NM_175612 NM_175613	152330	1.33	8.25E-03
FLJ11259	218627_at	NM_018370	NM_018370	55332	1.32	4.63E-03
CEPT1	1561884_at	AL833102	NM_00100779 4 NM_006090	10390	1.32	1.40E-04
AL049988	216614_at	AL049988	---	---	1.31	9.72E-03
CSPG6	1556925_at	AL360194	NM_005445	9126	1.31	8.99E-03
ASXL1	242439_s_at	AI819150	NM_015338	171023	1.31	1.22E-05
PVT1 LOC441378	1558290_a_at	BG200951	XM_372058 XM_499128	441378 5820	1.31	1.11E-04
TUBB6	209191_at	BC002654	NM_032525	84617	1.31	5.17E-04
IRAK1BP1	233290_at	AU145280	NM_001010844	134728	1.31	2.71E-03
AL137730	226999_at	AL137730	---	---	1.31	6.07E-03
PTEN	233314_at	AK021487	NM_000314	5728	1.31	7.60E-03
ZNF215	220214_at	NM_013250	NM_013250	7762	1.31	5.81E-03
LRPPRC	1557360_at	CA430402	NM_133259	10128	1.30	1.55E-03
DKFZP434C21:	231552_at	AW451785	NM_015635	26130	1.30	5.13E-04
AI651786	237945_at	AI651786	---	---	1.30	4.28E-03
AU155234	233289_at	AU155234	---	---	1.30	9.43E-03
AA648983	240478_at	AA648983	---	---	1.30	9.77E-05
AA412686	244608_at	AA412686	---	---	1.30	4.76E-03
RBMS3	240245_at	AW237264	NM_00100379 2 NM_00100379 3 NM_014483	27303	1.30	6.53E-03
AK021457	216682_s_at	AK021457	---	---	1.30	2.30E-04
SHPRH	243964_at	AI631201	NM_173082	257218	1.29	9.11E-03
METAP2	244185_at	AA921841	NM_006838	10988	1.29	5.27E-05
MAB21L2	210302_s_at	AF262032	NM_006439	10586	1.29	1.50E-04
AA543084	236480_at	AA543084	---	---	1.29	3.14E-04
AW271626	237441_at	AW271626	---	---	1.29	2.95E-05
SF3B14	1561923_a_at	AF147425	NM_016047	51639	1.29	7.66E-03
PRDX6	242751_at	N55072	NM_004905	9588	1.28	1.80E-03
SMU1	228180_at	AA805653	NM_018225	55234	1.28	6.63E-04
BF001773	241906_at	BF001773	---	---	1.28	9.10E-03
PFAAP5	221899_at	AI809961	NM_014887	10443	1.28	8.55E-03
FLJ13273	220063_at	NM_024751	NM_024751	79807	1.28	4.70E-04
HM13	1560297_at	BG928538	NM_030789 NM_178580 NM_178581 NM_178582	81502	1.28	3.78E-03

DRF1	206661_at	NM_025104	NM_025104 NM_145663	80174	1.28	5.80E-04
LOC284219	1556425_a_at	BF509747	---	284219	1.27	2.33E-03
ANXA2	213503_x_at	BE908217	NM_001002857 NM_001002858 NM_004039	302	1.27	2.58E-03
SPON1	213994_s_at	AI885290	NM_006108	10418	1.27	2.99E-03
M11S1	244778_x_at	N63691	NM_005898 NM_203364	4076	1.27	1.16E-03
LOC253981	226430_at	AI394438	---	253981	1.26	6.58E-04
FUBP1	240307_at	N54783	NM_003902	8880	1.26	5.57E-04
NKTR	231235_at	AA732581	NM_005385	4820	1.26	6.07E-03
ARHGAP24	223422_s_at	AI743534	NM_031305	83478	1.26	2.57E-03
KIAA1838	241152_at	BE466903	NM_032448	84498	1.26	4.94E-03
USP34	207365_x_at	NM_014709	NM_014709	9736	1.25	1.35E-04
DHX57	239311_at	AI367034	NM_144995 NM_145646 NM_198963	90957	1.25	7.92E-03
UBE2H	239721_at	AI280328	NM_003344 NM_182697	7328	1.25	7.22E-03
ID1	208937_s_at	D13889	NM_002165 NM_181353	3397	1.25	1.45E-03
MARK3	239166_at	R98192	NM_002376	4140	1.24	8.08E-04
APBB2	213419_at	U62325	NM_173075	323	1.24	5.44E-04
SVH	1558748_at	AL832759	NM_031905	83787	1.24	2.00E-03
ASXL1	242438_at	AI819150	NM_015338	171023	1.24	6.76E-05
P15RS	228566_at	AA778694	NM_018170	55197	1.24	2.39E-04
LOC115648	1558486_at	BC022394	NM_145326	115648	1.24	3.07E-04
CADPS	1568603_at	AI912173	NM_003716 NM_183393 NM_183394	8618	1.24	3.75E-03
AI291804	242856_at	AI291804	---	---	1.24	8.05E-05
TCTEL1	242109_at	AI038577	NM_006519	6993	1.23	3.41E-03
QKI	241938_at	AA935633	NM_006775 NM_206853 NM_206854 NM_206855	9444	1.23	1.41E-04
SCARA3	223842_s_at	AB007830	NM_016240 NM_182826	51435	1.22	3.50E-04
MRPS5	236779_at	BG539414	NM_031902	64969	1.22	1.33E-03
BE670307	227955_s_at	BE670307	---	---	1.22	9.05E-06
DNAPTP6	241812_at	AV648669	NM_015535	26010	1.22	8.50E-03
PCGF5	229194_at	AL045882	NM_032373	84333	1.22	2.28E-04
AU145679	233607_at	AU145679	---	---	1.21	4.54E-03
BE464799	214036_at	BE464799	---	---	1.21	5.03E-05
SLCO3A1	219229_at	NM_013272	NM_013272	28232	1.21	2.66E-03
BF433200	242467_at	BF433200	---	---	1.21	7.14E-03
PPARG	232331_at	AK027107	NM_005037 NM_015869 NM_138711 NM_138712	5468	1.21	6.85E-03
FNTA	240527_at	AI953011	NM_002027	2339	1.21	1.22E-03
TCF7L2	216035_x_at	AV721430	NM_030756	6934	1.21	2.15E-05
POLE	216026_s_at	AL080203	NM_006231	5426	1.21	2.59E-03
ZA20D3	238812_at	AA741296	NM_019006	54469	1.21	9.92E-03
SFRS2IP	232597_x_at	AK025132	NM_004719	9169	1.21	1.99E-03

TH	208291_s_at	NM_000360	NM_000360 NM_199292 NM_199293	7054	1.21	8.60E-04
NKTR	202380_s_at	NM_005385	NM_005385	4820	1.21	1.31E-03
PTPN13	243792_x_at	AI281371	NM_006264 NM_080683 NM_080684 NM_080685	5783	1.20	9.38E-03
UBE3B	232301_at	AK022019	NM_130466 NM_183414 NM_183415	89910	1.20	1.77E-04
RAB12	238714_at	AA504249	XM_113967	201475	1.20	7.92E-04
AW299775	235008_at	AW299775	---	---	1.20	1.71E-03
HSD17B12	242616_at	W80359	NM_016142	51144	1.19	8.50E-03
R16900	242514_at	R16900	---	---	1.19	2.39E-03
DST	232098_at	AK025142	NM_001723 NM_015548 NM_020388 NM_183380	667	1.19	4.65E-03
DKFZP564C18(	1559139_at	BC009786	NM_015658	26155	1.19	3.03E-03
C9orf3	233599_at	AK025151	NM_032823	84909	1.19	1.52E-03
AI859990	244197_x_at	AI859990	---	---	1.18	1.42E-03
SPON1	213993_at	AI885290	NM_006108	10418	1.18	8.98E-03
CENPF	207331_at	NM_016343	NM_016343	1063	1.18	6.92E-03
CDC2L5	232266_x_at	AK024379	NM_003718 NM_031267	8621	1.18	2.93E-03
EXT1	237310_at	AI743607	NM_000127	2131	1.18	4.88E-03
C1QDC1	218456_at	NM_023925	NM_00100225 9 NM_023925 NM_032156	65981	1.18	2.52E-06
FLJ45645	243038_at	AW292769	NM_198557	375287	1.18	6.22E-03
H43040	231108_at	H43040	---	---	1.18	2.07E-04
SEC63	242749_at	AI022173	NM_007214	11231	1.18	3.85E-03
KLF7	238482_at	AL120562	NM_003709	8609	1.17	4.23E-04
API5	214960_at	AF229253	NM_006595	8539	1.17	1.28E-04
ENC1	201341_at	NM_003633	NM_003633	8507	1.17	9.25E-04
SLC16A4	228455_at	AI092824	NM_004696	9122	1.17	3.54E-03
ANP32A	235954_at	AA972597	NM_006305	8125	1.17	4.73E-03
UBE2E1	236062_at	AI742722	NM_003341 NM_182666	7324	1.17	2.49E-03
EVL	227232_at	T58044	NM_016337	51466	1.17	1.12E-03
SLC6A2	210353_s_at	M65105	NM_001043	6530	1.17	3.19E-03
Cep63	238170_at	BE327727	NM_025180	80254	1.17	6.06E-05
AU147479	233359_at	AU147479	---	---	1.16	1.44E-03
AF010144	207953_at	AF010144	---	---	1.16	6.11E-05
TLE3	228340_at	BE967118	NM_005078	7090	1.16	2.16E-03
LOC338692	238642_at	AW367571	NM_207354	338692	1.16	6.72E-03
BF981643	214720_x_at	BF981643	NM_144710 NM_178584	151011	1.16	3.74E-03
AU152763	232939_at	AU152763	---	---	1.16	1.12E-03
COMMD10	1560349_at	BC036897	NM_016144	51397	1.16	7.89E-03
MDN1	1569484_s_at	AL603301	NM_014611	23195	1.16	1.37E-03
FLJ10213	219906_at	NM_018029	NM_018029	55096	1.16	2.68E-04
AF5Q31	1555436_a_at	BC025700	NM_014423	27125	1.16	4.10E-04
BE467787	243835_at	BE467787	---	---	1.16	3.16E-03
NOSTRIN	235506_at	AI076788	NM_052946	115677	1.16	5.52E-03

WWOX	242099_at	T83938	NM_016373 NM_018560 NM_130788 NM_130790 NM_130791 NM_130792 NM_130844	51741	1.16	1.72E-03
NKTR	202379_s_at	AI361805	NM_005385	4820	1.16	2.17E-03
TXNRD1	201266_at	NM_003330	NM_003330 NM_182729 NM_182742 NM_182743	7296	1.15	1.40E-04
STRA6	1569334_at	BC015881	NM_022369	64220	1.15	2.00E-03
DLEU2	215629_s_at	AA905286	NM_006021	8847	1.15	8.95E-03
MSH3	233263_at	AU147635	NM_002439	4437	1.15	3.30E-04
YAP	244803_at	AI335191	NM_018253 NM_139118 NM_139119 NM_139120 NM_139121	55249	1.14	3.17E-03
ANAPC5	235926_at	AI312527	NM_016237	51433	1.14	3.93E-03
LOC152573	229485_x_at	AI735586	XM_496688	152573	1.14	9.91E-03
VPS16	233313_at	AU158316	NM_022575 NM_080413 NM_080414	64601	1.14	1.33E-03
TNRC6	233836_at	AK025277	NM_014494 NM_020847	27327	1.14	4.69E-03
PCGF5	227935_s_at	AA522681	NM_032373	84333	1.13	1.23E-03
LOC255326	233271_at	AU145563	XM_497224	255326	1.13	9.42E-03
KIAA1881	207730_x_at	NM_017932	XM_375558	114782	1.13	8.71E-04
NAPE-PLD	233539_at	AK000801	NM_198990	222236	1.13	6.74E-03
PGAP1	220576_at	NM_024989	NM_024989	80055	1.13	4.35E-04
FLJ10707	239957_at	AW510793	XM_371614	55209	1.13	3.10E-03
SIVA	222030_at	AW024335	NM_006427 NM_021709	10572	1.13	8.59E-03
MGC34032	1552782_at	AK091400	NM_152697	204962	1.13	6.36E-03
TP53I3	210609_s_at	BC000474	NM_004881 NM_147184	9540	1.13	6.61E-03
SYT11	232677_at	AU146128	NM_152280	23208	1.13	3.78E-05
ZAK	1555259_at	AF465843	NM_016653 NM_133646	51776	1.13	4.30E-04
MTBP	233436_at	AK022122	NM_022045	27085	1.12	2.65E-03
SDHA SDHAL2	230077_at	W90764	NM_004168 XM_171032	255812 6389	1.12	7.47E-04
EIF4A1	214805_at	U79273	NM_001416	1973	1.12	7.09E-03
ZNF131	1557384_at	AL832081	---	7690	1.12	3.31E-03
TJP1	244476_at	R39769	NM_003257 NM_175610	7082	1.12	1.55E-03
NM_000575	208200_at	NM_000575	---	---	1.12	9.29E-03
SFI1	36545_s_at	AB011114	NM_00100746 7 NM_014775	9814	1.12	1.54E-03
GALNT7	222587_s_at	BF699855	NM_017423	51809	1.12	1.21E-03
AA176313	1566113_at	AA176313	---	---	1.12	7.32E-03
RABGAP1L	1565762_at	AK074233	NM_014857	9910	1.12	4.63E-03
MED6	207078_at	NM_005466	NM_005466	10001	1.12	8.69E-03
NDUFS1	1559691_at	BC032767	NM_005006	4719	1.11	7.49E-03
SYNCRIP	1555427_s_at	AY034482	NM_006372	10492	1.11	3.11E-03

TH1L	220607_x_at	NM_016397	NM_016397 NM_198976	51497	1.11	1.11E-03
SMURF2	230099_at	AI139993	NM_022739	64750	1.11	9.53E-03
KHDRBS3	209781_s_at	AF069681	NM_006558	10656	1.11	6.19E-04
LOC90799	223815_at	AF130069	NM_138363	90799	1.10	9.64E-03
ASCL1	209988_s_at	BC001638	NM_004316	429	1.10	6.04E-04
AA192765	238172_at	AA192765	---	---	1.10	7.54E-04
C7orf28B	215024_at	AK000993	NM_198097	221960	1.10	8.32E-03
SURF5	206593_s_at	NM_006752	NM_006752 NM_133640 NM_181491	6837	1.10	8.66E-03
SNTB2	232784_at	R42604	NM_006750 NM_130845	6645	1.10	1.54E-05
TD-60	243297_at	AI498610	NM_018715	55920	1.10	6.95E-03
HES1	203394_s_at	BE973687	NM_005524	3280	1.10	9.57E-05
CAS1	239545_at	AI335004	NM_022900	64921	1.10	4.20E-03
PSMB7	244801_at	AI248671	NM_002799	5695	1.10	1.35E-04
MBNL2	232138_at	AW276914	NM_144778 NM_207304	10150	1.10	6.31E-04
hSyn	231087_at	AL046412	NM_018157	55188	1.09	8.23E-03
LRRFIP1	238840_at	AW082668	NM_004735	9208	1.09	3.75E-03
SLC7A5	201195_s_at	AB018009	NM_003486	8140	1.09	1.06E-04
RDH11	217042_at	AL096716	NM_016026	51109	1.09	1.95E-03
LUC7L2	243852_at	AI963460	NM_016019	51631	1.09	4.04E-03
SEC8L1	216538_at	AL049351	NM_021807	60412	1.09	2.92E-04
NM_006896	206848_at	NM_006896	---	---	1.09	2.52E-04
PSMD7	244515_at	AI640348	NM_002811	5713	1.08	1.31E-05
SYMPK	1554595_at	BC030214	NM_004819	8189	1.08	6.40E-03
ELOVL5	1566079_at	AL833001	NM_021814	60481	1.08	7.71E-03
FLJ10357	241627_x_at	AI640434	NM_018071	55701	1.08	1.28E-03
PASK	213534_s_at	D50925	NM_015148	23178	1.08	6.82E-03
CALM2	235190_at	BF591288	NM_001743	805	1.08	1.73E-04
SEMA5A	205405_at	NM_003966	NM_003966	9037	1.08	7.59E-05
ITSN1	215791_at	AF003738	NM_00100113 2 NM_003024	6453	1.08	1.59E-03
PBX4	230536_at	AJ300182	NM_025245	80714	1.07	9.77E-04
MAN2A1	226538_at	AV700323	NM_002372	4124	1.07	2.26E-04
MGC2803	230213_at	BE220399	NM_024038	79002	1.07	9.35E-05
ABCD1	205142_x_at	NM_000033	NM_000033	215	1.07	8.99E-03
ZNF537	223392_s_at	BF510588	NM_020856	57616	1.07	1.32E-04
AI733583	243235_at	AI733583	---	---	1.07	3.45E-03
CROP	242389_at	BE887449	NM_006107 NM_016424	51747	1.07	1.26E-03
SSH2	230590_at	BE675486	NM_033389	85464	1.07	5.70E-04
NDUFS8	232169_x_at	AK002110	NM_002496	4728	1.06	6.64E-04
VAPA	242780_at	AI332536	NM_003574 NM_194434	9218	1.06	7.88E-03
FDFT1	238666_at	BF438300	NM_004462	2222	1.06	1.67E-03
NQO1	210519_s_at	BC000906	NM_000903	1728	1.06	4.23E-03
KLHL5	233866_at	AK001836	NM_00100707 5 NM_199039	51088	1.06	5.76E-03

SLC8A3	1562403_a_at	AK096553	NM_033262 NM_058240 NM_182932 NM_182933 NM_182936 NM_183002	6547	1.06	2.76E-05
DPF1	206531_at	NM_004647	NM_004647	8193	1.06	4.01E-03
MCCC2	1556345_s_at	AF086534	NM_022132	64087	1.06	2.60E-03
NOS1	239132_at	BE299830	NM_000620	4842	1.05	1.68E-03
DOK4	209691_s_at	BC003541	NM_018110	55715	1.05	9.53E-03
SESN2	223195_s_at	BF131886	NM_031459	83667	1.05	7.34E-03
AK025909	233814_at	AK025909	---	---	1.05	2.17E-06
FBN1	202766_s_at	NM_000138	NM_000138	2200	1.05	4.10E-03
UCHL1	201387_s_at	NM_004181	NM_004181	7345	1.05	2.84E-03
DIAPH1	209190_s_at	AF051782	NM_005219	1729	1.05	3.26E-04
KIAA0152	200616_s_at	BC000371	NM_014730	9761	1.04	2.72E-06
GAP43	204471_at	NM_002045	NM_002045	2596	1.04	4.27E-04
KIAA0528	240205_x_at	AW188170	NM_014802	9847	1.04	5.35E-03
AK025343	216176_at	AK025343	---	---	1.04	4.13E-04
WDR45	215553_x_at	AK024315	NM_007075	11152	1.04	3.37E-03
NLN	234762_x_at	AK026655	NM_020726	57486	1.03	6.21E-03
AI589594	238694_at	AI589594	---	---	1.03	1.36E-04
CTSL2	210074_at	AF070448	NM_001333	1515	1.03	7.07E-03
COBLL1	203642_s_at	NM_014900	NM_014900	22837	1.03	7.47E-03
MGC15407	235662_at	AI125867	NM_080667	112942	1.03	8.10E-03
TRNT1	223814_at	BC005184	NM_016000 NM_182916	51095	1.03	8.10E-04
AI377043	230722_at	AI377043	---	---	1.03	2.26E-03
MGC45866	232475_at	BC002881	NM_152259	90381	1.03	4.71E-03
KIAA2024	1566166_at	AL833423	NM_172070	130507	1.03	3.17E-04
SRGAP2	1556203_a_at	AI263819	XM_059095	23380	1.03	1.13E-03
CHTF18	226569_s_at	AK024476	NM_022092	63922	1.02	1.51E-03
TCF7L2	216511_s_at	AJ270770	NM_030756	6934	1.02	1.84E-07
SDFR1	228723_at	AL360198	NM_012428 NM_017455	27020	1.02	2.35E-04
CDCA7	230060_at	AI277642	NM_031942 NM_145810	83879	1.02	6.93E-03
CIAPIN1	230838_s_at	AW771492	NM_020313	57019	1.02	6.62E-03
SDC4	202071_at	NM_002999	NM_002999	6385	1.02	4.53E-03
STK36	234005_x_at	AK022692	NM_015690	27148	1.02	9.55E-05
DLGAP4	233056_x_at	AK024674	NM_014902 NM_183006	22839	1.02	5.12E-03
CNOT7	233019_at	AU145061	NM_013354 NM_054026	29883	1.02	3.38E-03
SKIL	217591_at	BF725121	NM_005414	6498	1.01	8.82E-06
GARNL1	215162_at	AB020691	NM_014990 NM_194301	253959	1.01	3.09E-04
RFC5	203210_s_at	NM_007370	NM_007370 NM_181578	5985	1.01	1.06E-03
AK024136	217152_at	AK024136	---	---	1.01	3.14E-03
ATP8B1	214594_x_at	BG252666	NM_005603	5205	1.01	6.15E-03
AL050032	216621_at	AL050032	---	---	1.01	1.08E-05
CKLFSF7	1560754_at	AL832450	NM_138410 NM_181472	112616	1.01	1.86E-03
KIAA1212	1562648_at	BC035848	NM_018084	55704	1.01	4.98E-03
CAPN1	232012_at	AV691296	NM_005186	823	1.01	1.96E-03
ZNF207	231848_x_at	AW192569	NM_003457	7756	1.01	7.04E-03
TRA2A	229574_at	AI268231	NM_013293	29896	1.01	7.43E-03

AU146021	232478_at	AU146021	---	---	1.01	7.34E-03
KNTC1	206316_s_at	NM_014708	NM_014708	9735	1.00	8.69E-06
DENR	238982_at	AW665791	NM_003677	8562	1.00	3.31E-03
DNCH2	1565149_at	AF288405	XM_370652	79659	1.00	2.59E-06
PRDX2	215067_x_at	AU147942	NM_005809	7001	1.00	5.62E-03
			NM_181737			
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PRDX6	238951_at	BF843343	NM_004905	9588	1.00	2.00E-04
RIOK3	215588_x_at	AK024958	NM_003831	8780	1.00	5.41E-04
			NM_145906			
MID1	203636_at	BE967532	NM_000381	4281	1.00	2.42E-03
			NM_033290			
			NM_033291			
E2-230K	1554814_at	BC007822	NM_022066	63893	1.00	2.86E-03
ZFOC1	1558816_at	BC037793	NM_152437	144348	1.00	1.23E-04
EFHC1	225656_at	AI564473	NM_018100	114327	1.00	7.26E-03
KIAA0999	242920_at	AW590838	NM_025164	23387	1.00	6.83E-03
GRK6	202848_s_at	BG423052	NM_00100410	2870	0.99	2.95E-03
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			NM_002082			
STS	243858_at	AA699970	NM_000351	412	0.99	1.31E-03
AZI2	223846_at	BC001139	NM_022461	64343	0.99	9.97E-05
			NM_203326			
AW069499	230886_at	AW069499	---	---	0.99	5.25E-04
NKTR	215338_s_at	AI688640	NM_005385	4820	0.99	6.23E-03
FLJ10408	220535_at	NM_018088	NM_018088	55138	0.99	2.76E-03
PDZRN3	232776_at	AU145289	NM_015009	23024	0.99	5.32E-03
ACVR2	244332_at	AW974077	NM_001616	92	0.99	5.39E-06
GLS	223080_at	AK025021	NM_014905	2744	0.99	2.09E-03
RAB35	205461_at	NM_006861	NM_006861	11021	0.99	8.15E-03
FLJ21415	218867_s_at	NM_024738	NM_024738	79794	0.99	4.67E-03
MTMR9	233101_at	AK022071	NM_015458	66036	0.98	3.57E-04
TDG	203742_s_at	BF674842	NM_00100841	6996	0.98	2.79E-04
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			NM_003211			
DKFZP434K04(	1570227_at	BC016065	NM_020312	57017	0.98	7.84E-03
RBL1	1555004_a_at	BC032247	NM_002895	5933	0.98	3.12E-03
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MYST3	242480_at	AA868356	NM_006766	7994	0.98	3.48E-03
TXNDC5	243405_at	AI097337	NM_022085	81567	0.98	1.17E-03
			NM_030810			
C14orf153	232814_x_at	AK024310	NM_032374	84334	0.98	2.05E-03
FLJ10569	237504_at	AW002398	NM_018142	55174	0.98	5.78E-05
AW451634	229470_at	AW451634	---	---	0.98	2.25E-03
ATP2B1	209281_s_at	M95541	NM_00100132	490	0.98	7.26E-05
			3			
			NM_001682			
CHPT1	1559739_at	AK025141	NM_020244	56994	0.98	1.14E-03
PFKFB4	228499_at	AL038787	NM_004567	5210	0.98	1.03E-04
AI435248	242837_at	AI435248	---	---	0.98	3.31E-03
AL567118	241388_at	AL567118	---	---	0.97	9.39E-03
ZNF274	232436_at	AI057616	NM_016324	10782	0.97	8.11E-03
			NM_016325			
			NM_133502			
SLCO3A1	229776_at	AW138118	NM_013272	28232	0.97	3.95E-03
DRIM	209725_at	AF072718	NM_014503	27340	0.97	6.32E-03

AARS	201000_at	NM_001605	NM_001605	16	0.97	3.59E-03
BE857972	243781_at	BE857972	---	---	0.97	2.71E-04
AU146017	234082_at	AU146017	---	---	0.97	1.73E-03
MGC20481	243513_at	AA971848	NM_052849	90416	0.96	3.69E-03
CPEB4	242384_at	AI452469	NM_030627	80315	0.96	8.12E-03
KDELC2	225128_at	AL548941	NM_153705	143888	0.96	3.31E-03
R84398	241993_x_at	R84398	---	---	0.96	3.54E-03
PR47	1560526_at	BQ880034	---	266671	0.96	4.91E-03
GTSE1	204315_s_at	AI340239	NM_016426	51512	0.96	1.04E-03
WDR11	229694_at	BF062828	NM_018117	55717	0.96	6.59E-03
CTNNB1	242558_at	AW362945	NM_001904	1499	0.96	4.14E-03
AI760298	244054_at	AI760298	---	---	0.96	2.18E-05
IQWD1	235613_at	BF476152	NM_018442	55827	0.96	6.64E-03
AW024890	229942_at	AW024890	---	---	0.96	6.64E-03
DDHD1	231165_at	BE857355	NM_030637	80821	0.96	8.45E-03
CDYL	240594_at	W86659	NM_004824	9425	0.96	4.83E-03
			NM_170751			
			NM_170752			
U2AF1	232141_at	AU144161	NM_006758	7307	0.96	2.17E-05
RAPGEF2	238176_at	T86196	XM_376350	9693	0.96	9.65E-03
C14orf135	1563259_at	AK024838	NM_022495	64430	0.95	1.91E-04
GPX3	214091_s_at	AW149846	NM_002084	2878	0.95	6.75E-03
DKFZp434P055	232398_at	AK001064	NM_173466	91531	0.95	1.46E-03
MATR3	242260_at	BG283790	NM_018834	9782	0.95	4.52E-04
STK36	231806_s_at	AL133630	NM_015690	27148	0.95	3.18E-03
DTX1	1559618_at	BQ188678	NM_004416	1840	0.95	2.32E-03
AL832061	1559436_x_at	AL832061	---	---	0.95	1.65E-03
VPS29	223026_s_at	AF201946	NM_016226	51699	0.95	6.16E-04
			NM_057180			
SEC61A2	228747_at	AI694646	NM_018144	55176	0.95	9.12E-03
USP7	230761_at	AI972599	NM_003470	7874	0.95	4.14E-06
STK32B	219686_at	NM_018401	NM_018401	55351	0.95	7.68E-03
SMO	218629_at	NM_005631	NM_005631	6608	0.95	6.28E-03
TCF7L2	212761_at	AI949687	NM_030756	6934	0.95	3.71E-03
PDK1	226452_at	AU146532	NM_002610	5163	0.94	7.99E-04
MAP3K1	225927_at	AA541479	XM_042066	4214	0.94	1.85E-03
PMAIP1	204286_s_at	NM_021127	NM_021127	5366	0.94	9.09E-04
AL049260	216524_x_at	AL049260	---	---	0.94	1.42E-03
GTF2H3	222104_x_at	AI569458	NM_001516	2967	0.94	2.18E-03
MGC13098	214740_at	BE676209	NM_032958	246721	0.94	6.48E-03
POLR2J2			NM_032959	84820		
			NM_145325			
			XM_379817			
			XM_499280			
FLJ31795	1566480_x_at	AK096357	NM_144609	124808	0.94	1.19E-03
MID1	203637_s_at	NM_000381	NM_000381	4281	0.94	8.91E-03
			NM_033290			
			NM_033291			
AI692624	1556352_at	AI692624	---	---	0.94	3.86E-03
AL035461	231827_at	AL035461	---	---	0.94	8.02E-03
NFKBIZ	223218_s_at	AB037925	NM_00100547	64332	0.93	9.02E-03
			4			
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R78413	240538_at	R78413	---	---	0.93	5.24E-03
UBXD4	235327_x_at	BG111015	NM_181713	165324	0.93	2.26E-06
PABPC1	236907_at	AI760366	NM_002568	26986	0.93	9.37E-03
RNF34	219035_s_at	NM_025126	NM_025126	80196	0.93	1.26E-05
			NM_194271			

FLJ11539	219791_s_at	NM_024748	XM_496724	79804	0.93	1.41E-03
FLJ10156	221591_s_at	BC005004	NM_019013	54478	0.93	4.68E-04
CREBL1	1554487_a_at	BC008394		1388	0.93	4.64E-05
			NM_004381			
RBBP4	239071_at	AI972451	NM_005610	5928	0.93	3.91E-03
SNRPA1	242146_at	AA872471	NM_003090	6627	0.93	4.37E-03
DERL3	231324_at	AW452134	NM_00100286	91319	0.93	9.94E-05
			2			
			NM_198440			
DDX50	1568815_a_at	AA903184	NM_024045	79009	0.93	3.15E-03
KCTD3	241903_at	AI688631	NM_016121	51133	0.93	1.35E-03
TBX3	225544_at	AI806338	NM_005996	6926	0.93	2.95E-03
			NM_016569			
EXOC7	214802_at	AK022397	NM_015219	23265	0.93	6.60E-03
ZDHHC13	243250_at	AI922173	NM_00100148	54503	0.93	7.75E-03
			3			
			NM_019028			
NSF	1566785_x_at	AK025172	NM_006178	4905	0.92	1.01E-03
C9orf3	237716_at	AA699673	NM_032823	84909	0.92	2.56E-03
GPR125	210473_s_at	M37712	NM_145290	166647	0.92	5.29E-07
ZNF160	214715_x_at	AK024789	NM_033288	90338	0.92	1.07E-03
			NM_198893			
CALU	238908_at	BG392414	NM_001219	813	0.92	2.85E-05
TCF7L2	216037_x_at	AA664011	NM_030756	6934	0.92	1.59E-04
MBNL2	232369_at	AF339768	NM_144778	10150	0.92	6.38E-03
			NM_207304			
DHX36	1559039_at	AK096808	NM_020865	170506	0.92	4.13E-03
BE563152	224806_at	BE563152	XM_498674	440448	0.92	7.47E-03
TM4SF8	232632_at	AU145719	NM_005724	10099	0.92	1.10E-05
			NM_198902			
BTBD14B	215587_x_at	AK023891	NM_052876	112939	0.92	2.11E-03
AI821721	241223_x_at	AI821721	---	---	0.91	3.84E-03
SREBF1	235862_at	AA954908	NM_00100529	6720	0.91	1.46E-03
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			NM_004176			
AI570571	236092_at	AI570571	---	---	0.91	2.41E-03
FLJ13491	219245_s_at	AI309636	NM_024623	79676	0.91	9.68E-06
MDH1	235374_at	AW952547	NM_005917	4190	0.91	1.14E-03
PASK	216945_x_at	U79240	NM_015148	23178	0.91	3.14E-03
DTYMK	1553983_at	AF258562	NM_012145	1841	0.90	9.36E-03
CLU	208792_s_at	M25915	NM_001831	1191	0.90	3.22E-05
			NM_203339			
C20orf172	219512_at	NM_024918	NM_024918	79980	0.90	1.35E-03
PTPN1	202716_at	NM_002827	NM_002827	5770	0.90	4.52E-04
ENTPD6	201704_at	NM_001247	NM_001247	955	0.90	9.65E-03
DKFZP564C19(	236367_at	N33174	XM_498825	284649	0.90	3.20E-03
GPT2	224839_s_at	BG328998	NM_133443	84706	0.89	2.50E-03
TH1L	225006_x_at	AJ238379	NM_016397	51497	0.89	1.75E-05
			NM_198976			
AW975183	244340_x_at	AW975183	---	---	0.89	1.08E-03
AW131450	235513_at	AW131450	---	---	0.89	1.09E-05
AK023783	215604_x_at	AK023783	---	---	0.89	6.48E-03
KIAA0582	239442_at	BF589179	NM_015147	23177	0.89	1.66E-03
BTBD7	217141_at	AL049394	NM_00100286	55727	0.89	2.17E-03
			0			
			NM_018167			
DNAPTP6	222154_s_at	AK002064	NM_015535	26010	0.89	1.33E-03
RNPEP	208270_s_at	NM_020216	NM_020216	6051	0.89	9.93E-04

KIAA0232	232595_at	AK023294	NM_014743	9778	0.89	2.09E-03
ZNF503	227195_at	AA603467	NM_032772	84858	0.88	1.25E-04
RABL4	213784_at	AL037167	NM_006860	11020	0.88	4.07E-03
KLF7	204334_at	AA488672	NM_003709	8609	0.88	5.59E-04
FLJ13611	234788_x_at	AK024819	NM_024941	80006	0.88	4.20E-03
TFF3	204623_at	NM_003226	NM_003226	7033	0.88	1.84E-03
C7orf24	239841_at	AA137038	NM_024051	79017	0.88	5.49E-05
FLJ14346	220720_x_at	NM_025029	NM_025029	80097	0.88	2.42E-03
PGF	215179_x_at	AK023843	NM_002632	5228	0.88	6.50E-04
BTBD9	233041_x_at	AK025009	NM_152733	114781	0.87	5.26E-03
ZFP64	242759_at	AI821726	NM_018197	55734	0.87	1.39E-03
			NM_022088			
			NM_199426			
			NM_199427			
AW139789	232134_at	AW139789	---	---	0.87	2.61E-05
KIAA1706	1563621_at	AL713724	NM_030636	80820	0.87	9.21E-03
GNAS	228173_at	AA810695	NM_000516	2778	0.87	1.14E-03
			NM_016592			
			NM_080425			
			NM_080426			
ESPL1	204817_at	NM_012291	NM_012291	9700	0.87	4.80E-03
AI791828	237868_x_at	AI791828	---	---	0.87	3.13E-05
RBM6	1556672_a_at	AI190489	NM_005777	10180	0.87	7.88E-04
SBNO1	216161_at	AK024128	NM_018183	55206	0.87	2.11E-03
BF056892	229024_at	BF056892	---	---	0.87	7.14E-06
CDC42BPA	215296_at	AK027000	NM_003607	8476	0.87	5.58E-03
			NM_014826			
BE727883	226495_at	BE727883	XM_498844	440752	0.87	7.67E-03
ANK2	216195_at	AF131823	NM_001148	287	0.86	2.02E-04
			NM_020977			
SFI1	215699_x_at	AL096768	NM_00100746	9814	0.86	4.61E-04
			7			
			NM_014775			
TH1L	225261_x_at	AJ238376	NM_016397	51497	0.86	4.08E-05
			NM_198976			
SEMA6A	215028_at	AB002438	NM_020796	57556	0.86	1.40E-04
LOC91431	228859_at	BF056790	NM_138698	91431	0.86	3.09E-03
FTHFSDC1	240552_at	AA811452	NM_015440	25902	0.86	8.65E-04
TRIM36	219736_at	NM_018700	NM_018700	55521	0.86	8.76E-03
DDX11	208159_x_at	NM_004399	NM_004399	1663	0.86	1.06E-03
			NM_030653			
			NM_030655			
NFATC2IP	212809_at	AA152202	NM_032815	84901	0.86	5.06E-04
M-RIP	231255_at	AI970090	NM_015134	23164	0.86	6.68E-04
			NM_201274			
PCNT1	218014_at	NM_024844	NM_024844	79902	0.86	7.48E-05
ADAM33	233868_x_at	AL117415	NM_025220	80332	0.85	1.87E-04
			NM_153202			
FLJ10569	229633_at	AA115512	NM_018142	55174	0.85	3.01E-04
AI734111	222284_at	AI734111	---	---	0.85	2.27E-03
RPL35A	215208_x_at	AK021571	NM_000996	6165	0.85	1.22E-03
SNCAIP	219511_s_at	NM_005460	NM_005460	9627	0.85	1.37E-03
GRIK2	1560265_at	BQ434382	NM_021956	2898	0.85	8.83E-04
			NM_175768			
CCND1	208711_s_at	BC000076	NM_053056	595	0.85	5.90E-05
NM_003349	201003_x_at	NM_003349	---	---	0.85	1.49E-04
FLJ13089	225888_at	N62802	NM_024953	80018	0.84	3.59E-04
SLB	226324_s_at	AB033005	NM_015662	26160	0.84	6.60E-03

SFRS15	222310_at	AA648521	NM_020706	57466	0.84	2.91E-03
AP3M2	1569053_at	BG110196	NM_006803	10947	0.84	9.81E-04
STRA6	1569335_a_at	BC015881	NM_022369	64220	0.83	1.47E-03
TH1L	225865_x_at	AJ238374	NM_016397	51497	0.83	3.21E-04
			NM_198976			
SLC2A4RG	218494_s_at	NM_020062	NM_020062	56731	0.83	8.97E-05
NCOA5	239815_at	R16784	NM_020967	57727	0.83	7.12E-03
AARSL	231845_at	AI721172	NM_020745	57505	0.83	4.13E-04
AA767373	236327_at	AA767373	---	---	0.83	1.12E-03
KIAA1434	230492_s_at	BE328402	NM_019593	56261	0.83	8.78E-04
RGMA	223468_s_at	AL136826	NM_020211	56963	0.83	2.26E-03
T86613	235804_at	T86613	---	---	0.83	9.52E-05
LMO4	209205_s_at	BC003600	NM_006769	8543	0.83	5.83E-04
AL044078	221860_at	AL044078	---	---	0.83	2.22E-04
AA824321	227547_at	AA824321	---	---	0.82	1.63E-03
C9orf64	223697_x_at	BC004407	NM_032307	84267	0.82	8.80E-05
EIF3S9	242550_at	AA628539	NM_003751	8662	0.82	2.91E-04
			NM_182712			
LOC144766	243986_at	BE409452	XM_378419	144766	0.82	2.37E-03
C14orf145	1557755_at	AW028337	XM_496002	145508	0.82	3.02E-03
FAM19A5	237094_at	AI953086	NM_015381	25817	0.82	1.93E-05
CDKN2C	211792_s_at	U17074	NM_001262	1031	0.82	7.21E-03
			NM_078626			
STMN3	222557_at	AL353715	NM_015894	50861	0.82	3.09E-03
C6orf111	230375_at	AI936531	NM_032870	25957	0.82	6.14E-04
CBWD1	226193_x_at	AV709992	NM_018491	150472	0.82	7.60E-03
CBWD2			NM_172003	220869		
LOC220869			NM_201453	389760		
DC36				55871		
ATF3	202672_s_at	NM_001674	NM_001674	467	0.82	4.70E-03
			NM_004024			
AW629478	244625_at	AW629478	---	---	0.82	1.02E-03
RAD51C	206066_s_at	NM_002876	NM_002876	5889	0.82	1.65E-03
			NM_058216			
			NM_058217			
C15orf25	220071_x_at	NM_018097	NM_018097	55142	0.82	5.19E-04
C22orf18	218741_at	NM_024053	NM_00100287	79019	0.81	7.04E-03
			6			
			NM_024053			
GSS	211630_s_at	L42531	NM_000178	2937	0.81	4.31E-03
IREB2	1563129_at	AL109710	NM_004136	3658	0.81	5.38E-03
EPIM	213434_at	H95263	NM_001980	2054	0.81	1.48E-05
			NM_194356			
DZIP1L	239785_at	BF340245	NM_173543	199221	0.81	7.64E-03
DHX37	223364_s_at	BC004463	NM_032656	57647	0.81	4.75E-03
BC041029	1569025_s_at	BC041029	XM_371697	389211	0.81	2.66E-03
NY-REN-7	214945_at	AW514267	NM_173663	285596	0.81	9.82E-03
LOC389347			XM_371783	389347		
AA778747	241941_at	AA778747	---	---	0.81	3.29E-04
PDE4C	206792_x_at	NM_000923	NM_000923	5143	0.81	3.77E-04
SYNCRIP	209025_s_at	AF037448	NM_006372	10492	0.81	1.94E-03
DRPLA	236961_at	AI539426	NM_00100702	1822	0.80	7.80E-03
			6			
			NM_001940			
ZNF611	208137_x_at	NM_030972	NM_030972	81856	0.80	1.06E-03
BACH2	215907_at	AK027193	NM_021813	60468	0.80	1.49E-03
AL038191	240271_at	AL038191	---	---	0.80	4.41E-04
FANCC	205189_s_at	NM_000136	NM_000136	2176	0.80	6.32E-04

RPL10A	232592_at	AU146731	NM_007104	4736	0.80	4.23E-03
GALNT7	218313_s_at	NM_017423	NM_017423	51809	0.80	5.54E-03
SCML1	222747_s_at	BF001786	NM_006746	6322	0.79	2.71E-03
DERA	218102_at	NM_015954	NM_015954	51071	0.79	1.87E-03
AF131796	231916_at	AF131796	---	---	0.79	4.14E-03
CCNE1	213523_at	AI671049	NM_001238 NM_057182	898	0.79	8.53E-03
WWOX	233161_at	AK022464	NM_016373 NM_018560 NM_130788 NM_130790 NM_130791 NM_130792 NM_130844	51741	0.79	2.29E-03
SRP54	1557504_at	AI076351	NM_003136	6729	0.79	7.25E-03
BG149337	229814_at	BG149337	---	---	0.79	7.38E-03
BE676171	237156_at	BE676171	---	---	0.79	4.22E-03
NR2C1	210530_s_at	M21985	NM_003297	7181	0.79	4.35E-03
NKTR	243055_at	BF514072	NM_005385	4820	0.78	9.55E-03
KIAA0152	200617_at	NM_014730	NM_014730	9761	0.78	6.41E-03
EMILIN3	228307_at	AL137580	NM_052846	90187	0.78	3.72E-03
TM4SF14	221002_s_at	NM_030927	NM_030927	81619	0.78	3.35E-03
AI151104	237475_x_at	AI151104	---	---	0.78	1.69E-03
NUP153	239948_at	AA004800	NM_005124	9972	0.78	1.85E-03
PELI2	219132_at	NM_021255	NM_021255	57161	0.78	9.97E-04
THOC4	226319_s_at	AF047002	NM_005782	10189	0.78	3.97E-03
HOXD4	1552337_s_at	NM_014621	NM_014621	3233	0.78	4.73E-03
PPM1B	232580_x_at	AL117553	NM_002706 NM_177968 NM_177969	5495	0.78	2.42E-03
AK000864	216290_x_at	AK000864	---	---	0.78	9.80E-03
KIFC1	209680_s_at	BC000712	XM_371813	3833	0.78	2.91E-03
GSS	201415_at	NM_000178	NM_000178	2937	0.78	7.64E-03
ACPL2	236908_at	BE550429	NM_152282	92370	0.78	2.99E-03
AA348683	240198_at	AA348683	---	---	0.77	1.02E-05
ORF1-FL49	224707_at	AL522667	NM_032412	84418	0.77	3.79E-04
LOC340085	232455_x_at	AU145408	---	340085	0.77	4.32E-04
CNP	1556053_at	AL556987	NM_033133	1267	0.77	2.24E-04
AK098337	1566144_at	AK098337	XM_496690	401131	0.77	1.47E-03
HEG	213069_at	AI148659	XM_087386	57493	0.77	1.93E-03
AI833186	242593_at	AI833186	---	---	0.77	9.83E-04
GPR51	217077_s_at	AF095723	NM_005458	9568	0.77	7.45E-03
KIAA1434	224826_at	AK001947	NM_019593	56261	0.77	3.37E-04
TYRO3	211432_s_at	U05682	NM_006293	7301	0.77	1.71E-03
GNB4	223488_s_at	BC000873	NM_021629	59345	0.77	9.63E-03
MPHOSPH9	237158_s_at	AW449069	NM_022782	10198	0.77	6.87E-03
FBXW12	215600_x_at	AK022174	NM_207102	285231	0.77	4.32E-03
PTK7	1555324_at	BC046109	NM_002821 NM_152880 NM_152881 NM_152882 NM_152883	5754	0.77	9.93E-03
KLHL5	226001_at	AK002174	NM_00100707 5 NM_199039	51088	0.77	7.30E-03
CRTAC1	221204_s_at	NM_018058	NM_018058	55118	0.76	5.35E-03
AK021514	215978_x_at	AK021514	---	---	0.76	7.15E-03
N53564	242280_x_at	N53564	---	---	0.76	1.02E-04

OLFML3	218162_at	NM_020190	NM_020190	56944	0.76	3.61E-04
PDCD2	243773_at	H65902	NM_002598 NM_144781	5134	0.76	9.35E-03
H09533	239748_x_at	H09533	---	---	0.76	6.06E-04
SH3MD1	224817_at	W93554	NM_014631	9644	0.76	1.12E-05
C9orf86	219828_at	NM_024718	NM_024718	55684	0.76	2.56E-03
TBX3	243234_at	BG055137	NM_005996 NM_016569	6926	0.76	4.38E-03
PHF20L1	1554472_a_at	BC015211	NM_016018 NM_024878 NM_032205 NM_198513	51105	0.76	3.06E-03
FLJ10404	243047_at	AV698751	NM_019057	54540	0.76	6.86E-03
SIRT2	1558331_at	BG722779	NM_012237 NM_030593	22933	0.76	6.78E-03
BRI3BP	231810_at	BG106919	NM_080626	140707	0.76	1.27E-03
C19orf14	215218_s_at	AC004144	NM_173636	284403	0.76	9.95E-03
AFG3L1	1552287_s_at	NM_001132	NM_001132	172	0.76	4.38E-03
MUM1	229033_s_at	AA143060	NM_032853	84939	0.76	1.74E-04
DHX35	218579_s_at	NM_021931	NM_021931	60625	0.76	1.36E-03
ESPL1	38158_at	D79987	NM_012291	9700	0.75	5.71E-03
WBSCR20C	213460_x_at	N29665	NM_032158 NM_148936 NM_148980 NM_149379	260294	0.75	3.30E-04
SFI1	213431_x_at	AB011114	NM_001007467 NM_014775	9814	0.75	3.65E-05
AI252004	242696_at	AI252004	---	---	0.75	1.12E-03
SLC15A4	225043_at	AW304786	NM_145648	121260	0.75	9.55E-03
PME-1	243443_at	AI076511	NM_016147	51400	0.75	4.15E-03
TUBGCP2	244842_x_at	AA235663	NM_006659	10844	0.75	5.81E-03
AI041522	228030_at	AI041522	---	---	0.75	8.68E-03
KIAA0992	234135_x_at	AK021652	NM_016081	23022	0.75	3.75E-04
NQO1	201467_s_at	AI039874	NM_000903	1728	0.75	9.53E-03
TJP2	243148_at	AA007423	NM_004817 NM_201629	9414	0.75	2.81E-03
IQGAP1	213446_s_at	AI679073	NM_003870	8826	0.75	1.44E-03
SEC11L3	223299_at	AF212233	NM_033280	90701	0.75	7.34E-04
LOC283871	222622_at	BG284709	XM_208887	283871	0.75	4.92E-03
T96555	243818_at	T96555	---	---	0.75	3.01E-03
TCEA1	1566207_at	BQ286789	NM_006756 NM_201437	6917	0.74	1.85E-03
ZNF44	233775_x_at	AK023304	NM_016264	51710	0.74	1.98E-04
AK024599	233702_x_at	AK024599	---	---	0.74	2.99E-03
C20orf44	244795_at	AV693986	NM_018244 NM_199487 NM_199513	55245	0.74	9.01E-03
N4BP2	231996_at	AB037834	NM_018177	55728	0.74	6.20E-06
CLIC4	201559_s_at	AF109196	NM_013943	25932	0.74	9.19E-03
SEC15L1	232599_at	AF220217	NM_019053	54536	0.74	7.90E-03
AU145662	233399_x_at	AU145662	XM_499131	441383	0.74	1.87E-03
RAD54L	204558_at	NM_003579	NM_003579	8438	0.74	1.24E-03
SLC4A8	207056_s_at	NM_004858	NM_004858	9498	0.74	5.18E-03
PLS3	201215_at	NM_005032	NM_005032	5358	0.74	9.88E-03
C10orf6	203482_at	AL133215	NM_018121	55719	0.74	9.76E-03

PDLIM7	1569150_x_at	BC023629	NM_005451 NM_203352 NM_203353 NM_213636	9260	0.73	1.56E-03
AI939447	241268_x_at	AI939447	---	---	0.73	2.79E-04
FLJ12649	219626_at	NM_024597	XM_291344	79649	0.73	8.01E-04
PPHLN1	234459_at	AK000186	NM_016488 NM_201438 NM_201439 NM_201440 NM_201515	51535	0.73	6.98E-03
DBT	205370_x_at	NM_001918	NM_001918	1629	0.73	4.67E-03
CBX3	230998_at	AV702506	NM_007276 NM_016587	11335	0.73	8.36E-03
ASAHL	214765_s_at	AK024677	NM_014435	27163	0.73	1.72E-05
AF130054	211452_x_at	AF130054	---	---	0.73	5.36E-04
CHKB	204193_at	NM_005198	NM_005198 NM_152253	1120	0.72	3.15E-04
IQGAP1	210840_s_at	D29640	NM_003870	8826	0.72	7.05E-05
ASAHL	232072_at	AK025371	NM_014435	27163	0.72	1.08E-03
MDS028	220590_at	NM_018463	NM_018463	55846	0.72	2.33E-04
SPCS3	222753_s_at	AL136660	NM_021928	60559	0.72	6.00E-03
TERT	207199_at	NM_003219	NM_003219 NM_198253 NM_198254 NM_198255	7015	0.72	3.23E-05
BI496583	1557675_at	BI496583	---	---	0.72	4.63E-03
KIAA1731	1565829_at	BU619319	XM_374922	85459	0.72	6.04E-03
UPF3A	206958_s_at	AF318575	NM_023011 NM_080687	65110	0.72	6.99E-04
GPR125	1555122_at	BC026009	NM_145290	166647	0.72	4.13E-03
FMNL2	1556656_at	BF477401	NM_00100441 7 NM_00100442 1 NM_00100442 2 NM_052905	114793	0.72	1.56E-03
UBE2J1	236528_at	N64079	NM_016021	51465	0.72	2.03E-03
AF15Q14	1552680_a_at	NM_020380	NM_020380 NM_144508 NM_170589	57082	0.71	8.46E-03
RAB11FIP3	228613_at	BF183535	NM_014700	9727	0.71	5.28E-03
GARNL1	234923_at	AK022988	NM_014990 NM_194301	253959	0.71	7.34E-03
TK1	1554408_a_at	BC007986	NM_003258	7083	0.71	4.05E-03
BE503981	229593_at	BE503981	---	---	0.71	2.45E-05
MARS	201475_x_at	NM_004990	NM_004990	4141	0.71	6.05E-03
IDH3B	210014_x_at	AF023266	NM_006899 NM_174855 NM_174856	3420	0.71	6.81E-03
ETV1	217061_s_at	AC004857	NM_004956	2115	0.71	4.82E-03
AI829569	236671_at	AI829569	---	---	0.71	5.08E-04
MCM4	212141_at	AA604621	NM_005914 NM_182746	4173	0.71	2.19E-03
HRPT2	215398_at	AF038194	NM_024529	79577	0.70	2.72E-03
SFRS14	212001_at	AV738039	NM_014884	10147	0.70	1.89E-04
GEMIN4	217099_s_at	AF258545	NM_015721	50628	0.70	2.89E-03

RRAGD	221524_s_at	AF272036	NM_021244	58528	0.70	4.52E-03
PSAT1	220892_s_at	NM_021154	NM_021154	29968	0.70	4.14E-03
			NM_058179			
NSUN5	213670_x_at	AI768378	NM_018044	155400	0.70	3.58E-05
WBSCR20B			NM_032158	260294		
WBSCR20C			NM_145645	55695		
			NM_148936			
			NM_148956			
			NM_148980			
			NM_149379			
KIAA0286	212621_at	AB006624	NM_015257	23306	0.70	5.42E-03
AFG3L1	236250_at	AI859065	NM_001132	172	0.70	4.29E-03
MAD2L2	223234_at	AF080398	NM_006341	10459	0.70	6.48E-03
BF062155	238279_x_at	BF062155	---	---	0.70	1.33E-03
PSMD7	238738_at	AW361702	NM_002811	5713	0.70	1.94E-03
TUBG1	201714_at	NM_001070	NM_001070	7283	0.69	9.09E-03
CSTF1	202190_at	NM_001324	NM_001324	1477	0.69	3.88E-03
T71269	234033_at	T71269	---	---	0.69	3.53E-03
CROP	241792_x_at	N36160	NM_006107	51747	0.69	2.36E-03
			NM_016424			
SLIT3	203813_s_at	NM_003062	NM_003062	6586	0.69	8.85E-03
AI857788	227126_at	AI857788	---	---	0.69	3.64E-04
FLJ12700	219627_at	NM_024910	NM_024910	79970	0.69	5.30E-04
FLJ40432	228810_at	AW135279	NM_152523	151195	0.69	9.81E-04
DGCR8	219811_at	NM_022720	NM_022720	54487	0.69	3.02E-03
SHMT1	209980_s_at	L23928	NM_004169	6470	0.68	2.17E-03
			NM_148918			
UPF3A	217596_at	AA649851	NM_023011	65110	0.68	3.51E-03
			NM_080687			
PPT2	209826_at	AF020544	NM_005155	9374	0.68	3.49E-04
			NM_138717			
			NM_138934			
THOC4	226320_at	AF047002	NM_005782	10189	0.68	4.54E-03
NDUFA5	215850_s_at	AK022209	NM_005000	4698	0.68	8.18E-03
DTYMK	203270_at	NM_012145	NM_012145	1841	0.68	7.28E-03
FLJ10199	218815_s_at	NM_018022	NM_018022	55092	0.68	3.91E-03
CRSP6	232483_at	AK022156	NM_004268	9440	0.68	5.79E-04
PTPRF	215066_at	AU158443	NM_002840	5792	0.68	3.31E-03
			NM_130440			
ADD1	214736_s_at	BE898639	NM_001119	118	0.68	1.78E-03
			NM_014189			
			NM_014190			
			NM_176801			
C9orf88	223019_at	BC001979	NM_022833	64855	0.68	9.03E-04
FLJ34443	241408_at	AA531337	NM_175918	285464	0.68	9.11E-03
TK2	208246_x_at	NM_017618	NM_004614	7084	0.67	5.00E-03
C10orf79	243896_at	AI809779	NM_025145	80217	0.67	4.78E-03
SRGAP2	1556202_at	AI263819	XM_059095	23380	0.67	9.56E-03
PANK2	218809_at	NM_024960	NM_024960	80025	0.67	2.17E-06
			NM_153637			
			NM_153638			
			NM_153639			
			NM_153640			
			NM_153641			
HOXD4	205522_at	NM_014621	NM_014621	3233	0.67	5.20E-03
NES	218678_at	NM_024609	NM_006617	10763	0.67	1.78E-03
MICAL3	229474_at	BF055090	XM_032996	57553	0.67	3.47E-03
			XM_032997			

TCF7L2	212762_s_at	AI375916	NM_030756	6934	0.67	3.83E-03
TPD52L2	201379_s_at	NM_003288	NM_003288 NM_199359 NM_199360 NM_199361 NM_199362 NM_199363	7165	0.66	4.00E-03
PVRL3	213325_at	AA129716	NM_015480	25945	0.66	2.59E-04
ASAHL	227135_at	AI436803	NM_014435	27163	0.66	2.36E-03
AI197932	229498_at	AI197932	---	---	0.66	6.38E-03
KIAA0931	213407_at	AB023148	NM_015020	23035	0.66	4.47E-03
AK057923	1556364_at	AK057923	XM_498935	440960	0.66	9.42E-03
ADRBK2	204183_s_at	AI478542	NM_005160	157	0.66	2.10E-04
SNX5	223666_at	BC002724	NM_014426 NM_152227	27131	0.66	5.32E-03
WBSCR23	221176_x_at	NM_025042	NM_025042	80112	0.66	5.53E-06
AK024901	234326_at	AK024901	---	---	0.65	1.50E-04
ZNF500	41113_at	AI871396	NM_021646	26048	0.65	1.77E-03
DMN	212730_at	AK026420	NM_015286 NM_145728	23336	0.65	3.64E-03
ANKH	239449_at	AV693734	NM_054027	56172	0.65	2.03E-03
C14orf120	216263_s_at	AK022215	XM_033371	25983	0.65	1.76E-03
ZNF291	215848_at	AW139369	NM_020843	49855	0.65	3.43E-03
RFC1	209085_x_at	L14922	NM_002913	5981	0.65	2.64E-04
SLIT2	209897_s_at	AF055585	NM_004787	9353	0.65	2.23E-03
LOC134147	234981_x_at	BE537881	NM_138809	134147	0.65	2.57E-03
GPR51	209991_x_at	AF069755	NM_005458	9568	0.65	6.51E-04
AL037473	1557780_at	AL037473	---	---	0.64	9.19E-03
C14orf111	215567_at	AU144919	NM_015962	51077	0.64	2.31E-03
CBX5	241875_at	AA204654	NM_012117	23468	0.64	8.07E-04
UCKL1	218533_s_at	NM_017859	NM_017859	54963	0.64	7.28E-03
BG231554	243179_at	BG231554	---	---	0.64	5.62E-04
PLK4	204887_s_at	NM_014264	NM_014264	10733	0.64	7.56E-04
OGG1	205760_s_at	NM_016821	NM_002542 NM_016819 NM_016820 NM_016821 NM_016826 NM_016827 NM_016828 NM_016829	4968	0.64	4.62E-04
PAICS	201014_s_at	NM_006452	NM_006452	10606	0.64	8.63E-05
RNF150	227657_at	AA722069	NM_020724	57484	0.64	2.38E-03
ETV1	217053_x_at	X87175	NM_004956	2115	0.64	6.17E-03
HRB2	232441_at	AU147079	NM_007043	11103	0.64	8.66E-03
CTNNBL1	221021_s_at	NM_030877	NM_030877	56259	0.64	2.56E-04
FLJ33915	229892_at	AW628843	NM_182613	347918	0.64	7.04E-03
TORC3	232879_at	AK024981	NM_022769	64784	0.64	5.57E-03
IPW	213447_at	AI672541	---	3653	0.64	3.46E-03
ZNF337	214760_at	AL049942	NM_015655	26152	0.64	6.30E-03
SNTA1	203516_at	NM_003098	NM_003098	6640	0.64	5.62E-03
STX1A	204729_s_at	NM_004603	NM_004603	6804	0.64	4.16E-04
RAN	200750_s_at	AF054183	NM_006325	5901	0.64	4.86E-04
FLJ11029	232215_x_at	AK000296	NM_018304	55771	0.63	8.93E-04
H2AFX	205436_s_at	NM_002105	NM_002105	3014	0.63	1.85E-03
LOC338799	1556042_s_at	BI912454	---	338799	0.63	2.22E-03
BC022346	1570210_x_at	BC022346	---	---	0.63	5.53E-03
C10orf58	224435_at	BC005871	NM_032333	84293	0.63	3.19E-06

LOC338799	226369_at	AW138760	---	338799	0.62	4.89E-03
C9orf81	1557985_s_at	AA248753	XM_095991	84131	0.62	4.31E-03
AK023870	233427_x_at	AK023870	---	---	0.62	7.36E-04
FLJ10504	218296_x_at	NM_018116	NM_018116	55154	0.62	1.11E-03
LOC155435	225839_at	AW290882	NM_001008408	155435	0.62	7.67E-03
GNG12	212294_at	BG111761	NM_018841	55970	0.62	4.81E-04
FLJ23342	236059_at	AW168168	NM_024631	79684	0.62	8.20E-03
LMO7	233646_at	AK027238	NM_005358	4008	0.62	7.32E-03
PHF20L1	222133_s_at	AK022280	NM_016018	51105	0.62	1.32E-03
			NM_024878			
			NM_032205			
			NM_198513			
C14orf143	214264_s_at	AI656610	NM_145231	90141	0.62	5.71E-03
LOC157627	1556046_a_at	AL832535	---	157627	0.62	4.24E-03
MAP3K13	206249_at	NM_004721	NM_004721	9175	0.62	4.38E-03
VGF	205586_x_at	NM_003378	NM_003378	7425	0.62	1.70E-03
BLCAP	201032_at	NM_006698	NM_006698	10904	0.62	1.91E-04
POLE2	205909_at	NM_002692	NM_002692	5427	0.62	9.76E-03
ZGPAT	221848_at	AL121845	NM_032527	84619	0.61	1.83E-03
			NM_181484			
			NM_181485			
STN2	227461_at	AA632295	NM_033104	85439	0.61	5.56E-03
SFRS11	213742_at	AW241752	NM_004768	9295	0.61	8.24E-03
GPR51	209990_s_at	AF056085	NM_005458	9568	0.61	8.69E-04
TGDS	237346_at	AA976208	NM_014305	23483	0.61	2.60E-03
PANK2	235130_at	AV703394	NM_024960	80025	0.61	2.05E-03
			NM_153637			
			NM_153638			
			NM_153639			
			NM_153640			
			NM_153641			
BAX	208478_s_at	NM_004324	NM_004324	581	0.61	2.28E-03
			NM_138761			
			NM_138762			
			NM_138763			
			NM_138764			
			NM_138765			
RNF10	207801_s_at	NM_014868	NM_014868	9921	0.61	9.50E-03
SPAG5	203145_at	NM_006461	NM_006461	10615	0.61	3.43E-03
TOP3A	204946_s_at	NM_004618	NM_004618	7156	0.61	4.78E-04
REC14	215156_at	AL109709	NM_025234	80349	0.61	9.61E-04
MGC4308	220612_at	NM_014135	NM_032359	84319	0.61	7.73E-03
AI144156	238670_at	AI144156	---	---	0.61	2.33E-03
TBPIP	205956_x_at	NM_013290	NM_013290	29893	0.61	9.34E-05
			NM_016556			
AW517479	242608_x_at	AW517479	---	---	0.60	4.70E-03
DXS9879E	219061_s_at	NM_006014	NM_006014	8270	0.60	7.83E-03
384D8-2	205086_s_at	NM_014551	NM_014551	29781	0.60	3.91E-03
			NM_152299			
)KFZP564K196	223170_at	AF132000	NM_015544	26022	0.60	2.90E-03
SOX2	213722_at	AW007161	NM_003106	6657	0.60	2.03E-03
CGI-96	33307_at	AL022316	NM_015703	27341	0.60	7.39E-03
BE464132	236841_at	BE464132	XM_496585	440897	0.60	1.92E-03
AK025048	1565705_x_at	AK025048	---	---	0.60	7.42E-03
HEXA	215155_at	J04178	NM_000520	3073	0.60	8.59E-03
NY-REN-41	226287_at	AI458313	NM_080654	91057	0.60	6.85E-03
AK023354	222252_x_at	AK023354	---	---	0.60	7.20E-03
KIAA0582	1559159_at	AK094069	NM_015147	23177	0.59	2.73E-03

PDE8A	212521_s_at	BE568219	NM_002605 NM_173454 NM_173455 NM_173456 NM_173457	5151	0.59	7.81E-03
BE671060	235901_at	BE671060	---	---	0.59	7.80E-03
KIAA1423	225127_at	BF217531	XM_376550	57583	0.59	2.86E-03
DDX54	219111_s_at	NM_024072	NM_024072	79039	0.59	5.24E-03
ADCYAP1	230237_at	BE220888	NM_001117	116	0.59	4.24E-03
CDKN1A	202284_s_at	NM_000389	NM_000389 NM_078467	1026	0.59	1.54E-03
PWP1	201606_s_at	BE796924	NM_007062	11137	0.59	3.48E-04
ZNF505	215758_x_at	AC007204	NM_00100412 6 NM_031218	81931	0.59	1.44E-03
FLJ00312	221971_x_at	BE672818	XM_374801	399761	0.59	7.23E-03
IGBP1	242337_at	AI347128	NM_001551	3476	0.59	9.36E-03
ANKRD11	219437_s_at	NM_013275	NM_013275	29123	0.59	5.45E-03
TRAF4	202871_at	NM_004295	NM_004295 NM_145751	9618	0.59	3.31E-03
FLJ10404	218920_at	NM_019057	NM_019057	54540	0.59	1.51E-03
SS18L1	213140_s_at	AB014593	NM_015558 NM_198935	26039	0.59	7.09E-05
C20orf161	236514_at	AI885067	NM_033421 NM_152897	90203	0.58	6.89E-03
CTNNB1	223679_at	AF130085	NM_001904	1499	0.58	7.83E-04
NSFL1C	220248_x_at	NM_018839	NM_016143 NM_018839 NM_182483	55968	0.58	4.26E-03
MGC15606	215968_at	AF055018	NM_145037	91775	0.58	2.12E-03
VTN	204534_at	NM_000638	NM_000638	7448	0.58	1.72E-03
SNX5	217792_at	NM_014426	NM_014426 NM_152227	27131	0.58	4.70E-03
LOC157627	214839_at	AF052108	---	157627	0.58	4.90E-03
NSFL1C	232520_s_at	AK023585	NM_016143 NM_018839 NM_182483	55968	0.58	7.68E-03
E2IG5	223193_x_at	AF201944	NM_014367	26355	0.58	3.89E-04
ANKFY1	224900_at	AK025960	NM_016376 NM_020740	51479	0.58	6.56E-03
HNRPA3	211931_s_at	BG505670	NM_194247	220988	0.58	1.97E-03
COH1	1553852_at	NM_152564	NM_015243 NM_017890 NM_152564 NM_181661 NM_184042	157680	0.58	8.57E-03
ZNF305	240181_at	AI939511	NM_014724	9753	0.58	6.71E-03
RFC5	203209_at	BC001866	NM_007370 NM_181578	5985	0.58	7.00E-03

Table 10. Decreased Gene Expression in Cell Lines H1 and BB10 vs. SiMa Cell Line in Undifferentiated State Using Microarray Analysis

Gene Symbol	Probe Set ID	Representative Public ID	RefSeq Transcript ID	Entrez Gene ID	Log2 Ratio	pvalue
HSPA1A	200799_at	NM_005345	NM_005345	3303	-6.50	8.44E-07
CYTL1	219837_s_at	NM_018659	NM_018659	54360	-5.69	4.29E-10
CYGB	226632_at	AL513673	NM_134268	114757	-5.62	1.77E-03
SYT13	226086_at	AB037848	NM_020826	57586	-5.23	2.54E-09
H39185	240433_x_at	H39185	---	---	-5.19	1.50E-07
AV724769	235118_at	AV724769	---	---	-5.15	5.31E-08
AW188087	226809_at	AW188087	---	---	-5.07	1.50E-07
IGFBP7	201162_at	NM_001553	NM_001553	3490	-4.97	1.64E-07
MEOX2	206201_s_at	NM_005924	NM_005924	4223	-4.95	5.73E-08
NNAT	204239_s_at	NM_005386	NM_005386 NM_181689	4826	-4.84	3.41E-07
CYGB	1553572_a_at	NM_134268	NM_134268	114757	-4.74	1.06E-03
IGSF4D	1552754_a_at	AA640422	NM_153184	253559	-4.44	9.24E-10
IGFBP7	201163_s_at	NM_001553	NM_001553	3490	-4.43	2.10E-04
CAP2	212554_at	N90755	NM_006366	10486	-4.40	7.38E-04
AF150317	243111_at	AF150317	---	---	-4.32	6.95E-07
FGF1	1552721_a_at	NM_033136	NM_000800 NM_033136 NM_033137	2246	-4.30	3.01E-04
LMCD1	218574_s_at	NM_014583	NM_014583	29995	-4.23	1.05E-04
TNFRSF10D	227345_at	AI738556	NM_003840	8793	-4.09	1.08E-04
IGFBP5	211959_at	AW007532	NM_000599	3488	-4.02	3.56E-04
CART	206339_at	NM_004291	NM_004291	9607	-4.01	4.51E-06
ASAM	226834_at	BG112263	NM_024769	79827	-3.99	9.02E-04
AI093492	237435_at	AI093492	---	---	-3.95	2.11E-04
FUCA2	223120_at	BC003060	NM_032020	2519	-3.94	2.55E-03
PAPPA	224942_at	BG434272	NM_002581	5069	-3.81	5.43E-06
PRAME	204086_at	NM_006115	NM_006115 NM_206953 NM_206954 NM_206955 NM_206956	23532	-3.67	4.15E-07
DHRS3	202481_at	NM_004753	NM_004753	9249	-3.66	8.82E-07
TRHDE	219937_at	NM_013381	NM_013381	29953	-3.59	4.97E-05
C9orf94	229585_at	AI803088	NM_152702	206938	-3.59	2.72E-04
DSCAM	237268_at	BE503065	NM_001389 NM_206887	1826	-3.57	1.08E-07
FGF13	205110_s_at	NM_004114	NM_004114 NM_033642	2258	-3.51	5.78E-05
FGF1	205117_at	X59065	NM_000800 NM_033136 NM_033137	2246	-3.50	1.90E-03
PTN	211737_x_at	BC005916	NM_002825	5764	-3.44	5.00E-04
GNAS	217057_s_at	AF107846	NM_000516 NM_016592 NM_080425 NM_080426	2778	-3.42	1.41E-03
FLJ45880	228538_at	BE671164	NM_207404	389114	-3.42	1.47E-04
ADAMTS3	214913_at	AB002364	NM_014243	9508	-3.41	2.23E-04
CYP2E1	1431_at	J02843	NM_000773	1571	-3.38	7.97E-04
AL353759	215071_s_at	AL353759	---	---	-3.37	9.25E-05
PAPPA	224940_s_at	BF107618	NM_002581	5069	-3.36	7.36E-06

BF941609	240218_at	BF941609	---	---	-3.35	3.21E-05
FGF1	208240_s_at	NM_013394	NM_000800 NM_033136 NM_033137	2246	-3.35	4.91E-04
TCEAL2	211276_at	AF063606	NM_080390	140597	-3.35	4.16E-05
TncRNA	224565_at	BE675516	---	283131	-3.34	1.99E-04
IGSF4D	1555544_a_at	AF538973	NM_153184	253559	-3.30	7.37E-07
MGC45474	228221_at	AA809640	NM_152369	126969	-3.27	7.37E-04
KIAA1598	221802_s_at	AU157109	NM_018330	57698	-3.25	5.86E-06
FGL1	205305_at	NM_004467	NM_004467 NM_147203 NM_201552 NM_201553	2267	-3.25	2.90E-06
AU157716	227051_at	AU157716	---	---	-3.23	7.84E-06
TMIE	1553601_a_at	NM_147196	NM_147196	259236	-3.22	3.71E-05
IGSF4D	1552752_a_at	NM_153184	NM_153184	253559	-3.21	2.78E-04
PAPPA	224941_at	BF107618	NM_002581	5069	-3.15	3.66E-05
CFC1	223753_s_at	AF312769	NM_032545	55997	-3.15	1.39E-05
PAPPA	228128_x_at	AI110886	NM_002581	5069	-3.07	9.98E-07
AA452540	232411_at	AA452540	---	---	-3.05	1.28E-04
AW003173	230746_s_at	AW003173	---	---	-3.03	3.62E-03
PAPPA	201981_at	AA148534	NM_002581	5069	-3.03	2.64E-07
BF432956	229057_at	BF432956	---	---	-3.01	5.34E-06
IL7	206693_at	NM_000880	NM_000880	3574	-3.01	6.79E-05
N92599	241421_at	N92599	---	---	-3.01	2.03E-05
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N95363	213183_s_at	N95363	---	---	-2.94	7.60E-03
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LOC56901	218484_at	NM_020142	NM_020142	56901	-2.88	8.77E-04
BACE2	217867_x_at	NM_012105	NM_012105 NM_138991 NM_138992	25825	-2.87	7.40E-04
BF110050	241100_at	BF110050	---	---	-2.81	1.52E-03
AU144437	232887_at	AU144437	---	---	-2.81	4.16E-03
GABRA5	206456_at	NM_000810	NM_000810	2558	-2.79	1.41E-03
SYNPR	230303_at	H11380	NM_144642	132204	-2.77	1.02E-03
CYP2E1	209975_at	AF182276	NM_000773	1571	-2.76	3.21E-03
GAL	214240_at	AL556409	NM_015973	51083	-2.75	1.20E-03
LOC51315	222585_x_at	BE326678	NM_016618	51315	-2.72	1.70E-05
CDH12	207149_at	L33477	NM_004061	1010	-2.72	1.51E-05
N39597	1555993_at	N39597	---	---	-2.70	1.39E-03
SYNPO2	227662_at	AA541622	NM_133477	171024	-2.69	4.62E-05
NPY	206001_at	NM_000905	NM_000905	4852	-2.68	9.89E-05
FGF19	223761_at	AF110400	NM_005117	9965	-2.65	8.85E-06
SLC35F3	229065_at	BF968270	NM_173508	148641	-2.64	8.85E-06
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PTPRR	206084_at	NM_002849	NM_002849 NM_130846	5801	-2.54	2.83E-04
BACE2	222446_s_at	AF178532	NM_012105 NM_138991 NM_138992	25825	-2.54	8.21E-05
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AA243659	209683_at	AA243659	---	---	-2.44	6.66E-07
LOC51315	233329_s_at	AK025986	NM_016618	51315	-2.44	4.58E-05
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AV719355	217554_at	AV719355	---	---	-2.36	2.61E-03
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HHLA3	220387_s_at	NM_007071	NM_007071	11147	-2.36	2.06E-03
SMARCA2	206542_s_at	AV725365	NM_003070 NM_139045	6595	-2.35	7.68E-04
CNGA3	207261_at	NM_001298	NM_001298	1261	-2.32	3.40E-05
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LOC339290	217506_at	H49382	XM_375527	339290	-2.30	8.85E-05
HTATIP2	209448_at	BC002439	NM_006410	10553	-2.30	6.50E-03
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LOC51315	218303_x_at	NM_016618	NM_016618	51315	-2.30	8.49E-07
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GAL	207466_at	NM_015973	NM_015973	51083	-2.25	6.61E-13
PTGER2	206631_at	NM_000956	NM_000956	5732	-2.25	2.22E-05
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TICAM2	228234_at	AI423165	NM_021649	353376	-2.22	4.67E-04
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IRS1	204686_at	NM_005544	NM_005544	3667	-2.22	2.74E-03
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AF085995	1561759_at	AF085995	---	---	-2.21	9.13E-03
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BF432875	235782_at	BF432875	XM_497668	388620	-2.20	1.92E-05
GPX7	213170_at	AA406605	NM_015696	2882	-2.19	2.99E-04
NLF1	241031_at	BE218239	NM_207322	145741	-2.18	8.81E-05
BE674309	230913_at	BE674309	---	---	-2.18	1.83E-04

CAP2	212551_at	NM_006366	NM_006366	10486	-2.17	5.50E-04
PRO1580	213550_s_at	AA993683	NM_018502	55374	-2.17	4.95E-03
CYB5R2	220230_s_at	NM_016229	NM_00100133 6 NM_016229	51700	-2.15	7.15E-04
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RAC2	207419_s_at	NM_002872	NM_002872	5880	-2.14	2.67E-03
LOC153682	232794_at	AL137383	---	153682	-2.13	5.45E-03
GRIA2	236538_at	BE219628	NM_000826	2891	-2.13	1.05E-03
IL20RA	219115_s_at	NM_014432	NM_014432	53832	-2.12	6.78E-03
SCN5A	207413_s_at	NM_000335	NM_000335	6331	-2.12	2.22E-04
TSAP6	218424_s_at	NM_018234	NM_198056 NM_00100841 0 NM_018234 NM_182915	55240	-2.12	1.68E-04
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SYNPO2	225720_at	AW009747	NM_133477	171024	-2.09	6.04E-03
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AI222435	230319_at	AI222435	---	---	-2.09	7.23E-05
MGC15668	229332_at	AI653050	NM_032756	84842	-2.08	1.02E-03
SCAP1	1560861_at	BG210619	NM_003726	8631	-2.08	5.32E-04
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SCN3A	210432_s_at	AF225986	NM_006922	6328	-2.07	3.67E-03
ADARB1	203865_s_at	NM_015833	NM_001112 NM_015833 NM_015834	104	-2.07	4.67E-06
AB051467	232738_at	AB051467	---	---	-2.06	1.71E-05
CREB5	205931_s_at	NM_004904	NM_004904 NM_182898 NM_182899	9586	-2.06	8.68E-04
ECHDC3	219298_at	NM_024693	NM_024693	79746	-2.05	6.42E-03
CRYGD	207532_at	NM_006891	NM_006891	1421	-2.05	2.10E-03
ICAM2	213620_s_at	AA126728	NM_000873	3384	-2.05	3.74E-04
CIP29	217498_at	BG389073	NM_033082	84324	-2.04	3.37E-04
AA700440	228329_at	AA700440	---	---	-2.04	4.62E-07
ATRNL1	213745_at	AW151108	NM_207303	26033	-2.04	9.28E-06
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RGAG4	227823_at	BE348679	XM_291322	340526	-2.03	2.13E-04
AW136654	240802_at	AW136654	---	---	-2.02	2.07E-03
MTL5	219786_at	NM_004923	NM_004923	9633	-2.02	3.30E-04
FBI4	1562953_s_at	BC019264	NM_205857	404201	-2.02	4.82E-03
ZNF91	238466_at	R43486	NM_003430	7644	-2.01	8.53E-04
LOC441168	229390_at	AV734646	XM_496823	441168	-2.01	1.83E-04
BF343672	227925_at	BF343672	XM_378321	399972	-2.01	1.32E-04
BC014056	1561906_at	BC014056	---	---	-2.01	8.02E-04

FGF18	206987_x_at	NM_003862	NM_003862 NM_033649	8817	-2.01	6.16E-03
CHST7	206756_at	NM_019886	NM_019886	56548	-2.00	1.29E-04
RAC2	213603_s_at	BE138888	NM_002872	5880	-2.00	2.89E-05
MCTP1	235740_at	BG250585	NM_00100279 6 NM_024717	79772	-2.00	2.38E-08
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SYNPO2	225894_at	AL589603	NM_133477	171024	-1.99	3.38E-04
FBI4	238081_at	AI694300	NM_205857	404201	-1.99	1.05E-03
GABRA5	215531_s_at	BF966183	NM_000810	2558	-1.98	6.28E-06
SORCS2	228720_at	AB037750	NM_020777	57537	-1.98	7.96E-05
MRAS	225185_at	BF343625	NM_012219	22808	-1.97	6.31E-04
BE962770	229032_at	BE962770	---	---	-1.97	6.94E-03
ATP2B3	242036_x_at	H09073	NM_00100134 4 NM_021949	492	-1.96	1.23E-03
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AA976778	230679_at	AA976778	---	---	-1.95	3.35E-04
LOC285878	1560692_at	BC037834	---	285878	-1.94	3.90E-04
BF114967	231067_s_at	BF114967	---	---	-1.93	1.31E-04
C10orf59	223824_at	BC005364	NM_018363	55328	-1.93	8.06E-03
ASAM	228082_at	BF056275	NM_024769	79827	-1.93	2.50E-04
OXTR	206825_at	NM_000916	NM_000916	5021	-1.93	2.27E-04
CNNM1	220166_at	NM_020348	NM_020348	26507	-1.92	1.23E-04
PLCD4	224505_s_at	BC006355	NM_032726	84812	-1.92	2.15E-05
NEFH	33767_at	X15306	NM_021076	4744	-1.92	2.20E-03
LOC339290	228160_at	AI433706	XM_375527	339290	-1.92	5.10E-03
EDG7	231192_at	AW274018	NM_012152	23566	-1.91	7.48E-04
BF002625	229530_at	BF002625	---	---	-1.90	4.09E-04
COL13A1	211343_s_at	M33653	NM_005203 NM_080798 NM_080799 NM_080800 NM_080801 NM_080802 NM_080803 NM_080804 NM_080805 NM_080806 NM_080807 NM_080808 NM_080809 NM_080810 NM_080811 NM_080812 NM_080813 NM_080814 NM_080815	1305	-1.90	5.01E-06
AI015847	1568838_at	AI015847	---	---	-1.90	6.44E-04
AA705933	239866_at	AA705933	---	---	-1.89	7.57E-04
NDFIP2	1568807_a_at	AI301081	NM_019080	54602	-1.89	6.50E-05
PRKACB	202742_s_at	NM_002731	NM_002731 NM_182948 NM_207578	5567	-1.88	2.83E-04
FLJ20449	1570153_at	BC013944	NM_017826	54937	-1.88	1.81E-03
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PRSS11	201185_at	NM_002775	NM_002775	5654	-1.87	2.45E-04

EBF	229487_at	W73890	NM_024007	1879	-1.86	2.25E-05
SLC16A14	238029_s_at	R15072	NM_152527	151473	-1.86	2.63E-05
LEPR	211356_x_at	U66495	NM_001003679 NM_001003680 NM_002303	3953	-1.86	9.14E-08
LOC339290	215283_at	U79248	XM_375527	339290	-1.85	3.14E-04
BE672499	230962_at	BE672499	---	---	-1.85	3.97E-04
AI435590	237193_s_at	AI435590	---	---	-1.84	4.11E-05
C10orf10	209183_s_at	AL136653	NM_007021	11067	-1.84	9.62E-05
ARTS-1	214012_at	BE551138	NM_016442	51752	-1.84	7.70E-04
M160	223655_at	AF264014	NM_174941	283316	-1.83	4.27E-03
AI803010	239503_at	AI803010	---	---	-1.83	6.21E-03
GLI2	228537_at	AI797248	NM_005270 NM_030379 NM_030380 NM_030381	2736	-1.83	6.30E-04
AI935541	236220_at	AI935541	---	---	-1.83	8.96E-04
HEBP2	203430_at	NM_014320	NM_014320	23593	-1.82	6.64E-03
)KFZp313N062	226688_at	AW003508	NM_173826	285343	-1.82	8.96E-06
EBF	232204_at	AF208502	NM_024007	1879	-1.81	6.25E-06
NT5E	203939_at	NM_002526	NM_002526	4907	-1.81	2.34E-05
D4S234E	209570_s_at	BC001745	NM_014392	27065	-1.80	1.14E-04
LOC133308	229491_at	BF433180	NM_178833	133308	-1.79	1.59E-03
BHLHB2	201170_s_at	NM_003670	NM_003670	8553	-1.79	7.17E-03
AI768374	228661_s_at	AI768374	---	---	-1.79	9.50E-04
AL355688	232081_at	AL355688	---	---	-1.79	5.36E-03
RPL39L	210115_at	L05096	NM_052969	116832	-1.79	6.47E-03
BCL2	203685_at	NM_000633	NM_000633 NM_000657	596	-1.78	4.07E-05
LRBA	214109_at	AI659561	NM_006726	987	-1.78	1.89E-03
C9orf150	227443_at	AI972386	NM_203403	286343	-1.78	2.50E-04
KCNAB1	210078_s_at	L39833	NM_003471 NM_172159 NM_172160	7881	-1.78	2.11E-03
PCDHB16	232099_at	AB046841	NM_020957	57717	-1.77	1.97E-03
SYNPO2	225895_at	AI634580	NM_133477	171024	-1.77	6.20E-04
AK000776	232060_at	AK000776	---	---	-1.75	1.44E-04
COL6A1	213428_s_at	AA292373	NM_001848	1291	-1.75	5.72E-04
LEPR	211355_x_at	U52914	NM_001003679 NM_001003680 NM_002303	3953	-1.74	2.06E-06
PABPC5	233136_at	AL122118	NM_080832	140886	-1.74	7.51E-04
PROM1	204304_s_at	NM_006017	NM_006017	8842	-1.74	6.03E-04
AGPAT3	223182_s_at	AI337300	NM_020132	56894	-1.73	3.62E-04
ANK3	209442_x_at	AL136710	NM_001149 NM_020987	288	-1.73	1.10E-03
CACNA1D	210108_at	BE550599	NM_000720	776	-1.72	3.20E-04
H2AFJ	220936_s_at	NM_018267	NM_018267 NM_177925	55766	-1.71	9.12E-04
LOC285878	230117_at	AI420977	---	285878	-1.71	1.65E-04
MGC70870	244125_at	AA837131	NM_203481	403340	-1.70	1.71E-03
LDB2	206481_s_at	NM_001290	NM_001290	9079	-1.70	9.86E-03
AI004009	222288_at	AI004009	XM_371647	389129	-1.70	6.64E-04

OPRM1	207989_at	NM_000914	NM_000914 NM_001008503 NM_001008504 NM_001008505	4988	-1.69	1.26E-05
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FGD5	226985_at	AW269340	NM_152536	152273	-1.68	4.08E-06
EBF	227646_at	BG435302	NM_024007	1879	-1.68	1.59E-04
KIAA0500	213839_at	AW028110	---	57237	-1.68	4.44E-03
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ARSD	223696_at	BC003660	NM_001669 NM_009589	414	-1.66	9.99E-03
C9orf94	239909_at	AI937348	NM_152702	206938	-1.66	7.20E-03
C6orf155	226810_at	BE500942	NM_024882	79940	-1.65	2.05E-03
LOC151194	1553743_at	NM_145280	NM_145280	151194	-1.65	6.80E-03
SYNPO2	225721_at	AI658662	NM_133477	171024	-1.64	9.76E-03
AL037414	230055_at	AL037414	---	---	-1.64	3.29E-04
AW572379	229569_at	AW572379	---	---	-1.63	2.80E-04
FRMD4B	213056_at	AU145019	XM_114303	23150	-1.63	2.55E-03
D4S234E	213533_at	M98528	NM_014392	27065	-1.63	1.82E-06
PTP4A3	209695_at	BC003105	NM_007079 NM_032611	11156	-1.62	4.14E-06
ACYP2	206833_s_at	NM_001108	NM_138448	98	-1.62	7.71E-04
MCTP1	220122_at	NM_024717	NM_001002796 NM_024717	79772	-1.62	6.95E-05
ALDH1A2	207016_s_at	AB015228	NM_003888 NM_170696 NM_170697	8854	-1.61	4.22E-04
CD302	203799_at	NM_014880	NM_014880	9936	-1.61	1.17E-05
F10269	1557746_at	F10269	---	---	-1.61	1.03E-03
FLJ20152	218532_s_at	NM_019000	NM_019000	54463	-1.61	2.67E-03
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PRKACB	202741_at	AA130247	NM_002731 NM_182948 NM_207578	5567	-1.59	1.12E-03
PDE4DIP	213388_at	H15535	NM_001002810 NM_001002811 NM_001002812 NM_014644 NM_022359	9659	-1.59	6.05E-04
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ST18	206135_at	NM_014682	NM_014682	9705	-1.58	4.56E-07
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SIX2	206510_at	AF332197	NM_016932	10736	-1.56	2.79E-05
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PCTK3	214797_s_at	BC000281	NM_002596 NM_212502 NM_212503	5129	-1.56	8.81E-03
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NEFH	204412_s_at	NM_021076	NM_021076	4744	-1.55	3.87E-03
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LOC285878	236308_at	D60436	---	285878	-1.53	2.60E-04
LRRN6A	227933_at	AI193252	NM_032808	84894	-1.53	5.09E-06
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EYA1	214608_s_at	AJ000098	NM_000503 NM_172058 NM_172059 NM_172060	2138	-1.53	5.85E-05
AI263044	214376_at	AI263044	---	---	-1.53	1.69E-04
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BF114745	235459_at	BF114745	---	---	-1.50	2.88E-03
TNFSF4	207426_s_at	NM_003326	NM_003326	7292	-1.49	1.01E-03
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TOX	204530_s_at	NM_014729	NM_014729	9760	-1.48	2.48E-03
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D4S234E	209569_x_at	NM_014392	NM_014392	27065	-1.47	3.74E-05
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LOC148418	229402_at	AI631824	NM_001010971	148418	-1.46	5.19E-04
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AI028528	241804_at	AI028528	---	---	-1.43	8.22E-04
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DMD	203881_s_at	NM_004010	NM_000109 NM_004006 NM_004007 NM_004009 NM_004010 NM_004011 NM_004012 NM_004013 NM_004014 NM_004015 NM_004016 NM_004017 NM_004018 NM_004019 NM_004020 NM_004021 NM_004022 NM_004023	1756	-1.43	1.85E-03
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C21orf86	228908_s_at	AW131553	NM_153454	257103	-1.42	1.26E-03
MYT1L	210016_at	BF223003	NM_015025	23040	-1.42	2.69E-04
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CAMK2B	209956_s_at	U23460	NM_001220 NM_172078 NM_172079 NM_172080 NM_172081 NM_172082 NM_172083 NM_172084	816	-1.42	1.44E-03
ST6GALNAC5	220979_s_at	NM_030965	NM_030965	81849	-1.41	5.22E-04
AI341823	239657_x_at	AI341823	---	---	-1.41	2.83E-03
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AW450420	236373_at	AW450420	---	---	-1.41	5.40E-03
PH-4	222125_s_at	BC000580	NM_017732 NM_177938 NM_177939	54681	-1.41	2.61E-03

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AI912571	228333_at	AI912571	---	---	-1.40	5.33E-03
BF059209	240214_at	BF059209	---	---	-1.40	2.18E-03
ARSD	232423_at	AU144083	NM_001669 NM_009589	414	-1.39	1.43E-03
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UNC5A	236448_at	R37358	XM_030300	90249	-1.38	1.31E-05
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LOC222070	51774_s_at	AW014299	---	222070	-1.38	4.64E-03
C6orf199	1552299_at	NM_145025	NM_145025	221264	-1.38	8.50E-03
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HOXD10	229400_at	AW299531	NM_002148	3236	-1.37	2.17E-03
GLIS3	229435_at	AW025602	NM_152629	169792	-1.37	1.72E-05
NAP1L3	204749_at	NM_004538	NM_004538	4675	-1.37	5.99E-03
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D59759	231560_at	D59759	---	---	-1.37	1.31E-06
ANK2	202920_at	BF726212	NM_001148 NM_020977	287	-1.35	3.09E-05
FLJ30655	236487_at	AW513286	NM_144643	132320	-1.35	3.30E-03
GLIS3	230258_at	AI277316	NM_152629	169792	-1.35	1.33E-03
SH3BGR	204979_s_at	NM_007341	NM_00100171 3 NM_007341	6450	-1.34	1.12E-04
RAI2	219440_at	NM_021785	NM_021785	10742	-1.34	2.50E-04
ATXN1	203232_s_at	NM_000332	NM_000332	6310	-1.34	8.99E-05
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AL117598	231964_at	AL117598	---	---	-1.33	5.64E-06
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N50117	240236_at	N50117	---	---	-1.33	1.78E-03
AK095719	1556696_s_at	AK095719	XM_499008	441094	-1.32	6.81E-03
W80446	231013_at	W80446	---	---	-1.32	9.26E-04
C21orf66	239407_at	AI793248	NM_013329 NM_016631 NM_058191 NM_145328	94104	-1.32	1.06E-03
RASGEF1B	230233_at	BF110534	NM_152545	153020	-1.32	5.98E-03
DCAMKL1	205399_at	NM_004734	NM_004734	9201	-1.32	8.09E-04
SCOTIN	222986_s_at	BC001463	NM_016479	51246	-1.32	7.27E-03
C21orf5	205248_at	NM_005128	NM_005128	9980	-1.32	2.95E-04
HEL308	228736_at	AW084661	NM_133636	113510	-1.32	6.40E-04
HDAC4	228813_at	AW206037	NM_006037	9759	-1.31	4.97E-04

ST7L	1552739_s_at	NM_138729	NM_017744 NM_138727 NM_138728 NM_138729 NM_198327 NM_198328	54879	-1.31	2.31E-03
DACH2	239738_at	AW780006	NM_053281	117154	-1.30	1.49E-03
RAB3-GAP150	243851_at	AI860647	NM_012414	25782	-1.29	9.51E-03
C9orf40	218904_s_at	NM_017998	NM_017998	55071	-1.29	9.53E-03
AK027226	232538_at	AK027226	---	---	-1.29	5.59E-03
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CEBPD	203973_s_at	NM_005195	NM_005195	1052	-1.28	2.94E-03
AA687479	242826_at	AA687479	---	---	-1.28	1.21E-04
SIAT7E	230482_at	AF131837	NM_030965	81849	-1.28	1.28E-03
AI694767	229768_at	AI694767	---	---	-1.28	5.06E-03
FLJ20753	229918_at	AB046860	XM_371082	55036	-1.28	9.34E-04
GUCY1A3	221942_s_at	AI719730	NM_000856	2982	-1.28	2.15E-03
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AI354636	235171_at	AI354636	---	---	-1.27	2.80E-03
STARD13	213103_at	AA128023	NM_052851 NM_178006 NM_178007 NM_178008	90627	-1.27	1.35E-05
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KLF9	203543_s_at	NM_001206	NM_001206	687	-1.27	1.17E-03
RAB6B	221792_at	AW118072	NM_016577	51560	-1.27	2.69E-03
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BBS7	219688_at	NM_018190	NM_018190 NM_176824	55212	-1.27	4.54E-05
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AK021551	232589_at	AK021551	---	---	-1.26	7.56E-05
BE894882	235681_at	BE894882	---	---	-1.26	2.96E-05
TOX	204529_s_at	AI961231	NM_014729	9760	-1.25	8.61E-05
STAR	204548_at	NM_000349	NM_000349 NM_001007243	6770	-1.25	2.94E-05
AL833383	1563776_at	AL833383	---	---	-1.25	1.41E-03
PPP3CA	202429_s_at	AL353950	NM_000944	5530	-1.25	1.86E-05
SUCLG2	215772_x_at	AL050226	NM_003848	8801	-1.25	6.75E-04
RAB26	219562_at	NM_014353	NM_014353	25837	-1.25	6.02E-04
GRIP2	216481_at	AF052177	XM_042936	80852	-1.25	7.55E-03
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PTPRD	214043_at	BF062299	NM_002839 NM_130391 NM_130392 NM_130393	5789	-1.25	5.77E-06
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CXorf32	229234_at	AW007160	NM_001010888	340554	-1.24	3.78E-03
ACAD8	238175_at	AI806909	NM_014384	27034	-1.24	8.68E-03
R71596	229580_at	R71596	---	---	-1.24	6.01E-03
H46176	237083_at	H46176	---	---	-1.24	1.64E-03
HPS3	227139_s_at	AA219354	NM_032383	84343	-1.24	1.38E-04

PTPRD	213362_at	N73931	NM_002839 NM_130391 NM_130392 NM_130393	5789	-1.23	1.49E-04
FLJ23861	230561_s_at	AA252512	NM_152519	151050	-1.23	2.64E-04
CD200	209582_s_at	H23979	NM_001004196 NM_001004197 NM_005944	4345	-1.23	2.09E-03
SDK2	242064_at	N23651	NM_019064	54549	-1.23	5.82E-04
AI051572	243310_at	AI051572	---	---	-1.23	7.64E-03
GFRA3	229936_at	AA694259	NM_001496	2676	-1.22	3.88E-03
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POU6F1	205878_at	NM_002702	NM_002702	5463	-1.22	2.77E-03
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SLC6A15	206376_at	NM_018057	NM_018057 NM_182767	55117	-1.21	3.32E-03
LGALS3BP	200923_at	NM_005567	NM_005567	3959	-1.21	2.42E-05
AI949265	229156_s_at	AI949265	XM_499089	441301	-1.21	9.17E-05
ANXA4	201302_at	NM_001153	NM_001153	307	-1.21	7.33E-03
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PTPRN2	203029_s_at	NM_002847	NM_002847 NM_130842 NM_130843	5799	-1.20	5.18E-04
RFPL1S	214120_at	AW157535	---	10740	-1.20	2.59E-05
IFNAR1	225661_at	AA811138	NM_000629	3454	-1.20	4.10E-04
GLIS1	244128_x_at	AA872588	NM_147193	148979	-1.20	6.88E-03
AGPAT3	223183_at	AI928403	NM_020132	56894	-1.20	5.35E-03
PPEF1	206547_s_at	NM_006240	NM_006240 NM_152223 NM_152224 NM_152225 NM_152226	5475	-1.20	2.16E-03
BCL6B	243825_at	T79768	NM_181844	255877	-1.20	2.18E-03
ABCG1	204567_s_at	NM_004915	NM_004915 NM_016818 NM_207174 NM_207627 NM_207628 NM_207629 NM_207630	9619	-1.19	4.03E-05
DJ462O23.2	225876_at	T84558	NM_020448	57185	-1.19	3.26E-03
CD200	209583_s_at	AF063591	NM_001004196 NM_001004197 NM_005944	4345	-1.19	1.77E-04

C10orf89	230129_at	BF589448	NM_153336	118672	-1.19	2.60E-03
MCPH1	219592_at	NM_024596	NM_024596	79648	-1.19	2.64E-03
LOC285705	226989_at	BE855765	---	285705	-1.19	2.15E-04
MANSC1	220945_x_at	NM_018050	NM_018050	54682	-1.19	1.43E-03
BF057799	236325_at	BF057799	---	---	-1.19	5.51E-03
OIP106	226013_at	AW451452	NM_014965	22906	-1.18	4.67E-03
RPL37	224763_at	BF724210	NM_000997	6167	-1.18	3.75E-03
N30152	229850_at	N30152	---	---	-1.18	6.56E-03
DTX3L	225415_at	AA577672	NM_138287	151636	-1.18	8.51E-04
RAB6B	225259_at	AI805050	NM_016577	51560	-1.18	4.83E-03
ROR1	205805_s_at	NM_005012	NM_005012	4919	-1.18	2.35E-05
DKFZp762K222	226822_at	AL512713	NM_020225	56977	-1.18	8.30E-04
AI631888	235532_at	AI631888	---	---	-1.17	3.83E-08
PDGFRB	202273_at	NM_002609	NM_002609	5159	-1.17	6.86E-03
TLE1	228284_at	BE302305	NM_005077	7088	-1.17	1.65E-03
APG5L	202512_s_at	NM_004849	NM_004849	9474	-1.17	3.29E-03
FLJ12572	219838_at	NM_022905	NM_022905	64927	-1.17	4.22E-04
BACH2	221234_s_at	NM_021813	NM_021813	60468	-1.17	1.76E-04
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ATF5	204998_s_at	NM_012068	NM_012068	22809	-1.09	5.15E-03
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IL17D	228977_at	AI669535	NM_138284	53342	-1.09	2.53E-03
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SIX3	242054_s_at	AW473656	NM_005413	6496	-1.07	3.51E-04
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BID	227143_s_at	AA706658	NM_001196 NM_197966 NM_197967	637	-1.07	1.25E-03
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LOC286052	241370_at	AA278233	---	286052	-1.04	1.43E-03
LRP16	219188_s_at	NM_014067	NM_014067	28992	-1.04	8.11E-03
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AW590679	229300_at	AW590679	---	---	-1.04	6.25E-06
BBS7	235007_at	AI683802	NM_018190 NM_176824	55212	-1.03	2.92E-03
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FLJ25168	1553400_a_at	NM_152466	NM_152466	147081	-1.01	1.66E-03
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IPP	241393_at	R78604	NM_005897	3652	-1.01	4.60E-03
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TMEM28	206299_at	NM_015686	NM_015686	27112	-1.00	3.66E-04
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SLICK	244455_at	AI732637	NM_198503	343450	-0.99	1.51E-03
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LOC340281	240194_at	AA406397	---	340281	-0.99	3.47E-03
LIPT1	205571_at	NM_015929	NM_015929 NM_145196 NM_145197 NM_145198 NM_145199	51601	-0.99	6.75E-03
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BTD	214116_at	AI767414	NM_000060	686	-0.98	4.23E-03
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C10orf104	229145_at	AA541762	NM_173473	119504	-0.98	9.01E-04
LOC222070	58900_at	AW025284	---	222070	-0.98	4.22E-04
ESRRG	207981_s_at	NM_001438	NM_001438 NM_206594 NM_206595	2104	-0.98	6.26E-03
PRPS2	203401_at	NM_002765	NM_002765	5634	-0.98	9.17E-04
TM4SF2	202242_at	NM_004615	NM_004615	7102	-0.98	4.04E-05
PCAF	203845_at	AV727449	NM_003884	8850	-0.98	3.42E-06
LOC284669	1559483_at	AK092251	---	284669	-0.98	1.08E-03
ARMCX5	1555902_at	BC022066	NM_022838	64860	-0.98	6.50E-03
AI862542	235696_at	AI862542	---	---	-0.98	7.90E-04
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ACSL4	202422_s_at	NM_022977	NM_004458 NM_022977	2182	-0.98	1.83E-03
PIN4	243226_at	N53548	NM_006223	5303	-0.97	9.48E-04
BF510890	243406_at	BF510890	---	---	-0.97	2.52E-03
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CACNA1B	235781_at	AA448208	NM_000718	774	-0.97	2.17E-03
LOC253982	214993_at	AF070642	NM_181718 NM_198907	253982	-0.97	5.64E-03
NOTCH4	205247_at	AI743713	NM_004557	4855	-0.96	5.91E-03
DACH1	205472_s_at	NM_004392	NM_004392 NM_080759 NM_080760	1602	-0.96	6.40E-04
C21orf25	212875_s_at	AP001745	NM_199050	25966	-0.96	1.81E-04
KIAA1377	235956_at	AI797063	NM_020802	57562	-0.96	2.43E-03
KIAA1729	230715_at	AI138969	NM_053042	85460	-0.96	2.87E-03
TMEM18	225487_at	AI074464	NM_152834	129787	-0.96	3.04E-04
CITED2	209357_at	AF109161	NM_006079	10370	-0.96	4.57E-03
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N50119	235635_at	N50119	---	---	-0.96	3.56E-03
AI802997	235211_at	AI802997	---	---	-0.96	4.66E-05
PRPH	213847_at	NM_006262	NM_006262	5630	-0.95	1.14E-03
C14orf167	227446_s_at	BF445127	---	55449	-0.95	4.86E-03
NEIL2	226585_at	BE466620	NM_145043	252969	-0.95	3.33E-04
LOC401020	1560475_at	AK092134	XM_379145	401020	-0.95	4.55E-03
CXorf45	205583_s_at	NM_024810	NM_024810	79868	-0.95	2.74E-03
MLLT4	238871_at	AI086124	NM_005936	4301	-0.95	6.94E-03
PPP3CA	202457_s_at	AA911231	NM_000944	5530	-0.95	7.65E-04
MTUS1	212095_s_at	BE552421	NM_001001924 NM_001001925 NM_001001927 NM_001001931 NM_020749	57509	-0.95	1.54E-03
CARD8	1554479_a_at	AF511652	NM_014959	22900	-0.95	1.49E-03
HS3ST5	240479_at	AW449310	NM_153612	222537	-0.95	4.10E-03
CDC42EP3	209286_at	AI754416	NM_006449	10602	-0.94	2.27E-05
CLDN12	223249_at	AL136770	NM_012129	9069	-0.94	7.31E-04
MGC70870	242136_x_at	T66145	NM_203481	403340	-0.94	4.23E-04
LIFR	225575_at	AI680541	NM_002310	3977	-0.94	2.42E-03
AA002140	241365_at	AA002140	---	---	-0.94	3.00E-03
LOC153364	230298_at	AI692906	NM_203406	153364	-0.94	5.23E-03
BRUNOL4	238966_at	AA678985	NM_020180	56853	-0.94	6.55E-04
AV700050	228835_at	AV700050	---	---	-0.94	3.53E-03
TRIM4	223384_s_at	BE501464	NM_033017 NM_033091	89122	-0.94	6.97E-03
FLJ23560	219487_at	NM_024685	NM_024685	79738	-0.94	1.67E-03
PDGFRL	205226_at	NM_006207	NM_006207	5157	-0.94	3.47E-03
BG502771	226397_s_at	BG502771	---	---	-0.94	6.49E-05
AI392908	230352_at	AI392908	---	---	-0.94	3.46E-03
LOC93622	225391_at	AL562398	NM_138699	93622	-0.94	5.23E-05
IMMP2L	227153_at	AI784580	NM_032549	83943	-0.94	1.01E-03
DACH1	205471_s_at	AW772082	NM_004392 NM_080759 NM_080760	1602	-0.94	4.97E-05
AI963605	230269_at	AI963605	---	---	-0.94	1.40E-03

R45950	229994_at	R45950	---	---	-0.93	1.97E-03
RGMB	227339_at	BE206621	NM_173670	285704	-0.93	3.25E-06
LOC285705				285705		
NIN	223981_at	AF223937	NM_016350	51199	-0.93	8.04E-03
			NM_020921			
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			NM_182946			
)KFZp313N062	241666_at	BG493222	NM_173826	285343	-0.93	6.42E-03
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CaMKIINalpha	218309_at	NM_018584	NM_018584	55450	-0.93	3.41E-05
MAPK10	237413_at	AI568447	NM_002753	5602	-0.93	2.01E-04
			NM_138980			
			NM_138981			
			NM_138982			
CXXC4	220277_at	NM_025212	NM_025212	80319	-0.93	1.90E-04
HEL308	1554341_a_at	BC011863	NM_133636	113510	-0.93	1.26E-04
SIGIRR	218921_at	NM_021805	NM_021805	59307	-0.92	3.82E-03
FBXL17	227203_at	AA115629	NM_022824	64839	-0.92	1.44E-03
ATXN1	203231_s_at	AW235612	NM_000332	6310	-0.92	5.79E-05
USP46	203869_at	AK024318	NM_022832	64854	-0.92	3.21E-04
CSE-C	224391_s_at	AF303378	NM_170601	54414	-0.92	2.82E-03
GGPS1	202321_at	AW299507	NM_004837	9453	-0.92	2.16E-03
MUTED	226543_at	AI768114	NM_201280	63915	-0.92	3.41E-03
KIAA0564	212946_at	AK025432	NM_00100981	23078	-0.92	4.42E-03
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			NM_015058			
JMY	226352_at	BF447037	NM_152405	133746	-0.92	2.68E-04
PALM2-AKAP2	202759_s_at	BE879367	NM_007203	445815	-0.92	1.79E-04
			NM_147150			
AI631072	228638_at	AI631072	---	---	-0.92	9.69E-03
MCAM	209087_x_at	AF089868	NM_006500	4162	-0.92	2.51E-03
PSD3	203355_s_at	NM_015310	NM_015310	23362	-0.92	4.84E-03
			NM_206909			
PTEN	228006_at	BG403361	NM_000314	5728	-0.92	3.02E-03
ABAT	209459_s_at	AF237813	NM_000663	18	-0.92	5.61E-03
			NM_020686			
AI887898	228423_at	AI887898	XM_374094	389237	-0.92	5.43E-04
MGC14595	238562_at	BE542779	NM_032334	84294	-0.92	1.59E-05
AA757630	236724_at	AA757630	---	---	-0.91	2.99E-04
BF510563	228561_at	BF510563	---	---	-0.91	1.65E-05
ETS2	201328_at	AL575509	NM_005239	2114	-0.91	6.50E-05
TRIM32	236233_at	AI768810	NM_012210	22954	-0.91	7.51E-03
CDC42EP3	209288_s_at	AL136842	NM_006449	10602	-0.91	1.33E-04
CNOT6L	227119_at	BF103856	NM_144571	246175	-0.91	2.60E-06
AI754871	229075_at	AI754871	---	---	-0.91	2.23E-03
PSD3	218613_at	NM_018422	NM_015310	23362	-0.91	2.81E-05
			NM_206909			
SLC20A2	229371_at	BF940010	NM_006749	6575	-0.91	2.66E-04
SNX10	218404_at	NM_013322	NM_013322	29887	-0.90	3.48E-03
KCTD18	226493_at	AI627249	NM_152387	130535	-0.90	7.20E-03
MGC31963	1558692_at	AW090182	NM_144580	112770	-0.90	9.19E-03
C21orf51	228239_at	AA148789	NM_058182	54065	-0.90	3.56E-03
T79639	243466_at	T79639	---	---	-0.90	3.38E-03
BE671727	244177_at	BE671727	---	---	-0.90	7.50E-03
WDR32	219001_s_at	NM_024345	NM_024345	79269	-0.90	1.46E-03
AW770320	242523_at	AW770320	---	---	-0.90	5.17E-03
FLJ31265	228341_at	AI809108	NM_152395	131870	-0.90	9.74E-03

TENS1	217853_at	NM_022748	NM_022748	64759	-0.90	3.93E-03
AFFX-BioB-3	AFFX-BioB-3_a	AFFX-BioB-3	---	---	-0.90	4.10E-03
AL359605	227318_at	AL359605	---	---	-0.90	4.75E-04
FIP1L1	1554424_at	BC017724	NM_030917	81608	-0.90	2.24E-05
MGC22773	235498_at	AI269596	NM_145258	127255	-0.89	3.93E-07
AI765014	224649_x_at	AI765014	---	---	-0.89	3.50E-03
ACSL6	229725_at	AV705292	NM_00100918 5 NM_015256	23305	-0.89	6.40E-03
HNRPR	208765_s_at	NM_005826	NM_005826	10236	-0.89	9.23E-05
GATM	216733_s_at	X86401	NM_001482	2628	-0.89	6.06E-03
SAT	213988_s_at	BE971383	NM_002970	6303	-0.89	6.15E-03
MGC16275	1558167_a_at	BM824870	---	85001	-0.89	3.24E-03
AI743452	237031_at	AI743452	---	---	-0.89	2.69E-03
FLJ11011	222656_at	AI625741	NM_00100148 1 NM_00100148 2 NM_018299	55284	-0.89	2.46E-03
BF510762	230262_at	BF510762	---	---	-0.89	7.78E-05
SOCS5	208127_s_at	NM_014011	NM_014011 NM_144949	9655	-0.89	2.64E-03
LTBP3	227308_x_at	AW515704	NM_021070	4054	-0.89	1.44E-04
AI826437	229975_at	AI826437	---	---	-0.89	3.65E-04
BRAF	236402_at	AW184034	NM_004333	673	-0.89	8.26E-03
LNX	227293_at	AI264003	NM_032622	84708	-0.88	1.56E-03
F3	204363_at	NM_001993	NM_001993	2152	-0.88	2.35E-03
COVA1	204643_s_at	NM_006375	NM_006375 NM_182314	10495	-0.88	9.34E-03
TPD52	201691_s_at	NM_005079	NM_005079	7163	-0.88	6.44E-04
GRIK2	1560142_at	AJ301610	NM_021956 NM_175768	2898	-0.88	5.49E-03
AI025829	235227_at	AI025829	---	---	-0.88	2.45E-03
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MAP3K5	203836_s_at	D84476	NM_005923	4217	-0.88	7.19E-03
NOX4	219773_at	NM_016931	NM_016931	50507	-0.88	6.53E-03
FBXL17	238174_at	AI694129	NM_022824	64839	-0.88	4.28E-04
ERCC6	207347_at	NM_000124	NM_000124	2074	-0.88	1.34E-03
TMEM34	219074_at	NM_018241	NM_018241	55751	-0.88	2.71E-03
MGC52110	226039_at	AW006441	NM_001008215	493753	-0.87	3.18E-05
SPHAR	206272_at	NM_006542	NM_006542	10638	-0.87	3.60E-03
FCMD	205283_at	NM_006731	NM_006731	2218	-0.87	3.96E-03
BAI3	205638_at	NM_001704	NM_001704	577	-0.87	8.83E-03
N29877	231169_at	N29877	---	---	-0.87	2.33E-03
MBNL1	201153_s_at	NM_021038	NM_021038 NM_207292 NM_207293 NM_207294 NM_207295 NM_207296 NM_207297	4154	-0.87	2.24E-05
CLCN3	201734_at	AI760629	NM_001829 NM_173872	1182	-0.87	7.31E-03
MGC13024	221864_at	AW517464	NM_152288	93129	-0.87	9.69E-03
XPR1	226615_at	BE439489	NM_004736	9213	-0.87	2.22E-04

CAMK2B	210404_x_at	AF078803	NM_001220 NM_172078 NM_172079 NM_172080 NM_172081 NM_172082 NM_172083 NM_172084	816	-0.87	1.66E-03
CHD2	228999_at	AW514564	NM_001271	1106	-0.86	2.91E-03
TMEM1	209412_at	U61500	NM_00100172 3 NM_003274	7109	-0.86	2.68E-03
FLJ32130	1554769_at	BC040642	NM_152458	146540	-0.86	3.30E-03
MCF2L	212935_at	AB002360	NM_024979	23263	-0.86	3.60E-04
PGRMC2	213227_at	BE879873	NM_006320	10424	-0.86	1.58E-03
BF434383	235473_at	BF434383	---	---	-0.86	5.25E-03
WARS2	222734_at	BF515963	NM_015836 NM_201263	10352	-0.86	9.52E-03
ASB13	218862_at	NM_024701	NM_024701	79754	-0.86	5.98E-03
ARSD	225280_x_at	N51673	NM_001669 NM_009589	414	-0.86	4.80E-03
HEL308	1554342_s_at	BC011863	NM_133636	113510	-0.86	8.97E-03
GLCE	213552_at	W87398	NM_015554	26035	-0.86	3.64E-03
ZNF25	235164_at	BG433539	NM_145011	219749	-0.86	8.82E-03
N56912	221944_at	N56912	XM_496112	440332	-0.86	2.61E-03
BMPR2	225144_at	AI457436	NM_001204 NM_033346	659	-0.86	9.23E-05
AI796858	236164_at	AI796858	---	---	-0.86	6.19E-05
HPS1	210112_at	U96721	NM_000195 NM_182637 NM_182638 NM_182639	3257	-0.86	9.98E-03
SCRN3	219234_x_at	NM_024583	NM_024583	79634	-0.86	1.04E-03
EFNB3	205031_at	NM_001406	NM_001406	1949	-0.86	4.69E-03
ZNF25	228185_at	N32599	NM_145011	219749	-0.85	9.68E-03
AW274846	228108_at	AW274846	---	---	-0.85	3.72E-03
STC1	204595_s_at	AI300520	NM_003155	6781	-0.85	1.72E-03
AW044658	229201_at	AW044658	---	---	-0.85	7.58E-05
CA442342	1556097_at	CA442342	---	---	-0.85	6.36E-03
FLJ21159	235550_at	AV751613	NM_024826	79884	-0.85	6.98E-04
PKNOX1	54051_at	H59033	NM_004571 NM_197976	5316	-0.85	1.84E-03
PDE2A	204134_at	NM_002599	NM_002599	5138	-0.85	1.09E-04
DHRSX	225503_at	AL547782	NM_145177	207063	-0.85	2.79E-03
SLC19A1	229489_at	AI681043	NM_003056 NM_194255	6573	-0.85	2.68E-03
C13orf24	213239_at	NM_006346	NM_006346	10464	-0.85	2.61E-04
SRGAP3	209794_at	AB007871	NM_014850	9901	-0.85	7.85E-03
C21orf127	234676_s_at	AK021678	NM_013240 NM_182749	29104	-0.85	8.73E-03
PARP11	229138_at	AV747166	NM_020367	57097	-0.84	1.23E-03
ELAC1	219325_s_at	NM_018696	NM_018696	55520	-0.84	9.17E-03
AV702357	229823_at	AV702357	---	---	-0.84	2.59E-04
FLRT1	210414_at	AF169675	NM_013280	23769	-0.84	8.98E-03
C2orf17	222129_at	AK026155	NM_024293	79137	-0.84	2.37E-03
PF6	1557593_at	AA250798	NM_206996	200162	-0.84	1.52E-03
BC040191	1568623_a_at	BC040191	---	---	-0.84	5.28E-03
H99038	227338_at	H99038	XM_498946	440983	-0.84	9.90E-03

MANBA	203778_at	NM_005908	NM_005908	4126	-0.84	4.77E-03
DELGEF	232983_s_at	AJ243951	NM_012139	26297	-0.84	7.32E-03
ATP2C1	209934_s_at	AF225981	NM_001001485 NM_001001486 NM_001001487 NM_014382	27032	-0.84	5.96E-03
LOC92249	212957_s_at	AU154785	XM_499179	92249	-0.83	7.94E-04
SPATA7	234929_s_at	AF144488	NM_018418	55812	-0.83	9.12E-03
AW269338	235691_at	AW269338	XM_378880	400764	-0.83	1.62E-03
ZNF295	225539_at	AP001745	NM_020727	49854	-0.83	1.11E-03
KIAA1223	225731_at	BF196876	XM_048747	57182	-0.83	1.79E-06
BF207861	239768_x_at	BF207861	---	---	-0.83	3.46E-03
BG236351	217598_at	BG236351	---	---	-0.83	1.23E-03
B3GTL	227083_at	N51325	NM_194318	145173	-0.83	2.95E-05
QPCT	205174_s_at	NM_012413	NM_012413	25797	-0.83	8.28E-03
AL045516	232166_at	AL045516	---	---	-0.83	2.57E-03
ZNF148	230821_at	AW594167	NM_021964	7707	-0.83	3.02E-03
GNG2	224964_s_at	AK026424	NM_053064	54331	-0.83	6.30E-03
CTPS2	219080_s_at	NM_019857	NM_019857	56474	-0.83	3.00E-04
CAMK2D	225019_at	BF797381	NM_175859 NM_001221 NM_172115 NM_172127 NM_172128	817	-0.83	8.53E-03
CYLD	213295_at	AA555096	NM_015247	1540	-0.83	7.35E-04
TMEM5	204808_s_at	NM_014254	NM_014254	10329	-0.83	2.63E-03
FLJ35036	225512_at	AI005245	XM_172341	253461	-0.83	6.24E-04
LOC51334	220014_at	NM_016644	NM_016644	51334	-0.82	5.21E-04
MGC34646	224996_at	N30209	NM_173519	157807	-0.82	6.97E-05
NDP52	235076_at	AA149539	NM_005831	10241	-0.82	2.69E-03
FLJ38991	227442_at	BG283902	NM_173827	285521	-0.82	2.38E-03
LOC144363	225469_at	AA015609	NM_001001660	144363	-0.82	6.00E-03
AI627803	236194_at	AI627803	---	---	-0.82	8.90E-03
EIF4E3	238461_at	AA228031	---	317649	-0.82	8.67E-03
LOC284262	227478_at	BF739885	---	284262	-0.82	1.50E-05
LRCH2	227688_at	AK022128	NM_020871	57631	-0.82	4.46E-04
AI635131	1557192_at	AI635131	XM_375410	400574	-0.82	2.14E-03
AA935515	242790_at	AA935515	---	---	-0.82	4.73E-04
ZNF423	214761_at	AW149417	NM_015069	23090	-0.82	6.45E-03
FBXO4	223493_at	AF129534	NM_012176 NM_033484	26272	-0.82	2.52E-03
AI417268	225028_at	AI417268	---	---	-0.82	8.20E-03
EIF2C1	228120_at	AW136032	NM_012199	26523	-0.81	1.09E-05
FLJ22313	236170_x_at	AI377423	NM_022373	64224	-0.81	4.47E-03
LOC401500	233946_at	AL512690	XM_379629	401500	-0.81	2.52E-03
AFFX-BioB-M	AFFX-BioB-M_a	AFFX-BioB-M	---	---	-0.81	3.21E-03
AI149508	228416_at	AI149508	---	---	-0.81	1.26E-04
ZNF287	220055_at	NM_020653	NM_020653	57336	-0.81	1.85E-04
FLJ30851	230435_at	BF108666	NM_198553	375190	-0.81	5.13E-03
BC042959	1556194_a_at	BC042959	---	---	-0.81	2.89E-03
CA5BL	238435_at	AA521288	XM_291346	340591	-0.81	4.85E-03
WIZ	221784_at	AI089655	XM_372716	58525	-0.81	1.35E-03
AW086077	232800_at	AW086077	---	---	-0.81	3.68E-03
FLJ22795	223327_x_at	AF316855	NM_025084	80154	-0.81	4.57E-03
AI075662	238038_at	AI075662	---	---	-0.81	4.28E-03

PCDHB14	231726_at	NM_018934	NM_018934	56122	-0.81	5.56E-03
LOC130355	227840_at	AA738440	XM_496588	130355	-0.81	2.33E-05
FLJ10378	231824_at	AK027164	NM_018078 NM_032239 NM_178043	55132	-0.81	7.52E-03
CAMK2B	211483_x_at	AF081924	NM_001220 NM_172078 NM_172079 NM_172080 NM_172081 NM_172082 NM_172083 NM_172084	816	-0.81	2.75E-04
RPL4	226556_at	BF431260	NM_000968	6124	-0.81	2.30E-07
C21orf108	212996_s_at	AI803485	---	9875	-0.81	4.93E-03
CYLD	39582_at	AL050166	NM_015247	1540	-0.81	8.02E-04
MBNL1	201151_s_at	BF512200	NM_021038 NM_207292 NM_207293 NM_207294 NM_207295 NM_207296 NM_207297	4154	-0.80	1.13E-03
HERC4	208055_s_at	NM_015601	NM_015601	26091	-0.80	1.46E-03
AI929792	236081_at	AI929792	---	---	-0.80	2.95E-03
SYNJ1	212990_at	AB020717	NM_003895 NM_203446	8867	-0.80	1.01E-03
C9orf123	224860_at	AL137489	XM_372075	90871	-0.80	8.84E-04
C21orf66	1556789_a_at	AK056384	NM_013329 NM_016631 NM_058191 NM_145328	94104	-0.80	4.85E-03
BMPR2	231873_at	AL046696	NM_001204 NM_033346	659	-0.80	1.31E-04
PCBP3	230486_at	BG025371	NM_020528	54039	-0.80	5.61E-04
JAM2	229127_at	BF195118	NM_021219	58494	-0.80	4.44E-03
COG6	225769_at	AF116827	NM_020751	57511	-0.80	4.32E-03
FLJ21159	220145_at	NM_024826	NM_024826	79884	-0.80	5.05E-03
HSD17B12	217869_at	NM_016142	NM_016142	51144	-0.80	5.67E-03
SMAP-5	224953_at	AW001618	NM_030799	81555	-0.80	5.29E-03
SAV1	218276_s_at	NM_021818	NM_021818	60485	-0.80	1.52E-03
PPID	204186_s_at	AI014573	NM_005038	5481	-0.80	5.72E-04
AZI2	227905_s_at	BF000175	NM_022461 NM_203326	64343	-0.79	9.88E-05
BE219874	236111_at	BE219874	---	---	-0.79	6.26E-03
KPNA1	202057_at	BC002374	NM_002264	3836	-0.79	5.21E-03
LOC339803	227940_at	N90774	---	339803	-0.79	1.13E-04
ALKBH	236721_at	AI922200	NM_006020	8846	-0.79	2.25E-03
AW237752	229699_at	AW237752	---	---	-0.79	8.75E-03
SLC22A17	218675_at	NM_020372	NM_016609 NM_020372	51310	-0.79	1.71E-04
TOB1	228834_at	BF240286	NM_005749	10140	-0.79	7.87E-04
MED28	224416_s_at	AF358829	NM_025205	80306	-0.79	1.39E-04
ZNF277	1555193_a_at	BC020626	NM_021994	11179	-0.79	9.56E-03
WDFY3	212598_at	BE348236	NM_014991 NM_178583 NM_178585	23001	-0.79	6.62E-03

SGNE1	203889_at	NM_003020	NM_003020	6447	-0.78	3.31E-04
ANKRD32	223542_at	AL136560	NM_032290	84250	-0.78	2.09E-04
CLCN3	201733_at	AA902971	NM_001829 NM_173872	1182	-0.78	1.25E-06
EIF4E3	225939_at	AL161983	---	317649	-0.78	2.79E-03
CARF	218929_at	NM_017632	NM_017632	55602	-0.78	2.99E-03
DCX	204851_s_at	AF040254	NM_000555 NM_178151 NM_178152 NM_178153	1641	-0.78	7.79E-03
C1orf25	220992_s_at	NM_030934	NM_030934	81627	-0.78	2.30E-03
TNFRSF25	219423_x_at	NM_003790	NM_003790 NM_148965 NM_148966 NM_148967 NM_148968 NM_148969 NM_148970 NM_148971 NM_148972 NM_148973 NM_148974	8718	-0.78	8.35E-03
AOF2	212348_s_at	AB011173	NM_00100999 9 NM_015013	23028	-0.78	3.47E-03
AW025980	241864_x_at	AW025980	XM_371647	389129	-0.78	5.72E-04
ACBD5	225663_at	AL047650	NM_145698	91452	-0.78	1.80E-03
FRS2	226045_at	AW264515	NM_006654	10818	-0.78	5.02E-03
MYOZ3	213955_at	BE673151	NM_133371	91977	-0.78	7.08E-03
DBT	205369_x_at	J03208	NM_001918	1629	-0.78	5.34E-03
AI061377	235233_s_at	AI061377	---	---	-0.78	2.35E-03
ENOSF1	204142_at	NM_017512	NM_017512	55556	-0.78	2.12E-03
CA5BL	239106_at	AI801563	XM_291346	340591	-0.77	3.87E-03
GTDC1	219770_at	NM_024659	NM_00100663 6 NM_024659	79712	-0.77	5.30E-04
RAB18	243496_at	AW367507	NM_021252	22931	-0.77	5.05E-03
AK025253	227009_at	AK025253	---	---	-0.77	2.24E-03
MRPS6	212944_at	AK024896	NM_032476	64968	-0.77	9.32E-03
AFAP	203563_at	NM_021638	NM_021638 NM_198595	60312	-0.77	4.32E-04
RGS7	1554500_a_at	AF493931	NM_002924	6000	-0.77	5.33E-04
QSCN6	201482_at	NM_002826	NM_00100412 8 NM_002826	5768	-0.77	5.46E-04
C21orf57	227421_at	BF026326	NM_00100611 4 NM_058181	54059	-0.77	2.03E-03
PLEKHA3	227658_s_at	BE550332	NM_019091	65977	-0.77	2.93E-04
FLJ10980	225327_at	AB037791	NM_019600	56204	-0.77	3.59E-03
PURA	229167_at	AI129941	NM_005859	5813	-0.77	7.80E-03
FFX-r2-Ec-bioC-5	X-r2-Ec-bioC-5	AFFX-r2-Ec-bioC-5	---	---	-0.77	1.36E-03
HSPA12A	214434_at	AB007877	XM_048898	259217	-0.77	5.03E-03
ZNF250	213858_at	BE350026	NM_021061	58500	-0.77	2.48E-03
FFX-r2-Ec-bioB-5	X-r2-Ec-bioB-5	AFFX-r2-Ec-bioB-5	---	---	-0.77	4.87E-03
PDXK	222492_at	AW262867	NM_003681	8566	-0.77	7.16E-03
H09780	230869_at	H09780	---	---	-0.76	5.31E-03
LOC283481	230351_at	AW070248	---	283481	-0.76	1.35E-04

LOC128153	1552269_at	NM_138796	NM_138796	128153	-0.76	8.35E-03
PTP4A2	208617_s_at	AF208850	NM_003479 NM_080391 NM_080392	8073	-0.76	8.88E-05
AB029551	201845_s_at	AB029551	---	---	-0.76	1.96E-04
KIAA1387	226230_at	AA541716	NM_020463	57223	-0.76	1.87E-03
C21orf86	226995_at	AV705934	NM_153454	257103	-0.76	5.79E-05
ISYNA1	222240_s_at	AL137749	NM_016368	51477	-0.76	3.08E-03
RNF13	201780_s_at	NM_007282	NM_007282 NM_183381 NM_183382 NM_183383 NM_183384	11342	-0.76	6.77E-04
JMJD2C	209984_at	AB037901	NM_015061	23081	-0.76	3.62E-03
GTDC1	238585_at	AW407668	NM_00100663 6 NM_024659	79712	-0.76	1.71E-03
AI955713	227193_at	AI955713	---	---	-0.76	2.70E-03
FKBP1A	210187_at	BC005147	NM_000801 NM_054014	2280	-0.76	7.11E-03
AW117322	239415_at	AW117322	XM_374094	389237	-0.76	5.02E-03
BBP	213883_s_at	AA012917	NM_032027	83941	-0.76	5.76E-03
LOC284804	1559161_at	AI871356	---	284804	-0.75	6.44E-03
DJ159A19.3	205002_at	NM_015699	XM_372774	27245	-0.75	8.45E-04
AFFX-BioDn-3	AFFX-BioDn-3_a	AFFX-BioDn-3	---	---	-0.75	2.83E-03
LAMB1	201505_at	NM_002291	NM_002291	3912	-0.75	9.18E-03
POLR3A	227872_at	AA527570	NM_007055	11128	-0.75	9.27E-04
CDC2L6	212899_at	AB028951	NM_015076	23097	-0.75	2.97E-05
GRK4	241989_at	AW269179	NM_00100405 6 NM_00100405 7 NM_005307 NM_182982	2868	-0.75	9.15E-03
FEV	207260_at	NM_017521	NM_017521	54738	-0.75	5.52E-04
MGC35274	226748_at	AI674731	NM_153374	256586	-0.75	6.51E-03
PRKCB1	209685_s_at	M13975	NM_002738 NM_212535	5579	-0.75	4.16E-03
OXR1	222553_x_at	AL541048	NM_181354	55074	-0.75	3.29E-03
ARP3BETA	218868_at	NM_020445	NM_020445	57180	-0.75	9.91E-03
PFN2	237116_at	AI262277	NM_002628 NM_053024	5217	-0.74	8.35E-03
LZTFL1	218437_s_at	NM_020347	NM_020347	54585	-0.74	3.96E-03
C6orf96	220329_s_at	NM_017909	NM_017909	55005	-0.74	1.80E-03
BE890365	222738_at	BE890365	---	---	-0.74	9.64E-03
BG112359	225785_at	BG112359	---	---	-0.74	2.08E-03
ICA1	204002_s_at	NM_022307	NM_004968 NM_022307 NM_022308	3382	-0.74	2.94E-03
ENOSF1	213645_at	AF305057	NM_017512	55556	-0.74	4.62E-03
CAMK2D	228555_at	AA029441	NM_001221 NM_172115 NM_172127 NM_172128	817	-0.74	1.79E-03
AI889373	227414_at	AI889373	---	---	-0.74	1.82E-03
GPR27	227769_at	AI703476	NM_018971	2850	-0.74	8.05E-03
AK055769	1558801_at	AK055769	---	---	-0.74	7.07E-03
AFFX-BioB-5	AFFX-BioB-5_a	AFFX-BioB-5	---	---	-0.73	3.91E-03

AA928542	226831_at	AA928542	---	---	-0.73	8.48E-04
PAM	202336_s_at	NM_000919	NM_000919 NM_138766 NM_138821 NM_138822	5066	-0.73	2.84E-03
THNSL1	222931_s_at	AI809864	NM_024838	79896	-0.73	3.88E-03
MGC14595	227836_at	AI859767	NM_032334	84294	-0.73	6.40E-03
PRKCE	226101_at	AI093546	NM_005400	5581	-0.73	3.23E-03
LOC92482	213224_s_at	AK025724	XM_378250	92482	-0.73	5.89E-03
AKAP14	228493_at	T87628	NM_00100853 4 NM_00100853 5 NM_178813	158798	-0.73	8.43E-03
DUSP16	224336_s_at	AB052156	NM_030640	80824	-0.73	4.69E-04
IRF2BP2	224571_at	BF968057	NM_182972	359948	-0.73	6.05E-03
C6orf117	243177_at	AI912225	NM_138409	112609	-0.73	7.88E-03
ADD2	205268_s_at	NM_017488	NM_001617 NM_017482 NM_017483 NM_017484 NM_017485 NM_017486 NM_017487 NM_017488	119	-0.73	4.20E-07
PCSK6	207414_s_at	NM_002570	NM_002570 NM_138319 NM_138320 NM_138321 NM_138322 NM_138323 NM_138324 NM_138325	5046	-0.73	3.49E-03
H62221	243414_at	H62221	---	---	-0.73	2.65E-03
AFFX-BioC-5	AFFX-BioC-5_a	AFFX-BioC-5	---	---	-0.73	6.02E-04
BF342524	235074_at	BF342524	---	---	-0.73	2.25E-03
LOC96610	226802_s_at	W87523	NM_080926	96610	-0.73	9.29E-03
BE645776	227288_at	BE645776	XM_068632	133993	-0.73	7.66E-04
KIAA0423	213304_at	AI823592	NM_015091	23116	-0.73	2.19E-03
ENOSF1	204143_s_at	NM_017512	NM_017512	55556	-0.73	2.84E-05
DSCR5	221689_s_at	AB035745	NM_016430 NM_153681 NM_153682	51227	-0.73	4.01E-05
MGC54289	225228_at	AI474054	NM_178454	128338	-0.72	2.77E-05
AK026379	232687_at	AK026379	---	---	-0.72	1.93E-04
MGC72075	228600_x_at	BE220330	NM_199136	340277	-0.72	5.28E-04
ASH1L	226447_at	BG290742	NM_018489	55870	-0.72	2.78E-03
KIAA0974	213463_s_at	AW300504	---	317662	-0.72	4.74E-04
C6orf157	227790_at	AV692609	NM_198920	90025	-0.72	3.66E-03
CLCN4	214769_at	AF052117	NM_001830	1183	-0.72	3.22E-04
LOC440360	236838_at	H11609	XM_498641	440360	-0.72	2.56E-03
SYNCRIP	217833_at	AL520908	NM_006372	10492	-0.72	4.62E-04
FX-r2-Ec-bioB-	X-r2-Ec-bioB-M	AFFX-r2-Ec-bioB-M	---	---	-0.72	7.96E-03
AKT3	212609_s_at	U79271	NM_005465 NM_181690	10000	-0.72	5.74E-03
PP1057	220968_s_at	NM_031285	---	83441	-0.72	6.75E-03
GM2A	1559776_at	H41167	NM_000405	2760	-0.72	1.46E-03

FLJ37228	1556641_at	AK094547	---	285264	-0.72	6.35E-03
NAV1	227584_at	BF339566	NM_020443	89796	-0.71	9.22E-05
MGC10198	225574_at	BE613081	NM_152682	201965	-0.71	1.36E-03
PPP2R5C	201877_s_at	NM_002719	NM_002719 NM_178586 NM_178587 NM_178588	5527	-0.71	1.25E-03
RAFTLIN	212646_at	D42043	NM_015150	23180	-0.71	7.61E-06
DKFZP564O243	210006_at	BC002571	NM_015407	25864	-0.71	5.84E-03
SLC35A5	218519_at	NM_017945	NM_017945	55032	-0.71	5.19E-03
BF526978	227125_at	BF526978	---	---	-0.71	2.88E-03
RBM16	227866_at	AI743557	NM_014892	22828	-0.71	4.70E-04
gm117	239038_at	AW015063	NM_198077	148423	-0.71	2.85E-05
AB058893	223973_at	AB058893	---	---	-0.71	3.00E-03
DUSP16	224832_at	AB051487	NM_030640	80824	-0.71	8.84E-04
FFX-r2-Ec-bioC-3	X-r2-Ec-bioC-3	AFFX-r2-Ec-bioC-3	---	---	-0.71	2.47E-03
AL355532	213845_at	AL355532	---	---	-0.71	1.72E-03
LOC284409	242016_at	BE857296	XM_211447	284409	-0.70	7.46E-03
PAK1	226507_at	AU154408	NM_002576	5058	-0.70	1.89E-03
BC015852	1560570_a_at	BC015852	---	---	-0.70	5.93E-04
EPM2AIP1	227847_at	BF432224	NM_014805	9852	-0.70	6.03E-03
13CDNA73	204072_s_at	NM_023037	NM_023037	10129	-0.70	1.50E-04
DECR1	202447_at	NM_001359	NM_001359	1666	-0.70	7.20E-03
USP38	223288_at	AW977401	NM_032557	84640	-0.70	6.63E-03
RAB4A	203581_at	BC002438	NM_004578	5867	-0.70	1.97E-03
PLEKHA3	223370_at	AF286162	NM_019091	65977	-0.70	4.19E-03
AFFX-BioC-3	AFFX-BioC-3_a	AFFX-BioC-3	---	---	-0.70	1.62E-03
PPID	204185_x_at	NM_005038	NM_005038	5481	-0.70	5.63E-04
PAM	214620_x_at	BF038548	NM_000919 NM_138766 NM_138821 NM_138822	5066	-0.70	2.61E-04
ARL7	202207_at	BG435404	NM_005737	10123	-0.70	1.62E-03
DNAJC6	204720_s_at	AV729634	NM_014787	9829	-0.70	2.00E-04
SYNCOILIN	225396_at	AI928212	NM_030786	81493	-0.70	5.70E-03
ANXA5	200782_at	NM_001154	NM_001154	308	-0.70	5.88E-03
MGC14595	238561_s_at	BE542779	NM_032334	84294	-0.70	6.39E-05
SELM	226051_at	BF973568	NM_080430	140606	-0.70	4.02E-03
AA489100	228390_at	AA489100	---	---	-0.70	5.43E-03
AA740675	244032_at	AA740675	---	---	-0.70	9.18E-04
ALDH5A1	203608_at	AL031230	NM_001080 NM_170740	7915	-0.69	3.13E-03
BE646451	235893_at	BE646451	---	---	-0.69	9.91E-03
DUSP7	213848_at	AI655015	NM_001947	1849	-0.69	9.16E-03
MGC42174	242539_at	AW665509	NM_152383	129563	-0.69	2.67E-03
FBXO25	225591_at	AA749085	NM_012173 NM_183420 NM_183421	26260	-0.69	4.48E-03
CNOT6L	226153_s_at	AW514857	NM_144571	246175	-0.69	4.37E-04
NPR2	204310_s_at	NM_003995	NM_000907 NM_003995	4882	-0.69	5.97E-03
DEPDC6	218858_at	NM_022783	NM_022783	64798	-0.69	2.62E-03
GARNL4	213280_at	AK000478	NM_015085	23108	-0.69	5.49E-03
ANKH	223093_at	T99215	NM_054027	56172	-0.69	3.95E-03
NUDT11	219855_at	NM_018159	NM_018159	55190	-0.69	1.75E-03
IFNAR2	204785_x_at	NM_000874	NM_000874 NM_207584 NM_207585	3455	-0.69	7.44E-05

ZNF148	235166_at	T08836	NM_021964	7707	-0.68	9.51E-03
LOC377064	229986_at	AW205616	XM_496648	377064	-0.68	3.34E-03
RSL1D1	212019_at	AK025446	NM_015659	26156	-0.68	2.80E-03
C10orf22	212500_at	AL049319	NM_032804	84890	-0.68	8.22E-03
DAZAP2	214334_x_at	N34846	NM_014764	9802	-0.68	2.12E-03
WDFY3	212606_at	AL536319	NM_014991 NM_178583 NM_178585	23001	-0.68	8.12E-05
PTPN23	223150_s_at	AF290614	NM_015466	25930	-0.68	2.67E-03
SNAP91	204953_at	NM_014841	NM_014841	9892	-0.68	1.47E-04
DSU	232682_at	BG167210	NM_018000	55686	-0.68	2.28E-04
ZNF490	231988_x_at	AB033024	NM_020714	57474	-0.68	8.43E-04
FFX-r2-Ec-bioD-3	X-r2-Ec-bioD-3	AFFX-r2-Ec-bioD-3	---	---	-0.68	8.66E-03
ZBTB1	242258_at	AW168154	NM_014950	22890	-0.68	7.93E-03
FFX-r2-Ec-bioB-3	X-r2-Ec-bioB-3	AFFX-r2-Ec-bioB-3	---	---	-0.68	4.88E-03
DLG3	212727_at	AB033058	NM_021120	1741	-0.68	2.75E-05
P15RS	225953_at	AI684281	NM_018170	55197	-0.68	4.56E-03
LRBA	212692_s_at	W60686	NM_006726	987	-0.68	1.07E-06
ZBED3	228402_at	AI679968	NM_032367	84327	-0.68	2.51E-03
DNASE1L1	203912_s_at	NM_006730	NM_001009932 NM_001009933 NM_001009934 NM_006730	1774	-0.68	4.97E-03
ABR	212895_s_at	AL527773	NM_001092 NM_021962	29	-0.68	9.54E-04
AF147335	1557518_a_at	AF147335	---	---	-0.68	3.85E-03
HNRPD	229129_at	AI948456	NM_001003810 NM_002138 NM_031369 NM_031370	3184	-0.68	9.99E-03
LOC387895	243905_at	AI652676	XM_373553	387895	-0.68	4.51E-03
PLCE1	205111_s_at	NM_016341	NM_016341	51196	-0.68	3.83E-04
ANTXR2	228573_at	BE673665	NM_058172	118429	-0.68	3.75E-03
MGC48625	1569039_s_at	BC029855	NM_182609	342926	-0.68	2.30E-04
MGC47869	229888_at	AA861435	NM_175874	144608	-0.68	3.57E-03
ZNF197	233070_at	AL117657	NM_006991	10168	-0.68	1.50E-04
DYRK2	202969_at	AI216690	NM_003583 NM_006482	8445	-0.68	3.24E-03
LOC285513	1556697_at	AI819722	NM_198281	285513	-0.67	1.21E-05
CRYZL1	219767_s_at	NM_005111	NM_005111 NM_145311 NM_145858	9946	-0.67	6.15E-03
AA935461	242579_at	AA935461	---	---	-0.67	3.50E-04
FLJ30990	1554588_a_at	BC033795	NM_152517	150737	-0.67	7.72E-03
RIPK5	229017_s_at	N31717	NM_015375 NM_199462	25778	-0.67	5.71E-03
N63920	226179_at	N63920	---	---	-0.67	9.08E-03
NM_022335	206936_x_at	NM_022335	---	---	-0.67	1.76E-04
SLC25A12	203340_s_at	NM_003705	NM_003705	8604	-0.67	6.85E-03
MED28	218438_s_at	NM_025205	NM_025205	80306	-0.67	1.38E-03
RAD52	236042_at	AI700506	NM_002879 NM_134422 NM_134423 NM_134424	5893	-0.67	1.28E-04

EPHA8	231796_at	AL035703	NM_00100694 3 NM_020526	2046	-0.67	5.79E-03
DSU	219648_at	NM_018000	NM_018000	55686	-0.67	3.20E-04
AA843541	229710_at	AA843541	---	---	-0.67	9.95E-04
AA461190	244294_at	AA461190	---	---	-0.67	9.45E-03
JAM2	219213_at	NM_021219	NM_021219	58494	-0.66	1.52E-03
CDK6	224847_at	AW051349	NM_001259	1021	-0.66	3.40E-03
MCM3APAS	1560542_at	BC016306	---	114044	-0.66	9.71E-03
LOC157657	244569_at	N92755	NM_177965	157657	-0.66	1.12E-04
LOC286334	226590_at	AA910497	---	286334	-0.66	5.51E-03
C3orf6	225331_at	BF941088	NM_174908 NM_178335	152137	-0.66	4.75E-03
KIAA1579	231851_at	AL359613	NM_018211	55225	-0.66	4.44E-03
KIAA0241	212474_at	D87682	NM_015060	23080	-0.66	2.52E-03
TFAP2B	214451_at	NM_003221	NM_003221	7021	-0.66	6.69E-04
AI218542	236089_at	AI218542	---	---	-0.66	8.36E-03
EEF2K	225546_at	W68180	NM_013302	29904	-0.66	1.99E-03
KIAA0999	204157_s_at	NM_025164	NM_025164	23387	-0.65	3.68E-05
FXR1	201637_s_at	NM_005087	NM_005087	8087	-0.65	8.08E-03
AA406435	230747_s_at	AA406435	---	---	-0.65	6.70E-03
ZNF626	235687_at	AA908777	NM_145297	199777	-0.65	5.29E-03
KIAA0582	212675_s_at	AB011154	NM_015147	23177	-0.65	7.85E-03
DTNA	227084_at	AW339310	NM_001390 NM_001391 NM_001392 NM_032975 NM_032978 NM_032979 NM_032980 NM_032981	1837	-0.65	3.98E-03
C9orf109	229059_at	AI765785	XM_379665	286333	-0.65	1.91E-03
TBC1D12	1557609_s_at	AW188458	XM_051081	23232	-0.65	4.03E-03
LIN7C	223350_x_at	N63709	NM_018362	55327	-0.65	3.22E-03
PIK3R2	1568629_s_at	BC033311	NM_005027	5296	-0.65	7.91E-05
AU151635	232111_at	AU151635	---	---	-0.65	6.09E-04
NM_018678	220494_s_at	NM_018678	---	---	-0.65	4.32E-03
FAM8A1	203420_at	NM_016255	NM_016255	51439	-0.65	8.87E-03
AL136588	223614_at	AL136588	---	---	-0.65	3.95E-04
KIAA0179	212846_at	AA811192	NM_015056	23076	-0.65	7.52E-03
BF509796	229318_at	BF509796	---	---	-0.65	2.51E-03
SEC31L1	200945_s_at	NM_014933	NM_014933 NM_016211	22872	-0.65	8.63E-04
KIAA0711	204301_at	NM_014867	NM_014867	9920	-0.65	1.44E-03
AW025141	228400_at	AW025141	---	---	-0.64	6.23E-03
SERP1	235475_at	AI580135	NM_014445	27230	-0.64	8.89E-03
C2orf32	226751_at	AW193693	NM_015463	25927	-0.64	6.94E-04
KIAA1935	228336_at	AW511595	XM_087672	114825	-0.64	2.59E-03
PDE4D	228962_at	BF507941	NM_006203	5144	-0.64	2.48E-03
CDC14B	221556_at	BF792631	NM_003671 NM_033331 NM_033332	8555	-0.64	2.02E-03
FANCF	218689_at	NM_022725	NM_022725	2188	-0.64	5.25E-03
BCAR3	204032_at	NM_003567	NM_003567	8412	-0.64	3.94E-03

UBE2D3	200667_at	BF448062	NM_003340 NM_181886 NM_181887 NM_181888 NM_181889 NM_181890 NM_181891 NM_181892 NM_181893	7323	-0.64	2.05E-03
MGC29463	238115_at	T03492	NM_152686	202052	-0.64	4.51E-03
AFFX-BioDn-5	AFFX-BioDn-5_a	AFFX-BioDn-5	---	---	-0.64	1.45E-03
TPD52	201690_s_at	AA524023	NM_005079	7163	-0.64	8.25E-04
HPSE	222881_at	AF155510	NM_006665	10855	-0.64	2.12E-03
MAN1A2	217920_at	H97940	NM_006699	10905	-0.64	2.61E-03
HRMT1L1	221564_at	AL570294	NM_001535 NM_206962	3275	-0.64	5.66E-03
C22orf9	227144_at	AA476916	NM_00100988 0 NM_015264	23313	-0.63	8.11E-03
RGS12	1555022_at	AF464736	NM_002926 NM_198227 NM_198229 NM_198230 NM_198430 NM_198432 NM_198587	6002	-0.63	3.89E-05
FFX-r2-Ec-bioD	X-r2-Ec-bioD-5	AFFX-r2-Ec-bioD-5	---	---	-0.63	3.52E-03
AI766065	224647_at	AI766065	---	---	-0.63	4.41E-04
TDRD3	1569069_s_at	BC020604	NM_030794	81550	-0.63	4.16E-03
SOS1	227426_at	AV702692	NM_005633	6654	-0.63	3.92E-03
SMAD2	203077_s_at	NM_005901	NM_00100365 2 NM_005901	4087	-0.63	7.24E-03
MED28	228992_at	BF064162	NM_025205	80306	-0.63	2.06E-05
BICD1	1556051_a_at	CA777994	NM_00100339 8 NM_001714	636	-0.63	6.24E-04
GOLPH3L	218361_at	NM_018178	NM_018178	55204	-0.63	9.58E-04
MBNL1	201152_s_at	N31913	NM_021038 NM_207292 NM_207293 NM_207294 NM_207295 NM_207296 NM_207297	4154	-0.63	4.11E-05
LZTFL1	222632_s_at	AA843132	NM_020347	54585	-0.63	4.52E-04
RUFY1	233380_s_at	AA429145	NM_025158	80230	-0.63	8.27E-04
RBM18	238963_at	BG106093	NM_033117	92400	-0.63	1.19E-03
UBXD1	220757_s_at	NM_025241	NM_025241	80700	-0.63	9.92E-04
NCAM1	227394_at	W94001	NM_000615 NM_181351	4684	-0.63	2.48E-03
C14orf4	223474_at	AI932310	NM_024496	64207	-0.63	3.20E-04
PEX11A	205161_s_at	NM_003847	NM_003847	8800	-0.63	1.24E-04
BF692729	1558044_s_at	BF692729	---	---	-0.62	1.31E-03
AW290940	226773_at	AW290940	---	---	-0.62	4.57E-04
DDHD1	225970_at	AA029818	NM_030637	80821	-0.62	2.27E-03
C9orf10OS	239391_at	AA195528	NM_198841	158293	-0.62	7.21E-03
AI694544	235215_at	AI694544	---	---	-0.62	3.54E-03

TMEM45A	219410_at	NM_018004	NM_018004	55076	-0.62	1.39E-03
CXorf38	228700_at	AA063608	NM_144970	159013	-0.62	5.45E-03
LOC57149	203897_at	BE963444	NM_020424	57149	-0.62	2.10E-03
LOC54499	208715_at	BF002031	NM_019026	54499	-0.62	1.19E-03
SCAMP1	212425_at	AL049223	NM_004866	9522	-0.62	8.35E-03
			NM_052822			
IMPACT	222698_s_at	AF208694	NM_018439	55364	-0.62	7.05E-03
TRPM1	243741_at	AW665484	NM_002420	4308	-0.62	7.71E-03
TMAP1	227326_at	BE966768	NM_00100852	439921	-0.62	4.82E-03
			8			
			NM_00100852			
			9			
			NM_198530			
NLK	222589_at	AI967933	NM_016231	51701	-0.62	9.48E-03
KIAA0280	36612_at	D87470	XM_370635	23201	-0.62	7.88E-03
SYNCRIP	236146_at	BF593158	NM_006372	10492	-0.62	2.46E-04
NAV1	224772_at	AB032977	NM_020443	89796	-0.61	1.83E-03
AI216347	242087_x_at	AI216347	---	---	-0.61	7.98E-03
RTN4R	228550_at	NM_023004	NM_023004	65078	-0.61	2.34E-03
TLOC1	225352_at	AI763287	NM_003262	7095	-0.61	1.21E-03
AL137344	232390_at	AL137344	---	---	-0.61	8.75E-06
COMMD2	226910_at	AW008502	NM_016094	51122	-0.61	9.68E-03
LOC57228	209679_s_at	BC003379	NM_020467	57228	-0.61	9.52E-03
AW873330	225674_at	AW873330	---	---	-0.61	7.46E-03
RAD50	208393_s_at	NM_005732	NM_005732	10111	-0.61	2.10E-06
			NM_133482			
ZFY	230760_at	BF592062	NM_003411	7544	-0.61	8.36E-05
C21orf33	202217_at	NM_004649	NM_004649	8209	-0.61	9.07E-03
			NM_198155			
PAM	212958_x_at	AI022882	NM_000919	5066	-0.61	1.54E-03
			NM_138766			
			NM_138821			
			NM_138822			
PDCD2	204025_s_at	NM_002598	NM_002598	5134	-0.61	4.97E-03
			NM_144781			
AHI1	221569_at	AL136797	NM_017651	54806	-0.61	2.59E-03
TPD52	201689_s_at	BE974098	NM_005079	7163	-0.61	5.72E-03
AV721564	227620_at	AV721564	---	---	-0.61	9.48E-03
ZNF540	229328_at	T90358	NM_152606	163255	-0.61	8.93E-03
DKFZp761D19			XM_375608	400692		
18						
GAB1	226002_at	AK022142	NM_002039	2549	-0.60	4.32E-04
			NM_207123			
R02709	242149_at	R02709	---	---	-0.60	8.54E-03
DCX	204850_s_at	NM_000555	NM_000555	1641	-0.60	4.23E-03
			NM_178151			
			NM_178152			
			NM_178153			
PPARG	208510_s_at	NM_015869	NM_005037	5468	-0.60	1.82E-03
			NM_015869			
			NM_138711			
			NM_138712			
PCYOX1	225274_at	BF247054	NM_016297	51449	-0.60	6.39E-03
M17S2	201384_s_at	NM_005899	NM_005899	4077	-0.60	9.84E-04
			NM_031858			
			NM_031862			
KBTBD7	223412_at	AL136782	NM_032138	84078	-0.60	3.40E-03
AK094546	1556205_at	AK094546	---	---	-0.60	8.73E-03

GAJ	223700_at	AY028916	NM_032117	84057	-0.60	2.55E-03
BACE1	222462_s_at	AI653425	NM_012104 NM_138971 NM_138972 NM_138973	23621	-0.60	5.62E-04
RAB26	50965_at	AI690165	NM_014353	25837	-0.60	2.77E-03
AGPAT4	228667_at	AI733330	NM_020133	56895	-0.60	7.61E-03
LOC134147	227522_at	AA209487	NM_138809	134147	-0.60	9.04E-03
MRPS30	222275_at	AI039469	NM_016640	10884	-0.60	1.13E-03
AV699883	230782_at	AV699883	---	---	-0.60	1.72E-03
DJ122O8.2	227797_x_at	AI652464	NM_020466	57226	-0.60	5.64E-03
ULK2	204062_s_at	BG526973	NM_014683	9706	-0.60	2.35E-03
AL552727	244080_at	AL552727	---	---	-0.60	4.85E-03
DDEF1	224791_at	AW513835	NM_018482	50807	-0.60	1.40E-04
TIAM1	213135_at	U90902	NM_003253	7074	-0.60	7.17E-03
HOXC6	206858_s_at	NM_004503	NM_004503 NM_153693	3223	-0.60	3.44E-03
POFUT2	209578_s_at	BC000626	NM_015227 NM_133634 NM_133635	23275	-0.60	1.08E-03
ZFP36L2	201368_at	U07802	NM_006887	678	-0.60	1.13E-03
BC016176	1561529_at	BC016176	---	---	-0.60	5.78E-03
CNOT8	202163_s_at	NM_004779	NM_004779	9337	-0.60	7.52E-03
LOC124220	228058_at	AI559190	NM_145252	124220	-0.59	4.64E-03
ZC3HDC1	218543_s_at	NM_022750	NM_022750	64761	-0.59	7.38E-03
KIAA1126	225598_at	AB032952	XM_050325	57210	-0.59	1.48E-03
W26593	213048_s_at	W26593	---	---	-0.59	5.40E-03
FLJ20534	218646_at	NM_017867	NM_017867	54969	-0.59	1.34E-04
LOC126167	1560779_a_at	AK092139	XM_058997	126167	-0.59	2.41E-03
AA449838	241411_at	AA449838	---	---	-0.59	3.04E-03
FLJ38451	235052_at	AV758821	NM_175872	126375	-0.59	3.59E-03
MAP2	225540_at	BF342661	NM_002374 NM_031845 NM_031846 NM_031847	4133	-0.59	2.90E-03
CPD	201941_at	BE349147	NM_001304	1362	-0.59	3.19E-04
RP42	218583_s_at	NM_020640	NM_020640	54165	-0.59	3.27E-06
RBMX	213762_x_at	AI452524	NM_002139	27316	-0.59	2.27E-04
LRIG2	238653_at	BF967997	NM_014813	9860	-0.59	4.27E-03
BF431965	213567_at	BF431965	---	---	-0.59	7.58E-03
TRIM23	204732_s_at	AI021991	NM_001656 NM_033227 NM_033228	373	-0.59	9.14E-03
C9orf67	224506_s_at	BC006362	NM_032728	84814	-0.58	1.45E-03
AB002295	204307_at	AB002295	---	---	-0.58	2.09E-03
KIAA1546	227624_at	AB046766	XM_042301	57667	-0.58	4.89E-07
PPM1A	227728_at	AA886888	NM_021003 NM_177951 NM_177952	5494	-0.58	7.82E-03
ZNF148	239024_at	AI478771	NM_021964	7707	-0.58	2.84E-04
MARCH-I	235385_at	AI935334	NM_017923	55016	-0.58	6.65E-03
AB033091	225295_at	AB033091	---	---	-0.58	3.88E-03
IRF2BP2	224570_s_at	AA166696	NM_182972	359948	-0.58	4.89E-04
D31763	231864_at	D31763	---	---	-0.58	1.86E-03
LOC151146	227604_at	BG292251	---	151146	-0.58	8.00E-03

UBE2D3	229355_at	AU150386	NM_003340 NM_181886 NM_181887 NM_181888 NM_181889 NM_181890 NM_181891 NM_181892 NM_181893	7323	-0.58	6.55E-06
CUTL1	214743_at	BE046521	NM_001913 NM_181500 NM_181552	1523	-0.58	3.01E-04
LOC152485	228046_at	AA741243	NM_178835	152485	-0.58	8.28E-03
CLPX	223507_at	AL136922	NM_006660	10845	-0.58	6.77E-03
MAPKAP1	222426_at	BG499947	NM_00100661 7 NM_00100661 8 NM_00100661 9 NM_00100662 0 NM_00100662 1 NM_024117	79109	-0.58	3.51E-03
BRUNOL4	223654_s_at	BC004167	NM_020180	56853	-0.58	2.18E-03
ARFIP1	218230_at	AL044651	NM_014447	27236	-0.58	3.04E-03
SEC5L1	226270_at	AL562686	NM_018303	55770	-0.58	8.15E-06

Table 11. Increased Gene Expression in Cell Lines H1 and BB10 vs. SiMa Cell Line in Differentiated State Using Microarray Analysis

Gene Symbol	Probe Set ID	Representative Public ID	RefSeq Transcript ID	Entrez Gene	Log2 Ratio	pvalue
)KFZp667G211	214030_at	BE501352	XM_376254	131544	5.13	6.09E-05
BF476109	1556300_s_at	BF476109	---	---	5.09	2.02E-05
H99792	225710_at	H99792	---	---	4.92	2.07E-08
SLITRK5	214930_at	AW449813	NM_015567	26050	4.63	3.87E-06
DAZ1	207909_x_at	U21663	NM_00100537	1617	4.60	2.31E-03
DAZ3			5	57054		
DAZ2			NM_00100578	57055		
DAZ4			5	57135		
			NM_00100578			
			6			
			NM_004081			
			NM_020363			
			NM_020364			
			NM_020420			
RGS5	218353_at	NM_025226	NM_003617	8490	4.54	1.63E-03
SIM1	206876_at	AL121948	NM_005068	6492	4.53	2.11E-04
KCTD12	212192_at	AI718937	NM_138444	115207	4.51	4.17E-05
RGS5	1555725_a_at	AF493929	NM_003617	8490	4.49	3.25E-05
FLJ39639	243547_at	BE176531	XM_370932	283876	4.37	2.87E-03
DAZ1	208282_x_at	NM_020363	NM_00100537	1617	4.32	3.54E-03
DAZ3			5	57054		
DAZ2			NM_00100578	57055		
DAZ4			5	57135		
			NM_00100578			
			6			
			NM_004081			
			NM_020363			
			NM_020364			
			NM_020420			
PCDH9	219737_s_at	AI524125	NM_020403	5101	4.30	1.19E-03
			NM_203487			
RGS5	209071_s_at	AF159570	NM_003617	8490	4.10	1.32E-04
RGS5	209070_s_at	AI183997	NM_003617	8490	4.07	1.28E-04
)KFZp761O201	232313_at	AL122107	XM_044062	92293	4.01	2.30E-06
MAB21L2	210302_s_at	AF262032	NM_006439	10586	3.99	2.81E-04
ALCAM	240655_at	BE502785	NM_001627	214	3.98	3.07E-05
DAZ1	207912_s_at	NM_004081	NM_00100537	1617	3.96	1.79E-03
DAZ3			5	57054		
DAZ2			NM_00100578	57055		
DAZ4			5	57135		
			NM_00100578			
			6			
			NM_004081			
			NM_020363			
			NM_020364			
			NM_020420			
GRP	206326_at	NM_002091	NM_002091	2922	3.94	1.52E-05
PDZRN3	233442_at	AU147500	NM_015009	23024	3.92	2.66E-03
MAB21L1	206163_at	NM_005584	NM_005584	4081	3.91	6.73E-06
TIMP3	201149_s_at	U67195	NM_000362	7078	3.84	5.07E-03
TIMP3	201147_s_at	BF347089	NM_000362	7078	3.61	7.18E-03
PDZRN3	212915_at	AL569804	NM_015009	23024	3.58	7.05E-03

LOC440738	221697_at	AF276659	NM_001004343	440738	3.54	3.13E-03
GNG11	204115_at	NM_004126	NM_004126	2791	3.52	6.00E-04
PLK2	201939_at	NM_006622	NM_006622	10769	3.49	8.48E-05
CXCR4	217028_at	AJ224869	NM_001008540 NM_003467	7852	3.49	2.53E-05
DLL1	224215_s_at	AF196571	NM_005618	28514	3.40	1.98E-05
LOC340109	1557765_at	BC039509	XM_379322	340109	3.33	4.27E-04
CCDC3	223316_at	AL136562	NM_031455	83643	3.32	3.45E-05
P2RY5	218589_at	NM_005767	NM_005767	10161	3.27	1.73E-03
QKI	212636_at	AL031781	NM_006775 NM_206853 NM_206854 NM_206855	9444	3.23	3.28E-03
DAZ1 DAZ3 DAZ2 DAZ4	208281_x_at	NM_020364	NM_001005375 57054 NM_001005785 57135 NM_001005786 NM_004081 NM_020363 NM_020364 NM_020420	1617 57055	3.19	3.17E-03
PCDH9	238919_at	R49295	NM_020403 NM_203487	5101	3.15	4.07E-03
AI242023	240458_at	AI242023	---	---	3.11	1.45E-04
SLC4A11	223748_at	AF336127	NM_032034	83959	3.10	1.45E-03
RPL10A	242188_at	AI743332	NM_007104	4736	3.09	2.35E-03
POLQ	207746_at	NM_014125	NM_006596 NM_199420	10721	3.07	7.89E-03
MGC24103	232568_at	AU145658	---	158295	3.07	8.38E-03
SPAG6	210033_s_at	AF079363	NM_012443 NM_172242	9576	3.06	1.67E-04
RNF182	230720_at	AI884906	NM_152737	221687	3.05	5.00E-05
LOC440928	235147_at	R56118	XM_498917	440928	3.04	2.36E-03
AL049260	216518_at	AL049260	---	---	3.01	8.57E-03
ITGA6	201656_at	NM_000210	NM_000210	3655	3.00	2.58E-04
KCTD12	212188_at	AA551075	NM_138444	115207	2.98	5.67E-04
CXCR4	211919_s_at	AF348491	NM_001008540 NM_003467	7852	2.98	7.80E-03
NEGR1	243357_at	AA115106	NM_173808	257194	2.98	6.99E-05
MGC34032	1569112_at	AW020413	NM_152697	204962	2.94	4.27E-04
PTPRG	1569323_at	BU853579	NM_002841	5793	2.92	3.90E-03
CXCR4	209201_x_at	L01639	NM_001008540 NM_003467	7852	2.90	6.72E-03
CBFA2T2	233243_at	AU144676	NM_005093 NM_175864	9139	2.88	2.26E-03

DAZ1 DAZ3 DAZ2 DAZ4	216922_x_at	AF271088	NM_00100537 5 NM_00100578 5 NM_00100578 6 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	2.88	7.32E-03
CGNL1	225817_at	AB051536	NM_032866	84952	2.86	3.83E-03
FBXL7	241457_at	AI821935	NM_012304	23194	2.84	1.42E-03
TIMP3	201148_s_at	AW338933	NM_000362	7078	2.79	6.12E-03
BNC2	233036_at	AU146418	NM_017637	54796	2.78	9.59E-03
EDG2	204036_at	AW269335	NM_001401 NM_057159	1902	2.73	5.34E-03
BE674460	237849_at	BE674460	---	---	2.73	7.55E-03
MAB21L2	210303_at	AF262032	NM_006439	10586	2.69	1.03E-03
PDE5A	227088_at	BF221547	NM_001083 NM_033430 NM_033431 NM_033437	8654	2.65	4.68E-03
BC043430	1558714_at	BC043430	---	---	2.65	4.03E-03
AA699443	241838_at	AA699443	---	---	2.64	9.15E-04
AL049337	215768_at	AL049337	---	---	2.62	9.86E-03
RASEF	1553986_at	BC023566	NM_152573	158158	2.61	4.66E-04
PTGFRN	224937_at	BF311866	NM_020440	5738	2.61	1.34E-06
AK025909	233814_at	AK025909	---	---	2.60	1.65E-03
CPVL	208146_s_at	NM_031311	NM_019029 NM_031311	54504	2.59	5.34E-04
TRIM36	219736_at	NM_018700	NM_018700	55521	2.59	6.52E-04
AI377043	230722_at	AI377043	---	---	2.58	7.06E-03
SLAC2-B	214734_at	AB014524	NM_015065	23086	2.58	1.44E-04
AI077566	243994_at	AI077566	---	---	2.57	2.62E-03
EFNA5	1559360_at	AL833045	NM_001962	1946	2.53	7.18E-04
BE464799	214036_at	BE464799	---	---	2.53	1.16E-03
MSN	200600_at	NM_002444	NM_002444	4478	2.52	1.01E-06
RAD23B	214422_at	T93562	NM_002874	5887	2.52	2.47E-03
TULP4	232372_at	AL157491	NM_00100746 6 NM_020245	56995	2.51	4.65E-03
SCN7A	239984_at	AI333640	NM_002976	6332	2.51	8.48E-03
ITGA6	215177_s_at	AV733308	NM_000210	3655	2.50	6.62E-04
NFIB	211466_at	U70862	NM_005596	4781	2.50	1.09E-05
EML1	204797_s_at	NM_004434	NM_00100870 7 NM_004434	2009	2.50	1.46E-03
BNC2	220272_at	NM_017637	NM_017637	54796	2.49	3.27E-04
BE348318	236167_at	BE348318	---	---	2.49	5.60E-03
AW963185	241700_at	AW963185	---	---	2.47	1.92E-04
ENC1	201340_s_at	AF010314	NM_003633	8507	2.47	8.66E-03
RBMS3	233608_at	AU146417	NM_00100379 2 NM_00100379 3 NM_014483	27303	2.44	5.92E-03

DACH1	1567101_at	AF147347	NM_004392 NM_080759 NM_080760	1602	2.42	9.28E-03
AA654772	241391_at	AA654772	---	---	2.41	7.59E-03
BG400570	1565689_at	BG400570	---	---	2.41	6.41E-03
PIAS1	222371_at	AI732802	NM_016166	8554	2.40	3.91E-03
EDD	232264_at	AK022204	NM_015902	51366	2.40	1.41E-03
NOL7	242143_at	BE674964	NM_016167	51406	2.39	4.55E-03
U80755	243820_at	U80755	---	---	2.39	2.59E-03
ASCL1	209985_s_at	BE797438	NM_004316	429	2.37	8.08E-03
AW052186	239942_at	AW052186	---	---	2.37	9.33E-03
THRAP2	238883_at	AW975051	NM_015335	23389	2.37	9.49E-03
ROBO2	226766_at	AB046788	XM_031246	6092	2.36	7.82E-03
INA	230859_at	BF111276	NM_032727	9118	2.36	2.50E-05
CHC1L	230292_at	AA868809	NM_001268	1102	2.36	6.84E-03
CHRNA7 CHRFAM7A	210123_s_at	U62436	NM_000746 NM_139320 NM_148911	1139 89832	2.33	2.81E-03
ARID1B	240008_at	AI955765	NM_017519 NM_020732 NM_175863	57492	2.32	7.87E-03
SSH2	230970_at	AA975530	NM_033389	85464	2.29	6.93E-03
BE670307	227955_s_at	BE670307	---	---	2.28	5.03E-04
EB-1	227441_s_at	AW005572	NM_020140 NM_152788 NM_181670	56899	2.28	6.31E-03
GNAI1	209576_at	AL049933	NM_002069	2770	2.27	8.26E-06
PIAS1	1559156_at	BC036508	NM_016166	8554	2.27	5.54E-03
CUGBP2	202158_s_at	NM_006561	NM_006561	10659	2.26	8.77E-03
LOC441157	1558795_at	AL833240	XM_499037	441157	2.25	6.17E-05
KIAA0265	238000_at	BF195340	NM_014997	23008	2.23	9.27E-03
SOX2	213721_at	L07335	NM_003106	6657	2.23	1.49E-03
ENC1	201341_at	NM_003633	NM_003633	8507	2.23	8.95E-03
PLXNA2	222159_at	AK023058	NM_025179	5362	2.21	5.06E-04
GNAI1	227692_at	AU153866	NM_002069	2770	2.21	2.84E-06
NRXN1	209915_s_at	AB035356	NM_004801 NM_138735	9378	2.21	3.08E-03
OLFML3	218162_at	NM_020190	NM_020190	56944	2.19	8.33E-04
CBLB	233614_at	AU145361	NM_170662	868	2.19	8.28E-03
CG012	215318_at	AL049782	---	116829	2.19	4.30E-03
SESN3	235150_at	AW376955	NM_144665	143686	2.18	1.58E-03
SOX2	228038_at	AI669815	NM_003106	6657	2.18	1.19E-03
C1orf43	1555225_at	BC008306	NM_015449 NM_138740	25912	2.17	1.21E-05
SPAG6	210032_s_at	AI651156	NM_012443 NM_172242	9576	2.16	1.98E-03
ASCL1	209987_s_at	BC002341	NM_004316	429	2.15	4.18E-03
RASEF	235144_at	AA826324	NM_152573	158158	2.14	2.84E-04
OSBPL3	209626_s_at	AI202969	NM_015550 NM_145320 NM_145321 NM_145322 NM_145323 NM_145324	26031	2.14	4.14E-04

HGF	210997_at	M77227	NM_000601 NM_00101093 1 NM_00101093 2 NM_00101093 3 NM_00101093 4	3082	2.13	3.66E-03
SLC7A2	225516_at	AA876372	NM_00100853 9 NM_003046	6542	2.13	9.92E-04
EDG3	228176_at	AA534817	NM_005226	1903	2.13	4.95E-04
EFNB2	202668_at	BF001670	NM_004093	1948	2.13	5.45E-03
BF513404	239469_at	BF513404	---	---	2.12	1.51E-03
LRRC16	219573_at	NM_017640	NM_017640	55604	2.11	8.45E-04
ARHGAP20	228368_at	AI936560	NM_020809	57569	2.11	3.27E-04
ZFHX4	219779_at	NM_024721	NM_024721	79776	2.10	3.71E-04
AW953794	230968_at	AW953794	---	---	2.09	6.43E-03
LOC23117	238341_at	BF677084	XM_290670	23117	2.09	3.42E-03
AK022040	233445_at	AK022040	---	---	2.08	3.85E-03
TOP1	238988_at	AI863675	NM_003286	7150	2.08	5.99E-03
ALCAM	1569362_at	BC041127	NM_001627	214	2.07	5.59E-04
XPO1	1560386_at	BC041656	NM_003400	7514	2.07	4.79E-04
SPAG9	1554543_at	BC007524	NM_003971 NM_172345	9043	2.07	1.57E-04
RAF1	244373_at	AI740571	NM_002880	5894	2.07	9.16E-04
GFRA2	205721_at	U97145	NM_001495	2675	2.06	4.42E-03
CXCL12	209687_at	U19495	NM_000609 NM_199168	6387	2.04	2.46E-04
MGC34032	235763_at	AA001450	NM_152697	204962	2.04	3.86E-03
AI671885	230494_at	AI671885	XM_379123	400999	2.01	7.61E-03
GPR125	1569542_at	BC020926	NM_145290	166647	1.99	8.83E-03
BF057073	231310_at	BF057073	---	---	1.97	9.44E-04
PGAP1	233479_at	AU148008	NM_024989	80055	1.95	7.98E-03
LOC440265	1569476_at	BC033224	XM_378506	440265	1.95	1.83E-03
TFPI2	209278_s_at	L27624	NM_006528	7980	1.95	3.05E-03
KIAA1713	233536_at	AI202664	XM_290811	80816	1.94	5.70E-05
H37807	241060_x_at	H37807	---	---	1.94	5.73E-03
AA417878	243463_s_at	AA417878	---	---	1.93	4.35E-04
ZNF537	223392_s_at	BF510588	NM_020856	57616	1.93	5.36E-04
PTPRG	204944_at	NM_002841	NM_002841	5793	1.93	4.06E-07
MAOA	204388_s_at	NM_000240	NM_000240	4128	1.92	2.34E-03
TFPI2	209277_at	AL574096	NM_006528	7980	1.91	9.47E-03
ASCL1	213768_s_at	AW950513	NM_004316	429	1.91	9.81E-03
GFM1	232295_at	AK000780	NM_024996	85476	1.90	3.91E-03
AF131796	231916_at	AF131796	---	---	1.90	9.65E-06
SLCO3A1	219229_at	NM_013272	NM_013272	28232	1.89	6.98E-07
FLJ34154	1561130_at	AF086006	NM_173813	283450	1.89	4.96E-03
MSI2	239232_at	AA521410	NM_138962 NM_170721	124540	1.87	7.62E-03
MAOA	212741_at	AA923354	NM_000240	4128	1.87	3.66E-04
PRKCBP1	207130_at	NM_018634	NM_012408 NM_183047 NM_183048	23613	1.87	5.52E-03
PPP3R1	1565811_at	BC033945	NM_000945	5534	1.86	2.12E-03
CUGBP2	202157_s_at	U89546	NM_006561	10659	1.86	4.76E-03
AW024890	229942_at	AW024890	---	---	1.86	2.32E-04

NOS1	239132_at	BE299830	NM_000620	4842	1.85	4.05E-05
AI733341	240911_at	AI733341	---	---	1.83	2.70E-06
MAOA	204389_at	NM_000240	NM_000240	4128	1.83	5.67E-03
AI919519	235092_at	AI919519	---	---	1.83	1.25E-03
HGF	210755_at	U46010	NM_000601	3082	1.83	4.16E-03
			NM_00101093 1			
			NM_00101093 2			
			NM_00101093 3			
			NM_00101093 4			
EB-1	227439_at	AI806510	NM_020140	56899	1.83	4.67E-03
			NM_152788			
			NM_181670			
NRG3	229233_at	H05240	NM_001010848	10718	1.81	5.10E-03
IREB2	1563130_a_at	AL109710	NM_004136	3658	1.81	4.45E-05
ASCL1	209988_s_at	BC001638	NM_004316	429	1.81	9.72E-03
BF509781	238970_at	BF509781	---	---	1.81	5.78E-03
AI651786	237945_at	AI651786	---	---	1.80	9.11E-04
AW206536	243470_at	AW206536	---	---	1.79	9.87E-03
CAS1	239545_at	AI335004	NM_022900	64921	1.78	2.35E-04
FLJ11259	218627_at	NM_018370	NM_018370	55332	1.78	3.98E-03
TPBG	203476_at	NM_006670	NM_006670	7162	1.78	3.60E-03
IGSF4	244345_at	AI627453	NM_014333	23705	1.78	1.19E-03
LOC441157	1558796_a_at	AL833240	XM_499037	441157	1.78	6.11E-04
C10orf18	216211_at	AL049233	XM_374765	54906	1.78	5.69E-03
TRIM68	219405_at	NM_018073	NM_018073	55128	1.77	9.35E-03
NM_018616	220702_at	NM_018616	---	---	1.76	8.03E-03
SF1	210172_at	D26121	NM_004630	7536	1.76	6.92E-03
			NM_201995			
			NM_201997			
			NM_201998			
AI140305	228849_at	AI140305	---	---	1.73	4.71E-03
BE856929	239349_at	BE856929	---	---	1.73	8.07E-03
CDC23	223651_x_at	BC005258	NM_004661	8697	1.73	3.36E-03
BG542611	1556277_a_at	BG542611	---	---	1.73	3.65E-03
LOC253981	226430_at	AI394438	---	253981	1.72	2.43E-04
FNDC5	226096_at	AI760132	NM_153756	252995	1.72	6.85E-03
VRK1	241737_x_at	T89693	NM_003384	7443	1.72	8.45E-04
PDE8B	243590_at	AA860184	NM_003719	8622	1.71	3.11E-03
SESN3	225123_at	BE883841	NM_144665	143686	1.71	4.09E-04
MAK3	244341_at	AA827728	NM_025146	80218	1.71	1.72E-03
FLJ35740	244297_at	AI806762	NM_147195	253650	1.70	9.74E-03
THOC3	236149_at	AA502999	NM_032361	84321	1.69	6.40E-03
INSM1	206502_s_at	NM_002196	NM_002196	3642	1.69	4.60E-03
SESN3	242899_at	N78412	NM_144665	143686	1.69	1.78E-03
PTGFRN	224950_at	BF476250	NM_020440	5738	1.69	3.70E-03
HIC2	1559600_at	AL831831	NM_015094	23119	1.69	1.03E-03
AI023295	237600_at	AI023295	---	---	1.67	3.22E-03
GLMN	236924_at	AA814383	NM_007070	11146	1.67	2.06E-03
			NM_053274			
N50083	229110_at	N50083	---	---	1.67	1.06E-03
BG542645	242793_at	BG542645	---	---	1.66	9.11E-03
FLJ37266	228973_at	AA057445	NM_175892	283225	1.65	3.82E-03
AK022258	233286_at	AK022258	---	---	1.64	4.08E-03
FNDC5	226097_at	AI686488	NM_153756	252995	1.64	5.89E-03

JJAZ1	1566191_at	AI907884	NM_015355	23512	1.63	6.56E-03
CNTN1	227202_at	AW072790	NM_001843 NM_175038	1272	1.63	3.78E-03
MYLIP	228098_s_at	AW292746	NM_013262	29116	1.63	2.87E-04
NM_024972	220898_at	NM_024972	---	---	1.63	5.35E-03
AL036662	235984_at	AL036662	---	---	1.62	1.89E-04
TIA1	1558922_at	CA776505	NM_022037 NM_022173	7072	1.62	3.98E-03
MYO6	203216_s_at	NM_004999	NM_004999	4646	1.62	5.80E-04
ZNF537	223393_s_at	AL136805	NM_020856	57616	1.62	7.69E-04
DNAPTP6	244597_at	AA701247	NM_015535	26010	1.61	2.65E-03
PIP5K1A	235646_at	BF515595	NM_003557	8394	1.61	1.66E-03
ANAPC7	225521_at	AL137586	NM_016238	51434	1.61	5.35E-03
AF5Q31	232865_at	N59653	NM_014423	27125	1.60	2.42E-04
C2orf31	221245_s_at	NM_030804	---	81561	1.60	3.45E-03
FAM55C	243011_at	BF317081	NM_145037	91775	1.59	1.18E-03
LHFPL2	212658_at	N66633	NM_005779	10184	1.59	1.64E-03
PSCD3	243752_s_at	AI870144	NM_004227	9265	1.59	2.84E-03
LOC90701	235676_at	BF055352	NM_033280	90701	1.59	6.05E-03
SMAD4	1565703_at	AL832789	NM_005359	4089	1.59	3.91E-03
PITPNB	242074_at	AA833902	NM_012399	23760	1.58	1.84E-03
DKFZp761D221	1569603_at	BC020900	NM_032291	84251	1.57	3.47E-03
MINA	213189_at	BE966695	NM_032778 NM_153182	84864	1.57	9.86E-05
YEATS2	236462_at	AA742310	NM_018023	55689	1.57	6.12E-04
ARIH1	242431_at	AI656728	NM_005744	25820	1.56	7.68E-03
XPO1	235927_at	BE350122	NM_003400	7514	1.56	1.83E-05
SPON1	213994_s_at	AI885290	NM_006108	10418	1.55	3.33E-03
SIMP	238303_at	AW070371	NM_178862	201595	1.55	2.24E-03
KLF12	243089_at	AA551114	NM_007249 NM_016285	11278	1.55	7.90E-03
MAK3	231199_at	AA701676	NM_025146	80218	1.55	2.30E-03
JARID2	232835_at	AA533080	NM_004973	3720	1.55	2.53E-03
H93038	241574_s_at	H93038	---	---	1.54	2.24E-03
TGFBR1	236561_at	AV700621	NM_004612	7046	1.54	4.78E-03
PRSS12	213802_at	AI810767	NM_003619	8492	1.53	6.28E-03
PLCL2	213309_at	AL117515	NM_015184	23228	1.52	6.87E-03
PIAS1	1558418_at	BC017507	NM_016166	8554	1.52	2.09E-03
USP48	229812_at	BE645018	NM_032236	84196	1.51	3.09E-05
SPOCK	202363_at	AF231124	NM_004598	6695	1.51	5.55E-05
MLL3	244010_at	AI057455	NM_021230 NM_170606	58508	1.50	4.50E-03
STRA6	1569335_a_at	BC015881	NM_022369	64220	1.50	2.05E-03
UCHL1	1555834_at	AW974143	NM_004181	7345	1.50	5.86E-03
AK025064	215221_at	AK025064	---	---	1.49	5.96E-03
MINA	213188_s_at	AI823896	NM_032778 NM_153182	84864	1.48	4.75E-05
PSME4	237180_at	T97717	NM_014614	23198	1.48	3.52E-03
SLC4A11	233550_s_at	AL109976	NM_032034	83959	1.48	5.66E-03
H04482	243287_s_at	H04482	---	---	1.48	5.28E-03
REPS1	215201_at	AW166925	NM_031922	85021	1.48	5.00E-03
OAZIN	240231_at	AI742383	NM_015878 NM_148174	51582	1.47	6.87E-03
CBLB	227900_at	AV701750	NM_170662	868	1.47	7.93E-03
SLC17A6	220551_at	NM_020346	NM_020346	57084	1.47	4.11E-04
CUGBP2	202156_s_at	N36839	NM_006561	10659	1.47	2.41E-03
R76828	1558877_at	R76828	---	---	1.46	4.33E-04
C9orf102	1557164_a_at	BM683657	NM_020207	56959	1.46	2.47E-03

CLSTN2	219414_at	NM_022131	NM_022131	64084	1.46	5.74E-03
FAM19A4	242348_at	AA757457	NM_001005527 NM_182522	151647	1.45	2.73E-05
HTR2B	206638_at	NM_000867	NM_000867	3357	1.44	5.90E-03
AW197616	230787_at	AW197616	---	---	1.44	1.22E-03
BC035170	1561079_at	BC035170	---	---	1.44	4.66E-03
CUGBP2	1557422_at	R49146	NM_006561	10659	1.44	7.71E-03
LCRISP1	223475_at	AF142573	NM_031461	83690	1.44	3.45E-03
SNCAIP	219511_s_at	NM_005460	NM_005460	9627	1.44	9.60E-03
RNF34	236288_at	AW572402	NM_025126 NM_194271	80196	1.44	1.55E-03
ALCAM	201951_at	BF242905	NM_001627	214	1.44	1.25E-03
FGD6	1555137_a_at	BC013319	NM_018351	55785	1.43	8.61E-03
AI821477	235985_at	AI821477	---	---	1.43	8.29E-04
SRPK2	239811_at	BF954306	NM_182691 NM_182692	6733	1.43	2.17E-03
CNTN1	227209_at	AI091445	NM_001843 NM_175038	1272	1.43	6.48E-03
PDLIM5	213684_s_at	BF671400	NM_001011513 NM_001011514 NM_001011515 NM_001011516 NM_006457	10611	1.43	4.72E-05
FLJ11710	244646_at	AW972881	---	79904	1.43	6.04E-03
MAPRE2	1564733_at	BC013931	NM_014268	10982	1.43	4.15E-03
DST	1558019_at	BC020911	NM_001723 NM_015548 NM_020388 NM_183380	667	1.42	5.60E-03
SCC-112	241798_at	AI339930	NM_015200	23244	1.42	4.68E-03
SPON1	209436_at	AB018305	NM_006108	10418	1.41	1.28E-03
PPP3R1	241786_at	AI380514	NM_000945	5534	1.41	8.09E-03
ARID1B	1556818_at	BE671639	NM_017519 NM_020732 NM_175863	57492	1.40	1.56E-03
ZA20D1	238994_at	AW022496	NM_020205	56957	1.40	1.24E-03
HIAT1	242374_at	AA747563	NM_033055	64645	1.40	9.78E-04
ZNF503	227195_at	AA603467	NM_032772	84858	1.40	1.14E-04
SMARCC2	1561973_at	AL833124	NM_003075 NM_139067	6601	1.39	4.39E-03
ZNF215	220214_at	NM_013250	NM_013250	7762	1.39	5.26E-03
KIAA0318	238817_at	BF063412	NM_015347	23504	1.39	3.46E-03
RAP80	233596_at	AF113675	NM_016290	51720	1.38	8.59E-03
ACY1L2	225421_at	AI654133	NM_001010852	135293	1.37	9.04E-04
UBE1C	1556338_at	BM353142	NM_003968 NM_198195 NM_198197	9039	1.37	4.28E-03
RASEF	1553186_x_at	NM_152573	NM_152573	158158	1.37	6.41E-03
MDN1	1569484_s_at	AL603301	NM_014611	23195	1.37	1.48E-03
E2-230K	1554814_at	BC007822	NM_022066	63893	1.36	5.24E-03
ZFOC1	1558816_at	BC037793	NM_152437	144348	1.35	1.76E-03
CAPZA2	240146_at	AW418562	NM_006136	830	1.35	1.22E-03
DLEU2	215629_s_at	AA905286	NM_006021	8847	1.35	3.10E-03

CLASP2	1558759_s_at	AA310888	NM_015097	23122	1.34	2.92E-03
KIAA1545	1557539_at	BC008052	XM_495939	57666	1.34	1.63E-03
FLJ45645	243038_at	AW292769	NM_198557	375287	1.34	4.56E-03
MGC34032	1552782_at	AK091400	NM_152697	204962	1.34	1.91E-03
ELOVL7	227180_at	AW138767	XM_371740	79993	1.33	4.90E-04
FLJ12666	215029_at	AL117451	NM_024595	79647	1.32	3.06E-03
AA156721	201952_at	AA156721	---	---	1.31	9.34E-05
IREB2	1555476_at	BC017880	NM_004136	3658	1.31	1.01E-03
SCML1	235652_at	AI431345	NM_006746	6322	1.31	1.08E-03
BTBD3	243462_s_at	BF590303	NM_014962 NM_181443	22903	1.31	1.87E-03
LRRTM1	243330_at	AW304000	NM_178839	347730	1.30	7.44E-03
RNF159	241956_at	AI521883	NM_032373	84333	1.30	2.94E-03
L3MBTL	242637_at	C14069	NM_015478 NM_032107	26013	1.30	2.01E-03
LRRFIP2	232704_s_at	AK025207	NM_006309 NM_017724	9209	1.29	1.87E-03
FLJ40773	1563933_a_at	AK091691	NM_152666	200150	1.29	6.62E-03
N46436	1556568_a_at	N46436	---	---	1.29	3.59E-03
TRIM33	239716_at	AA908970	NM_015906 NM_033020	51592	1.29	6.38E-03
RIP	1556088_at	AK098491	NM_032308	84268	1.29	7.36E-04
AK098258	1564175_at	AK098258	---	---	1.29	9.36E-03
WWOX	1556595_at	BQ025203	NM_016373 NM_018560 NM_130788 NM_130790 NM_130791 NM_130792 NM_130844	51741	1.29	9.57E-03
AW874669	239834_at	AW874669	---	---	1.29	1.39E-03
SYNCRIP	1555427_s_at	AY034482	NM_006372	10492	1.28	1.39E-03
ZNF198	1569091_at	BC039458	NM_003453 NM_197968	7750	1.28	9.19E-03
NOL7	244474_at	BE549780	NM_016167	51406	1.28	9.53E-03
C20orf23	232083_at	AB046810	NM_024704	55614	1.28	6.84E-03
THRAP1	236978_at	N51961	NM_005121	9969	1.28	5.36E-04
KIAA0217	241965_at	BF589232	NM_015155	23185	1.28	7.35E-03
ASXL1	242439_s_at	AI819150	NM_015338	171023	1.27	6.77E-03
ELOVL5	1566079_at	AL833001	NM_021814	60481	1.27	1.08E-03
XPO7	240168_at	AA679589	NM_015024	23039	1.26	3.43E-03
IREB2	1563129_at	AL109710	NM_004136	3658	1.26	2.34E-03
MMD	244523_at	AW104453	NM_012329	23531	1.26	1.24E-06
RASEF	1553185_at	NM_152573	NM_152573	158158	1.26	6.94E-03
ZA20D3	238812_at	AA741296	NM_019006	54469	1.26	5.79E-03
ARFGEF1	236742_at	AA132172	NM_006421	10565	1.25	6.55E-03
CUL3	242362_at	AI797788	NM_003590	8452	1.25	5.38E-03
THOC4	226319_s_at	AF047002	NM_005782	10189	1.25	5.54E-04
KLHL13	227875_at	AB037730	NM_033495	90293	1.25	1.10E-05
TAF15	241885_at	BF431050	NM_003487 NM_139215	8148	1.25	3.79E-03
C18965	242853_at	C18965	XM_379243	401106	1.24	2.00E-03
EZH2	203358_s_at	NM_004456	NM_004456 NM_152998	2146	1.24	4.13E-03
DLEU2	216870_x_at	AF264787	NM_006021	8847	1.24	3.31E-04
CABIN1	1557581_x_at	BC027347	NM_012295	23523	1.23	4.73E-03
HOXD4	205522_at	NM_014621	NM_014621	3233	1.23	7.69E-03
AW157450	235716_at	AW157450	---	---	1.23	1.18E-03

TPARL	1560622_at	AK000203	NM_018475	55858	1.23	3.89E-03
KDELC2	225128_at	AL548941	NM_153705	143888	1.23	6.61E-04
PTPRK	203038_at	NM_002844	NM_002844	5796	1.23	1.53E-03
SFRS2IP	1570507_at	BC020736	NM_004719	9169	1.23	3.26E-03
ZNF326	227680_at	AI057121	NM_181781 NM_182975 NM_182976	284695	1.23	1.88E-03
NM_000575	208200_at	NM_000575	---	---	1.23	1.37E-03
GPI	232002_at	AW843302	NM_000175	2821	1.23	2.05E-03
CAPN1	232012_at	AV691296	NM_005186	823	1.22	3.25E-05
XPO7	235796_at	AI927957	NM_015024	23039	1.22	8.08E-03
PITPNB	239978_at	BF109370	NM_012399	23760	1.22	8.12E-03
DENR	238982_at	AW665791	NM_003677	8562	1.22	1.47E-05
PFKFB3	202464_s_at	NM_004566	NM_004566	5209	1.22	3.62E-04
AA343057	234997_x_at	AA343057	XM_496451	388760	1.21	9.45E-03
RB1CC1	237626_at	AI801666	NM_014781	9821	1.21	5.81E-03
NR2C1	210530_s_at	M21985	NM_003297	7181	1.21	1.06E-06
PLXNA2	213030_s_at	AI688418	NM_025179	5362	1.21	7.50E-03
AI857788	227126_at	AI857788	---	---	1.20	3.82E-05
MYO6	210480_s_at	U90236	NM_004999	4646	1.20	3.13E-03
TH1L	225865_x_at	AJ238374	NM_016397 NM_198976	51497	1.20	3.35E-05
AL044078	221860_at	AL044078	---	---	1.19	1.28E-05
ZGPAT	221848_at	AL121845	NM_032527 NM_181484 NM_181485	84619	1.19	7.13E-04
HGF	209960_at	X16323	NM_000601 NM_001010931 NM_001010932 NM_001010933 NM_001010934	3082	1.18	7.95E-03
MGC47869	243056_at	AI301111	NM_175874	144608	1.18	5.95E-03
NKTR	1557737_s_at	AI880383	NM_005385	4820	1.18	1.36E-03
TRA2A	229574_at	AI268231	NM_013293	29896	1.18	1.72E-03
ITGB5	201125_s_at	NM_002213	NM_002213	3693	1.18	5.48E-04
ARIH1	1558710_at	BI791845	NM_005744	25820	1.18	7.13E-03
GOLGA4	215203_at	AW438464	NM_002078	2803	1.18	3.99E-03
BASP1	202391_at	NM_006317	NM_006317	10409	1.18	3.05E-03
TM4SF14	223314_at	BF025955	NM_030927	81619	1.18	1.52E-03
SYNCRIP	209025_s_at	AF037448	NM_006372	10492	1.17	3.35E-03
TH1L	220607_x_at	NM_016397	NM_016397 NM_198976	51497	1.15	2.89E-04
COBRA1	1556434_at	BQ777552	NM_015456	25920	1.15	3.42E-03
SPATS2	1570130_at	BC032441	NM_023071	65244	1.15	6.79E-03
GATA2	210358_x_at	BC002557	NM_032638	2624	1.15	2.50E-03
MYST3	242480_at	AA868356	NM_006766	7994	1.15	9.06E-03
TH1L	225261_x_at	AJ238376	NM_016397 NM_198976	51497	1.15	2.80E-05
PTK2	241387_at	AW276701	NM_005607 NM_153831	5747	1.14	7.90E-03
C9orf39	1559005_s_at	AK098502	NM_017738	54875	1.14	4.61E-03
SFRS8	240078_at	BG434474	NM_004592 NM_152235	6433	1.14	2.74E-03
TBC1D5	215612_at	AU147983	NM_014744	9779	1.14	2.73E-03

TCTEL1	242109_at	AI038577	NM_006519	6993	1.14	1.48E-06
SMC5L1	1562948_at	BC035661	NM_015110	23137	1.14	9.50E-03
PLS3	201215_at	NM_005032	NM_005032	5358	1.13	6.23E-03
TM4SF14	221002_s_at	NM_030927	NM_030927	81619	1.13	1.20E-03
SSB4	229929_at	AL563476	NM_080862	92369	1.13	8.19E-03
THOC4	226320_at	AF047002	NM_005782	10189	1.13	6.76E-04
EB-1	227440_at	AW005572	NM_020140	56899	1.13	5.86E-03
			NM_152788			
			NM_181670			
PCBP2	213517_at	AW103422	NM_005016	5094	1.13	2.39E-05
			NM_031989			
C9orf100	230522_s_at	BG028209	NM_032818	84904	1.12	5.16E-03
BNC2	235723_at	AA843242	NM_017637	54796	1.12	8.45E-03
UBE1C	1556339_a_at	BM353142	NM_003968	9039	1.12	2.60E-03
			NM_198195			
			NM_198197			
C20orf58	228017_s_at	BF593263	NM_152864	128414	1.12	4.82E-03
AW978811	242080_at	AW978811	---	---	1.12	5.08E-03
EXT1	1564378_a_at	AK025101	NM_000127	2131	1.12	4.78E-03
KIAA1423	225127_at	BF217531	XM_376550	57583	1.11	7.59E-05
CCAR1	236566_at	AI291189	NM_018237	55749	1.11	5.91E-03
SMG1	244766_at	BG180003	NM_014006	23049	1.11	2.54E-03
KIAA0220			NM_015092	283846		
LOC440345			XM_496125	440345		
TMP21	239851_at	AW629289	NM_006827	10972	1.11	9.85E-03
NOS1	207309_at	NM_000620	NM_000620	4842	1.11	4.13E-03
EIF4ENIF1	242983_at	AI806626	NM_019843	56478	1.11	2.41E-03
ANAPC5	239651_at	BE671583	NM_016237	51433	1.11	8.65E-03
FLJ20186	219646_at	NM_017702	NM_017702	54849	1.11	7.86E-03
			NM_207514			
BF196475	241529_at	BF196475	---	---	1.11	6.33E-03
FRMD4A	208476_s_at	NM_018027	NM_018027	55691	1.11	5.78E-03
SDHA	230077_at	W90764	NM_004168	255812	1.10	2.82E-03
SDHAL2			XM_171032	6389		
CHCHD3	216170_at	AK025271	NM_017812	54927	1.10	4.90E-03
SLC30A9	237051_at	AI890591	NM_006345	10463	1.10	3.32E-03
ANP32A	235954_at	AA972597	NM_006305	8125	1.10	6.96E-04
AV752058	244574_at	AV752058	---	---	1.09	1.04E-03
CTGLF1	1565620_at	BG621044	NM_133446	119016	1.09	8.36E-03
ZCCHC11	230713_at	BF115786	NM_00100988	23318	1.09	6.14E-03
			1			
			NM_00100988			
			2			
			NM_015269			
KIAA1219	242233_at	AI739332	NM_020336	57148	1.09	6.47E-03
PDGFD	219304_s_at	NM_025208	NM_025208	80310	1.09	1.44E-03
			NM_033135			
AA743413	236985_at	AA743413	---	---	1.08	9.66E-03
RNF10	237062_at	BE222109	NM_014868	9921	1.08	5.28E-03
ORC6L	219105_x_at	NM_014321	NM_014321	23594	1.08	3.86E-03
TH1L	225006_x_at	AJ238379	NM_016397	51497	1.08	3.76E-05
			NM_198976			
KIAA2024	1566166_at	AL833423	NM_172070	130507	1.07	9.88E-03
LOC283871	222622_at	BG284709	XM_208887	283871	1.06	3.90E-03
BE856960	242712_x_at	BE856960	---	---	1.06	1.22E-03
RPUSD3	1566603_s_at	AK094587	NM_173659	285367	1.05	1.31E-03
LOC284244	214162_at	AF070541	---	284244	1.05	6.69E-03
AI817960	239649_at	AI817960	---	---	1.05	8.05E-03

TRA2A	213593_s_at	AW978896	NM_013293	29896	1.05	1.05E-03
SBNO1	216161_at	AK024128	NM_018183	55206	1.05	2.06E-03
SIRT2	1558331_at	BG722779	NM_012237 NM_030593	22933	1.05	4.53E-04
AF090944	233995_at	AF090944	---	---	1.05	9.19E-03
C20orf58	230668_at	AI758937	NM_152864	128414	1.04	8.75E-03
HM13	1560297_at	BG928538	NM_030789 NM_178580 NM_178581 NM_178582	81502	1.04	7.20E-03
SLCO3A1	227367_at	AW976431	NM_013272	28232	1.04	1.11E-03
PAN3	239393_at	AW510927	NM_175854	255967	1.04	2.63E-03
CNTN4	229084_at	R42166	NM_175607 NM_175612 NM_175613	152330	1.04	7.84E-03
LOC51760	205613_at	NM_016524	NM_016524	51760	1.04	6.90E-03
APC	216933_x_at	S67788	NM_000038	324	1.04	6.77E-03
H43040	231108_at	H43040	---	---	1.03	6.01E-04
C9orf10	241242_at	BE503118	NM_014612	23196	1.03	9.13E-03
C13orf25	232291_at	AA256157	NM_213723 NM_213724	407975	1.03	4.81E-03
HAN11	233782_at	AU147133	NM_00100372 5 NM_005828	10238	1.03	2.43E-04
FLJ43654	235376_at	BF125564	NM_198562	375341	1.03	1.61E-03
RTN4	1556049_at	CA428769	NM_007008 NM_020532 NM_153828 NM_207520 NM_207521	57142	1.02	3.35E-03
CSE1L	210765_at	AF053640	NM_001316 NM_177436	1434	1.02	6.67E-05
CBLB	209682_at	U26710	NM_170662	868	1.02	1.33E-06
FLJ12750	236889_at	AI911084	NM_024667	79720	1.02	9.90E-03
PEG10	212094_at	AL582836	XM_496907 XM_499343	23089	1.02	4.05E-03
T40928	241913_at	T40928	XM_498972	441028	1.02	9.84E-03
FLJ11783	220546_at	NM_024891	NM_024891	79951	1.02	9.99E-04
NM_018627	220410_s_at	NM_018627	---	---	1.01	5.37E-03
CSPG6	1556925_at	AL360194	NM_005445	9126	1.01	1.34E-03
DERA	218102_at	NM_015954	NM_015954	51071	1.01	3.80E-03
DLL3	219537_x_at	NM_016941	NM_016941 NM_203486	10683	1.01	2.97E-04
CNOT7	233019_at	AU145061	NM_013354 NM_054026	29883	1.01	2.14E-03
HIVEP2	243254_at	T08739	NM_006734	3097	1.01	2.67E-03
MGC33926	229302_at	AA058832	NM_152390	130733	1.01	3.60E-03
LRRN5	216167_at	AK024867	NM_006338 NM_201630	10446	1.01	6.96E-03
API5	214960_at	AF229253	NM_006595	8539	1.00	5.16E-04
EAF2	219551_at	NM_018456	NM_018456	55840	1.00	5.97E-05
C2orf23	204364_s_at	BE535746	NM_022912	65055	1.00	9.51E-04
EVL	227232_at	T58044	NM_016337	51466	1.00	6.72E-04
MAP4K3	242448_at	AI800895	NM_003618	8491	1.00	4.16E-03
GLS	223080_at	AK025021	NM_014905	2744	1.00	5.50E-03
ST8SIA1	210073_at	L32867	NM_003034	6489	1.00	2.41E-03
SNAG1	226683_at	AU146771	NM_052870	112574	0.99	1.15E-03

TDG	203742_s_at	BF674842	NM_00100841 1 NM_003211	6996	0.99	1.56E-03
GALNT7	216756_at	AK024995	NM_017423	51809	0.99	7.57E-03
DCP2	244777_at	AA504595	NM_152624	167227	0.99	7.31E-03
HIPK2	224016_at	AF111850	NM_022740	28996	0.99	3.36E-03
BE467787	243835_at	BE467787	---	---	0.99	6.62E-03
C9orf39	239989_at	AW170610	NM_017738	54875	0.99	7.75E-05
AI655229	243497_at	AI655229	---	---	0.99	6.76E-03
WSB1	227501_at	AI377135	NM_015626 NM_134264 NM_134265	26118	0.99	6.53E-03
NM_025120	220728_at	NM_025120	---	---	0.98	1.00E-03
PCBP2	229467_at	AA504356	NM_005016 NM_031989	5094	0.98	8.91E-03
EIF4A1	214805_at	U79273	NM_001416	1973	0.98	7.43E-03
MGEA5	214972_at	AU144791	NM_012215	10724	0.97	7.74E-03
FLJ10579	230843_at	AA482037	NM_018145	55177	0.97	2.54E-03
ZCWPW2	243863_at	BF575233	XM_087384	152098	0.97	4.74E-03
RNF111	241413_at	W80457	NM_017610	54778	0.97	1.29E-03
PLEKHA6	205093_at	NM_014935	NM_014935	22874	0.97	1.50E-04
SEZ6L	207873_x_at	NM_021115	NM_021115	23544	0.97	2.35E-04
FLJ10213	219906_at	NM_018029	NM_018029	55096	0.97	6.80E-03
WTAP	1558783_at	AK024805	NM_004906 NM_152857 NM_152858	9589	0.97	2.62E-04
CTNNB1	242558_at	AW362945	NM_001904	1499	0.96	7.55E-03
AA830545	235730_at	AA830545	---	---	0.96	3.70E-05
MGC33846	231430_at	AW205640	NM_175885	220382	0.95	1.36E-03
ZNF238	207164_s_at	NM_006352	NM_006352 NM_205768	10472	0.95	2.86E-03
AF5Q31	232864_s_at	N59653	NM_014423	27125	0.95	4.59E-04
SFRS2	200753_x_at	BE866585	NM_003016	6427	0.95	2.39E-04
H40696	236122_at	H40696	XM_370722	387921	0.95	4.70E-03
AW971254	222369_at	AW971254	---	---	0.94	4.58E-03
DKFZp547A023	214731_at	AB037854	NM_018704	55917	0.94	7.37E-03
AK022388	233017_x_at	AK022388	---	---	0.94	7.06E-03
PRDX2	215067_x_at	AU147942	NM_005809 NM_181737 NM_181738	7001	0.94	2.97E-03
RET	215771_x_at	X15786	NM_020630 NM_020975	5979	0.94	8.55E-03
ACTR6	239679_at	AI871160	NM_022496	64431	0.94	4.88E-03
HNRPA1	222040_at	AI144007	NM_002136 NM_031157	3178	0.93	4.24E-03
TMEM4	209797_at	BC001027	NM_014255	10330	0.93	5.35E-04
CIAPIN1	230838_s_at	AW771492	NM_020313	57019	0.93	9.30E-04
PRPF4B	202126_at	AA156948	NM_003913 NM_176800	8899	0.93	2.94E-03
ETV3	1552423_at	NM_005240	NM_005240	2117	0.92	5.12E-03
KCNQ1OT1	243435_at	AI023707	---	10984	0.92	5.64E-03
HNRPA2B1	205292_s_at	NM_002137	NM_002137 NM_031243	3181	0.92	7.56E-04
AW138794	227283_at	AW138794	---	---	0.92	1.97E-03
HNRPU	236244_at	AI458297	NM_004501 NM_031844	3192	0.92	8.40E-04
TUBB6	209191_at	BC002654	NM_032525	84617	0.91	2.73E-03
SEZ6L	211894_x_at	AB041736	NM_021115	23544	0.91	9.29E-04

C2orf23	204365_s_at	NM_022912	NM_022912	65055	0.91	3.53E-04
HNRPM	238610_s_at	AI906424	NM_005968 NM_031203	4670	0.91	6.28E-03
NUP210	220035_at	NM_024923	NM_024923	23225	0.91	8.57E-03
RNF130	236292_at	AW196696	NM_018434	55819	0.91	5.09E-03
STMN3	222557_at	AL353715	NM_015894	50861	0.91	1.21E-04
KIAA0907	230028_at	BF508843	NM_014949	22889	0.91	1.57E-04
AI346432	229132_at	AI346432	---	---	0.91	6.45E-03
DLL3	222898_s_at	BE350882	NM_016941 NM_203486	10683	0.90	1.05E-03
CYB561	209164_s_at	BC002976	NM_001915	1534	0.90	8.80E-03
CBWD1	226193_x_at	AV709992	NM_018491	150472	0.90	5.40E-03
CBWD2			NM_172003	220869		
LOC220869			NM_201453	389760		
DC36				55871		
SFRS2	214882_s_at	BG254869	NM_003016	6427	0.90	2.75E-04
AK024901	234326_at	AK024901	---	---	0.90	3.19E-03
RAB12	238714_at	AA504249	XM_113967	201475	0.89	3.77E-03
BC001743	209446_s_at	BC001743	---	---	0.89	2.43E-05
CDK2AP1	201938_at	NM_004642	NM_004642	8099	0.89	4.50E-03
AF5Q31	1555436_a_at	BC025700	NM_014423	27125	0.89	2.72E-03
LOC144997	227289_at	AU119437	---	144997	0.88	6.49E-03
C10orf58	224435_at	BC005871	NM_032333	84293	0.88	3.29E-03
MAP3K13	211083_s_at	Z25428	NM_004721	9175	0.88	1.85E-03
CP110	1569353_at	BC030223	NM_014711	9738	0.88	1.17E-03
NDUFS1	1559691_at	BC032767	NM_005006	4719	0.88	5.87E-03
NUDT9	241489_at	BE671532	NM_024047 NM_198038 NM_198039	53343	0.88	3.25E-03
NFATC2IP	212808_at	AI884627	NM_032815	84901	0.88	1.28E-03
AW444985	243690_at	AW444985	---	---	0.87	3.30E-03
SYT11	232677_at	AU146128	NM_152280	23208	0.87	7.93E-03
PTPN1	202716_at	NM_002827	NM_002827	5770	0.87	7.56E-03
FLJ45983	240827_at	AA846824	NM_207423	399717	0.87	6.25E-03
BM041211	1562062_at	BM041211	---	---	0.87	8.38E-03
UQCRC2	241755_at	AI961429	NM_003366	7385	0.87	1.07E-03
WHSC2	1557300_s_at	AI741292	NM_005663	7469	0.87	7.80E-03
PDE7A	224046_s_at	U67932	NM_002603 NM_002604	5150	0.87	9.76E-03
PHF20	235389_at	BG168139	NM_016436	51230	0.87	1.49E-03
AW973410	244310_at	AW973410	XM_498613	440283	0.87	4.14E-03
FLJ10120	220220_at	NM_018001	---	55073	0.86	4.44E-03
ILF3	208931_s_at	AF147209	NM_004516 NM_012218 NM_153464	3609	0.86	4.15E-04
MARCKS	201670_s_at	M68956	NM_002356	4082	0.86	1.21E-03
U06715	217200_x_at	U06715	---	---	0.86	6.65E-03
182-FIP	224956_at	AI743689	NM_020772	57532	0.85	8.46E-03
FLJ13855	236107_at	AA147920	NM_023079	65264	0.85	4.95E-03
BI496583	1557675_at	BI496583	---	---	0.85	1.81E-03
C10orf58	228155_at	BF512388	NM_032333	84293	0.84	4.87E-03
SEZ6L	216047_x_at	AL050253	NM_021115	23544	0.84	6.17E-04
LOC254057	232370_at	AI635756	---	254057	0.84	3.35E-03
TCF7L2	216511_s_at	AJ270770	NM_030756	6934	0.84	7.95E-03
)KFZP564K196	223170_at	AF132000	NM_015544	26022	0.84	3.64E-03
SFRS2	200754_x_at	NM_003016	NM_003016	6427	0.83	7.20E-04
AA447714	244047_at	AA447714	---	---	0.83	8.79E-03
MARCKS	201668_x_at	AW163148	NM_002356	4082	0.83	5.34E-03

AF222691	216187_x_at	AF222691	---	---	0.83	8.37E-03
DCL-1	232371_at	AU155401	NM_014880	9936	0.83	8.82E-04
RPS24	1555878_at	AK094613	NM_001026 NM_033022	6229	0.83	7.05E-03
ZNF238	212774_at	AJ223321	NM_006352 NM_205768	10472	0.82	1.69E-03
NKTR	202379_s_at	AI361805	NM_005385	4820	0.82	2.20E-03
KIAA0485	242824_at	AW191647	---	57235	0.82	2.73E-03
CSE1L	201111_at	AF053641	NM_001316 NM_177436	1434	0.82	9.40E-03
NKTR	1557736_at	AI880383	NM_005385	4820	0.82	2.47E-03
MBD2	214397_at	AI827820	NM_003927 NM_015832	8932	0.82	8.51E-03
MCCC1	242223_at	AA505323	NM_020166	56922	0.82	5.18E-04
CREBBP	237239_at	AW183655	NM_004380	1387	0.82	1.36E-03
LOC129285	1554145_a_at	BC040721	NM_152994	129285	0.81	7.02E-03
SEZ6L	213609_s_at	AB023144	NM_021115	23544	0.81	8.59E-03
HNRPM	238611_at	AI906424	NM_005968 NM_031203	4670	0.81	5.61E-03
MYLIP	223129_x_at	T63512	NM_013262	29116	0.81	1.14E-03
AI476542	243032_at	AI476542	---	---	0.81	4.19E-03
HYPB	241458_at	AI868267	NM_012271 NM_014159	29072	0.81	8.29E-03
SNRPB2	1561965_at	BE466925	NM_003092 NM_198220	6629	0.81	8.93E-04
SMARCA4	217656_at	AW128846	NM_003072	6597	0.80	2.21E-03
MRPL4	223742_at	BC000756	NM_015956 NM_146387 NM_146388	51073	0.80	7.99E-05
HS6ST2	1552767_a_at	NM_147174	NM_147174 NM_147175	90161	0.80	2.64E-03
NEURL	243853_at	BF516539	NM_004210	9148	0.80	5.90E-04
SMARCD1	203183_s_at	NM_003076	NM_003076 NM_139071	6602	0.80	2.99E-03
HECTD1	242349_at	AW275658	NM_015382	25831	0.80	7.69E-04
GGA2	213772_s_at	BF196572	NM_015044 NM_138640	23062	0.80	3.58E-03
AA056145	227633_at	AA056145	---	---	0.79	9.47E-04
MAN2A1	235103_at	AA029155	NM_002372	4124	0.79	7.09E-03
SENP3	215114_at	AK000923	NM_015670	26168	0.79	2.65E-09
GULP1	223837_at	BC001103	NM_016315	51454	0.78	2.45E-03
JARID2	203297_s_at	BG029530	NM_004973	3720	0.78	9.88E-04
DNAPTP6	222154_s_at	AK002064	NM_015535	26010	0.78	5.12E-03
VPS29	223026_s_at	AF201946	NM_016226 NM_057180	51699	0.78	9.91E-03
AF279774	216967_at	AF279774	---	---	0.78	1.36E-03
COBLL1	203642_s_at	NM_014900	NM_014900	22837	0.78	1.12E-03
AI041522	228030_at	AI041522	---	---	0.78	4.80E-03
FLJ11029	219392_x_at	NM_018304	NM_018304	55771	0.78	4.83E-03
RNF34	219035_s_at	NM_025126	NM_025126 NM_194271	80196	0.77	2.35E-03
BF056892	229024_at	BF056892	---	---	0.77	3.47E-06
DKFZP564C186	1559139_at	BC009786	NM_015658	26155	0.77	3.20E-03
SFRS1	227164_at	AL521786	NM_006924	6426	0.77	1.00E-03
MR-1	225298_at	AA074597	NM_015488 NM_022572	25953	0.76	4.65E-03
ATP6V0A2	217603_at	AW444520	NM_012463	23545	0.76	2.94E-03

RECQL	210568_s_at	BC001052	NM_002907 NM_032941	5965	0.76	4.23E-03
YWHAB	208743_s_at	BC001359	NM_003404 NM_139323	7529	0.76	4.79E-03
ANKHD1	229457_at	AU148042	NM_017747 NM_017978 NM_024668	54882	0.76	4.26E-03
STRBP	233251_at	AK024960	NM_018387	55342	0.76	3.48E-03
AF147390	1562230_at	AF147390	---	---	0.76	2.73E-09
HIC2	212966_at	AL043112	NM_015094	23119	0.76	4.03E-03
LUC7L2	226758_at	AA043552	NM_016019	51631	0.76	5.54E-03
GNG2	224965_at	AU118419	NM_053064	54331	0.76	4.33E-03
USP7	230761_at	AI972599	NM_003470	7874	0.75	2.83E-03
SH3MD1	213252_at	AI739005	NM_014631	9644	0.75	1.10E-03
TLE4	204872_at	NM_007005	NM_007005	7091	0.75	4.50E-03
AA167167	243684_at	AA167167	---	---	0.75	4.31E-03
SLC25A13	229061_s_at	AW268880	NM_014251	10165	0.75	6.06E-03
NSD1	235760_at	AI421972	NM_022455 NM_172349	64324	0.75	9.51E-03
BTBD14A	243431_at	BF000597	NM_144653	138151	0.75	9.59E-03
AKR1B1	201272_at	NM_001628	NM_001628	231	0.74	2.19E-03
SDS3	233841_s_at	AK026749	NM_022491	64426	0.74	1.60E-04
ANAPC7	225554_s_at	AA131793	NM_016238	51434	0.74	4.31E-03
EPOR	215054_at	H16758	NM_000121	2057	0.74	9.06E-04
KHDRBS3	209781_s_at	AF069681	NM_006558	10656	0.74	6.64E-04
C6orf115	223361_at	AF116682	XM_371848	58527	0.73	1.49E-03
LOC157627	214839_at	AF052108	---	157627	0.73	8.43E-03
HS6ST2	230030_at	AI767756	NM_147174 NM_147175	90161	0.73	3.77E-03
DHX35	218579_s_at	NM_021931	NM_021931	60625	0.73	6.34E-06
AI700633	212812_at	AI700633	---	---	0.73	7.29E-03
ZNF281	222619_at	AU150752	NM_012482	23528	0.73	9.28E-04
NARG1	219158_s_at	NM_025085	NM_057175	80155	0.73	4.16E-03
C5orf13	201309_x_at	U36189	NM_004772	9315	0.73	6.38E-03
PBP	205353_s_at	NM_002567	NM_002567	5037	0.73	5.93E-04
KIAA0220	211996_s_at	BG256504	---	283846	0.72	1.81E-03
MYH10	212372_at	AK026977	NM_005964	4628	0.72	1.71E-03
AU147166	215212_at	AU147166	---	---	0.71	8.93E-03
BTBD3	202946_s_at	NM_014962	NM_014962 NM_181443	22903	0.71	8.99E-04
DNAJC9	213088_s_at	BE551340	NM_015190	23234	0.71	9.31E-03
MAN1A1	208116_s_at	NM_005907	NM_005907	4121	0.71	5.70E-03
ATP5G1	208972_s_at	AL080089	NM_00100202 7 NM_005175	516	0.71	3.03E-03
PAICS	201013_s_at	AA902652	NM_006452	10606	0.71	2.75E-03
AI378500	229821_at	AI378500	---	---	0.71	3.49E-03
KLHL5	226001_at	AK002174	NM_00100707 5 NM_199039	51088	0.71	2.63E-03
SFRS9	201698_s_at	NM_003769	NM_003769	8683	0.71	5.14E-04
PABPN1	213046_at	AI130920	NM_004643	8106	0.71	3.81E-04
GARNL1	234923_at	AK022988	NM_014990 NM_194301	253959	0.70	5.70E-03
MAN1A1	221760_at	BG287153	NM_005907	4121	0.70	7.22E-03
C5orf13	201310_s_at	NM_004772	NM_004772	9315	0.70	6.72E-03
NM_031221	208120_x_at	NM_031221	---	---	0.70	4.42E-04
CYHR1	213681_at	AW512817	NM_032687	50626	0.70	4.56E-03

BF437591	222026_at	BF437591	---	---	0.70	7.17E-03
SEZ6L	231650_s_at	BE672217	NM_021115	23544	0.70	9.10E-03
UFD1L	209103_s_at	BC001049	NM_005659	7353	0.70	1.25E-03
H37943	242311_x_at	H37943	---	---	0.70	2.95E-03
ACY1L2	225431_x_at	BE779764	NM_001010853	135293	0.70	3.20E-03
SCC-112	213983_s_at	AW991219	NM_015200	23244	0.70	8.02E-04
RPUSD3	1555916_at	BM670238	NM_173659	285367	0.70	1.32E-05
CCAR1	224736_at	BE617899	NM_018237	55749	0.69	8.03E-03
SNX1	1559154_at	AK098001	NM_003099	6642	0.69	5.03E-03
			NM_148955			
			NM_152826			
MGC52282	231638_at	AA400057	NM_178453	124221	0.69	4.60E-03
MAPKAPK3	202788_at	NM_004635	NM_004635	7867	0.69	3.76E-03
HNRPA3	211931_s_at	BG505670	NM_194247	220988	0.69	2.94E-04
AK024881	234723_x_at	AK024881	---	---	0.69	7.45E-03
PCIA1	218260_at	NM_024050	NM_024050	79016	0.69	9.77E-03
ANKRD36	238464_at	AA463221	XM_371540	375248	0.69	2.40E-03
N4BP2	231996_at	AB037834	NM_018177	55728	0.69	1.75E-03
EMID2	229080_at	BE741432	NM_133457	136227	0.68	1.65E-03
FLJ22490	242041_at	AI933671	NM_024790	79848	0.68	7.80E-03
IDH3B	210418_s_at	AF023265	NM_006899	3420	0.68	2.50E-03
			NM_174855			
			NM_174856			
MAN2A1	205105_at	NM_002372	NM_002372	4124	0.68	1.85E-03
BF055201	228242_at	BF055201	---	---	0.68	9.05E-03
IDH3B	210014_x_at	AF023266	NM_006899	3420	0.68	2.17E-03
			NM_174855			
			NM_174856			
GALNT4	231832_at	AI890347	NM_003774	8693	0.67	7.13E-03
OCIAD1	232644_x_at	AK024302	NM_017830	54940	0.67	5.83E-03
GPR51	211679_x_at	AF095784	NM_005458	9568	0.67	6.98E-03
SRC	213324_at	AK024281	NM_005417	6714	0.67	1.56E-03
			NM_198291			
PBP	210825_s_at	AF130103	NM_002567	5037	0.67	4.20E-03
THRAP4	213043_s_at	AI023317	NM_014815	9862	0.67	6.87E-04
ATAD3A	1552641_s_at	NM_031921	NM_018188	55210	0.66	7.21E-03
ATAD3B			NM_031921	83858		
FLJ20364	1559222_at	AA781731	NM_017785	54908	0.66	1.64E-03
TA-PP2C	225204_at	AA521311	NM_139283	160760	0.66	2.71E-03
EIF5A	201123_s_at	NM_001970	NM_001970	1984	0.66	8.31E-04
RECQL	212917_x_at	AI814728	NM_002907	5965	0.66	3.26E-03
			NM_032941			
ZC3HDC5	1562434_at	AL832312	XM_036115	85451	0.66	7.52E-03
BCR	202315_s_at	NM_004327	NM_004327	613	0.66	3.87E-03
			NM_021574			
C14orf2	242858_at	BF507638	NM_004894	9556	0.66	1.48E-03
MAP3K13	206249_at	NM_004721	NM_004721	9175	0.66	3.65E-03
SULT1A3	222094_at	AI580112	NM_003166	6818	0.66	3.16E-04
			NM_177552			
ZNF207	244153_at	AA521438	NM_003457	7756	0.65	8.57E-03
PEX26	219180_s_at	AI817074	NM_017929	55670	0.65	4.16E-03
RAN	200750_s_at	AF054183	NM_006325	5901	0.65	6.43E-03
EIF5A	213753_x_at	BF541557	NM_001970	1984	0.65	1.96E-05
C13orf6	235348_at	AA404347	NM_032859	84945	0.65	2.02E-03
EWSR1	210012_s_at	BC000527	NM_005243	2130	0.65	4.34E-03
			NM_013986			
SPG7	230885_at	BE670386	NM_003119	6687	0.65	7.60E-03
			NM_199367			

SCLY	59705_at	AA911739	NM_016510	51540	0.65	9.03E-03
KCTD10	223208_at	AF113208	NM_031954	83892	0.64	1.07E-04
FLJ13149	219016_at	NM_021826	NM_021826	60493	0.64	7.47E-04
ZNF217	203739_at	NM_006526	NM_006526	7764	0.64	2.22E-03
GGA2	208913_at	AA868560	NM_015044	23062	0.64	4.26E-03
			NM_138640			
DST	1560296_at	AV702787	NM_001723	667	0.64	8.16E-03
			NM_015548			
			NM_020388			
			NM_183380			
UBQLN1	222989_s_at	NM_013438	NM_013438	29979	0.64	9.49E-03
			NM_053067			
TOMM40	202264_s_at	NM_006114	NM_006114	10452	0.63	5.40E-03
VTI1A	235034_at	AW194969	NM_145206	143187	0.63	9.95E-03
TMEM33	222642_s_at	BC000948	NM_018126	55161	0.63	6.62E-03
KIAA1219	221738_at	BG236163	NM_020336	57148	0.63	1.93E-03
RPL23	215224_at	AK025200	NM_000978	9349	0.63	7.04E-04
ZNF43	222136_x_at	AK022905	NM_003423	7594	0.63	4.57E-03
BE671123	235798_at	BE671123	---	---	0.63	8.79E-03
WDR17	1552430_at	NM_170710	NM_170710	116966	0.63	5.45E-04
			NM_181265			
FUBP1	212847_at	AL036840	NM_003902	8880	0.63	6.95E-03
MBTD1	207115_x_at	NM_017643	NM_017643	54799	0.63	7.84E-03
PHC2	1557852_at	AW418842	NM_004427	1912	0.62	8.02E-03
			NM_198040			
AP1S2	228415_at	AA205444	NM_003916	8905	0.62	8.44E-03
GPR125	210473_s_at	M37712	NM_145290	166647	0.62	6.47E-03
SFRS6	208804_s_at	AL031681	NM_006275	6431	0.62	3.30E-03
AI216567	236754_at	AI216567	---	---	0.62	4.60E-03
C15orf25	220071_x_at	NM_018097	NM_018097	55142	0.62	9.64E-03
CDH2	203441_s_at	NM_001792	NM_001792	1000	0.62	5.11E-03
MRPL35	222775_s_at	AK026220	NM_016622	51318	0.62	1.89E-03
			NM_145644			
CNP	208912_s_at	BC001362	NM_033133	1267	0.62	3.84E-03
FLJ20331	218577_at	NM_017768	NM_017768	55631	0.62	6.26E-03
FLJ21415	218867_s_at	NM_024738	NM_024738	79794	0.62	3.36E-03
AF336882	224288_x_at	AF336882	---	---	0.62	3.59E-03
SSBP3	223635_s_at	BC003605	NM_00100995	23648	0.62	2.27E-03
			5			
			NM_018070			
			NM_145716			
ATF7IP	231825_x_at	AK025060	NM_018179	55729	0.62	7.81E-03
TOP1	208901_s_at	J03250	NM_003286	7150	0.61	6.28E-04
SYNCRIP	209024_s_at	AI472757	NM_006372	10492	0.61	1.15E-03
DHX30	239772_x_at	AI368527	NM_014966	22907	0.61	1.59E-04
			NM_138614			
			NM_138615			
BE878277	212829_at	BE878277	---	---	0.61	1.63E-03
FBXL10	226215_s_at	AI989996	NM_00100536	84678	0.61	7.38E-03
			6			
			NM_032590			
KIAA0251	1555347_at	BC033748	NM_015027	23042	0.61	2.52E-03
RBM14	204178_s_at	NM_006328	NM_006328	10432	0.61	3.59E-05
EXOSC1	1559044_at	BC012538	NM_016046	51013	0.61	7.00E-04
KIAA0992	234135_x_at	AK021652	NM_016081	23022	0.60	8.94E-03
EIF5A	201122_x_at	BC000751	NM_001970	1984	0.60	1.14E-03
R26456	243135_x_at	R26456	---	---	0.60	5.74E-03
TMEM33	218465_at	NM_018126	NM_018126	55161	0.60	8.99E-03

SFRS1	201741_x_at	M69040	NM_006924	6426	0.60	1.36E-03
RAB11FIP3	214999_s_at	AW243089	NM_014700	9727	0.60	1.50E-04
DDX46	228039_at	AI765169	NM_014829	9879	0.60	2.91E-03
HNRPU	200593_s_at	BC003621	NM_004501 NM_031844	3192	0.60	1.26E-05
HNRPU	200594_x_at	NM_004501	NM_004501 NM_031844	3192	0.59	1.74E-04
GNG12	212294_at	BG111761	NM_018841	55970	0.59	6.29E-03
ARS2	201680_x_at	NM_015908	NM_015908 NM_182800	51593	0.59	2.20E-04
FLJ37078	235880_at	BF593867	NM_153043	222183	0.59	7.82E-05
GPR51	209990_s_at	AF056085	NM_005458	9568	0.59	7.76E-03
MARCKS	201669_s_at	NM_002356	NM_002356	4082	0.59	4.74E-05
MAN2A1	226538_at	AV700323	NM_002372	4124	0.59	4.65E-03
HCFC1	202474_s_at	NM_005334	NM_005334	3054	0.59	2.12E-03
FLJ35709	242540_at	AI911330	NM_173589	283294	0.58	5.90E-03
MYO1B	212365_at	BF215996	NM_012223	4430	0.58	6.28E-04
PPP2CA	208652_at	BC000400	NM_002715	5515	0.58	3.88E-03
CDC5L	209055_s_at	AW268817	NM_001253	988	0.58	2.61E-04

Table 12. Decreased Gene Expression in Cell Lines H1 and BB10 vs.Cell Line SiMa in Differentiated State Using Microarray Analysis

Gene Symbol	Probe Set ID	Representative Public ID	RefSeq Transcript ID	Entrez Gene	Log2 Ratio	pvalue
CYTL1	219837_s_at	NM_018659	NM_018659	54360	-6.94	6.41E-06
GNAS	217057_s_at	AF107846	NM_000516 NM_016592 NM_080425 NM_080426	2778	-5.47	4.18E-03
CYGB	226632_at	AL513673	NM_134268	114757	-4.81	3.60E-03
TNFRSF10D	227345_at	AI738556	NM_003840	8793	-4.68	2.31E-06
ECEL1	219914_at	NM_004826	NM_004826	9427	-4.67	3.83E-05
SYT13	226086_at	AB037848	NM_020826	57586	-4.06	1.83E-04
TMIE	1553601_a_at	NM_147196	NM_147196	259236	-3.86	6.07E-05
NNAT	204239_s_at	NM_005386	NM_005386 NM_181689	4826	-3.83	5.67E-07
CNGA3	207261_at	NM_001298	NM_001298	1261	-3.76	4.84E-04
AU157716	227051_at	AU157716	---	---	-3.75	4.31E-03
AF150317	243111_at	AF150317	---	---	-3.69	9.83E-04
ASAM	226834_at	BG112263	NM_024769	79827	-3.61	5.78E-03
LOC254128	1557059_at	AK098264	---	254128	-3.51	1.95E-07
LOC339290	228160_at	AI433706	XM_375527	339290	-3.50	6.83E-05
FUCA2	223120_at	BC003060	NM_032020	2519	-3.47	8.50E-03
STX3A	209238_at	BE966922	NM_004177	6809	-3.45	8.83E-03
CYGB	1553572_a_at	NM_134268	NM_134268	114757	-3.43	4.93E-06
EDG7	231192_at	AW274018	NM_012152	23566	-3.39	1.39E-03
HTATIP2	207180_s_at	NM_006410	NM_006410	10553	-3.38	4.96E-04
HTATIP2	209448_at	BC002439	NM_006410	10553	-3.38	3.60E-04
LMCD1	218574_s_at	NM_014583	NM_014583	29995	-3.34	6.84E-03
BACE2	217867_x_at	NM_012105	NM_012105 NM_138991 NM_138992	25825	-3.33	5.05E-04
FLJ45880	228538_at	BE671164	NM_207404	389114	-3.28	4.82E-06
EDG7	220816_at	NM_012152	NM_012152	23566	-3.28	2.16E-03
CDC42EP1	204693_at	NM_007061	NM_007061 NM_152243	11135	-3.25	9.63E-03
TCEAL2	211276_at	AF063606	NM_080390	140597	-3.25	3.45E-04
MEOX2	206201_s_at	NM_005924	NM_005924	4223	-3.23	2.59E-06
FGF13	205110_s_at	NM_004114	NM_004114 NM_033642	2258	-3.22	4.26E-05
IGFBP7	201163_s_at	NM_001553	NM_001553	3490	-3.17	3.25E-03
BACE2	222446_s_at	AF178532	NM_012105 NM_138991 NM_138992	25825	-3.16	1.05E-04
SLC35F3	229065_at	BF968270	NM_173508	148641	-3.14	1.47E-06
TncRNA	224565_at	BE675516	---	283131	-3.11	3.26E-03
LGALS3	208949_s_at	BC001120	NM_002306	3958	-3.08	1.25E-03
GALIG			NM_194327	81625		
HSPA1A	200799_at	NM_005345	NM_005345	3303	-3.07	6.70E-03
AW136654	240802_at	AW136654	---	---	-3.06	1.56E-03
LOC56901	218484_at	NM_020142	NM_020142	56901	-3.02	3.26E-03
MMP14	202827_s_at	AU149305	NM_004995	4323	-3.01	1.34E-05
FLJ20701	219093_at	NM_017933	NM_017933	55022	-2.99	6.11E-03
CAP2	212554_at	N90755	NM_006366	10486	-2.95	3.40E-03
BF941609	240218_at	BF941609	---	---	-2.91	1.65E-08
SPINT2	210715_s_at	AF027205	NM_021102	10653	-2.90	6.36E-06

BG325630	234973_at	BG325630	---	---	-2.90	2.55E-03
)KFZp313N062	1555905_a_at	AI147556	NM_173826	285343	-2.87	1.28E-04
NPY	206001_at	NM_000905	NM_000905	4852	-2.85	5.26E-03
CYP2E1	1431_at	J02843	NM_000773	1571	-2.75	3.27E-03
HHLA3	220387_s_at	NM_007071	NM_007071	11147	-2.72	6.75E-04
IL13RA2	206172_at	NM_000640	NM_000640	3598	-2.66	6.71E-05
FLJ31295	226509_at	AV700302	NM_152320	121274	-2.65	7.10E-04
TncRNA	224566_at	AI042152	---	283131	-2.65	1.05E-04
)KFZP564I042:	223588_at	AL136607	NM_031435	83591	-2.64	1.28E-05
IGSF4D	1552754_a_at	AA640422	NM_153184	253559	-2.64	1.95E-03
PRKACB	235780_at	BE622723	NM_002731	5567	-2.63	2.35E-03
			NM_182948			
			NM_207578			
GNAS	214157_at	AA401492	NM_000516	2778	-2.61	1.23E-04
			NM_016592			
			NM_080425			
			NM_080426			
AW770245	236513_at	AW770245	---	---	-2.60	8.47E-05
LGI1	206349_at	NM_005097	NM_005097	9211	-2.60	8.58E-04
AI810266	235456_at	AI810266	---	---	-2.58	5.24E-03
HIST1H2BD	209911_x_at	BC002842	NM_021063	3017	-2.55	2.10E-03
			NM_138720			
AL353759	215071_s_at	AL353759	---	---	-2.51	9.79E-04
LOC339290	215283_at	U79248	XM_375527	339290	-2.51	3.84E-04
SLC16A3	202856_s_at	NM_004207	NM_004207	9123	-2.51	8.97E-03
LGALS1	201105_at	NM_002305	NM_002305	3956	-2.49	4.79E-03
N92599	241421_at	N92599	---	---	-2.47	1.03E-04
ECHDC3	219298_at	NM_024693	NM_024693	79746	-2.47	7.27E-04
NEBL	203961_at	AL157398	NM_006393	10529	-2.43	4.07E-04
			NM_213569			
RAC2	207419_s_at	NM_002872	NM_002872	5880	-2.42	2.93E-03
BF672306	229189_s_at	BF672306	---	---	-2.42	1.43E-03
CYP2E1	209975_at	AF182276	NM_000773	1571	-2.41	4.83E-03
NEBL	203962_s_at	NM_006393	NM_006393	10529	-2.40	9.78E-04
			NM_213569			
BE045392	243028_x_at	BE045392	---	---	-2.40	3.93E-03
LOC339290	217506_at	H49382	XM_375527	339290	-2.38	1.30E-05
PPAPDC1	236044_at	BF130943	XM_113641	196051	-2.35	1.18E-04
CYP2E1	209976_s_at	AF182276	NM_000773	1571	-2.34	7.08E-03
ASAM	228082_at	BF056275	NM_024769	79827	-2.32	6.80E-04
ICAM2	204683_at	NM_000873	NM_000873	3384	-2.32	7.89E-03
MEGF11	1552439_s_at	NM_032445	NM_032445	84465	-2.31	2.69E-03
CDS1	226185_at	AK026697	NM_001263	1040	-2.31	4.59E-05
ADARB1	203865_s_at	NM_015833	NM_001112	104	-2.30	2.34E-03
			NM_015833			
			NM_015834			
ELMO1	204513_s_at	NM_014800	NM_014800	9844	-2.30	9.13E-03
			NM_130442			
BC039553	1559544_s_at	BC039553	---	---	-2.29	2.32E-03
IGFBP5	211959_at	AW007532	NM_000599	3488	-2.27	8.27E-03
C6orf198	227834_at	AL589605	XM_371849	167838	-2.22	5.80E-03
AI826125	229866_at	AI826125	---	---	-2.20	1.50E-04
NLF1	241031_at	BE218239	NM_207322	145741	-2.19	3.17E-03
C6orf154	235935_at	AI539370	XM_168060	221424	-2.18	8.19E-04
GAL	214240_at	AL556409	NM_015973	51083	-2.17	3.60E-03
CFC1	223753_s_at	AF312769	NM_032545	55997	-2.17	1.16E-04
LOC344405	237291_at	AI695007	XM_293034	344405	-2.16	1.83E-03
PTN	211737_x_at	BC005916	NM_002825	5764	-2.13	4.30E-04

PTGER2	206631_at	NM_000956	NM_000956	5732	-2.12	3.45E-05
)KFZp761O011	207797_s_at	NM_018409	NM_018409	55805	-2.12	1.51E-03
C1GALT1C1	238989_at	BF749723	NM_00101155 1	29071	-2.11	6.52E-04
			NM_152692			
AA757630	236724_at	AA757630	---	---	-2.08	7.95E-06
PDLIM3	209621_s_at	AF002280	NM_014476	27295	-2.08	9.67E-03
KCNMA1	221584_s_at	U11058	NM_002247	3778	-2.08	1.62E-04
TSAP6	218424_s_at	NM_018234	NM_00100841 0	55240	-2.07	6.98E-03
			NM_018234			
			NM_182915			
ST3GAL3	1555702_a_at	AF425866	NM_006279	6487	-2.03	6.54E-03
			NM_174963			
			NM_174964			
			NM_174965			
			NM_174966			
			NM_174967			
			NM_174968			
			NM_174969			
			NM_174970			
			NM_174971			
			NM_174972			
ZNF346	232753_at	AU147613	NM_012279	23567	-2.03	2.80E-04
SYT5	206161_s_at	AI659957	NM_003180	6861	-2.02	8.93E-03
HEBP2	203430_at	NM_014320	NM_014320	23593	-2.02	4.86E-05
C9orf19	225604_s_at	AA284532	NM_022343	152007	-2.02	1.60E-03
AKAP12	227529_s_at	BF511276	NM_005100	9590	-2.02	6.85E-05
			NM_144497			
FLJ20152	218532_s_at	NM_019000	NM_019000	54463	-2.01	2.04E-03
SYNPR	230303_at	H11380	NM_144642	132204	-1.99	7.36E-03
UBE2D3	230171_at	AW662789	NM_003340	7323	-1.97	7.18E-06
			NM_181886			
			NM_181887			
			NM_181888			
			NM_181889			
			NM_181890			
			NM_181891			
			NM_181892			
			NM_181893			
STAC2	228888_at	AI821472	NM_198993	342667	-1.96	4.27E-04
BE894882	235681_at	BE894882	---	---	-1.95	5.54E-03
AKAP12	210517_s_at	AB003476	NM_005100	9590	-1.94	6.61E-05
			NM_144497			
ZNF91	238466_at	R43486	NM_003430	7644	-1.93	2.26E-05
HIST1H2BK	209806_at	BC000893	NM_080593	85236	-1.92	1.28E-04
BF432875	235782_at	BF432875	XM_497668	388620	-1.91	5.20E-03
TMEM4	202857_at	NM_014255	NM_014255	10330	-1.91	5.19E-03
FCRH1	243968_x_at	AI572979	NM_052938	115350	-1.90	4.72E-04
AKAP12	227530_at	BF511276	NM_005100	9590	-1.89	1.05E-04
			NM_144497			
COL16A1	204345_at	NM_001856	NM_001856	1307	-1.89	4.40E-03
FLJ32752	229631_at	AL040892	NM_144666	144132	-1.89	3.14E-03
GPX7	213170_at	AA406605	NM_015696	2882	-1.89	3.82E-04
BF000047	235736_at	BF000047	---	---	-1.88	9.64E-03
FLJ25952	243786_at	AA454190	NM_153251	253832	-1.87	9.52E-05
ARTS-1	214012_at	BE551138	NM_016442	51752	-1.87	5.76E-03
RAC2	213603_s_at	BE138888	NM_002872	5880	-1.86	2.55E-03

IL7	206693_at	NM_000880	NM_000880	3574	-1.86	7.63E-03
B3GNT5	225612_s_at	BE672260	NM_032047	84002	-1.86	1.01E-03
BCL2	203685_at	NM_000633	NM_000633 NM_000657	596	-1.85	3.00E-03
ZAP128	202982_s_at	NM_006821	NM_006821	10965	-1.84	2.07E-03
AF085995	1561759_at	AF085995	---	---	-1.84	4.44E-04
UCN	206072_at	NM_003353	NM_003353	7349	-1.84	1.79E-04
CDH10	220115_s_at	NM_006727	NM_006727	1008	-1.83	1.73E-03
BF114967	231067_s_at	BF114967	---	---	-1.83	6.70E-06
ADAMTS1	222162_s_at	AK023795	NM_006988	9510	-1.82	1.09E-04
PPFIA4	214978_s_at	AK023365	NM_015053	8497	-1.82	6.27E-03
BE674309	230913_at	BE674309	---	---	-1.81	1.25E-03
AL355688	232081_at	AL355688	---	---	-1.80	1.15E-03
AI698684	1558626_at	AI698684	---	---	-1.78	3.33E-03
PRPH	213847_at	NM_006262	NM_006262	5630	-1.78	3.01E-03
PTGES	210367_s_at	AF010316	NM_004878 NM_198797	9536	-1.78	4.71E-06
HPCAL1	205462_s_at	NM_002149	NM_002149 NM_134421	3241	-1.77	3.68E-03
INSIG1	229370_at	BF507344	NM_005542 NM_198336 NM_198337	3638	-1.77	3.55E-04
RAB6B	221792_at	AW118072	NM_016577	51560	-1.77	1.12E-04
AI733281	239994_at	AI733281	---	---	-1.75	1.40E-03
NDFIP2	1568807_a_at	AI301081	NM_019080	54602	-1.75	2.04E-04
KIAA1598	221802_s_at	AU157109	NM_018330	57698	-1.74	1.10E-03
CAP2	212551_at	NM_006366	NM_006366	10486	-1.74	7.36E-03
TICAM2	228234_at	AI423165	NM_021649	353376	-1.73	1.46E-03
DSCAM	237268_at	BE503065	NM_001389 NM_206887	1826	-1.73	5.66E-04
MATN3	230390_at	AI809899	NM_002381	4148	-1.72	2.82E-04
AL833383	1563776_at	AL833383	---	---	-1.71	6.57E-06
C21orf109	1553608_a_at	NM_138968	---	193629	-1.70	9.95E-03
FLJ35390	1569089_a_at	BC024303	---	255031	-1.70	2.94E-03
AF052119	214821_at	AF052119	---	---	-1.69	6.58E-04
M160	223655_at	AF264014	NM_174941	283316	-1.69	9.95E-03
AI588962	230477_at	AI588962	---	---	-1.69	8.76E-05
)KFZp313N062	1555906_s_at	AI147556	NM_173826	285343	-1.69	2.73E-04
DRD1IP	219896_at	NM_015722	NM_015722	50632	-1.69	4.68E-03
)KFZp313N062	226688_at	AW003508	NM_173826	285343	-1.68	8.18E-03
AW450420	236373_at	AW450420	---	---	-1.66	8.61E-03
LOC133308	1564746_at	BC009732	NM_178833	133308	-1.65	1.14E-04
AL037414	230055_at	AL037414	---	---	-1.63	9.73E-05
RGAG4	227823_at	BE348679	XM_291322	340526	-1.63	4.87E-05
APOBEC3G	204205_at	NM_021822	NM_021822	60489	-1.62	9.31E-03
BTN3A3	38241_at	U90548	NM_006994 NM_197974	10384	-1.62	2.24E-03
LOC133308	229491_at	BF433180	NM_178833	133308	-1.61	8.27E-04
C21orf66	239407_at	AI793248	NM_013329 NM_016631 NM_058191 NM_145328	94104	-1.61	6.82E-03
)KFZp761N111	229254_at	BE550027	NM_181644	148808	-1.60	3.14E-03
DSCAM	211484_s_at	AF023450	NM_001389 NM_206887	1826	-1.60	1.94E-04
ADAMTS1	222486_s_at	AF060152	NM_006988	9510	-1.59	4.21E-03
LOC286052	241370_at	AA278233	---	286052	-1.59	8.30E-05
MGC40157	239754_at	BE671886	NM_152350	125144	-1.59	9.45E-03

ZNF571	206648_at	NM_016536	NM_016536	51276	-1.59	1.41E-03
LIPT1	242053_at	AW665279	NM_015929 NM_145196 NM_145197 NM_145198 NM_145199	51601	-1.59	3.26E-04
FBI4	238081_at	AI694300	NM_205857	404201	-1.58	1.29E-03
FLJ11286	53720_at	AI862559	NM_018381	55337	-1.58	1.79E-03
FLJ30294	1553301_a_at	NM_144632	NM_144632	130827	-1.57	1.18E-04
HUMRGE/M10	UMRGE/M100	-HUMRGE/M100	---	---	-1.57	8.64E-03
HADHA	232590_at	AK025919	NM_000182	3030	-1.57	4.01E-03
NEDL1	243743_at	AI373512	NM_015052	23072	-1.56	9.50E-04
BF114745	235459_at	BF114745	---	---	-1.56	1.20E-03
FLJ13614	226521_s_at	AK023676	NM_139076	84142	-1.55	2.64E-03
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TBC1D10	226613_at	AI742029	NM_031937	83874	-1.53	5.51E-03
IL10RB	209575_at	BC001903	NM_000628	3588	-1.53	1.40E-05
GLT25D2	209883_at	AF288389	NM_015101	23127	-1.52	3.20E-05
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PDGFRB	202273_at	NM_002609	NM_002609	5159	-1.49	1.88E-03
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GPR123	239221_at	AI884909	NM_032422	84435	-1.48	1.25E-03
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HPCAL1	212552_at	BE617588	NM_002149 NM_134421	3241	-1.48	9.71E-04
LOC284361	229289_at	AL517395	NM_175063 NM_206538	284361	-1.48	2.00E-03
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LOC441422	236453_at	AW243154	XR_000264	441422	-1.47	2.36E-05
AA976778	230679_at	AA976778	---	---	-1.46	1.46E-05
FBI4	241401_at	BG496631	NM_205857	404201	-1.46	1.53E-03
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AI758408	227235_at	AI758408	---	---	-1.45	1.51E-03
TMEM5	204808_s_at	NM_014254	NM_014254	10329	-1.44	3.94E-03
BF111884	230491_at	BF111884	---	---	-1.44	3.82E-04
COL27A1	225293_at	AK021957	NM_032888	85301	-1.44	6.78E-03
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PTN	209466_x_at	M57399	NM_002825	5764	-1.43	9.60E-04
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DUSP22	226440_at	BE222746	NM_020185	56940	-1.40	2.32E-03
DUSP16	224336_s_at	AB052156	NM_030640	80824	-1.39	1.91E-03
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CAMK2D	228555_at	AA029441	NM_001221 NM_172115 NM_172127 NM_172128	817	-1.39	2.14E-04
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DISP1	228184_at	AK023679	NM_032890	84976	-1.39	2.54E-05
MAP3K5	203836_s_at	D84476	NM_005923	4217	-1.39	1.24E-03
H46176	237083_at	H46176	---	---	-1.38	8.44E-03
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TIMP1	201666_at	NM_003254	NM_003254	7076	-1.37	7.35E-03
PTGES	207388_s_at	NM_004878	NM_004878 NM_198797	9536	-1.37	6.78E-03
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LOC153682	232794_at	AL137383	---	153682	-1.36	2.78E-04
LOC146174	230721_at	BF436957	NM_173501	146174	-1.36	1.19E-04
DUSP22	218845_at	NM_020185	NM_020185	56940	-1.36	3.43E-06
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C1orf21	221272_s_at	NM_030806	NM_030806	81563	-1.34	5.15E-04
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C21orf57	227421_at	BF026326	NM_00100611 4 NM_058181	54059	-1.31	2.23E-06
C1orf21	223127_s_at	AW003850	NM_030806	81563	-1.31	2.69E-03
LOC91526	228471_at	AA744636	NM_153697	91526	-1.31	6.93E-03
FHL2	202949_s_at	NM_001450	NM_001450 NM_201555 NM_201556 NM_201557	2274	-1.31	1.03E-03
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AK001829	232594_at	AK001829	XM_498704	440498	-1.30	2.12E-03
BE551142	241091_at	BE551142	XM_497668	388620	-1.29	2.90E-03
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PCDHAC2	224539_s_at	AF152474	NM_018899 NM_031883	56134	-1.28	4.06E-03
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MGC39821	1555363_s_at	BC034236	XM_498465 XM_499595	284440	-1.28	1.45E-03
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NDUFV3	226616_s_at	NM_021075	NM_001001503 NM_021075	4731	-1.24	6.22E-04
NOTCH4	205247_at	AI743713	NM_004557	4855	-1.24	2.38E-03
LOC401321	1560371_at	BI823265	XM_379483 XM_380099	401321	-1.24	3.08E-03
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PHLDB3	1557948_at	BC007947	NM_198850	284345	-1.23	5.46E-04
PLRG1	227246_at	BF438014	NM_002669	5356	-1.23	4.56E-03
C9orf19	225602_at	H92988	NM_022343	152007	-1.23	4.21E-03
MGC16037	229050_s_at	AL533103	---	84973	-1.23	9.30E-03
PLP2	201136_at	NM_002668	NM_002668	5355	-1.21	2.30E-03
LOC91526	226641_at	AU157224	NM_153697	91526	-1.21	9.94E-03
ZNF404	239043_at	AA084273	XM_292765	342908	-1.21	8.85E-04
CNN1	203951_at	NM_001299	NM_001299	1264	-1.20	5.29E-03
AI862542	235696_at	AI862542	---	---	-1.19	2.30E-04
FHL3	218818_at	NM_004468	NM_004468	2275	-1.19	5.70E-03
LOC90246	233835_at	AK023635	---	90246	-1.19	1.62E-04
ARMCX5	1555902_at	BC022066	NM_022838	64860	-1.19	1.49E-04
LOC388227	229107_at	AW629461	XM_373670	388227	-1.19	5.59E-03
C6orf52	236504_x_at	BE670432	XM_371798	347744	-1.19	9.06E-03
ZNF606	219635_at	NM_025027	NM_025027	80095	-1.19	2.38E-03
C10orf39	233076_at	AL137551	NM_194303	282973	-1.19	6.97E-04
FVT1	1558279_a_at	BF666293	NM_002035	2531	-1.19	3.09E-03
TAF12	209463_s_at	D50544	NM_005644	6883	-1.18	3.00E-04
AI929792	236081_at	AI929792	---	---	-1.18	2.41E-05
PDCD2	228420_at	AW590850	NM_002598 NM_144781	5134	-1.18	9.07E-03
ETFDH	33494_at	S69232	NM_004453	2110	-1.18	6.70E-03
CD302	203799_at	NM_014880	NM_014880	9936	-1.17	9.28E-03
N30152	229850_at	N30152	---	---	-1.17	5.16E-03
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SPIN3	1554099_a_at	BC032490	NM_001010862	169981	-1.17	1.85E-05
PHKA1	229876_at	BE503584	NM_002637	5255	-1.17	2.72E-04
PCNXL2	1554256_a_at	BC008300	NM_014801 NM_024938	80003	-1.17	8.67E-05
LOC284409	239995_at	AI692774	XM_211447	284409	-1.17	1.43E-04
AV704017	222376_at	AV704017	---	---	-1.16	4.90E-03
AI767751	228084_at	AI767751	---	---	-1.16	6.90E-05
FLJ30294	238578_at	BF574691	NM_144632	130827	-1.16	2.44E-06
BTN3A1	209770_at	U90552	NM_007048 NM_194441	11119	-1.16	4.37E-03
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LOC285550	236321_at	AW439843	XM_209656	285550	-1.16	6.99E-03
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CYP2U1	226402_at	AK026498	NM_183075	113612	-1.15	2.05E-03
OPTN	202074_s_at	NM_021980	NM_00100821 1 NM_00100821 2 NM_00100821 3 NM_021980	10133	-1.15	7.05E-03
D4S234E	209569_x_at	NM_014392	NM_014392	27065	-1.15	1.26E-03
GUCY1A3	221942_s_at	AI719730	NM_000856	2982	-1.15	4.01E-04
C18orf18	229829_at	AA429735	---	147525	-1.14	7.95E-03
DUSP16	224832_at	AB051487	NM_030640	80824	-1.14	2.08E-04
C21orf25	212875_s_at	AP001745	NM_199050	25966	-1.13	2.32E-03
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AKT2	236664_at	AA448167	NM_001626	208	-1.13	5.51E-03
FGF7	1554741_s_at	AF523265	NM_002009	2252	-1.13	2.06E-03
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SPOCK2	202524_s_at	NM_014767	NM_014767	9806	-1.12	8.32E-03
ULK2	204063_s_at	NM_014683	NM_014683	9706	-1.12	5.36E-03
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BACE1	217904_s_at	NM_012104	NM_012104 NM_138971 NM_138972 NM_138973	23621	-1.12	1.17E-03
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AGA	216064_s_at	W27131	NM_000027	175	-1.12	8.70E-03
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AV714268	242323_at	AV714268	---	---	-1.11	2.68E-04
CXorf50	242292_at	H12084	NM_152693	203429	-1.11	4.02E-04
BC040287	1558605_at	BC040287	---	---	-1.11	7.41E-03
RSHL2	223713_at	AF353618	NM_031924	83861	-1.11	4.32E-05
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C21orf51	228239_at	AA148789	NM_058182	54065	-1.11	7.04E-06
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SAMD4	212845_at	AB028976	NM_015589	23034	-1.10	5.48E-03
CLCN3	201734_at	AI760629	NM_001829 NM_173872	1182	-1.10	9.57E-03

FLJ31265	238515_at	BF687577	NM_152395	131870	-1.10	7.24E-04
ITGB1BP1	203337_x_at	NM_004763	NM_004763 NM_022334	9270	-1.10	2.94E-03
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LIFR	225575_at	AI680541	NM_002310	3977	-1.09	6.39E-03
PCDHB16	232099_at	AB046841	NM_020957	57717	-1.09	5.69E-03
AI304870	236574_at	AI304870	---	---	-1.09	4.77E-03
LOC157378	241342_at	BG288115	NM_194291	157378	-1.09	7.42E-03
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LOC90693	228087_at	AK026684	NM_138771	90693	-1.08	6.62E-06
C10orf104	229145_at	AA541762	NM_173473	119504	-1.08	3.73E-03
KIAA1324	221874_at	AB037745	NM_020775	57535	-1.07	1.16E-04
FGF19	223761_at	AF110400	NM_005117	9965	-1.07	8.40E-03
AI768374	228661_s_at	AI768374	---	---	-1.07	9.53E-04
PLRG1	225194_at	NM_002669	NM_002669	5356	-1.07	8.76E-05
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DALRD3	221934_s_at	BF941492	NM_00100999 6 NM_018114	55152	-1.07	8.88E-03
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ABTB1	229164_s_at	AI337369	NM_032548 NM_172027 NM_172028	80325	-1.07	5.29E-03
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ZNF285	236328_at	AW513227	NM_152354	26974	-1.06	2.76E-04
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TAF1B	235673_at	AI436217	NM_005680	9014	-1.06	2.05E-03
BF002625	229530_at	BF002625	---	---	-1.06	6.62E-04
PEX6	204545_at	NM_000287	NM_000287	5190	-1.06	4.66E-05
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HCG8	215985_at	X92110	---	80869	-1.05	5.10E-03
PTPRD	214043_at	BF062299	NM_002839 NM_130391 NM_130392 NM_130393	5789	-1.05	2.37E-03
MAN2A2	219999_at	NM_018621	NM_006122	4122	-1.05	3.41E-03
CHC1	206499_s_at	NM_001269	NM_001269	1104	-1.05	3.22E-03
DUSP16	1558739_at	R30807	NM_030640	80824	-1.04	6.86E-04
PLEKHA2	238013_at	BF347859	XM_496973	59339	-1.04	7.63E-03
RODH	37512_at	U89281	NM_003725	8630	-1.04	2.71E-03
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LMNA	203411_s_at	NM_005572	NM_005572 NM_170707 NM_170708	4000	-1.04	6.43E-03
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ALLC	220365_at	NM_018436	NM_018436 NM_199232	55821	-1.04	3.61E-03
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AA156605	226798_at	AA156605	---	---	-1.04	1.65E-03
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HEL308	228736_at	AW084661	NM_133636	113510	-1.03	9.31E-04
LOC440388	228855_at	AI927964	XM_496170	440388	-1.03	2.15E-03
ANKRA2	218769_s_at	NM_023039	NM_023039	57763	-1.03	3.79E-04
SH3KBP1	223082_at	AF230904	NM_031892	30011	-1.03	5.39E-04
MAP7	202890_at	AW242297	NM_003980	9053	-1.03	9.43E-03
AI263044	214376_at	AI263044	---	---	-1.03	4.37E-03
D4S234E	209570_s_at	BC001745	NM_014392	27065	-1.03	5.33E-03
BF510563	228561_at	BF510563	---	---	-1.03	7.28E-03
LOC157378	238045_at	BG167675	NM_194291	157378	-1.02	9.58E-03
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SLC2A11	1558540_s_at	AK055523	NM_030807	66035	-1.01	5.49E-03
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CARD10	210026_s_at	AY028896	NM_014550	29775	-1.01	4.13E-03
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LOC401320	238540_at	AA933883	XM_379482 XM_380098	401320	-1.00	1.29E-03
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LOC400713	232315_at	AU149712	XR_000217	400713	-1.00	1.91E-03
DKFZP434H132	204494_s_at	AW516789	NM_015492	56905	-1.00	2.50E-04
DBT	231919_at	AK024946	NM_001918	1629	-1.00	3.13E-04
AI459157	225066_at	AI459157	---	---	-1.00	1.73E-03
WASL	227010_at	BF438330	NM_003941	8976	-1.00	3.51E-04
SH3KBP1	1554168_a_at	AF542051	NM_031892	30011	-0.99	9.41E-04
LOC339803	227941_at	AW327931	---	339803	-0.99	7.41E-04
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HMGCLL1	232305_at	AF131827	NM_019036	54511	-0.99	7.25E-06
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LIN7B	219760_at	NM_022165	NM_022165	64130	-0.99	6.61E-06
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PIGH	209625_at	BC004100	NM_004569	5283	-0.99	6.18E-04
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BE646451	235893_at	BE646451	---	---	-0.98	1.01E-03
KIAA1223	225735_at	AL110131	XM_048747	57182	-0.98	9.14E-04
SLC18A2	1553328_a_at	NM_003054	NM_003054	6571	-0.98	5.03E-03
C19orf4	219005_at	NM_012109	NM_012109	25789	-0.98	2.75E-03
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CAPN2	208683_at	M23254	NM_001748	824	-0.98	7.76E-03
TMEM23	212989_at	AI377497	NM_147156	259230	-0.98	5.42E-03
NEFH	204412_s_at	NM_021076	NM_021076	4744	-0.98	9.35E-03
ANXA5	200782_at	NM_001154	NM_001154	308	-0.98	5.17E-03
AI955713	227193_at	AI955713	---	---	-0.97	5.36E-08
LOC284422	231982_at	AF161441	XM_209196	284422	-0.97	7.92E-03
KCTD18	226493_at	AI627249	NM_152387	130535	-0.97	3.04E-05
LOC90024	228832_at	AI884670	XM_028217	90024	-0.97	7.03E-03
CA442342	1556097_at	CA442342	---	---	-0.97	3.17E-03
LOC90639	235533_at	AW021673	---	90639	-0.97	4.53E-03
HDAC4	228813_at	AW206037	NM_006037	9759	-0.96	3.30E-03

BC040901	1559535_s_at	BC040901	---	---	-0.96	6.19E-03
BBS7	235007_at	AI683802	NM_018190	55212	-0.96	1.86E-03
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MGC48625	1569039_s_at	BC029855	NM_182609	342926	-0.96	7.88E-05
MBNL1	201151_s_at	BF512200	NM_021038	4154	-0.96	4.33E-03
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CIB1	201953_at	NM_006384	NM_006384	10519	-0.96	2.33E-04
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CHC1	215747_s_at	X06130	NM_001269	1104	-0.96	4.49E-03
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KIAA0773	205368_at	NM_014690	NM_014690	9715	-0.95	1.39E-03
PDPK1	32029_at	AC005591	NM_002613	5170	-0.95	4.56E-04
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GNG8	234284_at	AF188179	NM_033258	94235	-0.95	5.33E-04
C14orf133	233140_s_at	AF111168	NM_022067	63894	-0.95	4.26E-04
ITR	231871_at	AU160685	NM_180989	160897	-0.95	5.11E-03
BC015852	1560570_a_at	BC015852	---	---	-0.95	6.20E-03
SNF1LK2	223430_at	AL136764	NM_015191	23235	-0.95	2.99E-03
CKLFSF1	235286_at	BG533580	NM_052999	113540	-0.95	5.78E-03
			NM_181268			
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BTN3A3	204821_at	NM_006994	NM_006994	10384	-0.95	7.79E-05
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PLEKHC1	209210_s_at	Z24725	NM_006832	10979	-0.94	2.90E-03
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NAP1L3	204749_at	NM_004538	NM_004538	4675	-0.94	2.43E-03
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PLEKHA2	217677_at	BF542055	XM_496973	59339	-0.94	7.55E-03
SIDT2	56256_at	AA150165	NM_015996	51092	-0.94	3.96E-04
STX12	212112_s_at	AI816243	NM_177424	23673	-0.94	7.35E-05

STX17	228091_at	AI800609	NM_017919	55014	-0.94	6.04E-03
C2orf17	221983_at	AL040896	NM_024293	79137	-0.94	4.85E-03
ZFP28	234937_x_at	AC007228	NM_020828	140612	-0.94	3.30E-03
HLA-G	210514_x_at	AF226990	NM_002127	3135	-0.94	1.71E-04
MGC14801	224443_at	BC005997	NM_032705	84791	-0.93	9.68E-03
N79601	242981_at	N79601	---	---	-0.93	4.16E-03
LOC284926	1556064_at	BQ575161	---	284926	-0.93	5.64E-03
WDR9	225446_at	AI638279	NM_00100724 6 NM_018963 NM_033656	54014	-0.93	3.04E-04
AI652546	228853_at	AI652546	---	---	-0.93	4.31E-03
EIF4E3	238461_at	AA228031	---	317649	-0.92	5.07E-03
AU151944	236916_at	AU151944	---	---	-0.92	1.50E-03
ZNF610	235953_at	AA776810	NM_173530	162963	-0.92	3.79E-04
RGS14	38290_at	AF037195	NM_006480	10636	-0.92	1.22E-03
WDR24	223293_at	AL136863	NM_032259	84219	-0.92	5.54E-04
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SIRT5	219185_at	NM_012241	NM_012241 NM_031244	23408	-0.91	1.64E-03
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LMNA	212089_at	M13452	NM_005572 NM_170707 NM_170708	4000	-0.91	7.00E-03
NINJ1	203045_at	NM_004148	NM_004148	4814	-0.91	3.51E-04
C9orf127	229729_at	BF507870	NM_016446	51754	-0.91	1.20E-04
LAF4	227198_at	AW085505	NM_002285	3899	-0.91	4.25E-05
ADPRHL2	223097_at	AF212236	NM_017825	54936	-0.91	1.91E-04
N21364	214202_at	N21364	---	---	-0.90	6.59E-06
LOC388727	231233_at	AI382195	XM_373881	388727	-0.90	1.97E-03
ALU Sequence	FFX-hum_alu_	AFFX-hum_alu	NM_000021 NM_000051 NM_000136 NM_000141 NM_000144 NM_000202 NM_00022 NM_000230 NM_000294 NM_000297 NM_000314 NM_000356 NM_000364 NM_000382 NM_000441 NM_000484 NM_000527 NM_000554	---	-0.90	2.52E-03
ACYP2	206833_s_at	NM_001108	NM_138448	98	-0.90	4.12E-03
EXOC7	212026_s_at	BE646386	NM_015219	23265	-0.90	1.03E-03
RPUSD3	225743_at	AI125996	NM_173659	285367	-0.90	3.62E-03
R15431	236440_at	R15431	---	---	-0.90	3.46E-05
AA194266	238728_at	AA194266	---	---	-0.90	8.94E-03
GNB5	207124_s_at	NM_006578	NM_006578 NM_016194	10681	-0.90	2.52E-04
TEX264	233350_s_at	AU158474	NM_015926	51368	-0.89	3.96E-04
TRIM32	1557315_a_at	AL134420	NM_012210	22954	-0.89	4.37E-03

BF342524	235074_at	BF342524	---	---	-0.89	2.65E-05
HADHA	236120_at	AW955973	NM_000182	3030	-0.89	8.56E-03
C21orf119	227424_x_at	AI800837	NM_032910	84996	-0.88	6.71E-03
CLN5	204085_s_at	NM_006493	NM_006493	1203	-0.88	6.71E-03
SAV1	218276_s_at	NM_021818	NM_021818	60485	-0.88	4.58E-03
HDHD3	221256_s_at	NM_031219	NM_031219	81932	-0.88	4.72E-03
EMID1	213779_at	AL031186	NM_133455	129080	-0.88	4.61E-05
GAL3ST3	1553257_at	AY026481	NM_033036	89792	-0.88	5.62E-03
USP44	224048_at	AL136825	NM_032147	84101	-0.88	1.11E-03
ACSL1	207275_s_at	NM_001995	NM_001995	2180	-0.87	9.24E-03
AK024681	231972_at	AK024681	---	---	-0.87	6.32E-03
AL527331	238716_at	AL527331	---	---	-0.87	3.42E-03
KIAA0711	204301_at	NM_014867	NM_014867	9920	-0.87	5.63E-07
NOL3	221566_s_at	AF043244	NM_003946	8996	-0.87	4.45E-03
AW236954	1557117_at	AW236954	---	---	-0.87	1.02E-03
MRPS33	218654_s_at	NM_016071	NM_016071	51650	-0.87	5.05E-03
SLC19A1	229489_at	AI681043	NM_053035 NM_003056 NM_194255	6573	-0.87	4.84E-04
ATP2C1	209935_at	AF225981	NM_001001485 NM_001001486 NM_001001487 NM_014382	27032	-0.87	1.03E-03
MBNL1	201153_s_at	NM_021038	NM_021038 NM_207292 NM_207293 NM_207294 NM_207295 NM_207296 NM_207297	4154	-0.87	2.49E-04
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OTUB2	219369_s_at	NM_023112	NM_023112	78990	-0.86	4.20E-03
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ANKH	229176_at	AI672354	NM_054027	56172	-0.86	8.12E-03
SYNE1	209447_at	AF043290	NM_015293 NM_033071 NM_133650 NM_182961	23345	-0.86	3.81E-03
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AI471969	239278_at	AI471969	---	---	-0.86	2.25E-03
OR6M1	227112_at	AW270037	NM_001005325	390261	-0.86	2.99E-04
DSCR3	217309_s_at	AJ001867	NM_006052	10311	-0.86	1.52E-04
VGLL4	212399_s_at	D50911	NM_014667	9686	-0.86	1.90E-03
RNH	206050_s_at	NM_002939	NM_002939 NM_203383 NM_203384 NM_203385 NM_203386 NM_203387 NM_203388 NM_203389	6050	-0.85	1.17E-03
EIF3S2	208756_at	U36764	NM_003757	8668	-0.85	3.95E-04
CHCHD5	235825_at	AI057238	NM_032309	84269	-0.85	2.48E-03
FLJ25715	231952_at	AU157271	NM_182570	284241	-0.85	4.49E-03
H28915	244359_s_at	H28915	XM_496692	441014	-0.85	2.81E-03

SVH	223328_at	BC003586	NM_031905	83787	-0.85	2.28E-03
BRD4	238612_at	AW298070	NM_014299 NM_058243	23476	-0.85	4.92E-04
PLEKHC1	209209_s_at	AW469573	NM_006832	10979	-0.85	9.05E-03
LOC220930	229090_at	AK026657	---	220930	-0.85	5.83E-04
AW665538	244532_x_at	AW665538	XM_496692	441014	-0.85	3.20E-03
DKFZp727A071	227348_at	AW409848	NM_152268	25973	-0.85	4.70E-05
STK19	36019_at	L26260	NM_004197 NM_032454	8859	-0.85	1.10E-03
DCTD	210137_s_at	BC001286	NM_001921	1635	-0.84	7.33E-03
AMT	204294_at	NM_000481	NM_000481	275	-0.84	1.21E-03
ERBB4	206794_at	NM_005235	NM_005235	2066	-0.84	7.70E-03
AI003508	244114_x_at	AI003508	XM_496690	401131	-0.84	2.43E-03
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TDRKH	221052_at	NM_006862	NM_006862	11022	-0.84	1.92E-03
BF340290	225220_at	BF340290	---	---	-0.84	8.97E-03
LNX	227293_at	AI264003	NM_032622	84708	-0.84	2.20E-03
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FLJ12716	218179_s_at	NM_021942	NM_021942 NM_199053	60684	-0.83	3.97E-04
ACP6	218795_at	NM_016361	NM_016361	51205	-0.83	7.19E-04
KIAA0543	226808_at	AW771007	XM_376720 XM_379967	23145	-0.83	2.42E-04
PAK6	1555310_a_at	BC035596	NM_020168	56924	-0.83	2.78E-03
TXNDC4	208958_at	AI827677	NM_015051	23071	-0.83	1.35E-03
PAM	202336_s_at	NM_000919	NM_000919 NM_138766 NM_138821 NM_138822	5066	-0.83	4.55E-03
LOC57149	203897_at	BE963444	NM_020424	57149	-0.82	1.05E-04
DCP1B	226093_at	AW204088	NM_152640	196513	-0.82	6.19E-04
FLJ12716	233558_s_at	AK023390	NM_021942 NM_199053	60684	-0.82	8.71E-04
TP53TG3	220167_s_at	NM_015369	NM_015369 NM_016212	24150	-0.82	3.88E-04
OCIAD2	225314_at	BG291649	NM_152398	132299	-0.82	8.74E-03
C14orf133	218431_at	NM_022067	NM_022067	63894	-0.82	9.75E-04
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DSCR3	203635_at	NM_006052	NM_006052	10311	-0.82	8.42E-04
PDCD2	204025_s_at	NM_002598	NM_002598 NM_144781	5134	-0.81	5.01E-04
DKFZP564D166	224952_at	BF115054	XM_371074	26115	-0.81	3.50E-04
FLJ13231	219381_at	NM_023073	NM_023073	65250	-0.81	9.78E-03
CDC37L1	235787_at	T65394	NM_017913	55664	-0.81	7.07E-04
WDTC1	215497_s_at	AK023778	NM_015023	23038	-0.81	5.43E-04
LOC94431	216908_x_at	AF001549	NM_145237	94431	-0.81	3.74E-06
SEC31L1	215009_s_at	U92014	NM_014933 NM_016211	22872	-0.81	2.06E-03
ZNF148	230821_at	AW594167	NM_021964	7707	-0.81	5.30E-03
DHRSX	225503_at	AL547782	NM_145177	207063	-0.81	8.16E-06
LYPLA3	204458_at	AL110209	NM_012320	23659	-0.81	3.93E-03

DCTD	201572_x_at	NM_001921	NM_001921	1635	-0.81	5.30E-04
FLJ31265	228341_at	AI809108	NM_152395	131870	-0.81	9.80E-04
TBC1D12	221858_at	N34407	XM_051081	23232	-0.81	2.80E-03
FLJ22795	223327_x_at	AF316855	NM_025084	80154	-0.81	6.81E-06
ZNF274	204937_s_at	NM_016325	NM_016324	10782	-0.81	2.65E-03
			NM_016325			
			NM_133502			
CSTB	201201_at	NM_000100	NM_000100	1476	-0.80	6.53E-04
LOC151146	227604_at	BG292251	---	151146	-0.80	2.89E-03
SLC18A2	205857_at	AI269290	NM_003054	6571	-0.80	3.73E-03
MANSC1	220945_x_at	NM_018050	NM_018050	54682	-0.80	2.89E-03
R44603	244113_at	R44603	---	---	-0.80	2.19E-03
PAK1	226507_at	AU154408	NM_002576	5058	-0.80	4.33E-03
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FBXL5	209005_at	AF157323	NM_012161	26234	-0.80	2.18E-04
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TM4SF2	202242_at	NM_004615	NM_004615	7102	-0.80	4.39E-03
EHD2	45297_at	AI417917	NM_014601	30846	-0.80	2.06E-05
UBE2D3	200667_at	BF448062	NM_003340	7323	-0.79	7.56E-06
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AA868896	226203_at	AA868896	---	---	-0.79	2.92E-03
DUSP24	233982_x_at	AF188204	NM_016086	51657	-0.79	9.14E-03
AU157441	226511_at	AU157441	---	---	-0.79	1.27E-03
AK2	205996_s_at	NM_013411	NM_001625	204	-0.79	2.76E-03
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			NM_172199			
AF086443	1560982_at	AF086443	---	---	-0.79	4.61E-03
C9orf9	220050_at	NM_018956	NM_018956	11092	-0.79	1.17E-03
ZNF23	213934_s_at	AL567808	NM_145911	7571	-0.79	3.42E-03
HLA-G	211529_x_at	M90684	NM_002127	3135	-0.79	1.15E-03
XPR1	226615_at	BE439489	NM_004736	9213	-0.79	8.43E-04
THAP9	230185_at	AW301218	NM_024672	79725	-0.79	4.10E-03
CCNDBP1	223084_s_at	AF246144	NM_012142	23582	-0.79	1.05E-04
			NM_037370			
AP3B2	205678_at	NM_004644	NM_004644	8120	-0.78	3.03E-03
CTHRC1	225681_at	AA584310	NM_138455	115908	-0.78	2.80E-03
LOC93622	225391_at	AL562398	NM_138699	93622	-0.78	8.43E-03
JAG2	209784_s_at	AF029778	NM_002226	3714	-0.78	7.94E-03
			NM_145159			
ZNF585A	229794_at	BE550717	NM_152655	199704	-0.78	4.45E-03
			NM_199126			
MGC2650	204985_s_at	NM_024108	NM_024108	79090	-0.78	4.43E-03
APRT	203219_s_at	NM_000485	NM_000485	353	-0.78	5.08E-04
USP36	220370_s_at	NM_025090	NM_025090	57602	-0.78	3.64E-03
INPP5A	203006_at	NM_005539	NM_005539	3632	-0.78	8.67E-03
ZNF197	205855_at	NM_006991	NM_006991	10168	-0.78	6.14E-03
PLEKHA2	225136_at	BF968578	XM_496973	59339	-0.78	4.19E-04
ARHGEF4	205109_s_at	NM_015320	NM_015320	50649	-0.77	7.05E-03
			NM_032995			

NETO1	1552736_a_at	NM_138966	NM_138966 NM_138999 NM_153181	81832	-0.77	2.29E-04
LRPAP1	201186_at	NM_002337	NM_002337	4043	-0.77	7.07E-03
MYST1	221820_s_at	AK024102	NM_032188	84148	-0.77	7.03E-03
FLJ12998	244734_at	W45568	NM_022764	64779	-0.77	1.04E-04
CLTC	238646_at	AA747756	NM_004859	1213	-0.77	8.00E-03
SLC30A5	1555334_s_at	AF439324	NM_022902 NM_024055	64924	-0.77	3.91E-03
PRKAG1	201805_at	NM_002733	NM_002733 NM_212461	5571	-0.77	2.24E-03
GPRASP1	204793_at	NM_014710	NM_014710	9737	-0.77	1.73E-03
NETO1	1562713_a_at	AL834354	NM_138966 NM_138999 NM_153181	81832	-0.77	2.38E-03
LOC89894	227172_at	BC000282	NM_138341	89894	-0.77	3.71E-04
STK19	204090_at	NM_004197	NM_004197 NM_032454	8859	-0.77	2.21E-03
LIPT1	205571_at	NM_015929	NM_015929 NM_145196 NM_145197 NM_145198 NM_145199	51601	-0.77	1.12E-03
ZCWCC3	213000_at	AP000693	NM_015358	23515	-0.77	1.90E-03
CLCN3	201735_s_at	NM_001829	NM_001829 NM_173872	1182	-0.77	8.06E-03
FLJ32370	226483_at	AI890761	NM_152417	137695	-0.76	2.24E-03
FYCO1	218204_s_at	NM_024513	NM_024513	79443	-0.76	1.16E-07
NEIL2	226585_at	BE466620	NM_145043	252969	-0.76	5.49E-04
KCNH2	205262_at	NM_000238	NM_000238 NM_172056 NM_172057	3757	-0.76	9.14E-06
BF966015	226787_at	BF966015	---	---	-0.76	3.80E-06
BBP	213882_at	AA012917	NM_032027	83941	-0.76	1.89E-03
GSTZ1	209531_at	BC001453	NM_001513 NM_145870 NM_145871	2954	-0.76	3.56E-03
EIF2C1	228120_at	AW136032	NM_012199	26523	-0.76	6.17E-03
PCTK2	206474_at	NM_002595	NM_002595	5128	-0.76	4.76E-03
C13orf21	243094_at	BF509416	NM_001010897	387923	-0.76	5.57E-03
MAPRE3	214270_s_at	AI885178	NM_012326	22924	-0.76	3.88E-03
BC017239	1558045_a_at	BC017239	---	---	-0.75	3.87E-03
COL27A1	225288_at	AI949136	NM_032888	85301	-0.75	9.38E-04
AI672159	226550_at	AI672159	---	---	-0.75	1.09E-04
MBNL1	201152_s_at	N31913	NM_021038 NM_207292 NM_207293 NM_207294 NM_207295 NM_207296 NM_207297	4154	-0.75	1.55E-04
TBN	1556178_x_at	BU618741	NM_138572	129685	-0.75	9.97E-03
TMAP1	227326_at	BE966768	NM_00100852 8 NM_00100852 9 NM_198530	439921	-0.75	4.09E-04

TNFRSF21	218856_at	NM_016629	NM_014452	27242	-0.75	6.87E-03
CHMP1.5	218177_at	AA293502	NM_020412	57132	-0.75	5.52E-05
SHFM3	221519_at	AF281859	NM_022039	6468	-0.75	1.33E-03
AU151635	232111_at	AU151635	---	---	-0.75	1.40E-07
PTK9L	202009_at	NM_007284	NM_007284	11344	-0.75	8.11E-03
PAM	214620_x_at	BF038548	NM_000919 NM_138766 NM_138821 NM_138822	5066	-0.75	3.40E-03
WDFY3	212606_at	AL536319	NM_014991 NM_178583 NM_178585	23001	-0.75	1.05E-03
KIAA1277	221885_at	AI131051	NM_015689	27147	-0.75	5.98E-03
DIRAS2	219619_at	NM_017594	NM_017594	54769	-0.74	6.42E-03
EXT2	202012_s_at	AA196245	NM_000401 NM_207122	2132	-0.74	5.88E-04
C18orf17	238480_at	AI871745	NM_153211	125488	-0.74	4.89E-04
SLC9A1	209453_at	M81768	NM_003047	6548	-0.74	5.21E-06
PCBD1	203557_s_at	NM_000281	NM_000281 NM_001001939	5092	-0.74	2.72E-04
C6orf83	225850_at	BF975327	NM_145169	113402	-0.74	6.67E-03
PIGV	219238_at	NM_017837	NM_017837	55650	-0.74	4.79E-04
KIAA0276	243691_at	AA150455	NM_015115	23142	-0.74	7.85E-03
PAM	212958_x_at	AI022882	NM_000919 NM_138766 NM_138821 NM_138822	5066	-0.74	9.54E-03
NM_152909	1553719_s_at	NM_152909	---	---	-0.74	1.13E-03
PKD1	216949_s_at	L39891	NM_000296 NM_001009944	5310	-0.74	1.43E-03
AI768895	231069_at	AI768895	---	---	-0.74	7.25E-03
MTMR7	228024_at	AW028100	NM_004686	9108	-0.74	3.76E-05
BRUNOL4	223653_x_at	AW593887	NM_020180	56853	-0.74	9.74E-03
LOH12CR1	227723_at	BF439234	NM_058169	118426	-0.74	7.19E-03
PTN	209465_x_at	AL565812	NM_002825	5764	-0.73	7.19E-03
RPL4	226556_at	BF431260	NM_000968	6124	-0.73	4.08E-03
MTRF1	219822_at	NM_004294	NM_004294	9617	-0.73	1.42E-04
PCCA	203860_at	NM_000282	NM_000282	5095	-0.73	9.56E-03
RPS4Y1	201909_at	NM_001008	NM_001008	6192	-0.73	2.03E-03
FLJ11273	222787_s_at	AV705186	NM_018374	54664	-0.73	7.27E-04
CSE-C	224391_s_at	AF303378	NM_170601	54414	-0.73	3.37E-03
KIAA0323	212356_at	AB002321	NM_015299	23351	-0.73	8.63E-03
AI061377	235232_at	AI061377	---	---	-0.73	9.74E-03
SH3YL1	204019_s_at	NM_015677	NM_015677	26751	-0.73	2.48E-03
LOC255458	1556180_at	BE646146	---	255458	-0.73	6.08E-05
JAGN1	223104_at	AF212230	NM_032492	84522	-0.73	2.17E-05
FLJ10038	205511_at	NM_017976	---	55056	-0.73	5.36E-03
FLJ13984	220007_at	NM_024770	NM_024770	79828	-0.73	6.13E-03
TMEM34	219074_at	NM_018241	NM_018241	55751	-0.73	8.00E-03
ARRDC1	226405_s_at	AK001822	NM_152285	92714	-0.72	2.87E-03
BF056746	228425_at	BF056746	---	---	-0.72	4.99E-04
P15RS	222559_s_at	T79568	NM_018170	55197	-0.72	1.36E-05
FLJ23560	219487_at	NM_024685	NM_024685	79738	-0.72	9.23E-03
ANKH	223093_at	T99215	NM_054027	56172	-0.72	3.35E-03
VAPA	225198_at	AL571942	NM_003574 NM_194434	9218	-0.72	2.38E-03

CCDC2	219174_at	NM_025103	NM_025103	80173	-0.72	2.41E-03
AA709148	243751_at	AA709148	---	---	-0.72	2.28E-04
GART	217445_s_at	AF008655	NM_000819 NM_175085	2618	-0.72	1.27E-03
LOC389906 LOC389910 LOC401625	1558046_x_at	BC017239	XM_372273 XM_374343 XM_377076	389906 389910 401625	-0.72	1.71E-03
SAV1	222573_s_at	AI679398	NM_021818	60485	-0.72	5.04E-04
BBS2	223227_at	AF342736	NM_031885	583	-0.72	2.39E-03
FLJ10726	218314_s_at	NM_018195	NM_018195	55216	-0.72	9.03E-04
AK055769	1558801_at	AK055769	---	---	-0.71	5.90E-03
R53065	240430_at	R53065	---	---	-0.71	6.12E-03
WDFY3	212602_at	AI806395	NM_014991 NM_178583 NM_178585	23001	-0.71	1.21E-03
CSNK2A2	203575_at	NM_001896	NM_001896	1459	-0.71	5.96E-03
KIAA0992	200907_s_at	AU157932	NM_016081	23022	-0.71	2.15E-03
LMNA	212086_x_at	AK026584	NM_005572 NM_170707 NM_170708	4000	-0.71	6.61E-03
BE502930	235124_at	BE502930	---	---	-0.71	3.16E-04
AI765014	224649_x_at	AI765014	---	---	-0.71	2.78E-03
TTC13	219481_at	NM_024525	NM_024525	79573	-0.71	1.48E-03
GAS5	224841_x_at	BF316352	---	60674	-0.71	6.06E-03
AI652899	228812_at	AI652899	---	---	-0.71	5.25E-05
PLCB1	213222_at	AL049593	NM_015192 NM_182734	23236	-0.71	7.21E-04
DET1	219641_at	NM_017996	NM_017996	55070	-0.71	1.63E-03
ACSL3	201660_at	AL525798	NM_004457 NM_203372	2181	-0.71	3.90E-04
MGC2749	200076_s_at	BC006479	NM_024069	79036	-0.71	6.49E-03
QPCT	205174_s_at	NM_012413	NM_012413	25797	-0.71	6.07E-03
PML	209640_at	M79462	NM_002675 NM_033238 NM_033239 NM_033240 NM_033242 NM_033244 NM_033245 NM_033246 NM_033247 NM_033249 NM_033250	5371	-0.70	3.55E-03
LRRC27	1558483_at	AK098652	NM_030626	80313	-0.70	3.75E-03
STK16	209622_at	AB020739	NM_00100891 0 NM_003691	8576	-0.70	2.64E-04
CRYZL1	219767_s_at	NM_005111	NM_005111 NM_145311 NM_145858	9946	-0.70	2.94E-03
TMEM43	217795_s_at	W74580	NM_024334	79188	-0.70	3.09E-03
DFFA	203277_at	NM_004401	NM_004401 NM_213566	1676	-0.70	4.51E-03
BF062875	230072_at	BF062875	---	---	-0.70	7.79E-04
AW974666	222365_at	AW974666	---	---	-0.70	3.83E-03
AA827878	223577_x_at	AA827878	---	---	-0.70	8.67E-03
TMEM43	222418_s_at	AA115485	NM_024334	79188	-0.70	3.97E-03

C14orf118	219720_s_at	NM_017972	NM_017926 NM_017972	55668	-0.70	1.92E-03
LOC285550	227270_at	BF593037	XM_209656	285550	-0.70	1.40E-03
LRRC28	227423_at	AI655972	NM_144598	123355	-0.70	6.98E-04
PFN2	237116_at	AI262277	NM_002628 NM_053024	5217	-0.70	2.39E-03
JMY	226352_at	BF447037	NM_152405	133746	-0.70	9.37E-04
TLOC1	225352_at	AI763287	NM_003262	7095	-0.69	2.60E-04
PPID	204186_s_at	AI014573	NM_005038	5481	-0.69	1.10E-03
FLJ38968	226383_at	AI652452	NM_152316	120534	-0.69	1.37E-03
KIAA0992	200897_s_at	NM_016081	NM_016081	23022	-0.69	1.00E-03
SLC30A5	232432_s_at	AK022818	NM_022902 NM_024055	64924	-0.69	2.34E-03
AIG1	230520_at	T78402	NM_016108	51390	-0.69	7.09E-05
FKBP9	212169_at	AL050187	NM_007270	11328	-0.69	3.13E-03
T1	56829_at	H61826	NM_031466	83696	-0.69	4.28E-03
AA813998	235837_at	AA813998	---	---	-0.69	7.10E-03
SNAP91	204953_at	NM_014841	NM_014841	9892	-0.69	8.76E-03
PLD3	201050_at	NM_012268	NM_012268	23646	-0.69	2.09E-03
CGI-41	218914_at	NM_015997	NM_015997	51093	-0.69	6.72E-03
RARA	228037_at	AA404273	NM_000964	5914	-0.69	9.78E-04
MYO9A	219027_s_at	NM_006901	NM_006901	4649	-0.68	3.06E-03
RDH13	1559190_s_at	AL833150	NM_138412	112724	-0.68	6.77E-03
RGS14	204280_at	NM_006480	NM_006480	10636	-0.68	1.43E-04
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BF434383	235473_at	BF434383	---	---	-0.68	8.03E-04
CDKL3	219831_at	NM_016508	NM_016508	51265	-0.68	4.12E-05
FRBZ1	226962_at	AW299558	NM_194314	360023	-0.68	3.75E-03
FLJ37953	241825_at	AI265967	NM_152382	129450	-0.68	8.57E-04
TRIM4	223384_s_at	BE501464	NM_033017 NM_033091	89122	-0.68	2.58E-03
SF3B3	200688_at	D13642	NM_012426	23450	-0.68	4.67E-03
PHF10	219126_at	NM_018288	NM_018288 NM_133325	55274	-0.68	2.92E-03
IL17RB	235531_at	AA928257	NM_018725 NM_172234	55540	-0.68	2.10E-03
BCL2L13	224035_s_at	AF183411	NM_015367	23786	-0.68	7.08E-04
MAN1A2	217922_at	AL157902	NM_006699	10905	-0.68	3.21E-03
ZNF232	236075_s_at	AI693543	NM_014519	7775	-0.68	6.78E-03
BC024246	1556301_at	BC024246	---	---	-0.68	2.06E-04
ZRANB1	225130_at	AW003734	NM_017580	54764	-0.67	1.84E-04
PP1665	32502_at	AL041124	NM_030792	81544	-0.67	9.49E-04
CAB39	224311_s_at	AF151824	NM_016289	51719	-0.67	2.14E-03
KRTAP4-7	225225_at	BF791544	NM_033061	85287	-0.67	8.80E-03
SLC30A5	218989_x_at	NM_022902	NM_022902 NM_024055	64924	-0.67	6.75E-03
RNF41	201961_s_at	AL583171	NM_005785 NM_194358 NM_194359	10193	-0.67	8.95E-03
C6orf168	232067_at	BC004869	NM_032511	84553	-0.67	2.42E-03
TNIP2	232160_s_at	AL137262	NM_024309	79155	-0.67	1.56E-03
DKFZP564D17:	212936_at	AI927701	NM_032042	83989	-0.67	5.18E-04
LOC439962	1560047_s_at	AA127813	XM_498479	439962	-0.67	3.91E-03
MCM3APAS	220459_at	NM_018118	---	114044	-0.67	2.26E-03
SLC35E1	229410_at	AI659219	NM_024881	79939	-0.67	5.75E-03
FBXW7	229419_at	BF222826	NM_018315 NM_033632	55294	-0.67	9.92E-04

C10orf22	212500_at	AL049319	NM_032804	84890	-0.67	3.49E-04
SURF2	205224_at	NM_017503	NM_017503	6835	-0.67	3.01E-04
MGC12966	224452_s_at	BC006110	NM_032706	84792	-0.67	4.02E-04
FLJ20195	223833_at	BC002482	NM_017706	54853	-0.67	5.69E-03
FLJ20542	233625_x_at	AK021939	NM_017871	54973	-0.67	8.46E-04
LRCH2	227688_at	AK022128	NM_032179 NM_020871	57631	-0.67	2.21E-04
SLC22A17	218675_at	NM_020372	NM_016609 NM_020372	51310	-0.67	3.50E-03
ARNT2	202986_at	NM_014862	NM_014862	9915	-0.67	1.18E-03
LOC440118	FX-M27830_M_AF	FX-M27830_M	XM_498554	440118	-0.67	5.77E-03
FLJ23518	223300_s_at	AI286012	NM_024725	79780	-0.66	7.90E-04
PROSC	209384_at	AA176833	NM_007198	11212	-0.66	1.14E-03
P15RS	222558_at	T79568	NM_018170	55197	-0.66	1.67E-04
PPP2R5C	201877_s_at	NM_002719	NM_002719 NM_178586 NM_178587 NM_178588	5527	-0.66	3.07E-06
SGNE1	203889_at	NM_003020	NM_003020	6447	-0.66	1.31E-04
CNOT6L	1553267_a_at	NM_144571	NM_144571	246175	-0.66	5.11E-03
TTLL1	205652_s_at	NM_012263	NM_00100857 2 NM_012263	25809	-0.66	3.38E-04
AD023	223411_at	AF225422	NM_020679	57409	-0.66	7.26E-06
KIF3C	203389_at	AF035621	NM_002254	3797	-0.66	2.70E-04
AI598222	235679_at	AI598222	---	---	-0.65	7.93E-03
PPP3CA	202457_s_at	AA911231	NM_000944	5530	-0.65	9.97E-03
RPIP8	213439_x_at	AI197870	NM_006695	10900	-0.65	1.89E-03
NSMCE1	224666_at	AF161451	NM_145080	197370	-0.65	3.16E-04
BACE1	222462_s_at	AI653425	NM_012104 NM_138971 NM_138972 NM_138973	23621	-0.65	3.25E-03
MPI	202472_at	NM_002435	NM_002435	4351	-0.65	8.59E-04
FBXW7	222729_at	BE551877	NM_018315 NM_033632	55294	-0.65	2.52E-03
NELF	221214_s_at	NM_015537	NM_015537	26012	-0.65	7.98E-04
HLA-A	215313_x_at	AA573862	NM_002116	3105	-0.65	7.23E-03
FGF2	204422_s_at	NM_002006	NM_002006	2247	-0.65	4.86E-07
P15RS	225953_at	AI684281	NM_018170	55197	-0.65	3.76E-04
GAS5	224741_x_at	BG329175	---	60674	-0.65	8.18E-03
IPO8	205701_at	NM_006390	NM_006390	10526	-0.65	7.25E-04
ECE2	230706_s_at	AI084921	NM_014693	9718	-0.65	4.71E-04
ZCSL3	213853_at	AL050199	NM_181706	120526	-0.65	6.76E-03
PSEN1	226577_at	N49844	NM_000021 NM_007318 NM_007319	5663	-0.65	3.44E-03
LOC284018	226901_at	AI214996	NM_181655 NM_181656	284018	-0.64	5.00E-04
FLJ32384	238547_at	AI972367	NM_144608	124790	-0.64	3.77E-03
LOC284106	230727_at	BE348515	XM_375449	284106	-0.64	7.65E-03
WDR32	219001_s_at	NM_024345	NM_024345	79269	-0.64	1.25E-04
RNF13	201779_s_at	AF070558	NM_007282 NM_183381 NM_183382 NM_183383 NM_183384	11342	-0.64	1.26E-04

VPS33B	218415_at	NM_018668	NM_018668	26276	-0.64	7.92E-03
SPTBN2	231311_at	AA725246	NM_006946	6712	-0.64	1.71E-03
LOC389906	1569629_x_at	BC017231	XM_372273	389906	-0.64	4.97E-04
C22orf9	227144_at	AA476916	NM_00100988 0 NM_015264	23313	-0.64	3.58E-03
PHKA1	205450_at	NM_002637	NM_002637	5255	-0.64	3.01E-03
COPS7A	209029_at	AF193844	NM_016319	50813	-0.64	6.55E-05
EIF2S3	205321_at	NM_001415	NM_001415	1968	-0.64	8.39E-03
TM6SF1	1558102_at	AK055438	NM_023003	53346	-0.64	2.18E-04
ATCAY	227365_at	AL566774	NM_033064	85300	-0.64	8.51E-03
CGI-119	223892_s_at	AF182414	NM_016056	51643	-0.64	1.66E-04
APG7L	224025_s_at	BC000091	NM_006395	10533	-0.64	4.74E-03
CIRBP	230142_s_at	AW088030	NM_001280	1153	-0.64	2.64E-03
C21orf127	220311_at	NM_013240	NM_013240 NM_182749	29104	-0.64	2.93E-03
)KFZP566D134	238597_at	BG028770	NM_030816	81573	-0.63	9.05E-03
WNT3	229103_at	AA463626	NM_030753	7473	-0.63	1.82E-03
C10orf88	219240_s_at	NM_024942	NM_024942	80007	-0.63	2.53E-03
KCNMB3	235980_at	AA767763	NM_014407 NM_171828 NM_171829 NM_171830	27094	-0.63	9.48E-04
LOC440360	236838_at	H11609	XM_498641	440360	-0.63	4.34E-03
AA868380	230569_at	AA868380	---	---	-0.63	7.44E-03
C3orf6	235051_at	BF696931	NM_174908 NM_178335	152137	-0.63	9.04E-03
BLP2	1552426_a_at	NM_078474	NM_025141 NM_078474	80213	-0.63	9.66E-03
PPID	204185_x_at	NM_005038	NM_005038	5481	-0.63	3.34E-03
CXorf12	204340_at	NM_003492	NM_003492	8269	-0.63	4.03E-03
PLCB1	211925_s_at	AY004175	NM_015192 NM_182734	23236	-0.63	8.12E-05
MYO7A	208189_s_at	NM_000260	NM_000260	4647	-0.63	1.17E-04
UBE2D3	229355_at	AU150386	NM_003340 NM_181886 NM_181887 NM_181888 NM_181889 NM_181890 NM_181891 NM_181892 NM_181893	7323	-0.63	6.20E-03
CYP2U1	226393_at	AW055161	NM_183075	113612	-0.63	7.35E-03
PFDN5	207132_x_at	NM_002624	NM_002624 NM_145896 NM_145897	5204	-0.63	9.53E-04
WSB1	201294_s_at	N24643	NM_015626 NM_134264 NM_134265	26118	-0.63	2.39E-03
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PROSC	214545_s_at	NM_007198	NM_007198	11212	-0.62	3.15E-04
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FLJ21919	202809_s_at	NM_023015	NM_023015	65123	-0.62	7.33E-03
MGC5356	220426_at	NM_024059	NM_024059	79025	-0.62	6.04E-03
KIAA1671	225525_at	AB051458	XM_371461	85379	-0.62	1.04E-03
SNX6	217789_at	NM_021249	NM_021249 NM_152233	58533	-0.62	4.75E-03

MPPE1	213727_x_at	AI743654	NM_023075 NM_138608	65258	-0.62	7.16E-04
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MAP7	215471_s_at	AJ242502	NM_003980	9053	-0.62	3.97E-04
FLJ11273	226529_at	BF513060	NM_018374	54664	-0.62	7.53E-03
ADCK2	44120_at	AI879381	NM_052853	90956	-0.62	3.67E-03
TST	209605_at	D87292	NM_003312	7263	-0.62	8.01E-03
NUDT2	218609_s_at	NM_001161	NM_001161 NM_147172 NM_147173	318	-0.62	7.23E-03
AI632010	244687_at	AI632010	---	---	-0.62	3.57E-04
PHC1	225958_at	AI554106	NM_004426	1911	-0.62	8.62E-05
PIK3CB	212688_at	BC003393	NM_006219	5291	-0.62	6.77E-04
LOC401466	1555241_at	BC032347	XM_376783	401466	-0.61	2.14E-03
KIAA1458	224843_at	AB040891	XM_044434	57606	-0.61	4.73E-04
AV756131	224915_x_at	AV756131	XM_497769	441951	-0.61	3.59E-03
APRT	213892_s_at	AA927724	NM_000485	353	-0.61	6.05E-04
WDR41	218055_s_at	NM_018268	NM_018268	55255	-0.61	5.04E-03
LOC143458	234985_at	AW043782	NM_174902	143458	-0.61	1.09E-04
MGC15429	224821_at	AL520200	NM_032750	84836	-0.61	1.73E-03
LOC387593	239715_at	AI374756	---	387593	-0.61	7.41E-03
MGC2494	219709_x_at	NM_023933	NM_023933	65990	-0.61	7.21E-03
SBF2	226169_at	AW276572	NM_030962	81846	-0.61	2.63E-03
CGI-119	222845_x_at	AF161526	NM_016056	51643	-0.61	6.18E-04
UBE2D3	200669_s_at	NM_003340	NM_003340 NM_181886 NM_181887 NM_181888 NM_181889 NM_181890 NM_181891 NM_181892 NM_181893	7323	-0.61	7.57E-04
NPC1L1	220106_at	NM_013389	NM_013389	29881	-0.61	9.81E-04
RNF13	201780_s_at	NM_007282	NM_007282 NM_183381 NM_183382 NM_183383 NM_183384	11342	-0.61	9.87E-04
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GAL	207466_at	NM_015973	NM_015973	51083	-0.59	6.79E-03
LOC92017	225608_at	H15273	NM_001009607	92017	-0.59	1.54E-05
WDR9	214820_at	AJ002572	NM_00100724 6 NM_018963 NM_033656	54014	-0.59	4.03E-04
PLEKHA3	223370_at	AF286162	NM_019091	65977	-0.59	4.77E-03
PPM1K	235061_at	AV706522	NM_152542	152926	-0.59	2.94E-03
MTL5	241466_at	AI275776	NM_004923	9633	-0.59	5.56E-04
DHX32	218198_at	NM_018180	NM_018180	55760	-0.59	7.21E-03

)KFZp451M211	231540_at	BF511274	NM_182585	285023	-0.59	1.28E-03
MTM1	36920_at	U46024	NM_000252	4534	-0.59	4.62E-03
ALKBH	236721_at	AI922200	NM_006020	8846	-0.59	7.70E-03
BC019017	1558128_at	BC019017	---	---	-0.59	1.03E-03
CDC42EP3	209288_s_at	AL136842	NM_006449	10602	-0.59	8.78E-04
FLJ20277	233638_s_at	AK026430	NM_017739	55624	-0.59	4.86E-03
AI766065	224647_at	AI766065	---	---	-0.59	1.11E-03
SETDB2	235339_at	W65369	NM_031915	83852	-0.59	5.43E-03
BE326214	229287_at	BE326214	---	---	-0.59	8.90E-04
HS2ST1	203285_s_at	NM_012262	NM_012262	9653	-0.58	4.84E-04
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GPR56	212070_at	AL554008	NM_005682	9289	-0.58	2.25E-03
			NM_201524			
			NM_201525			
LOC119710	228249_at	AA535128	NM_138787	119710	-0.58	7.12E-03
FLJ13576	234726_s_at	AK025482	NM_022484	64418	-0.58	5.50E-03
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			NM_145896			
			NM_145897			
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CHIC1	228345_at	AI745136	XR_000216	53344	-0.58	6.80E-03
BE645776	227288_at	BE645776	XM_068632	133993	-0.58	4.35E-04
CTBS	218923_at	AW304174	NM_004388	1486	-0.58	8.95E-03
TMF1	235566_at	AW591660	NM_007114	7110	-0.58	7.30E-03
PKNOX1	221883_at	AA133342	NM_004571	5316	-0.58	1.27E-03
			NM_197976			
ACTR1B	202135_s_at	NM_005735	NM_005735	10120	-0.58	2.50E-03
TNFRSF21	214581_x_at	BE568134	NM_014452	27242	-0.58	8.02E-03
PEX7	211033_s_at	BC006268	NM_000288	5191	-0.58	8.93E-03
EIF4E3	225941_at	AI935522	---	317649	-0.58	5.78E-03

What is claimed:

1. An established clonal cell line comprising cells susceptible to intoxication by BoNT/A,

   wherein the cells exhibits at least a 1.5-fold difference in gene expression levels of three or more genes as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164; and

   wherein the gene expression levels are selected from th group ADAMTS9, ASCL1, BASP1, DOK5, DPYD, GNB4, GNG11, GTSF1, MAOA, MINA, MSN, PEG3, PLK2, PRSS12, RNF182, SLC44A5, SPARC, TFPI2, and TPTE; and

   wherein the the clonal cell line comprises cells susceptible to BoNT/A intoxication by about 100 pM or less of a BoNT/A.

2. The established clonal cell line of Claim 1, wherein the the cells exhibit at least a 2.0-fold difference in gene expression levels of one or more genes as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164, at least a 3.0-fold difference in gene expression levels of one or more genes as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164, or at least a 4.0-fold difference in gene expression levels of one or more genes as compared to the expression levels of these genes in cells from the parental SiMa cell line DSMZ ACC 164.

3. The established clonal cell line of Claim 1, wherein the gene expression levels are measured before differentiation of the cell or after differentiation of the cell.

4. The established clonal cell line of Claim 1, wherein the cell from an established clonal cell line exhibits about 100 pM or less of a BoNT/A for at least 5 or more cell passages.

FIG. 1A.

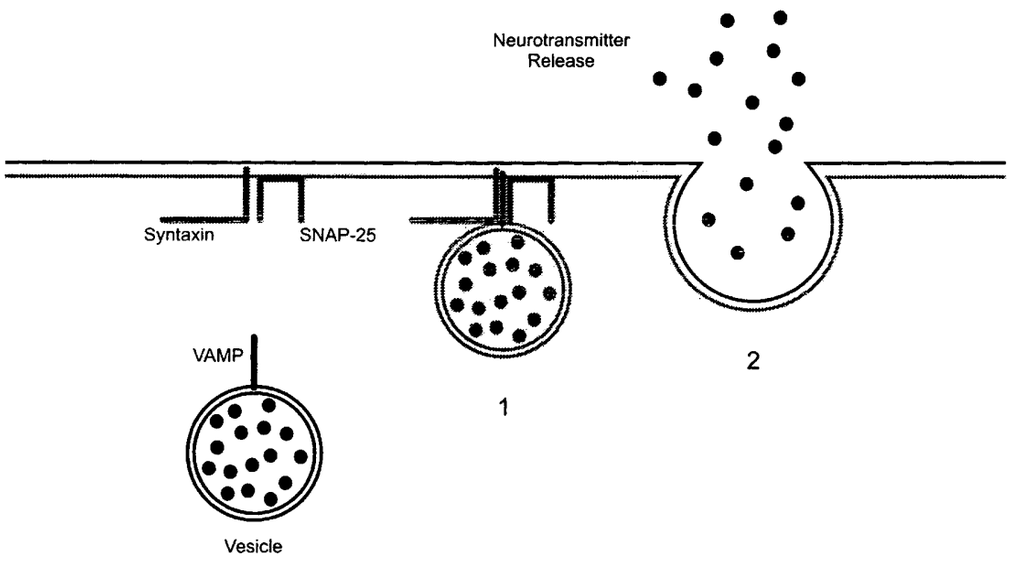

Neurotransmitter
Release
Syntaxin
SNAP-25
VAMP
Vesicle
1
2

FIG. 1B.

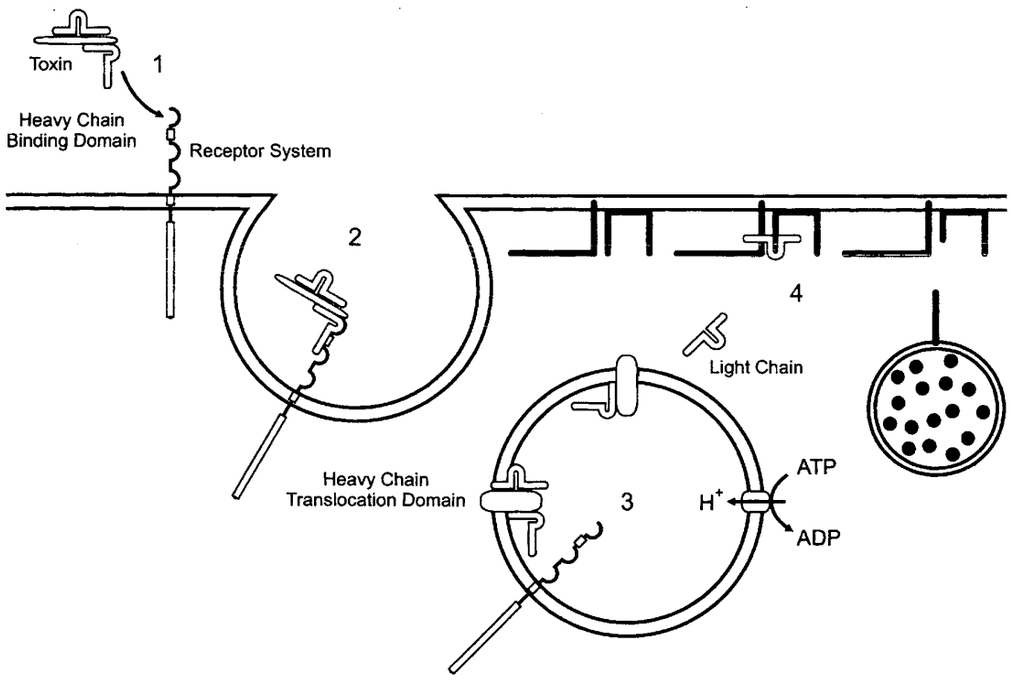

Toxin
1
Heavy Chain
Binding Domain
Receptor System
2
4
Light Chain
Heavy Chain
Translocation Domain
3
ATP
H+
ADP

FIG. 2A.

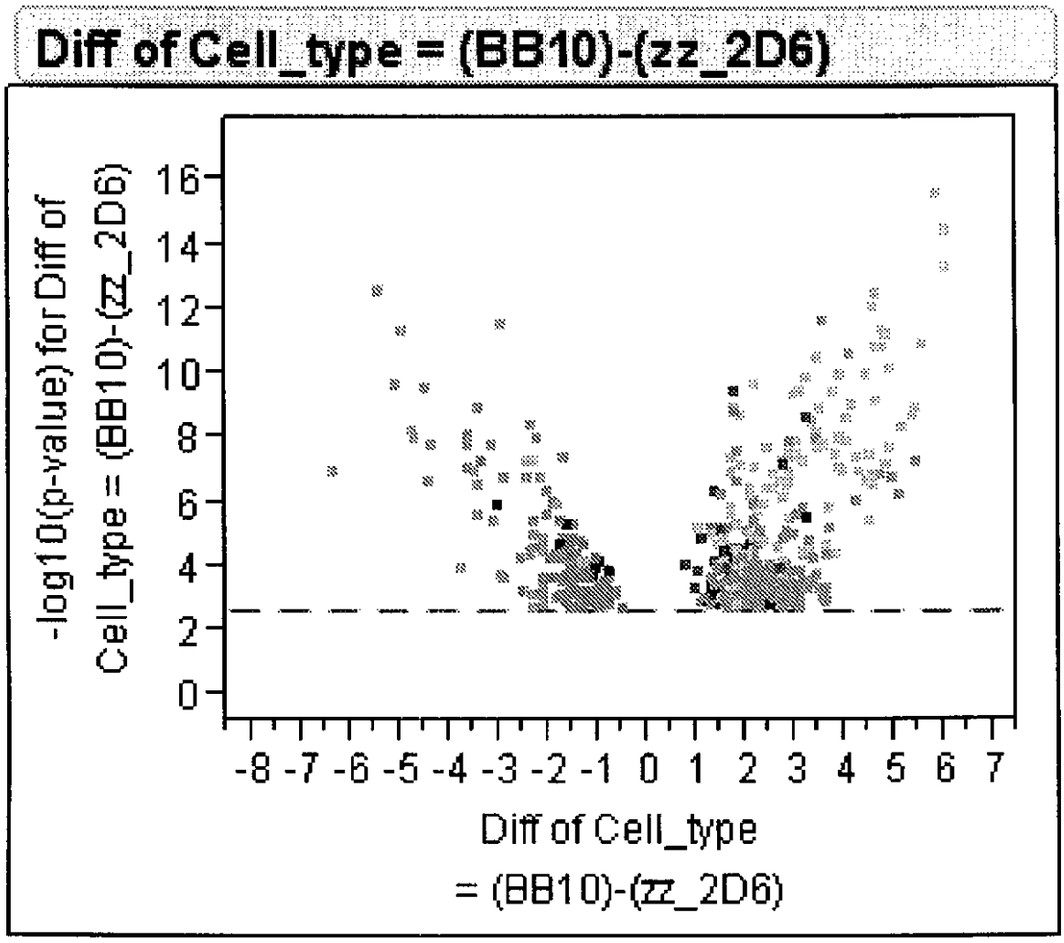

Diff of Cell_type = (BB10)-(zz_2D6)
-log10(p-value) for Diff of Cell_type = (BB10)-(zz_2D6)
16
14
12
10
8
6
4
2
0
-8 -7 -6 -5 -4 -3 -2 -1 0 1 2 3 4 5 6 7
Diff of Cell_type = (BB10)-(zz_2D6)

FIG. 2B.

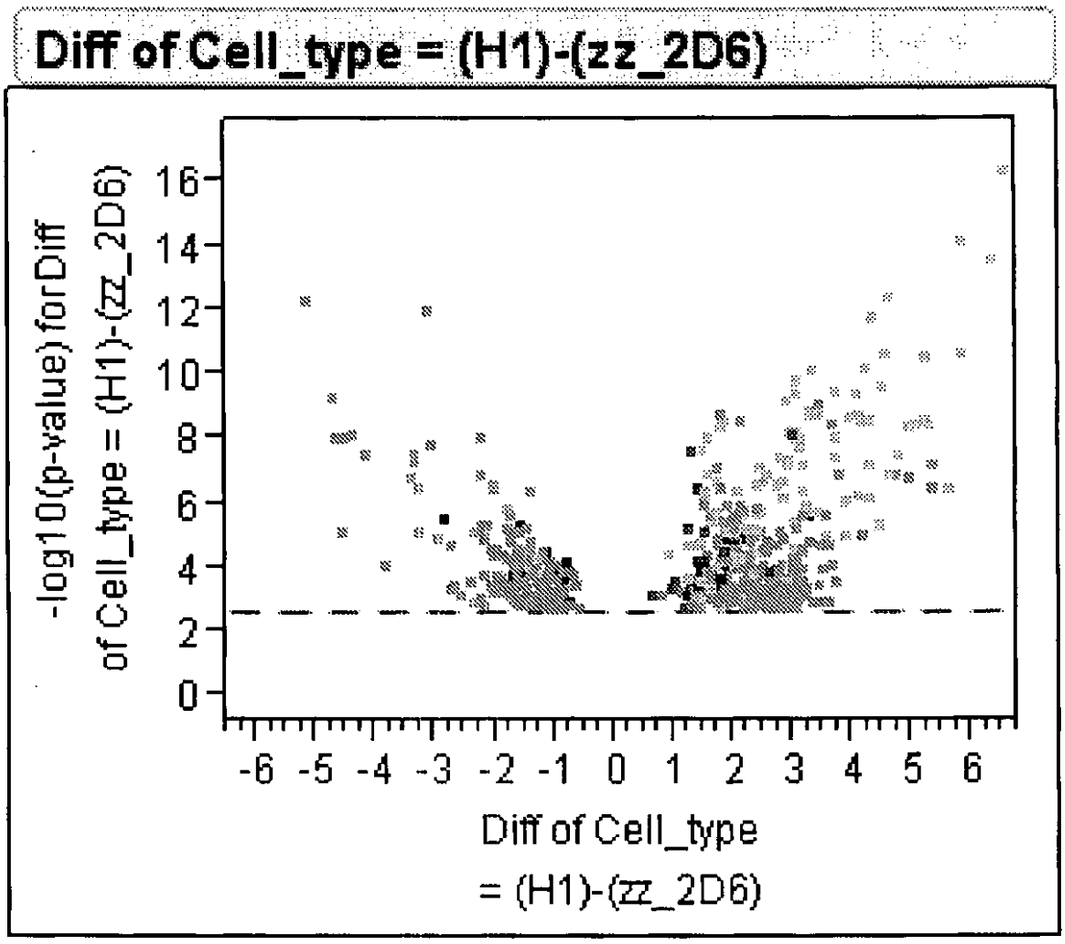

Diff of Cell_type = (H1)-(zz_2D6)
-log10(p-value) for Diff of Cell_type = (H1)-(zz_2D6)
16
14
12
10
8
6
4
2
0
-6 -5 -4 -3 -2 -1 0 1 2 3 4 5 6
Diff of Cell_type = (H1)-(zz_2D6)

FIG. 2C.

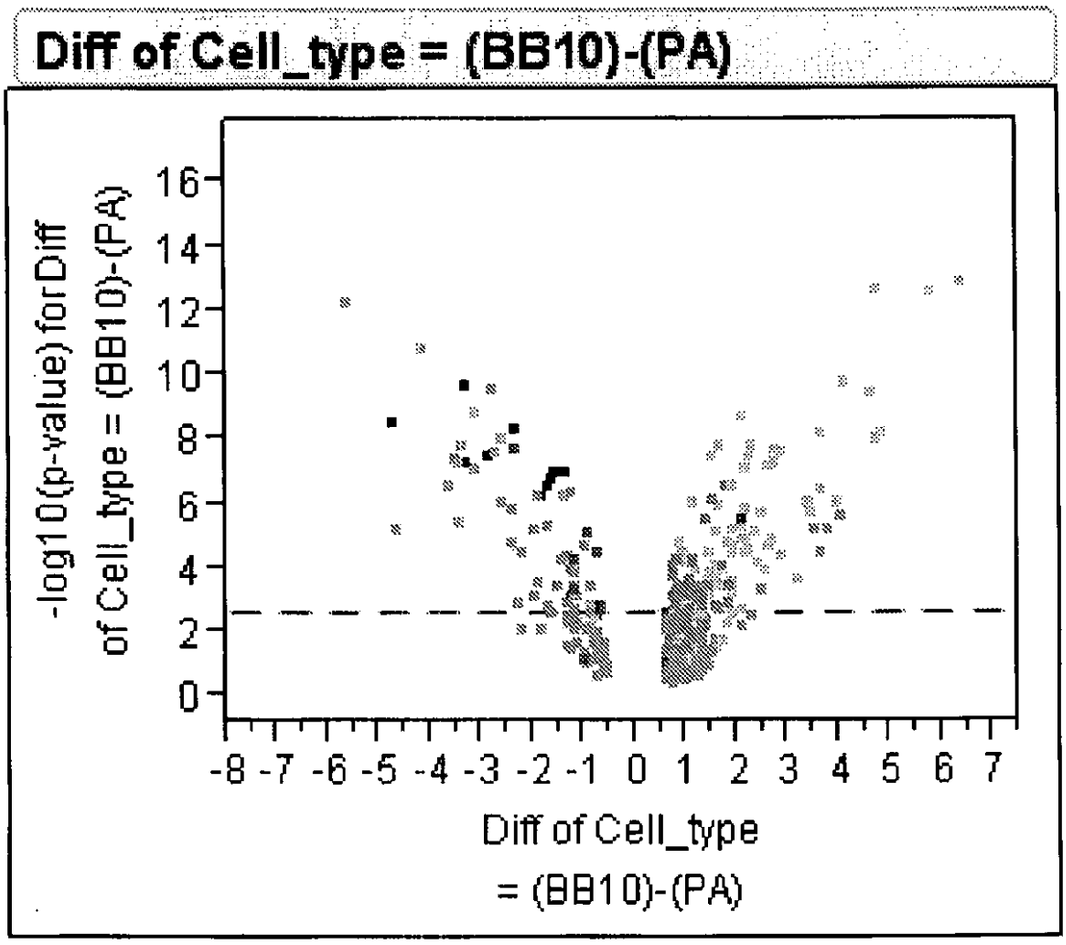

Diff of Cell_type = (BB10)-(PA)
-log10(p-value) for Diff of Cell_type = (BB10)-(PA)
16
14
12
10
8
6
4
2
0
-8 -7 -6 -5 -4 -3 -2 -1 0 1 2 3 4 5 6 7
Diff of Cell_type = (BB10)-(PA)

FIG. 2D.

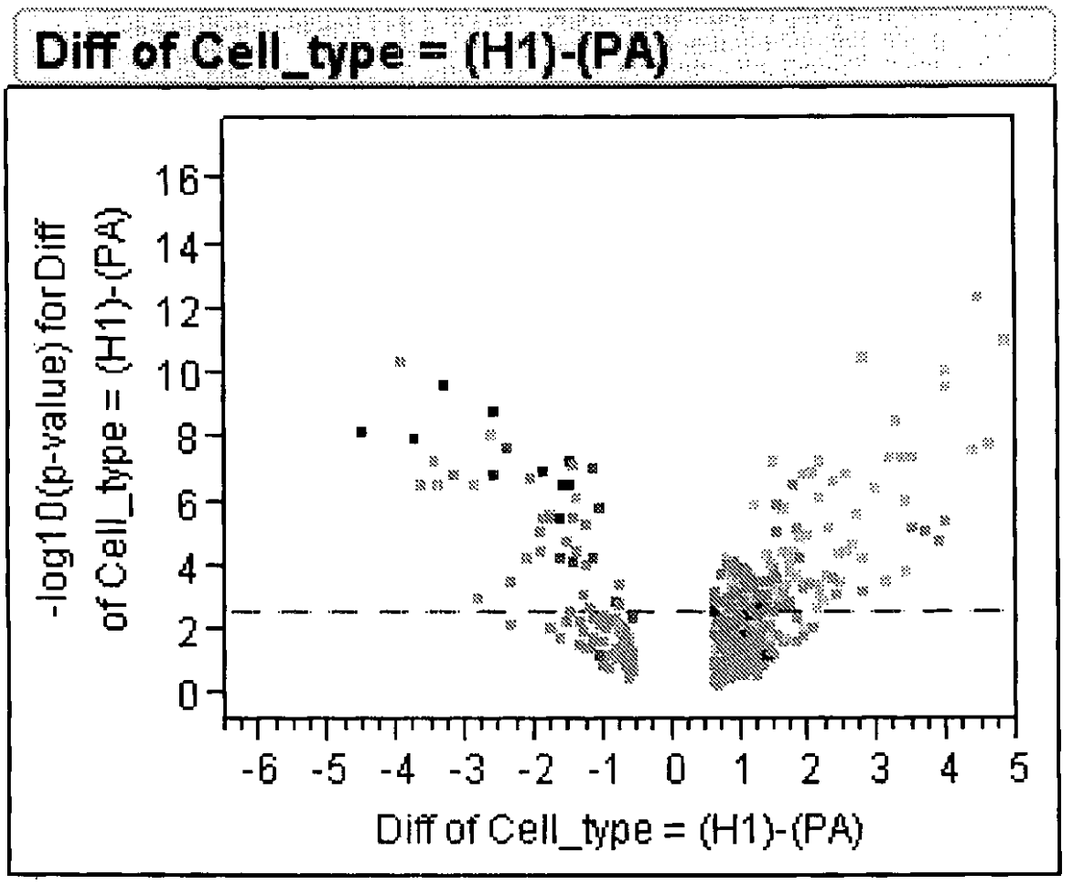

Diff of Cell_type = (H1)-(PA)
-log10(p-value) for Diff of Cell_type = (H1)-(PA)
16
14
12
10
8
6
4
2
0
-6 -5 -4 -3 -2 -1 0 1 2 3 4 5
Diff of Cell_type = (H1)-(PA)

FIG. 2E.

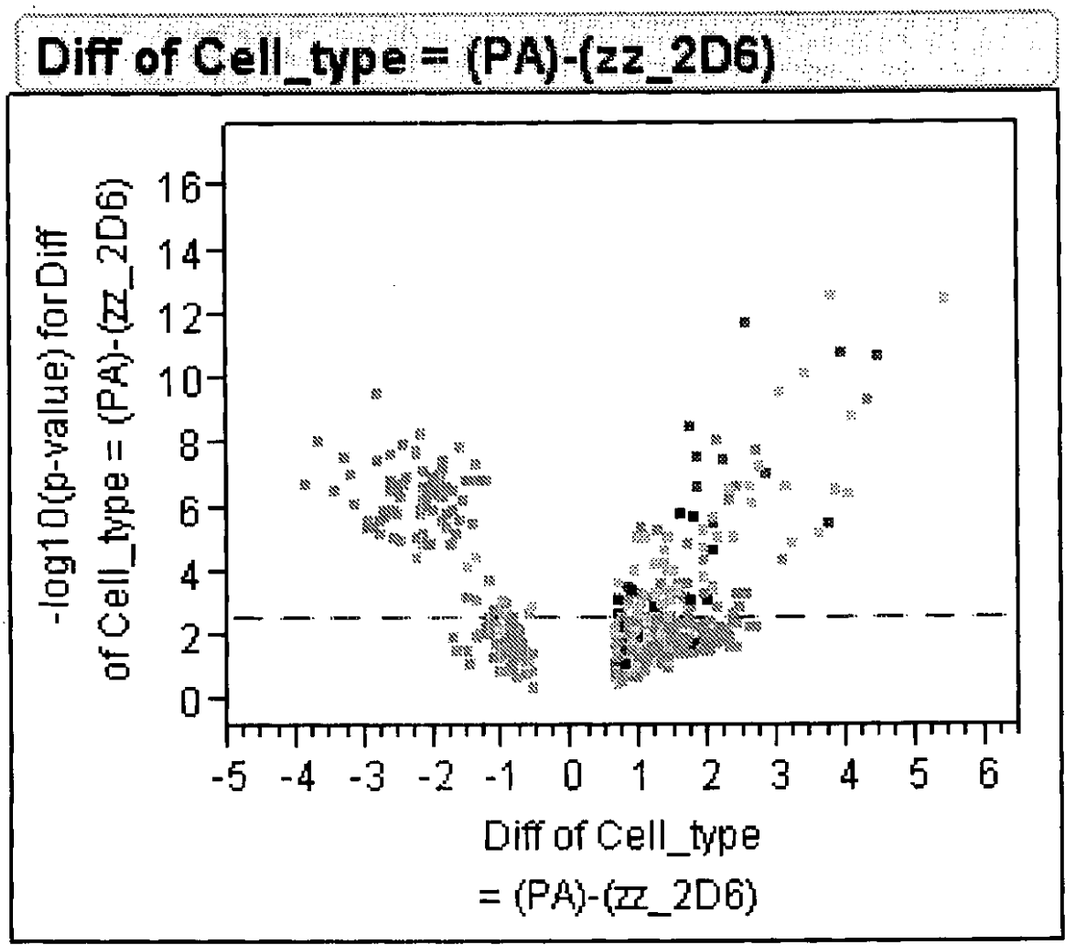
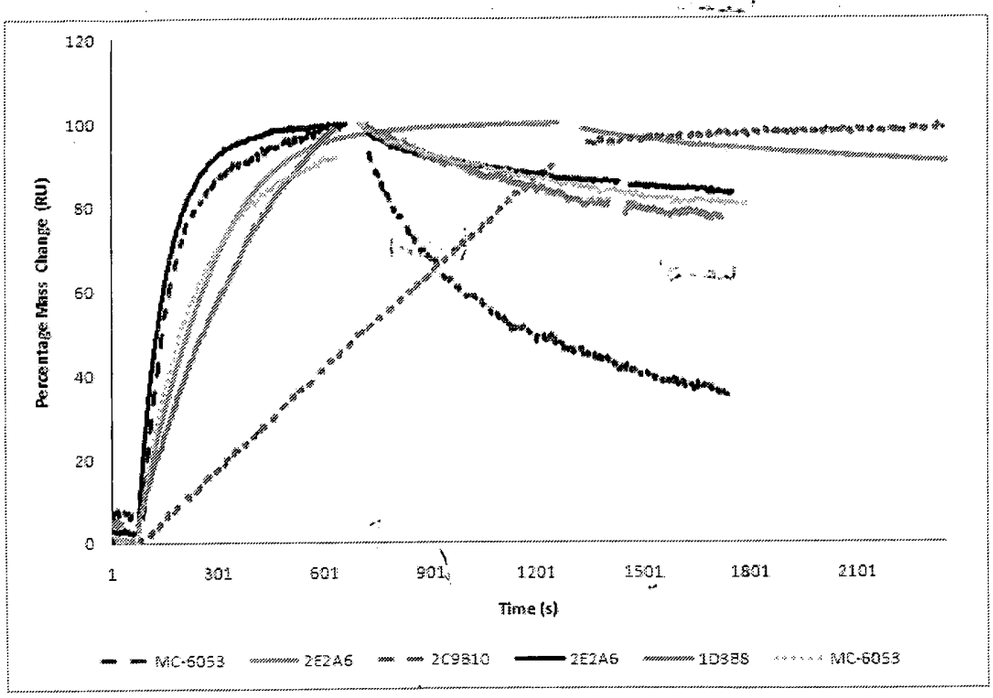
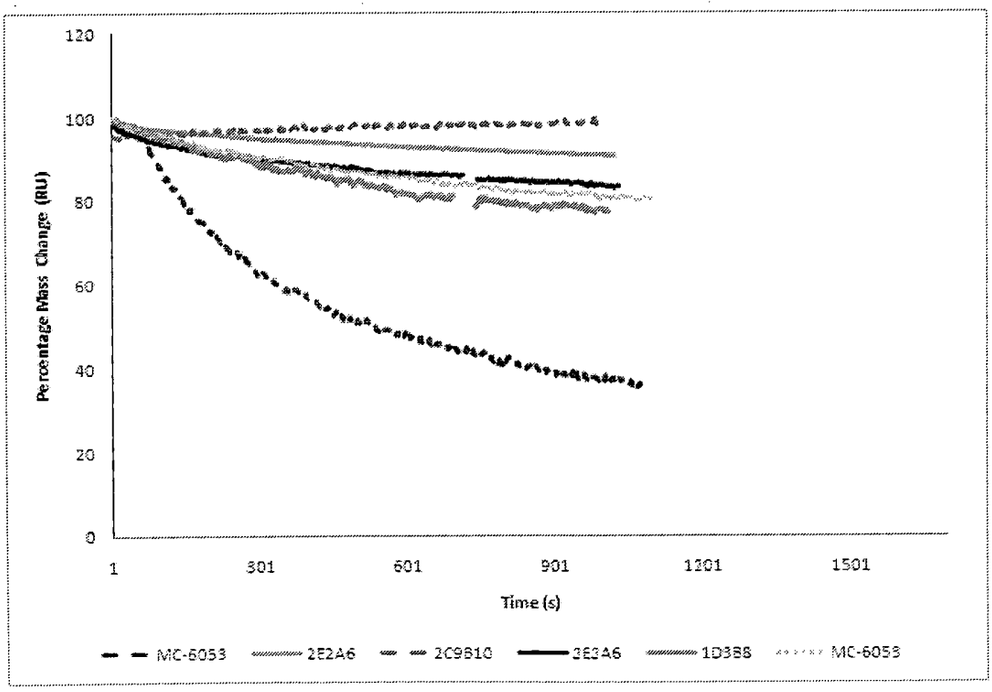

Diff of Cell_type = (PA)-(zz_2D6)
-log10(p-value) for Diff of Cell_type = (PA)-(zz_2D6)
16
14
12
10
8
6
4
2
0
-5 -4 -3 -2 -1 0 1 2 3 4 5 6
Diff of Cell_type = (PA)-(zz_2D6)

FIG. 3A.


120
100
80
60
40
20
0
Percentage Mass Change (RU)
1
301
601
901
1201
1501
1801
2101
Time (s)
MC-6053
2E2A6
2C9B10
2E2A6
1D3B8
MC-6053

450

FIG. 3B.


120
100
80
60
40
20
0
Percentage Mass Change (RU)
1
301
601
901
1201
1501
Time (s)
MC-6053
2E2A6
2C9B10
3E3A6
1D3B8
MC-6053

SEQUENCE LISTING

<110> Birgitte Jacky
Wang, Joanne
Zhu, Hong
Hodges, D. Dianne
Fernandez-Salas, Ester

<120> Cells Useful for Immuno-Based Botulinum
Toxin Serotype A Activity Assays

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            20                  25                  30
Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
        35                  40                  45
Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
    50                  55                  60
Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65                  70                  75                  80
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
                85                  90                  95
Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
            100                 105                 110
Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
        115                 120                 125
Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
    130                 135                 140
Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile
145                 150                 155                 160
Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr
                165                 170                 175
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
            180                 185                 190
Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
        195                 200                 205
Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
    210                 215                 220
Leu Ile His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225                 230                 235                 240
Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
                245                 250                 255
Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
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                260                 265                 270
Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
        275                 280                 285
Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
    290                 295                 300
Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305                 310                 315                 320
Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
                325                 330                 335
Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
            340                 345                 350
Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn
        355                 360                 365
Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr
    370                 375                 380
Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
385                 390                 395                 400
Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu
                405                 410                 415
Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
            420                 425                 430
Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Asp Lys Gly Tyr Asn Lys
        435                 440                 445
Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
    450                 455                 460
Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu
465                 470                 475                 480
Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
                485                 490                 495
Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro
            500                 505                 510
Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
        515                 520                 525
Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
    530                 535                 540
Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu
545                 550                 555                 560
His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu
                565                 570                 575
Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys
            580                 585                 590
Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu
        595                 600                 605
Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr
    610                 615                 620
Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala
625                 630                 635                 640
Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu
                645                 650                 655
Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala
            660                 665                 670
Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys
        675                 680                 685
Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu
    690                 695                 700
Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys
705                 710                 715                 720
Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu
                725                 730                 735
```

```
Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn
            740                 745                 750
Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp
        755                 760                 765
Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile
    770                 775                 780
Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met
785                 790                 795                 800
Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys
                805                 810                 815
Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly
            820                 825                 830
Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp
        835                 840                 845
Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser
    850                 855                 860
Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn
865                 870                 875                 880
Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser
                885                 890                 895
Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn
            900                 905                 910
Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu
        915                 920                 925
Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser
    930                 935                 940
Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn
945                 950                 955                 960
Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val
                965                 970                 975
Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu
            980                 985                 990
Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser
        995                 1000                1005
Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu
    1010                1015                1020
Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro
1025                1030                1035                1040
Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys
                1045                1050                1055
Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe
            1060                1065                1070
Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr
        1075                1080                1085
Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr
    1090                1095                1100
Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn
1105                1110                1115                1120
Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu
                1125                1130                1135
Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser
            1140                1145                1150
Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly
        1155                1160                1165
Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val
    1170                1175                1180
Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala
1185                1190                1195                1200
Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn
```

```
                1205                1210                1215
Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr
            1220                1225                1230
Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
        1235                1240                1245
Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser
    1250                1255                1260
Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys
1265                1270                1275                1280
Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu
                1285                1290                1295
```

<210> 2
<211> 1296
<212> PRT
<213> Clostridium botulinum

<400> 2

```
Met Pro Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp Pro Val Asn Gly
 1               5                  10                  15
Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Ala Gly Gln Met Gln Pro
            20                  25                  30
Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
        35                  40                  45
Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
    50                  55                  60
Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65                  70                  75                  80
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
                85                  90                  95
Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
            100                 105                 110
Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
        115                 120                 125
Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
    130                 135                 140
Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile
145                 150                 155                 160
Ile Gln Phe Glu Cys Lys Ser Phe Gly His Asp Val Leu Asn Leu Thr
                165                 170                 175
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
            180                 185                 190
Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
        195                 200                 205
Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
    210                 215                 220
Leu Ile His Ala Glu His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225                 230                 235                 240
Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
                245                 250                 255
Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
            260                 265                 270
Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
        275                 280                 285
Lys Phe Lys Asp Val Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Ile
    290                 295                 300
Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305                 310                 315                 320
```

```
Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
                325                 330                 335
Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
            340                 345                 350
Asn Phe Val Asn Phe Phe Lys Val Ile Asn Arg Lys Thr Tyr Leu Asn
        355                 360                 365
Phe Asp Lys Ala Val Phe Arg Ile Asn Ile Val Pro Asp Glu Asn Tyr
    370                 375                 380
Thr Ile Lys Asp Gly Phe Asn Leu Lys Gly Ala Asn Leu Ser Thr Asn
385                 390                 395                 400
Phe Asn Gly Gln Asn Thr Glu Ile Asn Ser Arg Asn Phe Thr Arg Leu
                405                 410                 415
Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
            420                 425                 430
Gly Ile Ile Pro Phe Lys Thr Lys Ser Leu Asp Glu Gly Tyr Asn Lys
        435                 440                 445
Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
    450                 455                 460
Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asp Lys Val Glu Glu
465                 470                 475                 480
Ile Thr Ala Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
                485                 490                 495
Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asp Phe Asp Asn Glu Pro
            500                 505                 510
Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
        515                 520                 525
Glu Pro Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
    530                 535                 540
Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu
545                 550                 555                 560
His Gly Asp Ser Arg Ile Ile Leu Thr Asn Ser Ala Glu Glu Ala Leu
                565                 570                 575
Leu Lys Pro Asn Val Ala Tyr Thr Phe Phe Ser Ser Lys Tyr Val Lys
            580                 585                 590
Lys Ile Asn Lys Ala Val Glu Ala Phe Met Phe Leu Asn Trp Ala Glu
        595                 600                 605
Glu Leu Val Tyr Asp Phe Thr Asp Glu Thr Asn Glu Val Thr Thr Met
    610                 615                 620
Asp Lys Ile Ala Asp Ile Thr Ile Ile Val Pro Tyr Ile Gly Pro Ala
625                 630                 635                 640
Leu Asn Ile Gly Asn Met Leu Ser Lys Gly Glu Phe Val Glu Ala Ile
                645                 650                 655
Ile Phe Thr Gly Val Val Ala Met Leu Glu Phe Ile Pro Glu Tyr Ala
            660                 665                 670
Leu Pro Val Phe Gly Thr Phe Ala Ile Val Ser Tyr Ile Ala Asn Lys
        675                 680                 685
Val Leu Thr Val Gln Thr Ile Asn Asn Ala Leu Ser Lys Arg Asn Glu
    690                 695                 700
Lys Trp Asp Glu Val Tyr Lys Tyr Thr Val Thr Asn Trp Leu Ala Lys
705                 710                 715                 720
Val Asn Thr Gln Ile Asp Leu Ile Arg Glu Lys Met Lys Lys Ala Leu
                725                 730                 735
Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn
            740                 745                 750
Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp
        755                 760                 765
Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Ser Ala Met Ile Asn Ile
    770                 775                 780
Asn Lys Phe Leu Asp Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met
```

785 790 795 800
Ile Pro Tyr Ala Val Lys Arg Leu Lys Asp Phe Asp Ala Ser Val Arg
805 810 815
Asp Val Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Val Leu
820 825 830
Gln Val Asp Arg Leu Lys Asp Glu Val Asn Asn Thr Leu Ser Ala Asp
835 840 845
Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Lys Lys Leu Leu Ser
850 855 860
Thr Phe Thr Glu Tyr Ile Lys Asn Ile Val Asn Thr Ser Ile Leu Ser
865 870 875 880
Ile Val Tyr Lys Lys Asp Asp Leu Ile Asp Leu Ser Arg Tyr Gly Ala
885 890 895
Lys Ile Asn Ile Gly Asp Arg Val Tyr Tyr Asp Ser Ile Asp Lys Asn
900 905 910
Gln Ile Lys Leu Ile Asn Leu Glu Ser Ser Thr Ile Glu Val Ile Leu
915 920 925
Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser
930 935 940
Phe Trp Ile Lys Ile Pro Lys Tyr Phe Ser Lys Ile Asn Leu Asn Asn
945 950 955 960
Glu Tyr Thr Ile Ile Asn Cys Ile Glu Asn Asn Ser Gly Trp Lys Val
965 970 975
Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Asn Lys Gln
980 985 990
Asn Ile Gln Arg Val Val Phe Lys Tyr Ser Gln Met Val Asn Ile Ser
995 1000 1005
Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu
1010 1015 1020
Thr Lys Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro
1025 1030 1035 1040
Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Lys Ile Met Phe Lys
1045 1050 1055
Leu Asp Gly Cys Arg Asp Pro Arg Arg Tyr Ile Met Ile Lys Tyr Phe
1060 1065 1070
Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr
1075 1080 1085
Asp Ser Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asn Tyr
1090 1095 1100
Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Phe Asp Pro Asn
1105 1110 1115 1120
Lys Tyr Val Asp Val Asn Asn Ile Gly Ile Arg Gly Tyr Met Tyr Leu
1125 1130 1135
Lys Gly Pro Arg Gly Ser Val Val Thr Thr Asn Ile Tyr Leu Asn Ser
1140 1145 1150
Thr Leu Tyr Glu Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly
1155 1160 1165
Asn Glu Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val
1170 1175 1180
Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala
1185 1190 1195 1200
Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn
1205 1210 1215
Leu Ser Gln Val Val Val Met Lys Ser Lys Asp Asp Gln Gly Ile Arg
1220 1225 1230
Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
1235 1240 1245
Phe Ile Gly Phe His Leu Tyr Asp Asn Ile Ala Lys Leu Val Ala Ser
1250 1255 1260

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Asn Trp Tyr Asn Arg Gln Val Gly Lys Ala Ser Arg Thr Phe Gly Cys
1265                1270                1275                1280
Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Ser Ser Leu
                1285                1290                1295


<210> 3
<211> 1292
<212> PRT
<213> Clostridium botulinum

<400> 3
Met Pro Phe Val Asn Lys Pro Phe Asn Tyr Arg Asp Pro Gly Asn Gly
 1               5                  10                  15
Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Ala Gly Gln Met Gln Pro
            20                  25                  30
Val Lys Ala Phe Lys Ile His Glu Gly Val Trp Val Ile Pro Glu Arg
        35                  40                  45
Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
    50                  55                  60
Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65                  70                  75                  80
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Ile Lys Leu Phe Asp
                85                  90                  95
Arg Ile Tyr Ser Thr Gly Leu Gly Arg Met Leu Leu Ser Phe Ile Val
            100                 105                 110
Lys Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
        115                 120                 125
Val Ile Asp Thr Asn Cys Ile Asn Val Ile Glu Pro Gly Gly Ser Tyr
    130                 135                 140
Arg Ser Glu Glu Leu Asn Leu Val Ile Thr Gly Pro Ser Ala Asp Ile
145                 150                 155                 160
Ile Gln Phe Glu Cys Lys Ser Phe Gly His Asp Val Phe Asn Leu Thr
                165                 170                 175
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
            180                 185                 190
Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
        195                 200                 205
Gly Ala Gly Thr Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
    210                 215                 220
Leu Ile His Ala Ala His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225                 230                 235                 240
Arg Val Leu Lys Val Lys Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
                245                 250                 255
Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly Asn Asp Thr Asn
            260                 265                 270
Phe Ile Asp Ser Leu Trp Gln Lys Lys Phe Ser Arg Asp Ala Tyr Asp
        275                 280                 285
Asn Leu Gln Asn Ile Ala Arg Ile Leu Asn Glu Ala Lys Thr Ile Val
    290                 295                 300
Gly Thr Thr Thr Pro Leu Gln Tyr Met Lys Asn Ile Phe Ile Arg Lys
305                 310                 315                 320
Tyr Phe Leu Ser Glu Asp Ala Ser Gly Lys Ile Ser Val Asn Lys Ala
                325                 330                 335
Ala Phe Lys Glu Phe Tyr Arg Val Leu Thr Arg Gly Phe Thr Glu Leu
            340                 345                 350
Glu Phe Val Asn Pro Phe Lys Val Ile Asn Arg Lys Thr Tyr Leu Asn
        355                 360                 365
Phe Asp Lys Ala Val Phe Arg Ile Asn Ile Val Pro Asp Glu Asn Tyr
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```
    370                 375                 380
Thr Ile Asn Glu Gly Phe Asn Leu Glu Gly Ala Asn Ser Asn Gly Gln
385                 390                 395                 400
Asn Thr Glu Ile Asn Ser Arg Asn Phe Thr Arg Leu Lys Asn Phe Thr
                405                 410                 415
Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg Gly Ile Ile Pro
            420                 425                 430
Phe Lys Thr Lys Ser Leu Asp Glu Gly Tyr Asn Lys Ala Leu Asn Tyr
        435                 440                 445
Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu
    450                 455                 460
Asp Asn Phe Thr Asn Asp Leu Asp Lys Val Glu Glu Ile Thr Ala Asp
465                 470                 475                 480
Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Ser Asp Leu Ile Gln
                485                 490                 495
Gln Tyr Tyr Leu Thr Phe Asp Phe Asp Asn Glu Pro Glu Asn Ile Ser
            500                 505                 510
Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu Glu Pro Met Pro
        515                 520                 525
Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu Leu Asp Lys Tyr
    530                 535                 540
Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu His Gly Asp Ser
545                 550                 555                 560
Arg Ile Ile Leu Thr Asn Ser Ala Glu Glu Ala Leu Leu Lys Pro Asn
                565                 570                 575
Val Ala Tyr Thr Phe Phe Ser Ser Lys Tyr Val Lys Lys Ile Asn Lys
            580                 585                 590
Ala Val Glu Ala Val Ile Phe Leu Ser Trp Ala Glu Glu Leu Val Tyr
        595                 600                 605
Asp Phe Thr Asp Glu Thr Asn Glu Val Thr Thr Met Asp Lys Ile Ala
    610                 615                 620
Asp Ile Thr Ile Ile Val Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly
625                 630                 635                 640
Asn Met Val Ser Lys Gly Glu Phe Val Glu Ala Ile Leu Phe Thr Gly
                645                 650                 655
Val Val Ala Leu Leu Glu Phe Ile Pro Glu Tyr Ser Leu Pro Val Phe
            660                 665                 670
Gly Thr Phe Ala Ile Val Ser Tyr Ile Ala Asn Lys Val Leu Thr Val
        675                 680                 685
Gln Thr Ile Asn Asn Ala Leu Ser Lys Arg Asn Glu Lys Trp Asp Glu
    690                 695                 700
Val Tyr Lys Tyr Thr Val Thr Asn Trp Leu Ala Lys Val Asn Thr Gln
705                 710                 715                 720
Ile Asp Leu Ile Arg Glu Lys Met Lys Lys Ala Leu Glu Asn Gln Ala
                725                 730                 735
Glu Ala Thr Arg Ala Ile Ile Asn Tyr Gln Tyr Asn Gln Tyr Thr Glu
            740                 745                 750
Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp Leu Ser Ser Lys
        755                 760                 765
Leu Asn Arg Ser Ile Asn Arg Ala Met Ile Asn Ile Asn Lys Phe Leu
    770                 775                 780
Asp Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile Pro Tyr Ala
785                 790                 795                 800
Val Lys Arg Leu Lys Asp Phe Asp Ala Ser Val Arg Asp Val Leu Leu
                805                 810                 815
Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Leu Gln Val Asp Arg
            820                 825                 830
Leu Lys Asp Glu Val Asn Asn Thr Leu Ser Ala Asp Ile Pro Phe Gln
        835                 840                 845
```

```
Leu Ser Lys Tyr Val Asn Asp Lys Lys Leu Leu Ser Thr Phe Thr Glu
    850                 855                 860
Tyr Ile Lys Asn Ile Val Asn Thr Ser Ile Leu Ser Ile Val Tyr Lys
865                 870                 875                 880
Lys Asp Asp Leu Ile Asp Leu Ser Arg Tyr Gly Ala Lys Ile Asn Ile
                885                 890                 895
Gly Asp Arg Val Tyr Tyr Asp Ser Ile Asp Lys Asn Gln Ile Lys Leu
            900                 905                 910
Ile Asn Leu Glu Ser Ser Thr Ile Glu Val Ile Leu Lys Asn Ala Ile
        915                 920                 925
Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Lys
    930                 935                 940
Ile Pro Lys Tyr Phe Ser Lys Ile Asn Leu Asn Asn Glu Tyr Thr Ile
945                 950                 955                 960
Ile Asn Cys Ile Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr
                965                 970                 975
Gly Glu Ile Ile Trp Thr Leu Gln Asp Asn Lys Gln Asn Ile Gln Arg
            980                 985                 990
Val Val Phe Lys Tyr Ser Gln Met Val Asn Ile Ser Asp Tyr Ile Asn
        995                 1000                1005
Arg Trp Met Phe Val Thr Ile Thr Asn Asn Arg Leu Thr Lys Ser Lys
    1010                1015                1020
Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu
1025                1030                1035                1040
Gly Asn Ile His Ala Ser Asn Lys Ile Met Phe Lys Leu Asp Gly Cys
                1045                1050                1055
Arg Asp Pro Arg Arg Tyr Ile Met Ile Lys Tyr Phe Asn Leu Phe Asp
            1060                1065                1070
Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp Ser Gln Ser
        1075                1080                1085
Asn Pro Gly Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Gln Tyr Asp
    1090                1095                1100
Lys Pro Tyr Tyr Met Leu Asn Leu Phe Asp Pro Asn Lys Tyr Val Asp
1105                1110                1115                1120
Val Asn Asn Ile Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg
                1125                1130                1135
Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Thr Leu Tyr Met
            1140                1145                1150
Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Glu Asp Asn
        1155                1160                1165
Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn
    1170                1175                1180
Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys
1185                1190                1195                1200
Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val
                1205                1210                1215
Val Val Met Lys Ser Lys Asp Asp Gln Gly Ile Arg Asn Lys Cys Lys
            1220                1225                1230
Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly Phe Val Gly Phe
        1235                1240                1245
His Leu Tyr Asp Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn
    1250                1255                1260
Arg Gln Val Gly Lys Ala Ser Arg Thr Phe Gly Cys Ser Trp Glu Phe
1265                1270                1275                1280
Ile Pro Val Asp Asp Gly Trp Gly Glu Ser Ser Leu
                1285                1290
```

<210> 4

<211> 1296
<212> PRT
<213> Clostridium botulinum

<400> 4

```
Met Pro Leu Val Asn Gln Gln Ile Asn Tyr Tyr Asp Pro Val Asn Gly
 1               5                  10                  15
Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Ala Gly Lys Met Gln Pro
            20                  25                  30
Val Lys Ala Phe Lys Ile His Asn Lys Val Trp Val Ile Pro Glu Arg
        35                  40                  45
Asp Ile Phe Thr Asn Pro Glu Glu Val Asp Leu Asn Pro Pro Pro Glu
    50                  55                  60
Ala Lys Gln Val Pro Ile Ser Tyr Tyr Asp Ser Ala Tyr Leu Ser Thr
65                  70                  75                  80
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Ile Lys Leu Phe Glu
                85                  90                  95
Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Ile Ser Ile Val
            100                 105                 110
Arg Gly Ile Pro Phe Trp Gly Gly Gly Lys Ile Asp Thr Glu Leu Lys
        115                 120                 125
Val Ile Asp Thr Asn Cys Ile Asn Ile Ile Gln Leu Asp Asp Ser Tyr
    130                 135                 140
Arg Ser Glu Glu Leu Asn Leu Ala Ile Ile Gly Pro Ser Ala Asn Ile
145                 150                 155                 160
Ile Glu Ser Gln Cys Ser Ser Phe Arg Asp Asp Val Leu Asn Leu Thr
                165                 170                 175
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
            180                 185                 190
Thr Val Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
        195                 200                 205
Gly Ala Gly Lys Phe Ala Gln Asp Pro Ala Val Ala Leu Ala His Glu
    210                 215                 220
Leu Ile His Ala Glu His Arg Leu Tyr Gly Ile Ala Ile Asn Thr Asn
225                 230                 235                 240
Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ala Gly Leu
                245                 250                 255
Glu Val Ser Leu Glu Glu Leu Ile Thr Phe Gly Gly Asn Asp Ala Lys
            260                 265                 270
Phe Ile Asp Ser Leu Gln Lys Lys Glu Phe Ser Leu Tyr Tyr Tyr Asn
        275                 280                 285
Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
    290                 295                 300
Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305                 310                 315                 320
Tyr Leu Leu Ser Glu Asp Ala Thr Gly Lys Phe Leu Val Asp Arg Leu
                325                 330                 335
Lys Phe Asp Glu Leu Tyr Lys Leu Leu Thr Glu Ile Tyr Thr Glu Asp
            340                 345                 350
Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn
        355                 360                 365
Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Asp Val Asn Tyr
    370                 375                 380
Thr Ile His Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
385                 390                 395                 400
Phe Asn Gly Gln Asn Ile Glu Ile Asn Asn Lys Asn Phe Asp Lys Leu
                405                 410                 415
Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
            420                 425                 430
```

```
Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Asp Glu Gly Tyr Asn Lys
        435                 440                 445
Ala Leu Asn Glu Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
    450                 455                 460
Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asp Lys Val Glu Glu
465                 470                 475                 480
Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
                485                 490                 495
Asp Leu Ile Gln Gln Tyr Tyr Leu Asn Phe Asn Phe Asp Asn Glu Pro
            500                 505                 510
Glu Asn Thr Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
        515                 520                 525
Glu Pro Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
    530                 535                 540
Leu Asn Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Lys
545                 550                 555                 560
His Ser Asn Ser Arg Ile Ile Leu Thr Asn Ser Ala Lys Glu Ala Leu
                565                 570                 575
Leu Lys Pro Asn Ile Val Tyr Thr Phe Phe Ser Ser Lys Tyr Ile Lys
            580                 585                 590
Ala Ile Asn Lys Ala Val Glu Ala Val Thr Phe Val Asn Trp Ile Glu
        595                 600                 605
Asn Leu Val Tyr Asp Phe Thr Asp Glu Thr Asn Glu Val Ser Thr Met
    610                 615                 620
Asp Lys Ile Ala Asp Ile Thr Ile Val Ile Pro Tyr Ile Gly Pro Ala
625                 630                 635                 640
Leu Asn Ile Gly Asn Met Ile Tyr Lys Gly Glu Phe Val Glu Ala Ile
                645                 650                 655
Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Ile Val Pro Glu Ile Ala
            660                 665                 670
Leu Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Val Ser Asn Lys
        675                 680                 685
Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu
    690                 695                 700
Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Ile
705                 710                 715                 720
Val Asn Thr Gln Ile Asn Leu Ile Arg Glu Lys Met Lys Lys Ala Leu
                725                 730                 735
Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn
            740                 745                 750
Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp
        755                 760                 765
Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Ser Ala Met Ile Asn Ile
    770                 775                 780
Asn Lys Phe Leu Asp Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met
785                 790                 795                 800
Ile Pro Tyr Ala Val Lys Arg Leu Lys Asp Phe Asp Ala Ser Val Arg
                805                 810                 815
Asp Val Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly
            820                 825                 830
Gln Val Asn Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Ala Asp
        835                 840                 845
Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Lys Lys Leu Leu Ser
    850                 855                 860
Thr Phe Thr Glu Tyr Ile Lys Asn Ile Thr Asn Ala Ser Ile Leu Ser
865                 870                 875                 880
Ile Val Tyr Lys Asp Asp Asp Leu Ile Asp Leu Ser Arg Tyr Gly Ala
                885                 890                 895
Glu Ile Tyr Asn Gly Asp Lys Val Tyr Tyr Asn Ser Ile Asp Lys Asn
```

```
            900                 905                 910
Gln Ile Arg Leu Ile Asn Leu Glu Ser Ser Thr Ile Glu Val Ile Leu
        915                 920                 925
Lys Lys Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser
    930                 935                 940
Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn
945                 950                 955                 960
Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val
                965                 970                 975
Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Phe Gln Asp Thr Gln Glu
            980                 985                 990
Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser
        995                 1000                1005
Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Ile
    1010                1015                1020
Thr Lys Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro
1025                1030                1035                1040
Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Lys Ile Met Phe Lys
                1045                1050                1055
Leu Asp Gly Cys Arg Asp Pro His Arg Tyr Ile Val Ile Lys Tyr Phe
            1060                1065                1070
Asn Leu Phe Asp Lys Glu Leu Ser Glu Lys Glu Ile Lys Asp Leu Tyr
        1075                1080                1085
Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr
    1090                1095                1100
Leu Gln Tyr Asp Lys Ser Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn
1105                1110                1115                1120
Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu
                1125                1130                1135
Lys Gly Pro Arg Asp Asn Val Met Thr Thr Asn Ile Tyr Leu Asn Ser
            1140                1145                1150
Ser Leu Tyr Met Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly
        1155                1160                1165
Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val
    1170                1175                1180
Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala
1185                1190                1195                1200
Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn
                1205                1210                1215
Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr
            1220                1225                1230
Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
        1235                1240                1245
Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser
    1250                1255                1260
Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys
1265                1270                1275                1280
Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Arg Glu Arg Pro Leu
                1285                1290                1295


<210> 5
<211> 206
<212> PRT
<213> Homo sapiens

<400> 5
Met Ala Glu Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg
 1               5                  10                  15
```

```
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
        35                  40                  45
Met Leu Asp Glu Gln Gly Glu Gln Leu Asp Arg Val Glu Glu Gly Met
    50                  55                  60
Asn His Ile Asn Gln Asp Met Lys Glu Ala Glu Lys Asn Leu Lys Asp
65                  70                  75                  80
Leu Gly Lys Cys Cys Gly Leu Phe Ile Cys Pro Cys Asn Lys Leu Lys
                85                  90                  95
Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
            100                 105                 110
Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
        115                 120                 125
Ile Ser Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn
    130                 135                 140
Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu
145                 150                 155                 160
Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
                165                 170                 175
Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile
            180                 185                 190
Asp Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
        195                 200                 205
```

<210> 6
<211> 206
<212> PRT
<213> Homo sapiens

<400> 6

```
Met Ala Glu Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg
 1               5                  10                  15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
        35                  40                  45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
    50                  55                  60
Asp Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp
65                  70                  75                  80
Leu Gly Lys Phe Cys Gly Leu Cys Val Cys Pro Cys Asn Lys Leu Lys
                85                  90                  95
Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
            100                 105                 110
Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
        115                 120                 125
Ile Ser Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn
    130                 135                 140
Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu
145                 150                 155                 160
Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
                165                 170                 175
Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile
            180                 185                 190
Asp Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
        195                 200                 205
```

<210> 7
<211> 206
<212> PRT
<213> Macaca mulatta

<400> 7
Met Ala Glu Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg
1 5 10 15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
20 25 30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
35 40 45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
50 55 60
Asp Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp
65 70 75 80
Leu Gly Lys Phe Cys Gly Leu Cys Val Cys Pro Cys Asn Lys Leu Lys
85 90 95
Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
100 105 110
Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
115 120 125
Ile Ser Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn
130 135 140
Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu
145 150 155 160
Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
165 170 175
Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile
180 185 190
Asp Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
195 200 205

<210> 8
<211> 206
<212> PRT
<213> Rattus norvegicus

<400> 8
Met Ala Glu Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg
1 5 10 15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
20 25 30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
35 40 45
Met Leu Asp Glu Gln Gly Glu Gln Leu Asp Arg Val Glu Glu Gly Met
50 55 60
Asn His Ile Asn Gln Asp Met Lys Glu Ala Glu Lys Asn Leu Lys Asp
65 70 75 80
Leu Gly Lys Cys Cys Gly Leu Phe Ile Cys Pro Cys Asn Lys Leu Lys
85 90 95
Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
100 105 110
Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
115 120 125
Ile Ser Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn
130 135 140

```
Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu
145                 150                 155                 160
Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
                165                 170                 175
Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile
            180                 185                 190
Asp Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
        195                 200                 205


<210> 9
<211> 206
<212> PRT
<213> Rattus norvegicus

<400> 9
Met Ala Glu Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg
 1               5                  10                  15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
        35                  40                  45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
    50                  55                  60
Asp Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp
65                  70                  75                  80
Leu Gly Lys Phe Cys Gly Leu Cys Val Cys Pro Cys Asn Lys Leu Lys
                85                  90                  95
Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
            100                 105                 110
Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
        115                 120                 125
Ile Ser Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn
    130                 135                 140
Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu
145                 150                 155                 160
Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
                165                 170                 175
Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile
            180                 185                 190
Asp Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
        195                 200                 205


<210> 10
<211> 206
<212> PRT
<213> Mus musculus

<400> 10
Met Ala Glu Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg
 1               5                  10                  15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
        35                  40                  45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
    50                  55                  60
Asp Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp
```

65 70 75 80
Leu Gly Lys Phe Cys Gly Leu Cys Val Cys Pro Cys Asn Lys Leu Lys
85 90 95
Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
100 105 110
Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
115 120 125
Ile Ser Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn
130 135 140
Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu
145 150 155 160
Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
165 170 175
Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile
180 185 190
Asp Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
195 200 205

<210> 11
<211> 206
<212> PRT
<213> Gallus gallus

<400> 11
Met Ala Glu Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg
1 5 10 15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
20 25 30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
35 40 45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
50 55 60
Asp Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp
65 70 75 80
Leu Gly Lys Phe Cys Gly Leu Cys Val Cys Pro Cys Asn Lys Leu Lys
85 90 95
Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
100 105 110
Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
115 120 125
Ile Ser Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn
130 135 140
Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu
145 150 155 160
Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
165 170 175
Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile
180 185 190
Asp Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
195 200 205

<210> 12
<211> 204
<212> PRT
<213> Carassius auratus

<400> 12

```
Met Ala Glu Asp Ala Asp Met Arg Asn Glu Leu Ser Asp Met Gln Gln
 1               5                  10                  15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
        35                  40                  45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
    50                  55                  60
Asp Gln Ile Asn Lys Asp Met Lys Asp Ala Glu Lys Asn Leu Asn Asp
65                  70                  75                  80
Leu Gly Lys Phe Cys Gly Leu Cys Ser Cys Pro Cys Asn Lys Met Lys
                85                  90                  95
Ser Gly Gly Ser Lys Ala Trp Gly Asn Asn Gln Asp Gly Val Val Ala
            100                 105                 110
Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala Ile Ser
        115                 120                 125
Gly Gly Phe Ile Arg Arg Val Thr Asp Asp Ala Arg Glu Asn Glu Met
    130                 135                 140
Asp Glu Asn Leu Glu Gln Val Gly Gly Ile Ile Gly Asn Leu Arg His
145                 150                 155                 160
Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg Gln Ile
                165                 170                 175
Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile Asp Glu
            180                 185                 190
Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
        195                 200
```

<210> 13
<211> 203
<212> PRT
<213> Carassius auratus

<400> 13

```
Met Ala Asp Glu Ala Asp Met Arg Asn Glu Leu Thr Asp Met Gln Ala
 1               5                  10                  15
Arg Ala Asp Gln Leu Gly Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
        35                  40                  45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
    50                  55                  60
Asp Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp
65                  70                  75                  80
Leu Gly Asn Leu Cys Gly Leu Cys Pro Cys Pro Cys Asn Lys Leu Lys
                85                  90                  95
Gly Gly Gly Gln Ser Trp Gly Asn Asn Gln Asp Gly Val Val Ser Ser
            100                 105                 110
Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala Ile Ser Gly
        115                 120                 125
Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn Glu Met Asp
    130                 135                 140
Glu Asn Leu Glu Gln Val Gly Ser Ile Ile Gly Asn Leu Arg His Met
145                 150                 155                 160
Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg Gln Ile Asp
                165                 170                 175
Arg Ile Met Asp Met Ala Asp Ser Asn Lys Thr Arg Ile Asp Glu Ala
            180                 185                 190
Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
```

195 200

<210> 14
<211> 204
<212> PRT
<213> Danio rerio

<400> 14
Met Ala Glu Asp Ser Asp Met Arg Asn Glu Leu Ala Asp Met Gln Gln
1 5 10 15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
20 25 30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
35 40 45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
50 55 60
Asp Gln Ile Asn Lys Asp Met Lys Asp Ala Glu Lys Asn Leu Asn Asp
65 70 75 80
Leu Gly Lys Phe Cys Gly Leu Cys Ser Cys Pro Cys Asn Lys Met Lys
85 90 95
Ser Gly Ala Ser Lys Ala Trp Gly Asn Asn Gln Asp Gly Val Val Ala
100 105 110
Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala Ile Ser
115 120 125
Gly Gly Phe Ile Arg Arg Val Thr Asp Asp Ala Arg Glu Asn Glu Met
130 135 140
Asp Glu Asn Leu Glu Gln Val Gly Gly Ile Ile Gly Asn Leu Arg His
145 150 155 160
Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg Gln Ile
165 170 175
Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile Asp Glu
180 185 190
Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
195 200

<210> 15
<211> 203
<212> PRT
<213> Danio rerio

<400> 15
Met Ala Asp Glu Ser Asp Met Arg Asn Glu Leu Asn Asp Met Gln Ala
1 5 10 15
Arg Ala Asp Gln Leu Gly Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
20 25 30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
35 40 45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
50 55 60
Asp Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp
65 70 75 80
Leu Gly Asn Leu Cys Gly Leu Cys Pro Cys Pro Cys Asn Lys Leu Lys
85 90 95
Gly Gly Gly Gln Ser Trp Gly Asn Asn Gln Asp Gly Val Val Ser Ser
100 105 110
Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala Ile Ser Gly
115 120 125

```
Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn Glu Met Asp
    130                 135                 140
Glu Asn Leu Glu Gln Val Gly Ser Ile Ile Gly Asn Leu Arg His Met
145                 150                 155                 160
Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg Gln Ile Asp
                165                 170                 175
Arg Ile Met Asp Met Ala Asp Ser Asn Lys Thr Arg Ile Asp Glu Ala
            180                 185                 190
Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
        195                 200
```

<210> 16
<211> 210
<212> PRT
<213> Torpedo marmorata

<400> 16

```
Met Glu Asn Ser Val Glu Asn Ser Met Asp Pro Arg Ser Glu Gln Glu
 1               5                  10                  15
Glu Met Gln Arg Cys Ala Asp Gln Ile Thr Asp Glu Ser Leu Glu Ser
            20                  25                  30
Thr Arg Arg Met Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile
        35                  40                  45
Arg Thr Leu Val Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile
    50                  55                  60
Glu Glu Gly Met Asp Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys
65                  70                  75                  80
Asn Leu Ser Asp Leu Gly Lys Cys Cys Gly Leu Cys Ser Cys Pro Cys
                85                  90                  95
Asn Lys Leu Lys Asn Phe Glu Ala Gly Gly Ala Tyr Lys Lys Val Trp
            100                 105                 110
Gly Asn Asn Gln Asp Gly Val Val Ala Ser Gln Pro Ala Arg Val Met
        115                 120                 125
Asp Asp Arg Glu Gln Met Ala Met Ser Gly Gly Tyr Ile Arg Arg Ile
    130                 135                 140
Thr Asp Asp Ala Arg Glu Asn Glu Met Glu Glu Asn Leu Asp Gln Val
145                 150                 155                 160
Gly Ser Ile Ile Gly Asn Leu Arg His Met Ala Leu Asp Met Ser Asn
                165                 170                 175
Glu Ile Gly Ser Gln Asn Ala Gln Ile Asp Arg Ile Val Val Lys Gly
            180                 185                 190
Asp Met Asn Lys Ala Arg Ile Asp Glu Ala Asn Lys His Ala Thr Lys
        195                 200                 205
Met Leu
    210
```

<210> 17
<211> 206
<212> PRT
<213> Xenopus laevis

<400> 17

```
Met Ala Asp Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg
 1               5                  10                  15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30
Leu Gln Tyr Val Glu Gly Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
```

```
        35                  40                  45
Met Leu Asp Glu Gln Gly Glu Gln Leu Asp Arg Val Glu Glu Gly Met
    50                  55                  60
Asn His Ile Asn Gln Asp Met Lys Glu Ala Glu Lys Asn Leu Lys Asp
65                  70                  75                  80
Leu Gly Lys Cys Cys Gly Leu Phe Ile Cys Pro Cys Asn Lys Leu Lys
                85                  90                  95
Ser Ser Gly Ala Tyr Asn Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
            100                 105                 110
Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
        115                 120                 125
Ile Ser Gly Gly Phe Val Arg Arg Val Thr Asn Asp Ala Arg Glu Thr
    130                 135                 140
Glu Met Asp Glu Asn Leu Glu Gln Val Gly Gly Ile Ile Gly Asn Leu
145                 150                 155                 160
Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
                165                 170                 175
Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Ala Arg Ile
            180                 185                 190
Asp Glu Ala Asn Lys His Ala Thr Lys Met Leu Gly Ser Gly
        195                 200                 205


<210> 18
<211> 206
<212> PRT
<213> Xenopus laevis

<400> 18
Met Ala Asp Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg
 1               5                  10                  15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30
Leu Gln Tyr Val Glu Gly Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
        35                  40                  45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
    50                  55                  60
Glu Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp
65                  70                  75                  80
Leu Gly Lys Phe Cys Gly Leu Cys Val Cys Pro Cys Asn Lys Leu Lys
                85                  90                  95
Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
            100                 105                 110
Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
        115                 120                 125
Ile Ser Gly Gly Phe Val Arg Arg Val Thr Asn Asp Ala Arg Glu Thr
    130                 135                 140
Glu Met Asp Glu Asn Leu Glu Gln Val Gly Gly Ile Ile Gly Asn Leu
145                 150                 155                 160
Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
                165                 170                 175
Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Ala Arg Ile
            180                 185                 190
Asp Glu Ala Asn Lys His Ala Thr Lys Met Leu Gly Ser Gly
        195                 200                 205


<210> 19
<211> 212
```

<212> PRT
<213> Strongylocentrotus purpuratus

<400> 19
Met Glu Asp Gln Asn Asp Met Asn Met Arg Ser Glu Leu Glu Glu Ile
1 5 10 15
Gln Met Gln Ser Asn Met Gln Thr Asp Glu Ser Leu Glu Ser Thr Arg
20 25 30
Arg Met Leu Gln Met Ala Glu Glu Ser Gln Asp Met Gly Ile Lys Thr
35 40 45
Leu Val Met Leu Asp Glu Gln Gly Glu Gln Leu Asp Arg Ile Glu Glu
50 55 60
Gly Met Asp Gln Ile Asn Thr Asp Met Arg Glu Ala Glu Lys Asn Leu
65 70 75 80
Thr Gly Leu Glu Lys Cys Cys Gly Ile Cys Val Cys Pro Trp Lys Lys
85 90 95
Leu Gly Asn Phe Glu Lys Gly Asp Asp Tyr Lys Lys Thr Trp Lys Gly
100 105 110
Asn Asp Asp Gly Lys Val Asn Ser His Gln Pro Met Arg Met Glu Asp
115 120 125
Asp Arg Asp Gly Cys Gly Gly Asn Ala Ser Met Ile Thr Arg Ile Thr
130 135 140
Asn Asp Ala Arg Glu Asp Glu Met Asp Glu Asn Leu Thr Gln Val Ser
145 150 155 160
Ser Ile Val Gly Asn Leu Arg His Met Ala Ile Asp Met Gln Ser Glu
165 170 175
Ile Gly Ala Gln Asn Ser Gln Val Gly Arg Ile Thr Ser Lys Ala Glu
180 185 190
Ser Asn Glu Gly Arg Ile Asn Ser Ala Asp Lys Arg Ala Lys Asn Ile
195 200 205
Leu Arg Asn Lys
210

<210> 20
<211> 212
<212> PRT
<213> Drosophila melanogaster

<400> 20
Met Pro Ala Asp Pro Ser Glu Glu Val Ala Pro Gln Val Pro Lys Thr
1 5 10 15
Glu Leu Glu Glu Leu Gln Ile Asn Ala Gln Gly Val Ala Asp Glu Ser
20 25 30
Leu Glu Ser Thr Arg Arg Met Leu Ala Leu Cys Glu Glu Ser Lys Glu
35 40 45
Ala Gly Ile Arg Thr Leu Val Ala Leu Asp Asp Gln Gly Glu Gln Leu
50 55 60
Asp Arg Ile Glu Glu Gly Met Asp Gln Ile Asn Ala Asp Met Arg Glu
65 70 75 80
Ala Glu Lys Asn Leu Ser Gly Met Glu Lys Cys Cys Gly Ile Cys Val
85 90 95
Leu Pro Cys Asn Lys Ser Gln Ser Phe Lys Glu Asp Asp Gly Thr Trp
100 105 110
Lys Gly Asn Asp Asp Gly Lys Val Val Asn Asn Gln Pro Gln Arg Val
115 120 125
Met Asp Asp Arg Asn Gly Met Met Ala Gln Ala Gly Tyr Ile Gly Arg
130 135 140
Ile Thr Asn Asp Ala Arg Glu Asp Glu Met Glu Glu Asn Met Gly Gln

145 150 155 160
Val Asn Thr Met Ile Gly Asn Leu Arg Asn Met Ala Leu Asp Met Gly
165 170 175
Ser Glu Leu Glu Asn Gln Asn Arg Gln Ile Asp Arg Ile Asn Arg Lys
180 185 190
Gly Glu Ser Asn Glu Ala Arg Ile Ala Val Ala Asn Gln Arg Ala His
195 200 205
Gln Leu Leu Lys
210

<210> 21
<211> 212
<212> PRT
<213> Hirudo medicinalis

<400> 21
Met Ala Lys Asp Ile Lys Pro Lys Pro Ala Asn Gly Arg Asp Ser Pro
1 5 10 15
Thr Asp Leu Gln Glu Ile Gln Leu Gln Met Asn Ala Ile Thr Asp Asp
20 25 30
Ser Leu Glu Ser Thr Arg Arg Met Leu Ala Met Cys Glu Glu Ser Lys
35 40 45
Asp Ala Gly Ile Arg Thr Leu Val Met Leu Asp Glu Gln Gly Glu Gln
50 55 60
Leu Asp Arg Ile Glu Glu Gly Met Asp Gln Ile Asn Gln Asp Met Arg
65 70 75 80
Asp Ala Glu Lys Asn Leu Glu Gly Met Glu Lys Cys Cys Gly Leu Cys
85 90 95
Ile Leu Pro Trp Lys Arg Thr Lys Asn Phe Asp Lys Gly Ala Glu Trp
100 105 110
Asn Lys Gly Asp Glu Gly Lys Val Asn Thr Asp Gly Pro Arg Leu Val
115 120 125
Val Gly Asp Gly Asn Met Gly Pro Ser Gly Gly Phe Ile Thr Lys Ile
130 135 140
Thr Asn Asp Ala Arg Glu Glu Glu Met Glu Gln Asn Met Gly Glu Val
145 150 155 160
Ser Asn Met Ile Ser Asn Leu Arg Asn Met Ala Val Asp Met Gly Ser
165 170 175
Glu Ile Asp Ser Gln Asn Arg Gln Val Asp Arg Ile Asn Asn Lys Met
180 185 190
Thr Ser Asn Gln Leu Arg Ile Ser Asp Ala Asn Lys Arg Ala Ser Lys
195 200 205
Leu Leu Lys Glu
210

<210> 22
<211> 212
<212> PRT
<213> Loligo pealei

<400> 22
Met Ser Ala Asn Gly Glu Val Glu Val Pro Lys Thr Glu Leu Glu Glu
1 5 10 15
Ile Gln Gln Gln Cys Asn Gln Val Thr Asp Asp Ser Leu Glu Ser Thr
20 25 30
Arg Arg Met Leu Asn Met Cys Glu Glu Ser Lys Glu Ala Gly Ile Arg
35 40 45

```
Thr Leu Val Met Leu Asp Glu Gln Gly Glu Gln Leu Asp Arg Ile Glu
    50                  55                  60
Glu Gly Leu Asp Gln Ile Asn Gln Asp Met Lys Asp Ala Glu Lys Asn
65                  70                  75                  80
Leu Glu Gly Met Glu Lys Cys Cys Gly Leu Cys Val Leu Pro Trp Lys
                85                  90                  95
Arg Gly Lys Ser Phe Glu Lys Ser Gly Asp Tyr Ala Asn Thr Trp Lys
            100                 105                 110
Lys Asp Asp Asp Gly Pro Thr Asn Thr Asn Gly Pro Arg Val Thr Val
        115                 120                 125
Gly Asp Gln Asn Gly Met Gly Pro Ser Ser Gly Tyr Val Thr Arg Ile
    130                 135                 140
Thr Asn Asp Ala Arg Glu Asp Asp Met Glu Asn Asn Met Lys Glu Val
145                 150                 155                 160
Ser Ser Met Ile Gly Asn Leu Arg Asn Met Ala Ile Asp Met Gly Asn
                165                 170                 175
Glu Ile Gly Ser Gln Asn Arg Gln Val Asp Arg Ile Gln Gln Lys Ala
            180                 185                 190
Glu Ser Asn Glu Ser Arg Ile Asp Glu Ala Asn Lys Lys Ala Thr Lys
        195                 200                 205
Leu Leu Lys Asn
    210
```

<210> 23
<211> 220
<212> PRT
<213> Lymnaea stagnalis

<400> 23

```
Met Thr Thr Asn Gly Glu Ile Leu Pro Val Gly Glu Glu Glu Glu Glu
 1               5                  10                  15
Glu Leu Gly Glu Asp Ala Leu Leu Arg Lys Gln Ile Asp Cys Asn Thr
            20                  25                  30
Asn Glu Ser Leu Glu Ser Thr Arg Arg Met Leu Ser Leu Cys Glu Glu
        35                  40                  45
Ser Lys Glu Ala Gly Ile Lys Thr Leu Val Met Leu Asp Glu Gln Gly
    50                  55                  60
Glu Gln Leu Asp Arg Ile Glu Glu Gly Met Gly Gln Ile Asn Gln Asp
65                  70                  75                  80
Met Arg Asp Ala Glu Lys Asn Leu Glu Gly Leu Glu Lys Cys Cys Gly
                85                  90                  95
Leu Cys Val Leu Pro Trp Lys Arg Ser Lys Asn Phe Glu Lys Gly Ser
            100                 105                 110
Asp Tyr Asn Lys Thr Trp Lys Ala Ser Glu Asp Gly Lys Ile Asn Thr
        115                 120                 125
Asn Gly Pro Arg Leu Val Val Asp Gln Gly Asn Gly Ser Gly Pro Thr
    130                 135                 140
Gly Gly Tyr Ile Thr Arg Ile Thr Asn Asp Ala Arg Glu Asp Glu Met
145                 150                 155                 160
Glu Gln Asn Ile Gly Glu Val Ala Gly Met Val Ser Asn Leu Arg Asn
                165                 170                 175
Met Ala Val Asp Met Gly Asn Glu Ile Glu Ser Gln Asn Lys Gln Leu
            180                 185                 190
Asp Arg Ile Asn Gln Lys Gly Gly Ser Leu Asn Val Arg Val Asp Glu
        195                 200                 205
Ala Asn Lys Arg Ala Asn Arg Ile Leu Arg Lys Gln
    210                 215                 220
```

<210> 24
<211> 207
<212> PRT
<213> Caenorhabditis elegans

<400> 24
Met Ser Gly Asp Asp Asp Ile Pro Glu Gly Leu Glu Ala Ile Asn Leu
 1   5   10   15
Lys Met Asn Ala Thr Thr Asp Asp Ser Leu Glu Ser Thr Arg Arg Met
            20   25   30
Leu Ala Leu Cys Glu Glu Ser Lys Glu Ala Gly Ile Lys Thr Leu Val
        35   40   45
Met Leu Asp Asp Gln Gly Glu Gln Leu Glu Arg Cys Glu Gly Ala Leu
    50   55   60
Asp Thr Ile Asn Gln Asp Met Lys Glu Ala Glu Asp His Leu Lys Gly
65   70   75   80
Met Glu Lys Cys Cys Gly Leu Cys Val Leu Pro Trp Asn Lys Thr Asp
                85   90   95
Asp Phe Glu Lys Thr Glu Phe Ala Lys Ala Trp Lys Lys Asp Asp Asp
            100   105   110
Gly Gly Val Ile Ser Asp Gln Pro Arg Ile Thr Val Gly Asp Ser Ser
        115   120   125
Met Gly Pro Gln Gly Gly Tyr Ile Thr Lys Ile Thr Asn Asp Ala Arg
    130   135   140
Glu Asp Glu Met Asp Glu Asn Val Gln Gln Val Ser Thr Met Val Gly
145   150   155   160
Asn Leu Arg Asn Met Ala Ile Asp Met Ser Thr Glu Val Ser Asn Gln
                165   170   175
Asn Arg Gln Leu Asp Arg Ile His Asp Lys Ala Gln Ser Asn Glu Val
            180   185   190
Arg Val Glu Ser Ala Asn Lys Arg Ala Lys Asn Leu Ile Thr Lys
        195   200   205

<210> 25
<211> 808
<212> PRT
<213> Homo sapiens

<400> 25
Met Gly Ala Pro Ala Cys Ala Leu Ala Leu Cys Val Ala Val Ala Ile
 1   5   10   15
Val Ala Gly Ala Ser Ser Glu Ser Leu Gly Thr Glu Gln Arg Val Val
            20   25   30
Gly Arg Ala Ala Glu Val Pro Gly Pro Glu Pro Gly Gln Gln Glu Gln
        35   40   45
Leu Val Phe Gly Ser Gly Asp Ala Val Glu Leu Ser Cys Pro Pro Pro
    50   55   60
Gly Gly Gly Pro Met Gly Pro Thr Val Trp Val Lys Asp Gly Thr Gly
65   70   75   80
Leu Val Pro Ser Glu Arg Val Leu Val Gly Pro Gln Arg Leu Gln Val
                85   90   95
Leu Asn Ala Ser His Glu Asp Ser Gly Ala Tyr Ser Cys Arg Gln Arg
            100   105   110
Leu Thr Gln Arg Val Leu Cys His Phe Ser Val Arg Val Thr Asp Ala
        115   120   125
Pro Ser Ser Gly Asp Asp Glu Asp Gly Glu Asp Glu Ala Glu Asp Thr
    130   135   140

```
Gly Val Asp Thr Gly Ala Pro Tyr Trp Thr Arg Pro Glu Arg Met Asp
145                 150                 155                 160
Lys Lys Leu Leu Ala Val Pro Ala Ala Asn Thr Val Arg Phe Arg Cys
                165                 170                 175
Pro Ala Ala Gly Asn Pro Thr Pro Ser Ile Ser Trp Leu Lys Asn Gly
            180                 185                 190
Arg Glu Phe Arg Gly Glu His Arg Ile Gly Gly Ile Lys Leu Arg His
        195                 200                 205
Gln Gln Trp Ser Leu Val Met Glu Ser Val Val Pro Ser Asp Arg Gly
    210                 215                 220
Asn Tyr Thr Cys Val Val Glu Asn Lys Phe Gly Ser Ile Arg Gln Thr
225                 230                 235                 240
Tyr Thr Leu Asp Val Leu Glu Arg Ser Pro His Arg Pro Ile Leu Gln
                245                 250                 255
Ala Gly Leu Pro Ala Asn Gln Thr Ala Val Leu Gly Ser Asp Val Glu
            260                 265                 270
Phe His Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Leu
        275                 280                 285
Lys His Val Glu Val Asn Gly Ser Lys Val Gly Pro Asp Gly Thr Pro
    290                 295                 300
Tyr Val Thr Val Leu Lys Ser Trp Ile Ser Glu Ser Val Glu Ala Asp
305                 310                 315                 320
Val Arg Leu Arg Leu Ala Asn Val Ser Glu Arg Asp Gly Gly Glu Tyr
                325                 330                 335
Leu Cys Arg Ala Thr Asn Phe Ile Gly Val Ala Glu Lys Ala Phe Trp
            340                 345                 350
Leu Ser Val His Gly Pro Arg Ala Ala Glu Glu Glu Leu Val Glu Ala
        355                 360                 365
Asp Glu Ala Gly Ser Val Tyr Ala Gly Ile Leu Ser Tyr Gly Val Gly
    370                 375                 380
Phe Phe Leu Phe Ile Leu Val Val Ala Ala Val Thr Leu Cys Arg Leu
385                 390                 395                 400
Arg Ser Pro Pro Lys Lys Gly Leu Gly Ser Pro Thr Val His Lys Ile
                405                 410                 415
Ser Arg Phe Pro Leu Lys Arg Gln Val Ser Leu Glu Ser Asn Ala Ser
            420                 425                 430
Met Ser Ser Asn Thr Pro Leu Val Arg Ile Ala Arg Leu Ser Ser Gly
        435                 440                 445
Glu Gly Pro Thr Leu Ala Asn Val Ser Glu Leu Glu Leu Pro Ala Asp
    450                 455                 460
Pro Lys Trp Glu Leu Ser Arg Ala Arg Leu Thr Leu Gly Lys Pro Leu
465                 470                 475                 480
Gly Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Ile Gly Ile
                485                 490                 495
Asp Lys Asp Arg Ala Ala Lys Pro Val Thr Val Ala Val Lys Met Leu
            500                 505                 510
Lys Asp Asp Ala Thr Asp Lys Asp Leu Ser Asp Leu Val Ser Glu Met
        515                 520                 525
Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu
    530                 535                 540
Gly Ala Cys Thr Gln Gly Gly Pro Leu Tyr Val Leu Val Glu Tyr Ala
545                 550                 555                 560
Ala Lys Gly Asn Leu Arg Glu Phe Leu Arg Ala Arg Arg Pro Pro Gly
                565                 570                 575
Leu Asp Tyr Ser Phe Asp Thr Cys Lys Pro Pro Glu Glu Gln Leu Thr
            580                 585                 590
Phe Lys Asp Leu Val Ser Cys Ala Tyr Gln Val Ala Arg Gly Met Glu
        595                 600                 605
Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn
```

610 615 620
Val Leu Val Thr Glu Asp Asn Val Met Lys Ile Ala Asp Phe Gly Leu
625 630 635 640
Ala Arg Asp Val His Asn Leu Asp Tyr Tyr Lys Lys Thr Thr Asn Gly
645 650 655
Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val
660 665 670
Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu
675 680 685
Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val Glu Glu
690 695 700
Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn
705 710 715 720
Cys Thr His Asp Leu Tyr Met Ile Met Arg Glu Cys Trp His Ala Ala
725 730 735
Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg
740 745 750
Val Leu Thr Val Thr Ser Thr Asp Glu Tyr Leu Asp Leu Ser Ala Pro
755 760 765
Phe Glu Gln Tyr Ser Pro Gly Gly Gln Asp Thr Pro Ser Ser Ser Ser
770 775 780
Ser Gly Asp Asp Ser Val Phe Ala His Asp Leu Leu Pro Pro Ala Pro
785 790 795 800
Pro Ser Ser Gly Gly Ser Arg Thr
805

<210> 26
<211> 806
<212> PRT
<213> Homo sapiens

<400> 26
Met Gly Ala Pro Ala Cys Ala Leu Ala Leu Cys Val Ala Val Ala Ile
1 5 10 15
Val Ala Gly Ala Ser Ser Glu Ser Leu Gly Thr Glu Gln Arg Val Val
20 25 30
Gly Arg Ala Ala Glu Val Pro Gly Pro Glu Pro Gly Gln Gln Glu Gln
35 40 45
Leu Val Phe Gly Ser Gly Asp Ala Val Glu Leu Ser Cys Pro Pro Pro
50 55 60
Gly Gly Gly Pro Met Gly Pro Thr Val Trp Val Lys Asp Gly Thr Gly
65 70 75 80
Leu Val Pro Ser Glu Arg Val Leu Val Gly Pro Gln Arg Leu Gln Val
85 90 95
Leu Asn Ala Ser His Glu Asp Ser Gly Ala Tyr Ser Cys Arg Gln Arg
100 105 110
Leu Thr Gln Arg Val Leu Cys His Phe Ser Val Arg Val Thr Asp Ala
115 120 125
Pro Ser Ser Gly Asp Asp Glu Asp Gly Glu Asp Glu Ala Glu Asp Thr
130 135 140
Gly Val Asp Thr Gly Ala Pro Tyr Trp Thr Arg Pro Glu Arg Met Asp
145 150 155 160
Lys Lys Leu Leu Ala Val Pro Ala Ala Asn Thr Val Arg Phe Arg Cys
165 170 175
Pro Ala Ala Gly Asn Pro Thr Pro Ser Ile Ser Trp Leu Lys Asn Gly
180 185 190
Arg Glu Phe Arg Gly Glu His Arg Ile Gly Gly Ile Lys Leu Arg His
195 200 205

Gln Gln Trp Ser Leu Val Met Glu Ser Val Val Pro Ser Asp Arg Gly
210 215 220
Asn Tyr Thr Cys Val Val Glu Asn Lys Phe Gly Ser Ile Arg Gln Thr
225 230 235 240
Tyr Thr Leu Asp Val Leu Glu Arg Ser Pro His Arg Pro Ile Leu Gln
245 250 255
Ala Gly Leu Pro Ala Asn Gln Thr Ala Val Leu Gly Ser Asp Val Glu
260 265 270
Phe His Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Leu
275 280 285
Lys His Val Glu Val Asn Gly Ser Lys Val Gly Pro Asp Gly Thr Pro
290 295 300
Tyr Val Thr Val Leu Lys Thr Ala Gly Ala Asn Thr Thr Asp Lys Glu
305 310 315 320
Leu Glu Val Leu Ser Leu His Asn Val Thr Phe Glu Asp Ala Gly Glu
325 330 335
Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Phe Ser His His Ser Ala
340 345 350
Trp Leu Val Val Leu Pro Ala Glu Glu Glu Leu Val Glu Ala Asp Glu
355 360 365
Ala Gly Ser Val Tyr Ala Gly Ile Leu Ser Tyr Gly Val Gly Phe Phe
370 375 380
Leu Phe Ile Leu Val Val Ala Ala Val Thr Leu Cys Arg Leu Arg Ser
385 390 395 400
Pro Pro Lys Lys Gly Leu Gly Ser Pro Thr Val His Lys Ile Ser Arg
405 410 415
Phe Pro Leu Lys Arg Gln Val Ser Leu Glu Ser Asn Ala Ser Met Ser
420 425 430
Ser Asn Thr Pro Leu Val Arg Ile Ala Arg Leu Ser Ser Gly Glu Gly
435 440 445
Pro Thr Leu Ala Asn Val Ser Glu Leu Glu Leu Pro Ala Asp Pro Lys
450 455 460
Trp Glu Leu Ser Arg Ala Arg Leu Thr Leu Gly Lys Pro Leu Gly Glu
465 470 475 480
Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Ile Gly Ile Asp Lys
485 490 495
Asp Arg Ala Ala Lys Pro Val Thr Val Ala Val Lys Met Leu Lys Asp
500 505 510
Asp Ala Thr Asp Lys Asp Leu Ser Asp Leu Val Ser Glu Met Glu Met
515 520 525
Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gly Ala
530 535 540
Cys Thr Gln Gly Gly Pro Leu Tyr Val Leu Val Glu Tyr Ala Ala Lys
545 550 555 560
Gly Asn Leu Arg Glu Phe Leu Arg Ala Arg Arg Pro Pro Gly Leu Asp
565 570 575
Tyr Ser Phe Asp Thr Cys Lys Pro Pro Glu Glu Gln Leu Thr Phe Lys
580 585 590
Asp Leu Val Ser Cys Ala Tyr Gln Val Ala Arg Gly Met Glu Tyr Leu
595 600 605
Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu
610 615 620
Val Thr Glu Asp Asn Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg
625 630 635 640
Asp Val His Asn Leu Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu
645 650 655
Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr
660 665 670
His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe

675 680 685
Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe
690 695 700
Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn Cys Thr
705 710 715 720
His Asp Leu Tyr Met Ile Met Arg Glu Cys Trp His Ala Ala Pro Ser
725 730 735
Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg Val Leu
740 745 750
Thr Val Thr Ser Thr Asp Glu Tyr Leu Asp Leu Ser Ala Pro Phe Glu
755 760 765
Gln Tyr Ser Pro Gly Gly Gln Asp Thr Pro Ser Ser Ser Ser Ser Gly
770 775 780
Asp Asp Ser Val Phe Ala His Asp Leu Leu Pro Pro Ala Pro Pro Ser
785 790 795 800
Ser Gly Gly Ser Arg Thr
805

<210> 27
<211> 694
<212> PRT
<213> Homo sapiens

<400> 27
Met Gly Ala Pro Ala Cys Ala Leu Ala Leu Cys Val Ala Val Ala Ile
1 5 10 15
Val Ala Gly Ala Ser Ser Glu Ser Leu Gly Thr Glu Gln Arg Val Val
20 25 30
Gly Arg Ala Ala Glu Val Pro Gly Pro Glu Pro Gly Gln Gln Glu Gln
35 40 45
Leu Val Phe Gly Ser Gly Asp Ala Val Glu Leu Ser Cys Pro Pro Pro
50 55 60
Gly Gly Gly Pro Met Gly Pro Thr Val Trp Val Lys Asp Gly Thr Gly
65 70 75 80
Leu Val Pro Ser Glu Arg Val Leu Val Gly Pro Gln Arg Leu Gln Val
85 90 95
Leu Asn Ala Ser His Glu Asp Ser Gly Ala Tyr Ser Cys Arg Gln Arg
100 105 110
Leu Thr Gln Arg Val Leu Cys His Phe Ser Val Arg Val Thr Asp Ala
115 120 125
Pro Ser Ser Gly Asp Asp Glu Asp Gly Glu Asp Glu Ala Glu Asp Thr
130 135 140
Gly Val Asp Thr Gly Ala Pro Tyr Trp Thr Arg Pro Glu Arg Met Asp
145 150 155 160
Lys Lys Leu Leu Ala Val Pro Ala Ala Asn Thr Val Arg Phe Arg Cys
165 170 175
Pro Ala Ala Gly Asn Pro Thr Pro Ser Ile Ser Trp Leu Lys Asn Gly
180 185 190
Arg Glu Phe Arg Gly Glu His Arg Ile Gly Gly Ile Lys Leu Arg His
195 200 205
Gln Gln Trp Ser Leu Val Met Glu Ser Val Val Pro Ser Asp Arg Gly
210 215 220
Asn Tyr Thr Cys Val Val Glu Asn Lys Phe Gly Ser Ile Arg Gln Thr
225 230 235 240
Tyr Thr Leu Asp Val Leu Glu Arg Ser Pro His Arg Pro Ile Leu Gln
245 250 255
Ala Gly Leu Pro Ala Asn Gln Thr Ala Val Leu Gly Ser Asp Val Glu
260 265 270

```
Phe His Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Leu
        275                 280                 285
Lys His Val Glu Val Asn Gly Ser Lys Val Gly Pro Asp Gly Thr Pro
    290                 295                 300
Tyr Val Thr Val Leu Lys Val Ser Leu Glu Ser Asn Ala Ser Met Ser
305                 310                 315                 320
Ser Asn Thr Pro Leu Val Arg Ile Ala Arg Leu Ser Ser Gly Glu Gly
                325                 330                 335
Pro Thr Leu Ala Asn Val Ser Glu Leu Glu Leu Pro Ala Asp Pro Lys
            340                 345                 350
Trp Glu Leu Ser Arg Ala Arg Leu Thr Leu Gly Lys Pro Leu Gly Glu
        355                 360                 365
Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Ile Gly Ile Asp Lys
    370                 375                 380
Asp Arg Ala Ala Lys Pro Val Thr Val Ala Val Lys Met Leu Lys Asp
385                 390                 395                 400
Asp Ala Thr Asp Lys Asp Leu Ser Asp Leu Val Ser Glu Met Glu Met
                405                 410                 415
Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gly Ala
            420                 425                 430
Cys Thr Gln Gly Gly Pro Leu Tyr Val Leu Val Glu Tyr Ala Ala Lys
        435                 440                 445
Gly Asn Leu Arg Glu Phe Leu Arg Ala Arg Arg Pro Pro Gly Leu Asp
    450                 455                 460
Tyr Ser Phe Asp Thr Cys Lys Pro Pro Glu Glu Gln Leu Thr Phe Lys
465                 470                 475                 480
Asp Leu Val Ser Cys Ala Tyr Gln Val Ala Arg Gly Met Glu Tyr Leu
                485                 490                 495
Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu
            500                 505                 510
Val Thr Glu Asp Asn Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg
        515                 520                 525
Asp Val His Asn Leu Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu
    530                 535                 540
Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr
545                 550                 555                 560
His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe
                565                 570                 575
Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe
            580                 585                 590
Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn Cys Thr
        595                 600                 605
His Asp Leu Tyr Met Ile Met Arg Glu Cys Trp His Ala Ala Pro Ser
    610                 615                 620
Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg Val Leu
625                 630                 635                 640
Thr Val Thr Ser Thr Asp Glu Tyr Leu Asp Leu Ser Ala Pro Phe Glu
                645                 650                 655
Gln Tyr Ser Pro Gly Gly Gln Asp Thr Pro Ser Ser Ser Ser Ser Gly
            660                 665                 670
Asp Asp Ser Val Phe Ala His Asp Leu Leu Pro Pro Ala Pro Pro Ser
        675                 680                 685
Ser Gly Gly Ser Arg Thr
    690
```

<210> 28
<211> 604
<212> PRT

<213> Homo sapiens

<400> 28

```
Ala Gln Arg Arg Lys Glu Arg Glu Glu Leu Ala Gln Gln Tyr Glu Ala
 1               5                  10                  15
Ile Leu Arg Glu Cys Gly His Gly Arg Phe Gln Trp Thr Leu Tyr Phe
            20                  25                  30
Val Leu Gly Leu Ala Leu Met Ala Asp Gly Val Glu Val Phe Val Val
        35                  40                  45
Gly Phe Val Leu Pro Ser Ala Glu Lys Asp Met Cys Leu Ser Asp Ser
    50                  55                  60
Asn Lys Gly Met Leu Gly Leu Ile Val Tyr Leu Gly Met Met Val Gly
65                  70                  75                  80
Ala Phe Leu Trp Gly Gly Leu Ala Asp Arg Leu Gly Arg Arg Gln Cys
                85                  90                  95
Leu Leu Ile Ser Leu Ser Val Asn Ser Val Phe Ala Phe Phe Ser Ser
            100                 105                 110
Phe Val Gln Gly Tyr Gly Thr Phe Leu Phe Cys Arg Leu Leu Ser Gly
        115                 120                 125
Val Gly Ile Gly Gly Ser Ile Pro Ile Val Phe Ser Tyr Phe Ser Glu
    130                 135                 140
Phe Leu Ala Gln Glu Lys Arg Gly Glu His Leu Ser Trp Leu Cys Met
145                 150                 155                 160
Phe Trp Met Ile Gly Gly Val Tyr Ala Ala Ala Met Ala Trp Ala Ile
                165                 170                 175
Ile Pro His Tyr Gly Trp Ser Phe Gln Met Gly Ser Ala Tyr Gln Phe
            180                 185                 190
His Ser Trp Arg Val Phe Val Leu Val Cys Ala Phe Pro Ser Val Phe
        195                 200                 205
Ala Ile Gly Ala Leu Thr Thr Gln Pro Glu Ser Pro Arg Phe Phe Leu
    210                 215                 220
Glu Asn Gly Lys His Asp Glu Ala Trp Met Val Leu Lys Gln Val His
225                 230                 235                 240
Asp Thr Asn Met Arg Ala Lys Gly His Pro Glu Arg Val Phe Ser Val
                245                 250                 255
Thr His Ile Lys Thr Ile His Gln Glu Asp Glu Leu Ile Glu Ile Gln
            260                 265                 270
Ser Asp Thr Gly Thr Trp Tyr Gln Arg Trp Gly Val Arg Ala Leu Ser
        275                 280                 285
Leu Gly Gly Gln Val Trp Gly Asn Phe Leu Ser Cys Phe Gly Pro Glu
    290                 295                 300
Tyr Arg Arg Ile Thr Leu Met Met Met Gly Val Trp Phe Thr Met Ser
305                 310                 315                 320
Phe Ser Tyr Tyr Gly Leu Thr Val Trp Phe Pro Asp Met Ile Arg His
                325                 330                 335
Leu Gln Ala Val Asp Tyr Ala Ser Arg Thr Lys Val Phe Pro Gly Glu
            340                 345                 350
Arg Val Glu His Val Thr Phe Asn Phe Thr Leu Glu Asn Gln Ile His
        355                 360                 365
Arg Gly Gly Gln Tyr Phe Asn Asp Lys Phe Ile Gly Leu Arg Leu Lys
    370                 375                 380
Ser Val Ser Phe Glu Asp Ser Leu Phe Glu Glu Cys Tyr Phe Glu Asp
385                 390                 395                 400
Val Thr Ser Ser Asn Thr Phe Phe Arg Asn Cys Thr Phe Ile Asn Thr
                405                 410                 415
Val Phe Tyr Asn Thr Asp Leu Phe Glu Tyr Lys Phe Val Asn Ser Arg
            420                 425                 430
Leu Ile Asn Ser Thr Phe Leu His Asn Lys Glu Gly Cys Pro Leu Asp
        435                 440                 445
```

```
Val Thr Gly Thr Gly Glu Gly Ala Tyr Met Val Tyr Phe Val Ser Phe
    450                 455                 460
Leu Gly Thr Leu Ala Val Leu Pro Gly Asn Ile Val Ser Ala Leu Leu
465                 470                 475                 480
Met Asp Lys Ile Gly Arg Leu Arg Met Leu Ala Gly Ser Ser Val Met
                485                 490                 495
Ser Cys Val Ser Cys Phe Phe Leu Ser Phe Gly Asn Ser Glu Ser Ala
            500                 505                 510
Met Ile Ala Leu Leu Cys Leu Phe Gly Gly Val Ser Ile Ala Ser Trp
        515                 520                 525
Asn Ala Leu Asp Val Leu Thr Val Glu Leu Tyr Pro Ser Asp Lys Arg
    530                 535                 540
Thr Thr Ala Phe Gly Phe Leu Asn Ala Leu Cys Lys Leu Ala Ala Val
545                 550                 555                 560
Leu Gly Ile Ser Ile Phe Thr Ser Phe Val Gly Ile Thr Lys Ala Ala
                565                 570                 575
Pro Ile Leu Phe Ala Ser Ala Ala Leu Ala Leu Gly Ser Ser Leu Ala
            580                 585                 590
Leu Lys Leu Pro Glu Thr Arg Gly Gln Val Leu Gln
        595                 600
```

<210> 29
<211> 683
<212> PRT
<213> Homo sapiens

<400> 29

```
Met Asp Asp Tyr Lys Tyr Gln Asp Asn Tyr Gly Gly Tyr Ala Pro Ser
 1               5                  10                  15
Asp Gly Tyr Tyr Arg Gly Asn Glu Ser Asn Pro Glu Glu Asp Ala Gln
            20                  25                  30
Ser Asp Val Thr Glu Gly His Asp Glu Glu Asp Glu Ile Tyr Glu Gly
        35                  40                  45
Glu Tyr Gln Gly Ile Pro His Pro Asp Asp Val Lys Ala Lys Gln Ala
    50                  55                  60
Lys Met Ala Pro Ser Arg Met Asp Ser Leu Arg Gly Gln Thr Asp Leu
65                  70                  75                  80
Met Ala Glu Arg Leu Glu Asp Glu Glu Gln Leu Ala His Gln Tyr Glu
                85                  90                  95
Thr Ile Met Asp Glu Cys Gly His Gly Arg Phe Gln Trp Ile Leu Phe
            100                 105                 110
Phe Val Leu Gly Leu Ala Leu Met Ala Asp Gly Val Glu Val Phe Val
        115                 120                 125
Val Ser Phe Ala Leu Pro Ser Ala Glu Lys Asp Met Cys Leu Ser Ser
    130                 135                 140
Ser Lys Lys Gly Met Leu Gly Met Ile Val Tyr Leu Gly Met Met Ala
145                 150                 155                 160
Gly Ala Phe Ile Leu Gly Gly Leu Ala Asp Lys Leu Gly Arg Lys Arg
                165                 170                 175
Val Leu Ser Met Ser Leu Ala Val Asn Ala Ser Phe Ala Ser Leu Ser
            180                 185                 190
Ser Phe Val Gln Gly Tyr Gly Ala Phe Leu Phe Cys Arg Leu Ile Ser
        195                 200                 205
Gly Ile Gly Ile Gly Gly Ala Leu Pro Ile Val Phe Ala Tyr Phe Ser
    210                 215                 220
Glu Phe Leu Ser Arg Glu Lys Arg Gly Glu His Leu Ser Trp Leu Gly
225                 230                 235                 240
Ile Phe Trp Met Thr Gly Gly Leu Tyr Ala Ser Ala Met Ala Trp Ser
```

```
                245                 250                 255
Ile Ile Pro His Tyr Gly Trp Gly Phe Ser Met Gly Thr Asn Tyr His
            260                 265                 270
Phe His Ser Trp Arg Val Phe Val Ile Val Cys Ala Leu Pro Cys Thr
        275                 280                 285
Val Ser Met Val Ala Leu Lys Phe Met Pro Glu Ser Pro Arg Phe Leu
    290                 295                 300
Leu Glu Met Gly Lys His Asp Glu Ala Trp Met Ile Leu Lys Gln Val
305                 310                 315                 320
His Asp Thr Asn Met Arg Ala Lys Gly Thr Pro Glu Lys Val Phe Thr
                325                 330                 335
Val Ser Asn Ile Lys Thr Pro Lys Gln Met Asp Glu Phe Ile Glu Ile
            340                 345                 350
Gln Ser Ser Thr Gly Thr Trp Tyr Gln Arg Trp Leu Val Arg Phe Lys
        355                 360                 365
Thr Ile Phe Lys Gln Val Trp Asp Asn Ala Leu Tyr Cys Val Met Gly
    370                 375                 380
Pro Tyr Arg Met Asn Thr Leu Ile Leu Ala Val Val Trp Phe Ala Met
385                 390                 395                 400
Ala Phe Ser Tyr Tyr Gly Leu Thr Val Trp Phe Pro Asp Met Ile Arg
                405                 410                 415
Tyr Phe Gln Asp Glu Glu Tyr Lys Ser Lys Met Lys Val Phe Phe Gly
            420                 425                 430
Glu His Val Tyr Gly Ala Thr Ile Asn Phe Thr Met Glu Asn Gln Ile
        435                 440                 445
His Gln His Gly Lys Leu Val Asn Asp Lys Phe Thr Arg Met Tyr Phe
    450                 455                 460
Lys His Val Leu Phe Glu Asp Thr Phe Phe Asp Glu Cys Tyr Phe Glu
465                 470                 475                 480
Asp Val Thr Ser Thr Asp Thr Tyr Phe Lys Asn Cys Thr Ile Glu Ser
                485                 490                 495
Thr Ile Phe Tyr Asn Thr Asp Leu Tyr Glu His Lys Phe Ile Asn Cys
            500                 505                 510
Arg Phe Ile Asn Ser Thr Phe Leu Glu Gln Lys Glu Gly Cys His Met
        515                 520                 525
Asp Leu Glu Gln Asp Asn Asp Phe Leu Ile Tyr Leu Val Ser Phe Leu
    530                 535                 540
Gly Ser Leu Ser Val Leu Pro Gly Asn Ile Ile Ser Ala Leu Leu Met
545                 550                 555                 560
Asp Arg Ile Gly Arg Leu Lys Met Ile Gly Gly Ser Met Leu Ile Ser
                565                 570                 575
Ala Val Cys Cys Phe Phe Leu Phe Phe Gly Asn Ser Glu Ser Ala Met
            580                 585                 590
Ile Gly Trp Gln Cys Leu Phe Cys Gly Thr Ser Ile Ala Ala Trp Asn
        595                 600                 605
Ala Leu Asp Val Ile Thr Val Glu Leu Tyr Pro Thr Asn Gln Arg Ala
    610                 615                 620
Thr Ala Phe Gly Ile Leu Asn Gly Leu Cys Lys Phe Gly Ala Ile Leu
625                 630                 635                 640
Gly Asn Thr Ile Phe Ala Ser Phe Val Gly Ile Thr Lys Val Val Pro
                645                 650                 655
Ile Leu Leu Ala Ala Ala Ser Leu Val Gly Gly Gly Leu Ile Ala Leu
            660                 665                 670
Arg Leu Pro Glu Thr Arg Glu Gln Val Leu Ile
        675                 680
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<210> 30
<211> 727

<212> PRT
<213> Homo sapiens

<400> 30

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Met Glu Asp Ser Tyr Lys Asp Arg Thr Ser Leu Met Lys Gly Ala Lys
 1               5                  10                  15
Asp Ile Ala Arg Glu Val Lys Lys Gln Thr Val Lys Lys Val Asn Gln
            20                  25                  30
Ala Val Asp Arg Ala Gln Asp Glu Tyr Thr Gln Arg Ser Tyr Ser Arg
        35                  40                  45
Phe Gln Asp Glu Glu Asp Asp Asp Asp Tyr Tyr Pro Ala Gly Glu Thr
    50                  55                  60
Tyr Asn Gly Glu Ala Asn Asp Asp Glu Gly Ser Ser Glu Ala Thr Glu
65                  70                  75                  80
Gly His Asp Glu Asp Asp Glu Ile Tyr Glu Gly Glu Tyr Gln Gly Ile
                85                  90                  95
Pro Ser Met Asn Gln Ala Lys Asp Ser Ile Val Ser Val Gly Gln Pro
            100                 105                 110
Lys Gly Asp Glu Tyr Lys Asp Arg Arg Glu Leu Glu Ser Glu Arg Arg
        115                 120                 125
Ala Asp Glu Glu Glu Leu Ala Gln Gln Tyr Glu Leu Ile Ile Gln Glu
    130                 135                 140
Cys Gly His Gly Arg Phe Gln Trp Ala Leu Phe Phe Val Leu Gly Met
145                 150                 155                 160
Ala Leu Met Ala Asp Gly Val Glu Val Phe Val Val Gly Phe Val Leu
                165                 170                 175
Pro Ser Ala Glu Thr Asp Leu Cys Ile Pro Asn Ser Gly Ser Gly Trp
            180                 185                 190
Leu Gly Ser Ile Val Tyr Leu Gly Met Met Val Gly Ala Phe Phe Trp
        195                 200                 205
Gly Gly Leu Ala Asp Lys Val Gly Arg Lys Gln Ser Leu Leu Ile Cys
    210                 215                 220
Met Ser Val Asn Gly Phe Phe Ala Phe Leu Ser Ser Phe Val Gln Gly
225                 230                 235                 240
Tyr Gly Phe Phe Leu Phe Cys Arg Leu Leu Ser Gly Phe Gly Ile Gly
                245                 250                 255
Gly Ala Ile Pro Thr Val Phe Ser Tyr Phe Ala Glu Val Leu Ala Arg
            260                 265                 270
Glu Lys Arg Gly Glu His Leu Ser Trp Leu Cys Met Phe Trp Met Ile
        275                 280                 285
Gly Gly Ile Tyr Ala Ser Ala Met Ala Trp Ala Ile Ile Pro His Tyr
    290                 295                 300
Gly Trp Ser Phe Ser Met Gly Ser Ala Tyr Gln Phe His Ser Trp Arg
305                 310                 315                 320
Val Phe Val Ile Val Cys Ala Leu Pro Cys Val Ser Ser Val Val Ala
                325                 330                 335
Leu Thr Phe Met Pro Glu Ser Pro Arg Phe Leu Leu Glu Val Gly Lys
            340                 345                 350
His Asp Glu Ala Trp Met Ile Leu Lys Leu Ile His Asp Thr Asn Met
        355                 360                 365
Arg Ala Arg Gly Gln Pro Glu Lys Val Phe Thr Val Asn Lys Ile Lys
    370                 375                 380
Thr Pro Lys Gln Ile Asp Glu Leu Ile Glu Ile Glu Ser Asp Thr Gly
385                 390                 395                 400
Thr Trp Tyr Arg Arg Cys Phe Val Arg Ile Arg Thr Glu Leu Tyr Gly
                405                 410                 415
Ile Trp Leu Thr Phe Met Arg Cys Phe Asn Tyr Pro Val Arg Asp Asn
            420                 425                 430
Thr Ile Lys Leu Thr Ile Val Trp Phe Thr Leu Ser Phe Gly Tyr Tyr
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        435                 440                 445
Gly Leu Ser Val Trp Phe Pro Asp Val Ile Lys Pro Leu Gln Ser Asp
    450                 455                 460
Glu Tyr Ala Leu Leu Thr Arg Asn Val Glu Arg Asp Lys Tyr Ala Asn
465                 470                 475                 480
Phe Thr Ile Asn Phe Thr Met Glu Asn Gln Ile His Thr Gly Met Glu
                485                 490                 495
Tyr Asp Asn Gly Arg Phe Ile Gly Val Lys Phe Lys Ser Val Thr Phe
            500                 505                 510
Lys Asp Ser Val Phe Lys Ser Cys Thr Phe Glu Asp Val Thr Ser Val
        515                 520                 525
Asn Thr Tyr Phe Lys Asn Cys Thr Phe Ile Asp Thr Val Phe Asp Asn
    530                 535                 540
Thr Asp Phe Glu Pro Tyr Lys Phe Ile Asp Ser Glu Phe Lys Asn Cys
545                 550                 555                 560
Ser Phe Phe His Asn Lys Thr Gly Cys Gln Ile Thr Phe Asp Asp Asp
                565                 570                 575
Tyr Ser Ala Tyr Trp Ile Tyr Phe Val Asn Phe Leu Gly Thr Leu Ala
            580                 585                 590
Val Leu Pro Gly Asn Ile Val Ser Ala Leu Leu Met Asp Arg Ile Gly
        595                 600                 605
Arg Leu Thr Met Leu Gly Gly Ser Met Val Leu Ser Gly Ile Ser Cys
    610                 615                 620
Phe Phe Leu Trp Phe Gly Thr Ser Glu Ser Met Met Ile Gly Met Leu
625                 630                 635                 640
Cys Leu Tyr Asn Gly Leu Thr Ile Ser Ala Trp Asn Ser Leu Asp Val
                645                 650                 655
Val Thr Val Glu Leu Tyr Pro Thr Asp Arg Arg Ala Thr Gly Phe Gly
            660                 665                 670
Phe Leu Asn Ala Leu Cys Lys Ala Ala Ala Val Leu Gly Asn Leu Ile
        675                 680                 685
Phe Gly Ser Leu Val Ser Ile Thr Lys Ser Ile Pro Ile Leu Leu Ala
    690                 695                 700
Ser Thr Val Leu Val Cys Gly Gly Leu Val Gly Leu Cys Leu Pro Asp
705                 710                 715                 720
Thr Arg Thr Gln Val Leu Met
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<210> 31
<211> 742
<212> PRT
<213> Homo sapiens

<400> 31

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Asp Ile Ala Lys Glu Val Lys Lys His Ala Ala Lys Lys Val Val Lys
            20                  25                  30
Gly Leu Asp Arg Val Gln Asp Glu Tyr Ser Arg Arg Ser Tyr Ser Arg
        35                  40                  45
Phe Glu Glu Glu Asp Asp Asp Asp Asp Phe Pro Ala Pro Ser Asp Gly
    50                  55                  60
Tyr Tyr Arg Gly Glu Gly Thr Gln Asp Glu Glu Glu Gly Gly Ala Ser
65                  70                  75                  80
Ser Asp Ala Thr Glu Gly His Asp Glu Asp Asp Glu Ile Tyr Glu Gly
                85                  90                  95
Glu Tyr Gln Asp Ile Pro Arg Ala Glu Ser Gly Gly Lys Gly Glu Arg
            100                 105                 110
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Met Ala Asp Gly Ala Pro Leu Ala Gly Val Arg Gly Gly Leu Ser Asp
        115                 120                 125
Gly Glu Gly Pro Pro Gly Gly Arg Gly Glu Ala Gln Arg Arg Lys Glu
    130                 135                 140
Arg Glu Glu Leu Ala Gln Gln Tyr Glu Ala Ile Leu Arg Glu Cys Gly
145                 150                 155                 160
His Gly Arg Phe Gln Trp Thr Leu Tyr Phe Val Leu Gly Leu Ala Leu
                165                 170                 175
Met Ala Asp Gly Val Glu Val Phe Val Val Gly Phe Val Leu Pro Ser
            180                 185                 190
Ala Glu Lys Asp Met Cys Leu Ser Asp Ser Asn Lys Gly Met Leu Gly
        195                 200                 205
Leu Ile Val Tyr Leu Gly Met Met Val Gly Ala Phe Leu Trp Gly Gly
    210                 215                 220
Leu Ala Asp Arg Leu Gly Arg Arg Gln Cys Leu Leu Ile Ser Leu Ser
225                 230                 235                 240
Val Asn Ser Val Phe Ala Phe Phe Ser Ser Phe Val Gln Gly Tyr Gly
                245                 250                 255
Thr Phe Leu Phe Cys Arg Leu Leu Ser Gly Val Gly Ile Gly Gly Ser
            260                 265                 270
Ile Pro Ile Val Phe Ser Tyr Phe Ser Glu Phe Leu Ala Gln Glu Lys
        275                 280                 285
Arg Gly Glu His Leu Ser Trp Leu Cys Met Phe Trp Met Ile Gly Gly
    290                 295                 300
Val Tyr Ala Ala Ala Met Ala Trp Ala Ile Ile Pro His Tyr Gly Trp
305                 310                 315                 320
Ser Phe Gln Met Gly Ser Ala Tyr Gln Phe His Ser Trp Arg Val Phe
                325                 330                 335
Val Leu Val Cys Ala Phe Pro Ser Val Phe Ala Ile Gly Ala Leu Thr
            340                 345                 350
Thr Gln Pro Glu Ser Pro Arg Phe Phe Leu Glu Asn Gly Lys His Asp
        355                 360                 365
Glu Ala Trp Met Val Leu Lys Gln Val His Asp Thr Asn Met Arg Ala
    370                 375                 380
Lys Gly His Pro Glu Arg Val Phe Ser Val Thr His Ile Lys Thr Ile
385                 390                 395                 400
His Gln Glu Asp Glu Leu Ile Glu Ile Gln Ser Asp Thr Gly Thr Trp
                405                 410                 415
Tyr Gln Arg Trp Gly Val Arg Ala Leu Ser Leu Gly Gly Gln Val Trp
            420                 425                 430
Gly Asn Phe Leu Ser Cys Phe Gly Pro Glu Tyr Arg Arg Ile Thr Leu
        435                 440                 445
Met Met Met Gly Val Trp Phe Thr Met Ser Phe Ser Tyr Tyr Gly Leu
    450                 455                 460
Thr Val Trp Phe Pro Asp Met Ile Arg His Leu Gln Ala Val Asp Tyr
465                 470                 475                 480
Ala Ser Arg Thr Lys Val Phe Pro Gly Glu Arg Val Gly His Val Thr
                485                 490                 495
Phe Asn Phe Thr Leu Glu Asn Gln Ile His Arg Gly Gly Gln Tyr Phe
            500                 505                 510
Asn Asp Lys Phe Ile Gly Leu Arg Leu Lys Ser Val Ser Phe Glu Asp
        515                 520                 525
Ser Leu Phe Glu Glu Cys Tyr Phe Glu Asp Val Thr Ser Ser Asn Thr
    530                 535                 540
Phe Phe Arg Asn Cys Thr Phe Ile Asn Thr Val Phe Tyr Asn Thr Asp
545                 550                 555                 560
Leu Phe Glu Tyr Lys Phe Val Asn Ser Arg Leu Ile Asn Ser Thr Phe
                565                 570                 575
Leu His Asn Lys Glu Gly Cys Pro Leu Asp Val Thr Gly Thr Gly Glu
```

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            580                 585                 590
Gly Ala Tyr Met Val Tyr Phe Val Ser Phe Leu Gly Thr Leu Ala Val
        595                 600                 605
Leu Pro Gly Asn Ile Val Ser Ala Leu Leu Met Asp Lys Ile Gly Arg
    610                 615                 620
Leu Arg Met Leu Ala Gly Ser Ser Val Met Ser Cys Val Ser Cys Phe
625                 630                 635                 640
Phe Leu Ser Phe Gly Asn Ser Glu Ser Ala Met Ile Ala Leu Leu Cys
                645                 650                 655
Leu Phe Gly Gly Val Ser Ile Ala Ser Trp Asn Ala Leu Asp Val Leu
            660                 665                 670
Thr Val Glu Leu Tyr Pro Ser Asp Lys Arg Thr Thr Ala Phe Gly Phe
        675                 680                 685
Leu Asn Ala Leu Cys Lys Leu Ala Ala Val Leu Gly Ile Ser Ile Phe
    690                 695                 700
Thr Ser Phe Val Gly Ile Thr Lys Ala Ala Pro Ile Leu Phe Ala Ser
705                 710                 715                 720
Ala Ala Leu Ala Leu Gly Ser Ser Leu Ala Leu Lys Leu Pro Glu Thr
                725                 730                 735
Arg Gly Gln Val Leu Gln
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<210> 32
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> SNAP-25 antigen having a free carboxyl-terminus at the P1 residue of the scissile bond of the BoNT/A cleavage site

<400> 32
Arg Ile Asp Glu Ala Asn Gln
 1   5

<210> 33
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> SNAP-25 antigen having a free carboxyl-terminus at the P1 residue of the scissile bond of the BoNT/A cleavage site

<400> 33
Thr Arg Ile Asp Glu Ala Asn Gln
 1   5

<210> 34
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> SNAP-25 antigen having a free carboxyl-terminus at the P1 residue of the scissile bond of the BoNT/A cleavage site

<400> 34
Lys Thr Arg Ile Asp Glu Ala Asn Gln
1 5

<210> 35
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> SNAP-25 antigen having a free carboxyl-terminus at the P1 residue of the scissile bond of the BoNT/A cleavage site

<400> 35
Asn Lys Thr Arg Ile Asp Glu Ala Asn Gln
1 5 10

<210> 36
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> SNAP-25 antigen having a free carboxyl-terminus at the P1 residue of the scissile bond of the BoNT/A cleavage site

<400> 36
Ser Asn Lys Thr Arg Ile Asp Glu Ala Asn Gln
1 5 10

<210> 37
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> SNAP-25 antigen having a free carboxyl-terminus at the P1 residue of the scissile bond of the BoNT/A cleavage site

<400> 37
Asp Ser Asn Lys Thr Arg Ile Asp Glu Ala Asn Gln
1 5 10

<210> 38
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> SNAP-25 antigen having a free carboxylated carboxyl-terminus at the P1 residue of the scissile bond of the BoNT/A cleavage site

<221> SITE
<222> (13)...(13)
<223> carboxylated glutamine

<400> 38
Cys Asp Ser Asn Lys Thr Arg Ile Asp Glu Ala Asn Gln
 1   5   10

<210> 39
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> SNAP-25 antigen having a free carboxyl-terminus at the P1 residue of the scissile bond of the BoNT/A cleavage site

<400> 39
Arg Ile Asp Glu Ala Asn Lys
 1   5

<210> 40
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> SNAP-25 antigen having a free carboxyl-terminus at the P1 residue of the scissile bond of the BoNT/A cleavage site

<400> 40
Ala Arg Ile Asp Glu Ala Asn Lys
 1   5

<210> 41
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> SNAP-25 antigen having a free carboxyl-terminus at the P1 residue of the scissile bond of the BoNT/A cleavage site

<400> 41
Lys Ala Arg Ile Asp Glu Ala Asn Lys
 1   5

<210> 42
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> SNAP-25 antigen having a free carboxyl-terminus at the P1 residue of the scissile bond of the BoNT/A cleavage site

<400> 42
Asn Lys Ala Arg Ile Asp Glu Ala Asn Lys
1 5 10

<210> 43
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> SNAP-25 antigen having a free carboxyl-terminus at the P1 residue of the scissile bond of the BoNT/A cleavage site

<400> 43
Met Asn Lys Ala Arg Ile Asp Glu Ala Asn Lys
1 5 10

<210> 44
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> SNAP-25 antigen having a free carboxyl-terminus at the P1 residue of the scissile bond of the BoNT/A cleavage site

<400> 44
Asp Met Asn Lys Ala Arg Ile Asp Glu Ala Asn Lys
1 5 10

<210> 45
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> SNAP-25 antigen having a free carboxylated carboxyl-terminus at the P1 residue of the scissile bond of the BoNT/A cleavage site

<221> SITE
<222> (13)...(13)
<223> Carboxylated lysine

<400> 45
Cys Asp Met Asn Lys Ala Arg Ile Asp Glu Ala Asn Lys
 1   5   10

<210> 46
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> SNAP-25 antigen

<400> 46
Cys Gly Gly Gly Arg Ile Asp Glu Ala Asn Gln
 1   5   10

<210> 47
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> SNAP-25 antigen

<400> 47
Cys Gly Gly Gly Arg Ile Asp Glu Ala Asn Lys
 1   5   10

<210> 48
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> BirA-HisTag?-SNAP-25-134-197

<400> 48
Met Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp
 1   5   10   15
His His His His His His His His Ile Arg Arg Val Thr Asn Asp Ala
            20   25   30
Arg Glu Asn Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile
        35   40   45
Gly Asn Leu Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr
    50   55   60
Gln Asn Arg Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys
65   70   75   80
Thr Arg Ile Asp Glu Ala Asn Gln
                85

<210> 49
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<223> BirA-HisTag?-SNAP-25-134-206

<400> 49
Met Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp
 1   5   10   15
His His His His His His His His Ile Arg Arg Val Thr Asn Asp Ala
            20   25   30
Arg Glu Asn Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile
        35   40   45
Gly Asn Leu Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr
    50   55   60
Gln Asn Arg Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys
65   70   75   80
Thr Arg Ile Asp Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser
                85   90   95
Gly

<210> 50
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> BirA peptide

<400> 50
Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His
 1   5   10   15

<210> 51
<211> 7570
<212> DNA
<213> Artificial Sequence

<220>
<223> pQBI-25/GFP-BoNT/A-LC expression construct.

<400> 51
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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
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gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 360
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<220>
<223> GFP-BoNT/A light chain amino acid sequence.

<400> 52

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60
Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160
Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
            180                 185                 190
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
        195                 200                 205
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
    210                 215                 220
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ile Asp
225                 230                 235                 240
Gly Gly Gly Gly Gly Pro Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp
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Pro Val Asn Gly Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Ala Gly
            260                 265                 270
Gln Met Gln Pro Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val
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Ile Pro Glu Arg Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn
    290                 295                 300
Pro Pro Pro Glu Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr
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Tyr Leu Ser Thr Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr
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Lys Leu Phe Glu Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu
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Thr Glu Leu Lys Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro
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Asp Gly Ser Tyr Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro
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Ser Ala Asp Ile Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val
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Leu Asn Leu Thr Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe
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His Asp Ala Lys Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu
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Thr Tyr Leu Asn Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro
    610                 615                 620
Lys Val Asn Tyr Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn
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Leu Ala Ala Asn Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn
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<210> 53
<211> 6259
<212> DNA
<213> Artificial Sequence

<220>
<223> pQBI-25/GFP expression construct.

<400> 53

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<213> Artificial Sequence

<220>
<223> GFP amino acid sequence.

<400> 54

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60
Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140
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Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160
Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
            180                 185                 190
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
        195                 200                 205
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
    210                 215                 220
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ile Asp
225                 230                 235                 240
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<210> 55
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<220>
<223> G-spacer flexible spacer

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<210> 56
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<210> 58
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<210> 59
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Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
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Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
100 105 110
Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
115 120 125
Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
130 135 140
Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145 150 155 160
Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
165 170 175
Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
180 185 190
Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
195 200 205
Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
210 215 220
Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225 230 235 240
Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
245 250 255
Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
260 265 270
Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
275 280 285
Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
290 295 300
Gly Leu Pro Tyr Leu Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr
305 310 315 320
Asp Lys Glu Ile Glu Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp
325 330 335
Ala Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe
340 345 350

```
His Ser Ala Trp Leu Thr Val Leu Pro Ala Pro Gly Arg Glu Lys Glu
        355                 360                 365
Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly
    370                 375                 380
Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met
385                 390                 395                 400
Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His
                405                 410                 415
Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala
            420                 425                 430
Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr
        435                 440                 445
Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser
    450                 455                 460
Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys
465                 470                 475                 480
Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val
                485                 490                 495
Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val
            500                 505                 510
Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu
        515                 520                 525
Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His
    530                 535                 540
Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu
545                 550                 555                 560
Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu
                565                 570                 575
Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg
            580                 585                 590
Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr
        595                 600                 605
Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His
    610                 615                 620
Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met
625                 630                 635                 640
Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr
                645                 650                 655
Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro
            660                 665                 670
Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser
        675                 680                 685
Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr
    690                 695                 700
Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His
705                 710                 715                 720
Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met
                725                 730                 735
Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln
            740                 745                 750
Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu
        755                 760                 765
Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro
    770                 775                 780
Asp Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro
785                 790                 795                 800
Asp Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn
                805                 810                 815
Gly Ser Val Lys Thr
```

<210> 60
<211> 822
<212> PRT
<213> Homo sapiens

<400> 60

```
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1               5                  10                  15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
            20                  25                  30
Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
        35                  40                  45
Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
    50                  55                  60
Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65                  70                  75                  80
Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
                85                  90                  95
Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
            100                 105                 110
Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
        115                 120                 125
Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
    130                 135                 140
Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145                 150                 155                 160
Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
                165                 170                 175
Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
            180                 185                 190
Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
        195                 200                 205
Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
    210                 215                 220
Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225                 230                 235                 240
Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
                245                 250                 255
Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
            260                 265                 270
Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
        275                 280                 285
Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
    290                 295                 300
Gly Leu Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser
305                 310                 315                 320
Asn Ala Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly
                325                 330                 335
Glu Tyr Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser
            340                 345                 350
Ala Trp Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys
        355                 360                 365
Glu Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile
    370                 375                 380
Gly Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg
385                 390                 395                 400
```

```
Met Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val
                405                 410                 415
His Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser
            420                 425                 430
Ala Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile
        435                 440                 445
Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val
    450                 455                 460
Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp
465                 470                 475                 480
Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val
                485                 490                 495
Val Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala
            500                 505                 510
Val Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp
        515                 520                 525
Leu Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys
    530                 535                 540
His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro
545                 550                 555                 560
Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr
                565                 570                 575
Leu Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn
            580                 585                 590
Arg Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr
        595                 600                 605
Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile
    610                 615                 620
His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val
625                 630                 635                 640
Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp
                645                 650                 655
Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala
            660                 665                 670
Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp
        675                 680                 685
Ser Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro
    690                 695                 700
Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly
705                 710                 715                 720
His Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met
                725                 730                 735
Met Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys
            740                 745                 750
Gln Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu
        755                 760                 765
Glu Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr
    770                 775                 780
Pro Asp Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser
785                 790                 795                 800
Pro Asp Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile
                805                 810                 815
Asn Gly Ser Val Lys Thr
            820
```

<210> 61
<211> 769
<212> PRT

<213> Homo sapiens

<400> 61

```
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1               5                  10                  15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
            20                  25                  30
Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
        35                  40                  45
Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
    50                  55                  60
Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65                  70                  75                  80
Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
                85                  90                  95
Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
            100                 105                 110
Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
        115                 120                 125
Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
    130                 135                 140
Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145                 150                 155                 160
Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
                165                 170                 175
Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
            180                 185                 190
Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
        195                 200                 205
Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
    210                 215                 220
Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225                 230                 235                 240
Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
                245                 250                 255
Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
            260                 265                 270
Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
        275                 280                 285
Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
    290                 295                 300
Gly Leu Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser
305                 310                 315                 320
Asn Ala Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly
                325                 330                 335
Glu Tyr Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser
            340                 345                 350
Ala Trp Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys
        355                 360                 365
Glu Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile
    370                 375                 380
Gly Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg
385                 390                 395                 400
Met Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val
                405                 410                 415
His Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser
            420                 425                 430
Ala Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile
        435                 440                 445
```

```
Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val
    450                 455                 460
Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp
465                 470                 475                 480
Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val
                485                 490                 495
Val Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala
            500                 505                 510
Val Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp
        515                 520                 525
Leu Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys
    530                 535                 540
His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro
545                 550                 555                 560
Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr
                565                 570                 575
Leu Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn
            580                 585                 590
Arg Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr
        595                 600                 605
Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile
    610                 615                 620
His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val
625                 630                 635                 640
Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp
                645                 650                 655
Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala
            660                 665                 670
Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp
        675                 680                 685
Ser Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro
    690                 695                 700
Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly
705                 710                 715                 720
His Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met
                725                 730                 735
Met Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys
            740                 745                 750
Gln Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu
        755                 760                 765
Ile
```

<210> 62
<211> 709
<212> PRT
<213> Homo sapiens

<400> 62

```
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1               5                  10                  15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
            20                  25                  30
Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
        35                  40                  45
Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
    50                  55                  60
Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
```

65 70 75 80
Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
85 90 95
Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
100 105 110
Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
115 120 125
Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
130 135 140
Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145 150 155 160
Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
165 170 175
Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
180 185 190
Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
195 200 205
Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
210 215 220
Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225 230 235 240
Asn His Thr Tyr His Leu Asp Val Val Ala Pro Gly Arg Glu Lys Glu
245 250 255
Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly
260 265 270
Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met
275 280 285
Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His
290 295 300
Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala
305 310 315 320
Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr
325 330 335
Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser
340 345 350
Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys
355 360 365
Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val
370 375 380
Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val
385 390 395 400
Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu
405 410 415
Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His
420 425 430
Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu
435 440 445
Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu
450 455 460
Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg
465 470 475 480
Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr
485 490 495
Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His
500 505 510
Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met
515 520 525
Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr
530 535 540

```
Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro
545                 550                 555                 560
Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser
                565                 570                 575
Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr
            580                 585                 590
Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His
        595                 600                 605
Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met
    610                 615                 620
Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln
625                 630                 635                 640
Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu
                645                 650                 655
Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro
            660                 665                 670
Asp Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro
        675                 680                 685
Asp Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn
    690                 695                 700
Gly Ser Val Lys Thr
705
```

<210> 63
<211> 707
<212> PRT
<213> Homo sapiens

<400> 63

```
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1               5                  10                  15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
            20                  25                  30
Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu Asp Asp Thr
        35                  40                  45
Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn Lys Arg Ala
    50                  55                  60
Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg Leu His Ala Val
65                  70                  75                  80
Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala Gly Gly Asn Pro
                85                  90                  95
Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu Phe Lys Gln Glu
            100                 105                 110
His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His Trp Ser Leu Ile
        115                 120                 125
Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr Thr Cys Val Val
    130                 135                 140
Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His Leu Asp Val Val
145                 150                 155                 160
Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly Leu Pro Ala Asn
                165                 170                 175
Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val Cys Lys Val Tyr
            180                 185                 190
Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His Val Glu Lys Asn
        195                 200                 205
Gly Ser Lys Tyr Gly Pro Asp Gly Leu Pro Tyr Leu Lys Val Leu Lys
    210                 215                 220
Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu Val Leu Tyr Ile
```

225 230 235 240
Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr Cys Leu Ala Gly
245 250 255
Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu Thr Val Leu Pro
260 265 270
Ala Pro Gly Arg Glu Lys Glu Ile Thr Ala Ser Pro Asp Tyr Leu Glu
275 280 285
Ile Ala Ile Tyr Cys Ile Gly Val Phe Leu Ile Ala Cys Met Val Val
290 295 300
Thr Val Ile Leu Cys Arg Met Lys Asn Thr Thr Lys Lys Pro Asp Phe
305 310 315 320
Ser Ser Gln Pro Ala Val His Lys Leu Thr Lys Arg Ile Pro Leu Arg
325 330 335
Arg Gln Val Thr Val Ser Ala Glu Ser Ser Ser Ser Met Asn Ser Asn
340 345 350
Thr Pro Leu Val Arg Ile Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr
355 360 365
Pro Met Leu Ala Gly Val Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys
370 375 380
Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu
385 390 395 400
Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Val Gly Ile Asp Lys
405 410 415
Asp Lys Pro Lys Glu Ala Val Thr Val Ala Val Lys Met Leu Lys Asp
420 425 430
Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val Ser Glu Met Glu Met
435 440 445
Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gly Ala
450 455 460
Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys
465 470 475 480
Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Arg Pro Pro Gly Met Glu
485 490 495
Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu Glu Gln Met Thr Phe Lys
500 505 510
Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu
515 520 525
Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu
530 535 540
Val Thr Glu Asn Asn Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg
545 550 555 560
Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu
565 570 575
Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr
580 585 590
His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Met Trp Glu Ile Phe
595 600 605
Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe
610 615 620
Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn Cys Thr
625 630 635 640
Asn Glu Leu Tyr Met Met Met Arg Asp Cys Trp His Ala Val Pro Ser
645 650 655
Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg Ile Leu
660 665 670
Thr Leu Thr Thr Asn Glu Glu Glu Lys Lys Val Ser Gly Ala Val Asp
675 680 685
Cys His Lys Pro Pro Cys Asn Pro Ser His Leu Pro Cys Val Leu Ala
690 695 700

Val Asp Gln
705

<210> 64
<211> 706
<212> PRT
<213> Homo sapiens

<400> 64

```
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1               5                  10                  15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
            20                  25                  30
Leu Glu Pro Glu Gly Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu
        35                  40                  45
Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys
    50                  55                  60
Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly
65                  70                  75                  80
Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn
                85                  90                  95
Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly
            100                 105                 110
Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr
        115                 120                 125
Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln
    130                 135                 140
Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu
145                 150                 155                 160
Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile
                165                 170                 175
Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp Gly Leu Pro
            180                 185                 190
Tyr Leu Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu
        195                 200                 205
Ile Glu Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu
    210                 215                 220
Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala
225                 230                 235                 240
Trp Leu Thr Val Leu Pro Ala Pro Gly Arg Glu Lys Glu Ile Thr Ala
                245                 250                 255
Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly Val Phe Leu
            260                 265                 270
Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met Lys Asn Thr
        275                 280                 285
Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His Lys Leu Thr
    290                 295                 300
Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Glu Ser Ser
305                 310                 315                 320
Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr Thr Arg Leu
                325                 330                 335
Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu
            340                 345                 350
Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu
        355                 360                 365
Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu
    370                 375                 380
Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val Thr Val Ala
```

385 390 395 400
Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu
405 410 415
Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile
420 425 430
Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile
435 440 445
Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg
450 455 460
Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu
465 470 475 480
Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala
485 490 495
Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu
500 505 510
Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met Lys Ile Ala
515 520 525
Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys
530 535 540
Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu
545 550 555 560
Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val
565 570 575
Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile
580 585 590
Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp
595 600 605
Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys
610 615 620
Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu
625 630 635 640
Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu Tyr Leu Asp
645 650 655
Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp Thr Arg
660 665 670
Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro Asp Pro Met
675 680 685
Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn Gly Ser Val
690 695 700
Lys Thr
705

<210> 65
<211> 705
<212> PRT
<213> Homo sapiens

<400> 65
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
1 5 10 15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
20 25 30
Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
35 40 45
Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
50 55 60
Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65 70 75 80

```
Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
                85                  90                  95
Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
            100                 105                 110
Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
        115                 120                 125
Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
    130                 135                 140
Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145                 150                 155                 160
Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
                165                 170                 175
Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
            180                 185                 190
Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
        195                 200                 205
Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
    210                 215                 220
Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225                 230                 235                 240
Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
                245                 250                 255
Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
            260                 265                 270
Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
        275                 280                 285
Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
    290                 295                 300
Gly Leu Pro Tyr Leu Lys Val Leu Lys Val Ser Ala Glu Ser Ser Ser
305                 310                 315                 320
Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr Thr Arg Leu Ser
                325                 330                 335
Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu Leu
            340                 345                 350
Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu Gly
        355                 360                 365
Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala
    370                 375                 380
Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val Thr Val Ala Val
385                 390                 395                 400
Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val
                405                 410                 415
Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile Ile
            420                 425                 430
Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val
        435                 440                 445
Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Arg
    450                 455                 460
Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu Glu
465                 470                 475                 480
Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala Arg
                485                 490                 495
Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala
            500                 505                 510
Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met Lys Ile Ala Asp
        515                 520                 525
Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys Thr
    530                 535                 540
Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe
```

545 550 555 560
Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val Leu
565 570 575
Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro
580 585 590
Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys
595 600 605
Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys Trp
610 615 620
His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp
625 630 635 640
Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu Tyr Leu Asp Leu
645 650 655
Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp Thr Arg Ser
660 665 670
Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro Asp Pro Met Pro
675 680 685
Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn Gly Ser Val Lys
690 695 700
Thr
705

<210> 66
<211> 704
<212> PRT
<213> Homo sapiens

<400> 66
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
1 5 10 15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
20 25 30
Leu Glu Pro Glu Gly Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu
35 40 45
Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys
50 55 60
Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly
65 70 75 80
Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn
85 90 95
Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly
100 105 110
Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr
115 120 125
Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln
130 135 140
Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu
145 150 155 160
Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile
165 170 175
Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp Gly Leu Pro
180 185 190
Tyr Leu Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu
195 200 205
Ile Glu Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu
210 215 220
Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala
225 230 235 240

```
Trp Leu Thr Val Leu Pro Ala Pro Gly Arg Glu Lys Glu Ile Thr Ala
                245                 250                 255
Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly Val Phe Leu
            260                 265                 270
Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met Lys Asn Thr
        275                 280                 285
Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His Lys Leu Thr
    290                 295                 300
Lys Arg Ile Pro Leu Arg Arg Gln Val Ser Ala Glu Ser Ser Ser Ser
305                 310                 315                 320
Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr Thr Arg Leu Ser Ser
                325                 330                 335
Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu Leu Pro
            340                 345                 350
Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu Gly Lys
        355                 360                 365
Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Val
    370                 375                 380
Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val Thr Val Ala Val Lys
385                 390                 395                 400
Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val Ser
                405                 410                 415
Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn
            420                 425                 430
Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val Glu
        435                 440                 445
Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Arg Pro
    450                 455                 460
Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu Glu Gln
465                 470                 475                 480
Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala Arg Gly
                485                 490                 495
Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala
            500                 505                 510
Arg Asn Val Leu Val Thr Glu Asn Asn Val Met Lys Ile Ala Asp Phe
        515                 520                 525
Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys Thr Thr
    530                 535                 540
Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp
545                 550                 555                 560
Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Met
                565                 570                 575
Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val
            580                 585                 590
Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro
        595                 600                 605
Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys Trp His
    610                 615                 620
Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu
625                 630                 635                 640
Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu Tyr Leu Asp Leu Ser
                645                 650                 655
Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp Thr Arg Ser Ser
            660                 665                 670
Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro Asp Pro Met Pro Tyr
        675                 680                 685
Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn Gly Ser Val Lys Thr
    690                 695                 700
```

<210> 67
<211> 680
<212> PRT
<213> Homo sapiens

<400> 67

```
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1               5                  10                  15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
            20                  25                  30
Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu Asp Asp Thr
        35                  40                  45
Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn Lys Arg Ala
    50                  55                  60
Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg Leu His Ala Val
65                  70                  75                  80
Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala Gly Gly Asn Pro
                85                  90                  95
Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu Phe Lys Gln Glu
            100                 105                 110
His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His Trp Ser Leu Ile
        115                 120                 125
Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr Thr Cys Val Val
    130                 135                 140
Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His Leu Asp Val Val
145                 150                 155                 160
Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly Leu Pro Ala Asn
                165                 170                 175
Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val Cys Lys Val Tyr
            180                 185                 190
Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His Val Glu Lys Asn
        195                 200                 205
Gly Ser Lys Tyr Gly Pro Asp Gly Leu Pro Tyr Leu Lys Val Leu Lys
    210                 215                 220
His Ser Gly Ile Asn Ser Ser Asn Ala Glu Val Leu Ala Leu Phe Asn
225                 230                 235                 240
Val Thr Glu Ala Asp Ala Gly Glu Tyr Ile Cys Lys Val Ser Asn Tyr
                245                 250                 255
Ile Gly Gln Ala Asn Gln Ser Ala Trp Leu Thr Val Leu Pro Lys Gln
            260                 265                 270
Gln Ala Pro Gly Arg Glu Lys Glu Ile Thr Ala Ser Pro Asp Tyr Leu
        275                 280                 285
Glu Ile Ala Ile Tyr Cys Ile Gly Val Phe Leu Ile Ala Cys Met Val
    290                 295                 300
Val Thr Val Ile Leu Cys Arg Met Lys Asn Thr Thr Lys Lys Pro Asp
305                 310                 315                 320
Phe Ser Ser Gln Pro Ala Val His Lys Leu Thr Lys Arg Ile Pro Leu
                325                 330                 335
Arg Arg Gln Val Thr Val Ser Ala Glu Ser Ser Ser Ser Met Asn Ser
            340                 345                 350
Asn Thr Pro Leu Val Arg Ile Thr Thr Arg Leu Ser Ser Thr Ala Asp
        355                 360                 365
Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu Leu Pro Glu Asp Pro
    370                 375                 380
Lys Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu Gly Lys Pro Leu Gly
385                 390                 395                 400
Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Val Gly Ile Asp
                405                 410                 415
```

```
Lys Asp Lys Pro Lys Glu Ala Val Thr Val Ala Val Lys Met Leu Lys
            420                 425                 430
Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val Ser Glu Met Glu
        435                 440                 445
Met Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gly
    450                 455                 460
Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val Glu Tyr Ala Ser
465                 470                 475                 480
Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Arg Pro Pro Gly Met
                485                 490                 495
Glu Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu Glu Gln Met Thr Phe
            500                 505                 510
Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala Arg Gly Met Glu Tyr
        515                 520                 525
Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Val
    530                 535                 540
Leu Val Thr Glu Asn Asn Val Met Lys Ile Ala Asp Phe Gly Leu Ala
545                 550                 555                 560
Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg
                565                 570                 575
Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr
            580                 585                 590
Thr His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Met Trp Glu Ile
        595                 600                 605
Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val Glu Glu Leu
    610                 615                 620
Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn Cys
625                 630                 635                 640
Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys Trp His Ala Val Pro
                645                 650                 655
Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg Ile
            660                 665                 670
Leu Thr Leu Thr Thr Asn Glu Ile
        675                 680
```

<210> 68
<211> 396
<212> PRT
<213> Homo sapiens

<400> 68

```
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1               5                  10                  15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
            20                  25                  30
Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
        35                  40                  45
Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
    50                  55                  60
Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65                  70                  75                  80
Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
                85                  90                  95
Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
            100                 105                 110
Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
        115                 120                 125
Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
```

```
    130                 135                 140
Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145                 150                 155                 160
Lys Thr Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
                165                 170                 175
Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
            180                 185                 190
Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
        195                 200                 205
Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
    210                 215                 220
Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225                 230                 235                 240
Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
                245                 250                 255
Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
            260                 265                 270
Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
        275                 280                 285
Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
    290                 295                 300
Gly Leu Pro Tyr Leu Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr
305                 310                 315                 320
Asp Lys Glu Ile Glu Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp
                325                 330                 335
Ala Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe
            340                 345                 350
His Ser Ala Trp Leu Thr Val Leu Pro Gly Ile Tyr Cys Ser Phe Ser
        355                 360                 365
Leu Gly Phe Phe Pro Phe Ser Trp Leu Thr Ala Ile Lys Leu Thr Gln
    370                 375                 380
Leu Leu Leu Ser Glu Met Ala Pro Phe Ile Leu Ala
385                 390                 395


<210> 69
<211> 317
<212> PRT
<213> Homo sapiens

<400> 69
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1                5                  10                  15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
            20                  25                  30
Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
        35                  40                  45
Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
    50                  55                  60
Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65                  70                  75                  80
Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
                85                  90                  95
Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
            100                 105                 110
Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
        115                 120                 125
Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
    130                 135                 140
```

```
Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145                 150                 155                 160
Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
                165                 170                 175
Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
            180                 185                 190
Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
        195                 200                 205
Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
    210                 215                 220
Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225                 230                 235                 240
Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
                245                 250                 255
Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
            260                 265                 270
Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
        275                 280                 285
Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
    290                 295                 300
Gly Leu Pro Tyr Leu Lys Val Leu Lys Val Arg Thr Phe
305                 310                 315
```

<210> 70
<211> 266
<212> PRT
<213> Homo sapiens

<400> 70

```
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1               5                  10                  15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
            20                  25                  30
Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
        35                  40                  45
Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
    50                  55                  60
Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65                  70                  75                  80
Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
                85                  90                  95
Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
            100                 105                 110
Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
        115                 120                 125
Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
    130                 135                 140
Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145                 150                 155                 160
Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
                165                 170                 175
Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
            180                 185                 190
Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
        195                 200                 205
Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
    210                 215                 220
Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
```

```
225                 230                 235                 240
Asn His Thr Tyr His Leu Asp Val Val Gly Glu Ser Ala Ser Pro Arg
                245                 250                 255
Val Ala Ala Ala Tyr Gln Pro Ile Leu Ala
            260                 265
```

<210> 71
<211> 336
<212> DNA
<213> Mus musculus

<400> 71
caggtgaagc tgcaggagtc tggcgctgag ttggtgaaac ctggggcttc agtgaagata 60
tcctgcaagg cttctggcta catcttcact gaccatgctc ttcactgggt gaggcagaag 120
cctgaacagg gcctggaatg gattgggtat atttttcccg gaaatggtaa tattgagtac 180
aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag tactgcctac 240
atgcagctca acagcctgac atctggagat tctgcaatgt atttctgtaa aaagatggac 300
tactggggcc aagggaccac ggtcaccgtc tcctca 336

<210> 72
<211> 112
<212> PRT
<213> Mus musculus

<400> 72
```
Gln Val Lys Leu Gln Glu Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp His
            20                  25                  30
Ala Leu His Trp Val Arg Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Phe Pro Gly Asn Gly Asn Ile Glu Tyr Asn Glu Lys Phe
    50                  55                  60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Asn Ser Leu Thr Ser Gly Asp Ser Ala Met Tyr Phe Cys
                85                  90                  95
Lys Lys Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
            100                 105                 110
```

<210> 73
<211> 336
<212> DNA
<213> Mus musculus

<400> 73
caggtgaagc tgcaggagtc tggcgctgag ttggtgaaac ctggggcttc agtgaagatc 60
tcctgcaagg cttctggtta caccttcact gaccattcta ttcactgggt gaagcagaag 120
cctggacagg gcctagaatg gattggatat ctttttcccg gaaatggtaa ttttgaatat 180
aatgagaaat tcaagggcaa ggccacactg actgcagaca aatcctccag cactgcctac 240
atgcacctca acagcctgac atctgaggat tctgcagtgt atttctgtaa aaagatggac 300
tactggggcc aagggaccac ggtcaccgtc tcctca 336

<210> 74
<211> 112
<212> PRT
<213> Mus musculus

<400> 74
Gln Val Lys Leu Gln Glu Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30
Ser Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Leu Phe Pro Gly Asn Gly Asn Phe Glu Tyr Asn Glu Lys Phe
    50   55   60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85   90   95
Lys Lys Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
            100   105   110

<210> 75
<211> 336
<212> DNA
<213> Mus musculus

<400> 75
caggttcagc tgcagcagtc cgacgctgag ttggtgaaac ctggggcttc agtgaagata 60
tcctgcaggg cttctggcta caccttcact gaccattcta ttcactgggt gaagcagcag 120
cctggccagg gcctggaatg gatcggatat atttttcccg gaaatggaaa tattgaatac 180
aatgacaaat tcaagggcaa ggccacactg actgcagaca aatcctccgg cactgcctac 240
atgcagctca acagcctgac atctgaggat tctgcagtgt atttctgtaa aaggatgggg 300
tactggggtc aaggaacctc agtcaccgtc tcctca   336

<210> 76
<211> 112
<212> PRT
<213> Mus musculus

<400> 76
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Ile Ser Cys Arg Ala Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30
Ser Ile His Trp Val Lys Gln Gln Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Phe Pro Gly Asn Gly Asn Ile Glu Tyr Asn Asp Lys Phe
    50   55   60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Gly Thr Ala Tyr
65   70   75   80
Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85   90   95
Lys Arg Met Gly Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
            100   105   110

<210> 77
<211> 336
<212> DNA
<213> Mus musculus

<400> 77

caggtcaagc tgcaggagtc tggcgctgag ttggtgaaac ctggggcttc agtgaagatc 60
tcctgcaagg cttctggcta caccttcact gaccattcta ttcactgggt gaagcagaag 120
cctggacagg gcctagaatg gattggatat ctttttcccg gaaatggtaa ttttgagtac 180
aatgaaaaat tcaagggcaa ggccacactg actgcagaca aatcctccag cactgtctac 240
atgtacctca acagcctgac atctgaggat tctgcagtgt atttctgtaa aaggatgggg 300
tactggggcc aagggaccac ggtcaccgtc tcctca 336

<210> 78
<211> 112
<212> PRT
<213> Mus musculus

<400> 78
Gln Val Lys Leu Gln Glu Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30
Ser Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Leu Phe Pro Gly Asn Gly Asn Phe Glu Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Val Tyr
65 70 75 80
Met Tyr Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95
Lys Arg Met Gly Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
100 105 110

<210> 79
<211> 336
<212> DNA
<213> Mus musculus

<400> 79
caggtcaagc tgcaggagtc tggacctgaa ctggtaaagc ctggggcttc agtgaagatg 60
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cctgggcagg gccttgagtg gattggatat attaatcctt acaatgatgg ctctaagtac 180
aatgagaagt tcaaaggcaa ggcctcactg acttcagaca aatcctccag cacagcctac 240
atggagctca gcagcctgac ctctgaggac tctgcggtct attactgtgc aagaatggac 300
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<210> 80
<211> 112
<212> PRT
<213> Mus musculus

<400> 80
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Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30
Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Lys Ala Ser Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr

65 70 75 80
Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Met Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
100 105 110

<210> 81
<211> 336
<212> DNA
<213> Mus musculus

<400> 81
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tcctgcaagg cttctggata cacattcact aactatgtta tacactgggt gaagcaaaag 120
cctgggcagg gccttgagtg gattggatat attaatcctt acaatgatgg ctctaagtac 180
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atggagctca gcagcctgac ctctgaggac tctgcggtct attactgtgc aagaatgggg 300
tactggggcc aagggaccac ggtcaccgtc tcctca 336

<210> 82
<211> 112
<212> PRT
<213> Mus musculus

<400> 82
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Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30
Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Lys Ala Ser Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Met Gly Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
100 105 110

<210> 83
<211> 342
<212> DNA
<213> Mus musculus

<400> 83
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tacctgcaga aaccaggcca gtctccaaag ctcctgatct acaaagtttc caaccgattt 180
tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
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<210> 84
<211> 113
<212> PRT

<213> Mus musculus

<400> 84
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Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
            20   25   30
Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35   40   45
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50   55   60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65   70   75   80
Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
                85   90   95
Ser His Val Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100   105   110
Arg

<210> 85
<211> 324
<212> DNA
<213> Mus musculus

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gggaccaggc tggaaataag acgg   324

<210> 86
<211> 108
<212> PRT
<213> Mus musculus

<400> 86
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Glu Thr Val Thr Ile Thr Cys Arg Thr Thr Glu Asn Ile Tyr Ser Tyr
            20   25   30
Phe Val Trp Ser Gln Gln Arg Gln Gly Lys Ser Pro Gln Leu Arg Val
        35   40   45
Tyr Asn Ala Lys Ser Leu Ala Glu Gly Val Pro Ser Ser Phe Asn Val
    50   55   60
Ser Val Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Gly Thr Tyr His Cys Gln His His Tyr Gly Thr Pro Tyr
                85   90   95
Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Arg Arg
            100   105

<210> 87
<211> 339
<212> DNA

<213> Mus musculus

<400> 87
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ttattccag aggccaggcca gtctccaaaa cgcctaatct atctggtgtc tgaattggac 180
tctggagtc cctgacaggtt cagtggcagt ggttcaggga cagatttcac actggaaatc 240
accagagtg gaggctgagga tttgggagtt tattactgct tgcagagtgc acattttcca 300
ttcacgttc ggctcgggcac caagctggaa atcaaacgg 339

<210> 88
<211> 113
<212> PRT
<213> Mus musculus

<400> 88
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Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Thr
            20   25   30
Asn Gly Lys Thr Tyr Leu Thr Trp Leu Phe Gln Arg Pro Gly Gln Ser
        35   40   45
Pro Lys Arg Leu Ile Tyr Leu Val Ser Glu Leu Asp Ser Gly Val Pro
    50   55   60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile
65   70   75   80
Thr Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Leu Gln Ser
                85   90   95
Ala His Phe Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100   105   110
Arg

<210> 89
<211> 339
<212> DNA
<213> Mus musculus

<400> 89
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tttacgttcg gctcgggcac caagctggaa atcaaacgg 339

<210> 90
<211> 113
<212> PRT
<213> Mus musculus

<400> 90
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Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Thr
            20   25   30
Asn Gly Lys Thr Tyr Leu Thr Trp Leu Ile Gln Arg Pro Gly Gln Ser
        35   40   45

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Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80
Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Leu Gln Ser
                85                  90                  95
Ser His Phe Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
Arg
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<210> 91
<211> 327
<212> DNA
<213> Mus musculus

<400> 91
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aggttcagtg gcagtggatc agtcacagat ttcactctca atatcaacag tgtggagact 240
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gggaccaagc tggagctgaa acgggct 327

<210> 92
<211> 108
<212> PRT
<213> Mus musculus

<400> 92
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Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Asn Ile Gly Asn Tyr
            20                  25                  30
Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
        35                  40                  45
Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Val Thr Asp Phe Thr Leu Asn Ile Asn Ser Val Glu Thr
65                  70                  75                  80
Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asp Thr Trp Pro Leu
                85                  90                  95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
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<210> 93
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<213> Mus musculus

<400> 93
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<210> 94
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<400> 94
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<210> 95
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<400> 95
Ile Phe Thr Asp His Ala Leu His
1 5

<210> 96
<211> 17
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<213> Mus musculus

<400> 96
Tyr Ile Phe Pro Gly Asn Gly Asn Ile Glu Tyr Asn Asp Lys Phe Lys
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<210> 97
<211> 17
<212> PRT
<213> Mus musculus

<400> 97
Tyr Leu Phe Pro Gly Asn Gly Asn Phe Glu Tyr Asn Glu Lys Phe Lys
1 5 10 15
Gly

<210> 98
<211> 17
<212> PRT
<213> Mus musculus

<400> 98
Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15
Gly

<210> 99
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<210> 100
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<400> 100
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<210> 101
<211> 5
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<400> 101
Lys Lys Met Asp Tyr
1 5

<210> 102
<211> 5
<212> PRT
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<400> 102
Ala Arg Met Asp Tyr
1 5

<210> 103
<211> 16
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<400> 103
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<210> 104
<211> 11
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<210> 105
<211> 16
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<213> Mus musculus

<400> 105
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1 5 10 15

<210> 106
<211> 16
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<400> 106
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<400> 107
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1 5 10

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<210> 109
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<400> 109
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<210> 111
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<400> 111
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<210> 112
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<210> 113
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<210> 114
<211> 9
<212> PRT
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<400> 114
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<210> 115
<211> 9
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<400> 115
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<210> 116
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<400> 116
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<210> 117

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<400> 117
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<210> 118
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<210> 120
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<210> 121
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<400> 121
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<400> 124
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<400> 129
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<210> 130
<211> 4654
<212> DNA
<213> Homo sapiens

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<211> 4657
<212> DNA
<213> Homo sapiens

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CÉLULAS ÚTILES PARA ENSAYOS DE ACTIVIDAD DEL SEROTIPO A DE LA TOXINA BOTULÍNICA BASADOS EN INMUNOENSAYOS

La presente solicitud de patente reivindica prioridad conforme al 35 U.S.C. § 119(e) de la Solicitud de Patente Provisional de Estados Unidos No. de serie 61/160,199, presentada el 13 de marzo de 2009, la cual se incorpora en su totalidad a la presente mediante esta referencia.

Las secuencias descritas en la presente memoria descriptiva están contenidas dentro del Listado de Secuencias presentado con la presente que se incorpora en su totalidad mediante esta referencia.

La capacidad de las toxinas clostridio tales como, por ej., neurotoxinas botulínicas (BoNT), BoNT/A, BoNT/B, BoNT/C1, BoNT/D, BoNT/E, BoNT/F y BoNT/G y neurotoxina del tétanos (TeNT) para inhibir la transmisión neuronal se explota en una amplia variedad de aplicaciones terapéuticas y cosméticas, véase por ej., William J. Lipham, Cosmetic and Clinical Applications of Botulinum Toxin (Slack, Inc., 2004). Las toxinas clostridio comercialmente disponibles como composiciones farmacéuticas incluyen preparaciones de BoNT/A, tales como, por ej., BOTOX® (Allergan, Inc., Irvine, CA),

DYSPORT®/RELOXIN®, (Ipsen Ltd., Slough, Inglaterra), PURTOX® (Mentor Corp., Santa Bárbara, CA), XEOMIN® (Merz Pharmaceuticals, GmbH., Frankfurt, Alemania), NEURONOX® (Medy-Tox, Inc., Ochang-myeon, Corea del Sur), BTX-A (Biogen-tech Ltd., University, Yantai, Shandong, China) y preparaciones de BoNT/B, tales como, por ej., MYOBLOC®/NEUROBLOC® (Solstice Neurosciences, Inc., San Francisco del Sur, CA). A modo de ejemplo, BOTOX® está actualmente aprobado en uno o más países para las siguientes indicaciones: acalasia, espasticidad en adultos, fisura anal, lumbalgia, blefaroespasmo, bruxismo, distonia cervical, temblor esencial, líneas en el entrecejo o líneas faciales hiperquinéticas, cefalea, espasmo hemifacial, hiperactividad de la vejiga, hiperhidrosis, parálisis cerebral juvenil, esclerosis múltiple, trastornos mioclónicos, líneas labiales y nasales, disfonía espasmódica, estrabismo y trastorno del nervio VII.

En la actualidad, el bioensayo LD_{50} de ratón, una prueba de letalidad, sigue siendo la prueba de criterio de referencia utilizada por todos los fabricantes farmacéuticos para expresar la potencia de sus preparaciones. S. S. Arnon et al., JAMA 285: 1059-1070 (2001). De hecho, las unidades en las etiquetas de las preparaciones farmacéuticas son unidades LD_{50} de ratón y la cantidad de animales que se necesitan para

producir datos de LD_{50} estadísticamente útiles es alta. La ventaja del bioensayo LD_{50} de ratón es que mide todas las etapas necesarias para la absorción de toxina botulínica (por ej., la unión de la toxina a un receptor de superficie celular, internalización del complejo toxina-receptor, translocación de cadena ligera al citoplasma, escisión de cadena ligera del sustrato), en lugar de simplemente determinar la actividad solo para una parte de este proceso de intoxicación, tal como, por ej., ensayos in vitro que solo miden la actividad enzimática de cadena ligera. Desafortunadamente, el bioensayo LD_{50} de ratón tiene muchas desventajas incluyendo un alto costo operativo debido a que se requiere una alta cantidad de animales de laboratorio, la falta de especificidad debido a que todos los serotipos de BoNT ocasionan el mismo criterio de valoración medible y el potencial de inexactitud a menos que se usen grupos grandes de animales. Además, los grupos de defensa de derechos animales han ejercido presión en las agencias reguladoras en Estados Unidos (FDA/NICEATM/ICCVAM) y Europa (MHRA y EDQM) y en las empresas farmacéuticas que fabrican productos de neurotoxina botulínica para reducir las pruebas en animales y, aun más importante, para reemplazar el bioensayo LD_{50} de ratón para el lanzamiento del producto. Las agencias reguladoras están comprometiendo a las empresas farmacéuticas para aplicar el principio de las tres "R" a las pruebas de

potencia de las neurotoxinas botulínicas: Reducir, Refinar, Reemplazar. D. Straughan, *Progress in Applying the Three Rs to the Potency Testing of Botulinum Toxin Type A*, Altern. Lab. Anim. 34(3): 305-313 (2006). En los últimos años, ya se han tomado varias medidas para reducir y refinar el bioensayo LD_{50} de ratón para poder estandarizar el protocolo y producir datos más consistentes usando menos animales por ensayo.

Por lo tanto, un ensayo de actividad de toxina botulínica simple, confiable, validado y aceptable para las agencias gubernamentales que pueda evaluar la integridad de todas las etapas necesarias para la absorción de toxina botulínica tendría un valor significativo debido a que tal ensayo que no está basado en animales aliviaría la necesidad de realizar pruebas en animales y todas las desventajas, costos y problemas éticos asociados con este tipo de ensayo basado en animales. La solicitud de patente acompañante de Ester Fernandez-Salas y otros, *Immuno-Based Botulinum Toxin Serotype A Activity Assays*, solicitud de patente estadounidense No. de serie: 12/403,531, proporciona composiciones, células y métodos novedosos para analizar la actividad de la BoNT/A útil para diversas industrias tales como, por ej., las industrias farmacéutica y alimenticia. Tales composiciones, células y métodos no usan animales vivos o tejidos extraídos de animales vivos, pero pueden evaluar

todas las etapas necesarias para la acción de neurotoxinas, a saber, unión y absorción celular de toxinas, translocación al citosol celular y actividad de la proteasa.

Uno de los componentes necesarios para los métodos descritos en la solicitud de patente estadounidense No. de serie: 12/403,531 es el uso de células de una línea celular establecida que son susceptibles de intoxicación a bajos niveles de BoNT/A debido a que la cantidad de BoNT/A contenida dentro de las composiciones farmacéuticas comercialmente disponibles es muy baja. Por ejemplo, la composición farmacéutica vendida como BOTOX® contiene aproximadamente 4 a 5 ng de un complejo de BoNT/A. Por lo tanto, existe una necesidad de identificar y crear líneas celulares establecidas que comprendan células susceptibles de intoxicación por BoNT/A solo cuando hay niveles muy bajos de neurotoxina presentes en la muestra. La presente memoria descriptiva proporciona células y composiciones celulares novedosas que son susceptibles de intoxicación por BoNT/A cuando solo están presentes cantidades muy bajas de BoNT/A y por lo tanto permiten el ensayo de composiciones farmacéuticas comercialmente disponibles que comprenden BoNT/A.

BREVE DESCRIPCIÓN DE LOS DIBUJOS

La FIG. 1 muestra un esquema del paradigma actual sobre la liberación de neurotransmisores e intoxicación por toxina clostridio en una neurona central y periférica. La FIG. 1A muestra un esquema para el mecanismo de liberación de neurotransmisores de una neurona central y periférica. El proceso de liberación se puede describir como que comprende dos pasos: 1) acoplamiento de vesícula, donde la proteína SNARE unida a la vesícula de una vesícula que contiene moléculas de neurotransmisores se asocia con las proteínas SNARE unidas a la membrana ubicadas en la membrana plasmática y 2) liberación de neurotransmisores, donde la vesícula se fusiona con la membrana plasmática y las moléculas de neurotransmisores se exocitan. La FIG. 1B muestra un esquema del mecanismo de intoxicación para la actividad de las toxinas del tétanos y botulínica en una neurona central y periférica. Este proceso de intoxicación se puede describir como que comprende cuatro pasos: 1) unión al receptor, donde la toxina clostridio se une a un complejo de receptor de clostridio e inicia el proceso de intoxicación; 2) internalización del complejo, donde luego de la unión de la toxina, una vesícula que contiene un complejo de sistema toxina/receptor se endocita a la célula; 3) translocación de

cadena ligera, donde se cree que ocurren múltiples eventos, incluyendo cambios en el pH interno de la vesícula, formación de un poro de canal que comprende el dominio H_N de la cadena pesada de toxina clostridio, separación de la cadena ligera de toxina clostridio de la cadena pesada y liberación de la cadena ligera y 4) modificación de la diana enzimática, donde la cadena ligera de la toxina clostridio escinde proteolíticamente sus sustratos SNARE diana, tales como, por ej., SNAP-25, VAMP o Sintaxina, y así previene el acoplamiento de vesícula y la liberación de neurotransmisores.

La FIG. 2 muestra gráficas tipo volcán de genes que son más de 4 veces ($\log_2(4) = 2$) regulados por aumento o por disminución en las líneas celulares BB10 y H1 en comparación con la línea celular 2D6. La FIG. 2A muestra los genes que se regulan por aumento en la línea celular BB10 en comparación con la línea celular 2D6. La FIG. 2B muestra los genes que se regulan por aumento en la línea celular H1 en comparación con la línea celular 2D6. La FIG. 2C muestra los genes que se regulan por aumento en la línea celular BB10 en comparación con la línea celular SiMa original (PA). La FIG. 2D muestra los genes que se regulan por aumento en la línea celular H1 en comparación con la línea celular SiMa original (PA). La FIG. 2E muestra los genes que se regulan por aumento en la

línea celular SiMa original (PA) en comparación con la línea celular 2D6. La FIG. 2F muestra los genes que se regulan por disminución en la línea celular BB10 en comparación con la línea celular 2D6. La FIG. 2G muestra los genes que se regulan por disminución en la línea celular H1 en comparación con la línea celular 2D6. La FIG. 2H muestra los genes que se regulan por disminución en la línea celular SiMa original (PA) en comparación con la línea celular 2D6. Cada punto representa un conjunto de sondas. La línea punteada marca un intervalo de confianza del 95%, $p \leq 0.05$. La mayoría de los genes que están sobreexpresados en BB10 y H1 en comparación con 2D6 (A y B) también están sobre o subexpresados en BB10 en comparación con PA (C), en H1 en comparación con PA (D) y en PA en comparación con 2D6 (E), sin embargo un número de estos está sobreexpresado menos de 4 veces y/o no pasan el intervalo de confianza del 95%.

La FIG. 3 muestra curvas SPR BIAcore normalizadas de 7.8 nM de los anticuerpos 2E2A6, 1D3B8, 3C1A5 y 2C9B10 y MC-6050 y MC-6053 comerciales. La FIG. 3A muestra los datos normalizados para la velocidad de asociación de cada anticuerpo. La FIG. 3B muestra los datos normalizados para la velocidad de disociación de cada anticuerpo.

DESCRIPCIÓN DETALLADA

La presente memoria descriptiva proporciona células y composiciones celulares novedosas que son susceptibles de intoxicación por BoNT/A para permitir analizar BoNT/A y composiciones de BoNT/A tales como, por ej., composiciones farmacéuticas comercialmente disponibles que comprenden BoNT/A. La célula y las composiciones celulares descritas en la presente memoria descriptiva son útiles para llevar adelante métodos que pueden detectar cantidades picomolares de BoNT/A en una muestra tales como los métodos descritos en, por ej., Ester Fernandez-Salas y otros, *Immuno-Based Botulinum Toxin Serotype A Activity Assays*, solicitud de patente estadounidense No. de serie: 12/403,531 que se incorpora en su totalidad a la presente mediante esta referencia. Las células y composiciones celulares y su uso en métodos para detectar la actividad de la BoNT/A reducen la necesidad de estudios de toxicidad en animales, pero sirven para analizar las múltiples etapas de intoxicación por BoNT/A, a saber, unión y absorción celular de toxinas, translocación a la célula de citosol y la actividad de proteasa. Tal como se discutirá con más detalle a continuación, las células y composiciones celulares novedosas de la presente memoria descriptiva se pueden usar en ensayos

que analizan muestras brutas y globales así como toxinas de doble cadena altamente purificadas y productos de toxina formulados y también se pueden someter a formatos de ensayo de alta producción automatizados.

Por lo tanto, los aspectos de la presente memoria descriptiva proporcionan una composición celular que comprende células de una línea celular clonal que son susceptibles de intoxicación por BoNT/A.

Otros aspectos de la presente memoria descriptiva proporcionan un método para detectar la actividad de la BoNT/A usando las líneas celulares clonales descritas en la presente memoria descriptiva.

Las toxinas clostridio producidas por *Clostridium botulinum*, *Clostridium tetani*, *Clostridium baratii* y *Clostridium butyricum* son las más usadas en los tratamientos terapéuticos y cosméticos de humanos y otros mamíferos. Las cepas de *C. botulinum* producen siete serotipos de toxinas botulínicas (BoNT) distintos desde el punto de vista de los antígenos, que han sido identificados al investigar los brotes de botulismo en el hombre (BoNT/A, BoNT/B, BoNT/E y BoNT/F), animales (BoNT/C1 y BoNT/D) o aislados de la tierra (BoNT/G). Mientras que los siete serotipos de toxina

botulínica tienen una estructura y propiedades biológicas similares, cada uno también manifiesta características heterogéneas, tales como, por ej., propiedades farmacológicas diferentes. Por el contrario, la toxina del tétanos (TeNT) es producida por un grupo uniforme de *C. tetani*. Otras dos especies de clostridio, *C. baratii* y *C. butyricum* también producen toxinas similares a BoNT/F y BoNT/E, respectivamente.

Cada una de las toxinas clostridio se traduce como un polipéptido de cadena simple de aproximadamente 150 kDa que luego es escindido por un corte proteolítico dentro de un bucle de disulfuro por una proteasa de origen natural tal como, por ej., una proteasa de toxina clostridio endógena o una proteasa de origen natural producida en el medio ambiente. Este procesamiento postraduccional proporciona una molécula de doble cadena que comprende una cadena ligera (LC) de aproximadamente 50 kDa y una cadena pesada (HC) de aproximadamente 100 kDa unidas por un solo enlace de disulfuro e interacciones no covalentes. Cada molécula de doble cadena madura comprende tres dominios funcionalmente diferentes: 1) un dominio enzimático ubicado en la LC que incluye una región de metaloproteasa que contiene actividad de endopeptidasa dependiente de cinc que se dirige específicamente a los componentes centrales del aparato de

liberación de neurotransmisores; 2) un dominio de translocación contenido dentro de la mitad del extremo aminoterminal de la HC (H_N) que facilita la liberación de la LC desde vesículas intracelulares al citoplasma de la célula diana y 3) un dominio de unión encontrado dentro de la mitad del extremo carboxiloterminal de la HC (H_C) que determina la actividad de unión y la especificidad de unión de la toxina al complejo de receptor ubicado en la superficie de la célula diana.

Tanto la unión como la translocación y la actividad enzimática de estos tres dominios funcionales son necesarios para la toxicidad. Mientras que los detalles de este proceso no se conocen aún con exactitud, el mecanismo de intoxicación celular global por el cual las toxinas clostridio ingresan a una neurona e inhiben la liberación de los neurotransmisores es similar, sin importar el serotipo o el subtipo. Pese a que los solicitantes no desean verse limitados por la siguiente descripción, el mecanismo de intoxicación se puede describir como que comprende al menos cuatro pasos: 1) unión al receptor, 2) internalización del complejo, 3) translocación de cadena ligera y 4) modificación de diana enzimática (FIG. 1). El proceso se inicia cuando el dominio de unión H_C de una toxina clostridio se une a un sistema de receptor específico para las toxinas que se ubica en la superficie de membrana

plasmática de una célula diana. Se cree que se logra la especificidad de unión de un complejo receptor, en parte, por combinaciones específicas de gangliósidos y receptores de proteína que parecen comprender claramente cada complejo de receptor de toxina clostridio. Una vez unidos, los complejos de toxina/receptor se internalizan por endocitosis y las vesículas internalizadas se clasifican en caminos intracelulares específicos. La etapa de translocación parece desencadenarse por la acidificación del compartimiento de vesícula. Este proceso parece iniciar nuevas disposiciones estructurales importantes dependientes del pH que aumentan la hidrofobicidad, promueven la formación de poros y facilitan la separación de las cadenas pesada y ligera de la toxina. Una vez separadas, la endopeptidasa de cadena ligera de la toxina se libera desde la vesícula intracelular al citosol donde parece que se dirige específicamente a los componentes centrales del aparato de liberación de neurotransmisores. Estas proteínas centrales, proteínas de membrana asociadas con la vesícula (VAMP)/sinaptobrevina, proteína asociada de forma sinaptosómica de 25 kDa (SNAP-25) y Sintaxina son necesarias para el acoplamiento y la fusión sináptica de la vesícula en el extremo del nervio y constituyen miembros de la familia de receptor de proteína de unión al factor sensible a N-etilmaleimida soluble (SNARE). BoNT/A y BoNT/E escinden la SNAP-25 en la región carboxiloterminal, y liberan

un fragmento de nueve o veintiséis aminoácidos, respectivamente, y BoNT/C1 también escinde la SNAP-25 cerca del extremo carboxiloterminal que libera un fragmento de ocho aminoácidos. Los serotipos botulínicos BoNT/B, BoNT/D, BoNT/F y BoNT/G y la toxina del tétanos actúan en la porción central conservada de VAMP y liberan la porción aminoterminal de VAMP al citosol. La BoNT/C1 escinde la sintaxina en un único sitio cerca de la superficie de la membrana citosólica. La proteólisis selectiva de SNARE sinápticas explica el bloqueo de la liberación de neurotransmisores causado por las toxinas clostridio in vivo. Las dianas de la proteína SNARE de las toxinas clostridio son comunes para la exocitosis en una variedad de tipos no neuronales; en estas células, como en las neuronas, la actividad de la peptidasa de cadena ligera inhibe la exocitosis, véase, por ej., Yann Humeau y otros, *How Botulinum and Tetanus Neurotoxins Block Neurotransmitter Release*, 82(5) Biochimi. 427-446 (2000); Kathryn Turton y otros, *Botulinum and Tetanus Neurotoxins: Structure, Function and Therapeutic Utility*, 27(11) Trends Biochem. Sci. 552-558. (2002); Giovanna Lalli y otros, *The Journey of Tetanus and Botulinum Neurotoxins in Neurons*, 11(9) Trends Microbiol. 431-437, (2003).

Los aspectos de la presente descripción comprenden, en parte, una célula de una línea celular establecida. Como se

usa en la presente, el término "célula" se refiere a una célula eucariótica susceptible de intoxicación por BoNT/A a causa de una BoNT/A o cualquier célula eucariota que puede absorber una BoNT/A. El término "célula" abarca células de una variedad de organismos, tales como, por ej., células murinas, de ratas, porcinos, bovinos, equinos, primates y humanas; de una variedad de tipos celulares tales como, por ej., neuronales y no neuronales y que se pueden aislar de una población, tejido u organismo celular heterogéneo o de una parte de estos. Tal como se usa en la presente, el término "línea celular establecida" es sinónimo de "línea celular inmortal" o "línea celular transformada" y se refiere a un cultivo celular de células seleccionadas para la propagación indefinida de una población celular derivada de una fuente de organismo, tejido u órgano. Por definición, una línea celular establecida excluye un cultivo celular de células primarias. Tal como se usa en la presente, el término "células primarias" se refiere a células recolectadas directamente de tejidos u órganos recién extraídos y no tienen el potencial de propagarse indefinidamente. Una línea celular establecida puede comprender una población heterogénea de células o una población uniforme de células. Una línea celular establecida derivada de una única célula se denomina línea celular clonal. Una línea celular establecida puede ser una cuyas células expresan de forma endógena todos los componentes

necesarios para que las células experimenten un mecanismo celular global por el cual la BoNT/A escinde proteolíticamente un sustrato de la SNAP-25 y abarca la unión de una BoNT/A a un receptor de BoNT/A, la internalización del complejo neurotoxina/receptor, la translocación de la cadena ligera de BoNT/A desde una vesícula intracelular al citoplasma y la escisión proteolítica de una SNAP-25. De manera alternativa, una línea celular establecida puede ser una a cuyas células se les haya introducido desde una fuente endógena al menos un componente necesario para que las células experimenten un mecanismo celular global por el cual una BoNT/A escinde proteolíticamente un sustrato de SNAP-25 y abarca la unión de una BoNT/A a un receptor de BoNT/A, la internalización del complejo neurotoxina/receptor, la translocación de la cadena ligera de la BoNT/A desde una vesícula intracelular al citoplasma y la escisión proteolítica de una SNAP-25. También se denominan línea celular genéticamente diseñada a las células de tal línea celular establecida que pueden, por ej., expresar un FGFR2 exógeno, un FGFR3 exógeno, un SV2 exógeno, una SNAP-25 exógena o cualquier combinación de los mismos. Tal como se usa en la presente, el término "línea celular clonal establecida" o "línea celular clonal" se refiere a un cultivo celular de células seleccionadas de una población heterogénea de tipos celulares que comprende una línea celular

establecida, que también puede ser denominado línea celular original. Por lo tanto, a modo de ejemplo no taxativo, las células de las líneas celulares clonales A6, A7, A9, A10, A11, B5, B10, C5, C11, C12, D7, D11, E11, F10, H1, H3, H8, H10, 1E3, 2B9, 2E4, 3B8, 3D5, 3G10, 4B5, 4C8, 5F3, AC9, AF4, BB3, BB10, BE3, BF8, CC11, CD6, CE6, CG8, CG10, DC4, DD10, DE7, YF5 y H1 1.4 se seleccionaron de la población heterogénea de tipos celulares que comprenden la línea celular SiMa (o línea celular SiMa original) DSMZ ACC 164.

Los aspectos de la presente descripción comprenden, en parte, una célula de una línea celular clonal establecida susceptible de intoxicación por BoNT/A. Tal como se usa en la presente, los términos "célula(s) susceptible(s) de intoxicación por BoNT/A", "célula(s) susceptible(s) de intoxicación por BoNT/A a causa de una BoNT/A" o "célula(s) de una línea celular clonal establecida susceptible(s) de intoxicación por BoNT/A a causa de una BoNT/A" se refieren a célula(s) que puede(n) experimentar el mecanismo celular global por el cual una BoNT/A escinde proteolíticamente un sustrato de SNAP-25 y abarca la unión de una BoNT/A a un receptor de BoNT/A, la internalización del complejo neurotoxina/receptor, la translocación de la cadena ligera de BoNT/A desde una vesícula intracelular al citoplasma y la escisión proteolítica de una SNAP-25. Por definición, las

células(s) susceptible(s) de intoxicación por BoNT/A debe(n) expresar, o estar diseñada(s) para expresar, al menos un receptor de BoNT/A y al menos un sustrato de SNAP-25. Los ejemplos no taxativos de una célula o células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A incluyen las líneas celulares clonales A6, A7, A9, A10, A11, B5, B10, C5, C11, C12, D7, D11, E11, F10, H1, H3, H8, H10, 1E3, 2B9, 2D2, 2D6, 2E4, 3B8, 3D5, 3G10, 4B5, 4C8, 4D3, 5C10, 5F3, AC9, AF4, BB3, BB10, BE3, BF8, CC11, CD6, CE6, CG8, CG10, DC4, DD10, DE7, DF5, YB7, YF5 y H1 1.4. Tal como se usa en la presente, los términos "célula(s) que puede(n) absorber una BoNT/A", "célula(s) que comprende(n) una línea celular clonal establecida que puede(n) absorber una BoNT/A" se refieren a las células que pueden experimentar el mecanismo celular global por el cual una BoNT/A escinde proteolíticamente un sustrato de SNAP-25 y abarca la unión de una BoNT/A a un receptor de BoNT/A, la internalización del complejo neurotoxina/receptor, la translocación de la cadena ligera de BoNT/A desde una vesícula intracelular al citoplasma y la escisión proteolítica de una SNAP-25. Por definición, la(s) células(s) que puede(n) absorber BoNT/A debe(n) expresar, o estar diseñada(s) para expresar, al menos un receptor de BoNT/A y al menos un sustrato de SNAP-25. Los ejemplos no taxativos de una célula o células de una línea celular clonal establecida que pueden absorber BoNT/A

incluyen las líneas celulares clonales A6, A7, A9, A10, A11, B5, B10, C5, C11, C12, D7, D11, E11, F10, H1, H3, H8, H10, 1E3, 2B9, 2D2, 2D6, 2E4, 3B8, 3D5, 3G10, 4B5, 4C8, 4D3, 5C10, 5F3, AC9, AF4, BB3, BB10, BE3, BF8, CC11, CD6, CE6, CG8, CG10, DC4, DD10, DE7, DF5, YB7, YF5 y H1 1.4. Las líneas celulares que comprenden célula(s) de una línea celular clonal establecida susceptible(s) de intoxicación por BoNT/A o célula(s) que pueden absorber BoNT/A se denominan "línea celular que responde".

Los aspectos de la presente descripción comprenden, en parte, células de una línea celular clonal establecida más susceptibles de intoxicación por BoNT/A. Tal como se usan en la presente, los términos "célula(s) más susceptible(s) de intoxicación por BoNT/A", "célula(s) más susceptible(s) de intoxicación por BoNT/A a causa de una BoNT/A" o "célula(s) de una línea celular clonal establecida más susceptible(s) de intoxicación por BoNT/A a causa de una BoNT/A" se refieren a célula(s) que experimentan el mecanismo celular global por el cual una BoNT/A escinde proteolíticamente un sustrato de la SNAP-25 en mayor medida que la(s) célula(s) que comprenden una línea celular SiMa original, tales como, por ej., línea celular SiMa original DSMZ ACC 164. Los ejemplos no taxativos de una célula o células de una línea celular clonal establecida más susceptibles de intoxicación por BoNT/A

incluyen una célula o células de las líneas celulares clonales A10, H1, 2E4, 3B8, 3D5, 5F3, AF4, BB3, BB10, DC4 o H1 1.4. Tal como se usan en la presente, los términos "célula(s) que absorbe(n) BoNT/A más" o "célula(s) que comprenden una línea celular clonal establecida que absorbe(n) BoNT/A más" se refiere a células que experimentan el mecanismo celular global por el cual una BoNT/A escinde proteolíticamente un sustrato de SNAP-25 en mayor medida en comparación con una o más células que comprenden una línea celular SiMa original, tal como, por ej., línea celular SiMa original DSMZ ACC 164. Los ejemplos no taxativos de una célula o células de una línea celular clonal establecida que pueden absorber BoNT/A más incluyen una célula o células de las líneas celulares clonales A10, H1, 2E4, 3B8, 3D5, 5F3, AF4, BB3, BB10, DC4 o H1 1.4. Las líneas celulares que comprenden célula(s) de una línea celular clonal establecida más susceptibles de intoxicación por BoNT/A o célula(s) que pueden absorber BoNT/A más se denominan "línea celular que responde en mayor medida".

Los aspectos de la presente descripción comprenden, en parte, células de una línea celular clonal establecida menos susceptibles de intoxicación por BoNT/A. Tal como se usan en la presente, los términos "célula(s) menos susceptibles de intoxicación por BoNT/A", "célula(s) menos susceptibles de

intoxicación por BoNT/A a causa de una BoNT/A" o "célula(s) de una línea celular clonal establecida menos susceptibles de intoxicación por BoNT/A a causa de una BoNT/A" se refieren a célula(s) que se someten al mecanismo celular global por el cual una BoNT/A escinde proteolíticamente un sustrato de la SNAP-25 en menor medida que la(s) célula(s) que comprenden una línea celular SiMa original, tal como, por ej., línea celular SiMa original DSMZ ACC 164. Los ejemplos no taxativos de una célula o células de una línea celular clonal establecida menos susceptibles de intoxicación por BoNT/A incluyen las líneas celulares clonales A7, B10, D11, H10, 2D2, 2D6, 4D3, 5C10, DF5 e YB7. Tal como se usan en la presente, los términos "célula(s) que absorben BoNT/A menos" o "célula(s) que comprenden una línea celular clonal establecida que absorben BoNT/A menos" se refieren a células que experimentan el mecanismo celular global por el cual BoNT/A escinde proteolíticamente un sustrato de la SNAP-25 en menor medida en comparación con una o más células que comprenden una línea celular SiMa original, tal como, por ej., línea celular SiMa original DSMZ ACC 164. Los ejemplos no taxativos de una célula o células de una línea celular clonal establecida que pueden absorber BoNT/A menos incluyen las líneas celulares clonales A7, B10, D11, H10, 2D2, 2D6, 4D3, 5C10, DF5 e YB7. Las líneas celulares que comprenden célula(s) de una línea celular clonal establecida menos

alrededor de 0.9 pM o menos, alrededor de 0.8 pM o menos, alrededor de 0.7 pM o menos, alrededor de 0.6 pM o menos, alrededor de 0.5 pM o menos, alrededor de 0.4 pM o menos, alrededor de 0.3 pM o menos, alrededor de 0.2 pM o menos o alrededor de 0.1 pM o menos de una BoNT/A. Tal como se usa en la presente, el término "alrededor", cuando califica un valor de un objeto, número, porcentaje o término establecido, se refiere a un intervalo de más o menos diez por ciento del valor del objeto, porcentaje, parámetro o término establecido.

En otra modalidad, las células que comprenden una línea celular clonal establecida pueden absorber una BoNT/A. En aspectos de esta modalidad, las células que comprenden una línea celular clonal establecida pueden absorber, por ej., alrededor de 500 pM o menos, alrededor de 400 pM o menos, alrededor de 300 pM o menos, alrededor de 200 pM o menos o alrededor de 100 pM o menos de una BoNT/A. En otros aspectos de esta modalidad, las células que comprenden una línea celular clonal establecida poseen la capacidad de absorber alrededor de 90 pM o menos, alrededor de 80 pM o menos, alrededor de 70 pM o menos, alrededor de 60 pM o menos, alrededor de 50 pM o menos, alrededor de 40 pM o menos, alrededor de 30 pM o menos, alrededor de 20 pM o menos o alrededor de 10 pM o menos de una BoNT/A. En aun otros

Por lo tanto, en una modalidad, las células de una línea celular clonal establecida son susceptibles de intoxicación por BoNT/A. En aspectos de esta modalidad, las células de una línea celular clonal establecida son susceptibles de intoxicación por BoNT/A por, por ej., alrededor de 500 pM o menos, alrededor de 400 pM o menos, alrededor de 300 pM o menos, alrededor de 200 pM o menos o alrededor de 100 pM o menos de una BoNT/A. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida son susceptibles de intoxicación por BoNT/A por, por ej., alrededor de 90 pM o menos, alrededor de 80 pM o menos, alrededor de 70 pM o menos, alrededor de 60 pM o menos, alrededor de 50 pM o menos, alrededor de 40 pM o menos, alrededor de 30 pM o menos, alrededor de 20 pM o menos o alrededor de 10 pM o menos de una BoNT/A. En aun otros aspectos, las células de una línea celular clonal establecida son susceptibles de intoxicación por BoNT/A por, por ej., alrededor de 9 pM o menos, alrededor de 8 pM o menos, alrededor de 7 pM o menos, alrededor de 6 pM o menos, alrededor de 5 pM o menos, alrededor de 4 pM o menos, alrededor de 3 pM o menos, alrededor de 2 pM o menos o alrededor de 1 pM o menos de una BoNT/A. En aun otros aspectos, las células de una línea celular clonal establecida son susceptibles de intoxicación por BoNT/A por, por ej.,

susceptibles de intoxicación por BoNT/A o célula(s) que pueden absorber BoNT/A menos se denominan "línea celular que responde en menor medida".

Los aspectos de la presente descripción comprenden, en parte, una célula de una línea celular clonal establecida no susceptibles de intoxicación por BoNT/A. Tal como se usan en la presente, los términos "célula(s) no susceptibles de intoxicación por BoNT/A", "célula(s) no susceptibles de intoxicación por BoNT/A a causa de una BoNT/A" o "célula(s) de una línea celular clonal establecida no susceptibles de intoxicación por BoNT/A a causa de una BoNT/A" se refieren a célula(s) que no pueden experimentar el mecanismo celular global por el cual una BoNT/A escinde proteolíticamente un sustrato de SNAP-25. Tal como se usan en la presente, los términos "célula(s) que no pueden absorber BoNT/A" o "célula(s) que comprenden una línea celular clonal establecida que no pueden absorber BoNT/A" se refieren a células que no pueden experimentar el mecanismo celular global por el cual una BoNT/A escinde proteolíticamente un sustrato de la SNAP-25. Las líneas celulares que comprenden célula(s) de una línea celular clonal establecida no susceptibles de intoxicación por BoNT/A o célula(s) que no pueden absorber BoNT/A se denominan "línea celular que no responde".

aspectos, las células que comprenden una línea celular clonal establecida poseen la capacidad de absorber alrededor de 9 pM o menos, alrededor de 8 pM o menos, alrededor de 7 pM o menos, alrededor de 6 pM o menos, alrededor de 5 pM o menos, alrededor de 4 pM o menos, alrededor de 3 pM o menos, alrededor de 2 pM o menos o alrededor de 1 pM o menos de una BoNT/A. En aun otros aspectos, las células que comprenden una línea celular clonal establecida poseen la capacidad de absorber alrededor de 0.9 pM o menos, alrededor de 0.8 pM o menos, alrededor de 0.7 pM o menos, alrededor de 0.6 pM o menos, alrededor de 0.5 pM o menos, alrededor de 0.4 pM o menos, alrededor de 0.3 pM o menos, alrededor de 0.2 pM o menos o alrededor de 0.1 pM o menos de una BoNT/A. En otros aspectos, las células que comprenden una línea celular clonal establecida pueden absorber BoNT/A de, por ejemplo, alrededor de 0.01 pM a alrededor de 100 pM, alrededor de 0.01 pM a alrededor de 75 pM, alrededor de 0.01 pM a alrededor de 50 pM, alrededor de 0.01 pM a alrededor de 25 pM, alrededor de 0.01 pM a alrededor de 20 pM, alrededor de 0.01 pM a alrededor de 15 pM, alrededor de 0.01 pM a alrededor de 10 pM, alrededor de 0.01 pM a alrededor de 5 pM, alrededor de 0.001 pM a alrededor de 100 pM, alrededor de 0.001 pM a alrededor de 75 pM, alrededor de 0.001 pM a alrededor de 50 pM, alrededor de 0.001 pM a alrededor de 25 pM, alrededor de 0.001 pM a alrededor de 20 pM, alrededor de 0.001 pM a

alrededor de 15 pM, alrededor de 0.001 pM a alrededor de 10 pM, alrededor de 0.001 pM a alrededor de 5 pM de BoNT/A.

En otra modalidad, las células de una línea celular clonal establecida no son susceptibles de intoxicación por BoNT/A. En aspectos de esta modalidad, las células de una línea celular clonal establecida no son susceptibles de intoxicación por BoNT/A por, por ej., alrededor de 500 pM o menos, alrededor de 400 pM o menos, alrededor de 300 pM o menos, alrededor de 200 pM o menos o alrededor de 100 pM o menos de una BoNT/A. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida son susceptibles de intoxicación por BoNT/A por, por ej., alrededor de 90 pM o menos, alrededor de 80 pM o menos, alrededor de 70 pM o menos, alrededor de 60 pM o menos, alrededor de 50 pM o menos, alrededor de 40 pM o menos, alrededor de 30 pM o menos, alrededor de 20 pM o menos o alrededor de 10 pM o menos de una BoNT/A. En aun otros aspectos, las células de una línea celular clonal establecida no son susceptibles de intoxicación por BoNT/A por, por ej., alrededor de 9 pM o menos, alrededor de 8 pM o menos, alrededor de 7 pM o menos, alrededor de 6 pM o menos, alrededor de 5 pM o menos, alrededor de 4 pM o menos, alrededor de 3 pM o menos, alrededor de 2 pM o menos o alrededor de 1 pM o menos de una BoNT/A. En aun otros

aspectos, las células de una línea celular clonal establecida no son susceptibles de intoxicación por BoNT/A por, por ej., alrededor de 0.9 pM o menos, alrededor de 0.8 pM o menos, alrededor de 0.7 pM o menos, alrededor de 0.6 pM o menos, alrededor de 0.5 pM o menos, alrededor de 0.4 pM o menos, alrededor de 0.3 pM o menos, alrededor de 0.2 pM o menos o alrededor de 0.1 pM o menos de una BoNT/A. En otros aspectos, las células de una línea celular clonal establecida no son susceptibles de intoxicación por BoNT/A de, por ejemplo, alrededor de 0.01 pM a alrededor de 100 pM, alrededor de 0.01 pM a alrededor de 75 pM, alrededor de 0.01 pM a alrededor de 50 pM, alrededor de 0.01 pM a alrededor de 25 pM, alrededor de 0.01 pM a alrededor de 20 pM, alrededor de 0.01 pM a alrededor de 15 pM, alrededor de 0.01 pM a alrededor de 10 pM, alrededor de 0.01 pM a alrededor de 5 pM, alrededor de 0.001 pM a alrededor de 100 pM, alrededor de 0.001 pM a alrededor de 75 pM, alrededor de 0.001 pM a alrededor de 50 pM, alrededor de 0.001 pM a alrededor de 25 pM, alrededor de 0.001 pM a alrededor de 20 pM, alrededor de 0.001 pM a alrededor de 15 pM, alrededor de 0.001 pM a alrededor de 10 pM o alrededor de 0.001 pM a alrededor de 5 pM de BoNT/A.

Los aspectos de la presente descripción comprenden, en parte, células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A que son más estables

que las células de una línea celular SiMa original tal como, por ej., la línea celular SiMa original DSMZ ACC 164. Tal como se usa en la presente, el término "estable" se refiere a células de una línea celular clonal establecida para una cantidad particular de pasajes que presentan una EC_{50} relativa, sensibilidad, eficacia, asíntota superior bien definida y/o curva de dosis-respuesta bien definida para la actividad de la BoNT/A que es similar a los valores de EC_{50} relativa, sensibilidad, eficacia, asíntota superior bien definida y/o curva de dosis-respuesta bien definida que presentan células de una línea celular SiMa original tal como, por ej., línea celular SiMa original DSMZ ACC 164, en el mismo número de pasajes, o un número similar, donde se usan las mismas condiciones de ensayo y la misma BoNT/A (o molécula) en ambos ensayos.

Por lo tanto, en una modalidad, las células de una línea celular clonal establecida son más estables en comparación con una línea celular SiMa original. En un aspecto de esta modalidad, las células de una línea celular clonal establecida son más estables en comparación con la línea celular SiMa original DSMZ ACC 164. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida son más estables para, por ej., al menos 5 pasajes más, al menos 10 pasajes más, al menos 15 pasajes

más, al menos 20 pasajes más, al menos 25 pasajes más o al menos 30 pasajes más, en comparación con una línea celular SiMa original. En aun otros aspectos de esta modalidad, las células de una línea celular clonal establecida son más estables, por ej., para al menos 5 pasajes más, al menos 10 pasajes más, al menos 15 pasajes más, al menos 20 pasajes más, al menos 25 pasajes más o al menos 30 pasajes más, en comparación con una línea celular SiMa original DSMZ ACC 164.

Los aspectos de la presente descripción comprenden, en parte, células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A que son estables para una pluralidad de pasajes celulares. Tal como se usa en la presente, el término "estable" se refiere a células de una línea celular clonal establecida para un número particular de pasajes que presentan una EC_{50} relativa, sensibilidad, eficacia, asíntota superior bien definida y/o curva de dosis-respuesta bien definida para la actividad de la BoNT/A que es similar a los valores de EC_{50} relativa, sensibilidad, eficacia, asíntota superior bien definida y/o curva de dosis-respuesta bien definida presentados por células de la misma línea celular clonal establecida pero de un pasaje o pasajes anteriores, donde se usan las mismas condiciones de ensayo y la misma BoNT/A (o molécula) en ambos ensayos.

Las células de una línea celular establecida descrita en la presente memoria descriptiva pueden presentar sensibilidad consistente con la actividad de la BoNT/A para una pluralidad de pasajes celulares. Tal como se usa en la presente, el término "sensibilidad a la actividad de la BoNT/A" se refiere a la dosis más baja que un ensayo puede medir consistentemente por encima de la señal detectada por una señal de referencia o de fondo que no es de tratamiento.

Por lo tanto, en una modalidad, las células de una línea celular clonal establecida presentan una sensibilidad a la actividad de la BoNT/A para cualquier número de pasajes dados que tengan por ej., 100 pM o menos, alrededor de 80 pM o menos, alrededor de 70 pM o menos, alrededor de 60 pM o menos, alrededor de 50 pM o menos, alrededor de 40 pM o menos, alrededor de 30 pM o menos, alrededor de 20 pM o menos, alrededor de 10 pM o menos, alrededor de 1 pM o menos, alrededor de 0.9 pM o menos, alrededor de 0.8 pM o menos, alrededor de 0.7 pM o menos, alrededor de 0.6 pM o menos, alrededor de 0.5 pM o menos, alrededor de 0.4 pM o menos, alrededor de 0.3 pM o menos, alrededor de 0.2 pM o menos o alrededor de 0.1 pM o menos de una BoNT/A. En aspectos de esta modalidad, las células de una línea celular clonal establecida presentan una sensibilidad a la actividad de la BoNT/A para cualquier número de pasajes dados, es decir, por

ejemplo, alrededor de 0.01 pM a alrededor de 100 pM, alrededor de 0.01 pM a alrededor de 75 pM, alrededor de 0.01 pM alrededor de 50 pM, alrededor de 0.01 pM a alrededor de 25 pM, alrededor de 0.01 pM a alrededor de 20 pM, alrededor de 0.01 pM a alrededor de 15 pM, alrededor de 0.01 pM a alrededor de 10 pM, alrededor de 0.01 pM a alrededor de 5 pM, alrededor de 0.001 pM a alrededor de 100 pM, alrededor de 0.001 pM a alrededor de 75 pM, alrededor de 0.001 pM a alrededor de 50 pM, alrededor de 0.001 pM a alrededor de 25 pM, alrededor de 0.001 pM a alrededor de 20 pM, alrededor de 0.001 pM a alrededor de 15 pM, alrededor de 0.001 pM a alrededor de 10 pM o alrededor de 0.001 pM a alrededor de 5 pM de BoNT/A.

En otra modalidad, las células de una línea celular clonal establecida presentan una sensibilidad a la actividad de la BoNT/A que es de alrededor de 100 pM o menos, alrededor de 75 pM o menos, alrededor de 50 pM o menos, alrededor de 25 pM o menos, alrededor de 20 o menos, alrededor de 15 pM o menos, alrededor de 10 pM o menos o alrededor de 1 pM o menos para, por ej., 5 o más pasajes celulares, 10 o más pasajes celulares, 15 o más pasajes celulares, 20 o más pasajes celulares, 25 o más pasajes celulares, 30 o más pasajes celulares, 35 o más pasajes celulares, 40 o más pasajes celulares, 45 o más pasajes celulares o 50 o más pasajes

celulares. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida presentan una sensibilidad a la actividad de la BoNT/A que es de alrededor de 100 pM o menos, alrededor de 75 pM o menos, alrededor de 50 pM o menos, alrededor de 25 pM o menos, alrededor de 20 pM o menos, alrededor de 15 pM o menos, alrededor de 10 pM o menos o alrededor de 1 pM o menos para, por ej., alrededor de 15 a alrededor de 60 pasajes, alrededor de 20 a alrededor de 60 pasajes, alrededor de 25 a alrededor de 60 pasajes, alrededor de 30 a alrededor de 60 pasajes, alrededor de 35 a alrededor de 60 pasajes, alrededor de 40 a alrededor de 60 pasajes, alrededor de 45 a alrededor de 60 pasajes, alrededor de 50 a alrededor de 60 pasajes, alrededor de 15 a alrededor de 50 pasajes, alrededor de 20 a alrededor de 50 pasajes, alrededor de 25 a alrededor de 50 pasajes, alrededor de 30 a alrededor de 50 pasajes, alrededor de 35 a alrededor de 50 pasajes, alrededor de 40 a alrededor de 50 pasajes, alrededor de 15 a alrededor de 40 pasajes, alrededor de 20 a alrededor de 40 pasajes, alrededor de 25 a alrededor de 40 pasajes, o alrededor de 30 a alrededor de 40 pasajes.

Las células de una línea celular establecida descrita en la presente memoria descriptiva pueden presentar una eficacia relativa consistente de absorción de BoNT/A, actividad de la BoNT/A o intoxicación por BoNT/A tras una

pluralidad de pasajes celular. Tal como se usa en la presente, el término "eficacia relativa" se refiere a cuán bien la asíntota superior para la actividad de la BoNT/A detectada en el presente ensayo se ejecuta en comparación con la asíntota superior para la actividad detectada de la BoNT/A en un estándar de referencia, una molécula de referencia o un número de pasajes de referencia usados en ese ensayo. Tal como se usa en la presente, el término "proporción de señal a ruido para la asíntota superior" se refiere a la señal detectada en un ensayo en el límite superior de detección dividida por la señal detectada por una señal de referencia o de fondo que no es de tratamiento. El límite superior de detección es la dosis más alta que un ensayo puede medir de forma consistente antes de que ocurra la saturación de la señal.

Por lo tanto, en una modalidad, las células de una línea celular establecida descrita en la presente memoria descriptiva pueden presentar una asíntota superior bien definida en una pluralidad de pasajes celulares y mantener una proporción de señal a ruido consistente y adecuada para el ensayo. En aspectos de esta modalidad, las células de una línea celular establecida descritas en la presente memoria descriptiva tienen que tener una proporción de señal a ruido para la asíntota superior para la actividad de la BoNT/A de,

por ej., al menos 3:1, al menos 4:1, al menos 5:1, al menos 6:1, al menos 7:1, al menos 8:1, al menos 9:1, al menos 10:1, al menos 15:1, al menos 20:1, al menos 25:1, al menos 30:1, al menos 35:1, al menos 40:1, al menos 45:1, al menos 50:1, al menos 60:1, al menos 70:1, al menos 80:1, al menos 90:1 o al menos 100:1, al menos 150:1, al menos 200:1, al menos 250:1, al menos 300:1, al menos 350:1, al menos 400:1, al menos 450:1, al menos 500:1, al menos 550:1 o al menos 600:1, en, por ej., 5 o más pasajes celulares, 10 o más pasajes celulares, 15 o más pasajes celulares, 20 o más pasajes celulares, 25 o más pasajes celulares, 30 o más pasajes celulares, 35 o más pasajes celulares, 40 o más pasajes celulares, 45 o más pasajes celulares o 50 o más pasajes celulares. En otros aspectos de esta modalidad, las células de una línea celular establecida descrita en la presente memoria descriptiva tienen que tener una proporción de señal a ruido para la asíntota superior para la actividad de la BoNT/A de, por ej., al menos 3:1, al menos 4:1, al menos 5:1, al menos 6:1, al menos 7:1, al menos 8:1, al menos 9:1, al menos 10:1, al menos 15:1, al menos 20:1, al menos 25:1, al menos 30:1, al menos 35:1, al menos 40:1, al menos 45:1, al menos 50:1, al menos 60:1, al menos 70:1, al menos 80:1, al menos 90:1 o al menos 100:1, al menos 150:1, al menos 200:1, al menos 250:1, al menos 300:1, al menos 350:1, al menos 400:1, al menos 450:1, al menos 500:1, al menos 550:1 o al

menos 600:1, en, por ej., alrededor de 15 a alrededor de 60 pasajes, alrededor de 20 a alrededor de 60 pasajes, alrededor de 25 a alrededor de 60 pasajes, alrededor de 30 a alrededor de 60 pasajes, alrededor de 35 a alrededor de 60 pasajes, alrededor de 40 a alrededor de 60 pasajes, alrededor de 45 a alrededor de 60 pasajes, alrededor de 50 a alrededor de 60 pasajes, alrededor de 15 a alrededor de 50 pasajes, alrededor de 20 a alrededor de 50 pasajes, alrededor de 25 a alrededor de 50 pasajes, alrededor de 30 a alrededor de 50 pasajes, alrededor de 35 a alrededor de 50 pasajes, alrededor de 40 a alrededor de 50 pasajes, alrededor de 15 a alrededor de 40 pasajes, alrededor de 20 a alrededor de 40 pasajes, alrededor de 25 a alrededor de 40 pasajes o alrededor de 30 a alrededor de 40 pasajes.

Las células de una línea celular establecida descrita en la presente memoria descriptiva pueden presentar una curva de dosis-respuesta bien definida para la actividad de la BoNT/A en una pluralidad de pasajes celulares. Tal como se usa en la presente, el término "curva de dosis-respuesta" se refiere a cuán bien los datos sin procesar se ajustan al modelo estadístico de elección para ese ensayo. Como un ejemplo no taxativo, una curva sigmoidal con un ajuste logístico de cuatro parámetros es una curva de dosis-respuesta para un ensayo de actividad enzimática tal como,

por ej., un ensayo de potencia. Como otro ejemplo no taxativo, un ligando que se une a un ajuste de saturación de sitio es una curva de dosis-respuesta para un ensayo de unión ligando/anticuerpo.

Por lo tanto, en una modalidad, las células de una línea celular establecida descritas en la presente memoria descriptiva presentan una curva de dosis-respuesta bien definida para la actividad de la BoNT/A en una pluralidad de pasajes celulares. En aspectos de esta modalidad, las células de una línea celular establecida descrita en la presente memoria descriptiva presentan una curva de dosis-respuesta bien definida para la actividad de la BoNT/A en, por ej., 5 o más pasajes celulares, 10 o más pasajes celulares, 15 o más pasajes celulares, 20 o más pasajes celulares, 25 o más pasajes celular, 30 o más pasajes celulares, 35 o más pasajes celulares, 40 o más pasajes celulares, 45 o más pasajes celulares o 50 o más pasajes celulares. En otros aspectos de esta modalidad, las células de una línea celular establecida descrita en la presente memoria descriptiva presentan una curva de dosis-respuesta bien definida para la actividad de la BoNT/A en, por ej., alrededor de 15 a alrededor de 60 pasajes, alrededor de 20 a alrededor de 60 pasajes, alrededor de 25 a alrededor de 60 pasajes, alrededor de 30 a alrededor de 60 pasajes, alrededor de 35 a alrededor de 60 pasajes,

alrededor de 40 a alrededor de 60 pasajes, alrededor de 45 a alrededor de 60 pasajes, alrededor de 50 a alrededor de 60 pasajes, alrededor de 15 a alrededor de 50 pasajes, alrededor de 20 a alrededor de 50 pasajes, alrededor de 25 a alrededor de 50 pasajes, alrededor de 30 a alrededor de 50 pasajes, alrededor de 35 a alrededor de 50 pasajes, alrededor de 40 a alrededor de 50 pasajes, alrededor de 15 a alrededor de 40 pasajes, alrededor de 20 a alrededor de 40 pasajes, alrededor de 25 a alrededor de 40 pasajes o alrededor de 30 a alrededor de 40 pasajes.

Las células de una línea celular establecida descrita en la presente memoria descriptiva pueden presentar un valor de EC_{50} relativa constante para la actividad de la BoNT/A en una pluralidad de pasajes celulares. Tal como se usa en la presente, el término "EC_{50} relativa" o "valor de EC_{50} relativa" se refiere a un valor de EC_{50} de actividad de la BoNT/A que se normaliza en comparación con la EC_{50} calculada para un estándar de referencia, una molécula de referencia o un número de pasajes de referencia usados en ese ensayo.

Por lo tanto, en una modalidad, las células de una línea celular clonal establecida presentan una EC_{50} relativa para la actividad de la BoNT/A en una pluralidad de pasajes celulares. En aspectos de esta modalidad, las células de una

línea celular clonal establecida presentan una EC_{50} relativa consistente para la actividad de la BoNT/A que es, por ej., alrededor de ± 10%, alrededor de ± 20%, alrededor de ± 30%, alrededor de ± 40%, alrededor de ± 50%, alrededor de 60%, alrededor de 70% o alrededor de ± 75%, la EC_{50} relativa para la actividad de la BoNT/A en, por ej., 5 o más pasajes celulares, 10 o más pasajes celulares, 15 o más pasajes celulares, 20 o más pasajes celulares, 25 o más pasajes celulares, 30 o más pasajes celulares, 35 o más pasajes celulares, 40 o más pasajes celulares, 45 o más pasajes celulares o 50 o más pasajes celulares. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida presentan una EC_{50} relativa para la actividad de la BoNT/A que es, por ej., de alrededor de ± 10% a alrededor de 75%, de alrededor de ± 10% a alrededor de 70%, de alrededor de ± 10% a alrededor de 60%, de alrededor de ± 10% a alrededor de 50%, de alrededor de ± 10% a alrededor de 40%, de alrededor de ± 10% a alrededor de 30% o de alrededor de ± 10% a alrededor de 20% de la EC_{50} relativa para la actividad de la BoNT/A en, por ej., 5 o más pasajes celulares, 10 o más pasajes celulares, 15 o más pasajes celulares, 20 o más pasajes celulares, 25 o más pasajes celulares, 30 o más pasajes celulares, 35 o más pasajes celulares, 40 o más pasajes celulares, 45 o más pasajes celulares o 50 o más pasajes celulares.

Los aspectos de la presente descripción comprenden, en parte, células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A que presentan al menos una diferencia de 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 5, 6, 7 u 8 en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptible de intoxicación por BoNT/A presentan una diferencia en los niveles de expresión genética de uno o más genes enumerados en las Tablas 5, 6, 7 u 8 de, por ej., al menos 1.5 veces, al menos 2.0 veces, al menos 2.5 veces, al menos 3.0 veces, al menos 3.5 veces, al menos 4.0 veces, al menos 4.5 veces, al menos 5.0 veces, al menos 5.5 veces, al menos 6.0 veces, al menos 7.0 veces o al menos 8.0 veces en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una diferencia en los niveles de expresión genética de, por ej., 2 o más genes, 3 o más genes, 4 o más genes, 5 o más genes, 6 o más genes, 7 o más genes, 8 o más genes, 9 o más genes, 10 o más genes, 20 o más genes, 30 o más genes, 40 o más genes, 50 o más genes, 60 o más genes, 70 o más genes, 80 o más genes, 90 o más genes o 100 o más genes enumerados en

las Tablas 5, 6, 7 u 8 en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6. En aun otros aspectos, las células de una línea celular clonal establecida susceptibles de intoxicación por BoTN/A presentan una diferencia en los niveles de expresión genética de, por ej., alrededor de 5 genes a alrededor de 100 genes, alrededor de 10 genes a alrededor de 100 genes, alrededor de 15 genes a alrededor de 100 genes, alrededor de 20 genes a alrededor de 100 genes, alrededor de 25 genes a alrededor de 100 genes, alrededor de 5 genes a alrededor de 75 genes, alrededor de 10 genes a alrededor de 75 genes, alrededor de 15 genes a alrededor de 75 genes, alrededor de 20 genes a alrededor de 75 genes, alrededor de 25 genes a alrededor de 75 genes, alrededor de 5 genes a alrededor de 50 genes, alrededor de 10 genes a alrededor de 50 genes, alrededor de 15 genes a alrededor de 50 genes, alrededor de 20 genes a alrededor de 50 genes o alrededor de 25 genes a alrededor de 50 genes enumerados en las Tablas 5, 6, 7 u 8 en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6. La proporción logarítmica en las Tablas 5, 6, 7 y 8 representan valores $\log_2$ donde 0.585 es $\log_2(1.5)$ que es una diferencia de 1.5 veces, 1 es $\log_2(2)$ que es una diferencia de 2 veces, 1.584 es $\log_2(3)$ que es una diferencia de 3 veces, 2 es $\log_2(4)$ que es una diferencia de 4 veces, 2.321 es $\log_2(5)$ que es una diferencia de 5 veces, 2.584 es

$\log_2(6)$ que es una diferencia de 6 veces, 2.807 es $\log_2(7)$ que es una diferencia de 7 veces, 3 es $\log_2(8)$ que es una diferencia de 8 veces, 3.169 es $\log_2(9)$ que es una diferencia de 9 veces y 3.321 es $\log_2(10)$ que es una diferencia de 10 veces.

En una modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 5 o 7 en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En aspectos de esta modalidad, las células de una línea celular clonal establecida susceptible de intoxicación por BoNT/A presentan un aumento en los niveles de expresión genética de uno o más genes enumerados en las Tablas 5 o 7 de, por ej., al menos 2.0 veces, al menos 2.5 veces, al menos 3.0 veces, al menos 3.5 veces, al menos 4.0 veces, al menos 4.5 veces, al menos 5.0 veces, al menos 5.5 veces, al menos 6.0 veces, al menos 7.0 veces o al menos 8.0 veces en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento en los niveles de expresión genética de, por ej., 2 o más genes, 3 o más genes, 4 o más

genes, 5 o más genes, 6 o más genes, 7 o más genes, 8 o más genes, 9 o más genes, 10 o más genes, 20 o más genes, 30 o más genes, 40 o más genes, 50 o más genes, 60 o más genes, 70 o más genes, 80 o más genes, 90 o más genes o 100 o más genes enumerados en las Tablas 5 o 7 en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6. En aun otros aspectos, las células de una línea celular clonal establecida susceptibles de intoxicación por BoTN/A presentan un aumento en los niveles de expresión genética de, por ej., alrededor de 5 genes a alrededor de 100 genes, alrededor de 10 genes a alrededor de 100 genes, alrededor de 15 genes a alrededor de 100 genes, alrededor de 20 genes a alrededor de 100 genes, alrededor de 25 genes a alrededor de 100 genes, alrededor de 5 genes a alrededor de 75 genes, alrededor de 10 genes a alrededor de 75 genes, alrededor de 15 genes a alrededor de 75 genes, alrededor de 20 genes a alrededor de 75 genes, alrededor de 25 genes a alrededor de 75 genes, alrededor de 5 genes a alrededor de 50 genes, alrededor de 10 genes a alrededor de 50 genes, alrededor de 15 genes a alrededor de 50 genes, alrededor de 20 genes a alrededor de 50 genes o alrededor de 25 genes a alrededor de 50 genes enumerados en las Tablas 5 o 7 en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6.

En una modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de A2BP1, ACO1, ACOT7, ACOT9, ACTL6A, ACTL6B, ADRBK2, AGPS, AIDA, AKAP13, ALCAM, ALDH7A1, AMOTL1, ANAPC7, ANKRD13A, ANKRD54, ANKS1B, ANLN, ANP32E, ANXA6, APAF1, APBB2, APOO, ARF3, ARHGAP11A, ARHGAP24, ARHGAP24, ARHGAP6, ARHGEF3, ARHGEF6, ARL13B, ARL6, ARL6IP1, ASCL1, ASF1A, ASF1B, ASXL3, ATAD2, ATP6V1A, AURKA, AURKB, BARD1, BASP1, BAX, BCL11A, BCR, BNC2, BOK, BRCA1, BRCA2, BRD4, BRI3BP, BRIP1, BTBD3, BTG3, BUB1, BUB1B, BUB3, BVES, C10ORF58, C10ORF78, C11ORF75, C12ORF48, C12ORF49, C14ORF106, C14ORF143, C15ORF23, C15ORF42, C18ORF54, C1ORF112, C1ORF183, C1ORF43, C1QL1, C20ORF108, C20ORF20, C20ORF7, C20ORF72, C22ORF28, C22ORF29, C22ORF39, C3ORF14, C3ORF70, C4ORF46, C4ORF49, C5ORF32, C6ORF115, C9ORF100, CARHSP1, CBLB, CBWD1, CBX5, CCDC109B, CCDC117, CCDC15, CCDC21, CCDC3, CCDC34, CCDC52, CCDC86, CCDC99, CCNB1, CCNE2, CCNF, CCNYL1, CD24, CD47, CD9, CDC2, CDC25B, CDC42EP4, CDC45L, CDC5L, CDC6, CDCA2, CDCA4, CDCA5, CDCA7, CDCA8, CDH2, CDK2, CDK2AP1, CDK6, CDKAL1, CDKN2C, CDKN2D, CDO1, CDS2, CECR5, CELSR3, CENPF, CENPH), CENPI, CENPJ, CENPK, CENPL, CENPM, CENPN, CENPO, CEP135, CEP152, CEP55, CEP78, CEP97, CHAF1A, CHD6, CHEK1, CHEK2, CHMP4B, CHRNA3, CHRNA7, CHST15, CIT, CKAP2, CKAP2L, CKLF, CKS1B, CLDND1, CLSTN2, CMTM7, CNN3,

CNOT4, CNP, CNTN1, CNTN4, COBLL1, COQ3, CPNE4, CPT1A, CPVL, CRISPLD1, CRTAC1, CRYBG3, CRYZ, CSE1L, CSRP2, CSRP2BP, CSTF1, CTDSPL2, CTNNBL1, CTSL2, CUGBP2, CXCR4, CYTSA, DACT1, DAZ1, DBF4B, DBH, DCLRE1B, DCPS, DDAH2, DDT, DEK, DENR, DEPDC1, DEPDC1B, DERA, DGCR14, DGKE, DHX15, DHX35, DIAPH1, DIAPH3, DKFZP434L187, DLEU2, DLGAP5, DLL3, DLX6, DNA2, DNM3, DNMT3B, DOCK10, DOK4, DOK5, DPF1, DPYD, DPYSL3, DRAM1, DRG1, DSCC1, DSN1, DTL, DTNBP1, DTYMK, DVL2, DYNLT3, DYRK4, E2F1, E2F2, E2F7, E2F8, EAF2, EBF1, ECT2, EFNA5, EFNB2, ELAVL4, ELOVL7, EME1, EMILIN2, EMILIN3, EML1, ENC1, EPB41L5, EPOR, ERCC6L, ESCO2, ESF1, ESPL1, ETS1, ETV1, EXO1, EXOC5, EXOSC6, EXPH5, EZH2, FAM101B, FAM105A, FAM110A, FAM114A1, FAM118A, FAM120C, FAM129B, FAM13A, FAM162B, FAM181B, FAM19A4, FAM19A5, FAM54A, FAM64A, FAM7A3, FAM83D, FANCG, FANCI, FANCL, FANCM, FARP1, FAT1, FBLN1, FBN1, FBP1, FBXO43, FBXO5, FEN1, FGFR2, FH, FIGNL1, FKBP5, FNDC5, FOXD1, FOXN3, FRMD6, FRZB, FSTL1, FZD2, FZD5, FZD8, G2E3, GABBR2, GAP43, GAP43, GAS2L3, GATM, GEMIN4, GFPT2, GFRA1, GFRA2, GGCX, GINS1, GINS3, GJC1, GLDC, GMNN, GNAI1, GNASAS, GNB4, GNG11, GNG12, GNG4, GPAM, GPN3, GPR125, GPR161, GPSM2, GPX3, GRP, GSG2, GSS, GSTCD, GTSE1, GTSF1, GXYLT1, H1F0, H2AFX, HAT1, HAUS6, HDAC8, HEG1, HES6, HGF, HIC2, HMG4L, HMGB1, HMGB2, HMGB3, HMGXB4, HMMR, HOOK3, HPS4, HRH3, HS3ST2, HS6ST2, HSPB11, HTATSF1, IDH2, IFI27L1, IQGAP1, ITGA6, ITGAV, ITGB5, ITPRIP, JARID2, KCNG3, KCNJ8, KCNN1, KCTD12, KDELC2, KHDRBS3, KIAA0101, KIAA0406, KIAA1211,

KIAA1524, KIF11, KIF14, KIF16B, KIF18A, KIF23, KIFC1, KLF7, KLHL13, KLHL5, KNTC1, KPNA2, LBH, LGR5, LHFPL2, LIFR, LIG3, LMF2, LMNB1, LOC100127983, LOC100128844, LOC100288551, LOC340109, LOC344595, LOC440288, LOC642597, LOC728052, LPAR1, LRFN2, LRRC1, LSM4, LUM, MAB21L1, MAB21L2, MAGEH1, MAN1A1, MAN2A1, MAOA, MAP3K13, MAPK11, MAPK12, MAPKAPK3, MASTL, MBD2, MCAM, MCM10, MCM3, MCM4, MCM5, MCM6, MCM7, MCM8, MDC1, MDM1, MED20, MEIS1, MEIS2, MELK, MEST, MFAP2, MGAT5B, MINA, MKI67, MKL1, MLF1IP, MMD, MNS1, MPHOSPH9, MPP5, MPPED2, MRC2, MRPL35, MRPL49, MRS2, MSN, MTF2, MTHFD1, MTUS1, MVK, MYBL1, MYBL2, MYD88, MYO1B, MYO6, MYST1, NAAA, NAGA, NANP, NARG1, NASP, NAT11, NAT13, NCAPD3, NCAPG, NCAPG2, NCAPH, NCAPH2, NDN, NEDD1, NEDD9, NEIL3, NELL2, NFIB, NOC4L, NOS1, NR3C1, NRG3, NRM, NRXN1, NSMCE4A, NTAN1, NUCKS1, NUDT1, NUF2, NUP107, NUP37, NUP43, NUP50, NUP93, NUSAP1, NXPH1, NXT2, ODZ3, ODZ4, OIP5, ORC1L, ORC6L, OSBPL3, PAICS, PANK2, PARP3, PASK, PBK, PCDH17, PCDH8, PCGF5, PCNA, PDCL, PDE5A, PDLIM5, PDRG1, PEG3, PELI2, PELO, PEX13, PEX26, PFKFB3, PGAM5, PGM2, PHF19, PHF20, PHF21B, PHF5A, PHLPP1, PHYHIPL, PI4KA, PIP4K2A, PIR, PKMYT1, PLCL2, PLD5, PLEKHF2, PLK2, PLK4, PLS3, PLXNA2, PLXNA4, PLXNB2, PM20D2, POLA1, POLA2, POLE, POLE2, POLQ, POSTN, PPAP2B, PPAT, PPIF, PPIL5, PPM1F, PPP1R13B, PPP1R3C, PPP2R2B, PPP3CB, PRIM1, PRIM2, PRLHR, PRPS1, PRSS12, PSMA7, PSMC3IP, PSMD5, PSMD9, PSRC1, PTER, PTGES2, PTGFRN, PTGR1, PTPRE, PTPRG, PTPRK, PTPRM, PTTG1, PVRL3, PXMP4, PXN, RAB35,

RAB3B, RAD18, RAD51, RAD51C, RALY, RAN, RANBP1, RANGAP1, RASEF, RBBP7, RBBP9, RBL1, RBPMS, RBX1, RECQL4, REEP1, RELB, RELL1, REXO2, RFC1, RFC2, RFC3, RFC4, RFC5, RGMA, RGS5, RILPL2, RIMBP2, RMI1, RNASEH2A, RNF182, RNF26, RNF34, RPA1, RPP30, RRM1, RRM2, RRP7A, RSRC1, S1PR3, SALL4, SAP30, SASS6, SBF2, SCD5, SCML1, SCML2, SDC1, SEC23A, SEC61A2, SELM, SEMA6A, SEMA6D, SESN3, SEZ6L, SFI1, SFRP1, SGOL2, SH3D19, SHCBP1, SHMT1, SHOX2, SIM1, SIVA1, SKA1, SKA2, SKA3, SKP2, SLC25A10, SLC26A2, SLC2A4RG, SLC2A8, SLC43A3, SLC44A5, SLC7A2, SLC8A1, SLCO3A1, SLIT3, SLITRK5, SLK, SLMO2, SMC1A, SMC2, SMC4, SMC6, SMO, SMYD5, SNAI2, SNAP29, SNCAIP, SNRPD3, SNX18, SNX5, SORD, SOX4, SPAG6, SPARC, SPATS2L, SPC24, SPC25, SPOCK1, SPSB4, SRGAP1, SRRD, SRRM4, SSH2, ST8SIA1, ST8SIA2, ST8SIA4, STARD4, STIL, STK17A, STMN3, STOM, STON2, STRA6, SUSD5, SUV39H1, SVIP, SYN2, SYNE2, SYNM, SYT17, SYTL4, TBC1D1, TBX3, TCF19, TCF7L2, TCFL5, TDRKH, TEAD3, TESC, TFDP1, TFDP2, TFPI2, TH1L, THOC4, TIFA, TIMP3, TLE3, TLE4, TMCC3, TMEM107, TMEM132C, TMEM151B, TMEM170B, TMEM178, TMEM194A, TMEM38B, TMEM48, TMEM56, TMEM98, TMPO, TMSB15B, TNFAIP8, TOB2, TOMM34, TPBG, TPTE, TPX2, TRIM29, TRIM36, TRIM68, TRIM9, TRIP13, TROAP, TSHZ3, TSPAN14, TSPAN4, TSPAN5, TTC28, TTC9, TUBA1B, TUBB, TWIST1, TXNRD1, TYMS, TYRO3, UBE2C, UBE2L3, UBE2V1, UBE3B, UCK1, UCP2, UFD1L, UHRF1, UNC119B, UNG, UQCC, USP1, USP48, UTP18, VAPB, VAV3, VPS29, VSTM2L, WDHD1, WDR51A, WDR53, WDR62, WDR67, WEE1, WEE1,

WHSC1, WRAP53, WWC3, XRCC4, XRCC6, ZAK, ZFHX4, ZFP82, ZGPAT, ZNF215, ZNF217, ZNF238, ZNF253, ZNF280B, ZNF367, ZNF43, ZNF443, ZNF503, ZNF521, ZNF560, ZNF608, ZNF626, ZNF681, ZNF71, ZNF823, ZNF85, ZNF92, ZNF93 y/o ZWINT, en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6.

En un aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 en los niveles de expresión genética de uno o más genes seleccionados de A2BP1, ACOT9, ALCAM, ANLN, ARHGAP24, ARHGAP6, ARHGEF3, ARHGEF6, ASCL1, ASF1B, ATAD2, AURKA, AURKB, BARD1, BASP1, BNC2, BRCA2, BRIP1, BTG3, BUB1, BUB1B, BVES, C11ORF75, C12ORF48, C14ORF106, C15ORF42, C18ORF54, C1ORF112, C3ORF70, C4ORF49, CCDC109B, CCDC3, CCNB1, CCNE2, CD9, CDC2, CDC25B, CDC45L, CDC6, CDCA2, CDCA5, CDCA8, CDK2, CDKN2D, CENPF, CENPI, CENPL, CENPN, CEP55, CHEK1, CHEK2, CHRNA7, CIT, CKAP2L, CLSTN2, CNTN1, CNTN4, CPVL, CRYBG3, CSRP2, CTSL2, CUGBP2, CXCR4, DAZ1, DEPDC1, DEPDC1B, DIAPH3, DLGAP5, DNA2, DOK5, DPYD, DPYSL3, DSCC1, DSN1, DTL, DYNLT3, E2F1, E2F2, E2F7, E2F8, ECT2, EFNB2, ELOVL7, EME1, EMILIN2, EMILIN3, EML1, ENC1, ERCC6L, ESCO2, ESPL1, ETV1, EXO1, EXPH5, FAM101B, FAM114A1, FAM54A, FAM64A, FAM7A3, FAM83D, FANCI, FAT1, FBLN1, FBP1, FBXO43, FGFR2, FNDC5, FOXD1, FRMD6, FRZB, FZD5, GAS2L3,

GFRA2, GINS1, GINS3, GNAI1, GNB4, GNG11, GNG12, GPSM2, GRP, GTSE1, GTSF1, HGF, HMMR, HS3ST2, ITGA6, ITPRIP, KCNG3, KCTD12, KDELC2, KIAA0101, KIAA1524, KIF11, KIF14, KIF18A, KIF23, KIFC1, LOC340109, LOC642597, LOC728052, LOC728052, LPAR1, LUM, MAB21L1, MAB21L2, MAOA, MCM10, MCM5, MELK, MINA, MKI67, MLF1IP, MPPED2, MRC2, MSN, MYBL1, MYBL2, MYO6, NCAPG, NCAPH, NDN, NEDD9, NEIL3, NR3C1, NRXN1, NUF2, NUSAP1, OIP5, ORC1L, OSBPL3, PBK, PCGF5, PDE5A, PEG3, PELO, PFKFB3, PHLPP1, PLD5, PLK2, PLK4, PLS3, POLA2, POLE2, POLQ, PPAP2B, PPP1R3C, PRLHR, PRSS12, PSRC1, PTGR1, PTPRE, PTPRK, PTPRM, PTTG1, PVRL3, RAD51, RBL1, RBPMS, RELL1, RFC5, RGMA, RGS5, RNF182, RRM2, S1PR3, SGOL2, SHCBP1, SHOX2, SIM1, SKA1, SLC43A3, SLC44A5, SLC7A2, SLITRK5, SMC2, SMC6, SPAG6, SPARC, SPC24, SPC25, ST8SIA4, STK17A, SUSD5, SYN2, SYNM, SYT17, TCF19, TESC, TFDP2, TFPI2, TIMP3, TLE3, TMEM132C, TMEM178, TNFAIP8, TPBG, TPTE, TPX2, TRIM29, TRIM36, TRIM68, TROAP, TWIST1, TYMS, UBE2C, UBE3B, UHRF1, WDHD1, WDR51A, WDR67, WEE1, ZFP82, ZNF367, ZNF521 y/o ZWINT, en comparación con los niveles de expresión de estos genes en células de línea celular 2D6.

En otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de A2BP1, ALCAM, ANLN, ARHGAP24, ARHGAP6,

ASCL1, ASF1B, ATAD2, AURKA, AURKB, BARD1, BASP1, BNC2, BRIP1, BUB1, BVES, C11ORF75, C12ORF48, C14ORF106, C18ORF54, C3ORF70, CCDC109B, CCDC3, CD9, CDC2, CDC45L, CDCA2, CDCA8, CDK2, CENPL, CEP55, CHEK2, CHRNA7, CKAP2L, CNTN1, CRYBG3, CUGBP2, CXCR4, DAZ1, DEPDC1, DIAPH3, DLGAP5, DOK5, DPYD, DTL, DYNLT3, E2F1, E2F7, E2F8, EFNB2, ELOVL7, EMILIN2, EML1, ENC1, ESPL1, ETV1, EXO1, EXPH5, FAM54A, FAM64A, FAM7A3, FAM83D, FANCI, FAT1, FBLN1, FBXO43, FGFR2, FZD5, GNAI1, GNB4, GNG11, GNG12, GPSM2, GRP, GTSE1, GTSF1, HGF, HMMR, ITGA6, ITPRIP, KCTD12, KDELC2, KIF11, KIF14, KIF18A, KIF23, KIFC1, LOC340109, LOC728052, LPAR1, LUM, MAB21L1, MAB21L2, MAOA, MCM10, MELK, MINA, MKI67, MSN, MYBL1, NCAPH, NDN, NEDD9, NEIL3, NRXN1, NUF2, NUSAP1, OIP5, ORC1L, OSBPL3, PBK, PCGF5, PEG3, PEG3, PHLPP1, PLD5, PLK2, PLK4, PLS3, POLE2, PPAP2B, PPP1R3C, PRLHR, PRSS12, PTPRE, PTPRK, PTPRM, RBPMS, RELL1, RGS5, RNF182, RRM2, S1PR3, SGOL2, SHCBP1, SHOX2, SIM1, SLC43A3, SLC44A5, SLC7A2, SLITRK5, SMC6, SPAG6, SPARC, SPC24, SPC25, ST8SIA4, STK17A, SYT17, TFPI2, TIMP3, TMEM132C, TMEM178, TPBG, TPTE, TPX2, TRIM36, TWIST1, UBE3B y/o ZNF367, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6.

En aun otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5

veces en los niveles de expresión genética de uno o más genes seleccionados de A2BP1, ARHGAP24, ARHGAP6, ASCL1, ASF1B, ATAD2, AURKA, BARD1, BASP1, BNC2, BUB1, BVES, C11ORF75, CCDC3, CHEK2, CHRNA7, CKAP2L, CNTN1, CRYBG3, CUGBP2, CUGBP2, CXCR4, DAZ1, DEPDC1, DIAPH3, DLGAP5, DOK5, DPYD, DTL, DYNLT3, E2F8, EFNB2, ELOVL7, ENC1, EXPH5, FAM7A3, FANCI, FAT1, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, GRP, GTSE1, GTSF1, HMMR, ITGA6, ITPRIP, KCTD12, KDELC2, LOC728052, LPAR1, LUM, MAB21L1, MAB21L2, MAOA, MCM10, MELK, MINA, MKI67, MSN, MYBL1, NDN, NEDD9, NRXN1, OSBPL3, PEG3, PLK2, PLS3, PRLHR, PRSS12, PTPRK, PTPRM, RBPMS, RGS5, RNF182, RRM2, SGOL2, SIM1, SLC43A3, SLC44A5, SLC7A2, SMC6, SPAG6, SPARC, STK17A, TFPI2, TIMP3, TMEM132C, TMEM178 y/o TPTE, en comparación con los niveles de expresión de los genes en las células de la línea celular 2D6.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presenta un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ADAMTS9, ATAD2, C11ORF82, CDC45L, CNTN1, CNTN4, Ciclina A, Ciclina E, E2F1, E2F2, E2F7, ELOVL7, EME1, FGFR, FGFR2, KIAA1524, MELK, MYBL1, MYBL2, NDC80, NDN, ORC1L, PLS3, PRIMA1, RAD54L, RBL1, RBPMS, RRM2, S1PR3, SCLY, SLCIA3, SPC24, SPC25, ST8SIA4, TFDP1, TFP12, TK1, TMEM35, TTK,

TWIST1, TYMS, TYK y/o ZWINT, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6.

En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de AURKB, BIRC5, BRCA1, BRCA2, BRIP1,BUB1B, CD9, DLGAP3, DYNLT3, ENC1, FBLN1, FOXM1, Gβγ, GNAI1, GNG11, GNG12, GPSM2, GUCY1B3, HGF, ITGA6, JNK, KCNJ5, KIF18A, KITLG, MMD, MSN, MYRIP, NEK2, NR3C1, NXPH1, OSBPL3, PKMYT1, PTPRM, RAD51, RAD51AP1, SLC7A2, SLC43A3, SMC6, SNAI2, SNCAIP, SSH2, STK17A, SYNPO2, TOP2A, TPTE, TRAF4, TSPAN, TSPAN4, UBE3, UBE3B, y/o VAV3, en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6. En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1,5 veces en los niveles de expresión genética de uno o más genes seleccionados de ALCAM, AURKA, CHEK, CIT, CSRP2, E2F, ECT2, EFNB2, ERK, ESPL1, GNAI, GPR161, HMMR, KIF4A, KIF14, KIF15, KIF22, KIF23, KIFC1, LPAR1, MK167, OIP5, PHLPP, PP1/PP2A, PPP1R3C, PRC1, PTTG1, RACGAP, RB, RGS5, SDC2 y/o TPX2, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ASCL1, HES6, MAPK, NMU, PEG3, PTPRK, PRLHR, PTPRK, SGOL2, SPARC y/o ZNF217, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ASF1B, BASP1, CHAF1A, NCAPH, PBK, PRAME, SMC2, UHRF1 y/o VRK1, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de C14ORF106, CEP72, KIF20A, PCNA, PEX13, PFC5, POLQ, SPAG5, SYTL4, TROAP y/o WDR51A, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En una modalidad adicional, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ANLN, ARHGAP24, ASPM, BUB1, CCDC99, CEP55,

CKAP2, DRAM, E2F8, PLXNA2, SLC16A10, UBE2C, UBE2S, y/o WDHD1, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ARHGEF3, CTSL2, DIAPH3, FBP1, KIF2C, KIF11, PFKFB3 y/o PLK4, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ARHGEF3, CTSL2, DIAPH3, FBP1, KIF2C, KIF11, PFKFB3 y/o PLK4, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de FNDC5, HSPC159, MAB21L2, SLITRK5, SYN2 y ZNF367, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En otra modalidad adicional, las células de una línea celular clonal establecida susceptibles de

intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de EXO1, KCTD12, MYO6, PHEBL1, SHCBP1, TPBG y/o TUBB6, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de BTG3, GABRA5, TR1P10 y/o ZNF521, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de BNC2, DPYD, EMILIN2, PPIL5 y/o TACC3, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una diferencia de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 14 o 16 en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En un aspecto

de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ACOT9, ADAMTS9, ARHGAP24, ARHGEF3, ASCL1, BARD1, BASP1, C3ORF70, C11ORF75, CCDC109B, CD9, CDCA7L, CDK2, CENPL, CLSTN2, CNTN1, CSRP2, CTSL2, CUGBP2, DEPDC1, DIAPH3, DOK5, DPYD, DYNLT3, EMILIN2, ETV1, FAM101B, FBLN1, FGFR2, FNDC5, GNAI1, GNB4, GNG11, GNG12, GPR177, GTSE1, HGF, KITLG, LPAR1, MAB21L2, MAOA, MCM10, MINA, MSN, MYO6, MYRIP, PAG1, PEG3, PLK2, POLA2, PPP1R3C, PRLHR, PRSS12, PTGR1, PTPRK, PVRL3, RAB32, RBPMS, SDC2, SGOL2, SLC43A3, SLC7A2, SMC2, SMC6, SPARC, SPC25, ST8SIA4, TCF7L1, TFPI2, TMEM35, TMEM178, TNFAIP8, TPTE, TRIP10, TWIST1 y/o ZNF521, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ADAMTS9, ARHGAP24, ASCL1, BARD1, BASP1, BVES, C11ORF75, CDCA7L, CNTN1, CUGBP2, DOK5, DPYD, DYNLT3, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, GTSE1, GTSF1, ITPRIP, KDELC2, LOC728052, LPAR1, MAB21L2, MAOA, MINA, MSN, PEG3, PLK2, PRLHR, PRSS12, PTPRK, RBPMS, RNF182, SGOL2, SLC43A3, SLC44A5, SLC7A2, SMC6, SPARC, TFPI2, TMEM178, y/o

TPTE, en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6. En aun otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ADAMTS9, ASCL1, BASP1, DOK5, DPYD, GNB4, GNG11, GTSF1, MAOA, MINA, MSN, PEG3, PLK2, PRSS12, RNF182, SLC44A5, SPARC, TFPI2 y/o TPTE, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6.

En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ADAMTS9, ARHGAP24, ARHGEF3, ASCL1, BARD1, CD9, CDK2, CSRP2, CTSL2, DIAPH3, DOK5, DYNLT3, EMILIN2, ETV1, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, HGF, KITLG, LPAR1, MCM10, MSN, PAG1, PEG3, PLK2, POLA2, PPP1R3C, PTPRK, RAB32, SDC2, SLC43A3, SLC7A2, SMC6, SPARC, SPC25, ST8SIA4, TCF7L1, TFPI2, TMEM35, TNFAIP8, TPTE, TRIP10 y/o TWIST1, en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6. En un aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos

1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ADAMTS9, ARHGAP24, ASCL1, BARD1, DOK5, DYNLT3, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, LPAR1, MSN, PEG3, PLK2, PTPRK, SLC43A3, SLC7A2, SMC6, SPARC, TFPI2 y/o TPTE, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En aun otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ADAMTS9, ASCL1, DOK5, GNB4, GNG11, MSN, PEG3, PLK2, SPARC, TFPI2 y/o TPTE, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6.

En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ACOT9, BASP1, C11ORF75, CCDC109B, CDCA7L, CLSTN2, CNTN1, CUGBP2, DEPDC1, DPYD, FAM101B, FNDC5, GTSE1, MAOA, MINA, MYO6, MYRIP, PLK2, PRLHR, PVRL3, RBPMS, SGOL2, SMC2, TFP12, TMEM178 y/o ZNF521, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En un aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan

un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de BASP1, C11ORF75, CDCA7L, CNTN1, CUGBP2, DPYD, GTSE1, MAOA, MINA, PLK2, PRLHR, RBPMS, SGOL2, TFPI2 y/o TMEM178, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de BASP1, DPYD, MAOA, MINA, PLK2 y/o TFPI2, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6.

En una modalidad adicional, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de C3ORF70, MAB21L2, PRSS12, CENPL, GPR177 y/o PTGR1, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En un aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de MAB21L2 y/o

PRSS12, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 6 u 8 en comparación con los niveles de expresión de estos genes en células de una línea celular 2D6. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptible de intoxicación por BoNT/A presentan una disminución en los niveles de expresión genética de uno o más genes enumerados en las Tablas 6 u 8 de, por ej., al menos 1.5 veces, al menos 2.0 veces, al menos 2.5 veces, al menos 3.0 veces, al menos 3.5 veces, al menos 4.0 veces, al menos 4.5 veces, al menos 5.0 veces, al menos 5.5 veces, al menos 6.0 veces, al menos 7.0 veces o al menos 8.0 veces en comparación con los niveles de expresión de estos genes en células de una línea celular 2D6. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución en los niveles de expresión genética de, por ej., 2 o más genes, 3 o más genes, 4 o más genes, 5 o más genes, 6 o más genes, 7 o más genes, 8 o más genes, 9 o más genes, 10 o más genes, 20 o más genes, 30 o

más genes, 40 o más genes, 50 o más genes, 60 o más genes, 70 o más genes, 80 o más genes, 90 o más genes o 100 o más genes enumerados en las Tablas 6 u 8 en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6. En aun otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoTN/A presentan una disminución en los niveles de expresión genética de, por ej., alrededor de 5 genes a alrededor de 100 genes, alrededor de 10 genes a alrededor de 100 genes, alrededor de 15 genes a alrededor de 100 genes, alrededor de 20 genes a alrededor de 100 genes, alrededor de 25 genes a alrededor de 100 genes, alrededor de 5 genes a alrededor de 75 genes, alrededor de 10 genes a alrededor de 75 genes, alrededor de 15 genes a alrededor de 75 genes, alrededor de 20 genes a alrededor de 75 genes, alrededor de 25 genes a alrededor de 75 genes, alrededor de 5 genes a alrededor de 50 genes, alrededor de 10 genes a alrededor de 50 genes, alrededor de 15 genes a alrededor de 50 genes, alrededor de 20 genes a alrededor de 50 genes o alrededor de 25 genes a alrededor de 50 genes enumerados en las Tablas 6 u 8 en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A

presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de AATK, ABCA2, ABCC5, ABCC8, ABR, ABTB1, ACOT1, ACRBP, ACRV1, ACYP2, ADARB1, ADCY1, ADM, AFF1, AGAP4, AGPAT3, AGXT2L2, AHI1, AKAP9, AKIRIN1, AKT2, AMH, ANK2, ANK3, ANKHD1, ANKRD17, ANKRD50, ANKS1A, AQP1, ARF1, ARHGAP1, ARHGAP23, ARL17A, ASAM, ASPHD1, ATP2B3, ATP2B3, ATP6V0A1, ATP8B2, ATP9A, BACE1, BACH2, BLZF1, BPTF, BRUNOL4, BRUNOL5, BRWD1, BRWD2, BTBD18, BTN3A3, BZRAP1, C14ORF159, C15ORF24, C15ORF57, C16ORF52, C17ORF28, C1ORF21, C1ORF21, C1ORF50, C21ORF57, C21ORF59, C21ORF66, C2CD2, C2CD4A, C2ORF60, C2ORF68, C3ORF23, C4ORF41, C5ORF42, C6ORF154, C6ORF52, C7ORF28B, C7ORF54, C9ORF150, C9ORF68, CACNA1D, CALY, CAMK2B, CAMK2N2, CAP2, CAPN2, CARTPT, CBS, CCDC104, CCDC50, CCDC76, CD151, CD163L1, CD302, CDC42EP1, CDH10, CDH12, CDKN1C, CDKN2A, CDS1, CFC1, CHD5, CLCN3, CLDN12, CLIP4, CLMN, CNGA3, CNNM1, CNOT6L, COL6A1, COPA, CPNE8, CRKRS, CRTC1, CRYGS, CSTB, CTSK, CUL4A, CYGB, CYLD, CYP2E1, CYP3A5, CYTL1, D4S234E, DCLK1, DCTD, DEPDC6, DHX36, DIP2A, DIS3, DKFZP547G183, DNAJC22, DTNA, DTWD1, DUSP16, DUSP5, DVL3, EFNB3, EIF3C, ELFN2, ENOSF1, ERAP1, ERBB2, ERBB4, ERMAP, ETFDH, EXOSC6, FADS3, FAM120AOS, FAM150B, FAM165B, FAM184B, FAM30A, FAM46A, FAM66C, FAT4, FBRSL1, FBXW7, FGD5, FGF13, FLJ33630, FNBP1, FOXO6, FUBP3, GAL, GAL, GLT25D2, GNAS, GOLGA8A, GPR123, GPX7, GRIA2, GRIP2, GRM5, GUCY1A3, H2AFY,

HCG 1776018, HCG 2022304, HCN4, HEATR1, HELQ, HERC4, HERPUD2, HEXDC, HGSNAT, HIST1H2AC, HIST1H2AE, HIST1H2BD, HIST1H2BK, HIST1H3I, HIST2H2BE, HIVEP3, HNRNPM, HNRNPR, HPCAL1, HPCAL4, HSPD1, IER3, IL10RB, IL17B, INTU, JMY, KAT2B, KATNB1, KBTBD11, KCNMA1, KCNQ2, KCNS2, KCTD13, KHDC1, KIAA0125, KIAA1370, KIAA1598, KIF1A, KIF5C, KIF5C, KISS1R, KLHDC1, LCORL, LGALS3BP, LOC100130097, LOC100130360, LOC100130522, LOC100272228, LOC284408, LOC399491, LOC401320, LOC641298, LOC642852, LOC90110, LOC94431, LONRF2, LRP2BP, LRRC37A2, LRRFIP1, LTBP3, LYPLAL1, LYRM5, MAP3K5, MAP7, MAP9, MCM3AP, MCM3APAS, MCTP1, MEOX2, METTL3, MFSD4, MGAT4A, MLXIP, MRPL1, MRPS33, MST1, MUC20, MXD1, MZF1, NAMPT, NAP1L3, NBPF1, NBPF10, NCOA7, NCRNA00171, NCRNA00182, NDRG1, NDUFA4L2, NDUFV3, NEBL, NELF, NHEDC2, NHEG1, NIPAL2, NIPAL3, NLRX1, NOL3, NSMAF, NUDT19, NUP153, NUP54, OLFM3, OR7D2, OSBP, PABPC1L, PABPC4, PACRGL, PAM, PAPPA, PAQR6, PARP12, PCBD2, PCNXL2, PDCD6, PDE4C, PDE9A, PDGFRB, PDIA2, PGAP1, PHF17, PHKA1, PHKA2, PHLDA2, PIGH, PION, PKD1, PLA2G4C, PLCB4, PLEKHH1, PLP2, PLRG1, PLXNC1, PNCK, PNMA3, POFUT2, POGK, PPAPDC1A, PPAPDC1B, PPID, PPIE, PPM1K, PPP1R2, PPP2R2C, PPT1, PRKACB, PRPH, PSMB7, PTCD1, PTGER2, PTGS1, PTN, PTPRD, PTPRN, RAB11FIP3, RAB6B, RAF1, RGAG4, RGS11, RGS8, RHBDL1, RHOQ, RHOU, RLF, RNASET2, RNF13, RNF149, RNF165, RNF207, RNF41, RPL37, RSL1D1, RUNDC3A, S100A6, SCMH1, SCN2A, SERP1, SETX, SFRS18, SFXN3, SGK3, SH3BP5, SH3GL2, SH3YL1, SHC2, SHC4,

SIGIRR, SIK1, SLC12A7, SLC1A2, SLC1A6, SLC22A17, SLC35F3, SLC38A5, SLCO1A2, SMAGP, SMAP2, SNCA, SOBP, SORCS1, SORL1, SPINT2, SPIRE2, SPOCK2, SRR, ST8SIA3, STAR, STEAP3, STOX2, STX3, SYNJ1, SYT13, SYT5, TAF10, TANC2, TCEA1, THBS2, THSD4, TIMP1, TM2D1, TMEM111, TMEM151A, TMEM184C, TMEM41B, TMEM43, TMEM5, TMEM59L, TMIE, TNFRSF25, TNFRSF25, TOX4, TP53BP1, TPM3, TRA2A, TRIM33, TRIM73, TRIM8, TRIT1, TSR1, TTC17, TTC3, TTC39C, TUSC3, TXLNB, U2AF1, UBE2D3, UBE2G2, UBN2, UBXN6, UCN, UGP2, UNC80, UNQ1887, USP36, USPL1, VN1R1, VPS13C, VPS53, VPS8, WDFY3, WDR27, WDR85, WSB1, YJEFN3, YLPM1, ZDHHC11, ZER1, ZG16B, ZNF275, ZNF440, ZNF573, ZNF641, ZNF662, ZNF785 y/o ZNF814, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6.

En un aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ACOT1, ADARB1, ADM, ANK2, AQP1, ASAM, C2CD4A, C3ORF23, CACNA1D, CAMK2B, CAP2, CARTPT, CD163L1, CDC42EP1, CDH10, CDKN1C, CDKN2A, CFC1, CLMN, CPNE8, CYGB, CYP2E1, CYTL1, DNAJC22, DUSP5, ENOSF1, ERAP1, FGF13, FOXO6, GAL, GNAS, GPX7, GRIA2, GRM5, HCG 1776018, HIST1H2AC, HIST1H2BD, HIST1H2BK, HIST2H2BE, IL17B, KIAA0125, KIAA1598, KISS1R, LRP2BP, MEOX2, NCRNA00182, NDRG1, NDUFA4L2, NIPAL2,

NUDT19, PDE4C, PHKA2, PHLDA2, PTGER2, RGS11, S100A6, SCN2A, SHC4, SIGIRR, SLC1A2, SLC1A6, SLC35F3, SLC38A5, SORCS1, SYT13, SYT5, THBS2, TIMP1 y/o TMEM111, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6.

En otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ACOT1, ADARB1, ANK2, AQP1, C3ORF23, CAP2, CARTPT, CD163L1, CDC42EP1, CDKN2A, CFC1, CPNE8, CYGB, CYP2E1, CYTL1, FGF13, FOXO6, GNAS, GRIA2, GRM5, HIST1H2AC, IL17B, KIAA0125, KIAA1598, KISS1R, MEOX2, NDRG1, NDUFA4L2, NIPAL2, PDE4C, PHKA2, RGS11, SCN2A, SLC1A2, SLC35F3, SLC38A5, SYT13 y/o THBS2, en comparación con los niveles de expresión de estos genes e las células de la línea celular 2D6.

En aun otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presenta una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de AQP1, CAP2, CARTPT, CD163L1, CDC42EP1, CFC1, CPNE8, CYGB, CYP2E1, CYTL1, FGF13, GNAS, GRIA2, GRM5, HIST1H2AC, IL17B, KIAA0125, MEOX2, NDUFA4L2, PDE4C, PHKA2,

RGS11, SLC1A2, SLC35F3, SLC38A5 y/o SYT13, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan al menos una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ANXA2, AQP1, ARHGAP9, CDH10, CDKN2A, CHPT1, CNTN2, ERAP1 y/o RGS11, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ABCC8, AELIM3, CAP2, IL17B, MEF2A, NEEBL, PHC, S100A6, SLC1A6, SMAD1, SMAD5, SMAD8, SYT13 y/o SYTL1, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de CSTB, GPCR, GRIM5, KISSR, SCN2A, SLC1A2 y/o THBS2, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ADARB1, ADM, PTPPH y/o SLCO1A2, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de CNGA3, HIST1H3E y/o PTGS1, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de HIST1H2BD y/o OSCAR, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En una modalidad adicional, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de CALY, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de COL5A1 y/o MICAL2, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de OLFML2A y/o SIGIRR, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de HPCAL1 y/o LPAR5, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6. En una modalidad adicional, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de HTR1E y/o SORCS1, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ANK2, CPNE8, CREB5, IL17B, KIAA0125, LOC100289109, LOC144571, NPAS4, SLC1A2, SORCS1, THBS2 y/o ZNF814, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6.

Los aspectos de la presente descripción comprenden, en parte, células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A que presentan una diferencia de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 9, 10, 11 o 12 en comparación con los niveles de expresión de estos genes en las células de la línea celular SiMa original. En aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una diferencia de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 9, 10, 11 o 12 en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptible de intoxicación por BoNT/A presentan una

diferencia en los niveles de expresión genética de uno o más genes enumerados en las Tablas 9, 10, 11 o 12 de, por ej., al menos 1.5 veces, al menos 2.0 veces, al menos 2.5 veces, al menos 3.0 veces, al menos 3.5 veces, al menos 4.0 veces, al menos 4.5 veces, al menos 5.0 veces, al menos 5.5 veces, al menos 6.0 veces, al menos 7.0 veces o al menos 8.0 veces en comparación con los niveles de expresión de estos genes en las células de la línea celular SiMa original DSMZ ACC 164. En aun otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una diferencia en los niveles de expresión genética de, por ej., 2 o más genes, 3 o más genes, 4 o más genes, 5 o más genes, 6 o más genes, 7 o más genes, 8 o más genes, 9 o más genes, 10 o más genes, 20 o más genes, 30 o más genes, 40 o más genes, 50 o más genes, 60 o más genes, 70 o más genes, 80 o más genes, 90 o más genes o 100 o más genes enumerados en las Tablas 9, 10, 11 o 12 en comparación con los niveles de expresión de estos genes en las células de la línea celular SiMa original DSMZ ACC 164. En aun otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoTN/A presentan una diferencia en los niveles de expresión genética de, por ej., alrededor de 5 genes a alrededor de 100 genes, alrededor de 10 genes a alrededor de 100 genes, alrededor de 15 genes a alrededor de 100 genes,

alrededor de 20 genes a alrededor de 100 genes, alrededor de 25 genes a alrededor de 100 genes, alrededor de 5 genes a alrededor de 75 genes, alrededor de 10 genes a alrededor de 75 genes, alrededor de 15 genes a alrededor de 75 genes, alrededor de 20 genes a alrededor de 75 genes, alrededor de 25 genes a alrededor de 75 genes, alrededor de 5 genes a alrededor de 50 genes, alrededor de 10 genes a alrededor de 50 genes, alrededor de 15 genes a alrededor de 50 genes, alrededor de 20 genes a alrededor de 50 genes o alrededor de 25 genes a alrededor de 50 genes enumerados en las Tablas 9, 10, 11 o 12 en comparación con los niveles de expresión de estos genes en las células de la línea celular SiMa original DSMZ ACC 164. La proporción logarítmica en las Tablas 9, 10, 11 o 12 representa valores $\log_2$ donde 0.585 es $\log_2(1.5)$ que es una diferencia de 1.5 veces, 1 es $\log_2(2)$ que es una diferencia de 2 veces, 1.584 es $\log_2(3)$ que es una diferencia de 3 veces, 2 es $\log_2(4)$ que es una diferencia de 4 veces, 2.321 es $\log_2(5)$ que es una diferencia de 5 veces, 2.584 es $\log_2(6)$ que es una diferencia de 6 veces, 2.807 es $\log_2(7)$ que es una diferencia de 7 veces, 3 es $\log_2(8)$ que es una diferencia de 8 veces, 3.169 es $\log_2(9)$ que es una diferencia de 9 veces y 3.321 es $\log_2(10)$ que es una diferencia de 10 veces.

En una modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una diferencia de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ACOT9, ADAMTS9, ARHGAP24, ARHGEF3, ASCL1, BARD1, BASP1, C3ORF70, C11ORF75, CCDC109B, CD9, CDCA7L, CDK2, CENPL, CLSTN2, CNTN1, CSRP2, CTSL2, CUGBP2, DEPDC1, DIAPH3, DOK5, DPYD, DYNLT3, EMILIN2, ETV1, FAM101B, FBLN1, FGFR2, FNDC5, GNAI1, GNB4, GNG11, GNG12, GPR177, GTSE1, HGF, KITLG, LPAR1, MAB21L2, MAOA, MCM10, MINA, MSN, MYO6, MYRIP, PAG1, PEG3, PLK2, POLA2, PPP1R3C, PRLHR, PRSS12, PTGR1, PTPRK, PVRL3, RAB32, RBPMS, SDC2, SGOL2, SLC43A3, SLC7A2, SMC2, SMC6, SPARC, SPC25, ST8SIA4, TCF7L1, TFPI2, TMEM35, TMEM178, TNFAIP8, TPTE, TRIP10, TWIST1 y/o ZNF521, en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164. En otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una diferencia de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ADAMTS9, ARHGAP24, ASCL1, BARD1, BASP1, BVES, C11ORF75, CDCA7L, CNTN1, CUGBP2, DOK5, DPYD, DYNLT3, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, GTSE1, GTSF1, ITPRIP, KDELC2, LOC728052, LPAR1, MAB21L2, MAOA, MINA, MSN, PEG3, PLK2, PRLHR, PRSS12, PTPRK, RBPMS, RNF182, SGOL2, SLC43A3, SLC44A5,

SLC7A2, SMC6, SPARC, TFPI2, TMEM178 y/o TPTE, en comparación con los niveles de expresión de estos genes en las células de la línea celular SiMa original DSZM ACC 164. En aun otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una diferencia de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ADAMTS9, ASCL1, BASP1, DOK5, DPYD, GNB4, GNG11, GTSF1, MAOA, MINA, MSN, PEG3, PLK2, PRSS12, RNF182, SLC44A5, SPARC, TFPI2 y/o TPTE, en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presenta un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 9 u 11 en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptible de intoxicación por BoNT/A presentan un aumento en los niveles de expresión genética de uno o más genes enumerados en las Tablas 9 u 11 de, por ej., al menos 1.5 veces, al menos 2.0 veces, al menos 2.5 veces, al menos 3.0 veces, al menos 3.5

veces, al menos 4.0 veces, al menos 4.5 veces, al menos 5.0 veces, al menos 5.5 veces, al menos 6.0 veces, al menos 7.0 veces o al menos 8.0 veces en comparación con los niveles de expresión de estos genes en células de una línea celular SiMa original DSMZ ACC 164. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento en los niveles de expresión genética de, por ej., 2 o más genes, 3 o más genes, 4 o más genes, 5 o más genes, 6 o más genes, 7 o más genes, 8 o más genes, 9 o más genes, 10 o más genes, 20 o más genes, 30 o más genes, 40 o más genes, 50 o más genes, 60 o más genes, 70 o más genes, 80 o más genes, 90 o más genes o 100 o más genes enumerados en las Tablas 9 u 11 en comparación con los niveles de expresión de estos genes en las células de la línea celular SiMa original DSMZ ACC 164. En aun otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoTN/A presentan un aumento en los niveles de expresión genética de, por ej., alrededor de 5 genes a alrededor de 100 genes, alrededor de 10 genes a alrededor de 100 genes, alrededor de 15 genes a alrededor de 100 genes, alrededor de 20 genes a alrededor de 100 genes, alrededor de 25 genes a alrededor de 100 genes, alrededor de 5 genes a alrededor de 75 genes, alrededor de 10 genes a alrededor de 75 genes, alrededor de 15 genes a alrededor de 75 genes, alrededor de

20 genes a alrededor de 75 genes, alrededor de 25 genes a alrededor de 75 genes, alrededor de 5 genes a alrededor de 50 genes, alrededor de 10 genes a alrededor de 50 genes, alrededor de 15 genes a alrededor de 50 genes, alrededor de 20 genes a alrededor de 50 genes o alrededor de 25 genes a alrededor de 50 genes enumerados en las Tablas 9 u 11 en comparación con los niveles de expresión de estos genes en las células de la línea celular SiMa original DSMZ ACC 164.

En una modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de A2BP1, ADRM1, AFF4, AGAP4, ALCAM, ANAPC7, ANKRD13D, ANKRD28, API5, ARF1, ARHGAP6, ARHGEF10, ARHGEF6, ARL17A, ASCL1, ASXL1, ASXL3, ATF7IP, B3GALNT2, BASP1, BLCAP, BNC2, C10ORF58, C12ORF49, C12ORF51, C1ORF43, C20ORF117, C20ORF7, CADM1, CADPS, CALCB, CAPN1, CAPRIN2, CBLB, CBLN2, CBWD1, CCDC150, CCDC3, CD9, CDC25B, CFDP1, CHRNA7, CIAPIN1, CLASP2, CNOT7, CPVL, CRYBG3, CSE1L, CTTNBP2NL, CUGBP2, CXCR4, DACT1, DAZ1, DBH, DCAF8, DENR, DHX35, DKFZP434L187, DLEU2, DLL1, DLL3, DYNC2H1, EAF2, EFNA5, EIF3B, EIF3C, ELOVL7, EML1, EML4, ENC1, EVL, EXOSC6, EXPH5, EZH2, FAM178A, FAM181B, FAM19A4, FAM7A3, FLJ10213, FUBP3, FUS, FZD5, GAP43, GFM1, GFRA2, GGA2, GNAI1, GNAS, GNB4, GNG11, GOLGA4, GPR125, GRM8, GRP, GSPT1, GSS,

GSTCD, GULP1, HAUS2, HEG1, HNRNPL, HNRNPM, HOXA7, HOXD4, ID2, IDH3B, IL1A, INSM1, IREB2, ITGA6, ITGB5, KCTD12, KDELC2, KHDRBS3, KIAA0907, KIAA1267, KIF16B, KLC1, KLHL13, LBH, LMO4, LOC100128844, LOC340109, LOC641298, LOC647190, LOC728052, LOC728153, LRPPRC, LRRFIP2, LSM3, LUM, MAB21L1, MAB21L2, MAN2A1, MAOA, MARS, MDN1, MED13L, MED22, MGC24103, MINA, MKLN1, MLEC, MMD, MORF4L2, MPZL1, MSH6, MSI2, MSN, MTMR9, MYO1B, MYO6, N4BP2, NAAA, NDUFS8, NEDD9, NFIB, NKTR, NLN, NOS1, NR2C1, NUFIP2, NUPL1, OSBPL3, PAPD4, PCBP2, PCDH9, PCGF5, PCNX, PDLIM5, PDZRN3, PELI2, PFKFB3, PGP, PHF20, PLK2, PLXNA2, PLXNA4, PM20D2, POLE, POLQ, PPP2R2A, PPP2R3C, PRDX2, PSMA7, PSME4, PTGFRN, PTK2, PTPN1, PTPRE, PTPRG, QKI, RAB12, RAB35, RAB3GAP2, RAD23B, RAF1, RALGAPA1, RAN, RASEF, RBL1, RDH11, RELL1, REPS1, RGS5, RIMBP2, RNF182, RNF34, RNPEP, ROBO2, RPAIN, RPL35A, RPRD1A, S1PR3, SALL4, SBNO1, SCARB2, SDHA, SEMA6A, SEZ6L, SF1, SFRS8, SIM1, SIRT2, SKIL, SLC20A1, SLC44A5, SLC7A2, SLCO3A1, SLITRK5, SMAD4, SMARCC2, SMC3, SNRPB2, SNRPN, SNX5, SOX2, SPAG6, SPAG9, SPATS2L, SPON1, SR140, SSBP2, ST8SIA1, STMN3, STRA6, SYNCRIP, SYTL3, TAF15, TCF7L2, TDG, TERT, TFPI2, TGFBR1, TH1L, THOC4, TIMP3, TLE3, TMEM132C, TMEM178, TMEM181, TNRC6A, TPBG, TRA2A, TRIM29, TRIM36, TSHZ3, TXNRD1, U2AF1, UBE2O, UBE2V1, UBE2Z, UBXN2A, UCHL1, USP25, USP32, USP34, VPS29, XPO1, XPO7, ZFAND6, ZFHX4, ZFYVE16, ZGPAT, ZNF217, ZNF451, ZNF503 y/o ZNF664, en

comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164.

En un aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ALCAM, ARHGAP6, ARHGEF6, ASCL1, BNC2, CBLN2, CCDC150, CCDC3, CHRNA7, CRYBG3, CUGBP2, CXCR4, DAZ1, DKFZP434L187, DLL1, EFNA5, ELOVL7, EML1, EML4, ENC1, EXPH5, FAM7A3, FZD5, GFRA2, GNAI1, GNB4, GNG11, GRP, ID2, ITGA6, KCTD12, LOC100128844, LOC340109, LOC728052, LUM, MAB21L1, MAB21L2, MAOA, MGC24103, MSN, NEDD9, NFIB, OSBPL3, PAPD4, PCDH9, PDZRN3, PLK2, POLQ, PTGFRN, PTPRE, PTPRG, RAD23B, RGS5, RNF182, ROBO2, SIM1, SLC20A1, SLC44A5, SLITRK5, SPAG6, SPAG9, SR140, TFPI2, TIMP3, TMEM132C, TPBG, TRIM29, TRIM36 y/o ZFAND6, en comparación con los niveles de expresión de estos genes en las células de la línea celular SiMa original DSMZ ACC 164.

En otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ALCAM, ARHGAP6, ARHGEF6, CBLN2, CCDC3,

CHRNA7, CRYBG3, CUGBP2, CXCR4, DAZ1, ELOVL7, EML1, EXPH5, FAM7A3, GNB4, GNG11, GRP, ITGA6, KCTD12, LOC340109, LUM, MAB21L1, MAB21L2, MGC24103, PCDH9, PLK2, POLQ, PTPRE, RGS5, RNF182, ROBO2, SIM1, SLC44A5, SLITRK5, SPAG6, TIMP3 y/o TMEM132C, en comparación con los niveles de expresión de estos genes en las células de la línea celular SiMa original DSMZ ACC 164.

En aun otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de CBLN2, CCDC3, CHRNA7, CRYBG3, CXCR4, DAZ1, EXPH5, FAM7A3, GNB4, GRP, KCTD12, LUM, MGC24103, PCDH9, PLK2, POLQ, PTPRE, RGS5, ROBO2, SIM1, SLITRK5, TIMP3 y/o TMEM132C, en comparación con los niveles de expresión de estos genes en las células de la línea celular SiMa original DSMZ ACC 164.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presenta un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 14 o 16 en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164. En aspectos de esta modalidad, las células de una

línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 14 o 16 en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptible de intoxicación por BoNT/A presentan un aumento en los niveles de expresión genética de uno o más genes enumerados en las Tablas 14 o 16 de, por ej., al menos 1.5 veces, al menos 2.0 veces, al menos 2.5 veces, al menos 3.0 veces, al menos 3.5 veces, al menos 4.0 veces, al menos 4.5 veces, al menos 5.0 veces, al menos 5.5 veces, al menos 6.0 veces, al menos 7.0 veces o al menos 8.0 veces en comparación con los niveles de expresión de estos genes en células de una línea celular SiMa original DSMZ ACC 164. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento en los niveles de expresión genética de, por ej., 2 o más genes, 3 o más genes, 4 o más genes, 5 o más genes, 6 o más genes, 7 o más genes, 8 o más genes, 9 o más genes, 10 o más genes, 20 o más genes, 30 o más genes, 40 o más genes, 50 o más genes, 60 o más genes, 70 o más genes, 80 o más genes, 90 o más genes o 100 o más genes enumerados en las Tablas 14 o 16 en comparación con los niveles de expresión de

estos genes en las células de la línea celular SiMa original DSMZ ACC 164. En aun otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoTN/A presentan un aumento en los niveles de expresión genética de, por ej., alrededor de 5 genes a alrededor de 100 genes, alrededor de 10 genes a alrededor de 100 genes, alrededor de 15 genes a alrededor de 100 genes, alrededor de 20 genes a alrededor de 100 genes, alrededor de 25 genes a alrededor de 100 genes, alrededor de 5 genes a alrededor de 75 genes, alrededor de 10 genes a alrededor de 75 genes, alrededor de 15 genes a alrededor de 75 genes, alrededor de 20 genes a alrededor de 75 genes, alrededor de 25 genes a alrededor de 75 genes, alrededor de 5 genes a alrededor de 50 genes, alrededor de 10 genes a alrededor de 50 genes, alrededor de 15 genes a alrededor de 50 genes, alrededor de 20 genes a alrededor de 50 genes o alrededor de 25 genes a alrededor de 50 genes enumerados en las Tablas 14 o 16 en comparación con los niveles de expresión de estos genes en las células de la línea celular SiMa original DSMZ ACC 164.

En aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes

seleccionados de ACOT9, ADAMTS9, ARHGAP24, ARHGEF3, ASCL1, BARD1, BASP1, C3ORF70, C11ORF75, CCDC109B, CD9, CDCA7L, CDK2, CENPL, CLSTN2, CNTN1, CSRP2, CTSL2, CUGBP2, DEPDC1, DIAPH3, DOK5, DPYD, DYNLT3, EMILIN2, ETV1, FAM101B, FBLN1, FGFR2, FNDC5, GNAI1, GNB4, GNG11, GNG12, GPR177, GTSE1, HGF, KITLG, LPAR1, MAB21L2, MAOA, MCM10, MINA, MSN, MYO6, MYRIP, PAG1, PEG3, PLK2, POLA2, PPP1R3C, PRLHR, PRSS12, PTGR1, PTPRK, PVRL3, RAB32, RBPMS, SDC2, SGOL2, SLC43A3, SLC7A2, SMC2, SMC6, SPARC, SPC25, ST8SIA4, TCF7L1, TFPI2, TMEM35, TMEM178, TNFAIP8, TPTE, TRIP10, TWIST1 y/o ZNF521, en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164. En otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ADAMTS9, ARHGAP24, ASCL1, BARD1, BASP1, BVES, C11ORF75, CDCA7L, CNTN1, CUGBP2, DOK5, DPYD, DYNLT3, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, GTSE1, GTSF1, ITPRIP, KDELC2, LOC728052, LPAR1, MAB21L2, MAOA, MINA, MSN, PEG3, PLK2, PRLHR, PRSS12, PTPRK, RBPMS, RNF182, SGOL2, SLC43A3, SLC44A5, SLC7A2, SMC6, SPARC, TFPI2, TMEM178 y/o TPTE, en comparación con los niveles de expresión de estos genes en las células de la línea celular SiMa original DSZM ACC 164. En aun otro aspecto de esta modalidad, las células de una línea celular clonal

establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ADAMTS9, ASCL1, BASP1, DOK5, DPYD, GNB4, GNG11, GTSF1, MAOA, MINA, MSN, PEG3, PLK2, PRSS12, RNF182, SLC44A5, SPARC, TFPI2 y/o TPTE, en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164.

En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ADAMTS9, ARHGAP24, ARHGEF3, ASCL1, BARD1, CD9, CDK2, CSRP2, CTSL2, DIAPH3, DOK5, DYNLT3, EMILIN2, ETV1, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, HGF, KITLG, LPAR1, MCM10, MSN, PAG1, PEG3, PLK2, POLA2, PPP1R3C, PTPRK, RAB32, SDC2, SLC43A3, SLC7A2, SMC6, SPARC, SPC25, ST8SIA4, TCF7L1, TFPI2, TMEM35, TNFAIP8, TPTE, TRIP10 y/o TWIST1, en comparación con los niveles de expresión de estos genes en las células de la línea celular SiMa original DSMZ ACC 164. En un aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ADAMTS9, ARHGAP24, ASCL1, BARD1, DOK5, DYNLT3, FBLN1, FGFR2, GNAI1,

GNB4, GNG11, GNG12, LPAR1, MSN, PEG3, PLK2, PTPRK, SLC43A3, SLC7A2, SMC6, SPARC, TFPI2 y/o TPTE, en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164. En otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ADAMTS9, ASCL1, DOK5, GNB4, GNG11, MSN, PEG3, PLK2, SPARC, TFPI2 y/o TPTE, en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164.

En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ACOT9, BASP1, C11ORF75, CCDC109B, CDCA7L, CLSTN2, CNTN1, CUGBP2, DEPDC1, DPYD, FAM101B, FNDC5, GTSE1, MAOA, MINA, MYO6, MYRIP, PLK2, PRLHR, PVRL3, RBPMS, SGOL2, SMC2, TFP12, TMEM178 y/o ZNF521, en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164. En un aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes

seleccionados de BASP1, C11ORF75, CDCA7L, CNTN1, CUGBP2, DPYD, GTSE1, MAOA, MINA, PLK2, PRLHR, RBPMS, SGOL2, TFPI2 y/o TMEM178, en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164. En otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de BASP1, DPYD, MAOA, MINA, PLK2 y/o TFPI2, en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164.

En una modalidad adicional, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de C3ORF70, MAB21L2, PRSS12, CENPL, GPR177 y/o PTGR1, en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164. En un aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de MAB21L2 y/o PRSS12, en comparación con los

niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presenta una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 10 o 12 en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original. En aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 10 o 12 en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptible de intoxicación por BoNT/A presentan una disminución en los niveles de expresión genética de uno o más genes enumerados en las Tablas 10 o 12 de, por ej., al menos 1.5 veces, al menos 2.0 veces, al menos 2.5 veces, al menos 3.0 veces, al menos 3.5 veces, al menos 4.0 veces, al menos 4.5 veces, al menos 5.0 veces, al menos 5.5 veces, al menos 6.0 veces, al menos 7.0 veces o al menos 8.0 veces en comparación con los niveles de expresión de estos genes en

células de la línea celular SiMa original DSMZ ACC 164. En otros aspectos, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución en los niveles de expresión genética de, por ej., 2 o más genes, 3 o más genes, 4 o más genes, 5 o más genes, 6 o más genes, 7 o más genes, 8 o más genes, 9 o más genes, 10 o más genes, 20 o más genes, 30 o más genes, 40 o más genes, 50 o más genes, 60 o más genes, 70 o más genes, 80 o más genes, 90 o más genes o 100 o más genes enumerados en las Tablas 10 o 12 en comparación con los niveles de expresión de estos genes en las células de la línea celular SiMa original DSMZ ACC 164. En aun otros aspectos, las células de una línea celular clonal establecida susceptibles de intoxicación por BoTN/A presentan una disminución en los niveles de expresión genética de, por ej., alrededor de 5 genes a alrededor de 100 genes, alrededor de 10 genes a alrededor de 100 genes, alrededor de 15 genes a alrededor de 100 genes, alrededor de 20 genes a alrededor de 100 genes, alrededor de 25 genes a alrededor de 100 genes, alrededor de 5 genes a alrededor de 75 genes, alrededor de 10 genes a alrededor de 75 genes, alrededor de 15 genes a alrededor de 75 genes, alrededor de 20 genes a alrededor de 75 genes, alrededor de 25 genes a alrededor de 75 genes, alrededor de 5 genes a alrededor de 50 genes, alrededor de 10 genes a alrededor de 50 genes, alrededor de 15 genes a alrededor de

50 genes, alrededor de 20 genes a alrededor de 50 genes o alrededor de 25 genes a alrededor de 50 genes enumerados en las Tablas 10 o 12 en comparación con los niveles de expresión de estos genes en las células de la línea celular SiMa original DSMZ ACC 164.

En una modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de 1-Mar, ABCG1, ABTB1, ACOT1, ACSL1, ACVR1, ACVR2A, ACYP2, ADAMTS1, ADAMTS3, ADAMTSL1, ADARB1, ADCY1, ADD2, ADO, AFF3, AKAP12, ALDH1A2, ALKBH1, ALLC, AMN1, ANKH, ANKRA2, ANKRD50, ANXA5, AP3B2, ARMC10, ARMCX5, ASAM, ASB13, ASPHD1, ATG5, ATL3, ATP2B3, ATP2C1, ATRNL1, B3GALTL, BACE1, BACE2, BBS10, BBS7, BCAP29, BCL2, BCORL1, BRUNOL4, BRUNOL6, BRWD1, BTN3A3, C10ORF10, C10ORF104, C11ORF57, C11ORF70, C14ORF167, C15ORF39, C16ORF52, C17ORF69, C18ORF18, C1GALT1C1, C1ORF21, C1ORF25, C1ORF97, C1RL, , C21ORF57, C2CD2, C2CD4A, C2ORF67, C2ORF68, C3ORF23, C4ORF12, C4ORF39, C4ORF41, C5ORF42, C6ORF120, C9ORF150, CADM2, CAMK2D, CAMK2N1, CAMK2N2, CAP2, CAPN2, CARTPT, CCDC126, CCDC40, CCDC50, CCNY, CD248, CD302, CDC2L6, CDC37L1, CDC42EP3, CDH12, CDKN1C, CDKN2A, CDS1, CFC1, CHMP1B, CLCN3, CLDN12, CLMN, CLN8, CNGA3, CNNM1, CNOT6L, COL27A1, COL5A1, COL6A1, COL6A2, COL6A3, COX18,

COX5B, CRYGD, CRYZL1, CTPS2, CTSC, CYB5R2, CYGB, CYLD, CYP2E1, CYP2U1, CYTL1, CYYR1, D4S234E, DAB1, DBT, DCAF10, DCLK1, DCTD, DDAH1, DHRSX, DISP1, DKFZP434I0714, DKK1, DNAJC12, DNAJC24, DNASE1L1, DNER, DOPEY2, DRAM2, DSCAM, DSCR3, DTX3L, DUSP16, DUSP22, ECEL1, ECHDC3, EEF1D, EEF2K, EFEMP2, EFNB3, EMID1, ENOX2, ERAP1, ERBB2, ERBB4, ETFDH, ETS2, EYA1, FAM13C, FAM162B, FAM165B, FAM172A, FAM175A, FAM190A, FAM26F, FAM46A, FAM49A, FAM71E1, FAM76A, FAM85A, FBXL5, FBXW7, FCRLB, FGD5, FGF1, FGF13, FGF19, FGF3, FGF7, FIP1L1, FKTN, FLJ10038, FLJ35220, FLJ35390, FLJ37798, FLJ39051, FOXO6, FSTL1, FUCA2, GAL, GART, GAS5, GDPD5, GLCE, GLI2, GLIS1, GLIS3, GLT25D2, GNA14, GNAS, GPR123, GPX7, GRM5, GTF2H5, GUCY1A3, H2AFJ, HCG 1776018, HDAC4, HEBP2, HELQ, HERPUD2, HHLA3, HIST1H2AC, HIST1H2BD, HIST1H2BK, HIST2H2BE, HMGCLL1, HNRNPR, HPCAL1, HPDL, HPS3, HSBP1L1, HSPA1A, HTATIP2, ICAM2, IFNAR1, IGFBP5, IGFBP7, IGSF5, IL10RB, IL13RA2, IL17D, IL20RA, IL7, IMMP2L, INSR, IRS1, ITGB1BP1, JMY, JRKL, KAT2B, KBTBD11, KCMF1, KCNMA1, KCNQ2, KCNQ5, KCTD18, KDM1A, KDSR, KHDC1, KIAA1109, KIAA1324, KIAA1598, KIAA1804, KIRREL3, KLHDC1, KRCC1, LGALS3, LGALS3BP, LIFR, LINGO1, LIPT1, LMAN2L, LMCD1, LOC100129195, LOC100129884, LOC100130522, LOC100130856, LOC100132167, LOC100216479, LOC100272217, LOC100287039, LOC151146, LOC153682, LOC220930, LOC254128, LOC255167, LOC283588, LOC285286, LOC285550, LOC285878, LOC286052, LOC339290, LOC401321, LOC645513,

LOC80154, LOC90246, LOC93622, LOC94431, LPAR3, LPHN2, LRCH2, LRP2BP, LYRM1, LYRM5, MAGI2, MANSC1, MAP3K13, MAP3K5, MAP9, MAPKAP1, MBD5, MBLAC2, MBNL1, MCTP1, MED6, MEGF11, MEOX2, MET, METT5D1, MFSD4, MFSD6, MFSD9, MGAT4A, MORC3, MREG, MRPS18C, MRPS33, MST1, MTMR3, MTUS2, MXRA7, N4BP3, NAP1L3, NCAM1, NCAM2, NCOA7, NCRNA00081, NCRNA00117, NCRNA00171, NDUFA4L2, NDUFV3, NEAT1, NEBL, NEIL2, NETO1, NFATC4, NHEDC2, NIPAL3, NLRX1, NNAT, NOTCH4, NPW, NPY, NR1H3, NR2F1, NT5E, NUDT19, NUDT6, OGFRL1, OLFM3, OMA1, OPRM1, OPTN, P4HTM, PABPC4L, PABPC5, PAK1, PAM, PAPOLG, PAPPA, PBX1, PCDHB10, PCDHB16, PCNX, PCNXL2, PDCD2, PDE4DIP, PDGFRB, PEX12, PEX6, PHKA1, PHLDB3, PIBF1, PID1, PIGH, PIGP, PIK3CB, PIWIL2, PKNOX1, PKNOX2, PLA2G12A, PLCB1, PLEKHA2, PLEKHA3, PLIN2, PLRG1, POLR3GL, POU6F1, PPAPDC1A, PPOX, PPP1R14A, PPP2R5C, PPP3CA, PRAME, PRKACB, PRMT2, PRPH, PSD3, PSTK, PTGER2, PTGES, PTN, PTP4A3, PTPRD, PTPRN2, PTPRR, QPCT, RAB4A, RAB6B, RAC2, RAI2, RCAN1, RCC1, RDH13, RFPL1S, RG9MTD2, RGAG4, RHBDD1, RHBDF2, RHOU, RNF13, RNF41, RNLS, RPL31, RPL37, RPRD1A, RRN3, RSL1D1, RSPH3, SAP30, SAV1, SCG5, SCN5A, SERTAD4, SGMS1, SH3BGR, SH3GL2, SH3KBP1, SH3YL1, SIAE, SIGIRR, SIK1, SIK3, SIX2, SLC12A7, SLC16A14, SLC22A17, SLC22A5, SLC25A12, SLC25A4, SLC35F3, SLC6A15, SLIT1, SMARCA2, SMEK2, SNAP91, SNCA, SOCS5, SORCS2, SPATA17, SPATA7, SPIN3, SPINT1, SPINT2, SPOCK2, SPRED1, SSPN, ST8SIA3, STAC2, STAR, STEAP3, STOX2, STX12, STXBP5L, SUCLG2, SYNJ1, SYNPR, SYT13,

TAF12, TAF1B, TBC1D12, TBC1D15, TCEAL2, TEX264, THAP2, TM2D1, TMCC1, TMEM182, TMEM184C, TMEM196, TMEM45B, TMEM5, TMEM59L, TMEM65, TMIE, TNC, TNFRSF10D, TNFSF4, TOX, TRAPPC9, TRHDE, TRIM61, TRIM69, TSPAN7, TSPAN9, TTC23, TTC39C, TUSC3, TXLNB, UBE2D3, UBE2W, UCN, UNC5A, UTP23, VPS37A, VSTM2A, WASF3, WDFY3, WDTC1, XPR1, XYLT1, ZBTB41, ZC3H12B, ZNF148, ZNF185, ZNF22, ZNF23, ZNF25, ZNF250, ZNF280D, ZNF285A, ZNF295, ZNF346, ZNF528, ZNF585A, ZNF610, ZNF641, ZNF662, ZNF677 y/o ZNF862, en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164.

En un aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ACOT1, ADARB1, ASAM, BACE2, C11ORF70, C2CD4A, C3ORF23, CADM2, CAP2, CARTPT, CDKN1C, CFC1, CNGA3, COL5A1, CYGB, CYP2E1, CYTL1, DSCAM, ECEL1, ECHDC3, FAM26F, FAM49A, FGF1, FGF13, FGF19, FLJ39051, FUCA2, GAL, GPX7, GRM5, HCG 1776018, HHLA3, HIST1H2AC, HIST1H2BD, HSPA1A, HTATIP2, ICAM2, IGFBP5, IGFBP7, IL13RA2, KCNMA1, KCNQ5, KIAA1598, KRCC1, LMCD1, LOC100216479, LOC254128, LOC339290, LPAR3, MEGF11, MEOX2, NCAM2, NDUFA4L2, NEAT1, NNAT, NPW, NPY, PABPC4L, PAPPA, PID1, PPAPDC1A, PRAME, PRKACB, PTGER2, PTN,

PTP4A3, RAC2, SLC35F3, SYT13, TCEAL2, THAP2, TMIE, TNFRSF10D, TRHDE, TXLNB y/o ZNF662, en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164.

En otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ACOT1, ASAM, BACE2, C11ORF70, C2CD4A, C3ORF23, CADM2, CAP2, CARTPT, CFC1, CNGA3, CYGB, CYP2E1, CYTL1, DSCAM, ECEL1, ECHDC3, FGF1, FGF13, FUCA2, GAL, GPX7, HSPA1A, HTATIP2, ICAM2, IGFBP5, IGFBP7, KIAA1598, KRCC1, LMCD1, LOC100216479, LOC254128, LOC339290, LPAR3, MEOX2, NDUFA4L2, NEAT1, NNAT, NPW, NPY, PAPPA, PID1, PPAPDC1A, PRAME, PTN, SLC35F3, SYT13, TCEAL2, TMIE, TNFRSF10D, TRHDE y/o ZNF662, en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164.

En aun otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de C11ORF70, CADM2, CAP2, CARTPT, CNGA3,

CYGB, CYP2E1, CYTL1, DSCAM, FGF13, FUCA2, GAL, HSPA1A, HTATIP2, ICAM2, IGFBP5, IGFBP7, LMCD1, LOC100216479, MEOX2, NDUFA4L2, NEAT1, NNAT, NPW, PID1, PRAME, SLC35F3, SYT13, TCEAL2, TMIE, TNFRSF10D y/o ZNF662, en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 5 o 7 en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6 y un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 9 u 11 en comparación con los niveles de expresión de estos genes en células de una línea celular SiMa original. En aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 5 o 7 en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6 y un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 9 u 11 en comparación con los

niveles de expresión de estos genes en células de una línea celular SiMa original DSMZ ACC 164. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento en los niveles de expresión genética de uno o más genes enumerados en las Tablas 5 o 7 de, por ej., al menos 1.5 veces, al menos 2.0 veces, al menos 2.5 veces, al menos 3.0 veces, al menos 3.5 veces, al menos 4.0 veces, al menos 4.5 veces, al menos 5.0 veces, al menos 5.5 veces, al menos 6.0 veces, al menos 7.0 veces o al menos 8.0 veces en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6 y presentan un aumento en los niveles de expresión genética de uno o más genes enumerados en las Tablas 9 u 11 de, por ej., al menos 1.5 veces, al menos 2.0 veces, al menos 2.5 veces, al menos 3.0 veces, al menos 3.5 veces, al menos 4.0 veces, al menos 4.5 veces, al menos 5.0 veces, al menos 5.5 veces, al menos 6.0 veces, al menos 7.0 veces o al menos 8.0 veces en comparación con los niveles de expresión de estos genes en las células de la línea celular SiMa original DSMZ ACC 164. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento en los niveles de expresión genética de, por ej., 2 o más genes, 3 o más genes, 4 o más genes, 5 o más genes, 6 o más genes, 7 o más genes, 8 o más genes, 9 o más

genes, 10 o más genes, 20 o más genes, 30 o más genes, 40 o más genes, 50 o más genes, 60 o más genes, 70 o más genes, 80 o más genes, 90 o más genes o 100 o más genes enumerados en las Tablas 5 o 7 en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6 y enumerados en las Tablas 9 u 11 en comparación con los niveles de expresión de estos genes de la línea celular SiMa original DSMZ ACC 164. En aun otros aspectos, las células de una línea celular clonal establecida susceptibles de intoxicación por BoTN/A presentan un aumento en los niveles de expresión genética de, por ej., alrededor de 5 genes a alrededor de 100 genes, alrededor de 10 genes a alrededor de 100 genes, alrededor de 15 genes a alrededor de 100 genes, alrededor de 20 genes a alrededor de 100 genes, alrededor de 25 genes a alrededor de 100 genes, alrededor de 5 genes a alrededor de 75 genes, alrededor de 10 genes a alrededor de 75 genes, alrededor de 15 genes a alrededor de 75 genes, alrededor de 20 genes a alrededor de 75 genes, alrededor de 25 genes a alrededor de 75 genes, alrededor de 5 genes a alrededor de 50 genes, alrededor de 10 genes a alrededor de 50 genes, alrededor de 15 genes a alrededor de 50 genes, alrededor de 20 genes a alrededor de 50 genes o alrededor de 25 genes a alrededor de 50 genes enumerados en las Tablas 5 o 7 en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6 y enumerados en las

Tablas 9 u 11 en comparación con los niveles de expresión de estos genes en las células de la línea celular SiMa original DSMZ ACC 164.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de A2BP1, ALCAM, ANAPC7, ARF1, ARHGAP6, ARHGEF6, ARL17A, ASCL1, ASXL3, BASP1, BNC2, C10ORF58, C12ORF49, C1ORF43, C20ORF7, CBLB, CBWD1, CCDC3, CD9, CDC25B, CHRNA7, CPVL, CRYBG3, CSE1L, CUGBP2, CXCR4, DACT1, DAZ1, DBH, DHX35, DKFZP434L187, DLEU2, DLL3, EAF2, EFNA5, EIF3C, ELOVL7, EML1, ENC1, EXOSC6, EXPH5, EZH2, FAM181B, FAM19A4, FAM7A3, FUBP3, FZD5, GAP43, GFRA2, GNAI1, GNB4, GNG11, GPR125, GRP, GSS, ITGA6, ITGA6, ITGB5, KCTD12, KDELC2, KHDRBS3, KIF16B, KLHL13, LBH, LOC100128844, LOC340109, LOC641298, LOC728052, LUM, MAB21L1, MAN2A1, MAOA, MINA, MMD, MSN, MYO1B, MYO6, NAAA, NEDD9, NOS1, OSBPL3, PCGF5, PELI2, PFKFB3, PHF20, PLK2, PLS3, PLXNA2, PLXNA4, PM20D2, POLE, PSMA7, PTGFRN, PTPRE, PTPRG, RAB35, RAF1, RAN, RASEF, RBL1, RELL1, RGS5, RIMBP2, RNF182, RNF34, S1PR3, SALL4, SEMA6A, SEZ6L, SIM1, SLC44A5, SLC7A2, SLCO3A1, SLITRK5, SPAG6, SPATS2L, ST8SIA1, STMN3, STRA6, TCF7L2, TFPI2, TH1L, THOC4, TIMP3, TLE3, TMEM132C, TMEM178, TPBG, TRA2A, TRIM29, TRIM36, TSHZ3, TXNRD1, U2AF1, UBE2V1, VPS29,

ZFHX4, ZGPAT, ZNF217 y/o ZNF503, en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6 y la línea celular SiMA original DSMZ ACC 164.

En un aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ALCAM, ARHGAP6, ARHGEF6, ASCL1, BNC2, CCDC3, CHRNA7, CRYBG3, CUGBP2, CXCR4, DAZ1, EFNA5, ELOVL7, EML1, ENC1, EXPH5, FAM7A3, FZD5, GFRA2, GNAI1, GNB4, GNG11, GRP, ITGA6, KCTD12, LOC100128844, LOC340109, LOC728052, LUM, MAB21L1, MAB21L2, MAOA, MSN, NEDD9, OSBPL3, PLK2, PTGFRN, PTPRE, RGS5, RNF182, SIM1, SLC44A5, SLITRK5, SPAG6, TFPI2, TIMP3, TMEM132C, TPBG, TRIM29 y/o TRIM36, en comparación con los niveles de expresión de estos genes en las células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ALCAM, ARHGAP6, ARHGEF6, CCDC3, CHRNA7,

CRYBG3, CUGBP2, CXCR4, DAZ1, ELOVL7, EML1, EXPH5, FAM7A3, GNB4, GNG11, GRP, ITGA6, KCTD12, LOC340109, LUM, MAB21L1, MAB21L2, PLK2, PTPRE, RGS5, RNF182, SIM1, SLC44A5, SLITRK5, SPAG6, TIMP3 y/o TMEM132C, en comparación con los niveles de expresión de estos genes en las células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En aun otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de CCDC3, CHRNA7, CRYBG3, CXCR4, DAZ1, EXPH5, FAM7A3, GNB4, GRP, KCTD12, LUM, PLK2, PTPRE, RGS5, SIM1, SLITRK5, TIMP3 y/o TMEM132C, en comparación con los niveles de expresión de estos genes tanto en las células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de A2BP1, ALCAM, ARF1, ARL17A, ASCL1, BASP1, CD9, CUGBP2, EAF2, EIF3C, FAM181B, FUBP3, GNAI1, GNB4, GNG11, KDELC2, KHDRBS3, KLHL13,

LOC641298, LOC728052, MAB21L2, MAOA, MINA, MSN, MYO6, PLK2, PLS3, RAF1, RELL1, RNF182, SEZ6L, SEZ6L, SIM1, SLC44A5, SLC7A2, SLCO3A1, SLITRK5, SPATS2L, TCF7L2, TFPI2, TMEM178, TRA2A, U2AF1 y/o ZNF217, en comparación con los niveles de expresión de estos genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En un aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de A2BP1, ALCAM, ARF1, ASCL1, BASP1, CD9, CUGBP2, EIF3C, FUBP3, GNAI1, GNB4, GNG11, KDELC2, KHDRBS3, LOC641298, LOC728052, MAB21L2, MAOA, MINA, MSN, MYO6, PLK2, PLS3, RELL1, RNF182, SIM1, SLC44A5, SLC7A2, SLCO3A1, SLITRK5, TCF7L2, TFPI2, TMEM178, TRA2A y/o ZNF217, en comparación con los niveles de expresión de estos genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ASCL1, CUGBP2, GNAI1, GNB4, GNG11,

LOC728052, MAB21L2, MAOA, MSN, PLK2, RNF182, SIM1, SLC44A5, SLITRK5 y/o TFPI2, en comparación con los niveles de expresión de estos genes tanto en células de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En aun otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de GNB4, GNG11, PLK2, RNF182, SIM1, SLC44A5 y/o SLITRK5, en comparación con los niveles de expresión de estos genes tanto en células de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En aun otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de GNB4, GNG11, PLK2, RNF182, SIM1, SLC44A5 y/o SLITRK5GNB4, PLK2, SIM1 y/o SLITRK5, en comparación con los niveles de expresión de estos genes tanto en células de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 6 u 8 en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6 y una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 10 o 12 en comparación con los niveles de expresión de estos genes en células de una línea celular SiMa original. En aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 6 u 8 en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6 y una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 10 o 12 en comparación con los niveles de expresión de estos genes en células de una línea celular SiMa original DSMZ ACC 164. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución en los niveles de expresión genética de uno o más genes enumerados en las Tablas 6 u 8 de, por ej., al menos 1.5 veces, al menos

2.0 veces, al menos 2.5 veces, al menos 3.0 veces, al menos 3.5 veces, al menos 4.0 veces, al menos 4.5 veces, al menos 5.0 veces, al menos 5.5 veces, al menos 6.0 veces, al menos 7.0 veces o al menos 8.0 veces en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6 y presentan una disminución en los niveles de expresión genética de uno o más genes enumerados en las Tablas 10 o 12 de, por ej., al menos 1.5 veces, al menos 2.0 veces, al menos 2.5 veces, al menos 3.0 veces, al menos 3.5 veces, al menos 4.0 veces, al menos 4.5 veces, al menos 5.0 veces, al menos 5.5 veces, al menos 6.0 veces, al menos 7.0 veces o al menos 8.0 veces en comparación con los niveles de expresión de estos genes en las células de la línea celular SiMa original DSMZ ACC 164. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución en los niveles de expresión genética de, por ej., 2 o más genes, 3 o más genes, 4 o más genes, 5 o más genes, 6 o más genes, 7 o más genes, 8 o más genes, 9 o más genes, 10 o más genes, 20 o más genes, 30 o más genes, 40 o más genes, 50 o más genes, 60 o más genes, 70 o más genes, 80 o más genes, 90 o más genes o 100 o más genes enumerados en las Tablas 6 u 8 en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6 y enumerados en las Tablas 10 o 12 en comparación con los

niveles de expresión de estos genes de la línea celular SiMa original DSMZ ACC 164. En aun otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoTN/A presentan una disminución en los niveles de expresión genética de, por ej., alrededor de 5 genes a alrededor de 100 genes, alrededor de 10 genes a alrededor de 100 genes, alrededor de 15 genes a alrededor de 100 genes, alrededor de 20 genes a alrededor de 100 genes, alrededor de 25 genes a alrededor de 100 genes, alrededor de 5 genes a alrededor de 75 genes, alrededor de 10 genes a alrededor de 75 genes, alrededor de 15 genes a alrededor de 75 genes, alrededor de 20 genes a alrededor de 75 genes, alrededor de 25 genes a alrededor de 75 genes, alrededor de 5 genes a alrededor de 50 genes, alrededor de 10 genes a alrededor de 50 genes, alrededor de 15 genes a alrededor de 50 genes, alrededor de 20 genes a alrededor de 50 genes o alrededor de 25 genes a alrededor de 50 genes enumerados en las Tablas 6 u 8 en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6 y enumerados en las Tablas 10 o 12 en comparación con los niveles de expresión de estos genes en las células de la línea celular SiMa original DSMZ ACC 164.

En una modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A

presentan una disminución de al menos 1.5 en los niveles de expresión genética de uno o más genes seleccionados de ABTB1, ACOT1, ACYP2, ADARB1, ADCY1, ANKRD50, ASAM, ASPHD1, ATP2B3, BACE1, BRUNOL4, BRWD1, BTN3A3, C16ORF52, C1ORF21, C21ORF57, C2CD2, C2CD4A, C3ORF23, C9ORF150, CAMK2N2, CAP2, CAPN2, CARTPT, CD302, CDH12, CDKN2A, CDS1, CFC1, CLCN3, CLDN12, CLMN, CNGA3, CNNM1, CNOT6L, COL6A1, CYGB, CYLD, CYP2E1, CYTL1, D4S234E, DCLK1, DCTD, DUSP16, EFNB3, ERAP1, ERBB2, ERBB4, ETFDH, FAM162B, FAM165B, FAM46A, FBXW7, FGD5, FGF13, FOXO6, FSTL1, GAL, GLT25D2, GNAS, GPR123, GPX7, GRM5, GUCY1A3, HCG 1776018, HELQ, HERPUD2, HIST1H2AC, HIST1H2BD, HIST1H2BK, HIST2H2BE, HNRNPR, HPCAL1, IL10RB, JMY, KAT2B, KBTBD11, KCNMA1, KCNQ2, KHDC1, KIAA1598, KLHDC1, LGALS3BP, LIFR, LOC100130522, LOC94431, LRP2BP, LYRM5, MAP3K5, MAP9, MCTP1, MEOX2, MFSD4, MGAT4A, MRPS33, MST1, NAP1L3, NCOA7, NCRNA00171, NDUFA4L2, NDUFV3, NEBL, NHEDC2, NIPAL3, NLRX1, NUDT19, OLFM3, PAM, PAPPA, PCNXL2, PDGFRB, PHKA1, PIGH, PLRG1, PLRG1, PPAPDC1A, PRKACB, PRPH, PTGER2, PTN, PTPRD, RAB6B, RGAG4, RHOU, RNF13, RNF41, RSL1D1, SH3GL2, SH3YL1, SIGIRR, SIK1, SLC12A7, SLC22A17, SLC35F3, SNCA, SPINT2, SPOCK2, ST8SIA3, STAR, STEAP3, STOX2, SYNJ1, SYT13, TM2D1, TMEM184C, TMEM5, TMEM59L, TMIE, TTC39C, TUSC3, TXLNB, UCN, WDFY3, WDFY3, ZNF641 y/o ZNF662, en comparación con los niveles de expresión de estos genes en células tanto de la

línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En aun otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ACOT1, ADARB1, ASAM, C2CD4A, C3ORF23, CAP2, CARTPT, CFC1, CNGA3, CYGB, CYP2E1, CYTL1, FGF13, GAL, GPX7, GRM5, HCG 1776018, HIST1H2AC, HIST1H2BD, KCNMA1, KIAA1598, MEOX2, NDUFA4L2, PPAPDC1A, PRKACB, PTGER2, PTN, SLC35F3, SYT13, TMIE, TXLNB y/o ZNF662, en comparación con los niveles de expresión de estos genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ACOT1, ASAM, C2CD4A, C3ORF23, CAP2, CARTPT, CFC1, CNGA3, CYGB, CYP2E1, CYTL1, FGF13, GAL, GPX7, KIAA1598, MEOX2, NDUFA4L2, PPAPDC1A, PTN, SLC35F3, SYT13, TMIE y/o ZNF662, en comparación con los niveles de expresión de estos

genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En aun otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de CAP2, CARTPT, CNGA3, CYGB, CYP2E1, CYTL1, FGF13, GAL, MEOX2, NDUFA4L2, SLC35F3, SYT13, TMIE y/o ZNF662, en comparación con los niveles de expresión de estos genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados CAP2, CDKN2A, CNGA3, FAM162B, FGF13, FOXO6, FSTL1, KCNMA1, KHDC1, LIFR, MCTP1, MEOX2, PPAPDC1A, PTN, SYT13, TMIE y/o ZNF662, en comparación con los niveles de expresión de estos genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En un aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación

por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados CAP2, CDKN2A, CNGA3, FGF13, FOXO6, FSTL1, KCNMA1, KHDC1, MCTP1, MEOX2, PPAPDC1A, PTN, SYT13, TMIE y/o ZNF662, en comparación con los niveles de expresión de estos genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados CNGA3, FGF13, KCNMA1, MEOX2, PPAPDC1A, PTN, SYT13, TMIE y/o ZNF662, en comparación con los niveles de expresión de estos genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En aun otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados CNGA3, FGF13, MEOX2, PPAPDC1A, PTN, SYT13, TMIE y/o ZNF662, en comparación con los niveles de expresión de estos genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En aun otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una disminución de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados CNGA3, FGF13, MEOX2, SYT13, TMIE y/o ZNF662, en comparación con los niveles de expresión de estos genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presenta una diferencia de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 14 o 16 en comparación con los niveles de expresión de estos genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164. En aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una diferencia de al menos 1.5 veces en los niveles de expresión genética de uno o más genes enumerados en las Tablas 14 o 16 en comparación con los niveles de expresión de estos genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptible de intoxicación por BoNT/A

presentan una diferencia en los niveles de expresión genética de uno o más genes enumerados en las Tablas 14 o 16 de, por ej., al menos 1.5 veces, al menos 2.0 veces, al menos 2.5 veces, al menos 3.0 veces, al menos 3.5 veces, al menos 4.0 veces, al menos 4.5 veces, al menos 5.0 veces, al menos 5.5 veces, al menos 6.0 veces, al menos 7.0 veces o al menos 8.0 veces en comparación con los niveles de expresión de estos genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento en los niveles de expresión genética de, por ej., 2 o más genes, 3 o más genes, 4 o más genes, 5 o más genes, 6 o más genes, 7 o más genes, 8 o más genes, 9 o más genes, 10 o más genes, 20 o más genes, 30 o más genes, 40 o más genes, 50 o más genes, 60 o más genes, 70 o más genes, 80 o más genes, 90 o más genes o 100 o más genes enumerados en las Tablas 14 o 16 en comparación con los niveles de expresión de estos genes en las células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164. En aun otros aspectos, las células de una línea celular clonal establecida susceptibles de intoxicación por BoTN/A presentan un aumento en los niveles de expresión genética de, por ej., alrededor de 5 genes a alrededor de 100 genes, alrededor de 10 genes a alrededor de 100 genes, alrededor de 15 genes a alrededor de

100 genes, alrededor de 20 genes a alrededor de 100 genes, alrededor de 25 genes a alrededor de 100 genes, alrededor de 5 genes a alrededor de 75 genes, alrededor de 10 genes a alrededor de 75 genes, alrededor de 15 genes a alrededor de 75 genes, alrededor de 20 genes a alrededor de 75 genes, alrededor de 25 genes a alrededor de 75 genes, alrededor de 5 genes a alrededor de 50 genes, alrededor de 10 genes a alrededor de 50 genes, alrededor de 15 genes a alrededor de 50 genes, alrededor de 20 genes a alrededor de 50 genes o alrededor de 25 genes a alrededor de 50 genes enumerados en las Tablas 14 o 16 en comparación con los niveles de expresión de estos genes en las células de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En una modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una diferencia de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ACOT9, ADAMTS9, ARHGAP24, ARHGEF3, ASCL1, BARD1, BASP1, C3ORF70, C11ORF75, CCDC109B, CD9, CDCA7L, CDK2, CENPL, CLSTN2, CNTN1, CSRP2, CTSL2, CUGBP2, DEPDC1, DIAPH3, DOK5, DPYD, DYNLT3, EMILIN2, ETV1, FAM101B, FBLN1, FGFR2, FNDC5, GNAI1, GNB4, GNG11, GNG12, GPR177, GTSE1, HGF, KITLG, LPAR1, MAB21L2, MAOA, MCM10, MINA, MSN, MYO6, MYRIP, PAG1, PEG3, PLK2, POLA2, PPP1R3C, PRLHR, PRSS12, PTGR1, PTPRK, PVRL3,

RAB32, RBPMS, SDC2, SGOL2, SLC43A3, SLC7A2, SMC2, SMC6, SPARC, SPC25, ST8SIA4, TCF7L1, TFPI2, TMEM35, TMEM178, TNFAIP8, TPTE, TRIP10, TWIST1 y/o ZNF521, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164. En otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una diferencia de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ADAMTS9, ARHGAP24, ASCL1, BARD1, BASP1, BVES, C11ORF75, CDCA7L, CNTN1, CUGBP2, DOK5, DPYD, DYNLT3, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, GTSE1, GTSF1, ITPRIP, KDELC2, LOC728052, LPAR1, MAB21L2, MAOA, MINA, MSN, PEG3, PLK2, PRLHR, PRSS12, PTPRK, RBPMS, RNF182, SGOL2, SLC43A3, SLC44A5, SLC7A2, SMC6, SPARC, TFPI2, TMEM178 y/o TPTE, en comparación con los niveles de expresión de estos genes en las células tanto de la línea celular 2D6 como de la línea celular SiMa original DSZM ACC 164. En aun otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una diferencia de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ADAMTS9, ASCL1, BASP1, DOK5, DPYD, GNB4, GNG11, GTSF1, MAOA, MINA, MSN, PEG3, PLK2, PRSS12, RNF182, SLC44A5, SPARC, TFPI2 y/o TPTE, en comparación con los niveles de expresión de

estos genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ADAMTS9, ARHGAP24, ARHGEF3, ASCL1, BARD1, CD9, CDK2, CSRP2, CTSL2, DIAPH3, DOK5, DYNLT3, EMILIN2, ETV1, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, HGF, KITLG, LPAR1, MCM10, MSN, PAG1, PEG3, PLK2, POLA2, PPP1R3C, PTPRK, RAB32, SDC2, SLC43A3, SLC7A2, SMC6, SPARC, SPC25, ST8SIA4, TCF7L1, TFPI2, TMEM35, TNFAIP8, TPTE, TRIP10 y/o TWIST1, en comparación con los niveles de expresión de estos genes en las células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164. En un aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ADAMTS9, ARHGAP24, ASCL1, BARD1, DOK5, DYNLT3, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, LPAR1, MSN, PEG3, PLK2, PTPRK, SLC43A3, SLC7A2, SMC6, SPARC, TFPI2 y/o TPTE, en comparación con los niveles de expresión de estos genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164. En otro aspecto de

esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ADAMTS9, ASCL1, DOK5, GNB4, GNG11, MSN, PEG3, PLK2, SPARC, TFPI2 y/o TPTE, en comparación con los niveles de expresión de estos genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de ACOT9, BASP1, C11ORF75, CCDC109B, CDCA7L, CLSTN2, CNTN1, CUGBP2, DEPDC1, DPYD, FAM101B, FNDC5, GTSE1, MAOA, MINA, MYO6, MYRIP, PLK2, PRLHR, PVRL3, RBPMS, SGOL2, SMC2, TFP12, TMEM178 y/o ZNF521, en comparación con los niveles de expresión de estos genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164. En un aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de BASP1, C11ORF75, CDCA7L, CNTN1, CUGBP2, DPYD, GTSE1, MAOA, MINA, PLK2, PRLHR, RBPMS, SGOL2, TFPI2 y/o TMEM178, en comparación con los

niveles de expresión de estos genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164. En otro aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de BASP1, DPYD, MAOA, MINA, PLK2 y/o TFPI2, en comparación con los niveles de expresión de estos genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

En aun otra modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de C3ORF70, MAB21L2, PRSS12, CENPL, GPR177 y/o PTGR1, en comparación con los niveles de expresión de estos genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164. En un aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan un aumento de al menos 1.5 veces en los niveles de expresión genética de uno o más genes seleccionados de MAB21L2 y/o PRSS12, en comparación con los niveles de expresión de estos

genes en células tanto de la línea celular 2D6 como de la línea celular SiMa original DSMZ ACC 164.

Los aspectos de la presente descripción comprenden, en parte, células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A que presentan una EC_{50} equivalente o menor para la actividad de la BoNT/A con respecto a la EC_{50} para la actividad de la BoNT/A de células de una línea celular SiMa original. En un aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles a intoxicación por BoNT/A que presentan una EC_{50} equivalente o menor para la actividad de la BoNT/A con respecto a la EC_{50} para la actividad de la BoNT/A de células de una línea celular SiMa original DSMZ ACC 164. En un aspecto de esta modalidad, las células de una línea celular clonal establecida susceptibles a intoxicación por BoNT/A presentan una EC_{50} equivalente para la actividad de la BoNT/A con respecto a la EC_{50} para la actividad de la BoNT/A de células de una línea celular SiMa original DSMZ ACC 164. En aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una EC_{50} menor para la actividad de la BoNT/A de, por ej., al menos 10%, al menos 20%, al menos 30%, al menos 40%, al menos 50%, al menos 60%, al menos 70%, al menos 80%, al menos 90% o al menos 100% con respecto a la EC_{50} para

la actividad de la BoNT/A de células de la línea celular SiMA original DSMZ ACC 164. En otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una EC_{50} menor para la actividad de la BoNT/A de, por ej., al menos 110%, al menos 120%, al menos 130%, al menos 140%, al menos 150%, al menos 160%, al menos 170%, al menos 180%, al menos 190% o al menos 200% con respecto a la EC_{50} para la actividad de la BoNT/A de células de la línea celular SiMA original DSMZ ACC 164. En aun otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una EC_{50} menor para la actividad de la BoNT/A de, por ej., al menos 225%, al menos 250%, al menos 275%, al menos 300%, al menos 325%, al menos 350%, al menos 375%, al menos 400%, al menos 425%, al menos 450%, al menos 475% o al menos 500% con respecto a la EC_{50} para la actividad de la BoNT/A de células de la línea celular SiMA original DSMZ ACC 164. En aun otros aspectos de esta modalidad, las células de una línea celular clonal establecida susceptibles de intoxicación por BoNT/A presentan una EC_{50} para actividad de la BoNT/A de, por ej., 10 pM o menos, 9 pM o menos, 8 pM o menos, 7 pM o menos, 6 pM o menos, 5 pM o menos, 4 pM o menos, 3.0 pM o menos, 2.9 pM o menos, 2.8 pM o menos, 2.7 pM o menos, 2.6 pM o menos, 2.5 pM o menos, 2.4 pM o menos, 2.3 pM o menos, 2.2 pM o menos, 2.1

pM o menos, 2.0 pM o menos, 1.9 pM o menos, 1.8 pM o menos, 1.7 pM o menos, 1.6 pM o menos, 1.5 pM o menos, 1.4 pM o menos, 1.3 pM o menos, 1.2 pM o menos, 1.1 pM o menos, 1.0 pM o menos, 0.9 pM o menos, 0.8 pM o menos, 0.7 pM o menos, 0.6 pM o menos, 0.5 pM o menos, 0.4 pM o menos, 0.3 pM o menos, 0.2 pM o menos o 0.1 pM o menos.

Los aspectos de la presente descripción comprenden, en parte, una BoNT/A. Como se utiliza en la presente, el término "BoNT/A" es sinónimo de "serotipo A de la neurotoxina botulínica" o "neurotoxina botulínica tipo A" y se refiere tanto a una BoNT/A de origen natural como a una BoNT/A de origen no natural de la misma e incluye un complejo de BoNT/A que comprende la neurotoxina BoNT/A de alrededor de 150 kDa y proteínas no asociadas con toxinas (NAP) asociadas, así como la neurotoxina BoNT/A de alrededor de 150 kDa sola. Los ejemplos no taxativos de complejos de BoNT/A incluyen, por ej., el complejo de BoNT/A de 900 kDa, el complejo de BoNT/A de 500 kDa y el complejo de BoNT/A de 300 kDa. Los ejemplos no taxativos de la neurotoxina BoNT/A de alrededor de 150 kDa incluyen, por ej., la SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4.

Como se utiliza en la presente, el término "BoNT/A de origen natural" se refiere a cualquier BoNT/A producida por

un proceso de origen natural, incluyendo, a modo no taxativo, isoformas de la BoNT/A producidas a partir de una modificación postraduccional, una transcripción alternativamente empalmada o una mutación espontánea y subtipos de la BoNT/A, como, por ej., un subtipo de la BoNT/A1, subtipo de la BoNT/A2, subtipo de la BoNT/A3, subtipo de la BoNT/A4 y subtipo de la BoNT/A5. Una BoNT/A de origen natural incluye, a modo no taxativo, la SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4 o una que sustituya, elimine o agregue, por ej., 1 o más, 2 o más, 3 o más, 4 o más, 5 o más, 6 o más, 7 o más, 8 o más, 9 o más, 10 o más, 20 o más, 30 o más, 40 o más, 50 o más o 100 aminoácidos de la SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3 o SEQ ID NO: 4. Las composiciones farmacéuticas comercialmente disponibles de una BoNT/A de origen natural incluyen, a modo no taxativo, BOTOX® (Allergan, Inc., Irvine, CA), DYSPORT®/RELOXIN®, (Ipsen Ltd., Slough, Inglaterra), PURTOX® (Mentor Corp., Santa Bárbara, CA), XEOMIN® (Merz Pharmaceuticals, GmbH., Frankfurt, Alemania), NEURONOX® (Medy-Tox, Inc., Ochang-myeon, Corea del Sur) y BTX-A.

Como se utiliza en la presente, el término "BoNT/A de origen no natural" se refiere a cualquier BoNT/A cuya estructura se modificó con la ayuda de la manipulación humana, incluyendo, a modo no taxativo, una BoNT/A con una

secuencia de aminoácidos alterada producida mediante modificación genética usando mutagénesis aleatoria o diseño racional y una BoNT/A producida mediante síntesis química in vitro. Ejemplos no taxativos de BoNT/A de origen no natural se describen, por ej., en Steward, L.E. et al., *Post-translational Modifications and Clostridial Neurotoxins*, patente estadounidense No. 7,223,577; Dolly, J.O. et al., *Activatable Clostridial Toxins*, patente estadounidense No. 7,419,676; Steward, L.E. et al., *Clostridial Neurotoxin Compositions and Modified Clostridial Neurotoxins*, US 2004/0220386; Steward, L.E. et al., *Modified Clostridial Toxins With Enhanced Targeting Capabilities For Endogenous Clostridial Toxin Receptor Systems*, publicación de patente estadounidense No. 2008/0096248; Steward, L.E. et al., *Modified Clostridial Toxins With Altered Targeting Capabilities For Clostridial Toxin Target Cells*, publicación de patente estadounidense No. 2008/0161543; Steward, L.E. et al., *Modified Clostridial Toxins With Enhanced Translocation Capabilities and Altered Targeting Activity For Clostridial Toxin Target Cells*, publicación de patente estadounidense No. 2008/0241881, cada una de las cuales se incorpora en su totalidad a la presente mediante esta referencia.

Por consiguiente, en una modalidad, la actividad de la BoNT/A que se detecta proviene de una BoNT/A de origen

natural. En aspectos de la presente modalidad, la actividad de la BoNT/A que se detecta proviene de una isoforma de la BoNT/A o un subtipo de la BoNT/A. En aspectos de la presente modalidad, la actividad de la BoNT/A que se detecta proviene de la BoNT/A de la SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3 o SEQ ID NO: 4. En otros aspectos de la presente modalidad, la actividad de la BoNT/A que se detecta proviene de una BoNT/A que tiene, por ej., al menos 70%, al menos 75%, al menos 80%, al menos 85%, al menos 90% o al menos 95% de identidad de aminoácidos con la SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3 o SEQ ID NO: 4. En otros aspectos de la presente modalidad, la actividad de la BoNT/A que se detecta proviene de BOTOX®, DYSPORT®/RELOXIN®, PURTOX®, XEOMIN®, NEURONOX® o BTX-A.

En otra modalidad, la actividad de la BoNT/A que se detecta proviene de una BoNT/A de origen no natural. En otros aspectos de la presente modalidad, la actividad de la BoNT/A que se detecta proviene de una variante de la BoNT/A de origen no natural que tiene, por ej., al menos 70%, al menos 75%, al menos 80%, al menos 85%, al menos 90% o al menos 95% de identidad de aminoácidos con la SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3 o SEQ ID NO: 4. En otros aspectos de la presente modalidad, la actividad de la BoNT/A que se detecta proviene de una variante de la BoNT/A de origen no natural que tiene, por ej., 1 o más, 2 o más, 3 o más, 4 o más, 5 o

más, 6 o más, 7 o más, 8 o más, 9 o más, 10 o más, 20 o más, 30 o más, 40 o más, 50 o más o 100 o más sustituciones, eliminaciones o adiciones de aminoácidos no contiguos con relación a la SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3 o SEQ ID NO: 4. En aun otros aspectos de la presente modalidad, la actividad de la BoNT/A que se detecta proviene de una variante de la BoNT/A de origen no natural que tiene, por ej., 1 o más, 2 o más, 3 o más, 4 o más, 5 o más, 6 o más, 7 o más, 8 o más, 9 o más, 10 o más, 20 o más, 30 o más, 40 o más, 50 o más o 100 o más sustituciones, eliminaciones o adiciones de aminoácidos contiguos con relación a la SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3 o SEQ ID NO: 4.

Los aspectos de la presente descripción comprenden, en parte, una SNAP-25. Como se utiliza en la presente, el término "SNAP-25" se refiere a una SNAP-25 de origen natural o una SNAP-25 de origen no natural que se escinde preferentemente mediante una BoNT/A. Como se utiliza en la presente, el término "se escinde preferentemente" se refiere a que la tasa de escisión de un sustrato de la BoNT/A mediante una BoNT/A es al menos un orden de magnitud mayor a la tasa de escisión de cualquier otro sustrato mediante una BoNT/A. En aspectos de la presente modalidad, la tasa de escisión de un sustrato de la BoNT/A mediante una BoNT/A es al menos dos órdenes de magnitud mayor, al menos tres órdenes

de magnitud mayor, al menos cuatro órdenes de magnitud mayor o al menos cinco órdenes de magnitud mayor que la tasa de escisión de cualquier otro sustrato mediante la BoNT/A.

Como se utiliza en la presente, el término "SNAP-25 de origen natural" se refiere a cualquier SNAP-25 producida mediante un proceso de origen natural, incluyendo, a modo no taxativo, isoformas de la SNAP-25 producidas a partir de una modificación postraduccional, una transcripción alternativamente empalmada o una mutación espontánea y subtipos de la SNAP-25. Una SNAP-25 de origen natural incluye, a modo no taxativo, la SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23 o SEQ ID NO: 24 o una que sustituya, elimine o agregue, por ej., 1 o más, 2 o más, 3 o más, 4 o más, 5 o más, 6 o más, 7 o más, 8 o más, 9 o más, 10 o más, 20 o más, 30 o más, 40 o más, 50 o más o 100 o más aminoácidos de la SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23 o SEQ ID NO: 24.

Como se utiliza en la presente, el término "SNAP-25 de origen no natural" se refiere a cualquier SNAP-25 cuya estructura se modificó con la ayuda de la manipulación humana, incluyendo, a modo no taxativo, una SNAP-25 producida mediante modificación genética usando mutagénesis aleatoria o diseño racional y una SNAP-25 producida mediante síntesis química in vitro. Los ejemplos no taxativos de SNAP-25 de origen no natural se describen, por ej., en Steward, L.E. et al., *FRET Protease Assays for Clostridial Toxins*, patente estadounidense 7,332,567; Fernandez-Salas et al., *Lipohilic Dye-based FRET Assays for Clostridial Toxin Activity*, publicación de patente estadounidense 2008/0160561, cada uno de los cuales se incorpora en su totalidad a la presente mediante esta referencia. Una SNAP-25 de origen no natural puede sustituir, eliminar o agregar, por ej., 1 o más, 2 o más, 3 o más, 4 o más, 5 o más, 6 o más, 7 o más, 8 o más, 9 o más, 10 o más, 20 o más, 30 o más, 40 o más, 50 o más o 100 o más aminoácidos de la SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23 o SEQ ID NO: 24.

Por consiguiente, en una modalidad, una SNAP-25 es una SNAP-25 de origen natural. En aspectos de la presente modalidad, la SNAP-25 es una isoforma de la SNAP-25 o un subtipo de la SNAP-25. En aspectos de la presente modalidad, la SNAP-25 de origen natural es la SNAP-25 de origen natural de la SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23 o SEQ ID NO: 24. En otros aspectos de la presente modalidad, la SNAP-25 es una SNAP-25 de origen natural que tiene, por ej., al menos 70% de identidad de aminoácidos, al menos 75%, al menos 80%, al menos 85%, al menos 90% o al menos 95% de identidad de aminoácidos con la SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23 o SEQ ID NO: 24.

En otra modalidad, una SNAP-25 es una SNAP-25 de origen no natural. En otros aspectos de la presente modalidad, la SNAP-25 es una SNAP-25 de origen no natural que tiene, por ej., al menos 70%, al menos 75%, al menos 80%, al menos 85%,

al menos 90% o al menos 95% de identidad de aminoácidos con la SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23 o SEQ ID NO: 24. En otros aspectos de la presente modalidad, la SNAP-25 es una SNAP-25 de origen no natural que tiene, por ej., 1 o más, 2 o más, 3 o más, 4 o más, 5 o más, 6 o más, 7 o más, 8 o más, 9 o más, 10 o más, 20 o más, 30 o más, 40 o más, 50 o más o 100 o más sustituciones, eliminaciones o adiciones de aminoácidos no contiguos con relación a la SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23 o SEQ ID NO: 24. En aun otros aspectos de la presente modalidad, la SNAP-25 es una SNAP-25 de origen no natural que tiene, por ej., 1 o más, 2 o más, 3 o más, 4 o más, 5 o más, 6 o más, 7 o más, 8 o más, 9 o más, 10 o más, 20 o más, 30 o más, 40 o más, 50 o más o 100 o más sustituciones, eliminaciones o adiciones de aminoácidos contiguos con relación a la SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID

NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23 o SEQ ID NO: 24.

Una SNAP-25 puede ser una SNAP-25 endógena o una SNAP-25 exógena. Como se utiliza en la presente, el término "SNAP-25 endógena" se refiere a una SNAP-25 que se encuentra naturalmente presente en la célula debido a que se codifica naturalmente en el genoma de la célula, de forma que la célula expresa inherentemente la SNAP-25 sin necesidad de una fuente externa de la SNAP-25 o una fuente externa de material genético que codifique una SNAP-25. La expresión de una SNAP-25 endógena puede producirse con o sin estimulación ambiental como, por ej., diferenciación celular. Por definición, una SNAP-25 endógena solo puede ser una SNAP-25 de origen natural o variantes de la misma. Por ejemplo, las siguientes líneas celulares establecidas expresan una SNAP-25 endógena: BE(2)-M17, Kelly, LA1-55n, N1E-115, N4TG3, N18, Neuro-2a, NG108-15, PC12, SH-SY5Y, SiMa y SK-N-BE(2)-C.

Como se utiliza en la presente, el término "SNAP-25 exógena" se refiere a una SNAP-25 expresada en una célula a través de la introducción de una fuente externa de la SNAP-25 o una fuente externa de material genético que codifica una SNAP-25 mediante manipulación humana. La expresión de una

SNAP-25 exógena se puede producir con o sin estimulación ambiental como, por ej., diferenciación celular. Como un ejemplo no taxativo, las células de una línea celular clonal establecida pueden expresar una SNAP-25 exógena mediante transfección transitoria o estable de una secuencia que codifica la SNAP-25. Como otro ejemplo no taxativo, las células de una línea celular clonal establecida pueden expresar una SNAP-25 exógena mediante la transfección de proteínas de una SNAP-25. Una SNAP-25 exógena puede ser una SNAP-25 de origen natural o variantes de la misma o una SNAP-25 de origen no natural o variantes de la misma.

Por consiguiente, en una modalidad, las células de una línea celular clonal establecida expresan una SNAP-25 endógena. En aspectos de la presente modalidad, la SNAP-25 endógena expresada por células de una línea celular clonal establecida es una SNAP-25 de origen natural. En otros aspectos de la presente modalidad, la SNAP-25 endógena expresada por células de una línea celular clonal establecida es la SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23 o SEQ ID NO: 24. En aun otros aspectos de la presente modalidad, la SNAP-25

endógena expresada por células de una línea celular clonal establecida es una SNAP-25 de origen natural, como, por ej., una isoforma de la SNAP-25 o un subtipo de la SNAP-25. En otros aspectos de la presente modalidad, la SNAP-25 endógena expresada por células de una línea celular clonal establecida es una SNAP-25 de origen natural que tiene, por ej., al menos 70% de identidad de aminoácidos, al menos 75%, al menos 80%, al menos 85%, al menos 90% o al menos 95% de identidad de aminoácidos con la SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23 o SEQ ID NO: 24.

En otra modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar una SNAP-25 exógena. En un aspecto de la presente modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar una SNAP-25 de origen natural. En otros aspectos de la presente modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar la SNAP-25 de origen natural de la SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ

ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23 o SEQ ID NO: 24. En aun otros aspectos de la presente modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar una SNAP-25 de origen natural, como, por ej., una isoforma de la SNAP-25 o un subtipo de la SNAP-25. En aun otros aspectos de la presente modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar una SNAP-25 de origen natural que tiene, por ej., al menos 70% de identidad de aminoácidos, al menos 75%, al menos 80%, al menos 85%, al menos 90% o al menos 95% de identidad de aminoácidos con la SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23 o SEQ ID NO: 24.

En otro aspecto de la modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar una SNAP-25 de origen no natural. En otros aspectos de la presente modalidad, las

células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar una SNAP-25 de origen no natural que tiene, por ej., al menos 70%, al menos 75%, al menos 80%, al menos 85%, al menos 90% o al menos 95% de identidad de aminoácidos con la SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23 o SEQ ID NO: 24. En otros aspectos de la presente modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar una SNAP-25 de origen no natural que tiene, por ej., 1 o más, 2 o más, 3 o más, 4 o más, 5 o más, 6 o más, 7 o más, 8 o más, 9 o más, 10 o más, 20 o más, 30 o más, 40 o más, 50 o más o 100 o más sustituciones, eliminaciones o adiciones de aminoácidos no contiguos con relación a la SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23 o SEQ ID NO: 24. En aun otros aspectos de la presente modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar una SNAP-25 de origen no

natural que tiene, por ej., 1 o más, 2 o más, 3 o más, 4 o más, 5 o más, 6 o más, 7 o más, 8 o más, 9 o más, 10 o más, 20 o más, 30 o más, 40 o más, 50 o más o 100 o más sustituciones, eliminaciones o adiciones de aminoácidos contiguos con relación a la SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23 o SEQ ID NO: 24.

Se pueden usar los ensayos que detectan la escisión del sustrato de la BoNT/A luego de la exposición a una BoNT/A para evaluar si una célula expresa una SNAP-25 endógena o exógena. En estos ensayos, se detectaría la generación de un producto de la escisión de la SNAP-25 en células que expresan una SNAP-25 luego del tratamiento con una BoNT/A. Los ejemplos no taxativos de un análisis de transferencia Western específico, así como reactivos, condiciones y protocolos bien caracterizados se encuentran fácilmente disponibles en vendedores comerciales que incluyen, a modo no taxativo, Amersham Biosciences, Piscataway, NJ; Bio-Rad Laboratories, Hercules, CA; Pierce Biotechnology, Inc., Rockford, IL; Promega Corporation, Madison, WI y Stratagene, Inc., La Jolla, CA. Se comprende que estos ensayos y ensayos similares

para la escisión de la SNAP-25 pueden ser útiles para identificar células que expresen una SNAP-25 endógena o exógena.

Como ejemplo no taxativo, se puede usar el análisis de transferencia Western utilizando un anticuerpo que reconoce el producto escindido de la SNAP-25 de la BoNT/A o las formas escindida y no escindida de la SNAP-25 para analizar la absorción de BoNT/A. Los ejemplos de anticuerpos α-SNAP-25 útiles para estos ensayos incluyen, a modo no taxativo, el anticuerpo monoclonal de ratón α-SNAP-25 SMI-81 (Sternberger Monoclonals Inc., Lutherville, MD), anticuerpo monoclonal α-SNAP-25 de ratón CI 71.1 (Synaptic Systems, Goettingen, Alemania), un anticuerpo monoclonal de ratón α-SNAP-25 CI 71.2 (Synaptic Systems, Goettingen, Alemania), anticuerpo monoclonal de ratón α-SNAP-25 SP12 (Abcam, Cambridge, MA), antisuero policlonal de conejo α-SNAP-25 (Synaptic Systems, Goettingen, Alemania), antisuero policlonal de conejo α-SNAP-25 (Abcam, Cambridge, MA) y antisuero policlonal de conejo α-SNAP-25 S9684 (Sigma, San Luis, MO).

Los aspectos de la presente descripción comprenden, en parte, un receptor de BoNT/A. Como se utiliza en la presente, el término "receptor de BoNT/A" se refiere a un receptor de BoNT/A de origen natural o un receptor de BoNT/A de origen no

natural que interactúa preferentemente con la BoNT/A de forma tal que provoca una respuesta a la intoxicación por BoNT/A. Como se utiliza en la presente, el término "interactúa preferentemente" se refiere a que la constante de disociación de equilibrio (KD) de la BoNT/A con respecto a un receptor de BoNT/A es al menos un orden de magnitud menor a la de la BoNT/A con respecto a cualquier otro receptor. La constante de disociación de equilibrio, es un tipo específico de constante de equilibrio que mide la propensión de un complejo de BoNT/A-receptor de BoNT/A a separarse (disociarse) de forma invertible en las moléculas que lo componen, a saber, el complejo de BoNT/A y el receptor de BoNT/A. La constante de disociación se define como KD=[L][R]/[C], donde [L] es igual a la concentración molar de la BoNT/A, [R] es la concentración molar de un receptor de BoNT/A y [C] es la concentración molar del complejo de BoNT/A-receptor de BoNT/A y donde todas las concentraciones se refieren a tales componentes cuando el sistema se encuentra en equilibrio. Cuanto menor es la constante de disociación, más estrecha es la unión de la BoNT/A con su receptor o mayor es la afinidad de unión entre la BoNT/A y el receptor de BoNT/A. En aspectos de la presente modalidad, la constante de disociación de la BoNT/A con respecto al receptor de BoNT/A es al menos dos órdenes de magnitud menor, al menos tres órdenes de magnitud menor, al menos cuatro órdenes de magnitud menor o al menos

cinco órdenes de magnitud menor que la de la BoNT/A con respecto a cualquier otro receptor. En otros aspectos de la presente modalidad, la afinidad de unión de una BoNT/A que interactúa preferentemente con un receptor de BoNT/A puede tener una constante de disociación de equilibrio, por ej., de 500 nM o menor, 400 nM o menor, 300 nM o menor, 200 o menor o 100 nM o menor. En otros aspectos de la presente modalidad, la afinidad de unión de una BoNT/A que interactúa preferentemente con un receptor de BoNT/A puede tener una constante de disociación de equilibrio, por ej., de 90 nM o menos, 80 nM o menos, 70 nM o menos, 60 o menos, 50 nM o menos, 40 nM o menos, 30 nM o menos, 20 nM o menos o 10 nM o menos. Como se utiliza en la presente, el término "provoca una respuesta a la intoxicación por BoNT/A" se refiere a la capacidad de un receptor de BoNT/A de interactuar con una BoNT/A para formar un complejo de neurotoxina/receptor y la posterior internalización de ese complejo en el citoplasma celular.

Como se utiliza en la presente, el término "receptor de BoNT/A de origen natural" se refiere a cualquier receptor de BoNT/A producido mediante un proceso de origen natural, incluyendo, a modo no taxativo, isoformas del receptor de BoNT/A producidas a partir de una modificación postraduccional, una transcripción alternativamente empalmada

o una mutación espontánea y subtipos del receptor de BoNT/A. Un receptor de BoNT/A de origen natural incluye, a modo no taxativo, un receptor del factor de crecimiento de fibroblastos 2 (FGFR2), un receptor del factor de crecimiento de fibroblastos 3 (FGFR3), una glucoproteína de vesícula sináptica 2 (SV2) y un ganglиósido complejo como GT1b, como los descritos en Ester Fernandez-Salas, et al., *Botulinum Toxin Screening Assays*, publicación de patente estadounidense 2008/0003240; Ester Fernandez-Salas, et al., *Botulinum Toxin Screening Assays*, publicación de patente estadounidense 2008/0182799; Min Dong et al., *SV2 is the Protein Receptor for Botulinum Neurotoxin A*, Science (2006); S. Mahrhold et al, *The Synaptic Vesicle Protein 2C Mediates the Uptake of Botulinum Neurotoxin A into Phrenic Nerves*, 580(8) FEBS Lett. 2011-2014 (2006), cada una de las cuales se incorpora en su totalidad a la presente mediante esta referencia. Un FGFR2 de origen natural incluye, a modo no taxativo, la SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69 y la SEQ ID NO: 70 o una que sustituya, elimine o agregue, por ej., 1 o más, 2 o más, 3 o más, 4 o más, 5 o más, 6 o más, 7 o más, 8 o más, 9 o más, 10 o más, 20 o más, 30 o más, 40 o más, 50 o más o 100 o más aminoácidos de la SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO:

65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69 y la SEQ ID NO: 70. Un FGFR3 de origen natural incluye, a modo no taxativo, la SEQ ID NO: 25, SEQ ID NO: 26 y la SEQ ID NO: 27 o una que sustituya, elimine o agregue, por ej., 1 o más, 2 o más, 3 o más, 4 o más, 5 o más, 6 o más, 7 o más, 8 o más, 9 o más, 10 o más, 20 o más, 30 o más, 40 o más, 50 o más o 100 o más aminoácidos de la SEQ ID NO: 25, SEQ ID NO: 26 y la SEQ ID NO: 27. Un SV2 de origen natural incluye, a modo no taxativo, la SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30 y la SEQ ID NO: 31 o una que sustituya, elimine o agregue, por ej., 1 o más, 2 o más, 3 o más, 4 o más, 5 o más, 6 o más, 7 o más, 8 o más, 9 o más, 10 o más, 20 o más, 30 o más, 40 o más, 50 o más o 100 o más aminoácidos de la SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30 y la SEQ ID NO: 31.

Como se utiliza en la presente, el término "variante del receptor de BoNT/A de origen no natural" se refiere a cualquier receptor de BoNT/A producido con la ayuda del diseño o la manipulación humana, incluyendo, a modo no taxativo, un receptor de BoNT/A producido mediante modificación genética usando mutagénesis aleatoria o diseño racional y un receptor de BoNT/A producido mediante síntesis química. Los ejemplos no taxativos de variantes de BoNT/A de origen no natural incluyen, por ej., variantes conservadoras del receptor de BoNT/A, variantes no conservadoras del

receptor de BoNT/A, variantes quiméricas del receptor de BoNT/A y fragmentos activos del receptor de BoNT/A.

Como se utiliza en la presente, el término "receptor de BoNT/A de origen no natural" se refiere a cualquier receptor de BoNT/A cuya estructura se modificó con la ayuda de la manipulación humana, incluyendo, a modo no taxativo, un receptor de BoNT/A producido mediante modificación genética usando mutagénesis aleatoria o diseño racional y un receptor de BoNT/A producido mediante síntesis química in vitro. Los ejemplos no taxativos de receptores de BoNT/A de origen no natural se describen, por ej., en Ester Fernandez-Salas, et al., *Botulinum Toxin Screening Assays*, publicación de patente estadounidense 2008/0003240; Ester Fernandez-Salas, et al., *Botulinum Toxin Screening Assays*, publicación de patente estadounidense 2008/0182799, cada una de las cuales se incorpora en su totalidad a la presente mediante esta referencia. Un receptor de BoNT/A de origen no natural puede sustituir, eliminar o agregar, por ej., 1 o más, 2 o más, 3 o más, 4 o más, 5 o más, 6 o más, 7 o más, 8 o más, 9 o más, 10 o más, 20 o más, 30 o más, 40 o más, 50 o más o 100 o más aminoácidos de la SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO:

66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69 o SEQ ID NO: 70.

Por consiguiente, en una modalidad, un receptor de BoNT/A es un receptor de BoNT/A de origen natural como, por ej., el FGFR2, el FGFR3 o el SV2. En aspectos de la presente modalidad, el receptor de BoNT/A es una isoforma del receptor de BoNT/A o un subtipo del receptor de BoNT/A. En aspectos de la presente modalidad, el receptor de BoNT/A de origen natural es el receptor de BoNT/A de origen natural de la SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69 o SEQ ID NO: 70. En otros aspectos de la presente modalidad, el receptor de BoNT/A es un receptor de BoNT/A de origen natural que tiene, por ej., al menos 70% de identidad de aminoácidos, al menos 75%, al menos 80%, al menos 85%, al menos 90% o al menos 95% de identidad de aminoácidos con la SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69 o SEQ ID NO: 70.

En otra modalidad, un receptor de BoNT/A es un receptor de BoNT/A de origen no natural, como, por ej., un FGFR2 modificado genéticamente, un FGFR3 modificado genéticamente o un SV2 modificado genéticamente. En otros aspectos de la presente modalidad, el receptor de BoNT/A es un receptor de BoNT/A de origen no natural que tiene, por ej., al menos 70%, al menos 75%, al menos 80%, al menos 85%, al menos 90% o al menos 95% de identidad de aminoácidos con la SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69 o SEQ ID NO: 70. En otros aspectos de la presente modalidad, el receptor de BoNT/A es un receptor de BoNT/A de origen no natural que tiene, por ej., 1 o más, 2 o más, 3 o más, 4 o más, 5 o más, 6 o más, 7 o más, 8 o más, 9 o más, 10 o más, 20 o más, 30 o más, 40 o más, 50 o más o 100 o más sustituciones, eliminaciones o adiciones de aminoácidos no contiguos con relación a la SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69 o SEQ ID NO: 70. En aun otros aspectos de la presente modalidad, el receptor de BoNT/A es un receptor de BoNT/A de

origen no natural que tiene, por ej., 1 o más, 2 o más, 3 o más, 4 o más, 5 o más, 6 o más, 7 o más, 8 o más, 9 o más, 10 o más, 20 o más, 30 o más, 40 o más, 50 o más o 100 o más sustituciones, eliminaciones o adiciones de aminoácidos contiguos con relación a la SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69 o SEQ ID NO: 70.

Un receptor de BoNT/A puede ser un receptor endógeno de BoNT/A o un receptor exógeno de BoNT/A. Como se utiliza en la presente, el término "receptor endógeno de BoNT/A" se refiere a un receptor de BoNT/A que se encuentra naturalmente presente en la célula debido a que está naturalmente codificado en el genoma celular, de forma que la célula exprese inherentemente el receptor de BoNT/A sin necesidad de una fuente externa de receptor de BoNT/A o una fuente externa de material genético que codifique el receptor de BoNT/A. La expresión de un receptor endógeno de BoNT/A puede producirse con o sin estimulación ambiental, como, por ej., diferenciación celular o activación de promotores. Por ejemplo, las siguientes líneas celulares clonales establecidas expresan al menos un receptor endógeno de

BoNT/A: BE(2)-M17, Kelly, LA1-55n, N1E-115, N4TG3, N18, Neuro-2a, NG108-15, PC12, SH-SY5Y, SiMa y SK-N-BE(2)-C. Un receptor endógeno de BoNT/A puede ser solamente un receptor de BoNT/A de origen natural o variantes de origen natural del mismo.

Como se utiliza en la presente, el término "receptor exógeno de BoNT/A" se refiere a un receptor de BoNT/A expresado en una célula a través de la introducción de una fuente externa de receptor de BoNT/A o una fuente externa de material genético que codifica un receptor de BoNT/A mediante manipulación humana. La expresión de un receptor exógeno de BoNT/A puede producirse con o sin estimulación ambiental como, por ej., diferenciación celular o activación de promotores. Como ejemplo no taxativo, las células de una línea celular clonal establecida pueden expresar uno o más receptores exógenos de BoNT/A mediante la transfección transitoria o estable de una molécula de polinucleótidos que codifique un receptor de BoNT/A como, por ej., un FGFR2, un FGFR3 o un SV2. Como otro ejemplo no taxativo, las células de una línea celular clonal establecida pueden expresar uno o más receptores exógenos de BoNT/A mediante la transfección proteica de receptores de BoNT/A como, por ej., un FGFR2, un FGFR3 o un SV2. Un receptor exógeno de BoNT/A puede ser un receptor de BoNT/A de origen natural o variantes de origen

natural del mismo o un receptor de BoNT/A de origen no natural o variantes de origen no natural del mismo.

Por consiguiente, en una modalidad, las células de una línea celular clonal establecida expresan un receptor endógeno de BoNT/A. En aspectos de la presente modalidad, el receptor endógeno de BoNT/A expresado por células de una línea celular clonal establecida es un receptor de BoNT/A de origen natural. En otros aspectos de la presente modalidad, el receptor endógeno de BoNT/A expresado por células de una línea celular clonal establecida es la SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69 o SEQ ID NO: 70. En aun otros aspectos de la presente modalidad, el receptor endógeno de BoNT/A expresado por células de una línea celular clonal establecida es un receptor de BoNT/A de origen natural como, por ej., una isoforma del receptor de BoNT/A o un subtipo del receptor de BoNT/A. En otros aspectos de la presente modalidad, el receptor endógeno de BoNT/A expresado por células de una línea celular clonal establecida es un receptor de BoNT/A de origen natural que tiene, por ej., al menos 70% de identidad de aminoácidos, al menos 75%, al menos 80%, al menos 85%, al

menos 90% o al menos 95% de identidad de aminoácidos con la SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69 o SEQ ID NO: 70.

En otra modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar un receptor exógeno de BoNT/A. En un aspecto de la presente modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar un receptor de BoNT/A de origen natural. En otros aspectos de la presente modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar el receptor de BoNT/A de origen natural de la SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69 o SEQ ID NO: 70. En aun otros aspectos de la presente modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar un receptor de BoNT/A de origen natural como, por

ej., una isoforma del receptor de BoNT/A o un subtipo del receptor de BoNT/A. En aun otros aspectos de la presente modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar un receptor de BoNT/A de origen natural que tiene, por ej., al menos 70% de identidad de aminoácidos, al menos 75%, al menos 80%, al menos 85%, al menos 90% o al menos 95% de identidad de aminoácidos con la SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69 o SEQ ID NO: 70.

En otro aspecto de la presente modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar un receptor de BoNT/A de origen no natural. En otros aspectos de la presente modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar un receptor de BoNT/A de origen no natural que tiene, por ej., al menos 70%, al menos 75%, al menos 80%, al menos 85%, al menos 90% o al menos 95% de identidad de aminoácidos con la SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO:

31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69 o SEQ ID NO: 70. En otros aspectos de la presente modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar un receptor de BoNT/A de origen no natural que tiene, por ej., 1 o más, 2 o más, 3 o más, 4 o más, 5 o más, 6 o más, 7 o más, 8 o más, 9 o más, 10 o más, 20 o más, 30 o más, 40 o más, 50 o más o 100 o más sustituciones, eliminaciones o adiciones de aminoácidos no contiguos con relación a la SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69 o SEQ ID NO: 70. En aun otros aspectos de la presente modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar un receptor de BoNT/A de origen no natural que tiene, por ej., 1 o más, 2 o más, 3 o más, 4 o más, 5 o más, 6 o más, 7 o más, 8 o más, 9 o más, 10 o más, 20 o más, 30 o más, 40 o más, 50 o más o 100 o más sustituciones, eliminaciones o adiciones de aminoácidos contiguos con relación a la SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID

NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69 o SEQ ID NO: 70

En otra modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar un FGFR2 exógeno, un FGFR3 exógeno, un SV2 exógeno o cualquier combinación de los mismos. En aspectos de la presente modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar un FGFR2 de origen natural, un FGFR3 de origen natural, un SV2 de origen natural o cualquier combinación de los mismos. En aun otros aspectos de la presente modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar un FGFR2 de origen no natural, un FGFR3 de origen no natural, un SV2 de origen no natural o cualquier combinación de los mismos. En aun otros aspectos de la presente modalidad, las células de una línea celular clonal establecida se modifican de forma transitoria o estable para expresar un FGFR2 de origen natural o un FGFR2 de origen no natural, un FGFR3 de origen natural o un FGFR3 de origen no natural, un SV2 de origen natural o un SV2 de origen no natural o cualquier combinación de los mismos.

Las células que expresan uno o más receptores endógenos o exógenos de BoNT/A se pueden identificar a través de métodos de rutina que incluyen ensayos directos e indirectos para analizar la absorción de toxinas. Los ensayos que determinan las propiedades de absorción o unión de la BoNT/A se pueden usar para evaluar si una célula expresa un receptor de BoNT/A. Tales ensayos incluyen, a modo no taxativo, ensayos de reticulación usando BoNT/A etiquetada, como, por ej., [^{125}I] BoNT/A, véase, por ej., Noriko Yokosawa et al., *Binding of Clostridium botulinum type C neurotoxin to different neuroblastoma cell lines*, 57(1) Infect. Immun. 272-277 (1989); Noriko Yokosawa et al., *Binding of botulinum type C1, D and E neurotoxins to neuronal cell lines and synaptosomes*, 29(2) Toxicon 261-264 (1991) y Tei-ichi Nishiki et al., *Identification of protein receptor for Clostridium botulinum type B neurotoxin in rat brain synaptosomes*, 269(14) J. Biol. Chem. 10498-10503 (1994). Otros ensayos no taxativos incluyen ensayos inmunocitoquímicos que detectan la unión a la BoNT/A usando anticuerpos etiquetados o no etiquetados, véase, por ej., Atsushi Nishikawa et al., *The receptor and transporter for internalization of Clostridium botulinum type C progenitor toxin into HT-29 cells*, 319(2) Biochem. Biophys. Res. Commun. 327-333 (2004) y ensayos de inmunoprecipitación, véase, por ej., Yukako Fujinaga et al., *Molecular characterization of binding subcomponents of*

Clostridium botulinum type C progenitor toxin for intestinal epithelial cells and erythrocytes, 150(Pt 5) Microbiology 1529-1538 (2004), que detectan la toxina unida usando anticuerpos etiquetados o no etiquetados. Los anticuerpos útiles para estos ensayos incluyen, a modo no taxativo, anticuerpos seleccionados en comparación con la BoNT/A, anticuerpos seleccionados en comparación con el receptor de BoNT/A como, por ej., el FGFR2, el FGFR3 o el SV2 y/o anticuerpos seleccionados en comparación con un ganglиósido, como, por ej., GD1a, GD1b, GD3, GQ1b o GT1b. Si el anticuerpo está etiquetado, la unión de la molécula se puede detectar mediante diversos medios, incluyendo análisis de transferencia Western, observación microscópica directa de la ubicación celular del anticuerpo, medición del anticuerpo unido a células o sustratos luego de una etapa de lavado, citometría de flujo, electroforesis o electroforesis capilar, utilizando métodos bien conocidos por los expertos en la técnica. Si el anticuerpo no está etiquetado, se puede emplear un anticuerpo secundario etiquetado para la detección indirecta de la molécula unida y la detección puede realizarse de la misma forma que para el anticuerpo etiquetado. Se comprende que estos ensayos y ensayos similares que determinan las características o propiedades de absorción de la BoNT/A pueden ser útiles para identificar

células que expresen receptores endógenos o exógenos de BoNT/A.

También se pueden usar los ensayos que controlan la liberación de una molécula luego de la exposición a la BoNT/A para evaluar si una célula expresa uno o más receptores endógenos o exógenos de BoNT/A. En estos ensayos, la inhibición de la liberación de molécula tendría lugar en células que expresan un receptor de BoNT/A luego del tratamiento con BoNT/A. Los ensayos bien conocidos incluyen métodos que miden la inhibición de liberación de catecolamina radioetiquetada desde las neuronas como, por ej., liberación de [3H] noradrenalina o [3H] dopamina, véase, por ej., A Fassio et al., *Evidence for calcium-dependent vesicular transmitter release insensitive to tetanus toxin and botulinum toxin type F*, 90(3) Neuroscience 893-902 (1999) y Sara Stigliani et al., *The sensitivity of catecholamine release to botulinum toxin C1 and E suggests selective targeting of vesicles set into the readily releasable pool*, 85(2) J. Neurochem. 409-421 (2003) o mide la liberación de catecolamina usando un procedimiento fluorométrico, véase, por ej., Anton de Paiva et al., *A role for the interchain disulfide or its participating thiols in the internalization of botulinum neurotoxin A revealed by a toxin derivative that binds to ecto-acceptors and inhibits transmitter release*

intracellularly, 268(28) J. Biol. Chem. 20838-20844 (1993); Gary W. Lawrence et al., *Distinct exocytotic responses of intact and permeabilised chromaffin cells after cleavage of the 25-kDa synaptosomal-associated protein (SNAP-25) or synaptobrevin by botulinum toxin A or B,* 236(3) Eur. J. Biochem. 877-886 (1996) y Patrick Foran et al., *Botulinum neurotoxin C1 cleaves both syntaxin and SNAP-25 in intact and permeabilized chromaffin cells: correlation with its blockade of catecholamine release,* 35(8) Biochemistry 2630-2636 (1996). Otros ejemplos no taxativos incluyen ensayos que miden la inhibición de liberación de hormonas desde células endócrinas, como, por ej., células pituitarias anteriores o células de ovario. Se comprende que estos ensayos y ensayos similares para la liberación de moléculas pueden ser útiles para identificar células que expresan receptores endógenos o exógenos de BoNT/A.

También se pueden usar los ensayos que detectan la escisión de un sustrato de BoNT/A luego de la exposición a BoNT/A para evaluar si una célula expresa uno o más receptores endógenos o exógenos de BoNT/A. En estos ensayos, se detectaría la generación de un producto de la escisión del sustrato de la BoNT/A o la desaparición del sustrato de la BoNT/A intacto en células que expresan un receptor de BoNT/A luego del tratamiento con BoNT/A. Los ejemplos no taxativos

de un análisis de transferencia Western específico, así como reactivos, condiciones y protocolos bien caracterizados se encuentra fácilmente disponible en vendedores comerciales que incluyen, a modo no taxativo, Amersham Biosciences, Piscataway, NJ; Bio-Rad Laboratories, Hercules, CA; Pierce Biotechnology, Inc., Rockford, IL; Promega Corporation, Madison, WI y Stratagene, Inc., La Jolla, CA. Se comprende que estos ensayos y ensayos similares que determinan la escisión del sustrato de la BoNT/A pueden ser útiles para identificar células que expresen receptores endógenos o exógenos de BoNT/A.

Como ejemplo no taxativo, se puede usar el análisis de transferencia Western utilizando un anticuerpo que reconoce el producto escindido de la SNAP-25 de la BoNT/A o las formas escindida y no escindida de la SNAP-25 para analizar la absorción de la BoNT/A. Los ejemplos de anticuerpos α-SNAP-25 útiles para estos ensayos incluyen, a modo no taxativo, el anticuerpo monoclonal de ratón α-SNAP-25 SMI-81 (Sternberger Monoclonals Inc., Lutherville, MD), anticuerpo monoclonal α-SNAP-25 de ratón CI 71.1 (Synaptic Systems, Goettingen, Alemania), anticuerpo monoclonal de ratón α-SNAP-25 CI 71.2 (Synaptic Systems, Goettingen, Alemania), anticuerpo monoclonal de ratón α-SNAP-25 SP12 (Abcam, Cambridge, MA), antisuero policlonal de conejo α-SNAP-25 (Synaptic Systems,

Goettingen, Alemania), antisuero policlonal de conejo α-SNAP-25 S9684 (Sigma, San Luis, MO) y antisuero policlonal de conejo α-SNAP-25 (Abcam, Cambridge, MA).

Aspectos de la presente descripción proporcionan células que se realizan a través de manipulación genética o modificación recombinante para expresar una SNAP-25 exógena y/o uno o más receptores exógenos de BoNT/A. Las células útiles para expresar una SNAP-25 exógena y/o uno o más receptores exógenos de BoNT/A a través de manipulación genética o modificación recombinante incluyen células neuronales y células no neuronales que pueden o no expresar una SNAP-25 endógena y/o uno o más receptores endógenos de BoNT/A. Se comprende adicionalmente que tales células manipuladas genéticamente o modificadas de forma recombinante pueden expresar una SNAP-25 exógena y uno o más receptores exógenos de BoNT/A bajo el control de un elemento promotor o elemento potenciador constitutivo, específico para el tejido, específico para la célula o inducible o ambos. Se comprende que toda célula es útil, siempre que la célula se pueda manipular genéticamente o modificar de forma recombinante para expresar una SNAP-25 exógena y/o uno o más receptores exógenos de BoNT/A y pueda someterse a intoxicación por BoNT/A.

Los métodos útiles para introducir en una célula una molécula exógena de polinucleótido que codifica un componente necesario para que las células experimenten el mecanismo celular global mediante el cual una BoNT/A escinde de forma proteolítica un sustrato de la SNAP-25, como, por ej., una SNAP-25, un FGFR2, un FGFR3 o un SV2 incluyen, a modo no taxativo, métodos de suministro mediados químicamente, como, por ej., mediados por fosfato de calcio, mediados por dietil-aminoetilo (DEAE) dextrano, mediados por lípidos, mediados por polietilenimina (PEI), mediados por polilisina y mediados por polibreno; métodos de suministro mediados físicamente, como, por ej., suministro biolístico de partículas, microinyección, electroporación y fusión de protoplastos y métodos de suministro mediados por virus, como, por ej., transfección mediada por retrovirus, véase, por ej., *Introducing Cloned Genes into Cultured Mammalian Cells*, pp. 16.1-16.62 (Sambrook & Russell, eds., Molecular Cloning A Laboratory Manual, Tomo 3, 3ª ed. 2001); Alessia Colosimo et al., *Transfer and Expression of Foreign Genes in Mammalian Cells*, 29(2) Biotechniques 314-318, 320-322, 324 (2000); Philip Washbourne & A. Kimberley McAllister, *Techniques for Gene Transfer into Neurons*, 12(5) Curr. Opin. Neurobiol. 566-573 (2002) y Current Protocols in Molecular Biology, John Wiley and Sons, pp 9.16.4-9.16.11 (2000), cada uno de los cuales se incorpora en su totalidad a modo de referencia. Un

experto en la técnica comprende que la selección de un método específico para introducir una molécula de polinucleótido en una célula dependerá, en parte, de si la célula contendrá de forma transitoria o estable un componente necesario para que las células experimenten el mecanismo celular global mediante el cual una BoNT/A escinde de forma proteolítica un sustrato de la SNAP-25. Ejemplos no taxativos de moléculas de polinucleótidos que codifican un componente necesario para que las células experimenten el mecanismo celular global mediante el cual una BoNT/A escinde de forma proteolítica un sustrato de la SNAP-25 como obra a continuación: una molécula de polinucleótido del FGFR2 de la SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 136, SEQ ID NO: 137 o SEQ ID NO: 138; una molécula de polinucleótido del FGFR3 de la SEQ ID NO: 139, SEQ ID NO: 140 o SEQ ID NO: 141; una molécula de polinucleótido del SV2 de la SEQ ID NO: 142, SEQ ID NO: 143 o SEQ ID NO: 144 y una molécula de polinucleótido de la SNAP-25 de la SEQ ID NO: 145 o SEQ ID NO: 146.

Los métodos de suministro mediados químicamente son bien conocidos por un experto en la técnica y se describen, por ej., en Martin Jordan & Florian Worm, *Transfection of Adherent and Suspended Cells by Calcium Phosphate*, 33(2) Métodos 136-143 (2004); Chun Zhang et al., *Polyethylenimine*

Strategies for Plasmid Delivery to Brain-Derived Cells, 33(2) Métodos 144-150 (2004), cada uno de los cuales se incorpora en su totalidad a la presente mediante esta referencia. Tales métodos de suministro mediados químicamente se pueden preparar mediante procedimientos estándar y se encuentran comercialmente disponibles, véase, por ej., kit de transfección CellPhect (Amersham Biosciences, Piscataway, NJ); kit de transfección en mamíferos, fosfato de calcio y DEAE Dextrano, (Stratagene, Inc., La Jolla, CA); reactivo de transfección Lipofectamine™ (Invitrogen, Inc., Carlsbad, CA); kit de transfección ExGen 500 (Fermentas, Inc., Hanover, MD) y los kits de transfección SuperFect y Effectene (Qiagen, Inc., Valencia, CA).

Los métodos de suministro mediados físicamente son bien conocidos por un experto en la técnica y se describen, por ej., en Jeike E. Biewenga et al., *Plasmid-Mediated Gene Transfer in Neurons using the Biolistics Technique*, 71(1) J. Neurosci. Métodos 67-75 (1997); John O'Brien & Sarah C. R. Lummis, *Biolistic and Diolistic Transfection: Using the Gene Gun to Deliver DNA and Lipophilic Dyes into Mammalian Cells*, 33(2) Métodos 121-125 (2004); M. Golzio et al., *In Vitro and In Vivo Electric Field-Mediated Permeabilization, Gene Transfer, and Expression*, 33(2) Métodos 126-135 (2004) y Oliver Greschet al., *New Non-Viral Method for Gene Transfer*

into Primary Cells, 33(2) Métodos 151-163 (2004), cada uno de los cuales se incorpora en su totalidad a la presente mediante esta referencia.

Los métodos de suministro mediados por virus son bien conocidos por un experto en la técnica y se describen, por ej., en Chooi M. Lai et al., *Adenovirus and Adeno-Associated Virus Vectors*, 21(12) DNA Cell Biol. 895-913 (2002); Ilya Frolov et al., *Alphavirus-Based Expression Vectors: Strategies and Applications*, 93(21) Proc. Natl. Acad. Sci. E.U.A. 11371-11377 (1996); Roland Wolkowicz et al., *Lentiviral Vectors for the Delivery of DNA into Mammalian Cells*, 246 Methods Mol. Biol. 391-411 (2004); A. Huser & C. Hofmann, *Baculovirus Vectors: Novel Mammalian Cell Gene-Delivery Vehicles and Their Applications*, 3(1) Am. J. Pharmacogenomics 53-63 (2003); Tiziana Tonini et al., *Transient Production of Retroviral- and Lentiviral-Based Vectors for the Transduction of Mammalian Cells*, 285 Methods Mol. Biol. 141-148 (2004); Manfred Gossen & Hermann Bujard, *Tight Control of Gene Expression in Eukaryotic Cells by Tetracycline-Responsive Promoters*, patente estadounidense No. 5,464,758; Hermann Bujard & Manfred Gossen, *Methods for Regulating Gene Expression*, patente estadounidense No. 5,814,618; David S. Hogness, *Polynucleotides Encoding Insect Steroid Hormone Receptor Polypeptides and Cells Transformed*

With Same, patente estadounidense No. 5,514,578; David S. Hogness, *Polynucleotide Encoding Insect Ecdysone Receptor*, patente estadounidense 6,245,531; Elisabetta Vegeto et al., *Progesterone Receptor Having C. Terminal Hormone Binding Domain Truncations*, patente estadounidense No. 5,364,791; Elisabetta Vegeto et al., *Mutated Steroid Hormone Receptors, Methods for Their Use and Molecular Switch for Gene Therapy*, patente estadounidense No. 5,874,534, cada una de las cuales se incorpora en su totalidad a la presente mediante esta referencia. Tales métodos de suministro mediados por virus se pueden preparar mediante procedimientos estándar y se encuentran comercialmente disponibles, véase, por ej., el sistema de expresión adenoviral VIRAPOWER™ (Invitrogen, Inc., Carlsbad, CA) y el manual de instrucción del sistema de expresión adenoviral VIRAPOWER™ 25-0543 versión A, Invitrogen, Inc., (15 de julio, 2002); el sistema de vector adenoviral ADEASY™ (Stratagene, Inc., La Jolla, CA) y el manual de instrucción del sistema de vector adenoviral ADEASY™ 064004f, Stratagene, Inc. Adicionalmente, tales sistemas de suministro virales se pueden preparar a través de métodos estándar y se encuentran comercialmente disponibles, véase, por ej., el sistema de expresión genética BD™ Tet-Off y Tet-On (BD Biosciences-Clonetech, Palo Alto, CA) y el manual del usuario del sistema de expresión genética BD™ Tet-Off y Tet-On, PT3001-1, BD Biosciences Clonetech, (14 de

marzo, 2003), Sistema GeneSwitch™ (Invitrogen, Inc., Carlsbad, CA); el sistema GENESWITCH™, un sistema de expresión regulado por mifepristona para células de mamíferos, versión D, 25-0313, Invitrogen, Inc., (4 de noviembre, 2002); el sistema de expresión lentiviral VIRAPOWER™ (Invitrogen, Inc., Carlsbad, CA) y el manual de instrucción del sistema de expresión lentivirual VIRAPOWER™ 25-0501 versión E, Invitrogen, Inc., (8 de diciembre, 2003); el sistema de expresión inducible retroviral en mamíferos COMPLETE CONTROL® (Stratagene, La Jolla, CA) y el manual de instrucción del sistema de expresión inducible retroviral en mamíferos COMPLETE CONTROL®, 064005e.

Como se mencionó anteriormente, se puede introducir en una célula un componente exógeno necesario para que las células experimenten el mecanismo celular global mediante el cual una BoNT/A escinde de forma proteolítica un sustrato de la SNAP-25, como, por ej., una SNAP-25, un FGFR2, un FGFR3 o un SV2 descritos en la presente memoria descriptiva. Todo y cualquier método útil para la introducción de tal componente exógeno con un agente de suministro en una población celular puede ser útil con la condición de que este método introduzca el componente exógeno descrito en la presente memoria descriptiva en al menos el 50% de las células en una población celular dada. Por consiguiente, los aspectos de la

presente modalidad pueden incluir una población celular donde, por ej., al menos el 50%, al menos 60%, al menos 70%, al menos 80% o al menos 90% de la población celular dada contiene un componente exógeno necesario para que las células experimenten el mecanismo celular global mediante el cual una BoNT/A escinde de forma proteolítica un sustrato de la SNAP-25, como, por ej., una SNAP-25, un FGFR2, un FGFR3 o un SV2 descritos en la presente memoria descriptiva. Como se utiliza en la presente, el término "agente de suministro" se refiere a cualquier molécula que permita o potencie la internalización de un enlazado de forma covalente, no enlazado de forma covalente o asociado de cualquier otra forma con un polipéptido en una célula [sic]. Por consiguiente, el término "agente de suministro" comprende, a modo no taxativo, proteínas, péptidos, peptidomiméticos, moléculas pequeñas, moléculas de polinucleótidos, liposomas, lípidos, virus, retrovirus y células que, a modo no taxativo, transportan una molécula unida de forma covalente o no covalente a la membrana celular, citoplasma celular o núcleo. Se comprende adicionalmente que el término "agente de suministro" comprende moléculas que se internalizan mediante cualquier mecanismo, incluyendo agentes de suministro que funcionan a través de endocitosis mediada por receptores y los que son independientes de la endocitosis mediada por receptores.

Un agente de suministro también puede ser un agente que permita o potencie la absorción celular de un componente enlazado de forma covalente, como el FGFR2, el FGFR3, el SV2 o la SNAP-25, como, por ej., mediante conjugación química o mediante proteínas de fusión producidas genéticamente. Los métodos que enlazan de forma covalente los agentes de suministro y los métodos de uso de tales agentes se describen, por ej., en Steven F. Dowdy, *Protein Transduction System and Methods of Use Thereof*, publicación internacional No WO 00/34308; Gérard Chassaing & Alain Prochiantz, *Peptides which can be Used as Vectors for the Intracellular Addressing of Active Molecules*, patente estadounidense No. 6,080,724; Alan Frankel et al., *Fusion Protein Comprising TAT-derived Transport Moiety*, patente estadounidense No. 5,674,980; Alan Frankel et al., *TAT-derived Transport Polypeptide Conjugates*, patente estadounidense No. 5,747,641; Alan Frankel et al., *TAT-derived Transport Polypeptides and Fusion Proteins*, patente estadounidense No. 5,804,604; Peter F. J. O'Hare et al., *Use of Transport Proteins*, patente estadounidense No. 6,734,167; Yao-Zhong Lin & Jack J. Hawiger, *Method for Importing Biologically Active Molecules into Cells*, patente estadounidense No. 5,807,746; Yao-Zhong Lin & Jack J. Hawiger, *Method for Importing Biologically Active Molecules into Cells*, patente estadounidense No. 6,043,339; Yao-Zhong

Lin et al., *Sequence and Method for Genetic Engineering of Proteins with Cell Membrane Translocating Activity*, patente estadounidense No. 6,248,558; Yao-Zhong Lin et al., Sequence and Method for Genetic *Engineering of Proteins with Cell Membrane Translocating Activity*, patente estadounidense No. 6,432,680; Jack J. Hawiger et al., *Method for Importing Biologically Active Molecules into Cells*, patente estadounidense No. 6,495,518; Yao-Zhong Lin et al., *Sequence and Method for Genetic Engineering of Proteins with Cell Membrane Translocating Activity*, patente estadounidense No. 6,780,843; Jonathan B. Rothbard & Paul A Wender, *Method and Composition for Enhancing Transport Across Biological Membranes*, patente estadounidense No. 6,306,993; Jonathan B. Rothbard & Paul A Wender, *Method and Composition for Enhancing Transport Across Biological Membranes*, patente estadounidense No. 6,495,663 y Pamela B. Davis et al., *Fusion Proteins for Protein Delivery*, patente estadounidense No. 6,287,817, cada una de las cuales se incorpora en su totalidad a modo de referencia.

Un agente de suministro también puede ser un agente que permita o potencie la absorción celular de un componente asociado de forma no covalente, como el FGFR2, el FGFR3, el SV2c o la SNAP-25. Los métodos que funcionan en ausencia de enlace covalente y los métodos de uso de tales agentes se

describen, por ej., en Gilles Divita et al, *Peptide-Mediated Transfection Agents and Methods of Use*, patente estadounidense No. 6,841,535; Philip L Felgner and Olivier Zelphati, *Intracellular Protein Delivery Compositions and Methods of Use*, publicación de patente estadounidense No. 2003/0008813 y Michael Karas, *Intracellular Delivery of Small Molecules, Proteins and Nucleic Acids*, publicación de patente estadounidense 2004/0209797, cada uno de los cuales se incorpora en su totalidad a modo de referencia. Tales agentes de suministro de péptidos se pueden preparar y utilizar a través de métodos estándar y se encuentran comercialmente disponibles, véase, por ej., el reactivo CHARIOT™ (Active Motif, Carlsbad, CA); reactivo BIO-PORTER® (Gene Therapy Systems, Inc., San Diego, CA), reactivo de suministro de proteínas BIO TREK™ (Stratagene, La Jolla, CA) y reactivo de transfección de proteínas PRO-JECT™ (Pierce Biotechnology Inc., Rockford, IL).

Los aspectos de la presente descripción también se pueden describir de la siguiente manera:

1. Una línea celular clonal establecida que comprende una célula susceptible de intoxicación por parte de una BoNT/A.

2. La línea celular clonal establecida del 1, donde la línea celular clonal se selecciona de una línea celular SiMa original.

3. La línea celular clonal establecida del 1 o el 2, donde la célula es susceptible de intoxicación por BoNT/A en alrededor de 100 pM o menos, en alrededor de 50 pM o menos, en alrededor de 10 pM o menos, en alrededor de 5 pM o menos, en alrededor de 1 pM o menos, en alrededor de 0.5 pM o menos o en alrededor de 0.1 pM o menos de una BoNT/A.

4. La línea celular clonal establecida del 1 o el 2, donde la susceptibilidad de intoxicación por BoNT/A se mide antes de la diferenciación de la célula.

5. La línea celular clonal establecida del 2, donde, en el estado no diferenciado, la célula presenta al menos un aumento de 1.5 veces en la expresión genética de uno o más genes con relación a la expresión del o los genes en una célula de una línea celular 2D6 y los genes se toman de la Tabla 5 o donde la célula presenta al menos una disminución de 1.5 veces en la expresión genética de uno o más genes con relación a la expresión del o los genes en una célula de la línea celular 2D6 y los genes se toman de la Tabla 6.

6. La línea celular clonal establecida del 2, donde, en el estado diferenciado, la célula presenta al menos un aumento de 1.5 veces en la expresión genética de uno o más genes con relación a la expresión del o los genes en una célula de una línea celular 2D6 y los genes se toman de la Tabla 9 o donde la célula presenta al menos una disminución de 1.5 veces en la expresión genética de uno o más genes con relación a la expresión del o los genes en una célula de la línea celular 2D6 y los genes se toman de la Tabla 10.

7. La línea celular clonal establecida del 2, donde, en el estado no diferenciado, la célula presenta al menos un aumento de 1.5 veces en la expresión genética de uno o más genes con relación a la expresión del o los genes en una célula de una línea celular SiMa original y los genes se toman de la Tabla 7 o donde la célula presenta al menos una disminución de 1.5 veces en la expresión genética de uno o más genes con relación a la expresión del o los genes en una célula de la línea celular SiMa original y los genes se toman de la Tabla 8.

8. La línea celular clonal establecida del 2, donde, en el estado diferenciado, la célula presenta al menos un aumento de 1.5 veces en la expresión genética de uno o más genes con relación a la expresión del o los genes en una

célula de una línea celular SiMa original y los genes se toman de la Tabla 11 o donde la célula presenta al menos una disminución de 1.5 veces en la expresión genética de uno o más genes con relación a la expresión del o los genes en una célula de la línea celular SiMa original y los genes se toman de la Tabla 12.

9. La línea celular clonal establecida del 1 o el 2, donde la célula presenta una sensibilidad hacia la actividad de la BoNT/A de 100 pM o menos o alrededor de 25 pM en 5 o más pasajes celulares, 10 o más pasajes celulares, 15 o más pasajes celulares, 20 o más pasajes celulares, 25 o más pasajes celulares, 30 o más pasajes celulares, 35 o más pasajes celulares, 40 o más pasajes celulares, 45 o más pasajes celulares, 50 o más pasajes celulares, 55 o más pasajes celulares o 60 o más pasajes celulares.

10. La línea celular clonal establecida del 1 o 2, donde la célula de una línea celular clonal establecida presenta una relación bien definida de señal a ruido de la asíntota superior para la actividad de la BoNT/A de al menos 3:1, al menos 4:1, al menos 5:1, al menos 6:1, al menos 7:1, al menos 8:1, al menos 9:1, al menos 10:1 en, por ej., 5 o más pasajes celulares, 10 o más pasajes celulares, 15 o más pasajes celulares, 20 o más pasajes celulares, 25 o más

pasajes celulares, 30 o más pasajes celulares, 35 o más pasajes celulares, 40 o más pasajes celulares, 45 o más pasajes celulares, 50 o más pasajes celulares, 55 o más pasajes celulares o 60 o más pasajes celulares.

11. Una línea celular clonal establecida que comprende una célula susceptible de intoxicación a causa de la BoNT/A producida a partir de una línea celular SiMa original, donde la célula es susceptible de intoxicación por BoNT/A en alrededor de 100 pM o menos, en alrededor de 50 pM o menos, en alrededor de 10 pM o menos, en alrededor de 5 pM o menos, en alrededor de 1 pM o menos, en alrededor de 0.5 pM o menos o en alrededor de 0.1 pM o menos de una BoNT/A.

12. Una línea celular clonal establecida que comprende células susceptibles de intoxicación por una BoNT/A,

donde la línea celular clonal se selecciona de una línea celular SiMa original y

donde la línea celular clonal comprende células susceptibles de intoxicación por BoNT/A en alrededor de 100 pM o menos de una BoNT/A.

13. La línea celular clonal establecida del 12, donde la línea celular SiMa original es la línea celular SiMa original DSMZ ACC 164.

14. La línea celular clonal establecida del 12, donde la célula presenta una sensibilidad hacia la actividad de la BoNT/A de 100 pM o menos o alrededor de 25 pM en 5 o más pasajes celulares, 10 o más pasajes celulares, 15 o más pasajes celulares, 20 o más pasajes celulares, 25 o más pasajes celulares, 30 o más pasajes celulares, 35 o más pasajes celulares, 40 o más pasajes celulares, 45 o más pasajes celulares, 50 o más pasajes celulares, 55 o más pasajes celulares o 60 o más pasajes celulares.

15. La línea celular clonal establecida del 12, donde la célula de una línea celular clonal establecida presenta una relación bien definida de señal a ruido de la asíntota superior para la actividad de la BoNT/A de al menos 3:1, al menos 4:1, al menos 5:1, al menos 6:1, al menos 7:1, al menos 8:1, al menos 9:1, al menos 10:1 en, por ej., 5 o más pasajes celulares, 10 o más pasajes celulares, 15 o más pasajes celulares, 20 o más pasajes celulares, 25 o más pasajes celulares, 30 o más pasajes celulares, 35 o más pasajes celulares, 40 o más pasajes celulares, 45 o más pasajes

celulares, 50 o más pasajes celulares, 55 o más pasajes celulares o 60 o más pasajes celulares.

16. La línea celular clonal establecida del 12, donde la susceptibilidad de intoxicación por BoNT/A se mide antes de la diferenciación de la célula o después de la diferenciación de la célula.

17. Una línea celular clonal establecida que comprende células susceptibles de intoxicación por una BoNT/A,

donde las células presentan al menos una diferencia de 1.5 veces en los niveles de expresión genética de tres o más genes, en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6;

donde los niveles de expresión genética se seleccionan del grupo de ADAMTS9, ASCL1, BASP1, DOK5, DPYD, GNB4, GNG11, GTSF1, MAOA, MINA, MSN, PEG3, PLK2, PRSS12, RNF182, SLC44A5, SPARC, TFPI2 y TPTE y

donde la línea celular clonal comprende células susceptibles de intoxicación por BoNT/A en alrededor de 100 pM o menos de una BoNT/A.

18. La línea celular clonal establecida del 17, donde las células presentan una diferencia de al menos 2.0 veces en los niveles de expresión genética de uno o más genes en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6, una diferencia de al menos 3.0 veces en los niveles de expresión genética de uno o más genes en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6 o una diferencia de al menos 4.0 veces en los niveles de expresión genética de uno o más genes en comparación con los niveles de expresión de estos genes en células de la línea celular 2D6.

19. La línea celular clonal establecida del 17, donde los niveles de expresión genética se miden antes de la diferenciación de la célula o después de la diferenciación de la célula.

20. La línea celular clonal establecida del 17, donde la célula presenta una sensibilidad hacia la actividad de la BoNT/A de 100 pM o menos o alrededor de 25 pM en 5 o más pasajes celulares, 10 o más pasajes celulares, 15 o más pasajes celulares, 20 o más pasajes celulares, 25 o más pasajes celulares, 30 o más pasajes celulares, 35 o más pasajes celulares, 40 o más pasajes celulares, 45 o más

pasajes celulares, 50 o más pasajes celulares, 55 o más pasajes celulares o 60 o más pasajes celulares.

21. La línea celular clonal establecida del 17, donde la célula de una línea celular clonal establecida presenta una relación bien definida de señal a ruido de la asíntota superior para la actividad de la BoNT/A de al menos 3:1, al menos 4:1, al menos 5:1, al menos 6:1, al menos 7:1, al menos 8:1, al menos 9:1, al menos 10:1 en, por ej., 5 o más pasajes celulares, 10 o más pasajes celulares, 15 o más pasajes celulares, 20 o más pasajes celulares, 25 o más pasajes celulares, 30 o más pasajes celulares, 35 o más pasajes celulares, 40 o más pasajes celulares, 45 o más pasajes celulares, 50 o más pasajes celulares, 55 o más pasajes celulares o 60 o más pasajes celulares.

EJEMPLOS

Ejemplo I

Análisis de líneas celulares que comprenden células susceptibles de intoxicación por BoNT/A

El siguiente ejemplo demuestra cómo identificar células clonales de una línea celular establecida original que son

susceptibles de intoxicación por BoNT/A o que tienen capacidad de absorción de neurotoxina.

1. Aislamiento de líneas celulares clonales.

La solicitud de patente acompañante de Ester Fernandez-Salas, et al., *Immuno-Based Botulinum Toxin Serotype A Activity Assays*, solicitud de patente estadounidense No. de serie: 12/403,531 identificó diversas líneas celulares establecidas útiles para llevar adelante los métodos basados en inmunoensayos descritos para detectar la actividad de la BoNT/A, incluyendo, por ej., LA1-55n (ECACC 06041203), N18 (ECACC 88112301), Neuro-2a (ATCC CCL-131), PC12 (ATCC CRL-1721), SH-SY5Y (ATCC CRL-2266) y SiMa (DSMZ ACC 164). Durante la caracterización de la línea celular SiMa, se descubrió que las células que comprenden esta línea celular establecida comprenden al menos cinco fenotipos celulares diferentes. Para determinar si alguno de estos tipos celulares fenotípicamente diferentes era responsable de la susceptibilidad de esta línea celular a la intoxicación por BoNT/A, se llevaron adelante dos análisis diferentes de dilución limitada para obtener aislados de colonia simple para cada tipo celular fenotípicamente diferente.

En ambos análisis, se cultivó una densidad adecuada de células de una solución madre de SiMa en medio RPMI 1640, que tenía 10% de suero bovino fetal, 1% de penicilina-estreptomicina, 2 mM de L-glutamina, contenido en un matraz recubierto con colágeno IV T175. Luego del segundo pasaje, las células se trataron con tripsina para producir una suspensión celular y se determinó la concentración celular. Alrededor de 4.0×10^6 células de esta suspensión celular se transfirieron a un tubo de 50 mL y las células se disociaron en células únicas por expulsión vigorosa repetida a través de una aguja de 18.5 de ancho usando una jeringa de 10 mL. Luego se diluyeron las células de esta suspensión disasociada de una célula a una concentración de 0.2×10^6 células/mL agregando 15 mL de medio de cultivo recién preparado y se agregaron 2.5 µL de esta dilución a 50 mL de medio de cultivo recién preparado para obtener una concentración de 10 células/mL. A partir de esta solución madre de dilución final, se agregaron 100 µL de medio de cultivo a cada pocillo de placas cubiertas con colágeno IV de 96 pocillos (densidad promedio final de una célula/pocillo) y las células se cultivaron de forma ininterrumpida en un incubador a 37°C con 5% de dióxido de carbono durante cuatro semanas. Se colocaron un total de diecinueve placas de 96 pocillos para el análisis. Las placas se examinaron microscópicamente de forma periódica para evaluar el crecimiento de colonias. Luego de

cuatro semanas, cada pocillo se examinó microscópicamente para identificar colonias en crecimiento y para cada colonia en crecimiento identificada, se agregaron 100 µL de medio de cultivo recién preparado a cada pocillo y las células se cultivaron ininterrumpidamente en un incubador a 37°C con 5% de dióxido de carbono durante dos semanas. Luego de dos semanas más de crecimiento, las colonias en crecimiento simples se trataron con tripsina y se transfirieron a una nueva placa de 96 pocillos para que siguiera creciendo. Una vez que las colonias crecieron hasta alrededor de 1,000 células, con base en la inspección visual, las células se trataron con tripsina y cada suspensión celular se transfirió a un nuevo pocillo de una placa recubierta con colágeno IV de 24 pocillos. Las células se cultivaron en un incubador a 37°C con 5% de dióxido de carbono con medio de cultivo recién preparado que se rellenó cada 2 a 3 días, en caso de ser necesario. Las células se cultivaron hasta que el cultivo alcanzó aproximadamente 60% de confluencia o más, momento en el cual las células se trataron con tripsina y cada suspensión celular se transfirió a un matraz recubierto con Colágeno IV de 25 cm^2. Las células se cultivaron en un incubador a 37°C con 5% de dióxido de carbono con medio de cultivo recién preparado que se rellenó cada 2 a 3 días, en caso de ser necesario. Una vez que las células en el matraz alcanzaron 70 a 80% de confluencia, se congelaron y

almacenaron en nitrógeno analizaron para determinar su susceptibilidad a la intoxicación por BoNT/A. De las 1,824 aislados de colonias inicialmente colocados para ambos análisis, se seleccionaron 130 líneas celulares clonales con base en criterios de viabilidad y crecimiento y se expandieron para llevar adelante procedimientos de análisis posteriores.

2. Análisis primario para determinar la susceptibilidad a la intoxicación por BoNT/A de células de una línea celular clonal usando un complejo de BoNT/A

Una forma de determinar si las células de una línea celular clonal eran susceptibles de intoxicación por BoNT/A fue llevar adelante un análisis primario usando un ensayo de viabilidad celular luminiscente CELLTITER-GLO® (Promega, Madison, WI) para normalizar el número de células en cada pocillo y un método basado en inmunoensayos para determinar la actividad de BoNT/A según se describe en Ester Fernandez-Salas, et al., *Immuno-Based Botulinum Toxin Serotype A Activity Assays*, solicitud de patente estadounidense No. de serie: 12/403,531, que se incorpora a la presente a modo de referencia en su totalidad. Se colocaron dos placas de 96 pocillos separadas, una para el ensayo de actividad de BoNT/A y otra para el ensayo de viabilidad celular.

Para llevar adelante el ensayo de actividad de la BoNT/A, se preparó un lisado a partir de células tratadas con BoNT/A por medio del recubrimiento de células de cada línea celular clonal aislada en un pocillo de una placa de 96 pocillos de poli-D-lisina (BD Biosciences, Bedford, MA). Los pocillos contenían 0.1 mL de un medio libre de suero que comprende medio esencial mínimo, 2 mM de GlutaMAX™ I con sales de Earle, 1 x de suplemento B27, 1 x de suplemento N2, 0.1 mM de aminoácidos no esenciales, 10 mM de HEPES y 25 µg/mL de GT1b (302-011-M005, Alexis Biochemicals, San Diego, CA). Estas células se incubaron en un incubador a 37°C con 5% de dióxido de carbono hasta que las células se diferenciaron, según se evaluó por criterios morfológicos estándar y de rutina, tal como la detención de crecimiento y la extensión de neuritas (aproximadamente 3 días). El medio de las células diferenciadas se aspiró de cada pocillo y se reemplazó con medio recién preparado que contenía 1 nM de un complejo de BoNT/A. Luego de una incubación de 24 hrs., las células se lavaron aspirando el medio de cultivo y enjuagando cada pocillo con 200 µL de 1 x de PBS. Para recolectar las células, se aspiró 1 x de PBS, las células se lisaron agregando 30 µl de amortiguador de lisis que comprendía 20 mM de Tris-HCl (pH 7.5), 150 mM de NaCl, 1 mM de EDTA, 1 mM de EGTA, 1% de Triton X-100 a cada pocillo y la placa se incubó en un agitador con rotación a 500 rpm durante 30 minutos 4°C.

La placa se centrifugó a 400 rpm durante 20 minutos a 4°C para sedimentar los residuos celulares y el sobrenadante se transfirió a una placa de 96 pocillos recubierta con anticuerpo de captura para llevar a cabo la etapa de detección.

Para preparar una solución de anticuerpo de captura α-SNAP-25, se purificó el anticuerpo monoclonal de ratón α-SNAP-25 contenido en las ascitis de la línea celular de hibridoma 2E2A6 (Ejemplo VII) usando un protocolo de purificación de proteína A estándar.

Para preparar una solución de anticuerpo de detección α-SNAP-25, se conjugó el anticuerpo policlonal de conejo α-SNAP-25 S9684 (Sigma, San Luis, MO) con el reactivo de etiquetado del éster de NHS Rutenio(II)-tris-bipiridina-(4-metilsulfonato) (Meso Scale Discovery, Gaithersburg, MD) de acuerdo con las instrucciones del fabricante (Meso Scale Discovery, Gaithersburg, MD). La reacción de conjugación se llevó a cabo agregando 30 µL de solución madre MSD SULFO-TAG™ reconstituida con agua destilada a 200 µL de 2 mg/mL de anticuerpos policlonales α-SNAP-25 e incubando la reacción a temperatura ambiente durante 2 horas en la oscuridad. Los anticuerpos etiquetados se purificaron usando un protocolo de columna de centrifugación estándar y la concentración de

proteína se determinó usando un ensayo de proteína colorimétrico. La absorbancia del conjugado del anticuerpo α-SNAP-25/MSD SULFO-TAG™ se midió a 455 nm usando un espectrofotómetro para determinar la concentración en moles por litro. La solución de anticuerpo de detección se almacenó a 4°C hasta que se necesitara.

Para preparar un soporte de fase sólida α-SNAP-25 que comprende un anticuerpo de captura α-SNAP-25, se agregaron aproximadamente 5 µL de la solución de anticuerpo monoclonal α-SNAP-25 apropiada (20 µg/mL en 1 x PBS) a cada pocillo de una placa MSD de alta unión de 96 pocillos y la solución se dejó secar al aire en un gabinete de seguridad biológica durante 2 a 3 horas para evaporar el líquido de la solución. Los pocillos unidos al anticuerpo de captura se sellaron y almacenaron a 4°C hasta que se necesitaran.

Para detectar la presencia de un producto de SNAP-25 escindida por ELISA tipo sándwich ECL, los pocillos de un soporte de fase sólida α-SNAP-25 se bloquearon luego agregando 150 µL de amortiguador de bloqueo que comprendía 2% de reactivo de bloqueo Amersham (GE Life Sciences, Piscataway, NJ) y 10% de suero de cabra (VWR, West Chester, PA) a temperatura ambiente durante 2 horas. El amortiguador de bloqueo se aspiró, se agregaron 25 µL de un lisado de

células tratadas con BoNT/A a cada pocillo y las placas se incubaron a 4°C durante la noche. Los pocillos de la placa se lavaron tres veces aspirando el lisado celular y enjuagando cada pocillo tres veces con 200 µL de 1 x de PBS, 0.1% de TWEEN-20® (monolaurato de sorbitán de polioxietileno (20)). Luego de lavar, se agregaron 25 µl de 5 µg/mL de solución de anticuerpo de detección α-SNAP-25 que comprendía 2% de reactivo de bloqueo Amersham en 1 x de PBS, 0.1% de TWEEN-20® (monolaurato de sorbitán de polioxietileno (20)) a cada pocillo, se sellaron e incubaron a temperatura ambiente durante 1 hora con agitación. Luego de la incubación del anticuerpo de detección α-SNAP-25, los pocillos se lavaron tres veces con 200 µL de 1 x de PBS, 0.1% de TWEEN-20® (monolaurato de sorbitán de polioxietileno (20)). Luego de lavar se agregaron 150 µL de 1 x de amortiguador Read (Meso Scale Discovery, Gaithersburg, MD) a cada pocillo y las placas se leyeron usando un lector de imágenes SECTOR™ Imager 6000 (Meso Scale Discovery, Gaithersburg, MD). Los datos sin procesar se recogieron usando el generador de imágenes ECL.

Para llevar a cabo un ensayo de viabilidad celular luminiscente, las células de cada línea celular clonal aislada se colocaron en placas y se diferenciaron como se describió anteriormente. El medio de las células diferenciadas se aspiró de cada pocillo y se reemplazó con

100 µl de la mezcla de reactivos que comprendía el sustrato CELLTITER-GLO® y el amortiguador CELLTITER-GLO® de acuerdo con las instrucciones del fabricante. Luego la placa se protegió de la luz y se mezcló durante dos minutos en un agitador orbital. La solución de la placa celular de 96 pocillos con fondo transparente se transfirió a una placa de luminómetro blanca y luego de 10 minutos la incubación se leyó en el luminómetro.

Estos resultados indicaron que las lecturas de viabilidad celular se ubicaban en el intervalo entre 9,838 a 10,423,188 y las señales de actividad de la BoNT/A se ubicaban en el intervalo entre 84 a 27,242 (Tabla 1). Además, una proporción de actividad de la BoNT/A sobre la viabilidad celular se calculó para normalizar los datos, pese a que no siempre hubo una proporción 1:1 de viabilidad y actividad. Siete líneas celulares clonales presentaron proporciones de actividad/viabilidad de alrededor de 0.2×10^{-2} o más: H1, A7, A11, F10, A9, A10 y C11 (Tabla 1). Nueve líneas celulares clonales presentaron proporciones de actividad/viabilidad de alrededor de 0.125×10^{-2} a alrededor de 0.150×10^{-2}: H3, H8, E11, H10, A6, C5, C12, D11 y B5 (Tabla 1). Dos líneas celulares presentaron proporciones de actividad/viabilidad de alrededor de 0.100×10^{-2}: D7 y B10 (Tabla 1). Con base en estas proporciones de actividad/viabilidad junto con las

mediciones de señal de viabilidad celular y de actividad de la BoNT/A, estas 18 líneas celulares clonales se seleccionaron para realizarles más pruebas llevando a cabo un análisis secundario usando el ensayo de actividad de la BoNT/A para generar una curva de dosis-respuesta de BoNT/A.

Tabla 1. Análisis primario para líneas celulares clonales susceptibles de intoxicación por BoNT/A usando señales de viabilidad y actividad

Pocillo	Lectura de viabilidad celular (RLU)	Señal de actividad de la BoNT/A (RLU)	Proporción de actividad/ viabilidad	Pocillo	Lectura de viabilidad celular (RLU)	Señal de actividad de la BoNT/A (RLU)	Proporción de actividad/ viabilidad
A1	2634417	2425	0.092×10^{-2}	A7	10132753	27242	0.269×10^{-2}
B1	731808	198	0.027×10^{-2}	B7	2977371	1642	0.055×10^{-2}
C1	4258160	1641	0.039×10^{-2}	C7	5746577	4878	0.085×10^{-2}
D1	6554606	4885	0.075×10^{-2}	D7	5861338	6044	0.103×10^{-2}
E1	2374483	897	0.038×10^{-2}	E7	2819910	1399	0.050×10^{-2}
F1	2801444	1842	0.066×10^{-2}	F7	23523	84	0.357×10^{-2}
G1	5094510	4579	0.090×10^{-2}	G7	6232344	4031	0.065×10^{-2}
H1	3808699	10861	0.285×10^{-2}	H7	4916756	2759	0.056×10^{-2}
A2	9593106	7090	0.074×10^{-2}	A8	5945833	5611	0.094×10^{-2}
B2	5374966	5673	0.106×10^{-2}	B8	4591002	2128	0.046×10^{-2}
C2	4170158	2972	0.071×10^{-2}	C8	5648241	8758	0.155×10^{-2}

D2	31283	88	0.281×10^{-2}	D8	4207887	3360	0.080×10^{-2}
E2	5706902	3743	0.066×10^{-2}	E8	5894699	3844	0.065×10^{-2}
F2	4884798	4568	0.094×10^{-2}	F8	5585487	4651	0.083×10^{-2}
G2	3552045	2190	0.062×10^{-2}	G8	4758800	4545	0.096×10^{-2}
H2	3743690	3421	0.091×10^{-2}	H8	5439137	8017	0.147×10^{-2}
A3	15372	89	0.579×10^{-2}	A9	10423188	20706	0.199×10^{-2}
B3	5381672	1551	0.029×10^{-2}	B9	6493893	4444	0.068×10^{-2}
C3	4270534	3959	0.093×10^{-2}	C9	5742047	5788	0.101×10^{-2}
D3	48702	97	0.199×10^{-2}	D9	3424405	1848	0.054×10^{-2}
E3	4707349	2671	0.057×10^{-2}	E9	5771943	8064	0.140×10^{-2}
F3	3053132	1539	0.050×10^{-2}	F9	24524	88	0.359×10^{-2}
G3	5518292	4195	0.076×10^{-2}	G9	7291510	6674	0.092×10^{-2}
H3	4156632	6339	0.153×10^{-2}	H9	4169883	6048	0.145×10^{-2}
A4	19793	89	0.450×10^{-2}	A10	9050811	17617	0.195×10^{-2}
B4	6224766	4299	0.069×10^{-2}	B10	5590113	5175	0.093×10^{-2}
C4	3212859	3202	0.100×10^{-2}	C10	2325807	1713	0.074×10^{-2}
D4	4376180	2367	0.054×10^{-2}	D10	2644116	2589	0.098×10^{-2}
E4	3931793	3975	0.101×10^{-2}	E10	4210945	2666	0.063×10^{-2}
F4	1150134	526	0.046×10^{-2}	F10	2932749	6390	0.218×10^{-2}
G4	19023	94	0.494×10^{-2}	G10	3980127	3114	0.078×10^{-2}
H4	3368425	2645	0.079×10^{-2}	H10	4519035	6187	0.137×10^{-2}
A5	8231689	7809	0.095×10^{-2}	A11	9870025	24690	0.250×10^{-2}
B5	5332004	6545	0.123×10^{-2}	B11	4973892	2235	0.045×10^{-2}
C5	3869441	5042	0.130×10^{-2}	C11	3326448	6405	0.193×10^{-2}
D5	2554300	1161	0.045×10^{-2}	D11	5747961	7169	0.125×10^{-2}

E5	3781403	764	0.020×10^{-2}	E11	5831546	8432	0.145×10^{-2}
F5	4608801	3720	0.081×10^{-2}	F11	5291803	4317	0.082×10^{-2}
G5	7105403	7330	0.103×10^{-2}	G11	3499587	2790	0.080×10^{-2}
H5	5585607	7544	0.135×10^{-2}	H11	3225750	4518	0.140×10^{-2}
A6	7698708	10152	0.132×10^{-2}	A12	9838	89	0.905×10^{-2}
B6	4706560	3196	0.068×10^{-2}	B12	3728293	2016	0.054×10^{-2}
C6	5866251	6145	0.105×10^{-2}	C12	4086862	5308	0.130×10^{-2}
D6	2285787	768	0.034×10^{-2}	D12	5044526	3860	0.077×10^{-2}
E6	2471979	1038	0.042×10^{-2}	E12	4787913	2719	0.057×10^{-2}
F6	10958	91	0.830×10^{-2}	F12	5101695	2585	0.051×10^{-2}
G6	19590	91	0.465×10^{-2}	G12	2887390	1622	0.056×10^{-2}
H6	2057687	2564	0.125×10^{-2}	H12	2829307	5105	0.180×10^{-2}

Para llevar a cabo un ensayo de actividad de la BoNT/A para generar una curva de dosis-respuesta de BoNT/A, las células de cada línea celular clonal aislada se sembraron en una placa de 96 pocillos de poli-D-lisina y se diferenciaron como se describió anteriormente. De las 18 líneas celulares clonales superiores seleccionadas para realizarles pruebas adicionales, solo 8 permanecieron viables, las otras 10 líneas celulares clonales no pudieron volver a crecer y se perdieron. El medio de las células diferenciadas se aspiró de cada pocillo y se reemplazó con sin tratar) 0.03 pM, 0.1 pM, 0.3 pM, 0.9 pM, 2.8 pM, 8.3 pM, y 25 pM de un complejo de

BoNT/A. Luego de 24 horas de tratamiento, las células se lavaron, incubaron por dos días más en un medio libre de suero sin toxina para permitir la escisión del sustrato de la SNAP-25 y se recolectaron como se describió anteriormente. El sobrenadante se transfirió a una placa de 96 pocillos recubiertos con anticuerpo de captura para realizar la etapa de detección.

La solución de anticuerpo de captura α-SNAP-25, la solución de anticuerpo de detección α-SNAP-25 y el soporte de fase sólida α-SNAP-25 se prepararon como se describió anteriormente. La detección de la presencia del producto de la SNAP-25 escindida por análisis ELISA tipo sándwich ECL se llevó a cabo como se describió anteriormente. Los datos sin procesar obtenidos del generador de imágenes ECL se transfirieron luego al SigmaPlot v. 9.0 y se usó un ajuste de logística de parámetro 4 para definir las curvas de respuesta a la dosis. No se usaron restricciones para la función de logística de parámetro 4 cuando se graficaron los datos. Los informes gráficos se generaron usando los siguientes análisis: R2 (coeficiente de correlación), a (máx. para el conjunto de datos), b (ladera) y X0 ± SE (valor de EC_{50} ± error estándar).

Estos resultados indicaron que de las 8 líneas celulares clonales analizadas, solo dos eran más susceptibles de intoxicación por BoNT/A en comparación con las células que comprenden la línea celular SiMa original (Tabla 2). Por ejemplo, las células que comprenden la línea celular SiMa original presentaron una actividad de EC_{50} para BoNT/A de 2.20 pM, mientras que las células que comprenden las líneas celulares H1 y A10 presentaron una actividad de EC_{50} para BoNT/A de 1.76 pM o menos. Por el contrario, las células que comprenden la línea celular H10 y D11 presentaron una actividad de EC_{50} para BoNT/A que era mayor a la observada para las células que comprenden la línea celular SiMa original, pero menor a 5.0 pM. Cabe destacar que cualquier línea celular clonal que presenta una actividad de EC_{50} para BoNT/A que es de 5.0 pM o menos (100 U/mL o menos) es útil para un método basado en inmunoensayos para determinar la actividad de la BoNT/A descrita en Ester Fernandez-Salas, et al., *Immuno-Based Botulinum Toxin Serotype A Activity Assays*, patente estadounidense No. de serie: 12/403,531.

Tabla 2. Análisis secundario para líneas celulares clonales susceptibles de intoxicación por BoNT/A

Clon	Actividad de la BoNT/A		
	EC_{50} (pM)	$Señal_{MIN}$ (RLU)	$Señal_{MAX}$ (RLU)
SiMa	2.20	123	47,611
H1	0.77	193	125,252
H3	ND	ND	ND
B5	>25.0	115	22,277
C5	ND	ND	ND
A6	ND	ND	ND
A7	5.59	153	100,412
D7	ND	ND	ND
H8	ND	ND	ND
A9	ND	ND	ND
A10	1.76	207	113,029
B10	6.35	147	101,935
F10	>25.0	111	32,663
H10	2.80	171	120,975
A11	ND	ND	ND
C11	ND	ND	ND
D11	4.4	1.84	105,527
E11	ND	ND	ND
C12	ND	ND	ND

ND = Sin determinar

3. Análisis primario para la susceptibilidad de intoxicación por BoNT/A de células de una línea celular clonal usando un producto farmacéutico de BoNT/A formulado.

Otra forma de determinar si las células de una línea celular clonal eran susceptibles de intoxicación por BoNT/A fue llevar adelante un análisis primario generando una curva de dosis-respuesta de BoNT/A y calcular el valor de EC_{50} usando un método basado en inmunoensayos para determinar la actividad de la BoNT/A según se describe en Ester Fernandez-Salas, et al., *Immuno-Based Botulinum Toxin Serotype A Activity Assays*, solicitud de patente estadounidense No. de serie: 12/403,531, que se incorpora a la presente a modo de referencia en su totalidad.

Al principio, se examinaron seis de 35 aislados de línea celular clonal usando una respuesta a la dosis completa de BoNT/A. Para preparar un lisado a partir de células tratadas con BoNT/A, se sembraron las células de seis líneas celulares clonales en una placa de 96 pocillos de poli-D-lisina y se diferenciaron según se describió anteriormente en la Sección 2 con la excepción de que el medio libre de suero comprendía 60 µg/mL de GT1b. Las líneas celulares clonales usadas fueron 3D8, YB8, 1D4, 2D6, 1E11 y 2F5. Las líneas celulares clonales H1 y H10 identificadas anteriormente,

junto con la línea celular SiMa original se usaron como referencias para identificar líneas celulares altamente susceptibles de intoxicación por BoNT/A. El medio de las células diferenciadas se aspiró de cada pocillo y se reemplazó con medio recién preparado que contenía 0 (muestra sin tratar), 0.98 U/mL, 1.9 U/mL, 3.91 U/mL, 7.81 U/mL, 15.6 U/mL, 31.3 U/mL, 62.5 U/mL, 125 U/mL, 250 U/mL o 500 U/mL de un producto farmacéutico de BoNT/A formulado. Luego de 24 horas de tratamiento, las células se lavaron, se incubaron durante dos días más en un medio libre de suero sin toxina para permitir la escisión del sustrato de SNAP-25. Para recolectar las células, se aspiró 1 x de PBS, las células se lisaron agregando 30 µl de amortiguador de lisis que comprendía 20 mM de Tris-HCl (pH 7.5), 150 mM de NaCl, 1 mM de EDTA, 1 mM de EGTA, 1% de Triton X-100 a cada pocillo y la placa se incubó en un agitador con rotación a 500 rpm durante 30 minutos 4°C. La placa se centrifugó a 4000 rpm durante 20 minutos a 4°C para sedimentar los residuos celulares. La concentración de proteína se determinó usando métodos estándar. El sobrenadante se transfirió a una placa de 96 pocillos recubierta con anticuerpo de captura para llevar a cabo la etapa de detección del método basado en inmunoensayos.

La solución de anticuerpo de captura α-SNAP-25, la solución de anticuerpo de detección α-SNAP-25 y el soporte de fase sólida α-SNAP-25 se prepararon como se describió anteriormente en la Sección 2. Se llevó adelante la detección de la presencia del producto de la escisión de la SNAP-25 por un análisis de ELISA tipo sándwich ECL, se analizaron los datos recogidos y se calcularon las EC_{50} como se describió anteriormente en la Sección 2, con la excepción de que se usó SigmaPlot v. 10.

Estos resultados muestran que la línea celular clonal H1 comprende células que son más susceptibles a la BoNT/A que la línea celular SiMa original (Tabla 3). Además, los resultados indican que pese a que todas las líneas celulares H10, 1D4, 1E11, 2D6, 2F5, 3D8 y YB8 comprenden células que son menos susceptibles a las BoNT/A que la línea celular SiMa original, todas tienen una EC_{50} de actividad de la BoNT/A menor a 30 U/mL (Tabla 3). Cabe destacar que cualquier línea celular clonal que presenta una actividad de EC_{50} para BoNT/A que es de 100 U/mL o menos (5.0 pM o menos) es útil para un método basado en inmunoensayos para determinar la actividad de la BoNT/A descrita en Ester Fernandez-Salas, et al., *Immuno-Based Botulinum Toxin Serotype A Activity Assays*, solicitud de patente estadounidense No. de serie: 12/403,531.

Tabla 3. Análisis primario para líneas celulares clonales susceptibles de intoxicación por BoNT/A

Clon	Actividad de la BoNT/A		
	EC_{50} (U/mL)	$Señal_{MIN}$ (RLU)	$Señal_{MAX}$ (RLU)
SiMa	10.8 ± 1.0	10,519	253,484
H1	10.2 ± 0.6	13,996	276,982
H10	22.2 ± 2.0	5,379	296,168
1D4	22.4 ± 0.8	6,064	239,096
1E11	14.2 ± 1.7	8,698	276,323
2D6	27.3 ± 1.8	3,347	179,454
2F5	15.8 ± 0.9	7,007	265,461
3D8	13.4 ± 0.6	11,658	266,279
YB8	19.7 ± 1.3	8,477	293,559

Este análisis primario inicial usando una curva de dosis-respuesta con las 10 concentraciones de BoNT/A diferentes identificó tres concentraciones que fueron útiles para un ensayo acortado usando 3 concentraciones de BoNT/A diferentes, donde una concentración es un poco mayor que la asíntota inferior (8 U/mL), una concentración se encuentra cerca de la EC50 (25 U/mL) y una concentración representa alrededor del 80% de la asíntota superior (80 U/mL). En estos análisis primarios posteriores los otros 29 aislados de línea celular clonal se probaron como se describió anteriormente

con la excepción de que las células se trataron con 0 (muestra sin tratar) 8 U/mL, 25 U/mL u 80 U/mL de un producto farmacéutico de BoNT/A formulado. Las líneas celulares clonales probadas fueron 1E3, 2B9, 2D2, 2E4, 3B8, 3D5, 3G10, 4B5, 4C8, 4D3, 5C10, 5F3, AC9, AF4, BB3, BB10, BE3, BF8, CC11, CD6, CE6, CG8, CG10, DC4, DD10, DE7, DF5, YB7 e YF5. Además, la línea celular SiMa original se usó como control positivo.

Estos resultados muestran que todas las líneas celulares clonales 2E4, 3B8, 3D5, 5F3, AF4, BB3, BB10 y DC4 comprenden células que son más susceptibles a BoNT/A que la línea celular SiMa original (Tabla 4). Además, estos resultados indican que todas las líneas celulares clonales 1E3, 2B9, 3G10, 4B5, 4C8, AC9, BE3, BF8, CC11, CD6, CE6, CG8, CG10, DD10, DE7 e YF5 comprenden células que tienen una susceptibilidad similar a la BoNT/A que la línea celular SiMa original (Tabla 4). Por último, estos resultados revelan que todas las líneas celulares clonales 2D2, 4D3, 5C10, DF5 e YB7 comprenden células que son menos susceptibles a la BoNT/A que la línea celular SiMa original (Tabla 4).

Tabla 4. Análisis primario para líneas celulares clonales susceptibles de intoxicación por BoNT/A

Clon	8 U/mL de BoNT/A		25 U/mL de BoNT/A		80 U/mL de BoNT/A	
	Señal de actividad (RLU)	Diferencia de veces	Señal de actividad (RLU)	Diferencia de veces	Señal de actividad (RLU)	Diferencia de veces
SiMa	75811/ 80562*	—	138952/ 175685*	—	173979/ 225768*	—
1E3	71040	0.9	128771	0.9	155107	0.9
2B9	66962	0.9	135006	1.0	166871	1.0
2D2	60224*	0.8	136947*	0.8	199786*	0.9
2E4	103680	1.4	217980	1.6	270463	1.6
3B8	123521	1.6	227367	1.6	249218	1.4
3D5	113532	1.5	201683	1.5	270578	1.6
3G10	83049	1.1	130930	0.9	175540	1.0
4B5	74344	1.0	137604	1.0	177363	1.0
4C8	87047	1.1	144395	1.0	185115	1.1
4D3	38063	0.5	80180	0.6	101724	0.6
5C10	16024*	0.2	49030	0.3	116396*	0.6
5F3	98263*	1.7	182902*	1.4	212275*	1.5
AC9	60016*	1.0	127030*	1.0	180384*	1.4
AF4	115460	1.5	179901	1.3	190867	1.1
BB3	74668	1.3	120966	1.4	170177	1.4
BB10	152748	2.0	232406	1.7	266555	1.5
BE3	100849	1.0	199487	0.9	236415	1.0
BF8	55763*	1.0	111746*	1.0	153074*	1.3
CC11	54421*	1.0	123576*	1.0	155337*	1.2

CD6	74970	1.0	151862	1.1	183377	1.1
CE6	70019	0.9	146292	1.1	208184	1.2
CG8	81790*	1.0	159098*	1.0	189209*	1.3
CG10	69503	0.9	141079	1.0	185801	1.1
DC4	112085	1.5	163319	1.2	169352	1.0
DD10	116325	1.5	205445	1.5	223473	1.3
DE7	60994*	0.9	131237*	0.9	174487*	0.9
DF5	34,165*	0.5	104,696*	0.7	179,314*	0.9
YB7	50433	0.7	103707	0.7	143423	0.8
YF5	65848	0.9	122487	0.9	146263	0.4

* Se realizaron dos análisis separados. En el primero, la señal detectada para la línea celular SiMa fue de 75811 RLU y este valor se usó para determinar la diferencia de veces para las líneas celulares clonales analizadas en este análisis (números sin asteriscos). Para el segundo análisis, la señal detectada para la línea celular SiMa fue de 80562 RLU y este valor se usó para determinar la diferencia de veces para las líneas celulares clonales analizadas en este análisis (números sin asteriscos).

Ejemplo II

Análisis de estabilidad de las líneas celulares clonales

El siguiente ejemplo demuestra cómo caracterizar la estabilidad de células de una línea celular clonal establecida que son susceptibles de intoxicación por BoNT/A o que tienen capacidad de absorción de neurotoxina.

Durante la caracterización de la línea celular SiMa, se determinó que la línea celular SiMa original se volvió inestable en términos de una pérdida significativa de sensibilidad a la BoNT/A. Por ejemplo, antes del pasaje 13, las células que comprenden la línea celular SiMa original presentaban de forma rutinaria una EC_{50} para la actividad de la BoNT/A inferior a 5.0 pM. Sin embargo, luego de los pasajes alrededor del 14 a alrededor del 20, las células que comprendían la línea celular SiMa presentaron una EC_{50} para la actividad de la BoNT/A que era, de forma rutinaria, superior a 25.0 pM. Una razón para esta reducción drástica en el valor de EC_{50} puede deberse a que la línea celular SiMa es heterogénea en naturaleza debido a que comprende al menos cinco tipos celulares diferentes. Con el tiempo, uno de estos tipos celulares podría sobrepasar el cultivo hasta la exclusión de los otro cuatro. Si el tipo celular que sobrepasa era menos susceptible de intoxicación por BoNT/A, o no era susceptible, entonces como este tipo celular se convirtió en el dominante en la línea celular, la EC_{50} para la actividad de la BoNT/A en esta línea celular SiMa sobrepasada

disminuiría. Por lo tanto, debido a que las líneas celulares clonales establecidas solo provenían de uno de estos tipos celulares, entonces la línea celular clonar presentaría una mayor estabilidad en términos de mantener una EC_{50} para la actividad de la BoNT/A que era de forma rutinaria menor a 5.0 pM.

Para determinar si las células de las líneas celulares clonales establecidas mostraban una mayor estabilidad con respecto a las células que comprenden la línea celular SiMa original, la EC_{50} para la actividad de la BoNT/A se determinó para las líneas celulares clonales BB10, H1, H10 y la línea celular SiMa original en diferentes números de pasajes usando un método basado en inmunoensayos para determinar la actividad de la BoNT/A. El medio de las células diferenciadas se aspiró de cada pocillo y se reemplazó con medio recién preparado que contenía 0 (muestra sin tratar), 0.98 U/mL, 1.9 U/mL, 3.91 U/mL, 7.81 U/mL, 15.6 U/mL, 31.3 U/mL, 62.5 U/mL, 125 U/mL, 250 U/mL o 500 U/mL de un producto farmacéutico de BoNT/A formulado. Luego de 24 horas de tratamiento, las células se lavaron, se incubaron por dos días más en un medio libre de suero sin toxina para permitir la escisión del sustrato de la SNAP-25 y se recolectaron como se describió anteriormente. El sobrenadante se transfirió a una placa de

96 pocillos recubiertos con anticuerpo de captura para llevar a cabo la etapa de detección.

De manera similar, la preparación de la solución de anticuerpo de captura α-SNAP-25, la solución de anticuerpo de detección α-SNAP-25 y el soporte de fase sólida que comprende un anticuerpo de captura α-SNAP-25 son como se describió en la Sección 3. Por último, se llevó adelante la detección de la presencia del producto de la escisión de la SNAP-25 por un análisis de ELISA tipo sándwich ECL, se analizaron los datos recogidos y se calculó la EC_{50} como se describió anteriormente en la Sección 2, con la excepción de que se usó PLA v. 2 para el ajuste de logística de parámetro 4.

Los resultados de estos experimentos de estabilidad indicaron que todas las líneas celulares BB10, H1 y H10 presentaron una mayor estabilidad en comparación con la línea celular SiMa original. Por ejemplo, en los casos en que las células de la línea celular SiMa original presentaron una EC_{50} para la actividad de la BoNT/A superior a 500 U/mL (o 25 pM) luego de los pasajes alrededor de 14 a alrededor de 20 pasajes, todas las células que comprenden las líneas celulares BB10, H1 y H10 presentaron una EC_{50} para la actividad de la BoNT/A inferior a 10 U/mL (o 0.5 pM) luego de los pasajes alrededor de 30.

Ejemplo III

Perfil de expresión genética de líneas celulares que comprenden células susceptibles de intoxicación por BoNT/A

El siguiente ejemplo demuestra cómo caracterizar las células de una línea celular clonal establecida que son susceptibles de intoxicación por BoNT/A o que tienen capacidad de absorción de neurotoxina por medio de la determinación de perfiles de expresión genética.

Para determinar los cambios en los niveles de transcripción genética en lo que respecta a los genomas en células susceptibles de intoxicación por BoNT/A, el análisis de expresión genética se llevó a cabo en células de las líneas celulares H1, BB10, 2D6 y SiMa original, tanto en los estados diferenciados como no diferenciados usando tecnología de micromatriz GENECHIP® U133 Plus 2 (Affymetrix, Inc., Santa Clara, CA) de acuerdo con las instrucciones del fabricante, véase, por ej., *GENECHIP® Expression Analysis Technical Manual*, 702232, Rev. 2 (2006) que se incorpora a la presente a modo de referencia en su totalidad.

Para preparar células diferenciadas para estas líneas celulares, una densidad adecuada de células de las líneas

celulares H1, BB10, 2D6 y SiMa se sembraron en matraces de cultivo de tejido T175 separados que contenían 50 mL de un medio libre de suero que comprende medio esencial mínimo mejorado, 10 mM de HEPES, 1 mM de piruvato de sodio, 0.1 mM de aminoácidos no esenciales, 1 x de suplemento B27, 1 x de suplemento N2 y 60 µg/mL de GT1b (302-011-M005, Alexis Biochemicals, San Diego, CA). Estas células se incubaron en un incubador a 37°C con 5% de dióxido de carbono hasta que las células se diferenciaron, según se evaluó por criterios morfológicos estándar y de rutina, tal como detención de crecimiento y extensión de neuritas y lograron una confluencia del 80% (aproximadamente 3 días). Luego las células se lavaron con 50 mL de 1 x PBS, se trataron con tripsina durante 5 minutos a temperatura ambiente y luego se agregaron 15 mL de medio de crecimiento al matraz para inactivar la tripsina. La suspensión celular se transfirió a un tubo de 50 mL y se centrifugó a 200 RCF durante 5 min a temperatura ambiente para sedimentar las células. El sedimento celular se lavó una vez en 50 mL de 1 x de PBS, se centrifugó a 200 RCF durante 5 min a temperatura ambiente para sedimentar las células y se retiró el sobrenadante. El sedimento celular se congeló rápidamente en hielo seco y se agitó a -80°C hasta que se necesitara.

Para preparar células no diferenciadas para estas líneas celulares, una densidad adecuada de células de las líneas celulares H1, BB10, 2D6 y SiMa se sembraron en matraces de cultivo de tejido T175 separados que contenían 50 mL de medio de crecimiento que comprende RPMI 1640, 10% de suero bovino fetal, 10 mM de HEPES, 1 mM de piruvato de sodio, 0.1 mM de aminoácidos no esenciales y 60 µg/mL de GT1b. Estas células se incubaron en un incubador a 37°C con 5% de dióxido de carbono hasta que las células lograron una confluencia del 80% (aproximadamente 3 días). Luego las células se procesaron como se describió anteriormente y los sedimentos celulares se congelaron rápidamente en hielo seco y se almacenaron a -80°C hasta que se necesitaran.

Para preparar ARN total, las células de cada línea celular se lisaron y se aisló ARN total y purificó usando un kit de aislamiento de ARN (QIAGEN, Valencia, CA) conforme a los protocolos del fabricante. Se digirió ADN usando un procedimiento de desoxirribonucleasa I en la columna (QIAGEN, Valencia, CA). Se cuantificó ARN fotoespectrométricamente a 260 nm y la pureza se evaluó para determinar la proporción A260A280 usando un espectrofotómetro. La integridad de ARN se evaluó usando un Bioanalyser 2100 (Agilent Technologies, Inc., Santa Clara, CA). Las alícuotas de ARN total extraídas

se congelaron instantáneamente in nitrógeno líquido y se almacenaron a -80°C.

Para preparar sondas de ADNc para los chips de micromatriz genética, alrededor de 1-15 µg se transcribió de forma inversa usando un cebador de promotor T7-Oligo(dT) en la reacción de síntesis de ADNc de primera cadena. Luego de la síntesis de ADNc de segunda cadena de ribonucleasa mediada por H, el ADNc de doble cadena se purificó y sirvió como plantilla para la posterior reacción de transcripción in vitro. La reacción de transcripción in vitro se llevó a cabo en presencia de polimerasa de ARN T7 y una mezcla de análogo de nucleótido biotinilado/ribonucleótico para amplificación de ARN complementario (ARNc) y etiquetado de biotina. Luego las dianas de ARNc biotinilado se limpiaron, fragmentaron e hibridaron en matrices de expresión de microchip durante 17 horas a 65°C de acuerdo con las instrucciones del fabricante, véase, por ej., Manual Técnico de Expresión de Análisis *GENECHIP®*, 702232, Rev. 2 (2006) que se incorpora a la presente a modo de referencia en su totalidad. Para identificar las diferencias de expresión genética reguladas por aumento o por disminución relacionadas con el tratamiento sustancial en comparación con líneas celulares de control, las diferencias mayores a 1.5 veces ($\log_2$ 0.58) se consideraron significativas y solo se tomaron en cuenta

aquellos genes que mostraron cambios consistentes en la expresión en el análisis triplicado (Tablas 5 a 12).

La determinación de perfiles de expresión para las líneas celulares H1, BB10 y 2D6 analizados en el estado no diferenciado reveló que 1,323 genes se identificaron como que tenían sus niveles de expresión aumentados en 1.5 veces ($\log_2$ 0.58) o más en las líneas celulares H1 y BB10 en comparación con los niveles de expresión genética obtenida de la línea celular 2D6 (Tabla 5). De estos, 686 genes presentaron un aumento en los niveles de expresión en las líneas celulares H1 y BB10 de 2 veces ($\log_2$ 1.0) o más en comparación con el nivel de expresión de estos genes determinada para la línea celular 2D6 y 231 genes presentaron un aumento en los niveles de expresión en las líneas celulares H1 y BB10 de 4 veces ($\log_2$ 2.0) o más en comparación con el nivel de expresión de estos genes determinados para la línea celular 2D6. Con respecto a la menor expresión, se identificaron 1,438 genes por tener sus niveles de expresión disminuidos de 1.5 veces ($\log_2$ 0.58) o más en las líneas celulares H1 y BB10 en comparación con los niveles de expresión genética obtenidos de la línea celular 2D6 (Tabla 6). De estos, 668 genes presentaron una disminución en los niveles de expresión en las líneas celulares H1 y BB10 de 2 veces ($\log_2$ 1.0) o más en comparación con el nivel de expresión de estos genes

determinados para la línea celular 2D6 y 107 genes presentaron una disminución en los niveles de expresión en las líneas celulares H1 y BB10 de 4 veces (log_2 2.0) o más en comparación con el nivel de expresión de estos genes determinados para la línea celular 2D6.

La determinación de perfiles de expresión para las líneas celulares H1, BB10 y 2D6 analizados en el estado diferenciado reveló que se identificaron 2,556 genes por tener sus niveles de expresión aumentados en 1.5 veces (log_2 0.58) o más en las líneas celulares H1 y BB10 en comparación con los niveles de expresión genética obtenida de la línea celular 2D6 (Tabla 7). De estos, 1,634 genes presentaron un aumento en los niveles de expresión en las líneas celulares H1 y BB10 de 2 veces (log_2 1.0) o más en comparación con el nivel de expresión de estos genes determinados para la línea celular 2D6 y 696 genes presentaron un aumento en los niveles de expresión en las líneas celulares H1 y BB10 de 4 veces (log_2 2.0) o más en comparación con el nivel de expresión de estos genes determinados para la línea celular 2D6. Con respecto a la menor expresión, se identificaron 2,087 genes por tener sus niveles de expresión disminuid osen 1.5 veces (log_2 0.58) o más en las líneas celulares H1 y BB10 en comparación con los niveles de expresión genética obtenidos de la línea celular 2D6 (Tabla 8). De estos, 1.215 genes

presentaron una disminución en los niveles de expresión en las líneas celulares H1 y BB10 de 2 veces (log_2 1.0) o más en comparación con el nivel de expresión de estos genes determinados para la línea celular 2D6 y 280 genes presentaron una disminución en los niveles de expresión en las líneas celulares H1 y BB10 de 4 veces (log_2 2.0) o más en comparación con el nivel de expresión de estos genes determinados para la línea celular 2D6.

La determinación de perfiles de expresión para las líneas celulares H1, BB10 y SiMa analizados en el estado no diferenciado reveló que se identificaron 1,232 genes por tener sus niveles de expresión aumentados en 1.5 veces (log_2 0.58) o más en las líneas celulares H1 y BB10 en comparación con los niveles de expresión genética obtenidos de la línea celular SiMa (Tabla 9). De estos, 764 genes presentaron un aumento en los niveles de expresión en las líneas celulares H1 y BB10 de 2 veces (log_2 1.0) o más en comparación con el nivel de expresión de estos genes determinados para la línea celular original SiMa y 228 genes presentaron un aumento en los niveles de expresión en las líneas celulares H1 y BB10 de 4 veces (log_2 2.0) o más en comparación con el nivel de expresión de estos genes determinados para la línea celular original SiMa. Con respecto a la expresión disminuida, se identificaron 1,265 genes por tener sus niveles de expresión

disminuidos en 1.5 veces (log_2 0.58) o más en las líneas celulares H1 y BB10 en comparación con los niveles de expresión genética obtenidos de la línea celular original SiMa (Tabla 10). De estos, 648 genes presentaron una disminución en los niveles de expresión en las líneas celulares H1 y BB10 de 2 veces (log_2 1.0) o más en comparación con el nivel de expresión de estos genes determinados para la línea celular original SiMa y 189 genes presentaron una disminución en los niveles de expresión en las líneas celulares H1 y BB10 de 4 veces (log_2 2.0) o más en comparación con el nivel de expresión de estos genes determinados para la línea celular original SiMa.

La determinación de perfiles de expresión para las líneas celulares H1, BB10 y SiMa analizados en el estado diferenciado reveló que se identificaron 756 genes por tener sus niveles de expresión aumentados en 1.5 veces (log_2 0.58) o más en las líneas celulares H1 y BB10 en comparación con los niveles de expresión genética obtenidos de la línea celular original SiMa (Tabla 11). De estos, 472 genes presentaron un aumento en los niveles de expresión en las líneas celulares H1 y BB10 de 2 veces (log_2 1.0) o más en comparación con el nivel de expresión de estos genes determinados para la línea celular original SiMa y 150 genes presentaron un aumento en los niveles de expresión en las

líneas celulares H1 y BB10 de 4 veces (log_2 2.0) o más en comparación con el nivel de expresión de estos genes determinados para la línea celular original SiMa. Con respecto a la expresión disminuida, se identificaron 912 genes por tener sus niveles de expresión disminuidos en 1.5 veces (log_2 0.58) o más en las líneas celulares H1 y BB10 en comparación con los niveles de expresión genética obtenidos de la línea celular original SiMa (Tabla 12). De estos, 411 genes presentaron una disminución en los niveles de expresión en las líneas celulares H1 y BB10 de 2 veces (log_2 1.0) o más en comparación con el nivel de expresión de estos genes determinados para la línea celular original SiMa y 108 genes presentaron una disminución en los niveles de expresión en las líneas celulares H1 y BB10 de 4 veces (log_2 2.0) o más en comparación con el nivel de expresión de estos genes determinados para la línea celular original SiMa.

Ejemplo IV

Análisis de senda de perfiles de expresión genética de líneas celulares clonales

El siguiente ejemplo demuestra cómo caracterizar los perfiles de expresión genética a partir de células clonales de una línea celular clonal establecida que son susceptibles

de intoxicación por BoNT/A o que tienen capacidad de absorción de neurotoxina para identificar redes o sendas biológicas asociadas con la intoxicación por BoNT/A.

Se llevó a cabo un análisis central del análisis de senda de habilidad (IPA) (Ingenuity Systems Inc., Redwood City, CA) para caracterizar el fenotipo de expresión de ARN de dos líneas celulares clonales únicas muy sensibles a BoNT/A independientemente derivadas, BB10 y H1, en comparación con una única línea celular clonal relacionada pero mucho menos sensible a BoNT/A, 2D6. El análisis se hizo para identificar el fenotipo de expresión genética específico de una línea celular sensible a BoNT/A. El resultado también se puede usar para predecir y potencialmente identificar proteínas que funcionan para mejorar la absorción de BoNT/A.

Se llevó a cabo un análisis central de análisis de senda de habilidad (IPA) que identificaba redes biológicamente relevantes para la intoxicación por BoNT/A con base en la conectividad entre los genes de una biblioteca de IPA y los genes que presentaban cambios significativos según se determina del establecimiento de perfiles de expresión discutido anteriormente. Para este análisis, todos los genes que presentaron un aumento o una disminución en los niveles de expresión en las líneas celulares H1 y BB10 de 4 veces

(log_2 2.0) o más en comparación con el nivel de expresión para estos genes determinados de la línea celular 2D6 se usaron junto con genes seleccionados con una relevancia conocida o sospechada a la intoxicación por BoNT/A, a los que se refiere en lo sucesivo como genes de perfil. La importancia de la asociación a una red dada se midió y clasificó según la proporción del número de genes de perfil que se mapearon a la red específica dividido por el número total de genes que se mapean a esa red. La prueba exacta de Fisher se usó para calcular los valores p, que representan la asociación entre los genes de perfil y la red y, con base en los valores p, se usaron los genes de los genes de perfil para clasificar las redes. Los valores p provinieron de los valores p. Si hay *n* genes en la red y *f* de esos son genes de perfil, entonces el valor p es la probabilidad de encontrar *f* o más genes de perfil en un conjunto de *n* genes seleccionados de forma aleatoria de la red global molecular. Debido a que los valores p significativos eran bastante bajos (por ej., 1 x 10^{-8}), una puntuación p se definió como el componente del valor p; puntuación p = -log10 (valor p). Las redes identificadas se revistieron con genes expresados de forma diferente que tenían una expresión diferencial de más de 1.5 veces y un valor p $\leq$ 0.001 ya sea antes o después de la diferenciación.

Usando el análisis central IPA los genes de perfil expresados de forma diferencial se conectaron a 26 redes. Diecinueve de estas incluían 10 o más genes de perfil (Tabla 13). Entre estas diecinueve redes, se identificaron tres grupos de redes globales llamados A, B y C (Tabla 13). Dentro de las redes en estos tres grupos había genes solapantes y la expresión para más de tres genes se aumentó luego de la diferenciación. Los genes del grupo A incluyen el receptor de FGFR2 que se ha mostrado que funciona en el proceso de intoxicación por BoNT/A como un receptor de una BoNT/A y son como sigue: genes que presentan una disminución de 1.5 veces o más en los niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en células de la línea celular 2D6, ANXA2, AQP1, ARHGAP9, CDH10, CDKN2A, CHPT1, CNTN2, ERAP1 y RGS11; genes que presentan un aumento de 1.5 veces o más en los niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea celular 2D6, ADAMTS9, ATAD2, C11ORF82, CDC45L, CNTN1, CNTN4, Ciclina A, Ciclina E, E2F1, E2F2, E2F7, ELOVL7, EME1, FGFR, FGFR2, KIAA1524, MELK, MYBL1, MYBL2, NDC80, NDN, ORC1L, PLS3, PRIMA1, RAD54L, RBL1, RBPMS, RRM2, S1PR3, SCLY, SLCIA3, SPC24, SPC25, ST8SIA4, TFDP1, TFP12, TK1, TMEM35, TTK, TWIST1, TYMS, TYK y ZWINT.

Los genes del grupo B incluyen el EGFR, un receptor que está regulado por el NGF que se ha mostrado que aumenta la absorción de BoNT/A en los experimentos de cultivo celular y son como sigue: genes que presentan una disminución de 1.5 veces o más en los niveles de expresión de las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea celular 2D6, ABCC8, AELIM3, CAP2, IL17B, MEF2A, NEEBL, PHC, S100A6, SLC1A6, SMAD1, SMAD5, SMAD8, SYT13 y SYTL1; genes que presentan un aumento de 1.5 veces o más en los niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea celular 2D6, AURKB, BIRC5, BRCA1, BRCA2, BRIP1,BUB1B, CD9, DLGAP3, DYNLT3, ENC1, FBLN1, FOXM1, Gβγ, GNAI1, GNG11, GNG12, GPSM2, GUCY1B3, HGF, ITGA6, JNK, KCNJ5, KIF18A, KITLG, MMD, MSN, MYRIP, NEK2, NR3C1, NXPH1, OSBPL3, PKMYT1, PTPRM, RAD51, RAD51AP1, SLC7A2, SLC43A3, SMC6, SNAI2, SNCAIP, SSH2, STK17A, SYNPO2, TOP2A, TPTE, TRAF4, TSPAN, TSPAN4, UBE3, UBE3B y VAV3.

Los genes del grupo C incluyen un número de proteínas motoras microtubulares de la familia cinesina que pueden funcionar en el tráfico intracelular de BoNT/A y son como sigue: genes que presentan una disminución de 1.5 veces o más en los niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea

celular 2D6, CSTB, GPCR, GRIM5, KISSR, SCN2A, SLC1A2 y THBS2; genes que presentan un aumento de 1.5 veces o más en los niveles de expresión de las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea celular 2D6, ALCAM, AURKA, CHEK, CIT, CSRP2, E2F, ECT2, EFNB2, ERK, ESPL1, GNAI, GPR161, HMMR, KIF4A, KIF14, KIF15, KIF22, KIF23, KIFC1, LPAR1, MK167, OIP5, PHLPP, PP1/PP2A, PPP1R3C, PRC1, PTTG1, RACGAP, RB, RGS5, SDC2 y TPX2.

Las redes restantes identificadas no compartían genes comunes con ninguna otra red. Para la red 3, los genes que presentan una disminución de 1.5 veces o más en los niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea celular 2D6, ADARB1, ADM, PTPPH y SLCO1A2; genes que presentan un aumento de 1.5 veces o más en los niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea celular 2D6, ASCL1,HES6, MAPK, NMU, PEG3, PTPRK, PRLHR, PTPRK, SGOL2, SPARC y ZNF217. Para la red 6, genes que presentan una disminución de 1.5 veces o más en niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea celular 2D6, CNGA3, HIST1H3E y PTGS1; genes que presentan un aumento de 1.5 veces o más en los niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en

las células de la línea celular 2D6, ASF1B, BASP1, CHAF1A, NCAPH, PBK, PRAME, SMC2, UHRF1 y VRK1. Para la red 9, genes que presentan una disminución de 1.5 veces o más en niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea celular 2D6, HIST1H2BD y OSCAR; genes que presentan un aumento de 1.5 veces o más en los niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea celular 2D6, C14ORF106, CEP72, KIF20A, PCNA, PEX13, PFC5, POLQ, SPAG5, SYTL4, TROAP y WDR51A. Para la red 12, genes que presentan un aumento de 1.5 veces o más en niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea celular 2D6, ANLN, ARHGAP24, ASPM, BUB1, CCDC99, CEP55, CKAP2, DRAM, E2F8, PLXNA2, SLC16A10, UBE2C, UBE2S y WDHD1. Para la red 13, genes que presentan una disminución de 1.5 veces o más en niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea celular 2D6, CALY; genes que presentan un aumento de 1.5 veces o más en los niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea celular 2D6, ARHGEF3, CTSL2, DIAPH3, FBP1, KIF2C, KIF11, PFKFB3 y PLK4. Para la red 14, los genes que presentan una disminución de 1.5 veces o más en niveles de expresión en las líneas celulares H1 y BB10 en comparación

con su expresión en las células de la línea celular 2D6, COL5A1 y MICAL2; genes que presentan un aumento de 1.5 veces o más en los niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en células de la línea celular 2D6, FNDC5, HSPC159, MAB21L2, SLITRK5, SYN2 y ZNF367. Para la red 15, genes que presentan una disminución de 1.5 veces o más en niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea celular 2D6, OLFML2A y SIGIRR; genes que presentan un aumento de 1.5 veces o más en los niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en células de la línea celular 2D6, EXO1, KCTD12, MYO6, PHEBL1, SHCBP1, TPBG y TUBB6. Para la red 17, genes que presentan una disminución de 1.5 veces o más en niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea celular 2D6, HPCAL1 y LPAR5; genes que presentan un aumento de 1.5 veces o más en los niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en células de la línea celular 2D6, BTG3, GABRA5, TR1P10 y ZNF521. Para la red 19, genes que presentan una disminución de 1.5 veces o más en niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea celular 2D6, HTR1E y SORCS1; genes que presentan un aumento de 1.5 veces o más en los niveles de expresión en las líneas

celulares H1 y BB10 en comparación con su expresión en células de la línea celular 2D6, BNC2, DPYD, EMILIN2, PPIL5 y TACC3.

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Tabla 13. Análisis central IPA de genes de perfil

Grupo	Red	Proteínas en la red	valor p	Número de gen de perfil	Estado de expresión no diferenciado		Estado de expresión diferenciado	
					Disminuido	Aumentado	Disminuido	Aumentado
		ADAMTS9, ATAD2, CDC45L, CDKN2A, CNTN1, CNTN2, Ciclina A, Ciclina E, DIRAS3, E2F1, E2F2, E2F7, FGFR2, HDAC, MYBL1, MYBL2, NDC80, NDN, NFkB, ORC1L, PLS3, RAD54L, RBL1, RRM2, S1PR3, SPC24, SPC25, TFDP1, TFPI2, TK1, TNFRSF10D, TTK, TYMS, TYK, ZWINT	551	330	CDKN2A	ADAMTS9, CNTN1, HDAC, NDN, PLS3, S1PR3,TFPI 2	CDKN2A, CNTN2,	ADAMTS9, ATAD2, CDC45L, CNTN1, Ciclina A, Ciclina E, E2F1, E2F2, E2F7, FGFR2, MYBL1, MYBL2, NDC80, NDN, ORC1L, PLS3, RAD54L, RBL1, RRM2,

								S1PR3, SPC24, SPC25, TFDP1, TFPI2, TK1, TTK, TYMS, TYK, ZWINT
		ALCAM, ANK2, ANK3, AURKA, DOK5, E2F, ERK, ESPL1, GDF15, GFRA2, HMMR, ITGA9, KIF15, KIF22, KISS1R, KPNA, KPNB, LGI1, MAFB, MAP2K1, MAP2K2, MKI67, NRG3, OIP5, PHKA2, PHLPP, POSTN, PP1/PP2A, PP2A, PPP1R3C, PPP2R2B, PPP2R2C, PTTG1, RAF1, RB, SCN2A, TPX2	46	28	ANK2, ANK3, PHKA2, PPP2R2C, SCN2A	ALCAM, DOK5, ERK, GFRA2, PP1/PP2A, PP2A, PPP1R3C, PPP2R2B	KISSR, SCN2A	ALCAM, AURKA, E2F, ERK, ESPL1, HMMR, KIF15, KIF22, MKI67, OIP5, PHLPP, PP1/PP2A, PPP1R3C, PTTG1, RB, TPX2
		ADARB1, ADM, AKAP12, ALP, ASCL1, BHLHB2, CRH, DLL1, FRZB, FSH, GRIA2, GRIP2, hCG, HES6, HTATIP2,	46	28	ADARB1, GRIP2, SLCO1A2	ASCL1, DLL1, FRZB, MAPK, PEG3, PLAT, PRLHR,	ADARB1, ADM, PTPPH, SLCO1A2	ASCL1, HES6, MAPK, NMU, PEG3,

		IL13RA2, MAPK, NMU, PDGF BB, PDLIM3, PEG3, PLAT, PPFIA4, PRLHR, PTPRH, PTPRK, SGOL2, SLCO1A2, SMAD6, SPARC, STC1, TEAD4, TGFB, VEGF, ZNF217				SMAD6, SPARC, ZNF217		PRLHR, PTPRK, SGOL2, SPARC, ZNF217
		AKT, ACTN1, ACTN2, ACTN3, ATF5, ATM/ATR, BDKRB2, CHEK1, CHEK2, CIT, CSRP2, CSTB, CTSH, ECT2, EFNB2, ELMO1, GNAI, GABBR2, GPCR, GPR161, GRM5, ICAM2, KIF4A, KIF14, KIF23, KIFC1, LPAR1, MMP, PDGFA PDGFB, PRC1, RAC, RAC2, RACGAP1, RGS5, SDC2, SLC1A2, THBS2	43	27	CSTB, GPCR, GRIM5, SLC1A2	GNAI, GPR161, LPAR1, RGS5	CSTB, GPCR, GRIM5, SLC1A2, THBS2	CIT, CSRP2, ECT2, EFNB2, CHEK, GNAI, GPR161, KIF4A, KIF14, KIF23, KIFC1, LPAR1, PRC1, RACGAP, RGS5, SDC2,
		ABLIM3, F-ACTF, G-ACT, CD9, CXCR4, DTNA, ENC1, FNBP1, Gβγ, GNAI1, GNG11,	38	25	SYT13, S100A6	CD9, CXCR4, ENC1, Gβγ, GNAI1,	AELIM3, S100A6, SYT13, SYTL1	CD9, ENC1, Gβγ, GNAI1,

		GNG12, GPSM2, ITG, ITA5, ITGA6, JNK, KCNJ4, MLC, MSN, MYRIP, NOX, NET1, NRXN1, NXPH1, PI3K, RHO, S100A6, STK17A, SYT13, SYTL1, TRAF4, TSPAN, TSPAN3, TSPAN4, VAV3				GNG11, GNG12, ITGA6, JNK, MSN, MYRIP, STK17A		GNG11, GNG12, GPSM2, ITGA6, JNK, KCNJ4, MSN, MYRIP, NXPH1, STK17A, TRAF4, TSPAN, TSPAN4, VAV3
		ADCY, ADCY1, AP1, ASF1B, ATP2B4, BASP1, BCL11B, CAM, CAMK2B, CHAF1A, CNGA3, CYP2E1, DACH1, HIST1H3E, HISH3, HRH3, HSP90, IL1, IL12, INS, INFA, ISG20, KCNN2, LDL, MMP14, NCAPH, PBK, PDGF, PIAS1, PRAME, PTGS1, SEC31A, SMC2, UHRF1, VRK1	36	24	CAMK2B	BASP1, HRH3	CNGA3, HIST1H3E, PTGS1	ASF1B, BASP1, CHAF1A, NCAPH, PBK, PRAME, SMC2, UHRF1, VRK1
		BARD1, BRCA1, BRCA2,	32	24	CAP2, CNA,	NR3C1,	CAP2,	BRCA1,

		BRIP1, BUB1B, CNA, CAP2, CK2, DLGAP5, FAT, GUCY1B3, HSP70, KITLG, MEF2A, NEK2, NFAT, NR3C1, NF1, PHLDA2, PKC(s), RAD51, RAD51AP1, TOP2, SAMD4A, SLC1A6, SMC6, SNAI2, SNCAIP, STAT5a, STAT5b, TCF7L2, UBE3, UBE3B, UBN, XPO1			PHLDA2, PKC(s)	SMC6, SNCAIP, TCF7L2	MEF2A, PKC(s), SLC1A6	BRCA2, BRIP1, BUB1B, DLGAP3, GUCY1B3, NEK2, KITLG, NR3C1, RAD51, RAD51AP1, SMC6, SNAI2, SNCAIP, UBE3, UBE3B
		CBP, AURKB, BIRC5, CACNA1D, CBP/p300, CD3, CREB, CREB5, DBH, EGR1, ERK1, ERK2, FBLN1, FBN1, FOXM1, HGF, INCENP, KCNMA1, LGALS1, MAOA, MEK, NDRG1, NID1, P38 MAPK, PKA, PKMYT1, PRKAC, PRKACB, RAF, RAP1, RAS, RGMA, RSK, SMAD1, SMAD5, SMAD8, SYNPO2,	30	21	KCNMA1, NDRG1, RAS	ERK1, ERK2, MAOA, P38 MAPK, RGMA	NDRG1, SMAD1, SMAD5, SMAD8	AURKB, BIRC5, ERK1, ERK2, FBLN1, FOXM1, HGF, MAOA, P38 MAPK, PKMYT1, SYNPO2, TOP2A

		TOP2A						
		C14ORF106, CDKN1A, CEP72, DHX8, FKBPL, HIST1H2BD, HNF4A, KIF20A, KRT18, MTHFS, OSCAR, PCGF5, PCNA, PELO, PEX13, PFC5, POLD4, POLK, POLL, POLM, POLQ, POLS, R3HDM1, RASL12, RFC5, SLC33A1, SPAG5, STAT4, SULT1A1, SULT1C2, SYTL4, TCEAL3, TROAP, VEZT, WDR51A, ZBTB16	19	15	—	PCGF5	HIST1H2BD, OSCAR	C14ORF106, CEP72, KIF20A, PCNA, PEX13, PFC5, POLQ, SPAG5, SYTL4, TROAP, WDR51A
	0	ARHGAP9, CDH10, CDS1, CDS2, CHPT1, CNTN4, ELOVL7, EME1, FGFR, GAS6, HAND1, IFI202B, ISL1, KIAA1524, KRT74, MIRN31, MUS81, MYF6, MYOD1, NFYB, OTX1, PRIMA1, QKI, RBM9, RBPMS, RORA, SHOX2, SLC39A8, SOX2, SOX15, ST8SIA4,	18	15	CHPT1	CNTN4, ELOVL7, HAND1, ODS2, SOX2, TWIST1	ARHGAP9, CDH10	CNTN4, ELOVL7, EME1, FGFR, KIAA1524, PRIMA1, RBPMS, ST8SIA4, TWIST1

		STAT3, TWIST1, VPS39, ZFHX3						
	1	ALDH3A2, B3GALT2, BAMBI, CNN2, CTNNAL1, CTNNB1, CTSC, CUGBP2, DYNLT3, IL13, KIF18A, LIN7C, MFI2, MPP5, MRC2, NDST1, PDGF-CC, PHLDA2, PLAU, PPM1J, PPP1CA, PTPN14, PTPRM, SLC16A3, SLC26A2, SLC43A3, SLC7A2, SSH2, STK17A, TAX1BP3, TCF7L1, TGFB1, TPTE, TSPAN8	18	15	PHLDA2	BAMBI, CUGBP2, DYNLT3, SLC7A2, SLC43A3, STK17A, TPTE	—	DYNLT3, KIF18A, PTPRM, SLC7A2, SLC43A3, SSH2, STK17A, TPTE
	2	AHR, AHRR, ANLN, APH1B, ARHGAP24, ASPM, BUB1, CCDC99, CEP55, CKAP2, DRAM, E2F8, HS3ST1, JPH1, MIRN124-1, NMT2, PDZRN3, PLXNA2, PMM1, PPP1R13L, PVRL3, RFFL, S100A2, SLC16A10, TP53, UBE2A, UBE2C,	17	15	HS3ST1	PDZRN3, PVRL3	—	ANLN, ARHGAP24, ASPM, BUB1, CCDC99, CEP55, CKAP2, DRAM, E2F8, PLXNA2, SLC16A10,

		UBE2D2, UBE2S, UBE2V1, UBE2V2, UBL3, VPS37C, WDHD1						UBE2C, UBE2S, WDHD1
	3	ARHGEF3, CALY, CSH2, CTSL2, DIAPH3, ECEL1, FBP1, FFAR2, FRAT2, GSK3B, HSD17B4, IL6, IL19, KIF11, KIF2C, KNG1, LARGE, LEFTY2, LGR5, LIF, LPAR3, MPZ, MSLN, ORM2, PFKFB3, PLK4, PMP22, PRPH, PRSS8, PTGER3, SCN7A, SCNN1B, SLC4A11, TAL1	17	14	CALY	ARHGEF3, GSK3B, RMP22	CALY	ARHGEF3, CTSL2, DIAPH3, FBP1, KIF2C, KIF11, PFKFB3, PLK4
	4	AGT, AGTRAP, Beta ARK, CADPS, CD160, COL5A1, CPNE8, FNDC5, HSPC159, INA, ITGA7, LIMA1, LPP, MAB21L2, MAPK1, MERTK, MICAL2, MIRN294, MIRN185, MIRN352, NTN1, PLCG1, PLCG2, PTGFR, RASGEF1B, RBM4B, RSU1, SKAP1, SLITRK5, SPRED1, ST8SIA2,	15	13	CPNE3	CADPS, FNDC5, MAB21L2, SLITRK5, ST8SIA2	COL5A1, MICAL2	FNDC5, HSPC159, MAB21L2, SLITRK5, SYN2, ZNF367

		SYN2, TGFB3, TNS1, ZNF367						
	5	ACT1, BAG5, CPVL, EXO1, GIPC1, GJC1, GPR37, HSPA5, HSPA1A, HSPBP1, IkBKB, KCTD12, MAP3K3, MAP3K14, MEKK3/NIK, MIRN30B, MYO6, OLFML2A, PELI3, RHEBL1, RNF126, RPL10A, RPN1, SEC16A, SHC1, SHCBP1, SIGIRR, TJP3, TPBG, TRAF6, TRAF2-TRAF5, TRAF2-TRAF5, TRAF6, TUBB6, TUBB2B	15	13	—	KCTD12, TPBG	OLFML2A, SIGIRR	EXO1, KCTD12, MYO6, PHEBL1, SHCBP1, TPBG, TUBB6
	6	ABCC8, BACE2, CLASP1, COLEC12, CXCR7, DACT1, ENTPD5, FGD6, FMO1, GSTT1, IL17B, KRT34, KYNU, LAMP3, LMCD1, MIRN101B, MMD, NEBL, NFRKB, OSBPL3, PCDH8, PEMT, RASAL2, SAMD4A, ST3GAL3, SYNGR3, SYNPO2,	15	13	IL17B	DACT1, PCDH8	ABCC8, IL17B, NEEBL	MMD, OSBPL3, SYNPO2

		TNF, TNNC1, TXN2, YWHAG, ZNF267, ZYX						
	7	ARPP-19, BTG3, CBFA2T2, CBLN1, CNGA2, EBF1, EGF, EGFR, GABA, GABRA5, GABRB3, GABRD, GABRR1, HDAC9, HPCAL1, HTT, IDS, INSL3, LPAR5, OPRL1, PCDH9, PDE10A, PDE11A, PDE1A, PDE1B, PDE2A, PDE4C, PDE6H, PPAP2B, PPP1R1B, ROBO2, SH3D2C1, TRIP10, ZNF521	14	13	HPCAL1	PPAP2B	HPCAL1, LPAR5	BTG3, GABRA5, TRIP10, ZNF521
	8	ANXA2, AQP1, C11ORF82, CCNI, CDKN2A, DEFB104A, DEFB4, EGLN3, ERAP1, FAM129A, GNAO1, IFNG, IL1B, IL1F7, INCA, LOC729687, MELK, MINA, MIRN210, MPA2L, MYC, NNAT, PDE5A, RGS11, RNASE7, RT1-B, SCLY, SCUBE1,	14	12	AQP1, CDKN2A	MINA, PDE5A	ANXA2, CDKN2A, ERAP1, RGS11	C11ORF82, MELK, MINA, PDE5A, SCLY, SLC1A3, TMEM35

		SLC11A1, SLC14A1, SLC1A3, ST18, TSH, TMEM35, TREM3						
	9	BIRC8, BNC2, CASP5, CASP10, CASP14, CASP, CBLN2, DEDD2, DNASE1L1, DPYD, DSG3, EIF4E, EMILIN2, HTR1D, HTR1E, HTR1F, HTR3A, IFT57, KHDC1, MIRN20A, MTCH1, NGFR, PLXNA4, PPIL5, RB1, RP11-257K9.7, SEMA6D, SERPINA3K, SORCS1, STK25, SYT5, TACC3, TERT	10	10	—	EMILIN2, PLXNA4	HTR1E, SORCS1	BNC2, DPYD, EMILIN2, PPIL5, TACC3
	0	EGFL7, GFI1B	2	1	—	—	—	—
	1	AGRN, PRSS12	2	1	—	—	—	—
	2	KCNB1, KCNG3	2	1	—	—	—	—
	3	NUP37, NUP43	2	1	—	—	—	—
	4	HS6ST1, HS6ST2	2	1	—	—	—	—
	5	FUCA1, FUCA2	2	1	—	—	—	—

	6	IQGAP, IQGAP3, MIRN339	2	1	—	—	—	—

Ejemplo V

Análisis de senda de perfiles de expresión genética de líneas celulares clonales

El siguiente ejemplo demuestra cómo caracterizar los perfiles de expresión genética a partir de células clonales de una línea celular clonal establecida que son susceptibles de intoxicación por BoNT/A o que tienen capacidad de absorción de neurotoxina para identificar redes o sendas biológicas asociadas con la intoxicación por BoNT/A.

El análisis informático se llevó a cabo para caracterizar el fenotipo de expresión de ARN de dos líneas celulares clonales únicas derivadas independientemente, BB10 y H1, muy sensibles a la actividad de la BoNT/A y una única línea celular clonal, 2D6, que era menos sensible a la actividad de la BoNT/A. Los resultados son útiles para identificar líneas celulares clonales seleccionadas de la línea celular SiMa original que son útiles para poner en práctica los métodos descritos en la presente memoria descriptiva.

Para identificar el fenotipo de expresión genética específico asociado con una línea celular sensible a BoNT/A, se analizaron los datos usando JMP Genomic (SAS Institute Inc., Cary, NC). Para llevar adelante un análisis JMP Genomics, los datos de expresión de ARN se importaron a JMP Genomics creando dos archivos SAS llamados "datos" y "diseño experimental". Se realizó un flujo de trabajo de expresión básico, incluyendo un análisis de varianza y un análisis de varianza de una vía (ANOVA de una vía) para identificar las diferencias en los valores de expresión medios. El análisis de varianza se usó para identificar las diferencias entre las líneas celulares y el estado de diferenciación de cada línea celular (diferenciada o no diferenciada). Los valores de expresión de las cuatro líneas celulares se compararon en pares, independientemente de su diferenciación y los genes que estaban sobreexpresados ≥ 4 veces en la línea celular H1 en comparación con la línea celular 2D6, en la línea celular BB10 en comparación con la línea celular 2D6 y en la línea celular SiMa original (PA) en comparación con la línea celular 2D6. El análisis de varianza trata todos los factores en el estudio como efectos aleatorios para descubrir cuál es su contribución a la proporción de la varianza explicada (varianza total = 100%). Cerca de la mitad de la varianza, el 46.9%, se asignó a las diferencias entre los diferentes tipos

celulares, mientras que el 26% se asignó a las diferencias antes y después de la diferenciación. Solo el 4.6% de la varianza se asignó a diferencias entre tipos celulares diferenciados y no diferenciados, lo que significa que los genes que se expresaron de forma diferencial luego de la diferenciación eran similares para todos los tipos celulares examinados, lo que sugiere que la diferencia en la sensibilidad a BoNT/A entre las líneas celulares no depende del estado de diferenciación. Como tal, se centró en los genes que eran diferentes entre los diferentes tipos celulares sin importar la diferenciación.

Con base en estos resultados del análisis de varianza, los valores de expresión de todas las líneas celulares se compararon en pares, sin importar la diferenciación (FIG. 2). Solo se muestran las sondas genéticas que estaban sobreexpresadas ≥ 4 veces en la línea celular H1 en comparación con la línea celular 2D6 y la línea celular BB10 en comparación con la línea celular 2D6. Las sondas genéticas se graficaron como valor de expresión (Log_2) en el eje x y el valor p ($-log_{10}$(valor p)) en el eje y. La línea punteada roja marca el intervalo de confianza del 95%. Las sondas genéticas que se sobreexpresaron ≥ 4 veces en la línea celular H1 en comparación con la línea celular 2D6 (FIG. 2A) y en la línea celular BB10 en comparación con la línea celular 2D6 (FIG.

2B) también se encontraban en gran medida entre los genes que se sobreexpresaron en la línea celular BB10 en comparación con la línea celular SiMa original (PA, FIG. 2C), en la línea celular H1 en comparación con la línea celular SiMa original (FIG. 2D) y en la línea celular original SiMa en comparación con la línea celular 2D6 (FIG. 2E). Estos datos sugieren que la sensibilidad a BoNT/A se relacionaba con un aumento gradual en la expresión de estos genes. Con base en este hallazgo, el número de sondas genéticas redujo aun más a 119 al incluir solo las sondas genéticas que también se sobreexpresaban en la línea celular SiMa original en comparación con la línea celular 2D6, basándose en el razonamiento de que sería incluso más probable que las sondas genéticas que se expresaban de forma diferencial a través de una línea celular fueran más importantes para la sensibilidad a BoNT/A. Como tal, el análisis JMP Genomic dio como resultado la identificación de 119 sondas genéticas, llamadas conjunto de sondas JMP.

El conjunto de sondas JMP se exportó al análisis central del análisis de senda de habilidad (IPA) (Ingenuity Systems Inc., Redwood City, CA) para caracterizar aun más el conjunto de sondas JMP. Usando este análisis, se identificaron las redes biológicamente importantes para la intoxicación por BoNT/A con base en la conectividad entre los

genes de una biblioteca IPA y las sondas genéticas contenidas en el conjunto de sondas JMP. La importancia de la asociación a una red dada se midió y clasificó por la proporción del número de sondas genéticas del conjunto de sondas JMP que se mapearon a la red específica dividido por el número total de genes que se mapean a esa red. Se usó la prueba exacta de Fisher para calcular las puntuaciones p y, basándose en las puntuaciones p, se usaron los genes del conjunto de sonda JMP para clasificar las redes. Las puntuaciones p provinieron de los valores p. Si hay *n* genes en la red y *f* de esos son sondas genéticas del conjunto de sondas JMP, entonces el valor p es la probabilidad de encontrar *f* o más sondas genéticas del conjunto de sondas JMP en un conjunto de *n* genes seleccionados de forma aleatoria de la red global molecular. Debido a que los valores p significativos son bastante bajos (por ej., 1×10^{-8}), una puntuación p se definió como el componente del valor p; puntuación p = -log10 (valor p). Las redes identificadas se revistieron con genes expresados de forma diferencial que tenían una expresión diferencial de más de 1.5 veces y un valor p $\leq$ 0.001 ya sea antes o después de la diferenciación. Usando el análisis central IPA, 111 de las 119 sondas genéticas del conjunto de sonda JMP se mapearon a las redes. Es más probable que las ocho sondas no mapeadas representen ya sea una sonda con una nomenclatura anticuada o una que representa un gen que no

tiene un producto genético conocido. Las 111 sondas genéticas correspondían a 79 genes que se expresaban de forma diferencial más de 4.0 veces en las líneas celulares H1 y BB10 en comparación con la línea celular 2D6 y que también se expresaban de forma diferencial mas de 4.0 veces en la línea celular SiMa original en comparación con la línea celular 2D6, cuando el corte del valor p se fijaba en 0.05 (Tabla 14).

Tabla 14. Genes identificados usando el Análisis de Núcleo IPA

Nombre del gen	Símbolo del gen	No. de ID de la sonda	Ubicación	Tipo	Proporción logarítmica
Homólogo del complejo achaete-scute 1	ASCL1	209985_s_at	Núcleo	regulador de transcripción	4.469
Homólogo del complejo achaete-scute 1	ASCL1	209988_s_at	Núcleo	regulador de transcripción	2.774
Homólogo del complejo achaete-scute 1	ASCL1	213768_s_at	Núcleo	regulador de transcripción	2.955
Acil-CoA tioesterasa 9	ACOT9	221641_s_at	Citoplasma	enzima	2.251
Metalopeptidasa ADAM con motivo de trombospondina tipo 1, 9	ADAMTS9	226814_at	Espacio extracelular	Peptidasa	4.034
Anquirina 2, neuronal	ANK2	216195_at	Membrana plasmática	Otro	-2.673
Anquirina 2, neuronal	ANK2	232606_at	Membrana plasmática	Otro	-2.621

Sustancia epicardial de los vasos sanguíneos	BVES	228783_at	Membrana plasmática	Otro	3.174
Proteína de señal 1 unida a la membrana y abundante en el cerebro	BASP1	202391_at	Membrana plasmática	Otro	4.549
Dominio RING 1 asociado a BRCA1	BARD1	205345_at	Núcleo	regulador de transcripción	3.44
Calsintenina 2	CLSTN2	219414_at	Membrana plasmática	Transportador	2.024
Proteína de unión 5 al elemento sensible al AMPc	CREB5	232555_at	Núcleo	Transcripción	-2.67
Catepsina L2	CTSL2	210074_at	Citoplasma	Peptidasa	2.119
molécula CD9	CD9	201005_at	Membrana plasmática	Otro	2.887
Asociado al ciclo de división celular tipo 7	CDCA7L	225081_s_at	Núcleo	Otro	3.737
Proteína de centrómero L	CENPL	1554271_a_at	Desconocida	Otro	2.582
Marco abierto de lectura 75 del cromosoma 11	C11ORF75	219806_s_at	Desconocida	Otro	3.914
Marco abierto de lectura 70 del cromosoma 3	C3ORF70	242447_at	Desconocida	Otro	2.705
Dominio de superhélice que contiene 109B	CCDC109B	218802_at	Desconocida	Otro	2.881
Contactina 1	CNTN1	211203_s_at	Membrana plasmática	enzima	3.684
Contactina 1	CNTN1	227202_at	Membrana	enzima	3.184

			plasmática		
Contactina 1	CNTN1	227209_at	Membrana plasmática	enzima	3.188
Copina VIII	CPNE8	228365_at	Desconocida	Otro	-3.355
Copina VIII	CPNE8	241706_at	Desconocida	Otro	-2.736
proteína 2 de unión al ARN y repetición de triplete CUG	CUGBP2	202157_s_at	Núcleo	Otro	3.588
Cinasa 2 dependiente de ciclina	CDK2	204252_at	Núcleo	Cinasa	2.744
Proteína 2 rica en cisteína y glicina	CSRP2	207030_s_at	Núcleo	Otro	2.487
Proteína 2 rica en cisteína y glicina	CSRP2	211126_s_at	Núcleo	Otro	2.109
Dominio DEP que contiene 1	DEPDC1	220295_x_at	Desconocida	Otro	2.795
Homólogo de diáfano 3	DIAPH3	232596_at	Citoplasma	enzima	2.434
Dihidropirimidina deshidrogenasa	DPYD	204646_at	Citoplasma	enzima	4.248
Proteína de acoplamiento 5	DOK5	214844_s_at	Membrana plasmática	Otro	4.56
Dineína, cadena ligera, Tctex tipo 3	DYNLT3	203303_at	Citoplasma	Otro	3.449
Interfaz de microfibrila de elastina 2	EMILIN2	224374_s_at	Espacio extracelular	Otro	2.603
Variante 1 de Ets	ETV1	206501_x_at	Núcleo	regulador de transcripción	2.578
Variante 1 de Ets	ETV1	217053_x_at	Núcleo	regulador de	2.499

				transcripción	
Variante 1 de Ets	ETV1	217061_s_at	Núcleo	regulador de transcripción	2.557
familia con similitud de secuencia 101, miembro B	FAM101B	226876_at	Desconocida	Otro	2.399
Receptor del factor de crecimiento de fibroblastos 2	FGFR2	203638_s_at	Membrana plasmática	Cinasa	2.306
Receptor del factor de crecimiento de fibroblastos 2	FGFR2	203639_s_at	Membrana plasmática	Cinasa	3.239
Receptor del factor de crecimiento de fibroblastos 2	FGFR2	208228_s_at	Membrana plasmática	Cinasa	2.151
dominio de fibronectina tipo III que contiene 5	FNDC5	226096_at	Desconocida	Otro	2.054
Fibulina 1	FBLN1	201787_at	Espacio extracelular	Otro	2.801
Fibulina 1	FBLN1	202994_s_at	Espacio extracelular	Otro	2.378
Fibulina 1	FBLN1	202995_s_at	Espacio extracelular	Otro	3.733
Receptor 117 acoplado a la proteína G	GPR177	221958_s_at	Desconocida	Otro	2.389
Receptor 117 acoplado a la proteína G	GPR177	228950_s_at	Desconocida	Otro	2.622
Expresado en G-2 y fase S 1	GTSE1	204317_at	Citoplasma	Otro	3.334
Factor 1 específico del gametocito	GTSF1	227711_at	Desconocida	Otro	6.407

proteína de unión al nucleótido de guanina (proteína G), polipéptido de actividad inhibidora alfa 1	GNAI1	227692_at	Membrana plasmática	enzima	3.123
proteína de unión al nucleótido de guanina (proteína G), polipéptido beta 4	GNB4	225710_at	Membrana plasmática	enzima	6.066
proteína de unión al nucleótido de guanina (proteína G), gamma 11	GNG11	204115_at	Membrana plasmática	enzima	4.251
proteína de unión al nucleótido de guanina (proteína G), gamma 12	GNG12	212294_at	Membrana plasmática	enzima	2.315
proteína de unión al nucleótido de guanina (proteína G), gamma 12	GNG12	222834_s_at	Membrana plasmática	enzima.	3.403
Factor de crecimiento de hepatocitos (hepapoyetina A)	HGF	209960_at	Espacio extracelular	factor de crecimiento	2.939
Proteína hipotética LOC100289109	LOC100289109	216189_at	Desconocida	Otro	-3.256
Proteína hipotética LOC144571	LOC144571	1564139_at	Desconocida	Otro	-2.394
Proteína de interacción con el receptor de 1,4,5-trifosfato de inositol	ITPRIP	225582_at	Desconocida	Otro	3.522
Interleucina 17B	IL17B	220273_at	Espacio extracelular	Citosina	-4.735
KDEL (Lys-Asp-Glu-Leu) que contiene 2	KDELC2	225128_at	Desconocida	Otro	3.003

KIAA0125	KIAA0125	206478_at	Desconocida	Otro	-8.436
Ligando KIT	KITLG	226534_at	Espacio extracelular	factor de crecimiento	2.59
Dominio LY6/PLAUR que contiene 6	LYPD6	227764_at	Espacio extracelular	Otro	2.64
receptor del ácido lisofosfatídico 1	LPAR1	204036_at	Membrana plasmática	Receptor	3.151
2 tipo mab-21	MAB21L2	210303_at	Desconocida	Otro	3.817
Componente del complejo de mantenimiento de minicromosoma 10	MCM10	223570_at	Núcleo	Otro	2.249
Moesina	MSN	200600_at	Membrana plasmática	Otro	5.842
monoaminooxidasa A	MAOA	204388_s_at	Citoplasma	enzima	4.029
monoaminooxidasa A	MAOA	204389_at	Citoplasma	enzima	3.355
monoaminooxidasa A	MAOA	212741_at	Citoplasma	enzima	4.157
antígeno nuclear inducido por MYC	MINA	213188_s_at	Núcleo	Otro	4.019
antígeno nuclear inducido por MYC	MINA	213189_at	Núcleo	Otro	4.636
miosina VI	MYO6	203216_s_at	Citoplasma	Otro	2.406
Miosina VIIA y proteína que interactúa con Rab	MYRIP	214156_at	Citoplasma	Otro	2.805
Proteína 4 de dominio PAS neuronal	NPAS4	1554299_at	Núcleo	regulador de transcripción	-2.515

Expresado paternalmente 3	PEG3	209242_at	Núcleo	Cinasa	5.896
Expresado paternalmente 3	PEG3	209243_s_at	Núcleo	Cinasa	4.556
Fosfoproteína asociada con microdominios de glucoesfingolípido 1	PAG1	225626_at	Membrana plasmática	Otro	2.193
Relacionado con el receptor de poliovirus 3	PVRL3	213325_at	Membrana plasmática	Otro	2.325
cinasa 2 tipo polo	PLK2	201939_at	Núcleo	Cinasa	4.93
Polimerasa (dirigida por ADN) alfa 2 (subunidad 70kD)	POLA2	204441_s_at	Núcleo	enzima	2.198
Receptor de la hormona liberadora de prolactina	PRLHR	231805_at	Membrana plasmática	Receptor	3.19
Prostaglandina reductasa 1	PTGR1	228824_s_at	Citoplasma	enzima	2.398
Prostaglandina reductasa 1	PTGR1	231897_at	Citoplasma	enzima	2.33
Proteasa, serina, 12 (neurotripsina, motopsina)	PRSS12	205515_at	Espacio extracelular	Peptidasa	5.146
Proteína fosfatasa 1, subunidad reguladora (inhibidora) 3C	PPP1R3C	204284_at	Citoplasma	Fosfatasa	2.827
Proteína tirosina fosfatasa, tipo receptor, K	PTPRK	203038_at	Membrana plasmática	Fosfatasa	3.451
RAB32, miembro de la familia del oncogén RAS	RAB32	204214_s_at	Citoplasma	Otro	2.192
1 tipo RELT	RELL1	226430_at	Desconocida	Otro	2.88
Proteína activadora de Rho GTPasa 24	ARHGAP24	223422_s_at	Citoplasma	Otro	3.043

Factor de intercambio de nucleótido guanina rho (GEF) 3	ARHGEF3	218501_at	Citoplasma	Otro	2.473
proteína del dedo anular 182	RNF182	230720_at	Desconocida	Otro	4.746
proteína de unión a ARN con múltiple corte y empalme	RBPMS	209487_at	Desconocida	Otro	2.329
proteína de unión a ARN con múltiple corte y empalme	RBPMS	209488_s_at	Desconocida	Otro	3.292
Proteína secretada, ácida, rica en cisteína (osteonectina)	SPARC	200665_s_at	Espacio extracelular	Otro	4.919
Proteína secretada, ácida, rica en cisteína (osteonectina)	SPARC	212667_at	Espacio extracelular	Otro	4.58
2 tipo shugoshina	SGOL2	230165_at	Núcleo	Otro	3.108
similar a hCG2031213	LOC728052	1558795_at	Desconocida	Otro	3.402
Familia de portador de soluto 1 (transportador de glutamato de alta afinidad glial), miembro 2	SLC1A2	225491_at	Membrana plasmática	Transportador	-4.354
familia de portador de soluto 43, miembro 3	SLC43A3	210692_s_at	Espacio extracelular	Otro	3.126
familia portadora de soluto 43, miembro 3	SLC43A3	213113_s_at	Espacio extracelular	Otro	2.804
familia portadora de soluto 44, miembro 5	SLC44A5	1569112_at	Desconocida	Otro	3.923
familia portadora de soluto 44, miembro 5	SLC44A5	235763_at	Desconocida	Otro	4.439
familia portadora de soluto 7	SLC7A2	225516_at	Membrana	Transportador	3.23

(sistema y+ transportador de aminoácidos catiónicos), miembro 2			plasmática		
Dominio VPS10 relacionado con la sortilina que contiene receptor 1	SORCS1	1556891_at	Membrana plasmática	Transportador	-2.424
homólogo de SPC25, componente del complejo cinetocoro NDC80	SPC25	209891_at	Desconocida	Otro	2.634
ST8 alfa-N-acetil-neuraminida alfa-2,8-sialiltransferasa 4	ST8SIA4	230836_at	Citoplasma	enzima	2.705
Mantenimiento estructural de cromosomas 2	SMC2	204240_s_at	Núcleo	Transportador	2.442
Mantenimiento estructural de cromosomas 6	SMC6	218781_at	Núcleo	Otro	3.327
Mantenimiento estructural de cromosomas 6	SMC6	236535_at	Núcleo	Otro	3.44
Sindecano 2	SDC2	212154_at	Membrana plasmática	Otro	2.367
Sindecano 2	SDC2	212158_at	Membrana plasmática	Otro	2.098
Trombospondina 2	THBS2	203083_at	Espacio extracelular	Otro	-2.81
Interactuador del receptor de hormona tiroidea 10	TRIP10	202734_at	Citoplasma	Otro	2.663
inhibidor 2 de la senda del factor tisular	TFPI2	209278_s_at	Espacio extracelular	Otro	4.666
1 tipo factor de transcripción 7	TCF7L1	221016_s_at	Núcleo	regulador de	2.835

(específico para células T, secuencia HMG)				transcripción	
Fosfatasa transmembrana con homología a tensina	TPTE	220205_at	Membrana plasmática	Fosfatasa	6.04
proteína transmembrana 178	TMEM178	229302_at	Desconocida	Otro	3.194
proteína transmembrana 35	TMEM35	219685_at	Desconocida	Otro	2.879
Factor de necrosis tumoral, proteína 8 inducida por alfa	TNFAIP8	210260_s_at	Citoplasma	Otro	2.389
Homólogo twist 1	TWIST1	213943_at	Núcleo	regulador de transcripción	2.573
proteína de dedos de cinc 521	ZNF521	226676_at	Núcleo	Otro	2.382
proteína de dedos de cinc 521	ZNF521	226677_at	Núcleo	Otro	2.943
proteína de dedos de cinc 814	ZNF814	1556204_a_at	Desconocida	Otro	-2.505

La proporción logarítmica representa valores $\log_2$ donde 0.585 es $\log_2(1.5)$ que es una diferencia de 1.5 veces, 1 es $\log_2(2)$ que es una diferencia de 2 veces, 1.584 es $\log_2(3)$ que es una diferencia de 3 veces, 2 es $\log_2(4)$ que es una diferencia de 4 veces, 2.321 es $\log_2(5)$ que es una diferencia de 5 veces, 2.584 es $\log_2(6)$ que es una diferencia de 6 veces, 2.807 es $\log_2(7)$ que es una diferencia de 7 veces, 3 es $\log_2(8)$ que es una diferencia de 8 veces, 3.169 es $\log_2(9)$ que es una diferencia de 9 veces y 3.321 es $\log_2(10)$ que es una diferencia de 10 veces.

Usando el análisis central IPA, 73 de los 79 genes se mapearon a 5 redes de proteína diferentes (Tabla 15). Con base en el mapeo genético solapante, 73 de los 79 genes que se regularon por aumento se podrían asociar con dos grupos principales de redes de proteínas llamados A y B (Tabla 15).

Las redes 1, 2 y 5 pertenecen al Grupo A y las Redes 3 y 4 pertenecen al Grupo B. De manera similar, todos los genes regulados por disminución se asociaron a una red llamada C (Tabla 15).

Los genes del grupo A incluyen el receptor de FGFR2 que se ha mostrado que funciona en el proceso de intoxicación por BoNT/A como un receptor de BoNT/A y son como sigue: genes que presentan un aumento de 1.5 veces o más en los niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea celular 2D6, ADAMTS9, ARHGAP24, ARHGEF3, ASCL1, BARD1, CD9, CDK2, CSRP2, CTSL2, DIAPH3, DOK5, DYNLT3, EMILIN2, ETV1, FBLN1, FGFR2, GNAI1, GNB4, GNG11, GNG12, HGF, KITLG, LPAR1, MCM10, MSN, PAG1, PEG3, PLK2, POLA2, PPP1R3C, PTPRK, RAB32, SDC2, SLC43A3, SLC7A2, SMC6, SPARC, SPC25, ST8SIA4, TCF7L1, TFPI2, TMEM35, TNFAIP8, TPTE, TRIP10 y TWIST1.

Los genes del grupo B son como sigue: genes que presentan un aumento de 1.5 veces o más en los niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea celular 2D6, ACOT9, BASP1, C11ORF75, CCDC109B, CDCA7L, CLSTN2, CNTN1, CUGBP2, DEPDC1, DPYD, FAM101B, FNDC5, GTSE1, MAOA, MINA,

MYO6, MYRIP, PLK2, PRLHR, PVRL3, RBPMS, SGOL2, SMC2, TFP12, TMEM178 y ZNF521

Los genes del grupo C son como sigue: genes que presentan una disminución de 1.5 veces o más en los niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea celular 2D6, ANK2, CPNE8, CREB5, IL17B, KIAA0125, LOC100289109, LOC144571, NPAS4, SLC1A2, SORCS1, THBS2 y ZNF814.

Las redes restantes identificadas no compartían genes comunes con ninguna otra red. Sin embargo, por separado, los genes que presentan un aumento de 1.5 veces o más en los niveles de expresión en las líneas celulares H1 y BB10 en comparación con su expresión en las células de la línea celular 2D6 fueron como sigue: C3ORF70 (Red 6), MAB21L2 (Red 7), PRSS12 (Red 8), CENPL (Red 9), GPR177 (Red 10) y PTGR1 (Red 11).

Tabla 15. Análisis central IPA de genes

Red	Grupo	Proteínas en la red	valor p	Número de gen JMP	Perfil de expresión	
					Aumentado	Disminuido
1	A	ADAMTS9, AKT, ASCL1, CDK2, CSRP2, CTSL2, DOK5, E2F, FBLN1, FSH, GNAI1, GNG11, hCG, HGF, KITLG, LPAR1, MAPK, MCM10, MEK, MSN, NFκB, P38, MAPK, PAG1, PDGF BB, PEG3, PLK2, RAC, RAS, SDC2, SPARC, TFPI2, TGFβ, TNFAIP8, TRIP10, VEGF	46	22	ADAMTS9, ASCL1, CDK2, CSRP2, CTSL2, DOK5, FBLN1, GNAI1, GNG11, HGF, KITLG, LPAR1, MCM10, MSN, PAG1, PEG3, PLK2, SDC2, SPARC, TFPI2, TNFAIP8, TRIP10	—
2	A	CASP3, Caspasa 3/7, CCL6, DIAPH3, DYNLT3, EMILIN2, EPM2A, ETV1, EYA2, FAM3B, FASTK, GNAI1, GNB4, GNG10, GNG11, GNG12, GSTM2, HK1, IGFBP3, IL13, PLCE1, POLA2, PPP1R3C, PTPRK, PTPRZ1, RAB32, SLC43A3, SLC7A2, SRC, ST8SIA4, TNF, TPTE, TWIST1	35	17	DIAPH3, DYNLT3, EMILIN2, ETV1, GNAI1, GNB4, GNG11, GNG12, POLA2, PPP1R3C, PTPRK, RAB32, SLC43A3, SLC7A2, ST8SIA4, TPTE, TWIST1	—
3	B	ACOT9, AR, ATXN7, BASP1, CCNE2, CCNK, CLSTN2, CNTN1, CUGBP2, DGKA, FNDC5, GTSE1, IL4, MAOA,	26	14	ACOT9, BASP1, CLSTN2, CNTN1, CUGBP2,	—

		MSH2, NOVA1, NF1, PICK1, PLK2, PNRC1, POM121, PRLHR, PTP4A1, PTP4A2, PVRL1, PVRL3, PVRL4, RBPMS, SERPINB5, SMARCA4, SPN, TFP12, TP53, ZNF521			FNDC5, GTSE1, MAOA, PLK2, PRLHR, PVRL3, RBPMS, TFP12, ZNF521	
4	B	ARHGAP17, AXL, C11ORF75, CAPN6, CCDC109B, CDCA7L, DEPDC1, DPYD, EIF4E, FAM101B, GRB2, HNRNPF, HTATIP2, MAOA, MINA, MIR124, MIRLET7A1, MYC, MYO6, MYRIP, NCAPD3, NF2, PPP2R5A, PPP2R5D, PPP2R5E, RPS16, RPS23, SGOL2, SLC25A12, SMC2, SMC4, TMEM178, TUSC2, TXNIP, ZBTB16	24	13	C11ORF75, CCDC109B, CDCA7L, DEPDC1, DPYD, FAM101B, MAOA, MINA, MYO6, MYRIP, SGOL2, SMC2, TMEM178	—
5	A	ARHGAP24, ARHGEF, ARHGEF3, BARD1, CD9, CD53, CTNNB1, DUSP3, ERK, ERM, FGF9, FGF18, FGF21, FGF23, FGFR2, IL1, IL6, IL17RD, Integrinaα6β1, KLB, LEF/TCF, LPAR1, MIRN297-2, PI3K, RAS homólogo, RNAPOLII, SLC26A2, SMC6, SPC25, SREBF1, TACC1, TCF7L1, TMEM35, TPT1, WISP1	17	10	ARHGAP24, ARHGEF3, BARD1, CD9, FGFR2, LPAR1, SMC6, SPC25, TCF7L1, TMEM35	—
6	—	C3ORF70, MIR31	2	1	C3ORF70	—
7	—	MAB21L2, MIRN294	2	1	MAB21L2	—
8	—	AGPN, PRSS12	2	1	PRSS12	—
9	—	CENPL, MIRN340	2	1	CENPL	—
10	—	GPR177, MIRN324	2	1	GPR177	—

11	—	ADH, PTGR1	2	1	PTGR1	—
12	C	ANK2, ATP2A2, BDNF, CEBPG, CPNE8, CREB5, GRM3, GRM5, IGFBP2, IL17B, ITPR, ITPR1, K+, L1CAM, MIRN330, Neurotrofina, NFE2L1, NGFR, NME1, NPAS4, citosina proinflamatoria, PSEN1, SCN2A, SCN3A, SCNN1B, SLC1A2, SLC8A1, SORCS1, SORT1, TGFA, THBS2, TNF, TNFAIP6	22	8	—	ANK2, CPNE8, CREB5, IL17B, KIAA0125, LOC100289109, LOC144571, NPAS4, SLC1A2, SORCS1, THBS2, ZNF814

El análisis informático se realizó como se muestra en el Ejemplo V con la excepción de que la lista de sondas reflejan los genes que se expresaban de forma diferencial más de 1.5 veces en las líneas celulares H1 y BB10 en comparación con las líneas celulares 2D6 y SiMa original. Al fijar el corte del valor p en 0.05, este análisis identificó 439 sondas genéticas que se podían clasificar en 369 genes (Tabla 16).

Tabla 16. Genes identificados usando el Análisis Central IPA

Nombre del gen	Símbolo del gen	No. de ID de la sonda	Ubicación	Tipo	Proporción logarítmica
6-fosfofructo-2-cinasa/fructosa-2,6-bifosfatasa 3	PFKFB3	202464_s_at	Citoplasma	cinasa	1.811
homólogo 1 del complejo achaete-scute	ASCL1	209985_s_at	Núcleo	regulador de transcripción	2.429
homólogo 1 del complejo	ASCL1	209987_s_at	Núcleo	regulador de	2.097

achaete-scute				transcripción	
homólogo 1 de complejo achaete-scute	ASCL1	209988_s_at	Núcleo	regulador de transcripción	1.446
homólogo 1 del complejo achaete-scute	ASCL1	213768_s_at	Núcleo	regulador de transcripción	1.578
molécula de adhesión celular del leucocito activado	ALCAM	1569362_at	Membrana plasmática	otro	2.612
molécula de adhesión celular del leucocito activado	ALCAM	201951_at	Membrana plasmática	otro	1.774
molécula de adhesión celular del leucocito activado	ALCAM	201952_at	Membrana plasmática	otro	1.521
Acil-CoA tioesterasa 1	ACOT1	202982_s_at	Citoplasma	enzima	-2.875
acilfosfatasa 2, tipo de músculo	ACYP2	206833_s_at	desconocida	enzima	-1.15
peines sexuales tipo 3 adicionales	ASXL3	233536_at	desconocida	otro	1.572
adenosina desaminasa, específica de ARN, B1	ADARB1	203865_s_at	Núcleo	enzima	-2.474
adenilato ciclasa 1	ADCY1	213245_at	Membrana plasmática	enzima	-1.935
molécula de adhesión específica de adipositos	ASAM	228082_at	Membrana plasmática	otro	-2.802
Factor de ADP-ribosilación 1	ARF1	1565651_at	Citoplasma	enzima	1.063
17A tipo factor de ADP-ribosilación	ARL17A	243899_at	desconocida	otro	0.741
subunidad 7 del complejo promotor de anafase	ANAPC7	225554_s_at	desconocida	otro	0.679
dominio de repetición de ankirina y de BTB (POZ) que	ABTB1	229164_s_at	Citoplasma	regulador de la traducción	-0.656

contiene 1					
dominio de repetición de ankirina 50	ANKRD50	225731_at	desconocida	otro	-0.654
dominio de repetición de ankirina 50	ANKRD50	225735_at	desconocida	otro	-1.114
dominio de aspartato beta-hidroxilasa que contiene 1	ASPHD1	214993_at	desconocida	otro	-0.763
proteína 1 de unión a la ataxina 2	A2BP1	1553422_s_at	Citoplasma	otro	1.453
proteína 1 de unión a la ataxina 2	A2BP1	221217_s_at	Citoplasma	otro	1.497
ATPasa, que transporta Ca++, membrana plasmática 3	ATP2B3	207026_s_at	Membrana plasmática	transportador	-1.248
ATPasa, que transporta Ca++, membrana plasmática 3	ATP2B3	242036_x_at	Membrana plasmática	transportador	-1.777
basonuclina 2	BNC2	220272_at	Núcleo	otro	2.466
basonuclina 2	BNC2	230722_at	Núcleo	otro	1.641
dominio de βγcristalina que contiene 3	CRYBG3	214030_at	desconocida	otro	4.74
Enzima 1 de escisión de APP del sitio β	BACE1	217904_s_at	Citoplasma	peptidasa	-1.57
proteína de señal 1 unida a la membrana y abundante en el cerebro	BASP1	202391_at	Membrana plasmática	otro	1.146
bromodominio y dominio de repetición de WD que contiene 1	BRWD1	225446_at	Núcleo	regulador de transcripción	-1.018
4 tipo bruno, proteína de unión a ARN	BRUNOL4	238966_at	Núcleo	regulador de la traducción	-0.81

butirofilina, subfamilia 3, miembro A3	BTN3A3	38241_at	desconocida	otro	-1.108
Dominio dependiente de calcio C2 que contiene 2	C2CD2	212875_s_at	desconocida	otro	-1.27
Dominio dependiente de calcio C2 que contiene 4A	C2CD4A	241031_at	desconocida	otro	-2.615
caderina 12, tipo 2 (N-caderina 2)	CDH12	207149_at	Membrana plasmática	otro	-1.408
inhibidor 2 de la proteína cinasa II dependiente de calcio/calmodulina	CAMK2N2	230706_s_at	Núcleo	otro	-0.692
calmina (transmembrana tipo calponina)	CLMN	213839_at	Citoplasma	otro	-1.911
calpaína 2 (m/II) subunidad grande	CAPN2	208683_at	Citoplasma	peptidasa	-1.429
CAP, proteína asociada con la adenilato ciclasa 2	CAP2	212551_at	Membrana plasmática	otro	-1.974
CAP, proteína asociada con la adenilato ciclasa 2	CAP2	212554_at	Membrana plasmática	otro	-3.68
carboxipeptidasa, tipo vitelogénica	CPVL	208146_s_at	desconocida	peptidasa	1.708
prepropéptido CART	CARTPT	206339_at	Espacio extracelular	otro	-4.676
secuencia b transformadora retroviral ecotrópica Cas-Br-M (murina)	CBLB	209682_at	Núcleo	otro	1.032
complejo de transcripción CCR-NOT, tipo subunidad 6	CNOT6L	227119_at	Citoplasma	otro	-0.785
molécula CD302	CD302	203799_at	Membrana plasmática	receptor	-1.518

molécula CD9	CD9	201005_at	Membrana plasmática	otro	1.415
sintasa CDP-diacilglicerol (fosfatidato citidililtransferasa) 1	CDS1	226185_at	Citoplasma	enzima	-1.74
homólogo B del ciclo de división celular 25 (S. pombe)	CDC25B	201853_s_at	núcleo	fosfatasa	1.453
receptor 4 de quimiocina (motivo C-X-C)	CXCR4	209201_x_at	Membrana plasmática	receptor	4.135
receptor 4 de quimiocina (motivo C-X-C)	CXCR4	211919_s_at	Membrana plasmática	receptor	3.957
receptor 4 de quimiocina (motivo C-X-C)	CXCR4	217028_at	Membrana plasmática	receptor	3.176
canal de cloruro 3	CLCN3	201733_at	Membrana plasmática	canal iónico	-0.908
canal de cloruro 3	CLCN3	201734_at	Membrana plasmática	canal iónico	-0.987
receptor colinérgico, nicotínico, alfa 7	CHRNA7	210123_s_at	Membrana plasmática	receptor	3.098
Marco abierto de lectura 21 del cromosoma 1	C1ORF21	221272_s_at	desconocida	otro	-0.74
Marco abierto de lectura 21 del cromosoma 1	C1ORF21	223127_s_at	desconocida	otro	-0.748
Marco abierto de lectura 43 del cromosoma 1	C1ORF43	1555225_at	desconocida	otro	1.604
Marco abierto de lectura 58 del cromosoma 10	C10ORF58	224435_at	Espacio extracelular	otro	0.918
Marco abierto de lectura 49 del cromosoma 12	C12ORF49	218867_s_at	desconocida	otro	0.692

Marco abierto de lectura 52 del cromosoma 16	C16ORF52	230721_at	desconocida	otro	-0.87
Marco abierto de lectura 7 del cromosoma 20	C20ORF7	227160_s_at	desconocida	otro	0.624
Marco abierto de lectura 57 del cromosoma 21	C21ORF57	227421_at	desconocida	otro	-1.086
Marco abierto de lectura 57 del cromosoma 21	C21ORF57	239208_s_at	desconocida	otro	-0.657
Marco abierto de lectura 23 del cromosoma 3	C3ORF23	1555905_a_at	Citoplasma	otro	-2.797
Marco abierto de lectura 23 del cromosoma 3	C3ORF23	1555906_s_at	Citoplasma	otro	-1.502
Marco abierto de lectura 23 del cromosoma 3	C3ORF23	241666_at	Citoplasma	otro	-1.017
Marco abierto de lectura 150 del cromosoma 9	C9ORF150	227443_at	desconocido	otro	-1.773
claudina 12	CLDN12	223249_at	Membrana plasmática	otro	-0.766
Dominio COBW que contiene 1	CBWD1	226193_x_at	desconocida	otro	0.849
Dominio de superhélice que contiene 3	CCDC3	223316_at	Citoplasma	otro	3.357
colágeno, tipo VI, alfa 1	COL6A1	213428_s_at	Espacio extracelular	otro	-1.638
cripto, FRL-1, familia críptica 1	CFC1	223753_s_at	Espacio extracelular	otro	-2.834
cripto, FRL-1, familia críptica 1	CFC1	236724_at	Espacio extracelular	otro	-1.636
tipo segregación de	CSE1L	210765_at	núcleo	transportador	1.581

cromosoma CSE1 1					
proteína 2 de unión al ARN y repetición de triplete CUG	CUGBP2	202156_s_at	núcleo	otro	1.318
proteína 2 de unión al ARN y repetición de triplete CUG	CUGBP2	202157_s_at	núcleo	otro	2.156
proteína 2 de unión al ARN y repetición de triplete CUG	CUGBP2	202158_s_at	núcleo	otro	2.539
canal modulado por nucleótidos cíclicos alfa 3	CNGA3	207261_at	Membrana plasmática	canal iónico	-3.182
Ciclina M1	CNNM1	220166_at	Membrana plasmática	otro	-1.214
inhibidor 2A de la cinasa dependiente de ciclina (melanoma, p16, inhibe la CDK4)	CDKN2A	209644_x_at	núcleo	regulador de transcripción	-1.277
cilindromatosis (síndrome de tumor turban)	CYLD	213295_at	núcleo	regulador de transcripción	-0.815
citocromo P450, familia 2, subfamilia E, polipéptido 1	CYP2E1	1431_at	Citoplasma	enzima	-4.466
citocromo P450, familia 2, subfamilia E, polipéptido 1	CYP2E1	209975_at	Citoplasma	enzima	-3.946
citocromo P450, familia 2, subfamilia E, polipéptido 1	CYP2E1	209976_s_at	Citoplasma	enzima	-3.429
citoglobina	CYGB	1553572_a_at	Citoplasma	transportador	-4.921
1 tipo citosina	CYTL1	219837_s_at	Espacio extracelular	citosina	-6.33
homólogo 1 de dapper, antagonista de beta catenina	DACT1	219179_at	Citoplasma	otro	1.682
desaminasa dCMP	DCTD	201572_x_at	desconocida	enzima	-0.649

polipéptido 35 de secuencia DEAH (Asp-Glu-Ala-His)	DHX35	218579_s_at	desconocida	enzima	0.735
eliminado en azoospermia 1	DAZ1	207909_x_at	núcleo	regulador de la traducción	6.92
eliminado en azoospermia 1	DAZ1	207912_s_at	núcleo	regulador de la traducción	5.558
eliminado en azoospermia 1	DAZ1	208281_x_at	núcleo	regulador de la traducción	5.258
eliminado en azoospermia 1	DAZ1	208282_x_at	núcleo	regulador de la traducción	7.008
eliminado en azoospermia 1	DAZ1	216351_x_at	núcleo	regulador de la traducción	3.596
eliminado en azoospermia 1	DAZ1	216922_x_at	núcleo	regulador de la traducción	5.185
eliminado en leucemia linfocítica 2 (codificación que no es de proteína)	DLEU2	216870_x_at	desconocida	otro	1.233
3 tipo delta (drosófila)	DLL3	219537_x_at	Espacio extracelular	otro	0.779
segmento de ADN en el cromosoma 4 (único) secuencia expresada 234	D4S234E	209569_x_at	Citoplasma	otro	-1.247
segmento de ADN en el cromosoma 4 (único) secuencia expresada 234	D4S234E	209570_s_at	Citoplasma	otro	-1.488
segmento de ADN en el cromosoma 4 (único) secuencia expresada 234	D4S234E	213533_at	Citoplasma	otro	-1.507
dopamina beta-hidroxilasa (dopamina beta-	DBH	206450_at	Citoplasma	enzima	1.311

monooxigenasa)					
cinasa 1 tipo doblecortina	DCLK1	215303_at	Citoplasma	cinasa	-1.62
fosfatasa 16 de especificidad dual	DUSP16	224832_at	núcleo	fosfatasa	-0.918
proteína asociada al microtúbulo equinodermo tipo 1	EML1	204797_s_at	Citoplasma	otro	2.668
corteza neural ectodérmica (con dominio tipo BTB)	ENC1	201340_s_at	núcleo	peptidasa	2.445
corteza neural ectodérmica (con dominio tipo BTB)	ENC1	201341_at	núcleo	peptidasa	1.91
deshidrogenasa flavoproteína que transfiere electrones	ETFDH	33494_at	Citoplasma	enzima	-0.807
Factor 2 asociado con ELL	EAF2	219551_at	núcleo	regulador de transcripción	0.693
miembro 7 de la familia ELOVL, alargamiento de ácidos grasos de cadena larga	ELOVL7	227180_at	desconocida	otro	2.644
aminopeptidasa de retículo endoplasmático 1	ERAP1	214012_at	Espacio extracelular	peptidasa	-1.885
potenciador del homólogo de zeste 2	EZH2	203358_s_at	núcleo	regulador de transcripción	0.94
efrina-A5	EFNA5	214036_at	Membrana plasmática	cinasa	2.041
efrina-A5	EFNA5	227955_s_at	Membrana plasmática	cinasa	1.84
efrina-A5	EFNA5	233814_at	Membrana plasmática	cinasa	1.805
efrina-B3	EFNB3	205031_at	Membrana	cinasa	-0.816

			plasmática		
Factor 3 de inicio de la traducción eucariota, subunidad C	EIF3C	236700_at	Citoplasma	regulador de la traducción	1.378
exofilina 5	EXPH5	214734_at	desconocida	otro	3.973
componente 6 del exosoma	EXOSC6	231916_at	núcleo	otro	1.057
familia con similitud de secuencia 162, miembro B	FAM162B	228875_at	desconocida	otro	-0.743
familia con similitud de secuencia 165, miembro B	FAM165B	228239_at	Membrana plasmática	otro	-0.822
familia con similitud de secuencia 181, miembro B	FAM181B	231430_at	desconocida	otro	0.794
familia con similitud de secuencia 19 (tipo quimiocina (motivo C-C)), miembro A4	FAM19A4	242348_at	Espacio extracelular	otro	1.282
familia con similitud de secuencia 46, miembro A	FAM46A	224973_at	desconocida	otro	-1.509
familia con similitud de secuencia 7, miembro A3	FAM7A3	243356_at	desconocida	otro	3.495
proteína 3 de unión al elemento corriente arriba (FUSE)	FUBP3	239193_at	núcleo	regulador de transcripción	1.192
dominio de repetición de WD y secuencia F que contiene 7	FBXW7	229419_at	núcleo	regulador de transcripción	-0.921
factor de crecimiento de fibroblastos 13	FGF13	205110_s_at	Espacio extracelular	factor de crecimiento	-3.522
1 tipo folistatina	FSTL1	208782_at	Espacio extracelular	otro	-1.275
secuencia cabeza de tenedor	FOXO6	239657_x_at	núcleo	otro	-1.512

O6					
homólogo frizzled 5	FZD5	221245_s_at	Membrana plasmática	receptor	2.347
dominio FYVE, RhoGEF y PH que contiene 5	FGD5	226985_at	Citoplasma	otro	-1.952
Receptor 123 acoplado a la proteína G	GPR123	239221_at	Membrana plasmática	receptor	-1.302
Receptor 125 acoplado a la proteína G	GPR125	210473_s_at	Membrana plasmática	receptor	0.714
galanina prepropéptido	GAL	207466_at	Espacio extracelular	otro	-1.434
galanina prepropéptido	GAL	214240_at	Espacio extracelular	otro	-3.128
péptido que libera gastrina	GRP	206326_at	Espacio extracelular	factor de crecimiento	4.698
receptor alfa 2 de la familia GDNF	GFRA2	205721_at	Membrana plasmática	receptor	1.847
receptor alfa 2 de la familia GDNF	GFRA2	205722_s_at	Membrana plasmática	receptor	2.265
receptor de glutamato, metabotrópico 5	GRM5	214217_at	Membrana plasmática	receptor	-2.231
glutationa peroxidasa 7	GPX7	213170_at	Citoplasma	enzima	-2.692
glutationa sintetasa	GSS	211630_s_at	Citoplasma	enzima	0.599
dominio de glucosiltransferasa 25 que contiene 2	GLT25D2	209883_at	desconocida	otro	-1.223
locus del complejo GNAS	GNAS	214157_at	Membrana plasmática	enzima	-1.794
proteína 43 asociada al crecimiento	GAP43	204471_at	Membrana plasmática	otro	0.869

proteína 43 asociada al crecimiento	GAP43	216963_s_at	Membrana plasmática	otro	1.151
proteína de unión al nucleótido de guanina (proteína G), polipéptido de actividad inhibidora alfa 1	GNAI1	209576_at	Membrana plasmática	enzima	2.225
proteína de unión al nucleótido de guanina (proteína G), polipéptido de actividad inhibidora alfa 1	GNAI1	227692_at	Membrana plasmática	enzima	2.111
proteína de unión al nucleótido de guanina (proteína G), polipéptido beta 4	GNB4	225710_at	Membrana plasmática	enzima	4.695
proteína de unión al nucleótido de guanina (proteína G), gamma 11	GNG11	204115_at	Membrana plasmática	enzima	2.587
guanilato ciclasa 1, soluble, alfa 3	GUCY1A3	221942_s_at	Citoplasma	enzima	-1.522
guanilato ciclasa 1, soluble, alfa 3	GUCY1A3	229530_at	Citoplasma	enzima	-1.696
helicasa tipo POLQ	HELQ	228736_at	núcleo	enzima	-1.28
miembro 2 de la familia HERPUD	HERPUD2	236170_x_at	desconocida	otro	-0.897
ribonucleoproteína R nuclear heterogénea	HNRNPR	208765_s_at	núcleo	otro	-0.64
1 tipo hipocalcina	HPCAL1	205462_s_at	Citoplasma	otro	-1.551
1 tipo hipocalcina	HPCAL1	212552_at	Citoplasma	otro	-1.387
grupo de histona 1, H2ac	HIST1H2AC	215071_s_at	núcleo	otro	-2.462
grupo de histona 1, H2bd	HIST1H2BD	209911_x_at	núcleo	otro	-2.036

grupo de histona 1, H2bk	HIST1H2BK	209806_at	núcleo	otro	-1.575
grupo de histona 2, H2be	HIST2H2BE	202708_s_at	núcleo	otro	-1.735
LOC100130522 hipotético	LOC100130522	230477_at	desconocida	otro	-0.928
LOC26082 hipotético	DKFZP434L187	230861_at	desconocida	otro	0.968
Proteína hipotética LOC100128844	LOC100128844	229110_at	desconocida	otro	2.106
proteína hipotética LOC643401	LOC340109	1557765_at	desconocida	otro	2.848
integrina, alfa 6	ITGA6	201656_at	Membrana plasmática	otro	2.822
integrina, alfa 6	ITGA6	215177_s_at	Membrana plasmática	otro	2.024
integrina, beta 5	ITGB5	201125_s_at	Membrana plasmática	otro	0.913
receptor de interleucina 10, beta	IL10RB	209575_at	Membrana plasmática	receptor de transmembrana	-1.444
proteína de unión de mediación y reguladora, cofactor p53	JMY	226352_at	núcleo	regulador de transcripción	-0.744
K(lisina) acetiltransferasa 2B	KAT2B	203845_at	núcleo	regulador de transcripción	-0.731
KDEL (Lys-Asp-Glu-Leu) que contiene 2	KDELC2	225128_at	desconocida	otro	1.085
Dominio kelch que contiene 1	KLHDC1	1552733_at	desconocida	otro	-0.952
dominio de repetición kelch y de BTB (POZ) que contiene 11	KBTBD11	204301_at	desconocida	otro	-0.733

13 tipo kelch (drosófila)	KLHL13	227875_at	desconocida	otro	0.902
transducción de señal de unión al ARN con dominio KH asociada a 3	KHDRBS3	209781_s_at	núcleo	otro	1.082
dominio de homología KH que contiene 1	KHDC1	230055_at	desconocida	otro	-1.656
KIAA1598	KIAA1598	221802_s_at	desconocida	otro	-2.811
miembro de la familia de cinesina 16B	KIF16B	232083_at	Citoplasma	otro	1.688
proteína de unión 3, lectina, unión a galactósida, soluble	LGALS3BP	200923_at	Membrana plasmática	receptor de transmembrana	-1.417
receptor del factor inhibidor de leucemia alfa	LIFR	225575_at	Membrana plasmática	receptor de transmembrana	-0.941
homólogo de desarrollo cardíaco y yema del miembro (ratón)	LBH	221011_s_at	núcleo	regulador de transcripción	0.788
proteína de unión a LRP2	LRP2BP	207797_s_at	desconocida	otro	-1.365
lumican	LUM	201744_s_at	Espacio extracelular	otro	5.638
motivo LYR que contiene 5	LYRM5	225469_at	desconocida	otro	-0.93
1 tipo mab-21	MAB21L1	206163_at	desconocida	otro	2.722
2 tipo mab-21	MAB21L2	210302_s_at	desconocida	otro	2.871
2 tipo mab-21	MAB21L2	210303_at	desconocida	otro	2.204
estimulador de macrófago 1 (tipo factor de crecimiento de hepatocitos)	MST1	216320_x_at	Espacio extracelular	factor de crecimiento	-1.012
dominio de superfamilia de facilitador principal que contiene 4	MFSD4	229254_at	desconocida	otro	-1.752

manosidasa, alfa, clase 2A, miembro 1	MAN2A1	226538_at	Citoplasma	enzima	0.864
manosil (alfa-1,3-)-glucoproteína beta-1,4-N-acetilglucosaminiltransferasa, isozima A	MGAT4A	226039_at	desconocida	enzima	-0.904
homeosecuencia mesenquimal 2	MEOX2	206201_s_at	núcleo	regulador de transcripción	-4.213
proteína 9 asociada a microtúbulos	MAP9	220145_at	desconocida	otro	-0.7
proteína 9 asociada a microtúbulos	MAP9	228423_at	desconocida	otro	-1.108
proteína 9 asociada a microtúbulos	MAP9	235550_at	desconocida	otro	-0.863
proteína ribosómica mitocondrial S33	MRPS33	218654_s_at	Citoplasma	otro	-0.609
cinasa 5 de cinasa de proteína cinasa activada por mitógeno	MAP3K5	203836_s_at	Citoplasma	cinasa	-1.159
moesina	MSN	200600_at	Membrana plasmática	otro	2.082
monoaminooxidasa A	MAOA	204388_s_at	Citoplasma	enzima	2.15
monoaminooxidasa A	MAOA	204389_at	Citoplasma	enzima	1.88
monoaminooxidasa A	MAOA	212741_at	Citoplasma	enzima	2.048
asociado a la diferenciación de macrófago a monocito	MMD	244523_at	Membrana plasmática	otro	1.045
dominios C2 múltiples, transmembrana 1	MCTP1	220122_at	desconocida	otro	-1.597
antígeno nuclear inducido por MYC	MINA	213188_s_at	núcleo	otro	1.391

antígeno nuclear inducido por MYC	MINA	213189_at	núcleo	otro	1.641
miosina IB	MYO1B	212365_at	Citoplasma	otro	0.71
miosina VI	MYO6	203216_s_at	Citoplasma	otro	1.104
miosina VI	MYO6	210480_s_at	Citoplasma	otro	1.41
dominio intercambiador de Na+/H+ que contiene 2	NHEDC2	1564746_at	Membrana plasmática	otro	-1.462
amidasa de ácido N-acetiletanolamina	NAAA	214765_s_at	Citoplasma	enzima	0.911
NADH deshidrogenasa (ubiquinona) 1 subcomplejo alfa, 2 tipo 4	NDUFA4L2	218484_at	desconocida	enzima	-3.507
NADH deshidrogenasa (ubiquinona) flavoproteína 3, 10kDa	NDUFV3	226616_s_at	Citoplasma	enzima	-0.875
nebulete	NEBL	203961_at	Citoplasma	otro	-1.359
célula precursora neuronal expresada, regulada por disminución embriológicamente 9	NEDD9	202150_s_at	núcleo	otro	2.41
dominio tipo NIPA que contiene 3	NIPAL3	225876_at	desconocida	otro	-1.203
sintasa de óxido nítrico 1 (neuronal)	NOS1	239132_at	Citoplasma	enzima	1.138
sintasa de óxido nítrico 1 (neuronal)	NOS1	240911_at	Citoplasma	enzima	1.187
miembro de la familia NLR X1	NLRX1	219680_at	desconocida	otro	-1.541
ARN que no codifica proteínas 171	NCRNA00171	215985_at	desconocida	otro	-0.692

coactivador del receptor nuclear 7	NCOA7	225344_at	núcleo	otro	-0.842
3 tipo proteína de disposición de nucleosoma 1	NAP1L3	204749_at	núcleo	otro	-1.53
motivo 19 tipo nudix (resto X unido a nucleósido difosfato)	NUDT19	235384_at	Citoplasma	otro	-1.685
olfactomedina 3	OLFM3	1554524_a_at	Citoplasma	otro	-0.927
3 tipo proteína de unión a oxisterol	OSBPL3	209626_s_at	Citoplasma	otro	2.083
2 tipo pecanex	PCNXL2	1554256_a_at	desconocida	otro	-0.728
homólogo de pelino 2	PELI2	219132_at	Citoplasma	otro	0.732
dominio de peptidasa M20 que contiene 2	PM20D2	225421_at	desconocida	otro	1.6
monooxigenasa de amidación de alfa peptidilglicina	PAM	202336_s_at	Membrana plasmática	enzima	-0.861
periferina	PRPH	213847_at	Membrana plasmática	otro	-1.417
proteína de dedo PHD 20	PHF20	235389_at	núcleo	otro	0.596
dominio tipo 2 de fosfatasas del ácido fosfatídico que contiene 1A	PPAPDC1A	236044_at	desconocida	fosfatasa	-2.621
biosíntesis de unión de fosfatidilinositol glicano, clase H	PIGH	209625_at	Citoplasma	enzima	-0.597
regulador que interactúa con fosfoinositida de canales potenciales del receptor transitorio	HCG 1776018	232887_at	desconocida	otro	-2.019
fosforilasa cinasa, alfa 1	PHKA1	229876_at	Citoplasma	cinasa	-1.2

(músculo)					
plastina 3 (isoforma T)	PLS3	201215_at	Citoplasma	otro	1.068
receptor del factor de crecimiento derivado de plaquetas, polipéptido beta	PDGFRB	202273_at	Membrana plasmática	cinasa	-1.373
pleiotrofina	PTN	209466_x_at	Espacio extracelular	factor de crecimiento	-1.426
pleiotrofina	PTN	211737_x_at	Espacio extracelular	factor de crecimiento	-2.929
regulador pleiotrópico 1	PLRG1	225194_at	núcleo	regulador de transcripción	-0.701
regulador pleiotrópico 1	PLRG1	227246_at	núcleo	regulador de transcripción	-1.228
plexina A2	PLXNA2	213030_s_at	Membrana plasmática	otro	0.946
plexina A4	PLXNA4	232317_at	Membrana plasmática	receptor	1.368
cinasa 2 tipo polo	PLK2	201939_at	núcleo	cinasa	3.606
anillo anular 5 del grupo polipeloso	PCGF5	227935_s_at	desconocida	otro	0.791
polimerasa (dirigida por ADN), epsilon	POLE	216026_s_at	núcleo	enzima	1.053
dominio de tetramerización de canal de potasio que contiene 12	KCTD12	212188_at	desconocida	canal iónico	3.396
dominio de tetramerisación de canal de potasio que contiene 12.	KCTD12	212192_at	desconocida	canal iónico	4.806
canal de potasio activado por	KCNMA1	221584_s_at	Membrana	canal iónico	-2.389

calcio de conductividad alta, subfamilia M, miembro alfa 1			plasmática		
canal de potasio dependiente de voltaje, subfamilia tipo KQT, miembro 2	KCNQ2	205737_at	Membrana plasmática	canal iónico	-1.246
proteína A plasmática asociada al embarazo, *papalisina 1*	PAPPA	201982_s_at	Espacio extracelular	peptidasa	-1.672
receptor 2 de prostaglandina E (subtipo EP2), 53kDa	PTGER2	206631_at	Membrana plasmática	receptor	-2.328
regulador negativo del receptor de prostaglandina F2	PTGFRN	224937_at	Membrana plasmática	otro	2.301
subunidad de proteasoma (prosoma, macropain), tipo alfa, 7	PSMA7	216088_s_at	Citoplasma	peptidasa	0.658
cinasa de proteína, dependiente de AMPc, catalítica, beta	PRKACB	235780_at	Citoplasma	cinasa	-2.17
Proteína tirosina fosfatasa, tipo receptor, D	PTPRD	214043_at	Membrana plasmática	fosfatasa	-1.16
Proteína tirosina fosfatasa, tipo receptor, E	PTPRE	221840_at	Membrana plasmática	fosfatasa	3.044
Proteína tirosina fosfatasa, tipo receptor, G	PTPRG	204944_at	Membrana plasmática	fosfatasa	1.237
RAB35, miembro de la familia del oncogén RAS	RAB35	205461_at	Citoplasma	enzima	0.737
RAB6B, miembro de la familia del oncogén RAS	RAB6B	225259_at	Citoplasma	enzima	-1.229
Factor de intercambio de nucleótido guanina Rac/Cdc42	ARHGEF6	209539_at	Citoplasma	otro	2.719

(GEF) 6					
RAN, miembro de la familia del oncogén RAS	RAN	200750_s_at	núcleo	enzima	0.59
que contiene el dominio de mano RAS y EF	RASEF	1553986_at	desconocida	otro	1.393
familia del gen homólogo de ras, miembro U	RHOU	223168_at	Citoplasma	enzima	-1.154
regulador de la señalización de la proteína G 5	RGS5	1555725_a_at	Membrana plasmática	otro	4.038
regulador de la señalización de la proteína G 5	RGS5	209070_s_at	Membrana plasmática	otro	3.729
regulador de la señalización de la proteína G 5	RGS5	209071_s_at	Membrana plasmática	otro	3.468
regulador de la señalización de la proteína G 5	RGS5	218353_at	Membrana plasmática	otro	3.65
1 tipo RELT	RELL1	226430_at	desconocida	otro	1.214
1 tipo retinoblastoma (p107)	RBL1	1559307_s_at	núcleo	otro	0.959
dominio gag de retrotransposón que contiene 4	RGAG4	227823_at	desconocida	otro	-1.775
Proteína 6 activadora de Rho GTPasa	ARHGAP6	206167_s_at	Citoplasma	otro	2.809
dominio L1 ribosómico que contiene 1	RSL1D1	213750_at	Citoplasma	otro	-0.816
proteína de unión a RIMS 2	RIMBP2	238817_at	Membrana plasmática	otro	1.679
proteína de dedo anular 13	RNF13	201780_s_at	núcleo	otro	-0.707
proteína de dedo anular 182	RNF182	230720_at	desconocida	otro	2.696
proteína de dedo anular 34	RNF34	219035_s_at	Citoplasma	enzima	0.85

proteína de dedo anular 41	RNF41	201962_s_at	Citoplasma	otro	-0.591
seudogén 1 del homólogo del factor de transcripción de polimerasa de ARN I	LOC94431	216908_x_at	desconocida	otro	-0.674
4 tipo sal	SALL4	229661_at	núcleo	otro	1.586
cinasa inducible por sal 1	SIK1	208078_s_at	Citoplasma	cinasa	-1.403
tipo homólogo 6 (ratón) relacionado con convulsiones	SEZ6L	207873_x_at	Membrana plasmática	otro	0.866
tipo homólogo 6 (ratón) relacionado con convulsiones	SEZ6L	211894_x_at	Membrana plasmática	otro	0.797
dominio sema, dominio transmembrana (TM) y dominio citoplásmico, (semaforina) 6A	SEMA6A	220454_s_at	Membrana plasmática	otro	1.356
inhibidor de la serina peptidasa, tipo Kunitz, 2	SPINT2	210715_s_at	Espacio extracelular	otro	-1.889
1 tipo Ysc84 que contiene dominio SH3	SH3YL1	204019_s_at	desconocida	otro	-0.859
2 tipo GRB2 de dominio SH3	SH3GL2	205751_at	Membrana plasmática	enzima	-1.605
similar a hCG2031213	LOC728052	1558795_at	desconocida	otro	2.239
similar a hCG2031213	LOC728052	1558796_a_at	desconocida	otro	1.887
dominio del receptor de interleucina 1 tipo toI (TIR) y de inmunoglobulina único	SIGIRR	52940_at	Membrana plasmática	receptor	-1.42
homólogo 1 "single-minded"	SIM1	1556300_s_at	núcleo	regulador de transcripción	6.36
homólogo 1 "single-minded"	SIM1	206876_at	núcleo	regulador de transcripción	5.737

familia de tipo SLIT y NTRK, miembro 5	SLITRK5	214930_at	desconocida	otro	4.094
seudogén de cinasa relacionado con la fosfatidilinositol 3 cinasa, homólogo de SMG1	LOC641298	244766_at	desconocida	otro	1.065
familia portadora de soluto 12 (transportadores de potasio/cloruro), miembro 7	SLC12A7	218066_at	Membrana plasmática	transportador	-1.258
familia portadora de solutos 22, miembro 17	SLC22A17	218675_at	Membrana plasmática	transportador	-0.724
familia portadora de soluto 35, miembro F3	SLC35F3	229065_at	desconocida	otro	-3.048
familia portadora de soluto 44, miembro 5	SLC44A5	1569112_at	desconocida	otro	2.738
familia portadora de soluto 44, miembro 5	SLC44A5	235763_at	desconocida	otro	1.845
familia portadora de solutos 7 (sistema y+ transportador de aminoácidos catiónicos), miembro 2	SLC7A2	225516_at	Membrana plasmática	transportador	1.892
familia transportadora de aniones orgánicos portadores de solutos, miembro 3A1	SLCO3A1	219229_at	Membrana plasmática	transportador	1.622
familia transportadora de aniones orgánicos portadores de solutos, miembro 3A1	SLCO3A1	227367_at	Membrana plasmática	transportador	1.045
sparc/osteonectina, dominios tipo cwcv y kazal proteoglicanos (testican)2	SPOCK2	202524_s_at	Espacio extracelular	otro	-0.83
antígeno asociado con el	SPAG6	210032_s_at	Citoplasma	otro	1.687

esperma 6					
antígeno asociado con el esperma 6	SPAG6	210033_s_at	Citoplasma	otro	2.774
tipo 2, rico en serina, asociado con la espermatogénesis	SPATS2L	222154_s_at	desconocida	otro	0.907
receptor 3 de esfingosina-1-fosfato	S1PR3	228176_at	Membrana plasmática	receptor	1.9
ST8 alfa-N-acetil-neuraminida alfa-2,8-sialiltransferasa 1	ST8SIA1	210073_at	Citoplasma	enzima	1.114
ST8 alfa-N-acetil-neuraminida alfa-2,8-sialiltransferasa 3	ST8SIA3	230262_at	Citoplasma	enzima	-1.039
3 tipo estatmina	STMN3	222557_at	núcleo	otro	0.788
miembro de la familia de STEAP 3	STEAP3	218424_s_at	Citoplasma	transportador	-1.827
proteína reguladora aguda esteroidogénica	STAR	204548_at	Citoplasma	transportador	-1.093
homólogo del gen 6 estimulado por ácido retinoico	STRA6	1569334_at	Membrana plasmática	otro	1.359
homólogo del gen 6 estimulado por ácido retinoico	STRA6	1569335_a_at	Membrana plasmática	otro	1.167
secuencia storkhead 2	STOX2	226822_at	desconocida	otro	-0.854
sinaptojanina 1	SYNJ1	212990_at	Citoplasma	fosfatasa	-0.624
sinaptotagmina XIII	SYT13	226086_at	desconocida	transportador	-4.754
sinucleína, alfa (componente del precursor amiloide que no es A4)	SNCA	236081_at	Citoplasma	otro	-0.935
taxilin beta	TXLNB	227834_at	Citoplasma	otro	-2.226
homeosecuencia 3 de dedo de cinc teashirt	TSHZ3	223392_s_at	núcleo	regulador de transcripción	1.472

homeosecuencia 3 de dedo de cinc teashirt	TSHZ3	223393_s_at	núcleo	regulador de transcripción	0.962
dominio de repetición de tetratricopéptido 39C	TTC39C	238480_at	desconocida	otro	-0.824
tipo TH1	TH1L	220607_x_at	núcleo	otro	1.027
tipo TH1	TH1L	225006_x_at	núcleo	otro	0.884
tipo TH1	TH1L	225261_x_at	núcleo	otro	0.883
tipo TH1	TH1L	225865_x_at	núcleo	otro	0.904
tioredoxina reductasa 1	TXNRD1	201266_at	Citoplasma	enzima	1.032
complejo THO 4	THOC4	226319_s_at	núcleo	regulador de transcripción	0.996
inhibidor 3 de la metalopeptidasa TIMP	TIMP3	201147_s_at	Espacio extracelular	otro	5.151
inhibidor 3 de la metalopeptidasa TIMP	TIMP3	201148_s_at	Espacio extracelular	otro	3.637
inhibidor 3 de la metalopeptidasa TIMP	TIMP3	201149_s_at	Espacio extracelular	otro	5.037
inhibidor 3 de la metalopeptidasa TIMP	TIMP3	201150_s_at	Espacio extracelular	otro	4.312
inhibidor 2 de la senda del factor tisular	TFPI2	209277_at	Espacio extracelular	otro	1.592
inhibidor 2 de la senda del factor tisular	TFPI2	209278_s_at	Espacio extracelular	otro	2.326
Dominio TM2 que contiene 1	TM2D1	213882_at	Membrana plasmática	receptor	-0.769
2 tipo factor de transcripción 7 (específico para células T, secuencia HMG)	TCF7L2	212761_at	núcleo	regulador de transcripción	1.005
2 tipo factor de transcripción 7	TCF7L2	212762_s_at	núcleo	regulador de	1.224

(específico para células T, secuencia HMG)				transcripción	
2 tipo factor de transcripción 7 (específico para células T, secuencia HMG)	TCF7L2	216035_x_at	núcleo	regulador de transcripción	1.072
2 tipo factor de transcripción 7 (específico para células T, secuencia HMG)	TCF7L2	216037_x_at	núcleo	regulador de transcripción	0.81
2 tipo factor de transcripción 7 (específico para células T, secuencia HMG)	TCF7L2	216511_s_at	núcleo	regulador de transcripción	1.003
potenciador de división tipo transducina 3	TLE3	212770_at	núcleo	otro	0.976
homólogo transformador alfa 2	TRA2A	213593_s_at	núcleo	otro	1.12
transmembrana del oído interno	TMIE	1553601_a_at	desconocida	otro	-3.334
proteína transmembrana 132C	TMEM132C	232313_at	desconocida	otro	4.02
proteína transmembrana 178	TMEM178	229302_at	desconocida	otro	1.697
proteína transmembrana 184C	TMEM184C	219074_at	desconocida	otro	-0.779
proteína transmembrana 5	TMEM5	204808_s_at	Membrana plasmática	otro	-1.074
tipo proteína transmembrana 59	TMEM59L	219005_at	Citoplasma	otro	-0.845
motivo tripartito que contiene 29	TRIM29	211002_s_at	Citoplasma	regulador de transcripción	2.005
motivo tripartito que contiene 36	TRIM36	219736_at	Citoplasma	otro	2.221
glucoproteína de trofoblasto	TPBG	203476_at	Membrana plasmática	otro	2.158

candidato 3 supresor de tumor	TUSC3	232770_at	Espacio extracelular	enzima	-1.407
factor auxiliar 1 del ARN pequeño nuclear U2	U2AF1	232141_at	núcleo	otro	0.776
variante 1 de la enzima E2 conjugadora de ubiquitina	UBE2V1	201003_x_at	núcleo	regulador de transcripción	0.663
urocortina	UCN	206072_at	Espacio extracelular	otro	-0.961
homólogo de clasificación de proteína vacuolar 29	VPS29	223026_s_at	Citoplasma	transportador	0.805
homólogo 4 del oncogén viral de leucemia eritroblástica v-erb-a	ERBB4	206794_at	Membrana plasmática	cinasa	-1.537
homólogo 4 del oncogén viral de leucemia eritroblástica v-erb-a	ERBB4	214053_at	Membrana plasmática	cinasa	-1.708
homólogo 2 del oncogén viral de leucemia eritroblástica v-erb-b2, homólogo de oncogén derivado de neuro/glioblastoma	ERBB2	216836_s_at	Membrana plasmática	cinasa	-0.698
homólogo 1 del oncogén viral de leucemia murina v-raf-1	RAF1	1557675_at	Citoplasma	cinasa	0.696
dominio de repetición de WD y FYVE que contiene 3	WDFY3	212602_at	Citoplasma	enzima	-0.626
dominio de repetición de WD y FYVE que contiene 3	WDFY3	212606_at	Citoplasma	enzima	-0.785
homeosecuencia 4 de dedo de cinc	ZFHX4	219779_at	desconocida	otro	1.36
homeosecuencia 4 de dedo de	ZFHX4	241700_at	desconocida	otro	1.234

cinc					
proteína de dedos de cinc 217	ZNF217	203739_at	núcleo	regulador de transcripción	1.096
proteína de dedos de cinc 503	ZNF503	227195_at	núcleo	otro	1.373
proteína de dedos de cinc 641	ZNF641	226509_at	desconocida	otro	-1.427
proteína de dedos de cinc 662	ZNF662	228538_at	desconocida	otro	-3.352
dedo de cinc, tipo CCCH con dominio de parche G	ZGPAT	221848_at	desconocida	otro	0.991

Se realizó análisis informático como en el Ejemplo V, salvo porque la lista de sondas refleja genes con un diferencial de más de 1.5 veces expresado en la línea celular H1 y la línea celular BB10, en comparación con las líneas celulares 2D6 y SiMa original, así como un diferencial de más de 1.5 veces expresado en la línea celular original SiMa, en comparación con la línea celular 2D6. Al fijar el corte del valor p en 0.05, este análisis identificó 94 sondas genéticas que se podían clasificar en 70 genes (Tabla 17).

Tabla 17. Genes identificados usando el análisis central IPA

Nombre del gen	Símbolo del gen	No. de ID de la sonda	Ubicación	Tipo	Proporción logarítmica
homólogo 1 del complejo	ASCL1	209985_s_at	Núcleo	regulador de	2.429

achaete-scute				transcripción	
homólogo 1 del complejo achaete-scute	ASCL1	209988_s_at	Núcleo	regulador de transcripción	1.446
homólogo 1 del complejo achaete-scute	ASCL1	213768_s_at	Núcleo	regulador de transcripción	1.578
molécula de adhesión celular del leucocito activado	ALCAM	201952_at	membrana plasmática	otro	1.521
factor 1 de ADP-ribosilación	ARF1	1565651_at	citoplasma	enzima	1.063
17A tipo factor de ADP-ribosilación	ARL17A	243899_at	desconocida	otro	0.741
proteína 1 de unión a la ataxina 2	A2BP1	1553422_s_at	citoplasma	otro	1.453
proteína 1 de unión a la ataxina 2	A2BP1	221217_s_at	citoplasma	otro	1.497
proteína de señal 1 unida a la membrana y abundante en el cerebro	BASP1	202391_at	membrana plasmática	otro	1.146
proteína asociada con la adenilato ciclasa CAP 2	CAP2	212551_at	membrana plasmática	otro	-1.974

molécula CD9	CD9	201005_at	membrana plasmática	otro	1.415
proteína 2 de unión al ARN y repetición de triplete CUG	CUGBP2	202157_s_at	núcleo	otro	2.156
canal modulado por nucleótidos cíclicos alfa 3	CNGA3	207261_at	membrana plasmática	canal iónico	-3.182
inhibidor de la cinasa dependiente de la ciclina 2A (melanoma, p16, inhibe la CDK4)	CDKN2A	209644_x_at	núcleo	regulador de transcripción	-1.277
factor 2 asociado con ELL	EAF2	219551_at	núcleo	regulador de transcripción	0.693
factor 3 de inicio de la traducción eucariota, subunidad C	EIF3C	236700_at	citoplasma	regulador de la traducción	1.378
familia con similitud de secuencia 162, miembro B	FAM162B	228875_at	desconocida	otro	-0.743
familia con similitud de secuencia 181, miembro B	FAM181B	231430_at	desconocida	otro	0.794

proteína 3 de unión al elemento corriente arriba (FUSE)	FUBP3	239193_at	núcleo	regulador de transcripción	1.192
factor de crecimiento de fibroblastos 13	FGF13	205110_s_at	espacio extracelular	factor de crecimiento	-3.522
1 tipo folistatina	FSTL1	208782_at	espacio extracelular	otro	-1.275
secuencia cabeza de tenedor O6	FOXO6	239657_x_at	núcleo	otro	-1.512
proteína de unión al nucleótido de guanina (proteína G), polipéptido 1 de actividad inhibidora alfa	GNAI1	227692_at	membrana plasmática	enzima	2.111
proteína de unión al nucleótido de guanina (proteína G), polipéptido 4 beta	GNB4	225710_at	membrana plasmática	enzima	4.695
proteína de unión al nucleótido de guanina (proteína G), gamma 11	GNG11	204115_at	membrana plasmática	enzima	2.587
KDEL (Lys-Asp-Glu-Leu)	KDELC2	225128_at	desconocida	otro	1.085

que contiene 2					
13 tipo kelch	KLHL13	227875_at	desconocida	otro	0.902
3 asociado a transducción de señal, unión al ARN, con dominio KH	KHDRBS3	209781_s_at	núcleo	otro	1.082
dominio de homología KH que contiene 1	KHDC1	230055_at	desconocida	otro	-1.656
receptor del factor inhibidor de leucemia alfa	LIFR	225575_at	membrana plasmática	receptor de transmembrana	-0.941
2 tipo mab-21	MAB21L2	210303_at	desconocida	otro	2.204
homeosecuencia mesenquimal 2	MEOX2	206201_s_at	núcleo	regulador de transcripción	-4.213
moesina	MSN	200600_at	membrana plasmática	otro	2.082
monoaminoxidasa A	MAOA	204388_s_at	citoplasma	enzima	2.15
monoaminoxidasa A	MAOA	204389_at	citoplasma	enzima	1.88
monoaminoxidasa A	MAOA	212741_at	citoplasma	enzima	2.048
dominios C2 múltiples,	MCTP1	220122_at	desconocida	otro	-1.597

transmembrana 1					
antígeno nuclear inducido por MYC	MINA	213188_s_at	núcleo	otro	1.391
antígeno nuclear inducido por MYC	MINA	213189_at	núcleo	otro	1.641
miosina VI	MYO6	203216_s_at	citoplasma	otro	1.104
dominio tipo 2 de fosfatasa del ácido fosfatídico que contiene 1A	PPAPDC1A	236044_at	desconocida	fosfatasa	-2.621
plastina 3 (isoforma T)	PLS3	201215_at	citoplasma	otro	1.068
pleiotrofina	PTN	209466_x_at	espacio extracelular	factor de crecimiento	-1.426
pleiotrofina	PTN	211737_x_at	espacio extracelular	factor de crecimiento	-2.929
cinasa 2 tipo polo (Drosófila)	PLK2	201939_at	núcleo	cinasa	3.606
canal de potasio activado por calcio de conductividad alta, subfamilia M, miembro	KCNMA1	221584_s_at	membrana plasmática	canal iónico	-2.389

alfa 1					
1 tipo RELT	RELL1	226430_at	desconocida	otro	1.214
proteína de dedo anular 182	RNF182	230720_at	desconocida	otro	2.696
tipo homólogo 6 relacionado con convulsiones	SEZ6L	207873_x_at	membrana plasmática	otro	0.866
tipo homólogo 6 (ratón) relacionado con convulsiones	SEZ6L	211894_x_at	membrana plasmática	otro	0.797
similar a hCG2031213	LOC728052	1558795_at	desconocida	otro	2.239
homólogo 1 "single-minded" (Drosófila)	SIM1	1556300_s_at	núcleo	regulador de transcripción	6.36
homólogo 1 "single-minded" (Drosófila)	SIM1	206876_at	núcleo	regulador de transcripción	5.737
familia de tipo SLIT y NTRK, miembro 5	SLITRK5	214930_at	desconocida	otro	4.094
seudogén de cinasa relacionado con la fosfatidilinositol 3 cinasa, homólogo de SMG1	LOC641298	244766_at	desconocida	otro	1.065

familia portadora de soluto 44, miembro 5	SLC44A5	1569112_at	desconocida	otro	2.738
familia portadora de soluto 44, miembro 5	SLC44A5	235763_at	desconocida	otro	1.845
familia portadora de soluto 7 (sistema y+ transportador de aminoácidos catiónicos), miembro 2	SLC7A2	225516_at	membrana plasmática	transportador	1.892
familia transportadora de aniones orgánicos portadores de solutos, miembro 3A1	SLCO3A1	219229_at	membrana plasmática	transportador	1.622
tipo 2, rico en serina, asociado con la espermatogénesis	SPATS2L	222154_s_at	desconocida	otro	0.907
sinaptotagmina XIII	SYT13	226086_at	desconocida	transportador	-4.754
inhibidor 2 de la senda del factor tisular	TFPI2	209278_s_at	espacio extracelular	otro	2.326
2 tipo factor de transcripción 7 (específico para células	TCF7L2	212761_at	Núcleo	regulador de transcripción	1.005

T, secuencia HMG)					
homólogo transformador 2 alfa	TRA2A	213593_s_at	Núcleo	otro	1.12
transmembrana del oído interno	TMIE	1553601_a_at	desconocida	otro	-3.334
proteína transmembrana 178	TMEM178	229302_at	desconocida	otro	1.697
factor auxiliar 1 del ARN pequeño nuclear U2	U2AF1	232141_at	Núcleo	otro	0.776
homólogo 1 del oncogén viral de leucemia murina v-raf-1	RAF1	1557675_at	Citoplasma	cinasa	0.696
proteína de dedos de cinc 217	ZNF217	203739_at	Núcleo	regulador de transcripción	1.096
proteína de dedos de cinc 662	ZNF662	228538_at	desconocida	otro	-3.352

La proporción logarítmica representa valores $\log_2$ donde 0.585 es $\log_2(1.5)$ que es una diferencia de 1.5 veces, 1 es $\log_2(2)$ que es una diferencia de 2 veces, 1.584 es $\log_2(3)$ que es una diferencia de 3 veces, 2 es $\log_2(4)$ que es una diferencia de 4 veces, 2.321 es $\log_2(5)$ que es una diferencia de 5 veces, 2.584 es $\log_2(6)$ que es una

diferencia de 6 veces, 2.807 es $\log_2(7)$ que es una diferencia de 7 veces, 3 es $\log_2(8)$ que es una diferencia de 8 veces, 3.169 es $\log_2(9)$ que es una diferencia de 9 veces y 3.321 es $\log_2(10)$ que es una diferencia de 10 veces.

Ejemplo VI

Método basado en inmunoensayos para detectar las cantidades picomolares de BoNT/A

El siguiente ejemplo ilustra cómo realizar métodos basados en inmunoensayos para detectar la actividad de BoNT/A que pueden detectar cantidades picomolares del producto farmacéutico de la BoNT/A como, por ej., BOTOX® DYSPORT®/RELOXIN®, PURTOX®, XEOMIN®, NEURONOX® o BTX-A.

1. Método basado en inmunoensayos para detectar BoNT/A usando un ELISA tipo sándwich ECL

Para preparar un lisado a partir de células tratadas con una BoNT/A, se colocaron en aproximadamente 150,000 células de una línea celular clonal establecida en los pocillos de placas de cultivo de tejido con poli-D-lisina de 96 pocillos que contenían 100 µL de un medio libre de suero

con medio esencial mínimo, 2 mM de GlutaMAX™ I con sales de Earle, 1 x de suplemento B27, 1 x de suplemento N2, 0.1 nM de aminoácidos no esenciales, 10 mM de HEPES y 60 µg/mL de GT1b. Las líneas celulares utilizadas fueron BB10, H1 y SiMa. Estas células se incubaron en un incubador a 37°C con 5% de dióxido de carbono hasta que las células se diferenciaran, según se evaluó según criterios morfológicos estándar y de rutina, como detención del crecimiento y extensión de neuritas (aproximadamente 3 días). Se aspiró el medio de las células diferenciadas de cada pocillo y se reemplazó con medio recién preparado que contenía uno de los siguientes: 1) línea celular SiMa, 0 (sin tratar), 0.98 U/mL, 1.9 U/mL, 3.91 U/mL, 7.81 U/mL, 15.6 U/mL, 31.3 U/mL, 62.5 U/mL, 125 U/mL, 250 U/mL o 500 U/mL de un producto farmacéutico de la BoNT/A reconstituido en un medio libre de cloruro de sodio; 2) BB10, 0 (sin tratar), 0.49 U/mL, 0.98 U/mL, 1.9 U/mL, 3.91 U/mL, 7.81 U/mL, 15.6 U/mL, 31.3 U/mL, 62.5 U/mL, 125 U/mL, 250 U/mL; 3) H1, 0 (sin tratar), 0.3 U/mL, 1 U/mL, 3 U/mL, 9 U/mL, 28 U/mL, 83 U/mL y 250 U/mL. Debido a que el producto farmacéutico de la BoNT/A contiene cloruro de sodio, su adición al medio de cultivo dio como resultado un medio hipertónico perjudicial para la viabilidad celular. Para evitar el problema de la hipertonicidad, se usaron 200 µL de medio MEM realizado sin cloruro de sodio para reconstituir el producto farmacéutico de la BoNT/A, lo que proporcionó una

concentración final de 25 pM de BoNT/A (500 U/Ml). La matriz se mantuvo constante para todas las concentraciones a lo largo de la curva de dosis-respuesta agregando cloruro de sodio al medio utilizado para hacer que las diluciones igualaran la cantidad de excipientes presentes en la mayor concentración utilizada (25 pM o 500 U/mL). Luego de un tratamiento de 24 h, las células se lavaron y se incubaron durante dos días adicionales sin toxina. Para recolectar las células, se aspiró 1 x de PBS, las células se lisaron agregando 75 µL de amortiguador de lisis con 50 mM de HEPES, 150 mM de NaCl, 1.5 mM de $MgCl_2$, 1 mM de EGTA y 1% de Tritón X-100 a cada pocillo y la placa se incubó en un agitador con rotación a 500 rpm durante 30 minutos a 4°C. La placa se centrifugó a 4000 rpm durante 20 minutos a 4°C para sedimentar los residuos celulares y el sobrenadante se transfirió a una placa de 96 pocillos recubierta con anticuerpo de captura para realizar la etapa de detección.

Para preparar la solución de anticuerpo de captura α-SNAP-25, el anticuerpo monoclonal α-SNAP-25 contenido en la ascitis de la línea celular de hibridoma 2E2A6 (Ejemplo VII) se purificó usando un protocolo de purificación de la proteína A estándar. Para preparar una solución de anticuerpo de detección α-SNAP-25, el anticuerpo policlonal de conejo α-SNAP-25 S9684 (Sigma, San Luis, MO) se conjugó con el

reactivo de etiquetado del éster de Rutenio(II)-tris-bipiridina-(4-metilsulfonato) de NHS (Meso Scale Discovery, Gaithersburg, MD) de acuerdo con las instrucciones del fabricante (Meso Scale Discovery, Gaithersburg, MD). La reacción de conjugación se llevó a cabo agregando 30 µL de solución madre MSD SULFO-TAG™ reconstituida de agua destilada a 200 µL de 2 mg/mL de anticuerpos policlonales α-SNAP-25 e incubando la reacción a temperatura ambiente durante 2 horas en la oscuridad. Los anticuerpos etiquetados se purificaron usando un protocolo de columna de centrifugación estándar y la concentración de proteína se determinó usando un ensayo de proteína colorimétrico estándar. La absorbancia del conjugado de anticuerpo α-SNAP-25/MSD SULFO-TAG™ se midió a 455 nm usando un espectrofotómetro para determinar la concentración en moles por litro. La solución de anticuerpo de detección se almacenó a 4°C hasta que se necesitara.

Para preparar el soporte de fase sólida que comprende el anticuerpo de captura específico para un producto escindido de la SNAP-25, se agregó aproximadamente 1 µL de solución de anticuerpo monoclonal α-SNAP-25 2E2A6 (45 µg/mL en 1 x de PBS, 750 µg/mL de BSA) a cada pocillo de una placa de alta unión de MSD de 96 pocillos (Meso Scale Discovery, Gaithersburg, MD) y la solución se dejó secar con aire en un gabinete de seguridad biológica durante 2-3 horas para que se

evaporara el líquido de la solución y luego las placas se sellaron y se almacenaron a 4°C hasta que se necesitaran. Los pocillos unidos con anticuerpo de captura secos luego se bloquearon agregando 150 µL de amortiguador de bloqueo con 1 x de PBS, 0.05% de Tween-20, 2% de reactivo de bloqueo ECL (GE Healthcare-Amersham) y 1% de suero de cabra (Rockland Immunochemicals, Gilbertsville, PA) a temperatura ambiente durante 2 horas con rotación a 600 rpm.

Para detectar la presencia de un producto de la escisión de la SNAP-25 mediante análisis de ELISA tipo sándwich ECL, se aspiró el amortiguador de bloqueo de las placas, se agregaron 25 µL de un lisado de células tratadas con BoNT/A a cada pocillo y las placas se incubaron a 4°C durante la noche. Los pocillos de la placa se lavaron tres veces aspirando el lisado celular y enjuagando cada pocillo tres veces con 200 µL de 1 x de PBS, 0.1% de TWEEN-20® (monolaurato de sorbitán de polioxietileno (20)). Luego de lavar, se agregaron 25 µl de 5 µg/mL de solución de anticuerpo de detección α-SNAP-25 con 2% de reactivo de bloqueo Amersham en 1 x de PBS, 0.1% de TWEEN-20® (monolaurato de sorbitán de polioxietileno (20)) a cada pocillo, la placa se selló e incubó a temperatura ambiente durante 1 hora con agitación. Luego de la incubación del anticuerpo de detección α-SNAP-25, los pocillos se lavaron

tres veces con 250 µL de 1 x de PBS, 0.1% de TWEEN-20® (monolaurato de sorbitán de polioxietileno (20)). Luego del lavado se agregaron 150 µL de 1 x de amortiguador Read (Meso Scale Discovery, Gaithersburg, MD) a cada pocillo y las placas se leyeron usando un lector de imágenes SECTOR™ Imager 6000 (Meso Scale Discovery, Gaithersburg, MD). Los datos sin procesar se transfirieron luego a SigmaPlot v. 10.0 y se usó un ajuste de logística de parámetro 4 para definir las curvas de respuesta a la dosis. No se usaron restricciones para la función de logística de parámetro 4 al graficar los datos. Los informes gráficos se generaron usando el siguiente análisis: R2 (coeficiente de correlación), a (máx. para el conjunto de datos), b (ladera) y X0 ± SE (valor de EC_{50} ± error estándar).

Estos resultados indicaron que, en promedio, las células que comprendían las líneas celulares clonales BB10 y H1 fueron más susceptibles de intoxicación por BoNT/A en comparación con las células que comprendían la línea celular SiMa original. Las células de una línea celular BB10 presentaron una EC_{50} para la actividad de la BoNT/A de 7 U/mL, las células de la línea celular H1 presentaron una EC_{50} para la actividad de la BoNT/A de 8 U/mL y las células de la línea celular SiMa original presentaron una EC_{50} para la actividad de la BoNT/A de 13 U/mL. Este método también se puede

realizar de forma múltiple como se describe en Ester Fernandez-Salas, et al., *Immuno-Based Botulinum Toxin Serotype A Activity Assays*, solicitud de patente estadounidense No. de serie: 12/403,531, que se incorpora en su totalidad a la presente mediante esta referencia.

Ejemplo VII

La transfección de ADN del receptor de BoNT/A en líneas celulares clonales sensibles mejora adicionalmente la sensibilidad de la línea celular clonal a la BoNT/A

El siguiente ejemplo ilustra cómo introducir una molécula de polinucleótido que codifica un receptor de BoNT/A en células de una línea celular clonal para mejorar adicionalmente la susceptibilidad de intoxicación por BoNT/A o mejorar la capacidad de absorción de BoNT/A.

Para introducir un receptor exógeno de BoNT/A en células que comprenden una línea celular clonal establecida, se transfectó una construcción de expresión en mamíferos que comprendía una molécula de polinucleótido de la SEQ ID NO: 139 que codificaba el FGFR3 de la SEQ ID NO: 25, en células de una línea celular clonal H1 mediante un método de lípidos catiónicos. Se colocó una densidad adecuada de células de una

línea celular clonal establecida (alrededor de 5 $x10^6$ células) en una placa de cultivo de tejido de 100 mm que contenía 5 mL de medio de cultivo completo y se cultivaron en un incubador a 37°C con 5% de dióxido de carbono hasta que las células alcanzaron una densidad apropiada para la transfección. Se preparó una solución de transfección de 3 mL agregando 1.5 mL de medio de suero reducido OPTI-MEM® que contenía 60 µL de LIPOFECTAMINE® 2000 (Invitrogen, Carlsbad, CA) incubado a temperatura ambiente durante 5 minutos hasta proporcionar 1.5 mL de medio de suero reducido OPTI-MEM® que contenía 24 µg de una construcción de expresión que codificaba el FGFR3 de la SEQ ID NO: 25. Esta mezcla de transfección se incubó a temperatura ambiente durante aproximadamente 30 minutos. El medio completo en las células se reemplazó con la solución de transfección de 3 mL y las células se incubaron en un incubador a 37°C con 5% de dióxido de carbono durante aproximadamente 8 horas. El medio de transfección se reemplazó con 3 mL de medio de cultivo completo recién preparado y las células se incubaron en un incubador a 37°C con dióxido de carbono durante aproximadamente 24 horas. El medio se reemplazó con 3 mL de medio de cultivo completo recién preparado que contenía aproximadamente 1 mM de G418 (Invitrogen, Carlsbad, CA) para la selección de células transfectadas. Las células se incubaron en un incubador a 37°C con 5% de dióxido de carbono

durante aproximadamente 1 semana, el medio anterior se reemplazó con medio de cultivo completo recién preparado que contenía 0.5 mM de G418 y las células se colocaron en una placa de 96 pocillos recubierta con colágeno IV a una densidad de placa de 0.5 células por pocillo. La viabilidad y el crecimiento celular se controlaron mediante examinación microscópica y, luego de alrededor de 3 semanas, aparecieron clones individuales en alrededor del 20% de los pocillos. Estos clones se cultivaron durante 2 semanas adicionales y luego se transfirieron a placas de 24 pocillos en duplicado recubiertas con colágeno IV, uno para mantener la línea celular clonal y el otro para evaluar la susceptibilidad a la BoNT/A.

Para determinar la susceptibilidad de las células que comprendían las líneas celulares clonales que sobreexpresaban un receptor de BoNT/A, se realizó un análisis de transferencia Western para determinar la sensibilidad y un ELISA de tipo sándwich ECL para determinar un valor de EC_{50}. Se evaluaron un total de ocho clones para las células H1 transfectadas de forma estable con el FGFR3.

Para preparar un lisado celular a partir del análisis de transferencia Western, las células de la línea celular clonal se colocaron en dos pocillos de placas de 96 pocillos

recubiertas con poli-D-lisina en medio libre de suero que contenía medio esencial mínimo, 2 mM de GLUTAMAX™ I con sales de Earle, 1 x de suplemento B27, 1 x de suplemento N2, 0.1 mM de aminoácidos no esenciales, 10 mM de HEPES y 25 µg/mL de GT1b (Alexis Biochemicals, Lausen, Suiza). Estas células se incubaron en un incubador a 37°C con 5% de dióxido de carbono hasta que las células se diferenciaron, según se evaluó con criterios morfológicos estándar y de rutina, como detención del crecimiento y extensión de neuritas (aproximadamente 3 días). Se aspiró el medio de las células diferenciadas de cada pocillo y se reemplazó con medio recién preparado que contenía 0 (sin tratar), 0.5 nM o 0.25 nM de un complejo de BoNT/A. Luego de un tratamiento de 6 h, las células se lavaron y se incubaron durante 18 h adicionales sin toxina. Luego de la incubación, las células se lavaron aspirando el medio de cultivo y enjuagando cada pocillo con 200 µL de 1 x de PBS. Para recolectar las células, se aspiró 1 x de PBS, las células se lisaron agregando 40 µL de 2 x de amortiguador de carga SDS y la placa se hizo girar para obtener un recubrimiento homogéneo del amortiguador de carga. El lisado se transfirió a una nueva placa de PCR de 96 pocillos (Axygen, Union City, CA) y la placa se calentó hasta 95°C durante 5 min para completar la lisis celular y desnaturalizar las proteínas.

Para detectar la presencia de sustrato de la SNAP-25 no escindida y productos de la SNAP-25 escindida, se analizó una alícuota de cada muestra recolectada mediante transferencia Western. En este análisis, se separó una alícuota de 12 µL de la muestra recolectada mediante electroforesis en gel de poliacrilamida MOPS usando geles de poliacrilamida precast Bis-Tris 12% NUPAGE® Novex (Invitrogen Inc., Carlsbad, CA) en condiciones de desnaturalización y reducción. Las proteínas separadas se transfirieron del gel a las membranas de nitrocelulosa (Bio-Rad Laboratories, Hercules, CA) mediante transferencia Western usando una cámara de transferencia "casetes +4 de transferencia y enfriador" (GE Healthcare, Piscataway, NJ). Las membranas se bloquearon mediante incubación a temperatura ambiente durante 1 h con agitación suave en una solución que contenía solución salina amortiguada con tris (TBS) (25 mM de ácido clorhídrico 2-amino-2-hidroximetil-1,3-propanodiol (Tris-HCl) (pH 7.4), 137 mM de cloruro de sodio, 2.7 mM de cloruro de potasio), 0.1% de TWEEN-20® (monolaureato de sorbitán polioxietileno (20)), 2% de albúmina de suero bovino (BSA) y 5% de leche en polvo descremada. Las membranas bloqueadas se incubaron a 4°C durante la noche en TBS, 0.1% de TWEEN-20® (monolaureato de sorbitán de polioxietileno (20)), 2% de BSA y 5% de leche en polvo descremada que contenía una dilución de 1:5,000 de antisuero policlonal de conejo α-SNAP-25 S9684 (Sigma, San

Luis, MO) como anticuerpo principal. Los anticuerpos policlonales de conejo α-SNAP-25 pueden detectar tanto el sustrato de la SNAP-25 no escindida como el producto de la escisión de la SNAP-25, lo que permitió la evaluación de la expresión general de la SNAP-25 en cada línea celular y el porcentaje de SNAP-25 escindida luego del tratamiento con BoNT/A como parámetro para evaluar la cantidad de absorción de BoNT/A. Las bandas sondadas con anticuerpo principal se lavaron tres veces durante 5 minutos cada vez en TBS, TWEEN-20® (monolaureato de sorbitán de polioxietileno (20)). Las membranas lavadas se incubaron a temperatura ambiente durante 2 horas en TBS, 0.1% de TWEEN-20® (monolaureato de sorbitán de polioxietileno (20)), 2% de BSA y 5% de leche en polvo descremada que contenía una dilución de 1:10,000 de inmunoglobulina G anti-conejo policlonal de cabra, anticuerpo de cadenas ligera y pesada (IgG, H+L) conjugado con peroxidasa de rábano picante (Invitrogen, Inc., Carlsbad, CA) como anticuerpo secundario. Las bandas sondadas con anticuerpo secundario se lavaron cinco veces durante 5 minutos cada vez en TBS y 0.1% de TWEEN-20® (monolaureato de sorbitán de polioxietileno (20)). La detección de señal de los productos de la SNAP-25 etiquetada se visualizó usando el sistema de detección de transferencia Western CL Plus™ (GE Healthcare, Amersham Biosciences, Piscataway, NJ), se tomaron imágenes de la membrana y se cuantificó el porcentaje de

productos de la SNAP-25 escindida con un software de análisis y generador de imágenes de modo variable Typhoon 9410 (GE Healthcare, Amersham Biosciences, Piscataway, NJ). La elección de tamaño de pixeles (100 a 200 pixeles) y los ajustes de voltaje de PMT (350 a 600, normalmente 400) dependió de la banda individual. Los volúmenes de las bandas que correspondían al producto de la SNAP-25 intacta y escindida se cuantificaron usando Image Quant TL y la cantidad total de SNAP-25 y el porcentaje de SNAP-25 escindida se calcularon con base en la intensidad de estas dos bandas de SNAP-25.

El clon H1 1.4 tuvo un porcentaje mayor de escisión de la SNAP-25 y niveles elevados de SNAP25 total y se seleccionó para análisis adicionales. El clon seleccionado se cultivó primero en una placa de 10 cm^2 y luego en matraces T175 para asegurarse de que se produjeran suficientes células para el ELISA de tipo sándwich ECL y las soluciones madre de congelación. Las soluciones madre congeladas se realizaron con 1 x 10^6 células y 1 mL de medio de congelamiento en cultivos celulares de recuperación (GIBCO-Invitrogen, medio de congelamiento #12648-010).

Para preparar un lisado celular para el ELISA de tipo sándwich ECL, se colocaron en placas aproximadamente 50,000

células de la línea celular clonal H1 y de la línea celular clonal H1 1.4 que sobreexpresaban el FGFR3 y se diferenciaron como se describió anteriormente. Se aspiró el medio de las células diferenciadas de cada pocillo y se reemplazó con medio recién preparado que contenía 0 (sin tratar), 0.27 pM, 0.82 pM, 2.47 pM, 7.4 pM, 22.2 pM, 66.6 pM y 200 pM de un complejo de BoNT/A. Luego de un tratamiento de 6 h, las células se lavaron y se incubaron durante la noche sin toxina. Luego de una incubación de 24 hrs., las células se lavaron aspirando el medio que contenía BoNT/A y enjuagando cada pocillo con 200 µL de 1 x de PBS. Las células lavadas se recolectaron lisándolas en amortiguador de lisis Tritón X-100 recién preparado (150 mM de NaCl, 20 mM de Tris-HCl (pH 7.5), 1 mM de EDTA, 1 mM de EGTA, 1% de Tritón X-100 más inhibidores de proteasa) a 4°C durante 30 minutos con agitación constante. Las células lisadas se centrifugaron a 4000 rpm durante 20 min a 4°C hasta proporcionar residuos de sedimentos.

La solución de anticuerpo de captura α-SNAP-25, la solución de anticuerpo de detección α-SNAP-25 y el soporte de fase sólida que comprendían el anticuerpo de captura específico para un producto escindido de la SNAP-25 se prepararon como se describió en el Ejemplo V. Para detectar la presencia de un producto de la SNAP-25 escindida mediante

ELISA de tipo sándwich ECL, se procesaron las placas, se recolectaron y analizaron los datos y se calculó la EC_{50} como se describió en el Ejemplo VI. La EC_{50} para las células H1 1.4 se estimó en alrededor de 1.7 pM, en comparación con una EC_{50} de alrededor de 8.7 pM para las células H1, lo que indicó que la línea celular H1 1.4 recientemente generada era alrededor de 5 veces más sensible que la línea celular H1 para la absorción de BoNT/A (promedio de dos experimentos independientes con resultados similares). La señal máxima para ambas líneas celulares fue idéntica, lo que indicó una eficacia similar hacia la escisión de la SNAP25. El aumento de sensibilidad fue especialmente prominente en concentraciones más bajas de BoNT/A, donde las células H1 1.4 fueron muchas veces más sensibles a la BoNT/A en comparación con células H1, lo que produjo una señal muy robusta sobre un fondo en una concentración de 0.27 pM. La sobreexpresión del FGFR3 se verificó en una transferencia Western usando anticuerpos α-FGFR3 sc-123 (Santa Cruz Biotechnologies, Santa Cruz, CA).

Ejemplo VIII

Desarrollo de anticuerpos monoclonales α-SNAP-25 que unen de forma selectiva un epítopo de la SNAP-25 con un extremo carboxiloterminal libre en el residuo de P_1 del enlace de

escísil del sitio de escisión de la BoNT/A

El siguiente ejemplo ilustra cómo realizar anticuerpos monoclonales α-SNAP-25 que se puedan unir de forma selectiva a un epítopo de la SNAP-25 con un extremo carboxiloterminal en el residuo de P_1 del enlace de escísil del sitio de escisión de la BoNT/A.

1. Generación de anticuerpos monoclonales α-SNAP-25

Se desarrollaron anticuerpos monoclonales α-SNAP-25 con mayor afinidad de unión a un producto de la escisión de la SNAP-25 y/o anticuerpos α-SNAP-25 con mayor especificidad de unión al producto de la escisión de la SNAP-25. Además, debido a que es preferible contar con una fuente permanente, estable y renovable de anticuerpos α-SNAP-25 para un ensayo aprobado por la FDA, se realizaron análisis de anticuerpos monoclonales aislados. Para desarrollar anticuerpos α-SNAP-25 monoclonales, se diseñó el péptido de 13 residuos $CDSNKTRIDEANQ_{COOH}$ (SEQ ID NO: 38) como un antígeno de la SNAP-25 con un extremo carboxiloterminal en el residuo P_1 del enlace de escísil del sitio de escisión de la BoNT/A. El péptido comprende una región enlazadora flexible y un residuo de cisteína N-terminal para la conjugación con KLH y los

aminoácidos 186-197 de la SNAP-25 humana (SEQ ID NO: 5) con una glutamina C-terminal carboxilada (SEQ ID NO: 38). La generación de anticuerpos monoclonales para secuencias peptídicas únicas bien seleccionadas proporciona un control sobre la especificidad de los epítopos, lo que permite la identificación de una subpoblación particular de proteínas entre un grupo de isoformas muy relacionadas. Las búsquedas de blastos revelaron que este péptido tenía una alta homología solamente con la SNAP-25 y casi ninguna reactividad cruzada posible con otras proteínas en células neuronales. La secuencia también se sometió a un cuidadoso escrutinio utilizando algoritmos informáticos para determinar índices de hidropatía, probabilidad de superficie proteica, regiones de flexibilidad y estructuras secundarias favorables, seguido de la orientación adecuada y la presentación de la secuencia peptídica elegida. El péptido se sintetizó y conjugó con hemocianina de lapa californiana (KLH) para aumentar la inmunogenicidad. Se inmunizaron seis ratones Balb/c con este péptido y, luego de tres inmunizaciones en alrededor de ocho semanas, los ratones se desangraron para su análisis. Se dejó que la sangre se coagulara mediante incubación a 4°C durante 60 minutos. La sangre coagulada se centrifugó a 10,000x g a 4°C durante 10 minutos para sedimentar los residuos celulares. La muestra de suero resultante se dispensó en alícuotas de 50 µL y se almacenó a -20°C hasta que se

necesitó.

Se utilizó una estrategia similar con base en otros antígenos de la SNAP-25 descritos en la presente memoria descriptiva para desarrollar anticuerpos monoclonales α-SNAP-25 que se pueden unir de forma selectiva a una SNAP-25 con un extremo carboxiloterminal en el residuo P_1 del enlace de escísil del sitio de escisión de la BoNT/A. Por ejemplo, el antígeno de la SNAP-25 de la SEQ ID NO: 45 se puede conjugar con KLH en lugar del antígeno de la SNAP-25 de la SEQ ID NO: 38. Como otro ejemplo, los aminoácidos 186-197 de la SNAP-25 humana del antígeno de la SNAP-25 de la SEQ ID NO: 38 se pueden reemplazar con la SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 147 o SEQ ID NO: 148.

2. Análisis para determinar la presencia de anticuerpos monoclonales α-SNAP-25

Para determinar la presencia de un anticuerpo monoclonal α-SNAP-25 que se pueda unir de forma selectiva a un antígeno de la SNAP-25 con un extremo carboxiloterminal en el residuo de P_1 del enlace de escísil del sitio de escisión de la BoNT/A, se realizaron ensayos de escisión basados en

células y ELISA comparativo usando el suero de ratón extraído. Para el ELISA comparativo, se construyeron dos proteínas de fusión: BIRA-HIS TAG®-SNAP-$25_{134-197}$ de la SEQ ID NO: 48 y el BIRA-HIS TAG®-SNAP-$25_{134-206}$ de la SEQ ID NO: 49. BIRA-HIS TAG®-SNAP-$25_{134-197}$ que comprendía un péptido BirA de 16 aminoácidos naturalmente biotinilado de la SEQ ID NO: 50, enlazado en el extremo aminoterminal a un péptido de la SNAP-25 que comprendía los aminoácidos 134-197 de la SEQ ID NO: 5. BIRA-HIS TAG®-SNAP-$25_{134-206}$ comprendía un péptido BirA de 16 aminoácidos naturalmente biotinilado de la SEQ ID NO: 50, enlazado en el extremo aminoterminal a un péptido de la SNAP-25 que comprendía los aminoácidos 134-206 de la SEQ ID NO: 5. Estos dos sustratos se suspendieron en 1 x de PBS a una concentración de 10 µg/mL de BIRA-HIS TAG®-SNAP-$25_{134-197}$ y el BIRA-HIS TAG®-SNAP-$25_{134-206}$. El BIRA-HIS TAG®-SNAP-$25_{134-197}$ y el BIRA-HIS TAG®-SNAP-$25_{134-206}$ se recubrieron en placas separadas agregando aproximadamente 100 µl de la solución de sustrato apropiada y las placas se incubaron a temperatura ambiente durante una hora. Las placas lavadas se incubaron a 37°C durante una hora en 0.5% de BSA en 1 x de TBS que contenía una dilución de 1:10 a 1:100 de un suero con anticuerpo derivado de uno a seis ratones inmunizados (Ratón 1, Ratón 2, Ratón 3, Ratón 4, Ratón 5 y Ratón 6). Las placas sondadas con anticuerpo principal se lavaron cuatro veces durante 5 minutos cada vez en 200 µl de TBS, 0.1% de TWEEN-20®

(monolaureato de sorbitán de polioxietileno (20)). Las placas lavadas se incubaron a 37°C durante 1 hora en 1 x de TBS que contenía una dilución de 1:10,000 de anticuerpo IgG anti-ratón policlonal de cabra conjugado con peroxidasa de rábano picante (Pierce Biotechnology, Rockford, IL) como anticuerpo secundario. Las placas sondadas con anticuerpo secundario se lavaron cuatro veces en 200 µl de TBS y 0.1% de TWEEN-20® (monolaureato de sorbitán de polioxietileno (20)). La detección cromogénica de los productos de la SNAP-25 etiquetada se visualizaron mediante detección cromogénica usando el kit de sustrato de TMB ImmunoPure (Pierce Biotechnology, Rockford, IL). La aparición de un color amarillo en las placas recubiertas con BIRA-HIS TAG®-SNAP-$25_{134-197}$, pero no en las placas recubiertas con BIRA-HIS TAG®-SNAP-$25_{134-206}$, indicó que el anticuerpo α-SNAP-25 reconocía preferentemente el producto de la escisión de la SNAP-25_{197}. El resultado indicó que de los seis ratones utilizados para la inmunización, tres ratones (Ratón 2, Ratón 3 y Ratón 4) tenían titulaciones más elevadas y mayor especificidad hacia un antígeno de la SNAP-25 con un extremo carboxiloterminal en el residuo de P_1 del enlace de escísil del sitio de escisión de la BoNT/A.

Estos resultados se confirmaron usando un ensayo de actividad de cadena ligera ELISA. Las placas de 96 pocillos

recubiertas con estreptavidina Reacti-Bind (Pierce Biotechnology, Rockford, IL) se prepararon agregando aproximadamente 100 µl de la siguiente solución de sustrato: Las filas A-C se recubrieron con 100 µl de BIRA-HIS TAG®-SNAP-$25_{134-197}$ en doce concentraciones diferentes, las filas D-H se recubrieron con 100 µl de BIRA-HIS TAG®-SNAP-$25_{134-206}$ a 10 µg/mL. Las placas se lavaron aspirando la solución de sustrato y enjuagando cada pocillo tres veces con 200 µL de TBS y 0.1% de TWEEN-20® (monolaurato de sorbitán de polioxietileno (20)). Las diluciones de BoNT/A se redujeron previamente a 37°C durante 20 minutos en amortiguador de incubación de BoNT/A (50 mM de HEPES, pH 7.4, 1% de suero bovino fetal, 10 µM de $ZnCl_2$, 10 mM de ditiotrietol) y se agregaron 100 µl de BoNT/A previamente reducida a las placas recubiertas con sustrato y se incubaron a 37°C durante 90 minutos. Las placas tratadas con BoNT/A se lavaron aspirando el amortiguador de incubación de BoNT/A y enjuagando cada placa tres veces con 200 µL de TBS y 0.1% de TWEEN-20® (monolaurato de sorbitán de polioxietileno (20)). Las placas lavadas se incubaron a 37°C durante una hora en 0.5% de BSA en 1 x de TBS que contenía una dilución de 1:10 a 1:100 del suero con anticuerpo que se analiza. Las placas sondadas con anticuerpo principal se lavaron cuatro veces durante 5 minutos cada vez en 200 µl de TBS, 0.1% de TWEEN-20® (monolaureato de sorbitán de polioxietileno (20)). Las placas

lavadas se incubaron a 37°C durante 1 hora en 1 x de TBS que contenía una dilución de 1:10,000 de anticuerpo IgG anti-ratón policlonal de cabra conjugado con peroxidasa de rábano picante (Pierce Biotechnology, Rockford, IL) como anticuerpo secundario. Las placas sondadas con anticuerpo secundario se lavaron cuatro veces en 200 µl de TBS y 0.1% de TWEEN-20® (monolaureato de sorbitán de polioxietileno (20)). La detección cromogénica de los productos de la SNAP-25 etiquetada se visualizó mediante detección cromogénica usando el kit de sustrato de TMB ImmunoPure (Pierce Biotechnology, Rockford, IL). Se detectó la aparición de un color amarillo, que tenía correlación con la presencia del producto de la escisión de la $SNAP\text{-}25_{197}$ en muestras tratadas con BoNT/A, pero no en los controles sin tratar, usando suero con anticuerpos derivado de los seis ratones inmunizados (Ratón 1, Ratón 2, Ratón 3, Ratón 4, Ratón 5 y Ratón 6). Por consiguiente, el análisis de ELISA comparativo indicó que de los ratones utilizados para la inmunización, tres ratones (Ratón 2, Ratón 3 y Ratón 4) tenían titulaciones más elevadas y mayor especificidad hacia un antígeno de la SNAP-25 con un extremo carboxiloterminal en el residuo de P_1 del enlace de escísil del sitio de escisión de la BoNT/A.

Para el ensayo de escisión basado en células, se colocaron densidades adecuadas de células PC12 en placas de

cultivo de tejido de 60 mm^2 que contenían 3 mL de un medio de suero apropiado (Tabla 1). Las células se cultivaron en un incubador a 37°C con 5% de dióxido de carbono hasta que las células alcanzaron la densidad apropiada. Se preparó una solución de transfección de 500 µL agregando 250 µL de medio de suero reducido OPTI-MEM® con 15 µL de LIPOFECTAINE® 2000 (Invitrogen Inc., Carlsbad, CA) y se incubó a temperatura ambiente durante 5 minutos hasta proporcionar 250 µL de medio de suero reducido OPTI-MEM® que contenía 10 µg de una construcción de expresión pQBI-25/GFP-BoNT/A-LC (SEQ ID NO: 51). La construcción de expresión pQBI-25/GFP-BoNT/A-LC comprende un vector de expresión pQBI-25 (Qbiogene Inc., Carlsbad, CA), cuyos elementos promotores están unidos de forma funcional a un polinucleótido que codifica la cadena ligera de GFP-BoNT/A de la SEQ ID NO: 52. Esta mezcla de transfección se incubó a temperatura ambiente durante aproximadamente 20 minutos. El medio se reemplazó con medio no complementado recién preparado y se agregó la solución de transfección de 500 µL a las células. Las células luego se incubaron en un incubador a 37°C con 5% de dióxido de carbono durante aproximadamente 6 a 18 horas. Las células se lavaron y recolectaron como se describió en el Ejemplo II. Para detectar la presencia del producto de la $SNAP\text{-}25_{197}$ escindida, se analizó una alícuota de cada muestra recolectada mediante transferencia Western como se describió en el Ejemplo II,

salvo porque el anticuerpo principal utilizado fue una dilución de 1:1,000 del suero con anticuerpo y el anticuerpo secundario fue un 1:20,000 de peroxidasa de rábano picante con α-IgG de ratón (Pierce Biotechnology, Rockford, IL). Se detectó una sola banda correspondiente al producto de la escisión de la $SNAP\text{-}25_{197}$ en las muestras tratadas con BoNT/A, pero no en los controles sin tratar, usando suero con anticuerpo derivado de tres ratones (Ratón 2, Ratón 3 y Ratón 4). Por consiguiente, el análisis de escisión basado en células indicó que de los ratones utilizados para la inmunización, tres ratones (Ratón 2, Ratón 3 y Ratón 4) tenían titulaciones más elevadas y mayor especificidad hacia un antígeno de la SNAP-25 con un extremo carboxiloterminal en el residuo de P_1 del enlace de escísil del sitio de escisión de la BoNT/A.

3. Producción de hibridomas

Para realizar hibridomas que produzcan anticuerpos monoclonales α-SNAP-25 que se puedan unir de forma selectiva a un antígeno de la SNAP-25 con un extremo carboxiloterminal en el residuo de P_1 de un enlace de escísil del sitio de escisión de la BoNT/A, se extrajo el bazo del Ratón 2 tres días después de una inmunización final "de refuerzo" y las células del bazo se fusionaron con células de mieloma P3-X63

Ag8.653 usando protocolos de hibridoma estándar. Estas células se colocaron en cinco placas de 96 pocillos y los híbridos se seleccionaron usando medio HAT. Dentro de los 8-14 días posteriores a la fusión, se realizó el primer análisis de los aproximadamente 480 clones progenitores usando un ELISA comparativo con los péptidos BIRA-HIS TAG®-SNAP-$25_{134-197}$ y BIRA-HIS TAG®-SNAP-$25_{134-206}$ recubiertos en dos placas separadas. El ELISA comparativo proporcionó un método de análisis rápido para identificar hibridomas que producen anticuerpos específicos para la SNAP-25_{197} escindida. Los 18 clones superiores se sometieron a un análisis adicional usando el ensayo de escisión basado en células descrito anteriormente e inmunotinción de las células transfectadas con LC/A. (Tabla 18)

Tabla 18. Análisis de sobrenadantes que contenían anticuerpo monoclonal α-SNAP-25

Clon	ELISA comparativo				Ensayo basado en células	
	OD SNAP-25_{197}	OD SNAP-25_{206}	Proporción$_{197/206}$	Proporción$_{206/197}$	SNAP-25_{197}	SNAP-25_{206}
1D3	1.805	0.225	8.02	0.13	+++	–
1F12	0.365	0.093	3.92	0.25	–	–
1G10	0.590	0.137	4.31	0.23	++	–

1H1	0.335	0.121	2.77	0.36	–	–
1H8	0.310	0.302	1.03	0.97	+	–
2C9	0.139	0.274	0.51	1.97	–	–
2E2	0.892	0.036	24.78	0.04	++	–
2E4	0.228	0.069	3.30	0.30	+	–
2F11	1.095	1.781	0.61	1.63	–	–
3C1	1.268	0.053	23.92	0.04	++	–
3C3	0.809	0.052	15.56	0.06	++	–
3E1	0.086	0.155	0.55	1.80	0	–
3E8	2.048	0.053	38.64	0.03	+++	–
3G2	0.053	0.158	0.34	2.98	–	–
4D1	0.106	0.218	0.49	2.06	–	–
4G6	0.061	0.159	0.38	2.61	–	–
5A5	0.251	0.106	2.37	0.42	+	–
5F11	0.243	0.061	3.98	0.25	–	–

Los clones 1D3, 1G10, 2E2, 3C1, 3C3 y 3E8 se clonaron adicionalmente limitando la dilución debido a que el medio

acondicionado producido mediante estos clones comprendía anticuerpos α-SNAP-25 con una especificidad de unión preferencial con una proporción$_{197/206}$ de al menos 4:1 para el producto de la escisión de la SNAP-25$_{197}$ con relación al sustrato no escindido de la SNAP-25$_{206}$ y se detectó el producto de la escisión de la SNAP-25$_{197}$ usando el ensayo de escisión basado en células y la inmunotinción de las células PC12 transfectadas con GFP-LC/A. De forma similar, los clones 2C9, 2F11, 3G2, 4D1 y 4G6 se clonaron adicionalmente limitando la dilución debido a que el medio acondicionado producido por esos clones comprendía anticuerpos α-SNAP-25 con una especificidad de unión preferencial con una proporción$_{206/197}$ de al menos 1.5:1 para el sustrato no escindido de la SNAP-25$_{206}$ con relación al producto de la escisión de la SNAP-25$_{197}$ y se detectó el sustrato no escindido de la SNAP-25$_{206}$ usando el ensayo de escisión basado en células. Estos clones derivados de células individuales se analizaron nuevamente usando un ELISA comparativo, escisión basada en células e inmunotinción para confirmar su afinidad y especificidad y los anticuerpos se separaron en isotipos usando procedimientos estándar. Se produjeron ascitis a partir de los clones 1D3B8 (IgM.k), 1G10A12 (IgG3.k), 2C9B10 (IgG3.k), 2E2A6 (IgG3.k), 2F11B6 (IgM.k), 3C1A5 (IgG2a.k) y 3C3E2 (IgG2a.k). El clon 3E8 dejó de producir anticuerpos durante el proceso de clonación y no se pudo evaluar

adicionalmente.

4. Evaluación de la especificidad de unión de los anticuerpos monoclonales α-SNAP-25

Para evaluar la especificidad de unión de un anticuerpo monoclonal α-SNAP-25 que se puede unir de forma selectiva a un antígeno de la SNAP-25 con un extremo carboxiloterminal en el residuo de P_1 del enlace de escísil del sitio de escisión de la BoNT/A se utilizaron ascitis de los clones 1D3B8, 1G10A12, 2C9B10, 2E2A6, 2F11B6, 3C1A5 y 3C3E2 para detectar el producto de la escisión de la SNAP-25 usando el ensayo de actividad basado en células, inmunocitoquímica e inmunoprecipitación.

Para el ensayo de actividad basado en células, se determinó la especificidad de unión analizando la capacidad de los ascitis que contenían anticuerpos de la α-SNAP-25 para detectar el sustrato de la $SNAP\text{-}25_{206}$ no escindida y el producto de la $SNAP\text{-}25_{197}$ escindida mediante análisis de transferencia Western. Se colocó una densidad adecuada de células PC12 en placas de cultivo de tejido de 60 mm^2 que contenían 3 mL de un medio de suero apropiado, se cultivó en un incubador a 37°C con 5% de dióxido de carbono hasta que se alcanzó una densidad celular apropiada y se transfectó con

una solución de transfección sin la construcción de expresión pQBI-25/GFP-BoNT/A-LC (células sin transfectar) o una solución de transfección con la construcción de expresión pQBI-25/GFP-BoNT/A-LC (células transfectadas), como se describió anteriormente. Las células se lavaron y recolectaron como se describió en el Ejemplo I. Para detectar la presencia del sustrato de la SNAP-25_{206} no escindida y el producto de la SNAP-25_{197} escindida, se analizó una alícuota de cada muestra recolectada mediante transferencia Western como se describió en el Ejemplo I, salvo porque el anticuerpo principal utilizado fue una dilución de 1:100 de la ascitis que contenía anticuerpo monoclonal α-SNAP-25 y el anticuerpo secundario utilizado fue un 1:20,000 de IgG α-ratón conjugada con peroxidasa de rábano picante (Pierce Biotechnology, Rockford, IL). Además, se analizaron tres anticuerpos monoclonales α-SNAP-25 de ratón comercialmente disponibles. Se usó el SMI-81 (Sternberger Monoclonals Inc., Lutherville, MD), un anticuerpo α-SNAP-25 que el fabricante indica que detecta tanto el sustrato de la SNAP-25_{206} no escindida como el producto se la SNAP-25_{197} escindida, en una dilución de 15,000 de acuerdo con las recomendaciones del fabricante. Se usó el MC-6050 (Research & Diagnostic Antibodies, Las Vegas, NV), un anticuerpo α-SNAP-25 que el fabricante indica que detecta tanto el sustrato de la SNAP-25_{206} no escindida como el producto se la SNAP-25_{197} escindida, en una dilución de

1:100 de acuerdo con las recomendaciones del fabricante. Se usó el MC-6053 (Research & Diagnostic Antibodies, Las Vegas, NV), un anticuerpo α-SNAP-25 que el fabricante indica que detecta solamente el producto de la SNAP-25_{197} escindida, en una dilución de 1:100 de acuerdo con las recomendaciones del fabricante.

La Tabla 19 indica las ascitis con anticuerpo α-SNAP-25 que detectaron solamente el producto de la escisión de la SNAP-25_{197}. El ensayo de escisión basado en células indicó que las ascitis producidas a partir de los clones 1D3B8, 2C9B10, 2E2A6, 3C1A5 y 3C3E2 sintetizan un anticuerpo monoclonal α-SNAP-25 con alta especificidad de unión al producto de la escisión de la SNAP-25_{197}, lo que permite el reconocimiento selectivo de este producto de escisión con relación al sustrato no escindido de la SNAP-25_{206}. El anticuerpo SMI-81 comercial detectó el sustrato no escindido de la SNAP-25_{206}, pero solo reconoció apenas el producto de la escisión de la SNAP-25_{197} (Tabla 19). De manera sorpresiva, el anticuerpo comercial MC-6050 detectó solamente el sustrato no escindido de la SNAP-25_{206} y no pudo reconocer el producto de la escisión de la SNAP-25_{197} (Tabla 19). De manera aun más sorprendente, el anticuerpo comercial MC-6050 solamente detectó el sustrato no escindido de la SNAP-25_{206} y no pudo reconocer el producto de la escisión de la SNAP-25_{197}, incluso

a pesar de que el fabricante afirma públicamente que este anticuerpo detecta de forma selectiva el producto de la escisión de la SNAP-25_{197} (Tabla 19). Por consiguiente, este análisis indica que mientras que 1D3B8, 2C9B10, 2E2A6, 3C1A5 y 3C3E2 presentan una selectividad adecuada para el producto de la escisión de la SNAP-25_{197}, no sucede lo mismo con 1G10A12 y 2F11B6. Además, los anticuerpos comerciales SMI-81, MC-6050 y MC-6053 no son adecuados para los métodos basados en inmunoensayos descritos en la presente solicitud, debido a que no pudieron detectar de forma selectiva el producto de la escisión de la SNAP-25_{197}.

Para el análisis de inmunocitoquímica, se determinó la especificidad de unión analizando la capacidad de las ascitis que contenían el anticuerpo α-SNAP-25 de detectar el sustrato de la SNAP-25_{206} no escindida y el producto de la SNAP-25_{197} escindida mediante inmunotinción. *Véase, por ej.*, Ester Fernandez-Salas et al., *Plasma Membrane Localization Signals in the Light Chain of Botulinum Neurotoxin*, Proc. Natl. Acad. Sci., E.U.A. 101(9): 3208-3213 (2004). Se colocó en placas una densidad adecuada de células PC12, se cultivó y se transfectó con una solución de transfección sin la construcción de expresión pQBI-25/GFP-BoNT/A-LC (células sin transfectar) o una solución de transfección que contenía la construcción de expresión pQBI-25/GFP-BoNT/A-LC (células

transfectadas), como se describió anteriormente. Las células se lavaron en 1 x de PBS y se fijaron en 5 mL de PAF a temperatura ambiente durante 30 minutos. Las células fijadas se lavaron en solución salina amortiguada con fosfato, se incubaron en 5 mL de 0.5% de Triton® X-100 (éter octilfenólico de polietilenglicol) en 1 x de PBS, se lavaron en 1 x de PBS y se permeabilizaron en 5 mL de metanol a -20°C durante seis minutos. Las células permeabilizadas se bloquearon en 5 mL de 100 mM de glicina a temperatura ambiente durante 30 minutos, se lavaron en 1 x de PBS y se bloquearon en 5 mL de 0.5% de BSA en 1 x de PBS a temperatura ambiente durante 30 minutos. Las células bloqueadas se lavaron en 1 x de PBS y se incubaron a temperatura ambiente durante dos horas en 0.5% de BSA en 1 x de PBS que contenía una dilución de 1:10 de una ascitis de una línea celular de hibridoma clonal que se analizaba. Las células sondadas con anticuerpo principal se lavaron tres veces durante 5 minutos cada vez en 1 x de PBS. Las células lavadas se incubaron a temperatura ambiente durante 2 horas en 1 x de PBS que contenía una dilución de 1:200 de inmunoglobulina G anti-ratón policlonal de cabra, anticuerpo de cadenas ligera y pesada (IgG, H+L) conjugado con ALEXA® FLUOR 568 (Invitrogen Inc., Carlsbad, CA) como anticuerpo secundario. Las células sondadas con anticuerpo secundario se lavaron tres veces durante 5 minutos cada vez en 1 x de PBS. Las células lavadas

se prepararon para la examinación microscópica colocándolas en medio de montaje VECTASHIELD® (Vector Laboratories, Burlingame, CA) y se cubrieron con un cubreobjetos. Las imágenes de la detección de señal se obtuvieron con un microscopio confocal Leica usando los ajustes de láser apropiados. La Tabla 19 indica las ascitis que contenían anticuerpo α-SNAP-25 que detectaron específicamente el producto de la escisión de la $SNAP\text{-}25_{197}$. El análisis de inmunocitoquímica indicó que las ascitis producidas a partir de los clones 1D3B8, 2C9B10, 2E2A6, 3C1A5 y 3C3E2 sintetizan un anticuerpo monoclonal α-SNAP-25 con alta especificidad de unión al producto de la escisión de la $SNAP\text{-}25_{197}$, lo que permite el reconocimiento preferencial de este producto de escisión con relación al sustrato no escindido de la $SNAP\text{-}25_{206}$.

Para el análisis de inmunoprecipitación, se determinó la especificidad de unión analizando la capacidad de anticuerpos monoclonales α-SNAP-25 purificados de la Proteína A (Proteína A HiTrap™ Columnas HP, GE Healthcare, Amersham, Piscataway, NJ) de precipitar el sustrato de la $SNAP\text{-}25_{206}$ no escindida y el producto de la $SNAP\text{-}25_{197}$ escindida. *Véase, por ej.*, Capítulo 8 *Storing and Purifying Antibodies*, pp. 309-311, Harlow & Lane, *supra*, 1998a. Se colocó en placas una densidad adecuada de células PC12, se cultivó y se transfectó

con una solución de transfección que contenía una construcción de expresión pQBI-25/GFP (células de referencia; SEQ ID NO: 53) o una solución de transfección que contenía la construcción de expresión pQBI-25/GFP-BoNT/A-LC (células experimentales), como se describió anteriormente. La construcción de expresión pQBI-25/GFP comprende un vector de expresión cuyos elementos promotores están enlazados funcionalmente a un polinucleótido que codifica la GFP de la SEQ ID NO: 54. Luego de incubación durante la noche, las células se lavaron aspirando el medio de cultivo y enjuagando cada pocillo con 200 µL de 1 x de PBS. Para recolectar las células, se aspiró el PBS, las células se lisaron agregando un amortiguador de lisis de inmunoprecipitación con 50 mM de HEPES, 150 mM de NaCl, 1.5 mM de $MgCl_2$, 1 mM de EGDT, 10% de glicerol, 1% de Triton® X-100 (éter octilfenólico de polietilenglicol) y 1 x de un cóctel inhibidor de proteasa COMPLETE™ (Roche Applied Biosciences, Indianápolis, IN) y se incubaron a 4°C durante una hora. Las células lisadas se centrifugaron a 3,000 x g a 4°C durante 10 minutos para retirar los residuos celulares y el sobrenadante se transfirió a un tubo limpio y se diluyó hasta proporcionar una concentración proteica de aproximadamente 1 mg/mL. Se agregaron aproximadamente 5 µg de anticuerpo monoclonal purificado a 0.5 mL de sobrenadante diluido y se incubaron a 4°C durante dos horas. Luego de la incubación del anticuerpo

principal, se agregaron aproximadamente 50 µl de Proteína G inmovilizada (Pierce Biotechnology, Rockford, IL) al sobrenadante diluido y se incubaron a 4°C durante una hora. El sobrenadante incubado se lavó tres veces durante 30 minutos cada vez agregando 0.5 mL de amortiguador de lisis de inmunoprecipitación, con centrifugación a 300 x g a 4°C durante un minuto para sedimentar la Proteína G inmovilizada y se decantó el sobrenadante. Luego del lavado, el sedimento se volvió a suspender en 30 µL de 1 x de amortiguador de carga SDS y la muestra se calentó hasta 95°C durante 5 minutos. Para detectar la presencia del sustrato de la SNAP-25_{206} no escindida y el producto de la SNAP-25_{197} escindida, se analizó una alícuota de cada muestra recolectada mediante transferencia Western, como se describió en el Ejemplo I, salvo porque el anticuerpo principal utilizado fue una dilución de 1:1,000 del suero de anticuerpo policlonal α-SNAP-25 (véase el Ejemplo IV) y el anticuerpo secundario utilizado fue un 1:20,000 de peroxidasa de rábano picante con α-IgG de conejo (Pierce Biotechnology, Rockford, IL). La Tabla 19 indica las ascitis que contenían anticuerpo α-SNAP-25 que disminuyeron específicamente el producto de la escisión de la SNAP-25_{197} mediante análisis de inmunoprecipitación. El análisis de inmunoprecipitación indicó que las ascitis producidas a partir de los clones 2E2A6 y 3C1A5 sintetizan un anticuerpo monoclonal α-SNAP-25

con alta especificidad de unión al producto de la escisión de la SNAP-25_{197}, lo que permite el reconocimiento preferencial de este producto de escisión con relación al sustrato no escindido de la SNAP-25_{206}.

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Tabla 19. Análisis de ascitis de clones que contienen anticuerpo monoclonal α-SNAP-25

Clon	Ensayo basado en células		Inmunocitoquímica		Inmunoprecipitación	
	SNAP-25_{197}	SNAP-25_{206}	SNAP-25_{197}	SNAP-25_{206}	SNAP-25_{197}	SNAP-25_{206}
1D3B8	++	–	++	-	Sin analizar	Sin analizar
1G10A12	++	++	Sin analizar	Sin analizar	Sin analizar	Sin analizar
2C9B10	++	–	++	-	Sin analizar	Sin analizar
2E2A6	++	–	++	-	++	–
2F11B6	+	+	+	+	Sin analizar	Sin analizar
3C1A5	++	–	++	–	++	–
3C3E2	+	–	Sin analizar	Sin analizar	Sin analizar	Sin analizar
MC-6050	–	+	Sin analizar	Sin analizar	Sin analizar	Sin analizar
MC-6053	–	+	Sin analizar	Sin analizar	Sin analizar	Sin analizar
SMI-81	-/+	++	Sin analizar	Sin analizar	Sin analizar	Sin analizar

5. Evaluación de la afinidad de unión de los anticuerpos monoclonales α-SNAP-25

Para determinar la afinidad de unión de un anticuerpo monoclonal α-SNAP-25 que muestra alta afinidad de unión al producto de la escisión de la $SNAP\text{-}25_{197}$ o el sustrato no escindido de la $SNAP\text{-}25_{206}$, se realizaron ensayos de afinidad de unión en un instrumento BIACORE 3000 usando chips sensores de carboximetil dextrán (CM5) (BIAcore, Inc., Piscataway, NJ). Las ejecuciones se realizaron a 25°C con amortiguador HBS-EP con 10 mM de HEPES (pH 7.4), 150 mM de cloruro de sodio, 3 mM de EDTA, 0.005% (v/v) de tensioactivo P20 a una velocidad de flujo de 10 µl/min. Los péptidos de la SNAP-25 que comprendían los aminoácidos 134-197 de la SEQ ID NO: 5 ($SNAP\text{-}25_{134\text{-}197}$) o los aminoácidos 134-206 de la SEQ ID NO: 5 ($SNAP\text{-}25_{134\text{-}206}$) se unieron de forma covalente a la superficie de los chips sensores CM5 usando acoplamiento estándar de amina. Brevemente, los chips CM5 se activaron mediante una inyección de 7 minutos de una mezcla de 1-etil-3-(3-dimetilaminopropil) carbodiimida 0.2 M y N-hidroxisuccinimida 0.05 M, luego los péptidos de la SNAP-25 se inyectaron en 10 mM de acetato de sodio (pH 4.0) durante 20 min a una velocidad de flujo de 10 µL/min y los ésteres de succinimida sin reaccionar se bloquearon mediante una inyección de 7 min de clorhidrato de etanolamina 1 M, pH 8.5. La cantidad

inmovilizada de SNAP-$25_{134-197}$ o SNAP-$25_{134-206}$ en los chips se reflejó mediante un aumento de 100-150 en las unidades de respuesta (alrededor de 0.10-0.15 ng/mm^2). Las muestras de anticuerpo que comprendían ascitis o anticuerpos monoclonales purificados producidos a partir de los clones 1D3B8, 2C9B10, 2E2A6, 3C1A5 y 3C3E2, así como los anticuerpos α-SNAP-25 comercialmente disponibles, se pasaron por una superficie de chips CM5, permitiendo un tiempo de asociación de 10 min y un tiempo de disociación de 20 min. Las superficies se regeneraron entre las ejecuciones mediante una inyección de 1 minuto de 10 mM de glicina-HCl (pH 2.5) a una velocidad de flujo de 15 µL/min. Las curvas del sensograma se ajustaron a un modelo de unión cinética 1:1 con el software BIAevaluation 3.0.

Los resultados indican que tanto 2E2A6 como 3C1A5 fueron altamente específicos para el producto de la SNAP-25_{197} escindida en comparación con el sustrato no escindido de la SNAP-25 (Tabla 20). Al compararlo con las afinidades de unión de MC-6050 y MC-6053, 1D3B6 tuvo una constante de disociación de equilibrio aproximadamente 10 veces más elevada para el producto de la escisión de la SNAP-25 en relación con estos anticuerpos comerciales (Tabla 20). De manera interesante, 2E2A6 tuvo una constante de disociación de equilibrio solo ligeramente menor para el producto de la escisión de la SNAP-

25 con relación a estos anticuerpos comerciales (0.405 nM en comparación con 0.497 y 0.508) (Tabla 20). Como ninguno de estos anticuerpos α-SNAP-25 comerciales reconoció de forma selectiva el producto de la escisión de la SNAP-25 (Tabla 19), una constante de disociación de equilibrio menor a alrededor de 0.5 nM parece, en parte, crítica para lograr dicha selectividad. De manera similar, al compararlo con las afinidades de unión de MC-6050 y MC-6053, 2E2A6 tuvo una constante de disociación/velocidad de disociación al menos una vez más lenta (6.74×10^{-5} en comparación con 8.82×10^{-4} s^{-1} y 1.18×10^{-3} s^{-1}) (Tabla 20). Esto sugiere adicionalmente que una constante de disociación/velocidad de disociación menor a alrededor de 8.82×10^{-4} parece, en parte, crítica para lograr la unión selectiva al producto de la escisión de la SNAP-25. Este resultado es coherente con 1D3B8, que tuvo una constante de disociación/velocidad de disociación de 5.78×10^{-5} s^{-1} (Tabla 20).

Tabla 20. Análisis de afinidad de unión de los anticuerpos monoclonales α-SNAP-25

Parámetro SPR	1D3B8		2E2A6	
	$SNAP\text{-}25_{197}$	$SNAP\text{-}25_{206}$[a]	$SNAP\text{-}25_{197}$	$SNAP\text{-}25_{206}$[b]

Ka (M^{-1} s^{-1})	1.06×10^{6}	—	1.70×10^{6} (1.66×10^{5})	— (—)
Kd (s^{-1})	5.78×10^{-5}	—	1.53×10^{-4} (6.74×10^{-5})	— (—)
KD (nM)	0.050	—	0.090 (0.405)	— (—)
Parámetro SPR	3C1A5		2C9B10	
	$SNAP\text{-}25_{197}$	$SNAP\text{-}25_{206}$[c]	$SNAP\text{-}25_{197}$	$SNAP\text{-}25_{206}$[d]
Ka (M^{-1} s^{-1})	2.17×10^{5}	—	1.15×10^{4}	—
Kd (s^{-1})	2.88×10^{-4}	—	3.11×10^{-4}	—
KD (nM)	1.33	—	27.1	—
Parámetro SPR	MC-6050		MC-6053	
	$SNAP\text{-}25_{197}$	$SNAP\text{-}25_{206}$	$SNAP\text{-}25_{197}$	$SNAP\text{-}25_{206}$
Ka (M^{-1} s^{-1})	1.78×10^{6}	3.06×10^{2}	2.32×10^{6}	1.06×10^{2}
Kd (s^{-1})	8.82×10^{-4}	6.07×10^{-3}	1.18×10^{-3}	2.56×10^{-5}
KD (nM)	0.497	19,800	0.508	240

[a] No se observó unión al pasar hasta 125 nM del anticuerpo monoclonal α-SNAP-25 1D3B8 por la superficie del chip sensor CM5 luego de un tiempo de asociación de 10 minutos.

[b] No se observó unión al pasar hasta 10 µM del anticuerpo monoclonal α-SNAP-25 2E2A6 por la superficie del chip sensor CM5 luego de un tiempo de asociación de 10 minutos.

[c] No se observó unión al pasar hasta 100 nM del anticuerpo monoclonal α-SNAP-25 3C1A5 por la superficie del chip sensor CM5 luego de un tiempo de asociación de 10 minutos.

[d] No se observó unión al pasar hasta 100 nM del anticuerpo monoclonal α-SNAP-25 2C9B10 por la superficie del chip sensor CM5 luego de un tiempo de asociación de 10 minutos.

Para comparar los seis anticuerpos diferentes, se normalizó la velocidad de asociación (ka) y la velocidad de disociación (kd) de cada uno, usando un programa del software BIA evaluation 4.1. Para la comparación de las velocidades de asociación, los datos primero se cortaron individualmente eliminando la parte de regeneración y las adiciones de inyecciones y luego se normalizaron hasta una escala de 0 a 100. Para la comparación de la velocidad de disociación, los datos se normalizaron hasta el punto superior/detención de la inyección. Este análisis mostró que 2C9B10 tenía un velocidad de asociación mucho más lenta que los otros anticuerpos (FIG. 3A) y que MC-6053 tenía una velocidad de disociación mucho más rápida que los otros anticuerpos (FIG. 3B). La velocidad de disociación rápida del MC-6053 indica que este anticuerpo

no tendrá una buena actuación en los métodos descritos en la presente memoria descriptiva, debido a que tendría dificultad para mantenerse unido al antígeno del sustrato durante las etapas de lavado.

6. Determinación de secuencias del epítopo de los anticuerpos monoclonales α-SNAP-25 aislados

Para determinar el epítopo de un anticuerpo monoclonal α-SNAP-25 aislado que se puede unir de forma selectiva a un antígeno de la SNAP-25 con un extremo carboxiloterminal en el residuo de P_1 del enlace de escísil del sitio de escisión de la BoNT/A, se determinaron las secuencias de la molécula de polinucleótido que codificaba las cadenas ligera variable (V_L) y pesada variable (V_H) del anticuerpo monoclonal α-SNAP-25 producido por los hibridomas 1D3B8, 2C9B10, 2E2A6, 3C1A5 y 3C3E2. Se extrajo el ARNm de cada hibridoma, se purificó usando protocolos estándar y se transcribió de forma inversa en ADNc usando un cebador antisentido oligo dT o un cebador anti-sentido específico para el gen (CH y kappa CL de IgG1 murina). Se usaron cebadores de dominio constante humano y murino específicos para amplificar el ADNc mediante PCR luego de la producción de ADNc para determinar el isotipo del anticuerpo. Los cebadores V_H y V_L redundantes se usaron para amplificar los dominios variables del ADNc. Para 5'RACE, se

agregó un residuo de dCTP homopolimérico al extremo 3' del ADNc. Las cadenas pesada y ligera luego se amplificaron con un cebador de sentido oligo dG y un cebador antisentido específico para el gen (CH/KC). Los productos de la PCR incluyeron la secuencia del péptido de señal, dominios variables y dominios constantes hasta el cebador antisentido. Los productos de la PCR se purificaron en gel para retirar fragmentos pequeños y se clonaron en un vector romo o TA para determinar las secuencias. Se determinaron las secuencias de cinco clones independientes para cada cadena y se determinaron los alineamientos de las cadenas V_H y VL y las secuencias de consenso. Los métodos utilizados para determinar las secuencias de aminoácidos de V_H y V_L se describen, por ej., en Roger A. Sabbadini, et al., *Novel Bioactive Lipid Derivatives and Methods of Making and Using Same*, publicación de patente estadounidense 2007/0281320 y Peter Amersdorfer, et al., *Molecular Characterization of Murine Humoral Immune Response to Botulinum Neurotoxin Type A Binding Domain as Assessed by Using Phage Antibody Libraries*, 65(9) Infect. Immun. 3743-3752, cada uno de los cuales se incorpora en su totalidad a la presente mediante esta referencia. Además, se encuentran disponibles servicios comerciales para determinar las secuencias de las cadenas pesada variable (V_H) y ligera variable (V_L) de un anticuerpo e identificar las regiones de CDR, véase, por ej., Fusion

Antibodies Ltd., Irlanda del Norte.

Las secuencias de polinucleótidos que comprendían las cadenas V_H y V_L del anticuerpo monoclonal α-SNAP-25 producido por los hibridomas descritos en la presente memoria descriptiva son como se indica a continuación: 1D3B8 V_H (SEQ ID NO: 71), 2C9B10 V_H (SEQ ID NO: 73), 2E2A6 V_H (SEQ ID NO: 75), 3C1A5 V_H (SEQ ID NO: 77), 3C3E2 V_H variante 1 (SEQ ID NO: 79), 3C3E2 V_H variante 2 (SEQ ID NO: 81), 3C3E2 V_H variante 3 (SEQ ID NO: 149), 1D3B8 V_L (SEQ ID NO: 83), 2C9B10 V_L (SEQ ID NO: 85), 2E2A6 V_L (SEQ ID NO: 87), 3C1A5 V_L (SEQ ID NO: 89) y 3C3E2 V_L (SEQ ID NO: 91). La secuencia de aminoácidos que comprendía las cadenas V_H y V_L del anticuerpo monoclonal α-SNAP-25 producido por los hibridomas descritos en la presente memoria descriptiva son como se indica a continuación: 1D3B8 V_H (SEQ ID NO: 72), 2C9B10 V_H (SEQ ID NO: 74), 2E2A6 V_H (SEQ ID NO: 76), 3C1A5 V_H (SEQ ID NO: 78), 3C3E2 V_H variante 1 (SEQ ID NO: 80), 3C3E2 V_H variante 2 (SEQ ID NO: 82); 3C3E2 V_H variante 2 (SEQ ID NO: 150), 1D3B8 V_L (SEQ ID NO: 84), 2C9B10 V_L (SEQ ID NO: 86), 2E2A6 V_L (SEQ ID NO: 88), 3C1A5 V_L (SEQ ID NO: 90) y 3C3E2 V_L (SEQ ID NO: 92). Las secuencias de aminoácidos que comprendían los dominios de CDR V_H y V_L del anticuerpo monoclonal α-SNAP-25 producidos por los hibridomas 1D3B8, 2C9B10, 2E2A6, 3C1A5 y 3C3E2 se indican en la Tabla 21.

Tabla 21. Secuencias de CDR de los dominios V_H y V_L de los anticuerpos monoclonales α-SNAP-25

CDR	Secuencia	Identificada en	SEQ ID NO:
CDR 1 V_H	TFTDHSIH	2E2A6 2C9B10 3C1A5	93
CDR 1 V_H	TFTNYVIH	3C3E2	94
CDR 1 V_H	IFTDHALH	1D3B8	95
CDR 2 V_H	YIFPGNGNIEYNDKFKG	2E2A6	96
CDR 2 V_H	YLFPGNGNFEYNEKFKG	2C9B10 3C1A5	97
CDR 2 V_H	YINPYNDGSKYNEKFKG	3C3E2	98
CDR 2 V_H	YIFPGNGNIEYNEKFKG	1D3B8	99
CDR 3 V_H	KRMGY	2E2A6 3C1A5	100
CDR 3 V_H	KKMDY	2C9B10 1D3B8	101
CDR 3 V_H	ARMDY	3C3E2var1	102

CDR 3 V_H	ARMGY	3C3E2var2	151
CDR 3 V_H	ARHLANTYYYFDY	3C3E2var3	152
CDR 1 V_L	RSSQSIVHSNGNTYLE	1D3B8	103
CDR 1 V_L	RTTENIYSYFV	2C9B10	104
CDR 1 V_L	KSSQSLLYTNGKTYLT	2E2A6	105
CDR 1 V_L	KSSQSLLNTNGKTYLT	3C1A5	106
CDR 1 V_L	RASQNIGNYLH	3C3E2	107
CDR 2 V_L	KVSNRFS	1D3B8	108
CDR 2 V_L	NAKSLAE	2C9B10	109
CDR 2 V_L	LVSELDS	2E2A6	110
CDR 2 V_L	LVSKLDS	3C1A5	111
CDR 2 V_L	YASQSIS	3C3E2	112
CDR 3 V_L	FQGSHVPPT	1D3B8	113
CDR 3 V_L	QHHYGTPYT	2C9B10	114
CDR 3 V_L	LQSAHFPFT	2E2A6	115
CDR 3 V_L	LQSSHFPFT	3C1A5	116
CDR 3 V_L	QQSDTWPLT	3C3E2	117

Ejemplos no taxativos de secuencias de aminoácidos que comprendían variantes de dominio de CDR V_H del anticuerpo monoclonal α-SNAP-25 producido por los hibridomas descritos en la presente memoria descriptiva incluyen la variante de CDR1 V_H de la SEQ ID NO: 118 para 1D3B8; variante de CDR1 V_H de la SEQ ID NO: 119 para 2C9B10, 2E2A6 y 3C1A5 V_H; variante de CDR1 V_H de la SEQ ID NO: 120 para 3C1A5 V_H y 3C3E2 variante 3; variante de CDR2 V_H de la SEQ ID NO: 121 para 1D3B8 y 2E2A6; variante de CDR2 V_H de la SEQ ID NO: 122 para 2C9B10 y 3C1A5 V_H; variante de CDR2 V_H de la SEQ ID NO: 123 para 3C1A5 V_H y 3C3E2 variante 3; variante de CDR3 V_H MDY para 1D3B8 y 2C9B10; variante de CDR3 V_H MGY para 2E2A6 y 3C1A5 V_H y variante de CDR3 V_H de la SEQ ID NO: 124 para 3C1A5 V_H y 3C3E2 variante 3. Ejemplos no taxativos de secuencias de aminoácidos que comprendían variantes de dominio de CDR V_L del anticuerpo monoclonal α-SNAP-25 producido por los hibridomas descritos en la presente memoria descriptiva incluyen la variante de CDR1 V_L de la SEQ ID NO: 125 para 1D3B8; variante de CDR1 V_L de la SEQ ID NO: 126 para 2C9B10; variante de CDR1 V_L de la SEQ ID NO: 127 para 2E2A6; variante de CDR1 V_L de la SEQ ID NO: 128 para 3C1A5; variante de CDR1 V_L de la SEQ ID NO: 129 para 3C3E2; variante de CDR2 V_L KVS para 1D3B8; variante de CDR2 V_L NAK para 2C9B10; variante de CDR2 V_L LVS para 2E2A6; variante de CDR2 V_L YAT para 3C1A5 y variante de CDR2 V_L YAS para 3C3E2.

Ejemplo IX

Desarrollo de anticuerpos policlonales α-SNAP-25 que unen de forma selectiva un epítopo de la SNAP-25 con un extremo carboxiloterminal libre en el residuo de P_1 del enlace de escísil del sitio de escisión de la BoNT/A

El siguiente ejemplo ilustra cómo realizar anticuerpos policlonales α-SNAP-25 que se puedan unir de forma selectiva a un epítopo de la SNAP-25 con un extremo carboxiloterminal en el residuo de P_1 del enlace de escísil del sitio de escisión de la BoNT/A.

Para desarrollar anticuerpos policlonales α-SNAP-25 que se unen a un epítopo que comprende un extremo carboxiloterminal en el residuo de P1 del enlace de escísil del sitio de escisión de la BoNT/A de un producto de la escisión de la SNAP-25, se diseñó el péptido de 10 residuos CGGGRIDEANQ (SEQ ID NO: 46) como un antígeno del producto de la escisión de la SNAP-25. Este péptido comprende un residuo de cisteína N terminal para la conjugación con KLH, un espaciador flexible espaciador G (GGG) enlazado a los aminoácido 191-197 de la SNAP-25 humana (SEQ ID NO: 5) y tiene una glutamina C terminal carboxilada. Las búsquedas de blastos revelaron que este péptido tenía una alta homología

solamente con la SNAP-25 y casi ninguna reactividad cruzada posible con otras proteínas en células neuronales. La secuencia también se sometió a un cuidadoso escrutinio utilizando algoritmos informáticos para determinar índices de hidropatía, probabilidad de superficie proteica, regiones de flexibilidad y estructuras secundarias favorables, seguido por la orientación adecuada y la presentación de la secuencia peptídica elegida. El péptido se sintetizó y conjugó con hemocianina de lapa californiana (KLH) para aumentar la inmunogenicidad. Antes de inmunizar los animales, primero se analizaron conejos sin tratar en comparación con lisados celulares de líneas celulares candidatas en una transferencia Western para identificar los animales que no tenían inmunorreactividad con las proteínas presentes en los lisados celulares. Se inmunizaron con este péptido dos conejos previamente analizados y, luego de tres inmunizaciones en alrededor de ocho semanas, los conejos se desangraron para su análisis. Se dejó que la sangre se coagulara mediante incubación a 4°C durante 60 minutos. La sangre coagulada se centrifugó a 10,000x g a 4°C durante 10 minutos para sedimentar los residuos celulares. La muestra de suero resultante se dispensó en alícuotas de 50 µL y se almacenó a -20°C hasta que se necesitó.

Se utilizó una estrategia similar con base en otros

antígenos de la SNAP-25 descritos en la presente memoria descriptiva para desarrollar anticuerpos policlonales α-SNAP-25 que se unen a un epítopo con un extremo carboxiloterminal en el residuo de P1 del enlace de escísil del sitio de escisión de la BoNT/A de un producto de la escisión de la SNAP-25. Por ejemplo, el antígeno de la SNAP-25 de la SEQ ID NO: 47 se puede conjugar con KLH en lugar del antígeno de la SNAP-25 de la SEQ ID NO: 46. Como otro ejemplo, los aminoácidos 191-197 de la SNAP-25 humana del antígeno de la SNAP-25 de la SEQ ID NO: 38 se pueden reemplazar con la SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43 o SEQ ID NO: 44.

2. Análisis para determinar la presencia de anticuerpos policlonales α-SNAP-25

Para determinar la presencia de anticuerpos policlonales α-SNAP-25 que se puedan unir de forma selectiva a un antígeno de la SNAP-25 con un extremo carboxiloterminal en el residuo de P_1 del enlace de escísil del sitio de escisión de la BoNT/A, se realizaron ensayos de escisión basados en células y ELISA comparativo usando el suero de conejo extraído como se describió en el Ejemplo VIII. El

suero de los dos conejos contenía anticuerpos policlonales α-SNAP-25 que se pueden unir de forma selectiva a un antígeno de la SNAP-25 con un extremo carboxilo en el residuo de P_1 del enlace de escísil del sitio de escisión de la BoNT/A. Los anticuerpos policlonales de conejo α-SNAP-25 se denominaron NTP 22 y NTP 23.

3. Purificación de anticuerpos policlonales α-SNAP-25

Para purificar anticuerpos policlonales α-SNAP-25 que se pueden unir de forma selectiva a un antígeno de la SNAP-25 con un extremo carboxiloterminal en el residuo de P_1 del enlace de escísil del sitio de escisión de la BoNT/A, se purificaron anticuerpos NTP 22 y NTP 23 de suero de conejo usando columnas de afinidad que contenían el antígeno de la SNAP-25 de la SEQ ID NO: 46.

4. Evaluación de la especificidad de unión de los anticuerpos policlonales α-SNAP-25

Para evaluar la especificidad de unión de un anticuerpo policlonal α-SNAP-25 que se puede unir de forma selectiva a un antígeno de la SNAP-25 con un extremo carboxiloterminal en el residuo de P_1 del enlace de escísil del sitio de escisión de la BoNT/A, se utilizaron anticuerpos policlonales α-SNAP-

25 NTP 22 y NTP 23 purificados para detectar el producto de la escisión usando el ensayo de actividad basado en células, inmunocitoquímica e inmunoprecipitación, como se describió en el Ejemplo VIII. El ensayo de escisión basado en células, el análisis de inmunocitoquímica y el análisis de inmunoprecipitación indicaron que los anticuerpos policlonales α-SNAP-25 NTP 22 y NTP 23 no reaccionaron de forma cruzada con la SNAP-25 no escindida. Por consiguiente, tanto la NTP 22 como la NTP 23 tienen alta especificidad de unión al producto de la escisión de la $SNAP\text{-}25_{197}$, lo que permite el reconocimiento preferencial de este producto de escisión con relación al sustrato no escindido de la $SNAP\text{-}25_{206}$. La afinidad a los antígenos se puede determinar usando SPR en el BiAcore como se describió en el Ejemplo VIII.

Salvo que se indique lo contrario, se debe comprender que todas las cifras que expresan cantidades de ingredientes, propiedades como peso molecular, condiciones de reacción y otras utilizadas en la presente memoria descriptiva y reivindicaciones se encuentran modificadas en todos los casos por el término "alrededor de". Por lo tanto, salvo que se indique lo contrario, los parámetros numéricos que se indican en la memoria descriptiva y en las reivindicaciones adjuntas son aproximaciones que pueden variar dependiendo de las

propiedades deseadas que se busque obtener con la presente invención. En última instancia y no como un intento de limitar la aplicación de la doctrina de equivalentes al alcance de las reivindicaciones, cada parámetro numérico se debería interpretar al menos en vista de la cantidad de dígitos significativos indicados y aplicando técnicas de redondeo normales. Sin perjuicio de que los intervalos y los parámetros numéricos que indican el amplio alcance de la invención sean aproximaciones, los valores numéricos que se indican en los ejemplos específicos se indican de la forma más precisa posible. No obstante, todo valor numérico contiene inherentemente algunos errores que resultan necesariamente de la desviación estándar que se encuentra en sus mediciones de análisis respectivas.

Los términos "un", "una", "el" y referentes similares utilizados en el contexto de la descripción de la invención (especialmente en el contexto de las siguientes reivindicaciones) se deben interpretar como abarcativos del singular y el plural, salvo que se indique lo contrario en la presente o que el contexto lo contradiga claramente. La mención de intervalos de valores en la presente pretende meramente servir como un método taquigráfico para referirse de forma individual a cada valor separado que se encuentra en el intervalo. Salvo que se indique lo contrario en la

presente, cada valor individual se incorpora en la memoria descriptiva como si se mencionara de forma individual en la presente. Todos los métodos descritos en la presente se pueden realizar en cualquier orden adecuado, salvo que se indique lo contrario en la presente o que el contexto lo contradiga claramente. El uso de todos y cualquiera de los ejemplos o las expresiones de ejemplo (por ej., "como") en la presente pretende meramente iluminar mejor la invención y no presenta una limitación al alcance de la invención reivindicada de otra forma. No se debe interpretar ningún lenguaje en la memoria descriptiva como una indicación de algún elemento no reivindicado esencial para la práctica de la invención.

Las agrupaciones de elementos o modalidades alternativos de la invención descritos en la presente no se deben interpretar como limitaciones. Cada miembro del grupo se puede referir y reivindicar de forma individual o en cualquier combinación con otros miembros del grupo u otros elementos que se encuentran en la presente. Se anticipa que uno o más miembros de un grupo se pueden incluir o eliminar de un grupo por razones de conveniencia y/o patentabilidad. Cuando ocurra una de tales inclusiones o eliminaciones, se considera que la memoria descriptiva contiene el grupo según se modificó y, por consiguiente, cumple con la descripción

escrita de todos los grupos Markush utilizados en las reivindicaciones adjuntas.

Algunas modalidades de la presente invención se describen en la presente, incluyendo la mejor forma conocida por los inventores para realizar la invención. Por supuesto, variaciones de estas modalidades descritas serán evidentes para los expertos en la técnica tras la lectura de la descripción que antecede. Los inventores esperan que los expertos utilicen tales variaciones según sea apropiado y pretenden que la invención se practique de una forma diferente a la que se describe específicamente en la presente. Por lo tanto, la presente invención incluye todas las modificaciones y los equivalentes de la materia mencionada en las reivindicaciones adjuntas a la presente según permita la ley. Adicionalmente, toda combinación de los elementos antedichos en todas las variaciones posibles de los mismos se encuentra incluida en la invención, salvo que se indique lo contrario en la presente o que lo contradiga claramente el contexto.

Las modalidades específicas descritas en la presente se pueden limitar adicionalmente en las reivindicaciones usando el vocabulario "que consiste en" o "que consiste esencialmente en". Cuando se utiliza en las reivindicaciones,

ya sea como se presentan o en adiciones a modo de corrección, el término de transición "que consiste en" excluye todo elemento, etapa o ingrediente que no se especifique en las reivindicaciones. El término de transición "que consiste esencialmente en" limita el alcance de una reivindicación a los materiales o las etapas especificados y a aquellos que no afectan de forma material la o las características básicas y novedosas. Las modalidades de la invención que se reivindican de tal forma se describen y permiten inherente o expresamente en la presente.

Adicionalmente, se han realizado diversas referencias a patentes y publicaciones impresas a lo largo de la presente memoria descriptiva. Cada una de las referencias y publicaciones impresas antedichas se incorporan de forma individual a la presente en su totalidad a modo de referencia.

Por último, se debe comprender que las modalidades de la invención descritas en la presente ilustran los principios de la presente invención. Otras modificaciones que se pueden utilizar se encuentran dentro del alance de la invención. Por consiguiente, a modo de ejemplo, pero de forma no taxativa, se pueden utilizar configuraciones alternativas de la presente invención de acuerdo con las enseñanzas que obran en

la presente. Por lo tanto, la presente invención no se limita a las mismas precisamente como se muestra y describe.

Tabla 5. Expresión genética aumentada en las líneas celulares H1 y BB10 en comparación con la línea celular 2D6 en estado no diferenciado usando análisis de micromatriz

Símbolo del gen	ID del conjunto de sondas	ID Pública representativa	ID de transcripción RefSec	ID del Gen Entrez	Proporción Log2	valor p
PLS3	201215_at	NM_005032	NM_005032	5358	6,56	2,91E-12
H99792	225710_at	H99792	---	---	6,46	1,81E-07
DAZ1 DAZ3 DAZ2 DAZ4	208282_x_at	NM_020363	NM_001005375 NM_001005785 NM_001005786 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	6,45	4,63E-04
TPTE	220205_at	NM_013315	NM_013315 NM_199259 NM_199260 NM_199261	7179	6,44	3,16E-08
DAZ1 DAZ3 DAZ2 DAZ4	207909_x_at	U21663	NM_001005375 NM_001005785 NM_001005786 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	6,20	2,48E-04
MSN	200600_at	NM_002444	NM_002444	4478	6,11	2,92E-09
CXCR4	217028_at	AJ224869	NM_001008540 NM_003467	7852	5,95	3,23E-04
NDN	209550_at	U35139	NM_002487	4692	5,81	3,18E-06
FLJ32942	227711_at	BG150433	NM_144594	121355	5,73	8,08E-09
AI197932	229498_at	AI197932	---	---	5,59	3,21E-08
PEG3	209242_at	AL042588	NM_006210	5178	5,58	1,13E-07
TIMP3	201149_s_at	U67195	NM_000362	7078	5,57	3,00E-05
NEDD9	202149_at	AL136139	NM_006403 NM_182966	4739	5,49	3,70E-09
TIMP3	201150_s_at	NM_000362	NM_000362	7078	5,40	1,53E-03
PRSS12	205515_at	NM_003619	NM_003619	8492	5,37	1,39E-06
LUM	201744_s_at	NM_002345	NM_002345	4060	5,37	1,04E-06
RGS5	1555725_a_at	AF493929	NM_003617	8490	5,22	2,23E-07
TFPI2	209278_s_at	L27624	NM_006528	7980	5,22	1,95E-05

CXCR4	211919_s_at	AF348491	NM_001008540 NM_003467	7852	5,18	9,56E-04
RGS5	218353_at	NM_025226	NM_003617	8490	5,15	1,82E-07
ASCL1	209985_s_at	BE797438	NM_004316	429	5,09	8,38E-06
KCTD12	212192_at	AI718937	NM_138444	115207	5,04	6,32E-06
SPARC	200665_s_at	NM_003118	NM_003118	6678	4,97	2,45E-06
CXCR4	209201_x_at	L01639	NM_001008540 NM_003467	7852	4,97	9,51E-04
TIMP3	201147_s_at	BF347089	NM_000362	7078	4,95	1,56E-04
DAZ1	207912_s_at	NM_004081	NM_001005375	1617	4,94	1,79E-03
DAZ3			NM_001005785	57054		
DAZ2			NM_001005786	57055		
DAZ4			NM_004081	57135		
			NM_020363			
			NM_020364			
			NM_020420			
MINA	213189_at	BE966695	NM_032778 NM_153182	84864	4,92	1,50E-08
CUGBP2	202157_s_at	U69546	NM_006561	10659	4,91	1,20E-06
BF000203	236385_at	BF000203	---	---	4,87	6,43E-06
GRP	206326_at	NM_002091	NM_002091	2922	4,82	1,83E-06
RGS5	209070_s_at	AI183997	NM_003617	8490	4,78	1,01E-07
AI183997	233858_at	AU144918	---	---	4,72	1,79E-05
RNF182	230720_at	AI884906	NM_152737	221687	4,72	4,74E-07
PEG3	209243_s_at	AF208967	NM_006210	5178	4,69	8,13E-06
RAM2	225081_s_at	AK022955	NM_018719	55536	4,52	1,18E-04
DKFZp667G2110	214030_at	BE501352	XM_376254	131544	4,52	6,37E-10
RGS5	209071_s_at	AF159570	NM_003617	8490	4,50	1,74E-07
VIP	206577_at	NM_003381	NM_003381 NM_194435	7432	4,44	2,77E-04
PRSS12	213802_at	AI810767	NM_003619	8492	4,41	1,46E-03
MGC34032	235763_at	AA001450	NM_152697	204962	4,40	3,84E-08
DAZ1	208281_x_at	NM_020364	NM_001005375	1617	4,39	5,53E-04
DAZ3			NM_001005785	57054		
DAZ2			NM_001005786	57055		
DAZ4			NM_004081	57135		
			NM_020363			
			NM_020364			
			NM_020420			

DAZ1 DAZ3 DAZ2 DAZ4	216922_x_at	AF271088	NM_001005375 NM_001005785 NM_001005786 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	4,35	6,79E-04
SPARC	212667_at	AL575922	NM_003118	6678	4,30	4,26E-05
MAB21L2	210302_s_at	AF262032	NM_006439	10586	4,28	1,96E-08
CCDC3	223316_at	AL136562	NM_031455	83643	4,21	1,24E-06
SLAC2-B	214734_at	AB014524	NM_015065	23086	4,20	1,64E-03
ARHGAP6	206167_s_at	NM_001174	NM_001174 NM_006125 NM_013422 NM_013423 NM_013427	395	4,19	1,68E-05
BASP1	202391_at	NM_006317	NM_006317	10409	4,18	3,67E-08
SIM1	206876_at	AL121948	NM_005068	6492	4,16	4,38E-05
SMC6L1	236535_at	AW069285	NM_024624	79677	4,09	2,41E-07
CUGBP2	202158_s_at	NM_006561	NM_006561	10659	4,09	8,95E-04
FAT	201579_at	NM_005245	NM_005245	2195	4,08	5,01E-03
GNG11	204115_at	NM_004126	NM_004126	2791	4,07	6,53E-04
ITGA6	201656_at	NM_000210	NM_000210	3655	3,98	4,23E-09
ACATE2	221641_s_at	AF241787	NM_012332	23597	3,97	4,71E-05
TCTE1L	203303_at	NM_006520	NM_006520	6990	3,96	2,11E-07
NEDD9	202150_s_at	U64317	NM_006403 NM_182966	4739	3,94	1,90E-06
DOK5	214844_s_at	AL050069	NM_018431 NM_177959	55816	3,83	1,64E-05
EDG2	204036_at	AW269335	NM_001401 NM_057159	1902	3,82	2,36E-08
MAOA	204388_s_at	NM_000240	NM_000240	4128	3,80	8,51E-05
SPAG6	210033_s_at	AF079363	NM_012443 NM_172242	9576	3,78	6,66E-06
BF476109	1556300_s_at	BF476109	---	---	3,78	7,77E-06
PTPRK	203038_at	NM_002844	NM_002844	5796	3,75	1,34E-03
GFRA2	205722_s_at	NM_001495	NM_001495	2675	3,74	7,15E-06
PTPRE	221840_at	AA775177	NM_006504 NM_130435	5791	3,72	2,12E-06
ADAMTS9	226814_at	AI431730	NM_020249 NM_182920 NM_182921	56999	3,70	9,69E-05
MINA	213188_s_at	AI823896	NM_032778 NM_153182	84864	3,69	3,36E-05
PLK2	201939_at	NM_006622	NM_006622	10769	3,69	1,39E-06
KIAA1754	225582_at	AA425726	NM_033397	85450	3,67	2,03E-04

FN5	219806_s_at	NM_020179	NM_020179	56935	3,65	2,97E-04
SMC6L1	218781_at	NM_024624	NM_024624	79677	3,64	1,72E-08
EML1	204797_s_at	NM_004434	NM_001008707 NM_004434	2009	3,64	6,58E-05
ADAMTS9	1562275_at	AL832835	NM_020249 NM_182920 NM_182921	56999	3,58	1,72E-06
LOC441157	1558795_at	AL833240	XM_499037	441157	3,56	7,55E-06
MAOA	212741_at	AA923354	NM_000240	4128	3,55	6,62E-04
TRIM29	211002_s_at	AF230389	NM_012101 NM_058193	23650	3,51	2,23E-07
MAOA	204389_at	NM_000240	NM_000240	4128	3,50	4,16E-07
MGC34032	1569112_at	AW020413	NM_152697	204962	3,50	9,78E-06
ELOVL7	227180_at	AW138767	XM_371740	79993	3,45	6,72E-04
TFPI2	209277_at	AL574096	NM_006528	7980	3,43	6,92E-06
ASCL1	213768_s_at	AW950513	NM_004316	429	3,36	5,80E-07
CHRNA7 CHRFAM7A	210123_s_at	U62436	NM_000746 NM_139320 NM_148911	1139 89832	3,33	4,22E-06
ASCL1	209987_s_at	BC002341	NM_004316	429	3,33	1,82E-08
FRZB	203697_at	U91903	NM_001463	2487	3,31	1,02E-05
SLC43A3	210692_s_at	BC003163	NM_014096 NM_017811 NM_199329	29015	3,31	7,81E-05
LOC253012	242601_at	AA600175	NM_198151	253012	3,30	2,75E-04
CD9	201005_at	NM_001769	NM_001769	928	3,26	3,31E-04
SMAD6	207069_s_at	NM_005585	NM_005585	4091	3,26	6,45E-06
PCGF5	226326_at	AI798098	NM_032373	84333	3,26	7,00E-07
MAB21L2	210303_at	AF262032	NM_006439	10586	3,26	6,74E-05
SLC7A2	225516_at	AA876372	NM_001008539 NM_003046	6542	3,22	1,59E-06
AL109791	233932_at	AL109791	---	---	3,20	1,60E-03
MGC33926	229302_at	AA058832	NM_152390	130733	3,20	1,16E-03
KCTD12	212188_at	AA551075	NM_138444	115207	3,19	7,60E-05
MAFB	218559_s_at	NM_005461	NM_005461	9935	3,16	7,22E-03
BNC2	220272_at	NM_017637	NM_017637	54796	3,14	3,14E-03
ASCL1	209988_s_at	BC001638	NM_004316	429	3,14	4,77E-08
CBLN2	242301_at	R60224	NM_182511	147381	3,14	3,35E-03
ALCAM	240655_at	BE502785	NM_001627	214	3,13	2,14E-04
AF131795	233139_at	AF131795	---	---	3,12	8,04E-03
AI656180	242447_at	AI656180	---	---	3,12	3,69E-05
LOC402524	242206_at	AW590588	XM_379850	402524	3,10	5,25E-04
EDG3	228176_at	AA534817	NM_005226	1903	3,10	4,81E-04
KDELC2	225128_at	AL548941	NM_153705	143888	3,09	2,21E-04
NEGR1	243357_at	AA115106	NM_173808	257194	3,09	1,42E-05
DACT1	219179_at	NM_016651	NM_016651	51339	3,09	2,14E-04

DAZ1 DAZ3 DAZ2 DAZ4	216351_x_at	AF248483	NM_001005375 NM_001005785 NM_001005786 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	3,06	4,06E-04
KIAA0527	214954_at	BF977837	XM_171054	26032	3,03	2,02E-04
TPBG	203476_at	NM_006670	NM_006670	7162	3,02	2,88E-05
LGR5	213880_at	AL524520	NM_003667	8549	3,02	2,16E-03
FLJ23091	228950_s_at	AL534095	NM_001002292 NM_024911	79971	3,01	2,38E-03
PLXNA4	232317_at	AB046770	XM_039393 XM_379927	57671	2,99	6,60E-07
FLJ20647	218802_at	NM_017918	NM_017918	55013	2,99	7,56E-03
CNTN4	229084_at	R42166	NM_175607 NM_175612 NM_175613	152330	2,96	2,55E-06
RBPMS	209488_s_at	D84109	NM_001008710 NM_001008711 NM_001008712 NM_006867	11030	2,96	5,32E-03
E2F7	228033_at	AI341146	NM_203394	144455	2,94	1,26E-03
TRIM29	202504_at	NM_012101	NM_012101 NM_058193	23650	2,93	6,42E-08
N26620	227503_at	N26620	---	---	2,93	1,14E-04
TIMP3	201148_s_at	AW338933	NM_000362	7078	2,91	1,23E-03
C2orf31	221245_s_at	NM_030804	---	81561	2,91	2,25E-05
DKFZp761O2018	232313_at	AL122107	XM_044062	92293	2,91	1,59E-06
BC041965	1560411_at	BC041965	---	---	2,91	8,58E-04
GNAI1	227692_at	AU153866	NM_002069	2770	2,90	2,00E-06
GPR10	231805_at	AL563031	NM_004248	2834	2,90	1,19E-04
LGR5	210393_at	AF062006	NM_003667	8549	2,89	4,97E-05
ENC1	201340_s_at	AF010314	NM_003633	8507	2,89	4,72E-05
LOC51760	205613_at	NM_016524	NM_016524	51760	2,88	9,54E-03
GNG12	222834_s_at	N32508	NM_018841	55970	2,88	1,98E-04
BARD1	205345_at	NM_000465	NM_000465	580	2,87	6,84E-03
A2BP1	1553422_s_at	NM_145892	NM_018723 NM_145891 NM_145892 NM_145893	54715	2,86	4,30E-03

PPP1R3C	204284_at	N26005	NM_005398	5507	2,84	1,93E-05
AF086027	1559697_a_at	AF086027	---	---	2,83	1,45E-03
PMP22	210139_s_at	L03203	NM_000304 NM_153321 NM_153322	5376	2,83	1,89E-04
GFRA2	205721_at	U97145	NM_001495	2675	2,83	4,80E-04
PFKFB3	202464_s_at	NM_004566	NM_004566	5209	2,82	3,61E-03
BF222929	242346_x_at	BF222929	---	---	2,82	2,87E-04
SLC43A3	213113_s_at	AI630178	NM_014096 NM_017611 NM_199329	29015	2,80	1,02E-06
PEX5L	1562473_at	BC037943	NM_016559	51555	2,79	1,76E-04
PELO	226731_at	AA156873	NM_015946	53918	2,76	4,84E-03
FBN1	202765_s_at	AI264196	NM_000138	2200	2,76	2,17E-03
PLEKHE1	212719_at	AB011178	NM_194449	23239	2,75	5,65E-03
MYRIP	214156_at	AL050090	NM_015460	25924	2,75	2,44E-06
BNC2	235723_at	AA843242	NM_017637	54796	2,74	2,24E-03
CPVL	208146_s_at	NM_031311	NM_019029 NM_031311	54504	2,73	2,87E-03
PLXNA4	228104_at	AL117427	XM_039393 XM_379927	57671	2,72	4,31E-04
BF940761	229427_at	BF940761	---	---	2,69	4,80E-03
ARHGEF6	209539_at	D25304	NM_004840	9459	2,68	2,81E-04
H17657	241444_at	H17657	---	---	2,67	2,17E-04
GNAI1	209576_at	AL049933	NM_002069	2770	2,65	1,06E-07
LOC441157	1558796_a_at	AL833240	XM_499037	441157	2,65	1,11E-03
CADPS	1568603_at	AI912173	NM_003716 NM_183393 NM_183394	8618	2,64	4,31E-04
POSTN	210809_s_at	D13665	NM_006475	10631	2,63	1,47E-03
PTPRR	210675_s_at	U77917	NM_002849 NM_130846	5801	2,60	4,53E-03
MGC24103	232568_at	AU145658	---	158295	2,59	3,96E-04
STK17A	202693_s_at	AW194730	NM_004760	9263	2,59	1,11E-04
LOC440738	221697_at	AF276659	NM_001004343	440738	2,58	1,85E-03
MYO6	203215_s_at	AA877789	NM_004999	4646	2,56	7,95E-03
CADPS	1568604_a_at	AI912173	NM_003716 NM_183393 NM_183394	8618	2,56	2,70E-07
NR3C1	211671_s_at	U01351	NM_000176	2908	2,56	2,36E-09
FRZB	203698_s_at	NM_001463	NM_001463	2487	2,56	3,80E-04
FLJ23091	221958_s_at	AA775681	NM_001002292 NM_024911	79971	2,54	5,86E-03
ADAMTS9	1554697_at	AF488803	NM_020249 NM_182920 NM_182921	56999	2,54	1,99E-04
AW130600	226865_at	AW130600	---	---	2,53	4,86E-04

ST8SIA4	230836_at	AI422986	NM_005668 NM_175052	7903	2,50	7,33E-03
CNTN1	211203_s_at	U07820	NM_001843 NM_175038	1272	2,49	1,34E-04
EMILIN2	224374_s_at	AF270513	NM_032048	84034	2,48	1,13E-04
HGF	210997_at	M77227	NM_000601 NM_001010931 NM_001010932 NM_001010933 NM_001010934	3082	2,46	4,58E-03
AI582818	229053_at	AI582818	---	---	2,44	6,88E-03
LOC253981	226430_at	AI394438	---	253981	2,44	3,85E-03
GNG12	212294_at	BG111761	NM_018841	55970	2,42	1,06E-06
C6orf148	220513_at	NM_030568	NM_030568	80759	2,41	5,89E-03
OSBPL3	209626_s_at	AI202969	NM_015550 NM_145320 NM_145321 NM_145322 NM_145323 NM_145324	26031	2,40	9,56E-04
SEMA6D	233882_s_at	AK022831	NM_020858 NM_024966 NM_153616 NM_153617 NM_153618 NM_153619	80031	2,39	1,02E-03
PCDH8	206935_at	NM_002590	NM_002590 NM_032949	5100	2,37	6,17E-07
MAB21L1	206163_at	NM_005584	NM_005584	4081	2,36	4,98E-03
TSC	218872_at	NM_017899	NM_017899	54997	2,36	1,01E-05
PPP2R2B	213849_s_at	AA974416	NM_004576 NM_181674 NM_181675 NM_181676 NM_181677 NM_181678	5521	2,35	2,05E-06
PDE5A	227088_at	BF221547	NM_001083 NM_033430 NM_033431 NM_033437	8654	2,35	2,27E-04
ZNF521	226676_at	AK021452	NM_015461	25925	2,34	1,55E-03
PVRL3	213325_at	AA129716	NM_015480	25945	2,34	3,70E-06
ENC1	201341_at	NM_003633	NM_003633	8507	2,33	3,06E-05
RGMA	223468_s_at	AL136826	NM_020211	56963	2,33	1,24E-07
ST8SIA2	239537_at	AW589904	NM_006011	8128	2,32	8,94E-07

FGFR2	203639_s_at	M80634	NM_000141 NM_022969 NM_022970 NM_022971 NM_022972 NM_022973 NM_022974 NM_022975 NM_022976 NM_023028 NM_023029 NM_023030 NM_023031	2263	2,29	4,06E-03
BAMBI	203304_at	NM_012342	NM_012342	25805	2,29	2,34E-08
ARHGAP6	1563386_at	AL079282	NM_001174 NM_006125 NM_013422 NM_013423 NM_013427	395	2,27	2,07E-03
PLCL2	213309_at	AL117515	NM_015184	23228	2,27	1,92E-03
A2BP1	221217_s_at	NM_018723	NM_018723 NM_145891 NM_145892 NM_145893	54715	2,26	5,56E-03
LOC340109	1557765_at	BC039509	XM_379322	340109	2,25	2,28E-05
SLC39A8	209267_s_at	AB040120	NM_022154	64116	2,25	4,91E-03
ITGA6	215177_s_at	AV733308	NM_000210	3655	2,23	2,05E-03
CNTN1	227209_at	AI091445	NM_001843 NM_175038	1272	2,23	4,31E-03
EGLN3	219232_s_at	NM_022073	NM_022073	112399	2,23	7,56E-03
ZFHX4	219779_at	NM_024721	NM_024721	79776	2,22	1,39E-03
AF086027	1559696_at	AF086027	---	---	2,21	1,05E-03
AL050204	213929_at	AL050204	---	---	2,20	2,15E-03
TPTE	233879_at	AL137389	NM_013315 NM_199259 NM_199260 NM_199261	7179	2,20	2,76E-03
TMEM35	219685_at	NM_021637	NM_021637	59353	2,20	8,17E-03
MSX2	205555_s_at	D31771	NM_002449	4488	2,20	6,02E-04
GPR51	211679_x_at	AF095784	NM_005458	9568	2,19	5,89E-03
BE856929	239349_at	BE856929	---	---	2,17	2,00E-03
SYN2	210247_at	AW139618	NM_003178 NM_133625	6854	2,15	5,68E-03
COLEC12	221019_s_at	NM_030781	NM_030781 NM_130386	81035	2,15	7,66E-03
TCF7L1	221016_s_at	NM_031283	NM_031283	83439	2,14	1,38E-03
NRXN1	228547_at	BF509242	NM_004801 NM_138735	9378	2,13	8,92E-03
CRH	205630_at	NM_000756	NM_000756	1392	2,13	1,12E-03

GPR161	230369_at	AI743151	NM_007369 NM_153832	23432	2,12	1,61E-04
ZNF217	203739_at	NM_006526	NM_006526	7764	2,12	3,18E-04
NEDD9	233223_at	AK000850	NM_006403 NM_182966	4739	2,11	4,23E-04
RASEF	235144_at	AA826324	NM_152573	158158	2,09	2,92E-03
PLAT	201860_s_at	NM_000930	NM_000930 NM_000931 NM_033011	5327	2,09	6,29E-04
GPR51	209990_s_at	AF056085	NM_005458	9568	2,05	1,33E-05
AL161982	1563494_at	AL161982	---	---	2,05	1,21E-03
SEMA6D	226492_at	AL036088	NM_020858 NM_024966 NM_153616 NM_153617 NM_153618 NM_153619	80031	2,05	1,22E-04
ORF1-FL49	224707_at	AL522667	NM_032412	84418	2,04	2,79E-05
NID	202007_at	BF940043	NM_002508	4811	2,04	2,24E-03
PCGF5	229194_at	AL045882	NM_032373	84333	2,02	2,51E-04
TCF7L2	216035_x_at	AV721430	NM_030756	6934	2,02	2,84E-07
AA156721	201952_at	AA156721	---	---	2,02	1,05E-06
FBN1	202766_s_at	NM_000138	NM_000138	2200	2,02	7,81E-04
DBH	206450_at	NM_000787	NM_000787	1621	2,01	2,59E-03
PTPRR	206084_at	NM_002849	NM_002849 NM_130846	5801	2,01	4,19E-03
CNTN1	227202_at	AW072790	NM_001843 NM_175038	1272	2,00	1,32E-03
ARHGEF3	218501_at	NM_019555	NM_019555	50650	2,00	4,42E-05
SLITRK5	214930_at	AW449813	NM_015567	26050	2,00	7,82E-06
ETV1	206501_x_at	NM_004956	NM_004956	2115	1,99	3,21E-03
SPAG6	210032_s_at	AI651156	NM_012443 NM_172242	9576	1,99	2,72E-04
LCRISP1	223475_at	AF142573	NM_031461	83690	1,99	3,27E-03
FGFR2	211401_s_at	AB030078	NM_000141 NM_022969 NM_022970 NM_022971 NM_022972 NM_022973 NM_022974 NM_022975 NM_022976 NM_023028 NM_023029 NM_023030 NM_023031	2263	1,99	1,83E-04
FLJ30058	238047_at	AA405456	NM_144967	158763	1,99	3,10E-03
BF434771	1568598_at	BF434771	XM_498494	440000	1,98	2,21E-03

TCF7L2	216511_s_at	AJ270770	NM_030756	6934	1,97	7,59E-05
MYO6	203216_s_at	NM_004999	NM_004999	4646	1,96	8,88E-05
ATP2B4	212136_at	AW517686	NM_001001396 NM_001684	493	1,96	7,81E-03
RAB32	204214_s_at	NM_006834	NM_006834	10981	1,96	3,53E-03
AI703256	231336_at	AI703256	---	---	1,95	4,67E-04
FLJ40773	1563933_a_at	AK091691	NM_152666	200150	1,95	1,13E-03
LOC92689	213455_at	W87466	NM_138389	92689	1,95	5,71E-04
TCF7L2	212761_at	AI949687	NM_030756	6934	1,94	5,52E-05
TDRD7	213361_at	AW129593	NM_014290	23424	1,93	4,13E-03
GFPT2	205100_at	NM_005110	NM_005110	9945	1,92	3,68E-04
FGFR2	203638_s_at	NM_022969	NM_000141 NM_022969 NM_022970 NM_022971 NM_022972 NM_022973 NM_022974 NM_022975 NM_022976 NM_023028 NM_023029 NM_023030 NM_023031	2263	1,92	3,46E-03
ALCAM	201951_at	BF242905	NM_001627	214	1,91	6,46E-06
ETV1	217053_x_at	X87175	NM_004956	2115	1,91	7,09E-03
NR3C1	201865_x_at	AI432196	NM_000176	2908	1,90	1,19E-05
PDLIM5	203242_s_at	BG054550	NM_001011513 NM_001011514 NM_001011515 NM_001011516 NM_006457	10611	1,89	7,00E-05
ST8SIA2	221285_at	NM_006011	NM_006011	8128	1,89	8,94E-04
TWIST1	213943_at	X99268	NM_000474	7291	1,88	3,85E-04
TLE4	216997_x_at	AL358975	NM_007005	7091	1,88	7,83E-03
GPR161	214104_at	AI703188	NM_007369 NM_153832	23432	1,88	5,85E-03
EDG2	204037_at	BF055366	NM_001401 NM_057159	1902	1,87	9,88E-08

PDLIM5	216804_s_at	AK027217	NM_001011513 NM_001011514 NM_001011515 NM_001011516 NM_006457	10611	1,87	2,39E-05
R39126	230932_at	R39126	---	---	1,87	2,27E-04
AI377043	230722_at	AI377043	---	---	1,87	1,53E-03
W93046	230068_s_at	W93046	---	---	1,86	2,03E-03
DMN	212730_at	AK026420	NM_015286 NM_145728	23336	1,86	2,15E-03
ARHGAP24	223422_s_at	AI743534	NM_031305	83478	1,86	1,60E-03
CCNE2	211814_s_at	AF112857	NM_004702 NM_057735 NM_057749	9134	1,85	5,31E-03
NRXN1	209914_s_at	AW149405	NM_004801 NM_138735	9378	1,84	2,88E-03
ETV1	217061_s_at	AC004857	NM_004956	2115	1,83	4,93E-04
FAM19A5	229459_at	AV723914	NM_015381	25817	1,82	1,07E-06
ITPR1	240052_at	AA648993	NM_002222	3708	1,82	7,08E-04
ZAK	222757_s_at	AB030034	NM_016653 NM_133646	51776	1,81	3,74E-04
FGFR2	208228_s_at	M87771	NM_000141 NM_022969 NM_022970 NM_022971 NM_022972 NM_022973 NM_022974 NM_022975 NM_022976 NM_023028 NM_023029 NM_023030 NM_023031	2263	1,81	1,44E-03
ZNF545	1555793_a_at	AL834267	NM_133466	284406	1,80	4,60E-04
AW024890	229942_at	AW024890	---	---	1,79	6,14E-05
AI733341	240911_at	AI733341	---	---	1,79	7,62E-04
PPAP2B	209355_s_at	AB000889	NM_003713 NM_177414	8613	1,79	4,28E-04
TBX3	222917_s_at	U69556	NM_005996 NM_016569	6926	1,79	9,78E-06
TRIP10	202734_at	NM_004240	NM_004240	9322	1,79	8,00E-03
TCF7L2	212762_s_at	AI375916	NM_030756	6934	1,79	3,86E-07
PELO	214660_at	X68742	NM_015946	53918	1,78	2,39E-03
GPR51	217077_s_at	AF095723	NM_005458	9568	1,78	3,16E-04

FBLN1	202994_s_at	Z95331	NM_001996 NM_006485 NM_006486 NM_006487	2192	1,77	2,59E-03
DOK5	1554863_s_at	BC008992	NM_018431 NM_177959	55816	1,77	3,36E-03
NRXN1	209915_s_at	AB035356	NM_004801 NM_138735	9378	1,76	7,05E-03
FLJ25067	243507_s_at	AV715251	NM_152504	149840	1,76	6,53E-07
DNAPTP6	222154_s_at	AK002064	NM_015535	26010	1,76	4,90E-04
MGC21654	1556429_a_at	BC026969	NM_145647	93594	1,76	6,54E-03
CPNE4	228796_at	BE645967	NM_130808	131034	1,75	4,64E-04
POSTN	1555778_a_at	AY140646	NM_006475	10631	1,75	4,56E-05
ATOH8	228890_at	BF434995	NM_032827	84913	1,75	7,05E-04
ALCAM	1569362_at	BC041127	NM_001627	214	1,75	9,54E-03
HTATSF1	202601_s_at	AI373539	NM_014500	27336	1,75	5,33E-05
MYD88	209124_at	U70451	NM_002468	4615	1,74	3,20E-04
PPAP2B	212230_at	AV725664	NM_003713 NM_177414	8613	1,74	1,11E-05
ZNF253 LOC114977	242919_at	AV683221	NM_021047	114977 56242	1,73	1,13E-03
DCLRE1B	219490_s_at	NM_022836	NM_022836	64858	1,73	3,54E-03
TBX3	229576_s_at	N29712	NM_005996 NM_016569	6926	1,72	6,02E-07
KHDRBS3	230249_at	AI650382	NM_006558	10656	1,72	3,44E-04
FLJ39609	1555980_a_at	CA447406	XM_379692	284598	1,72	9,03E-03
BF110268	238178_at	BF110268	---	---	1,71	1,80E-04
KLF7	238482_at	AL120562	NM_003709	8609	1,71	1,93E-03
ELL2	226099_at	AI924426	NM_012081	22936	1,71	8,96E-04
KHDRBS3	209781_s_at	AF069681	NM_006558	10656	1,71	3,55E-05
TRIM37	1569114_at	BC011742	NM_001005207 NM_015294	4591	1,71	3,38E-03
DLL3	222898_s_at	BE350882	NM_016941 NM_203486	10683	1,70	5,19E-07
SNAI2	213139_at	AI572079	NM_003068	6591	1,70	2,74E-03
FAM19A5	229655_at	N66656	NM_015381	25817	1,70	4,35E-05
ZNF560	1553276_at	NM_152476	NM_152476	147741	1,70	2,56E-04
TBX3	219682_s_at	NM_016569	NM_005996 NM_016569	6926	1,69	1,06E-06
C20orf23	232083_at	AB046810	NM_024704	55614	1,69	8,35E-06
AF131796	231916_at	AF131796	---	---	1,69	2,15E-03
NSE1	229546_at	AI378035	NM_145175	151354	1,69	2,85E-08
CXorf34	205238_at	NM_024917	NM_024917	79979	1,68	6,46E-03
CRH	205629_s_at	BC002599	NM_000756	1392	1,68	5,48E-03
NR3C1	216321_s_at	X03348	NM_000176	2908	1,68	5,45E-07
PTGFRN	224937_at	BF311866	NM_020440	5738	1,67	6,89E-04
ARG99	226322_at	BF109231	NM_031920 NM_175861	83857	1,67	4,14E-03

NXN	243503_at	AI632740	NM_022463	64359	1,67	2,57E-04
STK17A	202695_s_at	NM_004760	NM_004760	9263	1,66	2,52E-03
C11orf8	205413_at	NM_001584	NM_001584	744	1,66	1,85E-05
PI15	229947_at	AI088609	NM_015886	51050	1,66	1,62E-04
NXT2	209629_s_at	AF201942	NM_018698	55916	1,65	3,43E-04
CDC25B	201853_s_at	NM_021873	NM_004358 NM_021872 NM_021873 NM_021874 NM_212530	994	1,65	4,80E-05
TPST2	204079_at	NM_003595	NM_001008566 NM_003595	8459	1,65	2,97E-04
LOC344595	235606_at	AA417117	XM_298151	344595	1,64	2,58E-05
H22448	242530_at	H22448	---	---	1,64	2,20E-04
BF981643	214720_x_at	BF981643	NM_144710 NM_178584	151011	1,64	1,45E-04
LOC93349	214791_at	AK023116	NM_138402	93349	1,64	9,50E-05
DOK4	209690_s_at	BF591163	NM_018110	55715	1,64	7,06E-06
LZTS1	47550_at	N21184	NM_021020	11178	1,63	3,08E-04
TBX3	225544_at	AI806338	NM_005996 NM_016569	6926	1,63	5,24E-06
FSTL1	208782_at	BC000055	NM_007085	11167	1,63	2,00E-03
EMILIN3	228307_at	AL137580	NM_052846	90187	1,63	2,86E-03
ATP2B4	212135_s_at	AW517686	NM_001001396 NM_001684	493	1,63	4,64E-03
AL833029	1559444_at	AL833029	---	---	1,63	2,28E-03
PDLIM5	203243_s_at	NM_006457	NM_001011513 NM_001011514 NM_001011515 NM_001011516 NM_006457	10611	1,62	2,91E-05
TBC1D19	220260_at	NM_018317	NM_018317	55296	1,62	6,08E-05
FZD5	206136_at	NM_003468	NM_003468	7855	1,62	1,51E-03
PCDH9	219737_s_at	AI524125	NM_020403 NM_203487	5101	1,62	3,72E-03

PDLIM5	212412_at	AV715767	NM_001011513 NM_001011514 NM_001011515 NM_001011516 NM_006457	10611	1,61	7,77E-04
ZNF537	223393_s_at	AL136805	NM_020856	57616	1,61	2,15E-03
AW052186	239942_at	AW052186	---	---	1,61	5,57E-03
GPR51	209991_x_at	AF069755	NM_005458	9568	1,60	1,65E-06
BF509125	232198_at	BF509125	---	---	1,60	4,75E-03
C14orf31	225464_at	N30138	NM_152330	122786	1,60	3,92E-03
PARVA	217890_s_at	NM_018222	NM_018222	55742	1,59	6,06E-03
CBLB	227900_at	AV701750	NM_170662	868	1,59	2,60E-03
EB-1	227441_s_at	AW005572	NM_020140 NM_152788 NM_181670	56899	1,59	2,08E-04
NAGA	1555041_a_at	M29276	NM_000262	4668	1,59	2,23E-06
KIAA1713	233536_at	AI202664	XM_290811	80816	1,59	9,66E-04
HOMER3	215489_x_at	AI871287	NM_004838	9454	1,58	2,88E-04
NFIB	233304_at	AU145782	NM_005596	4781	1,58	6,95E-03
SOX5	238009_at	AI446064	NM_006940 NM_152989 NM_178010	6660	1,58	9,49E-06
TCF7L2	216037_x_at	AA664011	NM_030756	6934	1,57	2,43E-03
LOC152573	229485_x_at	AI735586	XM_496688	152573	1,57	6,34E-05
DCBLD2	213865_at	AI378788	NM_080927	131566	1,57	1,25E-04
NS5ATP13TP2	1558613_at	BC040647	NM_178507	220323	1,56	8,59E-03
SAMHD1	204502_at	NM_015474	NM_015474	25939	1,56	9,98E-05
N50083	229110_at	N50083	---	---	1,56	4,18E-04
LRRN3	209840_s_at	AI221950	NM_018334	54674	1,55	9,99E-07
CADPS	233950_at	AK000873	NM_003716 NM_183393 NM_183394	8618	1,55	1,09E-04
ELL2	226982_at	AI745624	NM_012081	22936	1,55	3,35E-03
HRH3	220447_at	NM_007232	NM_007232	11255	1,54	6,15E-04
LRRN3	209841_s_at	AL442092	NM_018334	54674	1,54	6,25E-07
PLK4	211088_s_at	Z25433	NM_014264	10733	1,53	1,15E-03
NOS1	239132_at	BE299830	NM_000620	4842	1,53	1,65E-03
PLEKHF2	218640_s_at	NM_024613	NM_024613	79666	1,53	1,36E-03
MGC72104	243689_s_at	AI681945	NM_207350	284802	1,52	1,75E-04
NOS1	207309_at	NM_000620	NM_000620	4842	1,52	2,45E-04
C1orf43	1555225_at	BC008306	NM_015449 NM_138740	25912	1,52	2,71E-03
GPR161	206972_s_at	NM_007369	NM_007369 NM_153832	23432	1,52	4,09E-03
ODZ3	219523_s_at	NM_018104	XM_371717	55714	1,51	2,29E-04

DOK4	209691_s_at	BC003541	NM_018110	55715	1,50	1,43E-04
TRIM68	219405_at	NM_018073	NM_018073	55128	1,50	2,70E-05
DPYSL3	201431_s_at	NM_001387	NM_001387	1809	1,50	7,17E-03
RBL1	1559307_s_at	BG387892	NM_002895 NM_183404	5933	1,50	2,27E-03
MYO6	210480_s_at	U90236	NM_004999	4646	1,50	1,85E-05
SYNGR1	210613_s_at	BC000731	NM_004711 NM_145731 NM_145738	9145	1,50	8,09E-03
CDO1	204154_at	NM_001801	NM_001801	1036	1,50	3,73E-04
NXT2	209628_at	AK023289	NM_018698	55916	1,49	1,70E-03
ACO1	207071_s_at	NM_002197	NM_002197	48	1,49	5,20E-03
STOM	201060_x_at	AI537887	NM_004099 NM_198194	2040	1,49	3,02E-04
ZNF503	227195_at	AA603467	NM_032772	84858	1,49	8,67E-07
CBX5	242069_at	BE568225	NM_012117	23468	1,48	3,23E-04
PPAP2B	212226_s_at	AA628586	NM_003713 NM_177414	8613	1,48	2,29E-03
C20orf102	226973_at	AA206763	NM_080607	128434	1,47	1,33E-04
CDKN2C	211792_s_at	U17074	NM_001262 NM_078626	1031	1,47	7,95E-03
PDZRN3	212915_at	AL569804	NM_015009	23024	1,47	5,49E-04
CRYGD	207532_at	NM_006891	NM_006891	1421	1,46	3,28E-03
AW207243	238617_at	AW207243	---	---	1,46	3,92E-09
EIF5A2	235296_at	BG500474	NM_020390	56648	1,46	5,19E-09
ANKRD5	220144_s_at	NM_022096	NM_022096 NM_198798	63926	1,45	8,13E-04
UNQ470	228403_at	AL541276	NM_198573	375704	1,45	3,48E-03
KCNJ8	205303_at	BF514158	NM_004982	3764	1,45	5,86E-05
ID1	208937_s_at	D13889	NM_002165 NM_181353	3397	1,45	1,41E-04
SALL4	229661_at	NM_020436	NM_020436	57167	1,44	2,91E-05
DPYSL3	201430_s_at	W72516	NM_001387	1809	1,44	2,58E-03
MSX2	210319_x_at	D89377	NM_002449	4488	1,44	1,48E-03
FNDC5	226096_at	AI760132	NM_153756	252995	1,44	7,61E-04
ZNF239	206261_at	NM_005674	NM_005674	8187	1,44	6,22E-05
COBLL1	203642_s_at	NM_014900	NM_014900	22837	1,44	6,55E-03
KIAA1524	1553810_a_at	NM_020890	NM_020890	57650	1,44	8,59E-03
AL038824	213676_at	AL038824	XM_496810	441151	1,44	6,78E-04
ARL6	235320_at	AL138043	NM_032146 NM_177976	84100	1,44	4,10E-07
MGC15937	227794_at	BF432254	NM_080661	92292	1,43	3,16E-03
BE671123	235798_at	BE671123	---	---	1,43	4,96E-06
ARL6	223735_at	AL136815	NM_032146 NM_177976	84100	1,43	7,57E-05
LOC221810	221911_at	BE881590	---	221810	1,43	2,72E-03
SEZ6L	207873_x_at	NM_021115	NM_021115	23544	1,42	2,45E-05
DOK4	207747_s_at	NM_018110	NM_018110	55715	1,42	3,44E-05
SLC1A1	206396_at	NM_004170	NM_004170	6505	1,42	4,65E-03

NSE1	225667_s_at	AI601101	NM_145175	151354	1,42	1,15E-03
ARHGAP24	230803_s_at	AI761947	NM_031305	83478	1,42	3,92E-03
C6orf152	242006_at	AI379143	NM_181714	167691	1,42	6,09E-03
LOC132671	229331_at	AI559300	NM_145263	132671	1,41	1,82E-03
TH	208291_s_at	NM_000360	NM_000360 NM_199292 NM_199293	7054	1,40	7,49E-04
RBL1	1555004_a_at	BC032247	NM_002895 NM_183404	5933	1,40	5,16E-03
SFRP1	202037_s_at	NM_003012	NM_003012	6422	1,40	5,74E-05
CTNNA1	1558214_s_at	BG330076	NM_001903	1495	1,40	5,25E-07
CPT1A	210688_s_at	BC000185	NM_001876	1374	1,40	1,43E-03
AI917901	243140_at	AI917901	---	---	1,40	1,50E-04
HES1	203394_s_at	BE973687	NM_005524	3280	1,40	4,39E-06
GALNT7	222587_s_at	BF699855	NM_017423	51809	1,40	1,79E-03
MGC33846	231430_at	AW205640	NM_175885	220382	1,39	1,42E-03
SEZ6L	211894_x_at	AB041736	NM_021115	23544	1,39	9,95E-07
CHML	206079_at	NM_001821	NM_001821	1122	1,39	8,74E-03
EGLN3	222847_s_at	AI378406	NM_022073	112399	1,39	3,90E-03
MDM1	213761_at	AW664850	NM_017440 NM_020128	56890	1,38	1,18E-04
SFRP1	202035_s_at	AI332407	NM_003012	6422	1,38	3,39E-03
CBLN1	205747_at	NM_004352	NM_004352	869	1,38	1,13E-03
PDLIM5	211681_s_at	AF116705	NM_001011513 NM_001011514 NM_001011515 NM_001011516 NM_006457	10611	1,38	1,41E-04
NQO1	210519_s_at	BC000906	NM_000903	1728	1,38	4,39E-03
ST8SIA1	210073_at	L32867	NM_003034	6489	1,38	9,29E-04
AL359594	1566867_at	AL359594	---	---	1,38	4,68E-03
DLEU2	216870_x_at	AF264787	NM_006021	8847	1,38	2,48E-04
BF966021	212698_s_at	BF966021	NM_144710 NM_178584	151011	1,37	4,75E-04
C14orf125	226510_at	BF435286	XM_113763 XM_370759	25938	1,37	5,78E-03
TRIM37	1554001_at	BC036012	NM_001005207 NM_015294	4591	1,37	1,10E-05
TLE3	228340_at	BE967118	NM_005078	7090	1,36	2,10E-03
SFRP1	202036_s_at	AF017987	NM_003012	6422	1,36	1,13E-03
C5orf13	222344_at	AW972765	NM_004772	9315	1,36	3,74E-03

SLC8A3	1562403_a_at	AK096553	NM_033262 NM_058240 NM_182932 NM_182933 NM_182936 NM_183002	6547	1,36	1,60E-04
FGFR2	208234_x_at	NM_022976	NM_000141 NM_022969 NM_022970 NM_022971 NM_022972 NM_022973 NM_022974 NM_022975 NM_022976 NM_023028 NM_023029 NM_023030 NM_023031	2263	1,36	2,95E-03
DLL3	219537_x_at	NM_016941	NM_016941 NM_203486	10683	1,35	4,38E-05
CUGBP2	202156_s_at	N36839	NM_006561	10659	1,35	2,49E-03
APBB2	213419_at	U62325	NM_173075	323	1,35	5,44E-04
DOCK10	219279_at	NM_017718	NM_014689	55619	1,34	5,78E-05
MAPK12	206106_at	AL022328	NM_002969	6300	1,34	2,33E-06
TLE3	212770_at	AW873621	NM_005078	7090	1,34	8,20E-04
BE670307	227955_s_at	BE670307	---	---	1,34	1,89E-05
HGF	210998_s_at	M77227	NM_000601 NM_001010931 NM_001010932 NM_001010933 NM_001010934	3082	1,34	9,86E-03
FLJ11259	218627_at	NM_018370	NM_018370	55332	1,33	4,22E-03
AI826125	229866_at	AI826125	---	---	1,33	4,02E-04
SEZ6L	240709_at	AW204757	NM_021115	23544	1,33	5,75E-03
RAB27B	228708_at	BF438386	NM_004163	5874	1,33	9,45E-03
MAP3K1	225927_at	AA541479	XM_042066	4214	1,33	1,90E-03
AL040051	225481_at	AL040051	---	---	1,33	5,84E-04
BE967311	226225_at	BE967311	---	---	1,32	2,96E-05
TLE4	204872_at	NM_007005	NM_007005	7091	1,32	4,50E-03
SNCAIP	219511_s_at	NM_005460	NM_005460	9627	1,32	3,58E-04
KIAA0376	212480_at	AB002374	NM_015330	23384	1,32	2,79E-05
LZTS1	219042_at	NM_021020	NM_021020	11178	1,32	3,07E-04
KIAA0318	238817_at	BF063412	NM_015347	23504	1,32	5,00E-04

RNF34	219035_s_at	NM_025126	NM_025126 NM_194271	80196	1,32	1,40E-03
STXBP4	244404_at	AI376134	NM_178509	252983	1,31	3,35E-05
AU144956	232501_at	AU144956	---	---	1,31	6,46E-06
FLJ11127	219694_at	NM_019018	NM_019018	54491	1,31	1,32E-03
MITF	226066_at	AL117653	NM_000248 NM_006722 NM_198158 NM_198159 NM_198177 NM_198178	4286	1,31	1,07E-03
ETS1	224833_at	BE218980	NM_005238	2113	1,31	2,75E-03
NANOS1	228523_at	AW970089	NM_001009553 NM_199461	340719	1,31	1,30E-03
FAM19A5	237094_at	AI953086	NM_015381	25817	1,31	2,32E-07
LBH	221011_s_at	NM_030915	NM_030915	81606	1,31	1,22E-04
PEX26	219180_s_at	AI817074	NM_017929	55670	1,30	3,74E-03
GALNT7	218313_s_at	NM_017423	NM_017423	51809	1,30	1,80E-04
C2orf23	204365_s_at	NM_022912	NM_022912	65055	1,30	5,58E-03
AL049709	216548_x_at	AL049709	---	---	1,30	5,30E-04
MGC34032	1552782_at	AK091400	NM_152697	204962	1,30	1,97E-03
DLL1	224215_s_at	AF196571	NM_005618	28514	1,30	1,62E-04
TMEM20	236219_at	AI452512	NM_153226	159371	1,30	3,29E-03
AW305300	238962_at	AW305300	---	---	1,30	4,31E-04
C20orf23	219570_at	NM_024704	NM_024704	55614	1,29	1,18E-03
DRIM	209725_at	AF072718	NM_014503	27340	1,29	1,99E-03
CBLB	209682_at	U26710	NM_170662	868	1,29	3,69E-03
STRA6	1569335_a_at	BC015881	NM_022369	64220	1,29	9,19E-04
CRTAC1	221204_s_at	NM_018058	NM_018058	55118	1,28	5,56E-04
AF070602	216214_at	AF070602	---	---	1,28	5,02E-03
NAGA	202943_s_at	M38083	NM_000262	4668	1,28	1,26E-03
AK025909	233814_at	AK025909	---	---	1,27	1,16E-04
AI141426	229898_at	AI141426	---	---	1,27	6,87E-05
SLC8A1	241752_at	AA094434	NM_021097	6546	1,27	6,10E-04
INSIG1	201625_s_at	BE300521	NM_005542 NM_198336 NM_198337	3638	1,26	8,33E-03
IQGAP1	210840_s_at	D29640	NM_003870	8826	1,26	2,60E-04
GAP43	204471_at	NM_002045	NM_002045	2596	1,26	5,02E-04
PDLIM5	213684_s_at	BF671400	NM_001011513 NM_001011514 NM_001011515 NM_001011516 NM_006457	10611	1,26	9,47E-04

GAP43	216963_s_at	AF279774	NM_002045	2596	1,26	5,66E-03
KLHL5	226001_at	AK002174	NM_001007075 NM_199039	51088	1,26	3,67E-04
RGS4	204339_s_at	BC000737	NM_005613	5999	1,25	4,16E-04
AF279774	216967_at	AF279774	---	---	1,25	9,39E-03
PTER	218967_s_at	NM_030664	NM_001001484 NM_030664	9317	1,25	1,22E-03
TLE3	212769_at	AI567426	NM_005078	7090	1,25	3,78E-03
TLE3	206472_s_at	NM_005078	NM_005078	7090	1,25	4,37E-03
RGS4	204338_s_at	NM_005613	NM_005613	5999	1,25	3,77E-04
CPT1A	203634_s_at	NM_001876	NM_001876	1374	1,25	1,93E-03
ASAHL	227135_at	AI436803	NM_014435	27163	1,25	9,20E-06
LOC344595	239466_at	AA463827	XM_298151	344595	1,25	4,65E-05
TH1L	225006_x_at	AJ238379	NM_016397 NM_198976	51497	1,24	9,26E-03
SEZ6L	216047_x_at	AL050253	NM_021115	23544	1,24	1,75E-05
NSE1	234331_s_at	AK025063	NM_145175	151354	1,24	1,19E-04
LRRIQ2	219886_at	NM_024548	NM_024548	79598	1,24	1,44E-03
GALNT10	207357_s_at	NM_017540	NM_017540 NM_198321	55568	1,24	2,18E-03
BF815640	238517_at	BF815640	---	---	1,23	4,48E-03
SLC30A9	229500_at	AI609256	NM_006345	10463	1,23	2,32E-03
LOC63929	227910_at	AI635379	NM_022098	63929	1,23	1,48E-04
CSE1L	210765_at	AF053640	NM_001316 NM_177436	1434	1,23	7,45E-03
BCL2L11	1558143_a_at	AK027160	NM_006538 NM_138621 NM_138622 NM_138623 NM_138624 NM_138625 NM_138626 NM_138627 NM_207002 NM_207003	10018	1,23	6,27E-03
TM4SF14	221002_s_at	NM_030927	NM_030927	81619	1,22	4,04E-03
SLIT3	203813_s_at	NM_003062	NM_003062	6586	1,22	1,58E-06
RAPGEF5	204681_s_at	NM_012294	XM_499059	9771	1,22	6,58E-04
ZNF184	213452_at	AI811577	NM_007149	7738	1,22	9,16E-03
PCYT2	209577_at	BC000351	NM_002861	5833	1,22	2,05E-03
WDR51A	234749_s_at	AL117629	NM_015426	25886	1,22	2,87E-03
MAN2A1	226538_at	AV700323	NM_002372	4124	1,21	3,05E-03
TLE4	233575_s_at	AA705845	NM_007005	7091	1,21	2,34E-04
AW665447	230113_at	AW665447	---	---	1,21	3,86E-03
SAP30	204899_s_at	BF247098	NM_003864	8819	1,21	2,33E-03
LOC221810	221910_at	BF131965	---	221810	1,21	8,18E-03
HOMER3	204647_at	NM_004838	NM_004838	9454	1,20	4,61E-03

SLC1A1	213664_at	AW235061	NM_004170	6505	1,20	5,98E-03
C20orf108	224690_at	BG432350	NM_080821	116151	1,20	8,73E-03
ZNF238	207164_s_at	NM_006352	NM_006352 NM_205768	10472	1,20	7,98E-03
PIR	207469_s_at	NM_003662	NM_003662	8544	1,20	1,53E-05
FLRT3	219250_s_at	NM_013281	NM_013281 NM_198391	23767	1,19	7,10E-04
SLIT3	203812_at	AB011538	NM_003062	6586	1,19	1,40E-03
TGIF	203313_s_at	NM_003244	NM_003244 NM_170695 NM_173207 NM_173208 NM_173209 NM_173210 NM_173211 NM_174886	7050	1,19	5,40E-05
CDKN2C	204159_at	NM_001262	NM_001262 NM_078626	1031	1,19	8,59E-05
MTUS1	212095_s_at	BE552421	NM_001001924 NM_001001925 NM_001001927 NM_001001931 NM_020749	57509	1,19	2,48E-04
SCARA3	223842_s_at	AB007830	NM_016240 NM_182826	51435	1,19	3,33E-04
HTATSF1	202602_s_at	NM_014500	NM_014500	27336	1,19	2,42E-05
TRAM2	202369_s_at	NM_012288	NM_012288	9697	1,18	7,27E-03
PTGFRN	224950_at	BF476250	NM_020440	5738	1,18	2,73E-03
DRD2	216938_x_at	S69899	NM_000795 NM_016574	1813	1,18	2,02E-03
TOP3B	215781_s_at	D87012	NM_003935	8940	1,18	2,21E-03
ACY1L2	225421_at	AI654133	NM_001010853	135293	1,18	7,34E-04
BC025350	1569418_at	BC025350	---	---	1,18	1,04E-06
KIAA1706	225630_at	AB051493	NM_030636	80820	1,18	1,55E-04
AW874669	239834_at	AW874669	---	---	1,18	7,57E-04
CPT1A	203633_at	BF001714	NM_001876	1374	1,17	1,23E-03
C2orf23	204364_s_at	BE535746	NM_022912	65055	1,17	2,59E-04
SMO	218629_at	NM_005631	NM_005631	6608	1,17	3,37E-05
RPH3A	205230_at	NM_014954	NM_014954	22895	1,17	6,35E-03
VIL2	208621_s_at	BF663141	NM_003379	7430	1,17	8,04E-04
SEC15L2	225900_at	AW294630	XM_039570	23233	1,17	7,12E-03
MCC	206132_at	NM_002387	NM_002387	4163	1,17	5,91E-04
C20orf108	224693_at	AI133137	NM_080821	116151	1,16	2,04E-05
RFC5	203209_at	BC001866	NM_007370 NM_181578	5985	1,16	9,74E-03

MAPK11	211499_s_at	U92268	NM_002751 NM_138993	5600	1,16	3,08E-04
EB-1	227439_at	AI806510	NM_020140 NM_152788 NM_181670	56899	1,16	9,25E-08
FBXL7	213249_at	AU145127	NM_012304	23194	1,16	5,25E-07
TTC9	213172_at	AW235608	XM_027236	23508	1,16	7,95E-04
SLC40A1	223044_at	AL136944	NM_014585	30061	1,16	6,08E-04
AI452715	229817_at	AI452715	---	---	1,16	3,41E-03
MAN2A1	235103_at	AA029155	NM_002372	4124	1,16	5,37E-04
VIL2	217234_s_at	AF199015	NM_003379	7430	1,16	3,24E-03
SEZ6L	213609_s_at	AB023144	NM_021115	23544	1,15	2,65E-06
TLX2	207410_s_at	NM_016170	NM_001534 NM_016170	3196	1,15	3,55E-05
CGI-96	202937_x_at	AL022316	NM_015703	27341	1,15	2,55E-03
KCNJ8	205304_s_at	NM_004982	NM_004982	3764	1,14	5,54E-03
ZNF537	223392_s_at	BF510588	NM_020856	57616	1,14	9,47E-06
DHX35	234728_s_at	AL023803	NM_021931	60625	1,14	6,62E-06
STRA6	1569334_at	BC015881	NM_022369	64220	1,14	5,40E-03
EAF2	219551_at	NM_018456	NM_018456	55840	1,14	9,77E-04
ITPR1	203710_at	NM_002222	NM_002222	3708	1,14	1,07E-03
LIFR	225575_at	AI680541	NM_002310	3977	1,13	4,19E-06
GJA7	208460_at	NM_005497	NM_005497	10052	1,13	4,63E-03
MBD2	214397_at	AI827820	NM_003927 NM_015832	8932	1,13	1,61E-03
ANKRD13	224810_s_at	AL569476	NM_033121	88455	1,13	2,65E-04
HDAC8	223908_at	AF212246	NM_018486	55869	1,13	1,96E-04
STN2	227461_at	AA632295	NM_033104	85439	1,12	4,18E-03
BE464799	214036_at	BE464799	---	---	1,12	1,37E-04
SOX2	228038_at	AI669815	NM_003106	6657	1,12	1,75E-04
GTF2E1	205930_at	NM_005513	NM_005513	2960	1,12	1,67E-03
H10661	242317_at	H10661	---	---	1,12	3,16E-04
HSZFP36	229732_at	AI417785	XM_375568	55552	1,12	2,16E-03
RBBP9	221440_s_at	NM_006606	NM_006606 NM_153328	10741	1,12	9,04E-04
DNAJB6	209015_s_at	BC002446	NM_005494 NM_058246	10049	1,12	2,51E-03
KNTC1	206316_s_at	NM_014708	NM_014708	9735	1,12	7,31E-03
FUT11	238551_at	BF541967	NM_173540	170384	1,12	1,14E-03
MAP2K6	205698_s_at	NM_002758	NM_002758 NM_031988	5608	1,11	8,00E-03
NRM	225592_at	D81048	NM_007243	11270	1,11	8,62E-03
STMN3	222557_at	AL353715	NM_015894	50861	1,11	1,13E-03
INSIG1	201626_at	BG292233	NM_005542 NM_198336 NM_198337	3638	1,11	1,47E-03
SH3MD2	225589_at	AB040927	NM_020870	57630	1,11	3,78E-04

BCL2L11	225606_at	AI949179	NM_006538 NM_138621 NM_138622 NM_138623 NM_138624 NM_138625 NM_138626 NM_138627 NM_207002 NM_207003	10018	1,11	4,77E-07
TYRO3	211432_s_at	U05682	NM_006293	7301	1,11	7,76E-03
APAF1	204859_s_at	NM_013229	NM_001160 NM_013229 NM_181861 NM_181868 NM_181869	317	1,11	8,54E-03
LRRC1	218816_at	NM_018214	NM_018214 NM_025168	55227	1,11	4,89E-03
DNM3	209839_at	AL136712	NM_015569	26052	1,11	5,67E-06
MAN2A1	205105_at	NM_002372	NM_002372	4124	1,11	6,81E-03
FLJ23322	220707_s_at	NM_024955	NM_024955	80020	1,10	2,15E-03
NDRG2	214279_s_at	W74452	NM_016250 NM_201535 NM_201536 NM_201537 NM_201538 NM_201539 NM_201540 NM_201541	57447	1,10	5,44E-03
SCAM-1	207788_s_at	NM_005775	NM_005775	10174	1,10	9,08E-03
LMO1	206718_at	NM_002315	NM_002315	4004	1,10	5,27E-04
ITPR1	216944_s_at	U23850	NM_002222	3708	1,10	8,15E-03
PCNXL2	39650_s_at	AB007895	NM_014801 NM_024938	80003	1,10	9,56E-05
RBBP9	232751_at	AL121893	NM_006606 NM_153328	10741	1,10	8,94E-04
AP3B1	203142_s_at	NM_003664	NM_003664	8546	1,09	2,19E-03
SNAP29	222597_at	AI346639	NM_004782	9342	1,09	1,46E-04
C20orf161	1553960_at	CA447177	NM_033421 NM_152897	90203	1,09	2,01E-03
LOC283464	232021_at	AI864273	XM_290597	283464	1,09	1,32E-03
AI589594	238694_at	AI589594	---	---	1,09	2,79E-05
SOX2	213721_at	L07335	NM_003106	6657	1,08	7,40E-04
ST3GAL6	210942_s_at	AB022918	NM_006100	10402	1,08	2,47E-04
BG231758	227615_at	BG231758	---	---	1,08	5,95E-08
FLJ33814	225644_at	BF060776	NM_173510	150275	1,08	2,63E-06
TYMS	1554696_s_at	AB077208	NM_001071	7298	1,08	7,83E-03
BOK	223349_s_at	BE614255	NM_032515	666	1,08	3,19E-06
C1QL1	205575_at	NM_006688	NM_006688	10882	1,08	1,06E-04

GMPS	236648_at	AI684467	NM_003875	8833	1,08	6,96E-04
AI733583	243235_at	AI733583	---	---	1,08	6,94E-03
BE066500	239729_at	BE066500	---	---	1,08	8,69E-04
ASAHL	232072_at	AK025371	NM_014435	27163	1,08	3,73E-04
SNX5	229981_at	AA131508	NM_014426 NM_152227	27131	1,08	1,66E-05
CYBA	203028_s_at	NM_000101	NM_000101	1535	1,07	5,76E-04
PTER	222798_at	BF112019	NM_001001484 NM_030664	9317	1,07	2,48E-03
LOC440820	226602_s_at	T30183	XM_496519	440820	1,07	2,20E-05
AA214369	238545_at	AA214369	---	---	1,07	3,48E-03
ELAVL4	241424_at	BF111117	NM_021952	1996	1,07	4,96E-03
C6orf189	228875_at	AI540210	---	221303	1,07	1,85E-04
PARG1	203910_at	NM_004815	NM_004815	9411	1,07	1,74E-04
OLFML3	218162_at	NM_020190	NM_020190	56944	1,07	4,22E-03
PI4K2B	222631_at	AI862887	NM_018323	55300	1,07	2,03E-03
PHYHIPL	226623_at	AI829726	NM_032439	84457	1,07	5,85E-05
AA156933	236141_at	AA156933	---	---	1,07	9,86E-04
AI346432	229132_at	AI346432	---	---	1,07	3,94E-04
AI919519	235092_at	AI919519	---	---	1,07	8,75E-03
ELK3	221773_at	AW575374	NM_005230	2004	1,07	2,45E-03
LPPR4	213496_at	AW592563	NM_014839	9890	1,07	1,23E-05
EZH2	203358_s_at	NM_004456	NM_004456 NM_152998	2146	1,06	5,13E-03
NS5ATP13TP2	225510_at	BG033561	NM_178507	220323	1,06	1,40E-04
KIAA1102	212325_at	AK027231	NM_014988	22998	1,06	1,82E-09
ZNF505	208119_s_at	NM_031218	NM_001004126 NM_031218	81931	1,06	5,75E-03
C20orf40	231200_at	BG222606	NM_144703	149986	1,06	1,73E-03
SLC8A1	238546_at	BF344961	NM_021097	6546	1,06	6,63E-03
PREX1	224909_s_at	BF308645	NM_020820	57580	1,06	7,16E-03
MAK3	222393_s_at	AU149868	NM_025146	80218	1,06	1,11E-05
TMPO	209753_s_at	BG391171	NM_003276	7112	1,06	3,02E-03
ADORA2A	205013_s_at	NM_000675	NM_000675	135	1,06	9,97E-03
MGC3040	223523_at	BC000568	NM_023943	66000	1,06	7,88E-07
AI700633	212812_at	AI700633	---	---	1,06	8,55E-03
TWSG1	219201_s_at	NM_020648	NM_020648	57045	1,06	9,70E-04
PPP3CB	209817_at	M29550	NM_021132	5532	1,06	2,71E-06
MAP3K13	206249_at	NM_004721	NM_004721	9175	1,06	3,52E-03
SKP2	210567_s_at	BC001441	NM_005983 NM_032637	6502	1,06	8,10E-04
SYN2	210315_at	AF077737	NM_003178 NM_133625	6854	1,05	9,08E-03
CGI-96	33307_at	AL022316	NM_015703	27341	1,05	7,16E-04
GNG12	1555240_s_at	AF493879	NM_018841	55970	1,05	6,35E-04
CUTL2	213920_at	AB006631	NM_015267	23316	1,04	1,63E-03

FLRT3	222853_at	N71923	NM_013281 NM_198391	23767	1,04	9,61E-07
FLJ13842	219877_at	NM_024645	NM_024645	79698	1,04	6,38E-03
ADRBK2	228771_at	AI651212	NM_005160	157	1,04	7,18E-05
SEC61A2	228747_at	AI694646	NM_018144	55176	1,04	4,56E-03
ST3GAL6	213355_at	AI989567	NM_006100	10402	1,04	1,38E-04
BF434228	235850_at	BF434228	---	---	1,04	4,97E-03
PCGF5	227935_s_at	AA522681	NM_032373	84333	1,04	8,11E-04
MYST1	214885_at	AL050395	NM_032188	84148	1,04	5,82E-03
PEX13	1558163_at	BC040953	NM_002618	5194	1,03	3,87E-03
INSIG1	201627_s_at	NM_005542	NM_005542 NM_198336 NM_198337	3638	1,03	2,57E-06
NELL2	203413_at	NM_006159	NM_006159	4753	1,03	1,75E-03
RND3	212724_at	BG054844	NM_005168	390	1,03	1,50E-03
TFDP2	203588_s_at	BG034328	NM_006286	7029	1,03	9,43E-03
CTNNBL1	221021_s_at	NM_030877	NM_030877	56259	1,03	3,20E-03
CHML	1565951_s_at	AJ293392	NM_001821	1122	1,03	8,52E-03
ITPR1	211323_s_at	L38019	NM_002222	3708	1,02	3,21E-05
DKFZP564O123	202536_at	AK002165	NM_014043	25978	1,02	9,94E-05
CKLF	219161_s_at	NM_016951	NM_016326 NM_016951 NM_181640 NM_181641	51192	1,02	8,63E-03
IQGAP1	213446_s_at	AI679073	NM_003870	8826	1,02	1,01E-03
C11orf8	215692_s_at	BE645386	NM_001584	744	1,02	1,49E-03
AL559474	235918_x_at	AL559474	---	---	1,02	2,13E-03
ADRBK2	204184_s_at	NM_005160	NM_005160	157	1,02	3,30E-04
LOC152185	234995_at	AA668779	NM_144718	152185	1,02	9,02E-04
XRCC4	205071_x_at	AB017445	NM_003401 NM_022406 NM_022550	7518	1,02	3,71E-03
GPR125	210473_s_at	M37712	NM_145290	166647	1,01	1,54E-08
SLCO3A1	219229_at	NM_013272	NM_013272	28232	1,01	7,19E-04
POLE	216026_s_at	AL080203	NM_006231	5426	1,01	8,50E-03
TMOD3	223078_s_at	AF177171	NM_014547	29766	1,01	2,98E-05
SKP2	203626_s_at	NM_005983	NM_005983 NM_032637	6502	1,01	9,59E-08
RBPMS	207836_s_at	NM_006867	NM_001008710 NM_001008711 NM_001008712 NM_006867	11030	1,00	5,05E-03
PHTF2	217097_s_at	AC004990	NM_020432	57157	1,00	4,53E-03
TM4SF14	223314_at	BF025955	NM_030927	81619	1,00	2,72E-03
SDC2	212157_at	BE048514	NM_002998	6383	1,00	6,35E-03

TP53I3	210609_s_at	BC000474	NM_004881 NM_147184	9540	1,00	8,78E-04
AL049385	232297_at	AL049385	---	---	1,00	1,36E-05
MTUS1	212096_s_at	AL096842	NM_001001924 NM_001001925 NM_001001927 NM_001001931 NM_020749	57509	1,00	1,43E-04
KLF7	1555420_a_at	BC012919	NM_003709	8609	1,00	1,21E-04
ZNF555	1556187_at	AF052118	NM_152791	148254	0,99	7,62E-03
GPAM	225424_at	AB046780	NM_020918	57678	0,99	5,06E-03
FLJ13273	1554518_at	BC032942	NM_024751	79807	0,99	2,86E-04
SAP30	204900_x_at	NM_003864	NM_003864	8819	0,99	3,10E-03
FBXL10	229855_at	AA779208	NM_001005366 NM_032590	84678	0,99	1,80E-03
NEUROD4	221318_at	NM_021191	NM_021191	58158	0,99	2,89E-03
FLJ12649	219626_at	NM_024597	XM_291344	79649	0,99	9,37E-05
TMPO	209754_s_at	AF113682	NM_003276	7112	0,99	6,52E-03
RASL11B	219142_at	NM_023940	NM_023940	65997	0,99	4,29E-03
ASAHL	214765_s_at	AK024677	NM_014435	27163	0,98	1,03E-05
ZNF238	212774_at	AJ223321	NM_006352 NM_205768	10472	0,98	6,70E-05
ITPR2	202662_s_at	NM_002223	NM_002223	3709	0,98	8,48E-03
SEZ6L	231650_s_at	BE672217	NM_021115	23544	0,98	1,12E-04
C10orf47	229801_at	AI640157	NM_153256	254427	0,98	7,31E-03
SNAG1	226683_at	AU146771	NM_052870	112574	0,98	1,70E-04
FGF11	227271_at	AU151265	NM_004112	2256	0,98	9,49E-03
DDT	202929_s_at	NM_001355	NM_001355	1652	0,98	3,16E-04
KLHL5	233866_at	AK001836	NM_001007075 NM_199039	51088	0,97	7,05E-03
PVRL3	241970_at	C14898	NM_015480	25945	0,97	5,02E-03
SEMA5A	205405_at	NM_003966	NM_003966	9037	0,97	2,27E-03
RFC1	209085_x_at	L14922	NM_002913	5981	0,97	6,24E-03
TRIM36	219736_at	NM_018700	NM_018700	55521	0,97	4,06E-03
FLJ23322	231846_at	AK026975	NM_024955	80020	0,97	3,27E-03
IMP-1	223689_at	AF198254	NM_006546	10642	0,97	1,78E-04
MDFI	205375_at	NM_005586	NM_005586	4188	0,97	7,23E-03
BE878277	212829_at	BE878277	---	---	0,97	1,51E-04
FLJ14451	227430_at	AI969773	NM_032786	84872	0,97	8,16E-03
NARG1	226998_at	AL556909	NM_057175	80155	0,96	1,89E-06
TMEM38B	222736_s_at	BC000049	NM_018112	55151	0,96	3,02E-05
LAMP2	203041_s_at	J04183	NM_002294 NM_013995	3920	0,96	1,13E-04

FANCL	218397_at	NM_018062	NM_018062	55120	0,96	3,05E-03
APOBEC3G	204205_at	NM_021822	NM_021822	60489	0,96	7,76E-03
NM_024853	220533_at	NM_024853	---	---	0,96	3,50E-03
UNG	202330_s_at	NM_003362	NM_003362 NM_080911	7374	0,96	2,31E-03
ACTL6A	202668_s_at	NM_004301	NM_004301 NM_177989 NM_178042	86	0,96	1,28E-03
N71074	238078_at	N71074	---	---	0,96	7,93E-04
FLJ40432	228810_at	AW135279	NM_152523	151195	0,96	4,18E-06
KIAA1102	212327_at	AK026815	NM_014988	22998	0,96	1,66E-05
C12orf2	225946_at	BG484552	NM_007211	11228	0,96	4,33E-06
FLJ11539	219791_s_at	NM_024748	XM_496724	79804	0,96	4,56E-04
MNS1	219703_at	NM_018365	NM_018365	55329	0,96	6,11E-04
SLC8A1	235518_at	AI741439	NM_021097	6546	0,95	4,16E-03
PSMD9	209334_s_at	BC002383	NM_002813	5715	0,95	5,08E-06
ACY1L2	225431_x_at	BE779764	NM_001010853	135293	0,95	7,73E-04
SOD2	215223_s_at	W46388	NM_000636	6648	0,95	3,07E-03
PPP1R3D	204554_at	AL109928	NM_006242	5509	0,95	2,56E-03
BF056892	229024_at	BF056892	---	---	0,95	1,67E-04
CHD6	225031_at	AL031667	NM_032221	84181	0,95	4,37E-05
MGC7036	227983_at	AI810244	NM_145058	196383	0,95	2,13E-04
CCBE1	243805_at	BG035826	NM_133459	147372	0,95	1,68E-03
AL110237	232959_at	AL110237	---	---	0,95	9,01E-04
LOC134111	226612_at	H17038	XM_059689	134111	0,94	3,88E-03
ELAVL4	234904_x_at	S73887	NM_021952	1996	0,94	1,21E-04
PANK2	238856_s_at	BG108346	NM_024960 NM_153637 NM_153638 NM_153639 NM_153640 NM_153641	80025	0,94	3,01E-05
CBX5	230752_at	AI638063	NM_012117	23468	0,94	6,48E-04
NDUFA6	202000_at	BC002772	NM_002490	4700	0,94	5,54E-04
HSPC117	200042_at	NM_014306	NM_014306	51493	0,94	6,59E-07
TLE4	235765_at	AI742932	NM_007005	7091	0,94	9,75E-04
SDC4	202071_at	NM_002999	NM_002999	6385	0,94	8,24E-05
CD47	211075_s_at	Z25521	NM_001777 NM_198793	961	0,94	1,46E-03
EGFR	224999_at	BE878463	NM_005228 NM_201282 NM_201283 NM_201284	1956	0,93	4,74E-03
TLX2	211049_at	BC006356	NM_001534 NM_016170	3196	0,93	6,56E-04
VIL2	208622_s_at	AA670344	NM_003379	7430	0,93	3,33E-03
JPH1	1553533_at	NM_020647	NM_020647	56704	0,93	2,57E-03
TEAD3	209454_s_at	AF142482	NM_003214	7005	0,93	5,72E-03
FKBP5	204560_at	NM_004117	NM_004117	2289	0,93	2,37E-03

SEC61A2	219499_at	NM_018144	NM_018144	55176	0,93	9,99E-03
PGM2	225366_at	AI652855	NM_018290	55276	0,93	6,09E-04
P4HA1	207543_s_at	NM_000917	NM_000917	5033	0,93	2,61E-04
SEC23A	204344_s_at	NM_006364	NM_006364	10484	0,93	3,24E-03
KIAA1102	212328_at	AB029025	NM_014988	22998	0,93	1,29E-05
RANBP1	202483_s_at	NM_002882	NM_002882	5902	0,93	7,82E-03
STARD4	226390_at	AA628398	NM_139164	134429	0,93	1,59E-04
B4GALT6	206232_s_at	NM_004775	NM_004775	9331	0,93	2,63E-03
AHI1	220842_at	NM_017651	NM_017651	54806	0,92	6,04E-03
MCM4	212142_at	AI936566	NM_005914 NM_182746	4173	0,92	7,62E-04
CHD6	225026_at	BF572029	NM_032221	84181	0,92	3,17E-03
HMGB2	208808_s_at	BC000903	NM_002129	3148	0,92	7,83E-03
DNMT3B	220668_s_at	NM_006892	NM_006892 NM_175848 NM_175849 NM_175850	1789	0,92	2,56E-03
AI095542	235759_at	AI095542	---	---	0,92	4,36E-03
SLC25A1	210010_s_at	U25147	NM_005984	6576	0,92	2,10E-03
ELAVL4	238073_at	R55745	NM_021952	1996	0,92	1,01E-03
BG149337	229814_at	BG149337	---	---	0,92	2,56E-03
R43103	243642_x_at	R43103	---	---	0,92	3,67E-03
NEDD1	1552417_a_at	NM_152905	NM_152905	121441	0,91	2,33E-03
MTUS1	212093_s_at	AI695017	NM_001001924 NM_001001925 NM_001001927 NM_001001931 NM_020749	57509	0,91	4,60E-04
ALG10	1552306_at	BC033730	NM_032834	84920	0,91	7,39E-04
ELAVL4	206051_at	NM_021952	NM_021952	1996	0,91	1,99E-03
MLF1	204783_at	AI911434	NM_022443	4291	0,91	1,31E-04
SLC2A8	218985_at	NM_014580	NM_014580	29988	0,91	6,78E-03
ITPR2	202660_at	AA834576	NM_002223	3709	0,91	9,15E-03
CISH	223377_x_at	AF035947	NM_013324 NM_145071	1154	0,91	4,28E-03
C3orf4	1554149_at	BC013610	NM_019895	56650	0,91	2,11E-05
LOC134111	226618_at	AW572911	XM_059689	134111	0,91	5,63E-04
BE857972	243781_at	BE857972	---	---	0,91	1,20E-03
Cep70	224150_s_at	AF289495	NM_024491	80321	0,91	4,27E-03
PP2447	232706_s_at	AW009248	NM_025204	80305	0,90	4,10E-03
RGS4	204337_at	AL514445	NM_005613	5999	0,90	1,42E-03
KLF7	204334_at	AA488672	NM_003709	8609	0,90	9,17E-04
SLCO3A1	227367_at	AW976431	NM_013272	28232	0,90	4,34E-03
FZD2	210220_at	L37882	NM_001466	2535	0,90	2,77E-04
SESTD1	226763_at	AW409611	NM_178123	91404	0,90	9,00E-04

DHX35	218579_s_at	NM_021931	NM_021931	60625	0,90	2,42E-05
PDLIM1	208690_s_at	BC000915	NM_020992	9124	0,90	6,24E-04
BICD1	1554020_at	BC010091	NM_001003398 NM_001714	636	0,90	3,41E-06
PXMP2	219076_s_at	NM_018663	NM_018663	5827	0,90	6,61E-03
SPOCK	202363_at	AF231124	NM_004598	6695	0,90	5,89E-03
AA581439	244650_at	AA581439	---	---	0,89	5,83E-03
BC003667	222487_s_at	BC003667	---	---	0,89	8,10E-03
NFYB	218128_at	AU151875	NM_006166	4801	0,89	2,19E-03
SYNJ2	212828_at	AA191573	NM_003898	8871	0,89	6,92E-03
ITGB5	201124_at	AL048423	NM_002213	3693	0,89	4,74E-03
SLC39A8	219869_s_at	NM_022154	NM_022154	64116	0,89	1,30E-03
AI333006	240432_x_at	AI333006	---	---	0,89	2,24E-03
BRD4	202103_at	AI991631	NM_014299 NM_058243	23476	0,89	3,39E-03
MCM8	233560_x_at	AA370141	NM_032485 NM_182802	84515	0,89	2,33E-03
PKIA	226864_at	BF245954	NM_006823 NM_181839	5569	0,89	4,86E-04
FAM43A	227410_at	AW264102	NM_153690	131583	0,89	4,81E-03
ZMYM1	220206_at	NM_024772	NM_024772	79830	0,89	5,27E-03
SLK	206875_s_at	NM_014720	NM_014720	9748	0,89	9,22E-06
EPB41L5	225855_at	AB046768	NM_020909	57669	0,89	8,39E-04
RAD18	223417_at	AF169796	NM_020165	56852	0,89	2,04E-04
MEIS2	207480_s_at	NM_020149	NM_002399 NM_020149 NM_170674 NM_170675 NM_170676 NM_170677 NM_172315 NM_172316	4212	0,89	4,23E-04
NFYA	204107_at	BF445142	NM_002505 NM_021705	4800	0,88	3,28E-06
SREBF2	201248_s_at	NM_004599	NM_004599	6721	0,88	4,75E-03
FLJ31842	237515_at	AA054642	NM_152487	148534	0,88	8,21E-04
ZFD25	205739_x_at	NM_016220	---	51427	0,88	8,79E-03
DLEU2	215629_s_at	AA905286	NM_006021	8847	0,88	6,43E-04
ZNF85	206572_x_at	NM_003429	NM_003429	7639	0,88	6,85E-06
PCDH17	228863_at	N69091	NM_014459	27253	0,88	6,70E-03
PTPRG	204944_at	NM_002841	NM_002841	5793	0,88	3,65E-03
AL833487	1562245_a_at	AL833487	---	---	0,88	8,59E-03
PCDH17	205656_at	NM_014459	NM_014459	27253	0,88	6,19E-03
ANAPC7	225554_s_at	AA131793	NM_016238	51434	0,88	8,37E-04
BE504215	228563_at	BE504215	---	---	0,88	1,17E-03
MLLT3	204917_s_at	AV756536	NM_004529	4300	0,88	5,47E-03
CD47	213857_s_at	BG230614	NM_001777 NM_198793	961	0,88	3,54E-04

PTK7	1555324_at	BC046109	NM_002821 NM_152880 NM_152881 NM_152882 NM_152883	5754	0,87	3,45E-03
EP300	1562921_at	BC040700	NM_001429	2033	0,87	3,55E-03
VPS29	223026_s_at	AF201946	NM_016226 NM_057180	51699	0,87	9,51E-03
EBF	227646_at	BG435302	NM_024007	1879	0,87	6,32E-04
GPC6	223730_at	AF111178	NM_005708	10082	0,87	7,72E-03
PHF5A	225309_at	AL008582	NM_032758	84844	0,87	1,93E-03
FLJ31842	234980_at	AI004375	NM_152487	148534	0,87	3,12E-04
AW953794	230968_at	AW953794	---	---	0,87	3,09E-03
AI888657	244189_at	AI888657	---	---	0,87	1,23E-03
FLJ21415	218867_s_at	NM_024738	NM_024738	79794	0,87	2,65E-03
MAK3	217745_s_at	NM_025146	NM_025146	80218	0,87	5,22E-04
SEC23A	212887_at	AI753659	NM_006364	10484	0,86	6,69E-03
PAX5	221969_at	BF510692	NM_016734	5079	0,86	4,37E-03
UNC84B	212144_at	AL021707	NM_015374	25777	0,86	9,44E-03
PRIM2A	205628_at	NM_000947	NM_000947	5558	0,86	1,80E-03
ISL1	206104_at	NM_002202	NM_002202	3670	0,86	2,89E-03
NAGA	202944_at	NM_000262	NM_000262	4668	0,86	1,12E-04
SCD4	224901_at	AL571375	NM_024906	79966	0,86	2,89E-04
PHYH	203335_at	NM_006214	NM_006214	5264	0,86	3,64E-05
HMGCS1	205822_s_at	NM_002130	NM_002130	3157	0,86	5,71E-04
GALNAC4S-6ST	203066_at	NM_014863	NM_015892	51363	0,86	1,55E-04
DKFZp762A217	235775_at	AI765006	NM_152588	160335	0,86	2,87E-03
ADRBK2	204183_s_at	AI478542	NM_005160	157	0,85	7,45E-05
BC002942	31837_at	U62317	NM_033200	91289	0,85	2,32E-03
KIAA1853	236151_at	BF315452	NM_194286	84530	0,85	8,93E-03
C10orf58	228155_at	BF512388	NM_032333	84293	0,85	4,55E-08
KIAA0286	212619_at	AW205215	NM_015257	23306	0,85	2,40E-03
AU146017	234082_at	AU146017	---	---	0,85	5,56E-03
GPR85	219898_at	NM_018970	NM_018970	54329	0,85	2,12E-03
KIAA1145	235146_at	N51717	NM_020698	57458	0,85	4,62E-05
CSTF1	202190_at	NM_001324	NM_001324	1477	0,85	2,75E-03
BF510533	228107_at	BF510533	---	---	0,85	7,13E-04
PANK2	218809_at	NM_024960	NM_024960 NM_153637 NM_153638 NM_153639 NM_153640 NM_153641	80025	0,85	5,93E-04
DHX37	223364_s_at	BC004463	NM_032656	57647	0,85	1,99E-03
HMGB3	203744_at	NM_005342	NM_005342	3149	0,85	6,52E-03
BNIP3	201848_s_at	U15174	NM_004052	664	0,85	1,65E-03
LOC284244	214162_at	AF070541	---	284244	0,85	2,94E-03
SV2C	216086_at	AB028977	XM_043493	22987	0,85	3,24E-03

MTP18	223172_s_at	AF060924	NM_001003704 NM_016498	51537	0,85	6,41E-03
SNAP29	218327_s_at	NM_004782	NM_004782	9342	0,85	4,67E-03
NFYA	204109_s_at	NM_002505	NM_002505 NM_021705	4800	0,85	4,40E-03
FLJ37858	227354_at	BF589359	NM_001007549	441357	0,84	6,04E-03
R58282	238557_at	R58282	---	---	0,84	5,38E-03
CDH2	203441_s_at	NM_001792	NM_001792	1000	0,84	1,55E-03
C20orf45	217851_s_at	NM_016045	NM_016045	51012	0,84	1,50E-03
MYO1B	212364_at	BF432550	NM_012223	4430	0,84	1,02E-03
PAICS	201014_s_at	NM_006452	NM_006452	10606	0,84	4,23E-04
ZNF505	215758_x_at	AC007204	NM_001004126 NM_031218	81931	0,84	1,32E-04
SEMA6A	215028_at	AB002438	NM_020796	57556	0,84	1,21E-04
SLIT2	209897_s_at	AF055585	NM_004787	9353	0,84	3,51E-03
CELSR3	40020_at	AB011536	NM_001407	1951	0,84	1,82E-06
DIRAS2	219619_at	NM_017594	NM_017594	54769	0,84	9,62E-03
TOB2	222243_s_at	AB051450	NM_016272	10766	0,84	3,84E-03
HAND1	220138_at	NM_004821	NM_004821	9421	0,84	8,36E-04
RAD18	224200_s_at	AB035274	NM_020165	56852	0,83	3,81E-03
LRIG3	226908_at	AI627704	NM_153377	121227	0,83	9,44E-03
AI150000	226671_at	AI150000	---	---	0,83	7,72E-04
EIF5A2	235289_at	AV747725	NM_020390	56648	0,83	2,77E-03
CDK2AP1	201938_at	NM_004642	NM_004642	8099	0,83	8,12E-03
MLF1	204784_s_at	NM_022443	NM_022443	4291	0,83	2,50E-03
MPP5	219321_at	NM_022474	NM_022474	64398	0,83	1,84E-03
TXNRD1	201266_at	NM_003330	NM_003330 NM_182729 NM_182742 NM_182743	7296	0,83	6,73E-05
C10orf58	224435_at	BC005871	NM_032333	84293	0,82	5,15E-06
EVE1	225162_at	BG285417	NM_001009555	152503	0,82	5,43E-03
RALY	201271_s_at	NM_016732	NM_007367 NM_016732	22913	0,82	1,71E-03
SEC10L1	228418_at	BF509391	NM_006544	10640	0,82	6,79E-06
MFAP2	203417_at	NM_017459	NM_002403 NM_017459	4237	0,82	9,64E-05
MYO1B	212365_at	BF215996	NM_012223	4430	0,82	2,49E-04
ACAA1	214274_s_at	AI860341	NM_001607	30	0,82	5,44E-03
KIAA0701	1554292_a_at	BC014891	NM_001006947 NM_015054	23074	0,81	5,60E-03
AK022598	232662_x_at	AK022598	---	---	0,81	5,55E-03
PLXNA2	213030_s_at	AI688418	NM_025179	5362	0,81	6,66E-03
BE501881	227565_at	BE501881	---	---	0,81	2,21E-03
BF447112	236192_at	BF447112	---	---	0,81	2,02E-03
LOC85028	228990_at	AI339426	XM_378848	85028	0,81	4,87E-04

BF511170	227332_at	BF511170	---	---	0,81	3,67E-03
KLF3	219657_s_at	NM_016531	NM_016531	51274	0,81	3,64E-03
GRIA1	209793_at	AL567302	NM_000827	2890	0,81	3,68E-03
SUHW2	229360_at	N22886	NM_080764	140883	0,81	8,50E-03
LOC401022	242042_s_at	AA406052	---	401022	0,81	5,97E-04
C3orf4	208925_at	AF161522	NM_019895	56650	0,81	1,42E-08
MRPL40	203152_at	NM_003776	NM_003776	64976	0,81	6,67E-03
PVT1 LOC441378	1558290_a_at	BG200951	XM_372058 XM_499128	441378 5820	0,81	2,88E-03
KELCHL	221837_at	BG325646	NM_032775	84861	0,81	3,12E-04
CELSR3	205165_at	NM_001407	NM_001407	1951	0,81	1,43E-04
RAB35	205461_at	NM_006861	NM_006861	11021	0,81	6,64E-03
MGC70857	226710_at	AI199072	NM_001001795	414919	0,81	3,76E-05
AA446953	241749_at	AA446953	XM_294592	347273	0,81	2,10E-04
PSMD5	203447_at	AU157008	NM_005047	5711	0,80	8,55E-04
NUP50	222583_s_at	AF116624	NM_007172 NM_153645 NM_153684	10762	0,80	2,54E-04
ARL6IP6	225707_at	AL581082	NM_152522	151188	0,80	4,86E-03
H1F0	208886_at	BC000145	NM_005318	3005	0,80	2,95E-04
RQCD1	1554080_at	BC007102	NM_005444	9125	0,80	5,80E-03
MVK	215649_s_at	AF217536	NM_000431	4598	0,80	4,39E-04
CDC5L	209055_s_at	AW268817	NM_001253	988	0,80	9,38E-03
LGR4	218326_s_at	NM_018490	NM_018490	55366	0,80	1,35E-04
C19orf32	226597_at	AI348159	NM_138393	92840	0,80	6,56E-03
HPS4	218402_s_at	NM_022081	NM_022081 NM_152840 NM_152841 NM_152842 NM_152843	89781	0,80	8,60E-04
MGC18216	243358_at	BF347362	---	145815	0,79	8,83E-03
ZNF43	222136_x_at	AK022905	NM_003423	7594	0,79	1,19E-06
DRG1	236537_at	AI760332	NM_004147	4733	0,79	9,05E-03
SLC2A4RG	218494_s_at	NM_020062	NM_020062	56731	0,79	1,26E-04
CHRNA3	211772_x_at	BC006114	NM_000743	1136	0,79	5,89E-03
UBE2L3	200683_s_at	BE964689	NM_003347 NM_198157	7332	0,79	2,55E-04
NUP43	238474_at	BF978064	NM_024647 NM_198887	348995	0,79	6,09E-03
EML5	1568777_at	BM677635	NM_183387	161436	0,79	2,74E-03
N24703	238637_at	N24703	---	---	0,79	1,03E-03
CHRNA3	211587_x_at	M37981	NM_000743	1136	0,79	2,09E-03
ZNF20	213916_at	AU154474	NM_021143	7568	0,79	2,24E-03
VAMP1	213326_at	AU150319	NM_014231 NM_016830 NM_199245	6843	0,79	2,99E-03
TMEM38B	222735_at	AW452608	NM_018112	55151	0,79	1,36E-05
MAPKAPK3	202788_at	NM_004635	NM_004635	7867	0,79	7,86E-03

GNB4	223488_s_at	BC000873	NM_021629	59345	0,79	5,46E-03
EPOR	209962_at	M34986	NM_000121	2057	0,78	2,19E-04
C6orf115	223361_at	AF116682	XM_371848	58527	0,78	1,07E-03
AK057923	1556364_at	AK057923	XM_498935	440960	0,78	4,56E-03
PGM2	225367_at	BF512139	NM_018290	55276	0,78	3,75E-04
CECR5	218592_s_at	NM_017829	NM_017829 NM_033070	27440	0,78	4,74E-03
CHRNA3	210221_at	BC000513	NM_000743	1136	0,78	2,56E-05
STMN3	218207_s_at	NM_015894	NM_015894	50861	0,78	8,10E-04
UCP2	208997_s_at	U82819	NM_003355	7351	0,78	3,02E-04
SFRS8	202773_s_at	AI023864	NM_004592 NM_152235	6433	0,78	4,72E-03
FIGNL1	1552921_a_at	NM_022116	NM_022116	63979	0,78	5,97E-03
MEST	202016_at	NM_002402	NM_002402 NM_177524 NM_177525	4232	0,78	9,96E-03
C20orf45	222441_x_at	BF032213	NM_016045	51012	0,78	2,01E-05
PLCXD2	235230_at	AW170015	NM_153268	257068	0,78	7,04E-03
UCK1	223142_s_at	AF237290	NM_031432	83549	0,78	3,34E-05
SNAP29	239084_at	BE896490	NM_004782	9342	0,78	7,09E-03
SNRPD3	202567_at	NM_004175	NM_004175	6634	0,78	8,05E-03
GABPB2	204618_s_at	NM_005254	NM_002041 NM_005254 NM_016654 NM_016655 NM_181427	2553	0,78	4,11E-04
RNF10	208632_at	AL578551	NM_014868	9921	0,77	7,94E-04
RFC1	208021_s_at	NM_002913	NM_002913	5981	0,77	9,34E-03
PAPPA	240295_at	AL045014	NM_002581	5069	0,77	2,94E-03
TM4SF9	225387_at	AA059445	NM_005723	10098	0,77	1,49E-03
PDCL	204448_s_at	AF031463	NM_005388	5082	0,77	8,07E-03
GNAZ	204993_at	NM_002073	NM_002073	2781	0,77	3,40E-03
STK39	202786_at	NM_013233	NM_013233	27347	0,77	5,82E-03
UBE2L3	200684_s_at	AI819709	NM_003347 NM_198157	7332	0,77	4,66E-06
BZRP	202096_s_at	NM_000714	NM_000714 NM_007311	706	0,77	2,65E-03
ELK3	206127_at	NM_005230	NM_005230	2004	0,77	2,08E-03
ZDHHC13	219296_at	NM_019028	NM_001001483 NM_019028	54503	0,77	9,19E-04
TIMP2	231579_s_at	BE968786	NM_003255	7077	0,77	2,80E-03
C8orf13	226614_s_at	BE856336	NM_053279	83648	0,77	3,12E-03
BAX	208478_s_at	NM_004324	NM_004324 NM_138761 NM_138762 NM_138763 NM_138764 NM_138765	581	0,77	5,20E-03

TCF8	239952_at	AI743662	NM_030751	6935	0,77	2,84E-04
LOC128977	227086_at	AA194312	NM_173793	128977	0,77	3,39E-03
PAICS	201013_s_at	AA902652	NM_006452	10606	0,76	3,48E-03
AKAP8	203848_at	AL050160	NM_005858	10270	0,76	6,90E-05
TWSG1	225406_at	AA195009	NM_020648	57045	0,76	1,41E-03
PDK1	206686_at	NM_002610	NM_002610	5163	0,76	4,33E-04
TIMP2	224560_at	BF107565	NM_003255	7077	0,76	7,63E-03
CDS2	212862_at	AL568982	NM_003818	8760	0,76	2,78E-05
384D8-2	205086_s_at	NM_014551	NM_014551 NM_152299	29781	0,76	4,69E-04
DTNBP1	223445_at	AF061734	NM_032122 NM_183040 NM_183041	84062	0,76	9,22E-04
BG492376	1557961_s_at	BG492376	---	---	0,76	3,56E-03
ARL6IP6	225711_at	AA654338	NM_152522	151188	0,76	8,52E-03
LRP10	201412_at	NM_014045	NM_014045	26020	0,75	8,53E-03
G22P1	200792_at	NM_001469	NM_001469	2547	0,75	1,40E-05
SDCBP	200958_s_at	NM_005625	NM_001007067 NM_001007068 NM_001007069 NM_001007070 NM_005625	6386	0,75	8,95E-04
PELI2	219132_at	NM_021255	NM_021255	57161	0,75	4,32E-04
NFYB	218129_s_at	NM_006166	NM_006166	4801	0,75	6,84E-03
BTBD3	202946_s_at	NM_014962	NM_014962 NM_181443	22903	0,75	2,02E-04
CSE1L	201111_at	AF053641	NM_001316 NM_177436	1434	0,75	9,19E-03
CAMKK1	223460_at	AL136576	NM_032294 NM_172206 NM_172207	84254	0,75	6,46E-03
TFDP2	244043_at	AI049824	NM_006286	7029	0,75	1,03E-03
AU154030	242141_at	AU154030	---	---	0,75	6,48E-03
C20orf20	218586_at	NM_018270	NM_018270	55257	0,75	4,07E-04
PPAT	209434_s_at	U00238	NM_002703	5471	0,75	4,18E-04
FH	203032_s_at	AI363836	NM_000143	2271	0,75	3,75E-04
USP28	231837_at	AB040948	NM_020886	57646	0,75	4,33E-04
COVA1	32042_at	S72904	NM_006375 NM_182314	10495	0,75	1,36E-03
KIAA1432	226221_at	AL138104	XM_039698	57589	0,75	1,64E-03
ZNF43	206695_x_at	NM_003423	NM_003423	7594	0,75	2,70E-03
MICAL-L1	55081_at	W46406	NM_033386	85377	0,75	4,38E-03
HPRP8BP	215905_s_at	AL157420	NM_004814	9410	0,74	1,02E-04
MAC30	214283_at	AU150186	NM_014573	27346	0,74	8,38E-06

C10orf78	238794_at	N23586	NM_001002759 NM_145247	119392	0,74	7,02E-03
Cep70	219036_at	NM_024491	NM_024491	80321	0,74	1,04E-03
CDKAL1	214877_at	BE794663	NM_017774	54901	0,74	7,46E-04
CUGBP2	227178_at	AI652861	NM_006561	10659	0,74	1,87E-03
SQLE	213562_s_at	BF979497	NM_003129	6713	0,74	1,93E-03
RABL3	226089_at	AI742028	NM_173825	285282	0,74	2,21E-03
TRAM2	202368_s_at	AI986461	NM_012288	9697	0,74	4,19E-03
CD47	227259_at	BF439618	NM_001777 NM_198793	961	0,74	6,22E-03
T87730	242500_at	T87730	---	---	0,74	5,92E-05
DGCR2	214198_s_at	AU150824	NM_005137	9993	0,74	5,08E-05
GIT2	209876_at	AF124491	NM_014776 NM_057169 NM_057170 NM_139201	9815	0,74	1,42E-03
MKKS	222530_s_at	AF275813	NM_018848 NM_170784	8195	0,74	8,92E-03
NFKBIE	203927_at	NM_004556	NM_004556	4794	0,73	7,87E-03
PTCH	209815_at	BG054916	NM_000264	5727	0,73	4,15E-07
SORT1	212807_s_at	BF447105	NM_002959	6272	0,73	6,06E-04
SKP2	203625_x_at	BG105365	NM_005983 NM_032637	6502	0,73	2,38E-03
B3GNT1	219326_s_at	NM_006577	NM_006577 NM_033252	10678	0,73	3,66E-03
TST	209605_at	D87292	NM_003312	7263	0,73	3,44E-03
RQCD1	1553510_s_at	NM_005444	NM_005444	9125	0,73	7,31E-03
LOC440928	235147_at	R56118	XM_498917	440928	0,73	8,09E-05
EPB41L5	220977_x_at	NM_020909	NM_020909	57669	0,73	9,69E-03
B4GALT6	206233_at	AF097159	NM_004775	9331	0,73	3,61E-04
MTHFD1	202309_at	NM_005956	NM_005956	4522	0,73	5,58E-03
SUHW2	230789_at	AI015954	NM_080764	140883	0,73	4,75E-03
TCF4	228837_at	BE857360	NM_003199	6925	0,73	1,23E-05
C20orf22	224742_at	BF570412	NM_015600	26090	0,73	5,04E-04
EIF4ENIF1	218626_at	NM_019843	NM_019843	56478	0,73	3,09E-06
ZNF141	206931_at	NM_003441	NM_003441	7700	0,73	1,09E-03
ZNF278	209494_s_at	AI807017	NM_014323 NM_032050 NM_032051 NM_032052	23598	0,73	1,80E-03
RNF26	224947_at	AL559247	NM_032015	79102	0,73	9,69E-04
GNG4	1555765_a_at	AF493872	NM_004485	2786	0,73	2,53E-03
BCR	202315_s_at	NM_004327	NM_004327 NM_021574	613	0,72	5,57E-03
FPGT	205140_at	NM_003838	NM_003838	8790	0,72	4,20E-05
FLJ13273	235387_at	AA740875	NM_024751	79807	0,72	2,00E-06
PRIM2A	215708_s_at	AL121975	NM_000947	5558	0,72	3,15E-03
TOMM22	217960_s_at	NM_020243	NM_020243	56993	0,72	3,02E-03

CDH2	203440_at	M34064	NM_001792	1000	0,72	1,27E-04
DENR	234915_s_at	BC000925	NM_003677	8562	0,72	5,52E-06
KIAA1280	219520_s_at	NM_018458	NM_015691	55841	0,72	1,98E-03
CDC5L	209056_s_at	NM_001253	NM_001253	988	0,72	5,21E-03
MYH9	211926_s_at	AI827941	NM_002473	4627	0,72	5,89E-03
SLC25A13	203775_at	NM_014251	NM_014251	10165	0,72	5,47E-03
SEMA6A	220454_s_at	NM_020796	NM_020796	57556	0,72	5,20E-04
SOX2	213722_at	AW007161	NM_003106	6657	0,72	3,52E-04
RP2	205191_at	NM_006915	NM_006915	6102	0,72	1,30E-03
AI291804	242856_at	AI291804	---	---	0,72	6,53E-03
SLC26A2	224963_at	AK025078	NM_000112	1836	0,72	3,23E-03
GRIA1	211520_s_at	M64752	NM_000827	2890	0,71	6,86E-04
SCD	211162_x_at	AF116616	NM_005063	6319	0,71	8,56E-03
TM4SF6	209109_s_at	U84895	NM_003270	7105	0,71	1,07E-04
CYB5-M	201634_s_at	NM_030579	NM_030579	80777	0,71	8,39E-03
AW025579	213429_at	AW025579	---	---	0,71	1,53E-04
CDW92	224595_at	AK022549	NM_022109 NM_080546	23446	0,71	4,42E-03
KIAA1853	230010_at	AA608629	NM_194286	84530	0,71	1,11E-03
GCLM	203925_at	NM_002061	NM_002061	2730	0,71	2,48E-03
TLK2	228627_at	AL041560	NM_006852	11011	0,71	1,99E-03
RNF144	204040_at	NM_014746	NM_014746	9781	0,71	3,67E-03
PAXIP1L	212825_at	AI357401	NM_007349	22976	0,71	7,70E-03
PHOX2B	207009_at	NM_003924	NM_003924	8929	0,71	1,10E-05
FAM19A2	241399_at	AI142028	NM_178538	338811	0,71	3,12E-03
RSN	210716_s_at	M97501	NM_002956 NM_198240	6249	0,71	1,47E-03
RB1	203132_at	NM_000321	NM_000321	5925	0,71	9,52E-03
AA603344	235964_x_at	AA603344	---	---	0,71	5,50E-03
ZNF278	211392_s_at	AF242522	NM_014323 NM_032050 NM_032051 NM_032052	23598	0,71	9,10E-03
DEK	200934_at	NM_003472	NM_003472	7913	0,71	7,14E-03
GPC6	227059_at	AI651255	NM_005708	10082	0,71	1,48E-03
KBTBD4	223765_s_at	AF151086	NM_016506 NM_018095	55709	0,71	2,77E-04
AA521504	235952_at	AA521504	---	---	0,71	7,68E-03
LOC163404	231397_at	AF131783	XM_375754	163404	0,71	9,06E-03
CHRNB4	207516_at	NM_000750	NM_000750	1143	0,70	2,92E-04
UBE2L3	200676_s_at	NM_003347	NM_003347 NM_198157	7332	0,70	3,80E-07
MAGEH1	218573_at	NM_014061	NM_014061	28986	0,70	8,04E-07
PKM2	201251_at	NM_002654	NM_002654 NM_182470 NM_182471	5315	0,70	5,34E-03
DVL2	57532_at	AW016304	NM_004422	1856	0,70	2,07E-03
AMMECR1	1553219_a_at	NM_015365	NM_015365	9949	0,70	2,11E-03

SLA/LP	235516_at	AI038867	NM_016955 NM_153825	51091	0,70	3,09E-03
PEPD	202108_at	NM_000285	NM_000285	5184	0,70	7,53E-04
LDHA	200650_s_at	NM_005566	NM_005566	3939	0,70	3,92E-03
MVK	204056_s_at	NM_000431	NM_000431	4598	0,70	3,92E-03
RAB22A	218360_at	NM_020673	NM_020673	57403	0,70	2,55E-03
MAP3K7IP1	203901_at	NM_006116	NM_006116 NM_153497	10454	0,70	4,29E-03
HMGCR	202540_s_at	NM_000859	NM_000859	3156	0,70	6,44E-04
AGPS	225113_at	BF688144	NM_003659	8540	0,70	1,13E-03
ZNF305	240181_at	AI939511	NM_014724	9753	0,70	2,45E-03
SATB2	213435_at	AB028957	NM_015265	23314	0,70	6,66E-03
HPS4	54037_at	AL041451	NM_022081 NM_152840 NM_152841 NM_152842 NM_152843	89781	0,70	1,86E-05
B4GALT4	210540_s_at	BC004523	NM_003778 NM_212543	8702	0,70	4,75E-03
ZNF555	1556188_a_at	AF052118	NM_152791	148254	0,70	9,31E-03
NEDD1	234984_at	AA236927	NM_152905	121441	0,70	9,72E-03
KIAA1648	213058_at	AL033538	---	284900	0,70	4,59E-03
MITF	207233_s_at	NM_000248	NM_000248 NM_006722 NM_198158 NM_198159 NM_198177 NM_198178	4286	0,69	9,18E-03
TM4SF9	225388_at	AI928507	NM_005723	10098	0,69	1,96E-05
GGA2	214190_x_at	AI799984	NM_015044 NM_138640	23062	0,69	5,04E-04
FLJ10199	218815_s_at	NM_018022	NM_018022	55092	0,69	5,48E-03
SAMHD1	234987_at	AV715309	NM_015474	25939	0,69	8,34E-03
IDH3B	210418_s_at	AF023265	NM_006899 NM_174855 NM_174856	3420	0,69	9,34E-05
BNIP3	201849_at	NM_004052	NM_004052	664	0,69	3,88E-03
CANP	1557129_a_at	AA960844	NM_198947	374393	0,69	8,06E-03
GNG4	205184_at	NM_004485	NM_004485	2786	0,69	4,91E-03
G3BP	201514_s_at	NM_005754	NM_005754 NM_198395	10146	0,69	7,45E-05
B3GNT1	222870_s_at	AF288208	NM_006577 NM_033252	10678	0,69	3,54E-03
CENTB2	212476_at	D26069	NM_012287	23527	0,69	1,34E-03
LBR	201795_at	NM_002296	NM_002296 NM_194442	3930	0,69	3,92E-04
EB-1	227440_at	AW005572	NM_020140 NM_152788 NM_181670	56899	0,69	8,38E-06

LANCL1	202019_s_at	AI935255	NM_006055	10314	0,69	4,49E-03
AI857788	227126_at	AI857788	---	---	0,69	9,75E-03
GPC1	202756_s_at	NM_002081	NM_002081	2817	0,69	1,42E-05
RBM14	204178_s_at	NM_006328	NM_006328	10432	0,69	2,67E-03
CRKL	212180_at	AK000311	NM_005207	1399	0,68	3,46E-07
SMC1L1	201589_at	D80000	NM_006306	8243	0,68	1,70E-03
NFIB	213032_at	AI186739	NM_005596	4781	0,68	4,95E-03
RBM14	1555639_a_at	AF315633	NM_006328	10432	0,68	5,28E-04
IDH3B	210014_x_at	AF023266	NM_006899 NM_174855 NM_174856	3420	0,68	2,88E-04
SC4MOL	209146_at	AV704962	NM_006745	6307	0,68	1,06E-05
SLC25A15	222705_s_at	BC002702	NM_014252	10166	0,68	5,67E-05
ESD	228162_at	AA193515	NM_001984	2098	0,68	7,72E-03
PPAT	209433_s_at	AI457120	NM_002703	5471	0,68	1,12E-03
ROD1	224618_at	BF059136	NM_005156	9991	0,68	6,34E-03
ATP7A	205197_s_at	BE567813	NM_000052	538	0,68	6,71E-03
AK022438	233508_at	AK022438	---	---	0,68	3,52E-03
BG337831	238065_at	BG337831	---	---	0,68	8,60E-03
CDS2	212864_at	Y16521	NM_003818	8760	0,68	1,15E-04
MGC34646	224996_at	N30209	NM_173519	157807	0,68	1,11E-04
RECK	205407_at	NM_021111	NM_021111	8434	0,67	8,99E-03
MCAM	211042_x_at	BC006329	NM_006500	4162	0,67	2,11E-04
LOC128977	1553974_at	BC030758	NM_173793	128977	0,67	2,13E-04
SNX5	222417_s_at	AF121855	NM_014426 NM_152227	27131	0,67	7,63E-04
C20orf22	228123_s_at	AW303865	NM_015600	26090	0,67	2,89E-04
PHF20	235389_at	BG168139	NM_016436	51230	0,67	9,09E-03
NM_014838	204799_at	NM_014838	---	---	0,67	1,84E-04
Cep70	1554489_a_at	BC016050	NM_024491	80321	0,67	5,84E-03
GCAT	205164_at	NM_014291	NM_014291	23464	0,67	9,67E-03
MGC20255	225257_at	AA534536	NM_052848	90324	0,67	2,25E-04
KIAA1715	225717_at	AI814587	NM_030650	80856	0,67	2,65E-03
SH3MD1	224817_at	W93554	NM_014631	9644	0,67	3,37E-04
NFYA	204108_at	AL031778	NM_002505 NM_021705	4800	0,67	6,22E-03
MGC10854	223456_s_at	BC004285	NM_032300	84260	0,67	2,49E-03
DNAJC13	212467_at	AB014578	NM_173823	23317	0,67	4,58E-05
SEMA6A	223449_at	AF225425	NM_020796	57556	0,67	7,98E-03
BC017932	1569283_at	BC017932	XM_495940	440122	0,67	1,88E-03
CDW92	224596_at	AI634866	NM_022109 NM_080546	23446	0,67	6,95E-03
HMGCS1	221750_at	BG035985	NM_002130	3157	0,67	5,27E-04
IDH3B	201509_at	NM_006899	NM_006899 NM_174855 NM_174856	3420	0,66	3,23E-04
CECR6	224393_s_at	AF307451	NM_031890	27439	0,66	3,23E-05
IPO11	222659_at	AK001696	NM_016338	51194	0,66	3,34E-03
ACTL6B	206013_s_at	NM_016188	NM_016188	51412	0,66	5,47E-03

D15Wsu75e	212527_at	BF057059	XM_039495	27351	0,66	1,32E-04
AL134573	228208_x_at	AL134573	---	---	0,66	1,64E-03
MLLT3	204918_s_at	NM_004529	NM_004529	4300	0,66	8,51E-03
GGA2	208913_at	AA868560	NM_015044 NM_138640	23062	0,66	2,22E-03
ROD1	224617_at	AI735576	NM_005156	9991	0,66	3,70E-03
SNN	218032_at	AF070673	NM_003498	8303	0,66	5,14E-03
CD47	213055_at	BF693956	NM_001777 NM_198793	961	0,66	2,63E-03
ENO1	217294_s_at	U88968	NM_001428	2023	0,66	2,43E-04
SESN3	235150_at	AW376955	NM_144665	143686	0,66	7,70E-04
CRY1	209674_at	D83702	NM_004075	1407	0,66	2,50E-03
NM_018243	201308_s_at	NM_018243	NM_018243	55752	0,66	3,72E-03
CBX5	241875_at	AA204654	NM_012117	23468	0,66	1,75E-03
ZFYVE16	203651_at	NM_014733	NM_014733	9765	0,66	1,76E-05
NRF1	204652_s_at	NM_005011	NM_005011	4899	0,66	2,20E-03
GALNT2	217788_s_at	NM_004481	NM_004481	2590	0,66	6,79E-06
SNX5	217792_at	NM_014426	NM_014426 NM_152227	27131	0,66	1,46E-03
ALK	208212_s_at	NM_004304	NM_004304	238	0,65	2,47E-03
WDR44	219297_at	NM_019045	NM_019045	54521	0,65	3,28E-04
ELMOD2	1553928_at	NM_153702	NM_153702	255520	0,65	1,79E-04
VAPB	202550_s_at	NM_004738	NM_004738	9217	0,65	3,71E-05
LOC129285	1553955_at	AY134855	NM_152994	129285	0,65	3,87E-03
MPHOSPH9	206205_at	NM_022782	NM_022782	10198	0,65	7,66E-05
SCML2	206147_x_at	NM_006089	NM_006089	10389	0,65	1,04E-03
HS6ST2	230030_at	AI767756	NM_147174 NM_147175	90161	0,65	3,43E-03
NUP43	219007_at	NM_024647	NM_024647 NM_198887	348995	0,65	6,58E-03
R12027	241836_x_at	R12027	---	---	0,65	6,67E-03
H16725	239138_at	H16725	---	---	0,65	7,65E-03
AGPS	205401_at	NM_003659	NM_003659	8540	0,65	1,27E-03
DKFZP564M082	204218_at	NM_014042	NM_014042	25906	0,65	2,63E-03
MCART1	214126_at	N39314	NM_033412	92014	0,65	6,73E-04
NUP50	218295_s_at	NM_007172	NM_007172 NM_153645 NM_153684	10762	0,65	4,08E-04
PDK1	226452_at	AU146532	NM_002610	5163	0,65	7,55E-03
GPR125	1555122_at	BC026009	NM_145290	166647	0,65	1,16E-03
KIAA0692	212200_at	AK025933	---	23141	0,65	3,35E-04
ZADH1	230774_at	BE465894	NM_152444	145482	0,65	1,11E-03
CD24	209772_s_at	X69397	NM_013230	934	0,65	3,11E-04
KIAA1715	225718_at	AL133768	NM_030650	80856	0,65	2,15E-03
MANEA	222805_at	AI587307	NM_024641	79694	0,65	3,26E-04
C10orf86	219067_s_at	NM_017615	NM_017615	54780	0,65	6,76E-03
AL524175	225479_at	AL524175	---	---	0,64	4,37E-05
MICAL-L1	221779_at	BC001090	NM_033386	85377	0,64	1,27E-03
AI708256	229342_at	AI708256	---	---	0,64	1,31E-05

G3BP	201503_at	BG500067	NM_005754 NM_198395	10146	0,64	3,53E-03
PLCXD1	222795_s_at	BE675241	NM_018390	55344	0,64	2,51E-03
CD47	226016_at	AL118798	NM_001777 NM_198793	961	0,64	1,22E-07
RAB8B	219210_s_at	NM_016530	NM_016530	51762	0,64	2,35E-04
RNF150	227657_at	AA722069	NM_020724	57484	0,64	5,51E-03
TEX261	212083_at	BG170659	NM_144582	113419	0,64	6,37E-03
BE893995	234983_at	BE893995	---	---	0,64	1,28E-03
MGC3731	222057_at	AW002578	NM_024313	79159	0,64	8,73E-03
LOC284801	225762_x_at	AL531683	XM_378973	284801	0,64	3,26E-03
SLC25A17	211754_s_at	BC005957	NM_006358	10478	0,64	9,76E-04
KIAA0692	212201_at	AW274877	---	23141	0,64	2,57E-03
PCDHB2	231725_at	NM_018936	NM_018936	56133	0,64	1,47E-03
ATP1A1	220948_s_at	NM_000701	NM_000701 NM_001001586	476	0,64	2,01E-03
CHKB	204193_at	NM_005198	NM_005198 NM_152253	1120	0,64	3,38E-03
MPHOSPH9	215731_s_at	X98258	NM_022782	10198	0,64	3,26E-03
KIAA0877	1560916_a_at	BI461155	XM_371891 XM_374422	23333	0,64	1,49E-03
MAC30	212279_at	BE779865	NM_014573	27346	0,64	1,07E-03
RPA1	201529_s_at	NM_002945	NM_002945	6117	0,64	4,43E-03
HADHSC	211569_s_at	AF001903	NM_005327	3033	0,64	4,68E-03
HNRPC	227110_at	AA126793	NM_004500 NM_031314	3183	0,64	8,86E-04
C2orf12	225269_s_at	BE384529	---	192137	0,64	5,65E-05
GSK3B	209945_s_at	BC000251	NM_002093	2932	0,64	8,48E-04
RCN3	61734_at	AI797684	NM_020650	57333	0,64	1,45E-03
MANEA	219003_s_at	NM_024641	NM_024641	79694	0,63	1,47E-04
LOC339448	238010_at	BF970340	NM_207356	339448	0,63	6,74E-03
U1SNRNPBP	205300_s_at	NM_022717	NM_007020 NM_022717 NM_180699 NM_180703	11066	0,63	7,93E-03
AB014540	209307_at	AB014540	---	---	0,63	5,07E-03
MKL1	212748_at	AB037859	NM_020831	57591	0,63	9,09E-04
NBS1	217299_s_at	AK001017	NM_002485	4683	0,63	5,38E-03
ACSL3	201662_s_at	D89053	NM_004457 NM_203372	2181	0,63	3,55E-04
GALNT2	223991_s_at	AF130059	NM_004481	2590	0,63	9,09E-04
FBXL10	226215_s_at	AI989996	NM_001005366 NM_032590	84678	0,63	6,47E-03
C1orf48	230592_at	BE501789	NM_015471	25936	0,63	6,21E-03
FSCN1	210933_s_at	BC004908	NM_003088	6624	0,63	7,38E-03
ALMS1	214221_at	AI825212	NM_015120	7840	0,63	6,34E-03
MGC3040	223524_s_at	BC000568	NM_023943	66000	0,63	8,05E-03

WDR5	223308_s_at	AL521101	NM_017588 NM_052821	11091	0,63	1,08E-03
RBMS1	203748_x_at	NM_016839	NM_002897 NM_016836 NM_016839	5937	0,63	4,92E-04
ACTR6	218395_at	NM_022496	NM_022496	64431	0,63	1,97E-06
TOMM22	222474_s_at	AB041906	NM_020243	56993	0,63	2,85E-03
LOC129138	231847_at	Z97630	NM_138797	129138	0,63	1,02E-04
LOC338799	226369_at	AW138760	---	338799	0,63	3,36E-03
SLC2A4RG	222650_s_at	BE898559	NM_020062	56731	0,63	7,06E-04
SCOC	224786_at	AL133580	NM_032547	60592	0,63	1,37E-05
MGC3731	219324_at	NM_024313	NM_024313	79159	0,62	1,54E-03
C10orf6	203481_at	AI655902	NM_018121	55719	0,62	2,18E-04
NUP133	233421_s_at	AU146738	NM_018230	55746	0,62	7,97E-03
CSRP2BP	228543_at	AA780252	NM_020536 NM_177926	57325	0,62	6,49E-04
HSPC129	1555106_a_at	BC035744	NM_016396	51496	0,62	1,80E-03
MGC5139	202365_at	BC004815	---	84747	0,62	1,02E-04
HIC2	212964_at	AI912206	NM_015094	23119	0,62	1,32E-04
FCHO2	228220_at	AI627666	NM_138782	115548	0,62	4,50E-03
CDK5RAP1	218315_s_at	NM_016408	NM_016082 NM_016408	51654	0,62	7,08E-05
FH	214170_x_at	AA669797	NM_000143	2271	0,62	9,05E-03
ENTPD6	201704_at	NM_001247	NM_001247	955	0,62	1,44E-03
NUP50	213682_at	AL036344	NM_007172 NM_153645 NM_153684	10762	0,62	2,73E-03
SNX5	229980_s_at	AA131508	NM_014426 NM_152227	27131	0,62	1,66E-04
B4GALT6	235333_at	BG503479	NM_004775	9331	0,62	4,18E-03
LOC150383	227590_at	BE501980	NM_001008917 NM_207327	150383	0,62	1,10E-03
SYNGR1	213854_at	BF511590	NM_004711 NM_145731 NM_145738	9145	0,62	3,40E-03
DZIP3	207231_at	NM_014648	NM_014648	9666	0,62	5,60E-05
CSRP2BP	228544_s_at	AA780252	NM_020536 NM_177926	57325	0,62	8,59E-03
SCC-112	212138_at	AK021757	NM_015200	23244	0,62	2,22E-06
TEAD1	224955_at	AI590088	NM_021961	7003	0,62	1,84E-03
DYRK4	212954_at	AF263541	NM_003845	8798	0,62	2,89E-04
RAPH1	243012_at	BF196252	NM_025252 NM_203365 NM_213589	65059	0,62	5,72E-03
SC5DL	211423_s_at	D85181	NM_006918	6309	0,61	1,75E-03
BUB3	201457_x_at	AF081496	NM_001007793 NM_004725	9184	0,61	5,81E-03

TMEM38B	218772_x_at	NM_018112	NM_018112	55151	0,61	1,91E-03
TPARL	218095_s_at	NM_018475	NM_018475	55858	0,61	1,44E-03
HRPT2	235196_at	AA447464	NM_024529	79577	0,61	2,37E-03
KIAA0406	212898_at	AB007866	NM_014657	9675	0,61	1,44E-03
FBXO30	226541_at	AI808182	NM_032145	84085	0,61	1,59E-03
EPOR	209963_s_at	M34986	NM_000121	2057	0,61	8,17E-03
AP3B1	203141_s_at	AW058575	NM_003664	8546	0,61	1,23E-04
FLJ33008	228954_at	AW452620	NM_152449	145748	0,61	3,98E-04
FLJ21908	1557984_s_at	BI464019	NM_024604	79657	0,61	1,58E-03
ALS2CR2	223266_at	AB038950	NM_018571	55437	0,61	6,51E-05
RPP30	203436_at	NM_006413	NM_006413	10556	0,61	4,85E-03
LOC388272	226608_at	AW157311	NM_001001436	388272	0,61	7,08E-03
AI421677	242964_at	AI421677	---	---	0,61	2,28E-04
HSDL1	223248_at	AK025626	NM_031463	83693	0,61	3,31E-04
GLT25D1	222644_s_at	AI924150	NM_024656	79709	0,61	3,50E-03
CBX5	209715_at	L07515	NM_012117	23468	0,61	7,77E-03
SCOC	223341_s_at	AF330205	NM_032547	60592	0,61	7,55E-03
FLJ22531	204922_at	NM_024650	NM_024650	79703	0,61	4,70E-03
TMOD3	220800_s_at	NM_014547	NM_014547	29766	0,61	1,32E-03
ZFP161	209724_s_at	AL534416	NM_003409	7541	0,61	7,01E-05
AL563613	226532_at	AL563613	---	---	0,61	3,89E-03
SESN3	242899_at	N78412	NM_144665	143686	0,61	2,87E-03
PGM2	223738_s_at	AL136705	NM_018290	55276	0,61	9,76E-05
ORC4L	203352_at	NM_002552	NM_002552 NM_181741 NM_181742	5000	0,60	3,05E-03
PANK3	218433_at	NM_024594	NM_024594	79646	0,60	9,11E-03
MGC13170	224468_s_at	BC006151	NM_199249 NM_199250	84798	0,60	2,79E-04
HABP4	209818_s_at	AF241831	NM_014282	22927	0,60	5,02E-04
RBMS1	225265_at	AI580100	NM_002897 NM_016836 NM_016839	5937	0,60	1,37E-03
SESN3	225123_at	BE883841	NM_144665	143686	0,60	3,28E-05
RG9MTD1	223267_at	AF226052	NM_017819	54931	0,60	4,25E-05
SEMA6A	225660_at	W92748	NM_020796	57556	0,60	3,33E-03
PPM1F	37384_at	D86995	NM_014634	9647	0,60	9,35E-04
BMP2K	219546_at	NM_017593	NM_017593 NM_198892	55589	0,60	7,82E-04
SCD	211708_s_at	BC005807	NM_005063	6319	0,60	3,69E-03
LOC286505	226421_at	AA707320	---	286505	0,60	6,02E-03
TOMM70A	201512_s_at	BC003633	NM_014820	9868	0,60	8,65E-03
ANXA11	206200_s_at	NM_001157	NM_001157 NM_145868 NM_145869	311	0,60	1,86E-03
AW971254	222369_at	AW971254	---	---	0,60	7,78E-04
AI754928	226347_at	AI754928	---	---	0,60	4,04E-03
NHLRC2	235356_at	AW297204	NM_198514	374354	0,60	4,48E-03
HDAC1	201209_at	NM_004964	NM_004964	3065	0,60	2,74E-05

MGC14141	225568_at	BE728983	NM_032928	85014	0,60	4,04E-04
NIT2	218557_at	NM_020202	NM_020202	56954	0,59	8,84E-03
SREBF2	201247_at	BE513151	NM_004599	6721	0,59	7,04E-03
MKKS	218138_at	NM_018848	NM_018848 NM_170784	8195	0,59	1,60E-04
EPIM	213434_at	H95263	NM_001980 NM_194356	2054	0,59	3,73E-03
NDRG3	221082_s_at	NM_022477	NM_022477 NM_032013	57446	0,59	7,59E-04
TIGD7	224365_s_at	AF251050	NM_033208	91151	0,59	8,93E-03
R68654	236971_at	R68654	---	---	0,59	5,73E-03
BE675101	236384_at	BE675101	---	---	0,59	2,31E-04
MAC30	212281_s_at	BF038366	NM_014573	27346	0,59	1,68E-04
FLJ12806	220199_s_at	NM_022831	NM_022831	64853	0,59	2,17E-05
ASF1A	203427_at	NM_014034	NM_014034	25842	0,59	1,25E-04
CTCF	202521_at	NM_006565	NM_006565	10664	0,59	4,94E-05
PSCD3	225147_at	AL521959	NM_004227	9265	0,59	9,96E-03
IQSEC3	213834_at	AB029033	XM_370667 XM_495902	440073	0,59	2,90E-04
MPHOSPH9	221965_at	AI990326	NM_022782	10198	0,58	9,17E-03
DNCI2	236698_at	AI823600	NM_001378	1781	0,58	1,70E-03
ZNRF3	226360_at	AK022809	XM_290972	84133	0,58	2,94E-03
OSBPL11	222586_s_at	AI884890	NM_022776	114885	0,58	2,49E-03
NIPSNAP3A	224436_s_at	BC005935	NM_015469	25934	0,58	3,38E-03
NBS1	202906_s_at	AF049895	NM_002485	4683	0,58	4,86E-03
MGC3162	218860_at	NM_024078	NM_024078	79050	0,58	3,07E-04
FLJ13149	219016_at	NM_021826	NM_021826	60493	0,58	8,95E-03
DIAPH1	213514_s_at	AU158818	NM_005219	1729	0,58	7,31E-03
IGSF4	209031_at	AL519710	NM_014333	23705	0,58	2,03E-03
ATP6V1A	201971_s_at	NM_001690	NM_001690	523	0,58	4,36E-04
FLJ25952	225365_at	BG249221	NM_153251	253832	0,58	2,88E-03

Tabla 6. Expresión genética disminuida en las líneas celulares H1 y BB10 en comparación con la línea celular 2D6 en estado no diferenciado usando análisis de micromatriz

Símbolo del gen	ID del conjunto de sondas	ID Pública representativa	ID de transcripción RefSec	ID de Gen Entrez	Proporción Log2	valor p
KIAA0125	206478_at	NM_014792	NM_014792	9834	-7,57	6,75E-06
CART	206339_at	NM_004291	NM_004291	9607	-6,35	6,05E-07
CPNE8	228365_at	AI765180	NM_153634	144402	-5,76	5,62E-09
MEOX2	206201_s_at	NM_005924	NM_005924	4223	-5,64	6,26E-06
CYTL1	219837_s_at	NM_018659	NM_018659	54360	-5,64	1,55E-10
CYGB	226632_at	AL513673	NM_134268	114757	-5,63	1,66E-03
FGF13	205110_s_at	NM_004114	NM_004114 NM_033642	2258	-5,18	1,42E-08
CPNE8	241706_at	AA431782	NM_153634	144402	-4,70	2,99E-10
CYGB	1553572_a_at	NM_134268	NM_134268	114757	-4,40	5,68E-05
BC036254	1557443_s_at	BC036254	---	---	-4,26	3,10E-05

SLC1A2	225491_at	AL157452	NM_004171	6506	-4,14	7,08E-13
CAP2	212554_at	N90755	NM_006366	10486	-4,08	3,14E-07
AL353759	215071_s_at	AL353759	---	---	-3,91	1,82E-05
GNAS	217057_s_at	AF107846	NM_000516 NM_016592 NM_080425 NM_080426	2778	-3,79	5,67E-04
CFC1	223753_s_at	AF312769	NM_032545	55997	-3,75	5,58E-06
GRM5	214217_at	D60132	NM_000842	2915	-3,73	3,90E-09
CYP2E1	1431_at	J02843	NM_000773	1571	-3,66	1,03E-03
LOC56901	218484_at	NM_020142	NM_020142	56901	-3,66	1,04E-04
PAPPA	224942_at	BG434272	NM_002581	5069	-3,64	2,15E-04
AQP1	209047_at	AL518391	NM_000385 NM_198098	358	-3,61	1,21E-05
BG325630	234973_at	BG325630	---	---	-3,57	9,05E-04
CDKN2A	209644_x_at	U38945	NM_000077 NM_058195 NM_058197	1029	-3,30	4,00E-06
CYP2E1	209975_at	AF182276	NM_000773	1571	-3,28	1,91E-03
BF432956	229057_at	BF432956	---	---	-3,21	2,21E-06
ANK3	237839_at	BF433975	NM_001149 NM_020987	288	-3,19	4,55E-03
AU144437	232887_at	AU144437	---	---	-3,17	9,97E-06
LOC158572	243017_at	AA032156	XM_379705	158572	-3,12	5,87E-07
SAMD4	212845_at	AB028976	NM_015589	23034	-3,12	2,46E-03
M160	223655_at	AF264014	NM_174941	283316	-3,12	3,65E-05
SYT13	226086_at	AB037848	NM_020826	57586	-3,11	1,85E-05
AI093492	237435_at	AI093492	---	---	-3,03	2,14E-03
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ASAM	226834_at	BG112263	NM_024769	79827	-2,98	6,28E-03
KIAA1598	221802_s_at	AU157109	NM_018330	57698	-2,94	8,29E-05
CDC42EP1	204693_at	NM_007061	NM_007061 NM_152243	11135	-2,90	4,19E-03
N92599	241421_at	N92599	---	---	-2,86	2,63E-05
GDF15	221577_x_at	AF003934	NM_004864	9518	-2,84	2,08E-03
AI341823	239657_x_at	AI341823	---	---	-2,82	2,19E-05
AW665665	237187_at	AW665665	---	---	-2,78	1,83E-03
SLC35F3	229065_at	BF968270	NM_173508	148641	-2,76	7,38E-06
AA151917	230503_at	AA151917	---	---	-2,73	3,30E-05
PAPPA	201982_s_at	NM_002581	NM_002581	5069	-2,70	2,76E-06
IL17B	220273_at	NM_014443	NM_014443	27190	-2,67	2,02E-04
KIAA0125	220377_at	NM_014151	NM_014792	9834	-2,65	1,07E-05
ANK2	232606_at	AK021894	NM_001148 NM_020977	287	-2,65	4,00E-08
AK021495	215571_at	AK021495	---	---	-2,65	9,41E-04
ANK3	239728_at	AI743588	NM_001149 NM_020987	288	-2,64	4,93E-04

ANK2	1561895_at	BC030740	NM_001148 NM_020977	287	-2,63	1,24E-04
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PAPPA	228128_x_at	AI110886	NM_002581	5069	-2,60	6,58E-04
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GRIA2	205358_at	NM_000826	NM_000826	2891	-2,54	3,09E-03
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PAPPA	224941_at	BF107618	NM_002581	5069	-2,50	1,61E-03
LOC283404	1558195_at	BG204230	---	283404	-2,49	1,03E-07
GRIP2	216481_at	AF052177	XM_042936	80852	-2,44	1,03E-04
BF000047	235736_at	BF000047	---	---	-2,43	2,70E-05
FGF1	1552721_a_at	NM_033136	NM_000800 NM_033136 NM_033137	2246	-2,43	2,69E-04
GRIA2	236538_at	BE219628	NM_000826	2891	-2,40	8,42E-04
BM977131	1557478_at	BM977131	---	---	-2,38	9,09E-05
BHLHB2	201170_s_at	NM_003670	NM_003670	8553	-2,37	5,35E-03
CAP2	212551_at	NM_006366	NM_006366	10486	-2,36	1,47E-03
PTN	211737_x_at	BC005916	NM_002825	5764	-2,35	1,99E-06
AI051127	231478_at	AI051127	---	---	-2,34	3,52E-03
PHLDA2	209803_s_at	AF001294	NM_003311	7262	-2,32	1,79E-05
RGS11	206107_at	NM_003834	NM_003834 NM_183337	8786	-2,31	1,17E-03
EGR1	201694_s_at	NM_001964	NM_001964	1958	-2,30	5,17E-03
DKK1	204602_at	NM_012242	NM_012242	22943	-2,29	9,68E-04
ZAP128	202982_s_at	NM_006821	NM_006821	10965	-2,29	2,38E-03
AK096401	1556204_a_at	AK096401	XM_375664	400721	-2,28	4,02E-05
AI459194	227404_s_at	AI459194	---	---	-2,28	8,03E-03
DKFZp313N0621	1555905_a_at	AI147556	NM_173826	285343	-2,26	6,00E-04
LOC51315	222585_x_at	BE326678	NM_016618	51315	-2,26	7,70E-05
HIST2H2BE	202708_s_at	NM_003528	NM_003528	8349	-2,25	5,90E-05
BC035768	1559987_at	BC035768	---	---	-2,24	2,82E-04
ERBB4	206794_at	NM_005235	NM_005235	2066	-2,24	7,92E-04
IL7	206693_at	NM_000880	NM_000880	3574	-2,20	1,47E-04
AA601031	228919_at	AA601031	---	---	-2,18	1,30E-03
HS3ST1	205466_s_at	NM_005114	NM_005114	9957	-2,18	6,77E-04
ANK3	215314_at	AU146646	NM_001149 NM_020987	288	-2,18	3,85E-04
LOC144571	1564139_at	AK056852	---	144571	-2,17	1,36E-03
ENOSF1	213645_at	AF305057	NM_017512	55556	-2,16	1,79E-06
RASGEF1B	230233_at	BF110534	NM_152545	153020	-2,16	7,76E-03
CREB5	205931_s_at	NM_004904	NM_004904 NM_182898 NM_182899	9586	-2,15	5,67E-03
CG018	213375_s_at	N80918	NM_052818	90634	-2,14	7,06E-03
GAL	214240_at	AL556409	NM_015973	51083	-2,12	7,95E-03

ANK2	202921_s_at	NM_001148	NM_001148 NM_020977	287	-2,11	3,33E-05
CAMK2B	209956_s_at	U23460	NM_001220 NM_172078 NM_172079 NM_172080 NM_172081 NM_172082 NM_172083 NM_172084	816	-2,10	8,15E-06
PHKA2	1560358_at	BC038597	NM_000292	5256	-2,08	2,64E-05
CACNA1D	210108_at	BE550599	NM_000720	776	-2,08	2,44E-03
AW954199	239331_at	AW954199	---	---	-2,08	1,68E-07
LOC150759	221973_at	AI983904	XM_498456 XM_499585	150759	-2,05	4,18E-04
ADCY1	235049_at	AA021120	NM_021116	107	-2,05	1,26E-03
AI435590	237193_s_at	AI435590	---	---	-2,02	9,66E-04
AQP1	207542_s_at	NM_000385	NM_000385 NM_198098	358	-2,02	1,79E-03
BE219849	240180_at	BE219849	---	---	-2,00	1,75E-03
BF111884	230491_at	BF111884	---	---	-2,00	8,24E-07
KIAA0251	1558430_at	R08650	NM_015027	23042	-2,00	5,90E-03
AI810266	235456_at	AI810266	---	---	-2,00	2,25E-07
PPP3CA	1562467_at	AK097085	NM_000944	5530	-1,97	1,35E-03
SYNPR	230303_at	H11380	NM_144642	132204	-1,96	6,12E-03
ADCY1	213245_at	AL120173	NM_021116	107	-1,96	8,54E-05
BCAR3	239908_at	AA496799	NM_003567	8412	-1,96	2,42E-03
BC025319	1568974_at	BC025319	---	---	-1,95	6,55E-05
DDEF1	1557685_at	AK054840	NM_018482	50807	-1,94	5,02E-04
NEURL	230767_at	BF448300	NM_004210	9148	-1,94	4,29E-04
STAR	204548_at	NM_000349	NM_000349 NM_001007243	6770	-1,93	5,97E-05
NAG8	210109_at	AF191492	NM_014411	27099	-1,92	7,56E-03
LOC55831	215250_at	AU147317	NM_018447	55831	-1,92	4,21E-04
AI927692	228528_at	AI927692	---	---	-1,91	1,93E-03
BC041941	1559597_at	BC041941	---	---	-1,90	9,44E-04
CLDN10	1556687_a_at	BE465772	NM_006984 NM_182848	9071	-1,90	2,11E-03
AI800713	235122_at	AI800713	---	---	-1,88	8,12E-04
ADARB1	203865_s_at	NM_015833	NM_001112 NM_015833 NM_015834	104	-1,87	6,53E-04
LOC92162	229452_at	AL544576	NM_203411	92162	-1,86	1,23E-03
AL049252	216527_at	AL049252	---	---	-1,85	4,62E-05
ARC	210090_at	AF193421	NM_015193	23237	-1,85	1,06E-04
FYN	1559101_at	AK090692	NM_002037 NM_153047 NM_153048	2534	-1,85	6,72E-04

AAK1	214956_at	AF090101	NM_014911	22848	-1,85	2,35E-03
FARP1	227996_at	BF725250	NM_001001715 NM_005766	10160	-1,85	2,09E-03
PTGER2	206631_at	NM_000956	NM_000956	5732	-1,84	5,50E-04
LOC360030	232744_x_at	BG485129	---	360030	-1,84	1,99E-03
TCEAL2	211276_at	AF063606	NM_080390	140597	-1,84	4,69E-04
SIGIRR	218921_at	NM_021805	NM_021805	59307	-1,83	2,45E-03
RAB7	239405_at	AI022632	NM_004637	7879	-1,83	1,40E-04
CAMK2B	210404_x_at	AF078803	NM_001220 NM_172078 NM_172079 NM_172080 NM_172081 NM_172082 NM_172083 NM_172084	816	-1,82	2,11E-06
ERBB4	214053_at	AW772192	NM_005235	2066	-1,82	9,63E-05
FLJ13955	227001_at	AI096706	NM_024759	79815	-1,81	1,39E-03
AI697701	243666_at	AI697701	---	---	-1,81	1,63E-04
AK024567	234597_at	AK024567	---	---	-1,81	4,51E-07
RHOQ	1559582_at	BC033251	NM_012249	23433	-1,81	2,02E-03
ATP2B3	207026_s_at	NM_021949	NM_001001344 NM_021949	492	-1,81	3,94E-03
BF055351	231205_at	BF055351	---	---	-1,79	3,90E-03
ACYP2	206833_s_at	NM_001108	NM_138448	98	-1,79	1,40E-04
CAMK2B	211483_x_at	AF081924	NM_001220 NM_172078 NM_172079 NM_172080 NM_172081 NM_172082 NM_172083 NM_172084	816	-1,78	7,39E-06
DUSP5	209457_at	U16996	NM_004419	1847	-1,77	7,59E-04
NLF1	241031_at	BE218239	NM_207322	145741	-1,77	1,06E-06
DTNA	240125_at	AI697494	NM_001390 NM_001391 NM_001392 NM_032975 NM_032978 NM_032979 NM_032980 NM_032981	1837	-1,77	2,09E-03
FLJ12671	233728_at	AU148213	NM_030980	81875	-1,77	1,42E-03
TM4SF2	234245_at	AL162055	NM_004615	7102	-1,76	3,16E-03
MGC13040	224463_s_at	BC006128	NM_032930	85016	-1,76	9,67E-03
IGFBP5	211959_at	AW007532	NM_000599	3488	-1,76	5,39E-03

COL9A2	213622_at	AI733465	NM_001852	1298	-1,76	2,66E-03
AB088847	1555547_at	AB088847	---	---	-1,76	4,05E-06
UGCGL2	1558467_a_at	BE156619	NM_020121	55757	-1,75	2,63E-03
GPX7	213170_at	AA406605	NM_015696	2882	-1,75	1,66E-03
RLF	241438_at	AI742686	NM_012421	6018	-1,75	3,53E-03
DUSP16	1558739_at	R30807	NM_030640	80824	-1,74	1,87E-04
SORCS1	1556891_at	BE328250	NM_052918	114815	-1,74	2,33E-03
ANK2	202920_at	BF726212	NM_001148 NM_020977	287	-1,73	1,72E-04
AL119491	244292_at	AL119491	---	---	-1,73	2,74E-03
ATP2B3	242036_x_at	H09073	NM_001001344 NM_021949	492	-1,72	2,83E-03
DRD1IP	219896_at	NM_015722	NM_015722	50632	-1,72	4,50E-04
KCNQ2	205737_at	NM_004518	NM_004518 NM_172106 NM_172107 NM_172108 NM_172109	3785	-1,72	4,02E-06
LOC51315	233329_s_at	AK025986	NM_016618	51315	-1,71	4,22E-05
PNCK	229411_at	AI986390	NM_198452	139728	-1,71	9,68E-05
AA007336	237586_at	AA007336	---	---	-1,71	5,37E-04
AI681941	237663_at	AI681941	---	---	-1,71	9,56E-04
SRPK2	242755_at	BE672140	NM_182691 NM_182692	6733	-1,71	3,64E-05
C9orf3	232783_at	AI147867	NM_032823	84909	-1,70	4,59E-03
RGAG4	227823_at	BE348679	XM_291322	340526	-1,70	6,60E-05
AK098781	1560814_a_at	AK098781	---	---	-1,69	7,73E-04
ERBB4	233498_at	AK024204	NM_005235	2066	-1,69	1,49E-03
C9orf10	241242_at	BE503118	NM_014612	23198	-1,68	1,66E-03
BF342356	238934_at	BF342356	---	---	-1,67	6,33E-06
IER3	201631_s_at	NM_003897	NM_003897 NM_052815	8870	-1,67	2,10E-06
AU147091	232818_at	AU147091	XM_097622	149297	-1,67	1,82E-05
SNX27	244349_at	AI807658	NM_030918	81609	-1,66	4,72E-04
ACSL4	1559663_at	AF090916	NM_004458 NM_022977	2182	-1,66	4,29E-04
AA705933	239866_at	AA705933	---	---	-1,66	1,19E-04
PRR3	244204_at	W87300	NM_025263	80742	-1,66	4,53E-03
TMP21	239851_at	AW629289	NM_006827	10972	-1,66	5,43E-03
DDHD1	231165_at	BE857355	NM_030637	80821	-1,65	5,85E-07
BRD4	232551_at	AA521443	NM_014299 NM_058243	23476	-1,65	1,19E-03
LRRC5	234148_at	AK025238	NM_018103	55144	-1,65	6,30E-04
BE674309	230913_at	BE674309	---	---	-1,64	9,40E-04
AI052447	236796_at	AI052447	---	---	-1,64	1,69E-05
BF513468	241505_at	BF513468	---	---	-1,63	7,53E-03
KIAA0754	215268_at	AW663712	---	23056	-1,62	1,40E-05

FLJ10378	242153_at	AW264125	NM_018078 NM_032239 NM_178043	55132	-1,62	6,22E-03
AGPAT3	223182_s_at	AI337300	NM_020132	56894	-1,62	7,22E-06
C9orf150	216769_x_at	AK025180	NM_203403	286343	-1,62	6,30E-03
LOC286411	1557133_at	AV753446	---	286411	-1,62	1,50E-03
HNRPD	213359_at	W74620	NM_001003810 NM_002138 NM_031369 NM_031370	3184	-1,61	9,97E-03
CKMT1	1561155_at	W76548	NM_020990	1159	-1,61	1,10E-03
BF433341	235977_at	BF433341	---	---	-1,61	3,15E-03
PRKACB	202742_s_at	NM_002731	NM_002731 NM_182948 NM_207578	5567	-1,61	2,42E-03
FLJ45880	228538_at	BE671164	NM_207404	389114	-1,59	3,25E-03
CRYGS	223643_at	AI762135	NM_017541	1427	-1,58	2,85E-05
BACH2	221234_s_at	NM_021813	NM_021813	60468	-1,58	2,32E-05
AW150212	1556038_at	AW150212	---	---	-1,58	7,16E-03
CDH12	207149_at	L33477	NM_004061	1010	-1,58	7,69E-03
AB062488	1555014_x_at	AB062488	---	---	-1,58	1,71E-03
RHOU	223168_at	AL096776	NM_021205	58480	-1,57	2,07E-07
C21orf66	239407_at	AI793248	NM_013329 NM_016631 NM_058191 NM_145328	94104	-1,57	4,80E-03
ENOSF1	204143_s_at	NM_017512	NM_017512	55556	-1,56	4,33E-04
BE894882	235681_at	BE894882	---	---	-1,55	4,33E-05
AW606588	239008_at	AW606588	---	---	-1,54	5,81E-03
SYTL1	227134_at	AI341537	NM_032872	84958	-1,54	6,41E-03
AK025360	216173_at	AK025360	---	---	-1,54	2,23E-04
DKFZP564D166	231799_at	AK021886	XM_371074	26115	-1,54	7,37E-03
LGALS3BP	200923_at	NM_005567	NM_005567	3959	-1,54	5,18E-09
AI768374	228661_s_at	AI768374	---	---	-1,54	1,48E-03
AA639707	243837_x_at	AA639707	---	---	-1,54	3,39E-03
AI821995	240201_at	AI821995	---	---	-1,54	1,51E-04
PHGDHL1	241932_at	AI073803	NM_177967	337867	-1,53	2,06E-03
LOC51315	218303_x_at	NM_016618	NM_016618	51315	-1,53	2,32E-05
C10orf10	209183_s_at	AL136653	NM_007021	11067	-1,52	3,47E-03
AI817960	239649_at	AI817960	---	---	-1,52	9,05E-05
CTBP2	215377_at	AK024129	NM_001329 NM_022802	1488	-1,52	3,37E-04
AI828075	230795_at	AI828075	---	---	-1,51	3,70E-05
ARHGAP20	228368_at	AI936560	NM_020809	57569	-1,51	1,86E-03
BC020585	1568817_at	BC020585	---	---	-1,51	6,55E-04
NDRG1	200632_s_at	NM_006096	NM_006096	10397	-1,51	1,79E-04
SLICK	234103_at	AU145191	NM_198503	343450	-1,51	8,70E-03
PROM1	204304_s_at	NM_006017	NM_006017	8842	-1,51	1,53E-04

THADA	233692_at	AK024928	NM_022065 NM_198554	63892	-1,51	8,55E-05
FBXL13	243057_at	AI923673	NM_145032	222235	-1,50	2,27E-03
LOC54103	222150_s_at	AK026747	XM_379881 XM_499340	54103	-1,50	3,51E-04
BE552011	230208_at	BE552011	---	---	-1,50	4,21E-03
MGC45477	1554250_s_at	BC033812	---	387277	-1,50	3,37E-04
AI521273	241702_at	AI521273	---	---	-1,49	2,58E-03
AL833239	1560082_at	AL833239	---	---	-1,49	2,21E-03
BACE1	217904_s_at	NM_012104	NM_012104 NM_138971 NM_138972 NM_138973	23621	-1,48	3,27E-05
PRSS11	201185_at	NM_002775	NM_002775	5654	-1,48	7,56E-04
PTPRH	208300_at	NM_002842	NM_002842	5794	-1,48	2,27E-03
C9orf150	227443_at	AI972386	NM_203403	286343	-1,48	1,85E-03
FLJ10159	236602_at	AA833813	---	55084	-1,48	1,23E-06
GLT25D2	209883_at	AF288389	NM_015101	23127	-1,47	9,47E-04
LOC133308	229491_at	BF433180	NM_178833	133308	-1,47	2,89E-03
KIAA1276	233823_at	AB033102	XM_039169	27146	-1,46	3,60E-04
GNRHR	1568661_at	BC039430	NM_000406	2798	-1,46	8,63E-03
RAB6B	221792_at	AW118072	NM_016577	51560	-1,46	2,71E-03
FLJ12666	215029_at	AL117451	NM_024595	79647	-1,45	1,46E-04
LOC23117	238342_at	BF677084	XM_290670	23117	-1,45	1,20E-05
BG430958	1559455_at	BG430958	---	---	-1,44	7,89E-04
C6orf148	237347_at	AL039379	NM_030568	80759	-1,44	3,82E-04
MAST4	225613_at	AI096389	XM_291141	23227	-1,44	4,89E-03
AL832439	1560661_x_at	AL832439	---	---	-1,44	3,31E-04
AA824624	239531_at	AA824624	---	---	-1,44	1,73E-05
AU146893	229858_at	AU146893	---	---	-1,44	1,74E-03
NDFIP2	1568807_a_at	AI301081	NM_019080	54602	-1,43	4,05E-06
SFRS1	239384_at	R18746	NM_006924	6426	-1,43	8,25E-03
STMN2	203001_s_at	NM_007029	NM_007029	11075	-1,43	6,36E-03
PTP4A3	209695_at	BC003105	NM_007079 NM_032611	11156	-1,43	3,11E-05
BE671117	243114_at	BE671117	---	---	-1,43	3,37E-04
AK021551	232589_at	AK021551	---	---	-1,43	2,58E-03
SRP54	1557505_a_at	AI076351	NM_003136	6729	-1,42	1,37E-03
KIAA1641	220940_at	NM_025190	NM_020970	57730	-1,42	1,31E-04
AW591282	231374_at	AW591282	---	---	-1,42	5,06E-03
MCM3AP	215581_s_at	AK022303	NM_003906	8888	-1,42	7,91E-04
TPD52	239862_at	W89022	NM_005079	7163	-1,42	1,59E-04
MGC15523	1563226_at	BC020925	NM_138570	124565	-1,42	3,66E-04
CEBPD	203973_s_at	NM_005195	NM_005195	1052	-1,42	2,21E-03
LOC133308	1564748_at	BC009732	NM_178833	133308	-1,41	9,96E-05
AI041215	242912_at	AI041215	---	---	-1,41	1,41E-03
BTN3A3 BTN3A2	204820_s_at	NM_006994	NM_006994 NM_007047 NM_197974	10384 11118	-1,41	3,26E-03

HIAT1	242374_at	AA747563	NM_033055	64645	-1,41	1,51E-03
KIAA0500	213839_at	AW028110	---	57237	-1,40	2,08E-04
C9orf41	1564690_at	BC022435	NM_152420	138199	-1,40	2,81E-04
AL832439	1560659_at	AL832439	---	---	-1,40	4,57E-05
ABR	214671_s_at	L19704	NM_001092 NM_021962	29	-1,40	1,63E-04
BE219187	237594_at	BE219187	---	---	-1,40	1,72E-03
HLCS	207833_s_at	NM_000411	NM_000411	3141	-1,39	7,33E-03
NFYC	1558782_a_at	BG390627	NM_014223	4802	-1,39	2,59E-03
SNF1LK	208078_s_at	NM_030751	NM_173354	150094	-1,39	3,83E-03
C9orf150	233112_at	AW301393	NM_203403	286343	-1,39	1,07E-03
SCFD1	243525_at	AA808051	NM_016106 NM_182835	23256	-1,39	5,74E-04
AA936428	244674_at	AA936428	---	---	-1,39	1,59E-03
DKFZp761N1114	229254_at	BE550027	NM_181644	148808	-1,39	3,32E-06
AI691075	229728_at	AI691075	---	---	-1,38	1,16E-04
FLJ11710	244646_at	AW972881	---	79904	-1,38	7,97E-03
AGPAT3	223183_at	AI928403	NM_020132	56894	-1,38	6,88E-04
BC037911	1568981_at	BC037911	---	---	-1,38	1,58E-05
RHOU	223169_s_at	AB051826	NM_021205	58480	-1,38	6,23E-03
AW172407	240908_at	AW172407	XM_373053	391733	-1,38	1,17E-04
HIST1H2BK	209806_at	BC000893	NM_080593	85236	-1,38	1,12E-04
BE046461	215303_at	BE046461	---	---	-1,38	7,47E-04
AA973100	230725_at	AA973100	---	---	-1,38	8,35E-07
SRP54	1557504_at	AI076351	NM_003136	6729	-1,38	5,06E-03
FLJ13197	219871_at	NM_024614	NM_024614	79667	-1,37	8,97E-03
OR7D2	1562337_at	AK095468	NM_175883	162998	-1,37	2,08E-04
TRIM32	1557315_a_at	AL134420	NM_012210	22954	-1,37	2,53E-03
AI394334	232696_at	AI394334	---	---	-1,37	2,28E-03
BIRC6	242068_at	AA608834	NM_016252	57448	-1,37	7,28E-03
ETFA	239830_at	AW850555	NM_000126	2108	-1,37	4,23E-04
PDGFRB	202273_at	NM_002609	NM_002609	5159	-1,37	1,64E-04
DDEF1	232952_at	AU146493	NM_018482	50807	-1,37	3,89E-03
AI912571	228333_at	AI912571	---	---	-1,36	9,03E-04
AW150212	1556039_s_at	AW150212	---	---	-1,36	2,10E-04
SLC16A14	238029_s_at	R15072	NM_152527	151473	-1,36	3,15E-04
COL6A1	212091_s_at	AI141603	NM_001848	1291	-1,35	4,35E-04
TMEM1	215269_at	AI922538	NM_001001723 NM_003274	7109	-1,35	7,34E-04
AA262583	238534_at	AA262583	---	---	-1,35	3,27E-03
AL037414	230055_at	AL037414	---	---	-1,35	3,69E-04
KIF1A	203849_s_at	BG473130	NM_004321	547	-1,35	3,10E-03
KIAA1904	1559072_a_at	BC032083	NM_052906	114794	-1,34	4,03E-03
ACSL4	1557418_at	W95007	NM_004458 NM_022977	2182	-1,34	4,22E-04
ATP1B4	243737_at	AI082610	NM_012069	23439	-1,34	4,77E-03

MAP2K5	244298_at	AA702999	NM_002757 NM_145160 NM_145161 NM_145162	5607	-1,34	3,13E-05
GAL	207466_at	NM_015973	NM_015973	51083	-1,33	8,78E-03
DOC2A	205744_at	NM_003586	NM_003586	8448	-1,33	3,98E-07
AV703843	1560775_at	AV703843	---	---	-1,33	4,77E-03
PCTK3	214797_s_at	BC000281	NM_002596 NM_212502 NM_212503	5129	-1,33	9,10E-04
DKFZp761O0113	207797_s_at	NM_018409	NM_018409	55805	-1,33	6,16E-03
RAC2	207419_s_at	NM_002872	NM_002872	5880	-1,33	4,07E-03
STMN2	203000_at	BF967657	NM_007029	11075	-1,32	8,36E-03
D4S234E	209569_x_at	NM_014392	NM_014392	27065	-1,32	1,21E-06
AV709727	225996_at	AV709727	---	---	-1,32	2,28E-03
C19orf4	219005_at	NM_012109	NM_012109	25789	-1,32	6,30E-06
AI276956	230766_at	AI276956	---	---	-1,32	5,11E-04
C13orf22	1562238_at	AL832776	NM_005800	10208	-1,32	1,46E-03
CRYZL1	243091_at	BF435599	NM_005111 NM_145311 NM_145858	9946	-1,32	7,89E-03
HR	241355_at	BF528433	NM_005144 NM_016411	55806	-1,32	3,52E-03
LOC285513	1564077_at	AK074440	NM_198281	285513	-1,32	8,81E-03
AI973085	239765_at	AI973085	---	---	-1,32	9,72E-03
DJ462O23.2	225876_at	T84558	NM_020448	57185	-1,31	3,81E-03
PKD1	216949_s_at	L39891	NM_000296 NM_001009944	5310	-1,31	4,56E-03
MAD	226275_at	AI188653	NM_002357	4084	-1,31	3,40E-03
MSI2	243579_at	BF029215	NM_138962 NM_170721	124540	-1,31	4,03E-03
UGCGL2	1558466_at	BE156619	NM_020121	55757	-1,31	7,77E-04
DDEF1	238193_at	W87434	NM_018482	50807	-1,31	6,32E-04
KIAA1277	221886_at	AL037701	NM_015689	27147	-1,31	3,41E-07
AI056683	228171_s_at	AI056683	---	---	-1,31	8,22E-04
FYN	243006_at	BG222258	NM_002037 NM_153047 NM_153048	2534	-1,31	1,31E-04
GART	236969_at	AI961651	NM_000819 NM_175085	2618	-1,30	9,66E-06
FLJ32130	242272_at	AI375066	NM_152458	146540	-1,30	2,75E-04
C6orf198	227834_at	AL589605	XM_371849	167838	-1,30	9,19E-03

DTNA	210736_x_at	U46746	NM_001390 NM_001391 NM_001392 NM_032975 NM_032978 NM_032979 NM_032980 NM_032981	1837	-1,30	5,47E-03
SERP1	235475_at	AI580135	NM_014445	27230	-1,30	1,39E-03
C21orf25	212875_s_at	AP001745	NM_199050	25966	-1,30	5,16E-05
MGC12488	211386_at	BC005372	---	84786	-1,30	2,63E-03
BM989131	1558075_at	BM989131	---	---	-1,30	1,86E-04
ENOSF1	204142_at	NM_017512	NM_017512	55556	-1,30	6,73E-04
AW014345	236229_at	AW014345	---	---	-1,29	1,23E-05
PKD1	202328_s_at	NM_000296	NM_000296 NM_001009944	5310	-1,29	5,93E-03
KIAA1276	227505_at	N64630	XM_039169	27146	-1,29	9,12E-04
AL390170	213904_at	AL390170	---	---	-1,29	4,93E-04
BE672499	230962_at	BE672499	---	---	-1,28	1,31E-05
FLJ20753	229918_at	AB046860	XM_371082	55036	-1,28	1,20E-05
SIGIRR	52940_at	AA085764	NM_021805	59307	-1,28	3,70E-04
S100A6	217728_at	NM_014624	NM_014624	6277	-1,28	5,27E-04
UCN	206072_at	NM_003353	NM_003353	7349	-1,28	1,49E-03
INSL3	214572_s_at	NM_005543	NM_005543	3640	-1,28	3,79E-03
TBX3	243234_at	BG055137	NM_005996 NM_016569	6926	-1,28	1,16E-04
LOC349136	242452_at	AI683911	NM_198285	349136	-1,28	4,80E-04
LOC440457	206088_at	NM_014834	XM_496239	440457	-1,28	1,40E-03
LONP	221833_at	AI971258	NM_031490	83752	-1,27	6,14E-03
LOC158301	239193_at	BF060981	---	158301	-1,27	2,55E-04
AW449624	239379_at	AW449624	---	---	-1,27	2,70E-03
KCTD13	45653_at	AW026481	NM_178863	253980	-1,27	2,70E-06
ST7L	216123_x_at	AK024158	NM_017744 NM_138727 NM_138728 NM_138729 NM_198327 NM_198328	54879	-1,27	1,64E-04
AA835417	243007_at	AA835417	---	---	-1,27	1,46E-03
FLJ40342	1558854_a_at	BG616498	NM_152347	124989	-1,27	5,60E-05

UBE2D3	233303_at	AL110175	NM_003340 NM_181886 NM_181887 NM_181888 NM_181889 NM_181890 NM_181891 NM_181892 NM_181893	7323	-1,26	6,81E-05
ZNF365	206448_at	NM_014951	NM_199450 NM_199451 NM_199452	22891	-1,26	1,40E-03
CDKN1C	213182_x_at	R78668	NM_000076	1028	-1,26	1,79E-03
FLJ32130	1554769_at	BC040642	NM_152458	146540	-1,26	3,10E-04
ICAM2	213620_s_at	AA126728	NM_000873	3384	-1,26	5,57E-03
KIAA0256	216278_at	AL109705	NM_014701	9728	-1,26	1,61E-03
BF432875	235782_at	BF432875	XM_497668	388620	-1,26	4,13E-04
PRKACB	202741_at	AA130247	NM_002731 NM_182948 NM_207578	5567	-1,25	3,74E-04
BG548427	235547_at	BG548427	---	---	-1,25	2,88E-03
MCF2L	35147_at	AB002360	NM_024979	23263	-1,25	1,29E-04
AGPAT3	223184_s_at	BC004219	NM_020132	56894	-1,25	7,98E-04
HSD17B1	205829_at	NM_000413	NM_000413	3292	-1,25	2,09E-03
AF086013	1556543_at	AF086013	---	---	-1,25	7,87E-04
FAH	202862_at	NM_000137	NM_000137	2184	-1,25	3,32E-03
FLJ23754	1553248_at	NM_152675	NM_152675	201252	-1,25	8,02E-03
RAB6B	225259_at	AI805050	NM_016577	51560	-1,25	8,67E-05
ZNF148	243559_at	BF515306	NM_021964	7707	-1,25	2,25E-03
HIAT1	230868_at	BF433103	NM_033055	64645	-1,24	2,21E-03
GAD2	243265_at	AW444497	NM_000818	2572	-1,24	4,66E-03
KCTD13	221889_at	AW026481	NM_178863	253980	-1,24	1,81E-04
PAN3	239597_at	AA993566	NM_175854	255967	-1,24	8,71E-03
RPIP8	206196_s_at	NM_006695	NM_006695	10900	-1,24	4,99E-03
FBXO22	215854_at	AU146050	NM_012170 NM_147188	26263	-1,24	8,97E-04
AI733281	239994_at	AI733281	---	---	-1,24	8,71E-03
COL6A1	213428_s_at	AA292373	NM_001848	1291	-1,23	1,41E-05
PHC3	215521_at	AK023029	NM_024947	80012	-1,23	2,90E-05
BF431902	228469_at	BF431902	---	---	-1,23	3,29E-03
SLC7A1	215401_at	AU147698	NM_003045	6541	-1,23	4,72E-05
ABCC5	226363_at	BE550362	NM_005688	10057	-1,23	1,08E-04
WDR9	225446_at	AI638279	NM_001007246 NM_018963 NM_033656	54014	-1,22	4,64E-03

C21orf18	213989_x_at	AB004853	NM_001007258 NM_001007259 NM_001007260 NM_001007261 NM_001007262 NM_017438	54093	-1,22	4,28E-04
FLJ11267	220216_at	NM_019607	NM_019607	56260	-1,22	2,57E-04
BE217890	240046_at	BE217890	---	---	-1,22	1,64E-03
UBE2D3	242403_at	AI459177	NM_003340 NM_181886 NM_181887 NM_181888 NM_181889 NM_181890 NM_181891 NM_181892 NM_181893	7323	-1,22	7,24E-05
AI697662	231465_at	AI697662	---	---	-1,22	6,05E-06
WDR9	1553227_s_at	NM_018963	NM_001007246 NM_018963 NM_033656	54014	-1,22	9,76E-03
AI985021	238918_at	AI985021	---	---	-1,22	3,05E-03
LOC387904	243760_at	AI739231	XM_370711	387904	-1,21	8,97E-04
GFRA3	214479_at	NM_001496	NM_001496	2676	-1,21	3,99E-03
BF196060	236521_at	BF196060	---	---	-1,21	8,75E-04
CDKN1C	219534_x_at	NM_000076	NM_000076	1028	-1,21	3,80E-04
FLJ10613	46947_at	T87245	NM_019067	54552	-1,21	6,49E-03
BG288330	235028_at	BG288330	---	---	-1,20	3,05E-03
PPP3CA	236545_at	AA532718	NM_000944	5530	-1,20	2,51E-03
EXT1	1564378_a_at	AK025101	NM_000127	2131	-1,20	9,41E-04
AI862542	235696_at	AI862542	---	---	-1,20	3,39E-04
D4S234E	213533_at	M98528	NM_014392	27065	-1,20	2,09E-05
AL353951	232601_at	AL353951	XM_498488	439987	-1,20	9,24E-03
DKFZp434O0527	1557879_at	BF110506	NM_194302	255101	-1,20	1,41E-03
MCTP1	220122_at	NM_024717	NM_001002796 NM_024717	79772	-1,20	2,83E-05
VN1R1	221412_at	NM_020633	NM_020633	57191	-1,20	1,29E-03
H29132	241658_at	H29132	---	---	-1,20	2,35E-03
MGC13057	232773_at	AI932618	NM_032321	84281	-1,20	2,72E-03
LOC51619	244046_at	BF939235	NM_015983	51619	-1,20	5,06E-03
HNRPR	232004_at	AK001846	NM_005826	10236	-1,20	5,41E-04
U80764	222128_at	U80764	---	---	-1,20	1,17E-04

RAB6IP2	1557738_at	BC041344	NM_015064 NM_178037 NM_178038 NM_178039 NM_178040	23085	-1,19	2,25E-03
LOC255326	239151_at	BG427809	XM_497224	255326	-1,19	4,72E-04
CTBP2	233315_at	AK024947	NM_001329 NM_022802	1488	-1,19	1,31E-03
MCF2L	212935_at	AB002360	NM_024979	23263	-1,19	4,90E-05
BF514509	239049_at	BF514509	---	---	-1,19	6,48E-03
AA678564	238620_at	AA678564	---	---	-1,19	9,54E-03
AW364675	239066_at	AW364675	---	---	-1,19	6,72E-04
BE856960	242712_x_at	BE856960	---	---	-1,18	8,35E-03
TYMS	217690_at	BG281679	NM_001071	7298	-1,18	3,35E-03
AL530703	231882_at	AL530703	XM_498570	440156	-1,18	1,80E-06
SH3BGR	204979_s_at	NM_007341	NM_001001713 NM_007341	6450	-1,18	6,25E-05
KIF5C	1557089_at	CA449408	XM_377774	3800	-1,18	8,52E-03
AP1GBP1	243667_at	AW977986	NM_007247 NM_080550	11276	-1,18	2,85E-04
DCAMKL1	205399_at	NM_004734	NM_004734	9201	-1,18	8,71E-03
JAG2	32137_at	Y14330	NM_002226 NM_145159	3714	-1,18	9,67E-03
TNFRSF25	219423_x_at	NM_003790	NM_003790 NM_148965 NM_148966 NM_148967 NM_148968 NM_148969 NM_148970 NM_148971 NM_148972 NM_148973 NM_148974	8718	-1,18	9,97E-05
R99939	239245_at	R99939	XM_498488	439987	-1,18	2,96E-03
KLF9	203542_s_at	AI690205	NM_001206	687	-1,18	9,74E-05
ZC3HDC1	218543_s_at	NM_022750	NM_022750	64761	-1,17	7,23E-04
IDS	1559136_s_at	AU140213	NM_000202 NM_006123	3423	-1,17	9,45E-03
CDKN1C	213348_at	N33167	NM_000076	1028	-1,17	3,74E-04
MLLT10	238257_at	N64035	NM_001009569 NM_004641	8028	-1,17	8,79E-03
LRRN6A	227933_at	AI193252	NM_032808	84894	-1,17	5,79E-05
IL10RB	209575_at	BC001903	NM_000628	3588	-1,17	2,48E-04
KIF1A	225482_at	AL533416	NM_004321	547	-1,17	1,50E-03
FAM46A	221766_s_at	AW246673	NM_017633	55603	-1,17	3,00E-04
D4S234E	209570_s_at	BC001745	NM_014392	27065	-1,17	3,84E-06

PDCD2	228420_at	AW590850	NM_002598 NM_144781	5134	-1,17	2,71E-03
DKFZp313N0621	1555906_s_at	AI147556	NM_173826	285343	-1,17	1,60E-05
TIMP1	201666_at	NM_003254	NM_003254	7076	-1,17	1,45E-03
LOC401074	1559826_a_at	BC039495	XM_376247	401074	-1,16	6,12E-03
AW300500	228907_at	AW300500	---	---	-1,16	9,31E-03
BACH2	227173_s_at	AW450901	NM_021813	60468	-1,16	1,95E-04
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AU146999	215986_at	AU146999	---	---	-1,15	4,17E-05
FLJ10404	243047_at	AV698751	NM_019057	54540	-1,15	3,32E-06
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UBE2D3	240383_at	AI239832	NM_003340 NM_181886 NM_181887 NM_181888 NM_181889 NM_181890 NM_181891 NM_181892 NM_181893	7323	-1,15	1,23E-03
YEATS2	236462_at	AA742310	NM_018023	55689	-1,15	9,25E-03
LTBP3	219922_s_at	NM_021070	NM_021070	4054	-1,15	3,83E-05
IREB2	1563130_a_at	AL109710	NM_004136	3658	-1,15	6,76E-04
CRYGS	223644_s_at	AF161703	NM_017541	1427	-1,15	2,33E-03
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KIAA0217	241965_at	BF589232	NM_015155	23185	-1,15	6,15E-04
AK024175	222152_at	AK024175	XM_373053	391733	-1,15	6,88E-04
DNAJB5	207453_s_at	NM_012266	NM_012266	25822	-1,14	8,99E-05
AI798680	227943_at	AI798680	---	---	-1,14	1,60E-03
VPS13C	235023_at	AA828371	NM_017684	54832	-1,14	2,37E-03
LAF4	232286_at	AA572675	NM_002285	3899	-1,14	5,79E-03
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SH3GL2	205751_at	NM_003026	NM_003026	6456	-1,14	7,99E-04
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AB037813	231969_at	AB037813	---	---	-1,12	9,92E-03
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MRAS	225185_at	BF343625	NM_012219	22808	-1,12	4,78E-04
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BTN3A3	204821_at	NM_006994	NM_006994 NM_197974	10384	-1,11	3,77E-04
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R3HDM	210714_at	BC001217	NM_015361	23518	-1,10	5,50E-03
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AU157716	227051_at	AU157716	---	---	-1,10	3,37E-03
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POFUT2	209578_s_at	BC000626	NM_015227 NM_133634 NM_133635	23275	-1,10	5,47E-04
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BF001773	241906_at	BF001773	---	---	-1,10	3,71E-03
TM4SF8	232632_at	AU145719	NM_005724 NM_198902	10099	-1,10	3,31E-04
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PCSK7 TAGLN	232521_at	AK027156	NM_001001522 NM_003186 NM_004716	6876 9159	-1,10	8,49E-03
HNRPD	236000_s_at	AA863112	NM_001003810 NM_002138 NM_031369 NM_031370	3184	-1,10	1,74E-03
FARP1	235501_at	AW961576	NM_001001715 NM_005766	10160	-1,10	2,99E-03
LOC255326	242393_x_at	AV708982	XM_497224	255326	-1,10	5,74E-03
IBTK	215086_at	AB037838	NM_015525	25998	-1,10	8,89E-03
DTNA	211493_x_at	U46744	NM_001390 NM_001391 NM_001392 NM_032975 NM_032978 NM_032979 NM_032980 NM_032981	1837	-1,10	3,03E-03
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LOC284408	1558809_s_at	AK094324	---	284408	-1,09	6,98E-05
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AW290940	226773_at	AW290940	---	---	-1,09	4,20E-05
TAGLN2	200916_at	NM_003564	NM_003564	8407	-1,09	2,34E-03
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AL833123	1559496_at	AL833123	---	---	-1,09	6,13E-04
AF138859	233037_at	AF138859	---	---	-1,09	4,93E-04
DUSP16	1558740_s_at	R30807	NM_030640	80824	-1,09	5,64E-04
NSUN6	242239_at	AW970888	NM_182543	221078	-1,09	1,80E-03
SLC39A14	1561886_a_at	R00975	NM_015359	23516	-1,09	3,24E-03

FMNL2	1556656_at	BF477401	NM_001004417 NM_001004421 NM_001004422 NM_052905	114793	-1,09	8,64E-03
MYO15B	219173_at	NM_024957	XR_000222	80022	-1,09	7,64E-03
MTSS1	232757_at	AV705679	NM_014751	9788	-1,09	4,23E-03
BCL6B	243825_at	T79768	NM_181844	255877	-1,09	2,13E-04
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CDKN1C	216894_x_at	D64137	NM_000076	1028	-1,09	8,38E-05
PGAP1	220576_at	NM_024989	NM_024989	80055	-1,09	4,32E-03
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STK17A	241410_at	AI949081	NM_004760	9263	-1,08	7,78E-03
FBLP-1	1555480_a_at	AF459643	NM_017556	54751	-1,08	4,80E-04
NDUFV3	226616_s_at	NM_021075	NM_001001503 NM_021075	4731	-1,08	7,94E-07
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PAK3	236277_at	H23551	NM_002578	5063	-1,08	7,40E-05
TP53BP1	1569098_s_at	BU508386	NM_005657	7158	-1,08	1,66E-05
FNBP1	230389_at	BE046511	NM_015033	23048	-1,08	1,40E-03
AK021973	234098_at	AK021973	---	---	-1,08	9,97E-03
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PPP2R2C	223574_x_at	AF086924	NM_020416 NM_181876	5522	-1,08	2,02E-05
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MYT1L	1554633_a_at	AF036943	NM_015025	23040	-1,08	2,26E-03
AVO3	237330_at	AA603494	XM_380173	253260	-1,08	2,23E-03
PTPN2	240843_at	N53696	NM_002828 NM_080422 NM_080423	5771	-1,07	1,44E-04
LUC7L2	242024_at	T90999	NM_016019	51631	-1,07	8,65E-03
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PDE9A	205593_s_at	NM_002606	NM_001001567 NM_001001568 NM_001001569 NM_001001570 NM_001001571 NM_001001572 NM_001001573 NM_001001574 NM_001001575 NM_001001576 NM_001001577 NM_001001578 NM_001001579 NM_001001580 NM_001001581 NM_001001582 NM_001001583 NM_001001584 NM_001001585 NM_002606	5152	-1,07	1,16E-05
LOC92154	1555894_s_at	AA829283	NM_138383	92154	-1,07	1,06E-03
CUL4A	232466_at	AU155661	NM_001008895 NM_003589	8451	-1,07	1,04E-04
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GSPT1	240452_at	AA580082	NM_002094	2935	-1,07	1,19E-03
PCAF	203845_at	AV727449	NM_003884	8850	-1,07	9,18E-05
TIGD4	232998_at	AK024235	NM_145720	201798	-1,07	1,44E-03
PCNXL2	1554256_a_at	BC008300	NM_014801 NM_024938	80003	-1,06	3,23E-03
AI950451	240971_x_at	AI950451	---	---	-1,06	6,35E-03
LOC57228	209679_s_at	BC003379	NM_020467	57228	-1,06	5,22E-04
ARFGEF1	236742_at	AA132172	NM_006421	10565	-1,06	8,57E-04
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FLJ22729	238295_at	N22706	NM_024683	79736	-1,06	4,49E-05

BICD1	242052_at	AW979272	NM_001003398 NM_001714	636	-1,06	1,94E-03
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BF476403	230218_at	BF476403	---	---	-1,06	9,08E-04
BIRC1 LOC441081	238446_at	AI970117	NM_004536 XM_496754	441081 4671	-1,06	3,30E-03
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P15RS	231502_at	BF591615	NM_018170	55197	-1,06	4,06E-03
JMJD1C	228793_at	BF002296	NM_004241	221037	-1,06	2,41E-05
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NM_014152	220694_at	NM_014152	---	---	-1,05	4,06E-04
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MYST4	215597_x_at	AU143799	NM_012330	23522	-1,05	4,35E-04
CAPZA1	238407_at	AI792880	NM_006135	829	-1,05	2,34E-07
KIAA1276	235288_at	AI627532	XM_039169	27146	-1,05	5,52E-05
CNNM1	220166_at	NM_020348	NM_020348	26507	-1,05	2,70E-05
RPH3AL	221614_s_at	BC005153	NM_006987	9501	-1,04	8,30E-04
MGC13098	60815_at	AA601208	XM_379817 XM_499280	84820	-1,04	3,22E-05
AI003508	244114_x_at	AI003508	XM_496690	401131	-1,04	2,52E-03
RAC2	213603_s_at	BE138888	NM_002872	5880	-1,04	2,21E-03
PLXNC1	206471_s_at	NM_005761	NM_005761	10154	-1,04	5,22E-03
C19orf30	223913_s_at	AB058892	NM_174947	284424	-1,04	1,45E-03
BF002625	229530_at	BF002625	---	---	-1,04	2,72E-03
ATP6V0A1	1559375_s_at	AV739195	NM_005177	535	-1,04	7,96E-03
BACE1	224335_s_at	AB050436	NM_012104 NM_138971 NM_138972 NM_138973	23621	-1,04	1,07E-03
MGC9850	224857_s_at	BE378670	NM_152705	219404	-1,04	1,09E-03
BC035958	1569540_at	BC035958	---	---	-1,04	3,88E-03
FLJ32130	1554770_x_at	BC040642	NM_152458	146540	-1,04	1,31E-05
GFRA3	229936_at	AA694259	NM_001496	2676	-1,04	1,40E-03
FKBP11	228308_at	AI452444	NM_016594	51303	-1,04	8,54E-03
AL137290	233724_at	AL137290	---	---	-1,04	4,79E-04
FRAS1	226145_s_at	AL157471	NM_020875 NM_025074 NM_032863 NM_206841	80144	-1,04	3,23E-04
AU145394	215370_at	AU145394	XM_496203	440423	-1,04	3,51E-06
BRUNOL6	227775_at	BE467313	NM_052840	60677	-1,04	1,58E-03
METAP2	240769_at	AI733395	NM_006838	10988	-1,04	8,99E-03
NDP52	238560_at	AI684710	NM_005831	10241	-1,04	2,82E-07
AW150065	217653_x_at	AW150065	---	---	-1,04	2,30E-04

C21orf57	227421_at	BF026326	NM_001006114 NM_058181	54059	-1,04	4,05E-06
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CLN8	219341_at	NM_018941	NM_018941	2055	-1,03	2,97E-03
CACNA1B	235781_at	AA448208	NM_000718	774	-1,03	6,51E-04
CPEB4	242384_at	AI452469	NM_030627	80315	-1,03	8,14E-03
BCAN	223632_s_at	AI739071	NM_021948 NM_198427	63827	-1,03	2,54E-03
KIAA0746	212314_at	AB018289	NM_015187	23231	-1,03	5,88E-05
PGAP1	233479_at	AU148008	NM_024989	80055	-1,03	2,96E-03
C1orf50	219406_at	NM_024097	NM_024097	79078	-1,03	7,42E-04
AF130084	1569538_at	AF130084	---	---	-1,03	5,41E-03
PCF11	239926_at	AI675753	NM_015885	51585	-1,03	2,46E-03
FNBP1	230086_at	AA937109	NM_015033	23048	-1,03	1,57E-04
AW117322	239415_at	AW117322	XM_374094	389237	-1,03	5,77E-03
BC033530	1560209_at	BC033530	---	---	-1,03	9,56E-05
AA888777	242740_at	AA888777	---	---	-1,03	1,32E-04
SFRS1	226419_s_at	AA046439	NM_006924	6426	-1,03	8,12E-03
HNRPD	229434_at	AA865357	NM_001003810 NM_002138 NM_031369 NM_031370	3184	-1,03	1,17E-04
LOC222070	51774_s_at	AW014299	---	222070	-1,03	7,32E-05
PHKA1	229876_at	BE503584	NM_002637	5255	-1,02	1,73E-05
NPY	206001_at	NM_000905	NM_000905	4852	-1,02	5,51E-03
CD302	203799_at	NM_014880	NM_014880	9936	-1,02	5,85E-04
UBE3A	1560741_at	AL832250	NM_000462 NM_130838 NM_130839	7337	-1,02	1,28E-03
AI582773	214373_at	AI582773	XM_498956	440996	-1,02	5,09E-03
C21orf66	240105_at	AI021902	NM_013329 NM_016631 NM_058191 NM_145328	94104	-1,02	3,11E-04
ICA1	204002_s_at	NM_022307	NM_004968 NM_022307 NM_022308	3382	-1,02	8,76E-05
CAPN2	208683_at	M23254	NM_001748	824	-1,02	7,34E-04
CYLD	213295_at	AA555096	NM_015247	1540	-1,02	8,54E-04
AK021477	232710_at	AK021477	---	---	-1,02	9,52E-03
AV658469	244699_at	AV658469	---	---	-1,02	6,27E-04
GUCY1A3	221942_s_at	AI719730	NM_000856	2982	-1,02	1,00E-03
FLJ10287	232489_at	AK001149	NM_019083	54482	-1,02	1,54E-03
PAQR6	219236_at	NM_024897	NM_024897 NM_198406	79957	-1,02	6,43E-04
PELI1	232304_at	AK026714	NM_020651	57162	-1,01	4,26E-04

AU152763	232939_at	AU152763	---	---	-1,01	1,50E-03
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SORL1	203509_at	NM_003105	NM_003105	6653	-1,01	7,27E-03
PPIE	210502_s_at	AF042386	NM_006112 NM_203456 NM_203457	10450	-1,01	7,51E-03
FNBP1	239453_at	AA262084	NM_015033	23048	-1,01	1,33E-05
C9orf126	233246_at	AI523450	NM_173690	286205	-1,01	4,78E-03
FAM13A1	232628_at	AI740629	NM_014883	10144	-1,01	2,51E-03
DDX31	236210_at	AW628575	NM_022779 NM_138620	64794	-1,01	3,89E-03
CRABP2	202575_at	NM_001878	NM_001878	1382	-1,01	3,16E-03
KIAA0746	212311_at	AA522514	NM_015187	23231	-1,01	2,25E-03
PDE4C	206791_s_at	BF511742	NM_000923	5143	-1,01	1,92E-03
BE669703	229541_at	BE669703	---	---	-1,01	8,81E-05
MLL	212079_s_at	AA715041	NM_005933	4297	-1,01	8,80E-04
ZDHHC11	221646_s_at	AF267859	NM_024786	79844	-1,01	2,90E-04
BC038589	1569311_at	BC038589	---	---	-1,01	9,76E-04
C21orf66	1555125_at	BC030539	NM_013329 NM_016631 NM_058191 NM_145328	94104	-1,00	1,94E-03
AK024879	216751_at	AK024879	---	---	-1,00	8,95E-06
EFNB3	205031_at	NM_001406	NM_001406	1949	-1,00	1,02E-03
AW188311	243281_at	AW188311	---	---	-1,00	1,13E-03
N95363	213183_s_at	N95363	---	---	-1,00	2,68E-05
RAB6IP2	232565_at	AK025052	NM_015064 NM_178037 NM_178038 NM_178039 NM_178040	23085	-1,00	3,56E-03
RASA4 FLJ21767	208534_s_at	NM_006989	NM_006989 XM_376602 XM_379820	10156 401331	-1,00	1,13E-03
DCTD	210137_s_at	BC001286	NM_001921	1635	-1,00	2,80E-03
EIF3S9	236274_at	AW129967	NM_003751 NM_182712	8662	-1,00	7,13E-04
PTP4A3	206574_s_at	NM_007079	NM_007079 NM_032611	11156	-1,00	8,68E-03
ARIH1	1558710_at	BI791845	NM_005744	25820	-1,00	2,71E-03
BF507816	240517_at	BF507816	---	---	-1,00	3,52E-04
C10orf42	243335_at	BE764796	NM_138357	90550	-0,99	5,78E-03
LNK	203320_at	NM_005475	NM_005475	10019	-0,99	9,93E-05

OPTN	202073_at	AV757675	NM_001008211 NM_001008212 NM_001008213 NM_021980	10133	-0,99	1,43E-03
AK022461	232472_at	AK022461	---	---	-0,99	8,48E-04
GRK4	241989_at	AW269179	NM_001004056 NM_001004057 NM_005307 NM_182982	2868	-0,99	1,24E-04
LOC200030 LOC400781 AG1	242191_at	AI701905	NM_183372 XM_371384 XM_378897 XM_496394	200030 400781 440673	-0,99	5,68E-07
RAB3-GAP150	240234_at	AI216539	NM_012414	25782	-0,99	3,46E-03
DHX57	239311_at	AI367034	NM_144995 NM_145646 NM_198963	90957	-0,99	3,00E-03
LRRN5	216187_at	AK024867	NM_006338 NM_201630	10446	-0,99	3,96E-03
GART	230097_at	AI207338	NM_000819 NM_175085	2618	-0,99	1,29E-03
KIAA2024	1566166_at	AL833423	NM_172070	130507	-0,99	2,85E-03
MLL3	244010_at	AI057455	NM_021230 NM_170606	58508	-0,99	1,91E-03
GSDML	215659_at	AK025174	NM_018530	55876	-0,99	4,78E-03
DSCAM	237268_at	BE503065	NM_001389 NM_206887	1826	-0,99	1,16E-03
AK057701	1558515_at	AK057701	---	---	-0,99	6,69E-03
MGC11332	213393_at	AI767210	NM_032718	84804	-0,99	7,13E-04
ISYNA1	222240_s_at	AL137749	NM_016368	51477	-0,99	2,38E-04
CLTC	220855_at	NM_014127	NM_004859	1213	-0,99	7,98E-03
COL6A2	209156_s_at	AY029208	NM_001849 NM_058174 NM_058175	1292	-0,98	2,04E-03
SUV420H1	242646_at	AA702946	NM_016028 NM_017635	51111	-0,98	1,65E-04
KIAA1223	225735_at	AL110131	XM_048747	57182	-0,98	5,36E-05
DNAJC12	218976_at	NM_021800	NM_021800 NM_201262	56521	-0,98	1,57E-06
RHBDL1	207383_s_at	NM_003961	NM_003961	9028	-0,98	6,79E-03
UBE2E1	236062_at	AI742722	NM_003341 NM_182666	7324	-0,98	5,85E-03
HEL308	228736_at	AW084681	NM_133636	113510	-0,98	1,68E-03
H28915	244359_s_at	H28915	XM_496692	441014	-0,98	5,93E-03

BRUNOL5	232416_at	AL390161	NM_021938	60680	-0,98	4,62E-03
RNF12	242121_at	AW973232	NM_016120 NM_183353	51132	-0,98	6,21E-03
SFRS15	222310_at	AA648521	NM_020706	57466	-0,98	2,65E-04
ACSL4	1557419_a_at	W95007	NM_004458 NM_022977	2182	-0,98	4,91E-03
SPOCK2	202524_s_at	NM_014767	NM_014767	9806	-0,98	6,88E-05
KIAA0999	242920_at	AW590838	NM_025164	23387	-0,97	3,05E-03
KCNK10	220727_at	NM_021161	NM_021161 NM_138317 NM_138318	54207	-0,97	9,90E-03
AATK	205986_at	NM_004920	---	9625	-0,97	2,81E-05
SERTAD4	230660_at	AU146709	NM_019605	56256	-0,97	5,49E-03
CDC2L5	242693_at	AW664859	NM_003718 NM_031267	8621	-0,97	6,26E-03
NM_025120	220728_at	NM_025120	---	---	-0,97	5,32E-03
SMG1 KIAA0220 LOC440345	244766_at	BG180003	NM_014006 NM_015092 XM_496125	23049 283846 440345	-0,97	2,50E-03
DNAJB5	212817_at	AK023253	NM_012266	25822	-0,97	1,18E-03
HIST3H2A	221582_at	BC001193	NM_033445	92815	-0,97	2,09E-03
SORL1	212560_at	AV728268	NM_003105	6653	-0,97	4,84E-03
BBP	213882_at	AA012917	NM_032027	83941	-0,97	7,60E-03
UGCGL2	218801_at	NM_020121	NM_020121	55757	-0,96	1,53E-03
TLE1	228284_at	BE302305	NM_005077	7088	-0,96	2,82E-06
CRYZL1	1552347_at	NM_145311	NM_005111 NM_145311 NM_145858	9946	-0,96	8,59E-03
KIAA1223	225731_at	BF196876	XM_048747	57182	-0,96	1,92E-04
CTNND1	238884_at	AW195351	NM_001331	1500	-0,96	7,20E-03
FLJ10980	225327_at	AB037791	NM_019600	56204	-0,96	4,11E-04
LOC255783	227325_at	AW172584	---	255783	-0,96	6,35E-03
SLICK	244455_at	AI732637	NM_198503	343450	-0,96	5,42E-04
MCM3AP	212269_s_at	AJ010089	NM_003906	8888	-0,96	2,03E-05
EMR3	1561042_at	AF086249	NM_032571 NM_152939	84658	-0,96	1,76E-03
OCIAD2	225314_at	BG291649	NM_152398	132299	-0,96	6,40E-05
BACE1	222463_s_at	AF190725	NM_012104 NM_138971 NM_138972 NM_138973	23621	-0,96	5,33E-04
DNAJC12	223721_s_at	AF176013	NM_021800 NM_201262	56521	-0,95	9,38E-05
CCNJ	1557830_at	AW063658	NM_019084	54619	-0,95	1,55E-03
KLF12	243089_at	AA551114	NM_007249 NM_016285	11278	-0,95	3,83E-03
RSL1D1	212019_at	AK025446	NM_015659	26156	-0,95	2,34E-04
AK022004	233003_at	AK022004	---	---	-0,95	3,09E-03
FTO	215385_at	AK022473	XM_051200	79068	-0,95	4,76E-03

AKAP10	236007_at	AU147278	NM_007202	11216	-0,95	8,23E-04
PDXK	202671_s_at	NM_003681	NM_003681	8566	-0,95	3,67E-06
TRIT1	218617_at	NM_017646	NM_017646	54802	-0,95	3,17E-07
MYT1L	210016_at	BF223003	NM_015025	23040	-0,95	8,33E-05
AA573901	227783_at	AA573901	---	---	-0,95	5,00E-04
AA804267	243185_at	AA804267	---	---	-0,95	9,14E-03
AW593330	237064_x_at	AW593330	---	---	-0,95	2,04E-03
HERC1	237632_at	AA765387	NM_003922	8925	-0,95	3,34E-04
INPP1	202794_at	NM_002194	NM_002194	3628	-0,95	1,43E-04
LOC169834	230876_at	AI827906	XM_095965	169834	-0,95	1,26E-04
C21orf5	205248_at	NM_005128	NM_005128	9980	-0,95	3,75E-04
FBXW7	222729_at	BE551877	NM_018315 NM_033632	55294	-0,95	4,83E-05
NFASC	214799_at	AI821777	NM_001005387 NM_001005388 NM_001005389 NM_015090	23114	-0,95	1,20E-03
LOC90639	235533_at	AW021673	---	90639	-0,95	6,72E-03
BRUNOL5	230497_at	BE503640	NM_021938	60680	-0,95	1,48E-06
CHPT1	1559739_at	AK025141	NM_020244	56994	-0,95	1,25E-05
APOC1	204416_x_at	NM_001645	NM_001645	341	-0,95	8,52E-03
TPD52	228818_at	BF110792	NM_005079	7163	-0,94	2,91E-03
HBXAP	215786_at	AK022170	NM_016578	51773	-0,94	8,66E-03
ATXN1	203232_s_at	NM_000332	NM_000332	6310	-0,94	1,93E-03
PDXK	218019_s_at	NM_021941	NM_003681	8566	-0,94	1,93E-04
FBXW7	218751_s_at	NM_018315	NM_018315 NM_033632	55294	-0,94	8,91E-05
ANKRD11	228866_at	BF514864	NM_013275	29123	-0,94	9,50E-03
LOC149297	1558113_at	BM545032	XM_097622	149297	-0,94	3,48E-03
FLJ20758	228512_at	AW138833	NM_017952	55037	-0,94	8,02E-05
BE552208	229359_at	BE552208	---	---	-0,94	3,55E-05
PDE4DIP	244511_at	AV700591	NM_001002810 NM_001002811 NM_001002812 NM_014644 NM_022359	9659	-0,94	2,74E-03
MGC9850	224874_at	N32181	NM_152705	219404	-0,94	2,65E-04
DUSP8	206374_at	NM_004420	NM_004420	1850	-0,94	1,10E-05
LOC400729 LOC440745	243021_at	AI344101	XM_378824 XM_498840	400729 440745	-0,94	5,94E-03
AI939586	237930_at	AI939586	---	---	-0,94	6,80E-03
PHF17	225820_at	AV646599	NM_024900 NM_199320	79960	-0,94	5,13E-03

LOC222070	58900_at	AW025284	---	222070	-0,93	6,09E-04
APOE	203381_s_at	N33009	NM_000041	348	-0,93	7,96E-03
AF086134	1561754_at	AF086134	XM_498989	441057	-0,93	4,00E-03
AMH	206516_at	NM_000479	NM_000479	268	-0,93	3,43E-04
SYT15	1560879_a_at	AI971263	NM_031912 NM_181519	83849	-0,93	1,08E-03
KCNJ12	207110_at	NM_021012	NM_021012	3768	-0,93	5,28E-03
ARHGEF4	205109_s_at	NM_015320	NM_015320 NM_032995	50649	-0,93	2,32E-03
PPM1B	232580_x_at	AL117553	NM_002706 NM_177968 NM_177969	5495	-0,93	7,12E-04
ZNF587	60794_f_at	AI400621	NM_032828	84914	-0,93	6,69E-06
HIPK2	224016_at	AF111850	NM_022740	28996	-0,93	8,37E-03
LOC133926	235628_x_at	BG025030	---	133926	-0,93	4,71E-03
AI681025	230220_at	AI681025	---	---	-0,93	2,78E-04
LOC64744	225282_at	AL137764	NM_022733	64744	-0,92	4,81E-05
ICA1	214191_at	W67992	NM_004968 NM_022307 NM_022308	3382	-0,92	2,91E-04
DKFZp451M2119	239240_at	AI814116	NM_182585	285023	-0,92	9,61E-03
SFRS15	222311_s_at	AA648521	NM_020706	57466	-0,92	6,79E-03
RNF111	241413_at	W80457	NM_017610	54778	-0,92	5,97E-04
KATNB1	203162_s_at	NM_005886	NM_005886	10300	-0,92	3,97E-04
PPM1K	235061_at	AV706522	NM_152542	152926	-0,92	2,02E-03
PHC3	233431_x_at	AU148142	NM_024947	80012	-0,92	1,61E-03
TJP1	244476_at	R39769	NM_003257 NM_175610	7082	-0,91	9,46E-04
ZDHHC11	232417_x_at	AU150300	NM_024786	79844	-0,91	3,90E-03
AKAP9	215483_at	AK000270	NM_005751 NM_147166 NM_147171 NM_147185	10142	-0,91	3,78E-03
PLRG1	227246_at	BF438014	NM_002669	5356	-0,91	4,23E-03
AL390216	234317_s_at	AL390216	---	---	-0,91	9,52E-03
METAP2	244185_at	AA921841	NM_006838	10988	-0,91	3,64E-04
PER1	36829_at	AF022991	NM_002616	5187	-0,91	3,45E-03
FLJ44796	230757_at	AA195276	NM_001001704	401209	-0,91	3,23E-03
R3HDM	240503_at	AW274946	NM_015361	23518	-0,91	3,05E-03
NME5	206197_at	NM_003551	NM_003551	8382	-0,91	1,53E-04
MGC5566	220449_at	NM_024049	---	79015	-0,90	2,88E-03
MGC13098	222208_s_at	W07700	XM_379817 XM_499280	84820	-0,90	1,93E-05
W90010	238271_x_at	W90010	---	---	-0,90	3,98E-03
DCTD	201572_x_at	NM_001921	NM_001921	1635	-0,90	3,11E-03
MGC42174	244304_at	AW129650	NM_152383	129563	-0,90	8,32E-03

DJ328E19.C1.1 LOC200030 MGC8902 LOC401967 AG1	214693_x_at	BE732345	NM_015383 NM_173638 NM_183372 XM_371384 XM_496394 XM_496406	200030 25832 284565 401967 440673	-0,90	2,29E-04
AA714835	1556646_at	AA714835	---	---	-0,90	8,70E-04
PPID	204186_s_at	AI014573	NM_005038	5481	-0,90	1,20E-03
ST18	206135_at	NM_014682	NM_014682	9705	-0,90	1,28E-03
ZNF275	225382_at	U82670	XM_372267	10838	-0,90	3,80E-03
W80446	231013_at	W80446	---	---	-0,90	2,17E-03
AI200555	228275_at	AI200555	---	---	-0,90	1,34E-05
CXorf43	1553646_at	NM_144657	NM_144657	139324	-0,90	5,46E-04
PAPD4	222282_at	AV761453	NM_173797	167153	-0,90	7,86E-03
AI015847	1568838_at	AI015847	---	---	-0,90	3,96E-03
CTGLF1	1565620_at	BG621044	NM_133446	119016	-0,90	3,42E-03
KIAA1838	241152_at	BE466903	NM_032448	84498	-0,90	1,43E-03
SLC22A17	218675_at	NM_020372	NM_016609 NM_020372	51310	-0,89	2,14E-04
FLJ21159	220145_at	NM_024826	NM_024826	79884	-0,89	6,77E-03
TRIP12	244659_at	AL120025	NM_004238	9320	-0,89	1,07E-03
FAM46A	224973_at	AL078599	NM_017633	55603	-0,89	5,88E-03
PPP2R2C	228010_at	AI669212	NM_020416 NM_181876	5522	-0,89	1,10E-03
MAST4	210958_s_at	BC003646	XM_291141	23227	-0,89	1,00E-03
KIDINS220	1557246_at	AA992480	NM_020738	57498	-0,89	4,66E-03
NOB1P	223018_at	BC000050	NM_014062	28987	-0,89	6,87E-03
AI469960	230653_at	AI469960	---	---	-0,89	4,89E-03
HCG8	215985_at	X92110	---	80869	-0,89	5,08E-03
BRUNOL4	238966_at	AA678985	NM_020180	56853	-0,89	1,12E-05
C21orf51	228239_at	AA148789	NM_058182	54065	-0,89	8,47E-04
MST1	216320_x_at	U37055	NM_020998	4485	-0,89	7,59E-03
DVL3	201908_at	NM_004423	NM_004423	1857	-0,89	2,80E-03
NR2F1	209506_s_at	BC004154	NM_005654	7025	-0,89	2,53E-05
STK19	243719_at	AI973206	NM_004197 NM_032454	8859	-0,89	3,23E-03
KLF9	203543_s_at	NM_001206	NM_001206	687	-0,89	1,00E-03
AA830545	235730_at	AA830545	---	---	-0,89	1,23E-03
AI949265	229156_s_at	AI949265	XM_499089	441301	-0,89	2,40E-04
SHANK2	213307_at	AF131790	NM_012309 NM_133266	22941	-0,88	1,79E-04
AI802997	235211_at	AI802997	---	---	-0,88	8,15E-06
GPR123	239221_at	AI884909	NM_032422	84435	-0,88	8,91E-04
ABCA2	212772_s_at	AL162060	NM_001606 NM_212533	20	-0,88	4,48E-04
AL049377	1562684_at	AL049377	---	---	-0,88	5,29E-05
SAT2	225272_at	AA128261	NM_133491	112483	-0,88	1,49E-03
ERMAP	219905_at	NM_018538	NM_018538	114625	-0,88	1,01E-03

C20orf103	219463_at	NM_012261	NM_012261	24141	-0,88	2,58E-03
CDS1	226185_at	AK026697	NM_001263	1040	-0,88	1,82E-04
AI459283	231220_at	AI459283	---	---	-0,88	1,08E-03
DKFZp313N0621	226688_at	AW003508	NM_173826	285343	-0,88	1,19E-03
AW235215	238913_at	AW235215	---	---	-0,87	7,73E-03
SLC27A2	205768_s_at	NM_003645	NM_003645	11001	-0,87	3,01E-03
AA975422	242829_x_at	AA975422	---	---	-0,87	5,23E-03
DEPDC6	218858_at	NM_022783	NM_022783	64798	-0,87	7,47E-04
CDC2L5	210965_x_at	BC001274	NM_003718 NM_031267	8621	-0,87	1,03E-03
AHSA2	212980_at	AL050376	NM_152392	130872	-0,87	8,94E-03
AK056212	1557215_at	AK056212	---	---	-0,87	4,38E-04
BF114733	236703_at	BF114733	---	---	-0,87	8,70E-03
AW628665	235555_at	AW628665	---	---	-0,87	4,04E-04
FXR1	229519_at	H48840	NM_005087	8087	-0,86	7,99E-03
AF5Q31	232865_at	N59653	NM_014423	27125	-0,86	2,34E-03
TAF15	241885_at	BF431050	NM_003487 NM_139215	8148	-0,86	2,03E-03
NM_001048	213921_at	NM_001048	---	---	-0,86	1,92E-03
PFAAP5	214753_at	AW084068	NM_014887	10443	-0,86	1,88E-03
FRMD4A	1560031_at	R19413	NM_018027	55691	-0,86	1,21E-04
NELF	221214_s_at	NM_015537	NM_015537	26012	-0,86	5,19E-05
MGC11332	213403_at	BF223370	NM_032718	84804	-0,86	5,38E-03
ETV3	1552423_at	NM_005240	NM_005240	2117	-0,86	4,99E-04
TMF1	242243_at	AI767435	NM_007114	7110	-0,86	4,40E-03
PIAS2	244633_at	AA404996	NM_004671 NM_173206	9063	-0,86	6,85E-03
SLC19A1	229489_at	AI681043	NM_003056 NM_194255	6573	-0,86	4,96E-03
ECE2	230706_s_at	AI084921	NM_014693	9718	-0,86	7,23E-04
HNRPM	238610_s_at	AI906424	NM_005968 NM_031203	4670	-0,86	2,13E-03
AW303888	1561346_at	AW303888	---	---	-0,86	5,89E-07
HNRPM	233605_x_at	AK022050	NM_005968 NM_031203	4670	-0,86	3,84E-05
FBXO15	231472_at	BE464323	NM_152676	201456	-0,86	5,46E-03
UBE2B	239163_at	AW364833	NM_003337	7320	-0,86	1,91E-03
BE467787	243835_at	BE467787	---	---	-0,86	3,40E-04
SORCS1	228194_s_at	AI675836	NM_052918	114815	-0,86	7,48E-05
ZDHHC11	1552283_s_at	NM_024786	NM_024786	79844	-0,86	1,80E-04
DEADC1	227213_at	AA706895	NM_182503	134637	-0,85	7,30E-04
RRAGC	218088_s_at	NM_022157	NM_022157	64121	-0,85	7,96E-03
UBE3C	242673_at	AA931284	NM_014671	9690	-0,85	2,73E-03
MGC13098	224517_at	BC006435	XM_379817 XM_499280	84820	-0,85	2,71E-05
FLJ23825	1555866_a_at	BM980844	NM_173620	284004	-0,85	2,22E-03
SLC16A1	1560579_s_at	BC023568	NM_003051	6566	-0,85	6,33E-04
RSNL2	226425_at	AU144247	NM_024692	79745	-0,85	1,24E-03
LOC283922	228688_at	AA843726	XM_208908	283922	-0,85	3,51E-04

GOLGIN-67	213650_at	AW006438	NM_015003 NM_181076 NM_181077	23015	-0,85	2,66E-03
FLJ37953	241825_at	AI265967	NM_152382	129450	-0,85	1,32E-03
AV700050	228835_at	AV700050	---	---	-0,85	2,40E-03
KIAA1915	1569706_at	BC017579	XM_055481	114803	-0,85	6,38E-03
CEPT1	1561884_at	AL833102	NM_001007794 NM_006090	10390	-0,85	1,37E-03
BF510762	230262_at	BF510762	---	---	-0,85	2,02E-06
TAGLN2	210978_s_at	BC002616	NM_003564	8407	-0,84	3,57E-03
DUSP6	208893_s_at	BC005047	NM_001946 NM_022652	1848	-0,84	1,45E-04
AI811800	241846_at	AI811800	---	---	-0,84	3,44E-03
AA167167	243684_at	AA167167	---	---	-0,84	3,92E-03
CNOT6L	227119_at	BF103856	NM_144571	246175	-0,84	2,79E-07
ARIH1	242431_at	AI656728	NM_005744	25820	-0,84	2,27E-03
BC037935	1569539_at	BC037935	---	---	-0,84	6,55E-04
DUSP6	208891_at	BC003143	NM_001946 NM_022652	1848	-0,84	3,81E-03
C15orf28	220710_at	NM_024970	---	80035	-0,84	9,94E-03
AA935515	242790_at	AA935515	---	---	-0,84	1,15E-03
MSI2	243010_at	BE000929	NM_138962 NM_170721	124540	-0,84	1,62E-03
CXorf45	205583_s_at	NM_024810	NM_024810	79868	-0,84	2,89E-03
PMS2L5	242201_at	AI418253	NM_174930	5383	-0,84	7,25E-04
AW000942	240230_s_at	AW000942	---	---	-0,84	6,90E-03
C9orf94	229585_at	AI803088	NM_152702	206938	-0,84	1,26E-03
FLJ20719	230712_at	AI634549	XM_373827	55672	-0,84	5,27E-03
GA17	215190_at	AV717062	NM_006360	10480	-0,84	6,82E-03
CD200	209582_s_at	H23979	NM_001004196 NM_001004197 NM_005944	4345	-0,84	7,62E-03
AA928506	213750_at	AA928506	---	---	-0,84	2,15E-04
AHI1	221569_at	AL136797	NM_017651	54806	-0,84	2,48E-05
RPIP8	213439_x_at	AI197870	NM_006695	10900	-0,84	1,33E-06
AI929792	236081_at	AI929792	---	---	-0,84	3,07E-04
CTNNB1	242558_at	AW362945	NM_001904	1499	-0,84	1,09E-04
ELOVL5	1566079_at	AL833001	NM_021814	60481	-0,83	1,76E-03
WDR11	229694_at	BF062828	NM_018117	55717	-0,83	2,23E-03
MAN2A2	219999_at	NM_018621	NM_006122	4122	-0,83	4,36E-03
AA825721	242228_at	AA825721	---	---	-0,83	8,71E-04
RAB12	238714_at	AA504249	XM_113967	201475	-0,83	4,32E-04
KCNMA1	221584_s_at	U11058	NM_002247	3778	-0,83	7,71E-04
BE467087	231075_x_at	BE467087	---	---	-0,83	4,80E-03
FGD5	226985_at	AW269340	NM_152536	152273	-0,83	5,34E-03
ProSAPiP1	204447_at	NM_014731	NM_014731	9762	-0,83	1,67E-04

ZNF539	1559449_a_at	BF679633	NM_203282	399655	-0,83	2,80E-04
NKX6-1	221366_at	NM_006168	NM_006168	4825	-0,83	7,76E-03
FLJ22624	236560_at	BE218020	NM_024808	79866	-0,83	7,40E-03
MGC72104	234949_at	AL117574	NM_207350	284802	-0,83	1,91E-03
GRIK2	1563754_at	AJ252246	NM_021956 NM_175768	2898	-0,83	6,46E-03
AI018235	240314_at	AI018235	---	---	-0,82	3,87E-03
ZNF518	242343_x_at	H57111	NM_014803	9849	-0,82	6,06E-03
FNBP4	235101_at	AV683244	NM_015308	23360	-0,82	3,49E-03
C21orf86	226995_at	AV705934	NM_153454	257103	-0,82	2,10E-03
AW148862	235217_at	AW148862	XM_380136	402582	-0,82	8,18E-03
AL559202	226458_at	AL559202	---	---	-0,82	5,40E-05
JMJD2C	214861_at	AI341811	NM_015061	23081	-0,82	2,97E-03
AOF2	212348_s_at	AB011173	NM_001009999 NM_015013	23028	-0,82	1,77E-05
TTC3	208663_s_at	AI652848	NM_001001894 NM_003316	7267	-0,82	7,37E-05
BE327722	239840_at	BE327722	---	---	-0,82	1,21E-06
AK021474	215892_at	AK021474	---	---	-0,82	9,46E-05
BF344235	242202_at	BF344235	XM_379855	402530	-0,82	5,35E-04
YLPM1	1557065_at	AA927802	XM_085151	56252	-0,82	8,82E-03
CaMKIINalpha	228302_x_at	AW162846	NM_018584	55450	-0,81	1,09E-03
AKT2	236664_at	AA448167	NM_001626	208	-0,81	3,20E-03
PRKCD	202545_at	NM_006254	NM_006254 NM_212539	5580	-0,81	2,09E-04
CYLD	39582_at	AL050166	NM_015247	1540	-0,81	1,26E-03
EIF4G1	208624_s_at	BE966878	NM_004953 NM_182917 NM_198241 NM_198242 NM_198244	1981	-0,81	7,60E-04
ACVR2	244332_at	AW974077	NM_001616	92	-0,81	1,17E-06
AI150690	228466_at	AI150690	---	---	-0,81	4,49E-04
AV700891	222303_at	AV700891	---	---	-0,81	1,60E-03
C20orf13	233719_s_at	AL121754	NM_017714	55617	-0,81	6,92E-04
SMURF2	230099_at	AI139993	NM_022739	64750	-0,81	2,36E-03
SHC2	213464_at	AV705938	XM_375550	25759	-0,81	4,62E-06
AW167298	228116_at	AW167298	XM_210856	283029	-0,80	5,41E-03
GPR56	206582_s_at	NM_005682	NM_005682 NM_201524 NM_201525	9289	-0,80	4,72E-03
ATXN7	209964_s_at	AF032105	NM_000333	6314	-0,80	2,95E-03
AK000995	215349_at	AK000995	---	---	-0,80	4,02E-03
AW086077	232800_at	AW086077	---	---	-0,80	1,60E-03
SLC37A1	218928_s_at	NM_018964	NM_018964	54020	-0,80	5,55E-03
PCNXL2	229202_at	AI768826	NM_014801 NM_024938	80003	-0,80	2,18E-04

SCMH1	221216_s_at	NM_012236	NM_012236	22955	-0,80	5,20E-06
FLJ31951	236322_at	AA830854	NM_144726	153830	-0,80	5,68E-03
CXXC5	233955_x_at	AK001782	NM_016463	51523	-0,80	9,43E-05
KIAA0220	231989_s_at	AC003007	---	283846	-0,80	5,47E-04
POLR3C	239383_at	AW023610	NM_006468	10623	-0,79	4,37E-03
SLC9A3R2	209830_s_at	AF035771	NM_004785	9351	-0,79	1,09E-04
CACNA1D	207998_s_at	NM_000720	NM_000720	776	-0,79	2,71E-03
AI417268	225028_at	AI417268	---	---	-0,79	5,37E-03
CTSB	213274_s_at	AA020826	NM_001908 NM_147780 NM_147781 NM_147782 NM_147783	1508	-0,79	2,12E-04
C9orf85	1557805_at	AF085969	NM_182505 NM_198394	138241	-0,79	4,15E-06
TNRC15	1560133_at	BC012484	NM_015575	26058	-0,79	1,04E-04
ARSD	225280_x_at	N51673	NM_001669 NM_009589	414	-0,79	8,39E-03
KLHDC1	1552733_at	NM_172193	NM_172193	122773	-0,79	8,55E-05
PRO0478	220696_at	NM_014129	---	29048	-0,79	7,62E-04
RAB40B	204547_at	NM_006822	NM_006822	10966	-0,79	3,04E-04
ETFDH	33494_at	S69232	NM_004453	2110	-0,79	1,02E-03
TGFBR1	236561_at	AV700621	NM_004612	7046	-0,79	6,33E-03
GPR18	233554_at	AF339764	NM_005292	2841	-0,79	2,72E-04
U2AF1	231904_at	AU122448	NM_006758	7307	-0,79	1,73E-03
DKFZP434I0714	231954_at	AL137273	---	54553	-0,79	1,34E-03
YAP	244803_at	AI335191	NM_018253 NM_139118 NM_139119 NM_139120 NM_139121	55249	-0,79	7,84E-05
LOC23117	238341_at	BF677084	XM_290670	23117	-0,79	1,63E-03
CLASP2	212308_at	AL137636	NM_015097	23122	-0,78	1,67E-03
C18orf17	238480_at	AI871745	NM_153211	125488	-0,78	8,79E-04
LOC51066	206741_at	NM_015931	NM_015931	51066	-0,78	3,65E-05
S100A13	202598_at	NM_005979	XM_371380	6284	-0,78	4,04E-03
FLJ39653	1553145_at	BC010030	NM_152684	202020	-0,78	4,89E-03
ANP32A	235954_at	AA972597	NM_006305	8125	-0,78	9,06E-03
TAF15	227884_at	AW296067	NM_003487 NM_139215	8148	-0,78	1,80E-03
HNRPR	208765_s_at	NM_005826	NM_005826	10236	-0,78	8,21E-05
AF194537	224549_x_at	AF194537	---	---	-0,78	6,16E-03
AF5Q31	1555436_a_at	BC025700	NM_014423	27125	-0,78	9,74E-05
MGC47869	229888_at	AA861435	NM_175874	144608	-0,78	5,64E-03
MEG3	235077_at	BF956762	XR_000277	55384	-0,78	2,12E-03
DKFZp547A023	214731_at	AB037854	NM_018704	55917	-0,78	1,66E-03
AI820796	217704_x_at	AI820796	---	---	-0,78	1,61E-04

CCNB1IP1	217988_at	NM_021178	NM_021178 NM_182849 NM_182851 NM_182852	57820	-0,77	9,59E-03
WDFY1	1562955_at	BC028181	NM_020830	57590	-0,77	2,91E-03
GPLD1	238752_at	AA780295	NM_001503 NM_177483	2822	-0,77	2,12E-04
CTSB	213275_x_at	W47179	NM_001908 NM_147780 NM_147781 NM_147782 NM_147783	1508	-0,77	2,40E-03
PLA2G4B	222256_s_at	AK000550	NM_005090	8681	-0,77	2,03E-03
BE856980	230961_at	BE856980	---	---	-0,77	2,41E-03
ABTB1	229164_s_at	AI337369	NM_032548 NM_172027 NM_172028	80325	-0,77	2,25E-03
AI702720	242309_at	AI702720	---	---	-0,77	2,84E-03
MGC4707	238161_at	AA813859	NM_001003676 NM_001003677 NM_001003678 NM_024113	79096	-0,77	2,25E-03
CD200	209583_s_at	AF063591	NM_001004196 NM_001004197 NM_005944	4345	-0,77	1,43E-03
GTF3C3	1555439_at	AF465407	NM_012086	9330	-0,77	3,57E-05
PTPRD	214043_at	BF062299	NM_002839 NM_130391 NM_130392 NM_130393	5789	-0,77	6,45E-05
MLR1	235970_at	AI807408	NM_153686	254251	-0,77	1,70E-03
AI305170	235747_at	AI305170	---	---	-0,77	8,11E-04
PLXNC1	213241_at	AF035307	NM_005761	10154	-0,77	8,27E-03
SP192	1569320_at	CA391618	NM_021639	60313	-0,77	2,71E-03
LRCH3	1559490_at	AL832278	NM_032773	84859	-0,77	7,53E-03
BC035170	1561079_at	BC035170	---	---	-0,77	3,38E-03
BC029480	1554447_at	BC029480	---	---	-0,77	1,93E-03
AI598222	235679_at	AI598222	---	---	-0,77	4,88E-04
SH3KBP1	223082_at	AF230904	NM_031892	30011	-0,77	9,30E-05
TNFSF13B	223502_s_at	AF134715	NM_006573	10673	-0,77	2,15E-06
AP3B2	205678_at	NM_004644	NM_004644	8120	-0,76	1,23E-04
MDS009	236649_at	AA907927	NM_020234	56986	-0,76	6,41E-04
CLIPR-59	212358_at	AL117468	NM_015526	25999	-0,76	2,11E-03
EDG4	206723_s_at	AF011466	NM_004720	9170	-0,76	2,87E-04

RNASET2	217984_at	NM_003730	NM_003730	8635	-0,76	7,52E-03
AI979338	229364_at	AI979338	---	---	-0,76	5,81E-03
KIAA1545	225704_at	AA527531	XM_495939	57666	-0,76	8,16E-03
MGC29898	235259_at	AA398590	NM_145048	133015	-0,76	3,12E-03
SIDT2	56256_at	AA150165	NM_015996	51092	-0,76	8,92E-03
MGC20741	232826_at	AU144129	NM_018561	25862	-0,76	2,64E-03
WBSCR19	232964_at	AL137266	NM_175064	285955	-0,76	3,56E-03
ACTR2	234210_x_at	AK025051	NM_001005386 NM_005722	10097	-0,76	2,63E-03
LOC92249	212957_s_at	AU154785	XM_499179	92249	-0,76	1,06E-03
JAK1	234193_at	AK025218	NM_002227	3716	-0,76	5,21E-03
PRH1	243389_at	AW663570	NM_006250	5554	-0,76	3,39E-03
AI523613	222358_x_at	AI523613	---	---	-0,76	4,89E-06
HSPA12A	214434_at	AB007877	XM_048898	259217	-0,76	6,62E-03
PIK3R2	1568629_s_at	BC033311	NM_005027	5296	-0,76	4,17E-03
MEG3	212732_at	AI950273	XR_000277	55384	-0,76	2,60E-03
AI743452	237031_at	AI743452	---	---	-0,76	8,51E-03
PVT1	222087_at	AW451806	XM_372058	5820	-0,76	1,17E-04
HNRPD	235999_at	AA863112	NM_001003810 NM_002138 NM_031369 NM_031370	3184	-0,75	2,35E-03
BG253162	242585_at	BG253162	---	---	-0,75	7,96E-04
LOC401320	238540_at	AA933883	XM_379482 XM_380098	401320	-0,75	9,69E-03
AK024681	231972_at	AK024681	---	---	-0,75	5,89E-05
FLJ14167	232289_at	BF237871	---	92080	-0,75	9,36E-03
FLJ10996	244648_at	AA007283	NM_019044	54520	-0,75	2,90E-03
TMEM25	226647_at	AL562445	NM_032780	84866	-0,75	1,43E-03
BC003629	210230_at	BC003629	---	---	-0,75	7,07E-03
DUSP6	208892_s_at	BC003143	NM_001946 NM_022652	1848	-0,75	5,05E-03
H63	1552719_at	NM_138423	NM_138423 NM_177974	113201	-0,75	2,02E-03
CXorf45	205584_at	NM_024810	NM_024810	79868	-0,75	2,96E-03
BG396868	1559957_a_at	BG396868	---	---	-0,75	1,66E-04
CLDN12	223249_at	AL136770	NM_012129	9069	-0,75	3,65E-04
UBE2G2	209042_s_at	BC001738	NM_003343 NM_182688	7327	-0,75	1,16E-05
BTN3A1	209770_at	U90552	NM_007048 NM_194441	11119	-0,75	8,21E-03
MRPL1	223154_at	AF212225	NM_020236	65008	-0,75	1,63E-03
SYNJ1	207594_s_at	NM_003895	NM_003895 NM_203446	8867	-0,75	9,53E-03
SORBS1	218087_s_at	NM_015385	NM_006434 NM_015385	10580	-0,75	9,17E-03

PORCN	219483_s_at	NM_022825	NM_022825 NM_203473 NM_203474 NM_203475 NM_203476	64840	-0,75	3,19E-05
ZRANB3	244092_at	AI670931	NM_032143	84083	-0,75	9,19E-03
MRPS30	231207_at	AW263539	NM_016640	10884	-0,75	6,93E-04
FLJ12666	217893_s_at	NM_024595	NM_024595	79647	-0,74	3,79E-03
DKFZp761L1417	238426_at	AV707703	NM_152913	222865	-0,74	8,47E-03
AI814750	1565692_at	AI814750	---	---	-0,74	2,10E-03
H2AFY	226840_at	AW291297	NM_004893 NM_138609 NM_138610	9555	-0,74	2,05E-04
LOC388312	238678_at	AI094787	XM_373704	388312	-0,74	3,88E-03
MCAM	209087_x_at	AF089868	NM_006500	4162	-0,74	6,99E-03
SH3YL1	204019_s_at	NM_015677	NM_015677	26751	-0,74	1,21E-03
KCNH2	210036_s_at	AB044806	NM_000238 NM_172056 NM_172057	3757	-0,74	6,86E-05
AW157450	235716_at	AW157450	---	---	-0,74	1,29E-03
LOC400099	230136_at	AI573252	XM_378399	400099	-0,74	3,10E-03
ASB13	239610_at	BF509210	NM_024701	79754	-0,74	1,28E-03
POU6F1	216330_s_at	L14482	NM_002702	5463	-0,74	2,20E-03
SH2D3C	1552667_a_at	NM_005489	NM_005489 NM_170600	10044	-0,74	7,58E-03
JAM2	219213_at	NM_021219	NM_021219	58494	-0,74	3,58E-05
AW665096	214188_at	AW665096	---	---	-0,74	2,49E-03
RIOK3	215588_x_at	AK024958	NM_003831 NM_145906	8780	-0,73	2,49E-04
AI963605	230269_at	AI963605	---	---	-0,73	8,73E-04
BE217923	228686_at	BE217923	---	---	-0,73	1,71E-03
C6orf111	226412_at	N66397	NM_032870	25957	-0,73	9,78E-03
BG109865	222459_at	BG109865	---	---	-0,73	1,83E-03
SP3	232529_at	AU144413	NM_003111	6670	-0,73	2,50E-03
RAB18	229398_at	AI769954	NM_021252	22931	-0,73	3,78E-03
KIAA1324	243349_at	AI672868	NM_020775	57535	-0,73	8,70E-03
CTSB	227961_at	AA130998	NM_001908 NM_147780 NM_147781 NM_147782 NM_147783	1508	-0,73	7,63E-04
AV733292	225444_at	AV733292	---	---	-0,73	1,88E-04
H73101	1556984_at	H73101	---	---	-0,73	1,17E-03
MGAT4A	219797_at	NM_012214	NM_012214	11320	-0,73	2,44E-03
EPOR	396_f_at	X97671	NM_000121	2057	-0,73	4,18E-03
LOC401394	231406_at	AW205664	XM_379512	401394	-0,73	2,54E-04
GPR153	221902_at	AL567940	NM_207370	387509	-0,73	2,83E-03
KIAA0241	1563452_at	AL833560	NM_015060	23080	-0,73	5,29E-04
BF114745	235459_at	BF114745	---	---	-0,73	8,34E-03

AA553722	243594_x_at	AA553722	---	---	-0,73	9,09E-04
AL359605	227318_at	AL359605	---	---	-0,73	3,65E-05
SMA4	214850_at	X75940	NM_021652	11039	-0,73	1,38E-03
ADFP	209122_at	BC005127	NM_001122	123	-0,73	5,72E-04
ETS2	201329_s_at	NM_005239	NM_005239	2114	-0,73	5,11E-03
AV761014	217667_at	AV761014	---	---	-0,73	4,49E-03
LOC283174	229734_at	BF507379	NM_001001873	283174	-0,73	1,27E-04
IGBP1	242337_at	AI347128	NM_001551	3476	-0,73	3,64E-03
TMEM1	209412_at	U61500	NM_001001723 NM_003274	7109	-0,73	3,07E-03
MGEA5	223494_at	AF307332	NM_012215	10724	-0,73	4,98E-03
PEX6	204545_at	NM_000287	NM_000287	5190	-0,73	9,95E-03
MGC42174	242539_at	AW665509	NM_152383	129563	-0,73	6,73E-04
KIF5C	203129_s_at	BF059313	XM_377774	3800	-0,73	3,45E-04
GPR56	212070_at	AL554008	NM_005682 NM_201524 NM_201525	9289	-0,72	1,51E-03
AMOTL2	203002_at	NM_016201	NM_016201	51421	-0,72	5,43E-04
LOC440360	236838_at	H11609	XM_498641	440360	-0,72	5,58E-03
MYEF2	222153_at	AK023133	NM_016132	50804	-0,72	2,99E-03
T82487	241759_at	T82487	---	---	-0,72	2,18E-03
CSTB	201201_at	NM_000100	NM_000100	1476	-0,72	9,61E-04
NGLY1	207492_at	NM_025105	NM_018297	55768	-0,72	9,68E-03
DUSP8	238594_x_at	AI864441	NM_004420	1850	-0,72	6,31E-03
LUZP1	1558173_a_at	AK093016	NM_033631	7798	-0,72	3,02E-04
BRUNOL4	223654_s_at	BC004167	NM_020180	56853	-0,72	3,06E-04
RGS8	234297_at	AL359941	NM_033345	85397	-0,72	8,24E-03
AI950023	244433_at	AI950023	---	---	-0,72	5,91E-03
AA327293	1566284_at	AA327293	---	---	-0,72	1,66E-03
CA442342	1556097_at	CA442342	---	---	-0,72	3,35E-03
PDE8B	243590_at	AA860184	NM_003719	8622	-0,72	9,18E-03
ARHGAP1	241419_at	AA709154	NM_004308	392	-0,72	4,95E-03
DKFZp547I014	207283_at	NM_020217	NM_020217	56969	-0,72	2,61E-03
DNASE1L1	203912_s_at	NM_006730	NM_001009932 NM_001009933 NM_001009934 NM_006730	1774	-0,72	1,52E-03
ANKRD17	225852_at	BE463523	NM_032217 NM_198889	26057	-0,72	7,58E-06
AI827550	229606_at	AI827550	---	---	-0,72	1,23E-04
AI538880	1558250_s_at	AI538880	---	---	-0,72	7,65E-05
AI040738	240730_at	AI040738	---	---	-0,72	7,11E-03
FBXW7	229419_at	BF222826	NM_018315 NM_033632	55294	-0,72	5,69E-04

ABCG1	204567_s_at	NM_004915	NM_004915 NM_016818 NM_207174 NM_207627 NM_207628 NM_207629 NM_207630	9619	-0,72	3,49E-04
TRA2A	213593_s_at	AW978896	NM_013293	29896	-0,72	4,15E-03
APC	215310_at	AF038181	NM_000038	324	-0,72	3,73E-03
CXXC5	222996_s_at	BC002490	NM_016463	51523	-0,71	8,07E-04
CSNK1A1	235464_at	AA010757	NM_001892	1452	-0,71	6,52E-04
USP7	230967_s_at	BF433061	NM_003470	7874	-0,71	1,69E-03
TAS2R14	235762_at	AI458566	NM_023922	50840	-0,71	1,07E-03
HNRPR	208766_s_at	BC001449	NM_005826	10236	-0,71	5,99E-04
CAPN1	232012_at	AV691298	NM_005186	823	-0,71	4,07E-03
AI825987	235889_at	AI825987	---	---	-0,71	1,70E-03
FLJ23867	226706_at	BE301252	---	200058	-0,71	5,23E-03
IGF2	202410_x_at	NM_000612	NM_000612	3481	-0,71	2,47E-03
AI887898	228423_at	AI887898	XM_374094	389237	-0,71	2,25E-03
MGC14801	224443_at	BC005997	NM_032705	84791	-0,71	1,76E-03
C1orf50	62212_at	W37846	NM_024097	79078	-0,71	1,18E-03
RLF	204243_at	NM_012421	NM_012421	6018	-0,71	2,22E-04
AW268719	236798_at	AW268719	---	---	-0,71	1,17E-04
AL080112	216858_x_at	AL080112	---	---	-0,71	6,17E-04
AI022648	242972_at	AI022648	---	---	-0,71	3,82E-04
AW072078	230959_at	AW072078	XM_496690	401131	-0,71	2,04E-05
PHKA1	205450_at	NM_002637	NM_002637	5255	-0,71	2,60E-05
AA694209	229066_at	AA694209	---	---	-0,71	1,09E-04
MAP1LC3B	208786_s_at	AF183417	NM_022818	81631	-0,71	4,58E-03
PABPC4	201064_s_at	NM_003819	NM_003819	8761	-0,71	2,02E-04
IGF2	210881_s_at	M17863	NM_000612	3481	-0,70	3,36E-03
C5orf16	1564031_a_at	AK054889	NM_173828	285613	-0,70	3,27E-03
UBXD1	223012_at	AF272894	NM_025241	80700	-0,70	2,81E-03
ANKRD28	229307_at	N32051	NM_015199	23243	-0,70	5,01E-03
UNQ1912	226752_at	AI816071	NM_198507	345757	-0,70	3,53E-03
ARHGAP1	202117_at	BG468434	NM_004308	392	-0,70	2,81E-03
C21orf59	218123_at	NM_017835	NM_017835 NM_021254	56683	-0,70	6,33E-07
MONDOA	225157_at	AW245631	NM_014938	22877	-0,70	1,12E-04
NM_024900	218517_at	NM_024900	---	---	-0,70	8,22E-04
C6orf133	215558_at	AK001118	NM_015255	23304	-0,70	6,83E-03
TRIM14	203147_s_at	BE962483	NM_014788 NM_033219 NM_033220 NM_033221	9830	-0,70	7,70E-03
NM_018678	220494_s_at	NM_018678	---	---	-0,70	1,04E-03
LOC144766	243986_at	BE409452	XM_378419	144766	-0,70	1,05E-03
PPP3CA	202429_s_at	AL353950	NM_000944	5530	-0,70	5,44E-04

RNF41	201962_s_at	NM_005785	NM_005785 NM_194358 NM_194359	10193	-0,70	4,15E-04
RPL35A	215208_x_at	AK021571	NM_000996	6165	-0,70	5,45E-03
CLSTN3	204375_at	NM_014718	NM_014718	9746	-0,70	4,42E-04
PTK2	241387_at	AW276701	NM_005607 NM_153831	5747	-0,70	5,63E-04
SYNJ1	212990_at	AB020717	NM_003895 NM_203446	8867	-0,69	1,15E-06
KIAA1276	227504_s_at	N64630	XM_039169	27146	-0,69	7,28E-06
MLR1	240592_at	AI939336	NM_153686	254251	-0,69	3,41E-04
LMNA	1554600_s_at	BC033088	NM_005572 NM_170707 NM_170708	4000	-0,69	9,76E-03
ZNF207	1556035_s_at	AI201248	NM_003457	7756	-0,69	3,42E-03
TM4SF2	202242_at	NM_004615	NM_004615	7102	-0,69	2,98E-03
AGRN	212285_s_at	AW008051	NM_198576	375790	-0,69	4,04E-03
AF116695	224254_x_at	AF116695	---	---	-0,69	4,32E-03
FLJ20758	228020_at	BG055431	NM_017952	55037	-0,69	3,97E-05
MYLIP	223130_s_at	AF212221	NM_013262	29116	-0,69	8,41E-03
PTPRD	213362_at	N73931	NM_002839 NM_130391 NM_130392 NM_130393	5789	-0,69	4,67E-03
UNC5A	236448_at	R37358	XM_030300	90249	-0,69	1,44E-05
USP36	224979_s_at	AU154368	NM_025090	57602	-0,69	1,61E-03
RBPMS2	228802_at	BE348466	XM_496072	348093	-0,69	1,05E-03
SENP2	222523_at	BE622841	NM_021627	59343	-0,69	4,48E-03
ATXN1	203231_s_at	AW235612	NM_000332	6310	-0,69	9,97E-03
AA630955	242133_s_at	AA630955	---	---	-0,69	1,82E-03
LOC285458	242577_at	BF109197	---	285458	-0,69	9,98E-03
ZNF573	217627_at	BE515346	NM_152360	126231	-0,69	5,61E-03
APC	216933_x_at	S67788	NM_000038	324	-0,69	1,03E-03
WDFY3	212598_at	BE348236	NM_014991 NM_178583 NM_178585	23001	-0,69	1,37E-05
FNBP1	244286_at	AI017983	NM_015033	23048	-0,69	3,21E-03
DSCR3	203635_at	NM_006052	NM_006052	10311	-0,68	1,64E-05
MONDOA	202519_at	NM_014938	NM_014938	22877	-0,68	3,72E-04
AI859990	244197_x_at	AI859990	---	---	-0,68	1,47E-03
C7orf19	1558426_x_at	BC016797	NM_032831	80228	-0,68	6,95E-04
MGC20419	225642_at	AL581536	NM_138417	112970	-0,68	5,44E-03
KIAA1644	221901_at	BF516072	XM_376018	85352	-0,68	3,43E-03
AI146751	242565_x_at	AI146751	---	---	-0,68	1,09E-03
PHF17	225816_at	AW138134	NM_024900 NM_199320	79960	-0,68	8,15E-04

NFASC	213438_at	AA995925	NM_001005387 NM_001005388 NM_001005389 NM_015090	23114	-0,68	1,25E-03
AI332346	225445_at	AI332346	---	---	-0,68	4,20E-03
PEX6	238672_at	AW953952	NM_000287	5190	-0,68	1,21E-05
PALM2-AKAP2	226694_at	BG540494	NM_007203 NM_147150	445815	-0,68	3,43E-04
AI821721	241223_x_at	AI821721	---	---	-0,68	5,48E-04
BF197705	230401_at	BF197705	---	---	-0,68	7,84E-03
BG527339	226457_at	BG527339	---	---	-0,68	2,91E-04
LOC146174	230721_at	BF436957	NM_173501	146174	-0,68	1,72E-03
C1orf21	223127_s_at	AW003850	NM_030806	81563	-0,68	6,33E-04
FBXO31	222352_at	BE465371	NM_024735	79791	-0,68	1,00E-04
TAF15	227891_s_at	AU144462	NM_003487 NM_139215	8148	-0,68	9,77E-03
ZNF207	231848_x_at	AW192569	NM_003457	7756	-0,68	1,45E-03
ZNF37A	228711_at	BF059259	NM_001007094 NM_003421	7587	-0,68	5,10E-04
ATP11A	1556055_at	U90905	NM_015205 NM_032189	23250	-0,68	4,26E-03
TIM14	225358_at	AI003794	NM_145261 NM_201259 NM_201260 NM_201261	131118	-0,68	2,38E-03
COL5A1	212489_at	AI983428	NM_000093	1289	-0,68	8,47E-03
MGC35274	226748_at	AI674731	NM_153374	256586	-0,68	1,32E-05
ST7L	238512_at	BF961733	NM_017744 NM_138727 NM_138728 NM_138729 NM_198327 NM_198328	54879	-0,67	2,66E-03
HUMPPA	213230_at	AI422335	NM_014603	30850	-0,67	7,14E-03
Cep164	204251_s_at	NM_014956	NM_014956	22897	-0,67	5,51E-03
C14orf159	218298_s_at	NM_024952	NM_024952	80017	-0,67	2,50E-03
MCTP1	235740_at	BG250585	NM_001002796 NM_024717	79772	-0,67	3,10E-03
ZNF451	215012_at	AU144775	NM_015555	26036	-0,67	3,81E-03
MAPT	225379_at	AA199717	NM_005910 NM_016834 NM_016835 NM_016841	4137	-0,67	6,84E-04
SMURF2	241900_at	AW195928	NM_022739	64750	-0,67	7,08E-03

FOXP1	235444_at	AI417897	NM_032682	27086	-0,67	5,32E-04
ZBED3	228402_at	AI679968	NM_032367	84327	-0,67	3,66E-03
ABCC8	210246_s_at	AF087138	NM_000352	6833	-0,67	5,10E-03
FLJ11016	219754_at	NM_018301	NM_018301	55285	-0,67	4,87E-03
AI344332	227227_at	AI344332	XM_373737	388397	-0,67	6,03E-05
HIS1	202814_s_at	AW193511	NM_006460	10614	-0,67	5,23E-04
LOC401394	217529_at	BE547674	XM_379512	401394	-0,67	1,35E-04
TMEM34	219074_at	NM_018241	NM_018241	55751	-0,67	2,81E-03
PPID	204185_x_at	NM_005038	NM_005038	5481	-0,67	2,92E-03
SFRS2IP	232597_x_at	AK025132	NM_004719	9169	-0,67	3,06E-03
SLC35E1	227518_at	AW051365	NM_024881	79939	-0,67	7,53E-03
C14orf118	229514_at	AB032978	NM_017926 NM_017972	55668	-0,67	8,14E-04
KIAA0913	212359_s_at	W89120	NM_015037	23053	-0,67	7,72E-03
C9orf85	238912_x_at	AA824363	NM_182505 NM_198394	138241	-0,67	1,86E-03
CaMKIINalpha	218309_at	NM_018584	NM_018584	55450	-0,67	1,94E-07
TAF1	227205_at	AW575233	NM_004606 NM_138923	6872	-0,67	3,47E-03
LOC144363	225469_at	AA015609	NM_001001660	144363	-0,66	4,42E-03
TNKS	233152_x_at	AL049979	NM_003747	8658	-0,66	2,23E-03
C1orf52	228135_at	AA738437	NM_198077	148423	-0,66	3,10E-03
BG502771	226397_s_at	BG502771	---	---	-0,66	6,19E-05
ELMO1	204513_s_at	NM_014800	NM_014800 NM_130442	9844	-0,66	6,47E-03
AI627803	236194_at	AI627803	---	---	-0,66	2,79E-03
AA604601	1570566_at	AA604601	---	---	-0,66	1,29E-04
RAMP1	204916_at	NM_005855	NM_005855	10267	-0,66	2,24E-06
AL137655	231886_at	AL137655	XM_373814	388572	-0,66	1,31E-04
PCDHB16	232099_at	AB046841	NM_020957	57717	-0,66	4,23E-03
KIAA0804	209553_at	BC001001	NM_001009921 NM_015303	23355	-0,66	2,61E-03
N63920	226179_at	N63920	---	---	-0,66	3,55E-04
MCPH1	219592_at	NM_024596	NM_024596	79648	-0,66	3,60E-03
MLLT6	224784_at	BG024886	NM_005937	4302	-0,66	6,68E-04
ARRDC1	226405_s_at	AK001822	NM_152285	92714	-0,66	2,73E-03
RAB11FIP4	224482_s_at	BC006240	NM_032932	84440	-0,66	3,11E-03
EFNA1	202023_at	NM_004428	NM_004428 NM_182685	1942	-0,66	2,72E-03
C18orf17	1552307_a_at	NM_153211	NM_153211	125488	-0,66	6,53E-03
MBTD1	207115_x_at	NM_017643	NM_017643	54799	-0,66	6,47E-03

ALG3	207396_s_at	NM_005787	NM_001006940 NM_001006941 NM_001006942 NM_005787	10195	-0,66	8,88E-04
IFNAR1	225661_at	AA811138	NM_000629	3454	-0,66	2,66E-03
FER1L4	222245_s_at	AF218012	---	80307	-0,66	3,17E-03
DDX50	1568815_a_at	AA903184	NM_024045	79009	-0,66	4,02E-03
ELK1	210376_x_at	M25269	NM_005229	2002	-0,66	8,45E-03
FBXO31	224162_s_at	BC002985	NM_024735	79791	-0,66	3,15E-03
RNF13	201779_s_at	AF070558	NM_007282 NM_183381 NM_183382 NM_183383 NM_183384	11342	-0,66	1,55E-03
LOC440345	238449_at	BG534511	XM_496125	440345	-0,66	1,28E-03
CXXC5	224516_s_at	BC006428	NM_016463	51523	-0,66	1,05E-05
MKNK2	223199_at	AA404592	NM_017572 NM_199054	2872	-0,66	2,26E-03
NFYC	202215_s_at	NM_014223	NM_014223	4802	-0,66	4,41E-04
RAB12	236019_at	AI076335	XM_113967	201475	-0,66	1,77E-03
ETFDH	205530_at	NM_004453	NM_004453	2110	-0,66	1,11E-03
LOC153364	230298_at	AI692906	NM_203406	153364	-0,66	1,11E-04
ELMO3	219411_at	NM_024712	NM_024712	79767	-0,66	2,82E-03
SERTAD4	229674_at	AL035414	NM_019605	56256	-0,66	3,57E-04
GPRASP1	204793_at	NM_014710	NM_014710	9737	-0,65	1,35E-03
SMAD4	1565703_at	AL832789	NM_005359	4089	-0,65	4,45E-03
ATP9A	216129_at	AL117659	XM_030577	10079	-0,65	3,73E-03
MGC21688	232806_s_at	AU158601	NM_144635	131408	-0,65	3,23E-03
LOC90410	210312_s_at	BC002640	NM_174887	90410	-0,65	1,34E-04
BE348430	230235_at	BE348430	---	---	-0,65	1,62E-04
UBE2G2	1557053_s_at	BC035653	NM_003343 NM_182688	7327	-0,65	1,15E-03
TRA2A	229574_at	AI268231	NM_013293	29896	-0,65	1,49E-03
MGC42174	238602_at	AL036541	NM_152383	129563	-0,65	9,27E-03
QSCN6	201482_at	NM_002826	NM_001004128 NM_002826	5768	-0,65	6,49E-03
C15orf24	217898_at	NM_020154	NM_020154	56851	-0,65	6,93E-03
SLCO1A2	211480_s_at	AF085224	NM_005075 NM_021094 NM_134431	6579	-0,65	3,46E-04

ATP2C1	230387_at	AL038450	NM_001001485 NM_001001486 NM_001001487 NM_014382	27032	-0,65	6,34E-03
AF5Q31	232864_s_at	N59653	NM_014423	27125	-0,65	1,51E-03
AL049975	234020_x_at	AL049975	---	---	-0,64	1,81E-03
AI634543	242208_at	AI634543	---	---	-0,64	1,23E-03
AI695743	244534_at	AI695743	---	---	-0,64	9,29E-03
CCNDBP1	223084_s_at	AF246144	NM_012142 NM_037370	23582	-0,64	1,19E-03
ZBED3	235109_at	AI887983	NM_032367	84327	-0,64	4,83E-03
BACE1	222462_s_at	AI653425	NM_012104 NM_138971 NM_138972 NM_138973	23621	-0,64	2,24E-05
SERTAD4	235337_at	AI276403	NM_019605	56256	-0,64	9,08E-04
ZNF596	240324_at	H50654	NM_173539	169270	-0,64	6,01E-04
AA845825	217534_at	AA845825	---	---	-0,64	1,19E-03
BE551142	241091_at	BE551142	XM_497668	388620	-0,64	2,87E-03
KIAA1181	224576_at	AK000752	NM_020462	57222	-0,64	9,10E-03
JMJD1C	221763_at	AI694023	NM_004241	221037	-0,64	1,29E-04
PPP2R5B	635_s_at	L42374	NM_006244	5526	-0,64	7,89E-04
FLJ31438	228316_at	AA905470	NM_152385	130162	-0,64	3,25E-05
AI524240	238863_x_at	AI524240	---	---	-0,64	3,04E-05
DJ971N18.2	240094_at	AL042660	NM_021156	56255	-0,64	7,59E-03
TTC3	208661_s_at	AW510696	NM_001001894 NM_003316	7267	-0,64	1,95E-04
JMJD3	41386_i_at	AB002344	XM_043272	23135	-0,64	6,66E-03
SEC6L1	228847_at	W69265	NM_007277	11336	-0,64	8,93E-03
C21orf106	227199_at	AW027812	NM_015151 NM_206889 NM_206890 NM_206891	23181	-0,64	1,63E-03
KIAA1919	242851_at	BE964989	NM_153369	91749	-0,64	1,22E-03
AI683552	217679_x_at	AI683552	---	---	-0,64	3,76E-03
ICA1	207949_s_at	NM_004968	NM_004968 NM_022307 NM_022308	3382	-0,64	3,58E-06
AI885665	238360_s_at	AI885665	---	---	-0,64	3,47E-04
AW511239	229765_at	AW511239	---	---	-0,64	7,38E-03
BI496583	1557675_at	BI496583	---	---	-0,63	3,19E-03
LOC253982	214993_at	AF070642	NM_181718 NM_198907	253982	-0,63	1,41E-04
ASB13	218862_at	NM_024701	NM_024701	79754	-0,63	2,48E-03
C18orf23	230143_at	BF433220	NM_152470	147341	-0,63	3,83E-03

WDFY3	212602_at	AI806395	NM_014991 NM_178583 NM_178585	23001	-0,63	3,16E-04
TMEM5	204808_s_at	NM_014254	NM_014254	10329	-0,63	4,54E-05
SPTBN1	200671_s_at	N92501	NM_003128 NM_178313	6711	-0,63	4,18E-04
AI216567	236754_at	AI216567	---	---	-0,63	2,90E-03
PTPRN2	203030_s_at	AF007555	NM_002847 NM_130842 NM_130843	5799	-0,63	7,43E-03
M17S2	1568857_a_at	BC012591	NM_005899 NM_031858 NM_031862	4077	-0,63	6,88E-03
C6orf170	1553726_s_at	NM_152730	NM_152730	221322	-0,63	2,53E-04
SON	201085_s_at	AA664291	NM_003103 NM_032195 NM_058183 NM_138925 NM_138926 NM_138927	6651	-0,63	2,20E-03
AA102332	240172_at	AA102332	---	---	-0,63	6,39E-03
MGC15416	225861_at	AW001250	NM_032371 NM_138418	84331	-0,63	4,24E-04
AK024602	222207_x_at	AK024602	---	---	-0,63	1,29E-03
AW945538	239208_s_at	AW945538	---	---	-0,63	2,53E-03
AI140364	221740_x_at	AI140364	XM_373737	388397	-0,63	1,10E-04
ARHGEF7	1562271_x_at	AL831814	NM_003899 NM_145735	8874	-0,63	5,76E-03
AG1	215434_x_at	AV684285	XM_371384 XM_496394	440673	-0,63	1,46E-03
BZRAP1	205839_s_at	NM_004758	NM_004758	9256	-0,63	3,66E-03
C14orf149	227699_at	BF511003	NM_144581	112849	-0,63	5,42E-03
U2AF1	232141_at	AU144161	NM_006758	7307	-0,63	2,12E-03
CAMK2B	213276_at	T15766	NM_001220 NM_172078 NM_172079 NM_172080 NM_172081 NM_172082 NM_172083 NM_172084	816	-0,63	7,05E-03
NRD1	229422_at	AA448346	NM_002525	4898	-0,63	5,72E-03
C10orf18	244165_at	AI809511	XM_374765	54906	-0,62	9,92E-03
TMPIT	234084_x_at	AU147104	NM_031925	83862	-0,62	7,32E-04
AI334297	225961_at	AI334297	---	---	-0,62	9,96E-03
MAPT	203929_s_at	AI056359	NM_005910 NM_016834 NM_016835 NM_016841	4137	-0,62	6,17E-04

XRN1	242995_at	AW976347	NM_019001	54464	-0,62	5,64E-03
NFIC	226377_at	AI093722	NM_005597 NM_205843	4782	-0,62	1,82E-03
FBXO9	212991_at	AL137520	NM_012347 NM_033480 NM_033481	26268	-0,62	1,09E-05
OSBPL6	223805_at	AF323728	NM_032523 NM_145739	114880	-0,62	1,05E-04
NRD1	242235_x_at	AW978721	NM_002525	4898	-0,62	6,13E-04
ATXN7L1	227732_at	AB033044	---	57485	-0,62	5,06E-03
PDPK1	32029_at	AC005591	NM_002613 NM_031268	5170	-0,62	8,86E-03
BF110411	221878_at	BF110411	XM_371506	388969	-0,62	4,02E-03
SNX1	1559154_at	AK098001	NM_003099 NM_148955 NM_152826	6642	-0,62	2,16E-03
LOC282965	230108_at	BF433475	---	282965	-0,62	7,42E-03
AA045233	224686_x_at	AA045233	XM_373737	388397	-0,62	1,42E-04
TIMM9	218316_at	NM_012460	NM_012460	26520	-0,62	9,93E-03
PTPRN2	203029_s_at	NM_002847	NM_002847 NM_130842 NM_130843	5799	-0,62	1,78E-04
MGC52110	226039_at	AW006441	NM_001008215	493753	-0,62	2,08E-04
SCN5A	207413_s_at	NM_000335	NM_000335 NM_198056	6331	-0,62	2,09E-03
ATF7	244473_at	R37637	NM_006856	11016	-0,62	6,77E-04
AL162054	1559420_x_at	AL162054	---	---	-0,62	2,91E-03
INHA	1569409_x_at	BC037812	NM_002191	3623	-0,62	9,67E-03
CTTN	214782_at	AU155105	NM_005231 NM_138565	2017	-0,62	3,85E-03
FLJ20758	228590_at	AA045257	NM_017952	55037	-0,62	1,29E-06
DTX3	221835_at	N92708	NM_178502	196403	-0,61	6,82E-03
AFG3L2	232919_at	AU147380	NM_006796	10939	-0,61	7,83E-03
NR2F1	209505_at	AI951185	NM_005654	7025	-0,61	1,18E-04
MYLIP	228098_s_at	AW292746	NM_013262	29116	-0,61	9,86E-05
FLJ00312	221971_x_at	BE672818	XM_374801	399761	-0,61	2,00E-05
STAT3	235680_at	AI914925	NM_003150 NM_139276 NM_213662	6774	-0,61	7,44E-04
PALM2-AKAP2	202759_s_at	BE879367	NM_007203 NM_147150	445815	-0,61	1,06E-05
AI692645	230206_at	AI692645	---	---	-0,61	7,26E-04
PPP3CA	202457_s_at	AA911231	NM_000944	5530	-0,61	1,76E-04
POM121 LOC340318	212178_s_at	AK022555	NM_172020 XM_290401 XM_379877	340318 9883	-0,61	6,29E-04
AK024255	232569_at	AK024255	---	---	-0,61	5,98E-03
TRIM8	223132_s_at	AF220034	NM_030912	81603	-0,61	5,53E-05
PDLIM4	211564_s_at	BC003096	NM_003687	8572	-0,61	4,83E-04

SHFM3	221519_at	AF281859	NM_022039	6468	-0,61	8,52E-06
RIC3	220282_at	NM_024557	NM_024557	79608	-0,61	3,26E-03
AK024881	234723_x_at	AK024881	---	---	-0,61	7,62E-03
DKFZP434H132	204494_s_at	AW516789	NM_015492	56905	-0,61	1,22E-04
SMA3	206565_x_at	NM_006780	NM_006780	10571	-0,61	8,06E-03
C21orf108	212996_s_at	AI803485	---	9875	-0,61	8,23E-04
MAP1LC3B	208785_s_at	BE893893	NM_022818	81631	-0,61	2,42E-03
PRKCZ	202178_at	NM_002744	NM_002744	5590	-0,61	2,33E-03
BICD1	214806_at	U90030	NM_001003398 NM_001714	636	-0,61	1,56E-03
MAP3K12	205447_s_at	BE222201	NM_006301	7786	-0,61	3,86E-03
PSIP1	232363_at	AK024516	NM_021144 NM_033222	11168	-0,61	2,71E-03
HPCAL1	205462_s_at	NM_002149	NM_002149 NM_134421	3241	-0,61	1,40E-05
PALM2-AKAP2	202760_s_at	NM_007203	NM_007203 NM_147150	445815	-0,61	4,74E-03
LOC282997	222307_at	AI695595	---	282997	-0,61	8,47E-03
BF339133	213296_at	BF339133	---	---	-0,60	3,76E-03
AI791303	238690_at	AI791303	---	---	-0,60	2,71E-03
KIAA1881	207730_x_at	NM_017932	XM_375558	114782	-0,60	1,50E-03
AL355532	213845_at	AL355532	---	---	-0,60	1,88E-04
ELOVL5	214153_at	BE467941	NM_021814	60481	-0,60	2,39E-03
FLJ38991	227442_at	BG283902	NM_173827	285521	-0,60	9,08E-05
C3orf6	226713_at	AI247881	NM_174908 NM_178335	152137	-0,60	6,70E-03
FNTA	230808_at	AA833870	NM_002027	2339	-0,60	3,58E-03
MGC54289	225228_at	AI474054	NM_178454	128338	-0,60	6,20E-03
KIAA1536	209002_s_at	BC003177	NM_020898	57658	-0,60	9,44E-03
CDK5R1	204995_at	AL567411	NM_003885	8851	-0,60	4,65E-04
SFXN3	1559993_at	AK091504	NM_030971	81855	-0,60	4,27E-03
AU157441	226511_at	AU157441	---	---	-0,60	3,90E-03
FLJ23861	231252_at	AI680874	NM_152519	151050	-0,60	5,09E-03
BE219067	243641_at	BE219067	---	---	-0,60	2,03E-06
BC042959	1556194_a_at	BC042959	---	---	-0,60	5,58E-03
PFAAP5	221899_at	AI809961	NM_014887	10443	-0,60	8,51E-03
PPP2R2C	223573_s_at	AW166283	NM_020416 NM_181876	5522	-0,60	4,24E-03
CLASP2	212309_at	AV725315	NM_015097	23122	-0,60	3,17E-04
INSR	226450_at	AV703054	NM_000208	3643	-0,60	8,36E-06
USP34	207365_x_at	NM_014709	NM_014709	9736	-0,60	8,70E-03
RUNX1	236114_at	AI798118	NM_001001890 NM_001754	861	-0,59	5,87E-03
VPS13C	218396_at	NM_017684	NM_017684	54832	-0,59	6,96E-03
KPNA1	202057_at	BC002374	NM_002264	3836	-0,59	3,30E-04
RPS6KL1	223534_s_at	BC004540	NM_031464	83694	-0,59	6,25E-04

CNNM3	240339_at	AA829860	NM_017623 NM_199078	26505	-0,59	2,25E-03
AK022428	234731_at	AK022428	---	---	-0,59	3,34E-04
NT5C3	223298_s_at	AF312735	NM_016489	51251	-0,59	8,53E-04
JMJD3	213146_at	AA521267	XM_043272	23135	-0,59	7,42E-03
NM_018289	219794_at	NM_018289	---	---	-0,59	4,18E-07
FCMD	205283_at	NM_006731	NM_006731	2218	-0,59	4,33E-03
C18orf17	1570552_at	AF363068	NM_153211	125488	-0,59	2,11E-03
FLJ23451	1569601_at	BF106979	NM_024766	79823	-0,59	1,13E-03
BF514509	239050_s_at	BF514509	---	---	-0,59	1,54E-03
LOC442647	229157_at	AI949265	XM_499544	442647	-0,59	2,37E-03
SLC24A5	228792_at	AU145100	NM_205850	283652	-0,59	1,36E-03
AI796076	243339_at	AI796076	---	---	-0,59	2,87E-03
BE857570	235677_at	BE857570	---	---	-0,59	2,57E-03
RALGDS	209051_s_at	AF295773	NM_006266	5900	-0,59	8,43E-03
SND1	242506_at	AI138785	NM_014390	27044	-0,59	1,79E-03
BM914560	1558220_at	BM914560	XM_496669	440993	-0,58	6,65E-03
SEZ6L2	218720_x_at	NM_012410	NM_012410 NM_201575	26470	-0,58	3,65E-03
AW294192	228040_at	AW294192	---	---	-0,58	3,57E-04
PCNT2	233387_s_at	AK024009	NM_006031	5116	-0,58	5,43E-03
CHST5	219182_at	NM_024533	NM_012126 NM_024533	23563	-0,58	9,75E-03
MGC15416	1553715_s_at	NM_032371	NM_032371 NM_138418	84331	-0,58	4,55E-03
ABAT	209460_at	AF237813	NM_000663 NM_020686	18	-0,58	5,91E-03
C9orf112	225586_at	BF222775	NM_138778	92715	-0,58	3,08E-03
DSCR3	217309_s_at	AJ001867	NM_006052	10311	-0,58	6,91E-03
IER2	202081_at	NM_004907	NM_004907	9592	-0,58	6,30E-03
MGC4796	223852_s_at	BC005169	NM_032017	83931	-0,58	7,87E-03
CD151	204306_s_at	NM_004357	NM_004357 NM_139030	977	-0,58	1,98E-03
MACF1	208633_s_at	W61052	NM_012090 NM_033044	23499	-0,58	1,19E-03
MGC16279	65585_at	AA527515	NM_032916	85002	-0,58	2,75E-03
ZBTB4	225629_s_at	AI669498	NM_020899	57659	-0,58	4,70E-05
GRIPAP1	1557562_at	AI984118	NM_020137 NM_207672	56850	-0,58	3,18E-03
AU145662	233399_x_at	AU145662	XM_499131	441383	-0,58	1,90E-03
SYNGAP1	230297_x_at	AW002361	NM_006772	8831	-0,58	5,57E-03
MGC15407	224968_at	AL518311	NM_080667	112942	-0,58	3,50E-03

Tabla 7. Expresión genética aumentada en las líneas celulares H1 y BB10 en comparación con la línea celular 2D6 en estado diferenciado usando análisis de micromatriz

Símbolo del gen	ID del conjunto de sondas	ID Pública representativa	ID de transcripción RefSec	ID de Gen Entrez	Proporción Log2	valor p
PLS3	201215_at	NM_005032	NM_005032	5358	6,46	2,18E-11
PEG3	209242_at	AL042588	NM_006210	5178	6,29	4,38E-07
FLJ32942	227711_at	BG150433	NM_144594	121355	6,29	3,26E-08
MSN	200600_at	NM_002444	NM_002444	4478	6,24	7,65E-10
DKFZp667G2110	214030_at	BE501352	XM_376254	131544	6,06	3,72E-05
MCM10	220651_s_at	NM_018518	NM_018518 NM_182751	55388	5,94	2,90E-06
TPTE	220205_at	NM_013315	NM_013315 NM_199259 NM_199260 NM_199261	7179	5,89	2,90E-07
DLG7	203764_at	NM_014750	NM_014750	9787	5,79	1,58E-05
PLK2	201939_at	NM_006622	NM_006622	10769	5,72	1,74E-08
HMMR	209709_s_at	U29343	NM_012484 NM_012485	3161	5,64	2,12E-07
BUB1	209642_at	AF043294	NM_004336	699	5,53	9,46E-06
RGS5	1555725_a_at	AF493929	NM_003617	8490	5,49	1,14E-04
NDN	209550_at	U35139	NM_002487	4692	5,42	1,66E-05
FLJ34013	225710_at	H99792	---	---	5,39	6,18E-08
FAT	201579_at	NM_005245	NM_005245	2195	5,36	1,20E-03
RGS5	218353_at	NM_025226	NM_003617	8490	5,29	4,83E-04
KCTD12	212192_at	AI718937	NM_138444	115207	5,28	1,26E-06
TFPI2	209278_s_at	L27624	NM_006528	7980	5,28	1,22E-05
AI813331	229097_at	AI813331	---	---	5,23	3,44E-07
GNG11	204115_at	NM_004126	NM_004126	2791	5,21	7,49E-06
AI197932	229498_at	AI197932	---	---	5,17	1,33E-07
RGS5	209070_s_at	AI183997	NM_003617	8490	5,14	3,20E-04
MKI67	212021_s_at	AU132185	NM_002417	4288	5,04	2,78E-05
PRSS12	205515_at	NM_003619	NM_003619	8492	5,01	3,19E-07
MCM10	222962_s_at	AB042719	NM_018518 NM_182751	55388	5,01	2,63E-07
BIRC5	210334_x_at	AB028869	NM_001168	332	5,00	5,51E-05
RAMP	222680_s_at	AK001261	NM_016448	51514	5,00	2,74E-05
ASF1B	218115_at	NM_018154	NM_018154	55723	4,97	3,08E-05
MKI67	212023_s_at	AU147044	NM_002417	4288	4,97	7,09E-06
MKI67	212020_s_at	AU152107	NM_002417	4288	4,97	3,98E-07
ATAD2	218782_s_at	NM_014109	NM_014109	29028	4,96	7,16E-07
BIRC5	202094_at	AA648913	NM_001168	332	4,96	3,70E-05
FLJ40629	229610_at	AW088063	NM_152515	150468	4,96	2,93E-05
EXO1	204603_at	NM_003686	NM_003686 NM_006027 NM_130398	9156	4,90	1,18E-05
DEPDC1	222958_s_at	AK000490	NM_017779	55635	4,89	2,51E-07
RGS5	209071_s_at	AF159570	NM_003617	8490	4,87	1,25E-04

RRM2	209773_s_at	BC001886	NM_001034	6241	4,86	4,36E-05
KIF14	236641_at	AW183154	XM_375825	9928	4,86	1,11E-05
OIP5	213599_at	BE045993	NM_007280	11339	4,85	5,98E-08
C10orf3	218542_at	NM_018131	NM_018131	55165	4,85	4,79E-06
BRRN1	212949_at	D38553	NM_015341	23397	4,85	2,87E-06
FLJ10719	223785_at	BC004277	NM_018193	55215	4,84	6,89E-06
CHEK2	210416_s_at	BC004207	NM_001005735 NM_007194 NM_145862	11200	4,81	1,17E-03
N31731	230165_at	N31731	---	---	4,80	2,02E-07
BRIP1	235609_at	BF056791	NM_032043	83990	4,80	3,95E-05
MELK	204825_at	NM_014791	NM_014791	9833	4,80	2,52E-04
KIF20A	218755_at	NM_005733	NM_005733	10112	4,71	2,34E-05
SPARC	200665_s_at	NM_003118	NM_003118	6678	4,71	6,23E-06
BUB1	215509_s_at	AL137654	NM_004336	699	4,69	2,73E-06
BASP1	202391_at	NM_006317	NM_006317	10409	4,68	5,50E-07
SULT1C2	1553321_a_at	NM_006588	NM_006588	27233	4,66	9,28E-06
GTSE1	204317_at	BF305380	NM_016426	51512	4,64	2,33E-08
DAZ1 DAZ3 DAZ2 DAZ4	208282_x_at	NM_020363	NM_001005375 NM_001005785 NM_001005786 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	4,64	4,44E-03
CDC45L	204126_s_at	NM_003504	NM_003504	8318	4,62	2,60E-04
PRSS12	213802_at	AI810767	NM_003619	8492	4,61	1,09E-05
BRIP1	221703_at	AF360549	NM_032043	83990	4,60	7,21E-06
RNF182	230720_at	AI884906	NM_152737	221687	4,59	1,15E-07
SLC1A3	202800_at	NM_004172	NM_004172	6507	4,55	1,78E-06
DAZ1 DAZ3 DAZ2 DAZ4	207912_s_at	NM_004081	NM_001005375 NM_001005785 NM_001005786 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	4,55	1,51E-03
GTSE1	204315_s_at	AI340239	NM_016426	51512	4,54	9,21E-06
NEIL3	219502_at	NM_018248	NM_018248	55247	4,54	8,88E-06
SPARC	212667_at	AL575922	NM_003118	6678	4,53	5,72E-05
FN5	219806_s_at	NM_020179	NM_020179	56935	4,53	2,58E-05
CENPA	204962_s_at	NM_001809	NM_001809	1058	4,53	1,46E-06

MYBL1	213906_at	AW592266	XM_034274	4603	4,52	2,33E-05
MAOA	212741_at	AA923354	NM_000240	4128	4,52	9,33E-07
HMMR	207165_at	NM_012485	NM_012484 NM_012485	3161	4,51	5,91E-06
ZNF367	229551_x_at	N62196	NM_153695	195828	4,50	2,65E-05
NMU	206023_at	NM_006681	NM_006681	10874	4,50	1,75E-04
CDCA8	221520_s_at	BC001651	NM_018101	55143	4,49	1,67E-06
FLJ10156	221591_s_at	BC005004	NM_019013	54478	4,48	1,61E-06
SHCBP1	219493_at	NM_024745	NM_024745	79801	4,47	1,26E-05
DIAPH3	232596_at	AL354829	NM_030932	81624	4,46	1,53E-06
DAZ1 DAZ3 DAZ2 DAZ4	207909_x_at	U21663	NM_001005375 NM_001005785 NM_001005786 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	4,46	3,63E-03
FOXM1	202580_x_at	NM_021953	NM_021953 NM_202002 NM_202003	2305	4,44	1,30E-04
MAB21L2	210302_s_at	AF262032	NM_006439	10586	4,43	9,15E-04
KIF18A	221258_s_at	NM_031217	NM_031217	81930	4,42	2,20E-07
STK6	204092_s_at	NM_003600	NM_003600 NM_198433 NM_198434 NM_198435 NM_198436 NM_198437	6790	4,41	1,58E-06
ANLN	1552619_a_at	NM_018685	NM_018685	54443	4,41	6,79E-05
MINA	213188_s_at	AI823896	NM_032778 NM_153182	84864	4,41	1,40E-04
CENPE	205046_at	NM_001813	NM_001813	1062	4,40	5,00E-07
FLJ20641	227928_at	AI224977	NM_017915	55010	4,40	5,48E-07
CDC2	203214_x_at	NM_001786	NM_001786 NM_033379	983	4,37	1,70E-06
KIF4A	218355_at	NM_012310	NM_012310	24137	4,36	5,88E-08
CDCA2	226661_at	T90295	NM_152562	157313	4,34	2,67E-07

BRCA1	211851_x_at	AF005068	NM_007294 NM_007295 NM_007296 NM_007297 NM_007298 NM_007299 NM_007300 NM_007301 NM_007302 NM_007303 NM_007304 NM_007305 NM_007306	672	4,34	1,52E-05
DEPDC1	235545_at	AI810054	NM_017779	55635	4,32	1,48E-07
MINA	213189_at	BE966695	NM_032778 NM_153182	84864	4,31	1,18E-06
CDKN3	209714_s_at	AF213033	NM_005192	1033	4,31	8,89E-05
PLK4	204887_s_at	NM_014264	NM_014264	10733	4,29	1,64E-04
RRM2	201890_at	BE966236	NM_001034	6241	4,28	5,37E-05
RAD51	205024_s_at	NM_002875	NM_002875 NM_133487	5888	4,27	1,40E-05
AURKB	209464_at	AB011446	NM_004217	9212	4,27	2,23E-05
TTK	204822_at	NM_003318	NM_003318	7272	4,27	7,61E-06
POLE2	205909_at	NM_002692	NM_002692	5427	4,27	9,18E-04
OSBPL3	209627_s_at	AY008372	NM_015550 NM_145320 NM_145321 NM_145322 NM_145323 NM_145324	26031	4,26	1,75E-05
PEG3	209243_s_at	AF208967	NM_006210	5178	4,26	3,95E-05
KIF11	204444_at	NM_004523	NM_004523	3832	4,25	4,91E-04
Spc24	235572_at	AI469788	NM_182513	147841	4,25	7,74E-09
FGFR2	203639_s_at	M80634	NM_000141 NM_022969 NM_022970 NM_022971 NM_022972 NM_022973 NM_022974 NM_022975 NM_022976 NM_023028 NM_023029 NM_023030 NM_023031	2263	4,24	9,58E-06
CDCA1	223381_at	AF326731	NM_031423 NM_145697	83540	4,22	1,90E-05
ANLN	222608_s_at	AK023208	NM_018685	54443	4,22	2,01E-04

MAB21L1	206163_at	NM_005584	NM_005584	4081	4,21	2,65E-05
CDC6	203967_at	U77949	NM_001254	990	4,20	1,21E-03
ESPL1	38158_at	D79987	NM_012291	9700	4,17	1,15E-06
MCM5	201755_at	NM_006739	NM_006739	4174	4,16	4,33E-04
MGC57827	225834_at	AL135396	NM_207418	389835	4,16	6,28E-06
STK6	208079_s_at	NM_003158	NM_003600 NM_198433 NM_198434 NM_198435 NM_198436 NM_198437	6790	4,16	1,80E-05
SLD5	211767_at	BC005995	NM_032336	84296	4,16	3,72E-03
RAMP	218585_s_at	NM_016448	NM_016448	51514	4,16	1,38E-04
KNTC2	204162_at	NM_006101	NM_006101	10403	4,14	1,03E-06
DEPDC1	220295_x_at	NM_017779	NM_017779	55635	4,14	6,26E-07
KNSL7	219306_at	NM_020242	NM_020242	56992	4,14	7,68E-06
CDCA2	236957_at	AI248208	NM_152562	157313	4,13	1,53E-05
MLF1IP	229305_at	AA460299	NM_024629	79682	4,13	2,13E-06
CDC2	210559_s_at	D88357	NM_001786 NM_033379	983	4,11	3,40E-06
CDKN3	1555758_a_at	AF213040	NM_005192	1033	4,10	5,09E-07
ATAD2	222740_at	AI925583	NM_014109	29028	4,10	1,44E-05
FAM54A	228069_at	AL138828	NM_138419	113115	4,10	8,67E-07
CDK2	204252_at	M68520	NM_001798 NM_052827	1017	4,10	1,46E-06
AI377043	230722_at	AI377043	---	---	4,10	2,84E-08
CDC25C	205167_s_at	NM_001790	NM_001790 NM_022809	995	4,09	1,38E-05
GTSE1	204318_s_at	NM_016426	NM_016426	51512	4,08	6,60E-06
UHRF1	225655_at	AK025578	NM_013282	29128	4,08	5,58E-05
FLJ23311	219990_at	NM_024680	NM_024680	79733	4,08	1,87E-05
PBK	219148_at	NM_018492	NM_018492	55872	4,08	2,74E-06
MGC34032	235763_at	AA001450	NM_152697	204962	4,07	4,96E-06
Spc25	209891_at	AF225416	NM_020675	57405	4,07	2,08E-04
ASPM	219918_s_at	NM_018123	NM_018136	259266	4,06	1,74E-06
IQGAP3	229538_s_at	AW271106	NM_178229	128239	4,04	3,66E-05
UBE3B	213822_s_at	BE856776	NM_130466 NM_183414 NM_183415	89910	4,03	1,32E-06
SMC2L1	204240_s_at	NM_006444	NM_006444	10592	4,02	1,45E-04
SYNPO2	225720_at	AW009747	NM_133477	171024	4,02	2,27E-04
FBLN1	202995_s_at	NM_006486	NM_001996 NM_006485 NM_006486 NM_006487	2192	4,01	1,34E-06
ITGA6	201656_at	NM_000210	NM_000210	3655	4,00	1,10E-06
CDC6	203968_s_at	NM_001254	NM_001254	990	4,00	3,34E-04
TK1	1554408_a_at	BC007986	NM_003258	7083	4,00	4,33E-07
FLJ25416	228281_at	BF343258	NM_145018	220042	3,99	1,36E-06

ORC1L	205085_at	NM_004153	NM_004153	4998	3,98	1,89E-05
CNTN1	211203_s_at	U07820	NM_001843 NM_175038	1272	3,97	1,43E-05
NUSAP1	218039_at	NM_016359	NM_016359 NM_018454	51203	3,97	2,83E-06
KIF23	204709_s_at	NM_004856	NM_004856 NM_138555	9493	3,96	7,58E-05
FBLN1	201787_at	NM_001996	NM_001996 NM_006485 NM_006486 NM_006487	2192	3,96	1,15E-04
RAD54L	204558_at	NM_003579	NM_003579	8438	3,95	6,59E-06
CENPF	209172_s_at	U30872	NM_016343	1063	3,95	2,98E-08
FGL1	205305_at	NM_004467	NM_004467 NM_147203 NM_201552 NM_201553	2267	3,94	2,35E-05
ARHGAP24	223422_s_at	AI743534	NM_031305	83478	3,94	2,71E-05
DKFZp564A232	1556300_s_at	BF476109	---	---	3,93	1,17E-03
DEPDC1	232278_s_at	AJ278112	NM_017779	55635	3,93	3,60E-05
GRP	206326_at	NM_002091	NM_002091	2922	3,92	5,54E-05
MAOA	204388_s_at	NM_000240	NM_000240	4128	3,92	3,38E-07
POLQ	219510_at	NM_006596	NM_006596 NM_199420	10721	3,91	8,49E-06
DKFZp762E1312	218726_at	NM_018410	NM_018410	55355	3,91	7,86E-06
GTSE1	215942_s_at	BF973178	NM_016426	51512	3,90	9,11E-06
TPX2	210052_s_at	AF098158	NM_012112	22974	3,90	3,85E-06
LOC440738	221697_at	AF276659	NM_001004343	440738	3,90	2,27E-03
LOC340109	1557765_at	BC039509	XM_379322	340109	3,89	2,74E-05
NUSAP1	219978_s_at	NM_018454	NM_016359 NM_018454	51203	3,89	3,26E-06
LOC253981	226430_at	AI394438	---	253981	3,88	6,06E-07
ESPL1	204817_at	NM_012291	NM_012291	9700	3,85	7,34E-05
KIFC1	209680_s_at	BC000712	XM_371813	3833	3,83	1,36E-06
KCTD12	212188_at	AA551075	NM_138444	115207	3,82	1,05E-05
KIF14	206364_at	NM_014875	XM_375825	9928	3,82	6,29E-07
SGOL2	235425_at	AW965339	NM_152524	151246	3,81	3,04E-05
KIAA0186	206102_at	NM_021067	XM_375911	9837	3,81	4,00E-06
C20orf129	225687_at	BC001068	NM_030919	81610	3,80	4,60E-05
DNA2L	213647_at	D42046	XM_166103	1763	3,79	4,96E-07
CCDC3	223316_at	AL136562	NM_031455	83643	3,78	9,80E-05
CIT	212801_at	AI861788	NM_007174	11113	3,78	9,25E-05
BUB1B	203755_at	NM_001211	NM_001211	701	3,78	6,66E-07
CDCA3	221436_s_at	NM_031299	NM_031299	83461	3,77	1,69E-04
MCM10	223570_at	AL136840	NM_018518 NM_182751	55388	3,76	8,71E-06
C18orf24	217640_x_at	BF038461	NM_145060	220134	3,76	7,58E-05
EMILIN2	224374_s_at	AF270513	NM_032048	84034	3,75	2,71E-05
C18orf54	229442_at	BF059556	NM_173529	162681	3,75	4,74E-08

MAB21L2	210303_at	AF262032	NM_006439	10586	3,73	4,97E-07
BNC2	238478_at	H97386	NM_017637	54796	3,73	6,40E-07
AI926924	239253_at	AI926924	---	---	3,73	3,76E-04
CDC2	203213_at	AL524035	NM_001786 NM_033379	983	3,73	5,41E-06
Pfs2	221521_s_at	BC003186	NM_016095	51659	3,73	2,20E-05
MGC34032	1569112_at	AW020413	NM_152697	204962	3,72	5,15E-06
NEK2	204641_at	NM_002497	NM_002497	4751	3,71	2,52E-05
MGC45871	226876_at	AI961778	NM_182705	359845	3,71	6,58E-06
DPYD	204646_at	NM_000110	NM_000110	1806	3,70	1,06E-04
BIRC5	202095_s_at	NM_001168	NM_001168	332	3,70	1,51E-06
ELOVL7	227180_at	AW138767	XM_371740	79993	3,69	9,47E-05
BF000203	236385_at	BF000203	---	---	3,69	1,75E-05
STK17A	202693_s_at	AW194730	NM_004760	9263	3,68	3,33E-04
CHEK1	205394_at	NM_001274	NM_001274	1111	3,67	2,79E-04
FLJ13912	45633_at	AI421812	NM_022770	64785	3,67	3,76E-06
FLJ10719	213008_at	BG403615	NM_018193	55215	3,67	4,86E-06
CENPF	207828_s_at	NM_005196	NM_016343	1063	3,65	1,58E-06
E2F2	228361_at	AL561296	NM_004091	1870	3,65	2,93E-06
NEGR1	243357_at	AA115106	NM_173808	257194	3,65	1,29E-06
CENPA	210821_x_at	BC002703	NM_001809	1058	3,65	7,15E-06
MGC40179	242560_at	AA579890	NM_173472	115795	3,64	1,89E-04
SPAG6	210033_s_at	AF079363	NM_012443 NM_172242	9576	3,64	3,09E-03
SLAC2-B	214734_at	AB014524	NM_015065	23086	3,64	3,42E-04
ASCL1	209985_s_at	BE797438	NM_004316	429	3,63	3,48E-04
ZNF521	226677_at	AF141339	NM_015461	25925	3,62	6,14E-07
NEK2	211080_s_at	Z25425	NM_002497	4751	3,62	4,42E-05
TK1	202338_at	NM_003258	NM_003258	7083	3,62	1,03E-05
CCNB1	214710_s_at	BE407516	NM_031966	891	3,62	5,65E-07
TCF7L1	221016_s_at	NM_031283	NM_031283	83439	3,61	1,36E-03
MYBL2	201710_at	NM_002466	NM_002466	4605	3,60	5,06E-05
BRCA2	208368_s_at	NM_000059	NM_000059	675	3,60	1,84E-05
TOP2A	201292_at	AL561834	NM_001067	7153	3,60	4,23E-06
CCNE2	205034_at	NM_004702	NM_004702 NM_057735 NM_057749	9134	3,60	1,96E-05
AI937080	244033_at	AI937080	---	---	3,59	1,30E-04
MKI67	212022_s_at	BF001806	NM_002417	4288	3,59	3,34E-05
dJ383J4.3	1554271_a_at	BC019022	NM_033319	91687	3,57	3,09E-05
SMC6L1	236535_at	AW069285	NM_024624	79677	3,56	3,19E-05
ECT2	219787_s_at	NM_018098	NM_018098	1894	3,56	7,41E-08
CDCA3	223307_at	BC002551	NM_031299	83461	3,56	9,80E-05
CDCA5	224753_at	BE614410	NM_080668	113130	3,56	1,86E-05
TRIP10	202734_at	NM_004240	NM_004240	9322	3,55	1,98E-05
C14orf106	226630_at	BF062175	NM_018353	55320	3,55	5,62E-07
TMEM35	219685_at	NM_021637	NM_021637	59353	3,55	9,24E-05
POLA2	204441_s_at	NM_002689	NM_002689	23649	3,54	5,49E-06
FLJ13912	218719_s_at	NM_022770	NM_022770	64785	3,52	1,92E-06

PDE5A	227088_at	BF221547	NM_001083 NM_033430 NM_033431 NM_033437	8654	3,52	7,25E-04
SIM1	206876_at	AL121948	NM_005068	6492	3,52	9,26E-04
WDR51A	226355_at	AW001089	NM_015426	25886	3,52	2,74E-05
TFPI2	209277_at	AL574096	NM_006528	7980	3,51	1,33E-04
CUGBP2	202158_s_at	NM_006561	NM_006561	10659	3,51	3,91E-03
ATAD2	235266_at	AI139629	NM_014109	29028	3,49	5,52E-05
DOK5	1554863_s_at	BC008992	NM_018431 NM_177959	55816	3,49	1,51E-03
ATAD2	228401_at	AI656807	NM_014109	29028	3,49	2,96E-06
WDHD1	204728_s_at	NM_007086	NM_001008396 NM_007086	11169	3,48	1,11E-05
BC002493	223274_at	BC002493	---	---	3,47	3,08E-05
BARD1	205345_at	NM_000465	NM_000465	580	3,46	1,90E-03
MGC45866	230021_at	AI638593	NM_152259	90381	3,46	1,66E-05
Cep152	239413_at	AI130715	NM_014985	22995	3,46	2,08E-07
DKFZp761O2018	232313_at	AL122107	XM_044062	92293	3,46	1,14E-04
TOP2A	201291_s_at	AU159942	NM_001067	7153	3,45	8,58E-06
TRAF4	202871_at	NM_004295	NM_004295 NM_145751	9618	3,44	2,74E-06
RBPMS	209488_s_at	D84109	NM_001008710 NM_001008711 NM_001008712 NM_006867	11030	3,44	6,92E-04
CNTN1	227202_at	AW072790	NM_001843 NM_175038	1272	3,44	1,89E-06
DCC1	219000_s_at	NM_024094	NM_024094	79075	3,43	2,54E-04
KIF2C	211519_s_at	AY026505	NM_006845	11004	3,42	9,85E-05
SLC43A3	210692_s_at	BC003163	NM_014096 NM_017611 NM_199329	29015	3,41	1,35E-04
KIAA0101	202503_s_at	NM_014736	NM_014736	9768	3,40	1,33E-05
FBP1	209696_at	D26054	NM_000507	2203	3,40	3,15E-04
AA224205	238075_at	AA224205	---	---	3,39	1,33E-05
ADAMTS9	226814_at	AI431730	NM_020249 NM_182920 NM_182921	56999	3,38	2,69E-06
FLJ10706	220840_s_at	NM_018186	NM_018186	55732	3,38	4,66E-05
HCAP-G	218662_s_at	NM_022346	NM_022346	64151	3,37	3,87E-06
SLC7A2	225516_at	AA876372	NM_001008539 NM_003046	6542	3,37	1,80E-08
BF477980	242775_at	BF477980	---	---	3,36	1,18E-04

UBE2C	202954_at	NM_007019	NM_007019 NM_181799 NM_181800 NM_181801 NM_181802 NM_181803	11065	3,36	1,60E-06
CSRP2	207030_s_at	NM_001321	NM_001321	1466	3,35	9,35E-07
PRC1	218009_s_at	NM_003981	NM_003981 NM_199413 NM_199414	9055	3,35	2,53E-06
GNG12	222834_s_at	N32508	NM_018841	55970	3,34	4,89E-06
AB040957	231855_at	AB040957	---	---	3,34	2,91E-07
DAZ1 DAZ3 DAZ2 DAZ4	208281_x_at	NM_020364	NM_001005375 NM_001005785 NM_001005786 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	3,34	4,52E-03
MCM5	216237_s_at	AA807529	NM_006739	4174	3,34	1,01E-04
CCNA2	203418_at	NM_001237	NM_001237	890	3,34	2,17E-04
FLJ20105	219650_at	NM_017669	NM_001009954 NM_017669	54821	3,34	1,12E-05
BF108778	235363_at	BF108778	---	---	3,33	1,13E-04
BM039	222118_at	AK023669	NM_018455	55839	3,33	1,47E-07
SDC2	212154_at	AI380298	NM_002998	6383	3,33	5,56E-04
LOC440928	235147_at	R56118	XM_498917	440928	3,33	1,32E-03
LOC146909	222039_at	AA292789	XM_085634	146909	3,31	2,57E-05
RAD51AP1	204146_at	BE966146	NM_006479	10635	3,31	4,07E-06
SMC6L1	218781_at	NM_024624	NM_024624	79677	3,30	2,52E-08
ZWINT	204026_s_at	NM_007057	NM_001005413 NM_001005414 NM_007057 NM_032997	11130	3,29	7,56E-06
KIAA1754	225582_at	AA425726	NM_033397	85450	3,29	3,22E-06
CCNB1	228729_at	N90191	NM_031966	891	3,29	3,59E-06
PRAME	204086_at	NM_006115	NM_006115 NM_206953 NM_206954 NM_206955 NM_206956	23532	3,28	3,84E-04

BRCA1	204531_s_at	NM_007295	NM_007294 NM_007295 NM_007296 NM_007297 NM_007298 NM_007299 NM_007300 NM_007301 NM_007302 NM_007303 NM_007304 NM_007305 NM_007306	672	3,28	2,73E-04
CNTN1	227209_at	AI091445	NM_001843 NM_175038	1272	3,27	3,23E-05
SLC43A3	213113_s_at	AI630178	NM_014096 NM_017611 NM_199329	29015	3,27	1,59E-06
TIMP3	201147_s_at	BF347089	NM_000362	7078	3,27	2,90E-04
LTB4DH	231897_at	AL135787	NM_012212	22949	3,27	4,25E-05
FLJ22624	219544_at	NM_024808	NM_024808	79866	3,27	4,96E-04
GNAI1	227692_at	AU153866	NM_002069	2770	3,26	1,36E-05
BC035780	1560258_a_at	BC035780	---	---	3,26	1,57E-07
CCNB2	202705_at	NM_004701	NM_004701	9133	3,24	2,06E-06
PTTG1	203554_x_at	NM_004219	NM_004219	9232	3,24	8,78E-06
LOC157570	235588_at	AA740849	XM_088331	157570	3,23	2,41E-04
BG391951	236852_at	BG391951	---	---	3,22	1,77E-04
MLF1IP	218883_s_at	NM_024629	NM_024629	79682	3,21	1,31E-05
MGC24665	226456_at	AW138157	NM_152308	116028	3,21	6,88E-05
GNAI1	209576_at	AL049933	NM_002069	2770	3,21	1,53E-06
PLK4	204886_at	AL043646	NM_014264	10733	3,20	2,80E-04
GPSM2	205240_at	NM_013296	NM_013296	29899	3,20	9,04E-07
TROAP	204649_at	NM_005480	NM_005480	10024	3,19	2,23E-05
SYNPO2	227662_at	AA541622	NM_133477	171024	3,19	1,95E-03
C14orf106	206500_s_at	NM_018353	NM_018353	55320	3,19	5,08E-04
HCAP-G	218663_at	NM_022346	NM_022346	64151	3,19	1,36E-04
FLJ10719	213007_at	W74442	NM_018193	55215	3,18	1,31E-05
LTB4DH	228824_s_at	BE566894	NM_012212	22949	3,17	2,71E-05
TRIM36	219736_at	NM_018700	NM_018700	55521	3,17	4,38E-05
HGF	209960_at	X16323	NM_000601 NM_001010931 NM_001010932 NM_001010933 NM_001010934	3082	3,17	6,34E-04
CHAF1A	203976_s_at	NM_005483	NM_005483	10036	3,17	3,20E-04

AK022040	233445_at	AK022040	---	---	3,17	1,50E-06
AA938184	236312_at	AA938184	---	---	3,17	1,06E-04
CTSL2	210074_at	AF070448	NM_001333	1515	3,17	5,51E-04
FKSG14	222848_at	BC005400	NM_022145	64105	3,16	3,35E-06
EME1	234465_at	AK021607	NM_152463	146956	3,16	8,50E-06
TCTE1L	203303_at	NM_006520	NM_006520	6990	3,15	2,23E-04
SBLF	213413_at	BG434174	NM_006873	11037	3,15	3,72E-03
MCM6	201930_at	NM_005915	NM_005915	4175	3,15	3,87E-06
LOC402524	242206_at	AW590588	XM_379850	402524	3,14	1,94E-07
INCENP	242787_at	AI924134	NM_020238	3619	3,14	7,83E-06
LTB4DH	228825_at	BE566894	NM_012212	22949	3,12	1,25E-04
FNDC5	226096_at	AI760132	NM_153756	252995	3,12	3,00E-04
P2RY5	218589_at	NM_005767	NM_005767	10161	3,12	2,25E-03
GABRA5	206456_at	NM_000810	NM_000810	2558	3,11	3,01E-04
E2F1	204947_at	NM_005225	NM_005225	1869	3,11	1,27E-05
E2F7	228033_at	AI341146	NM_203394	144455	3,11	9,10E-05
EDG2	204036_at	AW269335	NM_001401 NM_057159	1902	3,11	9,74E-05
RFC5	203210_s_at	NM_007370	NM_007370 NM_181578	5985	3,09	2,74E-05
BNC2	220272_at	NM_017637	NM_017637	54796	3,09	7,83E-06
DEPDC1B	226980_at	AK001166	NM_018369	55789	3,09	1,82E-06
PPAP2B	209355_s_at	AB000889	NM_003713 NM_177414	8613	3,09	1,33E-03
RBL1	1555004_a_at	BC032247	NM_002895 NM_183404	5933	3,09	1,25E-05
LOC132671	229331_at	AI559300	NM_145263	132671	3,09	2,77E-04
AI656180	242447_at	AI656180	---	---	3,09	6,33E-05
KCNG3	1552897_a_at	NM_133329	NM_133329 NM_172344	170850	3,09	1,62E-04
EFNB2	202668_at	BF001670	NM_004093	1948	3,08	7,07E-04
TACC3	218308_at	NM_006342	NM_006342	10460	3,07	1,21E-05
SHOX2	210135_s_at	AF022654	NM_003030 NM_006884	6474	3,07	2,01E-03
TYMS	1554696_s_at	AB077208	NM_001071	7298	3,07	2,09E-06
CDK2	211804_s_at	AB012305	NM_001798 NM_052827	1017	3,06	3,25E-06
MGC33887	213644_at	AI979276	NM_145036	201134	3,06	7,13E-03
BVES	228783_at	AA993518	NM_007073 NM_147147	11149	3,06	3,06E-04
C20orf172	219512_at	NM_024918	NM_024918	79980	3,05	1,03E-05
OSBPL3	209626_s_at	AI202969	NM_015550 NM_145320 NM_145321 NM_145322 NM_145323 NM_145324	26031	3,05	2,81E-04

CXCR4	211919_s_at	AF348491	NM_001008540 NM_003467	7852	3,05	2,72E-03
GAS2L3	235709_at	H37811	NM_174942	283431	3,04	8,83E-03
CENPJ	220885_s_at	NM_018451	NM_018451	55835	3,04	5,23E-04
TIMP3	201149_s_at	U67195	NM_000362	7078	3,03	3,76E-05
AW271106	229490_s_at	AW271106	---	---	3,03	3,24E-06
SPAG5	203145_at	NM_006461	NM_006461	10615	3,03	2,06E-06
CXCR4	217028_at	AJ224869	NM_001008540 NM_003467	7852	3,03	8,98E-04
PRIMA1	230087_at	AI823645	NM_178004 NM_178013	145270	3,02	1,47E-05
DDA3	201896_s_at	BC001425	NM_001005290 NM_032636	84722	3,02	5,61E-06
DAZ1 DAZ3 DAZ2 DAZ4	216922_x_at	AF271088	NM_001005375 NM_001005785 NM_001005786 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	3,02	8,33E-03
MYRIP	214156_at	AL050090	NM_015460	25924	3,02	2,47E-05
KITLG	226534_at	AI446414	NM_000899 NM_003994	4254	3,01	4,26E-04
GAS2L3	238756_at	AI860012	NM_174942	283431	3,00	7,34E-05
NRXN1	228547_at	BF509242	NM_004801 NM_138735	9378	3,00	1,59E-03
ORC6L	219105_x_at	NM_014321	NM_014321	23594	3,00	2,00E-07
CHEK1	205393_s_at	NM_001274	NM_001274	1111	2,99	6,29E-05
FLJ20641	220060_s_at	NM_017915	NM_017915	55010	2,98	3,74E-07
SLITRK5	214930_at	AW449813	NM_015567	26050	2,98	2,02E-05
BNC2	233036_at	AU146418	NM_017637	54796	2,98	6,17E-03
SYNPO2	225895_at	AI634580	NM_133477	171024	2,98	8,59E-04
UCP2	208998_at	U94592	NM_003355	7351	2,97	3,77E-05
ETV1	217061_s_at	AC004857	NM_004956	2115	2,96	6,17E-07
MNS1	219703_at	NM_018365	NM_018365	55329	2,96	3,49E-04
MGC11266	226118_at	BE326728	NM_024322	79172	2,95	4,33E-06
AW075105	228868_x_at	AW075105	---	---	2,95	2,52E-05
LOC91431	228859_at	BF056790	NM_138698	91431	2,95	1,95E-05
OSAP	223734_at	AF329088	NM_032623	84709	2,95	4,92E-04
ARHGAP11A	204492_at	NM_014783	NM_014783 NM_199357	9824	2,95	3,64E-08
C6orf173	226936_at	BG492359	---	---	2,95	2,93E-07
HSPA2	211538_s_at	U56725	NM_021979	3306	2,95	2,25E-03

MYO6	203216_s_at	NM_004999	NM_004999	4646	2,94	2,66E-07
MAOA	204389_at	NM_000240	NM_000240	4128	2,94	4,60E-06
ZNF521	226676_at	AK021452	NM_015461	25925	2,94	8,51E-04
ASPM	232238_at	AK001380	NM_018136	259266	2,94	4,78E-04
ENC1	201340_s_at	AF010314	NM_003633	8507	2,94	2,73E-05
KDELC2	225128_at	AL548941	NM_153705	143888	2,94	4,64E-05
SYNPO2	225894_at	AL589603	NM_133477	171024	2,93	8,98E-05
ENC1	201341_at	NM_003633	NM_003633	8507	2,93	2,30E-05
LOC441157	1558796_a_at	AL833240	XM_499037	441157	2,93	2,03E-03
SDC2	212158_at	AL577322	NM_002998	6383	2,92	7,40E-07
TROAP	1568596_a_at	AI199355	NM_005480	10024	2,92	8,12E-06
LOC253012	242601_at	AA600175	NM_198151	253012	2,92	1,02E-03
MGC24103	232568_at	AU145658	---	158295	2,91	1,01E-02
TFDP1	242939_at	AI950069	NM_007111	7027	2,91	4,17E-05
LOC441157	1558795_at	AL833240	XM_499037	441157	2,90	7,52E-07
C22orf18	218741_at	NM_024053	NM_001002876 NM_024053	79019	2,90	2,43E-05
TYMS	202589_at	NM_001071	NM_001071	7298	2,89	1,61E-06
CXCR4	209201_x_at	L01639	NM_001008540 NM_003467	7852	2,88	5,99E-03
MGC45871	226905_at	BG036514	NM_182705	359845	2,88	3,75E-04
KNTC1	206316_s_at	NM_014708	NM_014708	9735	2,87	5,79E-05
PCNA	201202_at	NM_002592	NM_002592 NM_182649	5111	2,87	8,09E-06
NEUROD4	221318_at	NM_021191	NM_021191	58158	2,86	1,12E-04
AF15Q14	1552680_a_at	NM_020380	NM_020380 NM_144508 NM_170589	57082	2,85	1,73E-04
AA699443	241838_at	AA699443	---	---	2,85	9,18E-05
CCNE1	213523_at	AI671049	NM_001238 NM_057182	898	2,85	3,52E-04
ST8SIA4	230836_at	AI422986	NM_005668 NM_175052	7903	2,85	4,72E-06
MGC33926	229302_at	AA058832	NM_152390	130733	2,84	2,64E-05
DDB2	203409_at	NM_000107	NM_000107	1643	2,84	2,16E-03
TWIST1	213943_at	X99268	NM_000474	7291	2,83	1,05E-05
DHRS6	218285_s_at	NM_020139	NM_020139	56898	2,82	4,65E-05
DHFR	202533_s_at	BC003584	NM_000791	1719	2,82	4,52E-05
FLJ11029	228273_at	BG165011	NM_018304	55771	2,82	6,55E-07
RNASEH2A	203022_at	NM_006397	NM_006397	10535	2,82	9,96E-07
DCLRE1B	222889_at	AI703304	NM_022836	64858	2,81	7,59E-05
C13orf3	227165_at	AI829603	NM_145061	221150	2,81	9,72E-05

RBPMS	209487_at	D84109	NM_001008710 NM_001008711 NM_001008712 NM_006867	11030	2,81	2,78E-06
ETV1	217053_x_at	X87175	NM_004956	2115	2,80	4,43E-07
CHRNA7 CHRFAM7A	210123_s_at	U62436	NM_000746 NM_139320 NM_148911	1139 89832	2,80	1,15E-04
MARLIN1	238600_at	AW157571	NM_144720	152789	2,80	1,18E-03
PLCL2	213309_at	AL117515	NM_015184	23228	2,80	1,93E-04
Cep152	238535_at	AW955956	NM_014985	22995	2,79	8,14E-06
RAB32	204214_s_at	NM_006834	NM_006834	10981	2,79	1,16E-03
MAD2L1	1554768_a_at	AF394735	NM_002358	4085	2,79	3,08E-06
ITGA6	215177_s_at	AV733308	NM_000210	3655	2,79	2,99E-04
ENDOG	204824_at	NM_004435	NM_004435	2021	2,78	3,20E-04
TFDP2	203588_s_at	BG034328	NM_006286	7029	2,78	7,51E-05
BTG3	1556213_a_at	BC028229	NM_006806	10950	2,78	5,93E-04
KIF2C	209408_at	U63743	NM_006845	11004	2,77	6,84E-05
CD9	201005_at	NM_001769	NM_001769	928	2,77	9,74E-06
TMPO	209754_s_at	AF113682	NM_003276	7112	2,77	9,71E-06
CDC25B	201853_s_at	NM_021873	NM_004358 NM_021872 NM_021873 NM_021874 NM_212530	994	2,77	2,17E-06
TMPO	209753_s_at	BG391171	NM_003276	7112	2,76	7,36E-06
AURKB	239219_at	N55457	NM_004217	9212	2,76	3,82E-04
TIFA	226117_at	AA195074	NM_052864	92610	2,75	2,55E-05
CDCA7	224428_s_at	AY029179	NM_031942 NM_145810	83879	2,75	2,27E-06
CDT1	209832_s_at	AF321125	NM_030928	81620	2,75	4,06E-04
HS3ST2	219697_at	NM_006043	NM_006043	9956	2,75	9,91E-05
C18orf54	244324_at	BG283921	NM_173529	162681	2,75	1,19E-05
PTPRM	1555579_s_at	BC029442	NM_002845	5797	2,74	5,55E-05
PLK1	202240_at	NM_005030	NM_005030	5347	2,74	4,99E-06
FBLN1	202994_s_at	Z95331	NM_001996 NM_006485 NM_006486 NM_006487	2192	2,74	5,20E-04
RAD54B	219494_at	NM_012415	NM_012415 NM_134434	25788	2,74	3,14E-04
C14orf31	225464_at	N30138	NM_152330	122786	2,74	6,69E-06
EDG3	228176_at	AA534817	NM_005226	1903	2,73	2,38E-04
UBL3	243072_at	AI733828	NM_007106	5412	2,72	2,94E-04
ASCL1	213768_s_at	AW950513	NM_004316	429	2,71	5,62E-05
RHEBL1	1570253_a_at	BC014155	NM_144593	121268	2,70	1,21E-05

FLJ40773	1563933_a_at	AK091691	NM_152666	200150	2,70	3,08E-04
ALCAM	240655_at	BE502785	NM_001627	214	2,70	9,75E-04
BRCA2	214727_at	X95152	NM_000059	675	2,70	4,89E-03
SCAP1	1560861_at	BG210619	NM_003726	8631	2,70	9,27E-05
CCNA2	213226_at	AI346350	NM_001237	890	2,69	3,29E-05
PKMYT1	204267_x_at	NM_004203	NM_004203 NM_182687	9088	2,69	2,26E-05
VRK1	203856_at	NM_003384	NM_003384	7443	2,69	6,68E-06
ARHGEF3	218501_at	NM_019555	NM_019555	50650	2,69	2,18E-04
ASPM	239002_at	AA748494	NM_018136	259266	2,69	7,18E-03
H17657	241444_at	H17657	---	---	2,69	3,92E-04
TNFAIP8	210260_s_at	BC005352	NM_014350	25816	2,68	5,03E-05
Cep72	219531_at	NM_018140	NM_018140	55722	2,68	5,02E-05
FGFR2	203638_s_at	NM_022969	NM_000141 NM_022969 NM_022970 NM_022971 NM_022972 NM_022973 NM_022974 NM_022975 NM_022976 NM_023028 NM_023029 NM_023030 NM_023031	2263	2,68	4,60E-05
CSRP2	211126_s_at	U46006	NM_001321	1466	2,68	6,18E-07
FAM49A	208092_s_at	NM_030797	NM_030797	81553	2,68	1,51E-03
CHAF1A	214426_x_at	BF062223	NM_005483	10036	2,67	2,14E-07
LOC387816	241360_at	BG413368	XM_370664	387816	2,67	1,92E-05
MTB	219588_s_at	NM_017760	NM_017760	54892	2,67	4,22E-05
EML1	204797_s_at	NM_004434	NM_001008707 NM_004434	2009	2,67	3,68E-03
MAD2L1	203362_s_at	NM_002358	NM_002358	4085	2,67	1,55E-06
RBL1	205296_at	AL365505	NM_002895 NM_183404	5933	2,66	2,73E-05
SYNPO2	225721_at	AI658662	NM_133477	171024	2,66	4,01E-04
SYNE2	202761_s_at	NM_015180	NM_015180 NM_182910 NM_182912 NM_182913 NM_182914	23224	2,66	1,44E-06
RASSF2	203185_at	NM_014737	NM_014737 NM_170773 NM_170774	9770	2,65	1,34E-04
AI001880	242723_at	AI001880	---	---	2,65	9,66E-04
PTPRK	203038_at	NM_002844	NM_002844	5796	2,65	5,22E-06
ETV1	206501_x_at	NM_004956	NM_004956	2115	2,65	2,26E-07

WDHD1	216228_s_at	AK001538	NM_001008396 NM_007086	11169	2,64	9,95E-04
ZNF505	1569241_a_at	BC020837	NM_001004126 NM_031218	81931	2,64	6,40E-03
SESN3	235683_at	BF685808	NM_144665	143686	2,63	1,07E-03
BLM	205733_at	NM_000057	NM_000057	641	2,63	3,91E-03
MYO6	210480_s_at	U90236	NM_004999	4646	2,62	1,11E-06
SIL	205339_at	NM_003035	NM_003035	6491	2,61	1,15E-04
CENPH	231772_x_at	AL572471	NM_022909	64946	2,60	1,04E-05
GUCY1B3	211555_s_at	AF020340	NM_000857	2983	2,60	8,17E-05
MLF1IP	229304_s_at	AA460299	NM_024629	79682	2,60	9,56E-06
ASCL1	209987_s_at	BC002341	NM_004316	429	2,60	2,04E-04
BF111626	228559_at	BF111626	---	---	2,60	2,36E-05
GAJ	223700_at	AY028916	NM_032117	84057	2,60	2,48E-05
LOC494143	235117_at	AI191897	NM_001008708	494143	2,59	9,30E-04
BG252802	229641_at	BG252802	---	---	2,58	2,53E-05
AA406603	230002_at	AA406603	---	---	2,58	3,50E-06
AW024890	229942_at	AW024890	---	---	2,58	9,80E-04
GPR10	231805_at	AL563031	NM_004248	2834	2,58	2,33E-04
Cep152	215170_s_at	AB020719	NM_014985	22995	2,58	6,05E-06
EB-1	227441_s_at	AW005572	NM_020140 NM_152788 NM_181670	56899	2,57	1,57E-03
TLE3	206472_s_at	NM_005078	NM_005078	7090	2,57	3,99E-04
WEE1	215711_s_at	AJ277546	NM_003390	7465	2,56	8,25E-05
BM039	219555_s_at	NM_018455	NM_018455	55839	2,56	9,17E-08
TMSNB	205347_s_at	NM_021992	NM_021992	11013	2,56	1,86E-04
KIAA1524	1553810_a_at	NM_020890	NM_020890	57650	2,55	1,25E-06
ACATE2	221641_s_at	AF241787	NM_012332	23597	2,54	6,19E-04
AF15Q14	228323_at	BF248364	NM_020380 NM_144508 NM_170589	57082	2,54	2,09E-04
CDC7	204510_at	NM_003503	NM_003503	8317	2,54	7,24E-04
PTPRM	203329_at	NM_002845	NM_002845	5797	2,53	3,83E-04
PLEKHE1	212719_at	AB011178	NM_194449	23239	2,52	1,61E-05
MYO6	203215_s_at	AA877789	NM_004999	4646	2,51	2,63E-04
AL035461	231827_at	AL035461	---	---	2,51	3,24E-04
BF509125	232198_at	BF509125	---	---	2,51	3,41E-03
TIMP3	201150_s_at	NM_000362	NM_000362	7076	2,51	1,89E-05
NRXN1	209915_s_at	AB035356	NM_004801 NM_138735	9378	2,51	9,30E-04
LOC221810	221911_at	BE881590	---	221810	2,51	4,94E-06
SLC16A10	222939_s_at	N30257	NM_018593	117247	2,51	2,79E-04
PPAP2B	212230_at	AV725664	NM_003713 NM_177414	8613	2,50	1,17E-04
C14orf143	214264_s_at	AI656610	NM_145231	90141	2,50	1,62E-05
FLJ11259	218627_at	NM_018370	NM_018370	55332	2,50	3,56E-04

FAM46C	226811_at	AL046017	NM_017709	54855	2,50	6,18E-03
CLSTN2	219414_at	NM_022131	NM_022131	64084	2,50	2,54E-04
OVOS LOC440080	228245_s_at	AW594320	XM_495907 XM_495909	408186 440080	2,49	1,90E-04
MCM8	224320_s_at	BC005170	NM_032485 NM_182802	84515	2,49	1,61E-05
ARG99	226322_at	BF109231	NM_031920 NM_175861	83857	2,49	6,26E-04
SUV39H1	218619_s_at	NM_003173	NM_003173	6839	2,49	1,39E-03
BG109249	1558750_a_at	BG109249	---	---	2,48	6,02E-05
CKAP2	218252_at	NM_018204	NM_018204	26586	2,48	9,73E-07
MGC17791	227420_at	BF338045	NM_152362	126282	2,48	2,52E-04
AK025909	233814_at	AK025909	---	---	2,48	3,30E-04
MGC20533	226308_at	AA099118	NM_001011699 NM_033417	93323	2,48	8,23E-06
GATM	216733_s_at	X86401	NM_001482	2628	2,48	4,09E-04
TPBG	203476_at	NM_006670	NM_006670	7162	2,47	4,81E-05
PTER	222798_at	BF112019	NM_001001484 NM_030664	9317	2,47	8,26E-04
FGFR2	208228_s_at	M87771	NM_000141 NM_022969 NM_022970 NM_022971 NM_022972 NM_022973 NM_022974 NM_022975 NM_022976 NM_023028 NM_023029 NM_023030 NM_023031	2263	2,47	2,00E-05
SMC4L1	201663_s_at	NM_005496	NM_001002799 NM_001002800 NM_005496	10051	2,47	1,52E-06
AW963185	241700_at	AW963185	---	---	2,46	2,26E-04
RFC3	204128_s_at	NM_002915	NM_002915 NM_181558	5983	2,46	3,05E-05
GLDC	204836_at	NM_000170	NM_000170	2731	2,46	4,48E-04
BF432331	242519_at	BF432331	---	---	2,46	1,67E-04
AW151660	239744_at	AW151660	---	---	2,46	4,79E-05
HRH3	220447_at	NM_007232	NM_007232	11255	2,46	1,62E-03
VAV3	218807_at	NM_006113	NM_006113	10451	2,46	6,79E-08
MCM6	238977_at	R54683	NM_005915	4175	2,45	1,80E-04
KIF22	202183_s_at	NM_007317	NM_007317	3835	2,44	1,23E-04

HSPC150	223229_at	AB032931	NM_014176	29089	2,44	1,16E-05
QKI	212636_at	AL031781	NM_006775 NM_206853 NM_206854 NM_206855	9444	2,43	4,26E-03
MGC21654	1556429_a_at	BC026969	NM_145647	93594	2,43	3,09E-06
ASCL1	209988_s_at	BC001638	NM_004316	429	2,43	1,00E-04
FLJ37034	229622_at	H16258	---	151176	2,42	4,51E-03
FSHPRH1	207590_s_at	NM_006733	NM_006733	2491	2,42	3,10E-03
PPP1R3C	204284_at	N26005	NM_005398	5507	2,42	2,95E-04
MASTL	228468_at	BF108964	NM_032844	84930	2,42	1,20E-05
DPYSL3	201430_s_at	W72516	NM_001387	1809	2,41	3,61E-06
AW052186	239942_at	AW052186	---	---	2,41	9,52E-03
RAM2	225081_s_at	AK022955	NM_018719	55536	2,40	3,44E-03
PCSK1	205825_at	NM_000439	NM_000439	5122	2,40	1,58E-03
TMPO	203432_at	AW272611	NM_003276	7112	2,40	5,20E-05
CUGBP2	202157_s_at	U69546	NM_006561	10659	2,40	6,84E-03
C19orf14	215218_s_at	AC004144	NM_173636	284403	2,38	1,41E-03
TRIM68	219405_at	NM_018073	NM_018073	55128	2,38	3,90E-03
TEX15	221448_s_at	NM_031271	NM_031271	56154	2,38	6,78E-03
AU156421	233413_at	AU156421	---	---	2,37	1,88E-03
CDKN2D	210240_s_at	U20498	NM_001800 NM_079421	1032	2,36	8,95E-04
PTGFRN	224937_at	BF311866	NM_020440	5738	2,36	4,21E-05
DERA	218102_at	NM_015954	NM_015954	51071	2,36	4,21E-04
VAV3	218806_s_at	AF118887	NM_006113	10451	2,35	2,50E-04
RASEF	1553986_at	BC023566	NM_152573	158158	2,34	4,65E-04
TNFSF13B	223502_s_at	AF134715	NM_006573	10673	2,34	3,38E-03
STN2	235852_at	BE379761	NM_033104	85439	2,34	2,91E-03
SLC4A11	223748_at	AF336127	NM_032034	83959	2,34	7,89E-03
C20orf72	225890_at	AI678096	NM_052865	92667	2,33	7,53E-05
CPVL	208146_s_at	NM_031311	NM_019029 NM_031311	54504	2,33	1,12E-03
HMGB2	208808_s_at	BC000903	NM_002129	3148	2,33	5,57E-07
FLJ13215	220466_at	NM_025004	NM_025004	80071	2,32	1,61E-04
PLK4	211088_s_at	Z25433	NM_014264	10733	2,31	1,24E-05
MRC2	37408_at	AB014609	NM_006039	9902	2,31	4,86E-03
ZNF488	229901_at	AI056483	NM_153034	118738	2,31	3,12E-03
TM4SF7	209264_s_at	AF054841	NM_003271	7106	2,31	1,36E-04
CCNF	204827_s_at	U17105	NM_001761	899	2,31	1,47E-04
RECQL4	1553015_a_at	NM_004260	NM_004260	9401	2,31	2,02E-04
CDR2	209501_at	AL582414	NM_001802	1039	2,31	1,41E-05

HGF	210997_at	M77227	NM_000601 NM_001010931 NM_001010932 NM_001010933 NM_001010934	3082	2,30	3,55E-03
WHSC1	209052_s_at	BF111870	NM_007331 NM_014919 NM_133330 NM_133331 NM_133332 NM_133333 NM_133334 NM_133335 NM_133336	7468	2,30	2,39E-03
CDCA7	230060_at	AI277642	NM_031942 NM_145810	83879	2,30	9,28E-03
SNAI2	213139_at	AI572079	NM_003068	6591	2,30	9,13E-04
NM_004260	213520_at	NM_004260	---	---	2,30	1,47E-04
DIRAS3	215506_s_at	AK021882	NM_004675	9077	2,30	2,88E-03
FLJ32363	229886_at	AA502768	NM_198566	375444	2,30	4,42E-04
KCNJ4	208359_s_at	NM_004981	NM_004981 NM_152868	3761	2,30	6,70E-04
PLCXD2	235230_at	AW170015	NM_153268	257068	2,29	2,14E-03
GALNAC4S-6ST	203066_at	NM_014863	NM_015892	51363	2,29	8,81E-05
TREX2	207891_s_at	NM_017518	---	11219	2,29	6,18E-05
DHFR	202534_x_at	NM_000791	NM_000791	1719	2,29	3,70E-05
dJ383J4.3	232065_x_at	N29457	NM_033319	91687	2,29	1,75E-05
ITGA9	227297_at	AI479176	NM_002207	3680	2,29	1,72E-03
NUP43	238474_at	BF978064	NM_024647 NM_198887	348995	2,28	1,07E-03
SSB4	229929_at	AL563476	NM_080862	92369	2,28	5,85E-04
GNG12	212294_at	BG111761	NM_018841	55970	2,28	2,93E-05
POLD1	203422_at	NM_002691	NM_002691	5424	2,27	8,87E-04
SHMT1	209980_s_at	L23928	NM_004169 NM_148918	6470	2,27	6,54E-05
DMN	212730_at	AK026420	NM_015286 NM_145728	23336	2,27	9,70E-05
EB-1	227439_at	AI806510	NM_020140 NM_152788 NM_181670	56899	2,27	3,41E-05
SGOL1	231938_at	AK024292	NM_138484	151648	2,26	2,13E-07
ARG99	226931_at	AU151239	NM_031920 NM_175861	83857	2,26	3,38E-04
U79256	37577_at	U79256	---	---	2,26	3,97E-05

HS6ST2	1552766_at	NM_147174	NM_147174 NM_147175	90161	2,26	2,22E-04
AW305300	238962_at	AW305300	---	---	2,25	3,89E-05
CCNF	204826_at	NM_001761	NM_001761	899	2,25	6,97E-06
CNAP1	201774_s_at	AK022511	NM_014865	9918	2,25	6,86E-05
AA019836	241733_at	AA019836	---	---	2,25	3,30E-04
SPAG6	210032_s_at	AI651156	NM_012443 NM_172242	9576	2,24	1,37E-03
PEX13	1558163_at	BC040953	NM_002618	5194	2,24	3,22E-04
AW953794	230968_at	AW953794	---	---	2,24	1,52E-03
TBPIP	213951_s_at	BE964655	NM_013290 NM_016556	29893	2,24	3,20E-05
SESN3	235150_at	AW376955	NM_144665	143686	2,24	4,11E-05
JPH1	229139_at	AI202201	NM_020647	56704	2,24	3,22E-03
CTSH	202295_s_at	NM_004390	NM_004390 NM_148979	1512	2,24	4,20E-03
NRG3	229233_at	H05240	NM_001010848	10718	2,24	1,44E-03
DPYSL3	201431_s_at	NM_001387	NM_001387	1809	2,23	2,10E-06
RACGAP1	222077_s_at	AU153848	NM_013277	29127	2,23	3,69E-06
BF222929	242346_x_at	BF222929	---	---	2,23	1,34E-03
FBXO5	218875_s_at	NM_012177	NM_012177	26271	2,23	3,85E-05
LOC143381	227550_at	AW242720	---	143381	2,23	7,49E-03
KIAA0056	212789_at	AI796581	NM_015261	23310	2,22	1,47E-05
GSG2	223759_s_at	AB039834	NM_031965	83903	2,22	7,72E-05
ZNF537	223392_s_at	BF510588	NM_020856	57616	2,22	4,48E-06
ADAMTS9	1554697_at	AF488803	NM_020249 NM_182920 NM_182921	56999	2,21	5,03E-04
CHAF1A	203975_s_at	BF000239	NM_005483	10036	2,21	6,39E-04
TEAD4	41037_at	U63824	NM_003213 NM_201441 NM_201443	7004	2,21	6,00E-03
PTER	218967_s_at	NM_030664	NM_001001484 NM_030664	9317	2,21	8,86E-03
ARHGAP20	228368_at	AI936560	NM_020809	57569	2,20	2,69E-04
GMNN	218350_s_at	NM_015895	NM_015895	51053	2,20	1,84E-05
RAD18	224200_s_at	AB035274	NM_020165	56852	2,20	8,40E-08
CCNE2	211814_s_at	AF112857	NM_004702 NM_057735 NM_057749	9134	2,20	8,82E-03
RAD18	223417_at	AF169796	NM_020165	56852	2,19	2,68E-06

HGF	210755_at	U46010	NM_000601 NM_001010931 NM_001010932 NM_001010933 NM_001010934	3082	2,19	4,99E-03
ALCAM	1569362_at	BC041127	NM_001627	214	2,19	3,28E-04
RFC3	204127_at	BC000149	NM_002915 NM_181558	5983	2,19	1,51E-04
KIF22	216969_s_at	AC002301	NM_007317	3835	2,18	7,12E-04
SALL4	229661_at	NM_020436	NM_020436	57167	2,18	3,50E-03
BNC2	235723_at	AA843242	NM_017637	54796	2,18	6,54E-03
VMP	239293_at	R38624	NM_080723	140767	2,18	7,44E-03
AU154486	213253_at	AU154486	---	---	2,18	1,78E-04
EBF	229487_at	W73890	NM_024007	1879	2,17	1,69E-03
CDC25A	204696_s_at	NM_001789	NM_001789 NM_201567	993	2,17	7,52E-04
FLJ23091	221958_s_at	AA775681	NM_001002292 NM_024911	79971	2,17	1,84E-06
MGC33846	231430_at	AW205640	NM_175885	220382	2,17	4,57E-05
BG028209	230521_at	BG028209	---	---	2,17	1,18E-04
FLJ20920	218844_at	NM_025149	NM_025149	80221	2,16	2,85E-04
AF131796	231916_at	AF131796	---	---	2,16	7,81E-05
RFC5	203209_at	BC001866	NM_007370 NM_181578	5985	2,16	3,16E-06
ATP2B4	212136_at	AW517686	NM_001001396 NM_001684	493	2,16	8,96E-03
AI653240	240247_at	AI653240	XM_496059	440261	2,16	3,06E-03
SNCAIP	219511_s_at	NM_005460	NM_005460	9627	2,15	6,77E-04
DHFR	48808_at	AI144299	NM_000791	1719	2,14	6,65E-05
KCNN2	220116_at	NM_021614	NM_021614 NM_170775	3781	2,14	8,09E-03
AI144156	238670_at	AI144156	---	---	2,14	4,87E-06
C15orf20	228252_at	AF108138	NM_025049	80119	2,14	6,49E-04
AA287223	238748_at	AA287223	---	---	2,13	7,76E-04
CKS1B	201897_s_at	NM_001826	NM_001826	1163	2,13	2,30E-06
RHEBL1	1553713_a_at	NM_144593	NM_144593	121268	2,13	1,90E-05
PVRL3	213325_at	AA129716	NM_015480	25945	2,13	3,03E-03
H2AFX	212525_s_at	AA760862	NM_002105	3014	2,13	2,86E-04
XRCC4	205071_x_at	AB017445	NM_003401 NM_022406 NM_022550	7518	2,13	6,87E-07
STK17A	202695_s_at	NM_004760	NM_004760	9263	2,12	4,96E-04
MCM2	202107_s_at	NM_004526	NM_004526	4171	2,12	7,65E-06

DHFR	202532_s_at	BC000192	NM_000791	1719	2,12	1,71E-04
INCENP	219769_at	NM_020238	NM_020238	3619	2,12	7,09E-03
CBLN1	205747_at	NM_004352	NM_004352	869	2,11	1,51E-03
ZNF545	1555793_a_at	AL834267	NM_133466	284406	2,11	5,39E-07
GGH	203560_at	NM_003878	NM_003878	8836	2,10	7,91E-06
FLJ23091	228950_s_at	AL534095	NM_001002292 NM_024911	79971	2,10	5,48E-05
TLE3	212769_at	AI567426	NM_005078	7090	2,09	4,14E-03
BE464799	214036_at	BE464799	---	---	2,09	9,39E-04
ANP32E	208103_s_at	NM_030920	NM_030920	81611	2,09	1,57E-05
NXPH1	232377_at	N62902	NM_152745	30010	2,08	8,71E-05
CDC25A	1555772_a_at	AY137580	NM_001789 NM_201567	993	2,08	1,17E-03
PPAP2B	212226_s_at	AA628586	NM_003713 NM_177414	8613	2,08	2,24E-03
FABP6	210445_at	U19869	NM_001445	2172	2,08	2,58E-03
T96523	237469_at	T96523	---	---	2,08	5,67E-03
KIAA0286	212621_at	AB006624	NM_015257	23306	2,08	1,03E-05
DTYMK	203270_at	NM_012145	NM_012145	1841	2,08	4,74E-05
NRM	225592_at	D81048	NM_007243	11270	2,08	4,53E-05
FLJ25067	243507_s_at	AV715251	NM_152504	149840	2,08	2,73E-04
ZNF215	220214_at	NM_013250	NM_013250	7762	2,08	6,34E-05
SEMA6A	220454_s_at	NM_020796	NM_020796	57556	2,07	4,90E-04
SEMA6A	223449_at	AF225425	NM_020796	57556	2,07	1,30E-03
PPIL5	235113_at	AA742244	NM_152329 NM_203466 NM_203467	122769	2,07	2,13E-05
SMC4L1	201664_at	AL136877	NM_001002799 NM_001002800 NM_005496	10051	2,06	2,53E-06
MPHOSPH1	205235_s_at	NM_016195	NM_016195	9585	2,06	3,99E-06
SKP2	210567_s_at	BC001441	NM_005983 NM_032637	6502	2,06	9,75E-05
ZNF537	223393_s_at	AL136805	NM_020856	57616	2,06	1,76E-04
PLEKHK1	230469_at	AW665138	NM_145307	219790	2,06	6,70E-04
ALCAM	201951_at	BF242905	NM_001627	214	2,06	1,36E-03
AI733341	240911_at	AI733341	---	---	2,06	4,21E-04
C14orf94	218383_at	NM_017815	NM_017815	54930	2,05	4,04E-05
HES6	226446_at	AW249678	NM_018645	55502	2,05	1,20E-04
EAF2	219551_at	NM_018456	NM_018456	55840	2,05	1,74E-04
GJA7	208460_at	NM_005497	NM_005497	10052	2,05	2,33E-03
PHF21B	1560091_a_at	AK092243	NM_138415	112885	2,04	6,65E-04
SEMA6A	225660_at	W92748	NM_020796	57556	2,04	7,90E-04
BF593263	228018_at	BF593263	---	---	2,03	4,92E-03
FLJ20647	218802_at	NM_017918	NM_017918	55013	2,03	1,70E-03
C20orf58	228017_s_at	BF593263	NM_152864	128414	2,03	1,08E-04

NET1	201830_s_at	NM_005863	NM_005863	10276	2,03	1,27E-03
FNDC5	226097_at	AI686488	NM_153756	252995	2,03	1,40E-03
HSDL2	209513_s_at	BC004331	NM_032303	84263	2,03	3,49E-05
NRXN1	209914_s_at	AW149405	NM_004801 NM_138735	9378	2,02	6,83E-03
CXorf34	205238_at	NM_024917	NM_024917	79979	2,02	5,46E-03
SYTL4	227703_s_at	AL391688	NM_080737	94121	2,02	3,25E-04
FGFR2	211401_s_at	AB030078	NM_000141 NM_022969 NM_022970 NM_022971 NM_022972 NM_022973 NM_022974 NM_022975 NM_022976 NM_023028 NM_023029 NM_023030 NM_023031	2263	2,01	3,92E-04
LOC440288	239792_at	N75594	XM_496075	440288	2,01	5,78E-04
TEX15	232760_at	AL133653	NM_031271	56154	2,00	9,86E-04
C6orf189	228875_at	AI540210	---	221303	2,00	1,16E-05
NSE1	229546_at	AI378035	NM_145175	151354	2,00	2,29E-04
KLHL13	227875_at	AB037730	NM_033495	90293	2,00	3,06E-06
ARHGAP24	230803_s_at	AI761947	NM_031305	83478	2,00	2,48E-04
RFC4	204023_at	NM_002916	NM_002916 NM_181573	5984	1,99	1,39E-05
TFDP2	203589_s_at	NM_006286	NM_006286	7029	1,99	1,73E-06
THBS4	204776_at	NM_003248	NM_003248	7060	1,99	4,42E-03
EMILIN3	228307_at	AL137580	NM_052846	90187	1,99	6,67E-03
SESN3	242906_at	BE787063	NM_144665	143686	1,99	2,42E-04
TLE4	216997_x_at	AL358975	NM_007005	7091	1,99	1,02E-02
MYH11	227249_at	AI857685	NM_002474 NM_022844	4629	1,99	3,80E-04
SMTN	209427_at	AF064238	NM_006932 NM_134269 NM_134270	6525	1,99	3,97E-03
FLJ11127	219694_at	NM_019018	NM_019018	54491	1,99	1,47E-03
AA156721	201952_at	AA156721	---	---	1,98	1,86E-04
LOC338773	227300_at	AL521682	NM_181724	338773	1,98	1,37E-03
SDC1	201286_at	Z48199	NM_001006946 NM_002997	6382	1,98	1,62E-04
LYN	202625_at	AI356412	NM_002350	4067	1,98	1,63E-05
TLE3	212770_at	AW873621	NM_005078	7090	1,98	1,14E-04
LOX	204298_s_at	NM_002317	NM_002317	4015	1,96	7,97E-04
KIAA0286	212619_at	AW205215	NM_015257	23306	1,96	2,89E-06
LHFPL2	212658_at	N66633	NM_005779	10184	1,96	3,29E-05

C11orf8	205413_at	NM_001584	NM_001584	744	1,96	1,73E-06
Cep70	1554489_a_at	BC016050	NM_024491	80321	1,96	2,05E-06
GPR155	231166_at	AI733474	NM_152529	151556	1,96	8,30E-05
POLA	204835_at	NM_016937	NM_016937	5422	1,96	2,08E-04
ZAK	225665_at	AI129320	NM_016653 NM_133646	51776	1,96	2,36E-06
DKFZP564K1964	223170_at	AF132000	NM_015544	26022	1,96	2,12E-05
TPST2	204079_at	NM_003595	NM_001008566 NM_003595	8459	1,95	1,43E-03
TRIP	205598_at	NM_005879	NM_005879	10293	1,95	1,00E-05
TPTE	233879_at	AL137389	NM_013315 NM_199259 NM_199260 NM_199261	7179	1,94	3,31E-03
FLJ10408	220535_at	NM_018088	NM_018088	55138	1,94	9,00E-03
DNAPTP6	222154_s_at	AK002064	NM_015535	26010	1,94	2,39E-07
DKFZp434P055	232398_at	AK001064	NM_173466	91531	1,93	5,72E-03
FBXO5	234863_x_at	AK026197	NM_012177	26271	1,93	2,02E-05
STRA6	1569335_a_at	BC015881	NM_022369	64220	1,93	3,41E-04
PASK	213534_s_at	D50925	NM_015148	23178	1,93	6,33E-04
DRF1	238508_at	BG026951	NM_025104 NM_145663	80174	1,93	4,54E-04
R71596	229580_at	R71596	---	---	1,93	8,51E-03
TTF2	204407_at	AF080255	NM_003594	8458	1,93	3,06E-03
KIAA0635	206003_at	NM_014645	NM_025009	9662	1,93	1,09E-05
OLFML3	218162_at	NM_020190	NM_020190	56944	1,93	7,36E-03
GPSM2	221922_at	AW195581	NM_013296	29899	1,92	1,45E-05
AW022607	226806_s_at	AW022607	---	---	1,92	6,78E-03
OPN3	219032_x_at	NM_014322	NM_014322	23596	1,92	2,34E-03
DTYMK	1553983_at	AF258562	NM_012145	1841	1,92	1,06E-04
NY-REN-41	226287_at	AI458313	NM_080654	91057	1,92	1,77E-04
RGMA	223468_s_at	AL136826	NM_020211	56963	1,91	2,31E-03
EBF	232204_at	AF208502	NM_024007	1879	1,91	4,36E-05
C9orf140	225777_at	AW250904	NM_178448	89958	1,91	8,55E-05
HPCA	205454_at	BC001777	NM_002143	3208	1,91	2,09E-04
RFC2	1053_at	M87338	NM_002914 NM_181471	5982	1,91	2,20E-06
GUCY1B3	203817_at	W93728	NM_000857	2983	1,91	1,10E-03
SEZ6L	207873_x_at	NM_021115	NM_021115	23544	1,90	4,82E-07
CUGBP2	202156_s_at	N36839	NM_006561	10659	1,90	8,07E-04
AF15Q14	1552682_a_at	NM_144508	NM_020380 NM_144508 NM_170589	57082	1,90	2,18E-04
CENPJ	223513_at	AF139625	NM_018451	55835	1,90	1,64E-05
SEZ6L	211894_x_at	AB041736	NM_021115	23544	1,90	1,44E-05
SDC1	201287_s_at	NM_002997	NM_001006946 NM_002997	6382	1,90	6,29E-05

PLAUR	210845_s_at	U08839	NM_001005376 NM_001005377 NM_002659	5329	1,90	5,08E-03
CBLN2	242301_at	R60224	NM_182511	147381	1,90	4,25E-03
DCLRE1B	219490_s_at	NM_022836	NM_022836	64858	1,89	2,44E-04
ZFHX4	219779_at	NM_024721	NM_024721	79776	1,89	6,77E-05
CYBA	203028_s_at	NM_000101	NM_000101	1535	1,89	3,82E-05
DOCK10	219279_at	NM_017718	NM_014689	55619	1,88	9,11E-04
MCM3	201555_at	NM_002388	NM_002388	4172	1,88	1,06E-05
ECT2	234992_x_at	BG170335	NM_018098	1894	1,87	2,46E-04
ADA	204639_at	NM_000022	NM_000022	100	1,87	8,91E-04
SOX4	213668_s_at	AI989477	NM_003107	6659	1,87	2,08E-04
STN2	227461_at	AA632295	NM_033104	85439	1,87	6,01E-04
HS6ST2	230030_at	AI767756	NM_147174 NM_147175	90161	1,87	6,20E-07
NAGA	1555041_a_at	M29276	NM_000262	4668	1,87	2,11E-04
GCHFR	204867_at	NM_005258	NM_005258	2644	1,86	8,27E-03
KIAA1596	234733_s_at	AK001672	XM_048128	57697	1,86	9,32E-05
RFC2	203696_s_at	NM_002914	NM_002914 NM_181471	5982	1,86	8,69E-06
HUNK	1555935_s_at	T58129	NM_014586	30811	1,86	2,81E-04
PEX13	1558164_s_at	BC040953	NM_002618	5194	1,85	9,05E-05
DTYMK	1553984_s_at	AF258562	NM_012145	1841	1,85	4,47E-04
TCF3	209151_x_at	AA768906	NM_003200	6929	1,85	2,01E-04
LOC91614	228293_at	AJ245600	NM_139160	91614	1,85	4,22E-03
CDCA4	218399_s_at	NM_017955	NM_017955 NM_145701	55038	1,84	3,08E-04
Cep152	215882_at	AK025247	NM_014985	22995	1,84	1,38E-03
TIMELESS	203046_s_at	NM_003920	NM_003920	8914	1,84	2,25E-04
ZNF505	208119_s_at	NM_031218	NM_001004126 NM_031218	81931	1,84	1,87E-04
SESN3	242899_at	N78412	NM_144665	143686	1,84	2,44E-03
FLJ14146	218546_at	NM_024709	NM_024709	79762	1,83	4,55E-04
PHF19	225533_at	AL117477	NM_001009936 NM_015651	26147	1,83	6,38E-04
C19orf32	226597_at	AI348159	NM_138393	92840	1,83	5,57E-05
SATB2	213435_at	AB028957	NM_015265	23314	1,83	9,07E-03
PASK	216945_x_at	U79240	NM_015148	23178	1,83	1,22E-03
MSH5	210410_s_at	AF034759	NM_002441 NM_025259 NM_172165 NM_172166	4439	1,83	2,29E-04
CBLB	227900_at	AV701750	NM_170662	868	1,82	5,23E-03
AI984541	235434_at	AI984541	---	---	1,82	1,15E-03
NEDD1	1552417_a_at	NM_152905	NM_152905	121441	1,82	2,63E-03

KDELR3	204017_at	NM_006855	NM_006855 NM_016657	11015	1,82	4,53E-03
TYMS	228989_at	AW291159	NM_001071	7298	1,82	3,40E-03
PCNXL2	39650_s_at	AB007895	NM_014801 NM_024938	80003	1,82	9,16E-05
HS6ST2	1552767_a_at	NM_147174	NM_147174 NM_147175	90161	1,82	8,21E-07
KIF23	244427_at	AW192521	NM_004856 NM_138555	9493	1,81	8,25E-03
EBF	227646_at	BG435302	NM_024007	1879	1,81	2,17E-05
BE466145	227041_at	BE466145	---	---	1,81	5,47E-05
KCNJ8	205303_at	BF514158	NM_004982	3764	1,81	1,32E-06
TRIP13	204033_at	NM_004237	NM_004237	9319	1,80	1,65E-04
SMAD3	218284_at	NM_015400	NM_005902	4088	1,80	2,69E-03
AI582818	229053_at	AI582818	---	---	1,80	1,03E-03
TBC1D1	212350_at	AB029031	NM_015173	23216	1,80	1,24E-04
FEN1	204768_s_at	NM_004111	NM_004111	2237	1,79	7,12E-05
HELLS	223556_at	AF155827	NM_018063	3070	1,79	4,87E-04
SFI1	36545_s_at	AB011114	NM_001007467 NM_014775	9814	1,78	8,13E-03
WASPIP	202664_at	AW058622	NM_003387	7456	1,78	6,38E-03
RASEF	235144_at	AA826324	NM_152573	158158	1,78	9,50E-04
NOS1	239132_at	BE299830	NM_000620	4842	1,78	9,36E-04
DNMT3B	220668_s_at	NM_006892	NM_006892 NM_175848 NM_175849 NM_175850	1789	1,78	3,32E-05
H10545	242137_at	H10545	---	---	1,77	7,47E-04
PKP4	214874_at	AL050364	NM_001005476 NM_003628	8502	1,76	7,22E-04
T86830	227835_at	T86830	XM_374317	389831	1,76	2,76E-03
HSDL2	209512_at	BC004331	NM_032303	84263	1,76	1,97E-03
AI146450	228073_at	AI146450	---	---	1,76	4,60E-06
BC041029	1569025_s_at	BC041029	XM_371697	389211	1,76	4,47E-06
AMOTL1	225459_at	AU157155	NM_130847	154810	1,76	8,01E-05
C2orf31	221245_s_at	NM_030804	---	81561	1,75	5,43E-05
STK3	204068_at	NM_006281	NM_006281	6788	1,75	3,93E-05
FAM19A4	242348_at	AA757457	NM_001005527 NM_182522	151647	1,75	6,22E-07
CHTF18	226569_s_at	AK024476	NM_022092	63922	1,75	5,44E-06
SOX4	201417_at	AL136179	NM_003107	6659	1,75	6,42E-05
RRM1	201476_s_at	AI692974	NM_001033	6240	1,74	5,08E-04
AV717623	212738_at	AV717623	---	---	1,74	2,87E-04
FGD4	227948_at	AI949549	NM_139241	121512	1,74	3,49E-04

NTRK2	221796_at	AA707199	NM_001007097 NM_006180	4915	1,74	2,14E-04
SOX4	201416_at	BG528420	NM_003107	6659	1,73	5,20E-04
SESN3	225123_at	BE883841	NM_144665	143686	1,73	4,70E-04
C6orf139	219294_at	NM_018132	NM_018132	55166	1,73	3,59E-05
SRGAP1	233888_s_at	AK023899	NM_020762	57522	1,73	7,93E-04
CDK6	235287_at	AW192700	NM_001259	1021	1,73	2,32E-03
TNFAIP8	208296_x_at	NM_014350	NM_014350	25816	1,73	9,57E-04
TUBG1	201714_at	NM_001070	NM_001070	7283	1,73	1,25E-04
LOC221810	221910_at	BF131965	---	221810	1,73	1,75E-04
AI220427	230696_at	AI220427	---	---	1,73	4,25E-03
AI685824	244565_at	AI685824	XM_370580	387716	1,73	2,27E-04
AL566034	224944_at	AL566034	---	---	1,72	1,01E-05
WEE1	212533_at	X62048	NM_003390	7465	1,72	1,55E-05
RRM1	201477_s_at	NM_001033	NM_001033	6240	1,72	1,46E-04
EZH2	203358_s_at	NM_004456	NM_004456 NM_152998	2146	1,72	4,30E-06
WHSC1	222777_s_at	AI770166	NM_007331 NM_014919 NM_133330 NM_133331 NM_133332 NM_133333 NM_133334 NM_133335 NM_133336	7468	1,72	4,09E-04
H2AFX	205436_s_at	NM_002105	NM_002105	3014	1,72	4,53E-05
DKFZP434L0117	227818_at	AL133609	NM_022778	64793	1,72	2,15E-04
C9orf100	230522_s_at	BG028209	NM_032818	84904	1,72	3,63E-04
ANKRD9	230972_at	AW194999	NM_152326	122416	1,71	5,46E-06
ACTA2	200974_at	NM_001613	NM_001613	59	1,71	1,89E-03
GALNT10	212256_at	BE906572	NM_017540 NM_198321	55568	1,71	2,83E-03
AI826125	229866_at	AI826125	---	---	1,71	1,06E-03
LRRC20	218550_s_at	NM_018205	NM_018205 NM_018239 NM_207119	55222	1,70	6,18E-03
C6orf213	1562443_at	AK095527	NM_001010852	134829	1,70	2,22E-07
EDG2	204037_at	BF055366	NM_001401 NM_057159	1902	1,69	2,85E-03
DLL3	222898_s_at	BE350882	NM_016941 NM_203486	10683	1,69	3,90E-05
TBPIP	205956_x_at	NM_013290	NM_013290 NM_016556	29893	1,69	8,09E-05
GFRA2	205721_at	U97145	NM_001495	2675	1,69	3,03E-03
AI140305	228849_at	AI140305	---	---	1,69	5,44E-03
MBD2	214397_at	AI827820	NM_003927 NM_015832	8932	1,68	7,38E-05

POLE	216026_s_at	AL080203	NM_006231	5426	1,68	1,73E-04
TIMP3	201148_s_at	AW338933	NM_000362	7078	1,68	3,70E-06
RBMS3	206767_at	NM_014483	NM_001003792 NM_001003793 NM_014483	27303	1,68	5,38E-04
BE670307	227955_s_at	BE670307	---	---	1,68	3,67E-04
LAMA4	202202_s_at	NM_002290	NM_002290	3910	1,68	8,97E-03
NUDT1	204766_s_at	NM_002452	NM_002452 NM_198948 NM_198949 NM_198950 NM_198952 NM_198953 NM_198954	4521	1,68	4,44E-03
LOC81691	208107_s_at	NM_030941	NM_030941	81691	1,68	6,55E-05
PKP4	201927_s_at	BG292559	NM_001005476 NM_003628	8502	1,68	8,23E-03
AI919519	235092_at	AI919519	---	---	1,68	4,50E-04
KPNA2	211762_s_at	BC005978	NM_002266	3838	1,67	1,78E-06
ZNF519	1568873_at	BC010705	NM_145287	162655	1,67	8,56E-03
PELO	226731_at	AA156873	NM_015946	53918	1,67	5,20E-03
HIRIP3	204504_s_at	NM_003609	NM_003609	8479	1,67	1,47E-05
RAD54B	235846_at	AI208616	NM_012415 NM_134434	25788	1,67	2,55E-03
DKFZP761M1511	225355_at	AK026748	---	54492	1,67	5,04E-03
SYN2	210247_at	AW139618	NM_003178 NM_133625	6854	1,67	7,92E-04
SNAG1	226683_at	AU146771	NM_052870	112574	1,67	1,69E-04
CDC25A	204695_at	AI343459	NM_001789 NM_201567	993	1,66	4,73E-04
MEST	202016_at	NM_002402	NM_002402 NM_177524 NM_177525	4232	1,66	1,55E-04
HPSE	222881_at	AF155510	NM_006665	10855	1,66	3,24E-04
AI673553	203061_s_at	AI673553	---	---	1,66	1,97E-05
SANG	232881_at	AI500353	---	149775	1,66	2,02E-04
HGF	210998_s_at	M77227	NM_000601 NM_001010931 NM_001010932 NM_001010933 NM_001010934	3082	1,66	6,82E-03
SCD4	224901_at	AL571375	NM_024906	79966	1,66	1,68E-03

RDH10	226021_at	AW150720	NM_172037	157506	1,66	1,99E-03
SYNPO2	232119_at	BF984227	NM_133477	171024	1,66	5,45E-03
LSM4	202737_s_at	NM_012321	NM_012321	25804	1,65	5,27E-05
BE857972	243781_at	BE857972	---	---	1,65	7,56E-04
NET1	201829_at	AW263232	NM_005863	10276	1,65	7,05E-05
LYN	210754_s_at	M79321	NM_002350	4067	1,65	3,45E-05
DACH1	228915_at	AI650353	NM_004392 NM_080759 NM_080760	1602	1,65	6,68E-03
LIG1	202726_at	NM_000234	NM_000234	3978	1,65	3,00E-04
LYN	202626_s_at	NM_002350	NM_002350	4067	1,64	1,87E-05
ST8SIA2	221285_at	NM_006011	NM_006011	8128	1,64	2,88E-03
FLJ23322	233250_x_at	AL022313	NM_024955	80020	1,64	1,54E-04
GNG12	1555240_s_at	AF493879	NM_018841	55970	1,64	9,06E-05
BC025350	1569418_at	BC025350	---	---	1,63	1,39E-03
EVE1	225162_at	BG285417	NM_001009555	152503	1,63	1,62E-03
SCML1	222747_s_at	BF001786	NM_006746	6322	1,63	2,63E-04
C20orf100	228737_at	AA211909	NM_032883	84969	1,63	9,04E-04
LMNB1	203276_at	NM_005573	NM_005573	4001	1,63	1,56E-04
TNFSF13B	223501_at	AW151360	NM_006573	10673	1,63	2,45E-03
ZAK	225662_at	H28667	NM_016653 NM_133646	51776	1,63	2,26E-05
N36085	227221_at	N36085	---	---	1,63	2,85E-04
SOX4	201418_s_at	NM_003107	NM_003107	6659	1,62	4,87E-04
LOC342892	244640_at	AW440392	XM_292740	342892	1,62	9,38E-05
MCM4	222037_at	AI859865	NM_005914 NM_182746	4173	1,62	4,15E-03
RAD51C	206066_s_at	NM_002876	NM_002876 NM_058216 NM_058217	5889	1,62	2,63E-04
SORT1	212807_s_at	BF447105	NM_002959	6272	1,62	7,88E-04
AV687517	228498_at	AV687517	---	---	1,62	4,00E-03
FLJ44635	227618_at	AI250910	NM_207422	392490	1,62	4,08E-03
HMG2L1	212597_s_at	AL079310	NM_001003681 NM_005487 NM_014250	10042	1,62	1,26E-04
PLXNA2	213030_s_at	AI688418	NM_025179	5362	1,62	1,87E-04
ST8SIA2	239537_at	AW589904	NM_006011	8128	1,61	3,33E-06
SCML1	218793_s_at	NM_006746	NM_006746	6322	1,61	6,46E-07
KIAA1754L	240037_at	R37132	NM_001008949 NM_178495	150771	1,61	8,33E-03
COBLL1	203642_s_at	NM_014900	NM_014900	22837	1,61	1,06E-03
N26620	227503_at	N26620	---	---	1,61	1,67E-03
RPA3	209507_at	BC005264	NM_002947	6119	1,61	2,30E-04
RODH	205700_at	NM_003725	NM_003725	8630	1,61	9,72E-03
CARHSP1	224910_at	AL575747	NM_014316	23589	1,61	7,34E-03
AL049709	216548_x_at	AL049709	---	---	1,61	2,85E-04

POLD3	212836_at	D26018	NM_006591	10714	1,61	3,76E-04
BZRP	202096_s_at	NM_000714	NM_000714 NM_007311	706	1,61	7,10E-03
LOC286044	222662_at	W60806	---	286044	1,60	2,19E-04
MICAL3	229474_at	BF055090	XM_032996 XM_032997	57553	1,60	4,74E-03
C1QL1	205575_at	NM_006688	NM_006688	10882	1,60	1,17E-03
EGFR	224999_at	BE878463	NM_005228 NM_201282 NM_201283 NM_201284	1956	1,60	1,02E-02
AL040051	225481_at	AL040051	---	---	1,60	1,85E-03
GLRX	209276_s_at	AF162769	NM_002064	2745	1,59	8,29E-03
CDC25C	217010_s_at	AF277724	NM_001790 NM_022809	995	1,59	8,33E-03
DNM3	209839_at	AL136712	NM_015569	26052	1,59	3,88E-04
LOC81691	215215_s_at	AC004381	NM_030941	81691	1,59	1,47E-05
SCD4	224018_s_at	BC004936	NM_024906	79968	1,59	5,27E-04
PAG	225626_at	AK000680	NM_018440	55824	1,59	7,40E-03
SLC8A1	235518_at	AI741439	NM_021097	6546	1,58	5,49E-04
W93046	230068_s_at	W93046	---	---	1,58	3,19E-03
Cep70	224150_s_at	AF289495	NM_024491	80321	1,58	1,32E-03
DACH1	205471_s_at	AW772082	NM_004392 NM_080759 NM_080760	1602	1,58	3,93E-03
FLJ12484	219361_s_at	NM_022767	NM_022767	64782	1,58	3,84E-04
IMP-1	223689_at	AF198254	NM_006546	10642	1,57	2,37E-03
AI697657	229128_s_at	AI697657	---	---	1,57	1,62E-05
LOC90139	227307_at	AL565381	NM_130783	90139	1,57	2,80E-03
SEZ6L	216047_x_at	AL050253	NM_021115	23544	1,57	1,21E-04
CENPC1	204739_at	NM_001812	NM_001812	1060	1,57	4,21E-04
CKS2	204170_s_at	NM_001827	NM_001827	1164	1,57	6,57E-04
LOC92689	213455_at	W87466	NM_138389	92689	1,57	6,69E-04
ROR1	211057_at	BC006374	NM_005012	4919	1,57	9,11E-04
PHF19	227211_at	BE544837	NM_001009936 NM_015651	26147	1,56	3,54E-04
PHF21B	1562309_s_at	AK092243	NM_138415	112885	1,56	5,12E-05
USP48	229812_at	BE645018	NM_032236	84196	1,56	4,62E-03
LOC221362	213248_at	AL577024	---	221362	1,56	9,52E-06
CRYZ	202950_at	NM_001889	NM_001889	1429	1,56	3,29E-04
GATM	203178_at	NM_001482	NM_001482	2628	1,56	1,90E-05
NM_014641	203062_s_at	NM_014641	---	---	1,55	5,41E-05
FLJ38964	235699_at	H19232	NM_173527	161253	1,55	4,09E-03
SPA17	205406_s_at	NM_017425	NM_017425	53340	1,55	1,75E-03
NRP1	212298_at	BE620457	NM_003873	8829	1,55	7,51E-03
NXN	243503_at	AI632740	NM_022463	64359	1,55	1,68E-04
TCFL5	235694_at	N49233	NM_006602	10732	1,55	7,24E-05

UNG	202330_s_at	NM_003362	NM_003362 NM_080911	7374	1,54	5,21E-06
TREX2	213334_x_at	BE676218	---	11219	1,54	6,50E-04
WHSC1	209053_s_at	BE793789	NM_007331 NM_014919 NM_133330 NM_133331 NM_133332 NM_133333 NM_133334 NM_133335 NM_133336	7468	1,54	1,93E-04
ITGB3BP	205176_s_at	NM_014288	NM_014288	23421	1,54	1,06E-04
LSM4	202736_s_at	AA112507	NM_012321	25804	1,54	8,14E-05
MPP5	226092_at	BF115203	NM_022474	64398	1,54	7,77E-03
MGC21654	214061_at	AI017564	NM_145647	93594	1,54	4,22E-04
C9orf76	218979_at	NM_024945	NM_024945	80010	1,54	2,48E-04
KLF7	238482_at	AL120562	NM_003709	8609	1,54	5,35E-03
LZTS1	47550_at	N21184	NM_021020	11178	1,54	9,06E-03
SLC8A1	238546_at	BF344961	NM_021097	6546	1,54	1,55E-03
FGD4	242445_at	AA296351	NM_139241	121512	1,54	9,73E-03
ZNF217	203739_at	NM_006526	NM_006526	7764	1,54	4,11E-06
TM4SF14	221002_s_at	NM_030927	NM_030927	81619	1,54	1,44E-03
NAGA	202943_s_at	M38083	NM_000262	4668	1,53	1,02E-03
RAI14	202052_s_at	NM_015577	NM_015577	26064	1,53	4,59E-04
PARD6G	227204_at	AI817448	NM_032510	84552	1,53	7,67E-04
MMD	203414_at	NM_012329	NM_012329	23531	1,53	7,58E-05
C15orf23	225300_at	BF792864	NM_033286	90417	1,53	6,24E-04
ACO1	207071_s_at	NM_002197	NM_002197	48	1,53	6,67E-03
FLJ10514	218365_s_at	AI765051	NM_018122	55157	1,53	2,72E-03
RAB3B	227123_at	AU156710	NM_002867	5865	1,52	1,25E-03
TCFL5	204849_at	NM_006602	NM_006602	10732	1,52	8,79E-04
GEMIN4	205527_s_at	NM_015487	NM_015721	50628	1,52	2,20E-03
CBLB	209682_at	U26710	NM_170662	868	1,52	9,18E-07
HMG2L1	212596_s_at	AJ010070	NM_001003681 NM_005487 NM_014250	10042	1,52	1,65E-04
CARHSP1	218384_at	NM_014316	NM_014316	23589	1,52	1,20E-03
PTPRR	210675_s_at	U77917	NM_002849 NM_130846	5801	1,51	6,84E-03
ZNF85	1554445_at	BC008688	NM_003429	7639	1,51	8,78E-03
C20orf58	230668_at	AI758937	NM_152864	128414	1,51	2,35E-04
AK098258	1564175_at	AK098258	---	---	1,51	4,42E-03
ADPN	220675_s_at	NM_025225	NM_025225	80339	1,51	6,52E-04
RANBP1	202483_s_at	NM_002882	NM_002882	5902	1,51	9,75E-06
CDK6	224851_at	AW274756	NM_001259	1021	1,51	3,51E-04
GPR161	206972_s_at	NM_007369	NM_007369 NM_153832	23432	1,51	3,61E-05

MCFP	205716_at	NM_018843	NM_018843	55972	1,51	5,29E-03
RTN4IP1	224509_s_at	BC006399	NM_032730	84816	1,51	1,29E-03
RANGAP1	212125_at	NM_002883	NM_002883	5905	1,50	4,37E-04
BF057492	221871_s_at	BF057492	---	---	1,50	2,08E-03
MMD	244523_at	AW104453	NM_012329	23531	1,50	4,38E-05
PHF19	227212_s_at	BE544837	NM_001009936 NM_015651	26147	1,50	4,91E-05
HMGB3	203744_at	NM_005342	NM_005342	3149	1,50	1,38E-06
RODH	37512_at	U89281	NM_003725	8630	1,50	6,29E-03
AW665447	230113_at	AW665447	---	---	1,50	8,13E-03
RANGAP1	1553535_a_at	NM_002883	NM_002883	5905	1,50	6,68E-05
PRIM1	205053_at	NM_000946	NM_000946	5557	1,49	7,62E-05
FEN1	204767_s_at	BC000323	NM_004111	2237	1,49	2,41E-04
MAN1A1	208116_s_at	NM_005907	NM_005907	4121	1,49	2,54E-03
SLC1A1	213664_at	AW235061	NM_004170	6505	1,49	1,97E-04
LOC283027	1562527_at	AF519622	---	283027	1,49	6,56E-03
BUB3	201457_x_at	AF081496	NM_001007793 NM_004725	9184	1,49	1,77E-05
GPR161	230369_at	AI743151	NM_007369 NM_153832	23432	1,49	2,32E-04
TRIM59	235476_at	AW182459	NM_173084	286827	1,49	9,48E-03
TLE4	204872_at	NM_007005	NM_007005	7091	1,48	3,51E-05
LOC401022	242042_s_at	AA406052	---	401022	1,48	1,50E-03
ZAK	238613_at	AI475164	NM_016653 NM_133646	51776	1,48	7,42E-03
DHRS10	228713_s_at	AI742586	NM_016246	51171	1,48	3,31E-03
FLJ10747 LOC159090	222673_x_at	AI582192	NM_018202 NM_145284	159090 55219	1,48	4,86E-05
MGC13186	223272_s_at	BC005102	NM_032324	84284	1,47	5,80E-03
FLJ11535	220798_x_at	NM_024888	NM_024888	79948	1,47	8,54E-03
C9orf81	228774_at	AW268594	XM_095991	84131	1,47	2,00E-04
DHX35	234728_s_at	AL023803	NM_021931	60625	1,47	9,46E-04
EPOR	209962_at	M34986	NM_000121	2057	1,47	4,25E-03
DUT	208955_at	AB049113	NM_001948	1854	1,47	1,77E-03
KHDRBS3	209781_s_at	AF069681	NM_006558	10656	1,47	5,70E-06
AA218973	237245_at	AA218973	XM_372330	390009	1,47	2,67E-03
PVT1 LOC441378	1558290_a_at	BG200951	XM_372058 XM_499128	441378 5820	1,47	4,77E-04
MCM7	210983_s_at	AF279900	NM_005916 NM_182776	4176	1,47	5,48E-05
POLR3K	218866_s_at	NM_016310	NM_016310	51728	1,47	2,20E-03
LOC159090	225361_x_at	AI348001	NM_145284	159090	1,47	4,60E-05
CNP	208912_s_at	BC001362	NM_033133	1267	1,47	7,89E-04
LOC201725	235088_at	AI276683	NM_001008393	201725	1,46	1,25E-03
CHRNA3	211772_x_at	BC006114	NM_000743	1136	1,46	8,95E-04
LOC126295	1554628_at	BC028974	NM_173480	126295	1,46	8,70E-03

FARP1	201911_s_at	NM_005766	NM_001001715 NM_005766	10160	1,46	7,82E-05
PAX5	221969_at	BF510692	NM_016734	5079	1,46	8,27E-04
HTR2B	206638_at	NM_000867	NM_000867	3357	1,46	5,49E-03
SLC25A10	218275_at	NM_012140	NM_012140	1468	1,46	6,48E-03
HELLS	242890_at	AI650364	NM_018063	3070	1,46	2,08E-03
CCBE1	243805_at	BG035826	NM_133459	147372	1,46	3,38E-03
BE877357	228314_at	BE877357	---	---	1,46	3,26E-03
MAK3	222393_s_at	AU149868	NM_025146	80218	1,46	4,59E-03
BE222344	226034_at	BE222344	---	---	1,46	5,03E-04
FLJ10375	243230_at	AA918375	NM_018075	55129	1,46	6,10E-03
BRI3BP	231810_at	BG106919	NM_080626	140707	1,46	5,53E-04
LCRISP1	223475_at	AF142573	NM_031461	83690	1,46	8,87E-04
ARHGAP6	206167_s_at	NM_001174	NM_001174 NM_006125 NM_013422 NM_013423 NM_013427	395	1,45	6,89E-03
TLX3	208495_at	NM_021025	NM_021025	30012	1,45	3,06E-04
H2AFV	202487_s_at	NM_012412	NM_012412 NM_138635 NM_201436 NM_201516 NM_201517	94239	1,45	4,29E-03
BIRC5	1555826_at	BQ021146	NM_001168	332	1,45	3,48E-03
AI357639	225716_at	AI357639	---	---	1,44	3,04E-04
ARMC7	229906_at	BF194773	NM_024585	79637	1,44	2,42E-03
OSBPL10	219073_s_at	NM_017784	NM_017784	114884	1,44	1,05E-03
TUBB4	212664_at	AL567012	NM_006087	10382	1,44	2,03E-03
LRRIQ2	219886_at	NM_024548	NM_024548	79598	1,44	8,76E-04
CUGBP2	1557422_at	R49146	NM_006561	10659	1,44	7,78E-03
SRGAP2	213329_at	AA742261	XM_059095	23380	1,44	1,39E-03
NUP93	202188_at	NM_014669	NM_014669	9688	1,44	2,68E-06
LOC440288	238511_at	BF982733	XM_496075	440288	1,44	3,83E-04
AI346432	229132_at	AI346432	---	---	1,44	3,77E-04
HSZFP36	229732_at	AI417785	XM_375568	55552	1,43	1,60E-04
DLG2	206253_at	NM_001364	NM_001364	1740	1,43	7,70E-04
PTX3	206157_at	NM_002852	NM_002852	5806	1,43	3,96E-04
FIGNL1	1552921_a_at	NM_022116	NM_022116	63979	1,43	3,50E-04
CHML	206079_at	NM_001821	NM_001821	1122	1,43	7,71E-03
AI889959	227350_at	AI889959	---	---	1,43	3,94E-04
TLE4	233575_s_at	AA705845	NM_007005	7091	1,43	5,78E-04
LOC388272	226608_at	AW157311	NM_001001436	388272	1,43	2,91E-03
MGC2603	220011_at	NM_024037	NM_024037	79000	1,43	1,24E-04
KIAA1853	230010_at	AA608629	NM_194286	84530	1,43	8,35E-04
LOC51760	205613_at	NM_016524	NM_016524	51760	1,42	1,17E-03
CSE1L	210766_s_at	AF053640	NM_001316 NM_177436	1434	1,42	1,06E-05

FAD158	223533_at	AL136919	NM_032270	84230	1,42	2,21E-04
FAM54A	234944_s_at	AL138828	NM_138419	113115	1,42	4,74E-03
UNC84B	212144_at	AL021707	NM_015374	25777	1,42	1,88E-03
BICD1	1554020_at	BC010091	NM_001003398 NM_001714	636	1,42	9,68E-03
GNG2	1555766_a_at	AF493870	NM_053064	54331	1,42	1,16E-06
WDR51A	234749_s_at	AL117629	NM_015426	25886	1,42	5,03E-03
EME1	234464_s_at	AK021607	NM_152463	146956	1,42	1,54E-05
TNFRSF19L	227060_at	AW571669	NM_032871 NM_152222	84957	1,42	3,79E-03
TSC	218872_at	NM_017899	NM_017899	54997	1,42	3,16E-03
LOC201725	238015_at	BE620598	NM_001008393	201725	1,42	7,24E-05
FAM33A	225686_at	BE048371	NM_182620	348235	1,42	9,89E-05
GTF2E1	205930_at	NM_005513	NM_005513	2960	1,42	2,50E-04
TYRO3	211432_s_at	U05682	NM_006293	7301	1,42	1,33E-03
GFPT2	205100_at	NM_005110	NM_005110	9945	1,42	1,08E-03
SNX10	218404_at	NM_013322	NM_013322	29887	1,41	4,80E-04
BU077901	1557214_at	BU077901	---	---	1,41	2,12E-04
KPNA2	201088_at	NM_002266	NM_002266	3838	1,41	1,16E-05
LZTS1	219042_at	NM_021020	NM_021020	11178	1,41	5,78E-03
NOS1	207309_at	NM_000620	NM_000620	4842	1,41	5,32E-04
CGI-96	33307_at	AL022316	NM_015703	27341	1,41	4,76E-04
WDR34	224715_at	BG338983	NM_052844	89891	1,40	1,09E-03
RAB3B	205924_at	BC005035	NM_002867	5865	1,40	2,80E-03
GCH1	204224_s_at	NM_000161	NM_000161	2643	1,40	2,84E-03
C14orf145	1557755_at	AW028337	XM_496002	145508	1,40	1,22E-03
PDLIM5	203242_s_at	BG054550	NM_001011513 NM_001011514 NM_001011515 NM_001011516 NM_006457	10611	1,40	6,09E-03
MPP5	219321_at	NM_022474	NM_022474	64398	1,40	2,21E-05
CDO1	204154_at	NM_001801	NM_001801	1036	1,40	3,42E-05
CHAF1B	204775_at	NM_005441	NM_005441	8208	1,40	9,66E-04
RECQL	210568_s_at	BC001052	NM_002907 NM_032941	5965	1,40	3,54E-03
MAPK12	206106_at	AL022328	NM_002969	6300	1,40	1,10E-06
PTTG3	208511_at	NM_021000	---	26255	1,39	1,10E-03
HAT1	203138_at	NM_003642	NM_003642	8520	1,39	2,54E-05
MYD88	209124_at	U70451	NM_002468	4615	1,39	2,89E-03
NUDT15	219347_at	NM_018283	NM_018283	55270	1,39	1,29E-04
PCDH9	219737_s_at	AI524125	NM_020403 NM_203487	5101	1,39	7,01E-03
182-FIP	243119_at	AA810156	NM_020772	57532	1,39	2,92E-04

MCM4	212141_at	AA604621	NM_005914 NM_182746	4173	1,39	3,82E-03
RAB23	229504_at	AI810826	NM_016277 NM_183227	51715	1,39	1,82E-05
C9orf88	223019_at	BC001979	NM_022833	64855	1,39	2,37E-03
DLX6	242940_x_at	AA040332	XM_376652 XM_379892	1750	1,39	2,34E-06
FLJ13909	219556_at	NM_025108	NM_025108	80178	1,39	5,95E-04
CDKN2C	204159_at	NM_001262	NM_001262 NM_078626	1031	1,39	5,88E-04
MEIS1	1559477_s_at	AL832770	NM_002398	4211	1,39	3,54E-04
STRA6	1569334_at	BC015881	NM_022369	64220	1,39	6,72E-03
AW069181	223519_at	AW069181	---	---	1,39	9,35E-04
SEZ6L	213609_s_at	AB023144	NM_021115	23544	1,38	5,40E-04
FKBP14	235311_at	BG110260	NM_017946	55033	1,38	1,16E-04
BG231758	227615_at	BG231758	---	---	1,38	1,85E-04
GEMIN4	217099_s_at	AF258545	NM_015721	50628	1,38	2,18E-03
H2AFV	227085_at	AI823792	NM_012412 NM_138635 NM_201436 NM_201516 NM_201517	94239	1,38	1,65E-04
KLF10	202393_s_at	NM_005655	NM_005655	7071	1,38	4,37E-03
MRE11A	205395_s_at	NM_005590	NM_005590 NM_005591	4361	1,38	9,90E-04
FDXR	207813_s_at	NM_004110	NM_004110 NM_024417	2232	1,38	6,17E-04
GNG4	205184_at	NM_004485	NM_004485	2786	1,38	2,86E-05
MYOHD1	219320_at	NM_025109	NM_025109	80179	1,38	6,52E-04
CTL2	224609_at	AI264216	NM_020428	57153	1,37	2,31E-03
FLJ13273	235387_at	AA740875	NM_024751	79807	1,37	1,76E-05
EDA2R	221399_at	NM_021783	NM_021783	60401	1,37	4,37E-03
MGC10744	238590_x_at	BF981428	NM_032354 NM_183085	84314	1,37	6,04E-03
ACYP1	205260_s_at	NM_001107	NM_001107 NM_203488	97	1,37	7,99E-03
MGC12197	1555501_s_at	BC010357	NM_016625	51319	1,37	1,22E-03
MGC13186	226813_at	AA883980	NM_032324	84284	1,37	9,86E-04
MRE11A	242456_at	AA931565	NM_005590 NM_005591	4361	1,37	6,99E-03
BCR	202315_s_at	NM_004327	NM_004327 NM_021574	613	1,36	1,69E-04
CHRNA3	211587_x_at	M37981	NM_000743	1136	1,36	8,91E-04
GPR161	235961_at	BF248385	NM_007369 NM_153832	23432	1,36	5,62E-05
DUSP4	204015_s_at	BC002671	NM_001394 NM_057158	1846	1,36	6,68E-04
GNG4	1555765_a_at	AF493872	NM_004485	2786	1,36	8,13E-05
FLJ11712	219056_at	NM_024570	NM_024570	79621	1,36	2,93E-03

BUB3	209974_s_at	AF047473	NM_001007793 NM_004725	9184	1,36	2,12E-06
LOC93081	213346_at	BE748563	NM_138779	93081	1,36	2,01E-05
UNQ470	228403_at	AL541276	NM_198573	375704	1,36	9,85E-03
FLJ20364	221685_s_at	AF269167	NM_017785	54908	1,36	4,22E-05
LOC283454	242715_at	AA331548	---	283454	1,36	8,25E-04
LOC388272	242555_at	AW578854	NM_001001436	388272	1,35	7,50E-03
SELM	226051_at	BF973568	NM_080430	140606	1,35	1,09E-04
PAQR4	212858_at	AL520675	NM_152341	124222	1,35	3,60E-05
C20orf7	222894_x_at	AI640582	NM_024120 NM_199052	79133	1,35	1,37E-04
PKP4	201929_s_at	NM_003628	NM_001005476 NM_003628	8502	1,35	6,66E-05
CBX5	242069_at	BE568225	NM_012117	23468	1,35	1,98E-03
CPNE4	228796_at	BE645967	NM_130808	131034	1,35	4,28E-03
CSE1L	201112_s_at	NM_001316	NM_001316 NM_177436	1434	1,35	2,61E-06
TBC1D1	227945_at	BE882538	NM_015173	23216	1,34	4,34E-03
B4GALT1	201883_s_at	D29805	NM_001497	2683	1,34	1,44E-03
TAF5	1553528_a_at	NM_139052	NM_006951	6877	1,34	9,10E-04
CEP1	205642_at	NM_007018	NM_007018	11064	1,34	3,35E-04
STOM	201061_s_at	M81635	NM_004099 NM_198194	2040	1,34	1,41E-04
C6orf182	1554019_s_at	BC033448	NM_173830	285753	1,34	1,74E-05
LOC284465	229382_at	AW149270	---	284465	1,34	3,05E-03
C20orf108	224690_at	BG432350	NM_080821	116151	1,34	1,10E-03
TDRD7	213361_at	AW129593	NM_014290	23424	1,34	5,01E-03
CDK6	224847_at	AW051349	NM_001259	1021	1,33	2,41E-04
C20orf102	226973_at	AA206763	NM_080607	128434	1,33	2,65E-03
TMPO	227578_at	H28597	NM_003276	7112	1,33	1,51E-03
TUBB6	209191_at	BC002654	NM_032525	84617	1,33	1,57E-04
ANP32E	221505_at	AW612574	NM_030920	81611	1,33	1,41E-05
FLJ20516	219258_at	NM_017858	NM_017858	54962	1,33	1,05E-03
DC13	218447_at	NM_020188	NM_020188	56942	1,33	3,60E-03
CKLF	219161_s_at	NM_016951	NM_016326 NM_016951 NM_181640 NM_181641	51192	1,33	6,08E-05
DLL3	219537_x_at	NM_016941	NM_016941 NM_203486	10683	1,33	1,14E-05
DOCK4	205003_at	NM_014705	NM_014705	9732	1,33	1,67E-03
UBAP2L	201377_at	NM_014847	NM_014847	9898	1,33	1,35E-05
FLJ10036	218349_s_at	NM_017975	NM_017975	55055	1,33	1,50E-03
SERPING1	200986_at	NM_000062	NM_000062	710	1,33	3,17E-03
SCML2	206147_x_at	NM_006089	NM_006089	10389	1,33	2,97E-05
BE877775	1568955_at	BE877775	---	---	1,33	1,57E-05
LOC440820	226602_s_at	T30183	XM_496519	440820	1,33	3,16E-05

FKBP5	224856_at	W86302	NM_004117	2289	1,33	1,42E-03
PPM1D	230330_at	AI312083	NM_003620	8493	1,33	4,50E-04
DKFZp313A2432	226278_at	AI150224	---	258010	1,32	1,69E-04
MAN1A1	221760_at	BG287153	NM_005907	4121	1,32	1,75E-05
RFWD3	218564_at	BC002574	---	55159	1,32	4,99E-04
C10orf78	238794_at	N23586	NM_001002759 NM_145247	119392	1,32	9,64E-05
NEGR1	229461_x_at	AI123532	NM_173808	257194	1,32	1,20E-03
DCK	203302_at	NM_000788	NM_000788	1633	1,32	3,62E-05
K-ALPHA-1	211072_x_at	BC006481	NM_006082	10376	1,32	6,06E-06
AI092265	228088_at	AI092265	---	---	1,32	9,95E-04
UCHL5	220083_x_at	NM_016017	NM_015984	51377	1,32	2,96E-04
TRIM37	1554001_at	BC036012	NM_001005207 NM_015294	4591	1,32	8,08E-04
MGC39900	214051_at	BF677486	NM_194324	286527	1,32	7,28E-03
NFYB	218129_s_at	NM_006166	NM_006166	4801	1,32	5,07E-03
FAS	204781_s_at	NM_000043	NM_000043 NM_152871 NM_152872 NM_152873 NM_152874 NM_152875 NM_152876 NM_152877	355	1,32	1,70E-03
C2orf23	204364_s_at	BE535746	NM_022912	65055	1,31	8,43E-05
YPEL1	228296_at	AW450686	NM_013313	29799	1,31	7,66E-03
TRAF4	211899_s_at	AF082185	NM_004295 NM_145751	9618	1,31	4,10E-03
GLS	203158_s_at	AF097493	NM_014905	2744	1,31	9,13E-04
FARP1	201910_at	BF213279	NM_001001715 NM_005766	10160	1,31	6,05E-04
C9orf40	222781_s_at	BF590861	NM_017998	55071	1,31	1,00E-02
ADCY3	235441_at	BF217471	NM_004036	109	1,31	9,61E-03
ZNF253 LOC114977	242919_at	AV683221	NM_021047	114977 56242	1,31	1,27E-03
NASP	201970_s_at	NM_002482	NM_002482 NM_152298 NM_172164	4678	1,31	8,90E-05
ACTL6A	202666_s_at	NM_004301	NM_004301 NM_177989 NM_178042	86	1,30	1,03E-07
HOXD3	206601_s_at	BC005124	NM_006898	3232	1,30	3,02E-04
SORD	201563_at	L29008	NM_003104	6652	1,30	6,16E-05
COQ3	223515_s_at	AL136726	NM_017421	51805	1,30	1,20E-05
SKP2	203626_s_at	NM_005983	NM_005983 NM_032637	6502	1,30	9,20E-03

CDK6	224848_at	AA922068	NM_001259	1021	1,30	3,32E-03
BOK	223349_s_at	BE614255	NM_032515	666	1,30	4,78E-06
PCDH17	205656_at	NM_014459	NM_014459	27253	1,30	1,41E-03
BCAS4	220588_at	NM_017843	NM_001010974 NM_017843 NM_198799	55653	1,30	3,33E-04
TDP1	219715_s_at	NM_018319	NM_001008744 NM_018319	55775	1,30	5,37E-05
LOC283683 LOC339003	217520_x_at	BG396614	XM_290660	283683 339003	1,30	9,14E-03
C6orf152	242006_at	AI379143	NM_181714	167691	1,30	2,64E-03
AA824298	222606_at	AA824298	---	---	1,30	2,38E-03
PRPS1	208447_s_at	NM_002764	NM_002764	5631	1,30	1,12E-04
AA401256	230537_at	AA401256	---	---	1,30	2,49E-03
SUV39H2	1554572_a_at	BC029360	NM_024670	79723	1,29	2,41E-05
LOC284244	214162_at	AF070541	---	284244	1,29	9,39E-03
WDR53	227814_at	AA789329	NM_182627	348793	1,29	5,37E-06
CPT1A	210688_s_at	BC000185	NM_001876	1374	1,29	5,31E-03
RFC1	208021_s_at	NM_002913	NM_002913	5981	1,29	1,61E-06
MGC10812	223469_at	BC004942	---	83542	1,29	3,11E-04
CSE1L	201111_at	AF053641	NM_001316 NM_177436	1434	1,29	1,01E-03
PPFIBP2	212841_s_at	AI692180	NM_003621	8495	1,29	4,46E-04
CHRNA3	210221_at	BC000513	NM_000743	1136	1,29	6,31E-03
RBL1	1559307_s_at	BG387892	NM_002895 NM_183404	5933	1,29	5,93E-05
ZNF43	206695_x_at	NM_003423	NM_003423	7594	1,28	2,30E-04
TM4SF7	209263_x_at	BC000389	NM_003271	7106	1,28	2,01E-04
PDLIM5	216804_s_at	AK027217	NM_001011513 NM_001011514 NM_001011515 NM_001011516 NM_006457	10611	1,28	1,45E-03
KCNJ8	205304_s_at	NM_004982	NM_004982	3764	1,28	8,99E-05
NLN	225943_at	BF222737	NM_020726	57486	1,28	6,53E-03
ORF1-FL49	224707_at	AL522667	NM_032412	84418	1,28	6,23E-05
AL833487	1562244_at	AL833487	---	---	1,28	1,81E-04
EB-1	227440_at	AW005572	NM_020140 NM_152788 NM_181670	56899	1,28	2,28E-03
MEIS1	204069_at	NM_002398	NM_002398	4211	1,28	3,15E-04
SESTD1	226763_at	AW409611	NM_178123	91404	1,27	1,35E-03
GNG2	224964_s_at	AK026424	NM_053064	54331	1,27	1,89E-05

DPF1	231599_x_at	AI939563	NM_004647	8193	1,27	1,45E-03
STMN1	200783_s_at	NM_005563	NM_005563 NM_203399 NM_203401	3925	1,27	5,04E-04
AF279774	216967_at	AF279774	---	---	1,27	8,55E-03
DUSP4	204014_at	NM_001394	NM_001394 NM_057158	1846	1,27	1,77E-04
MCM4	222036_s_at	AI859865	NM_005914 NM_182746	4173	1,27	2,04E-03
C6orf151	1553274_a_at	NM_152551	NM_152551	154007	1,27	8,31E-03
RRM2B	223342_at	AB036063	NM_015713	50484	1,27	4,55E-04
TDRKH	223530_at	AF227192	NM_006862	11022	1,27	1,02E-06
PRIM2A	215708_s_at	AL121975	NM_000947	5558	1,26	1,78E-03
GPR161	214104_at	AI703188	NM_007369 NM_153832	23432	1,26	1,74E-05
NR3C1	211671_s_at	U01351	NM_000176	2908	1,26	1,39E-04
TCF7L2	212761_at	AI949687	NM_030756	6934	1,26	8,24E-03
HECA	218603_at	NM_016217	NM_016217	51696	1,26	8,85E-03
KREMEN1	227250_at	BF221745	NM_032045 NM_153379	83999	1,26	3,46E-04
RBMS3	241789_at	AW338699	NM_001003792 NM_001003793 NM_014483	27303	1,26	7,52E-03
PLAUR	211924_s_at	AY029180	NM_001005376 NM_001005377 NM_002659	5329	1,26	2,35E-03
FLJ25059	229025_s_at	AW008627	NM_144981	196294	1,26	2,34E-03
FKBP5	204560_at	NM_004117	NM_004117	2289	1,26	5,68E-03
HOMER3	215489_x_at	AI871287	NM_004838	9454	1,26	3,85E-03
ZNF503	227195_at	AA603467	NM_032772	84858	1,26	6,66E-04
AL833634	1562699_at	AL833634	---	---	1,26	8,19E-05
BAX	211833_s_at	U19599	NM_004324 NM_138761 NM_138762 NM_138763 NM_138764 NM_138765	581	1,25	6,21E-04
SUHW2	229360_at	N22886	NM_080764	140883	1,25	5,46E-04
CNTN4	229084_at	R42166	NM_175607 NM_175612 NM_175613	152330	1,25	9,69E-04
ZNF184	213452_at	AI811577	NM_007149	7738	1,25	4,11E-05
MPP1	202974_at	NM_002436	NM_002436	4354	1,25	1,81E-03
LOC93349	214791_at	AK023116	NM_138402	93349	1,25	5,56E-06
TOP3B	215781_s_at	D87012	NM_003935	8940	1,25	1,49E-03

RTTN	227072_at	BG167480	NM_173630	25914	1,25	8,89E-06
ASK	204244_s_at	NM_006716	NM_006716	10926	1,25	3,89E-05
FANCG	203564_at	NM_004629	NM_004629	2189	1,25	1,29E-04
WIG1	1555609_a_at	AF355465	NM_022470 NM_152240	64393	1,25	2,45E-03
RFC1	209085_x_at	L14922	NM_002913	5981	1,24	3,75E-07
TRIM59	227801_at	N90779	NM_173084	286827	1,24	3,52E-03
KIAA1522	224746_at	AB040955	XM_036299	57648	1,24	8,59E-03
SLC17A6	220551_at	NM_020346	NM_020346	57084	1,24	4,19E-04
PFKFB3	202464_s_at	NM_004566	NM_004566	5209	1,24	4,76E-04
BF110268	238178_at	BF110268	---	---	1,24	1,57E-03
TCF3	209152_s_at	AI655986	NM_003200	6929	1,24	2,72E-03
AMOTL1	225450_at	AI433831	NM_130847	154810	1,24	5,65E-06
TUBA2	210527_x_at	L11645	NM_006001 NM_079836	7278	1,24	3,79E-05
AB033091	225295_at	AB033091	---	---	1,23	8,34E-06
Cep70	219036_at	NM_024491	NM_024491	80321	1,23	6,01E-03
RTN4IP1	1555679_a_at	AF439711	NM_032730	84816	1,23	3,15E-03
HTATSF1	202601_s_at	AI373539	NM_014500	27336	1,23	1,15E-03
CA773938	1558517_s_at	CA773938	---	---	1,23	7,86E-04
RAB27A	210951_x_at	AF125393	NM_004580 NM_183234 NM_183235 NM_183236	5873	1,23	4,76E-03
TLE3	228340_at	BE967118	NM_005078	7090	1,23	4,90E-03
AI452715	229817_at	AI452715	---	---	1,23	3,71E-03
AK022598	232662_x_at	AK022598	---	---	1,22	2,67E-03
RNF26	224947_at	AL559247	NM_032015	79102	1,22	2,05E-04
C2orf23	204365_s_at	NM_022912	NM_022912	65055	1,22	9,80E-05
KIAA0574	213997_at	AB011146	---	23359	1,22	4,46E-03
K-ALPHA-1	213646_x_at	BE300252	NM_006082	10376	1,22	1,24E-05
SKP2	203625_x_at	BG105365	NM_005983 NM_032637	6502	1,22	4,38E-06
ZNF443	205928_at	NM_005815	NM_005815	10224	1,22	2,72E-03
MAPKAPK3	202788_at	NM_004635	NM_004635	7867	1,22	1,73E-04
RUSC1	206949_s_at	NM_014328	NM_014328	23623	1,22	4,02E-04
FIGNL1	222843_at	AK023411	NM_022116	63979	1,22	1,26E-04
SENP1	1552812_a_at	NM_014554	NM_014554	29843	1,22	2,44E-03
AW874669	239834_at	AW874669	---	---	1,22	1,90E-04
USP1	202413_s_at	NM_003368	NM_003368	7398	1,22	3,61E-04
KIAA0318	238817_at	BF063412	NM_015347	23504	1,22	1,61E-03
MGC5576	201764_at	NM_024056	NM_024056	79022	1,22	1,26E-03
MGC34032	1552782_at	AK091400	NM_152697	204962	1,21	2,92E-03
septina 6	213666_at	AK026589	NM_015129 NM_145799 NM_145800 NM_145802	23157	1,21	5,69E-03
AI143124	212832_s_at	AI143124	---	---	1,21	2,67E-04
SLC2A4RG	218494_s_at	NM_020062	NM_020062	56731	1,21	6,93E-04

ZNF423	214761_at	AW149417	NM_015069	23090	1,21	8,23E-03
CSRP2BP	228543_at	AA780252	NM_020536 NM_177926	57325	1,21	9,19E-06
MTUS1	212095_s_at	BE552421	NM_001001924 NM_001001925 NM_001001927 NM_001001931 NM_020749	57509	1,21	2,45E-04
BF056092	242629_at	BF056092	---	---	1,21	6,11E-03
HPSE	219403_s_at	NM_006665	NM_006665	10855	1,21	1,02E-02
BF445001	238212_at	BF445001	---	---	1,21	2,00E-03
SRGAP2	1568957_x_at	BE877775	XM_059095	23380	1,21	1,43E-04
CDKN1A	202284_s_at	NM_000389	NM_000389 NM_078467	1026	1,21	1,36E-03
RAD51C	209849_s_at	AF029669	NM_002876 NM_058216 NM_058217	5889	1,21	2,70E-03
GTPBP1	219357_at	NM_014027	NM_004286	9567	1,20	7,29E-04
SLC25A1	210010_s_at	U25147	NM_005984	6576	1,20	5,15E-04
KIAA1713	233536_at	AI202664	XM_290811	80816	1,20	2,85E-03
APAF1	204859_s_at	NM_013229	NM_001160 NM_013229 NM_181861 NM_181868 NM_181869	317	1,20	5,73E-05
WHSC1	222778_s_at	AW024870	NM_007331 NM_014919 NM_133330 NM_133331 NM_133332 NM_133333 NM_133334 NM_133335 NM_133336	7468	1,20	4,19E-05
T87730	242500_at	T87730	---	---	1,20	1,38E-03
EHD4	209536_s_at	AF320070	NM_139265	30844	1,20	5,84E-03
WIG1	219628_at	NM_022470	NM_022470 NM_152240	64393	1,20	8,50E-04
BF977829	229067_at	BF977829	---	---	1,20	3,26E-04
NUP62	202153_s_at	NM_016553	NM_012346 NM_016553 NM_153718 NM_153719	23636	1,20	3,85E-04
N50083	229110_at	N50083	---	---	1,20	1,89E-03

ARL6	223735_at	AL136815	NM_032146 NM_177976	84100	1,20	5,56E-03
MGC2574	203119_at	NM_024098	NM_024098	79080	1,19	1,54E-04
FLJ10407	218073_s_at	NM_018087	NM_018087	55706	1,19	1,01E-02
DKFZp313A2432	230006_s_at	AI742358	---	258010	1,19	1,25E-04
C20orf7	227160_s_at	AW102828	NM_024120 NM_199052	79133	1,19	8,46E-04
MVK	215649_s_at	AF217536	NM_000431	4598	1,19	4,73E-03
PPP1R3D	204554_at	AL109928	NM_006242	5509	1,19	9,07E-04
MGC14560	218461_at	NM_016301	NM_016301	51184	1,19	2,49E-06
AC007277	216508_x_at	AC007277	---	---	1,19	1,79E-05
EPHA2	203499_at	NM_004431	NM_004431	1969	1,19	7,06E-04
UBE2L3	200684_s_at	AI819709	NM_003347 NM_198157	7332	1,19	4,60E-07
NFS1	218455_at	NM_021100	NM_021100 NM_181679	9054	1,19	2,24E-03
RELB	205205_at	NM_006509	NM_006509	5971	1,19	8,97E-03
GAS2L1	31874_at	Y07846	NM_006478 NM_152236 NM_152237	10634	1,19	1,72E-03
FLJ33814	225644_at	BF060776	NM_173510	150275	1,19	2,07E-05
K-ALPHA-1	211058_x_at	BC006379	NM_006082	10376	1,18	1,05E-05
NUP62	207740_s_at	NM_012346	NM_012346 NM_016553 NM_153718 NM_153719	23636	1,18	1,26E-04
K-ALPHA-1	201090_x_at	NM_006082	NM_006082	10376	1,18	1,13E-05
NLN	225944_at	AW006938	NM_020726	57486	1,18	5,24E-03
ALS2CR4	1553956_at	BG194770	NM_152388	65062	1,18	8,49E-04
FZD2	210220_at	L37882	NM_001466	2535	1,18	2,21E-05
RET	205879_x_at	BC004257	NM_020630 NM_020975	5979	1,18	2,08E-04
FLJ23322	231846_at	AK026975	NM_024955	80020	1,18	2,79E-04
BE878277	212829_at	BE878277	---	---	1,18	6,73E-04
ZNF286	239898_x_at	AI498484	NM_020652	57335	1,18	2,96E-03
HIVEP2	243254_at	T08739	NM_006734	3097	1,18	6,77E-04
SUCLG2	215772_x_at	AL050226	NM_003848	8801	1,18	3,77E-04
ARF4L	203586_s_at	NM_001661	NM_001661	379	1,18	3,10E-03
DDX11	213378_s_at	AI983033	NM_004399 NM_030653 NM_030655	1663	1,18	6,41E-03
PLEKHF2	218640_s_at	NM_024613	NM_024613	79666	1,18	2,90E-03
MCM7	208795_s_at	D55716	NM_005916 NM_182776	4176	1,18	2,26E-04
CDK6	207143_at	NM_001259	NM_001259	1021	1,18	4,14E-04

BAX	208478_s_at	NM_004324	NM_004324 NM_138761 NM_138762 NM_138763 NM_138764 NM_138765	581	1,17	5,30E-04
FLJ23322	220707_s_at	NM_024955	NM_024955	80020	1,17	2,10E-03
LOC139886	228654_at	AU145277	XM_066946	139886	1,17	1,82E-06
TANC	225308_s_at	AB051515	NM_033394	85461	1,17	1,16E-03
FBXO22	225736_at	BE966247	NM_012170 NM_147188	26263	1,17	3,53E-05
BE504215	228563_at	BE504215	---	---	1,17	2,17E-04
FAM43A	227410_at	AW264102	NM_153690	131583	1,17	2,24E-04
PXN	201087_at	NM_002859	NM_002859	5829	1,17	5,53E-04
BCLP	225536_at	AL545105	NM_033504	113452	1,16	9,28E-03
C1orf43	1555225_at	BC008306	NM_015449 NM_138740	25912	1,16	4,74E-04
CABYR	219928_s_at	NM_012189	NM_012189 NM_138643 NM_138644 NM_153768 NM_153769 NM_153770	26256	1,16	4,76E-04
SEZ6L	231650_s_at	BE672217	NM_021115	23544	1,16	9,63E-04
USP1	202412_s_at	AW499935	NM_003368	7398	1,16	9,85E-04
C21orf45	228597_at	AW151538	NM_018944	54069	1,16	9,08E-04
PDLIM5	203243_s_at	NM_006457	NM_001011513 NM_001011514 NM_001011515 NM_001011516 NM_006457	10611	1,16	3,70E-05
LGR4	218326_s_at	NM_018490	NM_018490	55366	1,16	1,79E-03
LOC284307	235773_at	AW029293	NM_001010879	284307	1,16	2,08E-03
ZCCHC4	220473_s_at	NM_014150	XM_376310	29063	1,16	2,21E-04
H10661	242317_at	H10661	---	---	1,16	4,34E-03
MFGE8	210605_s_at	BC003610	NM_005928	4240	1,16	5,08E-03
CDC5L	209055_s_at	AW268817	NM_001253	988	1,16	2,21E-06
ARL6IP	211935_at	D31885	NM_015161	23204	1,16	1,46E-04
NAGA	202944_at	NM_000262	NM_000262	4668	1,16	4,02E-05
RAB23	220955_x_at	NM_016277	NM_016277 NM_183227	51715	1,16	5,82E-04
KCNN1	206231_at	NM_002248	NM_002248	3780	1,16	4,89E-04
ch-TOG	1555278_a_at	BC035554	NM_001008938 NM_014756	9793	1,16	1,57E-04

MPHOSPH9	206205_at	NM_022782	NM_022782	10198	1,16	5,99E-04
AI141426	229898_at	AI141426	---	---	1,16	4,31E-04
POU2F1	206789_s_at	NM_002697	NM_002697	5451	1,15	5,40E-03
DKFZP434L187	230861_at	AA889613	XM_496054	26082	1,15	5,85E-05
C14orf160	224460_s_at	BC006117	NM_024884	79944	1,15	3,17E-03
PPM1D	204566_at	NM_003620	NM_003620	8493	1,15	1,21E-04
KIAA1853	236151_at	BF315452	NM_194286	84530	1,15	1,89E-03
GLS	203159_at	NM_014905	NM_014905	2744	1,15	4,23E-03
FLJ31842	234980_at	AI004375	NM_152487	148534	1,15	5,24E-03
FLJ20512	219219_at	NM_017854	NM_017854	54958	1,15	2,66E-03
C13orf7	219303_at	NM_024546	NM_024546	79596	1,15	1,92E-07
ADPN	233030_at	AK025665	NM_025225	80339	1,14	4,14E-03
FANCL	218397_at	NM_018062	NM_018062	55120	1,14	1,80E-04
MAK3	217745_s_at	NM_025146	NM_025146	80218	1,14	3,70E-06
H05254	244170_at	H05254	---	---	1,14	1,12E-03
FAM14B	230172_at	AL039706	NM_145249 NM_206949	122509	1,14	5,19E-03
NR3C1	216321_s_at	X03348	NM_000176	2908	1,14	4,77E-03
FH	203032_s_at	AI363836	NM_000143	2271	1,14	1,19E-03
SIVA	203489_at	NM_006427	NM_006427 NM_021709	10572	1,14	1,23E-04
C10orf58	224435_at	BC005871	NM_032333	84293	1,14	2,67E-05
MCAM	211042_x_at	BC006329	NM_006500	4162	1,14	2,97E-06
LOC144997	227289_at	AU119437	---	144997	1,14	8,41E-04
SAFB2	32099_at	D50928	NM_014649	9667	1,14	1,08E-03
MTUS1	212093_s_at	AI695017	NM_001001924 NM_001001925 NM_001001927 NM_001001931 NM_020749	57509	1,14	1,51E-04
SORD	201562_s_at	NM_003104	NM_003104	6652	1,14	8,56E-04
HMGB1	200679_x_at	BE311760	NM_002128	3146	1,14	4,89E-05
TUBB	212320_at	BC001002	NM_178014	203068	1,14	1,69E-04
CDC42EP4	218062_x_at	NM_012121	NM_012121	23580	1,13	4,75E-04
PACSIN1	227053_at	N47315	NM_020804	29993	1,13	8,60E-03
KIAA1712	228334_x_at	AI633734	NM_030633	80817	1,13	1,79E-03
CDK2AP1	201938_at	NM_004642	NM_004642	8099	1,13	4,73E-05
AI650582	226475_at	AI650582	---	---	1,13	9,58E-03
ZNF626	1552643_at	NM_145297	NM_145297	199777	1,13	4,93E-04
MAPKAPK3	202787_s_at	U43784	NM_004635	7867	1,13	2,06E-03
BTG3	205548_s_at	NM_006806	NM_006806	10950	1,13	3,73E-03
UBE2S	202779_s_at	NM_014501	NM_014501	27338	1,13	1,67E-04
TP53INP1	225912_at	AW341649	NM_033285	94241	1,13	6,83E-03
Cep192	218827_s_at	NM_018069	NM_018069 NM_032142	55125	1,13	3,17E-04

SUHW2	230789_at	AI015954	NM_080764	140883	1,13	1,79E-05
LOC128977	1553974_at	BC030758	NM_173793	128977	1,12	4,40E-04
CDH2	203441_s_at	NM_001792	NM_001792	1000	1,12	5,79E-03
ST8SIA1	210073_at	L32867	NM_003034	6489	1,12	1,10E-03
PTP4A1	200733_s_at	U48296	NM_003463	7803	1,12	2,69E-03
RNF34	219035_s_at	NM_025126	NM_025126 NM_194271	80196	1,12	2,20E-04
DDX11	208159_x_at	NM_004399	NM_004399 NM_030653 NM_030655	1663	1,12	2,66E-03
PTGES2	218083_at	NM_025072	NM_025072 NM_198938 NM_198939 NM_198940	80142	1,12	5,25E-05
PCCB	212694_s_at	NM_000532	NM_000532	5096	1,12	1,29E-03
ETV4	211603_s_at	U35622	NM_001986	2118	1,12	1,80E-03
MGC7036	227983_at	AI810244	NM_145058	196383	1,12	1,70E-05
GAP43	204471_at	NM_002045	NM_002045	2596	1,12	2,85E-05
DATF1	222595_s_at	AL578222	NM_022105 NM_080796 NM_080797	11083	1,12	9,82E-04
C1orf41	215691_x_at	AV702994	NM_016126	51668	1,11	6,15E-03
CHES1	218031_s_at	NM_018589	NM_005197	1112	1,11	3,51E-04
LOC89944	213713_s_at	R48779	NM_138342	89944	1,11	4,60E-03
AI807356	227349_at	AI807356	---	---	1,11	7,01E-03
RANGAP1	212127_at	BE379408	NM_002883	5905	1,11	1,65E-03
CHRNA5	206533_at	NM_000745	NM_000745	1138	1,11	2,14E-03
RNF138	239143_x_at	AW291944	NM_016271 NM_198128	51444	1,11	1,74E-04
LOC440145	225578_at	AI885466	XM_495961	440145	1,11	2,53E-04
FGF1	1552721_a_at	NM_033136	NM_000800 NM_033136 NM_033137	2246	1,11	1,39E-03
AL533234	225725_at	AL533234	---	---	1,11	7,91E-04
TM7SF3	222477_s_at	BC005176	NM_016551	51768	1,11	5,89E-04
FLJ90430	229533_x_at	AI963028	NM_178558	340252	1,11	7,02E-03
RPS27L	218007_s_at	NM_015920	NM_015920	51065	1,11	3,68E-03
CRTAC1	221204_s_at	NM_018058	NM_018058	55118	1,11	1,69E-03
SKD3	221845_s_at	AI655698	NM_030813	81570	1,11	1,33E-04
ZNF85	206572_x_at	NM_003429	NM_003429	7639	1,11	3,31E-03
XRCC3	216299_s_at	AK022829	NM_005432	7517	1,11	7,35E-05
AKAP13	222024_s_at	AK022014	NM_006738 NM_007200 NM_144767	11214	1,11	5,22E-03
C9orf81	1557985_s_at	AA248753	XM_095991	84131	1,11	6,85E-04
PDCL	204448_s_at	AF031463	NM_005388	5082	1,10	4,06E-03
RAPH1	243012_at	BF196252	NM_025252 NM_203365 NM_213589	65059	1,10	2,75E-03

DEK	200934_at	NM_003472	NM_003472	7913	1,10	5,01E-06
PPIF	201490_s_at	NM_005729	NM_005729	10105	1,10	3,89E-06
PTP4A1	200730_s_at	BF576710	NM_003463	7803	1,10	4,25E-03
AI888657	244189_at	AI888657	---	---	1,10	1,81E-05
TCF7L2	216037_x_at	AA664011	NM_030756	6934	1,10	1,01E-02
SNX5	222417_s_at	AF121855	NM_014426 NM_152227	27131	1,10	2,71E-03
SSH2	226080_at	BE676214	NM_033389	85464	1,10	4,02E-04
BE671123	235798_at	BE671123	---	---	1,10	2,84E-05
MSH6	211450_s_at	D89646	NM_000179	2956	1,10	4,87E-04
PDZRN3	212915_at	AL569804	NM_015009	23024	1,10	4,32E-03
PPP3CB	209817_at	M29550	NM_021132	5532	1,10	4,16E-04
FAM29A	218602_s_at	NM_017645	NM_017645	54801	1,09	1,73E-04
MINA	1554774_at	AB083191	NM_032778 NM_153182	84864	1,09	7,48E-03
SRGAP1	1569269_s_at	BM912471	NM_020762	57522	1,09	8,29E-03
LOC152185	234995_at	AA668779	NM_144718	152185	1,09	2,38E-04
LOC63929	227910_at	AI635379	NM_022098	63929	1,09	2,09E-03
ITPR2	202662_s_at	NM_002223	NM_002223	3709	1,09	4,74E-03
PCDH17	228863_at	N69091	NM_014459	27253	1,09	2,79E-04
ELAVL1	201727_s_at	NM_001419	NM_001419	1994	1,09	1,03E-02
PKP4	201928_at	AA194254	NM_001005476 NM_003628	8502	1,09	5,68E-05
MTUS1	212096_s_at	AL096842	NM_001001924 NM_001001925 NM_001001927 NM_001001931 NM_020749	57509	1,09	8,18E-06
SPOCK	202363_at	AF231124	NM_004598	6695	1,09	4,27E-04
DIAPH1	209190_s_at	AF051782	NM_005219	1729	1,09	3,00E-03
CKLFSF7	226017_at	AI708432	NM_138410 NM_181472	112816	1,09	7,48E-04
CORO6	1552301_a_at	NM_032854	NM_032854	84940	1,09	3,51E-03
C18orf9	219311_at	NM_024899	NM_024899	79959	1,09	7,95E-04
PDGFD	219304_s_at	NM_025208	NM_025208 NM_033135	80310	1,09	1,44E-03
UBE2L3	200676_s_at	NM_003347	NM_003347 NM_198157	7332	1,09	3,98E-06
SLA/LP	227982_at	AI806592	NM_016955 NM_153825	51091	1,08	6,59E-03
HOMER3	204647_at	NM_004838	NM_004838	9454	1,08	1,80E-04
SNRPD3	202567_at	NM_004175	NM_004175	6634	1,08	1,90E-05
3'HEXO	226416_at	AL137679	NM_153332	90459	1,08	3,50E-03
LMNB2	216952_s_at	M94363	NM_032737	84823	1,08	2,28E-04

CBX5	209715_at	L07515	NM_012117	23468	1,08	2,29E-03
ASF1A	203428_s_at	AB028628	NM_014034	25842	1,08	4,83E-05
UBE2L3	200682_s_at	BG531983	NM_003347 NM_198157	7332	1,08	7,87E-06
PDLIM5	212412_at	AV715767	NM_001011513 NM_001011514 NM_001011515 NM_001011516 NM_006457	10611	1,08	2,29E-03
PLEKHG3	212823_s_at	AI738980	NM_015549	26030	1,08	9,61E-03
ASXL1	244519_at	AI829840	NM_015338	171023	1,08	1,17E-03
HIST1H4C	205967_at	NM_003542	NM_003542	8364	1,08	4,91E-03
UBE2L3	200683_s_at	BE964689	NM_003347 NM_198157	7332	1,07	1,25E-06
DPYSL5	222797_at	BF508726	NM_020134	56896	1,07	7,59E-04
ZFP36L2	201368_at	U07802	NM_006887	678	1,07	1,86E-04
PUSL1	228733_at	AU154793	NM_153339	126789	1,07	3,30E-03
AA973128	242294_at	AA973128	---	---	1,07	3,63E-03
SAP30	204899_s_at	BF247098	NM_003864	8819	1,07	7,88E-05
ETV4	1554576_a_at	BC007242	NM_001986	2118	1,07	2,79E-03
RARA	203749_s_at	AI806984	NM_000964	5914	1,07	3,55E-03
TUBB	211714_x_at	BC005838	NM_178014	203068	1,07	3,33E-04
STARD4	226390_at	AA628398	NM_139164	134429	1,07	1,71E-05
TUBA6	211750_x_at	BC005946	NM_032704	84790	1,07	1,66E-05
CKLFSF8	235099_at	AW080832	NM_178868	152189	1,07	5,68E-03
THOC3	224623_at	BE614567	NM_032361	84321	1,07	3,08E-05
PRPS1	209440_at	BC001605	NM_002764	5631	1,07	2,15E-05
PRPS2	203401_at	NM_002765	NM_002765	5634	1,07	2,40E-03
CRY1	209674_at	D83702	NM_004075	1407	1,06	3,45E-03
DKFZP547N043	223511_at	AL512744	NM_001010984 NM_032018	83932	1,06	1,17E-03
FSTL1	208782_at	BC000055	NM_007085	11167	1,06	2,60E-03
NDRG2	214279_s_at	W74452	NM_016250 NM_201535 NM_201536 NM_201537 NM_201538 NM_201539 NM_201540 NM_201541	57447	1,06	7,80E-03
FLJ13273	1554518_at	BC032942	NM_024751	79807	1,06	4,36E-05
EPB41L1	212336_at	AA912711	NM_012156 NM_177996	2036	1,06	6,75E-05
FAM55C	243011_at	BF317081	NM_145037	91775	1,06	9,28E-03

TCF3	213730_x_at	BE962186	NM_003200	6929	1,06	4,18E-04
PLXNB2	208890_s_at	BC004542	XM_371474	23654	1,06	2,15E-04
BE218067	243662_at	BE218067	---	---	1,06	6,88E-03
PDRG1	225075_at	AL031658	NM_030815	81572	1,06	4,96E-03
BTG3	213134_x_at	AI765445	NM_006806	10950	1,06	2,21E-03
CDC42EP4	214721_x_at	AL162074	NM_012121	23580	1,06	6,10E-04
LOC96610	1569013_s_at	BC033148	NM_080926	96610	1,06	2,71E-03
BF510533	228107_at	BF510533	---	---	1,06	2,14E-03
TFDP1	204147_s_at	NM_007111	NM_007111	7027	1,06	2,66E-03
AI092770	230466_s_at	AI092770	---	---	1,06	1,88E-03
SFRP1	202037_s_at	NM_003012	NM_003012	6422	1,06	2,39E-04
FBXO22	225734_at	AW294765	NM_012170 NM_147188	26263	1,06	1,77E-05
TUBB	209026_x_at	AF141349	NM_178014	203068	1,06	6,65E-04
ELK3	221773_at	AW575374	NM_005230	2004	1,05	1,33E-05
APG4C	228190_at	BF197009	NM_032852 NM_178221	84938	1,05	3,09E-03
BCL11A	210347_s_at	AF080216	NM_018014 NM_022893 NM_138553 NM_138559	53335	1,05	4,33E-03
MFAP2	203417_at	NM_017459	NM_002403 NM_017459	4237	1,05	2,57E-04
C20orf108	224693_at	AI133137	NM_080821	116151	1,05	1,58E-03
CD24	209772_s_at	X69397	NM_013230	934	1,05	1,98E-04
FAS	204780_s_at	AA164751	NM_000043 NM_152871 NM_152872 NM_152873 NM_152874 NM_152875 NM_152876 NM_152877	355	1,05	3,67E-04
GGCX	214005_at	BE326952	NM_000821	2677	1,05	6,80E-03
SESN3	235684_s_at	BF685808	NM_144665	143686	1,05	8,56E-03
ANAPC7	225554_s_at	AA131793	NM_016238	51434	1,05	3,09E-06
INA	230859_at	BF111276	NM_032727	9118	1,05	1,36E-03
FKBP7	223667_at	AF092137	NM_016105 NM_181342	51661	1,05	1,99E-03
ESRRG	207981_s_at	NM_001438	NM_001438 NM_206594 NM_206595	2104	1,05	6,81E-03
RET	215771_x_at	X15786	NM_020630 NM_020975	5979	1,05	9,85E-04
CTNNAL1	202468_s_at	NM_003798	NM_003798	8727	1,05	1,23E-03
SMC1L1	201589_at	D80000	NM_006306	8243	1,05	3,76E-05
NFYB	218128_at	AU151875	NM_006166	4801	1,04	1,55E-04
NFYB	218127_at	AI804118	NM_006166	4801	1,04	2,59E-03
EPOR	209963_s_at	M34986	NM_000121	2057	1,04	9,69E-04

MGC10854	223455_at	BG493862	NM_032300	84260	1,04	2,09E-03
TCF3	210776_x_at	M31222	NM_003200	6929	1,04	6,32E-05
ELAVL4	238073_at	R55745	NM_021952	1996	1,04	6,02E-07
N66584	230593_at	N66584	---	---	1,04	1,67E-03
MGC13204	225836_s_at	AL528840	NM_031465	83695	1,04	4,81E-04
NUCKS	222424_s_at	BC000805	NM_022731	64710	1,04	1,65E-03
FBXO22	225737_s_at	BE966247	NM_012170 NM_147188	26263	1,04	2,33E-04
CXorf40	228809_at	AW006998	NM_178124	91966	1,04	6,72E-03
NEFL	221805_at	AL537457	NM_006158	4747	1,04	3,74E-03
MTHFD1	202309_at	NM_005956	NM_005956	4522	1,04	1,63E-04
SRD5A1	210959_s_at	AF113128	NM_001047	6715	1,04	3,17E-03
NASP	201969_at	AW003362	NM_002482 NM_152298 NM_172164	4678	1,04	8,40E-03
Septina 10	212698_s_at	BF966021	NM_144710 NM_178584	151011	1,04	4,13E-03
PLCXD1	218951_s_at	NM_018390	NM_018390	55344	1,04	2,13E-03
CD24	208650_s_at	BG327863	NM_013230	934	1,04	5,35E-03
ZNF92	235170_at	T52999	NM_007139 NM_152626	168374	1,04	1,71E-05
CENPF	207331_at	NM_016343	NM_016343	1063	1,03	3,14E-04
AA766126	244385_at	AA766126	---	---	1,03	2,59E-04
TENS1	217853_at	NM_022748	NM_022748	64759	1,03	1,28E-03
AL559474	235918_x_at	AL559474	---	---	1,03	7,29E-04
FLJ10407	234672_s_at	AL354612	NM_018087	55706	1,03	4,74E-05
SET8	220200_s_at	NM_020382	NM_020382	387893	1,03	5,39E-04
FLJ21125	226204_at	AI832193	NM_024627	79680	1,03	7,12E-03
PANK2	218809_at	NM_024960	NM_024960 NM_153637 NM_153638 NM_153639 NM_153640 NM_153641	80025	1,03	5,90E-06
TAF5	210053_at	AW138827	NM_006951	6877	1,03	3,76E-04
AI806853	225601_at	AI806853	---	---	1,03	2,08E-05
MMP11	203876_s_at	NM_005940	NM_005940	4320	1,03	2,69E-03
TUBA6	209251_x_at	BC004949	NM_032704	84790	1,03	2,38E-05
BCL2L11	225606_at	AI949179	NM_006538 NM_138621 NM_138622 NM_138623 NM_138624 NM_138625 NM_138626 NM_138627 NM_207002 NM_207003	10018	1,03	1,11E-04

ZGPAT	221848_at	AL121845	NM_032527 NM_181484 NM_181485	84619	1,03	4,13E-04
C14orf106	241816_at	AW103300	NM_018353	55320	1,03	2,05E-03
BCL3	204908_s_at	NM_005178	NM_005178	602	1,03	7,14E-04
CBFA2T2	209145_s_at	AF068266	NM_005093 NM_175864	9139	1,03	4,72E-03
MCFP	227012_at	AI823986	NM_018843	55972	1,03	1,94E-06
THAP10	219596_at	NM_020147	NM_020147	56906	1,03	7,28E-04
AW511319	227167_s_at	AW511319	---	---	1,03	6,48E-04
C2orf7	223312_at	BC005069	NM_032319	84279	1,03	8,00E-05
TTC9	213172_at	AW235608	XM_027236	23508	1,03	5,24E-03
DOT1L	231297_at	AI479899	NM_032482	84444	1,03	7,59E-03
TM7SF3	226478_at	BF540749	NM_016551	51768	1,02	1,16E-03
NFIA	224976_at	R37335	NM_005595	4774	1,02	4,91E-03
MGC72104	243689_s_at	AI681945	NM_207350	284802	1,02	6,29E-03
DGCR14	204383_at	NM_022719	NM_022719	8220	1,02	2,13E-03
TUBB2	208977_x_at	BC004186	NM_006088	10383	1,02	1,96E-05
ZNF505	215758_x_at	AC007204	NM_001004126 NM_031218	81931	1,02	1,93E-03
C6orf115	223361_at	AF116682	XM_371848	58527	1,02	3,11E-04
RAB3C	242328_at	BG055348	NM_138453	115827	1,02	5,07E-03
CECR5	218592_s_at	NM_017829	NM_017829 NM_033070	27440	1,02	1,72E-05
PSMD5	203447_at	AU157008	NM_005047	5711	1,02	3,28E-06
PHF6	225501_at	AK027039	NM_032335 NM_032458	84295	1,02	3,94E-05
CSRP2BP	228544_s_at	AA780252	NM_020536 NM_177926	57325	1,02	3,08E-03
M96	209704_at	AL523380	NM_007358	22823	1,01	2,10E-04
PELI2	219132_at	NM_021255	NM_021255	57161	1,01	2,52E-05
RPA1	201529_s_at	NM_002945	NM_002945	6117	1,01	1,36E-04
TCF3	213811_x_at	AW062341	NM_003200	6929	1,01	2,33E-03
C6orf151	226263_at	AA630674	NM_152551	154007	1,01	1,66E-03
C6orf4	215411_s_at	AL008730	NM_147200 NM_147686	10758	1,01	1,04E-02
DUSP6	208893_s_at	BC005047	NM_001946 NM_022652	1848	1,01	4,12E-03
PEG10	212094_at	AL582836	XM_496907 XM_499343	23089	1,01	4,74E-03
CTNNBL1	221021_s_at	NM_030877	NM_030877	56259	1,01	1,87E-05
MPHOSPH9	237158_s_at	AW449069	NM_022782	10198	1,01	8,39E-04
SCLY	221575_at	BC000586	NM_016510	51540	1,01	5,24E-04
NUP50	222583_s_at	AF116624	NM_007172 NM_153645 NM_153684	10762	1,01	9,47E-04
GSTO2	227163_at	AL162742	NM_183239	119391	1,01	9,87E-03

C20orf44	222470_s_at	AA033998	NM_018244 NM_199487 NM_199513	55245	1,01	9,65E-05
N56956	227254_at	N56956	---	---	1,01	6,12E-03
BAGE4 BAGE2	1555408_at	AF218570	NM_181704 NM_182482	85317 85319	1,01	6,41E-03
ARL2L1	228201_at	BE858032	NM_144996 NM_182896	200894	1,01	2,30E-03
TCF7L2	212762_s_at	AI375916	NM_030756	6934	1,01	2,14E-03
C21orf45	219004_s_at	NM_018944	NM_018944	54069	1,01	1,32E-03
C10orf58	228155_at	BF512388	NM_032333	84293	1,00	1,86E-05
LYK5	52169_at	AI302185	NM_001003786 NM_001003787 NM_001003788 NM_153335	92335	1,00	6,85E-04
PGF	209652_s_at	BC001422	NM_002632	5228	1,00	5,14E-03
FLJ14627	221908_at	AL120375	NM_032814	84900	1,00	7,78E-04
NUP37	218622_at	NM_024057	NM_024057	79023	1,00	2,06E-03
SYT3	223901_at	AL136594	NM_032298	84258	1,00	6,98E-05
NARG1	222837_s_at	AF327722	NM_057175	80155	1,00	1,83E-03
RNF144	204040_at	NM_014746	NM_014746	9781	1,00	1,07E-06
MRPL35	222775_s_at	AK026220	NM_016622 NM_145644	51318	1,00	1,64E-03
ROR1	205805_s_at	NM_005012	NM_005012	4919	1,00	3,27E-03
POP1	213449_at	D31765	NM_015029	10940	1,00	7,21E-03
ABTB2	213497_at	AL050374	NM_145804	25841	1,00	2,06E-03
ASCC3	212815_at	AA156961	NM_006828	10973	1,00	4,84E-03
HDGF	216484_x_at	L24521	NM_004494	3068	1,00	1,89E-03
DUSP6	208892_s_at	BC003143	NM_001946 NM_022652	1848	1,00	2,56E-03
DCPS	218774_at	NM_014026	NM_014026	28960	1,00	6,63E-03
AKIP	228600_x_at	BE463815	NM_017900	54998	1,00	1,79E-03
C6orf60	220150_s_at	NM_024581	NM_024581	79632	1,00	2,46E-03
NXT2	209629_s_at	AF201942	NM_018698	55916	1,00	6,17E-03
SEC61A2	219499_at	NM_018144	NM_018144	55176	1,00	1,35E-05
AI095542	235759_at	AI095542	---	---	1,00	3,08E-04
RPA1	201528_at	BG398414	NM_002945	6117	1,00	7,67E-06
FLJ14627	221909_at	AW299700	NM_032814	84900	1,00	1,91E-03
BE967311	226225_at	BE967311	---	---	0,99	6,96E-05
KIAA0841	213054_at	AA845355	XM_049237	23354	0,99	5,40E-05
GNG2	224965_at	AU118419	NM_053064	54331	0,99	5,01E-05
ZNF238	207164_s_at	NM_006352	NM_006352 NM_205768	10472	0,99	3,24E-03
PSMD9	209334_s_at	BC002383	NM_002813	5715	0,99	2,73E-04
SNX5	217792_at	NM_014426	NM_014426 NM_152227	27131	0,99	1,19E-05

PHLDA3	218634_at	NM_012396	NM_012396	23612	0,99	4,00E-04
ITGA2B	206494_s_at	NM_000419	NM_000419	3674	0,99	8,82E-03
SOX2	213722_at	AW007161	NM_003106	6657	0,99	7,14E-03
RALY	201271_s_at	NM_016732	NM_007367 NM_016732	22913	0,99	1,03E-05
PCNT1	218014_at	NM_024844	NM_024844	79902	0,99	2,81E-03
LOC400506	213237_at	AI652058	XM_375305	400506	0,99	8,09E-04
SLC6A15	240419_at	N25883	NM_018057 NM_182767	55117	0,99	6,25E-03
CBFA2T2	209144_s_at	AI810484	NM_005093 NM_175864	9139	0,99	5,43E-03
ASMTL	36554_at	Y15521	NM_004192	8623	0,99	2,79E-04
NARG1	226998_at	AL556909	NM_057175	80155	0,99	2,85E-05
KLHL5	226001_at	AK002174	NM_001007075 NM_199039	51088	0,99	5,50E-04
MGC59937	1569144_a_at	BC018787	NM_199001	375791	0,98	9,69E-03
NEDD4L	212445_s_at	AI357376	NM_015277	23327	0,98	3,46E-03
COVA1	32042_at	S72904	NM_006375 NM_182314	10495	0,98	1,78E-04
SWAP70	209306_s_at	AI139569	NM_015055	23075	0,98	1,45E-03
EPLIN	217892_s_at	NM_016357	NM_016357	51474	0,98	1,73E-03
TEF	225840_at	AA779795	NM_003216	7008	0,98	3,69E-03
KIAA0391	202713_s_at	AA129755	XM_375074	9692	0,98	7,23E-05
TXNRD1	201266_at	NM_003330	NM_003330 NM_182729 NM_182742 NM_182743	7296	0,98	7,52E-04
AI220627	213608_s_at	AI220627	XM_377713	402055	0,98	1,61E-04
SLC25A17	211754_s_at	BC005957	NM_006358	10478	0,98	1,22E-03
DDX11	208149_x_at	NM_030653	NM_004399 NM_030653 NM_030655	1663	0,98	2,49E-03
CD24	266_s_at	L33930	NM_013230	934	0,98	9,60E-04
SNAP29	218327_s_at	NM_004782	NM_004782	9342	0,98	4,38E-04
DDEFL1	219103_at	NM_017707	NM_017707	55616	0,98	8,35E-03
MTAP	211363_s_at	AF109294	NM_002451	4507	0,98	8,59E-03
H2AFJ	225245_x_at	BG386566	NM_018267 NM_177925	55766	0,98	9,29E-03
W91876	230240_at	W91876	---	---	0,98	6,38E-03
FLJ38973	227973_at	BF130937	NM_153689	205327	0,97	4,61E-03
ARL6	235320_at	AL138043	NM_032146 NM_177976	84100	0,97	9,35E-03

WWOX	219077_s_at	NM_016373	NM_016373 NM_018560 NM_130788 NM_130790 NM_130791 NM_130792 NM_130844	51741	0,97	2,03E-03
XTP3TPA	218069_at	NM_024096	NM_024096	79077	0,97	1,83E-04
NAPB	225111_s_at	AK022817	NM_022080	63908	0,97	1,32E-05
MRVI1	226047_at	N66571	NM_006069 NM_130385	10335	0,97	6,11E-03
H93038	241574_s_at	H93038	---	---	0,97	4,24E-03
AI700633	212812_at	AI700633	---	---	0,97	4,71E-04
DDAH2	215537_x_at	AJ012008	NM_013974	23564	0,97	4,32E-03
HSPC159	219998_at	NM_014181	NM_014181	29094	0,97	7,46E-04
GRK6	202849_x_at	NM_002082	NM_001004105 NM_001004106 NM_002082	2870	0,97	5,10E-03
ZNF219	219314_s_at	NM_016423	NM_016423	51222	0,97	2,40E-03
KLF3	219657_s_at	NM_016531	NM_016531	51274	0,97	2,90E-03
K03460	216323_x_at	K03460	---	---	0,96	1,11E-03
IER5	218611_at	NM_016545	NM_016545	51278	0,96	1,63E-03
BC040884	1560156_at	BC040884	---	---	0,96	8,01E-03
PROS1	207808_s_at	NM_000313	NM_000313	5627	0,96	4,30E-03
ALDH1B1	209645_s_at	NM_000692	NM_000692	219	0,96	5,95E-03
PEG10	212092_at	BE858180	XM_496907 XM_499343	23089	0,96	1,83E-03
GRK6	211543_s_at	AF040752	NM_001004105 NM_001004106 NM_002082	2870	0,96	4,44E-04
RPP30	203436_at	NM_006413	NM_006413	10556	0,96	4,98E-04
AD-003	223369_at	BC001396	NM_014064	28989	0,96	5,09E-03
BG026236	230166_at	BG026236	---	---	0,96	6,20E-03
KIAA2002	225913_at	AK025943	XM_370878	79834	0,96	8,75E-03
CD24	208651_x_at	M58664	NM_013230	934	0,96	1,62E-03
TCF3	209153_s_at	M31523	NM_003200	6929	0,96	1,74E-04
NMT1	201157_s_at	AF020500	NM_021079	4836	0,96	7,38E-03
SURB7	209363_s_at	U46837	NM_004264	9412	0,96	1,98E-04
PHYHIPL	226623_at	AI829726	NM_032439	84457	0,96	4,52E-06
HSPC117	200042_at	NM_014306	NM_014306	51493	0,96	2,37E-05
ALDH7A1	208950_s_at	BC002515	NM_001182	501	0,96	1,54E-05
TFDP2	226157_at	AI569747	NM_006286	7029	0,95	1,73E-03
SURB7	209362_at	AI688580	NM_004264	9412	0,95	3,64E-04
BC003636	222756_s_at	BC003636	---	---	0,95	1,07E-04
SCLY	59705_at	AA911739	NM_016510	51540	0,95	8,43E-04

MGC15634	242923_at	AW027457	---	84841	0,95	9,36E-03
KIBRA	216074_x_at	AK001727	NM_015238	23286	0,95	6,38E-03
CASP8AP2	222201_s_at	AB037736	NM_012115	9994	0,95	4,11E-04
AARS	201000_at	NM_001605	NM_001605	16	0,95	1,89E-03
LOC148203	229700_at	BE966267	---	148203	0,95	3,12E-04
CBLL1	220018_at	NM_024814	NM_024814	79872	0,95	1,63E-03
MRPL35	225255_at	AA810707	NM_016622 NM_145644	51318	0,95	4,17E-03
FAM29A	233655_s_at	AK022964	NM_017645	54801	0,95	1,14E-05
DKFZP566E144	223989_s_at	BC003502	NM_015523	25996	0,95	1,35E-04
PHF20	235389_at	BG168139	NM_016436	51230	0,95	7,86E-06
C20orf23	219570_at	NM_024704	NM_024704	55614	0,95	7,76E-04
MRS2L	228542_at	AI631209	NM_020662	57380	0,95	5,03E-04
GPX3	201348_at	NM_002084	NM_002084	2878	0,95	6,41E-03
PRIM2A	205628_at	NM_000947	NM_000947	5558	0,95	1,53E-04
PPAT	209433_s_at	AI457120	NM_002703	5471	0,95	1,26E-06
SLC9A3R1	201349_at	NM_004252	NM_004252	9368	0,95	3,16E-04
SNX5	229980_s_at	AA131508	NM_014426 NM_152227	27131	0,95	2,51E-04
C9orf122	1557014_a_at	BC041970	XM_379636	158228	0,95	9,32E-03
ETV6	235056_at	AV722693	NM_001987	2120	0,95	1,50E-03
ROD1	224617_at	AI735576	NM_005156	9991	0,95	5,78E-04
PPP2R5D	202513_s_at	NM_006245	NM_006245 NM_180976 NM_180977	5528	0,95	5,76E-03
AI392908	230352_at	AI392908	---	---	0,95	5,22E-03
PPAT	209434_s_at	U00238	NM_002703	5471	0,95	1,94E-06
HSPC129	1555106_a_at	BC035744	NM_016396	51496	0,94	1,87E-04
KIAA1333	223256_at	AW007694	NM_017769	55632	0,94	1,83E-05
GAP43	216963_s_at	AF279774	NM_002045	2596	0,94	8,23E-05
C6orf155	226810_at	BE500942	NM_024882	79940	0,94	3,25E-04
FKBP7	224002_s_at	AF100751	NM_016105 NM_181342	51661	0,94	7,01E-04
NIT2	218557_at	NM_020202	NM_020202	56954	0,94	8,71E-04
NTAN1	213061_s_at	AA643304	NM_173474	123803	0,94	3,59E-03
FBXL13	243057_at	AI923673	NM_145032	222235	0,94	1,12E-03
SURF5	206593_s_at	NM_006752	NM_006752 NM_133640 NM_181491	6837	0,94	1,04E-03
ASMTL	209394_at	BC002508	NM_004192	8623	0,94	7,15E-04
PXMP4	219428_s_at	BF057649	NM_007238 NM_183397	11264	0,94	1,03E-03
IGF1R	203627_at	AI830698	NM_000875	3480	0,94	5,54E-04
HN1	217755_at	NM_016185	NM_001002032 NM_001002033 NM_016185	51155	0,94	1,06E-03
AL833487	1562245_a_at	AL833487	---	---	0,94	2,02E-03

LIG3	204123_at	NM_013975	NM_002311 NM_013975	3980	0,93	1,64E-05
CSTF1	202180_at	NM_001324	NM_001324	1477	0,93	1,15E-03
KIAA0406	212898_at	AB007866	NM_014657	9675	0,93	4,37E-05
LIG3	207348_s_at	NM_002311	NM_002311 NM_013975	3980	0,93	5,83E-05
MAML3	242794_at	AI569476	NM_018717	55534	0,93	5,09E-03
SRD5A1	211056_s_at	BC006373	NM_001047	6715	0,93	1,03E-02
ELAVL4	206051_at	NM_021952	NM_021952	1996	0,93	8,90E-05
XRCC4	210813_s_at	BC005259	NM_003401 NM_022406 NM_022550	7518	0,93	5,17E-03
ALDH7A1	208951_at	BC002515	NM_001182	501	0,93	4,00E-06
SLCO3A1	227367_at	AW976431	NM_013272	28232	0,93	4,38E-03
OGFRL1	219582_at	NM_024576	NM_024576	79627	0,93	1,65E-04
CDH2	203440_at	M34064	NM_001792	1000	0,93	9,39E-06
FLJ31842	237515_at	AA054642	NM_152487	148534	0,93	6,73E-04
LOC283464	226868_at	BF977231	XM_290597	283464	0,93	1,55E-04
DNMT1	201697_s_at	NM_001379	NM_001379	1786	0,93	1,35E-04
H2AFZ	200853_at	NM_002106	NM_002106	3015	0,93	1,62E-06
GAS2L1	209729_at	BC001782	NM_006478 NM_152236 NM_152237	10634	0,93	6,61E-03
IDH2	210046_s_at	U52144	NM_002168	3418	0,93	2,00E-04
LOC51337	218500_at	NM_016647	NM_016647	51337	0,93	2,50E-03
DKFZp313A2432	230005_at	AI742358	---	258010	0,93	1,41E-03
CKLF	223451_s_at	AF096895	NM_016326 NM_016951 NM_181640 NM_181641	51192	0,93	7,64E-03
APEX2	204408_at	NM_014481	NM_014481	27301	0,92	5,63E-04
UBOX5	215544_s_at	AL121891	NM_014948 NM_199415	22888	0,92	5,63E-03
TMEM38B	222735_at	AW452608	NM_018112	55151	0,92	1,79E-03
GPX2	202831_at	NM_002083	NM_002083	2877	0,92	9,43E-04
MPHOSPH9	215731_s_at	X98258	NM_022782	10198	0,92	1,91E-04
HABP4	232341_x_at	AK025144	NM_014282	22927	0,92	1,03E-02
C20orf161	1553960_at	CA447177	NM_033421 NM_152897	90203	0,92	8,23E-03
FKBP5	224840_at	AI753747	NM_004117	2289	0,92	1,63E-03
MGC3162	218860_at	NM_024078	NM_024078	79050	0,92	6,27E-05
DKFZp313A2432	230285_at	BF447829	---	258010	0,92	4,30E-03
AA669799	36553_at	AA669799	---	---	0,92	2,04E-04
N93774	229671_s_at	N93774	---	---	0,92	3,48E-03
AW971254	222369_at	AW971254	---	---	0,92	3,06E-03
BF516305	230728_at	BF516305	---	---	0,92	9,61E-04
ALDH1A2	207016_s_at	AB015228	NM_003888 NM_170696 NM_170697	8854	0,92	7,68E-03

ZNF600	242463_x_at	AI620827	NM_198457	162966	0,92	6,82E-03
BUB3	201458_s_at	NM_004725	NM_001007793 NM_004725	9184	0,92	3,29E-04
FZD8	227405_s_at	AW340311	NM_031866	8325	0,92	7,53E-04
RAD1	228535_at	AI796010	NM_002853 NM_133282 NM_133377	5810	0,92	3,58E-04
GCAT	205164_at	NM_014291	NM_014291	23464	0,92	4,73E-03
DKFZp761A078	231895_at	AA501453	NM_194292	163786	0,92	1,89E-04
BE464337	229512_at	BE464337	---	---	0,92	2,81E-03
AI670824	238887_at	AI670824	---	---	0,91	4,22E-03
USP49	212872_s_at	AK023092	NM_004275	9477	0,91	1,13E-04
HTATSF1	202602_s_at	NM_014500	NM_014500	27336	0,91	3,64E-05
MAML3	228508_at	AI828006	NM_018717	55534	0,91	2,27E-04
UCHL5	219960_s_at	NM_015984	NM_015984	51377	0,91	1,62E-03
MKKS	222530_s_at	AF275813	NM_018848 NM_170784	8195	0,91	1,32E-04
C18orf9	52285_f_at	AW002970	NM_024899	79959	0,91	2,78E-06
ADRBK2	204183_s_at	AI478542	NM_005160	157	0,91	5,18E-03
LOC90313	225605_at	AL540867	NM_138349	90313	0,91	5,20E-03
FANCE	220255_at	NM_021922	NM_021922	2178	0,91	1,82E-03
SH3BGRL2	225354_s_at	AL035700	NM_031469	83699	0,91	3,32E-04
YEATS4	218911_at	NM_006530	NM_006530	8089	0,91	7,53E-05
FKBP14	219390_at	NM_017946	NM_017946	55033	0,91	3,85E-06
KIAA1712	231850_x_at	AB051499	NM_030633	80817	0,91	6,64E-03
C10orf78	236027_at	N23587	NM_001002759 NM_145247	119392	0,91	4,28E-03
BG261385	225906_at	BG261385	XM_499448	442703	0,91	2,60E-03
LOC339903	228721_at	AA225165	XM_291063	339903	0,91	2,86E-03
KIBRA	213085_s_at	AB020676	NM_015238	23286	0,91	5,30E-05
KIAA1333	223255_at	AA642341	NM_017769	55632	0,91	1,02E-03
H2AFJ	224301_x_at	BC003602	NM_018267 NM_177925	55766	0,91	8,07E-03
HRASLS	219984_s_at	NM_020386	NM_020386	57110	0,91	1,08E-03
TUBA3 K-ALPHA-1	212639_x_at	AL581768	NM_006009 NM_006082	10376 7846	0,91	2,50E-05
TOMM34	201870_at	NM_006809	NM_006809	10953	0,91	6,55E-05
RFX5	202964_s_at	NM_000449	NM_000449	5993	0,91	7,31E-04
AK1	202587_s_at	BC001116	NM_000476	203	0,91	7,38E-03
KATNA1	205526_s_at	NM_007044	NM_007044	11104	0,91	2,54E-03
PAICS	201014_s_at	NM_006452	NM_006452	10606	0,91	3,31E-03
KIAA1576	226415_at	AA156723	NM_020927	57687	0,90	4,18E-03
CHML	1565951_s_at	AJ293392	NM_001821	1122	0,90	1,84E-04
SLC2A8	218985_at	NM_014580	NM_014580	29988	0,90	1,85E-04
DKFZp779O175	238952_x_at	BF439163	XM_375606	374899	0,90	1,98E-03
FLJ43505	221477_s_at	BF575213	NM_207468	400823	0,90	2,64E-05
HTLF	226711_at	BF590117	NM_002158	3344	0,90	2,44E-05

FLJ10385	44563_at	AI858000	NM_018081	55135	0,90	1,42E-05
FLJ16517	229349_at	AL039884	NM_001004317	389421	0,90	7,06E-04
SIX5	229009_at	AA527770	NM_175875	147912	0,90	7,46E-03
STMN3	222557_at	AL353715	NM_015894	50861	0,90	3,11E-03
PPP2R5D	211159_s_at	AB000635	NM_006245 NM_180976 NM_180977	5528	0,90	3,08E-03
AI701857	243359_at	AI701857	---	---	0,90	7,55E-04
PHYH	203335_at	NM_006214	NM_006214	5264	0,90	1,50E-03
UFD1L	209103_s_at	BC001049	NM_005659	7353	0,90	7,15E-04
RAD1	204460_s_at	AF074717	NM_002853 NM_133282 NM_133377	5810	0,90	1,59E-03
MPHOSPH9	221965_at	AI990326	NM_022782	10198	0,90	5,47E-04
MLF1	204783_at	AI911434	NM_022443	4291	0,90	1,40E-03
THOC4	226319_s_at	AF047002	NM_005782	10189	0,90	3,55E-05
TM4SF15	218693_at	NM_012339	NM_012339	23555	0,90	1,06E-03
MSH6	202911_at	NM_000179	NM_000179	2956	0,90	8,89E-05
ANXA6	200982_s_at	NM_001155	NM_001155 NM_004033	309	0,90	2,34E-06
RAB23	223463_at	AF161486	NM_016277 NM_183227	51715	0,90	1,40E-03
PCTK1	207239_s_at	NM_006201	NM_006201 NM_033018	5127	0,90	2,68E-03
ZNF238	212774_at	AJ223321	NM_006352 NM_205768	10472	0,90	9,30E-04
HIP1R	209558_s_at	AB013384	NM_003959	9026	0,90	2,26E-04
UBAP2L	201378_s_at	NM_014847	NM_014847	9898	0,90	3,17E-04
FLJ32745	235644_at	BF213953	NM_144978	165055	0,90	2,95E-03
GGCX	214006_s_at	BE326952	NM_000821	2677	0,89	1,19E-03
HIP1	226364_at	AU145049	NM_005338	3092	0,89	1,85E-04
BG496998	225684_at	BG496998	---	---	0,89	7,38E-05
PIGX	1563111_a_at	AK000529	NM_017861	54965	0,89	1,57E-03
RAN	200750_s_at	AF054183	NM_006325	5901	0,89	7,04E-07
LOC128977	227086_at	AA194312	NM_173793	128977	0,89	7,56E-04
PRIM2A	1554885_a_at	BC017833	NM_000947	5558	0,89	1,97E-03
ACY1L2	225421_at	AI654133	NM_001010853	135293	0,89	1,02E-04
FLJ39582	239015_at	BE675073	XM_498459 XM_499589	439931	0,89	4,23E-03
CDK5RAP2	233540_s_at	AK025867	NM_001011649 NM_018249	55755	0,89	1,44E-03
HIP1	205425_at	NM_005338	NM_005338	3092	0,89	3,21E-04
RNF157	226433_at	BF056204	NM_052916	114804	0,89	4,40E-04
AL832468	1560116_a_at	AL832468	---	---	0,89	1,66E-04
CDC5L	209056_s_at	NM_001253	NM_001253	988	0,89	2,06E-05
C20orf17	235616_at	AI694059	NM_173485	128553	0,89	7,79E-03
STAU2	204226_at	NM_014393	NM_014393	27067	0,89	4,24E-05
TUBB2	213726_x_at	AA515698	NM_006088	10383	0,89	1,59E-04

TMEPAI	222449_at	AL035541	NM_020182 NM_199169 NM_199170 NM_199171	56937	0,89	8,38E-03
KIAA1958	239033_at	AI640482	NM_133465	158405	0,89	2,35E-04
TEAD3	209454_s_at	AF142482	NM_003214	7005	0,89	3,41E-03
KIAA1211	227231_at	AI991996	XM_044178	57482	0,88	1,97E-03
TMEFF1	205122_at	BF439316	NM_003692	8577	0,88	6,32E-03
SLC16A10	219915_s_at	NM_018593	NM_018593	117247	0,88	7,05E-04
ACPL2	226925_at	AW069729	NM_152282	92370	0,88	5,44E-07
C1orf41	203960_s_at	NM_016126	NM_016126	51668	0,88	6,92E-03
VPS29	223026_s_at	AF201946	NM_016226 NM_057180	51699	0,88	3,36E-04
FRAT2	209864_at	AB045118	NM_012083	23401	0,88	9,56E-03
IGSF4	209031_at	AL519710	NM_014333	23705	0,88	1,80E-03
PARP2	215773_x_at	AJ236912	NM_005484	10038	0,88	1,31E-03
SLCO3A1	219229_at	NM_013272	NM_013272	28232	0,88	8,63E-04
RNPC1	212430_at	AL109955	NM_017495 NM_183425	55544	0,88	4,48E-03
STAMBP	202811_at	NM_006463	NM_006463 NM_201647 NM_213622	10617	0,88	3,92E-04
RPS6KA1	203379_at	NM_002953	NM_001006665 NM_002953	6195	0,88	2,48E-03
BUB3	201456_s_at	AU160695	NM_001007793 NM_004725	9184	0,88	1,21E-04
LOC375295	228564_at	AI569804	XM_374020	375295	0,88	2,04E-03
KCNQ2	210508_s_at	D82346	NM_004518 NM_172106 NM_172107 NM_172108 NM_172109	3785	0,88	1,23E-04
EIF4E	201437_s_at	NM_001968	NM_001968	1977	0,88	2,52E-03
AGPS	225113_at	BF688144	NM_003659	8540	0,88	2,42E-03
BRD4	202103_at	AI991631	NM_014299 NM_058243	23476	0,88	2,06E-03
TOX	204529_s_at	AI961231	NM_014729	9760	0,88	4,56E-03
AI032121	227422_at	AI032121	---	---	0,88	5,07E-04
RAB3IP	223471_at	BC002556	NM_022456 NM_175623 NM_175624 NM_175625 NM_175626 NM_175627	117177	0,87	1,10E-03
DDT	202929_s_at	NM_001355	NM_001355	1652	0,87	4,60E-04
C10orf77	219745_at	NM_024789	NM_024789	79847	0,87	9,14E-03
NUCKS	224582_s_at	H09085	NM_022731	64710	0,87	2,99E-05

FBN1	202766_s_at	NM_000138	NM_000138	2200	0,87	9,90E-03
AA287457	226943_at	AA287457	---	---	0,87	2,30E-03
C10orf86	219067_s_at	NM_017615	NM_017615	54780	0,87	6,15E-05
MAGE:3604678	1555875_at	BU733713	---	---	0,87	7,23E-03
HSPA4L	205543_at	NM_014278	NM_014278	22824	0,87	7,62E-04
PLS1	205190_at	NM_002670	NM_002670	5357	0,87	7,93E-03
AW299815	241815_at	AW299815	---	---	0,87	5,59E-03
MRPL42	222466_s_at	AL136659	NM_014050 NM_172177 NM_172178	28977	0,87	3,61E-06
LYK5	221554_at	AF308302	NM_001003786 NM_001003787 NM_001003788 NM_153335	92335	0,87	5,17E-03
C6orf61	219673_at	NM_017696	---	54844	0,87	2,34E-04
NR3C1	201865_x_at	AI432196	NM_000176	2908	0,87	1,11E-03
KIAA1280	219520_s_at	NM_018458	NM_015691	55841	0,87	6,75E-05
HMG20B	209113_s_at	AF288679	NM_006339	10362	0,87	8,93E-05
KIAA1211	227230_s_at	BE855799	XM_044178	57482	0,87	4,76E-04
GAS6	202177_at	NM_000820	NM_000820	2621	0,87	1,87E-03
AKAP13	221718_s_at	M90360	NM_006738 NM_007200 NM_144767	11214	0,87	4,55E-04
H2AFZ	213911_s_at	BF718636	NM_002106	3015	0,87	6,81E-06
NYREN18	1569030_s_at	BC034716	NM_016118	51667	0,87	1,77E-03
C20orf20	218586_at	NM_018270	NM_018270	55257	0,86	1,58E-04
PAICS	201013_s_at	AA902652	NM_006452	10606	0,86	5,07E-04
HPS4	218402_s_at	NM_022081	NM_022081 NM_152840 NM_152841 NM_152842 NM_152843	89781	0,86	9,72E-04
GSS	211630_s_at	L42531	NM_000178	2937	0,86	3,22E-04
AL136980	222603_at	AL136980	---	---	0,86	1,97E-03
septina 11	201307_at	AL534972	NM_018243	55752	0,86	6,58E-05
PDLIM7	214266_s_at	AW206786	NM_005451 NM_203352 NM_203353 NM_213636	9260	0,86	8,67E-04
HIP1	205426_s_at	U79734	NM_005338	3092	0,86	1,59E-03
BF447112	236192_at	BF447112	---	---	0,86	6,78E-04
AW161909	232697_at	AW161909	---	---	0,86	1,71E-04
SEC61A2	228747_at	AI694646	NM_018144	55176	0,86	3,38E-04
PXMP2	219076_s_at	NM_018663	NM_018663	5827	0,86	2,72E-03
AU145336	233446_at	AU145336	---	---	0,86	2,61E-03

SIVA	210792_x_at	AF033111	NM_006427 NM_021709	10572	0,86	5,84E-04
NDUFA6	202000_at	BC002772	NM_002490	4700	0,86	2,77E-03
HMGB1	200680_x_at	NM_002128	NM_002128	3146	0,85	7,80E-05
septina8	209000_s_at	BC001329	XM_034872	23176	0,85	1,12E-03
EIF2B3	218488_at	NM_020365	NM_020365	8891	0,85	2,51E-06
DCX	204851_s_at	AF040254	NM_000555 NM_178151 NM_178152 NM_178153	1641	0,85	1,15E-03
TBC1D16	1554701_a_at	BC028290	NM_019020	125058	0,85	2,39E-03
CARD10	210026_s_at	AY028896	NM_014550	29775	0,85	2,51E-03
VAV2	205536_at	NM_003371	NM_003371	7410	0,85	2,59E-03
NES	218678_at	NM_024609	NM_006617	10763	0,85	8,46E-03
DRD2	216938_x_at	S69899	NM_000795 NM_016574	1813	0,85	7,98E-03
PARP2	214086_s_at	AK001980	NM_005484	10038	0,85	2,66E-03
MGC13204	225837_at	AL577977	NM_031465	83695	0,85	1,56E-03
SLC29A1	201802_at	NM_004955	NM_004955	2030	0,85	4,79E-03
DONSON	221677_s_at	AF232674	NM_017613 NM_145794 NM_145795	29980	0,85	3,72E-03
SLC37A4	217289_s_at	AF097831	NM_001467	2542	0,85	2,49E-03
HAND1	220138_at	NM_004821	NM_004821	9421	0,85	7,06E-03
ZGPAT	57539_at	AA535065	NM_032527 NM_181484 NM_181485	84619	0,85	3,82E-04
CGI-96	202937_x_at	AL022316	NM_015703	27341	0,85	4,33E-04
NUP107	218768_at	NM_020401	NM_020401	57122	0,84	7,62E-05
AL133101	228007_at	AL133101	---	---	0,84	1,62E-04
CALM3	200622_x_at	AV685208	NM_005184	808	0,84	4,45E-03
AW450360	222072_at	AW450360	---	---	0,84	4,39E-03
BTBD3	202946_s_at	NM_014962	NM_014962 NM_181443	22903	0,84	7,63E-04
RBBP8	203344_s_at	NM_002894	NM_002894 NM_203291 NM_203292	5932	0,84	2,62E-04
FH	203033_x_at	NM_000143	NM_000143	2271	0,84	2,23E-06
VAV2	226063_at	AA481141	NM_003371	7410	0,84	1,78E-04
MRPL49	201717_at	NM_004927	NM_004927	740	0,84	3,26E-03
TUBA3	209118_s_at	AF141347	NM_006009	7846	0,84	7,92E-05
CD24	216379_x_at	AK000168	NM_013230	934	0,84	4,53E-05
FLJ21415	218867_s_at	NM_024738	NM_024738	79794	0,84	3,59E-03
AA004210	229835_s_at	AA004210	---	---	0,84	1,26E-04
PIGX	1552291_at	NM_017861	NM_017861	54965	0,84	2,94E-03
L3MBTL2	1555815_a_at	AL136564	NM_001003689 NM_031488	83746	0,84	6,19E-03
SEC23A	212887_at	AI753659	NM_006364	10484	0,84	2,12E-03

AI589594	238694_at	AI589594	---	---	0,84	6,20E-04
C20orf45	222441_x_at	BF032213	NM_016045	51012	0,84	3,50E-03
C8orf20	218777_at	NM_025232	NM_025232	80346	0,84	8,62E-04
PREX1	224925_at	AL445192	NM_020820	57580	0,84	4,97E-03
RPA2	201756_at	NM_002946	NM_002946	6118	0,84	2,53E-03
RECQL	212918_at	AI962943	NM_002907 NM_032941	5965	0,83	5,17E-03
HOXD4	205522_at	NM_014621	NM_014621	3233	0,83	4,47E-03
AU144918	233858_at	AU144918	---	---	0,83	9,47E-03
DATF1	218325_s_at	NM_022105	NM_022105 NM_080796 NM_080797	11083	0,83	3,04E-03
EED	209572_s_at	AF080227	NM_003797 NM_152991	8726	0,83	6,60E-06
RIMS4	227644_at	AL049000	NM_182970	140730	0,83	1,04E-03
CHML	226350_at	AU155565	NM_001821	1122	0,83	1,58E-03
RAD21	200607_s_at	BG289967	NM_006265	5885	0,83	1,96E-03
ZNF555	1556188_a_at	AF052118	NM_152791	148254	0,83	3,68E-04
FSCN1	210933_s_at	BC004908	NM_003088	6624	0,83	1,24E-03
KIAA1467	213234_at	AB040900	XM_370682	57613	0,83	4,71E-03
DDX54	224433_s_at	BC005848	NM_024072	79039	0,83	4,90E-03
TERT	207199_at	NM_003219	NM_003219 NM_198253 NM_198254 NM_198255	7015	0,83	3,88E-03
HRASLS	219983_at	NM_020386	NM_020386	57110	0,83	7,17E-03
BACH	215728_s_at	AL031848	NM_007274 NM_181862 NM_181863 NM_181864 NM_181865 NM_181866	11332	0,83	3,84E-06
MSH5	221406_s_at	NM_025259	NM_002441 NM_025259 NM_172165 NM_172166	4439	0,83	9,50E-03
FLJ22955	221224_s_at	NM_024819	NM_024819	79877	0,83	2,19E-03
ATF7IP	218987_at	NM_018179	NM_018179	55729	0,83	8,71E-04
FLJ20508	218712_at	NM_017850	NM_017850	54955	0,82	1,46E-03
PHF5A	225309_at	AL008582	NM_032758	84844	0,82	1,72E-04
C20orf27	50314_i_at	AI761506	NM_017874	54976	0,82	7,41E-04
SET8	225094_at	AL578116	NM_020382	387893	0,82	8,35E-04
KCNS3	205968_at	NM_002252	NM_002252	3790	0,82	9,42E-03
CHES1	222494_at	AW051527	NM_005197	1112	0,82	1,04E-02
RCBTB1	218352_at	NM_018191	NM_018191	55213	0,82	8,95E-05
NM_024601	220033_at	NM_024601	---	---	0,82	1,30E-03
HCN3	228741_s_at	AA569959	NM_020897	57657	0,82	2,94E-03
ATP6V1A	201971_s_at	NM_001690	NM_001690	523	0,82	1,36E-03
RNF26	224338_s_at	AB055622	NM_032015	79102	0,82	2,45E-03

BC042916	1559111_a_at	BC042916	---	---	0,82	8,94E-03
PINX1	223907_s_at	AF205718	NM_017884	54984	0,82	1,62E-04
AW771952	242434_at	AW771952	---	---	0,82	2,95E-03
HNRPAB	201277_s_at	NM_004499	NM_004499 NM_031266	3182	0,82	1,19E-04
FH	214170_x_at	AA669797	NM_000143	2271	0,82	3,99E-05
LOC283852	238554_at	BE501733	---	283852	0,82	5,07E-03
ZNF79	214138_at	AA284829	NM_007135	7633	0,82	2,28E-04
C22orf19	209418_s_at	BC003615	NM_001002877 NM_001002878 NM_001002879 NM_003678	8563	0,82	2,69E-04
RAD21	200608_s_at	NM_006265	NM_006265	5885	0,82	1,40E-03
H1F0	208886_at	BC000145	NM_005318	3005	0,82	3,44E-03
MAPKAPK5	212871_at	NM_003668	NM_003668 NM_139078	8550	0,82	5,71E-04
PPP1R13B	216347_s_at	AK023188	NM_015316	23368	0,82	4,23E-04
ZNF278	211392_s_at	AF242522	NM_014323 NM_032050 NM_032051 NM_032052	23598	0,81	1,59E-03
ENC2	210307_s_at	AL136796	NM_022480	64410	0,81	6,42E-03
DACH1	1562342_at	AL713717	NM_004392 NM_080759 NM_080760	1602	0,81	4,53E-03
ADRBK2	204184_s_at	NM_005160	NM_005160	157	0,81	3,83E-04
JUP	201015_s_at	NM_021991	NM_002230 NM_021991	3728	0,81	5,55E-03
KIAA1333	223258_s_at	BC000973	NM_017769	55632	0,81	2,69E-03
ETAA16	219216_at	NM_019002	NM_019002	54465	0,81	1,33E-03
LOC387882	225105_at	BF969397	NM_207376	387882	0,81	9,88E-04
KIAA1648	213058_at	AL033538	---	284900	0,81	3,45E-03
DYRK4	212954_at	AF263541	NM_003845	8798	0,81	3,72E-03
LOC200008	229605_at	AI150848	NM_201546	200008	0,81	6,35E-06
GPX3	214091_s_at	AW149846	NM_002084	2878	0,81	1,38E-03
LRP10	201412_at	NM_014045	NM_014045	26020	0,81	4,50E-03
LOC55954	218752_at	NM_019103	NM_001003692 NM_019103	55954	0,81	9,27E-03
FLJ23441	219217_at	NM_024678	NM_024678	79731	0,81	5,14E-06
TH1L	220607_x_at	NM_016397	NM_016397 NM_198976	51497	0,81	1,63E-03
AD-003	223368_s_at	BC001396	NM_014064	28989	0,81	2,11E-03
HIP2	202347_s_at	AB022435	NM_005339	3093	0,80	1,48E-04
MGAT5B	238445_x_at	AI609043	NM_144677 NM_198955	146664	0,80	6,85E-04

EPOR	37986_at	M60459	NM_000121	2057	0,80	5,63E-03
HIC2	212966_at	AL043112	NM_015094	23119	0,80	3,15E-05
GJA7	228776_at	AA430014	NM_005497	10052	0,80	4,03E-05
DNAJC9	213088_s_at	BE551340	NM_015190	23234	0,80	2,60E-03
HMGN2	208668_x_at	BC003689	NM_005517	3151	0,80	1,11E-03
MRPL42	217919_s_at	BE782148	NM_014050 NM_172177 NM_172178	28977	0,80	2,11E-03
HSPC129	223270_at	AF161543	NM_016396	51496	0,80	1,61E-05
HNRPA2B1	205292_s_at	NM_002137	NM_002137 NM_031243	3181	0,80	3,05E-04
ANXA4	201301_s_at	BC000182	NM_001153	307	0,80	8,27E-03
SOX13	38918_at	AF083105	NM_005686	9580	0,80	3,55E-03
ACTR1A	200721_s_at	NM_005736	NM_005736	10121	0,80	2,85E-03
MEIS2	207480_s_at	NM_020149	NM_002399 NM_020149 NM_170674 NM_170675 NM_170676 NM_170677 NM_172315 NM_172316	4212	0,80	4,47E-04
APG3L	221482_s_at	AF202092	NM_022488	64422	0,80	1,43E-03
CDYL	203099_s_at	AF081258	NM_004824 NM_170751 NM_170752	9425	0,80	3,28E-03
ODZ3	219523_s_at	NM_018104	XM_371717	55714	0,80	1,87E-03
VAPB	202550_s_at	NM_004738	NM_004738	9217	0,80	8,33E-06
SAP30	204900_x_at	NM_003864	NM_003864	8819	0,80	1,56E-05
HOXD1	205975_s_at	NM_024501	NM_024501	3231	0,80	1,08E-03
FLJ10385	220258_s_at	NM_018081	NM_018081	55135	0,80	1,71E-03
LRRC1	218816_at	NM_018214	NM_018214 NM_025168	55227	0,80	5,23E-03
CD24	209771_x_at	AA761181	NM_013230	934	0,80	5,76E-04
SLC29A1	201801_s_at	AF079117	NM_004955	2030	0,80	7,75E-04
C10orf86	211376_s_at	BC005212	NM_017615	54780	0,80	2,32E-05
GNAZ	204993_at	NM_002073	NM_002073	2781	0,80	8,65E-05
C15orf25	229208_at	AK022939	NM_018097	55142	0,80	8,67E-03
CPT1A	203633_at	BF001714	NM_001876	1374	0,80	1,57E-03
LOC150383	227590_at	BE501980	NM_001008917 NM_207327	150383	0,80	1,76E-05
MGC18216	225330_at	AL044092	---	145815	0,80	7,91E-04
384D8-2	205086_s_at	NM_014551	NM_014551 NM_152299	29781	0,80	8,25E-05
USP28	231837_at	AB040948	NM_020886	57646	0,80	4,10E-04
G22P1	200792_at	NM_001469	NM_001469	2547	0,79	1,57E-06
TIMM50	224913_s_at	AA877820	NM_001001563	92609	0,79	1,54E-06
OSRF	219421_at	NM_012382	NM_012382	23548	0,79	1,38E-03

TIAF1 MYO18A	202039_at	NM_004740	NM_004740 NM_078471 NM_203318	399687 9220	0,79	7,17E-03
SNN	218032_at	AF070673	NM_003498	8303	0,79	3,27E-05
HPS4	54037_at	AL041451	NM_022081 NM_152840 NM_152841 NM_152842 NM_152843	89781	0,79	3,31E-05
AI339606	222852_at	AI339606	---	---	0,79	3,52E-03
CNN3	201445_at	NM_001839	NM_001839	1266	0,79	2,38E-05
C16orf34	212115_at	AK023154	NM_144570	90861	0,79	1,93E-04
DKFZP564K0822	208091_s_at	NM_030796	NM_030796	81552	0,79	4,71E-04
LETM2	1557415_s_at	AI023774	NM_144652	137994	0,79	1,29E-03
AW665227	229713_at	AW665227	---	---	0,79	2,47E-05
C14orf130	218108_at	NM_018108	NM_018108 NM_175748	55148	0,79	4,99E-03
NEDD1	234984_at	AA236927	NM_152905	121441	0,79	3,11E-04
LOC57168	227015_at	Z99714	NM_020437	57168	0,79	4,74E-06
ZNF267	219540_at	AU150728	NM_003414	10308	0,79	1,98E-03
HIC2	212964_at	AI912206	NM_015094	23119	0,79	6,64E-06
BG150301	230271_at	BG150301	---	---	0,79	9,81E-03
NM_014838	204799_at	NM_014838	---	---	0,79	1,18E-03
FLJ14827	221777_at	BE966197	NM_032848	84934	0,79	2,97E-05
NP	201695_s_at	NM_000270	NM_000270	4860	0,78	8,55E-03
BACH	208002_s_at	NM_007274	NM_007274 NM_181862 NM_181863 NM_181864 NM_181865 NM_181866	11332	0,78	1,62E-04
GPR155	244509_at	AW449728	NM_152529	151556	0,78	8,05E-03
EIF2S1	201144_s_at	NM_004094	NM_004094	1965	0,78	4,48E-06
CLEC11A	205131_x_at	NM_002975	NM_002975	6320	0,78	3,57E-03
BCL11A	219497_s_at	NM_022893	NM_018014 NM_022893 NM_138553 NM_138559	53335	0,78	8,37E-05
MRPL2	229884_s_at	AA187325	NM_015950	51069	0,78	6,69E-04
PRKAB2	1558027_s_at	AL552001	NM_005399	5565	0,78	1,67E-03
DTX1	227336_at	AW576405	NM_004416	1840	0,78	1,19E-03
M96	203347_s_at	NM_007358	NM_007358	22823	0,78	8,86E-03
ACN9	218981_at	NM_020186	NM_020186	57001	0,78	1,05E-03
IMP-1	227377_at	AK022784	NM_006546	10642	0,78	2,10E-04
DVL2	57532_at	AW016304	NM_004422	1856	0,78	1,49E-04
DKFZp547A023	239525_at	AI733041	NM_018704	55917	0,78	2,26E-04
LOC91431	1565935_at	AF075091	NM_138698	91431	0,78	1,72E-03
H1FX	204805_s_at	NM_006026	NM_006026	8971	0,78	2,36E-03
RNPEP	208270_s_at	NM_020216	NM_020216	6051	0,78	1,53E-03

LOC400960	227969_at	AI627636	XM_379102	400960	0,78	1,32E-04
PXMP4	224210_s_at	BC001147	NM_007238 NM_183397	11264	0,78	7,76E-03
MAP3K7IP1	203901_at	NM_006116	NM_006116 NM_153497	10454	0,78	2,33E-04
LSM2	209449_at	AF196468	NM_021177	57819	0,78	2,81E-03
ODF2	225617_at	AL138382	NM_002540 NM_153437	4957	0,78	1,50E-03
JARID2	203297_s_at	BG029530	NM_004973	3720	0,77	5,30E-03
C20orf27	218081_at	NM_017874	NM_017874	54976	0,77	1,93E-04
FLJ35779	227267_at	AI953478	NM_152408	134359	0,77	5,87E-03
FLJ38973	238974_at	N47077	NM_153689	205327	0,77	3,60E-03
LOC202181	232309_at	Y13871	---	202181	0,77	9,94E-04
DDX54	219111_s_at	NM_024072	NM_024072	79039	0,77	5,24E-03
NELL2	203413_at	NM_006159	NM_006159	4753	0,77	1,82E-04
AZI1	214742_at	AB029041	NM_001009811 NM_014984	22994	0,77	4,54E-04
C13orf6	235348_at	AA404347	NM_032859	84945	0,77	6,35E-07
MKL1	212748_at	AB037859	NM_020831	57591	0,77	1,75E-04
MLF1	204784_s_at	NM_022443	NM_022443	4291	0,77	4,84E-03
RPP25	219143_s_at	NM_017793	NM_017793	54913	0,77	2,33E-03
MRPL39	218558_s_at	NM_017446	NM_017446 NM_080794	54148	0,77	1,79E-03
MR-1	225298_at	AA074597	NM_015488 NM_022572	25953	0,77	9,47E-03
SCOC	223341_s_at	AF330205	NM_032547	60592	0,77	5,34E-06
GAMT	1552474_a_at	NM_138924	NM_000156 NM_138924	2593	0,77	8,68E-04
MGC61550	228791_at	BF434655	NM_182616	348110	0,77	5,38E-04
MGC4172	218756_s_at	NM_024308	NM_024308	79154	0,76	8,18E-04
IKIP	227295_at	AW182575	NM_153687 NM_201612 NM_201613 NM_201614	121457	0,76	1,09E-04
BCL11A	219498_s_at	NM_018014	NM_018014 NM_022893 NM_138553 NM_138559	53335	0,76	6,17E-05
LOC115098	225454_at	AW248770	NM_138442	115098	0,76	2,43E-03
NM_016534	219817_at	NM_016534	---	---	0,76	1,74E-03
H15087	238186_at	H15087	---	---	0,76	4,91E-03
D15Wsu75e	212527_at	BF057059	XM_039495	27351	0,76	5,47E-03
TMEM19	229126_at	AI597651	NM_018279	55266	0,76	9,91E-03
TCF3	215260_s_at	X52078	NM_003200	6929	0,76	3,41E-03
PEX19	201706_s_at	BC000496	NM_002857	5824	0,76	6,90E-07
HSPC132	218403_at	NM_016399	NM_016399	51499	0,76	1,21E-03
TMEM33	222642_s_at	BC000948	NM_018126	55161	0,76	1,16E-03
LOC58489	225436_at	AI339710	XM_051862	58489	0,76	6,79E-04

RAB3D	225001_at	AI744658	NM_004283	9545	0,76	1,35E-04
CBWD1 CBWD2 LOC220869 DC36	226193_x_at	AV709992	NM_018491 NM_172003 NM_201453	150472 220869 389760 55871	0,76	7,42E-06
C7orf31	229146_at	AA778668	NM_138811	136895	0,76	4,75E-04
ZNF569	1569366_a_at	BC038737	NM_152484	148266	0,76	2,84E-03
TOB2	222243_s_at	AB051450	NM_016272	10766	0,76	1,66E-04
BF978778	226832_at	BF978778	XM_374070	389188	0,75	2,91E-03
SULF2	233555_s_at	AL034418	NM_018837 NM_198596	55959	0,75	2,13E-03
D50683	208944_at	D50683	---	---	0,75	8,75E-04
TMEFF1	205123_s_at	NM_003692	NM_003692	8577	0,75	5,76E-04
CSNK2A1	206075_s_at	NM_001895	NM_001895 NM_177559 NM_177560	1457	0,75	8,62E-03
MYO1B	212364_at	BF432550	NM_012223	4430	0,75	1,60E-05
TBL1XR1	222634_s_at	AF314544	NM_024665	79718	0,75	8,23E-03
C20orf6	222765_x_at	AL161659	NM_016649	51575	0,75	2,08E-03
TRA16	226839_at	N25631	NM_176880	126382	0,75	4,39E-03
TH1L	225006_x_at	AJ238379	NM_016397 NM_198976	51497	0,75	3,15E-03
LANCL1	202019_s_at	AI935255	NM_006055	10314	0,75	3,29E-04
ZFYVE21	219929_s_at	NM_024071	NM_024071	79038	0,75	5,24E-04
BF697865	235018_at	BF697865	---	---	0,75	3,31E-05
RECQL	212917_x_at	AI814728	NM_002907 NM_032941	5965	0,75	1,03E-03
GPR158	232195_at	R41459	NM_020752	57512	0,75	9,00E-03
TH1L	225865_x_at	AJ238374	NM_016397 NM_198976	51497	0,75	5,42E-03
AW025579	213429_at	AW025579	---	---	0,75	2,61E-03
NDUFA3	218563_at	NM_004542	NM_004542	4696	0,75	1,05E-03
AI857788	227126_at	AI857788	---	---	0,75	3,17E-04
TRIM32	203846_at	BC003154	NM_012210	22954	0,75	9,18E-04
LZIC	226087_at	BG180887	NM_032368	84328	0,75	5,95E-03
CBX1	201518_at	NM_006807	NM_006807	10951	0,75	3,35E-03
TUB	228882_at	AL042088	NM_003320 NM_177972	7275	0,75	1,66E-03
EPOR	215054_at	H16758	NM_000121	2057	0,74	2,51E-03
PDXP	223290_at	BC000320	NM_020315	57026	0,74	3,77E-04
GSS	201415_at	NM_000178	NM_000178	2937	0,74	8,16E-04
SEC10L1	228418_at	BF509391	NM_006544	10640	0,74	1,01E-02
DNAJC9	213092_x_at	AW241779	NM_015190	23234	0,74	4,38E-03
SULF2	224724_at	AL133001	NM_018837 NM_198596	55959	0,74	7,10E-04
KIAA0082	212380_at	D43949	NM_015050	23070	0,74	9,43E-03
NM_003349	201003_x_at	NM_003349	---	---	0,74	2,17E-03
HH114	232506_s_at	AK026504	NM_032499	84529	0,74	2,32E-03
MAP3K13	211083_s_at	Z25428	NM_004721	9175	0,74	1,51E-03

SRR	222844_s_at	AF169974	NM_021947	63826	0,74	1,66E-03
SIP1	205063_at	NM_003616	NM_001009182 NM_001009183 NM_003616	8487	0,74	5,42E-03
SMPD3	219695_at	NM_024703	NM_018667	55512	0,74	8,85E-03
ARL6IP6	225707_at	AL581082	NM_152522	151188	0,74	3,27E-03
LOC90525	228922_at	AI760446	NM_138356	90525	0,74	8,81E-03
PARP2	204752_x_at	NM_005484	NM_005484	10038	0,74	8,00E-03
EPB41L5	225855_at	AB046768	NM_020909	57669	0,74	2,98E-04
BG492376	1557961_s_at	BG492376	---	---	0,74	8,26E-03
KLF3	225140_at	BF438116	NM_016531	51274	0,74	1,89E-03
R12027	241836_x_at	R12027	---	---	0,74	1,13E-03
MCM8	233560_x_at	AA370141	NM_032485 NM_182802	84515	0,74	7,31E-03
TFR2	210215_at	AF067864	NM_003227	7036	0,74	3,11E-04
EIF4E	201435_s_at	AW268640	NM_001968	1977	0,74	4,34E-05
AK001164	232752_at	AK001164	---	---	0,74	3,62E-03
FLJ21839	218480_at	NM_021831	NM_021831	60509	0,73	2,20E-04
DUT	209932_s_at	U90223	NM_001948	1854	0,73	1,26E-03
RBBP7	201092_at	NM_002893	NM_002893	5931	0,73	2,45E-03
SCOC	224786_at	AL133580	NM_032547	60592	0,73	1,16E-06
ELF2	210361_s_at	AF256223	NM_006874 NM_201999	1998	0,73	1,61E-04
BF315093	227617_at	BF315093	NM_001010866	199953	0,73	3,23E-03
C6orf125	224448_s_at	BC006007	NM_032340	84300	0,73	1,18E-03
AK025512	225514_at	AK025512	---	---	0,73	2,88E-03
TTLL4	203702_s_at	AL043927	NM_014640	9654	0,73	1,86E-03
PHOX2B	207009_at	NM_003924	NM_003924	8929	0,73	6,98E-04
PAK4	33814_at	AF005046	NM_005884	10298	0,73	6,87E-03
TTC8	226120_at	AW293939	NM_144596 NM_198309 NM_198310	123016	0,73	8,67E-04
SSBP3	217991_x_at	NM_018070	NM_001009955 NM_018070 NM_145716	23648	0,73	2,77E-03
PPIF	201489_at	BC005020	NM_005729	10105	0,73	5,19E-05
LOC155435	226732_at	AI823400	NM_001008408	155435	0,73	8,92E-03
RAD1	210216_x_at	AF084513	NM_002853 NM_133282 NM_133377	5810	0,73	1,61E-04
PDE7A	223358_s_at	AW269834	NM_002603 NM_002604	5150	0,73	1,04E-03
LOC284611	226568_at	AI478747	NM_001010883	284611	0,73	4,22E-03
MPHOSPH9	1558369_at	BC036600	NM_022782	10198	0,73	9,01E-03
AHCY	200903_s_at	NM_000687	NM_000687	191	0,73	6,38E-04
KIAA1393	221952_x_at	AB037814	NM_020810	57570	0,73	1,27E-03

WDR50	203721_s_at	NM_016001	NM_016001	51096	0,73	2,41E-06
NRF1	204651_at	AW003022	NM_005011	4899	0,72	2,06E-05
ATP6V1A	201972_at	AF113129	NM_001690	523	0,72	6,11E-06
ATP6V1C1	202872_at	AW024925	NM_001007254 NM_001695	528	0,72	5,21E-03
AP3M1	222517_at	AU152391	NM_012095 NM_207012	26985	0,72	8,61E-04
HIP1R	38340_at	AB014555	NM_003959	9026	0,72	9,01E-03
CDKAL1	214877_at	BE794663	NM_017774	54901	0,72	2,66E-07
C10orf119	222464_s_at	BC004183	NM_024834	79892	0,72	2,58E-04
QRSL1	218949_s_at	NM_018292	NM_018292	55278	0,72	1,91E-04
HSPC129	223271_s_at	AF161543	NM_016396	51496	0,72	1,33E-04
MTAP	204956_at	NM_002451	NM_002451	4507	0,72	9,35E-03
TNFRSF10B	210405_x_at	AF153687	NM_003842 NM_147187	8795	0,72	1,20E-05
NDUFS1	203039_s_at	NM_005006	NM_005006	4719	0,72	3,56E-06
SRPK1	202199_s_at	AW082913	NM_003137	6732	0,71	2,30E-04
B4GALT4	210540_s_at	BC004523	NM_003778 NM_212543	8702	0,71	3,68E-03
RBM9	213901_x_at	AW149379	NM_014309	23543	0,71	8,10E-03
DENR	234915_s_at	BC000925	NM_003677	8562	0,71	1,01E-02
CPOX	204172_at	NM_000097	NM_000097	1371	0,71	4,66E-04
HSPC121	217777_s_at	NM_016395	NM_016395	51495	0,71	2,24E-04
RFX5	202963_at	AW027312	NM_000449	5993	0,71	6,50E-03
SHD1	205449_at	NM_013299	NM_013299	29901	0,71	7,97E-03
ARF3	200734_s_at	BG341906	NM_001659	377	0,71	3,13E-05
ING1	208415_x_at	NM_005537	NM_005537 NM_198217 NM_198218 NM_198219	3621	0,71	1,86E-05
TH1L	225261_x_at	AJ238376	NM_016397 NM_198976	51497	0,71	2,65E-03
VCL	200931_s_at	NM_014000	NM_003373 NM_014000	7414	0,71	4,61E-03
ZNF545	235176_at	AA927918	NM_133466	284406	0,71	8,64E-03
UBOX5	204598_at	NM_014948	NM_014948 NM_199415	22888	0,71	5,08E-03
ELAVL1	201726_at	BC003376	NM_001419	1994	0,71	7,04E-03
ITGB5	201125_s_at	NM_002213	NM_002213	3693	0,71	2,15E-03
NUP205	212247_at	AW008531	NM_015135	23165	0,71	5,94E-04
SLC17A5	221041_s_at	NM_012434	NM_012434	26503	0,71	9,98E-03
AI939588	241156_at	AI939588	---	---	0,71	3,21E-03
SCRIB	212556_at	AI469403	NM_015356 NM_182706	23513	0,71	7,66E-03
SOCS4	226178_at	BF446961	NM_080867 NM_199421	122809	0,71	1,73E-04
C6orf211	218195_at	NM_024573	NM_024573	79624	0,71	6,55E-03

PSMA7	216088_s_at	AL078633	NM_002792 NM_152255	5688	0,71	2,39E-04
AKR1B1	201272_at	NM_001628	NM_001628	231	0,71	4,69E-04
HMG20B	210719_s_at	BC002552	NM_006339	10362	0,71	5,46E-03
DZIP3	213186_at	BG502305	NM_014648	9666	0,71	5,65E-03
MFI2	223723_at	BC001875	NM_005929 NM_033316	4241	0,71	2,36E-03
PPP1CC	200726_at	NM_002710	NM_002710	5501	0,71	1,35E-03
AL521247	225046_at	AL521247	XM_374317	389831	0,71	3,82E-03
KIAA0841	213053_at	AW189966	XM_049237	23354	0,71	9,24E-03
PDE7A	224046_s_at	U67932	NM_002603 NM_002604	5150	0,71	5,94E-03
FBXO30	226541_at	AI808182	NM_032145	84085	0,71	1,04E-02
SRC	213324_at	AK024281	NM_005417 NM_198291	6714	0,70	5,83E-05
LOC57168	227014_at	BE550881	NM_020437	57168	0,70	3,95E-04
CIB2	205008_s_at	NM_006383	NM_006383	10518	0,70	1,68E-03
GPAM	225420_at	AV699379	NM_020918	57678	0,70	5,07E-03
KLF7	1555420_a_at	BC012919	NM_003709	8609	0,70	6,45E-03
AA833830	230896_at	AA833830	---	---	0,70	7,62E-04
BTBD14A	243431_at	BF000597	NM_144653	138151	0,70	2,99E-03
MAPK11	211499_s_at	U92268	NM_002751 NM_138993	5600	0,70	9,93E-03
FSCN1	201564_s_at	NM_003088	NM_003088	6624	0,70	2,66E-03
PLAGL2	202924_s_at	AL562280	NM_002657	5326	0,70	3,13E-04
USP39	217829_s_at	NM_006590	NM_006590	10713	0,70	6,69E-04
ABHD10	222697_s_at	AI521709	NM_018394	55347	0,70	3,65E-04
C20orf142	233061_at	AL117382	XM_371399	128486	0,70	8,68E-03
GPR51	209990_s_at	AF056085	NM_005458	9568	0,70	1,26E-03
CELSR3	205165_at	NM_001407	NM_001407	1951	0,70	1,21E-03
SSBP2	210829_s_at	AF077048	NM_012446	23635	0,70	7,97E-04
POT1	204353_s_at	BC002923	NM_015450	25913	0,70	1,78E-04
B4GALT6	206233_at	AF097159	NM_004775	9331	0,70	1,09E-03
MARF (C3HC4) 2	210075_at	AF151074	NM_001005415 NM_001005416 NM_016496	51257	0,70	7,91E-03
MGC4825	221620_s_at	AF061264	NM_024122	79135	0,70	9,49E-03
CBLL1	227187_at	AI824009	NM_024814	79872	0,70	2,62E-03
RAB11A	200864_s_at	NM_004663	NM_004663	8766	0,70	7,58E-03
SLBP	206052_s_at	NM_006527	NM_006527	7884	0,70	1,28E-03
TBX3	229576_s_at	N29712	NM_005996 NM_016569	6926	0,70	1,56E-03
RNF10	207801_s_at	NM_014868	NM_014868	9921	0,69	2,04E-03
KIAA0153	1552257_a_at	NM_015140	NM_015140	23170	0,69	9,62E-04
THOC4	226320_at	AF047002	NM_005782	10189	0,69	2,92E-03
SDHA	201093_x_at	NM_004168	NM_004168	6389	0,69	1,14E-05
FKBPL	219187_at	NM_022110	NM_022110	63943	0,69	5,41E-03

EXOSC3	223489_x_at	AW015573	NM_001002269 NM_016042	51010	0,69	2,58E-04
COCH	1554242_a_at	BC007230	NM_004086	1690	0,69	4,57E-03
C16orf34	212109_at	AI590869	NM_144570	90861	0,69	1,30E-04
CITED1	207144_s_at	NM_004143	NM_004143	4435	0,69	6,40E-03
ZDHHC3	218077_s_at	BE542551	NM_016598	51304	0,69	1,09E-03
AW611729	228744_at	AW611729	---	---	0,69	1,38E-03
MBD4	209580_s_at	AF114784	NM_003925	8930	0,69	1,50E-04
CKLF	221058_s_at	NM_016326	NM_016326 NM_016951 NM_181640 NM_181641	51192	0,69	6,66E-03
PPM1F	37384_at	D86995	NM_014634	9647	0,69	9,40E-05
CSTF1	32723_at	L02547	NM_001324	1477	0,69	7,49E-04
KIAA1333	223257_at	AI823905	NM_017769	55632	0,69	1,45E-04
SHB	1557458_s_at	BU685917	NM_003028	6461	0,69	1,46E-03
AA608749	228095_at	AA608749	---	---	0,69	8,96E-03
MPST	203524_s_at	NM_021126	NM_021126	4357	0,69	4,69E-04
METRN	232269_x_at	BE965311	NM_024042	79006	0,69	7,29E-03
NUP43	219007_at	NM_024647	NM_024647 NM_198887	348995	0,69	8,85E-05
TTYH2	223741_s_at	BC004233	NM_032646 NM_052869	94015	0,69	9,46E-03
C20orf178	225119_at	AW299290	NM_176812	128866	0,69	9,97E-06
GTF3A	215091_s_at	BE542815	NM_002097	2971	0,69	1,55E-04
NIPSNAP1	201708_s_at	AW083371	NM_003634	8508	0,69	1,45E-03
C20orf44	217935_s_at	NM_018244	NM_018244 NM_199487 NM_199513	55245	0,68	2,08E-03
PNRC2	222406_s_at	AV738970	NM_017761	55629	0,68	5,58E-05
IGFBP2	202718_at	NM_000597	NM_000597	3485	0,68	8,62E-03
PDE6D	204091_at	NM_002601	NM_002601	5147	0,68	3,97E-04
KIAA0376	212480_at	AB002374	NM_015330	23384	0,68	1,42E-03
PLAGL2	202925_s_at	NM_002657	NM_002657	5326	0,68	1,26E-03
C6orf18	42361_g_at	AI588986	NM_019052	54535	0,68	4,87E-04
C16orf5	223960_s_at	AF195661	NM_013399	29965	0,68	1,19E-03
ZDHHC22	229875_at	AI363193	NM_174976	283576	0,68	8,32E-03
RetSat	1566472_s_at	AK098125	NM_017750	54884	0,68	8,62E-03
CD47	213857_s_at	BG230614	NM_001777 NM_198793	961	0,68	1,35E-04
ADRBK2	228771_at	AI651212	NM_005160	157	0,68	4,73E-04
KCTD9	218823_s_at	NM_017634	NM_017634	54793	0,68	1,27E-03
H49805	239911_at	H49805	---	---	0,68	6,32E-03
ZA20D3	221613_s_at	AL136598	NM_019006	54469	0,68	2,84E-04
KELCHL	221837_at	BG325646	NM_032775	84861	0,68	4,31E-03
HMOX2	218120_s_at	D21243	NM_002134	3163	0,68	2,33E-04
C22orf13	223039_at	BC004144	NM_031444	83606	0,68	2,45E-03
ZNF71	226514_at	W55975	NM_021216	58491	0,68	1,83E-03

MGC12466	223898_at	BC005360	NM_033213	93474	0,68	6,20E-03
HMGB1	224731_at	BF673940	NM_002128	3146	0,68	1,63E-03
TBC1D7	223461_at	AF151073	NM_016495	51256	0,68	8,95E-04
PDCL	204449_at	NM_005388	NM_005388	5082	0,68	1,36E-03
RAD1	235253_at	AI742925	NM_002853 NM_133282 NM_133377	5810	0,68	2,51E-03
CKB	200884_at	NM_001823	NM_001823	1152	0,68	3,63E-05
SRrp35	239295_at	AA889416	NM_080743	135295	0,68	5,74E-03
SARA2	218254_s_at	NM_016103	NM_016103	51128	0,68	7,27E-06
CBX2	226473_at	BE514414	---	876	0,68	2,77E-04
BLCAP	201032_at	NM_006698	NM_006698	10904	0,68	1,40E-04
MGC5139	202365_at	BC004815	---	84747	0,68	1,18E-03
HIBADH	224812_at	AL577446	NM_152740	11112	0,68	4,29E-05
MOBK1B	201298_s_at	BC003398	NM_018221	55233	0,68	1,42E-05
NIPSNAP1	201709_s_at	NM_003634	NM_003634	8508	0,67	3,88E-03
CSNK2A1	212072_s_at	AL049761	NM_001895 NM_177559 NM_177560	1457	0,67	4,08E-03
DUT	208956_x_at	U62891	NM_001948	1854	0,67	2,02E-03
HOOK3	224359_s_at	AF241830	NM_032410	84376	0,67	9,68E-04
CSTF3	229665_at	AI653037	NM_001326	1479	0,67	9,91E-03
RUVBL1	201614_s_at	NM_003707	NM_003707	8607	0,67	3,37E-03
PNRC2	217779_s_at	NM_017761	NM_017761	55629	0,67	1,36E-03
KIAA1893	227975_at	AW963386	NM_052899	114787	0,67	8,58E-03
KIAA1949	224927_at	BG251556	---	170954	0,67	8,52E-03
PSMB2	200039_s_at	NM_002794	NM_002794	5690	0,67	2,36E-04
RCOR2	236030_at	BF528119	NM_173587	283248	0,67	3,41E-03
AL157484	221861_at	AL157484	---	---	0,67	8,93E-03
RBX1	218117_at	NM_014248	NM_014248	9978	0,67	4,54E-03
SIPA1	204164_at	NM_006747	NM_006747 NM_153253	6494	0,67	5,05E-03
DHRS8	217989_at	NM_016245	NM_016245	51170	0,67	3,77E-03
FBXO45	225100_at	BF590021	XM_117294	200933	0,67	5,60E-03
C19orf25	226378_s_at	AI554705	NM_152482	148223	0,67	2,15E-03
E2F3	203693_s_at	NM_001949	NM_001949	1871	0,67	9,86E-04
SERAC1	232183_at	AA128978	NM_032861	84947	0,67	2,83E-05
LOC129138	231847_at	Z97630	NM_138797	129138	0,67	4,79E-04
AL524175	225479_at	AL524175	---	---	0,67	3,32E-04
CCDC5	225297_at	AV715391	NM_138443	115106	0,67	1,96E-04
KIAA1166	225784_s_at	AU150745	NM_018684	55906	0,67	4,05E-03
SH3BP4	222258_s_at	AF015043	NM_014521	23677	0,67	8,34E-05
YTHDF1	221741_s_at	AL096828	NM_017798	54915	0,66	8,07E-04
DKFZP566E144	218194_at	NM_015523	NM_015523	25996	0,66	9,77E-05
HADHSC	201035_s_at	BC000306	NM_005327	3033	0,66	2,93E-03
GALNT4	231832_at	AI890347	NM_003774	8693	0,66	6,21E-03
FLJ90709	243709_at	BG054799	NM_173514	153129	0,66	1,04E-02

SMARCB1	212167_s_at	AK021419	NM_001007468 NM_003073	6598	0,66	3,27E-05
NDUFC1	203478_at	NM_002494	NM_002494	4717	0,66	4,38E-03
ATP1A1	220948_s_at	NM_000701	NM_000701 NM_001001586	476	0,66	9,29E-05
KIAA0265	209256_s_at	AF277177	NM_014997	23008	0,66	5,63E-03
KIAA0153	216251_s_at	BF965437	NM_015140	23170	0,66	1,12E-04
CCNG1	208796_s_at	BC000196	NM_004060 NM_199246	900	0,66	7,05E-03
DT1P1A10	213079_at	AA223871	NM_058163	90121	0,66	1,80E-03
FLJ32065	223443_s_at	BC003669	NM_153032	201283	0,66	8,33E-04
CORO1C	222409_at	AL162070	NM_014325	23603	0,66	6,46E-05
GGA2	208914_at	BE646414	NM_015044 NM_138640	23062	0,66	1,84E-03
SNRPB	208821_at	J04564	NM_003091 NM_198216	6628	0,66	8,27E-05
NUCKS	224581_s_at	AI707721	NM_022731	64710	0,66	5,13E-06
FLJ40432	228810_at	AW135279	NM_152523	151195	0,66	7,36E-05
G6PC3	221759_at	AL583123	NM_138387	92579	0,66	9,07E-04
CAMTA1	225692_at	AV756867	NM_015215	23261	0,66	1,84E-03
CBX5	212126_at	BG391282	NM_012117	23468	0,66	2,40E-03
LIMK2	202193_at	NM_005569	NM_005569 NM_016733	3985	0,66	8,69E-03
MRPL40	203152_at	NM_003776	NM_003776	64976	0,66	7,24E-03
CBR4	244052_at	AI469277	NM_032783	84869	0,66	1,00E-03
NKIRAS1	225930_at	AI970120	NM_020345	28512	0,65	3,27E-04
ASH2L	209517_s_at	AB020982	NM_004674	9070	0,65	4,47E-04
KRAS	204009_s_at	W80678	NM_004985 NM_033360	3845	0,65	2,50E-04
KELCHL	221838_at	N38751	NM_032775	84861	0,65	6,67E-04
MRPL35	218890_x_at	NM_016622	NM_016622 NM_145644	51318	0,65	6,17E-03
NUDT3	221579_s_at	AF062530	NM_006703	11165	0,65	6,42E-03
MAGEH1	218573_at	NM_014061	NM_014061	28986	0,65	1,12E-04
CCNK C14orf65	225824_at	AA528091	NM_003858	317762 8812	0,65	1,32E-04
CPE	201117_s_at	NM_001873	NM_001873	1363	0,65	5,66E-03
GAMT	205354_at	NM_000156	NM_000156 NM_138924	2593	0,65	1,31E-03
KIAA1423	225127_at	BF217531	XM_376550	57583	0,65	2,39E-03
EXOSC3	227916_x_at	AA747303	NM_001002269 NM_016042	51010	0,65	9,83E-03
RNF166	227726_at	BF057084	NM_178841	115992	0,65	8,38E-04
SFI1	213431_x_at	AB011114	NM_001007467 NM_014775	9814	0,65	6,82E-03

FLJ14721	226487_at	BE551088	NM_032829	84915	0,65	9,93E-04
FLJ21908	1557984_s_at	BI464019	NM_024604	79657	0,65	4,41E-03
TNFRSF10B	209294_x_at	BC001281	NM_003842 NM_147187	8795	0,65	9,89E-05
FLJ14827	44065_at	AI937468	NM_032848	84934	0,65	1,53E-04
TMEM33	218465_at	NM_018126	NM_018126	55161	0,65	1,81E-03
PDHA1	1555864_s_at	AW057819	NM_000284	5160	0,65	2,47E-04
SDCBP	200958_s_at	NM_005625	NM_001007067 NM_001007068 NM_001007069 NM_001007070 NM_005625	6386	0,65	5,40E-03
TM4SF9	225387_at	AA059445	NM_005723	10098	0,65	2,21E-04
SARA2	1554482_a_at	BC002847	NM_016103	51128	0,65	1,82E-04
BE138575	214020_x_at	BE138575	---	---	0,65	1,59E-05
LOC440885	239624_at	AA725362	XM_498906	440885	0,65	3,36E-04
MGC4308	224523_s_at	BC006475	NM_032359	84319	0,65	5,54E-03
SSBP2	203787_at	NM_012446	NM_012446	23635	0,65	3,43E-03
ELMOD2	1553928_at	NM_153702	NM_153702	255520	0,65	3,72E-03
KIAA1043	215146_s_at	AB028968	---	23331	0,64	5,53E-04
BC015774	1569973_at	BC015774	XM_496867	441220	0,64	7,67E-03
FLJ14166	219227_at	NM_024565	NM_024565	79616	0,64	4,93E-03
BRMS1L	224484_s_at	BC006250	NM_032352	84312	0,64	1,03E-02
SIP1	211115_x_at	AB037703	NM_001009182 NM_001009183 NM_003616	8487	0,64	4,84E-05
RGS19	204336_s_at	NM_005873	NM_005873	10287	0,64	2,62E-03
HEMK1	52159_at	W93807	NM_016173	51409	0,64	4,05E-03
BCCIP	218264_at	NM_016567	NM_016567 NM_078468 NM_078469	56647	0,64	2,33E-04
RPL5	213689_x_at	AL137958	NM_000969	388650	0,64	1,28E-03
LOC388650			NM_001006605	6125		
CYCS	208905_at	BC005299	NM_018947	54205	0,64	6,99E-07
ARF3	211622_s_at	M33384	NM_001659	377	0,64	1,47E-04
C19orf14	1553125_x_at	NM_173636	NM_173636	284403	0,64	9,52E-03
MGC10433	205740_s_at	NM_024321	NM_024321	79171	0,64	3,28E-04
PRKDC	208694_at	U47077	NM_006904	5591	0,64	8,30E-03

SCDR10	1569905_at	BC018336	NM_198533 NM_198704 NM_198705 NM_198706 NM_198707 NM_198708	374875	0,64	8,71E-03
TGIF2	216262_s_at	AL050318	NM_021809	60436	0,64	1,37E-05
LOC90268	229268_at	AA723152	NM_138348	90268	0,64	3,05E-04
PARP1	208644_at	M32721	NM_001618	142	0,64	6,21E-05
RGMB LOC285705	227339_at	BE206621	NM_173670	285704 285705	0,64	2,63E-04
ZNF250	213858_at	BE350026	NM_021061	58500	0,64	6,68E-03
ACTR1A	200720_s_at	AL532341	NM_005736	10121	0,64	3,97E-03
FBXL10	229855_at	AA779208	NM_001005366 NM_032590	84678	0,64	5,29E-03
PIPPIN	209981_at	AL023553	NM_014460	27254	0,64	8,32E-03
C22orf16	224932_at	AI814909	NM_213720	400916	0,64	5,31E-03
DTNBP1	223445_at	AF061734	NM_032122 NM_183040 NM_183041	84062	0,63	1,32E-03
GRWD1	221549_at	AF337808	NM_031485	83743	0,63	8,09E-03
LARS2	34764_at	D21851	NM_015340	23395	0,63	1,98E-03
PPP5C	201979_s_at	NM_006247	NM_006247	5536	0,63	5,76E-05
AW051899	242602_x_at	AW051899	---	---	0,63	2,62E-03
FLJ21125	219560_at	NM_024627	NM_024627	79680	0,63	9,02E-03
MRPS28	219819_s_at	NM_014018	NM_014018	28957	0,63	1,73E-03
SENP1	226619_at	AW665440	NM_014554	29843	0,63	3,06E-03
CENTD2	34206_at	AB018325	NM_015242 NM_139181	116985	0,63	2,69E-04
TPM1	206117_at	NM_000366	NM_000366	7168	0,63	1,78E-03
RAP1GDS1	209444_at	BC001851	NM_021159	5910	0,63	2,24E-04
CELSR3	40020_at	AB011536	NM_001407	1951	0,63	6,88E-04
PPM1F	203063_at	NM_014634	NM_014634	9647	0,63	3,60E-05
HMGB1	214938_x_at	AF283771	NM_002128	3146	0,63	4,46E-04
AW294869	225227_at	AW294869	---	---	0,63	1,30E-03
AI417537	227739_at	AI417537	XM_372169	389822	0,63	9,49E-03
GTF3A	201338_x_at	NM_002097	NM_002097	2971	0,63	4,05E-04
EXOSC3	223490_s_at	AF281132	NM_001002269 NM_016042	51010	0,63	4,03E-05
HSPA14	219212_at	NM_016299	NM_016299	51182	0,63	2,58E-05
DHX15	201386_s_at	AF279891	NM_001358	1665	0,63	2,26E-05
CDK5RAP2	220935_s_at	NM_018249	NM_001011649 NM_018249	55755	0,62	1,12E-03
CBX5	231862_at	AK023520	NM_012117	23468	0,62	8,64E-03
AW024563	225712_at	AW024563	---	---	0,62	2,41E-03
NME4	212739_s_at	AL523860	NM_005009	4833	0,62	4,02E-04

EEF2K	225545_at	BF001312	NM_013302	29904	0,62	1,58E-06
ECHDC1	219974_x_at	NM_018479	NM_018479	55862	0,62	1,24E-03
SORT1	224818_at	BE622952	NM_002959	6272	0,62	6,15E-03
FKBP7	231130_at	AA683602	NM_016105 NM_181342	51661	0,62	6,59E-03
PPP4R2	225519_at	AA206408	NM_174907	151987	0,62	1,07E-03
JAG1	216268_s_at	U77914	NM_000214	182	0,62	3,91E-03
OSBPL1A	241693_at	BF246603	NM_018030 NM_080597 NM_133268	114876	0,62	3,59E-03
AP1B1	205423_at	NM_001127	NM_001127 NM_145730	162	0,62	5,15E-06
SNRPB	213175_s_at	AL049650	NM_003091 NM_198216	6628	0,62	1,16E-05
MYH9	211926_s_at	AI827941	NM_002473	4627	0,62	7,82E-06
BICD2	213154_s_at	AI934125	NM_001003800 NM_015250	23299	0,62	6,85E-03
SNX11	220140_s_at	NM_013323	NM_013323 NM_152244	29916	0,62	6,32E-03
ZNF354A	205427_at	NM_005649	NM_005649	6940	0,62	9,78E-03
ANK1	205390_s_at	NM_000037	NM_000037 NM_020475 NM_020476 NM_020477 NM_020478 NM_020479 NM_020480 NM_020481	286	0,62	1,01E-02
SNRPG	205644_s_at	NM_003096	NM_003096	6637	0,62	1,58E-03
15E1.2	214711_at	BE568184	NM_176818	283459	0,62	9,53E-03
PPOX	204788_s_at	NM_000309	NM_000309	5498	0,62	5,07E-03
GTF2F2	209595_at	BC001771	NM_004128	2963	0,62	6,89E-04
RAC3	206103_at	NM_005052	NM_005052	5881	0,62	8,05E-04
IRAK1BP1	213074_at	BG545769	NM_001010844	134728	0,62	1,38E-03
M96	203345_s_at	AI566096	NM_007358	22823	0,62	1,24E-03
CHPPR	203208_s_at	NM_014637	NM_014637	9650	0,62	5,77E-03
CBFB	206788_s_at	AF294326	NM_001755 NM_022845	865	0,62	3,44E-03
HIVEP2	212641_at	AL023584	NM_006734	3097	0,62	2,38E-03
FDPS	201275_at	NM_002004	NM_002004	2224	0,62	1,13E-03
SCC-112	213983_s_at	AW991219	NM_015200	23244	0,62	4,84E-03
NCOR2	207760_s_at	NM_006312	NM_006312	9612	0,62	2,28E-03
CIAPIN1	208424_s_at	NM_020313	NM_020313	57019	0,62	2,19E-05
STAT1	AFFX-HUMISGF3A/M97935_5_at	AFFX-HUMISGF3A/M97935_5	NM_007315 NM_139266	6772	0,62	9,80E-04
EIF5B	201027_s_at	NM_015904	NM_015904	9669	0,62	3,52E-04
FBXO45	225099_at	AA126446	XM_117294	200933	0,62	4,20E-03
COPS6	213504_at	W63732	NM_006833	10980	0,62	7,94E-03

ACO2	200793_s_at	NM_001098	NM_001098	50	0,61	1,19E-03
HADHSC	211569_s_at	AF001903	NM_005327	3033	0,61	1,58E-03
M6PRBP1	202122_s_at	NM_005817	NM_005817	10226	0,61	5,73E-03
GPR51	211679_x_at	AF095784	NM_005458	9568	0,61	2,47E-03
LOC63929	226501_at	BE966626	NM_022098	63929	0,61	5,18E-04
FLJ20331	218577_at	NM_017768	NM_017768	55631	0,61	7,70E-03
AI125670	231431_s_at	AI125670	XM_373626	388114	0,61	5,65E-04
RENT1	211168_s_at	D86988	NM_002911	5976	0,61	5,90E-03
COX7B	202110_at	NM_001866	NM_001866	1349	0,61	1,87E-03
RBMS1	209868_s_at	D28482	NM_002897 NM_016836 NM_016839	5937	0,61	1,58E-05
NAP1L4	1560339_s_at	AK095320	NM_005969	4676	0,61	7,56E-03
DTNBP1	223446_s_at	AF061734	NM_032122 NM_183040 NM_183041	84062	0,61	1,14E-03
SUHW3	235520_at	AA805654	NM_017666	55609	0,61	7,60E-03
RAD1	204461_x_at	NM_002853	NM_002853 NM_133282 NM_133377	5810	0,61	8,03E-03
NAP1L4	201414_s_at	NM_005969	NM_005969	4676	0,61	8,91E-03
DBN1	202806_at	NM_004395	NM_004395 NM_080881	1627	0,61	6,46E-03
LSM3	202209_at	NM_014463	NM_014463	27258	0,61	3,78E-04
ITGAV	202351_at	AI093579	NM_002210	3685	0,61	1,45E-03
PDCD8	205512_s_at	NM_004208	NM_004208 NM_145812 NM_145813	9131	0,61	3,22E-03
GLT28D1	219015_s_at	NM_018466	NM_018466	55849	0,61	1,02E-02
DKFZp586M1819	224776_at	BF513102	NM_178819	137964	0,61	3,28E-04
ZNF305	206507_at	NM_014724	NM_014724	9753	0,61	6,84E-03
MRPL37	222993_at	AF325707	NM_016491	51253	0,61	3,36E-03
MYO1B	212365_at	BF215996	NM_012223	4430	0,61	4,15E-06
XRCC5	208642_s_at	AA205834	NM_021141	7520	0,61	1,58E-05
AK096932	1564220_a_at	AK096932	---	---	0,60	2,76E-03
MGC50372	1558097_at	W21283	NM_173566	253143	0,60	1,75E-03
UBE2R2	226954_at	BE221883	NM_017811	54926	0,60	1,57E-04
LOC283484	1556940_at	AW665184	---	283484	0,60	6,08E-03
C20orf77	225024_at	AL117521	NM_021215	58490	0,60	4,10E-05
FLJ10350	217943_s_at	NM_018067	NM_018067	55700	0,60	2,33E-03
LOC84661	224129_s_at	AF226998	NM_032574	84661	0,60	6,46E-03
SMYD5	209516_at	U50383	NM_006062	10322	0,60	2,51E-04
H2AFJ	220936_s_at	NM_018267	NM_018267 NM_177925	55766	0,60	2,36E-03
XPNPEP1	208453_s_at	NM_006523	NM_020383	7511	0,60	2,47E-03
APG7L	218673_s_at	NM_006395	NM_006395	10533	0,60	7,62E-03
RASGRP1	205590_at	NM_005739	NM_005739	10125	0,60	8,56E-03
KIAA1333	223254_s_at	AA887053	NM_017769	55632	0,60	1,03E-02
C6orf79	220094_s_at	NM_022102	NM_022102	63933	0,60	1,45E-03

PHACTR3	227949_at	AL357503	NM_080672 NM_183244 NM_183246	116154	0,60	5,45E-04
CSPG6	209259_s_at	AF020043	NM_005445	9126	0,60	4,65E-03
C6orf108	204238_s_at	NM_006443	NM_006443 NM_199184	10591	0,60	6,02E-03
MGC15606	215968_at	AF055018	NM_145037	91775	0,60	6,84E-04
MGC13017	235006_at	AL571598	NM_080656	91368	0,60	6,97E-03
PA2G4	208676_s_at	U87954	NM_006191	5036	0,60	2,40E-03
MRPL2	218887_at	NM_015950	NM_015950	51069	0,60	4,44E-04
FUSIP1	206095_s_at	NM_006625	NM_006625 NM_054016	10772	0,60	6,03E-03
NUP98	203194_s_at	AA527238	NM_005387 NM_016320 NM_139131 NM_139132	4928	0,60	2,00E-03
G6PC3	44654_at	AI669655	NM_138387	92579	0,60	2,87E-03
BCR	217223_s_at	U07000	NM_004327 NM_021574	613	0,60	3,32E-03
AP3S2	202399_s_at	NM_005829	NM_005829	10239	0,59	2,43E-03
ZNF589	219968_at	NM_016089	NM_016089	51385	0,59	2,39E-03
AHCYL1	200850_s_at	NM_006621	NM_006621	10768	0,59	5,75E-04
SIN3A	225135_at	AI433017	NM_015477	25942	0,59	4,14E-03
CHCHD3	217972_at	NM_017812	NM_017812	54927	0,59	2,72E-03
SSBP3	223635_s_at	BC003605	NM_001009955 NM_018070 NM_145716	23648	0,59	1,16E-03
AI127452	228443_s_at	AI127452	---	---	0,59	2,59E-03
LOC113174	225614_at	AI815207	NM_138421	113174	0,59	4,60E-04
C20orf24	224376_s_at	AF274948	NM_018840 NM_199483 NM_199484 NM_199485	55969	0,59	1,49E-04
PITPNB	202522_at	AL031591	NM_012399	23760	0,59	1,72E-04
RPE	216574_s_at	J04742	NM_006916 NM_199229	6120	0,59	1,51E-03
AF061733	223477_s_at	AF061733	---	---	0,59	4,14E-03
ECHDC1	223088_x_at	BC003549	NM_018479	55862	0,59	2,67E-05
MRPL30	223996_s_at	AF151083	NM_016503 NM_145212 NM_145213	51263	0,59	5,32E-04
CNOT4	203291_at	NM_013316	NM_001008225 NM_013316	4850	0,59	1,86E-04
MGC32020	214816_x_at	BC003535	NM_152266	91442	0,59	1,21E-03
SLC4A7	209884_s_at	AF047033	NM_003615	9497	0,59	8,63E-03
ATXN10	208833_s_at	AF119662	NM_013236	25814	0,59	1,71E-06
POP7	209482_at	BC001430	NM_005837	10248	0,59	4,07E-04

LRRFIP1	223492_s_at	BC004958	NM_004735	9208	0,59	2,17E-03
HIG1	221896_s_at	BE739519	NM_014056	25994	0,58	3,91E-03
PBX3	204082_at	NM_006195	NM_006195	5090	0,58	7,63E-03
LZTR1	203412_at	NM_006767	NM_006767	8216	0,58	7,27E-03
SFI1	215699_x_at	AL096768	NM_001007467 NM_014775	9814	0,58	6,00E-03
TOP3B	213660_s_at	AA581879	NM_003935	8940	0,58	3,68E-03
PSMD12	202352_s_at	AI446530	NM_002816 NM_174871	5718	0,58	1,19E-03
RAB7L1	218700_s_at	BC002585	NM_003929	8934	0,58	7,31E-03
NM_016402	217946_s_at	NM_016402	---	---	0,58	3,60E-04
SIP1	211114_x_at	AB037702	NM_001009182 NM_001009183 NM_003616	8487	0,58	5,55E-03
COPS8	214260_at	AI079287	NM_006710 NM_198189	10920	0,58	9,44E-03
ZNF141	206931_at	NM_003441	NM_003441	7700	0,58	8,62E-05
LANCL1	202020_s_at	NM_006055	NM_006055	10314	0,58	6,88E-03
PXK	225796_at	AI684747	NM_017771	54899	0,58	6,08E-04
AMACR	209424_s_at	AI796120	NM_014324 NM_203382	23600	0,58	8,99E-03
RPE	225040_s_at	AV699857	NM_006916 NM_199229	6120	0,58	5,46E-04
GSPT1	215438_x_at	BE906054	NM_002094	2935	0,58	1,02E-02
ASXL1	212234_at	AL034550	NM_015338	171023	0,58	1,46E-03
EIF4ENIF1	218626_at	NM_019843	NM_019843	56478	0,58	1,12E-04
RIT1	239843_at	AI655057	NM_006912	6016	0,58	2,20E-03
TP53RK	225402_at	BG339450	NM_033550	112858	0,58	1,38E-04
MAT2B	217993_s_at	NM_013283	NM_013283 NM_182796	27430	0,58	2,85E-03
TMCC3	226489_at	BG177562	NM_020698	57458	0,58	3,41E-03
POLRMT	203782_s_at	NM_005035	NM_005035	5442	0,58	2,34E-03
BG109230	228567_at	BG109230	---	---	0,58	2,93E-04
RBMS1	203748_x_at	NM_016839	NM_002897 NM_016836 NM_016839	5937	0,58	1,17E-05
LOC96610	226802_s_at	W87523	NM_080926	96610	0,58	8,19E-03

Tabla 8. Expresión genética disminuida en las líneas celulares H1 y BB10 en comparación con la línea celular 2D6 en estado diferenciado usando análisis de micromatriz

Símbolo del gen	ID del conjunto de sondas	ID Pública representativa	ID de transcripción RefSec	ID de Gen Entrez	Proporción Log2	valor p
CYTL1	219837_s_at	NM_018659	NM_018659	54360	-6,87	8,62E-11
IL17B	220273_at	NM_014443	NM_014443	27190	-6,24	3,55E-08
KIAA0125	206478_at	NM_014792	NM_014792	9834	-5,76	4,88E-04
OLFML2A	213075_at	AL050002	NM_182487	169611	-5,40	4,32E-12
GNAS	217057_s_at	AF107846	NM_000516 NM_016592 NM_080425 NM_080426	2778	-5,37	6,02E-03
THBS2	203083_at	NM_003247	NM_003247	7058	-5,31	9,79E-08
CAP2	212554_at	N90755	NM_006366	10486	-5,29	4,85E-06
CYGB	226632_at	AL513673	NM_134268	114757	-5,15	2,38E-03
MEOX2	206201_s_at	NM_005924	NM_005924	4223	-4,96	9,77E-08
AI051127	231478_at	AI051127	---	---	-4,84	1,89E-03
CRH	205630_at	NM_000756	NM_000756	1392	-4,78	2,26E-03
NXF	1554299_at	AB049469	NM_178864	266743	-4,75	3,31E-05
SLC1A2	225491_at	AL157452	NM_004171	6506	-4,71	1,26E-09
FGF13	205110_s_at	NM_004114	NM_004114 NM_033642	2258	-4,65	6,61E-06
MICAL2	212473_s_at	BE965029	NM_014632	9645	-4,59	1,59E-05
CART	206339_at	NM_004291	NM_004291	9607	-4,59	4,64E-03
ADM	202912_at	NM_001124	NM_001124	133	-4,47	5,16E-07
OSCAR	1554503_a_at	BC035023	NM_130771 NM_133168 NM_133169 NM_206817 NM_206818	126014	-4,38	3,92E-04
HTR1E	207404_s_at	NM_000865	NM_000865	3354	-4,24	8,64E-04

BF681305	1561817_at	BF681305	---	---	-4,22	5,84E-04
EGFL7	218825_at	NM_016215	NM_016215 NM_201446	51162	-4,16	3,07E-05
SLC1A6	1554593_s_at	BC028721	NM_005071	6511	-4,16	8,15E-04
GPR54	242517_at	AI819198	NM_032551	84634	-4,15	1,40E-04
BC036254	1557443_s_at	BC036254	---	---	-4,14	5,46E-06
NDRG1	200632_s_at	NM_006096	NM_006096	10397	-4,10	8,60E-05
LOC56901	218484_at	NM_020142	NM_020142	56901	-4,10	1,79E-03
STX3A	209238_at	BE966922	NM_004177	6809	-4,02	4,71E-04
AQP1	209047_at	AL518391	NM_000385 NM_198098	358	-4,02	1,49E-03
AA530995	213832_at	AA530995	---	---	-4,00	2,31E-03
AL353759	215071_s_at	AL353759	---	---	-3,90	1,96E-05
ARHGAP9	224451_x_at	BC006107	NM_032496	64333	-3,89	8,61E-04
CAP2	212551_at	NM_006366	NM_006366	10486	-3,86	4,69E-07
LOC158572	243017_at	AA032156	XM_379705	158572	-3,85	1,09E-04
PDE4C	211818_s_at	U88712	NM_000923	5143	-3,78	3,71E-03
RaLP	230538_at	AI027957	NM_203349	399694	-3,67	1,39E-05
PTGS1	215813_s_at	S36219	NM_000962 NM_080591	5742	-3,65	1,09E-08
CYGB	1553572_a_at	NM_134268	NM_134268	114757	-3,65	2,42E-06
ANXA2	201590_x_at	NM_004039	NM_001002857 NM_001002858 NM_004039	302	-3,65	1,12E-05
NEBL	203961_at	AL157398	NM_006393 NM_213569	10529	-3,63	1,91E-05
ANXA2	210427_x_at	BC001388	NM_001002857 NM_001002858 NM_004039	302	-3,61	1,06E-05
BE219849	240180_at	BE219849	---	---	-3,60	1,29E-05

AU157716	227051_at	AU157716	---	---	-3,58	1,17E-07
RaLP	235238_at	BF676462	NM_203349	399694	-3,55	6,19E-07
RGS11	206107_at	NM_003834	NM_003834 NM_183337	8786	-3,53	1,56E-06
AI743780	229385_s_at	AI743780	---	---	-3,53	5,61E-08
CRH	205629_s_at	BC002599	NM_000756	1392	-3,52	2,27E-03
MGC4677	225799_at	BF209337	NM_052871	112597	-3,49	6,17E-05
AW954199	239331_at	AW954199	---	---	-3,49	1,64E-05
PTGS1	205128_x_at	NM_000962	NM_000962 NM_080591	5742	-3,48	3,62E-08
BF449053	238018_at	BF449053	---	---	-3,48	3,99E-07
CDC42EP1	204693_at	NM_007061	NM_007061 NM_152243	11135	-3,46	1,15E-04
CDH10	220115_s_at	NM_006727	NM_006727	1008	-3,43	5,86E-06
AI341823	239657_x_at	AI341823	---	---	-3,42	9,66E-07
HPCAL1	1560154_a_at	AK026500	NM_002149 NM_134421	3241	-3,40	3,33E-08
LOC283454	229552_at	AI698128	---	283454	-3,38	1,29E-03
ABLIM3	205730_s_at	NM_014945	NM_014945	22885	-3,34	4,32E-05
AI885066	239845_at	AI885066	---	---	-3,32	1,56E-05
AI810266	235456_at	AI810266	---	---	-3,31	6,67E-04
HIST1H3E	236278_at	AV705309	NM_003532	8353	-3,26	1,95E-05
SLC35F3	229065_at	BF988270	NM_173508	148641	-3,24	3,97E-06
BHLHB2	201170_s_at	NM_003670	NM_003670	8553	-3,22	2,22E-03
NEBL	203962_s_at	NM_006393	NM_006393 NM_213569	10529	-3,21	3,48E-05
ANXA2	213503_x_at	BE908217	NM_001002857 NM_001002858 NM_004039	302	-3,19	2,51E-07
PHKA2	1560358_at	BC038597	NM_000292	5256	-3,18	3,38E-03
GRM5	214217_at	D60132	NM_000842	2915	-3,18	2,84E-04

AL512727	215014_at	AL512727	---	---	-3,18	8,51E-04
STC1	204595_s_at	AI300520	NM_003155	6781	-3,16	9,00E-03
BG325630	234973_at	BG325630	---	---	-3,15	2,18E-03
SYTL1	227134_at	AI341537	NM_032872	84958	-3,14	1,02E-05
BC002465	216189_at	BC002465	---	---	-3,11	3,46E-03
C1orf24	217967_s_at	AF288391	NM_022083 NM_052966	116496	-3,11	5,38E-03
PDE4C	206791_s_at	BF511742	NM_000923	5143	-3,08	2,33E-03
HIST1H2BD	209911_x_at	BC002842	NM_021063 NM_138720	3017	-3,08	9,52E-06
SYT5	206161_s_at	AI659957	NM_003180	6861	-3,06	3,57E-03
LAMP3	205569_at	NM_014398	NM_014398	27074	-3,06	8,91E-03
ADARB1	203865_s_at	NM_015833	NM_001112 NM_015833 NM_015834	104	-3,06	2,79E-04
CYP2E1	1431_at	J02843	NM_000773	1571	-3,05	1,50E-03
LOC150759	221973_at	AI983904	XM_498456 XM_499585	150759	-3,03	2,56E-03
SORCS1	1556891_at	BE328250	NM_052918	114815	-3,03	3,14E-05
CREB5	232555_at	AI689210	NM_004904 NM_182898 NM_182899	9586	-3,03	1,60E-03
ISG20	204698_at	NM_002201	NM_002201	3669	-3,00	1,76E-03
AA417078	238619_at	AA417078	---	---	-2,99	5,87E-05
AW274468	242299_at	AW274468	---	---	-2,98	2,44E-05
PTPRH	208300_at	NM_002842	NM_002842	5794	-2,97	3,46E-04
BHLHB2	201169_s_at	BG326045	NM_003670	8553	-2,96	1,38E-03
AW270105	229413_s_at	AW270105	---	---	-2,92	9,07E-04
LOC390916	235384_at	AW963217	XM_372723	390916	-2,90	9,52E-08
SLCO1A2	211480_s_at	AF085224	NM_005075 NM_021094 NM_134431	6579	-2,88	2,29E-05
HIST1H2BK	209806_at	BC000893	NM_080593	85236	-2,88	3,64E-05

SYT5	206162_x_at	NM_003180	NM_003180	6861	-2,86	6,38E-04
DKFZp761O0113	207797_s_at	NM_018409	NM_018409	55805	-2,86	2,54E-05
CDKN1C	219534_x_at	NM_000076	NM_000076	1028	-2,86	3,17E-04
SCHIP1	1566772_at	AL832567	NM_014575	29970	-2,85	7,20E-03
CDKN1C	213182_x_at	R78668	NM_000076	1028	-2,85	3,87E-04
FLJ13955	227001_at	AI096706	NM_024759	79815	-2,82	9,16E-04
SYT13	226086_at	AB037848	NM_020826	57586	-2,80	7,99E-04
M160	223655_at	AF264014	NM_174941	283316	-2,79	3,27E-04
CDKN2A	209644_x_at	U38945	NM_000077 NM_058195 NM_058197	1029	-2,78	1,33E-06
AA954997	243436_at	AA954997	---	---	-2,77	1,59E-05
HIST2H2BE	202708_s_at	NM_003528	NM_003528	8349	-2,75	8,53E-04
GTF2IRD2	1557289_s_at	BU617476	NM_173537	84163	-2,75	3,68E-05
AI079543	236949_at	AI079543	XM_498613	440283	-2,75	7,55E-03
LONP	221833_at	AI971258	NM_031490	83752	-2,75	1,32E-03
AI681941	237663_at	AI681941	---	---	-2,74	1,15E-04
BE894882	235681_at	BE894882	---	---	-2,73	3,37E-06
GRIA2	205358_at	NM_000826	NM_000826	2891	-2,73	7,10E-03
MYO15B	219173_at	NM_024957	XR_000222	80022	-2,73	4,36E-05
BC042953	1561242_at	BC042953	---	---	-2,70	6,39E-03
GRIA2	236538_at	BE219628	NM_000826	2891	-2,69	3,27E-03
MYO15B	59375_at	AI825877	XR_000222	80022	-2,68	1,90E-06
AI927692	228528_at	AI927692	---	---	-2,67	6,22E-06
BC021677	1559631_at	BC021677	---	---	-2,67	4,72E-04
AA088430	242556_at	AA088430	---	---	-2,65	5,20E-07
AI769477	236875_at	AI769477	---	---	-2,65	2,18E-08
HSPA5	230031_at	AW052044	NM_005347	3309	-2,64	7,69E-03
HRK	206865_at	U76376	NM_003806	8739	-2,64	6,03E-03

BE671060	235901_at	BE671060	---	---	-2,63	9,58E-04
PLA2G4C	1554810_at	BC017956	NM_003706	8605	-2,63	4,54E-05
CYP2E1	209976_s_at	AF182276	NM_000773	1571	-2,63	4,37E-03
CDKN1C	213348_at	N33167	NM_000076	1028	-2,62	4,09E-04
ARHGAP9	232543_x_at	BE675685	NM_032496	64333	-2,62	7,93E-05
AI798680	227943_at	AI798680	---	---	-2,62	1,59E-05
BG430958	1559455_at	BG430958	---	---	-2,59	1,73E-06
PPP2R2C	1562290_at	AL157448	NM_020416 NM_181876	5522	-2,59	4,74E-04
ANK2	216195_at	AF131823	NM_001148 NM_020977	287	-2,59	2,14E-03
CYP2E1	209975_at	AF182276	NM_000773	1571	-2,58	3,47E-03
BG231712	230408_at	BG231712	---	---	-2,58	3,02E-03
ACRBP	223717_s_at	AB051833	NM_032489	84519	-2,58	1,02E-04
AU145981	232439_at	AU145981	---	---	-2,57	3,24E-05
SIK2	233648_at	AK026914	NM_015191	23235	-2,55	1,93E-03
ANK2	1561895_at	BC030740	NM_001148 NM_020977	287	-2,55	9,50E-04
RHOB	1553962_s_at	BI668074	NM_004040	388	-2,54	1,06E-03
BC040652	1559528_at	BC040652	---	---	-2,53	1,20E-03
CDKN1C	216894_x_at	D64137	NM_000076	1028	-2,52	2,77E-04
AQP1	207542_s_at	NM_000385	NM_000385 NM_198098	358	-2,52	6,49E-03
DKFZP434N1817	232257_s_at	AK022645	NM_032137	84077	-2,51	6,77E-03
CTBP1	243180_at	AW452392	NM_001328	1487	-2,51	1,14E-05
KIAA0500	213839_at	AW028110	---	57237	-2,51	5,06E-05
AW606588	239008_at	AW606588	---	---	-2,50	5,69E-04
AA903473	235666_at	AA903473	---	---	-2,50	1,43E-03
DKFZp313N0621	1555905_a_at	AI147556	NM_173826	285343	-2,49	1,95E-04

VEGF	211527_x_at	M27281	NM_003376	7422	-2,49	1,00E-03
FAM46A	224973_at	AL078599	NM_017633	55603	-2,48	2,76E-05
ZNF395 FBXO16	223216_x_at	BC001237	NM_018660 NM_172366	157574 55893	-2,48	7,42E-04
XPO1	230729_at	AI860764	NM_003400	7514	-2,48	1,68E-05
C20orf119	231838_at	AK026760	---	80336	-2,47	1,43E-06
ANK2	232606_at	AK021894	NM_001148 NM_020977	287	-2,46	1,49E-04
AV702101	238595_at	AV702101	---	---	-2,46	3,03E-04
AW364675	239066_at	AW364675	---	---	-2,45	3,80E-06
FAM46A	221766_s_at	AW246673	NM_017633	55603	-2,45	2,44E-06
AK096401	1556204_a_at	AK096401	XM_375664	400721	-2,44	7,27E-04
ZNF395	221123_x_at	NM_018660	NM_018660	55893	-2,44	8,86E-04
PTGER2	206631_at	NM_000956	NM_000956	5732	-2,43	2,99E-05
FLJ31295	226509_at	AV700302	NM_152320	121274	-2,43	2,75E-05
MEF2A	239571_at	AI123399	NM_005587	4205	-2,42	5,57E-04
AW298171	244346_at	AW298171	---	---	-2,41	1,16E-05
FLJ30594	235836_at	N51413	---	150622	-2,41	3,87E-03
AW205919	229830_at	AW205919	---	---	-2,40	1,33E-04
BE671519	242236_at	BE671519	---	---	-2,39	2,68E-03
SIGIRR	218921_at	NM_021805	NM_021805	59307	-2,39	3,99E-05
AW665665	237187_at	AW665665	---	---	-2,39	6,09E-04
GPR92	230252_at	AW183080	NM_020400	57121	-2,39	1,54E-05
MGC13040	224463_s_at	BC006128	NM_032930	85016	-2,39	2,97E-03
ANKS1	212747_at	AI990523	NM_015245	23294	-2,38	1,37E-03
ABCC8	210246_s_at	AF087138	NM_000352	6833	-2,38	2,60E-04
RHOB	212099_at	AI263909	NM_004040	388	-2,38	7,05E-04
SMOC2	223235_s_at	AB014737	NM_022138	64094	-2,37	1,05E-03
CENTG2	1559491_at	AL390180	NM_014914	116987	-2,36	1,41E-03

ARTS-1	214012_at	BE551138	NM_016442	51752	-2,36	4,64E-05
TM4SF8	232632_at	AU145719	NM_005724 NM_198902	10099	-2,36	2,15E-04
U66046	215057_at	U66046	---	---	-2,36	2,03E-04
KIAA0251	1558430_at	R08650	NM_015027	23042	-2,35	5,89E-03
TIMP1	201666_at	NM_003254	NM_003254	7076	-2,35	1,13E-05
AK024567	234597_at	AK024567	---	---	-2,34	1,59E-04
PPFIA4	214978_s_at	AK023365	NM_015053	8497	-2,34	1,46E-03
BCL11B	233302_at	AU146285	NM_022898 NM_138576	64919	-2,34	1,59E-04
C21orf4	228001_at	N51405	NM_006134	757	-2,34	7,50E-05
ATF5	204999_s_at	BC005174	NM_012068	22809	-2,34	1,08E-03
COL7A1	217312_s_at	L23982	NM_000094	1294	-2,33	2,40E-05
AL049252	216527_at	AL049252	---	---	-2,33	1,19E-03
VGCNL1	228608_at	N49852	NM_052867	259232	-2,32	3,07E-06
OLFM1	205591_at	NM_006334	NM_006334 NM_014279 NM_058199	10439	-2,32	9,85E-03
ZNF395 FBXO16	232693_s_at	AK021850	NM_018660 NM_172366	157574 55893	-2,32	2,21E-03
CNTN2	230045_at	BF740264	NM_005076	6900	-2,31	5,97E-04
ZNF395	239619_at	BF431867	NM_018660	55893	-2,31	2,70E-03
RASGEF1B	230233_at	BF110534	NM_152545	153020	-2,31	2,05E-03
AGPAT3	223182_s_at	AI337300	NM_020132	56894	-2,31	6,95E-03
ZNF395	236474_at	AI797677	NM_018660	55893	-2,30	6,29E-03
MPP5	242779_at	N36400	NM_022474	64398	-2,30	3,44E-08
AL512728	216813_at	AL512728	---	---	-2,30	1,89E-03
PLEKHH1	225727_at	AB033026	NM_020715	57475	-2,29	1,26E-06
PLEKHH1	225726_s_at	AB033026	NM_020715	57475	-2,29	3,43E-07
AI123416	227591_at	AI123416	---	---	-2,29	2,47E-04
ANK2	202921_s_at	NM_001148	NM_001148	287	-2,29	7,41E-03

			NM_020977			
CKMT1	1561155_at	W76548	NM_020990	1159	-2,28	6,30E-03
CFC1	223753_s_at	AF312769	NM_032545	55997	-2,27	1,79E-03
BF111884	230491_at	BF111884	---	---	-2,27	8,21E-06
SEC31L1	1556416_s_at	AF086242	NM_014933 NM_016211	22872	-2,27	7,06E-05
SCN2A2	206381_at	NM_021007	NM_021007	6326	-2,26	6,33E-06
PLEKHA5	237483_at	AI990790	NM_019012	54477	-2,25	8,37E-03
EDG7	231192_at	AW274018	NM_012152	23566	-2,24	1,41E-03
DTNA	240125_at	AI697494	NM_001390 NM_001391 NM_001392 NM_032975 NM_032978 NM_032979 NM_032980 NM_032981	1837	-2,23	6,58E-03
AF085937	1558695_at	AF085937	---	---	-2,22	8,05E-03
AI394334	232696_at	AI394334	---	---	-2,22	2,96E-03
UCN	206072_at	NM_003353	NM_003353	7349	-2,22	5,09E-07
DRD1IP	219896_at	NM_015722	NM_015722	50632	-2,22	1,17E-04
AA412686	244608_at	AA412686	---	---	-2,21	3,65E-03
TSAP6	218424_s_at	NM_018234	NM_00100841 0 NM_018234 NM_182915	55240	-2,21	8,31E-05
LOC201158	1560776_at	AU121725	NM_145301	201158	-2,21	7,37E-04
LAF4	244696_at	AI033582	NM_002285	3899	-2,21	6,82E-03
S100A6	217728_at	NM_014624	NM_014624	6277	-2,20	8,83E-05
BACH2	236307_at	AA085906	NM_021813	60468	-2,20	2,30E-03
KIAA1102	241459_at	AI494113	NM_014988	22998	-2,20	4,06E-03
COL5A1	212488_at	N30339	NM_000093	1289	-2,20	4,18E-06
ENOSF1	213645_at	AF305057	NM_017512	55556	-2,19	2,12E-04

LOC158863	232179_at	AL110203	---	158863	-2,19	1,08E-05
ECEL1	219914_at	NM_004826	NM_004826	9427	-2,19	1,99E-03
C21orf4	222907_x_at	BC000569	NM_006134	757	-2,18	3,97E-04
SMYD2	233713_at	AK022181	NM_020197	56950	-2,18	6,04E-04
PDZK6	228946_at	AW150229	NM_015693	27152	-2,18	3,60E-04
C21orf4	225182_at	AL355685	NM_006134	757	-2,17	1,19E-03
AA601031	228919_at	AA601031	---	---	-2,17	3,77E-03
N95363	213183_s_at	N95363	---	---	-2,17	3,77E-04
ARHGAP9	226906_s_at	AL548053	NM_032496	64333	-2,17	9,12E-04
ZNF395	222536_s_at	N36098	NM_018660	55893	-2,16	4,88E-03
FLJ12671	233728_at	AU148213	NM_030980	81875	-2,16	8,06E-04
AU146864	232659_at	AU146864	---	---	-2,16	2,93E-04
SERPINE1	202628_s_at	NM_000602	NM_000602	5054	-2,14	2,61E-05
TYRP1	242893_at	AW195492	NM_000550	7306	-2,14	1,35E-03
SLC33A1	1559232_a_at	BC029450	NM_004733	9197	-2,14	4,34E-03
AI695695	242051_at	AI695695	---	---	-2,13	1,12E-03
HRK	206864_s_at	NM_003806	NM_003806	8739	-2,12	4,70E-03
RLF	241438_at	AI742686	NM_012421	6018	-2,12	4,81E-03
CUL3	237376_at	BF115815	NM_003590	8452	-2,11	9,56E-06
BG704082	1556216_s_at	BG704082	---	---	-2,11	1,16E-03
AI968130	240327_at	AI968130	NM_015129 NM_145799 NM_145800 NM_145802	23157	-2,11	3,06E-04
CNGA3	207261_at	NM_001298	NM_001298	1261	-2,11	6,85E-04
AI803010	239503_at	AI803010	---	---	-2,11	1,53E-03
N73550	244112_x_at	N73550	---	---	-2,10	2,68E-03
BF110426	243237_at	BF110426	XM_114222	200373	-2,10	4,35E-04
BM977131	1557478_at	BM977131	---	---	-2,10	2,99E-03
AV685992	241376_at	AV685992	---	---	-2,09	4,64E-03

PAN3	239393_at	AW510927	NM_175854	255967	-2,08	1,36E-04
VEGF	210513_s_at	AF091352	NM_003376	7422	-2,08	7,20E-03
BDKRB2	205870_at	NM_000623	NM_000623	624	-2,08	2,97E-03
ZNF395	218149_s_at	NM_017606	NM_018660	55893	-2,07	6,79E-04
DEPDC6	218858_at	NM_022783	NM_022783	64798	-2,06	5,34E-04
EVER1	214958_s_at	AK021738	NM_007267	11322	-2,06	2,91E-03
LUC7L2	242024_at	T90999	NM_016019	51631	-2,06	2,82E-03
KIAA0804	1559500_at	BC036005	NM_00100992 1 NM_015303	23355	-2,06	1,55E-05
FOXP4 ASCC2	229763_at	BE504097	NM_032204 NM_138457	116113 84164	-2,05	6,69E-05
ATF5	204998_s_at	NM_012068	NM_012068	22809	-2,05	1,57E-03
AA452540	232411_at	AA452540	---	---	-2,04	3,30E-03
FNBP1	230389_at	BE046511	NM_015033	23048	-2,04	1,05E-03
AU144437	232887_at	AU144437	---	---	-2,04	2,07E-03
IDS	1569315_s_at	BC032484	NM_000202 NM_006123	3423	-2,03	1,16E-03
CSTB	236449_at	AI885390	NM_000100	1476	-2,03	8,87E-05
IGF2	210881_s_at	M17863	NM_000612	3481	-2,03	1,78E-04
LOC51315	222585_x_at	BE326678	NM_016618	51315	-2,03	7,77E-03
TRIM66	213748_at	AW271713	XM_084529	9866	-2,02	8,91E-03
AA705933	239866_at	AA705933	---	---	-2,02	3,47E-04
AI691075	229728_at	AI691075	---	---	-2,02	7,84E-03
HIST1H2AE	214469_at	NM_021052	NM_021052	3012	-2,02	1,08E-06
LOC402617	241353_s_at	AW471181	XM_380151	402617	-2,02	4,90E-04
SERPINE1	202627_s_at	AL574210	NM_000602	5054	-2,01	9,89E-06
SND1	228271_at	AW001186	NM_014390	27044	-2,01	5,63E-03
MIG-6	224657_at	AL034417	NM_018948	54206	-2,01	2,57E-04
NM_015583	208015_at	NM_015583	---	---	-2,01	1,80E-04

SMYD2	212921_at	AF070592	NM_020197	56950	-2,01	1,62E-06
S100A4	203186_s_at	NM_002961	NM_002961 NM_019554	6275	-2,01	6,07E-04
HIST2H2AA	214290_s_at	AI313324	NM_003516	8337	-2,01	7,64E-04
LOC360030	236404_at	AW197320	---	360030	-2,01	7,91E-03
AL119491	244292_at	AL119491	---	---	-2,00	8,84E-03
FNBP1	230086_at	AA937109	NM_015033	23048	-2,00	6,01E-03
LGALS3 GALIG	208949_s_at	BC001120	NM_002306 NM_194327	3958 81625	-1,99	1,10E-03
CPEB4	242384_at	AI452469	NM_030627	80315	-1,99	8,34E-03
AA278901	244055_at	AA278901	---	---	-1,99	1,31E-04
NSMAF	232148_at	BF056507	NM_003580	8439	-1,98	6,51E-03
HIST3H2A	221582_at	BC001193	NM_033445	92815	-1,98	3,01E-04
FLJ21657	1557828_a_at	BE675061	NM_022483	64417	-1,98	5,30E-03
EVER1	230526_at	BF515959	NM_007267	11322	-1,98	5,20E-08
SLITRK3	206732_at	NM_014926	NM_014926	22865	-1,97	7,66E-05
AW973410	244310_at	AW973410	XM_498613	440283	-1,97	3,35E-03
ZC3HDC1	218543_s_at	NM_022750	NM_022750	64761	-1,97	2,63E-03
GPR18	244791_at	AA835936	NM_005292	2841	-1,97	1,52E-03
LOC283666	226682_at	AW006185	---	283666	-1,96	1,61E-04
DUSP5	209457_at	U16996	NM_004419	1847	-1,96	3,92E-06
AL048861	1559148_at	AL048861	---	---	-1,96	2,90E-03
PKD2	240370_at	AI432451	NM_000297	5311	-1,96	3,38E-04
AI963079	236411_at	AI963079	---	---	-1,96	1,65E-03
AI758408	227235_at	AI758408	---	---	-1,96	1,28E-03
R63578	242818_x_at	R63578	---	---	-1,95	2,36E-03
AW189467	230183_at	AW189467	---	---	-1,95	3,15E-03
PNMA3	223621_at	AL136878	NM_013364	29944	-1,95	4,80E-07
LOC286411	1557133_at	AV753446	---	286411	-1,94	4,84E-04

RHOQ	1559582_at	BC033251	NM_012249	23433	-1,93	1,51E-03
AI817960	239649_at	AI817960	---	---	-1,93	8,93E-03
FLJ10359	232414_at	AA827672	XM_375853	55127	-1,92	2,24E-04
C16orf45	239971_at	AI298297	NM_033201	89927	-1,92	5,46E-03
MGC29875	220251_at	NM_024998	NM_014388	27042	-1,92	3,38E-03
FLJ10159	1563906_at	AK090879	---	55084	-1,92	4,66E-03
FLJ10159	236602_at	AA833813	---	55084	-1,92	2,30E-04
FAT4	219427_at	NM_024582	NM_024582	79633	-1,92	5,03E-03
MGC45477	1554250_s_at	BC033812	---	387277	-1,92	2,59E-03
ARMCX4	1552327_at	NM_152583	NM_152583	158947	-1,91	9,32E-07
IGF2	202410_x_at	NM_000612	NM_000612	3481	-1,91	1,38E-04
PRR3	244204_at	W87300	NM_025263	80742	-1,91	2,49E-03
FLJ20152	218510_x_at	AI816291	NM_019000	54463	-1,90	5,85E-04
PCBD2	240846_at	BF223271	NM_032151	84105	-1,90	3,18E-05
C6orf198	227834_at	AL589605	XM_371849	167838	-1,90	5,03E-03
MTX3	237681_at	AA699464	NM_001010891	345778	-1,89	3,91E-03
BF514509	239049_at	BF514509	---	---	-1,89	9,85E-04
C6orf148	237347_at	AL039379	NM_030568	80759	-1,89	9,86E-05
KIAA1904	1559072_a_at	BC032083	NM_052906	114794	-1,88	2,81E-04
C6orf154	235935_at	AI539370	XM_168080	221424	-1,88	2,76E-04
ATP2B3	242036_x_at	H09073	NM_001001344 NM_021949	492	-1,88	2,12E-05
BF433341	235977_at	BF433341	---	---	-1,88	2,48E-05
TMP21	239851_at	AW629289	NM_006827	10972	-1,88	5,43E-04
GFM1	232295_at	AK000780	NM_024996	85476	-1,88	3,27E-03
AAK1	214956_at	AF090101	NM_014911	22848	-1,87	3,23E-03
LOC283439	238636_at	BG430061	---	283439	-1,87	2,24E-03
FTHFSDC1	240552_at	AA811452	NM_015440	25902	-1,87	1,82E-03

AW296421	230064_at	AW296421	---	---	-1,87	6,51E-03
PAPPA	240295_at	AL045014	NM_002581	5069	-1,87	7,85E-05
LOC55831	215250_at	AU147317	NM_018447	55831	-1,87	3,85E-03
LOC253982	238142_at	AW029203	NM_181718 NM_198907	253982	-1,86	8,13E-03
NKTR	243055_at	BF514072	NM_005385	4820	-1,86	2,53E-03
AW294722	240246_at	AW294722	---	---	-1,86	7,82E-03
AK023394	232107_at	AK023394	---	---	-1,86	4,70E-05
VPS13C	235023_at	AA828371	NM_017684	54832	-1,85	5,51E-03
RHBDL1	207383_s_at	NM_003961	NM_003961	9028	-1,85	1,70E-04
C21orf4	219600_s_at	NM_006134	NM_006134	757	-1,85	1,43E-03
TPM3	238079_at	AV713323	NM_152263 NM_153649	7170	-1,85	1,29E-03
BACE2	217867_x_at	NM_012105	NM_012105 NM_138991 NM_138992	25825	-1,85	1,57E-03
VEGF	212171_x_at	H95344	NM_003376	7422	-1,84	1,68E-03
ID2	213931_at	AI819238	NM_002166	3398	-1,84	3,39E-03
LOC51315	218303_x_at	NM_016618	NM_016618	51315	-1,84	5,97E-03
TMIE	1553601_a_at	NM_147196	NM_147196	259236	-1,83	8,89E-04
TM4SF2	234245_at	AL162055	NM_004615	7102	-1,83	7,61E-03
FADS3	216080_s_at	AC004770	NM_021727	3995	-1,83	1,05E-04
SNF1LK	208078_s_at	NM_030751	NM_173354	150094	-1,83	2,37E-03
FGD5	226985_at	AW269340	NM_152536	152273	-1,83	1,69E-03
ATP2B3	207026_s_at	NM_021949	NM_00100134 4 NM_021949	492	-1,83	1,63E-04
LOC51315	233329_s_at	AK025986	NM_016618	51315	-1,83	5,27E-03
FLJ00310	1569664_at	BC035915	XM_496691	375010	-1,82	5,02E-04
FNBP1	244286_at	AI017983	NM_015033	23048	-1,82	1,10E-03
ASAM	228082_at	BF056275	NM_024769	79827	-1,82	4,85E-03

VN1R1	221412_at	NM_020633	NM_020633	57191	-1,82	4,74E-05
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FLJ23754	1553248_at	NM_152675	NM_152675	201252	-1,81	6,36E-03
HSD17B1	205829_at	NM_000413	NM_000413	3292	-1,81	5,39E-05
ZNF407	233239_at	AK024882	NM_017757	55628	-1,81	4,86E-03
ARTS-1	209788_s_at	AF183569	NM_016442	51752	-1,81	5,75E-03
GBE1	203282_at	NM_000158	NM_000158	2632	-1,81	2,17E-03
LONP	221834_at	AV700132	NM_031490	83752	-1,81	7,26E-03
SFXN3	217226_s_at	M95928	NM_030971	81855	-1,80	4,81E-04
AK021973	234098_at	AK021973	---	---	-1,80	1,25E-03
AA682539	235575_at	AA682539	---	---	-1,80	5,79E-03
AI950023	244433_at	AI950023	---	---	-1,80	3,52E-03
C13orf22	1562238_at	AL832776	NM_005800	10208	-1,80	5,58E-04
AI828075	230795_at	AI828075	---	---	-1,79	7,39E-05
AW172407	240908_at	AW172407	XM_373053	391733	-1,79	1,54E-03
ARG2	203946_s_at	U75667	NM_001172	384	-1,79	8,38E-05
AI582773	214373_at	AI582773	XM_498956	440996	-1,79	6,73E-03
C1orf21	221272_s_at	NM_030806	NM_030806	81563	-1,79	1,58E-06
BF431902	228469_at	BF431902	---	---	-1,79	8,24E-03
AI732874	241314_at	AI732874	---	---	-1,79	6,26E-03
AI521273	241702_at	AI521273	---	---	-1,79	2,16E-03
SFXN3	220974_x_at	NM_030971	NM_030971	81855	-1,78	5,28E-05
AA394039	229720_at	AA394039	---	---	-1,78	3,12E-04
AI765607	244631_at	AI765607	XM_374318	389834	-1,78	7,00E-03
PHACTR1	238297_at	AI884781	NM_030948	221692	-1,78	6,75E-03
BF000047	235736_at	BF000047	---	---	-1,78	2,66E-03
PPP1R7	1559054_a_at	BC027905	NM_002712	5510	-1,78	8,88E-04
SRP54	1557504_at	AI076351	NM_003136	6729	-1,77	3,30E-03

MLLT2	237006_at	AA703523	NM_005935	4299	-1,77	1,07E-03
KIAA1276	235288_at	AI627532	XM_039169	27146	-1,77	3,48E-04
LOC360030	1565804_at	AK025161	---	360030	-1,77	7,53E-03
PAQR6	219236_at	NM_024897	NM_024897 NM_198406	79957	-1,77	1,41E-03
KIAA2024	1566166_at	AL833423	NM_172070	130507	-1,77	1,09E-03
FLJ20152	218532_s_at	NM_019000	NM_019000	54463	-1,77	2,47E-03
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AI150690	228466_at	AI150690	---	---	-1,76	1,91E-03
AK098781	1560814_a_at	AK098781	---	---	-1,76	9,35E-06
FLJ11267	220216_at	NM_019607	NM_019607	56260	-1,76	2,56E-03
CPEB1	219578_s_at	NM_030594	NM_030594	64506	-1,76	3,75E-03
NIT1	202891_at	NM_005600	NM_005600	4817	-1,76	4,55E-04
ZDHHC11	221646_s_at	AF267859	NM_024786	79844	-1,76	1,39E-04
LASS5	1556783_a_at	AF088003	NM_147190	91012	-1,76	4,78E-03
FLJ13231	1562387_at	BU189724	NM_023073	65250	-1,76	4,71E-03
GNRHR	1568661_at	BC039430	NM_000406	2798	-1,76	1,78E-03
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PHLDA2	209803_s_at	AF001294	NM_003311	7262	-1,75	1,03E-03
GRM3	240004_at	BF436080	NM_000840	2913	-1,74	5,05E-03
ABI1	238563_at	AV762916	NM_005470	10006	-1,74	2,03E-03
RAB11FIP3	1563104_at	BC009036	NM_014700	9727	-1,74	2,52E-03
C6orf52	236504_x_at	BE670432	XM_371798	347744	-1,74	5,49E-03
AV658469	244699_at	AV658469	---	---	-1,74	6,93E-07
PLXNC1	206470_at	NM_005761	NM_005761	10154	-1,74	1,25E-03
NTNG2	233072_at	AI348745	NM_032536	84628	-1,74	2,30E-03
AMH	206516_at	NM_000479	NM_000479	268	-1,73	4,35E-04
AI814750	1565692_at	AI814750	---	---	-1,73	7,35E-03

NAG8	210109_at	AF181492	NM_014411	27099	-1,73	8,58E-04
PLXNC1	206471_s_at	NM_005761	NM_005761	10154	-1,73	1,82E-03
LOC283861	1554520_at	BC009860	---	283861	-1,73	1,36E-03
HNRPM	230392_at	AW298141	NM_005968 NM_031203	4670	-1,72	2,74E-04
AI802997	235211_at	AI802997	---	---	-1,72	4,84E-03
APOC1	204416_x_at	NM_001645	NM_001645	341	-1,72	7,65E-05
ADCY1	213245_at	AL120173	NM_021116	107	-1,71	4,24E-03
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B3GNT5	225612_s_at	BE672260	NM_032047	84002	-1,71	9,32E-03
ANK2	202920_at	BF726212	NM_001148 NM_020977	287	-1,71	6,21E-03
TTC3	1569472_s_at	BC026260	NM_001001894 NM_003316	7267	-1,71	1,33E-03
HSPD1	241716_at	BF965447	NM_002156 NM_199440	3329	-1,71	1,25E-04
RHOU	223168_at	AL096776	NM_021205	58480	-1,71	1,77E-05
AI733281	239994_at	AI733281	---	---	-1,71	1,76E-03
BC015455	1569724_at	BC015455	---	---	-1,71	1,78E-04
RGS16	209324_s_at	BF304996	NM_002928	6004	-1,71	4,44E-03
LOC285535	229130_at	AU145323	---	285535	-1,71	3,49E-03
PDIP	206691_s_at	NM_006849	NM_006849	64714	-1,71	2,28E-08
BE221330	241624_at	BE221330	XM_374318	389834	-1,71	4,44E-03
BF434212	237942_at	BF434212	---	---	-1,71	2,50E-03
FLJ14966	243611_at	BG231646	NM_032867	84953	-1,71	4,23E-03
MGC10850	223707_at	BC004284	---	84736	-1,71	9,45E-04
H15900	239833_at	H15900	---	---	-1,71	4,92E-05
SPPL3	1566897_at	AL834399	NM_139015	121665	-1,71	1,54E-04
LOC256273	229466_at	AU144187	---	256273	-1,70	7,69E-03
AI288679	242969_at	AI288679	---	---	-1,70	1,70E-04

LOC400988	230941_at	AI651340	XM_379112	400988	-1,70	2,26E-05
MYO15B	227743_at	AI671062	XR_000222	80022	-1,70	5,37E-03
FLJ10159	229034_at	BF511724	---	55084	-1,70	1,89E-03
ZNF42	40569_at	M58297	NM_003422 NM_198055	7593	-1,70	8,99E-05
TMP21	238886_at	BF056141	NM_006827	10972	-1,70	3,75E-03
CAMK2B	209956_s_at	U23460	NM_001220 NM_172078 NM_172079 NM_172080 NM_172081 NM_172082 NM_172083 NM_172084	816	-1,69	2,99E-03
SCFD1	233229_at	AU147042	NM_016106 NM_182835	23256	-1,69	1,27E-04
ERMAP	219905_at	NM_018538	NM_018538	114625	-1,69	9,14E-06
AI190292	240190_at	AI190292	---	---	-1,69	6,34E-04
VEGF	210512_s_at	AF022375	NM_003376	7422	-1,69	7,38E-04
DNAJB11	223054_at	BC001144	NM_016306	51726	-1,69	6,40E-03
LOC401320	239313_at	AI803568	XM_379482 XM_380098	401320	-1,69	6,47E-03
AL359574	234588_at	AL359574	---	---	-1,68	5,27E-03
GOPC	236862_at	AA279958	NM_020399	57120	-1,68	4,91E-05
MAP3K5	203836_s_at	D84476	NM_005923	4217	-1,68	3,70E-04
AW118878	230736_at	AW118878	XM_373451	387647	-1,68	2,03E-04
SLC7A1	215401_at	AU147698	NM_003045	6541	-1,68	3,38E-03
PDE4DIP	244511_at	AV700591	NM_001002810 NM_001002811 NM_001002812 NM_014644 NM_022359	9659	-1,68	1,87E-04
BLCAP	1557521_a_at	AA653638	NM_006698	10904	-1,68	7,83E-03

PNCK	229411_at	AI986390	NM_198452	139728	-1,68	1,49E-08
TUSC3	232770_at	AK026149	NM_006765 NM_178234	7991	-1,67	3,31E-04
FBXW7	222729_at	BE551877	NM_018315 NM_033632	55294	-1,67	6,18E-06
DKFZP564O0463	220843_s_at	NM_014156	NM_015420	25879	-1,67	4,38E-03
FYN	243006_at	BG222258	NM_002037 NM_153047 NM_153048	2534	-1,67	1,63E-03
PDGFA	205463_s_at	NM_002607	---	5154	-1,67	1,01E-03
ST7L	216123_x_at	AK024158	NM_017744 NM_138727 NM_138728 NM_138729 NM_198327 NM_198328	54879	-1,67	2,23E-03
ZNF42	204138_s_at	AI762174	NM_003422 NM_198055	7593	-1,67	1,08E-03
FNBP1	239453_at	AA262084	NM_015033	23048	-1,67	5,15E-04
GNAS	214157_at	AA401492	NM_000516 NM_016592 NM_080425 NM_080426	2778	-1,67	1,44E-03
BRD4	232551_at	AA521443	NM_014299 NM_058243	23476	-1,67	8,62E-04
FLJ10287	232489_at	AK001149	NM_019083	54482	-1,67	4,17E-03
TRIM2	214249_at	AK000179	NM_015271	23321	-1,66	3,49E-03
AK021423	232890_at	AK021423	---	---	-1,66	1,20E-03
FARSLB	223036_at	D84430	NM_005687	10056	-1,66	2,56E-03
BE891071	1569147_at	BE891071	XM_496749	441078	-1,66	2,82E-03
PRKACB	235780_at	BE622723	NM_002731 NM_182948 NM_207578	5567	-1,66	3,63E-04
SLC35D3	231341_at	BE670584	NM_001008783	340146	-1,66	8,93E-03
N92599	241421_at	N92599	---	---	-1,66	2,32E-03

DR1	227074_at	AA524669	NM_001938	1810	-1,66	1,72E-03
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SLCO1A2	207308_at	NM_021094	NM_005075 NM_021094 NM_134431	6579	-1,65	5,88E-03
HNRPD	236000_s_at	AA863112	NM_001003810 NM_002138 NM_031369 NM_031370	3184	-1,65	1,29E-03
LOC54103	222150_s_at	AK026747	XM_379881 XM_499340	54103	-1,65	2,42E-03
RORA	1562529_s_at	BC040965	NM_002943 NM_134260 NM_134261 NM_134262	6095	-1,65	6,52E-04
AFFX-HUMRGE/M10098_M	AFFX-HUMRGE/M10098_M_at	AFFX-HUMRGE/M10098_M	---	---	-1,65	3,90E-03
FLJ44968	229961_x_at	AI871270	NM_198537	374887	-1,65	6,71E-04
ARIH1	1558710_at	BI791845	NM_005744	25820	-1,64	1,02E-03
GPX7	213170_at	AA406605	NM_015696	2882	-1,64	8,64E-04
ERBB4	206794_at	NM_005235	NM_005235	2066	-1,64	1,93E-05
LOC57228	209679_s_at	BC003379	NM_020467	57228	-1,64	4,85E-04
UBE2D3	233303_at	AL110175	NM_003340 NM_181886 NM_181887 NM_181888 NM_181889 NM_181890 NM_181891 NM_181892 NM_181893	7323	-1,64	3,36E-03
AK000995	215349_at	AK000995	---	---	-1,64	4,56E-03
N70015	236510_at	N70015	---	---	-1,64	1,10E-03
BC031957	1565672_at	BC031957	XM_498823	440703	-1,63	8,75E-03
FLJ36674	228482_at	AV702789	NM_173622	284040	-1,63	1,14E-03
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AU153281	231937_at	AU153281	---	---	-1,63	1,84E-05
AI807627	239734_at	AI807627	---	---	-1,63	1,25E-03
SLC4A3	205918_at	NM_005070	NM_005070 NM_201574	6508	-1,63	6,65E-04
NME5	206197_at	NM_003551	NM_003551	8382	-1,63	2,24E-03
RGS16	209325_s_at	U94829	NM_002928	6004	-1,63	8,91E-03
H46176	237083_at	H46176	---	---	-1,62	2,84E-04
CDKN2A	207039_at	NM_000077	NM_000077 NM_058195 NM_058197	1029	-1,62	4,13E-03
GLT25D2	209883_at	AF288389	NM_015101	23127	-1,62	6,05E-05
BF002625	229530_at	BF002625	---	---	-1,62	1,45E-03
RIPK1	209941_at	U50062	NM_003804	8737	-1,62	6,97E-05
FLJ45880	228538_at	BE671164	NM_207404	389114	-1,62	5,47E-06
LOC286161	228615_at	AW291761	---	286161	-1,62	3,70E-03
FLJ32096	1555870_at	AK056658	NM_173795	148646	-1,62	9,30E-03
NUP54	215213_at	AU146949	NM_017426	53371	-1,61	3,52E-07
DKFZp313N0621	1555906_s_at	AI147556	NM_173828	285343	-1,61	1,21E-04
GOLGIN-67	213650_at	AW006438	NM_015003 NM_181076 NM_181077	23015	-1,61	4,39E-03
AHI1	221569_at	AL136797	NM_017651	54806	-1,61	1,18E-03
PLXNC1	213241_at	AF035307	NM_005761	10154	-1,61	1,31E-03
AMY2A	208498_s_at	NM_004038	NM_000699	279	-1,61	1,12E-05
C9orf41	1564690_at	BC022435	NM_152420	138199	-1,60	3,52E-05
MGC29898	235259_at	AA398590	NM_145048	133015	-1,60	1,34E-04
AV700050	228835_at	AV700050	---	---	-1,60	3,88E-05
LGALS3BP	200923_at	NM_005567	NM_005567	3959	-1,60	1,65E-06
CRYZL1	243091_at	BF435599	NM_005111 NM_145311 NM_145858	9946	-1,60	1,91E-03

ZDHHC11	1552283_s_at	NM_024786	NM_024786	79844	-1,60	2,31E-05
CENTG2	233225_at	AK000798	NM_014914	116987	-1,59	6,55E-03
CLCN3	240237_at	H23230	NM_001829 NM_173872	1182	-1,59	6,03E-03
WASL	216094_at	AK025323	NM_003941	8976	-1,59	7,27E-03
CDK3	229468_at	AI885421	NM_001258	1018	-1,59	7,50E-06
PRKWNK1	216022_at	AL049278	NM_018979	65125	-1,59	2,19E-03
CALR	214315_x_at	AI348935	NM_004343	811	-1,59	3,10E-03
NM_018289	219794_at	NM_018289	---	---	-1,59	2,26E-07
LOC392790	243171_at	AA570178	XM_374751	392790	-1,58	5,98E-03
AA166617	230198_at	AA166617	---	---	-1,58	3,03E-03
TP53BP1	1569098_s_at	BU508386	NM_005657	7158	-1,58	5,76E-04
C21orf66	240105_at	AI021902	NM_013329 NM_016631 NM_058191 NM_145328	94104	-1,58	4,09E-03
BC014200	1570061_at	BC014200	---	---	-1,58	7,06E-05
KIAA1045	213636_at	AB028968	XM_048592	23349	-1,57	2,94E-03
AK024175	222152_at	AK024175	XM_373053	391733	-1,57	8,76E-03
DDHD1	231165_at	BE857355	NM_030637	80821	-1,57	1,47E-03
DNAH5	243938_x_at	AI872645	NM_001369	1767	-1,57	4,06E-03
LSS	211018_at	D63807	NM_00100143 8 NM_002340	4047	-1,57	2,49E-03
BC026294	1569510_at	BC026294	---	---	-1,57	3,20E-06
FLJ32954	235349_at	AI261321	NM_144713	151393	-1,57	7,97E-05
ISG20	33304_at	U88964	NM_002201	3669	-1,56	1,82E-03
GPR89	1562412_at	BC020562	NM_016334	51463	-1,56	5,13E-05
AL122039	234260_at	AL122039	---	---	-1,56	3,46E-03
ARSD	225280_x_at	N51673	NM_001669 NM_009589	414	-1,56	3,54E-03
MKLN1	233219_at	AK023427	NM_013255	4289	-1,56	7,04E-03

LOC91526	228471_at	AA744636	NM_153697	91526	-1,56	1,49E-03
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FLJ12666	215029_at	AL117451	NM_024595	79647	-1,56	2,57E-03
BF512871	240174_at	BF512871	XM_373962	388903	-1,55	2,49E-04
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AI271434	243668_at	AI271434	---	---	-1,55	7,05E-03
CCPG1	221511_x_at	AB033080	NM_004748 NM_020739	9236	-1,55	8,33E-03
ENOSF1	204143_s_at	NM_017512	NM_017512	55556	-1,55	5,87E-03
ARG2	203945_at	NM_001172	NM_001172	384	-1,55	3,00E-03
AA583038	238498_at	AA583038	---	---	-1,55	5,09E-04
BG548427	235547_at	BG548427	---	---	-1,55	1,16E-03
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LOC286208	1560089_at	AL833509	XM_379668	286208	-1,54	2,16E-03
AA504346	242170_at	AA504346	---	---	-1,54	7,12E-03
T77543	237530_at	T77543	---	---	-1,54	9,66E-04
MLSTD1	1557224_at	BM682057	NM_018099	55711	-1,54	4,35E-03
SIGIRR	52940_at	AA085764	NM_021805	59307	-1,54	4,74E-03
T91323	241093_at	T91323	NM_015129 NM_145799 NM_145800 NM_145802	23157	-1,54	8,22E-03
GRM8	1556800_a_at	BC041397	NM_000845	2918	-1,54	5,54E-05
ILK	235906_at	BE962235	NM_004517	3611	-1,54	5,88E-04
LOC284408	1558809_s_at	AK094324	---	284408	-1,53	2,05E-03
PTPN23	1569104_a_at	BE646227	NM_015466	25930	-1,53	9,23E-04
N36832	226396_at	N36832	---	---	-1,53	1,87E-03
CALR	212953_x_at	BE251303	NM_004343	811	-1,53	1,01E-03
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KLF6	211610_at	U51869	NM_00100849 0 NM_001300	1316	-1,53	7,45E-04
TTC17	232323_s_at	AK026217	NM_018259	55761	-1,53	2,27E-05
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AK024879	216751_at	AK024879	---	---	-1,53	7,76E-03
WDFY3	238660_at	AI732512	NM_014991 NM_178583 NM_178585	23001	-1,53	4,22E-05
FLJ20719	230712_at	AI634549	XM_373827	55672	-1,52	3,20E-03
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LOC440078	1570397_x_at	BC034777	XM_498534	440078	-1,52	1,46E-03
BLZF1	1558560_s_at	AI002966	NM_003666	8548	-1,51	3,05E-08
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EVER1	204328_at	NM_007267	NM_007267	11322	-1,51	7,60E-03
LOC285989	235231_at	AI355709	NM_213603	285989	-1,51	9,23E-03
AW665096	214188_at	AW665096	---	---	-1,51	1,36E-03
LTBP3	219922_s_at	NM_021070	NM_021070	4054	-1,51	8,21E-06
H2BFS	208579_x_at	NM_017445	NM_017445	54145	-1,51	3,28E-04
PGAP1	220576_at	NM_024989	NM_024989	80055	-1,51	4,78E-04
ACTN4	232058_at	AU158358	NM_004924	81	-1,51	6,69E-03
FGD5	226984_at	H09596	NM_152536	152273	-1,50	8,21E-03
HPCAL4	219671_at	AL136591	NM_016257	51440	-1,50	7,58E-05
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RBM25	1557081_at	AA580691	NM_021239	58517	-1,50	1,01E-03
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AW241864	214353_at	AW241864	---	---	-1,49	4,23E-03
PTPRN	204945_at	NM_002846	NM_002846	5798	-1,49	4,07E-04
N75937	240072_at	N75937	---	---	-1,49	2,94E-03
FLJ10404	243047_at	AV698751	NM_019057	54540	-1,48	2,74E-03
LOC400729 LOC440745	243021_at	AI344101	XM_378824 XM_498840	400729 440745	-1,48	9,58E-03
AV709727	225996_at	AV709727	---	---	-1,48	1,09E-03
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AU146999	215986_at	AU146999	---	---	-1,48	7,62E-05
MAP3K5	203837_at	NM_005923	NM_005923	4217	-1,48	5,81E-04
AW300500	228907_at	AW300500	---	---	-1,48	3,51E-04
SORCS1	228194_s_at	AI675836	NM_052918	114815	-1,48	9,87E-06
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CDK3	207188_at	NM_001258	NM_001258	1018	-1,48	1,93E-05
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PRKACB	202741_at	AA130247	NM_002731 NM_182948 NM_207578	5567	-1,47	3,58E-03
AA868193	244031_at	AA868193	---	---	-1,47	1,71E-03
RCN1	201063_at	NM_002901	NM_002901	5954	-1,47	7,39E-03
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HIAT1	242374_at	AA747563	NM_033055	64645	-1,47	2,87E-03
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BG396868	1559957_a_at	BG396868	---	---	-1,47	8,59E-04
SMURF2	241900_at	AW195928	NM_022739	64750	-1,47	3,53E-05
SERP1	235475_at	AI580135	NM_014445	27230	-1,47	1,72E-03
BF347758	240222_at	BF347758	---	---	-1,47	2,67E-04
CAMK2B	210404_x_at	AF078803	NM_001220 NM_172078 NM_172079 NM_172080 NM_172081 NM_172082 NM_172083 NM_172084	816	-1,47	1,61E-03
MYO9A	242512_at	AI382029	NM_006901	4649	-1,47	5,15E-03
AKNA	225701_at	AK024431	NM_030767	80709	-1,47	5,81E-03
GPM6B	240286_at	AL041745	NM_001001994 NM_001001995 NM_001001996 NM_005278	2824	-1,46	1,79E-03
STK4	223746_at	BC005231	NM_006282	6789	-1,46	1,31E-04
BG178274	214757_at	BG178274	---	---	-1,46	2,61E-04
AW015870	240352_at	AW015870	---	---	-1,46	3,79E-05

C21orf66	239407_at	AI793248	NM_013329 NM_016631 NM_058191 NM_145328	94104	-1,46	4,76E-03
KIN	236887_at	AA768850	NM_012311	22944	-1,46	5,23E-03
PCNXL2	229202_at	AI768826	NM_014801 NM_024938	80003	-1,46	6,03E-04
KCNQ2	205737_at	NM_004518	NM_004518 NM_172106 NM_172107 NM_172108 NM_172109	3785	-1,46	2,13E-04
C2orf17	222129_at	AK026155	NM_024293	79137	-1,46	1,21E-03
FBXW7	218751_s_at	NM_018315	NM_018315 NM_033632	55294	-1,46	1,23E-07
U20648	216677_at	U20648	---	---	-1,46	7,32E-05
AGPAT3	223184_s_at	BC004219	NM_020132	56894	-1,46	2,96E-03
ACYP2	206833_s_at	NM_001108	NM_138448	98	-1,46	1,16E-04
TTC17	224852_at	BE964325	NM_018259	55761	-1,46	6,04E-05
FLJ10159	218974_at	NM_018013	---	55084	-1,46	5,54E-04
ZNF160	239954_at	AA701249	NM_033288 NM_198893	90338	-1,46	7,17E-03
SRP54	1557505_a_at	AI076351	NM_003136	6729	-1,45	1,01E-03
AK023798	216838_at	AK023798	---	---	-1,45	5,04E-04
HMGB2	243368_at	AI572938	NM_002129	3148	-1,45	8,71E-03
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DKFZp313N0621	226688_at	AW003508	NM_173826	285343	-1,45	6,50E-03
GUCY1A3	221942_s_at	AI719730	NM_000856	2982	-1,45	5,82E-05
LISCH7	208190_s_at	NM_015925	NM_015925 NM_205834 NM_205835	51599	-1,45	2,12E-03
AI140531	1557812_a_at	AI140531	---	---	-1,45	6,90E-03
KIAA1276	227505_at	N64630	XM_039169	27146	-1,45	1,75E-03

BC040287	1558605_at	BC040287	---	---	-1,44	4,22E-03
AI800713	235122_at	AI800713	---	---	-1,44	3,58E-04
BC033530	1560209_at	BC033530	---	---	-1,44	1,67E-03
HLCS	207833_s_at	NM_000411	NM_000411	3141	-1,44	7,21E-03
MCF2L	239636_at	W74618	NM_024979	23263	-1,44	1,41E-03
KIAA1276	233823_at	AB033102	XM_039169	27146	-1,44	3,24E-04
OR7D2	1562337_at	AK095468	NM_175883	162998	-1,44	7,48E-04
JAK2	1562031_at	BC043187	NM_004972	3717	-1,44	4,16E-04
PSMB7	244801_at	AI248671	NM_002799	5695	-1,44	4,98E-03
KIAA1411	233730_at	AL078591	NM_020819	57579	-1,43	3,20E-05
AL530703	231882_at	AL530703	XM_498570	440156	-1,43	5,81E-04
FLJ32731	227564_at	BF433005	XM_372038	138050	-1,43	7,92E-05
DUSP16	1563505_at	AL833073	NM_030640	80824	-1,43	4,10E-05
MGC4171	219722_s_at	NM_024307	NM_024307	79153	-1,43	5,72E-03
RGAG4	227823_at	BE348679	XM_291322	340526	-1,43	3,08E-05
MGC15875	226783_at	AI762154	NM_032921 NM_153373	85007	-1,43	1,81E-03
FIP1L1	233405_at	AU155384	NM_030917	81608	-1,43	3,48E-03
PKD1	202328_s_at	NM_000296	NM_000296 NM_00100994 4	5310	-1,43	1,82E-04
CRYGS	223643_at	AI762135	NM_017541	1427	-1,43	5,80E-03
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OFD1	241751_at	AW292752	NM_003611	8481	-1,42	4,86E-03
PHC3	233431_x_at	AU148142	NM_024947	80012	-1,42	1,22E-03
AK022100	233406_at	AK022100	---	---	-1,42	1,03E-03
PPARG	208510_s_at	NM_015869	NM_005037 NM_015869 NM_138711 NM_138712	5468	-1,42	1,45E-03
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WDR45	209217_s_at	BC000464	NM_007075	11152	-1,42	3,54E-03
BF512190	235406_x_at	BF512190	---	---	-1,41	1,37E-03
BE738279	242546_at	BE738279	XM_498570	440156	-1,41	1,24E-03
AI929077	244818_at	AI929077	---	---	-1,41	2,46E-03
T96555	243818_at	T96555	---	---	-1,41	1,37E-03
DUSP16	1558739_at	R30807	NM_030640	80824	-1,41	3,84E-04
LOC389087	243647_at	AI808306	XM_374028	389087	-1,41	9,78E-03
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AU155234	233289_at	AU155234	---	---	-1,41	2,99E-03
AI698684	1558626_at	AI698684	---	---	-1,40	3,33E-04
KIAA1102	1569208_a_at	BC020895	NM_014988	22998	-1,40	4,93E-03
AW150212	1556038_at	AW150212	---	---	-1,40	1,33E-03
ABCC5	226363_at	BE550362	NM_005688	10057	-1,40	4,83E-05
FLJ13105	233083_at	AV706915	XM_496701	80068	-1,40	1,72E-03
AI963605	230269_at	AI963605	---	---	-1,40	1,31E-03
ACHE	205377_s_at	AI190022	NM_000665 NM_015831	43	-1,40	2,24E-04
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ZNF596	240324_at	H50654	NM_173539	169270	-1,39	3,41E-04
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TSGA10	1555932_at	AK094208	NM_025244 NM_182911	80705	-1,38	2,99E-03
MST1	216320_x_at	U37055	NM_020998	4485	-1,38	1,28E-03
LOC440722	238503_at	AI142850	XM_498831	440722	-1,38	8,92E-04
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SMG1 KIAA0220 LOC440345	244766_at	BG180003	NM_014006 NM_015092 XM_496125	23049 283846 440345	-1,38	8,25E-03
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VPS13C	232386_at	AV703288	NM_017684	54832	-1,38	1,41E-04
ZNF42	210336_x_at	AF055078	NM_003422 NM_198055	7593	-1,38	7,52E-05
MCCC2	1560033_at	AK090834	NM_022132	64087	-1,37	6,91E-05
USP40	225089_at	AA127740	NM_018218	55230	-1,37	9,95E-03
ZNF589	1569108_a_at	BC028160	NM_016089	51385	-1,37	3,43E-03
CITED2	207980_s_at	NM_006079	NM_006079	10370	-1,37	6,11E-03
GAL	214240_at	AL556409	NM_015973	51083	-1,37	2,81E-03
RAGE	205130_at	NM_014226	NM_014226	5891	-1,37	8,58E-03
AA516469	236375_at	AA516469	---	---	-1,37	2,01E-03
AI915861	1557348_at	AI915861	---	---	-1,37	7,72E-04
AI861893	242888_at	AI861893	---	---	-1,37	5,02E-03
EDNRA	243555_at	AA573452	NM_001957	1909	-1,37	2,53E-03
C14orf92	232097_at	AA657818	NM_014828	9878	-1,37	1,70E-03
LOC92482	232885_at	AK021501	XM_378250	92482	-1,37	7,03E-04
KIAA0999	242920_at	AW590838	NM_025164	23387	-1,37	7,90E-03
KCNK12	220448_at	NM_022055	NM_022055	56660	-1,37	2,31E-05

TGFB1I4	237745_at	BE670165	NM_006022 NM_183422	8848	-1,37	1,15E-03
CDC2L5	242693_at	AW664859	NM_003718 NM_031267	8621	-1,37	7,67E-03
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BRUNOL5	232416_at	AL390161	NM_021938	60680	-1,36	9,03E-03
AKAP12	210517_s_at	AB003476	NM_005100 NM_144497	9590	-1,36	3,29E-03
RGS12	1555022_at	AF464736	NM_002926 NM_198227 NM_198229 NM_198230 NM_198430 NM_198432 NM_198587	6002	-1,36	1,77E-05
LOC401320	238540_at	AA933883	XM_379482 XM_380098	401320	-1,36	1,06E-04
CUL4A	232466_at	AU155661	NM_001008895 NM_003589	8451	-1,36	5,42E-03
SENP6	240016_at	AW273732	NM_015571	26054	-1,36	2,45E-03
NBR2	1553992_s_at	BC034248	NM_005821	10230	-1,36	5,37E-03
TBC1D8	221592_at	BC001663	NM_007063	11138	-1,36	4,54E-03
MBNL1	1556658_a_at	AA744622	NM_021038 NM_207292 NM_207293 NM_207294 NM_207295 NM_207296 NM_207297	4154	-1,35	6,66E-03
HIST2H2AA	218280_x_at	NM_003516	NM_003516	8337	-1,35	5,61E-04
HECTD1	242349_at	AW275658	NM_015382	25831	-1,35	3,14E-05
CSGlcA-T	221799_at	AB037823	NM_019015	54480	-1,35	9,13E-03
TD-60	243297_at	AI498610	NM_018715	55920	-1,35	3,64E-05
AW117322	239415_at	AW117322	XM_374094	389237	-1,35	5,46E-05
ERCC3	215545_at	AK024185	NM_000122	2071	-1,35	7,55E-03

AW148862	235217_at	AW148862	XM_380136	402582	-1,35	8,44E-03
NAP1L3	204749_at	NM_004538	NM_004538	4675	-1,35	1,79E-04
HIST1H2BD	222067_x_at	AL353759	NM_021063 NM_138720	3017	-1,34	1,71E-05
CITED2	209357_at	AF109161	NM_006079	10370	-1,34	3,87E-03
NM_024914	220450_at	NM_024914	---	---	-1,34	5,65E-04
USP36	220370_s_at	NM_025090	NM_025090	57602	-1,34	2,56E-03
ARMCX4	1564399_a_at	AK096955	NM_152583	158947	-1,34	8,99E-04
GOLGA4	215203_at	AW438464	NM_002078	2803	-1,34	1,95E-03
R92984	231088_at	R92984	---	---	-1,34	4,79E-04
LOC200030 LOC400781 AG1	242191_at	AI701905	NM_183372 XM_371384 XM_378897 XM_496394	200030 400781 440673	-1,34	1,70E-03
USP40	225085_at	AA522888	NM_018218	55230	-1,34	5,51E-03
AK026429	233038_at	AK026429	---	---	-1,34	8,07E-03
AW977516	235172_at	AW977516	---	---	-1,33	1,91E-03
AK023334	232975_at	AK023334	---	---	-1,33	3,06E-03
CPSF6	238651_at	BF512491	NM_007007	11052	-1,33	2,21E-03
LOC158301	239193_at	BF060981	---	158301	-1,33	9,50E-03
TJP2	232017_at	AK025185	NM_004817 NM_201629	9414	-1,33	4,30E-04
AW591282	231374_at	AW591282	---	---	-1,33	1,30E-04
C21orf2	203995_at	NM_004928	NM_004928	755	-1,33	2,28E-03
BF063821	230598_at	BF063821	---	---	-1,33	2,29E-03
AI743452	237031_at	AI743452	---	---	-1,33	6,25E-04
AI825068	239798_at	AI825068	---	---	-1,33	7,63E-03
SYVN1	225090_at	AA844682	NM_032431 NM_172230	84447	-1,32	5,82E-03
FLJ32731	1557064_s_at	AW328331	XM_372038	138050	-1,32	3,89E-06
SLC12A7	218066_at	NM_006598	NM_006598	10723	-1,32	7,75E-04

UBE2Q	231816_s_at	AI986085	NM_017582	55585	-1,32	6,59E-03
GOLGIN-67	208797_s_at	AI829170	NM_015003 NM_181076 NM_181077	23015	-1,32	1,73E-04
THRAP2	239561_at	AA780679	NM_015335	23389	-1,32	1,91E-03
PCDHB16	232099_at	AB046841	NM_020957	57717	-1,32	2,25E-03
GPR123	239221_at	AI884909	NM_032422	84435	-1,31	2,84E-03
C1orf21	223127_s_at	AW003850	NM_030806	81563	-1,31	8,71E-04
LOC54103	213142_x_at	AV700415	XM_379881 XM_499340	54103	-1,31	2,15E-03
LOC90408	1560081_at	AL702091	---	90408	-1,31	3,47E-04
HEMK1	1556092_s_at	BQ025558	NM_016173	51409	-1,31	2,82E-03
AW294192	228040_at	AW294192	---	---	-1,31	1,56E-03
ZNF207	1556035_s_at	AI201248	NM_003457	7756	-1,31	6,92E-03
BU680365	1562497_at	BU680365	---	---	-1,31	9,25E-03
MGC24132	1557991_at	AK057791	NM_152396	131965	-1,31	9,13E-04
CLCN3	201734_at	AI760629	NM_001829 NM_173872	1182	-1,31	2,96E-03
PPIB	200968_s_at	NM_000942	NM_000942	5479	-1,31	5,05E-03
MYNN	1566108_at	AK056483	NM_018657	55892	-1,31	3,79E-03
MFN1	236417_at	BE644770	NM_017927 NM_033540	55669	-1,31	5,74E-03
TTC17	224849_at	AK023161	NM_018259	55761	-1,31	2,03E-04
HNRPD	229434_at	AA865357	NM_00100381 0 NM_002138 NM_031369 NM_031370	3184	-1,30	4,38E-03
BE217923	228686_at	BE217923	---	---	-1,30	1,31E-04
WDR11	229694_at	BF062828	NM_018117	55717	-1,30	5,51E-03
AA703326	241863_x_at	AA703326	---	---	-1,30	3,55E-03
ZNF117	235408_x_at	AW058673	NM_024498	7670	-1,30	8,70E-03
COL5A1	212489_at	AI983428	NM_000093	1289	-1,30	8,41E-03

AKAP12	241679_at	AI672553	NM_005100 NM_144497	9590	-1,30	1,14E-03
DKFZp762K2 22	226822_at	AL512713	NM_020225	56977	-1,30	1,52E-04
PTBP2	236962_at	AA521018	NM_021190	58155	-1,30	3,82E-03
C7orf28B	215024_at	AK000993	NM_198097	221960	-1,29	6,75E-04
EFHC1	225656_at	AI564473	NM_018100	114327	-1,29	8,52E-03
KIAA1970	1568858_at	BC013247	NM_133451	124454	-1,29	1,47E-05
CAMK2B	211483_x_at	AF081924	NM_001220 NM_172078 NM_172079 NM_172080 NM_172081 NM_172082 NM_172083 NM_172084	816	-1,29	6,21E-03
LOC142678	226644_at	BE222279	NM_080875	142678	-1,29	4,59E-04
IGBP1	242337_at	AI347128	NM_001551	3476	-1,29	4,53E-03
MAP7	202890_at	AW242297	NM_003980	9053	-1,29	9,83E-04
AK3	230630_at	AI566130	NM_00100535 3 NM_013410 NM_203464	205	-1,29	3,77E-03
AI434790	239070_at	AI434790	---	---	-1,29	2,24E-04
CD302	203799_at	NM_014880	NM_014880	9936	-1,29	1,51E-04
VPS13C	218396_at	NM_017684	NM_017684	54832	-1,29	1,69E-04
CUL3	242362_at	AI797788	NM_003590	8452	-1,29	3,18E-03
AW971123	238446_at	AW971123	---	---	-1,28	3,31E-03
FLJ13150	219504_s_at	NM_024813	NM_024813	79871	-1,28	6,46E-06
EPAS1	230711_at	AA777349	NM_001430	2034	-1,28	7,58E-03
LOC91526	226641_at	AU157224	NM_153697	91526	-1,28	3,21E-03
AW467480	236202_at	AW467480	---	---	-1,28	1,77E-03
MTHFR	226929_at	AA524272	NM_005957	4524	-1,28	1,48E-04
MKLN1	1560145_at	BQ942131	NM_013255	4289	-1,28	4,90E-03

ZNF207	231848_x_at	AW192569	NM_003457	7756	-1,28	7,40E-03
AI796536	229810_at	AI796536	---	---	-1,28	5,96E-04
BF724558	241722_x_at	BF724558	---	---	-1,28	4,48E-03
AI825987	235889_at	AI825987	---	---	-1,27	2,27E-04
TXNDC4	208958_at	AI827677	NM_015051	23071	-1,27	7,53E-04
ADORA2B	205891_at	NM_000676	NM_000676	136	-1,27	7,80E-03
FLJ21159	220145_at	NM_024826	NM_024826	79884	-1,27	1,45E-05
WSB1	201294_s_at	N24643	NM_015626 NM_134264 NM_134265	26118	-1,27	4,68E-03
AK3	225342_at	AK026966	NM_001005353 NM_013410 NM_203464	205	-1,27	9,13E-03
PLCB4	203896_s_at	NM_000933	NM_000933 NM_182797	5332	-1,27	1,40E-04
RAPGEF2	215992_s_at	AL117397	XM_376350	9693	-1,27	1,92E-05
PDXK	218019_s_at	NM_021941	NM_003681	8566	-1,27	9,30E-03
DUSP16	224336_s_at	AB052156	NM_030640	80824	-1,27	3,94E-03
BACE2	222446_s_at	AF178532	NM_012105 NM_138991 NM_138992	25825	-1,27	4,30E-04
PUM2	216121_at	AL080106	NM_015317	23369	-1,27	1,02E-05
AVEN	219366_at	NM_020371	NM_020371	57099	-1,27	5,67E-03
NMB	205204_at	NM_021077	NM_021077 NM_205858	4828	-1,26	3,26E-05
EPOR	396_f_at	X97671	NM_000121	2057	-1,26	8,71E-04
CSRP1	200621_at	NM_004078	NM_004078	1465	-1,26	9,64E-03
MYT1L	1554633_a_at	AF036943	NM_015025	23040	-1,26	4,55E-03
TAPBP	208829_at	AF029750	NM_003190 NM_172208 NM_172209	6892	-1,26	8,92E-06
AI741597	230302_at	AI741597	---	---	-1,26	3,47E-03

C10orf10	209183_s_at	AL136653	NM_007021	11067	-1,26	1,25E-03
FLJ31951	236322_at	AA830854	NM_144726	153830	-1,26	1,23E-03
HERC4	225989_at	AB046813	NM_015601	26091	-1,26	1,35E-04
PTGS1	238669_at	BE613133	NM_000962 NM_080591	5742	-1,26	7,68E-05
GTPBP2	221050_s_at	NM_019096	NM_019096	54676	-1,26	5,82E-03
CNOT4	1559347_at	BI599409	NM_00100822 5 NM_013316	4850	-1,26	4,86E-03
BM914560	1558220_at	BM914560	XM_496669	440993	-1,26	9,16E-03
C6orf111	230375_at	AI936531	NM_032870	25957	-1,26	1,30E-03
WBSCR19	232964_at	AL137266	NM_175064	285955	-1,26	4,75E-04
AW104619	229754_at	AW104619	---	---	-1,26	3,59E-03
DISC1	244642_at	AI761381	NM_018662	27185	-1,26	7,13E-03
FLJ32130	1554770_x_at	BC040642	NM_152458	146540	-1,26	1,11E-03
AW192718	1559437_at	AW192718	XM_373180	392084	-1,25	5,77E-03
BC014318	1558236_at	BC014318	---	---	-1,25	1,70E-04
EVC	219432_at	NM_014556	NM_014556 NM_153717	2121	-1,25	3,41E-03
PPAPDC1	236044_at	BF130943	XM_113641	196051	-1,25	1,93E-04
AI732885	214388_at	AI732885	---	---	-1,25	1,01E-03
AI588962	230477_at	AI588962	---	---	-1,25	1,64E-04
HIST1H2BI	208523_x_at	NM_003525	NM_003525	8346	-1,25	1,67E-03
HRMT1L1	216069_at	AL050065	NM_001535 NM_206962	3275	-1,25	6,45E-05
DKFZP434I0 714	231954_at	AL137273	---	54553	-1,25	1,77E-03
ZNF654	219239_s_at	NM_018293	NM_018293	55279	-1,25	8,76E-04
BC035105	1569482_at	BC035105	---	---	-1,25	1,09E-03
ZFYVE16	240859_at	N20928	NM_014733	9765	-1,25	8,54E-03
AW303371	242096_at	AW303371	---	---	-1,25	8,48E-03

AK025360	216173_at	AK025360	---	---	-1,25	7,46E-03
LOC440157	1558139_at	BE730158	XM_495969	440157	-1,25	8,53E-03
MGC15407	224868_at	AL518311	NM_080667	112942	-1,25	1,67E-04
W18186	239842_x_at	W18186	---	---	-1,25	3,42E-04
FLJ32130	1554769_at	BC040642	NM_152458	146540	-1,25	1,81E-04
PER2	205251_at	NM_022817	NM_003894 NM_022817	8864	-1,25	4,90E-03
NOL3	221567_at	AF064599	NM_003946	8996	-1,25	1,02E-04
ORMDL1	228801_at	AI809749	NM_016467	94101	-1,25	1,54E-07
FLJ23825	1555866_a_at	BM980844	NM_173620	284004	-1,25	2,44E-03
ACRV1	207969_x_at	NM_020109	NM_001612 NM_020069 NM_020107 NM_020108 NM_020109 NM_020110 NM_020111 NM_020113 NM_020114 NM_020115	56	-1,24	3,48E-04
CHD5	213965_s_at	AL035406	NM_015557	26038	-1,24	1,51E-04
C17orf27	1569078_at	AF318359	NM_020914	57674	-1,24	4,95E-03
RAPGEF2	238176_at	T86196	XM_376350	9693	-1,24	9,33E-03
JMJD2B	1558448_a_at	BC032415	NM_015015	23030	-1,24	7,07E-03
SIPA1L2	1559489_s_at	BC006013	NM_020808	57568	-1,24	5,27E-03
AI018235	240314_at	AI018235	---	---	-1,24	4,83E-03
BC007626	1562946_at	BC007626	---	---	-1,24	5,88E-05
TIP120A	239771_at	BG399629	NM_018448	55832	-1,24	1,29E-03
BF507816	240517_at	BF507816	---	---	-1,24	6,12E-03
T79942	228465_at	T79942	---	---	-1,23	1,38E-03
RPIP8	206196_s_at	NM_006695	NM_006695	10900	-1,23	2,25E-03
SFRS12	243361_at	N51597	NM_139168	140890	-1,23	4,89E-03
FBXW7	229419_at	BF222826	NM_018315	55294	-1,23	3,99E-04

			NM_033632			
PRKCA	213093_at	AI471375	NM_002737	5578	-1,23	4,72E-04
AI042344	240121_x_at	AI042344	---	---	-1,23	3,31E-05
ABCA2	210100_s_at	AF327657	NM_001606 NM_212533	20	-1,23	2,95E-04
CHST1	205567_at	NM_003654	NM_003654	8534	-1,23	4,23E-03
GRIK2	1563754_at	AJ252246	NM_021956 NM_175768	2898	-1,23	1,60E-03
AI887898	228423_at	AI887898	XM_374094	389237	-1,23	7,61E-04
FADS3	204257_at	NM_021727	NM_021727	3995	-1,23	4,30E-04
BE551142	241091_at	BE551142	XM_497668	388620	-1,23	4,14E-03
BC014318	1558237_x_at	BC014318	---	---	-1,23	7,31E-04
TCEA1	1566207_at	BQ286789	NM_006756 NM_201437	6917	-1,23	9,86E-06
PLCE1	205111_s_at	NM_016341	NM_016341	51196	-1,23	4,76E-07
KIAA0125	220377_at	NM_014151	NM_014792	9834	-1,23	3,84E-04
PIK3C2A	241905_at	AA579047	NM_002645	5286	-1,22	8,81E-03
USP15	233473_x_at	AU156202	NM_006313	9958	-1,22	5,44E-03
DHX36	1559039_at	AK096808	NM_020865	170506	-1,22	5,13E-03
KIAA0368	236368_at	BF059292	XM_036708	23392	-1,22	1,71E-04
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ADAM8	205180_s_at	NM_001109	NM_001109	101	-1,22	7,63E-03
FGF7	230918_at	BE856598	NM_002009	2252	-1,22	1,18E-03
C21orf25	212875_s_at	AP001745	NM_199050	25966	-1,22	1,75E-03
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BF061976	243499_at	BF061976	---	---	-1,22	3,63E-03
RLF	204243_at	NM_012421	NM_012421	6018	-1,21	3,24E-05
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BE467577	228251_at	BE467577	---	---	-1,21	2,37E-03
WSB1	201295_s_at	BF111821	NM_015626 NM_134264 NM_134265	26118	-1,21	2,55E-03
PR47	1560526_at	BQ880034	---	266671	-1,21	4,02E-03
PRPH	213847_at	NM_006262	NM_006262	5630	-1,21	3,82E-03
H75391	1559515_at	H75391	---	---	-1,21	3,64E-04
AI740589	243515_at	AI740589	---	---	-1,21	7,40E-04
OLFM3	1554526_at	BC022531	NM_058170	118427	-1,21	1,84E-04
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AI631888	235532_at	AI631888	---	---	-1,21	1,03E-03
EXOC7	214802_at	AK022397	NM_015219	23265	-1,21	8,35E-03
SIPA1L2	225056_at	AB037810	NM_020808	57568	-1,20	7,73E-03
HSPC065	222890_at	BG054922	NM_014157	29070	-1,20	4,19E-03
IER3	201631_s_at	NM_003897	NM_003897 NM_052815	8870	-1,20	3,48E-04
BF059537	240020_at	BF059537	---	---	-1,20	2,65E-04
BE503598	1557659_a_at	BE503598	---	---	-1,20	1,58E-03
FLJ13710	222835_at	BG163478	NM_024817	79875	-1,20	8,19E-03
C14orf120	216263_s_at	AK022215	XM_033371	25983	-1,20	5,96E-07
FNBP1	212288_at	AB011126	NM_015033	23048	-1,20	9,04E-06
TTC11	244082_at	BF507959	NM_016068	51024	-1,20	7,10E-03
ABR	214671_s_at	L19704	NM_001092 NM_021962	29	-1,20	5,25E-03
ABTB1	229164_s_at	AI337369	NM_032548 NM_172027 NM_172028	80325	-1,20	3,15E-03
TRIM50C	1554182_at	BC033871	NM_198853	378108	-1,19	6,94E-05
ADAMTS1	222162_s_at	AK023795	NM_006988	9510	-1,19	1,75E-03
TIGD4	232998_at	AK024235	NM_145720	201798	-1,19	1,23E-04

KIAA0220	231989_s_at	AC003007	---	283846	-1,19	6,25E-03
AI435590	237192_at	AI435590	---	---	-1,19	7,36E-04
NOL3	59625_at	AI912351	NM_003946	8996	-1,19	4,25E-05
FOXR2	1569669_at	BM550294	NM_198451	139628	-1,19	6,60E-03
AW628665	235555_at	AW628665	---	---	-1,19	7,01E-03
LOC285831	228857_at	AA775731	---	285831	-1,19	2,24E-04
C15orf28	220710_at	NM_024970	---	80035	-1,19	7,83E-03
KIAA1967	240721_at	BE672858	NM_021174 NM_199205	57805	-1,19	4,55E-04
BRPF3	225217_s_at	AB033112	NM_015695	27154	-1,19	3,39E-04
PPP3CA	236545_at	AA532718	NM_000944	5530	-1,18	1,89E-03
BF514509	239050_s_at	BF514509	---	---	-1,18	8,62E-03
AA639707	243837_x_at	AA639707	---	---	-1,18	1,88E-04
WSB1	210561_s_at	AL110243	NM_015626 NM_134264 NM_134265	26118	-1,18	7,42E-04
AA888777	242740_at	AA888777	---	---	-1,18	1,23E-03
BMPR2	238393_at	AL047534	NM_001204 NM_033346	659	-1,18	5,95E-03
BACH2	1556451_at	AL833645	NM_021813	60468	-1,18	2,17E-04
CRELD1	203368_at	NM_015513	NM_015513	78987	-1,18	3,92E-03
RPL37	224766_at	AW008221	NM_000997	6167	-1,18	6,73E-06
CSTB	201201_at	NM_000100	NM_000100	1476	-1,18	2,39E-06
MGC12458	211200_s_at	BC002836	NM_032328	84288	-1,18	4,74E-03
C9orf111	228383_at	AK024443	NM_152286	375775	-1,18	4,27E-03
PLRG1	227246_at	BF438014	NM_002669	5356	-1,18	8,04E-04
ZFYVE9	208446_s_at	NM_007323	NM_004799 NM_007323 NM_007324	9372	-1,18	3,59E-03
ZNF226	224004_at	AF246126	NM_015919 NM_016444	7769	-1,17	2,52E-04
NM_015437	207799_x_at	NM_015437	---	---	-1,17	7,74E-04

AFTIPHILIN	244312_at	AW195572	NM_001002243 NM_017657 NM_203437	54812	-1,17	6,11E-03
AL137378	216144_at	AL137378	---	---	-1,17	1,87E-03
NUP153	239948_at	AA004800	NM_005124	9972	-1,17	4,63E-03
OLFM3	1554524_a_at	AF397394	NM_058170	118427	-1,17	4,35E-05
N30152	229850_at	N30152	---	---	-1,17	1,02E-03
AI934828	227116_at	AI934828	XM_375373	400547	-1,17	4,08E-03
LRRFIP2	230082_at	AW137053	NM_006309 NM_017724	9209	-1,17	1,78E-03
HPCAL1	212552_at	BE617588	NM_002149 NM_134421	3241	-1,17	1,73E-04
DRPLA	236961_at	AI539426	NM_001007026 NM_001940	1822	-1,17	2,23E-03
CLCN3	201732_s_at	AF029346	NM_001829 NM_173872	1182	-1,17	2,63E-03
RFX2	226872_at	AK024288	NM_000635 NM_134433	5990	-1,17	2,24E-03
HNRPD	235999_at	AA863112	NM_001003810 NM_002138 NM_031369 NM_031370	3184	-1,17	1,28E-04
WNK1	211993_at	AI768512	NM_018979	65125	-1,17	1,66E-03
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KIAA1040	242225_at	AI569482	NM_015026	23041	-1,17	5,75E-03
C9orf68	220218_at	NM_017985	NM_017985	55064	-1,16	4,90E-03
C21orf66	1555125_at	BC030539	NM_013329 NM_016631 NM_058191 NM_145328	94104	-1,16	3,17E-05
GAD2	243265_at	AW444497	NM_000818	2572	-1,16	1,34E-04

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CENTB2	240759_at	AW593931	NM_012287	23527	-1,16	5,67E-03
CAPN2	208683_at	M23254	NM_001748	824	-1,16	3,02E-04
TMEM5	204808_s_at	NM_014254	NM_014254	10329	-1,16	1,28E-04
HIST1H2BF	208490_x_at	NM_003522	NM_003522	8343	-1,16	7,03E-04
BCAP29	230150_at	N57499	NM_001008405 NM_001008406 NM_001008407 NM_018844	55973	-1,16	2,32E-03
PERLD1	55616_at	AI703342	NM_033419	93210	-1,16	4,41E-03
DTNA	227084_at	AW339310	NM_001390 NM_001391 NM_001392 NM_032975 NM_032978 NM_032979 NM_032980 NM_032981	1837	-1,16	3,40E-03
CHD9	220586_at	NM_025134	NM_025134	80205	-1,16	3,15E-03
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AI693178	228101_at	AI693178	---	---	-1,15	1,78E-06
ZNF587	242564_at	AI703142	NM_032828	84914	-1,15	8,15E-04
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AK3	204348_s_at	NM_013410	NM_001005353 NM_013410 NM_203464	205	-1,15	4,21E-03

EFNB3	205031_at	NM_001406	NM_001406	1949	-1,15	1,14E-04
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AI022648	242972_at	AI022648	---	---	-1,15	6,12E-03
AA651954	236626_at	AA651954	---	---	-1,14	1,11E-04
TAGLN2	200916_at	NM_003564	NM_003564	8407	-1,14	7,20E-03
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AKAP14	228493_at	T87628	NM_001008534 NM_001008535 NM_178813	158798	-1,14	3,57E-03
NEDD5	232637_at	AK025163	NM_001008491 NM_001008492 NM_004404 NM_006155	4735	-1,14	1,03E-04

COH1	236254_at	BE048857	NM_015243 NM_017890 NM_152564 NM_181661 NM_184042	157680	-1,14	9,97E-04
COLEC11	219873_at	NM_024027	NM_024027 NM_199235	78989	-1,14	2,80E-04
TMPIT	234084_x_at	AU147104	NM_031925	83862	-1,14	4,48E-03
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PDGFRB	202273_at	NM_002609	NM_002609	5159	-1,13	4,37E-03
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GNPTG	224887_at	AF302786	NM_032520	84572	-1,13	7,70E-05
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BF940997	239857_at	BF940997	---	---	-1,12	2,17E-03
SFRS11	237746_at	AI168187	NM_004768	9295	-1,12	3,42E-03
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ADAMTS20	220717_at	NM_025003	NM_025003 NM_175851	80070	-1,12	3,36E-03
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C1orf8	241018_at	BF446758	NM_004872	9528	-1,12	3,93E-03
CLTC	220855_at	NM_014127	NM_004859	1213	-1,11	8,87E-04
BC035773	1569665_at	BC035773	---	---	-1,11	8,41E-03
KDELR2	242725_at	BG026159	NM_006854	11014	-1,11	8,62E-03
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SIRT5	221010_s_at	NM_031244	NM_012241 NM_031244	23408	-1,11	4,63E-03
MAD	226275_at	AI188653	NM_002357	4084	-1,11	1,65E-03
ARSD	223695_s_at	BC003660	NM_001669 NM_009589	414	-1,11	8,01E-03
LOC284361	224727_at	AL045545	NM_175063 NM_206538	284361	-1,11	1,48E-03
DMPK	37996_s_at	L08835	NM_004409	1760	-1,11	9,75E-05
HCG8	215985_at	X92110	---	80869	-1,11	6,05E-03
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PLD3	201050_at	NM_012268	NM_012268	23646	-1,11	9,93E-04
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AA573901	227783_at	AA573901	---	---	-1,11	5,51E-04
PROX1	242119_at	AW451938	NM_002763	5629	-1,11	2,23E-03
AI862542	235696_at	AI862542	---	---	-1,11	2,47E-03
ZNF596	232641_at	AC004908	NM_173539	169270	-1,11	3,61E-03
GOLGIN-67	210424_s_at	AF163441	NM_015003 NM_181076 NM_181077	23015	-1,10	3,73E-04
JMY	226352_at	BF447037	NM_152405	133746	-1,10	1,15E-05
APXL2	239435_x_at	AA588854	NM_133456	134549	-1,10	2,97E-03
BC004287	223366_at	BC004287	---	---	-1,10	3,09E-03
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BF510762	230262_at	BF510762	---	---	-1,10	2,62E-04
AI741900	239140_at	AI741900	---	---	-1,10	7,72E-05
INADL	223681_s_at	AB044807	NM_005799 NM_170605 NM_176877 NM_176878	10207	-1,10	3,79E-04
PCDHB14	231726_at	NM_018934	NM_018934	56122	-1,10	7,91E-03
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NPIP	204538_x_at	NM_006985	NM_006985	9284	-1,10	2,65E-04
SR140	236696_at	BE464843	XM_031553	23350	-1,09	5,65E-03
CCNL2	221427_s_at	NM_030937	NM_030937	81669	-1,09	1,71E-03
GFRA3	214479_at	NM_001496	NM_001496	2676	-1,09	9,83E-03
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C20orf103	219463_at	NM_012261	NM_012261	24141	-1,09	5,61E-03
HERC1	240703_s_at	AW591969	NM_003922	8925	-1,09	1,25E-03

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AK023264	233068_at	AK023264	---	---	-1,08	5,48E-03
UBE2D3	230171_at	AW662789	NM_003340 NM_181886 NM_181887 NM_181888 NM_181889 NM_181890 NM_181891 NM_181892 NM_181893	7323	-1,08	3,01E-03
PRKCSH	200707_at	NM_002743	NM_00100132 9 NM_002743	5589	-1,08	1,56E-03
BRUNOL5	230497_at	BE503640	NM_021938	60680	-1,08	1,26E-03
FLJ35390	1558123_at	AK092709	---	255031	-1,08	6,65E-03
IPO9	225728_at	AI659533	NM_018085	55705	-1,08	2,88E-03
HNRPC	1568941_a_at	BC022884	NM_004500 NM_031314	3183	-1,08	3,18E-03
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LOC399491	215921_at	AC002544	---	399491	-1,08	2,25E-04
SMU1	228180_at	AA805653	NM_018225	55234	-1,08	3,97E-03
AKT2	236664_at	AA448167	NM_001626	208	-1,08	1,98E-03
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INADL	214705_at	AJ001306	NM_005799 NM_170605 NM_176877 NM_176878	10207	-1,08	9,90E-04
C9orf10OS	1558761_a_at	AK093641	NM_198841	158293	-1,08	2,09E-05
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AL390216	234317_s_at	AL390216	---	---	-1,07	4,32E-05
PLA2G4B	219095_at	NM_005090	NM_005090	8681	-1,07	7,70E-05
AF131844	222184_at	AF131844	---	---	-1,07	1,01E-03

AI939452	240892_at	AI939452	---	---	-1,07	2,32E-03
ANKHD1	229457_at	AU148042	NM_017747 NM_017978 NM_024668	54882	-1,07	1,15E-03
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AA033699	229111_at	AA033699	---	---	-1,07	9,78E-03
GOLGIN-67	208798_x_at	AF204231	NM_015003 NM_181076 NM_181077	23015	-1,07	8,11E-04
SYNE1	209447_at	AF043290	NM_015293 NM_033071 NM_133650 NM_182961	23345	-1,07	2,21E-03
AL080112	216858_x_at	AL080112	---	---	-1,07	8,82E-03
MAP7	215471_s_at	AJ242502	NM_003980	9053	-1,07	7,77E-04
BC025319	1568974_at	BC025319	---	---	-1,06	9,12E-03
DJ328E19.C1 .1 LOC200030 MGC8902 LOC401967 AG1	214693_x_at	BE732345	NM_015383 NM_173638 NM_183372 XM_371384 XM_496394 XM_496406	200030 25832 284565 401967 440673	-1,06	3,98E-04
PIGF	239258_at	BE551407	NM_002643 NM_173074	5281	-1,06	3,15E-04
NPIP LOC339047 LOC440341	214870_x_at	AC002045	NM_006985 XM_290671 XM_352159	339047 440341 9284	-1,06	2,19E-04
KIF5C	203129_s_at	BF059313	XM_377774	3800	-1,06	2,07E-03
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AK3 AK3L2	204347_at	AI653169	NM_00100292 1 NM_00100535 3 NM_013410 NM_203464	205 387851	-1,06	8,16E-03

BACE1	217904_s_at	NM_012104	NM_012104 NM_138971 NM_138972 NM_138973	23621	-1,06	1,51E-04
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PPIE	229375_at	AL526713	NM_006112 NM_203456 NM_203457	10450	-1,06	2,02E-06
C10orf57	218174_s_at	NM_025125	NM_025125	80195	-1,06	8,98E-04
PEX6	238672_at	AW953952	NM_000287	5190	-1,06	6,15E-04
BDH	211715_s_at	BC005844	NM_004051 NM_203314 NM_203315	622	-1,06	4,14E-04
BF110411	221878_at	BF110411	XM_371506	388969	-1,05	8,17E-03
R93413	236590_at	R93413	---	---	-1,05	6,60E-04
FLJ36674	244698_at	AW297656	NM_173622	284040	-1,05	4,58E-03
AA729232	241359_at	AA729232	---	---	-1,05	9,24E-03
FLJ21159	235550_at	AV751613	NM_024826	79884	-1,05	4,53E-03
SMPD1	209420_s_at	M59916	NM_000543 NM_00100759 3	6609	-1,05	8,56E-04
AA281853	239505_at	AA281853	---	---	-1,05	8,55E-04
KCNMA1	221584_s_at	U11058	NM_002247	3778	-1,05	7,34E-05
LOC439928	1569519_at	BC039454	XM_498427	439928	-1,05	2,09E-03
PAM	202336_s_at	NM_000919	NM_000919 NM_138766 NM_138821 NM_138822	5066	-1,05	1,27E-03
DCTD	201571_s_at	AI656493	NM_001921	1635	-1,05	9,35E-05
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WDR19	232163_at	AI982884	NM_025132	57728	-1,05	4,32E-04
ETFDH	33494_at	S69232	NM_004453	2110	-1,05	1,51E-03
RRAGC	222514_at	AK023373	NM_022157	64121	-1,05	7,18E-03
C14orf139	219563_at	NM_024633	NM_024633	79686	-1,05	7,66E-03
DNASE1	1560536_at	BC035759	NM_005223	1773	-1,05	1,80E-03
D17262	1567997_x_at	D17262	---	---	-1,04	5,43E-03
BTG3	215425_at	AL049332	NM_006806	10950	-1,04	5,78E-04
ATE1	238252_at	AI040743	NM_001001976 NM_007041	11101	-1,04	5,92E-04
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RRAGC	218088_s_at	NM_022157	NM_022157	64121	-1,04	8,27E-04
ZZEF1	212601_at	AB007859	NM_015113	23140	-1,04	4,08E-03
BCL11B	222895_s_at	AA918317	NM_022898 NM_138576	64919	-1,04	6,07E-04
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NSUN6	242239_at	AW970888	NM_182543	221078	-1,04	8,03E-03
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AA910371	212952_at	AA910371	---	---	-1,04	3,15E-03
C21orf51	228239_at	AA148789	NM_058182	54065	-1,04	6,43E-06
PPT1	200975_at	NM_000310	NM_000310	5538	-1,04	2,75E-05
TTC3	208663_s_at	AI652848	NM_001001894 NM_003316	7267	-1,04	9,53E-06
ZCSL3	1570048_at	BC036571	NM_181706	120526	-1,04	6,02E-03
ZNF3	232497_at	AF217988	NM_017715 NM_032924	7551	-1,04	7,84E-04
RRN3	230328_at	BF057656	NM_018427	54700	-1,04	1,78E-03
FTH1	214211_at	AA083483	NM_002032	2495	-1,03	2,78E-03
SERF2	226692_at	AI092931	NM_005770	10169	-1,03	3,64E-03

MTCP1	239236_at	BE465277	NM_014221	4515	-1,03	2,24E-03
PDCD2	228420_at	AW590850	NM_002598 NM_144781	5134	-1,03	8,82E-03
SPOCK2	202524_s_at	NM_014767	NM_014767	9806	-1,03	2,19E-06
CYLD	221905_at	BF516433	NM_015247	1540	-1,03	1,43E-04
IREB2	1563130_a_at	AL109710	NM_004136	3658	-1,03	3,66E-03
HRMT1L1	221564_at	AL570294	NM_001535 NM_206962	3275	-1,03	1,20E-06
DDOST	208674_x_at	BC002594	NM_005216	1650	-1,03	1,01E-03
LOC339047	214682_at	AK023376	XM_290671	339047	-1,02	4,06E-03
MGC15875	226519_s_at	AL561859	NM_032921 NM_153373	85007	-1,02	1,51E-03
HNRPM	233605_x_at	AK022050	NM_005968 NM_031203	4670	-1,02	3,07E-03
LOC144363	225469_at	AA015609	NM_001001660	144363	-1,02	6,55E-04
ZNF346	232753_at	AU147613	NM_012279	23567	-1,02	9,40E-04
C3orf6	228693_at	AI681307	NM_174908 NM_178335	152137	-1,02	2,49E-03
AK024681	231972_at	AK024681	---	---	-1,02	1,17E-03
UBXD1	223012_at	AF272894	NM_025241	80700	-1,02	3,65E-04
HERC4	225988_at	AI819938	NM_015601	26091	-1,02	2,15E-03
MYO5A	227761_at	AW235548	NM_000259	4644	-1,02	8,53E-03
LTBP3	227308_x_at	AW515704	NM_021070	4054	-1,02	6,79E-07
C14orf118	229520_s_at	BF060678	NM_017926 NM_017972	55668	-1,02	4,18E-03
RHOU	223169_s_at	AB051826	NM_021205	58480	-1,02	9,28E-03
SH3BGR	204979_s_at	NM_007341	NM_001001713 NM_007341	6450	-1,02	1,78E-03
BC014481	1569368_at	BC014481	---	---	-1,02	3,54E-03
LOC158230	243595_at	AI589280	---	158230	-1,02	4,74E-04
BC031322	1555900_at	BC031322	---	---	-1,02	1,29E-03

SPG3A	223340_at	AF131801	NM_015915 NM_181598	51062	-1,02	7,49E-03
AA448858	238948_at	AA448858	---	---	-1,02	3,09E-03
MGC33486	235614_at	AI215667	NM_153266	256472	-1,01	2,05E-05
M78162	217536_x_at	M78162	---	---	-1,01	4,51E-03
PHKA1	229876_at	BE503584	NM_002637	5255	-1,01	4,38E-04
STX6	244041_at	AI884934	NM_005819	10228	-1,01	8,65E-03
FLJ23518	233400_at	AU158247	NM_024725	79780	-1,01	3,50E-03
PPIE	210502_s_at	AF042386	NM_006112 NM_203456 NM_203457	10450	-1,01	4,24E-03
DDOST	208675_s_at	D29643	NM_005216	1650	-1,01	2,59E-03
OPTN	202073_at	AV757675	NM_00100821 1 NM_00100821 2 NM_00100821 3 NM_021980	10133	-1,01	2,57E-05
Cep164	1558953_s_at	BC000602	NM_014956	22897	-1,01	1,37E-03
SLC19A2	1556602_at	AW614839	NM_006996	10560	-1,00	2,90E-03
DMPK	217066_s_at	M87313	NM_004409	1760	-1,00	8,62E-03
SFRS15	222311_s_at	AA648521	NM_020706	57466	-1,00	2,57E-03
LYPLAL1	230174_at	AI953360	NM_138794	127018	-1,00	3,17E-03
AK000970	215512_at	AK000970	NM_005885	10299	-1,00	2,13E-03
LOC492304	202409_at	X07868	NM_00100713 9	492304	-1,00	1,87E-03
PIGH	209625_at	BC004100	NM_004569	5283	-1,00	6,00E-07
MEIS3	1569402_at	BC014430	NM_00100981 3 NM_020160	56917	-1,00	8,61E-03
DDX52	1570415_at	BC012557	NM_007010 NM_152300	11056	-1,00	1,89E-03

DTNA	211493_x_at	U46744	NM_001390 NM_001391 NM_001392 NM_032975 NM_032978 NM_032979 NM_032980 NM_032981	1837	-1,00	7,35E-03
EIF5	208707_at	BE552334	NM_001969 NM_183004	1983	-1,00	8,81E-03
ADRBK2 ALDH3B1 ALDH3A2 ANXA2 BIRC4 APP ATM ATOX1 ATP1B3 ATP5D BAD BCAT2 BDNF BMPR2 BRCA1 C11orf3 C21orf4 CACNB2 CCM1 CD47 CDK6 CHKA CHRNB1 AP3S1 SLC31A1 CP	AFFX-hum_alu_at	AFFX-hum_alu	NM_000021 NM_000051 NM_000136 NM_000141 NM_000144 NM_000202 NM_000227 NM_000230 NM_000294 NM_000297 NM_000314 NM_000356 NM_000364 NM_000382 NM_000441 NM_000484 NM_000527 NM_000554	10001 10020 10045 10160 10197 10198 10206 10207 1021 10225 10277 10402 10457 10513 10524 10606 10609 10611 10712 10730 10801 10806 10848 10921 11011 11019	-1,00	5,84E-04
DJ462O23.2	225876_at	T84558	NM_020448	57185	-1,00	6,61E-04
BE467087	231075_x_at	BE467087	---	---	-1,00	8,51E-03
ITSN1	216472_at	AF003737	NM_00100113 2 NM_003024	6453	-1,00	2,41E-03
DMWD	213231_at	L19267	XM_496318	1762	-1,00	1,12E-03
RPL37	224767_at	AL044126	NM_000997	6167	-1,00	1,07E-03
LMO4	229537_at	AI694521	NM_006769	8543	-1,00	2,20E-03

ACE	227463_at	AW057540	NM_000789 NM_152830 NM_152831	1636	-1,00	1,34E-03
KIAA1345	234936_s_at	AK023876	XM_106386	57545	-0,99	1,60E-03
AG1	215434_x_at	AV684285	XM_371384 XM_496394	440673	-0,99	1,70E-03
BE645588	243429_at	BE645588	---	---	-0,99	7,12E-03
PAM	214620_x_at	BF038548	NM_000919 NM_138766 NM_138821 NM_138822	5066	-0,99	4,07E-03
LRRFIP1	201861_s_at	BF965566	NM_004735	9208	-0,99	7,92E-06
RAD50	238656_at	AA877043	NM_005732 NM_133482	10111	-0,99	8,65E-03
LOC338758	238893_at	AI377324	---	338758	-0,99	2,11E-03
BE856007	238676_at	BE856007	---	---	-0,99	5,32E-06
Lrp2bp	227337_at	AA886870	NM_181726	353322	-0,99	6,37E-04
SMURF2	227489_at	BE962027	NM_022739	64750	-0,99	4,11E-04
PGRMC2	213227_at	BE879873	NM_006320	10424	-0,99	1,98E-03
TMEM41B	212623_at	AU153138	---	23027	-0,99	8,63E-03
BE670056	226663_at	BE670056	---	---	-0,99	6,70E-03
MYO9B	242742_at	AI863135	NM_004145	4650	-0,99	3,16E-03
DKFZp313N0621	241666_at	BG493222	NM_173826	285343	-0,99	1,70E-03
HK2	202934_at	AI761561	NM_000189	3099	-0,99	4,09E-03
DKFZp547I014	207283_at	NM_020217	NM_020217	56969	-0,99	6,98E-04
MAP1LC3B	208786_s_at	AF183417	NM_022818	81631	-0,99	3,39E-03
AKAP12	227530_at	BF511276	NM_005100 NM_144497	9590	-0,99	7,30E-03
AB014532	222796_at	AB014532	---	---	-0,98	6,13E-04
C1orf50	219406_at	NM_024097	NM_024097	79078	-0,98	2,14E-04
RPL13	1565759_at	BG396520	NM_000977	6137	-0,98	2,65E-04

			NM_033251			
MGC43690	235298_at	AW194823	NM_182552	253769	-0,98	3,94E-04
AF086554	1558504_at	AF086554	XM_373889	440721	-0,98	2,45E-03
FLJ11196	218651_s_at	NM_018357	NM_018357 NM_197958	55323	-0,98	1,86E-03
C17orf28	225981_at	AW139549	NM_030630	283987	-0,98	3,41E-04
SFXN3	1559993_at	AK091504	NM_030971	81855	-0,98	4,54E-03
C6orf111	226412_at	N66397	NM_032870	25957	-0,98	1,98E-03
RPL13	229590_at	AI369389	NM_000977 NM_033251	6137	-0,98	1,00E-03
LOC133308	1564746_at	BC009732	NM_178833	133308	-0,98	1,21E-04
AK027185	232102_at	AK027185	---	---	-0,98	1,28E-04
AW290940	226773_at	AW290940	---	---	-0,98	1,34E-04
AB040946	222564_at	AB040946	---	---	-0,98	1,34E-03
ILVBL	202993_at	NM_006844	NM_006844 NM_176826	10994	-0,97	1,11E-03
NPR2	204310_s_at	NM_003995	NM_000907 NM_003995	4882	-0,97	1,05E-03
PAM	212958_x_at	AI022882	NM_000919 NM_138766 NM_138821 NM_138822	5066	-0,97	2,87E-03
F11066	242973_at	F11066	---	---	-0,97	5,82E-03
SPIN3	1554099_a_at	BC032490	NM_001010862	169981	-0,97	4,95E-05
AA167167	243684_at	AA167167	---	---	-0,97	1,78E-03
LANCL2	218219_s_at	NM_018697	NM_018697	55915	-0,97	9,88E-03
AFFX-BioB-3	AFFX-BioB-3_at	AFFX-BioB-3	---	---	-0,97	1,52E-04
AHI1	220841_s_at	NM_017651	NM_017651	54806	-0,97	4,15E-04
AI675308	1569154_a_at	AI675308	---	---	-0,97	2,61E-03
AI339837	241741_at	AI339837	---	---	-0,97	9,92E-03

HNLF	238525_at	BF987157	NM_182547	222068	-0,97	3,73E-05
NM_024658	218305_at	NM_024658	---	---	-0,97	8,21E-03
FLJ30294	238867_at	AI298041	NM_144632	130827	-0,97	9,74E-03
FBXO9	1559096_x_at	AK095307	NM_012347 NM_033480 NM_033481	26268	-0,97	6,38E-05
PLP2	201136_at	NM_002668	NM_002668	5355	-0,97	1,29E-04
ZNF542	229187_at	AI026708	NM_194319	147947	-0,97	7,05E-03
TTLL3	210129_s_at	AF078842	NM_015644	26140	-0,97	6,31E-03
D4S234E	213533_at	M98528	NM_014392	27065	-0,97	1,57E-04
SHC2	213464_at	AV705938	XM_375550	25759	-0,97	4,07E-06
GCC1	243306_s_at	BE276093	NM_024523	79571	-0,97	2,70E-07
TSGA2	230093_at	AI683428	NM_080860	89765	-0,97	4,32E-03
HDLBP	222916_s_at	AF116718	NM_005336 NM_203346	3069	-0,97	5,58E-03
C9orf91	221865_at	BF969986	NM_153045	203197	-0,96	6,15E-03
CYorf15B	223646_s_at	AF332225	NM_032576	84663	-0,96	4,37E-03
LTB4R	236172_at	AW206817	NM_181657	1241	-0,96	5,00E-03
MGC11332	213403_at	BF223370	NM_032718	84804	-0,96	5,81E-03
SPIRE2	227706_at	AI215798	NM_032451	84501	-0,96	7,98E-05
AU146901	233264_at	AU146901	---	---	-0,96	1,84E-03
BG000693	1559932_at	BG000693	---	---	-0,96	1,63E-04
FLJ20758	228512_at	AW138833	NM_017952	55037	-0,96	1,99E-03
UNC5D	231325_at	AI802048	NM_080872	137970	-0,96	4,13E-05
THRAP2	242911_at	AW999644	NM_015335	23389	-0,96	5,60E-03
CLDN15	219640_at	NM_014343	NM_014343 NM_138429	24146	-0,96	1,04E-03
DUSP16	1558740_s_at	R30807	NM_030640	80824	-0,96	9,85E-03
TMEM1	209412_at	U61500	NM_001001723 NM_003274	7109	-0,96	5,34E-03

DDX26	222239_s_at	AL117626	NM_012141	26512	-0,95	1,60E-03
LOC388526	235322_at	BF038869	XM_371157	388526	-0,95	1,09E-04
OS-9	215399_s_at	AI683900	NM_006812	10956	-0,95	7,81E-03
PRKCSH	214080_x_at	AI815793	NM_001001329 NM_002743	5589	-0,95	2,14E-04
BF976290	238768_at	BF976290	XM_371506	388969	-0,95	9,91E-04
FLJ14107	207287_at	NM_025026	NM_025026	80094	-0,95	1,43E-05
ARHGAP23	226638_at	AV701292	XM_290799	57636	-0,95	3,20E-04
AI252004	242696_at	AI252004	---	---	-0,95	2,67E-03
TGFB1I1	209651_at	BC001830	NM_015927	7041	-0,95	7,45E-03
AI598222	235679_at	AI598222	---	---	-0,95	1,26E-03
AA131302	236032_at	AA131302	---	---	-0,95	5,35E-04
AI929792	236081_at	AI929792	---	---	-0,95	6,74E-05
N45312	228159_at	N45312	---	---	-0,95	5,76E-04
MONDOA	202519_at	NM_014938	NM_014938	22877	-0,95	6,48E-04
PLCB4	203895_at	AL535113	NM_000933 NM_182797	5332	-0,95	8,09E-05
RNF149	225414_at	AL558987	NM_173647	284996	-0,95	9,45E-03
DNASE1	1557189_at	AW468509	NM_005223	1773	-0,95	4,38E-04
OS-9	200714_x_at	NM_006812	NM_006812	10956	-0,95	4,30E-03
CCNL2	222999_s_at	AF251294	NM_030937	81669	-0,95	5,76E-03
NPD014	209006_s_at	AF247168	NM_020317 NM_207035	57035	-0,95	1,08E-03
LOC154822	243261_at	BF530486	---	154822	-0,94	6,74E-03
TARSL2	227611_at	AA442856	NM_152334	123283	-0,94	4,59E-03
AA827805	241364_at	AA827805	---	---	-0,94	9,38E-03
KRT18	201596_x_at	NM_000224	NM_000224 NM_199187	3875	-0,94	2,40E-03
CYLD	213295_at	AA555096	NM_015247	1540	-0,94	2,37E-04
BC011119	1569723_a_at	BC011119	---	---	-0,94	7,41E-03

PHF17	225820_at	AV646599	NM_024900 NM_199320	79960	-0,94	3,79E-03
C10orf104	229145_at	AA541762	NM_173473	119504	-0,94	1,46E-03
BF062399	240141_at	BF062399	---	---	-0,94	1,03E-03
LOC286437	239762_at	AI080505	---	286437	-0,94	1,26E-04
AA714835	1556646_at	AA714835	---	---	-0,94	6,42E-04
MGC3222	233480_at	AK026869	NM_024334	79188	-0,94	1,32E-03
NEDD4	213012_at	D42055	NM_006154 NM_198400	4734	-0,94	3,31E-03
MGC26979	232023_at	AL575584	NM_153704	91147	-0,94	2,50E-03
BE669703	229541_at	BE669703	---	---	-0,94	5,09E-04
AW665287	243725_at	AW665287	---	---	-0,94	8,33E-04
SPG7	202104_s_at	NM_003119	NM_003119 NM_199367	6687	-0,94	4,93E-03
AFFX-r2-Ec-bioB-5	AFFX-r2-Ec-bioB-5_at	AFFX-r2-Ec-bioB-5	---	---	-0,94	1,31E-04
AG1	212854_x_at	AB051480	XM_371384 XM_496394	440673	-0,94	2,84E-03
BF478154	242620_at	BF478154	---	---	-0,94	2,31E-03
PPM1K	235061_at	AV706522	NM_152542	152926	-0,94	2,87E-04
MDS010	218587_s_at	NM_020231	NM_020231 NM_152305	56983	-0,94	7,79E-03
RNF13	201779_s_at	AF070558	NM_007282 NM_183381 NM_183382 NM_183383 NM_183384	11342	-0,93	1,21E-06
ATP8B2	226771_at	AB032963	NM_001005855 NM_020452	57198	-0,93	1,31E-06
DCTD	210137_s_at	BC001286	NM_001921	1635	-0,93	4,45E-04
LOC286260	232420_x_at	AA706480	---	286260	-0,93	3,00E-04
IDS	217432_s_at	AF179281	NM_000202 NM_006123	3423	-0,93	1,24E-03

ANKRD10	223251_s_at	BC001727	NM_017664	55608	-0,93	6,05E-05
AK098354	1555824_a_at	AK098354	---	---	-0,93	2,66E-04
DOCK9	212538_at	AL576253	NM_015296	23348	-0,93	3,70E-03
DRE1	206551_x_at	NM_017644	NM_017644	54800	-0,93	7,84E-04
SNF1LK2	213221_s_at	AB018324	NM_015191	23235	-0,93	7,54E-03
KIAA1546	227624_at	AB046766	XM_042301	57667	-0,93	7,15E-03
AI417992	240513_at	AI417992	---	---	-0,93	7,71E-03
U2AF1	231904_at	AU122448	NM_006758	7307	-0,92	7,45E-04
KIAA0492	215109_at	R02172	XM_378914	57238	-0,92	3,40E-03
LOC158563	226273_at	AA218974	---	158563	-0,92	1,79E-04
AF130054	211452_x_at	AF130054	---	---	-0,92	4,58E-03
NCOA7	225344_at	AL035689	NM_181782	135112	-0,92	1,11E-03
LOC284356	1555842_at	BM978026	---	284356	-0,92	8,07E-03
EXOSC3	242590_at	BE464643	NM_001002269 NM_016042	51010	-0,92	4,59E-03
MALAT1	224558_s_at	AI446756	---	378938	-0,92	8,89E-03
C20orf44	229672_at	AA707125	NM_018244 NM_199487 NM_199513	55245	-0,92	1,02E-03
N64760	212622_at	N64760	---	---	-0,92	3,14E-04
HRMT1L1	202098_s_at	NM_001535	NM_001535 NM_206962	3275	-0,92	5,36E-05
NEU1	208926_at	U84246	NM_000434	4758	-0,92	6,42E-03
AF131777	215504_x_at	AF131777	---	---	-0,92	7,86E-03
PS1TP4	226381_at	AW450329	---	414327	-0,92	9,25E-03
C3orf6	235051_at	BF696931	NM_174908 NM_178335	152137	-0,92	9,12E-03
MAP1LC3B	208785_s_at	BE893893	NM_022818	81631	-0,91	1,87E-03
NM_024900	218517_at	NM_024900	---	---	-0,91	8,37E-03
P4HA2	202733_at	NM_004199	NM_004199	8974	-0,91	4,34E-03

MBTD1	207115_x_at	NM_017643	NM_017643	54799	-0,91	1,43E-03
BF476403	230218_at	BF476403	---	---	-0,91	2,19E-03
AL080160	217446_x_at	AL080160	---	---	-0,91	1,65E-03
C19orf4	219005_at	NM_012109	NM_012109	25789	-0,91	5,96E-04
LOC399491	214035_x_at	AA308853	---	399491	-0,91	6,27E-04
CHPT1	1559739_at	AK025141	NM_020244	56994	-0,91	6,26E-03
U2AF1L1	206512_at	NM_005083	---	7310	-0,91	8,01E-03
C20orf44	244795_at	AV693986	NM_018244 NM_199487 NM_199513	55245	-0,91	4,26E-04
LOC339047	221501_x_at	AF229069	XM_290671	339047	-0,91	2,33E-04
FLJ35093	235125_x_at	AI078279	NM_198549	374986	-0,91	2,80E-03
SLC22A17	218675_at	NM_020372	NM_016609 NM_020372	51310	-0,91	2,67E-06
EIF4A1	214805_at	U79273	NM_001416	1973	-0,91	7,74E-03
Cep164	204251_s_at	NM_014956	NM_014956	22897	-0,91	4,21E-03
AK2	212172_at	AW277253	NM_001625 NM_013411 NM_172199	204	-0,91	1,68E-04
NFKB1	209239_at	M55643	NM_003998	4790	-0,91	2,66E-03
AL833666	1566854_at	AL833666	---	---	-0,91	3,74E-03
BE857570	235677_at	BE857570	---	---	-0,91	6,67E-04
KIAA1276	227504_s_at	N64630	XM_039169	27146	-0,91	9,00E-05
KIAA0590	204792_s_at	NM_014714	NM_014714	9742	-0,91	2,73E-03
AV733292	225444_at	AV733292	---	---	-0,91	9,09E-04
BF057855	236829_at	BF057855	---	---	-0,91	4,03E-03
BC020820	1562962_at	BC020820	---	---	-0,91	1,89E-04
AFFX-r2-Ec-bioB-3	AFFX-r2-Ec-bioB-3_at	AFFX-r2-Ec-bioB-3	---	---	-0,91	4,89E-04
AF086478	1558948_a_at	AF086478	---	---	-0,91	5,21E-03

PHF20L1	222133_s_at	AK022280	NM_016018 NM_024878 NM_032205 NM_198513	51105	-0,90	9,98E-03
HERC4	208055_s_at	NM_015601	NM_015601	26091	-0,90	1,92E-03
R42552	239718_at	R42552	---	---	-0,90	1,67E-03
FBXO9	1559094_at	AK095307	NM_012347 NM_033480 NM_033481	26268	-0,90	1,55E-04
OSBP	1563051_at	BC017975	NM_002556	5007	-0,90	8,83E-03
GPR27	227769_at	AI703476	NM_018971	2850	-0,90	3,33E-03
C21orf33	202217_at	NM_004649	NM_004649 NM_198155	8209	-0,90	2,00E-03
RGS8	234297_at	AL359941	NM_033345	85397	-0,90	4,04E-03
AFFX-BioB-M	AFFX-BioB-M_at	AFFX-BioB-M	---	---	-0,90	9,42E-05
POLR3E	233458_at	AB040885	NM_018119	55718	-0,90	1,75E-03
DKFZp761B107	226139_at	BE670598	NM_173463	91050	-0,90	4,14E-03
AA923289	236666_s_at	AA923289	XM_372416	390205	-0,90	1,19E-03
BE247450	244443_at	BE247450	XM_498623	440309	-0,90	3,66E-03
SEMA4B	234725_s_at	AK026133	NM_020210 NM_198925	10509	-0,90	1,81E-03
WDFY3	212606_at	AL536319	NM_014991 NM_178583 NM_178585	23001	-0,90	3,35E-04
NM_018336	205955_at	NM_018336	---	---	-0,90	5,74E-04
SELS	223209_s_at	AF328864	NM_018445 NM_203472	55829	-0,90	2,33E-03
CDH20	243657_at	AW593060	NM_031891	28316	-0,90	7,78E-03
KIAA1223	225735_at	AL110131	XM_048747	57182	-0,90	7,05E-04
BE502826	231550_at	BE502826	---	---	-0,90	5,25E-03
DDX26	218819_at	NM_012141	NM_012141	26512	-0,90	1,74E-03
FLJ32731	218017_s_at	NM_025070	XM_372038	138050	-0,90	3,84E-07

FLJ32499	1552711_a_at	NM_144607	NM_144607	124637	-0,90	6,17E-05
AFFX-BioB-5	AFFX-BioB-5_at	AFFX-BioB-5	---	---	-0,89	2,50E-05
TMEM17	1557137_at	AA084725	NM_198276	200728	-0,89	9,22E-04
R26456	243135_x_at	R26456	---	---	-0,89	2,43E-03
AFFX-r2-Ec-bioC-3	AFFX-r2-Ec-bioC-3_at	AFFX-r2-Ec-bioC-3	---	---	-0,89	1,35E-04
RAB5A	215956_at	AK022065	NM_004162	5868	-0,89	3,52E-03
AFFX-r2-Ec-bioB-M	AFFX-r2-Ec-bioB-M_at	AFFX-r2-Ec-bioB-M	---	---	-0,89	3,74E-05
NXPH4	221967_at	AI933199	NM_007224	11247	-0,89	1,39E-05
PERLD1	221811_at	BF033007	NM_033419	93210	-0,89	3,44E-04
WDR21	214758_at	AL080157	NM_015604 NM_181340 NM_181341	26094	-0,89	2,29E-04
MDS009	236649_at	AA907927	NM_020234	56986	-0,89	1,30E-03
DISP1	228184_at	AK023679	NM_032890	84976	-0,89	6,47E-05
HIST1H2BH	208546_x_at	NM_003524	NM_003524	8345	-0,89	5,00E-03
MLR1	240592_at	AI939336	NM_153686	254251	-0,89	2,34E-03
AF088033	1556228_a_at	AF088033	---	---	-0,89	7,95E-05
FLJ10815	228951_at	AI631572	NM_018231	55238	-0,89	1,85E-03
UTP14A	221514_at	BC001149	NM_006649	10813	-0,89	9,63E-03
BBP	213882_at	AA012917	NM_032027	83941	-0,89	3,54E-05
NCSTN	208759_at	AF240468	NM_015331	23385	-0,89	6,91E-06
LOC283922	228688_at	AA843726	XM_208908	283922	-0,88	3,60E-03
Cep164	204250_s_at	AI655714	NM_014956	22897	-0,88	2,74E-03
ZFYVE26	213073_at	AB002319	NM_015346	23503	-0,88	1,02E-03
AI525856	239016_at	AI525856	---	---	-0,88	4,67E-05
IREB2	1555476_at	BC017880	NM_004136	3658	-0,88	1,40E-03
W80462	242194_at	W80462	---	---	-0,88	2,61E-03
C13orf21	228044_at	AI420319	NM_00101089	387923	-0,88	1,82E-03

WTAP	1560274_at	BF679507	NM_004906 NM_152857 NM_152858	9589	-0,88	2,07E-04
MGC4278	220352_x_at	NM_024305	---	79151	-0,88	6,74E-03
PHF17	225816_at	AW138134	NM_024900 NM_199320	79960	-0,88	3,82E-03
LOC401551	243900_at	AI190548	XM_376909	401551	-0,88	6,97E-03
FLJ35630	229603_at	AA971753	NM_152618	166379	-0,88	2,21E-03
KIAA1008	218362_s_at	NM_014953	NM_014953	22894	-0,88	7,57E-04
SON	201085_s_at	AA664291	NM_003103 NM_032195 NM_058183 NM_138925 NM_138926 NM_138927	6651	-0,88	5,49E-03
AK021474	215892_at	AK021474	---	---	-0,88	5,75E-03
DCTD	201572_x_at	NM_001921	NM_001921	1635	-0,88	1,87E-04
H73101	1556984_at	H73101	---	---	-0,87	3,73E-03
USP34	230148_at	AI831431	NM_014709	9736	-0,87	8,65E-03
Ufc1	217797_at	NM_016406	NM_016406	51506	-0,87	7,99E-05
BE044193	229384_at	BE044193	---	---	-0,87	8,85E-03
VMP1	224917_at	BF674052	NM_030938	81671	-0,87	8,73E-03
KIAA0711	204301_at	NM_014867	NM_014867	9920	-0,87	4,26E-05
C21orf66	218515_at	NM_016631	NM_013329 NM_016631 NM_058191 NM_145328	94104	-0,87	2,26E-04
D4S234E	209569_x_at	NM_014392	NM_014392	27065	-0,87	6,40E-03
TJP2	202085_at	NM_004817	NM_004817 NM_201629	9414	-0,87	5,83E-04
MAN1A2	217282_at	AK001970	NM_006699	10905	-0,87	5,09E-03
C15orf17	224798_s_at	AI079857	NM_020447	57184	-0,87	5,80E-03
SLC20A2	231818_x_at	AK023965	NM_006749	6575	-0,87	8,22E-03

C14orf103	222840_at	H96715	NM_018036	55102	-0,87	2,43E-03
AFFX-BioC-3	AFFX-BioC-3_at	AFFX-BioC-3	---	---	-0,87	3,17E-05
MGLL	211026_s_at	BC006230	NM_001003794 NM_007283	11343	-0,87	3,12E-03
FZD6	203987_at	NM_003506	NM_003506	8323	-0,87	9,59E-03
AFFX-BioC-5	AFFX-BioC-5_at	AFFX-BioC-5	---	---	-0,87	1,11E-04
ENPP2	210839_s_at	D45421	NM_006209	5168	-0,87	1,49E-04
DKFZP564D166	231799_at	AK021886	XM_371074	26115	-0,87	1,88E-04
ANKRD20A LOC440841	1569608_x_at	BC016022	NM_032250 XM_496541	440841 84210	-0,87	2,10E-03
AW341304	237332_at	AW341304	---	---	-0,87	1,73E-03
USP36	224979_s_at	AU154368	NM_025090	57602	-0,87	8,89E-04
FLJ10980	225327_at	AB037791	NM_019600	56204	-0,87	3,59E-05
AI768374	228661_s_at	AI768374	---	---	-0,87	3,95E-04
CANX	200068_s_at	M94859	NM_001746	821	-0,87	7,71E-03
MED6	207078_at	NM_005466	NM_005466	10001	-0,87	9,36E-03
C3orf6	226713_at	AI247881	NM_174908 NM_178335	152137	-0,87	4,87E-03
DJ328E19.C1.1 LOC200030 MGC8902 AG1	201104_x_at	NM_015383	NM_015383 NM_173638 NM_183372 XM_371384 XM_496394	200030 25832 284565 440673	-0,87	9,45E-04
CARD14	240392_at	BF752351	NM_024110 NM_052819	79092	-0,87	6,29E-03
FKBP2	203391_at	NM_004470	NM_004470 NM_057092	2286	-0,86	6,91E-03
CBS	212816_s_at	BE613178	NM_000071	875	-0,86	6,44E-03
AI695743	244534_at	AI695743	---	---	-0,86	1,23E-04
NGLY1	220742_s_at	NM_018297	NM_018297	55768	-0,86	4,72E-04

H19	224997_x_at	AL575306	---	283120	-0,86	2,98E-03
DYRK1B	204954_s_at	NM_004714	NM_004714 NM_006483 NM_006484	9149	-0,86	6,27E-03
IDS	202439_s_at	NM_000202	NM_000202 NM_006123	3423	-0,86	1,14E-03
LOC284267	228453_at	AW004076	---	284267	-0,86	6,01E-03
JUN	201466_s_at	NM_002228	NM_002228	3725	-0,86	6,35E-03
TRAP1	228929_at	AI341246	NM_016292	10131	-0,86	7,28E-03
TSC1	209390_at	AF013168	NM_000368 NM_001008567	7248	-0,86	1,82E-03
MLR1	235970_at	AI807408	NM_153686	254251	-0,86	7,89E-04
AI086530	217604_at	AI086530	---	---	-0,86	1,82E-03
DVL3	201908_at	NM_004423	NM_004423	1857	-0,86	2,67E-04
HIST1H3D	214522_x_at	NM_021065	NM_003530	8351	-0,86	4,36E-05
AFFX-HUMRGE/M10098_5	AFFX-HUMRGE/M10098_5_at	AFFX-HUMRGE/M10098_5	---	---	-0,86	2,30E-03
TPP1	200742_s_at	BG231932	NM_000391	1200	-0,86	7,91E-03
TTC3	208664_s_at	AU131711	NM_001001894 NM_003316	7267	-0,86	7,07E-03
RFPL2	207227_x_at	NM_006605	NM_006605	10739	-0,86	3,03E-03
D4S234E	209570_s_at	BC001745	NM_014392	27065	-0,86	1,12E-04
LOC146174	230721_at	BF436957	NM_173501	146174	-0,86	5,19E-04
C9orf68	1554708_s_at	BC034293	NM_017985	55064	-0,86	1,35E-03
R3HDM	240503_at	AW274946	NM_015361	23518	-0,86	6,04E-03
SNCA	204467_s_at	NM_000345	NM_000345 NM_007308	6622	-0,85	9,17E-05
AK094546	1556205_at	AK094546	---	---	-0,85	6,76E-04
KIAA1450	225924_at	AI478634	---	57600	-0,85	6,97E-03
SKP1A	200719_at	BE964043	NM_006930	6500	-0,85	3,06E-03

			NM_170679			
PGK1	228483_s_at	BE856250	NM_000291	5230	-0,85	2,17E-03
LOC200030	229447_x_at	N32025	NM_183372	200030	-0,85	8,99E-04
PRKCA	1560074_at	AL119889	NM_002737	5578	-0,85	1,54E-03
AI332346	225445_at	AI332346	---	---	-0,85	1,78E-03
COG1	231813_s_at	AV746580	NM_018714	9382	-0,85	1,02E-03
FLJ20203	219846_at	NM_025174	NM_032292	54856	-0,85	1,98E-03
GALNS	206335_at	NM_000512	NM_000512	2588	-0,85	9,33E-03
CASP9	203984_s_at	U60521	NM_001229 NM_032996	842	-0,85	1,05E-03
AU147777	232145_at	AU147777	XM_371506	388969	-0,85	7,96E-03
MGC52110	226039_at	AW006441	NM_00100821 5	493753	-0,85	9,51E-06
MACF1	208634_s_at	AB029290	NM_012090 NM_033044	23499	-0,85	2,09E-03
FLJ41603	227717_at	BF939317	NM_00100166 9	389337	-0,84	5,48E-03
FLJ12716	233558_s_at	AK023390	NM_021942 NM_199053	60684	-0,84	1,27E-03
BE676062	231249_at	BE676062	---	---	-0,84	2,18E-03
KIAA0415	209913_x_at	AB007875	XM_166527 XM_379771 XM_499251 XM_499396	9907	-0,84	3,69E-03
PCAF	203845_at	AV727449	NM_003884	8850	-0,84	4,85E-03
MONDOA	211789_s_at	AF312918	NM_014938	22877	-0,84	4,65E-03
C6orf70	227656_at	AW968493	XM_376556	55780	-0,84	1,48E-03
PTPN21	226380_at	N21442	NM_007039	11099	-0,84	1,06E-03
PNMT	206793_at	NM_002686	NM_002686	5409	-0,84	2,71E-03
ALG5	218203_at	NM_013338	NM_013338	29880	-0,84	8,89E-03
LOC90110	226842_at	AV694039	---	90110	-0,84	5,28E-03
CYLD	39582_at	AL050166	NM_015247	1540	-0,84	4,04E-03

LOC150271	228658_at	R54042	---	150271	-0,84	6,95E-03
FER1L4	222245_s_at	AF218012	---	80307	-0,84	5,44E-05
MECT1	213091_at	AB014516	NM_015321 NM_025021	23373	-0,84	2,37E-04
AL359605	227318_at	AL359605	---	---	-0,84	4,99E-06
SH3GL2	205751_at	NM_003026	NM_003026	6456	-0,84	3,31E-04
MUC1	213693_s_at	AI610869	NM_002456 NM_182741	4582	-0,84	6,09E-04
RSHL2	223713_at	AF353618	NM_031924	83861	-0,84	3,80E-03
MRPS33	218654_s_at	NM_016071	NM_016071 NM_053035	51650	-0,83	2,36E-03
FBLP-1	1554795_a_at	BC019895	NM_017556	54751	-0,83	5,75E-03
XPOT	227117_at	AW242820	NM_007235	11260	-0,83	5,63E-03
ACRV1	206776_x_at	NM_001612	NM_001612 NM_020069 NM_020107 NM_020108 NM_020109 NM_020110 NM_020111 NM_020113 NM_020114 NM_020115	56	-0,83	7,51E-03
AI334297	225961_at	AI334297	---	---	-0,83	5,29E-04
TMEM34	219074_at	NM_018241	NM_018241	55751	-0,83	1,81E-03
AI494500	241448_at	AI494500	---	---	-0,83	9,31E-04
LOC440160	239010_at	AI744280	XM_498571	440160	-0,83	6,65E-03
PPID	204186_s_at	AI014573	NM_005038	5481	-0,83	2,63E-04
PAK3	236277_at	H23551	NM_002578	5063	-0,83	1,34E-04
NPM1	221923_s_at	AA191576	NM_002520 NM_199185	4869	-0,83	5,74E-03
ProSAPIP1	204447_at	NM_014731	NM_014731	9762	-0,83	4,47E-04
NSMAF	232149_s_at	BF056507	NM_003580	8439	-0,83	6,67E-03
MGC21881	1555874_x_at	BC019880	NM_203448	389741	-0,83	1,97E-03

FLJ37953	241825_at	AI265967	NM_152382	129450	-0,83	2,38E-03
INPP5A	203006_at	NM_005539	NM_005539	3632	-0,83	5,00E-04
SLC25A16	210686_x_at	BC001407	NM_152707	8034	-0,83	2,87E-03
CBS	1553972_a_at	BC007257	NM_000071	875	-0,83	5,27E-03
KIAA0804	209553_at	BC001001	NM_001009921 NM_015303	23355	-0,83	9,90E-04
AW945538	239208_s_at	AW945538	---	---	-0,83	3,44E-04
AK021583	232931_at	AK021583	---	---	-0,82	4,13E-03
BDP1	224227_s_at	AF298152	NM_018429	55814	-0,82	4,88E-03
SPG7	214494_s_at	NM_005200	NM_003119 NM_199367	6687	-0,82	9,51E-03
ZNF599	1558390_at	BC033354	NM_001007247 NM_001007248	148103	-0,82	1,18E-03
AFFX-r2-Ec-bioC-5	AFFX-r2-Ec-bioC-5_at	AFFX-r2-Ec-bioC-5	---	---	-0,82	2,81E-04
KIAA0690	1559127_x_at	BC042908	NM_015179	23223	-0,82	1,09E-04
KIAA1546	1569385_s_at	BC019007	XM_042301	57667	-0,82	3,51E-04
SSR4	201004_at	NM_006280	NM_006280	6748	-0,82	1,83E-03
TRIT1	218617_at	NM_017646	NM_017646	54802	-0,82	5,10E-05
MAPK10	204813_at	NM_002753	NM_002753 NM_138980 NM_138981 NM_138982	5602	-0,82	2,98E-03
CGI-119	219206_x_at	NM_016056	NM_016056	51643	-0,82	3,02E-03
GPRASP1	204793_at	NM_014710	NM_014710	9737	-0,82	2,03E-04
ARHGAP1	241419_at	AA709154	NM_004308	392	-0,82	2,43E-03
KIAA0934	212504_at	N31807	NM_014974	22982	-0,82	2,71E-04
LOC51619	240014_at	AI821720	NM_015983	51619	-0,82	7,64E-03
MEF2A	212535_at	AA142929	NM_005587	4205	-0,81	8,41E-04
AI859463	242111_at	AI859463	---	---	-0,81	3,79E-03

KLF15	231015_at	AW014734	NM_014079	28999	-0,81	3,05E-03
MGC8902 AG1	213612_x_at	AI800419	NM_173638 XM_371384 XM_496394	284565 440673	-0,81	1,93E-03
FLJ10038	205511_at	NM_017976	---	55056	-0,81	1,24E-03
PCDHA2	210572_at	BC003126	NM_018905 NM_031495 NM_031496	56146	-0,81	3,16E-04
EYA1	214608_s_at	AJ000098	NM_000503 NM_172058 NM_172059 NM_172060	2138	-0,81	3,74E-03
CENTG1	229917_at	BE551002	NM_014770	116986	-0,81	1,70E-03
PLRG1	225194_at	NM_002669	NM_002669	5356	-0,81	2,39E-03
DUSP16	236511_at	AI798976	NM_030640	80824	-0,81	8,12E-03
LRRFIP1	201862_s_at	NM_004735	NM_004735	9208	-0,81	2,88E-04
AI393706	238944_at	AI393706	---	---	-0,81	3,70E-03
TNIP1	207196_s_at	NM_006058	NM_006058	10318	-0,81	3,18E-03
SYNCRIP	236146_at	BF593158	NM_006372	10492	-0,81	3,42E-03
TAS2R5	231757_at	NM_018980	NM_018980	54429	-0,81	1,10E-03
PABPC4	201064_s_at	NM_003819	NM_003819	8761	-0,81	1,63E-03
AW367380	236408_at	AW367380	---	---	-0,81	6,92E-03
C21orf127	234676_s_at	AK021678	NM_013240 NM_182749	29104	-0,81	6,83E-03
NM_018678	220494_s_at	NM_018678	---	---	-0,81	9,98E-03
AF5Q31	232864_s_at	N59653	NM_014423	27125	-0,81	5,40E-03
LTB4R	216388_s_at	U33448	NM_181657	1241	-0,80	3,43E-03
ENPP2	209392_at	L35594	NM_006209	5168	-0,80	1,95E-05
SMURF2	205596_s_at	AY014180	NM_022739	64750	-0,80	2,21E-04
STS	243858_at	AA699970	NM_000351	412	-0,80	1,20E-03
KLHDC1	1552733_at	NM_172193	NM_172193	122773	-0,80	1,05E-03

ASTN2	215407_s_at	AK024064	NM_014010 NM_198186 NM_198187 NM_198188	23245	-0,80	2,08E-03
BQ008117	1556659_at	BQ008117	---	---	-0,80	5,03E-03
FLJ10534	239042_at	AI282511	NM_018128	55720	-0,80	2,54E-03
RABL5	218785_s_at	NM_022777	NM_022777	64792	-0,80	2,32E-03
RNASET2	217983_s_at	NM_003730	NM_003730	8635	-0,80	7,39E-04
BTBD14B	215587_x_at	AK023891	NM_052876	112939	-0,80	3,30E-03
FALZ	232909_s_at	AU146870	NM_004459 NM_182641	2186	-0,80	7,77E-03
NEUGRIN	228541_x_at	AI049608	NM_016645	51335	-0,80	2,24E-03
UNC5B	213100_at	AA127885	NM_170744	219699	-0,80	6,29E-03
LOC439987 LOC439993	229609_at	BF224281	XM_495841 XM_498488	439987 439993	-0,80	7,79E-04
RPIP8	213439_x_at	AI197870	NM_006695	10900	-0,80	3,47E-05
LOC285949	1563781_at	AK096687	---	285949	-0,80	3,61E-03
FLJ22313	236170_x_at	AI377423	NM_022373	64224	-0,80	5,62E-04
AQP3	39248_at	N74607	NM_004925	360	-0,80	4,75E-03
FALZ	209271_at	AB032251	NM_004459 NM_182641	2186	-0,80	9,58E-03
LOC440118	AFFX-M27830_M_at	AFFX-M27830_M	XM_498554	440118	-0,80	9,04E-04
ARF1	232175_at	AI972094	NM_001658	375	-0,80	1,30E-04
ERBB2	216836_s_at	X03363	NM_001005862 NM_004448	2064	-0,80	1,70E-04
LOC440823	227168_at	BF475488	XM_498878	440823	-0,80	8,41E-03
DUSP8	206374_at	NM_004420	NM_004420	1850	-0,80	9,45E-04
ARHGAP1	202117_at	BG468434	NM_004308	392	-0,79	5,77E-04
CYLD	221903_s_at	BE046443	NM_015247	1540	-0,79	4,50E-05
AFFX-BioDn-5	AFFX-BioDn-5_at	AFFX-BioDn-5	---	---	-0,79	2,95E-05

CARS	202402_s_at	NM_001751	NM_001751 NM_139273	833	-0,79	7,28E-03
ASTN2	209693_at	AF116574	NM_014010 NM_198186 NM_198187 NM_198188	23245	-0,79	9,79E-04
AK025546	232161_x_at	AK025546	---	---	-0,79	4,20E-03
PTPRD	214043_at	BF062299	NM_002839 NM_130391 NM_130392 NM_130393	5789	-0,79	8,45E-03
ATP6V0A1	212383_at	AL096733	NM_005177	535	-0,79	9,12E-04
AIG1	223136_at	AF151861	NM_016108	51390	-0,79	8,00E-03
ANXA7	242027_at	AI732079	NM_001156 NM_004034	310	-0,79	8,52E-04
HDLBP	225012_at	BE378479	NM_005336 NM_203346	3069	-0,79	4,04E-04
C10orf51	231196_x_at	AI333226	---	387644	-0,79	1,33E-05
WASL	227010_at	BF438330	NM_003941	8976	-0,79	1,01E-03
RSNL2	226425_at	AU144247	NM_024692	79745	-0,79	4,96E-05
ATP9A	216129_at	AL117659	XM_030577	10079	-0,79	2,42E-04
AA888098	244426_at	AA888098	---	---	-0,79	7,13E-04
DYM	220774_at	NM_017653	NM_017653	54808	-0,79	1,83E-03
C2orf17	221983_at	AL040896	NM_024293	79137	-0,79	6,51E-03
MGC4618	223462_at	BC005158	NM_032326	84286	-0,78	2,33E-03
RSL1D1	212019_at	AK025446	NM_015659	26156	-0,78	3,44E-03
LOC200030 MGC8902 AG1	201103_x_at	BE299495	NM_173638 NM_183372 XM_371384 XM_496394	200030 284565 440673	-0,78	1,09E-03
WDR13	222138_s_at	AF158978	NM_017883	64743	-0,78	1,22E-03
SERP1	200971_s_at	NM_014445	NM_014445	27230	-0,78	1,90E-03
KIAA1049	213311_s_at	BF000251	NM_014972	22980	-0,78	2,49E-03
BG502771	226397_s_at	BG502771	---	---	-0,78	2,83E-03

AI652868	225811_at	AI652868	---	---	-0,78	5,96E-03
AL559202	226458_at	AL559202	---	---	-0,78	8,12E-03
R15431	236440_at	R15431	---	---	-0,78	1,66E-05
SLC43A1	204394_at	NM_003627	NM_003627	8501	-0,78	3,44E-03
C18orf17	238480_at	AI871745	NM_153211	125488	-0,78	7,85E-04
C11orf31	228331_at	AA526939	NM_170746	280636	-0,78	1,80E-03
SLC9A3	226125_at	BF346665	NM_004174	6550	-0,78	1,02E-03
EPC2	225838_at	AK002010	NM_015630	26122	-0,78	1,65E-04
KIAA0934	212503_s_at	N22859	NM_014974	22982	-0,78	2,51E-04
EFHC1	231026_at	AW451135	NM_018100	114327	-0,78	9,28E-03
AA883831	244042_x_at	AA883831	---	---	-0,78	9,44E-03
NIN	225921_at	AL359571	NM_016350 NM_020921 NM_182944 NM_182945 NM_182946	51199	-0,78	1,33E-04
AW502656	240800_x_at	AW502656	---	---	-0,77	2,82E-05
SMYD2	212922_s_at	AI809870	NM_020197	56950	-0,77	4,17E-03
NDUFV3	226616_s_at	NM_021075	NM_001001503 NM_021075	4731	-0,77	3,48E-03
LSS	202245_at	AW084510	NM_001001438 NM_002340	4047	-0,77	1,95E-04
TTC3	208662_s_at	AI885338	NM_001001894 NM_003316	7267	-0,77	1,75E-04
IL10RB	209575_at	BC001903	NM_000628	3588	-0,77	1,78E-05
PLTP	202075_s_at	NM_006227	NM_006227 NM_182676	5360	-0,77	6,25E-03
ANKRD17	225852_at	BE463523	NM_032217 NM_198889	26057	-0,77	1,79E-05
LOC283981	232463_at	T77995	---	283981	-0,77	9,63E-03
AI146751	242565_x_at	AI146751	---	---	-0,77	1,83E-03

GDF1 LASS1	206397_x_at	NM_001492	NM_001492 NM_021267 NM_198207	10715 2657	-0,77	1,04E-04
FLJ10276	218004_at	NM_018045	NM_018045	55108	-0,77	1,60E-03
BF223556	229376_at	BF223556	---	---	-0,77	3,00E-03
KIAA1109	212779_at	AB029032	XM_371706	84162	-0,77	8,29E-04
AI983303	237877_at	AI983303	---	---	-0,77	2,54E-05
JMJD2A	203204_s_at	BC002558	NM_014663	9682	-0,77	5,29E-03
RBM8A	217856_at	AF182415	NM_005105	9939	-0,77	1,77E-03
FLJ12716	218179_s_at	NM_021942	NM_021942 NM_199053	60684	-0,77	4,05E-04
CGI-119	222845_x_at	AF161526	NM_016056	51643	-0,77	4,64E-05
BI520422	1559467_at	BI520422	---	---	-0,77	6,79E-03
AA134418	232150_at	AA134418	---	---	-0,77	3,88E-03
ZNF323	222016_s_at	AW086021	NM_030899 NM_145909	64288	-0,77	3,58E-03
GLG1	214730_s_at	AK025457	NM_012201	2734	-0,77	8,94E-05
AK024602	222207_x_at	AK024602	---	---	-0,76	4,03E-03
BE964222	226589_at	BE964222	---	---	-0,76	2,53E-04
GNAS	228173_at	AA810695	NM_000516 NM_016592 NM_080425 NM_080426	2778	-0,76	5,49E-03
MONDOA	225157_at	AW245631	NM_014938	22877	-0,76	3,06E-04
KIAA2010	215607_x_at	AU144530	NM_017936 NM_032560	55671	-0,76	3,17E-03
DJ328E19.C1 .1 LOC200030 MGC8902 LOC439928 AG1	226740_x_at	BF740216	NM_015383 NM_173638 NM_183372 XM_371384 XM_496394 XM_498427	200030 25832 284565 439928 440673	-0,76	1,09E-03
LEAP-2	1552362_a_at	NM_052971	NM_052971	116842	-0,76	5,61E-03
BRUNOL4	238966_at	AA678985	NM_020180	56853	-0,76	8,60E-03

AA827878	223577_x_at	AA827878	---	---	-0,76	5,84E-03
CDKL1	244670_at	AI767697	NM_004196	8814	-0,76	4,97E-03
NALP1	218380_at	NM_021730	NM_014922 NM_033004 NM_033006 NM_033007	22861	-0,76	2,51E-03
MAN1B1	65884_at	AA631254	NM_016219	11253	-0,76	3,92E-04
GOSR2	235041_at	AW005457	NM_004287 NM_054022	9570	-0,76	9,63E-04
BI496583	1557675_at	BI496583	---	---	-0,76	7,35E-03
AA194266	238728_at	AA194266	---	---	-0,76	2,48E-03
EFEMP2	209356_x_at	AB030655	NM_016938	30008	-0,76	5,52E-03
NM_018705	220572_at	NM_018705	---	---	-0,76	3,25E-03
MGC2747	224712_x_at	AI656658	NM_024104	79086	-0,76	2,38E-04
PIK3R1	212239_at	AI680192	NM_181504 NM_181523 NM_181524	5295	-0,76	7,57E-03
RAB11B	34478_at	X79780	NM_004218	9230	-0,76	5,20E-04
FLJ23867	226706_at	BE301252	---	200058	-0,76	2,32E-03
NELF	221214_s_at	NM_015537	NM_015537	26012	-0,76	9,78E-05
MAP2K7	216206_x_at	BC005365	NM_145185	5609	-0,75	1,08E-03
FLJ43806	213752_at	BF111846	NM_201628	399563	-0,75	3,92E-03
CHMP1.5	218177_at	AA293502	NM_020412	57132	-0,75	3,04E-04
KNDC1	230359_at	N45097	NM_033404 NM_152643	85442	-0,75	6,69E-04
HNRPU	236244_at	AI458297	NM_004501 NM_031844	3192	-0,75	7,10E-03
C1orf50	62212_at	W37846	NM_024097	79078	-0,75	7,56E-04
KIAA0913	212359_s_at	W89120	NM_015037	23053	-0,75	2,87E-05
PPP2CA	215628_x_at	AL049285	NM_002715	5515	-0,75	2,81E-04
C6orf160	225155_at	BG339050	XM_499041	441164	-0,75	3,83E-03
CD151	204306_s_at	NM_004357	NM_004357 NM_139030	977	-0,75	1,69E-06

HLCS	209399_at	D87328	NM_000411	3141	-0,75	2,42E-04
AA017536	242270_at	AA017536	---	---	-0,75	2,11E-05
FLJ43663	215330_at	AL049991	XM_379520 XM_380146	378805	-0,75	1,78E-05
MRRF	225126_at	BF438352	NM_138777 NM_199176 NM_199177	92399	-0,75	5,23E-03
WNK1	211992_at	AI445745	NM_018979	65125	-0,75	3,85E-03
AI870959	244877_at	AI870959	---	---	-0,75	1,78E-03
LOC94431	216908_x_at	AF001549	NM_145237	94431	-0,75	2,16E-03
BG527339	226457_at	BG527339	---	---	-0,75	3,79E-03
AA928506	213750_at	AA928506	---	---	-0,74	4,38E-04
GP1BB	206655_s_at	NM_000407	NM_000407	2812	-0,74	4,60E-04
AA629075	236653_at	AA629075	---	---	-0,74	1,35E-04
TTC3	208661_s_at	AW510696	NM_001001894 NM_003316	7267	-0,74	1,79E-05
TNRC6C	227149_at	AB046802	NM_018996	57690	-0,74	5,66E-03
POFUT2	209578_s_at	BC000626	NM_015227 NM_133634 NM_133635	23275	-0,74	1,92E-03
CLDN12	223249_at	AL136770	NM_012129	9069	-0,74	2,31E-03
PICALM	239102_s_at	AW293296	NM_001008660 NM_007166	8301	-0,74	3,04E-03
SKIV2L	203727_at	NM_006929	NM_006929	6499	-0,74	4,08E-04
LOC125150	228719_at	BE645222	---	125150	-0,74	7,64E-03
AA026666	235611_at	AA026666	---	---	-0,74	3,78E-03
KIAA0323	212356_at	AB002321	NM_015299	23351	-0,74	1,24E-03
BC031035	1569503_at	BC031035	---	---	-0,74	1,39E-05
UNC5B	226899_at	AK022859	NM_170744	219699	-0,74	6,84E-03
KCNRG	239098_at	W68737	NM_173605 NM_199464	283518	-0,74	5,28E-03

DPCD	226009_at	AI129328	NM_015448	25911	-0,74	8,18E-03
LEPREL2	204854_at	NM_014262	NM_014262	10536	-0,74	3,69E-03
AW341225	1556690_s_at	AW341225	---	---	-0,74	1,25E-06
DPP7	224814_at	NM_013379	NM_013379	29952	-0,74	2,41E-04
GAS5	224841_x_at	BF316352	---	60674	-0,74	1,39E-03
TRIM8	223132_s_at	AF220034	NM_030912	81603	-0,73	1,24E-05
BF056548	232140_at	BF056548	XM_499148	441443	-0,73	8,09E-03
PPT2 EGFL8	208469_s_at	NM_030652	NM_005155 NM_030652 NM_138717 NM_138934	80864 9374	-0,73	3,43E-03
SH3YL1	204019_s_at	NM_015677	NM_015677	26751	-0,73	4,63E-04
EXOSC6	227696_at	AI701408	NM_058219	118460	-0,73	1,43E-03
SNIP	232547_at	BF062187	NM_025248	80725	-0,73	8,20E-06
AL833564	1563638_at	AL833564	---	---	-0,73	4,87E-05
MACF1	208633_s_at	W61052	NM_012090 NM_033044	23499	-0,73	9,23E-04
CIB1	201953_at	NM_006384	NM_006384	10519	-0,73	5,74E-04
RAMP1	204916_at	NM_005855	NM_005855	10267	-0,73	1,63E-03
AA694209	229066_at	AA694209	---	---	-0,73	9,44E-03
NOTCH4	205247_at	AI743713	NM_004557	4855	-0,73	5,43E-03
BF000009	243952_at	BF000009	---	---	-0,73	9,42E-03
NR2F1	209506_s_at	BC004154	NM_005654	7025	-0,73	4,54E-03
LOC92154	1555894_s_at	AA829283	NM_138383	92154	-0,73	9,70E-03
C9orf94	229585_at	AI803088	NM_152702	206938	-0,73	2,44E-03
MAN1A2	217922_at	AL157902	NM_006699	10905	-0,73	1,21E-03
CGI-119	223892_s_at	AF182414	NM_016056	51643	-0,73	1,67E-03
STAF65(gamma)	201836_s_at	AU154740	NM_014860	9913	-0,73	6,03E-03
PLXNA3	203623_at	AI675453	NM_017514	55558	-0,73	4,76E-04
SPATA11	223318_s_at	BC004393	NM_032306	84266	-0,73	9,26E-03

BE674055	236109_at	BE674055	---	---	-0,73	8,42E-03
KIAA2026	228446_at	BF062203	XM_088551	158358	-0,73	2,23E-03
CLN3	210859_x_at	AF077973	NM_000086	1201	-0,72	4,13E-03
AW129145	238992_at	AW129145	---	---	-0,72	3,88E-03
LOC201158	1552377_s_at	NM_145301	NM_145301	201158	-0,72	2,76E-03
FLJ31265	228341_at	AI809108	NM_152395	131870	-0,72	1,87E-03
BF111169	230820_at	BF111169	---	---	-0,72	1,14E-04
D8S2298E	215983_s_at	D83768	NM_005671	7993	-0,72	6,50E-03
AI424847	243218_at	AI424847	---	---	-0,72	4,14E-03
PCDHA9 PCDHAC2 PCDHAC1 PCDHA13 PCDHA12 PCDHA11 PCDHA10 PCDHA8 PCDHA7 PCDHA6 PCDHA5 PCDHA4 PCDHA3 PCDHA2 PCDHA1	224212_s_at	AF169689	NM_014005 NM_018898 NM_018899 NM_018900 NM_018901 NM_018902 NM_018903 NM_018904 NM_018905 NM_018906 NM_018907 NM_018908 NM_018909 NM_018910 NM_018911 NM_031410 NM_031411 NM_031495	56134 56135 56136 56137 56138 56139 56140 56141 56142 56143 56144 56145 56146 56147 9752	-0,72	5,55E-04
RBM5	201394_s_at	U23946	NM_005778	10181	-0,72	2,11E-03
AFFX-BioDn-3	AFFX-BioDn-3_at	AFFX-BioDn-3	---	---	-0,72	1,31E-04
WBSCR16	1554409_at	BC040695	NM_030798 NM_148842	81554	-0,72	5,09E-04
SYNJ1	212990_at	AB020717	NM_003895 NM_203446	8867	-0,72	6,07E-05
C19orf2	222266_at	BF796940	NM_003796 NM_134447	8725	-0,72	1,36E-03
RAPGEF2	203097_s_at	NM_014247	XM_376350	9693	-0,72	7,01E-03

PQBP1	207769_s_at	NM_005710	NM_005710 NM_144494 NM_144495	10084	-0,72	2,58E-03
LOC162967 FLJ38482	1555790_a_at	BC036301	NM_152681	162967 201931	-0,72	3,31E-03
EGFL4	214778_at	AB011541	NM_001410	1954	-0,72	3,38E-05
FLJ21148	219751_at	NM_024860	NM_024860	79918	-0,72	3,93E-04
KIAA0773	205368_at	NM_014690	NM_014690	9715	-0,72	3,08E-03
FBLP-1	1555480_a_at	AF459643	NM_017556	54751	-0,71	6,08E-03
PCDHA3	211870_s_at	AF152481	NM_018906 NM_031497	56145	-0,71	8,36E-04
ULK3	225067_at	AL117482	NM_015518	25989	-0,71	5,76E-04
ALS4	201965_s_at	NM_015046	NM_015046	23064	-0,71	1,86E-03
RASEF	243862_at	AW205358	NM_152573	158158	-0,71	2,57E-03
C16orf45	212736_at	BE299456	NM_033201	89927	-0,71	9,07E-06
PAK7	213990_s_at	BF056517	NM_020341 NM_177990	57144	-0,71	5,12E-03
SF3B3	200688_at	D13642	NM_012426	23450	-0,71	6,09E-04
BRSK1	1552504_a_at	NM_032430	NM_032430	84446	-0,71	8,13E-04
C14orf103	226684_at	AI217906	NM_018036	55102	-0,71	3,88E-03
SLC35E1	229410_at	AI659219	NM_024881	79939	-0,71	9,27E-04
NFYC	202215_s_at	NM_014223	NM_014223	4802	-0,71	1,98E-03
MRPL53	225523_at	AV726817	NM_053050	116540	-0,71	8,44E-04
C5orf14	220495_s_at	NM_024715	NM_024715	79770	-0,71	8,19E-03
RUFY1	218243_at	NM_025158	NM_025158	80230	-0,71	4,37E-04
C11orf11	214128_at	AB014559	NM_006133	747	-0,71	6,28E-03
ZNF404	239043_at	AA084273	XM_292765	342908	-0,71	6,01E-03
TTC3	208073_x_at	NM_003316	NM_00100189 4 NM_003316	7267	-0,71	3,39E-04
RNASET2	217984_at	NM_003730	NM_003730	8635	-0,71	8,81E-04
AI200555	228275_at	AI200555	---	---	-0,71	1,65E-03

NM_021031	220452_x_at	NM_021031	---	---	-0,71	1,15E-03
MGC16169	240269_at	BF590274	NM_033115	93627	-0,71	5,80E-03
BF590958	226243_at	BF590958	XM_372919	391356	-0,71	5,37E-05
RNF139	209510_at	AF064801	NM_007218	11236	-0,71	5,26E-04
CNOT4	210203_at	R64001	NM_001008225 NM_013316	4850	-0,71	8,35E-05
MCM3APAS	220459_at	NM_018118	---	114044	-0,70	3,02E-03
MGC42090	236705_at	AA017245	NM_152774	256130	-0,70	8,57E-03
KIAA2026	238490_at	BG109896	XM_088551	158358	-0,70	5,75E-03
SLC35E1	235035_at	BF342223	NM_024881	79939	-0,70	2,86E-03
KIAA0690	1559126_at	BC042908	NM_015179	23223	-0,70	2,78E-04
TIM14	225359_at	BF666961	NM_145261 NM_201259 NM_201260 NM_201261	131118	-0,70	5,32E-04
PHKA1	205450_at	NM_002637	NM_002637	5255	-0,70	2,40E-03
RNF13	201780_s_at	NM_007282	NM_007282 NM_183381 NM_183382 NM_183383 NM_183384	11342	-0,70	6,65E-03
CLASP2	212309_at	AV725315	NM_015097	23122	-0,70	9,41E-03
VPS11	203292_s_at	NM_021729	NM_021729	55823	-0,70	2,21E-03
AI791187	241724_x_at	AI791187	---	---	-0,70	4,52E-03
DCTN4	233490_at	AI985890	NM_016221	51164	-0,70	4,12E-03
LASS5	224951_at	BE348305	NM_147190	91012	-0,70	5,49E-04
SLC35E1	227518_at	AW051365	NM_024881	79939	-0,70	4,70E-03
SPPL3	224638_at	AI338356	NM_139015	121665	-0,70	2,98E-03
C11orf1	231530_s_at	BG150085	NM_022761	64776	-0,70	2,09E-04
RNF103	202636_at	NM_005667	NM_005667	7844	-0,69	5,99E-04
LOC134218	230893_at	AI223870	NM_194283	134218	-0,69	5,69E-03

C21orf59	218123_at	NM_017835	NM_017835 NM_021254	56683	-0,69	2,83E-04
C19orf12	227704_at	N21279	NM_031448	83636	-0,69	4,72E-03
ZF	213584_s_at	AI432137	NM_021212	58487	-0,69	2,28E-04
MGC4796	223852_s_at	BC005169	NM_032017	83931	-0,69	5,00E-03
C9orf112	225586_at	BF222775	NM_138778	92715	-0,69	2,74E-06
AK023354	222252_x_at	AK023354	---	---	-0,69	9,83E-04
AW873330	225674_at	AW873330	---	---	-0,69	9,10E-04
INSR	213792_s_at	AA485908	NM_000208	3643	-0,69	6,19E-03
C6orf111	212179_at	AW157501	NM_032870	25957	-0,69	2,41E-03
AY094612	1566887_x_at	AY094612	XM_499198	441699	-0,69	9,34E-03
ZNF275	225383_at	BF793625	XM_372267	10838	-0,68	4,76E-03
AA811371	238098_at	AA811371	---	---	-0,68	6,60E-03
RABGAP1L	203020_at	NM_014857	NM_014857	9910	-0,68	1,28E-04
ARHGEF2	235595_at	AW299534	NM_004723	9181	-0,68	2,77E-03
C6orf52	239417_x_at	AW103116	XM_371798	347744	-0,68	7,21E-05
DCL-1	232371_at	AU165401	NM_014880	9936	-0,68	4,13E-03
PPID	204185_x_at	NM_005038	NM_005038	5481	-0,68	1,13E-03
TP53	201746_at	NM_000546	NM_000546	7157	-0,68	6,97E-03
DHRSX	225503_at	AL547782	NM_145177	207063	-0,68	8,56E-05
ATF6	226941_at	BF439325	NM_007348	22926	-0,68	1,77E-03
PIK3R1	212240_s_at	AI679268	NM_181504 NM_181523 NM_181524	5295	-0,68	2,27E-03
AFFX-r2-Ec-bioD-5	AFFX-r2-Ec-bioD-5_at	AFFX-r2-Ec-bioD-5	---	---	-0,68	7,51E-04
CCNL1	220046_s_at	NM_020307	NM_020307	57018	-0,68	5,67E-04
BC017431	1570087_at	BC017431	---	---	-0,68	5,92E-03
P29	202553_s_at	NM_015484	NM_015484 NM_207170	25949	-0,68	7,53E-03
KIAA0256	212451_at	N52532	NM_014701	9728	-0,68	2,25E-03

PPP3CA	202425_x_at	NM_000944	NM_000944	5530	-0,68	4,15E-03
QTRT1	221270_s_at	NM_031209	NM_031209	81890	-0,68	7,11E-04
C21orf2	203994_s_at	U84569	NM_004928	755	-0,67	4,72E-06
KCNAB1	210471_s_at	U33428	NM_003471 NM_172159 NM_172160	7881	-0,67	3,93E-03
ASB6	222524_s_at	AF151697	NM_017873 NM_177999	140459	-0,67	1,52E-04
BF438106	228045_at	BF438106	---	---	-0,67	9,75E-03
NFYC	211797_s_at	U62296	NM_014223	4802	-0,67	5,31E-04
AI344253	238412_at	AI344253	---	---	-0,67	1,27E-03
ZNF551	211721_s_at	BC005868	NM_138347	90233	-0,67	3,58E-03
TETRAN	209215_at	L11669	NM_001120	10227	-0,67	2,16E-05
C9orf60	202452_at	AI991574	NM_006336	10444	-0,67	7,13E-04
IGF2AS	220561_at	NM_016412	NM_016412	51214	-0,67	8,13E-03
ERO1L	225750_at	BE966748	NM_014584	30001	-0,67	2,29E-06
MGC16028	226196_s_at	AW827281	NM_052873	112752	-0,67	6,84E-03
KIF1A	225482_at	AL533416	NM_004321	547	-0,67	2,15E-03
CAMTA1	213268_at	Z98884	NM_015215	23261	-0,67	4,84E-03
MAPT	203930_s_at	NM_016835	NM_005910 NM_016834 NM_016835 NM_016841	4137	-0,67	2,43E-03
MGC8721	200847_s_at	NM_016127	NM_016127	51669	-0,67	2,91E-03
LOC158563	226274_at	AK025562	---	158563	-0,67	3,76E-04
MAN1B1	218636_s_at	NM_016219	NM_016219	11253	-0,67	1,77E-05
SFRS7	213649_at	AA524053	NM_006276	6432	-0,67	7,31E-05
AK024117	234969_s_at	AK024117	---	---	-0,67	8,03E-04
AF336878	211454_x_at	AF336878	---	---	-0,67	4,04E-03
SPTBN1	212071_s_at	BE968833	NM_003128 NM_178313	6711	-0,67	1,01E-04

PCBD1	203557_s_at	NM_000281	NM_000281 NM_001001939	5092	-0,67	1,83E-04
CNOT6L	227119_at	BF103856	NM_144571	246175	-0,67	7,28E-04
SLC19A1	229489_at	AI681043	NM_003056 NM_194255	6573	-0,67	1,83E-03
C11orf1	222785_x_at	AJ250229	NM_022761	64776	-0,67	1,97E-04
ACOX1	227962_at	BF435852	NM_004035 NM_007292	51	-0,67	9,83E-03
VGLL4	214004_s_at	AI806207	NM_014667	9686	-0,67	1,59E-04
FBXL6	219189_at	NM_024555	NM_012162 NM_024555	26233	-0,67	5,47E-04
EIF3S9	242550_at	AA628539	NM_003751 NM_182712	8662	-0,67	2,25E-03
CYHR1	223421_at	BC005073	NM_032687	50626	-0,67	2,88E-03
PQBP1	214527_s_at	AB041836	NM_005710 NM_144494 NM_144495	10084	-0,67	7,86E-03
AA813998	235837_at	AA813998	---	---	-0,67	9,41E-03
MYST4	211874_s_at	AF119230	NM_012330	23522	-0,66	1,12E-03
CXXC5	233955_x_at	AK001782	NM_016463	51523	-0,66	8,92E-03
LOC54499	208715_at	BF002031	NM_019026	54499	-0,66	3,49E-04
LOC286437	229531_at	AW182938	---	286437	-0,66	9,60E-03
LOC283970	221992_at	AI925734	XM_498469	283970	-0,66	7,97E-05
PPT2	209826_at	AF020544	NM_005155 NM_138717 NM_138934	9374	-0,66	6,89E-03
GPR85	234303_s_at	AL161959	NM_018970	54329	-0,66	2,74E-03
KIAA0350	242728_at	AA705118	NM_015226	23274	-0,66	8,55E-03
C18orf23	230143_at	BF433220	NM_152470	147341	-0,66	6,22E-03
LOC493856	226689_at	AI749451	NM_001008388	493856	-0,66	3,86E-04
L1CAM	204584_at	AI653981	NM_000425 NM_024003	3897	-0,66	3,46E-03

FLNA	214752_x_at	AI625550	NM_001456	2316	-0,66	5,06E-03
CSNK1G1	220640_at	NM_022048	NM_001011664 NM_022048	53944	-0,66	7,24E-03
C19orf24	221587_s_at	BC000890	NM_017914	55009	-0,66	1,58E-03
KIF5C	203130_s_at	NM_004522	XM_377774	3800	-0,66	3,64E-03
CNOT4	210867_at	AF180475	NM_001008225 NM_013316	4850	-0,66	2,10E-03
ZNF502	229532_at	AI056364	NM_033210	91392	-0,66	4,74E-03
PCDHA9 PCDHAC2 PCDHAC1 PCDHA13 PCDHA12 PCDHA11 PCDHA10 PCDHA8 PCDHA7 PCDHA6 PCDHA5 PCDHA4 PCDHA3 PCDHA2 PCDHA1	210674_s_at	AF152308	NM_014005 NM_018898 NM_018899 NM_018900 NM_018901 NM_018902 NM_018903 NM_018904 NM_018905 NM_018906 NM_018907 NM_018908 NM_018909 NM_018910 NM_018911 NM_031410 NM_031411 NM_031495	56134 56135 56136 56137 56138 56139 56140 56141 56142 56143 56144 56145 56146 56147 9752	-0,66	1,36E-03
INPP5B	213804_at	AI039084	NM_005540	3633	-0,66	6,73E-03
RNF41	201962_s_at	NM_005785	NM_005785 NM_194358 NM_194359	10193	-0,66	3,92E-04
MLL2	227528_s_at	AI394529	NM_003482	8085	-0,66	1,08E-03
EPC1	223875_s_at	AF277374	NM_025209	80314	-0,66	6,07E-03
CLCN5	232127_at	AK021494	NM_000084	1184	-0,66	4,77E-03
BE549909	228172_at	BE549909	---	---	-0,66	4,49E-03
DTX3	49049_at	N92708	NM_178502	196403	-0,66	9,76E-03
AA491228	242176_at	AA491228	---	---	-0,66	3,24E-03

USP16	222616_s_at	AI806796	NM_001001992 NM_006447	10600	-0,66	3,36E-03
FLJ10824 LOC387680	212370_x_at	AL080183	NM_001005751 XM_290482	387680 55747	-0,66	2,44E-04
NFX1	1553103_at	NM_147134	NM_002504 NM_147133 NM_147134	4799	-0,66	5,66E-04
MAPRE3	203841_x_at	BG222594	NM_012326	22924	-0,66	1,69E-04
AW025023	228503_at	AW025023	---	---	-0,66	6,46E-03
EIF4G3	201935_s_at	AI768122	NM_003760	8672	-0,65	2,11E-03
KIAA1223	225731_at	BF196876	XM_048747	57182	-0,65	2,55E-03
RUFY1	233380_s_at	AA429145	NM_025158	80230	-0,65	2,87E-03
TMEM43	222418_s_at	AA115485	NM_024334	79188	-0,65	6,70E-03
SCMH1	221216_s_at	NM_012236	NM_012236	22955	-0,65	1,81E-06
NSMAF	203269_at	NM_003580	NM_003580	8439	-0,65	4,56E-03
TPP1	200743_s_at	NM_000391	NM_000391	1200	-0,65	7,89E-04
BSCL2	208906_at	BC004911	NM_032667	26580	-0,65	1,19E-03
SNCA	204466_s_at	BG260394	NM_000345 NM_007308	6622	-0,65	3,00E-06
AW452971	231152_at	AW452971	---	---	-0,65	2,61E-03
YWHAZ	214848_at	U79277	NM_003406 NM_145690	7534	-0,65	2,64E-04
MANSC1	220945_x_at	NM_018050	NM_018050	54682	-0,65	8,05E-04
SELT	225561_at	BF692332	NM_016275	51714	-0,65	1,05E-03
CHD2	228999_at	AW514564	NM_001271	1106	-0,65	1,05E-04
AI458020	238026_at	AI458020	---	---	-0,65	6,28E-04
MGC35048	216135_at	AK000122	NM_153208	124152	-0,65	3,59E-03
AI937687	232218_at	AI937687	---	---	-0,65	1,85E-03
PSENEN	218302_at	NM_018468	NM_172341	55851	-0,65	3,74E-03
LEMD3	218604_at	NM_014319	NM_014319	23592	-0,65	8,61E-05

KIAA0368	212427_at	AB002366	XM_036708	23392	-0,65	3,72E-04
CTSB	213275_x_at	W47179	NM_001908 NM_147780 NM_147781 NM_147782 NM_147783	1508	-0,65	8,91E-03
USP32	244871_s_at	AW268357	NM_032582	84669	-0,65	2,06E-03
GAS5	224741_x_at	BG329175	---	60674	-0,65	2,74E-03
ATP13A1	218052_s_at	NM_020410	NM_020410	57130	-0,65	1,62E-03
AA973100	230725_at	AA973100	---	---	-0,65	1,61E-03
MBD3 FLJ25976	222183_x_at	AL390153	NM_003926 NM_174943	283579 53615	-0,64	1,72E-03
CD248	219025_at	NM_020404	NM_020404	57124	-0,64	8,85E-04
PERQ1	228755_at	NM_022574	NM_022574	64599	-0,64	4,85E-03
FLJ10618	237741_at	AW514168	NM_018155	55186	-0,64	7,33E-03
TGFBRAP1	205210_at	NM_004257	NM_004257	9392	-0,64	3,31E-03
SNAP91	204953_at	NM_014841	NM_014841	9892	-0,64	7,24E-03
AI631833	227396_at	AI631833	---	---	-0,64	8,39E-03
MICAL2	212472_at	BE965029	NM_014632	9645	-0,64	2,60E-04
KIAA0592	211068_x_at	BC006456	NM_015262	253725	-0,64	1,32E-03
RBM8A	213852_at	BG289199	NM_005105	9939	-0,64	9,90E-03
TMAP1	227326_at	BE966768	NM_001008528 NM_001008529 NM_198530	439921	-0,64	8,06E-03
MRPL1	223154_at	AF212225	NM_020236	65008	-0,64	1,18E-03
IDS	1559136_s_at	AU140213	NM_000202 NM_006123	3423	-0,64	1,45E-03
TRIM8	221012_s_at	NM_030912	NM_030912	81603	-0,64	3,17E-04
C1orf27	222720_x_at	W72877	NM_017847	54953	-0,64	2,02E-04
TPP1	214196_s_at	AA602532	NM_000391	1200	-0,64	2,31E-03
PMS2L2	215412_x_at	AB017007	NM_002679	5380	-0,64	9,44E-03

KIAA0276	243691_at	AA150455	NM_015115	23142	-0,63	1,60E-03
AV736334	237561_x_at	AV736334	---	---	-0,63	5,35E-03
LOC148189	235191_at	BE780373	---	148189	-0,63	7,40E-03
FBXL2	214436_at	AF176518	NM_012157	25827	-0,63	6,41E-03
HT036	223769_x_at	AF284750	NM_031207	81888	-0,63	1,42E-04
MLX	217910_x_at	NM_013383	NM_170607 NM_198204 NM_198205	6945	-0,62	8,02E-03
C5orf5	218518_at	NM_016603	NM_016603	51306	-0,62	3,54E-03
AI652919	230581_at	AI652919	---	---	-0,62	3,52E-03
BF196255	229921_at	BF196255	---	---	-0,62	4,55E-03
KCNF1	210263_at	AF029780	NM_002236	3754	-0,62	7,86E-03
LKAP	202386_s_at	NM_019081	NM_014647 NM_019081	9665	-0,62	2,93E-05
AU151222	227526_at	AU151222	---	---	-0,62	1,49E-04
ZNF266	214686_at	AA868898	NM_006631 NM_198058	10781	-0,62	3,90E-03
MAGI-3	226770_at	AI692181	NM_020985 NM_152900	260425	-0,62	8,14E-04
HNRPR	208765_s_at	NM_005826	NM_005826	10236	-0,62	1,26E-03
TSTA3	36936_at	U58766	NM_003313	7264	-0,62	6,42E-03
AK001513	233642_s_at	AK001513	---	---	-0,62	2,84E-04
OGT	212307_s_at	BF001665	NM_003605 NM_181672. NM_181673	8473	-0,62	2,58E-03
POMT2	225560_at	AK023804	NM_013382	29954	-0,62	4,78E-03
KIAA1340	225732_at	AU146850	NM_020782	57542	-0,62	5,78E-03
FLJ21148	1554555_a_at	BC022451	NM_024860	79918	-0,61	3,94E-04
ZFX	229022_at	AI745209	NM_003410	7543	-0,61	5,57E-03
GPR56	212070_at	AL554008	NM_005682 NM_201524 NM_201525	9289	-0,61	6,44E-03

PTEN	225363_at	AK024986	NM_000314	5728	-0,64	4,41E-03
C15orf24	217898_at	NM_020154	NM_020154	56851	-0,64	1,32E-03
SELT	217811_at	NM_016275	NM_016275	51714	-0,64	1,82E-04
URB	225242_s_at	AW303375	NM_199511 NM_199512	151887	-0,64	6,81E-03
EFHC1	219833_s_at	NM_018100	NM_018100	114327	-0,64	1,22E-03
AW970002	235660_at	AW970002	---	---	-0,64	4,41E-03
C14orf43	225980_at	AV740879	NM_194278	91748	-0,64	1,54E-03
DKFZP564J102	214890_s_at	AL080065	NM_001006655 NM_015398	25854	-0,63	7,10E-03
STARD7	236484_at	AW850611	NM_020151 NM_139267	56910	-0,63	1,49E-04
AW519141	227444_at	AW519141	---	---	-0,63	1,87E-03
TTC3	210645_s_at	D83077	NM_001001894 NM_003316	7267	-0,63	2,39E-03
SCN3B	204722_at	AW007335	NM_018400	55800	-0,63	5,01E-05
ATF6	217550_at	AA576497	NM_007348	22926	-0,63	5,13E-03
OFD1	203569_s_at	NM_003611	NM_003611	8481	-0,63	4,46E-04
ITPK1	210740_s_at	AF279372	NM_014216	3705	-0,63	7,31E-04
CCNDBP1	223084_s_at	AF246144	NM_012142 NM_037370	23582	-0,63	1,14E-04
BEX2	224367_at	AF251053	NM_032621	84707	-0,63	5,01E-03
KIAA1387	226230_at	AA541716	NM_020463	57223	-0,63	8,30E-03
DND1	222070_at	AW090043	NM_194249	373863	-0,63	9,36E-03
MLL2	227527_at	AI394529	NM_003482	8085	-0,63	6,88E-03
C5orf14	227873_at	BE547587	NM_024715	79770	-0,63	3,10E-03
TMED4	224680_at	AL539253	NM_182547	222068	-0,63	6,32E-04
MTMR1	216095_x_at	AF057354	NM_003828 NM_176789	8776	-0,63	7,62E-03
MAP3K12	205448_s_at	NM_006301	NM_006301	7786	-0,63	1,84E-03

BBS7	235007_at	AI683802	NM_018190 NM_176824	55212	-0,61	9,30E-03
EIF2C4	227930_at	AI669957	NM_017629	192670	-0,61	7,32E-03
FLJ13868	222190_s_at	BC000822	NM_022744	64755	-0,61	6,09E-03
AI524240	238863_x_at	AI524240	---	---	-0,61	5,90E-03
AI140364	221740_x_at	AI140364	XM_373737	388397	-0,61	5,62E-03
PRO1853	220943_s_at	NM_018607	NM_018607 NM_144736	55471	-0,61	4,64E-04
FLJ20850	51200_at	AI744084	NM_017967	55049	-0,61	7,02E-05
TGDS	237346_at	AA976208	NM_014305	23483	-0,61	7,82E-03
COMMD10	240595_at	AA928078	NM_016144	51397	-0,61	3,63E-04
FLJ31340	235301_at	AI797353	NM_152748	222223	-0,61	4,73E-04
C2orf17	221984_s_at	AL040896	NM_024293	79137	-0,61	7,61E-03
VPS54	222627_at	AK002205	NM_001005739 NM_016516	51542	-0,61	8,85E-03
WDR9	225446_at	AI638279	NM_001007246 NM_018963 NM_033656	54014	-0,61	6,06E-03
LOC157697	227016_at	AA767385	NM_207332	157697	-0,61	8,34E-03
SLC35E1	79005_at	AA504646	NM_024881	79939	-0,61	2,09E-03
RFX1	226786_at	BF507952	NM_002918	5989	-0,61	1,11E-03
MDS028	220589_s_at	NM_018463	NM_018463	55846	-0,61	4,18E-04
RNF111	241413_at	W80457	NM_017610	54778	-0,61	4,93E-03
RPL10	221989_at	AW057781	NM_006013	6134	-0,61	8,66E-03
NR1H2	218215_s_at	NM_007121	NM_007121	7376	-0,61	3,22E-05
TSPYL2	218012_at	NM_022117	NM_022117	64061	-0,61	4,00E-03
COG7	213190_at	R61519	NM_153603	91949	-0,60	1,96E-03
NM_018507	219599_at	NM_018507	---	---	-0,60	7,03E-03
ZNF638	213775_x_at	AI357871	NM_014497	27332	-0,60	9,27E-03

ABCD4	203981_s_at	AL574660	NM_005050 NM_020323 NM_020324 NM_020325 NM_020326	5826	-0,60	1,48E-04
MKLN1	243959_at	N35099	NM_013255	4289	-0,60	8,87E-04
AFFX-r2-Ec-bioD-3	AFFX-r2-Ec-bioD-3_at	AFFX-r2-Ec-bioD-3	---	---	-0,60	1,47E-03
KIAA1277	53991_at	AA127623	NM_015689	27147	-0,60	1,38E-03
RAB11B	217793_at	AL575337	NM_004218	9230	-0,60	8,56E-04
KRTCAP3	235148_at	BF680458	NM_173853	200634	-0,60	6,87E-03
ILVBL	210624_s_at	BC000109	NM_006844 NM_176826	10994	-0,60	9,87E-03
CACNB1	210185_at	AB054985	NM_000723 NM_199247 NM_199248	782	-0,60	3,90E-04
ZFYVE28	1569369_at	BC035793	NM_020972	57732	-0,60	2,58E-05
C21orf127	220311_at	NM_013240	NM_013240 NM_182749	29104	-0,60	3,00E-03
SNAPC3	229712_at	AI066599	NM_003084	6619	-0,60	8,08E-04
JAM3	212813_at	AA149644	NM_032801	83700	-0,60	2,27E-05
KPNA1	202057_at	BC002374	NM_002264	3836	-0,60	8,33E-03
HEL308	1554342_s_at	BC011863	NM_133636	113510	-0,60	9,43E-03
ET	221192_x_at	NM_024311	NM_024311	79157	-0,60	2,02E-03
SNRPB2	1561965_at	BE466925	NM_003092 NM_198220	6629	-0,60	2,74E-03
MLL	212080_at	AV714029	NM_005933	4297	-0,60	4,11E-03
FAIM2	203618_at	AB023167	NM_012308	23017	-0,60	3,14E-03
RASA2	230669_at	W38444	NM_006506	5922	-0,59	4,05E-03
GRIK5	214966_at	S40369	NM_002088	2901	-0,59	4,00E-03
PARP6	234710_s_at	AK021790	NM_020213 NM_020214	56965	-0,59	2,29E-04
DXYS155E	203624_at	NM_005088	NM_005088	8227	-0,59	9,05E-03

DUSP3	201536_at	AL048503	NM_004090	1845	-0,59	5,91E-03
FLJ10324	223693_s_at	AL136731	NM_018059	55698	-0,59	4,22E-04
KATNB1	203163_at	NM_005886	NM_005886	10300	-0,59	1,72E-03
C12orf10	218220_at	NM_021640	NM_021640	60314	-0,59	4,83E-03
SCN3B	204723_at	AB032984	NM_018400	55800	-0,59	5,81E-04
IL17D	227401_at	BE856748	NM_138284	53342	-0,59	5,23E-04
TUSC3	209228_x_at	U42349	NM_006765 NM_178234	7991	-0,59	8,59E-05
ATP6AP1	207809_s_at	NM_001183	NM_001183	537	-0,59	3,60E-03
DKFZP564D166	224952_at	BF115054	XM_371074	26115	-0,59	7,36E-06
SFRS5	203380_x_at	NM_006925	NM_006925	6430	-0,59	3,73E-03
MRX85	225867_at	BE741869	NM_138440	114990	-0,59	2,02E-03
SBF2	226169_at	AW276572	NM_030962	81846	-0,59	9,95E-04
CDC16	209658_at	AF164598	NM_003903	8881	-0,59	7,37E-03
LOC493856	226686_at	AI188518	NM_001008388	493856	-0,59	3,94E-03
LAMB2	216264_s_at	X79683	NM_002292	3913	-0,59	5,67E-03
FLJ10826	225110_at	AK024314	NM_018233	55239	-0,59	4,75E-03
TLOC1	208942_s_at	BE866511	NM_003262	7095	-0,59	2,74E-03
VPS24	222436_s_at	AF219226	NM_001005753 NM_016079	51652	-0,59	9,34E-04
ECE2	230706_s_at	AI084921	NM_014693	9718	-0,59	5,56E-04
ZNF292	212368_at	AA972711	XM_048070	23036	-0,59	8,05E-04
AK022413	233658_at	AK022413	---	---	-0,59	7,17E-03
FLNA	200859_x_at	NM_001456	NM_001456	2316	-0,59	6,02E-03
TIGD1	1553099_at	NM_145702	NM_145702	200765	-0,59	5,58E-03
HUMPPA	213230_at	AI422335	NM_014603	30850	-0,59	2,36E-04
NUDT13	214136_at	W80642	NM_015901	25961	-0,58	8,37E-03
NMT2	215069_at	AK025065	NM_004808	9397	-0,58	5,28E-03

LOC51255	223064_at	AF151072	NM_016494	51255	-0,58	8,47E-04
NPD014	209007_s_at	AF267856	NM_020317 NM_207035	57035	-0,58	6,29E-03
DGKD	208072_s_at	NM_003648	NM_003648 NM_152879	8527	-0,58	5,37E-04
FLJ10824 LOC387680	212929_s_at	W68158	NM_00100575 1 XM_290482	387680 55747	-0,58	9,32E-03
AL049985	215507_x_at	AL049985	---	---	-0,58	4,06E-03
PCNXL2	1554256_a_at	BC008300	NM_014801 NM_024938	80003	-0,58	9,20E-03
MGC54289	225228_at	AI474054	NM_178454	128338	-0,58	2,51E-04
FBXL14	213145_at	BF001666	NM_152441	144699	-0,58	2,17E-03
TFG	239385_at	AI150613	NM_00100756 5 NM_006070	10342	-0,58	1,31E-03
MACF1	215222_x_at	AK023406	NM_012090 NM_033044	23499	-0,58	6,16E-03
AW268719	236798_at	AW268719	---	---	-0,58	1,80E-04
BRUNOL6	227775_at	BE467313	NM_052840	60677	-0,58	7,34E-03
CLN3	209275_s_at	AF015593	NM_000086	1201	-0,58	5,20E-04
CKLFSF3	224733_at	AL574900	NM_144601 NM_181553 NM_181554 NM_181555	123920	-0,58	6,40E-04
DSCR1	208370_s_at	NM_004414	NM_004414 NM_203417 NM_203418	1827	-0,58	2,94E-03
PFDN5	210908_s_at	AB055804	NM_002624 NM_145896 NM_145897	5204	-0,58	9,12E-04
AA206016	228191_at	AA206016	---	---	-0,58	2,94E-03
IDS	212221_x_at	AV703259	NM_000202 NM_006123	3423	-0,58	7,55E-06
ZNF295	225539_at	AP001745	NM_020727	49854	-0,58	4,67E-03
AW292996	236330_at	AW292996	---	---	-0,58	3,90E-03

LOC253982	214993_at	AF070642	NM_181718 NM_198907	253982	-0,58	6,71E-04
USP24	212388_at	AB028980	XM_371254	23358	-0,58	1,07E-03
AW237752	229699_at	AW237752	---	---	-0,58	7,54E-03
UNQ1912	226752_at	AI816071	NM_198507	345757	-0,58	1,56E-03
PHC1	225958_at	AI554106	NM_004426	1911	-0,58	2,64E-03
PAN3	225563_at	AI970788	NM_175854	255967	-0,58	1,42E-04

Tabla 9. Expresión genética aumentada en las líneas celulares H1 y BB10 en comparación con la línea celular SIMa en estado no diferenciado usando análisis de micromatriz

Símbolo del gen	**ID del conjunto de sondas**	**ID Pública representativa**	**ID de transcripción RefSec**	**ID de Gen Entrez**	**Proporción Log2**	**valor p**
DAZ1 DAZ3 DAZ2 DAZ4	208282_x_at	NM_020363	NM_001005375 NM_001005785 NM_001005786 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	6,15	6,22E-05
BF476109	1556300_s_at	BF476109	---	---	6,07	4,58E-08
DAZ1 DAZ3 DAZ2 DAZ4	207909_x_at	U21663	NM_001005375 NM_001005785 NM_001005786 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	6,03	3,64E-05
TIMP3	201147_s_at	BF347089	NM_000362	7078	5,78	9,00E-07
LUM	201744_s_at	NM_002345	NM_002345	4060	5,28	9,11E-07
SIM1	206876_at	AL121948	NM_005068	6492	5,13	3,40E-06
TIMP3	201149_s_at	U67195	NM_000362	7078	5,09	4,07E-05
CXCR4	209201_x_at	L01639	NM_001008540 NM_003467	7852	4,91	1,18E-03

GRP	206326_at	NM_002091	NM_002091	2922	4,77	1,84E-06
MGC24103	232568_at	AU145658	---	158295	4,71	1,34E-05
CXCR4	211919_s_at	AF348491	NM_001008540 NM_003467	7852	4,65	1,78E-03
KCTD12	212192_at	AI718937	NM_138444	115207	4,61	1,59E-05
DAZ1 DAZ3 DAZ2 DAZ4	207912_s_at	NM_004081	NM_001005375 NM_001005785 NM_001005786 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	4,39	5,11E-04
DAZ1 DAZ3 DAZ2 DAZ4	216922_x_at	AF271088	NM_001005375 NM_001005785 NM_001005786 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	4,30	4,72E-04
DAZ1 DAZ3 DAZ2 DAZ4	208281_x_at	NM_020364	NM_001005375 NM_001005785 NM_001005786 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	4,30	3,22E-04
PTPRE	221840_at	AA775177	NM_006504 NM_130435	5791	4,28	4,00E-07
AF086027	1559697_a_at	AF086027	---	---	4,28	1,11E-04
BNC2	233036_at	AU146418	NM_017637	54796	4,20	2,05E-04
H99792	225710_at	H99792	---	---	4,20	1,70E-06
DKFZp667G2110	214030_at	BE501352	XM_376254	131544	4,19	1,81E-09
AL049260	216518_at	AL049260	---	---	4,16	8,81E-04
AU144918	233858_at	AU144918	---	---	4,15	1,87E-05
GPC6	233090_at	AU144140	NM_005708	10082	4,08	1,76E-03
TIMP3	201150_s_at	NM_000362	NM_000362	7078	4,04	7,75E-05
ALCAM	240655_at	BE502785	NM_001627	214	3,98	1,71E-04
SSBP2	1557813_at	BF724621	NM_012446	23635	3,98	1,18E-03

C1orf1	233306_at	AK021509	---	711	3,97	8,32E-06
ARHGAP6	206167_s_at	NM_001174	NM_001174 NM_006125 NM_013422 NM_013423 NM_013427	395	3,91	9,85E-05
TFPI2	209278_s_at	L27624	NM_006528	7980	3,87	1,53E-06
AL049337	215768_at	AL049337	---	---	3,87	3,23E-03
FLJ39639	243547_at	BE176531	XM_370932	283876	3,83	3,19E-04
KIAA1944	236377_at	AW166133	NM_133448	121256	3,80	2,79E-03
AF086027	1559696_at	AF086027	---	---	3,77	3,26E-05
VIP	206577_at	NM_003381	NM_003381 NM_194435	7432	3,72	1,05E-03
CCDC3	223316_at	AL136562	NM_031455	83643	3,72	8,39E-06
POLQ	207746_at	NM_014125	NM_006596 NM_199420	10721	3,54	1,20E-04
SLAC2-B	214734_at	AB014524	NM_015065	23086	3,53	2,59E-03
GPC6	232453_at	AF339813	NM_005708	10082	3,52	8,95E-04
MBNL1	241681_at	AW296451	NM_021038 NM_207292 NM_207293 NM_207294 NM_207295 NM_207296 NM_207297	4154	3,50	2,40E-03
EML4	233940_at	AK022801	NM_019063	27436	3,49	4,67E-03
AW974642	1558410_s_at	AW974642	XM_499534	442612	3,49	1,47E-03
RGS5	1555725_a_at	AF493929	NM_003617	8490	3,47	3,83E-03
TIMP3	201148_s_at	AW338933	NM_000362	7078	3,46	9,21E-03
AI939547	243004_at	AI939547	---	---	3,45	6,37E-03
SLITRK5	214930_at	AW449813	NM_015567	26050	3,42	1,80E-05
GFRA2	205722_s_at	NM_001495	NM_001495	2675	3,38	1,70E-03
RGS5	209070_s_at	AI183997	NM_003617	8490	3,32	3,17E-03
EML1	204797_s_at	NM_004434	NM_001008707 NM_004434	2009	3,29	2,09E-04
FBXL7	241457_at	AI821935	NM_012304	23194	3,27	1,14E-03
PLK2	201939_at	NM_006622	NM_006622	10769	3,27	1,65E-06
NEGR1	243357_at	AA115106	NM_173808	257194	3,26	2,19E-06
ELOVL7	227180_at	AW138767	XM_371740	79993	3,26	3,23E-03
SPAG6	210033_s_at	AF079363	NM_012443 NM_172242	9576	3,23	3,60E-05
FLJ39660	1553459_at	NM_173646	NM_173646	284992	3,22	5,48E-03
NEDD9	202150_s_at	U64317	NM_006403 NM_182966	4739	3,22	1,70E-04
PDZRN3	233442_at	AU147500	NM_015009	23024	3,21	2,82E-05
TRIM29	211002_s_at	AF230389	NM_012101 NM_058193	23650	3,18	3,79E-05

PCDH9	219737_s_at	AI524125	NM_020403 NM_203487	5101	3,13	7,67E-06
FAT	201579_at	NM_005245	NM_005245	2195	3,11	4,81E-03
NEDD9	202149_at	AL136139	NM_006403 NM_182966	4739	3,08	2,64E-04
ITGA6	201656_at	NM_000210	NM_000210	3655	3,07	8,91E-05
DAZ1 DAZ3 DAZ2 DAZ4	216351_x_at	AF248483	NM_001005375 NM_001005785 NM_001005786 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	3,06	3,84E-04
FLJ37266	1566948_at	AL831894	NM_175892	283225	3,06	3,09E-03
EFNA5	1559360_at	AL833045	NM_001962	1946	3,03	1,65E-05
RPL10A	242188_at	AI743332	NM_007104	4736	3,03	2,49E-03
BE466926	217671_at	BE466926	---	---	3,02	9,00E-03
PTPRG	1569323_at	BU853579	NM_002841	5793	3,01	1,51E-05
CUGBP2	202158_s_at	NM_006561	NM_006561	10659	3,01	8,47E-05
TULP4	232372_at	AL157491	NM_001007466 NM_020245	56995	3,01	6,44E-03
BC043430	1558714_at	BC043430	---	---	2,99	6,39E-03
LOC340109	1557765_at	BC039509	XM_379322	340109	2,99	6,58E-05
DKFZp761O2018	232313_at	AL122107	XM_044062	92293	2,98	3,82E-05
RGS5	218353_at	NM_025226	NM_003617	8490	2,96	3,43E-03
CHRNA7 CHRFAM7A	210123_s_at	U62436	NM_000746 NM_139320 NM_148911	1139 89832	2,96	5,22E-06
LOC440265	1569476_at	BC033224	XM_378506	440265	2,90	2,51E-03
ARHGEF6	209539_at	D25304	NM_004840	9459	2,90	7,95E-05
AL049277	234839_at	AL049277	---	---	2,89	4,82E-03
KIAA0265	238000_at	BF195340	NM_014997	23008	2,85	2,90E-04
DACT1	219179_at	NM_016651	NM_016651	51339	2,85	4,31E-04
KCTD12	212188_at	AA551075	NM_138444	115207	2,84	1,79E-04
RGS5	209071_s_at	AF159570	NM_003617	8490	2,84	3,29E-03
AL832561	1561689_at	AL832561	---	---	2,84	3,60E-05
AA872187	230332_at	AA872187	---	---	2,82	1,50E-03
BG542611	1556277_a_at	BG542611	---	---	2,81	2,09E-03
PIAS2	244633_at	AA404996	NM_004671 NM_173206	9063	2,80	3,93E-05
AI630830	243150_at	AI630830	---	---	2,79	2,12E-03
UCHL1	1555834_at	AW974143	NM_004181	7345	2,77	3,11E-03
TRIO	235705_at	BF676361	NM_007118	7204	2,76	4,51E-04
AK022040	233445_at	AK022040	---	---	2,76	7,74E-04
CBLN2	242301_at	R60224	NM_182511	147381	2,76	3,83E-03

MID1	242671_at	BF055144	NM_000381 NM_033290 NM_033291	4281	2,74	4,62E-04
BC041991	1561690_at	BC041991	---	---	2,73	2,25E-03
EML4	232587_at	AI208611	NM_019063	27436	2,72	8,16E-03
TRIM29	202504_at	NM_012101	NM_012101 NM_058193	23650	2,70	1,08E-03
AW139261	243934_at	AW139261	---	---	2,69	5,92E-03
ROBO2	226709_at	BE858548	XM_031246	6092	2,69	1,07E-04
MEF2A	239571_at	AI123399	NM_005587	4205	2,68	1,53E-04
KIAA1128	240499_at	AA482221	NM_018999	54462	2,68	8,42E-03
KLF7	239809_at	BF197708	NM_003709	8609	2,65	5,01E-03
CALCA	217561_at	BF447272	NM_001741	796	2,62	2,08E-03
LOC51760	205613_at	NM_016524	NM_016524	51760	2,61	5,89E-03
EDD	232264_at	AK022204	NM_015902	51366	2,61	7,50E-04
LOC440161	243241_at	AW341473	XM_498572	440161	2,61	2,72E-04
SCHIP1	1566772_at	AL832567	NM_014575	29970	2,61	1,17E-03
TFPI2	209277_at	AL574096	NM_006528	7980	2,61	6,75E-04
EML4	1556732_at	BC039354	NM_019063	27436	2,59	2,34E-03
AA808231	242025_at	AA808231	---	---	2,59	1,52E-04
CUGBP2	202157_s_at	U69546	NM_006561	10659	2,59	6,58E-06
PAPD4	222282_at	AV761453	NM_173797	167153	2,57	4,37E-03
MGC14161	240502_at	AW015920	NM_032892	84978	2,55	2,58E-03
UBE3A	1560741_at	AL832250	NM_000462 NM_130838 NM_130839	7337	2,54	5,57E-03
LRRC5	234148_at	AK025238	NM_018103	55144	2,54	8,12E-04
PEX5L	1562473_at	BC037943	NM_016559	51555	2,54	7,14E-04
IMP-2	218847_at	NM_006548	NM_001007225 NM_006548	10644	2,54	9,50E-05
C2orf31	221245_s_at	NM_030804	---	81561	2,51	8,63E-05
AK024882	233228_at	AK024882	---	---	2,50	4,73E-04
TAS2R45	234042_at	AF264628	NM_176886	259291	2,50	4,78E-04
KIAA1102	241459_at	AI494113	NM_014988	22998	2,48	4,62E-05
BC041965	1560411_at	BC041965	---	---	2,47	7,60E-03
USP31	239348_at	AI285970	NM_020718	57478	2,47	5,27E-03
AU144294	215574_at	AU144294	---	---	2,47	3,25E-03
RNF152	233180_at	AU147152	NM_173557	220441	2,46	7,81E-03
LOC440738	221697_at	AF276659	NM_001004343	440738	2,45	2,37E-03
KATNAL1	243828_at	AA758906	NM_032116	84056	2,44	1,32E-03
MGC39558	1562391_at	AK091497	NM_152490	148789	2,44	7,21E-03
GNG11	204115_at	NM_004126	NM_004126	2791	2,43	1,79E-04
AI076172	236355_s_at	AI076172	XM_495841	439993	2,42	3,12E-03
ITPR1	240052_at	AA648993	NM_002222	3708	2,42	1,52E-04
IARS	239794_at	AI356405	NM_002161 NM_013417	3376	2,42	2,89E-04

PLXNA4	232317_at	AB046770	XM_039393 XM_379927	57671	2,41	8,26E-05
AURKB	239219_at	N55457	NM_004217	9212	2,41	5,13E-04
FBXL7	233276_at	AU146390	NM_012304	23194	2,41	3,40E-04
CDH2	237305_at	AW450381	NM_001792	1000	2,40	2,95E-03
SPRY4	1566968_at	AK024556	NM_030964	81848	2,40	1,67E-05
SYT4	223529_at	AB037763	NM_020783	6860	2,40	4,26E-04
PPP4R2	1560926_at	AF085924	NM_174907	151987	2,38	6,45E-03
BE674460	237849_at	BE674460	---	---	2,38	7,15E-04
AK024956	232726_at	AK024956	---	---	2,37	2,24E-03
PITPNB	242074_at	AA833902	NM_012399	23760	2,37	2,45E-04
KIAA0485	214295_at	AW129056	---	57235	2,36	6,51E-04
BF000203	236385_at	BF000203	---	---	2,33	1,55E-03
BNC2	220272_at	NM_017637	NM_017637	54796	2,33	3,96E-04
SDFR1	242865_at	AI332638	NM_012428 NM_017455	27020	2,31	1,45E-04
DTNA	1557803_at	AF086074	NM_001390 NM_001391 NM_001392 NM_032975 NM_032978 NM_032979 NM_032980 NM_032981	1837	2,31	3,61E-04
NRCAM	233401_at	BF723605	NM_005010	4897	2,31	1,07E-03
FOXO3A	1569477_at	BC025999	NM_001455 NM_201559	2309	2,31	5,92E-03
MSN	200600_at	NM_002444	NM_002444	4478	2,30	1,14E-05
AL832142	1561195_at	AL832142	---	---	2,30	2,10E-03
EDG3	228176_at	AA534817	NM_005226	1903	2,29	2,67E-03
ASCL1	209985_s_at	BE797438	NM_004316	429	2,28	9,42E-05
LOC146174	233832_at	AK021824	NM_173501	146174	2,27	3,37E-04
PLXNA4	228104_at	AL117427	XM_039393 XM_379927	57671	2,26	7,59E-04
KIDINS220	1557246_at	AA992480	NM_020738	57498	2,26	5,87E-03
GFRA2	205721_at	U97145	NM_001495	2675	2,25	3,08E-03
LOC440092	1570571_at	BC035168	XM_498540	440092	2,25	3,18E-05
ROBO2	226766_at	AB046788	XM_031246	6092	2,25	3,58E-05
GAB2	1566959_at	AL049273	NM_012296 NM_080491	9846	2,24	9,27E-03
ARHGAP6	1563386_at	AL079282	NM_001174 NM_006125 NM_013422 NM_013423 NM_013427	395	2,24	2,24E-03
PCNX	215175_at	AB023212	NM_014982	22990	2,24	3,95E-03
C10orf18	216211_at	AL049233	XM_374765	54906	2,23	1,64E-03
AI678013	240165_at	AI678013	---	---	2,22	1,17E-03
AI653240	240247_at	AI653240	XM_496059	440261	2,21	1,90E-04

GFM1	232295_at	AK000780	NM_024996	85476	2,20	4,88E-03
AF116659	210717_at	AF116659	---	---	2,20	2,72E-03
NM_018611	220666_at	NM_018611	---	---	2,20	3,83E-03
PFKFB3	202464_s_at	NM_004566	NM_004566	5209	2,20	1,42E-03
AI671885	230494_at	AI671885	XM_379123	400999	2,20	4,83E-04
TPBG	203476_at	NM_006670	NM_006670	7162	2,20	1,21E-07
ITGA6	215177_s_at	AV733308	NM_000210	3655	2,19	2,48E-03
AW008791	240315_at	AW008791	XM_294019	345930	2,19	7,20E-03
C10orf18	244165_at	AI809511	XM_374765	54906	2,18	1,55E-03
FLJ21148	231005_at	T91195	NM_024860	79918	2,18	3,18E-04
DEFB32	243311_at	BE044548	NM_207469	400830	2,18	1,71E-03
THRAP2	232307_at	AK021554	NM_015335	23389	2,18	7,79E-04
BF057073	231310_at	BF057073	---	---	2,16	3,16E-05
CFDP1	210701_at	D85939	NM_006324	10428	2,16	1,15E-03
SYNE2	242774_at	AI684761	NM_015180 NM_182910 NM_182912 NM_182913 NM_182914	23224	2,16	3,57E-03
RNF182	230720_at	AI884906	NM_152737	221687	2,15	1,49E-04
PAPD4	242144_at	AW104325	NM_173797	167153	2,15	8,28E-03
DKFZp761D221	241872_at	AI149963	NM_032291	84251	2,15	7,56E-03
NFIB	230791_at	AU146924	NM_005596	4781	2,14	1,39E-03
PTGFRN	224937_at	BF311866	NM_020440	5738	2,14	1,95E-03
FOXO3A	242320_at	AI435586	NM_001455 NM_201559	2309	2,13	1,69E-03
SSBP2	1557814_a_at	BF724621	NM_012446	23635	2,13	6,51E-03
KLF12	243089_at	AA551114	NM_007249 NM_016285	11278	2,13	1,78E-03
EXT1	232174_at	AA480392	NM_000127	2131	2,13	2,01E-04
MGC4504	219270_at	NM_024111	NM_024111	79094	2,13	2,30E-03
TTL	244078_at	AI438957	NM_153712	150465	2,12	1,97E-04
ODZ3	233291_at	AU145618	XM_371717	55714	2,11	2,81E-04
MSI2	239232_at	AA521410	NM_138962 NM_170721	124540	2,11	7,13E-04
ZNF403	233937_at	AK024883	NM_024835	79893	2,11	2,80E-04
FRZB	203698_s_at	NM_001463	NM_001463	2487	2,10	6,12E-03
ATP1B4	243737_at	AI082610	NM_012069	23439	2,10	3,38E-03
AI077566	243994_at	AI077566	---	---	2,09	3,50E-03
GATA4	243692_at	AW181962	NM_002052	2626	2,09	2,75E-03
ID2	213931_at	AI819238	NM_002166	3398	2,09	3,49E-04
N21631	231329_at	N21631	---	---	2,08	3,60E-03
GNAI1	209576_at	AL049933	NM_002069	2770	2,08	4,56E-05
ZNF292	236435_at	BE219036	XM_048070	23036	2,08	7,00E-03
NEDD9	233223_at	AK000850	NM_006403 NM_182966	4739	2,07	4,93E-04
UBE2E3	232528_at	AI338705	NM_006357 NM_182678	10477	2,06	7,31E-03
PAN3	239393_at	AW510927	NM_175854	255967	2,05	4,66E-03

SMARCC1	239238_at	AI208857	NM_003074	6599	2,04	7,80E-04
MTMR2	231057_at	AU144266	NM_016156 NM_201278 NM_201281	8898	2,04	8,90E-05
MGC33926	229302_at	AA058832	NM_152390	130733	2,04	4,33E-05
DREV1	230395_at	AI536637	NM_016025	51108	2,04	3,23E-03
AF238870	215811_at	AF238870	---	---	2,04	1,97E-03
DMXL2	215761_at	AK000156	NM_015263	23312	2,04	2,78E-04
MAOA	204388_s_at	NM_000240	NM_000240	4128	2,04	7,48E-04
OSBPL3	209626_s_at	AI202969	NM_015550 NM_145320 NM_145321 NM_145322 NM_145323 NM_145324	26031	2,04	1,76E-03
AL161982	1563494_at	AL161982	---	---	2,03	1,29E-03
SALL4	229661_at	NM_020436	NM_020436	57167	2,03	2,39E-03
DJ971N18.2	240094_at	AL042660	NM_021156	56255	2,03	1,10E-03
GOLPH4	233877_at	AK000777	NM_014498	27333	2,02	1,37E-03
MSX2	205555_s_at	D31771	NM_002449	4488	2,02	2,73E-03
SR140	236696_at	BE464843	XM_031553	23350	2,02	1,40E-03
PSCD3	243752_s_at	AI870144	NM_004227	9265	2,02	5,25E-05
JMJD2C	239285_at	AI341227	NM_015061	23081	2,02	1,02E-03
THRAP2	238883_at	AW975051	NM_015335	23389	2,01	3,31E-03
BF508839	239907_at	BF508839	---	---	2,01	1,50E-03
VRK1	241737_x_at	T89693	NM_003384	7443	2,01	4,67E-05
AA417878	243463_s_at	AA417878	---	---	2,01	4,39E-03
RAP1GDS1	237856_at	AI052055	NM_021159	5910	1,99	6,70E-03
BF724206	244457_at	BF724206	---	---	1,99	5,28E-03
MAOA	212741_at	AA923354	NM_000240	4128	1,98	7,12E-04
TPTE	233879_at	AL137389	NM_013315 NM_199259 NM_199260 NM_199261	7179	1,97	6,72E-03
SPAG6	210032_s_at	AI651156	NM_012443 NM_172242	9576	1,97	2,71E-04
VDP	222316_at	AW973253	NM_003715	8615	1,97	8,98E-03
FLJ35740	244297_at	AI806762	NM_147195	253650	1,97	7,86E-03
SPPL3	1554565_x_at	BC011943	NM_139015	121665	1,96	5,95E-04
BC028185	1569609_at	BC028185	XM_496328	440546	1,96	4,09E-05
MYH10	237491_at	AA700633	NM_005964	4628	1,96	3,02E-03
TMP21	238886_at	BF056141	NM_006827	10972	1,96	1,48E-03
TFCP2	242859_at	BE156563	NM_005653	7024	1,95	8,85E-03
BE856929	239349_at	BE856929	---	---	1,95	4,12E-03
LOC151878	222372_at	AW971248	---	151878	1,95	1,02E-03
SEC15L2	1569202_x_at	BF847120	XM_039570	23233	1,94	2,05E-05
SCFD1	243525_at	AA808051	NM_016106 NM_182835	23256	1,94	1,42E-03

RTN4	243031_at	N90377	NM_007008 NM_020532 NM_153828 NM_207520 NM_207521	57142	1,94	3,06E-03
TRA1	239451_at	AI684643	NM_003299	7184	1,93	2,01E-03
CSE1L	210765_at	AF053640	NM_001316 NM_177436	1434	1,93	2,75E-04
ATXN2	238589_s_at	AW601184	NM_002973	6311	1,93	1,04E-03
GNAI1	227692_at	AU153866	NM_002069	2770	1,93	7,06E-05
TCF12	235925_at	AW057520	NM_003205 NM_207036 NM_207037 NM_207038 NM_207040	6938	1,93	2,43E-03
LASS5	238299_at	AW005866	NM_147190	91012	1,93	1,53E-04
AA766886	239171_at	AA766886	---	---	1,92	7,67E-03
KIAA1102	1569208_a_at	BC020895	NM_014988	22998	1,92	1,80E-03
SARS	237689_at	BF111108	NM_006513	6301	1,92	5,62E-03
VTI1A	233323_at	AK024973	NM_145206	143187	1,91	6,85E-04
B4GALT5	1559391_s_at	AI084451	NM_004776	9334	1,91	9,95E-03
AA804267	243185_at	AA804267	---	---	1,91	1,67E-03
MGC34032	1569112_at	AW020413	NM_152697	204962	1,90	1,85E-03
AL050204	213929_at	AL050204	---	---	1,90	5,32E-03
FLJ31951	236322_at	AA830854	NM_144726	153830	1,89	9,55E-03
ASCL1	209987_s_at	BC002341	NM_004316	429	1,89	1,70E-06
LOC441157	1558795_at	AL833240	XM_499037	441157	1,89	7,22E-05
NOL7	242143_at	BE674964	NM_016167	51406	1,89	1,62E-03
XPO1	235927_at	BE350122	NM_003400	7514	1,88	1,14E-04
FOXP1	240666_at	AI732568	NM_032682	27086	1,88	6,71E-03
CD9	201005_at	NM_001769	NM_001769	928	1,87	3,75E-03
TNKS	238108_at	AI401627	NM_003747	8658	1,87	8,80E-03
NID	202007_at	BF940043	NM_002508	4811	1,87	3,81E-03
MARS	213672_at	AA621558	NM_004990	4141	1,86	2,54E-04
C20orf23	232083_at	AB046810	NM_024704	55614	1,86	1,17E-04
KIAA1713	233536_at	AI202664	XM_290811	80816	1,86	3,15E-05
U80755	243820_at	U80755	---	---	1,85	8,97E-05
AA700817	241997_at	AA700817	---	---	1,85	4,70E-03
UBE2E1	215577_at	AU146791	NM_003341 NM_182666	7324	1,85	2,95E-03
AP2B1	233800_at	AA805082	NM_001282	163	1,84	4,55E-05
AGTPBP1	242008_at	BE350312	NM_015239	23287	1,83	9,60E-03
RPL4	1562440_at	BC026249	NM_000968	6124	1,83	1,24E-03
LOC441157	1558796_a_at	AL833240	XM_499037	441157	1,83	3,63E-06
EIF3S8	236700_at	AI377875	NM_003752	8663	1,82	1,24E-07
ZDHHC2	243528_at	AW014108	NM_016353	51201	1,82	8,62E-05
WSB1	227501_at	AI377135	NM_015626 NM_134264 NM_134265	26118	1,82	2,98E-03

PTPN12	244356_at	AL079909	NM_002835	5782	1,81	5,18E-03
RB1CC1	237626_at	AI801666	NM_014781	9821	1,81	2,19E-03
PCTK2	243993_at	AA436887	NM_002595	5128	1,80	9,68E-03
PIP5K1A	235646_at	BF515595	NM_003557	8394	1,80	5,13E-03
AU146318	232355_at	AU146318	---	---	1,80	7,55E-03
N59650	244265_at	N59650	---	---	1,80	8,30E-03
YARS	238760_at	AW452122	NM_003680	8565	1,80	4,51E-03
RNF159	241956_at	AI521883	NM_032373	84333	1,80	5,20E-05
AI820961	240331_at	AI820961	---	---	1,79	7,22E-03
FLJ30058	238047_at	AA405456	NM_144967	158763	1,79	5,67E-03
GULP1	223837_at	BC001103	NM_016315	51454	1,79	6,85E-04
CGI-26	230892_at	AI912194	NM_015954	51071	1,79	1,73E-03
LRCH3	1559490_at	AL832278	NM_032773	84859	1,79	6,87E-03
HIRA	240451_at	AA004844	NM_003325	7290	1,79	2,21E-05
SRPK2	239811_at	BF954306	NM_182691 NM_182692	6733	1,78	5,28E-03
C9orf33	217130_at	AF072164	---	90477	1,78	1,23E-04
AI916641	242471_at	AI916641	---	---	1,78	4,35E-04
SCC-112	241798_at	AI339930	NM_015200	23244	1,78	1,62E-03
SLC33A1	1559232_a_at	BC029450	NM_004733	9197	1,78	1,37E-04
ATRX	236778_at	AA826176	NM_000489 NM_138270 NM_138271	546	1,78	2,50E-03
ZFYVE16	1554638_at	BC032227	NM_014733	9765	1,78	1,30E-03
FLJ13089	236816_at	BF110370	NM_024953	80018	1,78	9,12E-03
SLC7A2	225516_at	AA876372	NM_001008539 NM_003046	6542	1,78	2,48E-06
DBH	206450_at	NM_000787	NM_000787	1621	1,77	5,25E-04
H15073	236685_at	H15073	---	---	1,77	1,63E-04
R45137	238304_at	R45137	---	---	1,77	4,97E-03
FBXW8	237317_at	AW136338	NM_012174 NM_153348	26259	1,76	4,78E-03
MLL3	244010_at	AI057455	NM_021230 NM_170606	58508	1,76	5,04E-05
SLC37A3	1569666_s_at	BC035773	NM_032295 NM_207113	84255	1,76	1,21E-05
CNOT2	222313_at	AW972359	NM_014515	4848	1,76	1,85E-04
NS5ATP13TP2	1558613_at	BC040647	NM_178507	220323	1,75	7,91E-04
MBNL1	1556657_at	AA744622	NM_021038 NM_207292 NM_207293 NM_207294 NM_207295 NM_207296 NM_207297	4154	1,74	1,02E-04
AU152272	1556650_at	AU152272	---	---	1,74	2,69E-03
AI372879	237134_at	AI372879	---	---	1,73	1,97E-03
N23846	1557804_at	N23846	---	---	1,72	6,11E-03

C10orf47	229801_at	AI640157	NM_153256	254427	1,72	6,95E-03
W72466	231467_at	W72466	---	---	1,72	2,85E-05
MAPRE2	1564733_at	BC013931	NM_014268	10982	1,72	1,15E-03
R38403	240425_x_at	R38403	---	---	1,72	2,69E-03
AF090944	233995_at	AF090944	---	---	1,72	3,50E-04
RANBP17	234137_s_at	AK022022	NM_022897	64901	1,71	3,68E-03
OAZIN	240231_at	AI742383	NM_015878 NM_148174	51582	1,71	1,34E-07
L3MBTL	242637_at	C14069	NM_015478 NM_032107	26013	1,71	6,68E-03
AB062477	1555303_at	AB062477	---	---	1,71	6,75E-03
AA682539	235575_at	AA682539	---	---	1,70	8,28E-03
AL353942	216147_at	AL353942	NM_018243	55752	1,70	3,06E-04
VPS26	243316_x_at	AA004710	NM_004896	9559	1,70	1,14E-04
LAF4	243967_at	AI424899	NM_002285	3899	1,70	8,24E-03
SEZ6L	240709_at	AW204757	NM_021115	23544	1,70	9,27E-04
AVO3	237330_at	AA603494	XM_380173	253260	1,70	6,44E-04
TPARL	1560622_at	AK000203	NM_018475	55858	1,69	1,26E-03
PDLIM5	213684_s_at	BF671400	NM_001011513 NM_001011514 NM_001011515 NM_001011516 NM_006457	10611	1,69	6,08E-03

SOS2	233369_at	AU146027	NM_006939	6655	1,69	9,57E-03
IREB2	1563130_a_at	AL109710	NM_004136	3658	1,68	7,14E-06
MPZL1	210210_at	AF181660	NM_003953 NM_024569	9019	1,68	5,09E-05
AW206536	243470_at	AW206536	---	---	1,68	4,56E-03
TOP1	239404_at	BF840360	NM_003286	7150	1,67	5,17E-04
AA936428	244674_at	AA936428	---	---	1,67	1,91E-03
PUM2	235138_at	AA565051	NM_015317	23369	1,67	8,24E-04
MINA	213189_at	BE966695	NM_032778 NM_153182	84864	1,67	9,49E-05
LOC152185	239091_at	AA497043	NM_144718	152185	1,67	4,23E-04
SEC31L1	1556416_s_at	AF086242	NM_014933 NM_016211	22872	1,67	6,36E-04
MAOA	204389_at	NM_000240	NM_000240	4128	1,66	2,78E-04
ALCAM	1569362_at	BC041127	NM_001627	214	1,66	8,23E-03
KRT18	201596_x_at	NM_000224	NM_000224 NM_199187	3875	1,66	1,32E-03
N73550	244112_x_at	N73550	---	---	1,66	5,23E-03
MKLN1	1560145_at	BQ942131	NM_013255	4289	1,65	4,78E-03
ARHGAP5	242110_at	AV735587	NM_001173	394	1,65	8,85E-03
GPI	232002_at	AW843302	NM_000175	2821	1,65	6,38E-04

STAU	1569527_at	BC017275	NM_004602 NM_017452 NM_017453 NM_017454	6780	1,65	2,32E-04
BF512254	242695_at	BF512254	---	---	1,65	2,52E-03
EIF4ENIF1	242983_at	AI806626	NM_019843	56478	1,65	4,13E-03
AU144781	233300_at	AU144781	---	---	1,65	2,25E-03
DKFZp547A023	214731_at	AB037854	NM_018704	55917	1,65	8,41E-03
LBH	221011_s_at	NM_030915	NM_030915	81606	1,64	3,86E-05
KIAA0217	241965_at	BF589232	NM_015155	23185	1,64	3,53E-04
MED31	243319_at	AI274981	NM_016060	51003	1,64	2,26E-04
DLEU2	1556821_x_at	H48516	NM_006021	8847	1,64	8,43E-03
AA195014	243769_at	AA195014	---	---	1,63	9,11E-03
N50083	229110_at	N50083	---	---	1,63	1,73E-03
N46436	1556568_a_at	N46436	---	---	1,63	4,33E-04
RAPGEF5	204680_s_at	AI263837	XM_499059	9771	1,62	1,84E-03
AW003140	227576_at	AW003140	---	---	1,62	5,17E-03
AL119001	233440_at	AL119001	---	---	1,62	5,61E-03
CPSF6	238651_at	BF512491	NM_007007	11052	1,62	4,97E-03
RBM5	230742_at	AA742596	NM_005778	10181	1,62	6,51E-03
CADPS	233950_at	AK000873	NM_003716 NM_183393 NM_183394	8618	1,62	3,44E-04
SPON1	209437_s_at	AB051390	NM_006108	10418	1,62	1,60E-03
SCFD1	241775_at	AW298119	NM_016106 NM_182835	23256	1,61	2,89E-03
CDC14A	210742_at	AF064103	NM_003672 NM_033312 NM_033313	8556	1,61	4,92E-03
FZD5	206136_at	NM_003468	NM_003468	7855	1,61	1,56E-03
ZNF451	215012_at	AU144775	NM_015555	26036	1,61	9,28E-03
PCGF5	226326_at	AI798098	NM_032373	84333	1,61	2,79E-05
PTGFRN	224950_at	BF476250	NM_020440	5738	1,61	8,83E-03
TSC	218872_at	NM_017899	NM_017899	54997	1,61	5,32E-04
GRM8	216255_s_at	AC000099	NM_000845	2918	1,60	3,03E-05
MGC47869	243056_at	AI301111	NM_175874	144608	1,60	1,26E-03
DNAPTP6	244597_at	AA701247	NM_015535	26010	1,60	2,38E-03
BC028606	1555485_s_at	BC028606	---	---	1,60	5,40E-03
ARID1B	1558822_at	AF147412	NM_017519 NM_020732 NM_175863	57492	1,60	2,93E-03
BF841212	232096_x_at	BF841212	---	---	1,60	1,12E-03
AU144005	232797_at	AU144005	---	---	1,60	2,27E-03
LOC158160	244075_at	BF224218	NM_182829	158160	1,60	3,37E-03
MYO6	210480_s_at	U90236	NM_004999	4646	1,59	6,83E-04
MBNL2	236699_at	AL566294	NM_144778 NM_207304	10150	1,59	3,46E-03
BI868311	1565651_at	BI868311	---	---	1,59	4,00E-03
LETMD1	242424_at	AA345855	NM_015416	25875	1,59	5,03E-04

N75937	240072_at	N75937	---	---	1,59	6,26E-03
H04482	243287_s_at	H04482	---	---	1,59	3,04E-03
NFIB	233304_at	AU145782	NM_005596	4781	1,59	6,80E-03
PPP3R1	1565811_at	BC033945	NM_000945	5534	1,59	6,08E-05
DLEU2	216870_x_at	AF264787	NM_006021	8847	1,59	2,46E-04
COBRA1	1556434_at	BQ777552	NM_015456	25920	1,59	2,75E-04
C6orf60	1558523_at	AJ420563	NM_024581	79632	1,58	6,89E-03
MAK3	231199_at	AA701676	NM_025146	80218	1,58	3,34E-03
KIAA0485	242824_at	AW191647	---	57235	1,57	3,46E-05
CTBP2	233315_at	AK024947	NM_001329 NM_022802	1488	1,57	2,17E-05
AA935659	240321_at	AA935659	---	---	1,57	9,78E-03
TAF15	227884_at	AW296067	NM_003487 NM_139215	8148	1,56	6,85E-03
KIF5C	1557089_at	CA449408	XM_377774	3800	1,56	2,83E-04
KIAA0143	232356_at	AW003230	NM_015137	23167	1,56	7,00E-03
CPVL	208146_s_at	NM_031311	NM_019029 NM_031311	54504	1,56	4,48E-03
DMXL1	241472_at	N74444	NM_005509	1657	1,55	8,84E-04
SNX5	229981_at	AA131508	NM_014426 NM_152227	27131	1,55	1,33E-05
ALCAM	201951_at	BF242905	NM_001627	214	1,55	2,09E-06
ANKRD11	228866_at	BF514864	NM_013275	29123	1,55	2,95E-04
ID2	201565_s_at	NM_002166	NM_002166	3398	1,55	9,49E-04
PFAAP5	214753_at	AW084068	NM_014887	10443	1,55	8,30E-04
KIAA0318	238817_at	BF063412	NM_015347	23504	1,55	8,89E-05
SR140	236431_at	AI674977	XM_031553	23350	1,54	8,08E-03
API5	229692_at	AW135003	NM_006595	8539	1,54	1,07E-03
AA516469	236375_at	AA516469	---	---	1,54	6,79E-03
NUPL1	241425_at	AA769986	NM_001008564 NM_001008565 NM_014089	9818	1,54	4,72E-05
AI791138	242968_at	AI791138	---	---	1,54	8,93E-03
JAK1	234193_at	AK025218	NM_002227	3716	1,54	3,33E-04
AW052186	239942_at	AW052186	---	---	1,53	6,32E-03
KIF23	244427_at	AW192521	NM_004856 NM_138555	9493	1,53	7,98E-03
AI800470	242836_at	AI800470	---	---	1,53	5,90E-04
BF509125	232198_at	BF509125	---	---	1,52	1,16E-04
SPON1	209436_at	AB018305	NM_006108	10418	1,52	2,06E-04
DLEU2	1556820_a_at	H48516	NM_006021	8847	1,52	1,57E-03
AK025105	232476_at	AK025105	---	---	1,52	2,32E-03
AA228366	236251_at	AA228366	---	---	1,52	4,86E-03
H37807	241060_x_at	H37807	---	---	1,52	4,23E-03
BNC2	238478_at	H97386	NM_017637	54796	1,52	2,14E-05

CADPS	1568604_a_at	AI912173	NM_003716 NM_183393 NM_183394	8618	1,51	7,84E-07
SCARB2	215754_at	AU148040	NM_005506	950	1,51	1,21E-03
MBNL1	238558_at	AI445833	NM_021038 NM_207292 NM_207293 NM_207294 NM_207295 NM_207296 NM_207297	4154	1,51	1,09E-03
BC003528	210920_x_at	BC003528	---	---	1,51	2,78E-03
GPR18	233554_at	AF339764	NM_005292	2841	1,51	8,61E-03
UBE3B	213822_s_at	BE856776	NM_130466 NM_183414 NM_183415	89910	1,51	8,72E-03
WWOX	1556595_at	BQ025203	NM_016373 NM_018560 NM_130788 NM_130790 NM_130791 NM_130792 NM_130844	51741	1,51	1,78E-03
AI740589	243515_at	AI740589	---	---	1,51	4,92E-04
N26620	227503_at	N26620	---	---	1,51	2,93E-03
C18965	242853_at	C18965	XM_379243	401106	1,51	5,39E-03
CPNE4	239890_at	AI821426	NM_130808	131034	1,50	1,95E-03
FBXL11	215191_at	AW836210	NM_012308	22992	1,50	3,06E-03
CHD1L	238070_at	AA573217	NM_004284	9557	1,50	8,83E-03
JARID2	232835_at	AA533080	NM_004973	3720	1,50	3,50E-04
MIB1	240446_at	AI798164	NM_020774	57534	1,50	4,01E-04
Z39232	1560924_at	Z39232	---	---	1,49	6,88E-04
PLEKHE1	212719_at	AB011178	NM_194449	23239	1,49	2,28E-04
UBE1C	1556339_a_at	BM353142	NM_003968 NM_198195 NM_198197	9039	1,49	7,82E-04
NM_030892	220969_s_at	NM_030892	---	---	1,49	4,83E-04
TBX3	219682_s_at	NM_016569	NM_005996 NM_016569	6926	1,48	2,65E-03
PHGDHL1	241932_at	AI073803	NM_177967	337867	1,48	5,92E-03
LOC158301	239193_at	BF060981	---	158301	1,48	1,36E-03
FLJ10579	230843_at	AA482037	NM_018145	55177	1,48	6,04E-04
RPL10A	234224_at	AL137541	NM_007104	4736	1,48	5,43E-03
C10orf119	242167_at	AA703310	NM_024834	79892	1,48	9,08E-06
CORO6	1552301_a_at	NM_032854	NM_032854	84940	1,48	5,48E-03
MGC15912	239635_at	BF510708	NM_032886	84972	1,47	4,46E-03

DTNB	233727_at	AL157472	NM_021907 NM_033147 NM_033148 NM_183360 NM_183361	1838	1,47	4,45E-03
FLJ22955	232447_at	AU147405	NM_024819	79877	1,46	3,56E-03
LOC151194	236607_at	AI921882	NM_145280	151194	1,46	8,35E-04
BC035170	1561079_at	BC035170	---	---	1,46	5,42E-03
XPO7	240168_at	AA679589	NM_015024	23039	1,46	3,12E-03
EZH2	215006_at	AK023816	NM_004456 NM_152998	2146	1,46	2,64E-03
LTB4DH	228825_at	BE566894	NM_012212	22949	1,46	1,02E-03
BBX	1557240_a_at	BU689085	NM_020235	56987	1,46	5,33E-03
ARIH2	1559121_s_at	AI767566	NM_006321	10425	1,46	8,11E-04
ANKRD28	229307_at	N32051	NM_015199	23243	1,45	2,51E-03
LRRFIP2	232704_s_at	AK025207	NM_006309 NM_017724	9209	1,45	2,05E-03
PHLDA1	218000_s_at	NM_007350	NM_007350	22822	1,45	5,61E-03
AF070602	216214_at	AF070602	---	---	1,44	3,75E-03
C6orf133	215558_at	AK001118	NM_015255	23304	1,44	1,76E-04
AW083060	243274_x_at	AW083060	---	---	1,44	6,61E-03
ATOH8	228890_at	BF434995	NM_032827	84913	1,43	9,99E-03
CHC1L	230292_at	AA868809	NM_001268	1102	1,43	2,15E-03
SMG1 KIAA0220 LOC440345	244766_at	BG180003	NM_014006 NM_015092 XM_496125	23049 283846 440345	1,43	1,93E-03
T98846	239654_at	T98846	---	---	1,43	7,51E-05
ZA20D3	222186_at	AL109684	NM_019006	54469	1,43	2,35E-03
SMC5L1	1562948_at	BC035661	NM_015110	23137	1,43	7,05E-03
SMC4L1	237246_at	AI797163	NM_001002799 NM_001002800 NM_005496	10051	1,43	7,94E-03
SLD5	1554356_at	BC027454	NM_032336	84296	1,43	1,24E-03
AW451426	244480_at	AW451426	---	---	1,42	1,53E-04
ZSWIM6	1560199_x_at	AU120130	XM_035299	57688	1,42	2,96E-04
H06497	243211_at	H06497	---	---	1,42	1,88E-03
ENC1	201340_s_at	AF010314	NM_003633	8507	1,42	8,83E-03
AW963544	238580_at	AW963544	---	---	1,42	1,14E-04
IGSF4	232793_at	AL359567	NM_014333	23705	1,42	6,90E-04
AK022100	233406_at	AK022100	---	---	1,41	8,65E-03
CENTB2	240759_at	AW593931	NM_012287	23527	1,41	8,75E-04
PTPRK	203038_at	NM_002844	NM_002844	5796	1,41	2,80E-04
LOC286109	243304_at	AI733824	---	286109	1,41	8,07E-03
ASCL1	213768_s_at	AW950513	NM_004316	429	1,40	2,65E-05
AW293174	244290_at	AW293174	XM_499534	442612	1,40	2,89E-05
MGC15937	227794_at	BF432254	NM_080661	92292	1,40	2,78E-03

PTK2	1559529_at	BC043202	NM_005607 NM_153831	5747	1,40	3,63E-03
MAN2A1	205105_at	NM_002372	NM_002372	4124	1,39	3,32E-04
CBLB	233614_at	AU145361	NM_170662	868	1,39	9,21E-04
KIAA0998	215898_at	AK021879	NM_015072	23093	1,39	5,01E-03
PMAIP1	204285_s_at	AI857639	NM_021127	5366	1,39	3,88E-06
FNBP1L	242310_at	AA665058	NM_017737	54874	1,38	4,27E-03
AI755057	233055_at	AI755057	---	---	1,38	1,05E-03
RAB3-GAP150	240234_at	AI216539	NM_012414	25782	1,38	7,73E-03
ACSL4	1557418_at	W95007	NM_004458 NM_022977	2182	1,38	5,61E-04
FAM13A1	232628_at	AI740629	NM_014883	10144	1,37	4,61E-03
FLJ23451	1569601_at	BF106979	NM_024766	79823	1,37	4,24E-05
ZNF217	203739_at	NM_006526	NM_006526	7764	1,37	5,73E-03
BF197705	230401_at	BF197705	---	---	1,37	9,92E-04
HEG	212822_at	AA121502	XM_087386	57493	1,37	2,43E-04
MGC15523	1563226_at	BC020925	NM_138570	124565	1,37	7,40E-03
AA156721	201952_at	AA156721	---	---	1,37	1,55E-04
AL110237	232959_at	AL110237	---	---	1,37	7,09E-03
PSME4	237180_at	T97717	NM_014614	23198	1,37	1,78E-03
IGSF4	244345_at	AI627453	NM_014333	23705	1,36	7,17E-03
MRPS25	244019_at	T89845	NM_022497	64432	1,36	2,01E-03
BF801735	238712_at	BF801735	---	---	1,36	2,63E-03
SPRY4	221489_s_at	W48843	NM_030964	81848	1,35	7,35E-04
SCN7A	239984_at	AI333640	NM_002976	6332	1,35	8,33E-04
HIVEP2	243254_at	T08739	NM_006734	3097	1,35	5,09E-03
PTPN11	241930_x_at	AA223204	NM_002834	5781	1,35	9,28E-04
AW235215	238913_at	AW235215	---	---	1,35	9,92E-03
C10orf6	1553909_x_at	NM_144592	NM_018121	55719	1,35	2,80E-04
ZFHX4	219779_at	NM_024721	NM_024721	79776	1,35	1,82E-05
MEST	202016_at	NM_002402	NM_002402 NM_177524 NM_177525	4232	1,34	2,65E-04
TRIO	231403_at	N21108	NM_007118	7204	1,34	9,69E-03
UBE3C	242673_at	AA931284	NM_014671	9690	1,34	3,34E-04
PPP2R2A	236492_at	AI934447	NM_002717	5520	1,34	4,98E-03
HIAT1	230868_at	BF433103	NM_033055	64645	1,34	7,24E-04
LOC440971	1556744_a_at	AI732587	XM_496651	440971	1,33	3,92E-03
CUGBP2	202156_s_at	N36839	NM_006561	10659	1,33	2,42E-03
CNTN4	229084_at	R42166	NM_175607 NM_175612 NM_175613	152330	1,33	8,25E-03
FLJ11259	218627_at	NM_018370	NM_018370	55332	1,32	4,63E-03
CEPT1	1561884_at	AL833102	NM_001007794 NM_006090	10390	1,32	1,40E-04
AL049988	216614_at	AL049988	---	---	1,31	9,72E-03
CSPG6	1556925_at	AL360194	NM_005445	9126	1,31	8,99E-03
ASXL1	242439_s_at	AI819150	NM_015338	171023	1,31	1,22E-05

PVT1 LOC441378	1558290_a_at	BG200951	XM_372058 XM_499128	441378 5820	1,31	1,11E-04
TUBB6	209191_at	BC002654	NM_032525	84617	1,31	5,17E-04
IRAK1BP1	233290_at	AU145280	NM_001010844	134728	1,31	2,71E-03
AL137730	226999_at	AL137730	---	---	1,31	6,07E-03
PTEN	233314_at	AK021487	NM_000314	5728	1,31	7,60E-03
ZNF215	220214_at	NM_013250	NM_013250	7762	1,31	5,81E-03
LRPPRC	1557360_at	CA430402	NM_133259	10128	1,30	1,55E-03
DKFZP434C212	231552_at	AW451785	NM_015635	26130	1,30	5,13E-04
AI651786	237945_at	AI651786	---	---	1,30	4,28E-03
AU155234	233289_at	AU155234	---	---	1,30	9,43E-03
AA648983	240478_at	AA648983	---	---	1,30	9,77E-05
AA412686	244608_at	AA412686	---	---	1,30	4,76E-03
RBMS3	240245_at	AW237264	NM_001003792 NM_001003793 NM_014483	27303	1,30	6,53E-03
AK021457	216682_s_at	AK021457	---	---	1,30	2,30E-04
SHPRH	243964_at	AI631201	NM_173082	257218	1,29	9,11E-03
METAP2	244185_at	AA921841	NM_006838	10988	1,29	5,27E-05
MAB21L2	210302_s_at	AF262032	NM_006439	10586	1,29	1,50E-04
AA543084	236480_at	AA543084	---	---	1,29	3,14E-04
AW271626	237441_at	AW271626	---	---	1,29	2,95E-05
SF3B14	1561923_a_at	AF147425	NM_016047	51639	1,29	7,66E-03
PRDX6	242751_at	N55072	NM_004905	9588	1,28	1,80E-03
SMU1	228180_at	AA805653	NM_018225	55234	1,28	6,63E-04
BF001773	241906_at	BF001773	---	---	1,28	9,10E-03
PFAAP5	221899_at	AI809961	NM_014887	10443	1,28	8,55E-03
FLJ13273	220063_at	NM_024751	NM_024751	79807	1,28	4,70E-04
HM13	1560297_at	BG928538	NM_030789 NM_178580 NM_178581 NM_178582	81502	1,28	3,78E-03
DRF1	206661_at	NM_025104	NM_025104 NM_145663	80174	1,28	5,80E-04
LOC284219	1556425_a_at	BF509747	---	284219	1,27	2,33E-03
ANXA2	213503_x_at	BE908217	NM_001002857 NM_001002858 NM_004039	302	1,27	2,58E-03
SPON1	213994_s_at	AI885290	NM_006108	10418	1,27	2,99E-03
M11S1	244778_x_at	N63691	NM_005898 NM_203364	4076	1,27	1,16E-03
LOC253981	226430_at	AI394438	---	253981	1,26	6,58E-04
FUBP1	240307_at	N54783	NM_003902	8880	1,26	5,57E-04
NKTR	231235_at	AA732581	NM_005385	4820	1,26	6,07E-03
ARHGAP24	223422_s_at	AI743534	NM_031305	83478	1,26	2,57E-03

KIAA1838	241152_at	BE466903	NM_032448	84498	1,26	4,94E-03
USP34	207365_x_at	NM_014709	NM_014709	9736	1,25	1,35E-04
DHX57	239311_at	AI367034	NM_144995 NM_145646 NM_198963	90957	1,25	7,92E-03
UBE2H	239721_at	AI280328	NM_003344 NM_182697	7328	1,25	7,22E-03
ID1	208937_s_at	D13889	NM_002165 NM_181353	3397	1,25	1,45E-03
MARK3	239166_at	R98192	NM_002376	4140	1,24	8,08E-04
APBB2	213419_at	U62325	NM_173075	323	1,24	5,44E-04
SVH	1558748_at	AL832759	NM_031905	83787	1,24	2,00E-03
ASXL1	242438_at	AI819150	NM_015338	171023	1,24	6,76E-05
P15RS	228566_at	AA778694	NM_018170	55197	1,24	2,39E-04
LOC115648	1558486_at	BC022394	NM_145326	115648	1,24	3,07E-04
CADPS	1568603_at	AI912173	NM_003716 NM_183393 NM_183394	8618	1,24	3,75E-03
AI291804	242856_at	AI291804	---	---	1,24	8,05E-05
TCTEL1	242109_at	AI038577	NM_006519	6993	1,23	3,41E-03
QKI	241938_at	AA935633	NM_006775 NM_206853 NM_206854 NM_206855	9444	1,23	1,41E-04
SCARA3	223842_s_at	AB007830	NM_016240 NM_182826	51435	1,22	3,50E-04
MRPS5	236779_at	BG539414	NM_031902	64969	1,22	1,33E-03
BE670307	227955_s_at	BE670307	---	---	1,22	9,05E-06
DNAPTP6	241812_at	AV648669	NM_015535	26010	1,22	8,50E-03
PCGF5	229194_at	AL045882	NM_032373	84333	1,22	2,28E-04
AU145679	233607_at	AU145679	---	---	1,21	4,54E-03
BE464799	214036_at	BE464799	---	---	1,21	5,03E-05
SLCO3A1	219229_at	NM_013272	NM_013272	28232	1,21	2,66E-03
BF433200	242467_at	BF433200	---	---	1,21	7,14E-03
PPARG	232331_at	AK027107	NM_005037 NM_015869 NM_138711 NM_138712	5468	1,21	6,85E-03
FNTA	240527_at	AI953011	NM_002027	2339	1,21	1,22E-03
TCF7L2	216035_x_at	AV721430	NM_030756	6934	1,21	2,15E-05
POLE	216026_s_at	AL080203	NM_006231	5426	1,21	2,59E-03
ZA20D3	238812_at	AA741296	NM_019006	54469	1,21	9,92E-03
SFRS2IP	232597_x_at	AK025132	NM_004719	9169	1,21	1,99E-03
TH	208291_s_at	NM_000360	NM_000360 NM_199292 NM_199293	7054	1,21	8,60E-04
NKTR	202380_s_at	NM_005385	NM_005385	4820	1,21	1,31E-03

PTPN13	243792_x_at	AI281371	NM_006264 NM_080683 NM_080684 NM_080685	5783	1,20	9,38E-03
UBE3B	232301_at	AK022019	NM_130466 NM_183414 NM_183415	89910	1,20	1,77E-04
RAB12	238714_at	AA504249	XM_113987	201475	1,20	7,92E-04
AW299775	235008_at	AW299775	---	---	1,20	1,71E-03
HSD17B12	242616_at	W80359	NM_016142	51144	1,19	8,50E-03
R16900	242514_at	R16900	---	---	1,19	2,39E-03
DST	232098_at	AK025142	NM_001723 NM_015548 NM_020388 NM_183380	667	1,19	4,65E-03
DKFZP564C186	1559139_at	BC009786	NM_015658	26155	1,19	3,03E-03
C9orf3	233599_at	AK025151	NM_032823	84909	1,19	1,52E-03
AI859990	244197_x_at	AI859990	---	---	1,18	1,42E-03
SPON1	213993_at	AI885290	NM_006108	10418	1,18	8,98E-03
CENPF	207331_at	NM_016343	NM_016343	1063	1,18	6,92E-03
CDC2L5	232266_x_at	AK024379	NM_003718 NM_031267	8621	1,18	2,93E-03
EXT1	237310_at	AI743607	NM_000127	2131	1,18	4,88E-03
C1QDC1	218456_at	NM_023925	NM_001002259 NM_023925 NM_032156	65981	1,18	2,52E-06
FLJ45645	243038_at	AW292769	NM_198557	375287	1,18	6,22E-03
H43040	231108_at	H43040	---	---	1,18	2,07E-04
SEC63	242749_at	AI022173	NM_007214	11231	1,18	3,85E-03
KLF7	238482_at	AL120562	NM_003709	8609	1,17	4,23E-04
API5	214960_at	AF229253	NM_006595	8539	1,17	1,28E-04
ENC1	201341_at	NM_003633	NM_003633	8507	1,17	9,25E-04
SLC16A4	228455_at	AI092824	NM_004696	9122	1,17	3,54E-03
ANP32A	235954_at	AA972597	NM_006305	8125	1,17	4,73E-03
UBE2E1	236062_at	AI742722	NM_003341 NM_182666	7324	1,17	2,49E-03
EVL	227232_at	T58044	NM_016337	51466	1,17	1,12E-03
SLC6A2	210353_s_at	M65105	NM_001043	6530	1,17	3,19E-03
C6p63	238170_at	BE327727	NM_025180	80254	1,17	6,06E-05
AU147479	233359_at	AU147479	---	---	1,16	1,44E-03
AF010144	207953_at	AF010144	---	---	1,16	6,11E-05
TLE3	228340_at	BE967118	NM_005078	7090	1,16	2,16E-03
LOC338692	238642_at	AW367571	NM_207354	338692	1,16	6,72E-03
BF981643	214720_x_at	BF981643	NM_144710 NM_178584	151011	1,16	3,74E-03
AU152763	232939_at	AU152763	---	---	1,16	1,12E-03
COMMD10	1560349_at	BC036897	NM_016144	51397	1,16	7,89E-03
MDN1	1569484_s_at	AL603301	NM_014611	23195	1,16	1,37E-03

FLJ10213	219906_at	NM_018029	NM_018029	55096	1,16	2,68E-04
AF5Q31	1555436_a_at	BC025700	NM_014423	27125	1,16	4,10E-04
BE467787	243835_at	BE467787	---	---	1,16	3,16E-03
NOSTRIN	235506_at	AI076788	NM_052946	115677	1,16	5,52E-03
WWOX	242099_at	T83938	NM_016373 NM_018560 NM_130788 NM_130790 NM_130791 NM_130792 NM_130844	51741	1,16	1,72E-03
NKTR	202379_s_at	AI361805	NM_005385	4820	1,16	2,17E-03
TXNRD1	201266_at	NM_003330	NM_003330 NM_182729 NM_182742 NM_182743	7296	1,15	1,40E-04
STRA6	1569334_at	BC015881	NM_022369	64220	1,15	2,00E-03
DLEU2	215629_s_at	AA905286	NM_006021	8847	1,15	8,95E-03
MSH3	233263_at	AU147635	NM_002439	4437	1,15	3,30E-04
YAP	244803_at	AI335191	NM_018253 NM_139118 NM_139119 NM_139120 NM_139121	55249	1,14	3,17E-03
ANAPC5	235926_at	AI312527	NM_016237	51433	1,14	3,93E-03
LOC152573	229485_x_at	AI735586	XM_496688	152573	1,14	9,91E-03
VPS16	233313_at	AU158316	NM_022575 NM_080413 NM_080414	64601	1,14	1,33E-03
TNRC6	233836_at	AK025277	NM_014494 NM_020847	27327	1,14	4,69E-03
PCGF5	227935_s_at	AA522681	NM_032373	84333	1,13	1,23E-03
LOC255326	233271_at	AU145563	XM_497224	255326	1,13	9,42E-03
KIAA1881	207730_x_at	NM_017932	XM_375558	114782	1,13	8,71E-04
NAPE-PLD	233539_at	AK000801	NM_198990	222236	1,13	6,74E-03
PGAP1	220576_at	NM_024989	NM_024989	80055	1,13	4,35E-04
FLJ10707	239957_at	AW510793	XM_371614	55209	1,13	3,10E-03
SIVA	222030_at	AW024335	NM_006427 NM_021709	10572	1,13	8,59E-03
MGC34032	1552782_at	AK091400	NM_152697	204962	1,13	6,36E-03
TP53I3	210609_s_at	BC000474	NM_004881 NM_147184	9540	1,13	6,61E-03
SYT11	232677_at	AU146128	NM_152280	23208	1,13	3,78E-05
ZAK	1555259_at	AF465843	NM_016653 NM_133646	51776	1,13	4,30E-04
MTBP	233436_at	AK022122	NM_022045	27085	1,12	2,65E-03
SDHA	230077_at	W90764	NM_004168	255812	1,12	7,47E-04
SDHAL2			XM_171032	6389		
EIF4A1	214805_at	U79273	NM_001416	1973	1,12	7,09E-03

ZNF131	1557384_at	AL832081	---	7690	1,12	3,31E-03
TJP1	244476_at	R39769	NM_003257 NM_175610	7082	1,12	1,55E-03
NM_000575	208200_at	NM_000575	---	---	1,12	9,29E-03
SFI1	36545_s_at	AB011114	NM_001007467 NM_014775	9814	1,12	1,54E-03
GALNT7	222587_s_at	BF699855	NM_017423	51809	1,12	1,21E-03
AA176313	1566113_at	AA176313	---	---	1,12	7,32E-03
RABGAP1L	1565762_at	AK074233	NM_014857	9910	1,12	4,63E-03
MED6	207078_at	NM_005466	NM_005466	10001	1,12	8,69E-03
NDUFS1	1559691_at	BC032767	NM_005006	4719	1,11	7,49E-03
SYNCRIP	1555427_s_at	AY034482	NM_006372	10492	1,11	3,11E-03
TH1L	220607_x_at	NM_016397	NM_016397 NM_198976	51497	1,11	1,11E-03
SMURF2	230099_at	AI139993	NM_022739	64750	1,11	9,53E-03
KHDRBS3	209781_s_at	AF069681	NM_006558	10656	1,11	6,19E-04
LOC90799	223815_at	AF130069	NM_138363	90799	1,10	9,64E-03
ASCL1	209988_s_at	BC001638	NM_004316	429	1,10	6,04E-04
AA192765	238172_at	AA192765	---	---	1,10	7,54E-04
C7orf28B	215024_at	AK000993	NM_198097	221960	1,10	8,32E-03
SURF5	206593_s_at	NM_006752	NM_006752 NM_133640 NM_181491	6837	1,10	8,66E-03
SNTB2	232784_at	R42604	NM_006750 NM_130845	6645	1,10	1,54E-05
TD-60	243297_at	AI498610	NM_018715	55920	1,10	6,95E-03
HES1	203394_s_at	BE973687	NM_005524	3280	1,10	9,57E-05
CAS1	239545_at	AI335004	NM_022900	64921	1,10	4,20E-03
PSMB7	244801_at	AI248671	NM_002799	5695	1,10	1,35E-04
MBNL2	232138_at	AW276914	NM_144778 NM_207304	10150	1,10	6,31E-04
hSyn	231087_at	AL046412	NM_018157	55188	1,09	8,23E-03
LRRFIP1	238840_at	AW082668	NM_004735	9208	1,09	3,75E-03
SLC7A5	201195_s_at	AB018009	NM_003486	8140	1,09	1,06E-04
RDH11	217042_at	AL096716	NM_016026	51109	1,09	1,95E-03
LUC7L2	243852_at	AI963460	NM_016019	51631	1,09	4,04E-03
SEC8L1	216538_at	AL049351	NM_021807	60412	1,09	2,92E-04
NM_006896	206848_at	NM_006896	---	---	1,09	2,52E-04
PSMD7	244515_at	AI640348	NM_002811	5713	1,08	1,31E-05
SYMPK	1554595_at	BC030214	NM_004819	8189	1,08	6,40E-03
ELOVL5	1566079_at	AL833001	NM_021814	60481	1,08	7,71E-03
FLJ10357	241627_x_at	AI640434	NM_018071	55701	1,08	1,28E-03
PASK	213534_s_at	D50925	NM_015148	23178	1,08	6,82E-03
CALM2	235190_at	BF591288	NM_001743	805	1,08	1,73E-04
SEMA5A	205405_at	NM_003966	NM_003966	9037	1,08	7,59E-05
ITSN1	215791_at	AF003738	NM_001001132 NM_003024	6453	1,08	1,59E-03

PBX4	230536_at	AJ300182	NM_025245	80714	1,07	9,77E-04
MAN2A1	226538_at	AV700323	NM_002372	4124	1,07	2,26E-04
MGC2803	230213_at	BE220399	NM_024038	79002	1,07	9,35E-05
ABCD1	205142_x_at	NM_000033	NM_000033	215	1,07	8,99E-03
ZNF537	223392_s_at	BF510588	NM_020856	57616	1,07	1,32E-04
AI733583	243235_at	AI733583	---	---	1,07	3,45E-03
CROP	242389_at	BE887449	NM_006107 NM_016424	51747	1,07	1,26E-03
SSH2	230590_at	BE675486	NM_033389	85464	1,07	5,70E-04
NDUFS8	232169_x_at	AK002110	NM_002496	4728	1,06	6,64E-04
VAPA	242780_at	AI332536	NM_003574 NM_194434	9218	1,06	7,88E-03
FDFT1	238666_at	BF438300	NM_004462	2222	1,06	1,67E-03
NQO1	210519_s_at	BC000906	NM_000903	1728	1,06	4,23E-03
KLHL5	233866_at	AK001836	NM_001007075 NM_199039	51088	1,06	5,76E-03
SLC8A3	1562403_a_at	AK096553	NM_033262 NM_058240 NM_182932 NM_182933 NM_182936 NM_183002	6547	1,06	2,76E-05
DPF1	206531_at	NM_004647	NM_004647	8193	1,06	4,01E-03
MCCC2	1556345_s_at	AF086534	NM_022132	64087	1,06	2,60E-03
NOS1	239132_at	BE299830	NM_000620	4842	1,05	1,68E-03
DOK4	209691_s_at	BC003541	NM_018110	55715	1,05	9,53E-03
SESN2	223195_s_at	BF131886	NM_031459	83667	1,05	7,34E-03
AK025909	233814_at	AK025909	---	---	1,05	2,17E-06
FBN1	202766_s_at	NM_000138	NM_000138	2200	1,05	4,10E-03
UCHL1	201387_s_at	NM_004181	NM_004181	7345	1,05	2,84E-03
DIAPH1	209190_s_at	AF051782	NM_005219	1729	1,05	3,26E-04
KIAA0152	200616_s_at	BC000371	NM_014730	9761	1,04	2,72E-06
GAP43	204471_at	NM_002045	NM_002045	2596	1,04	4,27E-04
KIAA0528	240205_x_at	AW188170	NM_014802	9847	1,04	5,35E-03
AK025343	216176_at	AK025343	---	---	1,04	4,13E-04
WDR45	215553_x_at	AK024315	NM_007075	11152	1,04	3,37E-03
NLN	234762_x_at	AK026655	NM_020726	57486	1,03	6,21E-03
AI589594	238694_at	AI589594	---	---	1,03	1,36E-04
CTSL2	210074_at	AF070448	NM_001333	1515	1,03	7,07E-03
COBLL1	203642_s_at	NM_014900	NM_014900	22837	1,03	7,47E-03
MGC15407	235662_at	AI125867	NM_080667	112942	1,03	8,10E-03
TRNT1	223814_at	BC005184	NM_016000 NM_182916	51095	1,03	8,10E-04
AI377043	230722_at	AI377043	---	---	1,03	2,26E-03
MGC45866	232475_at	BC002881	NM_152259	90381	1,03	4,71E-03
KIAA2024	1566166_at	AL833423	NM_172070	130507	1,03	3,17E-04
SRGAP2	1556203_a_at	AI263819	XM_059095	23380	1,03	1,13E-03
CHTF18	226569_s_at	AK024476	NM_022092	63922	1,02	1,51E-03

TCF7L2	216511_s_at	AJ270770	NM_030756	6934	1,02	1,84E-07
SDFR1	228723_at	AL360198	NM_012428 NM_017455	27020	1,02	2,35E-04
CDCA7	230060_at	AI277642	NM_031942 NM_145810	83879	1,02	6,93E-03
CIAPIN1	230838_s_at	AW771492	NM_020313	57019	1,02	6,62E-03
SDC4	202071_at	NM_002999	NM_002999	6385	1,02	4,53E-03
STK36	234005_x_at	AK022692	NM_015690	27148	1,02	9,55E-05
DLGAP4	233056_x_at	AK024674	NM_014902 NM_183006	22839	1,02	5,12E-03
CNOT7	233019_at	AU145061	NM_013354 NM_054026	29883	1,02	3,38E-03
SKIL	217591_at	BF725121	NM_005414	6498	1,01	8,82E-06
GARNL1	215162_at	AB020691	NM_014990 NM_194301	253959	1,01	3,09E-04
RFC5	203210_s_at	NM_007370	NM_007370 NM_181578	5985	1,01	1,06E-03
AK024136	217152_at	AK024136	---	---	1,01	3,14E-03
ATP8B1	214594_x_at	BG252666	NM_005603	5205	1,01	6,15E-03
AL050032	216621_at	AL050032	---	---	1,01	1,08E-05
CKLFSF7	1560754_at	AL832450	NM_138410 NM_181472	112616	1,01	1,86E-03
KIAA1212	1562848_at	BC035848	NM_018084	55704	1,01	4,98E-03
CAPN1	232012_at	AV691296	NM_005186	823	1,01	1,96E-03
ZNF207	231848_x_at	AW192569	NM_003457	7756	1,01	7,04E-03
TRA2A	229574_at	AI268231	NM_013293	29896	1,01	7,43E-03
AU146021	232478_at	AU146021	---	---	1,01	7,34E-03
KNTC1	206316_s_at	NM_014708	NM_014708	9735	1,00	8,69E-06
DENR	238982_at	AW665791	NM_003677	8562	1,00	3,31E-03
DNCH2	1565149_at	AF288405	XM_370652	79659	1,00	2,59E-06
PRDX2	215067_x_at	AU147942	NM_005809 NM_181737 NM_181738	7001	1,00	5,62E-03
PRDX6	238951_at	BF843343	NM_004905	9588	1,00	2,00E-04
RIOK3	215588_x_at	AK024958	NM_003831 NM_145906	8780	1,00	5,41E-04
MID1	203636_at	BE967532	NM_000381 NM_033290 NM_033291	4281	1,00	2,42E-03
E2-230K	1554814_at	BC007822	NM_022066	63893	1,00	2,86E-03
ZFOC1	1558816_at	BC037793	NM_152437	144348	1,00	1,23E-04
EFHC1	225656_at	AI564473	NM_018100	114327	1,00	7,26E-03
KIAA0999	242920_at	AW590838	NM_025164	23387	1,00	6,83E-03
GRK6	202848_s_at	BG423052	NM_001004105 NM_001004106 NM_002082	2870	0,99	2,95E-03
STS	243858_at	AA699970	NM_000351	412	0,99	1,31E-03

AZI2	223846_at	BC001139	NM_022461 NM_203326	64343	0,99	9,97E-05
AW069499	230886_at	AW069499	---	---	0,99	5,25E-04
NKTR	215338_s_at	AI688640	NM_005385	4820	0,99	6,23E-03
FLJ10406	220535_at	NM_018088	NM_018088	55138	0,99	2,76E-03
PDZRN3	232776_at	AU145289	NM_015009	23024	0,99	5,32E-03
ACVR2	244332_at	AW974077	NM_001616	92	0,99	5,39E-06
GLS	223080_at	AK025021	NM_014905	2744	0,99	2,09E-03
RAB35	205461_at	NM_006861	NM_006861	11021	0,99	8,15E-03
FLJ21415	218867_s_at	NM_024738	NM_024738	79794	0,99	4,67E-03
MTMR9	233101_at	AK022071	NM_015458	66036	0,98	3,57E-04
TDG	203742_s_at	BF674842	NM_001008411 NM_003211	6996	0,98	2,79E-04
DKFZP434K046	1570227_at	BC016065	NM_020312	57017	0,98	7,84E-03
RBL1	1555004_a_at	BC032247	NM_002895 NM_183404	5933	0,98	3,12E-03
MYST3	242480_at	AA868356	NM_006766	7994	0,98	3,48E-03
TXNDC5	243405_at	AI097337	NM_022085 NM_030810	81567	0,98	1,17E-03
C14orf153	232814_x_at	AK024310	NM_032374	84334	0,98	2,05E-03
FLJ10569	237504_at	AW002398	NM_018142	55174	0,98	5,78E-05
AW451634	229470_at	AW451634	---	---	0,98	2,25E-03
ATP2B1	209281_s_at	M95541	NM_001001323 NM_001682	490	0,98	7,26E-05
CHPT1	1559739_at	AK025141	NM_020244	56994	0,98	1,14E-03
PFKFB4	228499_at	AL038787	NM_004567	5210	0,98	1,03E-04
AI435248	242837_at	AI435248	---	---	0,98	3,31E-03
AL567118	241388_at	AL567118	---	---	0,97	9,39E-03
ZNF274	232436_at	AI057616	NM_016324 NM_016325 NM_133502	10782	0,97	8,11E-03
SLCO3A1	229776_at	AW138118	NM_013272	28232	0,97	3,95E-03
DRIM	209725_at	AF072718	NM_014503	27340	0,97	6,32E-03
AARS	201000_at	NM_001605	NM_001605	16	0,97	3,59E-03
BE857972	243781_at	BE857972	---	---	0,97	2,71E-04
AU146017	234082_at	AU146017	---	---	0,97	1,73E-03
MGC20481	243513_at	AA971848	NM_052849	90416	0,96	3,69E-03
CPEB4	242364_at	AI452469	NM_030627	80315	0,96	8,12E-03
KDELC2	225128_at	AL548941	NM_153705	143888	0,96	3,31E-03
R84398	241993_x_at	R84398	---	---	0,96	3,54E-03
PR47	1560526_at	BQ880034	---	266671	0,96	4,91E-03
GTSE1	204315_s_at	AI340239	NM_016426	51512	0,96	1,04E-03
WDR11	229694_at	BF062828	NM_018117	55717	0,96	6,59E-03
CTNNB1	242558_at	AW362945	NM_001904	1499	0,96	4,14E-03
AI760298	244054_at	AI760298	---	---	0,96	2,18E-05
IQWD1	235613_at	BF476152	NM_018442	55827	0,96	6,64E-03
AW024890	229942_at	AW024890	---	---	0,96	6,64E-03

DDHD1	231165_at	BE857355	NM_030637	80821	0,96	8,45E-03
CDYL	240594_at	W86659	NM_004824 NM_170751 NM_170752	9425	0,96	4,83E-03
U2AF1	232141_at	AU144161	NM_006758	7307	0,96	2,17E-05
RAPGEF2	238176_at	T86196	XM_376350	9693	0,96	9,65E-03
C14orf135	1563259_at	AK024838	NM_022495	64430	0,95	1,91E-04
GPX3	214091_s_at	AW149846	NM_002084	2878	0,95	6,75E-03
DKFZp434P055	232398_at	AK001064	NM_173466	91531	0,95	1,46E-03
MATR3	242260_at	BG283790	NM_018834	9782	0,95	4,52E-04
STK36	231806_s_at	AL133630	NM_015690	27148	0,95	3,18E-03
DTX1	1559618_at	BQ188678	NM_004416	1840	0,95	2,32E-03
AL832061	1559436_x_at	AL832061	---	---	0,95	1,65E-03
VPS29	223026_s_at	AF201946	NM_016226 NM_057180	51699	0,95	6,16E-04
SEC61A2	228747_at	AI694646	NM_018144	55176	0,95	9,12E-03
USP7	230761_at	AI972599	NM_003470	7874	0,95	4,14E-06
STK32B	219686_at	NM_018401	NM_018401	55351	0,95	7,68E-03
SMO	218629_at	NM_005631	NM_005631	6608	0,95	6,28E-03
TCF7L2	212761_at	AI949687	NM_030756	6934	0,95	3,71E-03
PDK1	226452_at	AU146532	NM_002610	5163	0,94	7,99E-04
MAP3K1	225927_at	AA541479	XM_042066	4214	0,94	1,85E-03
PMAIP1	204286_s_at	NM_021127	NM_021127	5366	0,94	9,09E-04
AL049260	216524_x_at	AL049260	---	---	0,94	1,42E-03
GTF2H3	222104_x_at	AI569458	NM_001516	2967	0,94	2,18E-03
MGC13098 POLR2J2	214740_at	BE676209	NM_032958 NM_032959 NM_145325 XM_379817 XM_499280	246721 84820	0,94	6,48E-03
FLJ31795	1566480_x_at	AK096357	NM_144609	124808	0,94	1,19E-03
MID1	203637_s_at	NM_000381	NM_000381 NM_033290 NM_033291	4281	0,94	8,91E-03
AI692624	1556352_at	AI692624	---	---	0,94	3,86E-03
AL035461	231827_at	AL035461	---	---	0,94	8,02E-03
NFKBIZ	223218_s_at	AB037925	NM_001005474 NM_031419	64332	0,93	9,02E-03
R78413	240538_at	R78413	---	---	0,93	5,24E-03
UBXD4	235327_x_at	BG111015	NM_181713	165324	0,93	2,26E-06
PABPC1	236907_at	AI760366	NM_002568	26986	0,93	9,37E-03
RNF34	219035_s_at	NM_025126	NM_025126 NM_194271	80196	0,93	1,26E-05
FLJ11539	219791_s_at	NM_024748	XM_496724	79804	0,93	1,41E-03
FLJ10156	221591_s_at	BC005004	NM_019013	54478	0,93	4,68E-04
CREBL1	1554487_a_at	BC008394	NM_004381	1388	0,93	4,64E-05
RBBP4	239071_at	AI972451	NM_005610	5928	0,93	3,91E-03

SNRPA1	242146_at	AA872471	NM_003090	6627	0,93	4,37E-03
DERL3	231324_at	AW452134	NM_001002862 NM_198440	91319	0,93	9,94E-05
DDX50	1568815_a_at	AA903184	NM_024045	79009	0,93	3,15E-03
KCTD3	241903_at	AI688631	NM_016121	51133	0,93	1,35E-03
TBX3	225544_at	AI806338	NM_005996 NM_016569	6926	0,93	2,95E-03
EXOC7	214802_at	AK022397	NM_015219	23265	0,93	6,60E-03
ZDHHC13	243250_at	AI922173	NM_001001483 NM_019028	54503	0,93	7,75E-03
NSF	1566785_x_at	AK025172	NM_006178	4905	0,92	1,01E-03
C9orf3	237716_at	AA699673	NM_032823	84909	0,92	2,56E-03
GPR125	210473_s_at	M37712	NM_145290	166647	0,92	5,29E-07
ZNF160	214715_x_at	AK024789	NM_033288 NM_198893	90338	0,92	1,07E-03
CALU	238908_at	BG392414	NM_001219	813	0,92	2,85E-05
TCF7L2	216037_x_at	AA664011	NM_030756	6934	0,92	1,59E-04
MBNL2	232369_at	AF339768	NM_144778 NM_207304	10150	0,92	6,38E-03
DHX36	1559039_at	AK096808	NM_020865	170506	0,92	4,13E-03
BE563152	224806_at	BE563152	XM_498674	440448	0,92	7,47E-03
TM4SF8	232632_at	AU145719	NM_005724 NM_198902	10099	0,92	1,10E-05
BTBD14B	215587_x_at	AK023891	NM_052876	112939	0,92	2,11E-03
AI821721	241223_x_at	AI821721	---	---	0,91	3,84E-03
SREBF1	235862_at	AA954908	NM_001005291 NM_004176	6720	0,91	1,46E-03
AI570571	236092_at	AI570571	---	---	0,91	2,41E-03
FLJ13491	219245_s_at	AI309636	NM_024623	79676	0,91	9,68E-06
MDH1	235374_at	AW952547	NM_005917	4190	0,91	1,14E-03
PASK	216945_x_at	U79240	NM_015148	23178	0,91	3,14E-03
DTYMK	1553983_at	AF258562	NM_012145	1841	0,90	9,36E-03
CLU	208792_s_at	M25915	NM_001831 NM_203339	1191	0,90	3,22E-05
C20orf172	219512_at	NM_024918	NM_024918	79980	0,90	1,35E-03
PTPN1	202716_at	NM_002827	NM_002827	5770	0,90	4,52E-04
ENTPD6	201704_at	NM_001247	NM_001247	955	0,90	9,65E-03
DKFZP564C196	236367_at	N33174	XM_498825	284649	0,90	3,20E-03
GPT2	224839_s_at	BG328998	NM_133443	84706	0,89	2,50E-03
TH1L	225006_x_at	AJ238379	NM_016397 NM_198976	51497	0,89	1,75E-05
AW975183	244340_x_at	AW975183	---	---	0,89	1,08E-03
AW131450	235513_at	AW131450	---	---	0,89	1,09E-05
AK023783	215604_x_at	AK023783	---	---	0,89	6,48E-03
KIAA0582	239442_at	BF589179	NM_015147	23177	0,89	1,66E-03

BTBD7	217141_at	AL049394	NM_001002860 NM_018167	55727	0,89	2,17E-03
DNAPTP6	222154_s_at	AK002064	NM_015535	26010	0,89	1,33E-03
RNPEP	208270_s_at	NM_020216	NM_020216	6051	0,89	9,93E-04
KIAA0232	232595_at	AK023294	NM_014743	9778	0,89	2,09E-03
ZNF503	227195_at	AA603467	NM_032772	84858	0,88	1,25E-04
RABL4	213784_at	AL037167	NM_006860	11020	0,88	4,07E-03
KLF7	204334_at	AA488672	NM_003709	8609	0,88	5,59E-04
FLJ13611	234788_x_at	AK024819	NM_024941	80006	0,88	4,20E-03
TFF3	204623_at	NM_003226	NM_003226	7033	0,88	1,84E-03
C7orf24	239841_at	AA137038	NM_024051	79017	0,88	5,49E-05
FLJ14346	220720_x_at	NM_025029	NM_025029	80097	0,88	2,42E-03
PGF	215179_x_at	AK023843	NM_002632	5228	0,88	6,50E-04
BTBD9	233041_x_at	AK025009	NM_152733	114781	0,87	5,26E-03
ZFP64	242759_at	AI821726	NM_018197 NM_022088 NM_199426 NM_199427	55734	0,87	1,39E-03
AW139789	232134_at	AW139789	---	---	0,87	2,61E-05
KIAA1706	1563621_at	AL713724	NM_030636	80820	0,87	9,21E-03
GNAS	228173_at	AA810695	NM_000516 NM_016592 NM_080425 NM_080426	2778	0,87	1,14E-03
ESPL1	204817_at	NM_012291	NM_012291	9700	0,87	4,80E-03
AI791828	237868_x_at	AI791828	---	---	0,87	3,13E-05
RBM6	1556672_a_at	AI190489	NM_005777	10180	0,87	7,88E-04
SBNO1	216161_at	AK024128	NM_018183	55206	0,87	2,11E-03
BF056892	229024_at	BF056892	---	---	0,87	7,14E-06
CDC42BPA	215296_at	AK027000	NM_003607 NM_014826	8476	0,87	5,58E-03
BE727883	226495_at	BE727883	XM_498844	440752	0,87	7,67E-03
ANK2	216195_at	AF131823	NM_001148 NM_020977	287	0,86	2,02E-04
SFI1	215699_x_at	AL096768	NM_001007467 NM_014775	9814	0,86	4,61E-04
TH1L	225261_x_at	AJ238376	NM_016397 NM_198976	51497	0,86	4,08E-05
SEMA6A	215028_at	AB002438	NM_020796	57556	0,86	1,40E-04
LOC91431	228859_at	BF056790	NM_138698	91431	0,86	3,09E-03
FTHFSDC1	240552_at	AA811452	NM_015440	25902	0,86	8,65E-04
TRIM36	219736_at	NM_018700	NM_018700	55521	0,86	8,76E-03
DDX11	208159_x_at	NM_004399	NM_004399 NM_030653 NM_030655	1663	0,86	1,06E-03
NFATC2IP	212809_at	AA152202	NM_032815	84901	0,86	5,06E-04

M-RIP	231255_at	AI970090	NM_015134 NM_201274	23164	0,86	6,68E-04
PCNT1	218014_at	NM_024844	NM_024844	79902	0,86	7,48E-05
ADAM33	233868_x_at	AL117415	NM_025220 NM_153202	80332	0,85	1,87E-04
FLJ10569	229633_at	AA115512	NM_018142	55174	0,85	3,01E-04
AI734111	222284_at	AI734111	---	---	0,85	2,27E-03
RPL35A	215208_x_at	AK021571	NM_000996	6165	0,85	1,22E-03
SNCAIP	219511_s_at	NM_005460	NM_005460	9627	0,85	1,37E-03
GRIK2	1560265_at	BQ434382	NM_021956 NM_175768	2898	0,85	8,83E-04
CCND1	208711_s_at	BC000076	NM_053056	595	0,85	5,90E-05
NM_003349	201003_x_at	NM_003349	---	---	0,85	1,49E-04
FLJ13089	225888_at	N62802	NM_024953	80018	0,84	3,59E-04
SLB	226324_s_at	AB033005	NM_015662	26160	0,84	6,60E-03
SFRS15	222310_at	AA648521	NM_020706	57466	0,84	2,91E-03
AP3M2	1569053_at	BG110196	NM_006803	10947	0,84	9,81E-04
STRA6	1569335_a_at	BC015881	NM_022369	64220	0,83	1,47E-03
TH1L	225865_x_at	AJ238374	NM_016397 NM_198976	51497	0,83	3,21E-04
SLC2A4RG	218494_s_at	NM_020062	NM_020062	56731	0,83	8,97E-05
NCOA5	239815_at	R16784	NM_020967	57727	0,83	7,12E-03
AARSL	231845_at	AI721172	NM_020745	57505	0,83	4,13E-04
AA767373	236327_at	AA767373	---	---	0,83	1,12E-03
KIAA1434	230492_s_at	BE328402	NM_019593	56261	0,83	8,78E-04
RGMA	223468_s_at	AL136826	NM_020211	56963	0,83	2,26E-03
T86613	235804_at	T86613	---	---	0,83	9,52E-05
LMO4	209205_s_at	BC003600	NM_006769	8543	0,83	5,83E-04
AL044078	221860_at	AL044078	---	---	0,83	2,22E-04
AA824321	227547_at	AA824321	---	---	0,82	1,63E-03
C9orf64	223697_x_at	BC004407	NM_032307	84267	0,82	8,80E-05
EIF3S9	242550_at	AA628539	NM_003751 NM_182712	8662	0,82	2,91E-04
LOC144766	243986_at	BE409452	XM_378419	144766	0,82	2,37E-03
C14orf145	1557755_at	AW028337	XM_496002	145508	0,82	3,02E-03
FAM19A5	237094_at	AI953086	NM_015381	25817	0,82	1,93E-05
CDKN2C	211792_s_at	U17074	NM_001262 NM_078626	1031	0,82	7,21E-03
STMN3	222557_at	AL353715	NM_015894	50861	0,82	3,09E-03
C6orf111	230375_at	AI936531	NM_032870	25957	0,82	6,14E-04
CBWD1 CBWD2 LOC220869 DC36	226193_x_at	AV709992	NM_018491 NM_172003 NM_201453	150472 220869 389760 55871	0,82	7,60E-03
ATF3	202672_s_at	NM_001674	NM_001674 NM_004024	467	0,82	4,70E-03
AW629478	244625_at	AW629478	---	---	0,82	1,02E-03

RAD51C	206066_s_at	NM_002876	NM_002876 NM_058216 NM_058217	5889	0,82	1,65E-03
C15orf25	220071_x_at	NM_018097	NM_018097	55142	0,82	5,19E-04
C22orf18	218741_at	NM_024053	NM_001002876 NM_024053	79019	0,81	7,04E-03
GSS	211630_s_at	L42531	NM_000178	2937	0,81	4,31E-03
IREB2	1563129_at	AL109710	NM_004136	3658	0,81	5,38E-03
EPIM	213434_at	H95263	NM_001980 NM_194356	2054	0,81	1,48E-05
DZIP1L	239785_at	BF340245	NM_173543	199221	0,81	7,64E-03
DHX37	223364_s_at	BC004463	NM_032656	57647	0,81	4,75E-03
BC041029	1569025_s_at	BC041029	XM_371697	389211	0,81	2,66E-03
NY-REN-7 LOC389347	214945_at	AW514267	NM_173663 XM_371783	285596 389347	0,81	9,82E-03
AA778747	241941_at	AA778747	---	---	0,81	3,29E-04
PDE4C	206792_x_at	NM_000923	NM_000923	5143	0,81	3,77E-04
SYNCRIP	209025_s_at	AF037448	NM_006372	10492	0,81	1,94E-03
DRPLA	236961_at	AI539426	NM_001007026 NM_001940	1822	0,80	7,80E-03
ZNF611	208137_x_at	NM_030972	NM_030972	81856	0,80	1,06E-03
BACH2	215907_at	AK027193	NM_021813	60468	0,80	1,49E-03
AL038191	240271_at	AL038191	---	---	0,80	4,41E-04
FANCC	205189_s_at	NM_000136	NM_000136	2176	0,80	6,32E-04
RPL10A	232592_at	AU146731	NM_007104	4736	0,80	4,23E-03
GALNT7	218313_s_at	NM_017423	NM_017423	51809	0,80	5,54E-03
SCML1	222747_s_at	BF001786	NM_006746	6322	0,79	2,71E-03
DERA	218102_at	NM_015954	NM_015954	51071	0,79	1,87E-03
AF131796	231916_at	AF131796	---	---	0,79	4,14E-03
CCNE1	213523_at	AI671049	NM_001238 NM_057182	898	0,79	8,53E-03
WWOX	233161_at	AK022464	NM_016373 NM_018560 NM_130788 NM_130790 NM_130791 NM_130792 NM_130844	51741	0,79	2,29E-03
SRP54	1557504_at	AI076351	NM_003136	6729	0,79	7,25E-03
BG149337	229814_at	BG149337	---	---	0,79	7,38E-03
BE676171	237156_at	BE676171	---	---	0,79	4,22E-03
NR2C1	210530_s_at	M21985	NM_003297	7181	0,79	4,35E-03
NKTR	243055_at	BF514072	NM_005385	4820	0,78	9,55E-03
KIAA0152	200617_at	NM_014730	NM_014730	9761	0,78	6,41E-03
EMILIN3	228307_at	AL137580	NM_052846	90187	0,78	3,72E-03
TM4SF14	221002_s_at	NM_030927	NM_030927	81619	0,78	3,35E-03
AI151104	237475_x_at	AI151104	---	---	0,78	1,69E-03

NUP153	239948_at	AA004800	NM_005124	9972	0,78	1,85E-03
PELI2	219132_at	NM_021255	NM_021255	57161	0,78	9,97E-04
THOC4	226319_s_at	AF047002	NM_005782	10189	0,78	3,97E-03
HOXD4	1552337_s_at	NM_014621	NM_014621	3233	0,78	4,73E-03
PPM1B	232580_x_at	AL117553	NM_002706 NM_177968 NM_177969	5495	0,78	2,42E-03
AK000864	216290_x_at	AK000864	---	---	0,78	9,80E-03
KIFC1	209680_s_at	BC000712	XM_371813	3833	0,78	2,91E-03
GSS	201415_at	NM_000178	NM_000178	2937	0,78	7,64E-03
ACPL2	236908_at	BE550429	NM_152282	92370	0,78	2,99E-03
AA348683	240198_at	AA348683	---	---	0,77	1,02E-05
ORF1-FL49	224707_at	AL522667	NM_032412	84418	0,77	3,79E-04
LOC340085	232455_x_at	AU145408	---	340085	0,77	4,32E-04
CNP	1556053_at	AL556987	NM_033133	1267	0,77	2,24E-04
AK098337	1566144_at	AK098337	XM_496690	401131	0,77	1,47E-03
HEG	213069_at	AI148659	XM_087386	57493	0,77	1,93E-03
AI833186	242593_at	AI833186	---	---	0,77	9,83E-04
GPR51	217077_s_at	AF095723	NM_005458	9568	0,77	7,45E-03
KIAA1434	224826_at	AK001947	NM_019593	56261	0,77	3,37E-04
TYRO3	211432_s_at	U05682	NM_006293	7301	0,77	1,71E-03
GNB4	223488_s_at	BC000873	NM_021629	59345	0,77	9,63E-03
MPHOSPH9	237158_s_at	AW449069	NM_022782	10198	0,77	6,87E-03
FBXW12	215600_x_at	AK022174	NM_207102	285231	0,77	4,32E-03
PTK7	1555324_at	BC046109	NM_002821 NM_152880 NM_152881 NM_152882 NM_152883	5754	0,77	9,93E-03
KLHL5	226001_at	AK002174	NM_001007075 NM_199039	51088	0,77	7,30E-03
CRTAC1	221204_s_at	NM_018058	NM_018058	55118	0,76	5,35E-03
AK021514	215978_x_at	AK021514	---	---	0,76	7,15E-03
N53564	242280_x_at	N53564	---	---	0,76	1,02E-04
OLFML3	218162_at	NM_020190	NM_020190	56944	0,76	3,61E-04
PDCD2	243773_at	H65902	NM_002598 NM_144781	5134	0,76	9,35E-03
H09533	239748_x_at	H09533	---	---	0,76	6,06E-04
SH3MD1	224817_at	W93554	NM_014631	9644	0,76	1,12E-05
C9orf86	219828_at	NM_024718	NM_024718	55684	0,76	2,56E-03
TBX3	243234_at	BG055137	NM_005996 NM_016569	6926	0,76	4,38E-03
PHF20L1	1554472_a_at	BC015211	NM_016018 NM_024878 NM_032205 NM_198513	51105	0,76	3,06E-03
FLJ10404	243047_at	AV698751	NM_019057	54540	0,76	6,86E-03

SIRT2	1556331_at	BG722779	NM_012237 NM_030593	22933	0,76	6,78E-03
BRI3BP	231810_at	BG106919	NM_080626	140707	0,76	1,27E-03
C19orf14	215218_s_at	AC004144	NM_173636	284403	0,76	9,95E-03
AFG3L1	1552287_s_at	NM_001132	NM_001132	172	0,76	4,38E-03
MUM1	229033_s_at	AA143060	NM_032853	84939	0,76	1,74E-04
DHX35	218579_s_at	NM_021931	NM_021931	60625	0,76	1,36E-03
ESPL1	38158_at	D79987	NM_012291	9700	0,75	5,71E-03
WBSCR20C	213460_x_at	N29665	NM_032158 NM_148936 NM_148980 NM_149379	260294	0,75	3,30E-04
SFI1	213431_x_at	AB011114	NM_001007467 NM_014775	9814	0,75	3,65E-05
AI252004	242696_at	AI252004	---	---	0,75	1,12E-03
SLC15A4	225043_at	AW304786	NM_145648	121260	0,75	9,55E-03
PME-1	243443_at	AI076511	NM_016147	51400	0,75	4,15E-03
TUBGCP2	244842_x_at	AA235663	NM_006659	10844	0,75	5,81E-03
AI041522	228030_at	AI041522	---	---	0,75	8,68E-03
KIAA0992	234135_x_at	AK021652	NM_016081	23022	0,75	3,75E-04
NQO1	201467_s_at	AI039874	NM_000903	1728	0,75	9,53E-03
TJP2	243148_at	AA007423	NM_004817 NM_201629	9414	0,75	2,81E-03
IQGAP1	213446_s_at	AI679073	NM_003870	8826	0,75	1,44E-03
SEC11L3	223299_at	AF212233	NM_033280	90701	0,75	7,34E-04
LOC283871	222622_at	BG284709	XM_208887	283871	0,75	4,92E-03
T96555	243818_at	T96555	---	---	0,75	3,01E-03
TCEA1	1566207_at	BQ286789	NM_006756 NM_201437	6917	0,74	1,85E-03
ZNF44	233775_x_at	AK023304	NM_016264	51710	0,74	1,98E-04
AK024599	233702_x_at	AK024599	---	---	0,74	2,99E-03
C20orf44	244795_at	AV693986	NM_018244 NM_199487 NM_199513	55245	0,74	9,01E-03
N4BP2	231996_at	AB037834	NM_018177	55728	0,74	6,20E-06
GLIG4	201559_s_at	AF109196	NM_013943	25932	0,74	9,19E-03
SEC15L1	232599_at	AF220217	NM_019053	54536	0,74	7,90E-03
AU145662	233399_x_at	AU145662	XM_499131	441383	0,74	1,87E-03
RAD54L	204558_at	NM_003579	NM_003579	8438	0,74	1,24E-03
SLC4A8	207056_s_at	NM_004858	NM_004858	9498	0,74	5,18E-03
PLS3	201215_at	NM_005032	NM_005032	5358	0,74	9,88E-03
C10orf6	203482_at	AL133215	NM_018121	55719	0,74	9,76E-03
PDLIM7	1569150_x_at	BC023629	NM_005451 NM_203352 NM_203353 NM_213636	9260	0,73	1,56E-03
AI939447	241268_x_at	AI939447	---	---	0,73	2,79E-04
FLJ12649	219626_at	NM_024597	XM_291344	79649	0,73	8,01E-04

PPHLN1	234459_at	AK000186	NM_016488 NM_201438 NM_201439 NM_201440 NM_201515	51535	0,73	6,98E-03
DBT	205370_x_at	NM_001918	NM_001918	1629	0,73	4,67E-03
CBX3	230998_at	AV702506	NM_007276 NM_016587	11335	0,73	8,36E-03
ASAHL	214765_s_at	AK024677	NM_014435	27163	0,73	1,72E-05
AF130054	211452_x_at	AF130054	---	---	0,73	5,36E-04
CHKB	204193_at	NM_005198	NM_005198 NM_152253	1120	0,72	3,15E-04
IQGAP1	210840_s_at	D29640	NM_003870	8826	0,72	7,05E-05
ASAHL	232072_at	AK025371	NM_014435	27163	0,72	1,08E-03
MDS028	220590_at	NM_018463	NM_018463	55846	0,72	2,33E-04
SPCS3	222753_s_at	AL136660	NM_021928	60559	0,72	6,00E-03
TERT	207199_at	NM_003219	NM_003219 NM_198253 NM_198254 NM_198255	7015	0,72	3,23E-05
BI496583	1557675_at	BI496583	---	---	0,72	4,63E-03
KIAA1731	1565829_at	BU619319	XM_374922	85459	0,72	6,04E-03
UPF3A	206958_s_at	AF318575	NM_023011 NM_080687	65110	0,72	6,99E-04
GPR125	1555122_at	BC026009	NM_145290	166647	0,72	4,13E-03
FMNL2	1556656_at	BF477401	NM_001004417 NM_001004421 NM_001004422 NM_052905	114793	0,72	1,56E-03
UBE2J1	236528_at	N64079	NM_016021	51465	0,72	2,03E-03
AF15Q14	1552680_a_at	NM_020380	NM_020380 NM_144508 NM_170589	57082	0,71	8,46E-03
RAB11FIP3	228613_at	BF183535	NM_014700	9727	0,71	5,28E-03
GARNL1	234923_at	AK022988	NM_014990 NM_194301	253959	0,71	7,34E-03
TK1	1554408_a_at	BC007986	NM_003258	7083	0,71	4,05E-03
BE503981	229593_at	BE503981	---	---	0,71	2,45E-05
MARS	201475_x_at	NM_004990	NM_004990	4141	0,71	6,05E-03
IDH3B	210014_x_at	AF023266	NM_006899 NM_174855 NM_174856	3420	0,71	6,81E-03
ETV1	217061_s_at	AC004857	NM_004956	2115	0,71	4,82E-03
AI829569	236671_at	AI829569	---	---	0,71	5,08E-04
MCM4	212141_at	AA604621	NM_005914 NM_182746	4173	0,71	2,19E-03

HRPT2	215398_at	AF038194	NM_024529	79577	0,70	2,72E-03
SFRS14	212001_at	AV738039	NM_014884	10147	0,70	1,89E-04
GEMIN4	217099_s_at	AF258545	NM_015721	50628	0,70	2,89E-03
RRAGD	221524_s_at	AF272036	NM_021244	58528	0,70	4,52E-03
PSAT1	220892_s_at	NM_021154	NM_021154 NM_058179	29968	0,70	4,14E-03
NSUN5 WBSCR20B WBSCR20C	213670_x_at	AI768378	NM_018044 NM_032158 NM_145645 NM_148936 NM_148956 NM_148980 NM_149379	155400 260294 55695	0,70	3,58E-05
KIAA0286	212621_at	AB006624	NM_015257	23306	0,70	5,42E-03
AFG3L1	236250_at	AI859065	NM_001132	172	0,70	4,29E-03
MAD2L2	223234_at	AF080398	NM_006341	10459	0,70	6,48E-03
BF062155	238279_x_at	BF062155	---	---	0,70	1,33E-03
PSMD7	238738_at	AW361702	NM_002811	5713	0,70	1,94E-03
TUBG1	201714_at	NM_001070	NM_001070	7283	0,69	9,09E-03
CSTF1	202190_at	NM_001324	NM_001324	1477	0,69	3,88E-03
T71269	234033_at	T71269	---	---	0,69	3,53E-03
CROP	241792_x_at	N36160	NM_006107 NM_016424	51747	0,69	2,36E-03
SLIT3	203813_s_at	NM_003062	NM_003062	6586	0,69	8,85E-03
AI857788	227126_at	AI857788	---	---	0,69	3,64E-04
FLJ12700	219627_at	NM_024910	NM_024910	79970	0,69	5,30E-04
FLJ40432	228810_at	AW135279	NM_152523	151195	0,69	9,81E-04
DGCR8	219811_at	NM_022720	NM_022720	54487	0,69	3,02E-03
SHMT1	209980_s_at	L23928	NM_004169 NM_148918	6470	0,68	2,17E-03
UPF3A	217596_at	AA649851	NM_023011 NM_080687	65110	0,68	3,51E-03
PPT2	209826_at	AF020544	NM_005155 NM_138717 NM_138934	9374	0,68	3,49E-04
THOC4	226320_at	AF047002	NM_005782	10189	0,68	4,54E-03
NDUFA5	215850_s_at	AK022209	NM_005000	4698	0,68	8,18E-03
DTYMK	203270_at	NM_012145	NM_012145	1841	0,68	7,28E-03
FLJ10199	218815_s_at	NM_018022	NM_018022	55092	0,68	3,91E-03
CRSP6	232483_at	AK022156	NM_004268	9440	0,68	5,79E-04
PTPRF	215066_at	AU158443	NM_002840 NM_130440	5792	0,68	3,31E-03
ADD1	214736_s_at	BE898639	NM_001119 NM_014189 NM_014190 NM_176801	118	0,68	1,78E-03
C9orf88	223019_at	BC001979	NM_022833	64855	0,68	9,03E-04
FLJ34443	241408_at	AA531337	NM_175918	285464	0,68	9,11E-03
TK2	208246_x_at	NM_017618	NM_004614	7084	0,67	5,00E-03

C10orf79	243896_at	AI809779	NM_025145	80217	0,67	4,78E-03
SRGAP2	1556202_at	AI263819	XM_059095	23380	0,67	9,56E-03
PANK2	218809_at	NM_024960	NM_024960 NM_153637 NM_153638 NM_153639 NM_153640 NM_153641	80025	0,67	2,17E-06
HOXD4	205522_at	NM_014621	NM_014621	3233	0,67	5,20E-03
NES	218678_at	NM_024609	NM_006617	10763	0,67	1,78E-03
MICAL3	229474_at	BF055090	XM_032998 XM_032997	57553	0,67	3,47E-03
TCF7L2	212762_s_at	AI375916	NM_030756	6934	0,67	3,83E-03
TPD52L2	201379_s_at	NM_003288	NM_003288 NM_199359 NM_199360 NM_199361 NM_199362 NM_199363	7165	0,66	4,00E-03
PVRL3	213325_at	AA129716	NM_015480	25945	0,66	2,59E-04
ASAHL	227135_at	AI436803	NM_014435	27163	0,66	2,36E-03
AI197932	229498_at	AI197932	---	---	0,66	6,38E-03
KIAA0931	213407_at	AB023148	NM_015020	23035	0,66	4,47E-03
AK057923	1556364_at	AK057923	XM_498935	440960	0,66	9,42E-03
ADRBK2	204183_s_at	AI478542	NM_005160	157	0,66	2,10E-04
SNX5	223666_at	BC002724	NM_014426 NM_152227	27131	0,66	5,32E-03
WBSCR23	221176_x_at	NM_025042	NM_025042	80112	0,66	5,53E-06
AK024901	234326_at	AK024901	---	---	0,65	1,50E-04
ZNF500	41113_at	AI871396	NM_021646	26048	0,65	1,77E-03
DMN	212730_at	AK026420	NM_015286 NM_145728	23336	0,65	3,64E-03
ANKH	239449_at	AV693734	NM_054027	56172	0,65	2,03E-03
C14orf120	216263_s_at	AK022215	XM_033371	25983	0,65	1,76E-03
ZNF291	215848_at	AW139369	NM_020843	49855	0,65	3,43E-03
RFC1	209085_x_at	L14922	NM_002913	5981	0,65	2,64E-04
SLIT2	209897_s_at	AF055585	NM_004787	9353	0,65	2,23E-03
LOC134147	234981_x_at	BE537881	NM_138809	134147	0,65	2,57E-03
GPR51	209991_x_at	AF069755	NM_005458	9568	0,65	6,51E-04
AL037473	1557780_at	AL037473	---	---	0,64	9,19E-03
C14orf111	215567_at	AU144919	NM_015962	51077	0,64	2,31E-03
CBX5	241875_at	AA204654	NM_012117	23468	0,64	8,07E-04
UCKL1	218533_s_at	NM_017859	NM_017859	54963	0,64	7,28E-03
BG231554	243179_at	BG231554	---	---	0,64	5,62E-04
PLK4	204887_s_at	NM_014264	NM_014264	10733	0,64	7,56E-04

OGG1	205760_s_at	NM_016821	NM_002542 NM_016819 NM_016820 NM_016821 NM_016826 NM_016827 NM_016828 NM_016829	4968	0,64	4,62E-04
PAICS	201014_s_at	NM_006452	NM_006452	10606	0,64	8,63E-05
RNF150	227657_at	AA722069	NM_020724	57484	0,64	2,38E-03
ETV1	217053_x_at	X87175	NM_004956	2115	0,64	6,17E-03
HRB2	232441_at	AU147079	NM_007043	11103	0,64	8,66E-03
CTNNBL1	221021_s_at	NM_030877	NM_030877	56259	0,64	2,56E-04
FLJ33915	229892_at	AW628843	NM_182613	347918	0,64	7,04E-03
TORC3	232879_at	AK024981	NM_022769	64784	0,64	5,57E-03
IPW	213447_at	AI672541	---	3653	0,64	3,46E-03
ZNF337	214760_at	AL049942	NM_015855	26152	0,64	6,30E-03
SNTA1	203516_at	NM_003098	NM_003098	6640	0,64	5,62E-03
STX1A	204729_s_at	NM_004603	NM_004603	6804	0,64	4,16E-04
RAN	200750_s_at	AF054183	NM_006325	5901	0,64	4,86E-04
FLJ11029	232215_x_at	AK000296	NM_018304	55771	0,63	8,93E-04
H2AFX	205436_s_at	NM_002105	NM_002105	3014	0,63	1,85E-03
LOC338799	1556042_s_at	BI912454	---	338799	0,63	2,22E-03
BC022346	1570210_x_at	BC022346	---	---	0,63	5,53E-03
C10orf58	224435_at	BC005871	NM_032333	84293	0,63	3,19E-06
LOC338799	226369_at	AW138760	---	338799	0,62	4,89E-03
C9orf81	1557985_s_at	AA248753	XM_095991	84131	0,62	4,31E-03
AK023870	233427_x_at	AK023870	---	---	0,62	7,36E-04
FLJ10504	218296_x_at	NM_018116	NM_018116	55154	0,62	1,11E-03
LOC155435	225839_at	AW290882	NM_001008408	155435	0,62	7,67E-03
GNG12	212294_at	BG111761	NM_018841	55970	0,62	4,81E-04
FLJ23342	236059_at	AW168168	NM_024631	79684	0,62	8,20E-03
LMO7	233646_at	AK027238	NM_005358	4008	0,62	7,32E-03
PHF20L1	222133_s_at	AK022280	NM_016018 NM_024878 NM_032205 NM_198513	51105	0,62	1,32E-03
C14orf143	214264_s_at	AI656610	NM_145231	90141	0,62	5,71E-03
LOC157627	1556046_a_at	AL832535	---	157627	0,62	4,24E-03
MAP3K13	206249_at	NM_004721	NM_004721	9175	0,62	4,38E-03
VGF	205586_x_at	NM_003378	NM_003378	7425	0,62	1,70E-03
BLCAP	201032_at	NM_006698	NM_006698	10904	0,62	1,91E-04
POLE2	205909_at	NM_002692	NM_002692	5427	0,62	9,76E-03
ZGPAT	221848_at	AL121845	NM_032527 NM_181484 NM_181485	84619	0,61	1,83E-03
STN2	227461_at	AA632295	NM_033104	85439	0,61	5,56E-03
SFRS11	213742_at	AW241752	NM_004768	9295	0,61	8,24E-03
GPR51	209990_s_at	AF056085	NM_005458	9568	0,61	8,69E-04

TGDS	237346_at	AA976208	NM_014305	23483	0,61	2,60E-03
PANK2	235130_at	AV703394	NM_024960 NM_153637 NM_153638 NM_153639 NM_153640 NM_153641	80025	0,61	2,05E-03
BAX	208478_s_at	NM_004324	NM_004324 NM_138761 NM_138762 NM_138763 NM_138764 NM_138765	581	0,61	2,28E-03
RNF10	207801_s_at	NM_014868	NM_014868	9921	0,61	9,50E-03
SPAG5	203145_at	NM_006461	NM_006461	10615	0,61	3,43E-03
TOP3A	204946_s_at	NM_004618	NM_004618	7156	0,61	4,78E-04
REC14	215156_at	AL109709	NM_025234	80349	0,61	9,61E-04
MGC4308	220612_at	NM_014135	NM_032359	84319	0,61	7,73E-03
AI144156	238670_at	AI144156	---	---	0,61	2,33E-03
TBPIP	205956_x_at	NM_013290	NM_013290 NM_016556	29893	0,61	9,34E-05
AW517479	242608_x_at	AW517479	---	---	0,60	4,70E-03
DXS9879E	219061_s_at	NM_006014	NM_006014	8270	0,60	7,83E-03
384D8-2	205086_s_at	NM_014551	NM_014551 NM_152299	29781	0,60	3,91E-03
DKFZP564K1964	223170_at	AF132000	NM_015544	26022	0,60	2,90E-03
SOX2	213722_at	AW007161	NM_003106	6657	0,60	2,03E-03
CGI-96	33307_at	AL022316	NM_015703	27341	0,60	7,39E-03
BE464132	236841_at	BE464132	XM_496585	440897	0,60	1,92E-03
AK025048	1566705_x_at	AK025048	---	---	0,60	7,42E-03
HEXA	215155_at	J04178	NM_000520	3073	0,60	8,59E-03
NY-REN-41	226287_at	AI458313	NM_080654	91057	0,60	6,85E-03
AK023354	222252_x_at	AK023354	---	---	0,60	7,20E-03
KIAA0582	1559159_at	AK094069	NM_015147	23177	0,59	2,73E-03
PDE8A	212521_s_at	BE568219	NM_002605 NM_173454 NM_173455 NM_173456 NM_173457	5151	0,59	7,81E-03
BE671060	235901_at	BE671060	---	---	0,59	7,80E-03
KIAA1423	225127_at	BF217531	XM_376550	57583	0,59	2,86E-03
DDX54	219111_s_at	NM_024072	NM_024072	79039	0,59	5,24E-03
ADCYAP1	230237_at	BE220888	NM_001117	116	0,59	4,24E-03
CDKN1A	202284_s_at	NM_000389	NM_000389 NM_078467	1026	0,59	1,54E-03
PWP1	201606_s_at	BE796924	NM_007062	11137	0,59	3,48E-04
ZNF505	215758_x_at	AC007204	NM_001004126 NM_031218	81931	0,59	1,44E-03

FLJ00312	221971_x_at	BE672818	XM_374801	399761	0,59	7,23E-03
IGBP1	242337_at	AI347128	NM_001551	3476	0,59	9,36E-03
ANKRD11	219437_s_at	NM_013275	NM_013275	29123	0,59	5,45E-03
TRAF4	202871_at	NM_004295	NM_004295 NM_145751	9618	0,59	3,31E-03
FLJ10404	218920_at	NM_019057	NM_019057	54540	0,59	1,51E-03
SS18L1	213140_s_at	AB014593	NM_015558 NM_198935	26039	0,59	7,09E-05
C20orf161	236514_at	AI885067	NM_033421 NM_152897	90203	0,58	6,89E-03
CTNNB1	223679_at	AF130085	NM_001904	1499	0,58	7,83E-04
NSFL1C	220248_x_at	NM_018839	NM_016143 NM_018839 NM_182483	55968	0,58	4,26E-03
MGC15606	215968_at	AF055018	NM_145037	91775	0,58	2,12E-03
VTN	204534_at	NM_000638	NM_000638	7448	0,58	1,72E-03
SNX5	217792_at	NM_014426	NM_014426 NM_152227	27131	0,58	4,70E-03
LOC157627	214839_at	AF052108	---	157627	0,58	4,90E-03
NSFL1C	232520_s_at	AK023585	NM_016143 NM_018839 NM_182483	55968	0,58	7,68E-03
E2IG5	223193_x_at	AF201944	NM_014367	26355	0,58	3,89E-04
ANKFY1	224900_at	AK025960	NM_016376 NM_020740	51479	0,58	6,56E-03
HNRPA3	211931_s_at	BG505670	NM_194247	220988	0,58	1,97E-03
COH1	1553852_at	NM_152564	NM_015243 NM_017890 NM_152564 NM_181661 NM_184042	157680	0,58	8,57E-03
ZNF305	240181_at	AI939511	NM_014724	9753	0,58	6,71E-03
RFC5	203209_at	BC001866	NM_007370 NM_181578	5985	0,58	7,00E-03

Tabla 10. Expresión genética disminuida en las líneas celulares H1 y BB10 en comparación con la línea celular SiMa en estado no diferenciado usando análisis de micromatriz

Símbolo del gen	ID del conjunto de sondas	ID Pública representativa	ID de transcripción RefSec	ID de Gen Entrez	Proporción Log2	valor p
HSPA1A	200799_at	NM_005345	NM_005345	3303	-6,50	8,44E-07
CYTL1	219837_s_at	NM_018659	NM_018659	54360	-5,69	4,29E-10
CYGB	226632_at	AL513673	NM_134268	114757	-5,62	1,77E-03
SYT13	226086_at	AB037848	NM_020826	57586	-5,23	2,54E-09
H39185	240433_x_at	H39185	---	---	-5,19	1,50E-07
AV724769	235118_at	AV724769	---	---	-5,15	5,31E-08
AW188087	226809_at	AW188087	---	---	-5,07	1,50E-07
IGFBP7	201162_at	NM_001553	NM_001553	3490	-4,97	1,64E-07
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AF150317	243111_at	AF150317	---	---	-4,32	6,95E-07
FGF1	1552721_a_at	NM_033136	NM_000800 NM_033136 NM_033137	2246	-4,30	3,01E-04
LMCD1	218574_s_at	NM_014583	NM_014583	29995	-4,23	1,05E-04
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FUCA2	223120_at	BC003060	NM_032020	2519	-3,94	2,55E-03
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PRAME	204086_at	NM_006115	NM_006115 NM_206953 NM_206954 NM_206955 NM_206956	23532	-3,67	4,15E-07
DHRS3	202481_at	NM_004753	NM_004753	9249	-3,66	8,82E-07
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C9orf94	229585_at	AI803088	NM_152702	206938	-3,59	2,72E-04
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TncRNA	224565_at	BE675516	---	283131	-3,34	1,99E-04
IGSF4D	1555544_a_at	AF538973	NM_153184	253559	-3,30	7,37E-07
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FGL1	205305_at	NM_004467	NM_004467 NM_147203 NM_201552 NM_201553	2267	-3,25	2,90E-06
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TMIE	1553601_a_at	NM_147196	NM_147196	259236	-3,22	3,71E-05
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GAL	214240_at	AL556409	NM_015973	51083	-2,75	1,20E-03
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N39597	1555993_at	N39597	---	---	-2,70	1,39E-03
SYNPO2	227662_at	AA541622	NM_183477	171024	-2,69	4,62E-05
NPY	206001_at	NM_000905	NM_000905	4852	-2,68	9,89E-

FGF19	223761_at	AF110400	NM_005117	9965	-2,65	8,85E-05
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AA243659	209683_at	AA243659	---	---	-2,44	6,66E-07
LOC51315	233329_s_at	AK025986	NM_016618	51315	-2,44	4,58E-05
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FLJ20701	219093_at	NM_017933	NM_017933	55022	-2,43	3,02E-03
ICAM2	204683_at	NM_000873	NM_000873	3384	-2,41	3,71E-04
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AI767727	229815_at	AI767727	---	---	-2,40	5,54E-04
BF591692	231532_at	BF591692	---	---	-2,39	6,45E-04
GRM5	214217_at	D60132	NM_000842	2915	-2,39	1,63E-06
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ANK3	206385_s_at	NM_020987	NM_001149 NM_020987	288	-2,37	4,86E-04
AI810266	235456_at	AI810266	---	---	-2,36	7,31E-07
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AV719355	217554_at	AV719355	---	---	-2,36	2,61E-03
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HHLA3	220387_s_at	NM_007071	NM_007071	11147	-2,36	2,06E-03
SMARCA2	206542_s_at	AV725365	NM_003070 NM_139045	6595	-2,35	7,68E-04
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HTATIP2	209448_at	BC002439	NM_006410	10553	-2,30	6,50E-03
FLJ31659	1553710_at	NM_153027	NM_153027	152756	-2,30	6,35E-06
LOC51315	218303_x_at	NM_016618	NM_016618	51315	-2,30	8,49E-07
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GAL	207466_at	NM_015973	NM_015973	51083	-2,25	6,61E-13
PTGER2	206631_at	NM_000956	NM_000956	5732	-2,25	2,22E-05
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TICAM2	228234_at	AI423165	NM_021649	353376	-2,22	4,67E-04
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IRS1	204686_at	NM_005544	NM_005544	3667	-2,22	2,74E-03
TRIM61	238990_x_at	AI763262	XM_373038	391712	-2,21	1,88E-04
AF085995	1561759_at	AF085995	---	---	-2,21	9,13E-03
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GPX7	213170_at	AA406605	NM_015696	2882	-2,19	2,99E-04
NLF1	241031_at	BE218239	NM_207322	145741	-2,18	8,81E-05
BE674309	230913_at	BE674309	---	---	-2,18	1,83E-04
CAP2	212551_at	NM_006366	NM_006366	10486	-2,17	5,50E-04
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CYB5R2	220230_s_at	NM_016229	NM_001001336 NM_016229	51700	-2,15	7,15E-04
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RAC2	207419_s_at	NM_002872	NM_002872	5880	-2,14	2,67E-03
LOC153682	232794_at	AL137383	---	153682	-2,13	5,45E-03
GRIA2	236538_at	BE219628	NM_000826	2891	-2,13	1,05E-03
IL20RA	219115_s_at	NM_014432	NM_014432	53832	-2,12	6,78E-03
SCN5A	207413_s_at	NM_000335	NM_000335 NM_198056	6331	-2,12	2,22E-04
TSAP6	218424_s_at	NM_018234	NM_001008410 NM_018234 NM_182915	55240	-2,12	1,68E-04
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HIST2H2BE	202708_s_at	NM_003528	NM_003528	8349	-2,10	6,97E-05
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LOC441422	236453_at	AW243154	XR_000264	441422	-2,09	2,02E-04
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AI222435	230319_at	AI222435	---	---	-2,09	7,23E-05
MGC15668	229332_at	AI653050	NM_032756	84842	-2,08	1,02E-03
SCAP1	1560861_at	BG210619	NM_003726	8631	-2,08	5,32E-04
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ADARB1	203865_s_at	NM_015833	NM_001112 NM_015833 NM_015834	104	-2,07	4,67E-06
AB051467	232738_at	AB051467	---	---	-2,06	1,71E-05
CREB5	205931_s_at	NM_004904	NM_004904 NM_182898 NM_182899	9586	-2,06	8,68E-04
ECHDC3	219298_at	NM_024693	NM_024693	79746	-2,05	6,42E-03
GRYGD	207532_at	NM_006891	NM_006891	1421	-2,05	2,10E-03
ICAM2	213620_s_at	AA126728	NM_000873	3384	-2,05	3,74E-04
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AA700440	228329_at	AA700440	---	---	-2,04	4,62E-07
ATRNL1	213745_at	AW151108	NM_207303	26033	-2,04	9,28E-06
SLC6A15	239352_at	AI368909	NM_018057 NM_182767	55117	-2,03	1,76E-04
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MTL5	219786_at	NM_004923	NM_004923	9633	-2,02	3,30E-04
FBI4	1562953_s_at	BC019264	NM_205857	404201	-2,02	4,82E-03
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LOC441168	229390_at	AV734646	XM_496823	441168	-2,01	1,83E-04
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BC014056	1561906_at	BC014056	---	---	-2,01	8,02E-04
FGF18	206987_x_at	NM_003862	NM_003862 NM_033649	8817	-2,01	6,16E-03
CHST7	206756_at	NM_019886	NM_019886	56548	-2,00	1,29E-04
RAC2	213603_s_at	BE138888	NM_002872	5880	-2,00	2,89E-05
MCTP1	235740_at	BG250585	NM_001002796 NM_024717	79772	-2,00	2,38E-08
C6orf198	227834_at	AL589605	XM_371849	167838	-2,00	1,53E-03
SYNPO2	225894_at	AL589603	NM_133477	171024	-1,99	3,38E-04
FBI4	238081_at	AI694300	NM_205857	404201	-1,99	1,05E-03
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SORCS2	228720_at	AB037750	NM_020777	57537	-1,98	7,96E-05
MRAS	225185_at	BF343625	NM_012219	22808	-1,97	6,31E-04
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ATP2B3	242036_x_at	H09073	NM_001001344 NM_021949	492	-1,96	1,23E-03
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AA976778	230679_at	AA976778	---	---	-1,95	3,35E-04
LOC285878	1560692_at	BC037834	---	285878	-1,94	3,90E-04
BF114967	231067_s_at	BF114967	---	---	-1,93	1,31E-04
C10orf59	223824_at	BC005364	NM_018363	55328	-1,93	8,06E-03
ASAM	228082_at	BF056275	NM_024769	79827	-1,93	2,50E-04
OXTR	206825_at	NM_000916	NM_000916	5021	-1,93	2,27E-04
CNNM1	220166_at	NM_020348	NM_020348	26507	-1,92	1,23E-04
PLCD4	224505_s_at	BC006355	NM_032726	84812	-1,92	2,15E-05
NEFH	33767_at	X15306	NM_021076	4744	-1,92	2,20E-03
LOC339290	228160_at	AI433706	XM_375527	339290	-1,92	5,10E-03
EDG7	231192_at	AW274018	NM_012152	23566	-1,91	7,48E-04
BF002625	229530_at	BF002625	---	---	-1,90	4,09E-04
COL13A1	211343_s_at	M33653	NM_005203 NM_080798 NM_080799 NM_080800 NM_080801 NM_080802 NM_080803 NM_080804 NM_080805 NM_080806 NM_080807 NM_080808 NM_080809 NM_080810 NM_080811 NM_080812 NM_080813 NM_080814 NM_080815	1305	-1,90	5,01E-06

AI015847	1568838_at	AI015847	---	---	-1,90	6,44E-04
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NDFIP2	1568807_a_at	AI301081	NM_019080	54602	-1,89	6,50E-05
PRKACB	202742_s_at	NM_002731	NM_002731 NM_182948 NM_207578	5567	-1,88	2,83E-04
FLJ20449	1570153_at	BC013944	NM_017826	54937	-1,88	1,81E-03
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PRSS11	201185_at	NM_002775	NM_002775	5654	-1,87	2,45E-04
EBF	229487_at	W73890	NM_024007	1879	-1,86	2,25E-05
SLC16A14	238029_s_at	R15072	NM_152527	151473	-1,86	2,63E-05
LEPR	211356_x_at	U66495	NM_001003679 NM_001003680 NM_002303	3953	-1,86	9,14E-08
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BE672499	230962_at	BE672499	---	---	-1,85	3,97E-04
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C10orf10	209183_s_at	AL136653	NM_007021	11067	-1,84	9,62E-05
ARTS-1	214012_at	BE551138	NM_016442	51752	-1,84	7,70E-04
M160	223655_at	AF264014	NM_174941	283316	-1,83	4,27E-03
AI803010	239503_at	AI803010	---	---	-1,83	6,21E-03
GLI2	228537_at	AI797248	NM_005270 NM_030379 NM_030380 NM_030381	2736	-1,83	6,30E-04
AI935541	236220_at	AI935541	---	---	-1,83	8,96E-04
HEBP2	203430_at	NM_014320	NM_014320	23593	-1,82	6,64E-03
DKFZp313N0621	226688_at	AW003508	NM_173826	285343	-1,82	8,96E-06
EBF	232204_at	AF208502	NM_024007	1879	-1,81	6,25E-06
NT5E	203939_at	NM_002526	NM_002526	4907	-1,81	2,34E-05
D4S234E	209570_s_at	BC001745	NM_014392	27065	-1,80	1,14E-04
LOC133308	229491_at	BF433180	NM_178833	133308	-1,79	1,59E-03
BHLHB2	201170_s_at	NM_003670	NM_003670	8553	-1,79	7,17E-03

AI768374	228661_s_at	AI768374	---	---	-1,79	9,50E-04
AL355688	232081_at	AL355688	---	---	-1,79	5,36E-03
RPL39L	210115_at	L05096	NM_052969	116832	-1,79	6,47E-03
BCL2	203685_at	NM_000633	NM_000633 NM_000657	596	-1,78	4,07E-05
LRBA	214109_at	AI659561	NM_006726	987	-1,78	1,89E-03
C9orf150	227443_at	AI972386	NM_203403	286343	-1,78	2,50E-04
KCNAB1	210078_s_at	L39833	NM_003471 NM_172159 NM_172160	7881	-1,78	2,11E-03
PCDHB16	232099_at	AB046841	NM_020957	57717	-1,77	1,97E-03
SYNPO2	225895_at	AI634580	NM_133477	171024	-1,77	6,20E-04
AK000776	232060_at	AK000776	---	---	-1,75	1,44E-04
COL6A1	213428_s_at	AA292373	NM_001848	1291	-1,75	5,72E-04
LEPR	211355_x_at	U52914	NM_001003679 NM_001003680 NM_002303	3953	-1,74	2,06E-06
PABPC5	233136_at	AL122118	NM_080832	140886	-1,74	7,51E-04
PROM1	204304_s_at	NM_006017	NM_006017	8842	-1,74	6,03E-04
AGPAT3	223182_s_at	AI337300	NM_020132	56894	-1,73	3,62E-04
ANK3	209442_x_at	AL136710	NM_001149 NM_020987	288	-1,73	1,10E-03
CACNA1D	210108_at	BE550599	NM_000720	776	-1,72	3,20E-04
H2AFJ	220936_s_at	NM_018267	NM_018267 NM_177925	55766	-1,71	9,12E-04
LOC285878	230117_at	AI420977	---	285878	-1,71	1,65E-04
MGC70870	244125_at	AA837131	NM_203481	403340	-1,70	1,71E-03
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AI004009	222288_at	AI004009	XM_371647	389129	-1,70	6,64E-04
OPRM1	207989_at	NM_000914	NM_000914 NM_001008503 NM_001008504 NM_001008505	4988	-1,69	1,26E-05

OPN3	224392_s_at	AF303588	NM_014322	23596	-1,69	6,03E-04
FGD5	226985_at	AW269340	NM_152536	152273	-1,68	4,08E-06
EBF	227646_at	BG435302	NM_024007	1879	-1,68	1,59E-04
KIAA0500	213839_at	AW028110	---	57237	-1,68	4,44E-03
BF342356	238934_at	BF342356	---	---	-1,68	6,92E-03
PRKCH	218764_at	NM_024064	NM_006255	5583	-1,67	7,79E-05
ARSD	223686_at	BC003660	NM_001669 NM_009589	414	-1,66	8,89E-03
C9orf94	239909_at	AI937348	NM_152702	206938	-1,66	7,20E-03
C6orf155	226810_at	BE500942	NM_024882	79940	-1,65	2,05E-03
LOC151194	1553743_at	NM_145280	NM_145280	151194	-1,65	6,80E-03
SYNPO2	225721_at	AI658662	NM_133477	171024	-1,64	9,76E-03
AL037414	230055_at	AL037414	---	---	-1,64	3,29E-04
AW572379	229569_at	AW572379	---	---	-1,63	2,80E-04
FRMD4B	213056_at	AU145016	XM_114303	23150	-1,63	2,55E-03
D4S234E	213533_at	M98528	NM_014392	27065	-1,63	1,82E-06
PTP4A3	209695_at	BC003105	NM_007079 NM_032611	11156	-1,62	4,14E-06
ACYP2	206833_s_at	NM_001108	NM_138448	98	-1,62	7,71E-04
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ALDH1A2	207016_s_at	AB015228	NM_003888 NM_170696 NM_170697	8854	-1,61	4,22E-04
CD302	203799_at	NM_014880	NM_014880	9936	-1,61	1,17E-05
F10269	1557746_at	F10269	---	---	-1,61	1,03E-03
FLJ20152	218532_s_at	NM_019000	NM_019000	54463	-1,61	2,67E-03
FBI4	241401_at	BG496631	NM_205857	404201	-1,60	1,55E-03
BC031271	1569785_at	BC031271	---	---	-1,60	4,07E-04
BE046461	215303_at	BE046461	---	---	-1,60	5,17E-04
FLJ10970	219230_at	NM_018286	NM_018286	55273	-1,59	1,10E-04
CA336272	1558512_at	CA336272	---	---	-1,59	1,57E-04

PRKACB	202741_at	AA130247	NM_002731 NM_182948 NM_207578	5567	-1,59	1,12E-03
PDE4DIP	213388_at	H15535	NM_001002810 NM_001002811 NM_001002812 NM_014644 NM_022359	9659	-1,59	6,05E-04
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ST18	206135_at	NM_014682	NM_014682	9705	-1,58	4,56E-07
DBT	231919_at	AK024946	NM_001918	1629	-1,58	1,11E-03
STMN2	203001_s_at	NM_007029	NM_007029	11075	-1,58	5,47E-03
SIX2	206510_at	AF332197	NM_016932	10736	-1,56	2,79E-05
NEBL	203961_at	AL157398	NM_006393 NM_213569	10529	-1,56	7,89E-03
PCTK3	214797_s_at	BC000281	NM_002596 NM_212502 NM_212503	5129	-1,56	8,81E-03
DOC1	1554966_a_at	AF329092	NM_014890 NM_182909	11259	-1,56	5,32E-04
AI800713	235122_at	AI800713	---	---	-1,56	7,94E-04
NEFH	204412_s_at	NM_021076	NM_021076	4744	-1,55	3,87E-03
MEGF11	1552439_s_at	NM_032445	NM_032445	84465	-1,55	7,12E-04
AI796536	229810_at	AI796536	---	---	-1,55	6,60E-04
MGC11332	213393_at	AI767210	NM_032718	84804	-1,54	1,06E-04
RBMS3	237860_at	AI821998	NM_001003792 NM_001003793 NM_014483	27303	-1,54	9,15E-03
LOC285878	236308_at	D80436	---	285878	-1,53	2,60E-04
LRRN6A	227933_at	AI193252	NM_032808	84894	-1,53	5,09E-06
NHS	228933_at	BF111819	NM_198270	4810	-1,53	3,83E-03
EYA1	214608_s_at	AJ000098	NM_000503 NM_172058 NM_172059 NM_172060	2138	-1,53	5,85E-06
AI263044	214376_at	AI263044	---	---	-1,53	1,69E-

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ANKH	220076_at	NM_019847	NM_054027	56172	-1,52	2,18E-03
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LOC133308	1564746_at	BC009732	NM_178833	133308	-1,52	3,24E-03
AA747287	242273_at	AA747287	---	---	-1,52	3,10E-04
IL10RB	209575_at	BC001903	NM_000628	3588	-1,52	4,38E-05
BACE1	217904_s_at	NM_012104	NM_012104 NM_138971 NM_138972 NM_138973	23621	-1,51	1,09E-04
DISP1	228184_at	AK023679	NM_032890	84976	-1,51	7,96E-03
KIAA1277	221886_at	AL037701	NM_015689	27147	-1,51	1,64E-03
AI276956	230766_at	AI276956	---	---	-1,51	4,00E-04
FAM13C1	1554547_at	BC036453	NM_001001971 NM_198215	220965	-1,51	4,02E-03
AKAP12	227529_s_at	BF511276	NM_005100 NM_144497	9590	-1,50	2,52E-04
POSTN	1555778_a_at	AY140646	NM_006475	10631	-1,50	1,94E-04
BF114745	235459_at	BF114745	---	---	-1,50	2,88E-03
TNFSF4	207426_s_at	NM_003326	NM_003326	7292	-1,49	1,01E-03
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NR2F1	209505_at	AI951185	NM_005654	7025	-1,49	3,03E-04
PTN	209466_x_at	M57399	NM_002825	5764	-1,49	6,92E-06
AI821995	240201_at	AI821995	---	---	-1,49	2,74E-03
MGC11332	213403_at	BF223370	NM_032718	84804	-1,49	1,36E-03
KCNJ6	210454_s_at	U24660	NM_002240	3763	-1,49	5,76E-03
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T87730	242500_at	T87730	---	---	-1,48	1,37E-05
LAF4	227198_at	AW085505	NM_002285	3899	-1,48	1,11E-04
AL137538	232679_at	AL137538	---	---	-1,48	6,18E-03
TOX	204530_s_at	NM_014729	NM_014729	9760	-1,48	2,48E-03
SB145	232283_at	AL122088	NM_212551	388695	-1,48	8,90E-03
PPP1R14A	227006_at	AA156998	NM_033256	94274	-1,47	1,25E-04

CRABP2	202575_at	NM_001878	NM_001878	1382	-1,47	1,13E-03
AV723260	1560425_s_at	AV723260	---	---	-1,47	8,62E-03
D4S234E	209569_x_at	NM_014392	NM_014392	27065	-1,47	3,74E-05
CDKN1C	213348_at	N33167	NM_000076	1028	-1,47	5,81E-05
LOC148418	229402_at	AI631824	NM_001010971	148418	-1,46	5,19E-04
DKFZP434H132	204494_s_at	AW516789	NM_015492	56905	-1,46	5,88E-04
ZNF528	215019_x_at	AW474158	NM_032423	84438	-1,46	4,78E-07
GCH1	204224_s_at	NM_000161	NM_000161	2643	-1,46	8,78E-04
PCSK1	205825_at	NM_000439	NM_000439	5122	-1,46	1,15E-03
WDR9	225446_at	AI638279	NM_001007246 NM_018963 NM_033656	54014	-1,44	6,32E-05
DOC1	204135_at	NM_014890	NM_014890 NM_182909	11259	-1,44	6,57E-03
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AI028528	241804_at	AI028528	---	---	-1,43	8,22E-04
LOC253012	242601_at	AA600175	NM_198151	253012	-1,43	1,56E-03
DMD	203881_s_at	NM_004010	NM_000109 NM_004006 NM_004007 NM_004009 NM_004010 NM_004011 NM_004012 NM_004013 NM_004014 NM_004015 NM_004016 NM_004017 NM_004018 NM_004019 NM_004020 NM_004021 NM_004022 NM_004023	1756	-1,43	1,85E-03
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C21orf86	228908_s_at	AW131553	NM_153454	257103	-1,42	1,26E-03
MYT1L	210016_at	BF223003	NM_015025	23040	-1,42	2,69E-04

C1GALT1C1	238989_at	BF749723	NM_001011551 NM_152692	29071	-1,42	2,08E-03
LOC402524	242206_at	AW590588	XM_379850	402524	-1,42	6,10E-04
CAMK2B	209956_s_at	U23460	NM_001220 NM_172078 NM_172079 NM_172080 NM_172081 NM_172082 NM_172083 NM_172084	816	-1,42	1,44E-03
ST6GALNAC5	220979_s_at	NM_030965	NM_030965	81849	-1,41	5,22E-04
AI341823	239657_x_at	AI341823	---	---	-1,41	2,83E-03
AI733281	239994_at	AI733281	---	---	-1,41	8,41E-03
SH3GL2	205751_at	NM_003026	NM_003026	6456	-1,41	6,60E-04
AW450420	236373_at	AW450420	---	---	-1,41	5,40E-03
PH-4	222125_s_at	BC000580	NM_017732 NM_177938 NM_177939	54681	-1,41	2,61E-03
CDKN2A	209644_x_at	U38945	NM_000077 NM_058195 NM_058197	1029	-1,40	1,98E-05
AI912571	228333_at	AI912571	---	---	-1,40	5,33E-03
BF059209	240214_at	BF059209	---	---	-1,40	2,18E-03
ARSD	232423_at	AU144083	NM_001669 NM_009589	414	-1,39	1,43E-03
NEDL1	243743_at	AI373512	NM_015052	23072	-1,39	2,52E-03
FRAS1	226145_s_at	AL157471	NM_020875 NM_025074 NM_032863 NM_206841	80144	-1,39	8,77E-06
UNC5A	236448_at	R37358	XM_030300	90249	-1,38	1,31E-05
FLJ35808	230924_at	AI698574	NM_173623	284076	-1,38	5,69E-04
LOC222070	51774_s_at	AW014299	---	222070	-1,38	4,64E-03
C6orf199	1552299_at	NM_145025	NM_145025	221264	-1,38	8,50E-03
CAPN2	208683_at	M23254	NM_001748	824	-1,38	1,58E-03
BE503598	1557658_at	BE503598	---	---	-1,38	5,77E-03
HOXD10	229400_at	AW299531	NM_002148	3236	-1,37	2,17E-03

GLIS3	229435_at	AW025602	NM_152629	169792	-1,37	1,72E-05
NAP1L3	204749_at	NM_004538	NM_004538	4675	-1,37	5,99E-03
FLJ45244	229227_at	BF511219	NM_207443	400242	-1,37	6,16E-03
D59759	231560_at	D59759	---	---	-1,37	1,31E-06
ANK2	202920_at	BF726212	NM_001148 NM_020977	287	-1,35	3,09E-05
FLJ30655	236487_at	AW513286	NM_144643	132320	-1,35	3,30E-03
GLIS3	230258_at	AI277316	NM_152629	169792	-1,35	1,33E-03
SH3BGR	204979_s_at	NM_007341	NM_001001713 NM_007341	6450	-1,34	1,12E-04
RAI2	219440_at	NM_021785	NM_021785	10742	-1,34	2,50E-04
ATXN1	203232_s_at	NM_000332	NM_000332	6310	-1,34	8,99E-05
CRSP2	215167_at	BE567032	NM_004229	9282	-1,34	6,26E-03
AI740460	236856_x_at	AI740460	---	---	-1,34	3,19E-03
MGC42090	236705_at	AA017245	NM_152774	256130	-1,34	3,46E-04
SNF1LK	208078_s_at	NM_030751	NM_173354	150094	-1,33	4,49E-03
N4BP3	214775_at	AW139448	XM_038920	23138	-1,33	8,59E-05
AL117598	231964_at	AL117598	---	---	-1,33	5,64E-06
NT5E	227486_at	AI086864	NM_002526	4907	-1,33	9,12E-04
AL390170	213904_at	AL390170	---	---	-1,33	7,47E-04
N50117	240236_at	N50117	---	---	-1,33	1,78E-03
AK095719	1556896_s_at	AK095719	XM_499008	441094	-1,32	6,81E-03
W80446	231013_at	W80446	---	---	-1,32	9,26E-04
C21orf66	239407_at	AI793248	NM_013329 NM_016631 NM_058191 NM_145328	94104	-1,32	1,06E-03
RASGEF1B	230233_at	BF110534	NM_152545	153020	-1,32	5,98E-03
DCAMKL1	205399_at	NM_004734	NM_004734	9201	-1,32	8,09E-04
SCOTIN	222986_s_at	BC001463	NM_016479	51246	-1,32	7,27E-03
C21orf5	205248_at	NM_005128	NM_005128	9980	-1,32	2,95E-04
HEL308	228736_at	AW084661	NM_133636	113510	-1,32	6,40E-04
HDAC4	228813_at	AW206037	NM_006037	9759	-1,31	4,97E-04

ST7L	1552739_s_at	NM_138729	NM_017744 NM_138727 NM_138728 NM_138729 NM_198327 NM_198328	54879	-1,31	2,31E-03
DACH2	239738_at	AW780006	NM_053281	117154	-1,30	1,49E-03
RAB3-GAP150	243851_at	AI860647	NM_012414	25782	-1,29	9,51E-03
C9orf40	218904_s_at	NM_017998	NM_017998	55071	-1,29	9,53E-03
AK027226	232538_at	AK027226	---	---	-1,29	5,59E-03
ZSWIM5	232336_at	AI479419	XM_046581	57643	-1,28	1,68E-03
CEBPD	203973_s_at	NM_005195	NM_005195	1052	-1,28	2,94E-03
AA687479	242826_at	AA687479	---	---	-1,28	1,21E-04
SIAT7E	230482_at	AF131837	NM_030965	81849	-1,28	1,28E-03
AI694767	229768_at	AI694767	---	---	-1,28	5,06E-03
FLJ20753	229918_at	AB046860	XM_371082	55036	-1,28	9,34E-04
GUCY1A3	221942_s_at	AI719730	NM_000856	2982	-1,28	2,15E-03
PTP4A3	206574_s_at	NM_007079	NM_007079 NM_032611	11156	-1,27	9,96E-03
AI354636	235171_at	AI354636	---	---	-1,27	2,80E-03
STARD13	213103_at	AA128023	NM_052851 NM_178006 NM_178007 NM_178008	90627	-1,27	1,35E-05
AKAP12	227530_at	BF511276	NM_005100 NM_144497	9590	-1,27	1,01E-04
AI825987	235889_at	AI825987	---	---	-1,27	9,63E-04
KLF9	203543_s_at	NM_001206	NM_001206	687	-1,27	1,17E-03
RAB6B	221792_at	AW118072	NM_016577	51560	-1,27	2,69E-03
HR	241355_at	BF528433	NM_005144 NM_018411	55806	-1,27	2,35E-03
BBS7	219688_at	NM_018190	NM_018190 NM_176824	55212	-1,27	4,54E-05
BE467383	228932_at	BE467383	XM_497668	388620	-1,27	3,12E-03
HPCA	205454_at	BC001777	NM_002143	3208	-1,26	1,22E-03
KIAA1223	225735_at	AL110131	XM_048747	57182	-1,26	2,58E-04
AK021551	232589_at	AK021551	---	---	-1,26	7,56E-05

BE894882	235681_at	BE894882	---	---	-1,26	2,96E-05
TOX	204529_s_at	AI961231	NM_014729	9760	-1,25	8,61E-05
STAR	204548_at	NM_000349	NM_000349 NM_001007243	6770	-1,25	2,94E-05
AL833383	1563776_at	AL833383	---	---	-1,25	1,41E-03
PPP3CA	202429_s_at	AL353950	NM_000944	5530	-1,25	1,86E-05
SUCLG2	215772_x_at	AL050226	NM_003848	8801	-1,25	6,75E-04
RAB26	219562_at	NM_014353	NM_014353	25837	-1,25	6,02E-04
GRIP2	216481_at	AF052177	XM_042936	80852	-1,25	7,55E-03
AA135722	237419_at	AA135722	---	---	-1,25	3,44E-04
PTPRD	214043_at	BE062299	NM_002839 NM_130391 NM_130392 NM_130393	5789	-1,25	5,77E-06
CDS1	226185_at	AK026697	NM_001263	1040	-1,24	5,63E-04
CXorf32	229234_at	AW007160	NM_001010888	340554	-1,24	3,78E-03
ACAD8	238175_at	AI806909	NM_014384	27034	-1,24	8,68E-03
R71596	229580_at	R71596	---	---	-1,24	6,01E-03
H46176	237083_at	H46176	---	---	-1,24	1,64E-03
HPS3	227139_s_at	AA219354	NM_032383	84343	-1,24	1,38E-04
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GFRA3	229936_at	AA694259	NM_001496	2676	-1,22	3,88E-03
SUCLG2	212459_x_at	BF593940	NM_003848	8801	-1,22	2,39E-04
POU6F1	205878_at	NM_002702	NM_002702	5463	-1,22	2,77E-03

NRP2	229225_at	N90777	NM_003872 NM_018534 NM_201264 NM_201266 NM_201267 NM_201279	8828	-1,22	2,35E-03
H2AFJ	228213_at	AW241813	NM_018267 NM_177925	55766	-1,22	1,63E-03
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ANXA4	201302_at	NM_001153	NM_001153	307	-1,21	7,33E-03
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PTPRN2	203029_s_at	NM_002847	NM_002847 NM_130842 NM_130843	5799	-1,20	5,18E-04
RFPL1S	214120_at	AW157535	---	10740	-1,20	2,59E-05
IFNAR1	225661_at	AA811138	NM_000629	3454	-1,20	4,10E-04
GLIS1	244128_x_at	AA872588	NM_147193	148979	-1,20	6,88E-03
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PPEF1	206547_s_at	NM_006240	NM_006240 NM_152223 NM_152224 NM_152225 NM_152226	5475	-1,20	2,16E-03
BCL6B	243825_at	T79768	NM_181844	255877	-1,20	2,18E-03
ABCG1	204567_s_at	NM_004915	NM_004915 NM_016818 NM_207174 NM_207627 NM_207628 NM_207629 NM_207630	9619	-1,19	4,03E-05
DJ462O23.2	225876_at	T84558	NM_020448	57185	-1,19	3,26E-03
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LOC285705	226989_at	BE855765	---	285705	-1,19	2,15E-04
MANSC1	220945_x_at	NM_018050	NM_018050	54682	-1,19	1,43E-03
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OIP106	226013_at	AW451452	NM_014965	22906	-1,18	4,67E-03
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DTX3L	225415_at	AA577672	NM_138287	151636	-1,18	8,51E-04
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ROR1	205805_s_at	NM_005012	NM_005012	4919	-1,18	2,35E-05
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PDGFRB	202273_at	NM_002609	NM_002609	5159	-1,17	6,86E-03
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BACH2	221234_s_at	NM_021813	NM_021813	60468	-1,17	1,76E-04
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CDKN1C	213182_x_at	R78668	NM_000076	1028	-1,16	2,89E-03
BC040901	1559534_at	BC040901	---	---	-1,15	6,40E-03
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RUNX1	209360_s_at	D43968	NM_001001890 NM_001754	861	-1,15	9,21E-03
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OMA1	226019_at	AI927931	NM_145243	115209	-1,14	7,48E-03
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BID	229321_s_at	AK026026	NM_001196 NM_197966 NM_197967	637	-1,14	6,39E-03
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BBP	213882_at	AA012917	NM_032027	83941	-1,13	2,41E-03
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AKAP12	210517_s_at	AB003476	NM_005100 NM_144497	9590	-1,13	3,33E-04
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MARCH-I	229383_at	AI707896	NM_017923	55016	-1,12	2,06E-03
KCNQ2	205737_at	NM_004518	NM_004518 NM_172106 NM_172107 NM_172108 NM_172109	3785	-1,12	1,40E-04

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PLXNC1	206471_s_at	NM_005761	NM_005761	10154	-1,12	3,43E-05
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CDKN1C	219534_x_at	NM_000076	NM_000076	1028	-1,11	7,81E-05
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FBXO3	238686_at	AA130258	NM_012175 NM_033406	26273	-1,11	1,55E-03
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AK097571	1556261_a_at	AK097571	---	---	-1,10	2,59E-03
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NFIB	243933_at	AI096634	NM_005596	4781	-1,10	5,38E-03
FLJ32954	235349_at	AI261321	NM_144713	151393	-1,10	6,76E-03
KCNK10	220727_at	NM_021161	NM_021161 NM_138317 NM_138318	54207	-1,10	5,91E-04
SORL1	212560_at	AV728268	NM_003105	6653	-1,10	4,61E-03
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SH3KBP1	1554168_a_at	AF542051	NM_031892	30011	-1,10	5,41E-04

OPTN	202073_at	AV757675	NM_001008211 NM_001008212 NM_001008213 NM_021980	10133	-1,09	5,67E-03
ATF5	204998_s_at	NM_012068	NM_012068	22809	-1,09	5,15E-03
LOC401264	227298_at	AI806330	XM_379417	401264	-1,09	6,06E-03
NSE1	229546_at	AI378035	NM_145175	151354	-1,09	5,14E-03
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IL17D	228977_at	AI669535	NM_138284	53342	-1,09	2,53E-03
RG9MTD2	230243_at	BE671949	NM_152292	93587	-1,09	7,55E-03
PLXNC1	213241_at	AF035307	NM_005761	10154	-1,09	3,36E-03
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CSPG3	205143_at	NM_004386	NM_004386	1463	-1,08	3,42E-03
INSL3	214572_s_at	NM_005543	NM_005543	3640	-1,08	9,70E-03
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DNAJC12	218976_at	NM_021800	NM_021800 NM_201262	56521	-1,08	9,46E-05
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BF476403	230218_at	BF476403	---	---	-1,08	8,15E-04
AI798680	227943_at	AI798680	---	---	-1,08	2,18E-03
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AB037765	226747_at	AB037765	---	---	-1,08	2,32E-03
SIX3	242054_s_at	AW473656	NM_005413	6496	-1,07	3,51E-04
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BID	227143_s_at	AA706658	NM_001196 NM_197966 NM_197967	637	-1,07	1,25E-03
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FBXW7	229419_at	BF222826	NM_018315 NM_033632	55294	-1,07	8,90E-07
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MAP6	228943_at	AW003666	NM_033063 NM_207577	4135	-1,07	6,70E-03
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H16409	227623_at	H16409	---	---	-1,06	9,62E-05
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KIAA1324	221874_at	AB037745	NM_020775	57535	-1,06	6,36E-04
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RPH3AL	221614_s_at	BC005153	NM_006987	9501	-1,05	1,97E-03
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R53065	240430_at	R53065	---	---	-1,04	1,68E-04
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AW590679	229300_at	AW590679	---	---	-1,04	6,25E-06
BBS7	235007_at	AI683802	NM_018190 NM_176824	55212	-1,03	2,92E-03
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HPCAL1	212552_at	BE617588	NM_002149 NM_134421	3241	-1,03	6,95E-10
PHKB	238601_at	AI798207	NM_000293	5257	-1,03	3,11E-03
NF2	211017_s_at	AF123570	NM_000268 NM_016418 NM_181825 NM_181826 NM_181827 NM_181828 NM_181829 NM_181830 NM_181831 NM_181832 NM_181833 NM_181834 NM_181835	4771	-1,02	2,45E-03

NFASC	213438_at	AA995925	NM_001005387 NM_001005388 NM_001005389 NM_015090	23114	-1,02	2,89E-05
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CTSC	225646_at	AI246687	NM_001814 NM_148170	1075	-1,02	7,92E-03
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FLJ25168	1553400_a_at	NM_152466	NM_152466	147081	-1,01	1,66E-03
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BG150485	228754_at	BG150485	---	---	-1,01	3,89E-04
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BF512183	229885_at	BF512183	---	---	-1,01	4,33E-04
KIAA1573	225627_s_at	AK024256	NM_020925	57685	-1,01	1,13E-03
GPR123	239221_at	AI884909	NM_032422	84435	-1,01	2,88E-03
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AV723984	230403_at	AV723984	---	---	-1,01	9,06E-04
AI672159	226550_at	AI672159	---	---	-1,00	3,25E-03
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SLIT1	213601_at	AB011537	NM_003061	6585	-1,00	3,09E-04
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LOC169834	230876_at	AI827906	XM_095965	169834	-1,00	1,27E-04
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VPS41	235625_at	AW963328	NM_014396 NM_080631	27072	-1,00	3,16E-03
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LRRTM2	206408_at	NM_015564	NM_015564	26045	-1,00	5,75E-03
PHF10	221787_at	BF431618	NM_018288 NM_133325	55274	-1,00	3,14E-06
PHKA2	1560358_at	BC036597	NM_000292	5256	-0,99	4,51E-03
NM_015492	204495_s_at	NM_015492	---	---	-0,99	2,51E-03
AU151107	230650_at	AU151107	---	---	-0,99	3,88E-03
SLICK	244455_at	AI732637	NM_198503	343450	-0,99	1,51E-03
FLJ30294	238867_at	AI298041	NM_144632	130827	-0,99	9,15E-04
LOC340281	240194_at	AA406397	---	340281	-0,99	3,47E-03
LIPT1	205571_at	NM_015929	NM_015929 NM_145196 NM_145197 NM_145198 NM_145199	51601	-0,99	6,75E-03
DKFZP434H132	215087_at	AL109730	NM_015492	56905	-0,99	7,16E-06
RAPGEF6	210051_at	U78166	NM_006105	10411	-0,98	7,80E-03
BTD	214116_at	AI767414	NM_000060	686	-0,98	4,23E-03
ZCCHC7	226496_at	BG291039	NM_032226	84186	-0,98	5,34E-03
C10orf104	229145_at	AA541762	NM_173473	119504	-0,98	9,01E-04
LOC222070	58900_at	AW025284	---	222070	-0,98	4,22E-04
ESRRG	207981_s_at	NM_001438	NM_001438 NM_206594 NM_206595	2104	-0,98	6,26E-03
PRPS2	203401_at	NM_002765	NM_002765	5634	-0,98	9,17E-04
TM4SF2	202242_at	NM_004615	NM_004615	7102	-0,98	4,04E-05
PCAF	203845_at	AV727449	NM_003884	8850	-0,98	3,42E-06
LOC284669	1559483_at	AK092251	---	284669	-0,98	1,08E-03
ARMCX5	1555902_at	BC022066	NM_022838	64860	-0,98	6,50E-03
AI862542	235696_at	AI862542	---	---	-0,98	7,90E-04

PLEKHA2	225136_at	BF968578	XM_496973	59339	-0,98	1,31E-03
ACSL4	202422_s_at	NM_022977	NM_004458 NM_022977	2182	-0,98	1,83E-03
PIN4	243226_at	N53548	NM_006223	5303	-0,97	9,48E-04
BF510890	243406_at	BF510890	---	---	-0,97	2,52E-03
FLJ11000	235159_at	AW296028	NM_018295	55281	-0,97	8,58E-03
TPMT	203672_x_at	U12387	NM_000367	7172	-0,97	3,95E-03
NCOA7	225344_at	AL035689	NM_181782	135112	-0,97	1,02E-03
NUDT6	220183_s_at	NM_007083	NM_007083 NM_198041	11162	-0,97	1,63E-05
CACNA1B	235781_at	AA448208	NM_000718	774	-0,97	2,17E-03
LOC253982	214993_at	AF070642	NM_181718 NM_198907	253982	-0,97	5,64E-03
NOTCH4	205247_at	AI743713	NM_004557	4855	-0,96	5,91E-03
DACH1	205472_s_at	NM_004392	NM_004392 NM_080759 NM_080760	1602	-0,96	6,40E-04
C21orf25	212875_s_at	AP001745	NM_199050	25966	-0,96	1,81E-04
KIAA1377	235956_at	AI797063	NM_020802	57562	-0,96	2,43E-03
KIAA1729	230715_at	AI138969	NM_053042	85460	-0,96	2,87E-03
TMEM18	225487_at	AI074464	NM_152834	129787	-0,96	3,04E-04
CITED2	209357_at	AF109161	NM_006079	10370	-0,96	4,57E-03
AI768895	231069_at	AI768895	---	---	-0,96	4,30E-03
DKFZp451M2119	239240_at	AI814116	NM_182585	285023	-0,96	8,59E-03
N50119	235635_at	N50119	---	---	-0,96	3,56E-03
AI802997	235211_at	AI802997	---	---	-0,96	4,66E-05
PRPH	213847_at	NM_006262	NM_006262	5630	-0,95	1,14E-03
C14orf167	227446_s_at	BF445127	---	55449	-0,95	4,86E-03
NEIL2	226585_at	BE466620	NM_145043	252969	-0,95	3,33E-04
LOC401020	1560475_at	AK092134	XM_379145	401020	-0,95	4,55E-03
CXorf45	205583_s_at	NM_024810	NM_024810	79868	-0,95	2,74E-03
MLLT4	238871_at	AI086124	NM_005936	4301	-0,95	6,84E-03
PPP3CA	202457_s_at	AA911231	NM_000944	5530	-0,95	7,65E-04

MTUS1	212095_s_at	BE552421	NM_001001924 NM_001001925 NM_001001927 NM_001001931 NM_020749	57509	-0,95	1,54E-03
CARD8	1554479_a_at	AF511652	NM_014959	22900	-0,95	1,49E-03
HS3ST5	240479_at	AW449310	NM_153612	222537	-0,95	4,10E-03
CDC42EP3	209286_at	AI754416	NM_006449	10602	-0,94	2,27E-05
CLDN12	223249_at	AL136770	NM_012129	9069	-0,94	7,31E-04
MGC70870	242136_x_at	T66145	NM_203481	403340	-0,94	4,23E-04
LIFR	225575_at	AI680541	NM_002310	3977	-0,94	2,42E-03
AA002140	241365_at	AA002140	---	---	-0,94	3,00E-03
LOC153364	230298_at	AI692906	NM_203406	153364	-0,94	5,23E-03
BRUNOL4	238966_at	AA678985	NM_020180	56853	-0,94	6,55E-04
AV700050	228835_at	AV700050	---	---	-0,94	3,53E-03
TRIM4	223384_s_at	BE501464	NM_033017 NM_033091	89122	-0,94	6,97E-03
FLJ23560	219487_at	NM_024685	NM_024685	79738	-0,94	1,67E-03
PDGFRL	205226_at	NM_006207	NM_006207	5157	-0,94	3,47E-03
BG502771	226397_s_at	BG502771	---	---	-0,94	6,49E-05
AI392908	230352_at	AI392908	---	---	-0,94	3,46E-03
LOC93622	225391_at	AL562398	NM_138699	93622	-0,94	5,23E-05
MMP2L	227153_at	AI784580	NM_032549	83943	-0,94	1,01E-03
DACH1	205471_s_at	AW772082	NM_004392 NM_080759 NM_080760	1602	-0,94	4,97E-05
AI963605	230269_at	AI963605	---	---	-0,94	1,40E-03
R45950	229994_at	R45950	---	---	-0,93	1,97E-03
RGMB LOC285705	227339_at	BE206621	NM_173670	285704 285705	-0,93	3,25E-06

NIN	223981_at	AF223937	NM_016350 NM_020921 NM_182944 NM_182945 NM_182946	51199	-0,93	8,04E-03
DKFZp313N0621	241666_at	BG493222	NM_173826	285343	-0,93	6,42E-03
DKFZP564D172	212936_at	AI927701	NM_032042	83989	-0,93	2,49E-05
CaMKIINalpha	218309_at	NM_018584	NM_018584	55450	-0,93	3,41E-05
MAPK10	237413_at	AI568447	NM_002753 NM_138980 NM_138981 NM_138982	5602	-0,93	2,01E-04
CXXC4	220277_at	NM_025212	NM_025212	80319	-0,93	1,90E-04
HEL308	1554341_a_at	BC011983	NM_133636	113510	-0,93	1,26E-04
SIGIRR	218921_at	NM_021805	NM_021805	59307	-0,92	3,82E-03
FBXL17	227203_at	AA115629	NM_022824	64839	-0,92	1,44E-03
ATXN1	203231_s_at	AW235612	NM_000332	6310	-0,92	5,79E-05
USP46	203869_at	AK024318	NM_022832	64854	-0,92	3,21E-04
CSE-C	224391_s_at	AF303378	NM_170601	54414	-0,92	2,82E-03
GGPS1	202321_at	AW299507	NM_004837	9453	-0,92	2,16E-03
MUTED	226543_at	AI768114	NM_201280	63915	-0,92	3,41E-03
KIAA0564	212946_at	AK025432	NM_001009814 NM_015058	23078	-0,92	4,42E-03
JMY	226352_at	BF447037	NM_152405	133746	-0,92	2,68E-04
PALM2-AKAP2	202759_s_at	BE879367	NM_007203 NM_147150	445815	-0,92	1,79E-04
AI631072	228638_at	AI631072	---	---	-0,92	9,69E-03
MCAM	209087_x_at	AF089868	NM_006500	4162	-0,92	2,51E-03
PSD3	203355_s_at	NM_015310	NM_015310 NM_206909	23362	-0,92	4,84E-03
PTEN	228006_at	BG403361	NM_000314	5728	-0,92	3,02E-03
ABAT	209459_s_at	AF237813	NM_000663 NM_020686	18	-0,92	5,61E-03
AI887898	228423_at	AI887898	XM_374094	389237	-0,92	5,43E-04
MGC14595	238562_at	BE542779	NM_032334	84294	-0,92	1,59E-05
AA757630	236724_at	AA757630	---	---	-0,91	2,99E-04

BF510563	228561_at	BF510563	---	---	-0,91	1,65E-05
ETS2	201328_at	AL575509	NM_005239	2114	-0,91	6,50E-05
TRIM32	236233_at	AI768810	NM_012210	22954	-0,91	7,51E-03
CDC42EP3	209288_s_at	AL136842	NM_006449	10602	-0,91	1,33E-04
CNOT6L	227119_at	BF103856	NM_144571	246175	-0,91	2,60E-06
AI754871	229075_at	AI754871	---	---	-0,91	2,23E-03
PSD3	219513_at	NM_019422	NM_015310 NM_206909	23362	-0,91	2,81E-05
SLC20A2	229371_at	BF940010	NM_006749	6575	-0,91	2,66E-04
SNX10	218404_at	NM_013322	NM_013322	29887	-0,90	3,48E-03
KCTD18	226493_at	AI627249	NM_152387	130535	-0,90	7,20E-03
MGC31963	1558692_at	AW090182	NM_144580	112770	-0,90	9,19E-03
C21orf51	228239_at	AA148789	NM_058182	54065	-0,90	3,56E-03
T79639	243466_at	T79639	---	---	-0,90	3,38E-03
BE671727	244177_at	BE671727	---	---	-0,90	7,60E-03
WDR32	219001_s_at	NM_024345	NM_024345	79269	-0,90	1,46E-03
AW770320	242523_at	AW770320	---	---	-0,90	5,17E-03
FLJ31265	228341_at	AI809108	NM_152395	131870	-0,90	9,74E-03
TENS1	217853_at	NM_022748	NM_022748	64759	-0,90	3,93E-03
AFFX-BioB-3	AFFX-BioB-3_at	AFFX-BioB-3	---	---	-0,90	4,10E-03
AL359605	227318_at	AL359605	---	---	-0,90	4,75E-04
FIP1L1	1554424_at	BC017724	NM_030917	81608	-0,90	2,24E-05
MGC22773	235498_at	AI269596	NM_145258	127255	-0,89	3,93E-07
AI765014	224649_x_at	AI765014	---	---	-0,89	3,50E-03
ACSL6	229725_at	AV705292	NM_001009185 NM_015256	23305	-0,89	6,40E-03
HNRPR	208765_s_at	NM_005826	NM_005826	10236	-0,89	9,23E-05
GATM	216733_s_at	X86401	NM_001482	2628	-0,89	6,06E-03
SAT	213988_s_at	BE971383	NM_002970	6303	-0,89	6,15E-03
MGC16275	1558167_a_at	BM824870	---	85001	-0,89	3,24E-03
AI743452	237031_at	AI743452	---	---	-0,89	2,69E-03

FLJ11011	222656_at	AI625741	NM_001001481 NM_001001482 NM_018299	55284	-0,89	2,46E-03
BF510762	230262_at	BF510762	---	---	-0,89	7,78E-05
SOCS5	208127_s_at	NM_014011	NM_014011 NM_144949	9655	-0,89	2,64E-03
LTBP3	227308_x_at	AW515704	NM_021070	4054	-0,89	1,44E-04
AI826437	229975_at	AI826437	---	---	-0,89	3,65E-04
BRAF	236402_at	AW184034	NM_004333	673	-0,89	8,26E-03
LNX	227293_at	AI264003	NM_032622	84708	-0,88	1,56E-03
F3	204363_at	NM_001993	NM_001993	2152	-0,88	2,35E-03
COVA1	204643_s_at	NM_006375	NM_006375 NM_182314	10495	-0,88	9,34E-03
TPD52	201691_s_at	NM_005079	NM_005079	7163	-0,88	6,44E-04
GRIK2	1560142_at	AJ301610	NM_021956 NM_175768	2898	-0,88	5,49E-03
AI025829	235227_at	AI025829	---	---	-0,88	2,45E-03
AI761584	229654_at	AI761584	---	---	-0,88	9,83E-03
MAP3K5	203836_s_at	D84476	NM_005923	4217	-0,88	7,19E-03
NOX4	219773_at	NM_016931	NM_016931	50507	-0,88	6,53E-03
FBXL17	238174_at	AI694129	NM_022824	64839	-0,88	4,28E-04
ERCC6	207347_at	NM_000124	NM_000124	2074	-0,88	1,34E-03
TMEM34	219074_at	NM_018241	NM_018241	55751	-0,88	2,71E-03
MGC52110	226039_at	AW006441	NM_001008215	493753	-0,87	3,18E-05
SPHAR	206272_at	NM_006542	NM_006542	10638	-0,87	3,60E-03
FCMD	205283_at	NM_006731	NM_006731	2218	-0,87	3,96E-03
BAI3	205638_at	NM_001704	NM_001704	577	-0,87	8,83E-03
N29877	231169_at	N29877	---	---	-0,87	2,33E-03
MBNL1	201153_s_at	NM_021038	NM_021038 NM_207292 NM_207293 NM_207294 NM_207295 NM_207296 NM_207297	4154	-0,87	2,24E-05

CLCN3	201734_at	AI760629	NM_001829 NM_173872	1182	-0,87	7,31E-03
MGC13024	221864_at	AW517464	NM_152288	93129	-0,87	9,69E-03
XPR1	226615_at	BE439489	NM_004736	9213	-0,87	2,22E-04
CAMK2B	210404_x_at	AF078803	NM_001220 NM_172078 NM_172079 NM_172080 NM_172081 NM_172082 NM_172083 NM_172084	816	-0,87	1,66E-03
CHD2	228999_at	AW514564	NM_001271	1106	-0,86	2,91E-03
TMEM1	209412_at	U61500	NM_001001723 NM_003274	7109	-0,86	2,68E-03
FLJ32130	1554769_at	BC040642	NM_152458	146540	-0,86	3,30E-03
MCF2L	212935_at	AB002360	NM_024979	23263	-0,86	3,60E-04
PGRMC2	213227_at	BE879873	NM_006320	10424	-0,86	1,58E-03
BF434383	235473_at	BF434383	---	---	-0,86	5,25E-03
WARS2	222734_at	BF515963	NM_015836 NM_201263	10352	-0,86	9,52E-03
ASB13	218862_at	NM_024701	NM_024701	79754	-0,86	5,98E-03
ARSD	225280_x_at	N51673	NM_001669 NM_009589	414	-0,86	4,80E-03
HEL308	1554342_s_at	BC011863	NM_133636	113510	-0,86	8,97E-03
GLCE	213552_at	W87398	NM_015554	26035	-0,86	3,64E-03
ZNF25	235164_at	BG433539	NM_145011	219749	-0,86	8,82E-03
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BMPR2	225144_at	AI457436	NM_001204 NM_033346	659	-0,86	9,23E-05
AI796858	236164_at	AI796858	---	---	-0,86	6,19E-05
HPS1	210112_at	U96721	NM_000195 NM_182637 NM_182638 NM_182639	3257	-0,86	9,98E-03
SCRN3	219234_x_at	NM_024583	NM_024583	79634	-0,86	1,04E-03
EFNB3	205031_at	NM_001406	NM_001406	1949	-0,86	4,69E-03
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AW274846	228108_at	AW274846	---	---	-0,85	3,72E-03
STC1	204595_s_at	AI300520	NM_003155	6781	-0,85	1,72E-03
AW044658	229201_at	AW044658	---	---	-0,85	7,58E-05
CA442342	1556097_at	CA442342	---	---	-0,85	6,36E-03
FLJ21159	235550_at	AV751613	NM_024826	79884	-0,85	6,98E-04
PKNOX1	54051_at	H59033	NM_004571 NM_197976	5316	-0,85	1,84E-03
PDE2A	204134_at	NM_002599	NM_002599	5138	-0,85	1,09E-04
DHRSX	225503_at	AL547782	NM_145177	207063	-0,85	2,79E-03
SLC19A1	229489_at	AI681043	NM_003056 NM_194255	6573	-0,85	2,68E-03
C13orf24	213239_at	NM_006346	NM_006346	10464	-0,85	2,61E-04
SRGAP3	209794_at	AB007871	NM_014850	9901	-0,85	7,85E-03
C21orf127	234676_s_at	AK021678	NM_013240 NM_182749	29104	-0,85	8,73E-03
PARP11	229138_at	AV747166	NM_020367	57097	-0,84	1,23E-03
ELAC1	219325_s_at	NM_018696	NM_018696	55520	-0,84	9,17E-03
AV702357	229823_at	AV702357	---	---	-0,84	2,59E-04
FLRT1	210414_at	AF169675	NM_013280	23769	-0,84	8,98E-03
C2orf17	222129_at	AK026155	NM_024293	79137	-0,84	2,37E-03
PF6	1557593_at	AA250798	NM_206996	200162	-0,84	1,52E-03
BC040191	1568623_a_at	BC040191	---	---	-0,84	5,28E-03
H99038	227338_at	H99038	XM_498946	440983	-0,84	9,90E-03
MANBA	203778_at	NM_005908	NM_005908	4126	-0,84	4,77E-03
DELGEF	232983_s_at	AJ243951	NM_012139	26297	-0,84	7,32E-03
ATP2C1	209934_s_at	AF225981	NM_001001485 NM_001001486 NM_001001487 NM_014382	27032	-0,84	5,96E-03
LOC92249	212957_s_at	AU154785	XM_499179	92249	-0,83	7,94E-04
SPATA7	234929_s_at	AF144488	NM_018418	55812	-0,83	9,12E-03
AW269338	235691_at	AW269338	XM_378880	400764	-0,83	1,62E-03

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KIAA1223	225731_at	BF196876	XM_048747	57182	-0,83	1,79E-06
BF207861	239768_x_at	BF207861	---	---	-0,83	3,46E-03
BG236351	217598_at	BG236351	---	---	-0,83	1,23E-03
B3GTL	227083_at	N51325	NM_194318	145173	-0,83	2,95E-05
QPCT	205174_s_at	NM_012413	NM_012413	25797	-0,83	8,28E-03
AL045516	232166_at	AL045516	---	---	-0,83	2,57E-03
ZNF148	230821_at	AW594167	NM_021964	7707	-0,83	3,02E-03
GNG2	224964_s_at	AK026424	NM_053064	54331	-0,83	6,30E-03
CTPS2	219080_s_at	NM_019857	NM_019857 NM_175859	56474	-0,83	3,00E-04
CAMK2D	225019_at	BF797381	NM_001221 NM_172115 NM_172127 NM_172128	817	-0,83	8,53E-03
CYLD	213295_at	AA555096	NM_015247	1540	-0,83	7,35E-04
TMEM5	204808_s_at	NM_014254	NM_014254	10329	-0,83	2,63E-03
FLJ35036	225512_at	AI005245	XM_172341	253461	-0,83	6,24E-04
LOC51334	220014_at	NM_016644	NM_016644	51334	-0,82	5,21E-04
MGC34646	224996_at	N30209	NM_173519	157807	-0,82	6,97E-05
NDP52	235076_at	AA149539	NM_005831	10241	-0,82	2,69E-03
FLJ38991	227442_at	BG283902	NM_173827	285521	-0,82	2,38E-03
LOC144363	225469_at	AA015609	NM_001001660	144363	-0,82	6,00E-03
AI627803	236194_at	AI627803	---	---	-0,82	8,90E-03
EIF4E3	238461_at	AA228031	---	317649	-0,82	8,67E-03
LOC284262	227478_at	BF739885	---	284262	-0,82	1,50E-05
LRCH2	227688_at	AK022128	NM_020871	57631	-0,82	4,46E-04
AI635131	1557192_at	AI635131	XM_375410	400574	-0,82	2,14E-03
AA935515	242790_at	AA935515	---	---	-0,82	4,73E-04
ZNF423	214761_at	AW149417	NM_015069	23090	-0,82	6,45E-03
FBXO4	223493_at	AF129534	NM_012176 NM_033484	26272	-0,82	2,52E-03
AI417268	225028_at	AI417268	---	---	-0,82	8,20E-03
EIF2C1	228120_at	AW136032	NM_012199	26523	-0,81	1,09E-

FLJ22313	236170_x_at	AI377423	NM_022373	64224	-0,81	4,47E-05
LOC401500	233946_at	AL512690	XM_379629	401500	-0,81	2,52E-03
AFFX-BioB-M	AFFX-BioB-M_at	AFFX-BioB-M	---	---	-0,81	3,21E-03
AI149508	228416_at	AI149508	---	---	-0,81	1,26E-03
ZNF287	220055_at	NM_020653	NM_020653	57336	-0,81	1,85E-04
FLJ30851	230435_at	BF108666	NM_198553	375190	-0,81	5,13E-04
BC042959	1556194_a_at	BC042959	---	---	-0,81	2,89E-03
CA5BL	238435_at	AA521288	XM_291346	340591	-0,81	4,85E-03
WIZ	221784_at	AI089655	XM_372716	58525	-0,81	1,35E-03
AW086077	232800_at	AW086077	---	---	-0,81	3,68E-03
FLJ22795	223327_x_at	AF316855	NM_025084	80154	-0,81	4,57E-03
AI075662	238038_at	AI075662	---	---	-0,81	4,28E-03
PCDHB14	231726_at	NM_018934	NM_018934	56122	-0,81	5,56E-03
LOC130355	227840_at	AA738440	XM_496588	130355	-0,81	2,33E-05
FLJ10378	231824_at	AK027164	NM_018078 NM_032239 NM_178043	55132	-0,81	7,52E-03
CAMK2B	211483_x_at	AF081924	NM_001220 NM_172078 NM_172079 NM_172080 NM_172081 NM_172082 NM_172083 NM_172084	816	-0,81	2,75E-04
RPL4	226556_at	BF431260	NM_000968	6124	-0,81	2,30E-07
C21orf108	212996_s_at	AI803485	---	9875	-0,81	4,93E-03
CYLD	39582_at	AL050166	NM_015247	1540	-0,81	8,02E-04
MBNL1	201151_s_at	BF512200	NM_021038 NM_207292 NM_207293 NM_207294 NM_207295 NM_207296 NM_207297	4154	-0,80	1,13E-03
HERC4	208055_s_at	NM_015601	NM_015601	26091	-0,80	1,46E-03
AI929792	236081_at	AI929792	---	---	-0,80	2,95E-

SYNJ1	212990_at	AB020717	NM_003895 NM_203446	8867	-0,80	1,01E-03
C9orf123	224860_at	AL137489	XM_372075	90871	-0,80	8,84E-04
C21orf66	1556789_a_at	AK056384	NM_013329 NM_016631 NM_058191 NM_145328	94104	-0,80	4,85E-03
BMPR2	231873_at	AL046696	NM_001204 NM_033346	659	-0,80	1,31E-04
PCBP3	230486_at	BG025371	NM_020528	54039	-0,80	5,61E-04
JAM2	229127_at	BF195118	NM_021219	58494	-0,80	4,44E-03
COG6	225769_at	AF116827	NM_020751	57511	-0,80	4,32E-03
FLJ21159	220145_at	NM_024826	NM_024826	79884	-0,80	5,05E-03
HSD17B12	217869_at	NM_016142	NM_016142	51144	-0,80	5,67E-03
SMAP-5	224953_at	AW001618	NM_030799	81555	-0,80	5,29E-03
SAV1	218276_s_at	NM_021818	NM_021818	60485	-0,80	1,52E-03
PPID	204186_s_at	AI014573	NM_005038	5481	-0,80	5,72E-04
AZI2	227905_s_at	BF000175	NM_022461 NM_203326	64343	-0,79	9,88E-05
BE219874	236111_at	BE219874	---	---	-0,79	6,26E-03
KPNA1	202057_at	BC002374	NM_002264	3836	-0,79	5,21E-03
LOC339803	227940_at	N90774	---	339803	-0,79	1,13E-04
ALKBH	236721_at	AI922200	NM_006020	8846	-0,79	2,25E-03
AW237752	229699_at	AW237752	---	---	-0,79	8,75E-03
SLC22A17	218675_at	NM_020372	NM_016609 NM_020372	51310	-0,79	1,71E-04
TOB1	228834_at	BF240286	NM_005749	10140	-0,79	7,87E-04
MED28	224416_s_at	AF358829	NM_025205	80306	-0,79	1,39E-04
ZNF277	1555193_a_at	BC020626	NM_021994	11179	-0,79	9,56E-03
WDFY3	212598_at	BE348236	NM_014991 NM_178583 NM_178585	23001	-0,79	6,62E-03
SGNE1	203889_at	NM_003020	NM_003020	6447	-0,78	3,31E-04
ANKRD32	223542_at	AL136560	NM_032290	84250	-0,78	2,09E-04
CLCN3	201733_at	AA902971	NM_001829 NM_173872	1182	-0,78	1,25E-06

EIF4E3	225939_at	AL161983	---	317649	-0,78	2,79E-03
CARF	218929_at	NM_017632	NM_017632	55602	-0,78	2,99E-03
DCX	204851_s_at	AF040254	NM_000555 NM_178151 NM_178152 NM_178153	1641	-0,78	7,79E-03
C1orf25	220992_s_at	NM_030934	NM_030934	81627	-0,78	2,30E-03
TNFRSF25	219423_x_at	NM_003790	NM_003790 NM_148965 NM_148966 NM_148967 NM_148968 NM_148969 NM_148970 NM_148971 NM_148972 NM_148973 NM_148974	8718	-0,78	8,35E-03
AOF2	212348_s_at	AB011173	NM_001009999 NM_015013	23028	-0,78	3,47E-03
AW025980	241864_x_at	AW025980	XM_371647	389129	-0,78	5,72E-04
ACBD5	225663_at	AL047650	NM_145698	91452	-0,78	1,80E-03
FRS2	226045_at	AW264515	NM_006654	10818	-0,78	5,02E-03
MYOZ3	213955_at	BE673151	NM_133371	91977	-0,78	7,08E-03
DBT	205369_x_at	J03208	NM_001918	1629	-0,78	5,34E-03
AI061377	235233_s_at	AI061377	---	---	-0,78	2,35E-03
ENOSF1	204142_at	NM_017512	NM_017512	55556	-0,78	2,12E-03
CA5BL	239106_at	AI801563	XM_291346	340591	-0,77	3,87E-03
GTDC1	219770_at	NM_024659	NM_001006636 NM_024659	79712	-0,77	5,30E-04
RAB18	243496_at	AW367507	NM_021252	22931	-0,77	5,05E-03
AK025253	227009_at	AK025253	---	---	-0,77	2,24E-03
MRPS6	212944_at	AK024896	NM_032476	64968	-0,77	9,32E-03
AFAP	203563_at	NM_021638	NM_021638 NM_198595	60312	-0,77	4,32E-04
RGS7	1554500_a_at	AF493931	NM_002924	6000	-0,77	5,33E-04

QSCN6	201482_at	NM_002826	NM_001004128 NM_002826	5768	-0,77	5,46E-04
C21orf57	227421_at	BF026326	NM_001006114 NM_058181	54059	-0,77	2,03E-03
PLEKHA3	227658_s_at	BE550332	NM_019091	65977	-0,77	2,93E-04
FLJ10980	225327_at	AB037791	NM_019600	56204	-0,77	3,59E-03
PURA	229167_at	AI129941	NM_005859	5813	-0,77	7,80E-03
AFFX-r2-Ec-bioC-5	AFFX-r2-Ec-bioC-5_at	AFFX-r2-Ec-bioC-5	---	---	-0,77	1,36E-03
HSPA12A	214434_at	AB007877	XM_048898	259217	-0,77	5,03E-03
ZNF250	213858_at	BE350026	NM_021061	58500	-0,77	2,48E-03
AFFX-r2-Ec-bioB-5	AFFX-r2-Ec-bioB-5_at	AFFX-r2-Ec-bioB-5	---	---	-0,77	4,87E-03
PDXK	222492_at	AW262867	NM_003681	8566	-0,77	7,16E-03
H09780	230869_at	H09780	---	---	-0,76	5,31E-03
LOC283481	230351_at	AW070248	---	283481	-0,76	1,35E-04
LOC128153	1552269_at	NM_138796	NM_138796	128153	-0,76	8,35E-03
PTP4A2	208617_s_at	AF208850	NM_003479 NM_080391 NM_080392	8073	-0,76	8,88E-05
AB029551	201845_s_at	AB029551	---	---	-0,76	1,96E-04
KIAA1387	226230_at	AA541716	NM_020463	57223	-0,76	1,87E-03
C21orf86	226995_at	AV705934	NM_153454	257103	-0,76	5,79E-05
ISYNA1	222240_s_at	AL137749	NM_016368	51477	-0,76	3,08E-03
RNF13	201780_s_at	NM_007282	NM_007282 NM_183381 NM_183382 NM_183383 NM_183384	11342	-0,76	6,77E-04
JMJD2C	209984_at	AB037901	NM_015061	23081	-0,76	3,62E-03
GTDC1	238585_at	AW407668	NM_001006636 NM_024659	79712	-0,76	1,71E-03
AI955713	227193_at	AI955713	---	---	-0,76	2,70E-03
FKBP1A	210187_at	BC005147	NM_000801 NM_054014	2280	-0,76	7,11E-03
AW117322	239415_at	AW117322	XM_374094	389237	-0,76	5,02E-03
BBP	213883_s_at	AA012917	NM_032027	83941	-0,76	5,78E-

LOC284804	1559161_at	AI871356	---	284804	-0,75	6,44E-03
DJ159A19.3	205002_at	NM_015699	XM_372774	27245	-0,75	8,45E-04
AFFX-BioDn-3	AFFX-BioDn-3_at	AFFX-BioDn-3	---	---	-0,75	2,83E-03
LAMB1	201505_at	NM_002291	NM_002291	3912	-0,75	9,18E-03
POLR3A	227872_at	AA527570	NM_007055	11128	-0,75	9,27E-04
CDC2L6	212899_at	AB028951	NM_015076	23097	-0,75	2,97E-05
GRK4	241989_at	AW269179	NM_001004056 NM_001004057 NM_005307 NM_182982	2868	-0,75	9,15E-03
FEV	207260_at	NM_017521	NM_017521	54738	-0,75	5,52E-04
MGC35274	226748_at	AI674731	NM_153374	256586	-0,75	6,51E-03
PRKCB1	209685_s_at	M13975	NM_002738 NM_212535	5579	-0,75	4,16E-03
OXR1	222553_x_at	AL541048	NM_181354	55074	-0,75	3,29E-03
ARP3BETA	218868_at	NM_020445	NM_020445	57180	-0,75	9,91E-03
PFN2	237116_at	AI262277	NM_002628 NM_053024	5217	-0,74	8,35E-03
LZTFL1	218437_s_at	NM_020347	NM_020347	54585	-0,74	3,96E-03
C6orf96	220329_s_at	NM_017909	NM_017909	55005	-0,74	1,80E-03
BE890365	222738_at	BE890365	---	---	-0,74	9,64E-03
BG112359	225785_at	BG112359	---	---	-0,74	2,08E-03
ICA1	204002_s_at	NM_022307	NM_004968 NM_022307 NM_022308	3382	-0,74	2,94E-03
ENOSF1	213645_at	AF305057	NM_017512	55556	-0,74	4,62E-03
CAMK2D	228555_at	AA029441	NM_001221 NM_172115 NM_172127 NM_172128	817	-0,74	1,79E-03
AI889373	227414_at	AI889373	---	---	-0,74	1,82E-03
GPR27	227769_at	AI703476	NM_018971	2850	-0,74	8,05E-03
AK055769	1558801_at	AK055769	---	---	-0,74	7,07E-03
AFFX-BioB-5	AFFX-BioB-5_at	AFFX-BioB-5	---	---	-0,73	3,91E-03

AA928542	226831_at	AA928542	---	---	-0,73	8,48E-04
PAM	202336_s_at	NM_000919	NM_000919 NM_138766 NM_138821 NM_138822	5066	-0,73	2,84E-03
THNSL1	222931_s_at	AI809864	NM_024838	79896	-0,73	3,88E-03
MGC14595	227836_at	AI859767	NM_032334	84294	-0,73	6,40E-03
PRKCE	226101_at	AI093546	NM_005400	5581	-0,73	3,23E-03
LOC92482	213224_s_at	AK025724	XM_378250	92482	-0,73	5,89E-03
AKAP14	228493_at	T87628	NM_001008534 NM_001008535 NM_178813	158798	-0,73	8,43E-03
DUSP16	224336_s_at	AB052156	NM_030640	80824	-0,73	4,69E-04
IRF2BP2	224571_at	BF968057	NM_182972	359948	-0,73	6,05E-03
C6orf117	243177_at	AI912225	NM_138409	112609	-0,73	7,88E-03
ADD2	205268_s_at	NM_017488	NM_001617 NM_017482 NM_017483 NM_017484 NM_017485 NM_017486 NM_017487 NM_017488	119	-0,73	4,20E-07
PCSK6	207414_s_at	NM_002570	NM_002570 NM_138319 NM_138320 NM_138321 NM_138322 NM_138323 NM_138324 NM_138325	5046	-0,73	3,49E-03
H62221	243414_at	H62221	---	---	-0,73	2,65E-03
AFFX-BioC-5	AFFX-BioC-5_at	AFFX-BioC-5	---	---	-0,73	6,02E-04
BF342524	235074_at	BF342524	---	---	-0,73	2,25E-03
LOC96610	226802_s_at	W87523	NM_080926	96610	-0,73	9,29E-03
BE645776	227288_at	BE645776	XM_068832	133993	-0,73	7,66E-04
KIAA0423	213304_at	AI823592	NM_015091	23116	-0,73	2,19E-03
ENOSF1	204143_s_at	NM_017512	NM_017512	55556	-0,73	2,84E-

DSCR5	221689_s_at	AB035745	NM_016430 NM_153681 NM_153682	51227	-0,73	4,01E-05
MGC54289	226228_at	AI474054	NM_178454	126338	-0,72	2,77E-05
AK026379	232687_at	AK026379	---	---	-0,72	1,93E-04
MGC72075	228600_x_at	BE220330	NM_199136	340277	-0,72	5,28E-04
ASH1L	226447_at	BG290742	NM_018489	55870	-0,72	2,78E-03
KIAA0974	213463_s_at	AW300504	---	317662	-0,72	4,74E-04
C6orf157	227790_at	AV692609	NM_198920	80025	-0,72	3,66E-03
CLCN4	214769_at	AF052117	NM_001830	1183	-0,72	3,22E-04
LOC440360	236838_at	H11609	XM_498641	440360	-0,72	2,56E-03
SYNCRIP	217833_at	AL520908	NM_006372	10492	-0,72	4,62E-04
AFFX-r2-Ec-bioB-M	AFFX-r2-Ec-bioB-M_at	AFFX-r2-Ec-bioB-M	---	---	-0,72	7,96E-03
AKT3	212609_s_at	U79271	NM_005465 NM_181690	10000	-0,72	5,74E-03
PP1057	220968_s_at	NM_031285	---	83441	-0,72	6,75E-03
GM2A	1559776_at	H41167	NM_000405	2760	-0,72	1,46E-03
FLJ37228	1556641_at	AK094547	---	285264	-0,72	6,35E-03
NAV1	227584_at	BF339566	NM_020443	89796	-0,71	9,22E-05
MGC10198	225574_at	BE613081	NM_152682	201965	-0,71	1,36E-03
PPP2R5C	201877_s_at	NM_002719	NM_002719 NM_178586 NM_178587 NM_178588	5527	-0,71	1,25E-03
RAFTLIN	212646_at	D42043	NM_015150	23180	-0,71	7,61E-06
DKFZP564O243	210006_at	BC002571	NM_015407	25864	-0,71	5,84E-03
SLC35A5	218519_at	NM_017945	NM_017945	55032	-0,71	5,19E-03
BF526978	227125_at	BF526978	---	---	-0,71	2,88E-03
RBM16	227866_at	AI743557	NM_014892	22828	-0,71	4,70E-04
gm117	239038_at	AW015063	NM_198077	148423	-0,71	2,85E-05
AB058893	223973_at	AB058893	---	---	-0,71	3,00E-03
DUSP16	224832_at	AB051487	NM_030640	80824	-0,71	8,84E-04
AFFX-r2-Ec-bioC-3	AFFX-r2-Ec-bioC-3_at	AFFX-r2-Ec-bioC-3	---	---	-0,71	2,47E-03

AL355532	213845_at	AL355532	---	---	-0,71	1,72E-03
LOC284409	242016_at	BE857296	XM_211447	284409	-0,70	7,46E-03
PAK1	226507_at	AU154408	NM_002576	5058	-0,70	1,89E-03
BC015852	1560570_a_at	BC015852	---	---	-0,70	5,93E-04
EPM2AIP1	227847_at	BF432224	NM_014805	9852	-0,70	6,03E-03
13CDNA73	204072_s_at	NM_023037	NM_023037	10129	-0,70	1,50E-04
DECR1	202447_at	NM_001359	NM_001359	1666	-0,70	7,20E-03
USP38	223288_at	AW977401	NM_032557	84640	-0,70	6,63E-03
RAB4A	203581_at	BC002438	NM_004578	5867	-0,70	1,97E-03
PLEKHA3	223370_at	AF286162	NM_019091	65977	-0,70	4,19E-03
AFFX-BioC-3	AFFX-BioC-3_at	AFFX-BioC-3	---	---	-0,70	1,62E-03
PPID	204185_x_at	NM_005038	NM_005038	5481	-0,70	5,63E-04
PAM	214620_x_at	BF038548	NM_000919 NM_138766 NM_138821 NM_138822	5066	-0,70	2,61E-04
ARL7	202207_at	BG435404	NM_005737	10123	-0,70	1,62E-03
DNAJC6	204720_s_at	AV729634	NM_014787	9829	-0,70	2,00E-04
SYNCOILIN	225396_at	AI928212	NM_030786	81493	-0,70	5,70E-03
ANXA5	200782_at	NM_001154	NM_001154	308	-0,70	5,88E-03
MGC14595	238561_s_at	BE542779	NM_032334	84294	-0,70	6,39E-05
SELM	226051_at	BF973568	NM_080430	140606	-0,70	4,02E-03
AA489100	228390_at	AA489100	---	---	-0,70	5,43E-03
AA740675	244032_at	AA740675	---	---	-0,70	9,18E-04
ALDH5A1	203608_at	AL031230	NM_001080 NM_170740	7915	-0,69	3,13E-03
BE646451	235893_at	BE646451	---	---	-0,69	9,91E-03
DUSP7	213848_at	AI655015	NM_001947	1849	-0,69	9,16E-03
MGC42174	242539_at	AW665509	NM_152383	129563	-0,69	2,67E-03
FBXO25	225591_at	AA749085	NM_012173 NM_183420 NM_183421	26260	-0,69	4,48E-03
CNOT6L	226153_s_at	AW514857	NM_144571	246175	-0,69	4,37E-04

NPR2	204310_s_at	NM_003995	NM_000907 NM_003995	4882	-0,69	5,97E-03
DEPDC6	218858_at	NM_022783	NM_022783	64798	-0,69	2,62E-03
GARNL4	213280_at	AK000478	NM_015085	23108	-0,69	5,49E-03
ANKH	223093_at	T99215	NM_054027	56172	-0,69	3,95E-03
NUDT11	219855_at	NM_018159	NM_018159	55190	-0,69	1,75E-03
IFNAR2	204785_x_at	NM_000874	NM_000874 NM_207584 NM_207585	3455	-0,69	7,44E-05
ZNF148	235166_at	T08836	NM_021964	7707	-0,68	9,51E-03
LOC377064	229986_at	AW205616	XM_496648	377064	-0,68	3,34E-03
RSL1D1	212019_at	AK025446	NM_015659	26156	-0,68	2,80E-03
C10orf22	212500_at	AL049319	NM_032804	84890	-0,68	8,22E-03
DAZAP2	214334_x_at	N34846	NM_014764	9802	-0,68	2,12E-03
WDFY3	212606_at	AL536319	NM_014991 NM_178583 NM_178585	23001	-0,68	8,12E-05
PTPN23	223150_s_at	AF290614	NM_015466	25930	-0,68	2,67E-03
SNAP91	204953_at	NM_014841	NM_014841	9892	-0,68	1,47E-04
DSU	232682_at	BG167210	NM_018000	55686	-0,68	2,28E-04
ZNF490	231988_x_at	AB033024	NM_020714	57474	-0,68	8,43E-04
AFFX-r2-Ec-bioD-3	AFFX-r2-Ec-bioD-3_at	AFFX-r2-Ec-bioD-3	---	---	-0,68	8,66E-03
ZBTB1	242258_at	AW168154	NM_014950	22890	-0,68	7,93E-03
AFFX-r2-Ec-bioB-3	AFFX-r2-Ec-bioB-3_at	AFFX-r2-Ec-bioB-3	---	---	-0,68	4,86E-03
DLG3	212727_at	AB033058	NM_021120	1741	-0,68	2,75E-05
P15RS	225953_at	AI684281	NM_018170	55197	-0,68	4,56E-03
LRBA	212692_s_at	W60686	NM_006726	987	-0,68	1,07E-06
ZBED3	228402_at	AI679868	NM_032367	84327	-0,68	2,61E-03
DNASE1L1	203912_s_at	NM_006730	NM_001009932 NM_001009933 NM_001009934 NM_006730	1774	-0,68	4,97E-03
ABR	212895_s_at	AL527773	NM_001092 NM_021962	29	-0,68	9,54E-04

AF147335	1557518_a_at	AF147335	---	---	-0,68	3,85E-03
HNRPD	229129_at	AI948456	NM_001003810 NM_002138 NM_031369 NM_031370	3184	-0,68	9,99E-03
LOC387895	243905_at	AI652676	XM_373553	387895	-0,68	4,51E-03
PLCE1	205111_s_at	NM_016341	NM_016341	51196	-0,68	3,83E-04
ANTXR2	228573_at	BE673665	NM_058172	118429	-0,68	3,75E-03
MGC48625	1569039_s_at	BC029855	NM_182609	342926	-0,68	2,30E-04
MGC47869	229888_at	AA861435	NM_175874	144608	-0,68	3,57E-03
ZNF197	233070_at	AL117657	NM_006991	10168	-0,68	1,50E-04
DYRK2	202999_at	AI216690	NM_003583 NM_006482	8445	-0,68	3,24E-03
LOC285513	1556697_at	AI819722	NM_198281	285513	-0,67	1,21E-05
CRYZL1	219767_s_at	NM_005111	NM_005111 NM_145311 NM_145858	9946	-0,67	6,15E-03
AA935461	242579_at	AA935461	---	---	-0,67	3,50E-04
FLJ30990	1554588_a_at	BC033795	NM_152517	150737	-0,67	7,72E-03
RIPK5	229017_s_at	N31717	NM_015375 NM_199462	25778	-0,67	5,71E-03
N63920	226179_at	N63920	---	---	-0,67	9,08E-03
NM_022335	206936_x_at	NM_022335	---	---	-0,67	1,76E-04
SLC25A12	203340_s_at	NM_003705	NM_003705	8604	-0,67	6,85E-03
MED28	218438_s_at	NM_025205	NM_025205	80306	-0,67	1,38E-03
RAD52	236042_at	AI700506	NM_002879 NM_134422 NM_134423 NM_134424	5893	-0,67	1,28E-04
EPHA8	231796_at	AL035703	NM_001006943 NM_020526	2046	-0,67	5,79E-03
DSU	219648_at	NM_018000	NM_018000	55686	-0,67	3,20E-04
AA843541	229710_at	AA843541	---	---	-0,67	9,95E-04
AA461190	244294_at	AA461190	---	---	-0,67	9,45E-03
JAM2	219213_at	NM_021219	NM_021219	58494	-0,66	1,52E-03
CDK6	224847_at	AW051349	NM_001259	1021	-0,66	3,40E-

MCM3APAS	1560542_at	BC016306	---	114044	-0,66	9,71E-03
LOC157657	244569_at	N92755	NM_177965	157657	-0,66	1,12E-03
LOC286334	226590_at	AA910497	---	286334	-0,66	5,51E-04
C3orf6	225331_at	BF941088	NM_174908 NM_178335	152137	-0,66	4,75E-03
KIAA1579	231851_at	AL359613	NM_018211	55225	-0,66	4,44E-03
KIAA0241	212474_at	D87682	NM_015060	23080	-0,66	2,52E-03
TFAP2B	214451_at	NM_003221	NM_003221	7021	-0,66	6,69E-04
AI218542	236089_at	AI218542	---	---	-0,66	8,36E-03
EEF2K	225546_at	W68180	NM_013302	29904	-0,66	1,99E-03
KIAA0999	204157_s_at	NM_025164	NM_025164	23387	-0,65	3,68E-05
FXR1	201637_s_at	NM_005087	NM_005087	8087	-0,65	8,08E-03
AA406435	230747_s_at	AA406435	---	---	-0,65	6,70E-03
ZNF626	235687_at	AA908777	NM_145297	199777	-0,65	5,29E-03
KIAA0582	212675_s_at	AB011154	NM_015147	23177	-0,65	7,85E-03
DTNA	227084_at	AW339310	NM_001390 NM_001391 NM_001392 NM_032975 NM_032978 NM_032979 NM_032980 NM_032981	1837	-0,65	3,98E-03
C9orf109	229059_at	AI765785	XM_379665	286333	-0,65	1,91E-03
TBC1D12	1557609_s_at	AW188458	XM_051081	23232	-0,65	4,03E-03
LIN7C	223350_x_at	N63709	NM_018362	55327	-0,65	3,22E-03
PIK3R2	1568629_s_at	BC033311	NM_005027	5296	-0,65	7,91E-05
AU151635	232111_at	AU151635	---	---	-0,65	6,09E-04
NM_018678	220494_s_at	NM_018678	---	---	-0,65	4,32E-03
FAM8A1	203420_at	NM_016255	NM_016255	51439	-0,65	8,87E-03
AL136588	223614_at	AL136588	---	---	-0,65	3,95E-04
KIAA0179	212846_at	AA811192	NM_015056	23076	-0,65	7,52E-03
BF509796	229318_at	BF509796	---	---	-0,65	2,51E-03

SEC31L1	200945_s_at	NM_014933	NM_014933 NM_016211	22872	-0,65	8,63E-04
KIAA0711	204301_at	NM_014867	NM_014867	9920	-0,65	1,44E-03
AW025141	228400_at	AW025141	---	---	-0,64	6,23E-03
SERP1	235475_at	AI580135	NM_014445	27230	-0,64	8,89E-03
C2orf32	226751_at	AW193693	NM_015463	25927	-0,64	6,94E-04
KIAA1935	228336_at	AW511595	XM_087672	114825	-0,64	2,59E-03
PDE4D	228962_at	BF507941	NM_006203	5144	-0,64	2,48E-03
CDC14B	221556_at	BF792631	NM_003671 NM_033331 NM_033332	8555	-0,64	2,02E-03
FANCF	218689_at	NM_022725	NM_022725	2188	-0,64	5,25E-03
BCAR3	204032_at	NM_003567	NM_003567	8412	-0,64	3,94E-03
UBE2D3	200667_at	BF448062	NM_003340 NM_181886 NM_181887 NM_181888 NM_181889 NM_181890 NM_181891 NM_181892 NM_181893	7323	-0,64	2,05E-03
MGC29463	238115_at	T03492	NM_152686	202052	-0,64	4,51E-03
AFFX-BioDn-5	AFFX-BioDn-5_at	AFFX-BioDn-5	---	---	-0,64	1,45E-03
TPD52	201690_s_at	AA524023	NM_005079	7163	-0,64	8,25E-04
HPSE	222881_at	AF155510	NM_006665	10855	-0,64	2,12E-03
MAN1A2	217920_at	H97940	NM_006699	10905	-0,64	2,61E-03
HRMT1L1	221564_at	AL570294	NM_001535 NM_206962	3275	-0,64	5,66E-03
C22orf9	227144_at	AA476916	NM_001009880 NM_015264	23313	-0,63	8,11E-03
RGS12	1555022_at	AF464736	NM_002926 NM_198227 NM_198229 NM_198230 NM_198430 NM_198432 NM_198587	6002	-0,63	3,89E-05
AFFX-r2-Ec-bioD-5	AFFX-r2-Ec-bioD-5_at	AFFX-r2-Ec-bioD-5	---	---	-0,63	3,52E-03

AI766065	224647_at	AI766065	---	---	-0,63	4,41E-04
TDRD3	1569069_s_at	BC020604	NM_030794	81550	-0,63	4,16E-03
SOS1	227426_at	AV702692	NM_005633	6654	-0,63	3,92E-03
SMAD2	203077_s_at	NM_005901	NM_001003652 NM_005901	4087	-0,63	7,24E-03
MED28	228992_at	BF064162	NM_025205	80306	-0,63	2,06E-05
BICD1	1556051_a_at	CA777994	NM_001003398 NM_001714	636	-0,63	6,24E-04
GOLPH3L	218361_at	NM_018178	NM_018178	55204	-0,63	9,58E-04
MBNL1	201152_s_at	N31913	NM_021038 NM_207292 NM_207293 NM_207294 NM_207295 NM_207296 NM_207297	4154	-0,63	4,11E-05
LZTFL1	222632_s_at	AA843132	NM_020347	54585	-0,63	4,52E-04
RUFY1	233380_s_at	AA429145	NM_025158	80230	-0,63	8,27E-04
RBM18	238963_at	BG106093	NM_033117	92400	-0,63	1,19E-03
UBXD1	220757_s_at	NM_025241	NM_025241	80700	-0,63	9,92E-04
NCAM1	227394_at	W94001	NM_000615 NM_181351	4684	-0,63	2,48E-03
C14orf4	223474_at	AI932310	NM_024496	64207	-0,63	3,20E-04
PEX11A	205161_s_at	NM_003847	NM_003847	8800	-0,63	1,24E-04
BF692729	1558044_s_at	BF692729	---	---	-0,62	1,31E-03
AW290940	226773_at	AW290940	---	---	-0,62	4,57E-04
DDHD1	225970_at	AA029818	NM_030637	80821	-0,62	2,27E-03
C9orf10OS	239391_at	AA195528	NM_198841	158293	-0,62	7,21E-03
AI694544	235215_at	AI694544	---	---	-0,62	3,54E-03
TMEM45A	219410_at	NM_018004	NM_018004	55076	-0,62	1,39E-03
CXorf38	228700_at	AA063608	NM_144970	159013	-0,62	5,45E-03
LOC57149	203897_at	BE963444	NM_020424	57149	-0,62	2,10E-03
LOC54499	208715_at	BF002031	NM_019026	54499	-0,62	1,19E-03
SCAMP1	212425_at	AL049223	NM_004866 NM_052822	9522	-0,62	8,35E-03

IMPACT	222698_s_at	AF208694	NM_018439	55364	-0,62	7,05E-03
TRPM1	243741_at	AW665484	NM_002420	4308	-0,62	7,71E-03
TMAP1	227326_at	BE966768	NM_001008528 NM_001008529 NM_198530	439921	-0,62	4,82E-03
NLK	222589_at	AI967933	NM_016231	51701	-0,62	9,48E-03
KIAA0280	36612_at	D87470	XM_370635	23201	-0,62	7,88E-03
SYNCRIP	236146_at	BF593158	NM_006372	10492	-0,62	2,46E-04
NAV1	224772_at	AB032977	NM_020443	89796	-0,61	1,83E-03
AI216347	242087_x_at	AI216347	---	---	-0,61	7,98E-03
RTN4R	228550_at	NM_023004	NM_023004	65078	-0,61	2,34E-03
TLOC1	225352_at	AI763287	NM_003262	7095	-0,61	1,21E-03
AL137344	232390_at	AL137344	---	---	-0,61	8,75E-06
COMMD2	226910_at	AW008502	NM_016094	51122	-0,61	9,68E-03
LOC57228	209679_s_at	BC003379	NM_020467	57228	-0,61	9,52E-03
AW873330	225674_at	AW873330	---	---	-0,61	7,46E-03
RAD50	208393_s_at	NM_005732	NM_005732 NM_133482	10111	-0,61	2,10E-06
ZFY	230760_at	BF592062	NM_003411	7544	-0,61	8,36E-05
C21orf33	202217_at	NM_004649	NM_004649 NM_198155	8209	-0,61	9,07E-03
PAM	212958_x_at	AI022882	NM_000919 NM_138766 NM_138821 NM_138822	5066	-0,61	1,54E-03
PDCD2	204025_s_at	NM_002598	NM_002598 NM_144781	5134	-0,61	4,97E-03
AHI1	221569_at	AL136797	NM_017651	54806	-0,61	2,59E-03
TPD52	201689_s_at	BE974098	NM_005079	7163	-0,61	5,72E-03
AV721564	227620_at	AV721564	---	---	-0,61	9,48E-03
ZNF540 DKFZp761D1918	229328_at	T90358	NM_152606 XM_375608	163255 400692	-0,61	8,93E-03
GAB1	226002_at	AK022142	NM_002039 NM_207123	2549	-0,60	4,32E-04
R02709	242149_at	R02709	---	---	-0,60	8,54E-03

DGX	204850_s_at	NM_000555	NM_000555 NM_178151 NM_178152 NM_178153	1641	-0,60	4,23E-03
PPARG	208510_s_at	NM_015869	NM_005037 NM_015869 NM_138711 NM_138712	5468	-0,60	1,82E-03
PCYOX1	225274_at	BF247054	NM_016297	51449	-0,60	6,39E-03
M17S2	201384_s_at	NM_005899	NM_005899 NM_031858 NM_031862	4077	-0,60	9,84E-04
KBTBD7	223412_at	AL136782	NM_032138	84078	-0,60	3,40E-03
AK094546	1556205_at	AK094546	---	---	-0,60	8,73E-03
GAJ	223700_at	AY028916	NM_032117	84057	-0,60	2,55E-03
BACE1	222462_s_at	AI653425	NM_012104 NM_138971 NM_138972 NM_138973	23621	-0,60	5,62E-04
RAB26	50965_at	AI690165	NM_014353	25837	-0,60	2,77E-03
AGPAT4	228667_at	AI733330	NM_020133	56895	-0,60	7,61E-03
LOC134147	227522_at	AA209487	NM_138809	134147	-0,60	9,04E-03
MRPS30	222275_at	AI039469	NM_016640	10884	-0,60	1,13E-03
AV699883	230782_at	AV699883	---	---	-0,60	1,72E-03
DJ122O8.2	227797_x_at	AI652464	NM_020466	57226	-0,60	5,64E-03
ULK2	204062_s_at	BG526973	NM_014683	9706	-0,60	2,35E-03
AL552727	244080_at	AL552727	---	---	-0,60	4,85E-03
DDEF1	224791_at	AW513835	NM_018482	50807	-0,60	1,40E-04
TIAM1	213135_at	U90902	NM_003253	7074	-0,60	7,17E-03
HOXC6	206858_s_at	NM_004503	NM_004503 NM_153693	3223	-0,60	3,44E-03
POFUT2	209578_s_at	BC000626	NM_015227 NM_133634 NM_133635	23275	-0,60	1,08E-03
ZFP36L2	201368_at	U07802	NM_006887	678	-0,60	1,13E-03
BC016176	1561529_at	BC016176	---	---	-0,60	5,78E-03
CNOT8	202163_s_at	NM_004779	NM_004779	9337	-0,60	7,52E-03
LOC124220	228058_at	AI559190	NM_145252	124220	-0,59	4,64E-03

ZC3HDC1	218543_s_at	NM_022750	NM_022750	64761	-0,59	7,38E-03
KIAA1126	225598_at	AB032952	XM_050325	57210	-0,59	1,48E-03
W26593	213048_s_at	W26593	---	---	-0,59	5,40E-03
FLJ20534	218646_at	NM_017867	NM_017867	54969	-0,59	1,34E-04
LOC126167	1560779_a_at	AK092139	XM_058997	126167	-0,59	2,41E-03
AA449838	241411_at	AA449838	---	---	-0,59	3,04E-03
FLJ38451	235052_at	AV758821	NM_175872	120376	-0,59	3,69E-03
MAP2	225540_at	BF342661	NM_002374 NM_031845 NM_031846 NM_031847	4133	-0,59	2,90E-03
CPD	201941_at	BE349147	NM_001304	1362	-0,59	3,19E-04
RP42	218583_s_at	NM_020640	NM_020640	54165	-0,59	3,27E-06
RBMX	213762_x_at	AI452524	NM_002139	27316	-0,59	2,27E-04
LRIG2	238653_at	BF967997	NM_014813	9860	-0,59	4,27E-03
BF431965	213567_at	BF431965	---	---	-0,59	7,58E-03
TRIM23	204732_s_at	AI021991	NM_001656 NM_033227 NM_033228	373	-0,59	9,14E-03
C9orf67	224506_s_at	BC006362	NM_032728	84814	-0,58	1,45E-03
AB002295	204307_at	AB002295	---	---	-0,58	2,09E-03
KIAA1546	227624_at	AB046766	XM_042301	57667	-0,58	4,89E-07
PPM1A	227728_at	AA886888	NM_021003 NM_177951 NM_177952	5494	-0,58	7,82E-03
ZNF148	239024_at	AI478771	NM_021964	7707	-0,58	2,84E-04
MARCH-I	235385_at	AI935334	NM_017923	55016	-0,58	6,65E-03
AB033091	225295_at	AB033091	---	---	-0,58	3,88E-03
IRF2BP2	224570_s_at	AA166696	NM_182972	359948	-0,58	4,89E-04
D31763	231864_at	D31763	---	---	-0,58	1,86E-03
LOC151146	227604_at	BG292251	---	151146	-0,58	8,00E-03

UBE2D3	229355_at	AU150386	NM_003340 NM_181886 NM_181887 NM_181888 NM_181889 NM_181890 NM_181891 NM_181892 NM_181893	7323	-0,58	6,55E-06
CUTL1	214743_at	BE046521	NM_001913 NM_181500 NM_181552	1523	-0,58	3,01E-04
LOC152485	228046_at	AA741243	NM_178835	152485	-0,58	8,28E-03
CLPX	223507_at	AL136922	NM_006660	10845	-0,58	6,77E-03
MAPKAP1	222426_at	BG499947	NM_001006617 NM_001006618 NM_001006619 NM_001006620 NM_001006621 NM_024117	79109	-0,58	3,51E-03
BRUNOL4	223654_s_at	BC004167	NM_020180	56853	-0,58	2,18E-03
ARFIP1	218230_at	AL044651	NM_014447	27236	-0,58	3,04E-03
SEC5L1	226270_at	AL562686	NM_018303	55770	-0,58	8,15E-06

Tabla 11. Expresión genética aumentada en las líneas celulares H1 y BB10 en comparación con la línea celular SIMa en estado diferenciado usando análisis de micromatriz

Símbolo del gen	ID del conjunto de sondas	ID Pública representativa	ID de transcripción RefSec	ID de Gen Entrez	Proporción Log2	valor p
DKFZp667G2110	214030_at	BE501352	XM_376254	131544	5,13	6,09E-05
BF476109	1556300_s_at	BF476109	---	---	5,09	2,02E-05
H99792	225710_at	H99792	---	---	4,92	2,07E-08
SLITRK5	214930_at	AW449813	NM_015567	26050	4,63	3,87E-06
DAZ1	207909_x_at	U21663	NM_001005375	1617	4,60	2,31E-03
DAZ3			NM_001005785	57054		
DAZ2			NM_001005786	57055		
DAZ4			NM_004081	57135		
			NM_020363			
			NM_020364			
			NM_020420			
RGS5	218353_at	NM_025226	NM_003617	8490	4,54	1,63E-03
SIM1	206876_at	AL121948	NM_005068	6492	4,53	2,11E-04
KCTD12	212192_at	AI718937	NM_138444	115207	4,51	4,17E-05
RGS5	1555725_a_at	AF493929	NM_003617	8490	4,49	3,25E-05
FLJ39639	243547_at	BE176531	XM_370932	283876	4,37	2,67E-03
DAZ1	208282_x_at	NM_020363	NM_001005375	1617	4,32	3,54E-03
DAZ3			NM_001005785	57054		
DAZ2			NM_001005786	57055		
DAZ4			NM_004081	57135		
			NM_020363			
			NM_020364			
			NM_020420			
PCDH9	219737_s_at	AI524125	NM_020403	5101	4,30	1,19E-03
			NM_203487			
RGS5	209071_s_at	AF159570	NM_003617	8490	4,10	1,32E-04
RGS5	209070_s_at	AI183997	NM_003617	8490	4,07	1,28E-04
DKFZp761O2018	232313_at	AL122107	XM_044062	92293	4,01	2,30E-06
MAB21L2	210302_s_at	AF262032	NM_006439	10586	3,99	2,81E-04
ALCAM	240655_at	BE502785	NM_001627	214	3,98	3,07E-05

DAZ1 DAZ3 DAZ2 DAZ4	207912_s_at	NM_004081	NM_001005375 NM_001005785 NM_001005786 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	3,96	1,79E-03
GRP	206326_at	NM_002091	NM_002091	2922	3,94	1,52E-05
PDZRN3	233442_at	AU147500	NM_015009	23024	3,92	2,66E-03
MAB21L1	206163_at	NM_005584	NM_005584	4081	3,91	6,73E-06
TIMP3	201149_s_at	U67195	NM_000362	7078	3,84	5,07E-03
TIMP3	201147_s_at	BF347089	NM_000362	7078	3,61	7,18E-03
PDZRN3	212915_at	AL569804	NM_015009	23024	3,58	7,05E-03
LOC440738	221697_at	AF276659	NM_001004343	440738	3,54	3,13E-03
GNG11	204115_at	NM_004126	NM_004126	2791	3,52	6,00E-04
PLK2	201939_at	NM_006622	NM_006622	10769	3,49	8,48E-05
CXCR4	217028_at	AJ224869	NM_001008540 NM_003467	7852	3,49	2,53E-05
DLL1	224215_s_at	AF196571	NM_005618	28514	3,40	1,98E-05
LOC340109	1557765_at	BC039509	XM_379322	340109	3,33	4,27E-04
CCDC3	223316_at	AL136562	NM_031455	83643	3,32	3,45E-05
P2RY5	218589_at	NM_005767	NM_005767	10161	3,27	1,73E-03
QKI	212636_at	AL031781	NM_006775 NM_206853 NM_206854 NM_206855	9444	3,23	3,28E-03
DAZ1 DAZ3 DAZ2 DAZ4	208281_x_at	NM_020364	NM_001005375 NM_001005785 NM_001005786 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	3,19	3,17E-03
PCDH9	238919_at	R49295	NM_020403 NM_203487	5101	3,15	4,07E-03
AI242023	240458_at	AI242023	---	---	3,11	1,45E-04
SLC4A11	223748_at	AF336127	NM_032034	83959	3,10	1,45E-03
RPL10A	242188_at	AI743332	NM_007104	4736	3,09	2,35E-03
POLQ	207746_at	NM_014125	NM_006596 NM_199420	10721	3,07	7,89E-03
MGC24103	232568_at	AU145658	---	158295	3,07	8,38E-03

SPAG6	210033_s_at	AF079363	NM_012443 NM_172242	9576	3,06	1,67E-04
RNF182	230720_at	AI884906	NM_152737	221687	3,05	5,00E-05
LOC440928	235147_at	R56118	XM_498917	440928	3,04	2,36E-03
AL049260	216518_at	AL049260	---	---	3,01	8,57E-03
ITGA6	201656_at	NM_000210	NM_000210	3655	3,00	2,58E-04
KCTD12	212188_at	AA551075	NM_138444	115207	2,98	5,67E-04
CXCR4	211919_s_at	AF348491	NM_001008540 NM_003467	7852	2,98	7,80E-03
NEGR1	243357_at	AA115106	NM_173808	257194	2,96	6,99E-05
MGC34032	1569112_at	AW020413	NM_152697	204962	2,94	4,27E-04
PTPRG	1569323_at	BU853579	NM_002841	5793	2,92	3,90E-03
CXCR4	209201_x_at	L01639	NM_001008540 NM_003467	7852	2,90	6,72E-03
CBFA2T2	233243_at	AU144676	NM_005093 NM_175864	9139	2,88	2,26E-03
DAZ1 DAZ3 DAZ2 DAZ4	216922_x_at	AF271088	NM_001005375 NM_001005785 NM_001005786 NM_004081 NM_020363 NM_020364 NM_020420	1617 57054 57055 57135	2,88	7,32E-03
CGNL1	225817_at	AB051536	NM_032866	84952	2,86	3,83E-03
FBXL7	241457_at	AI821935	NM_012304	23194	2,84	1,42E-03
TIMP3	201148_s_at	AW338933	NM_000362	7078	2,79	6,12E-03
BNC2	233036_at	AU146418	NM_017637	54796	2,78	9,59E-03
EDG2	204036_at	AW269335	NM_001401 NM_057159	1902	2,73	5,34E-03
BE674460	237849_at	BE674460	---	---	2,73	7,55E-03
MAB21L2	210303_at	AF262032	NM_006439	10586	2,69	1,03E-03
PDE5A	227088_at	BF221547	NM_001083 NM_033430 NM_033431 NM_033437	8654	2,65	4,68E-03
BC043430	1558714_at	BC043430	---	---	2,65	4,03E-03
AA699443	241838_at	AA699443	---	---	2,64	9,15E-04
AL049337	215768_at	AL049337	---	---	2,62	9,86E-03
RASEF	1553986_at	BC023566	NM_152573	158158	2,61	4,66E-04
PTGFRN	224937_at	BF311866	NM_020440	5738	2,61	1,34E-06
AK025909	233814_at	AK025909	---	---	2,60	1,65E-03
CPVL	208146_s_at	NM_031311	NM_019029 NM_031311	54504	2,59	5,34E-04
TRIM36	219736_at	NM_018700	NM_018700	55521	2,59	6,52E-04

AI377043	230722_at	AI377043	---	---	2,58	7,06E-03
SLAC2-B	214734_at	AB014524	NM_015065	23086	2,58	1,44E-04
AI077566	243994_at	AI077566	---	---	2,57	2,62E-03
EFNA5	1559360_at	AL833045	NM_001962	1946	2,53	7,18E-04
BE464799	214036_at	BE464799	---	---	2,53	1,16E-03
MSN	200600_at	NM_002444	NM_002444	4478	2,52	1,01E-06
RAD23B	214422_at	T93562	NM_002874	5887	2,52	2,47E-03
TULP4	232372_at	AL157491	NM_001007466 NM_020245	56995	2,51	4,65E-03
SCN7A	239984_at	AI333640	NM_002976	6332	2,51	8,48E-03
ITGA6	215177_s_at	AV733308	NM_000210	3655	2,50	6,62E-04
NFIB	211466_at	U70862	NM_005596	4781	2,50	1,09E-05
EML1	204797_s_at	NM_004434	NM_001008707 NM_004434	2009	2,50	1,46E-03
BNC2	220272_at	NM_017637	NM_017637	54796	2,49	3,27E-04
BE348318	236167_at	BE348318	---	---	2,49	5,60E-03
AW963185	241700_at	AW963185	---	---	2,47	1,92E-04
ENC1	201340_s_at	AF010314	NM_003633	8507	2,47	8,66E-03
RBMS3	233608_at	AU146417	NM_001003792 NM_001003793 NM_014483	27303	2,44	5,92E-03
DACH1	1567101_at	AF147347	NM_004392 NM_080759 NM_080760	1602	2,42	9,28E-03
AA654772	241391_at	AA654772	---	---	2,41	7,59E-03
BG400570	1565689_at	BG400570	---	---	2,41	6,41E-03
PIAS1	222371_at	AI732802	NM_016166	8554	2,40	3,91E-03
EDD	232264_at	AK022204	NM_015902	51366	2,40	1,41E-03
NOL7	242143_at	BE674964	NM_016167	51406	2,39	4,55E-03
U80755	243820_at	U80755	---	---	2,39	2,59E-03
ASCL1	209985_s_at	BE797438	NM_004316	429	2,37	8,08E-03
AW052166	239942_at	AW052166	---	---	2,37	9,33E-03
THRAP2	238883_at	AW975051	NM_015335	23389	2,37	9,49E-03
ROBO2	226766_at	AB046788	XM_031246	6092	2,36	7,82E-03
INA	230859_at	BF111276	NM_032727	9118	2,36	2,50E-05
CHC1L	230292_at	AA868809	NM_001268	1102	2,36	6,84E-03
CHRNA7 CHRFAM7A	210123_s_at	U62436	NM_000746 NM_139320 NM_148911	1139 89832	2,33	2,81E-03
ARID1B	240008_at	AI955765	NM_017519 NM_020732 NM_175863	57492	2,32	7,87E-03
SSH2	230970_at	AA975530	NM_033389	85464	2,29	6,93E-03
BE670307	227955_s_at	BE670307	---	---	2,26	5,03E-04

EB-1	227441_s_at	AW005572	NM_020140 NM_152788 NM_181670	56899	2,28	6,31E-03
GNAI1	209576_at	AL049933	NM_002069	2770	2,27	8,26E-06
PIAS1	1559156_at	BC036508	NM_016166	8554	2,27	5,54E-03
CUGBP2	202158_s_at	NM_006561	NM_006561	10659	2,26	8,77E-03
LOC441157	1558795_at	AL833240	XM_499037	441157	2,25	6,17E-05
KIAA0265	238000_at	BF195340	NM_014997	23008	2,23	9,27E-03
SOX2	213721_at	L07335	NM_003106	6657	2,23	1,49E-03
ENC1	201341_at	NM_003633	NM_003633	8507	2,23	8,95E-03
PLXNA2	222159_at	AK023056	NM_025179	5362	2,21	5,06E-04
GNAI1	227692_at	AU153866	NM_002069	2770	2,21	2,84E-06
NRXN1	209915_s_at	AB035356	NM_004801 NM_138735	9378	2,21	3,08E-03
OLFML3	218162_at	NM_020190	NM_020190	56944	2,19	8,33E-04
CBLB	233614_at	AU145361	NM_170662	868	2,19	8,28E-03
CG012	215318_at	AL049782	---	116829	2,19	4,30E-03
SESN3	235150_at	AW376955	NM_144665	143686	2,18	1,58E-03
SOX2	228038_at	AI669815	NM_003106	6657	2,18	1,19E-03
C1orf43	1555225_at	BC008306	NM_015449 NM_138740	25912	2,17	1,21E-05
SPAG6	210032_s_at	AI651156	NM_012443 NM_172242	9576	2,16	1,98E-03
ASCL1	209987_s_at	BC002341	NM_004316	429	2,15	4,18E-03
RASEF	235144_at	AA826324	NM_152573	158158	2,14	2,84E-04
OSBPL3	209626_s_at	AI202969	NM_015550 NM_145320 NM_145321 NM_145322 NM_145323 NM_145324	26031	2,14	4,14E-04
HGF	210997_at	M77227	NM_000601 NM_001010931 NM_001010932 NM_001010933 NM_001010934	3082	2,13	3,66E-03
SLC7A2	225516_at	AA876372	NM_001008539 NM_003046	6542	2,13	9,92E-04
EDG3	228176_at	AA534817	NM_005226	1903	2,13	4,95E-04
EFNB2	202666_at	BF001670	NM_004093	1948	2,13	5,45E-03
BF513404	239469_at	BF513404	---	---	2,12	1,51E-03
LRRC16	219573_at	NM_017640	NM_017640	55604	2,11	8,45E-04
ARHGAP20	228368_at	AI936560	NM_020809	57569	2,11	3,27E-04
ZFHX4	219779_at	NM_024721	NM_024721	79776	2,10	3,71E-04

AW953794	230968_at	AW953794	---	---	2,09	6,43E-03
LOC23117	238341_at	BF677084	XM_290670	23117	2,09	3,42E-03
AK022040	233445_at	AK022040	---	---	2,08	3,85E-03
TOP1	238988_at	AI863675	NM_003286	7150	2,08	5,99E-03
ALCAM	1569362_at	BC041127	NM_001627	214	2,07	5,59E-04
XPO1	1560386_at	BC041658	NM_003400	7514	2,07	4,79E-04
SPAG9	1554543_at	BC007524	NM_003971 NM_172345	9043	2,07	1,57E-04
RAF1	244373_at	AI740571	NM_002880	5894	2,07	9,16E-04
GFRA2	205721_at	U97145	NM_001495	2675	2,06	4,42E-03
CXCL12	209687_at	U19495	NM_000609 NM_199168	6387	2,04	2,46E-04
MGC34032	235763_at	AA001450	NM_152697	204962	2,04	3,86E-03
AI671885	230494_at	AI671885	XM_379123	400999	2,01	7,81E-03
GPR125	1569542_at	BC020926	NM_145290	166647	1,99	8,83E-03
BF057073	231310_at	BF057073	---	---	1,97	9,44E-04
PGAP1	233479_at	AU148008	NM_024989	80055	1,95	7,98E-03
LOC440265	1569476_at	BC033224	XM_378506	440265	1,95	1,83E-03
TFPI2	209278_s_at	L27624	NM_006528	7980	1,95	3,05E-03
KIAA1713	233536_at	AI202664	XM_290811	80816	1,94	5,70E-05
H37807	241060_x_at	H37807	---	---	1,94	5,73E-03
AA417878	243463_s_at	AA417878	---	---	1,93	4,35E-04
ZNF537	223392_s_at	BF510566	NM_020856	57616	1,93	5,36E-04
PTPRG	204944_at	NM_002841	NM_002841	5793	1,93	4,06E-07
MAOA	204388_s_at	NM_000240	NM_000240	4128	1,92	2,34E-03
TFPI2	209277_at	AL574096	NM_006528	7980	1,91	9,47E-03
ASCL1	213768_s_at	AW950513	NM_004316	429	1,91	9,81E-03
GFM1	232295_at	AK000780	NM_024996	85476	1,90	3,91E-03
AF131796	231916_at	AF131796	---	---	1,90	9,65E-06
SLCO3A1	219229_at	NM_013272	NM_013272	28232	1,89	6,98E-07
FLJ34154	1561130_at	AF086006	NM_173813	283450	1,89	4,96E-03
MSI2	239232_at	AA521410	NM_138962 NM_170721	124540	1,87	7,62E-03
MAOA	212741_at	AA923354	NM_000240	4128	1,87	3,66E-04
PRKCBP1	207130_at	NM_018634	NM_012408 NM_183047 NM_183048	23613	1,87	5,52E-03
PPP3R1	1565811_at	BC033945	NM_000945	5534	1,86	2,12E-03
CUGBP2	202157_s_at	U69546	NM_006561	10659	1,86	4,76E-03
AW024890	229942_at	AW024890	---	---	1,86	2,32E-04
NOS1	239132_at	BE299830	NM_000620	4842	1,85	4,05E-05
AI733341	240911_at	AI733341	---	---	1,83	2,70E-06
MAOA	204389_at	NM_000240	NM_000240	4128	1,83	5,67E-03
AI919519	235092_at	AI919519	---	---	1,83	1,25E-03

HGF	210755_at	U46010	NM_000601 NM_001010931 NM_001010932 NM_001010933 NM_001010934	3082	1,83	4,16E-03
EB-1	227439_at	AI806510	NM_020140 NM_152788 NM_181670	56899	1,83	4,67E-03
NRG3	229233_at	H05240	NM_001010848	10718	1,81	5,10E-03
IREB2	1563130_a_at	AL109710	NM_004136	3658	1,81	4,45E-05
ASCL1	209988_s_at	BC001638	NM_004316	429	1,81	9,72E-03
BF509781	238970_at	BF509781	---	---	1,81	5,78E-03
AI651786	237945_at	AI651786	---	---	1,80	9,11E-04
AW206536	243470_at	AW206536	---	---	1,79	9,87E-03
CAS1	239545_at	AI335004	NM_022900	64921	1,78	2,35E-04
FLJ11259	218627_at	NM_018370	NM_018370	55332	1,78	3,96E-03
TPBG	203476_at	NM_006670	NM_006670	7162	1,78	3,60E-03
IGSF4	244345_at	AI627453	NM_014333	23705	1,78	1,19E-03
LOC441157	1558796_a_at	AL833240	XM_499037	441157	1,78	6,11E-04
C10orf18	216211_at	AL049233	XM_374765	54906	1,78	5,69E-03
TRIM68	219405_at	NM_018073	NM_018073	55128	1,77	9,35E-03
NM_018616	220702_at	NM_018616	---	---	1,76	8,03E-03
SF1	210172_at	D26121	NM_004630 NM_201995 NM_201997 NM_201998	7536	1,76	6,92E-03
AI140305	228849_at	AI140305	---	---	1,73	4,71E-03
BE856929	239349_at	BE856929	---	---	1,73	8,07E-03
CDC23	223651_x_at	BC005258	NM_004661	8697	1,73	3,36E-03
BG542611	1556277_a_at	BG542611	---	---	1,73	3,65E-03
LOC253981	226430_at	AI394438	---	253981	1,72	2,43E-04
FNDC5	226096_at	AI760132	NM_153756	252995	1,72	6,85E-03
VRK1	241737_x_at	T89693	NM_003384	7443	1,72	8,45E-04
PDE6B	243590_at	AA860184	NM_003719	8622	1,71	3,11E-03
SESN3	225123_at	BE883841	NM_144665	143686	1,71	4,09E-04
MAK3	244341_at	AA827728	NM_025146	80218	1,71	1,72E-03
FLJ35740	244297_at	AI806762	NM_147195	253650	1,70	9,74E-03
THOC3	236149_at	AA502999	NM_032361	84321	1,69	6,40E-03
INSM1	206502_s_at	NM_002196	NM_002196	3642	1,69	4,60E-03
SESN3	242899_at	N78412	NM_144665	143686	1,69	1,78E-03
PTGFRN	224950_at	BF476250	NM_020440	5738	1,69	3,70E-03
HIC2	1559600_at	AL831831	NM_015094	23119	1,69	1,03E-03
AI023295	237600_at	AI023295	---	---	1,67	3,22E-03
GLMN	236924_at	AA814383	NM_007070 NM_053274	11146	1,67	2,06E-03

N50083	229110_at	N50083	---	---	1,67	1,06E-03
BG542645	242793_at	BG542645	---	---	1,66	9,11E-03
FLJ37266	228973_at	AA057445	NM_175892	283225	1,65	3,82E-03
AK022258	233286_at	AK022258	---	---	1,64	4,08E-03
FNDC5	226097_at	AI686488	NM_153756	252995	1,64	5,69E-03
JJAZ1	1566191_at	AI907884	NM_015355	23512	1,63	6,56E-03
CNTN1	227202_at	AW072790	NM_001843	1272	1,63	3,78E-03
MYLIP	228098_s_at	AW292746	NM_175038 NM_013262	29116	1,63	2,87E-04
NM_024972	220898_at	NM_024972	---	---	1,63	5,35E-03
AL036662	235984_at	AL036662	---	---	1,62	1,89E-04
TIA1	1558922_at	CA776505	NM_022037	7072	1,62	3,98E-03
MYO6	203216_s_at	NM_004999	NM_022173 NM_004999	4646	1,62	5,80E-04
ZNF537	223393_s_at	AL136805	NM_020856	57616	1,62	7,69E-04
DNAPTP6	244597_at	AA701247	NM_015535	26010	1,61	2,65E-03
PIP5K1A	235646_at	BF515595	NM_003557	8394	1,61	1,66E-03
ANAPC7	225521_at	AL137586	NM_016238	51434	1,61	5,35E-03
AF5Q31	232865_at	N59653	NM_014423	27125	1,60	2,42E-04
C2orf31	221245_s_at	NM_030804	---	81561	1,60	3,45E-03
FAM55C	243011_at	BF317081	NM_145037	91775	1,59	1,18E-03
LHFPL2	212658_at	N66633	NM_005779	10184	1,59	1,64E-03
PSCD3	243752_s_at	AI870144	NM_004227	9265	1,59	2,64E-03
LOC90701	235676_at	BF055352	NM_033280	90701	1,59	6,05E-03
SMAD4	1565703_at	AL832789	NM_005359	4089	1,59	3,91E-03
PITPNB	242074_at	AA833902	NM_012399	23760	1,58	1,84E-03
DKFZp761D221	1569603_at	BC020900	NM_032291	84251	1,57	3,47E-03
MINA	213189_at	BE966695	NM_032778 NM_153182	84864	1,57	9,86E-05
YEATS2	236462_at	AA742310	NM_018023	55689	1,57	6,12E-04
ARIH1	242431_at	AI656728	NM_005744	25820	1,56	7,68E-03
XPO1	235927_at	BE350122	NM_003400	7514	1,56	1,83E-05
SPON1	213994_s_at	AI885290	NM_006108	10418	1,55	3,33E-03
SIMP	238303_at	AW070371	NM_178862	201595	1,55	2,24E-03
KLF12	243089_at	AA551114	NM_007249 NM_016285	11278	1,55	7,90E-03
MAK3	231199_at	AA701676	NM_025146	80218	1,55	2,30E-03
JARID2	232835_at	AA533080	NM_004973	3720	1,55	2,53E-03
H93038	241574_s_at	H93038	---	---	1,54	2,24E-03
TGFBR1	236561_at	AV700621	NM_004612	7046	1,54	4,78E-03
PRSS12	213602_at	AI810767	NM_003619	8492	1,53	6,26E-03
PLCL2	213309_at	AL117515	NM_015184	23228	1,52	6,87E-03
PIAS1	1558418_at	BC017507	NM_016166	8554	1,52	2,09E-03
USP48	229812_at	BE645018	NM_032236	84196	1,51	3,09E-05
SPOCK	202363_at	AF231124	NM_004598	6695	1,51	5,55E-05
MLL3	244010_at	AI057455	NM_021230 NM_170606	58508	1,50	4,50E-03
STRA6	1569335_a_at	BC015881	NM_022369	64220	1,50	2,05E-03
UCHL1	1555834_at	AW974143	NM_004181	7345	1,50	5,86E-03

AK025064	215221_at	AK025064	---	---	1,49	5,96E-03
MINA	213188_s_at	AI823896	NM_032778 NM_153182	84864	1,48	4,75E-05
PSME4	237180_at	T97717	NM_014614	23198	1,48	3,52E-03
SLC4A11	233550_s_at	AL109976	NM_032034	83959	1,48	5,66E-03
H04482	243287_s_at	H04482	---	---	1,48	5,28E-03
REPS1	215201_at	AW166925	NM_031922	85021	1,48	5,00E-03
OAZIN	240231_at	AI742383	NM_015878 NM_148174	51582	1,47	6,87E-03
CBLB	227900_at	AV701750	NM_170662	868	1,47	7,93E-03
SLC17A6	220551_at	NM_020346	NM_020346	57084	1,47	4,11E-04
CUGBP2	202156_s_at	N36839	NM_006561	10659	1,47	2,41E-03
R76828	1558877_at	R76828	---	---	1,46	4,33E-04
C9orf102	1557164_a_at	BM683657	NM_020207	56959	1,46	2,47E-03
CLSTN2	219414_at	NM_022131	NM_022131	64084	1,46	5,74E-03
FAM19A4	242348_at	AA757457	NM_001005527 NM_182522	151647	1,45	2,73E-05
HTR2B	206638_at	NM_000867	NM_000867	3357	1,44	5,90E-03
AW197616	230787_at	AW197616	---	---	1,44	1,22E-03
BC035170	1561079_at	BC035170	---	---	1,44	4,66E-03
CUGBP2	1557422_at	R49146	NM_006561	10659	1,44	7,71E-03
LCRISP1	223475_at	AF142573	NM_031461	83690	1,44	3,45E-03
SNCAIP	219511_s_at	NM_005460	NM_005460	9627	1,44	9,60E-03
RNF34	236288_at	AW572402	NM_025126 NM_194271	80196	1,44	1,55E-03
ALCAM	201951_at	BF242905	NM_001627	214	1,44	1,25E-03
FGD6	1555137_a_at	BC013319	NM_018351	55785	1,43	8,61E-03
AI821477	235985_at	AI821477	---	---	1,43	8,29E-04
SRPK2	239811_at	BF954306	NM_182691 NM_182692	6733	1,43	2,17E-03
CNTN1	227209_at	AI091445	NM_001843 NM_175038	1272	1,43	6,48E-03
PDLIM5	213684_s_at	BF671400	NM_001011513 NM_001011514 NM_001011515 NM_001011516 NM_006457	10611	1,43	4,72E-05
FLJ11710	244646_at	AW972881	---	79904	1,43	6,04E-03
MAPRE2	1564733_at	BC013931	NM_014268	10982	1,43	4,15E-03
DST	1558019_at	BC020911	NM_001723 NM_015548 NM_020388 NM_183380	667	1,42	5,60E-03
SCG-112	241798_at	AI339930	NM_015200	23244	1,42	4,68E-03

SPON1	209436_at	AB018305	NM_006108	10418	1,41	1,28E-03
PPP3R1	241786_at	AI380514	NM_000945	5534	1,41	8,09E-03
ARID1B	1556818_at	BE671639	NM_017519 NM_020732 NM_175863	57492	1,40	1,56E-03
ZA20D1	238994_at	AW022496	NM_020205	56957	1,40	1,24E-03
HIAT1	242374_at	AA747563	NM_033055	64645	1,40	9,78E-04
ZNF503	227195_at	AA603467	NM_032772	84858	1,40	1,14E-04
SMARCC2	1561973_at	AL833124	NM_003075 NM_139067	6601	1,39	4,39E-03
ZNF215	220214_at	NM_013250	NM_013250	7762	1,39	5,26E-03
KIAA0318	238817_at	BF063412	NM_015347	23504	1,39	3,46E-03
RAP80	233596_at	AF113675	NM_016290	51720	1,38	8,59E-03
ACY1L2	225421_at	AI654133	NM_001010853	135293	1,37	9,04E-04
UBE1C	1556338_at	BM353142	NM_003968 NM_198195 NM_198197	9039	1,37	4,28E-03
RASEF	1553186_x_at	NM_152573	NM_152573	158158	1,37	6,41E-03
MDN1	1569484_s_at	AL603301	NM_014611	23195	1,37	1,48E-03
E2-230K	1554814_at	BC007822	NM_022066	63893	1,36	5,24E-03
ZFOC1	1558816_at	BC037793	NM_152437	144348	1,35	1,76E-03
CAPZA2	240146_at	AW418562	NM_006136	830	1,35	1,22E-03
DLEU2	215629_s_at	AA905286	NM_006021	8847	1,35	3,10E-03
CLASP2	1558759_s_at	AA310888	NM_015097	23122	1,34	2,92E-03
KIAA1545	1557539_at	BC008052	XM_495939	57666	1,34	1,63E-03
FLJ45645	243038_at	AW292769	NM_198557	375287	1,34	4,56E-03
MGC34032	1552782_at	AK091400	NM_152697	204962	1,34	1,91E-03
ELOVL7	227180_at	AW138767	XM_371740	79993	1,33	4,90E-04
FLJ12666	215029_at	AL117451	NM_024595	79647	1,32	3,06E-03
AA156721	201952_at	AA156721	---	---	1,31	9,34E-05
IREB2	1555476_at	BC017880	NM_004136	3658	1,31	1,01E-03
SCML1	235652_at	AI431345	NM_006746	6322	1,31	1,08E-03
BTBD3	243462_s_at	BF590303	NM_014962 NM_181443	22903	1,31	1,87E-03
LRRTM1	243330_at	AW304000	NM_178839	347730	1,30	7,44E-03
RNF159	241956_at	AI521883	NM_032373	84333	1,30	2,94E-03
L3MBTL	242637_at	C14069	NM_015478 NM_032107	26013	1,30	2,01E-03
LRRFIP2	232704_s_at	AK025207	NM_006309 NM_017724	9209	1,29	1,87E-03
FLJ40773	1563933_a_at	AK091691	NM_152666	200150	1,29	6,62E-03
N46436	1556568_a_at	N46436	---	---	1,29	3,59E-03
TRIM33	239716_at	AA908970	NM_015906 NM_033020	51592	1,29	6,38E-03
RIP	1556088_at	AK098491	NM_032308	84268	1,29	7,36E-04
AK098258	1564175_at	AK098258	---	---	1,29	9,36E-03

WWOX	1556595_at	BQ025203	NM_016373 NM_018560 NM_130788 NM_130790 NM_130791 NM_130792 NM_130844	51741	1,29	9,57E-03
AW874669	239834_at	AW874669	---	---	1,29	1,39E-03
SYNCRIP	1555427_s_at	AY034482	NM_006372	10492	1,28	1,39E-03
ZNF198	1569091_at	BC039458	NM_003453 NM_197968	7750	1,28	9,19E-03
NOL7	244474_at	BE549780	NM_016167	51406	1,28	9,53E-03
C20orf23	232083_at	AB046810	NM_024704	55614	1,28	6,84E-03
THRAP1	236978_at	N51961	NM_005121	9969	1,28	5,36E-04
KIAA0217	241965_at	BF589232	NM_015155	23185	1,28	7,35E-03
ASXL1	242439_s_at	AI819150	NM_015338	171023	1,27	6,77E-03
ELOVL5	1566079_at	AL833001	NM_021814	60481	1,27	1,08E-03
XPO7	240168_at	AA679589	NM_015024	23039	1,26	3,43E-03
IREB2	1563129_at	AL109710	NM_004136	3658	1,26	2,34E-03
MMD	244523_at	AW104453	NM_012329	23531	1,26	1,24E-06
RASEF	1553185_at	NM_152573	NM_152573	158158	1,26	6,94E-03
ZA20D3	238812_at	AA741296	NM_019006	54469	1,26	5,79E-03
ARFGEF1	236742_at	AA132172	NM_006421	10565	1,25	6,55E-03
CUL3	242362_at	AI797788	NM_003590	8452	1,25	5,38E-03
THOC4	226319_s_at	AF047002	NM_005782	10189	1,25	5,54E-04
KLHL13	227875_at	AB037730	NM_033495	90293	1,25	1,10E-05
TAF15	241885_at	BF431050	NM_003487 NM_139215	8148	1,25	3,79E-03
C18965	242853_at	C18965	XM_379243	401106	1,24	2,00E-03
EZH2	203358_s_at	NM_004456	NM_004456 NM_152998	2146	1,24	4,13E-03
DLEU2	216870_x_at	AF264787	NM_006021	8847	1,24	3,31E-04
CABIN1	1557581_x_at	BC027347	NM_012295	23523	1,23	4,73E-03
HOXD4	205522_at	NM_014621	NM_014621	3233	1,23	7,69E-03
AW157450	235716_at	AW157450	---	---	1,23	1,18E-03
TPARL	1560622_at	AK000203	NM_018475	55858	1,23	3,89E-03
KDELC2	225128_at	AL548941	NM_153705	143888	1,23	6,61E-04
PTPRK	203038_at	NM_002844	NM_002844	5796	1,23	1,53E-03
SFRS2IP	1570507_at	BC020736	NM_004719	9169	1,23	3,26E-03
ZNF326	227660_at	AI057121	NM_181781 NM_182975 NM_182976	284695	1,23	1,88E-03
NM_000575	208200_at	NM_000575	---	---	1,23	1,37E-03
GPI	232002_at	AW843302	NM_000175	2821	1,23	2,05E-03
CAPN1	232012_at	AV691296	NM_005186	823	1,22	3,25E-05
XPO7	235796_at	AI927957	NM_015024	23039	1,22	8,08E-03
PITPNB	239978_at	BF109370	NM_012399	23760	1,22	8,12E-03
DENR	238982_at	AW665791	NM_003677	8562	1,22	1,47E-05
PFKFB3	202464_s_at	NM_004566	NM_004566	5209	1,22	3,62E-04

AA343057	234997_x_at	AA343057	XM_496451	388760	1,21	9,45E-03
RB1CC1	237626_at	AI801666	NM_014781	9821	1,21	5,81E-03
NR2C1	210530_s_at	M21985	NM_003297	7181	1,21	1,06E-06
PLXNA2	213030_s_at	AI688418	NM_025179	5362	1,21	7,50E-03
AI857766	227126_at	AI857766	---	---	1,20	3,82E-05
MYO6	210480_s_at	U90236	NM_004999	4646	1,20	3,13E-03
TH1L	225865_x_at	AJ238374	NM_016397 NM_198976	51497	1,20	3,35E-05
AL044078	221860_at	AL044078	---	---	1,19	1,28E-05
ZGPAT	221848_at	AL121845	NM_032527 NM_181484 NM_181485	84619	1,19	7,13E-04
HGF	209960_at	X16323	NM_000601 NM_001010931 NM_001010932 NM_001010933 NM_001010934	3082	1,18	7,95E-03

MGC47869	243056_at	AI301111	NM_175874	144608	1,18	5,95E-03
NKTR	1557737_s_at	AI880383	NM_005385	4820	1,18	1,36E-03
TRA2A	229574_at	AI268231	NM_013293	29896	1,18	1,72E-03
ITGB5	201125_s_at	NM_002213	NM_002213	3693	1,18	5,48E-04
ARIH1	1558710_at	BI791845	NM_005744	25820	1,18	7,13E-03
GOLGA4	215203_at	AW438464	NM_002078	2803	1,18	3,99E-03
BASP1	202391_at	NM_006317	NM_006317	10409	1,18	3,05E-03
TM4SF14	223314_at	BF025955	NM_030927	81619	1,18	1,52E-03
SYNCRIP	209025_s_at	AF037448	NM_006372	10492	1,17	3,35E-03
TH1L	220607_x_at	NM_016397	NM_016397 NM_198976	51497	1,15	2,89E-04
COBRA1	1556434_at	BQ777552	NM_015456	25920	1,15	3,42E-03
SPATS2	1570130_at	BC032441	NM_023071	65244	1,15	6,79E-03
GATA2	210358_x_at	BC002557	NM_032638	2624	1,15	2,50E-03
MYST3	242480_at	AA868356	NM_006766	7994	1,15	9,06E-03
TH1L	225261_x_at	AJ238376	NM_016397 NM_198976	51497	1,15	2,80E-05
PTK2	241387_at	AW276701	NM_005607 NM_153831	5747	1,14	7,90E-03
C9orf39	1559005_s_at	AK098502	NM_017738	54875	1,14	4,61E-03
SFRS8	240078_at	BG434474	NM_004592 NM_152235	6433	1,14	2,74E-03
TBC1D5	215612_at	AU147983	NM_014744	9779	1,14	2,73E-03
TCTEL1	242109_at	AI038577	NM_006519	6993	1,14	1,48E-06
SMC5L1	1562948_at	BC035661	NM_015110	23137	1,14	9,50E-03
PLS3	201215_at	NM_005032	NM_005032	5358	1,13	6,23E-03
TM4SF14	221002_s_at	NM_030927	NM_030927	81619	1,13	1,20E-03
SSB4	229929_at	AL563476	NM_080862	92369	1,13	8,19E-03

THOC4	226320_at	AF047002	NM_005782	10189	1,13	6,76E-04
EB-1	227440_at	AW005572	NM_020140 NM_152788 NM_181670	56899	1,13	5,86E-03
PCBP2	213517_at	AW103422	NM_005016 NM_031989	5094	1,13	2,39E-05
C9orf100	230522_s_at	BG028209	NM_032818	84904	1,12	5,16E-03
BNC2	235723_at	AA843242	NM_017637	54796	1,12	8,45E-03
UBE1C	1556339_a_at	BM353142	NM_003968 NM_198195 NM_198197	9039	1,12	2,60E-03
C20orf58	228017_s_at	BF593263	NM_152864	128414	1,12	4,82E-03
AW978811	242080_at	AW978811	---	---	1,12	5,08E-03
EXT1	1564378_a_at	AK025101	NM_000127	2131	1,12	4,78E-03
KIAA1423	225127_at	BF217531	XM_376550	57583	1,11	7,59E-05
CCAR1	236566_at	AI291189	NM_018237	55749	1,11	5,91E-03
SMG1 KIAA0220 LOC440345	244766_at	BG180003	NM_014006 NM_015092 XM_496125	23049 283846 440345	1,11	2,54E-03
TMP21	239851_at	AW629289	NM_006827	10972	1,11	9,85E-03
NOS1	207309_at	NM_000620	NM_000620	4842	1,11	4,13E-03
EIF4ENIF1	242983_at	AI806626	NM_019843	56478	1,11	2,41E-03
ANAPC5	239651_at	BE671583	NM_016237	51433	1,11	8,65E-03
FLJ20186	219646_at	NM_017702	NM_017702 NM_207514	54849	1,11	7,86E-03
BF196475	241529_at	BF196475	---	---	1,11	6,33E-03
FRMD4A	208476_s_at	NM_018027	NM_018027	55691	1,11	5,78E-03
SDHA SDHAL2	230077_at	W90764	NM_004168 XM_171032	255812 6389	1,10	2,82E-03
CHCHD3	216170_at	AK025271	NM_017812	54927	1,10	4,90E-03
SLC30A9	237051_at	AI890591	NM_006345	10463	1,10	3,32E-03
ANP32A	235954_at	AA972597	NM_006305	8125	1,10	6,96E-04
AV752058	244574_at	AV752058	---	---	1,09	1,04E-03
CTGLF1	1565620_at	BG621044	NM_133446	119016	1,09	8,36E-03
ZCCHC11	230713_at	BF115786	NM_001009881 NM_001009882 NM_015269	23318	1,09	6,14E-03
KIAA1219	242233_at	AI739332	NM_020336	57148	1,09	6,47E-03
PDGFD	219304_s_at	NM_025208	NM_025208 NM_033135	80310	1,09	1,44E-03
AA743413	236985_at	AA743413	---	---	1,08	9,66E-03
RNF10	237062_at	BE222109	NM_014868	9921	1,08	5,28E-03
ORC6L	219105_x_at	NM_014321	NM_014321	23594	1,08	3,86E-03
TH1L	225006_x_at	AJ238379	NM_016397 NM_198976	51497	1,08	3,76E-05
KIAA2024	1566166_at	AL833423	NM_172070	130507	1,07	9,88E-03
LOC283871	222622_at	BG284709	XM_208887	283871	1,06	3,90E-03

BE856960	242712_x_at	BE856960	---	---	1,06	1,22E-03
RPUSD3	1566603_s_at	AK094587	NM_173659	285367	1,05	1,31E-03
LOC284244	214162_at	AF070541	---	284244	1,05	6,69E-03
AI817960	239649_at	AI817960	---	---	1,05	8,05E-03
TRA2A	213593_s_at	AW976696	NM_013293	29696	1,05	1,05E-03
SBNO1	216161_at	AK024128	NM_018183	55206	1,05	2,06E-03
SIRT2	1558331_at	BG722779	NM_012237 NM_030593	22933	1,05	4,53E-04
AF090944	233995_at	AF090944	---	---	1,05	9,19E-03
C20orf58	230668_at	AI758937	NM_152864	128414	1,04	8,75E-03
HM13	1560297_at	BG928536	NM_030769 NM_178580 NM_178581 NM_178582	61502	1,04	7,20E-03
SLCO3A1	227367_at	AW976431	NM_013272	28232	1,04	1,11E-03
PAN3	239393_at	AW510927	NM_175854	255967	1,04	2,63E-03
CNTN4	229084_at	R42166	NM_175607 NM_175612 NM_175613	152330	1,04	7,84E-03
LOC51760	205613_at	NM_016524	NM_016524	51760	1,04	6,90E-03
APC	216933_x_at	S67788	NM_000038	324	1,04	6,77E-03
H43040	231108_at	H43040	---	---	1,03	6,01E-04
C9orf10	241242_at	BE503118	NM_014612	23196	1,03	9,13E-03
C13orf25	232291_at	AA256157	NM_213723 NM_213724	407975	1,03	4,81E-03
HAN11	233782_at	AU147133	NM_001003725 NM_005828	10238	1,03	2,43E-04
FLJ43654	235376_at	BF125564	NM_198562	375341	1,03	1,61E-03
RTN4	1556049_at	CA428769	NM_007008 NM_020532 NM_153828 NM_207520 NM_207521	57142	1,02	3,35E-03
CSE1L	210765_at	AF053640	NM_001316 NM_177436	1434	1,02	6,67E-05
CBLB	209682_at	U26710	NM_170662	868	1,02	1,33E-06
FLJ12750	236889_at	AI911084	NM_024667	79720	1,02	9,90E-03
PEG10	212094_at	AL582836	XM_496907 XM_499343	23089	1,02	4,05E-03
T40928	241913_at	T40928	XM_498972	441028	1,02	9,84E-03
FLJ11783	220546_at	NM_024891	NM_024891	79951	1,02	9,99E-04
NM_018627	220410_s_at	NM_018627	---	---	1,01	5,37E-03
CSPG6	1556925_at	AL360194	NM_005445	9126	1,01	1,34E-03
DERA	218102_at	NM_015954	NM_015954	51071	1,01	3,80E-03
DLL3	219537_x_at	NM_016941	NM_016941 NM_203486	10683	1,01	2,97E-04
GNOT7	233019_at	AU145061	NM_013354 NM_054026	29883	1,01	2,14E-03

HIVEP2	243254_at	T08739	NM_006734	3097	1,01	2,67E-03
MGC33926	229302_at	AA058832	NM_152390	130733	1,01	3,60E-03
LRRN5	216167_at	AK024867	NM_006338 NM_201630	10446	1,01	6,96E-03
API5	214960_at	AF229253	NM_006595	8539	1,00	5,16E-04
EAF2	219551_at	NM_018456	NM_018456	55840	1,00	5,97E-05
C2orf23	204364_s_at	BE535746	NM_022912	65055	1,00	9,51E-04
EVL	227232_at	T58044	NM_016337	51466	1,00	6,72E-04
MAP4K3	242448_at	AI800895	NM_003618	8491	1,00	4,16E-03
GLS	223080_at	AK025021	NM_014905	2744	1,00	5,50E-03
ST8SIA1	210073_at	L32667	NM_003034	6489	1,00	2,41E-03
SNAG1	226683_at	AU146771	NM_052870	112574	0,99	1,15E-03
TDG	203742_s_at	BF674842	NM_001008411 NM_003211	6996	0,99	1,56E-03
GALNT7	216756_at	AK024995	NM_017423	51809	0,99	7,57E-03
DCP2	244777_at	AA504595	NM_152624	167227	0,99	7,31E-03
HIPK2	224016_at	AF111850	NM_022740	28996	0,99	3,36E-03
BE467787	243835_at	BE467787	---	---	0,99	6,62E-03
C9orf39	239989_at	AW170610	NM_017738	54875	0,99	7,75E-05
AI655229	243497_at	AI655229	---	---	0,99	6,76E-03
WSB1	227501_at	AI377135	NM_015626 NM_134264 NM_134265	26118	0,99	6,53E-03
NM_025120	220728_at	NM_025120	---	---	0,98	1,00E-03
PCBP2	229467_at	AA504356	NM_005016 NM_031989	5094	0,98	8,91E-03
EIF4A1	214805_at	U79273	NM_001416	1973	0,98	7,43E-03
MGEA5	214972_at	AU144791	NM_012215	10724	0,97	7,74E-03
FLJ10579	230843_at	AA482037	NM_018145	55177	0,97	2,54E-03
ZCWPW2	243863_at	BF575233	XM_087384	152098	0,97	4,74E-03
RNF111	241413_at	W80457	NM_017610	54778	0,97	1,29E-03
PLEKHA6	205093_at	NM_014935	NM_014935	22874	0,97	1,50E-04
SEZ6L	207873_x_at	NM_021115	NM_021115	23544	0,97	2,35E-04
FLJ10213	219906_at	NM_018029	NM_018029	55096	0,97	6,80E-03
WTAP	1558783_at	AK024805	NM_004906 NM_152857 NM_152858	9589	0,97	2,62E-04
CTNNB1	242558_at	AW362945	NM_001904	1499	0,96	7,55E-03
AA830545	235730_at	AA830545	---	---	0,96	3,70E-05
MGC33846	231430_at	AW205640	NM_175885	220382	0,95	1,36E-03
ZNF238	207164_s_at	NM_006352	NM_006352 NM_205768	10472	0,95	2,86E-03
AF5Q31	232864_s_at	N59653	NM_014423	27125	0,95	4,59E-04
SFRS2	200753_x_at	BE866585	NM_003016	6427	0,95	2,39E-04
H40696	236122_at	H40696	XM_370722	387921	0,95	4,70E-03
AW971254	222369_at	AW971254	---	---	0,94	4,56E-03
DKFZp547A023	214731_at	AB037854	NM_018704	55917	0,94	7,37E-03
AK022388	233017_x_at	AK022388	---	---	0,94	7,08E-03

PRDX2	215067_x_at	AU147942	NM_005809 NM_181737 NM_181738	7001	0,94	2,97E-03
RET	215771_x_at	X15786	NM_020630 NM_020975	5979	0,94	8,55E-03
ACTR6	239679_at	AI871160	NM_022496	64431	0,94	4,88E-03
HNRPA1	222040_at	AI144007	NM_002136 NM_031157	3178	0,93	4,24E-03
TMEM4	209797_at	BC001027	NM_014255	10330	0,93	5,35E-04
CIAPIN1	230838_s_at	AW771492	NM_020313	57019	0,93	9,30E-04
PRPF4B	202126_at	AA156946	NM_003913 NM_176800	8899	0,93	2,94E-03
ETV3	1552423_at	NM_005240	NM_005240	2117	0,92	5,12E-03
KCNQ1OT1	243435_at	AI023707	---	10984	0,92	5,64E-03
HNRPA2B1	205292_s_at	NM_002137	NM_002137 NM_031243	3181	0,92	7,56E-04
AW138794	227283_at	AW138794	---	---	0,92	1,97E-03
HNRPU	236244_at	AI458297	NM_004501 NM_031844	3192	0,92	8,40E-04
TUBB6	209191_at	BC002654	NM_032525	84617	0,91	2,73E-03
SEZ6L	211894_x_at	AB041736	NM_021115	23544	0,91	9,29E-04
C2orf23	204365_s_at	NM_022912	NM_022912	65055	0,91	3,53E-04
HNRPM	238610_s_at	AI906424	NM_005968 NM_031203	4670	0,91	6,26E-03
NUP210	220035_at	NM_024923	NM_024923	23225	0,91	8,57E-03
RNF130	236292_at	AW196696	NM_018434	55819	0,91	5,09E-03
STMN3	222557_at	AL353715	NM_015894	50861	0,91	1,21E-04
KIAA0907	230028_at	BF508843	NM_014949	22889	0,91	1,57E-04
AI346432	229132_at	AI346432	---	---	0,91	6,45E-03
DLL3	222898_s_at	BE350882	NM_016941 NM_203486	10683	0,90	1,05E-03
CYB561	209164_s_at	BC002976	NM_001915	1534	0,90	8,80E-03
CBWD1 CBWD2 LOC220969 DC36	226193_x_at	AV709992	NM_018491 NM_172003 NM_201453	150472 220869 389760 55871	0,90	5,40E-03
SFRS2	214882_s_at	BG254869	NM_003016	6427	0,90	2,75E-04
AK024901	234326_at	AK024901	---	---	0,90	3,19E-03
RAB12	238714_at	AA504249	XM_113967	201475	0,89	3,77E-03
BC001743	209446_s_at	BC001743	---	---	0,89	2,43E-05
CDK2AP1	201938_at	NM_004642	NM_004642	8099	0,89	4,50E-03
AF5Q31	1555436_a_at	BC025700	NM_014423	27125	0,89	2,72E-03
LOC144997	227289_at	AU119437	---	144997	0,88	6,49E-03
C10orf58	224435_at	BC005871	NM_032333	84293	0,88	3,29E-03
MAP3K13	211083_s_at	Z25428	NM_004721	9175	0,88	1,85E-03
CP110	1569353_at	BC030223	NM_014711	9738	0,88	1,17E-03
NDUFS1	1559691_at	BC032767	NM_005006	4719	0,88	5,67E-03

NUDT9	241489_at	BE671532	NM_024047 NM_198038 NM_198039	53343	0,88	3,25E-03
NFATC2IP	212808_at	AI884627	NM_032815	84901	0,88	1,28E-03
AW444985	243690_at	AW444985	---	---	0,87	3,30E-03
SYT11	232677_at	AU146128	NM_152280	23208	0,87	7,93E-03
PTPN1	202716_at	NM_002827	NM_002827	5770	0,87	7,56E-03
FLJ45983	240827_at	AA846824	NM_207423	399717	0,87	6,25E-03
BM041211	1562062_at	BM041211	---	---	0,87	8,38E-03
UQCRC2	241755_at	AI961429	NM_003366	7385	0,87	1,07E-03
WHSC2	1557300_s_at	AI741292	NM_005663	7469	0,87	7,80E-03
PDE7A	224046_s_at	U67932	NM_002603 NM_002604	5150	0,87	9,76E-03
PHF20	235389_at	BG168139	NM_016436	51230	0,87	1,49E-03
AW973410	244310_at	AW973410	XM_498613	440283	0,87	4,14E-03
FLJ10120	220220_at	NM_018001	---	55073	0,86	4,44E-03
ILF3	208931_s_at	AF147209	NM_004516 NM_012218 NM_153464	3609	0,86	4,15E-04
MARCKS	201670_s_at	M68956	NM_002356	4082	0,86	1,21E-03
U06715	217200_x_at	U06715	---	---	0,86	6,65E-03
182-FIP	224956_at	AI743689	NM_020772	57532	0,85	8,46E-03
FLJ13855	236107_at	AA147920	NM_023079	65264	0,85	4,95E-03
BI496583	1557675_at	BI496583	---	---	0,85	1,81E-03
C10orf58	228155_at	BF512388	NM_032333	84293	0,84	4,87E-03
SEZ6L	216047_x_at	AL050253	NM_021115	23544	0,84	6,17E-04
LOC254057	232370_at	AI635756	---	254057	0,84	3,35E-03
TCF7L2	216511_s_at	AJ270770	NM_030756	6934	0,84	7,95E-03
DKFZP564K1964	223170_at	AF132000	NM_015544	26022	0,84	3,64E-03
SFRS2	200754_x_at	NM_003016	NM_003016	6427	0,83	7,20E-04
AA447714	244047_at	AA447714	---	---	0,83	8,79E-03
MARCKS	201668_x_at	AW163148	NM_002356	4082	0,83	5,34E-03
AF222691	216187_x_at	AF222691	---	---	0,83	8,37E-03
DCL-1	232371_at	AU155401	NM_014880	9936	0,83	8,82E-04
RPS24	1555878_at	AK094613	NM_001026 NM_033022	6229	0,83	7,05E-03
ZNF238	212774_at	AJ223321	NM_006352 NM_205768	10472	0,82	1,69E-03
NKTR	202379_s_at	AI361805	NM_005385	4820	0,82	2,20E-03
KIAA0485	242824_at	AW191647	---	57235	0,82	2,73E-03
CSE1L	201111_at	AF053641	NM_001316 NM_177436	1434	0,82	9,40E-03
NKTR	1557736_at	AI880383	NM_005385	4820	0,82	2,47E-03
MBD2	214397_at	AI827820	NM_003927 NM_015832	8932	0,82	8,51E-03
MCCC1	242223_at	AA505323	NM_020166	56922	0,82	5,18E-04
CREBBP	237239_at	AW183655	NM_004380	1387	0,82	1,36E-03
LOC129285	1554145_a_at	BG040721	NM_152994	129285	0,81	7,02E-03
SEZ6L	213609_s_at	AB023144	NM_021115	23544	0,81	8,59E-03

HNRPM	238611_at	AI906424	NM_005968 NM_031203	4670	0,81	5,61E-03
MYLIP	223129_x_at	T63512	NM_013262	29116	0,81	1,14E-03
AI476542	243032_at	AI476542	---	---	0,81	4,19E-03
HYPB	241456_at	AI866267	NM_012271 NM_014159	29072	0,81	8,29E-03
SNRPB2	1561965_at	BE466925	NM_003092 NM_198220	6629	0,81	8,93E-04
SMARCA4	217656_at	AW128846	NM_003072	6597	0,80	2,21E-03
MRPL4	223742_at	BC000756	NM_015956 NM_146387 NM_146388	51073	0,80	7,99E-05
HS6ST2	1552767_a_at	NM_147174	NM_147174 NM_147175	90161	0,80	2,64E-03
NEURL	243853_at	BF516539	NM_004210	9148	0,80	5,90E-04
SMARCD1	203183_s_at	NM_003076	NM_003076 NM_139071	6602	0,80	2,99E-03
HECTD1	242349_at	AW275658	NM_015382	25831	0,80	7,69E-04
GGA2	213772_s_at	BF196572	NM_015044 NM_138640	23062	0,80	3,58E-03
AA056145	227633_at	AA056145	---	---	0,79	9,47E-04
MAN2A1	235103_at	AA029155	NM_002372	4124	0,79	7,09E-03
SENP3	215114_at	AK000923	NM_015670	26168	0,79	2,65E-09
GULP1	223837_at	BC001103	NM_016315	51454	0,78	2,45E-03
JARID2	203297_s_at	BG029530	NM_004973	3720	0,78	9,88E-04
DNAPTP6	222154_s_at	AK002064	NM_015535	26010	0,78	5,12E-03
VPS29	223026_s_at	AF201946	NM_016226 NM_057180	51699	0,78	9,91E-03
AF279774	216967_at	AF279774	---	---	0,78	1,36E-03
COBLL1	203642_s_at	NM_014900	NM_014900	22837	0,78	1,12E-03
AI041522	228030_at	AI041522	---	---	0,78	4,80E-03
FLJ11029	219392_x_at	NM_018304	NM_018304	55771	0,78	4,83E-03
RNF34	219035_s_at	NM_025126	NM_025126 NM_194271	80196	0,77	2,35E-03
BF056892	229024_at	BF056892	---	---	0,77	3,47E-06
DKFZP564C186	1559139_at	BC009786	NM_015658	26155	0,77	3,20E-03
SFRS1	227164_at	AL521786	NM_006924	6426	0,77	1,00E-03
MR-1	225298_at	AA074597	NM_015488 NM_022572	25953	0,76	4,65E-03
ATP6V0A2	217603_at	AW444520	NM_012463	23545	0,76	2,94E-03
RECQL	210566_s_at	BC001052	NM_002907 NM_032941	5965	0,76	4,23E-03
YWHAB	208743_s_at	BC001359	NM_003404 NM_139323	7529	0,76	4,79E-03
ANKHD1	229457_at	AU148042	NM_017747 NM_017978 NM_024668	54882	0,76	4,26E-03
STRBP	233251_at	AK024960	NM_018387	55342	0,76	3,48E-03
AF147390	1562230_at	AF147390	---	---	0,76	2,73E-09

HIC2	212966_at	AL043112	NM_015094	23119	0,76	4,03E-03
LUC7L2	226758_at	AA043552	NM_016019	51631	0,76	5,54E-03
GNG2	224965_at	AU118419	NM_053064	54331	0,76	4,33E-03
USP7	230761_at	AI972599	NM_003470	7874	0,75	2,83E-03
SH3MD1	213252_at	AI739005	NM_014631	9644	0,75	1,10E-03
TLE4	204872_at	NM_007005	NM_007005	7091	0,75	4,50E-03
AA167167	243684_at	AA167167	---	---	0,75	4,31E-03
SLC25A13	229061_s_at	AW268880	NM_014251	10165	0,75	6,06E-03
NSD1	235760_at	AI421972	NM_022455 NM_172349	64324	0,75	9,51E-03
BTBD14A	243431_at	BF000597	NM_144653	136151	0,75	9,59E-03
AKR1B1	201272_at	NM_001628	NM_001628	231	0,74	2,19E-03
SDS3	233841_s_at	AK026749	NM_022491	64426	0,74	1,60E-04
ANAPC7	225554_s_at	AA131793	NM_016238	51434	0,74	4,31E-03
EPOR	215054_at	H16758	NM_000121	2057	0,74	9,06E-04
KHDRBS3	209781_s_at	AF069681	NM_006558	10656	0,74	6,64E-04
C6orf115	223361_at	AF116682	XM_371848	58527	0,73	1,49E-03
LOC157627	214839_at	AF052108	---	157627	0,73	8,43E-03
HS6ST2	230030_at	AI767756	NM_147174 NM_147175	90161	0,73	3,77E-03
DHX35	218579_s_at	NM_021931	NM_021931	60625	0,73	6,34E-06
AI700633	212812_at	AI700633	---	---	0,73	7,29E-03
ZNF281	222619_at	AU150752	NM_012482	23528	0,73	9,26E-04
NARG1	219158_s_at	NM_025085	NM_057175	80155	0,73	4,16E-03
C5orf13	201309_x_at	U36189	NM_004772	9315	0,73	6,38E-03
PBP	205353_s_at	NM_002567	NM_002567	5037	0,73	5,93E-04
KIAA0220	211996_s_at	BG256504	---	283846	0,72	1,81E-03
MYH10	212372_at	AK026977	NM_005964	4628	0,72	1,71E-03
AU147166	215212_at	AU147166	---	---	0,71	8,93E-03
BTBD3	202946_s_at	NM_014962	NM_014962 NM_181443	22903	0,71	8,99E-04
DNAJC9	213088_s_at	BE551340	NM_015190	23234	0,71	9,31E-03
MAN1A1	208116_s_at	NM_005907	NM_005907	4121	0,71	5,70E-03
ATP5G1	208972_s_at	AL080089	NM_001002027 NM_005175	516	0,71	3,03E-03
PAICS	201013_s_at	AA902652	NM_006452	10606	0,71	2,75E-03
AI378500	229821_at	AI378500	---	---	0,71	3,49E-03
KLHL5	226001_at	AK002174	NM_001007075 NM_199039	51088	0,71	2,63E-03
SFRS9	201698_s_at	NM_003769	NM_003769	8683	0,71	5,14E-04
PABPN1	213046_at	AI130920	NM_004643	8106	0,71	3,81E-04
GARNL1	234923_at	AK022988	NM_014990 NM_194301	253959	0,70	5,70E-03
MAN1A1	221760_at	BG287153	NM_005907	4121	0,70	7,22E-03
C5orf13	201310_s_at	NM_004772	NM_004772	9315	0,70	6,72E-03
NM_031221	208120_x_at	NM_031221	---	---	0,70	4,42E-04
CYHR1	213681_at	AW512817	NM_032687	50626	0,70	4,56E-03

BF437591	222026_at	BF437591	---	---	0,70	7,17E-03
SEZ6L	231650_s_at	BE672217	NM_021115	23544	0,70	9,10E-03
UFD1L	209103_s_at	BC001049	NM_005659	7353	0,70	1,25E-03
H37943	242311_x_at	H37943	---	---	0,70	2,95E-03
ACY1L2	225431_x_at	BE779764	NM_001010853	135293	0,70	3,20E-03
SCC-112	213983_s_at	AW991219	NM_015200	23244	0,70	8,02E-04
RPUSD3	1555916_at	BM670238	NM_173659	285367	0,70	1,32E-05
CCAR1	224736_at	BE617899	NM_018237	55749	0,69	8,03E-03
SNX1	1559154_at	AK098001	NM_003099 NM_148955 NM_152826	6642	0,69	5,03E-03
MGC52282	231638_at	AA400057	NM_178453	124221	0,69	4,60E-03
MAPKAPK3	202788_at	NM_004635	NM_004635	7867	0,69	3,76E-03
HNRPA3	211931_s_at	BG505670	NM_194247	220988	0,69	2,94E-04
AK024881	234723_x_at	AK024881	---	---	0,69	7,45E-03
PCIA1	218260_at	NM_024050	NM_024050	79016	0,69	9,77E-03
ANKRD36	238464_at	AA463221	XM_371640	375248	0,69	2,40E-03
N4BP2	231996_at	AB037834	NM_018177	55728	0,69	1,75E-03
EMID2	229080_at	BE741432	NM_133457	136227	0,68	1,65E-03
FLJ22490	242041_at	AI933671	NM_024790	79848	0,68	7,80E-03
IDH3B	210418_s_at	AF023265	NM_006899 NM_174855 NM_174856	3420	0,68	2,50E-03
MAN2A1	205105_at	NM_002372	NM_002372	4124	0,68	1,85E-03
BF055201	228242_at	BF055201	---	---	0,68	9,05E-03
IDH3B	210014_x_at	AF023266	NM_006899 NM_174855 NM_174856	3420	0,68	2,17E-03
GALNT4	231832_at	AI690347	NM_003774	8693	0,67	7,13E-03
OCIAD1	232644_x_at	AK024302	NM_017830	54940	0,67	5,83E-03
GPR51	211679_x_at	AF095784	NM_005458	9568	0,67	6,98E-03
SRC	213324_at	AK024281	NM_005417 NM_198291	6714	0,67	1,56E-03
PBP	210825_s_at	AF130103	NM_002567	5037	0,67	4,20E-03
THRAP4	213043_s_at	AI023317	NM_014815	9862	0,67	6,87E-04
ATAD3A ATAD3B	1552641_s_at	NM_031921	NM_018188 NM_031921	55210 83858	0,66	7,21E-03
FLJ20364	1559222_at	AA781731	NM_017785	54908	0,66	1,64E-03
TA-PP2C	225204_at	AA521311	NM_139283	160760	0,66	2,71E-03
EIF5A	201123_s_at	NM_001970	NM_001970	1984	0,66	8,31E-04
RECQL	212917_x_at	AI614728	NM_002907 NM_032941	5965	0,66	3,26E-03
ZC3HDC5	1562434_at	AL832312	XM_036115	85451	0,66	7,52E-03
BCR	202315_s_at	NM_004327	NM_004327 NM_021574	613	0,66	3,87E-03
C14orf2	242858_at	BF507638	NM_004894	9556	0,66	1,48E-03
MAP3K13	206249_at	NM_004721	NM_004721	9175	0,66	3,65E-03
SULT1A3	222094_at	AI580112	NM_003166 NM_177552	6818	0,66	3,16E-04

ZNF207	244153_at	AA521438	NM_003457	7756	0,65	8,57E-03
PEX26	219180_s_at	AI817074	NM_017929	55670	0,65	4,16E-03
RAN	200750_s_at	AF054183	NM_006325	5901	0,65	6,43E-03
EIF5A	213753_x_at	BF541557	NM_001970	1984	0,65	1,96E-05
C13orf6	235348_at	AA404347	NM_032859	84945	0,65	2,02E-03
EWSR1	210012_s_at	BC000527	NM_005243 NM_013986	2130	0,65	4,34E-03
SPG7	230885_at	BE670386	NM_003119 NM_199367	6687	0,65	7,60E-03
SCLY	59705_at	AA911739	NM_016510	51540	0,65	9,03E-03
KCTD10	223208_at	AF113208	NM_031954	83892	0,64	1,07E-04
FLJ13149	219016_at	NM_021826	NM_021826	60493	0,64	7,47E-04
ZNF217	203739_at	NM_006526	NM_006526	7764	0,64	2,22E-03
GGA2	208913_at	AA868560	NM_015044 NM_138640	23062	0,64	4,26E-03
DST	1560296_at	AV702787	NM_001723 NM_015548 NM_020388 NM_183380	667	0,64	8,16E-03
UBQLN1	222989_s_at	NM_013438	NM_013438 NM_053067	29979	0,64	9,49E-03
TOMM40	202264_s_at	NM_006114	NM_006114	10452	0,63	5,40E-03
VTI1A	235034_at	AW194969	NM_145206	143187	0,63	9,95E-03
TMEM33	222642_s_at	BC000948	NM_018126	55161	0,63	6,62E-03
KIAA1219	221738_at	BG236163	NM_020336	57148	0,63	1,93E-03
RPL23	215224_at	AK025200	NM_000978	9349	0,63	7,04E-04
ZNF43	222136_x_at	AK022905	NM_003423	7594	0,63	4,57E-03
BE671123	235798_at	BE671123	---	---	0,63	8,79E-03
WDR17	1552430_at	NM_170710	NM_170710 NM_181265	116966	0,63	5,45E-04
FUBP1	212847_at	AL036840	NM_003902	8880	0,63	6,95E-03
MBTD1	207115_x_at	NM_017643	NM_017643	54799	0,63	7,84E-03
PHC2	1557852_at	AW418842	NM_004427 NM_198040	1912	0,62	8,02E-03
AP1S2	228415_at	AA205444	NM_003916	8905	0,62	8,44E-03
GPR125	210473_s_at	M37712	NM_145290	166647	0,62	6,47E-03
SFRS6	208804_s_at	AL031681	NM_006275	6431	0,62	3,30E-03
AI216567	236754_at	AI216567	---	---	0,62	4,60E-03
C15orf25	220071_x_at	NM_018097	NM_018097	55142	0,62	9,64E-03
CDH2	203441_s_at	NM_001792	NM_001792	1000	0,62	5,11E-03
MRPL35	222775_s_at	AK026220	NM_016622 NM_145644	51318	0,62	1,89E-03
CNP	208912_s_at	BC001362	NM_033133	1267	0,62	3,84E-03
FLJ20331	218577_at	NM_017768	NM_017768	55631	0,62	6,26E-03
FLJ21415	218867_s_at	NM_024738	NM_024738	79794	0,62	3,36E-03
AF336662	224268_x_at	AF336662	---	---	0,62	3,59E-03

SSBP3	223635_s_at	BC003605	NM_001009955 NM_018070 NM_145716	23648	0,62	2,27E-03
ATF7IP	231825_x_at	AK025060	NM_018179	55729	0,62	7,81E-03
TOP1	208901_s_at	J03250	NM_003286	7150	0,61	6,28E-04
SYNCRIP	209024_s_at	AI472757	NM_006372	10492	0,61	1,15E-03
DHX30	239772_x_at	AI368527	NM_014966 NM_138614 NM_138615	22907	0,61	1,59E-04
BE676277	212829_at	BE676277	---	---	0,61	1,63E-03
FBXL10	226215_s_at	AI989996	NM_001005366 NM_032590	84678	0,61	7,38E-03
KIAA0251	1555347_at	BC033748	NM_015027	23042	0,61	2,52E-03
RBM14	204178_s_at	NM_006328	NM_006328	10432	0,61	3,59E-05
EXOSC1	1559044_at	BC012536	NM_016046	51013	0,61	7,00E-04
KIAA0992	234135_x_at	AK021652	NM_016081	23022	0,60	8,94E-03
EIF5A	201122_x_at	BC000751	NM_001970	1984	0,60	1,14E-03
R26456	243135_x_at	R26456	---	---	0,60	5,74E-03
TMEM33	218465_at	NM_018126	NM_018126	55161	0,60	8,99E-03
SFRS1	201741_x_at	M69040	NM_006924	6426	0,60	1,36E-03
RAB11FIP3	214999_s_at	AW243089	NM_014700	9727	0,60	1,50E-04
DDX46	228039_at	AI765169	NM_014829	9879	0,60	2,91E-03
HNRPU	200593_s_at	BC003621	NM_004501 NM_031844	3192	0,60	1,26E-05
HNRPU	200594_x_at	NM_004501	NM_004501 NM_031844	3192	0,59	1,74E-04
GNG12	212294_at	BG111761	NM_018841	55970	0,59	6,29E-03
ARS2	201680_x_at	NM_015908	NM_015908 NM_182800	51593	0,59	2,20E-04
FLJ37078	235880_at	BF593867	NM_153043	222183	0,59	7,82E-05
GPR51	209990_s_at	AF056085	NM_005458	9568	0,59	7,76E-03
MARCKS	201669_s_at	NM_002356	NM_002356	4082	0,59	4,74E-05
MAN2A1	226536_at	AV700323	NM_002372	4124	0,59	4,65E-03
HCFC1	202474_s_at	NM_005334	NM_005334	3054	0,59	2,12E-03
FLJ35709	242540_at	AI911330	NM_173589	283294	0,58	5,90E-03
MYO1B	212365_at	BF215996	NM_012223	4430	0,58	6,28E-04
PPP2CA	208652_at	BC000400	NM_002715	5515	0,58	3,88E-03
CDC5L	209055_s_at	AW268817	NM_001253	988	0,58	2,61E-04

Tabla 12. Expresión genética disminuida en las líneas celulares H1 y BB10 en comparación con la línea celular SIMa en estado diferenciado usando análisis de micromatriz

Símbolo del gen	ID del conjunto de sondas	ID Pública representativa	ID de transcripción RefSec	ID de Gen Entrez	Proporción Log2	valor p
CYTL1	219837_s_at	NM_018659	NM_018659	54360	-6,94	6,41E-06
GNAS	217057_s_at	AF107846	NM_000516 NM_016592 NM_080425 NM_080426	2778	-5,47	4,18E-03
CYGB	226632_at	AL513673	NM_134268	114757	-4,81	3,60E-03
TNFRSF10D	227345_at	AI738556	NM_003840	8793	-4,68	2,31E-06
ECEL1	219914_at	NM_004826	NM_004826	9427	-4,67	3,83E-05
SYT13	226086_at	AB037848	NM_020826	57586	-4,06	1,83E-04
TMIE	1553601_a_at	NM_147196	NM_147196	259236	-3,86	6,07E-05
NNAT	204239_s_at	NM_005386	NM_005386 NM_181689	4826	-3,63	5,67E-07
CNGA3	207261_at	NM_001298	NM_001298	1261	-3,76	4,84E-04
AU157716	227051_at	AU157716	---	---	-3,75	4,31E-03
AF150317	243111_at	AF150317	---	---	-3,69	9,83E-04
ASAM	226834_at	BG112263	NM_024769	79827	-3,61	5,78E-03
LOC254128	1557059_at	AK096264	---	254128	-3,51	1,95E-07
LOC339290	228160_at	AI433706	XM_375527	339290	-3,50	6,83E-05
FUCA2	223120_at	BC003060	NM_032020	2519	-3,47	8,50E-03
STX3A	209238_at	BE966922	NM_004177	6809	-3,45	8,83E-03
CYGB	1553572_a_at	NM_134268	NM_134268	114757	-3,43	4,93E-06
EDG7	231192_at	AW274018	NM_012152	23566	-3,39	1,39E-03
HTATIP2	207180_s_at	NM_006410	NM_006410	10553	-3,36	4,96E-04
HTATIP2	209448_at	BC002439	NM_006410	10553	-3,38	3,60E-04
LMCD1	218574_s_at	NM_014583	NM_014583	29995	-3,34	6,84E-03
BACE2	217867_x_at	NM_012105	NM_012105 NM_138991 NM_138992	25825	-3,33	5,05E-04
FLJ46860	228538_at	BE671164	NM_207404	389114	-3,28	4,62E-06
EDG7	220816_at	NM_012152	NM_012152	23566	-3,28	2,18E-03
CDC42EP1	204693_at	NM_007061	NM_007061 NM_152243	11135	-3,25	9,63E-03
TCEAL2	211276_at	AF063606	NM_080390	140597	-3,25	3,45E-04
MEOX2	206201_s_at	NM_005924	NM_005924	4223	-3,23	2,59E-06
FGF13	205110_s_at	NM_004114	NM_004114 NM_033642	2258	-3,22	4,26E-05
IGFBP7	201163_s_at	NM_001553	NM_001553	3490	-3,17	3,25E-03
BACE2	222446_s_at	AF178532	NM_012105 NM_138991 NM_138992	25825	-3,16	1,05E-04
SLC35F3	229065_at	BF966270	NM_173508	148641	-3,14	1,47E-06
TncRNA	224565_at	BE675516	---	283131	-3,11	3,26E-03
LGALS3 GALIG	208949_s_at	BC001120	NM_002306 NM_194327	3958 81625	-3,08	1,25E-03

HSPA1A	200799_at	NM_005345	NM_005345	3303	-3,07	6,70E-03
AW136654	240802_at	AW136654	---	---	-3,06	1,56E-03
LOC56901	218484_at	NM_020142	NM_020142	56901	-3,02	3,26E-03
MMP14	202827_s_at	AU149305	NM_004995	4323	-3,01	1,34E-05
FLJ20701	219093_at	NM_017933	NM_017933	55022	-2,99	6,11E-03
CAP2	212554_at	N90755	NM_006366	10486	-2,95	3,40E-03
BF941609	240218_at	BF941609	---	---	-2,91	1,65E-08
SPINT2	210715_s_at	AF027205	NM_021102	10653	-2,90	6,36E-06
BG325630	234973_at	BG325630	---	---	-2,90	2,55E-03
DKFZp313N0621	1555905_a_at	AI147556	NM_173826	285343	-2,87	1,28E-04
NPY	206001_at	NM_000905	NM_000905	4852	-2,85	5,26E-03
CYP2E1	1431_at	J02843	NM_000773	1571	-2,75	3,27E-03
HHLA3	220387_s_at	NM_007071	NM_007071	11147	-2,72	6,75E-04
IL13RA2	206172_at	NM_000640	NM_000640	3598	-2,66	6,71E-05
FLJ31295	226509_at	AV700302	NM_152320	121274	-2,65	7,10E-04
TncRNA	224566_at	AI042152	---	283131	-2,65	1,05E-04
DKFZP564I0422	223588_at	AL136607	NM_031435	83591	-2,64	1,28E-05
IGSF4D	1552754_a_at	AA640422	NM_153184	253559	-2,64	1,95E-03
PRKACB	235780_at	BE622723	NM_002731 NM_182948 NM_207578	5567	-2,63	2,35E-03
GNAS	214157_at	AA401492	NM_000516 NM_016592 NM_080425 NM_080426	2778	-2,61	1,23E-04
AW770245	236513_at	AW770245	---	---	-2,60	8,47E-05
LGI1	206349_at	NM_005097	NM_005097	9211	-2,60	8,58E-04
AI810266	235456_at	AI810266	---	---	-2,58	5,24E-03
HIST1H2BD	209911_x_at	BC002842	NM_021063 NM_138720	3017	-2,55	2,10E-03
AL353759	215071_s_at	AL353759	---	---	-2,51	9,79E-04
LOC339290	215283_at	U79248	XM_375527	339290	-2,51	3,84E-04
SLC16A3	202856_s_at	NM_004207	NM_004207	9123	-2,51	8,97E-03
LGALS1	201105_at	NM_002305	NM_002305	3956	-2,49	4,79E-03
N92599	241421_at	N92599	---	---	-2,47	1,03E-04
ECHDC3	219298_at	NM_024693	NM_024693	79746	-2,47	7,27E-04
NEBL	203961_at	AL157398	NM_006393 NM_213569	10529	-2,43	4,07E-04
RAC2	207418_s_at	NM_002872	NM_002872	5880	-2,42	2,93E-03
BF672306	229189_s_at	BF672306	---	---	-2,42	1,43E-03
CYP2E1	209975_at	AF182276	NM_000773	1571	-2,41	4,83E-03
NEBL	203962_s_at	NM_006393	NM_006393 NM_213569	10529	-2,40	9,78E-04
BE045392	243028_x_at	BE045392	---	---	-2,40	3,93E-03
LOC339290	217506_at	H49382	XM_375527	339290	-2,38	1,30E-05
PPAPDC1	236044_at	BF130943	XM_113641	196051	-2,35	1,18E-04
CYP2E1	209976_s_at	AF182276	NM_000773	1571	-2,34	7,08E-03
ASAM	228082_at	BF056275	NM_024769	79827	-2,32	6,80E-04

ICAM2	204683_at	NM_000873	NM_000873	3384	-2,32	7,89E-03
MEGF11	1552439_s_at	NM_032445	NM_032445	84465	-2,31	2,69E-03
CDS1	226185_at	AK026697	NM_001263	1040	-2,31	4,59E-05
ADARB1	203865_s_at	NM_015833	NM_001112 NM_015833 NM_015834	104	-2,30	2,34E-03
ELMO1	204513_s_at	NM_014800	NM_014800 NM_130442	9844	-2,30	9,13E-03
BC039553	1559544_s_at	BC039553	---	---	-2,29	2,32E-03
IGFBP5	211959_at	AW007532	NM_000599	3488	-2,27	8,27E-03
C6orf168	227834_at	AL589605	XM_371849	167838	-2,22	5,80E-03
AI826125	229866_at	AI826125	---	---	-2,20	1,50E-04
NLF1	241031_at	BE218239	NM_207322	145741	-2,19	3,17E-03
C6orf154	235935_at	AI539370	XM_168060	221424	-2,18	8,19E-04
GAL	214240_at	AL556409	NM_015973	51083	-2,17	3,60E-03
CFC1	223753_s_at	AF312769	NM_032545	55997	-2,17	1,16E-04
LOC344405	237291_at	AI695007	XM_293034	344405	-2,16	1,63E-03
PTN	211737_x_at	BC005916	NM_002825	5764	-2,13	4,30E-04
PTGER2	206631_at	NM_000956	NM_000956	5732	-2,12	3,45E-05
DKFZp761O0113	207797_s_at	NM_018409	NM_018409	55805	-2,12	1,51E-03
C1GALT1C1	238989_at	BF749723	NM_001011551 NM_152692	29071	-2,11	6,52E-04
AA757630	236724_at	AA757630	---	---	-2,08	7,95E-06
PDLIM3	209621_s_at	AF002280	NM_014476	27295	-2,08	9,67E-03
KCNMA1	221584_s_at	U11058	NM_002247	3778	-2,08	1,62E-04
TSAP6	218424_s_at	NM_018234	NM_001008410 NM_018234 NM_182915	55240	-2,07	6,98E-03
ST3GAL3	1555702_a_at	AF425866	NM_006279 NM_174963 NM_174964 NM_174965 NM_174966 NM_174967 NM_174968 NM_174969 NM_174970 NM_174971 NM_174972	6487	-2,03	6,54E-03
ZNF346	232753_at	AU147613	NM_012279	23567	-2,03	2,80E-04
SYT5	206161_s_at	AI659957	NM_003180	6861	-2,02	8,93E-03
HEBP2	203430_at	NM_014320	NM_014320	23593	-2,02	4,86E-05
C9orf19	225604_s_at	AA284532	NM_022343	152007	-2,02	1,60E-03
AKAP12	227529_s_at	BF511276	NM_005100 NM_144497	9590	-2,02	6,85E-05
FLJ20152	218532_s_at	NM_019000	NM_019000	54463	-2,01	2,04E-03
SYNPR	230303_at	H11380	NM_144642	132204	-1,99	7,36E-03

UBE2D3	230171_at	AW662789	NM_003340 NM_181886 NM_181887 NM_181888 NM_181889 NM_181890 NM_181891 NM_181892 NM_181893	7323	-1,97	7,18E-06
STAC2	228888_at	AI821472	NM_198993	342667	-1,96	4,27E-04
BE894882	235681_at	BE894882	---	---	-1,95	5,54E-03
AKAP12	210517_s_at	AB003476	NM_005100 NM_144497	9590	-1,94	6,61E-05
ZNF91	238466_at	R43486	NM_003430	7644	-1,93	2,26E-05
HIST1H2BK	209806_at	BC000893	NM_080593	85236	-1,92	1,28E-04
BF432875	235782_at	BF432875	XM_497668	388620	-1,91	5,20E-03
TMEM4	202857_at	NM_014255	NM_014255	10330	-1,91	5,19E-03
FCRH1	243968_x_at	AI572979	NM_052938	115350	-1,90	4,72E-04
AKAP12	227530_at	BF511276	NM_005100 NM_144497	9590	-1,89	1,05E-04
COL16A1	204345_at	NM_001856	NM_001856	1307	-1,89	4,40E-03
FLJ32752	229631_at	AL040892	NM_144666	144132	-1,89	3,14E-03
GPX7	213170_at	AA406605	NM_015696	2882	-1,89	3,82E-04
BF000047	235736_at	BF000047	---	---	-1,88	9,64E-03
FLJ25952	243786_at	AA454190	NM_153251	253832	-1,87	9,52E-05
ARTS-1	214012_at	BE551138	NM_016442	51752	-1,87	5,76E-03
RAC2	213603_s_at	BE138888	NM_002872	5880	-1,86	2,55E-03
IL7	206693_at	NM_000880	NM_000880	3574	-1,86	7,63E-03
B3GNT5	225612_s_at	BE672260	NM_032047	84002	-1,86	1,01E-03
BCL2	203685_at	NM_000633	NM_000633 NM_000657	596	-1,85	3,00E-03
ZAP128	202982_s_at	NM_006821	NM_006821	10965	-1,84	2,07E-03
AF085995	1561759_at	AF085995	---	---	-1,84	4,44E-04
UCN	206072_at	NM_003353	NM_003353	7349	-1,84	1,79E-04
CDH10	220115_s_at	NM_006727	NM_006727	1008	-1,83	1,73E-03
BF114967	231067_s_at	BF114967	---	---	-1,83	6,70E-06
ADAMTS1	222162_s_at	AK023795	NM_006988	9510	-1,82	1,09E-04
PPFIA4	214978_s_at	AK023365	NM_015053	8497	-1,82	6,27E-03
BE674309	230913_at	BE674309	---	---	-1,81	1,25E-03
AL355688	232081_at	AL355688	---	---	-1,80	1,15E-03
AI698684	1558626_at	AI698684	---	---	-1,78	3,33E-03
PRPH	213847_at	NM_006262	NM_006262	5630	-1,78	3,01E-03
PTGES	210367_s_at	AF010316	NM_004878 NM_198797	9536	-1,78	4,71E-06
HPCAL1	205462_s_at	NM_002149	NM_002149 NM_134421	3241	-1,77	3,68E-03
INSIG1	229370_at	BF507344	NM_005542 NM_198336 NM_198337	3638	-1,77	3,55E-04

RAB6B	221792_at	AW118072	NM_016577	51560	-1,77	1,12E-04
AI733281	239994_at	AI733281	---	---	-1,75	1,40E-03
NDFIP2	1568807_a_at	AI301081	NM_019080	54602	-1,75	2,04E-04
KIAA1598	221802_s_at	AU157109	NM_018330	57698	-1,74	1,10E-03
CAP2	212551_at	NM_006366	NM_006366	10486	-1,74	7,36E-03
TICAM2	228234_at	AI423165	NM_021649	353376	-1,73	1,46E-03
DSCAM	237268_at	BE503065	NM_001389 NM_206887	1826	-1,73	5,66E-04
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AL833383	1563776_at	AL833383	---	---	-1,71	6,57E-06
C21orf109	1553606_a_at	NM_138966	---	163629	-1,70	9,95E-03
FLJ35390	1569089_a_at	BC024303	---	255031	-1,70	2,94E-03
AF052119	214821_at	AF052119	---	---	-1,69	6,58E-04
M160	223655_at	AF264014	NM_174941	283316	-1,69	9,95E-03
AI588962	230477_at	AI588962	---	---	-1,69	8,76E-05
DKFZp313N0621	1555906_s_at	AI147556	NM_173826	285343	-1,69	2,73E-04
DRD1IP	219896_at	NM_015722	NM_015722	50632	-1,69	4,68E-03
DKFZp313N0621	226688_at	AW003508	NM_173826	285343	-1,68	8,18E-03
AW450420	236373_at	AW450420	---	---	-1,66	8,61E-03
LOC133308	1564746_at	BC009732	NM_178833	133308	-1,65	1,14E-04
AL037414	230055_at	AL037414	---	---	-1,63	9,73E-05
RGAG4	227823_at	BE348679	XM_291322	340526	-1,63	4,87E-05
APOBEC3G	204205_at	NM_021822	NM_021822	60489	-1,62	9,31E-03
BTN3A3	38241_at	U90548	NM_006994 NM_197974	10384	-1,62	2,24E-03
LOC133308	229491_at	BF433180	NM_178833	133308	-1,61	8,27E-04
C21orf66	239407_at	AI793248	NM_013329 NM_016631 NM_058191 NM_145328	94104	-1,61	6,82E-03
DKFZp761N1114	229254_at	BE550027	NM_181644	148808	-1,60	3,14E-03
DSCAM	211484_s_at	AF023450	NM_001389 NM_206887	1826	-1,60	1,94E-04
ADAMTS1	222486_s_at	AF060152	NM_006988	9510	-1,59	4,21E-03
LOC286052	241370_at	AA278233	---	286052	-1,59	8,30E-05
MGC40157	239754_at	BE671886	NM_152350	125144	-1,59	9,45E-03
ZNF571	206648_at	NM_016536	NM_016536	51276	-1,59	1,41E-03
LIPT1	242053_at	AW665279	NM_015929 NM_145196 NM_145197 NM_145198 NM_145199	51601	-1,59	3,26E-04
FBI4	238081_at	AI694300	NM_205857	404201	-1,58	1,29E-03
FLJ11286	53720_at	AI962559	NM_018391	55337	-1,58	1,79E-03
FLJ30294	1553301_a_at	NM_144632	NM_144632	130827	-1,57	1,18E-04
AFFX-HUMRGE/M10098_M	AFFX-HUMRGE/M10098_M_at	AFFX-HUMRGE/M10098_M	---	---	-1,57	8,64E-03

HADHA	232590_at	AK025919	NM_000182	3030	-1,57	4,01E-03
NEDL1	243743_at	AI373512	NM_015052	23072	-1,56	9,50E-04
BF114745	235459_at	BF114745	---	---	-1,56	1,20E-03
FLJ13614	226521_s_at	AK023676	NM_139076	84142	-1,55	2,64E-03
AI276956	230766_at	AI276956	---	---	-1,54	4,30E-03
AI765942	243914_at	AI765942	---	---	-1,54	6,05E-03
TBC1D10	226613_at	AI742029	NM_031937	83874	-1,53	5,51E-03
IL10RB	209575_at	BC001903	NM_000628	3588	-1,53	1,40E-05
GLT25D2	209883_at	AF288389	NM_015101	23127	-1,52	3,20E-05
AI971535	229626_at	AI971535	XM_370691	387856	-1,52	8,91E-03
FLJ13614	233543_s_at	AK021562	NM_139076	84142	-1,51	9,66E-03
BF432855	237364_at	BF432855	---	---	-1,51	2,88E-05
AI590198	243418_at	AI590198	---	---	-1,50	5,83E-03
B7	206076_at	NM_006992	NM_006992 NM_201650	10233	-1,50	3,23E-03
PDGFRB	202273_at	NM_002609	NM_002609	5159	-1,49	1,88E-03
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GPR123	239221_at	AI884909	NM_032422	84435	-1,48	1,25E-03
C10orf57	222545_s_at	AA029276	NM_025125	80195	-1,48	3,36E-03
HPCAL1	212552_at	BE617588	NM_002149 NM_134421	3241	-1,48	9,71E-04
LOC284361	229289_at	AL517395	NM_175063 NM_206538	284361	-1,48	2,00E-03
PDE4DIP	213388_at	H15535	NM_001002810 NM_001002811 NM_001002812 NM_014644 NM_022359	9659	-1,47	1,48E-03
LOC441422	236453_at	AW243154	XR_000264	441422	-1,47	2,36E-05
AA976778	230679_at	AA976778	---	---	-1,46	1,46E-05
FBI4	241401_at	BG496631	NM_205857	404201	-1,46	1,53E-03
C14orf149	227699_at	BF511003	NM_144581	112849	-1,45	1,61E-03
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AI758408	227235_at	AI758408	---	---	-1,45	1,51E-03
TMEM5	204808_s_at	NM_014254	NM_014254	10329	-1,44	3,94E-03
BF111884	230491_at	BF111884	---	---	-1,44	3,82E-04
COL27A1	225293_at	AK021957	NM_032888	85301	-1,44	6,78E-03
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PTN	209466_x_at	M57399	NM_002825	5764	-1,43	9,60E-04
COL6A1	213428_s_at	AA292373	NM_001848	1291	-1,43	7,05E-03
DKFZp313N062 1	241666_at	BG493222	NM_173826	285343	-1,43	8,80E-04
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DKFZP434I071 4	231954_at	AL137273	---	54553	-1,42	2,11E-03
AI927692	228528_at	AI927692	---	---	-1,41	9,58E-04
SH3GL2	205751_at	NM_003026	NM_003026	6456	-1,41	1,80E-05
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LGALS3BP	200923_at	NM_005567	NM_005567	3959	-1,40	1,13E-05
AI796536	229810_at	AI796536	---	---	-1,40	2,02E-03
DUSP22	226440_at	BE222746	NM_020185	56940	-1,40	2,32E-03
DUSP16	224336_s_at	AB052156	NM_030640	80824	-1,39	1,91E-03
BF591692	231532_at	BF591692	---	---	-1,39	3,15E-04
CAMK2D	228555_at	AA029441	NM_001221 NM_172115 NM_172127 NM_172128	817	-1,39	2,14E-04
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DISP1	226184_at	AK023679	NM_032890	84976	-1,39	2,54E-05
MAP3K5	203836_s_at	D84476	NM_005923	4217	-1,39	1,24E-03
H46176	237083_at	H46176	---	---	-1,38	8,44E-03
RPL37	224767_at	AL044126	NM_000997	6167	-1,37	1,60E-03
TIMP1	201666_at	NM_003254	NM_003254	7076	-1,37	7,35E-03
PTGES	207388_s_at	NM_004878	NM_004878 NM_198797	9536	-1,37	6,78E-03
SCRG1	205475_at	NM_007281	NM_007281	11341	-1,37	1,72E-03
LOC153682	232794_at	AL137383	---	153682	-1,36	2,78E-04
LOC146174	230721_at	BF436957	NM_173501	146174	-1,36	1,19E-04
DUSP22	218845_at	NM_020185	NM_020185	56940	-1,36	3,43E-06
PH-4	222125_s_at	BC000580	NM_017732 NM_177938 NM_177939	54681	-1,35	5,67E-04
DJ462O23.2	225876_at	T84558	NM_020448	57185	-1,35	1,26E-03
CDKN2A	209644_x_at	U38945	NM_000077 NM_058195 NM_058197	1029	-1,35	1,67E-04
DNER	226261_at	BF059512	NM_139072	92737	-1,35	1,29E-04
ANKH	220076_at	NM_019847	NM_054027	56172	-1,34	4,18E-03
TBC1D10	233528_s_at	AC004997	NM_031937	83874	-1,34	1,10E-03
C1orf21	221272_s_at	NM_030806	NM_030806	81563	-1,34	5,15E-04
NMB	205204_at	NM_021077	NM_021077 NM_205858	4828	-1,33	1,42E-04
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BE672499	230962_at	BE672499	---	---	-1,32	7,98E-03
C21orf57	227421_at	BF026326	NM_001006114 NM_058181	54059	-1,31	2,23E-06
C1orf21	223127_s_at	AW003850	NM_030806	81563	-1,31	2,69E-03
LOC91526	228471_at	AA744636	NM_153697	91526	-1,31	6,93E-03

FHL2	202949_s_at	NM_001450	NM_001450 NM_201555 NM_201556 NM_201557	2274	-1,31	1,03E-03
NM_024599	219202_at	NM_024599	---	---	-1,31	6,35E-03
C10orf57	218174_s_at	NM_025125	NM_025125	80195	-1,31	7,96E-03
LOC196394	226258_at	BG031897	NM_207337	196394	-1,30	8,09E-04
AK001829	232594_at	AK001829	XM_498704	440498	-1,30	2,12E-03
BE551142	241091_at	BE551142	XM_497668	388620	-1,29	2,90E-03
ZFP28	234300_s_at	AF226995	NM_020828	140612	-1,29	6,22E-04
BE046461	215303_at	BE046461	---	---	-1,29	9,65E-03
PCDHAC2	224539_s_at	AF152474	NM_018899 NM_031883	56134	-1,28	4,06E-03
RPL37	224763_at	BF724210	NM_000997	6167	-1,28	6,11E-03
AI631072	228638_at	AI631072	---	---	-1,28	1,12E-03
MGC39821	1555363_s_at	BC034236	XM_498465 XM_499595	284440	-1,28	1,45E-03
ATP6V1E2	1552286_at	NM_080653	NM_080653	90423	-1,28	2,19E-03
DTX3L	225415_at	AA577672	NM_138287	151636	-1,26	6,35E-03
ZNF258	213698_at	AI805560	NM_007167 NM_145310	9204	-1,26	4,04E-03
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RFX2	226872_at	AK024288	NM_000635 NM_134433	5990	-1,25	5,59E-03
LOC402524	242206_at	AW590588	XM_379850	402524	-1,25	2,69E-04
NEFH	33767_at	X15306	NM_021076	4744	-1,25	4,29E-03
HRMT1L1	228722_at	AI928367	NM_001535 NM_206962	3275	-1,25	1,86E-03
AI963605	230269_at	AI963605	---	---	-1,24	2,72E-03
NDUFV3	226616_s_at	NM_021075	NM_001001503 NM_021075	4731	-1,24	6,22E-04
NOTCH4	205247_at	AI743713	NM_004557	4855	-1,24	2,38E-03
LOC401321	1560371_at	BI823265	XM_379483 XM_380099	401321	-1,24	3,08E-03
SMPD1	209420_s_at	M59916	NM_000543 NM_001007593	6609	-1,24	2,86E-03
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BRUNOL6	227775_at	BE467313	NM_052840	60677	-1,24	2,38E-04
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PHLDB3	1557948_at	BC007947	NM_198850	284345	-1,23	5,46E-04
PLRG1	227246_at	BF438014	NM_002669	5356	-1,23	4,56E-03
C9orf19	225602_at	H92988	NM_022343	152007	-1,23	4,21E-03
MGC16037	229050_s_at	AL533103	---	84973	-1,23	9,30E-03
PLP2	201136_at	NM_002668	NM_002668	5355	-1,21	2,30E-03

LOC91526	226641_at	AU157224	NM_153697	91526	-1,21	9,94E-03
ZNF404	239043_at	AA084273	XM_292765	342908	-1,21	8,85E-04
CNN1	203951_at	NM_001299	NM_001299	1264	-1,20	5,29E-03
AI862542	235696_at	AI862542	---	---	-1,19	2,30E-04
FHL3	218616_at	NM_004468	NM_004468	2275	-1,19	5,70E-03
LOC90246	233835_at	AK023635	---	90246	-1,19	1,62E-04
ARMCX5	1555902_at	BC022066	NM_022838	64860	-1,19	1,49E-04
LOC388227	229107_at	AW629461	XM_373670	388227	-1,19	5,59E-03
C6orf52	236504_x_at	BE670432	XM_371798	347744	-1,19	9,06E-03
ZNF606	219635_at	NM_025027	NM_025027	80095	-1,19	2,38E-03
C10orf39	233076_at	AL137551	NM_194303	282973	-1,19	6,97E-04
FVT1	1558279_a_at	BF666293	NM_002035	2531	-1,19	3,09E-03
TAF12	209463_s_at	D50544	NM_005644	6883	-1,18	3,00E-04
AI929792	236081_at	AI929792	---	---	-1,18	2,41E-05
PDCD2	228420_at	AW590850	NM_002598 NM_144781	5134	-1,18	9,07E-03
ETFDH	33494_at	S69232	NM_004453	2110	-1,18	6,70E-03
CD302	203799_at	NM_014880	NM_014880	9936	-1,17	9,28E-03
N30152	229850_at	N30152	---	---	-1,17	5,16E-03
MGC11332	213403_at	BF223370	NM_032718	84804	-1,17	1,04E-03
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PHKA1	229876_at	BE503584	NM_002637	5255	-1,17	2,72E-04
PCNXL2	1554256_a_at	BC008300	NM_014801 NM_024938	80003	-1,17	8,67E-05
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AV704017	222376_at	AV704017	---	---	-1,16	4,90E-03
AI767751	228084_at	AI767751	---	---	-1,16	6,90E-05
FLJ30294	238578_at	BF574691	NM_144632	130827	-1,16	2,44E-06
BTN3A1	209770_at	U90552	NM_007048 NM_194441	11119	-1,16	4,37E-03
ZC3HDC6	241372_at	R34135	NM_198581	376940	-1,16	4,27E-05
LOC285550	236321_at	AW439843	XM_209656	285550	-1,16	6,99E-03
MGC11332	213393_at	AI767210	NM_032718	84804	-1,15	7,85E-03
CYP2U1	226402_at	AK026498	NM_183075	113612	-1,15	2,05E-03
OPTN	202074_s_at	NM_021980	NM_001008211 NM_001008212 NM_001008213 NM_021980	10133	-1,15	7,05E-03
D4S234E	209569_x_at	NM_014392	NM_014392	27065	-1,15	1,26E-03
GUCY1A3	221942_s_at	AI719730	NM_000856	2982	-1,15	4,01E-04
C18orf18	229829_at	AA429735	---	147525	-1,14	7,95E-03
DUSP16	224832_at	AB051487	NM_030640	80824	-1,14	2,08E-04
C21orf25	212875_s_at	AP001745	NM_199050	25966	-1,13	2,32E-03
DKFZP434B172	232124_at	AL117530	XM_046264	26172	-1,13	1,47E-03
AKT2	236664_at	AA448167	NM_001626	208	-1,13	5,51E-03

FGF7 FLJ30435	1554741_s_at	AF523265	NM_002009 NM_174950	2252 387628	-1,13	2,06E-03
SPOCK2	202524_s_at	NM_014767	NM_014767	9806	-1,12	8,32E-03
ULK2	204063_s_at	NM_014683	NM_014683	9706	-1,12	5,36E-03
DCTD	201671_s_at	AI656493	NM_001921	1635	-1,12	9,66E-05
BACE1	217904_s_at	NM_012104	NM_012104 NM_138971 NM_138972 NM_138973	23621	-1,12	1,17E-03
BC006438	224519_at	BC006438	XR_000264	441422	-1,12	9,10E-04
AW192692	227917_at	AW192692	---	---	-1,12	3,83E-06
AGA	216064_s_at	W27131	NM_000027	175	-1,12	8,70E-03
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AV714268	242323_at	AV714268	---	---	-1,11	2,68E-04
CXorf50	242292_at	H12084	NM_152693	203429	-1,11	4,02E-04
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RSHL2	223713_at	AF353618	NM_031924	83861	-1,11	4,32E-05
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GTDC1	239390_at	BE327650	NM_001006636 NM_024659	79712	-1,11	5,93E-03
MGC14425	1552665_at	NM_032903	---	84989	-1,11	1,79E-03
ERBB2	216836_s_at	X03363	NM_001005862 NM_004448	2064	-1,11	1,73E-05
C21orf51	228239_at	AA148789	NM_058182	54065	-1,11	7,04E-06
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SAMD4	212845_at	AB028976	NM_015589	23034	-1,10	5,48E-03
CLCN3	201734_at	AI760629	NM_001829 NM_173872	1182	-1,10	9,57E-03
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ITGB1BP1	203337_x_at	NM_004763	NM_004763 NM_022334	9270	-1,10	2,94E-03
AW467480	236202_at	AW467480	---	---	-1,09	3,18E-03
LIFR	225575_at	AI680541	NM_002310	3977	-1,09	6,39E-03
PCDHB16	232099_at	AB046841	NM_020957	57717	-1,09	5,69E-03
AI304870	236574_at	AI304870	---	---	-1,09	4,77E-03
LOC157378	241342_at	BG288115	NM_194291	157378	-1,09	7,42E-03
M19720	214058_at	M19720	---	---	-1,09	6,67E-03
LOC90693	228087_at	AK026684	NM_138771	90693	-1,08	6,62E-06
C10orf104	229145_at	AA541762	NM_173473	119504	-1,08	3,73E-03
KIAA1324	221874_at	AB037745	NM_020775	57535	-1,07	1,16E-04
FGF19	223761_at	AF110400	NM_005117	9965	-1,07	8,40E-03
AI768374	228661_s_at	AI768374	---	---	-1,07	9,53E-04
PLRG1	225194_at	NM_002669	NM_002669	5356	-1,07	8,76E-05
AI821995	240201_at	AI821995	---	---	-1,07	5,19E-03
LOC400924	226956_at	AW025389	XM_376003	400924	-1,07	6,57E-04
SLC22A5	205074_at	NM_003060	NM_003060	6584	-1,07	4,71E-03

DALRD3	221934_s_at	BF941492	NM_001009996 NM_018114	55152	-1,07	8,88E-03
AL122040	232429_at	AL122040	---	---	-1,07	1,70E-06
FLJ10490	220151_at	NM_018111	NM_018111	55150	-1,07	4,45E-04
ABTB1	229164_s_at	AI337369	NM_032548 NM_172027 NM_172028	80325	-1,07	5,29E-03
AI569997	242610_x_at	AI569997	---	---	-1,06	7,58E-03
ZNF285	236328_at	AW513227	NM_152354	26974	-1,06	2,76E-04
FSTL1	208782_at	BC000055	NM_007085	11167	-1,06	9,38E-03
TAF1B	235673_at	AI436217	NM_005680	9014	-1,06	2,05E-03
BF002625	228530_at	BF002625	---	---	-1,06	6,62E-04
PEX6	204545_at	NM_000287	NM_000287	5190	-1,06	4,66E-05
ZNF258	219924_s_at	NM_007167	NM_007167 NM_145310	9204	-1,06	5,59E-03
BE467383	228932_at	BE467383	XM_497668	388620	-1,06	3,42E-03
TIGD4	232998_at	AK024235	NM_145720	201798	-1,06	7,64E-04
HCG8	215985_at	X92110	---	80869	-1,05	5,10E-03
PTPRD	214043_at	BF062299	NM_002839 NM_130391 NM_130392 NM_130393	5789	-1,05	2,37E-03
MAN2A2	219999_at	NM_018621	NM_006122	4122	-1,05	3,41E-03
CHC1	206499_s_at	NM_001269	NM_001269	1104	-1,05	3,22E-03
DUSP16	1558739_at	R30807	NM_030640	80824	-1,04	6,86E-04
PLEKHA2	238013_at	BF347859	XM_496973	59339	-1,04	7,63E-03
RODH	37512_at	U89281	NM_003725	8630	-1,04	2,71E-03
TMEM42	226361_at	BF056095	NM_144638	131616	-1,04	2,56E-03
MGC4655	226058_at	AI651445	NM_033309	84752	-1,04	4,77E-04
LMNA	203411_s_at	NM_005572	NM_005572 NM_170707 NM_170708	4000	-1,04	6,43E-03
AL552727	244060_at	AL552727	---	---	-1,04	1,69E-03
ALLC	220365_at	NM_018436	NM_018436 NM_199232	55821	-1,04	3,61E-03
KIAA0543	213444_at	AB011115	XM_376720 XM_379967	23145	-1,04	3,24E-07
TRIM61	238990_x_at	AI763262	XM_373038	391712	-1,04	3,91E-03
AA156605	226798_at	AA156605	---	---	-1,04	1,65E-03
STX12	212111_at	AA628051	NM_177424	23673	-1,03	9,08E-07
PHF17	225816_at	AW138134	NM_024900 NM_199320	79960	-1,03	9,73E-03
AL042817	225553_at	AL042817	---	---	-1,03	2,32E-04
HEL308	228736_at	AW084661	NM_133636	113510	-1,03	9,31E-04
LOC440388	228855_at	AI927964	XM_496170	440388	-1,03	2,15E-03
ANKRA2	218769_s_at	NM_023039	NM_023039	57763	-1,03	3,79E-04
SH3KBP1	223082_at	AF230904	NM_031892	30011	-1,03	5,39E-04
MAP7	202890_at	AW242297	NM_003980	9053	-1,03	9,43E-03

AI263044	214376_at	AI263044	---	---	-1,03	4,37E-03
D4S234E	209570_s_at	BC001745	NM_014392	27065	-1,03	5,33E-03
BF510563	228561_at	BF510563	---	---	-1,03	7,28E-03
LOC157378	238045_at	BG167675	NM_194291	157378	-1,02	9,58E-03
BF510762	230262_at	BF510762	---	---	-1,02	3,17E-03
SLC2A11	1558540_s_at	AK055523	NM_030807	66035	-1,01	5,49E-03
INPP5A	1554757_a_at	AF273055	NM_005539	3632	-1,01	3,78E-03
CARD10	210026_s_at	AY028896	NM_014550	29775	-1,01	4,13E-03
EFNB3	205031_at	NM_001406	NM_001406	1949	-1,01	2,94E-03
SVH	1554480_a_at	AY150851	NM_031905	83787	-1,01	4,33E-05
PP1057	220968_s_at	NM_031285	---	83441	-1,01	3,02E-04
LOC401320	238540_at	AA933883	XM_379482 XM_380098	401320	-1,00	1,29E-03
GNB5	211871_x_at	AF300650	NM_006578 NM_016194	10681	-1,00	2,54E-03
BE549742	230724_s_at	BE549742	---	---	-1,00	3,40E-03
MGC34648	228604_at	AI805069	NM_152660	199870	-1,00	2,70E-03
AL390170	213904_at	AL390170	---	---	-1,00	4,30E-03
LOC400713	232315_at	AU149712	XR_000217	400713	-1,00	1,91E-03
DKFZP434H132	204494_s_at	AW516789	NM_015492	56905	-1,00	2,50E-04
DBT	231919_at	AK024946	NM_001918	1629	-1,00	3,13E-04
AI459157	225066_at	AI459157	---	---	-1,00	1,73E-03
WASL	227010_at	BF438330	NM_003941	8976	-1,00	3,51E-04
SH3KBP1	1554168_a_at	AF542051	NM_031892	30011	-0,99	9,41E-04
LOC339803	227941_at	AW327931	---	339803	-0,99	7,41E-04
NM_017923	219574_at	NM_017923	---	---	-0,99	1,05E-04
HMGCLL1	232305_at	AF131827	NM_019036	54511	-0,99	7,25E-06
MGC29898	235259_at	AA398590	NM_145048	133015	-0,99	2,85E-03
LIN7B	219760_at	NM_022165	NM_022165	64130	-0,99	6,61E-06
AI161338	65472_at	AI161338	XM_371506	388969	-0,99	7,88E-03
PIGH	209625_at	BC004100	NM_004569	5283	-0,99	6,18E-04
RRN3	216902_s_at	AF001549	NM_018427	54700	-0,98	1,48E-05
BE646451	235893_at	BE646451	---	---	-0,98	1,01E-03
KIAA1223	225735_at	AL110131	XM_048747	57182	-0,98	9,14E-04
SLC18A2	1553328_a_at	NM_003054	NM_003054	6571	-0,98	5,03E-03
C19orf4	219005_at	NM_012109	NM_012109	25789	-0,98	2,75E-03
D4S234E	213533_at	M98528	NM_014392	27065	-0,98	2,97E-04
CAPN2	208683_at	M23254	NM_001748	824	-0,98	7,76E-03
TMEM23	212989_at	AI377497	NM_147156	259230	-0,98	5,42E-03
NEFH	204412_s_at	NM_021076	NM_021076	4744	-0,98	9,35E-03
ANXA5	200782_at	NM_001154	NM_001154	308	-0,98	5,17E-03
AI955713	227193_at	AI955713	---	---	-0,97	5,36E-08
LOC284422	231982_at	AF161441	XM_209196	284422	-0,97	7,92E-03
KCTD18	226493_at	AI627249	NM_152387	130535	-0,97	3,04E-05
LOC90024	228832_at	AI884670	XM_028217	90024	-0,97	7,03E-03
CA442342	1556097_at	CA442342	---	---	-0,97	3,17E-03
LOC90639	235533_at	AW021673	---	90639	-0,97	4,53E-03
HDAC4	228813_at	AW206037	NM_006037	9759	-0,96	3,30E-03
BC040901	1559535_s_at	BC040901	---	---	-0,96	6,19E-03

BBS7	235007_at	AI683802	NM_018190 NM_176824	55212	-0,96	1,86E-03
MGC48625	1569039_s_at	BC029855	NM_182609	342926	-0,96	7,88E-05
MBNL1	201151_s_at	BF512200	NM_021038 NM_207292 NM_207293 NM_207294 NM_207295 NM_207296 NM_207297	4154	-0,96	4,33E-03
CIB1	201953_at	NM_006384	NM_006384	10519	-0,96	2,33E-04
RPP21	218836_at	NM_024839	NM_024839	79897	-0,96	2,49E-03
CHC1	215747_s_at	X06130	NM_001269	1104	-0,96	4,49E-03
ACSL1	201963_at	NM_021122	NM_001995	2180	-0,95	5,71E-04
RHOU	223169_s_at	AB051826	NM_021205	58480	-0,95	1,29E-03
KIAA0773	205388_at	NM_014690	NM_014690	9715	-0,95	1,39E-03
PDPK1	32029_at	AC005591	NM_002613 NM_031268	5170	-0,95	4,56E-04
GNG8	234284_at	AF188179	NM_033258	94235	-0,95	5,33E-04
C14orf133	233140_s_at	AF111168	NM_022067	63894	-0,95	4,26E-04
ITR	231871_at	AU160685	NM_180989	160897	-0,95	5,11E-03
BC015852	1560570_a_at	BC015852	---	---	-0,95	6,20E-03
SNF1LK2	223430_at	AL136764	NM_015191	23235	-0,95	2,99E-03
CKLFSF1	235286_at	BG533580	NM_052999 NM_181268 NM_181269 NM_181270 NM_181271 NM_181272 NM_181283 NM_181285 NM_181286 NM_181287 NM_181288 NM_181289 NM_181290 NM_181292 NM_181293 NM_181294 NM_181295 NM_181296 NM_181297 NM_181298 NM_181299 NM_181300 NM_181301	113540	-0,95	5,78E-03
BTN3A3	204821_at	NM_006994	NM_006994 NM_197974	10384	-0,95	7,79E-05
PLEKHC1	209210_s_at	Z24725	NM_006832	10979	-0,94	2,90E-03

RNF41	201962_s_at	NM_005785	NM_005785 NM_194358 NM_194359	10193	-0,94	3,16E-03
NAP1L3	204749_at	NM_004538	NM_004538	4675	-0,94	2,43E-03
ZNF251	226754_at	W93231	XM_291262	90967	-0,94	1,04E-03
PLEKHA2	217677_at	BF542055	XM_496973	59339	-0,94	7,55E-03
SIDT2	56256_at	AA150165	NM_015996	51092	-0,94	3,96E-04
STX12	212112_s_at	AI816243	NM_177424	23673	-0,94	7,35E-05
STX17	228091_at	AI800609	NM_017919	55014	-0,94	6,04E-03
C2orf17	221983_at	AL040896	NM_024293	79137	-0,94	4,85E-03
ZFP28	234937_x_at	AC007228	NM_020628	140612	-0,94	3,30E-03
HLA-G	210514_x_at	AF226990	NM_002127	3135	-0,94	1,71E-04
MGC14801	224443_at	BC005997	NM_032705	84791	-0,93	9,68E-03
N79601	242981_at	N79601	---	---	-0,93	4,16E-03
LOC284926	1556064_at	BQ575161	---	284926	-0,93	5,64E-03
WDR9	225446_at	AI638279	NM_001007246 NM_018963 NM_033656	54014	-0,93	3,04E-04
AI652546	228853_at	AI652546	---	---	-0,93	4,31E-03
EIF4E3	238461_at	AA228031	---	317649	-0,92	5,07E-03
AU151944	236916_at	AU151944	---	---	-0,92	1,50E-03
ZNF610	235953_at	AA776810	NM_173530	162963	-0,92	3,79E-04
RGS14	38290_at	AF037195	NM_006480	10636	-0,92	1,22E-03
WDR24	223293_at	AL136863	NM_032259	84219	-0,92	5,54E-04
T87730	242500_at	T87730	---	---	-0,92	7,27E-03
AW615274	229423_at	AW615274	---	---	-0,92	8,89E-03
SIRT5	219185_at	NM_012241	NM_012241 NM_031244	23408	-0,91	1,64E-03
MGC54289	225230_at	AI735261	NM_178454	128338	-0,91	9,98E-03
LMNA	212089_at	M13452	NM_005572 NM_170707 NM_170708	4000	-0,91	7,00E-03
NINJ1	203045_at	NM_004148	NM_004148	4814	-0,91	3,51E-04
C9orf127	229729_at	BF507870	NM_016446	51754	-0,91	1,20E-04
LAF4	227198_at	AW085505	NM_002285	3899	-0,91	4,25E-05
ADPRHL2	223097_at	AF212236	NM_017825	54936	-0,91	1,91E-04
N21364	214202_at	N21364	---	---	-0,90	6,59E-06
LOC388727	231233_at	AI382195	XM_373881	388727	-0,90	1,97E-03

ALU Sequence	AFFX-hum_alu_at	AFFX-hum_alu	NM_000021 NM_000051 NM_000136 NM_000141 NM_000144 NM_000202 NM_00022 NM_000230 NM_000294 NM_000297 NM_000314 NM_000356 NM_000364 NM_000382 NM_000441 NM_000484 NM_000527 NM_000554	---	-0,90	2,52E-03
ACYP2	206833_s_at	NM_001108	NM_138448	98	-0,90	4,12E-03
EXOC7	212026_s_at	BE646386	NM_015219	23265	-0,90	1,03E-03
RPUSD3	225743_at	AI125996	NM_173659	285367	-0,90	3,62E-03
R15431	236440_at	R15431	---	---	-0,90	3,46E-05
AA194266	236728_at	AA194266	---	---	-0,90	8,94E-03
GNB5	207124_s_at	NM_006578	NM_006578 NM_016194	10681	-0,90	2,52E-04
TEX264	233350_s_at	AU158474	NM_015926	51368	-0,89	3,96E-04
TRIM32	1557315_a_at	AL134420	NM_012210	22954	-0,89	4,37E-03
BF342524	235074_at	BF342524	---	---	-0,89	2,65E-05
HADHA	236120_at	AW955973	NM_000182	3030	-0,89	8,56E-03
C21orf119	227424_x_at	AI800837	NM_032910	84996	-0,88	6,71E-03
CLN5	204085_s_at	NM_006493	NM_006493	1203	-0,88	6,71E-03
SAV1	218276_s_at	NM_021818	NM_021818	60485	-0,88	4,58E-03
HDHD3	221256_s_at	NM_031219	NM_031219	81932	-0,88	4,72E-03
EMID1	213779_at	AL031186	NM_133455	129080	-0,88	4,61E-05
GAL3ST3	1553257_at	AY026481	NM_033036	89792	-0,88	5,62E-03
USP44	224048_at	AL136825	NM_032147	84101	-0,88	1,11E-03
ACSL1	207275_s_at	NM_001995	NM_001995	2180	-0,87	9,24E-03
AK024681	231972_at	AK024681	---	---	-0,87	6,32E-03
AL527331	238716_at	AL527331	---	---	-0,87	3,42E-03
KIAA0711	204301_at	NM_014867	NM_014867	9920	-0,87	5,63E-07
NOL3	221566_s_at	AF043244	NM_003946	8996	-0,87	4,45E-03
AW236954	1557117_at	AW236954	---	---	-0,87	1,02E-03
MRPS33	218654_s_at	NM_016071	NM_016071 NM_053035	51650	-0,87	5,05E-03
SLC19A1	229489_at	AI681043	NM_003056 NM_194255	6573	-0,87	4,84E-04

ATP2C1	209935_at	AF225981	NM_001001485 NM_001001486 NM_001001487 NM_014382	27032	-0,87	1,03E-03
MBNL1	201153_s_at	NM_021038	NM_021038 NM_207292 NM_207293 NM_207294 NM_207295 NM_207296 NM_207297	4154	-0,87	2,49E-04
MGC52110	226039_at	AW006441	NM_001008215	493753	-0,86	1,48E-03
OTUB2	219369_s_at	NM_023112	NM_023112	78990	-0,86	4,20E-03
ZNF558	227810_at	AW119060	NM_144693	148156	-0,86	1,86E-04
ANKH	229176_at	AI672354	NM_054027	56172	-0,86	8,12E-03
SYNE1	209447_at	AF043290	NM_015293 NM_033071 NM_133650 NM_182961	23345	-0,86	3,61E-03
MGC35097	225755_at	AI160540	NM_173546	200942	-0,86	6,77E-03
AI471969	239278_at	AI471969	---	---	-0,86	2,25E-03
OR6M1	227112_at	AW270037	NM_001005325	390261	-0,86	2,99E-04
DSCR3	217309_s_at	AJ001867	NM_006052	10311	-0,86	1,52E-04
VGLL4	212399_s_at	D50911	NM_014667	9686	-0,86	1,90E-03
RNH	206050_s_at	NM_002939	NM_002939 NM_203383 NM_203384 NM_203385 NM_203386 NM_203387 NM_203388 NM_203389	6050	-0,85	1,17E-03
EIF3S2	208756_at	U36764	NM_003757	8668	-0,85	3,95E-04
CHCHD5	235825_at	AI057238	NM_032309	84269	-0,85	2,48E-03
FLJ25715	231952_at	AU157271	NM_182570	284241	-0,85	4,49E-03
H28915	244359_s_at	H28915	XM_496692	441014	-0,85	2,81E-03
SVH	223328_at	BC003586	NM_031905	83787	-0,85	2,28E-03
BRD4	238612_at	AW298070	NM_014299 NM_058243	23476	-0,85	4,92E-04
PLEKHC1	209209_s_at	AW469573	NM_006832	10979	-0,85	9,05E-03
LOC220930	229090_at	AK026657	---	220930	-0,85	5,83E-04
AW665538	244532_x_at	AW665538	XM_496692	441014	-0,85	3,20E-03
DKFZp727A071	227348_at	AW409848	NM_152268	25973	-0,85	4,70E-05
STK19	36019_at	L26260	NM_004197 NM_032454	8859	-0,85	1,10E-03

DCTD	210137_s_at	BC001286	NM_001921	1635	-0,84	7,33E-03
AMT	204294_at	NM_000481	NM_000481	275	-0,84	1,21E-03
ERBB4	206794_at	NM_005235	NM_005235	2066	-0,84	7,70E-03
AI003508	244114_x_at	AI003508	XM_496690	401131	-0,84	2,43E-03
CNOT6L	227119_at	BF103856	NM_144571	246175	-0,84	1,58E-04
LRRC14	32062_at	D25216	NM_014665	9684	-0,84	1,85E-03
AI796858	236164_at	AI796858	---	---	-0,84	8,09E-03
SUMF2	225002_s_at	BE349022	NM_015411	25870	-0,84	1,85E-03
CLN8	229958_at	W93695	NM_018941	2055	-0,84	1,34E-03
TDRKH	221052_at	NM_006862	NM_006862	11022	-0,84	1,92E-03
BF340290	225220_at	BF340290	---	---	-0,84	8,97E-03
LNX	227293_at	AI264003	NM_032622	84708	-0,84	2,20E-03
ADCK1	227482_at	AI097656	NM_020421	57143	-0,83	4,63E-03
FLJ31340	235301_at	AI797353	NM_152748	222223	-0,83	9,27E-04
FLJ12716	218179_s_at	NM_021942	NM_021942 NM_199053	60684	-0,83	3,97E-04
ACP6	218795_at	NM_016361	NM_016361	51205	-0,83	7,19E-04
KIAA0543	226808_at	AW771007	XM_376720 XM_379967	23145	-0,83	2,42E-04
PAK6	1555310_a_at	BC035596	NM_020168	56924	-0,83	2,78E-03
TXNDC4	208958_at	AI827677	NM_015051	23071	-0,83	1,35E-03
PAM	202336_s_at	NM_000919	NM_000919 NM_138766 NM_138821 NM_138822	5066	-0,83	4,55E-03
LOC57149	203897_at	BE963444	NM_020424	57149	-0,82	1,05E-04
DCP1B	226093_at	AW204088	NM_152640	196513	-0,82	6,19E-04
FLJ12716	233558_s_at	AK023390	NM_021942 NM_199053	60684	-0,82	8,71E-04
TP53TG3	220167_s_at	NM_015369	NM_015369 NM_016212	24150	-0,82	3,88E-04
OCIAD2	225314_at	BG291649	NM_152398	132299	-0,82	8,74E-03
C14orf133	218431_at	NM_022067	NM_022067	63894	-0,82	9,75E-04
FLJ38991	227442_at	BG283902	NM_173827	285521	-0,82	2,25E-03
FLJ31340	244317_at	BF035563	NM_152748	222223	-0,82	5,35E-03
DSCR3	203635_at	NM_006052	NM_006052	10311	-0,82	8,42E-04
PDCD2	204025_s_at	NM_002598	NM_002598 NM_144781	5134	-0,81	5,01E-04
DKFZP564D166	224952_at	BF115054	XM_371074	26115	-0,81	3,50E-04
FLJ13231	219381_at	NM_023073	NM_023073	65250	-0,81	9,78E-03
CDC37L1	235787_at	T65394	NM_017913	55664	-0,81	7,07E-04
WDTC1	215497_s_at	AK023778	NM_015023	23038	-0,81	5,43E-04
LOC94431	216908_x_at	AF001549	NM_145237	94431	-0,81	3,74E-06
SEC31L1	215009_s_at	U92014	NM_014933 NM_016211	22872	-0,81	2,06E-03
ZNF148	230821_at	AW594167	NM_021964	7707	-0,81	5,30E-03
DHRSX	225503_at	AL547782	NM_145177	207063	-0,81	8,16E-06
LYPLA3	204458_at	AL110209	NM_012320	23659	-0,81	3,93E-03
DCTD	201572_x_at	NM_001921	NM_001921	1635	-0,81	5,30E-04

FLJ31265	228341_at	AI809108	NM_152395	131870	-0,81	9,80E-04
TBC1D12	221858_at	N34407	XM_051081	23232	-0,81	2,80E-03
FLJ22795	223327_x_at	AF316855	NM_025084	80154	-0,81	6,81E-06
ZNF274	204937_s_at	NM_016325	NM_016324 NM_016325 NM_133502	10782	-0,81	2,65E-03
CSTB	201201_at	NM_000100	NM_000100	1476	-0,80	6,53E-04
LOC151146	227604_at	BG292251	---	151146	-0,80	2,89E-03
SLC18A2	205857_at	AI269290	NM_003054	6571	-0,80	3,73E-03
MANSC1	220945_x_at	NM_018050	NM_018050	54682	-0,80	2,89E-03
R44603	244113_at	R44603	---	---	-0,80	2,19E-03
PAK1	226507_at	AU154408	NM_002576	5058	-0,80	4,33E-03
KIRREL3	240402_at	H05918	NM_032531	84623	-0,80	2,61E-03
AW516665	227571_at	AW516665	---	---	-0,80	4,02E-03
FBXL5	209005_at	AF157323	NM_012161 NM_033535	26234	-0,80	2,18E-04
TM4SF2	202242_at	NM_004615	NM_004615	7102	-0,80	4,39E-03
EHD2	45297_at	AI417917	NM_014601	30846	-0,80	2,06E-05
UBE2D3	200667_at	BF448062	NM_003340 NM_181886 NM_181887 NM_181888 NM_181889 NM_181890 NM_181891 NM_181892 NM_181893	7323	-0,79	7,56E-06
AA868896	226203_at	AA868896	---	---	-0,79	2,92E-03
DUSP24	233982_x_at	AF188204	NM_016086	51657	-0,79	9,14E-03
AU157441	226511_at	AU157441	---	---	-0,79	1,27E-03
AK2	205996_s_at	NM_013411	NM_001625 NM_013411 NM_172199	204	-0,79	2,76E-03
AF086443	1560982_at	AF086443	---	---	-0,79	4,61E-03
C9orf9	220050_at	NM_018956	NM_018956	11092	-0,79	1,17E-03
ZNF23	213934_s_at	AL567808	NM_145911	7571	-0,79	3,42E-03
HLA-G	211529_x_at	M90684	NM_002127	3135	-0,79	1,15E-03
XPR1	226615_at	BE439489	NM_004736	9213	-0,79	8,43E-04
THAP9	230185_at	AW301218	NM_024672	79725	-0,79	4,10E-03
CCNDBP1	223084_s_at	AF246144	NM_012142 NM_037370	23582	-0,79	1,05E-04
AP3B2	205678_at	NM_004644	NM_004644	8120	-0,78	3,03E-03
CTHRC1	225681_at	AA584310	NM_138455	115908	-0,78	2,80E-03
LOC93622	225391_at	AL562398	NM_138699	93622	-0,78	8,43E-03
JAG2	209784_s_at	AF029778	NM_002226 NM_145159	3714	-0,78	7,94E-03
ZNF585A	229794_at	BE550717	NM_152655 NM_199126	199704	-0,78	4,45E-03
MGC2650	204985_s_at	NM_024108	NM_024108	79090	-0,78	4,43E-03

APRT	203219_s_at	NM_000485	NM_000485	353	-0,78	5,08E-04
USP36	220370_s_at	NM_025090	NM_025090	57602	-0,78	3,64E-03
INPP5A	203006_at	NM_005539	NM_005539	3632	-0,78	8,67E-03
ZNF197	205855_at	NM_006991	NM_006991	10168	-0,78	6,14E-03
PLEKHA2	225136_at	BF968578	XM_496973	59339	-0,78	4,19E-04
ARHGEF4	205109_s_at	NM_015320	NM_015320 NM_032995	50649	-0,77	7,05E-03
NETO1	1552736_a_at	NM_138966	NM_138966 NM_138999 NM_153181	81832	-0,77	2,29E-04
LRPAP1	201186_at	NM_002337	NM_002337	4043	-0,77	7,07E-03
MYST1	221820_s_at	AK024102	NM_032188	84148	-0,77	7,03E-03
FLJ12998	244734_at	W45568	NM_022764	64779	-0,77	1,04E-04
CLTC	238646_at	AA747756	NM_004859	1213	-0,77	8,00E-03
SLC30A5	1555334_s_at	AF439324	NM_022902 NM_024055	64924	-0,77	3,91E-03
PRKAG1	201805_at	NM_002733	NM_002733 NM_212461	5571	-0,77	2,24E-03
GPRASP1	204793_at	NM_014710	NM_014710	9737	-0,77	1,73E-03
NETO1	1562713_a_at	AL834354	NM_138966 NM_138999 NM_153181	81832	-0,77	2,38E-03
LOC89894	227172_at	BC000282	NM_138341	89894	-0,77	3,71E-04
STK19	204090_at	NM_004197	NM_004197 NM_032454	8859	-0,77	2,21E-03
LIPT1	205571_at	NM_015929	NM_015929 NM_145196 NM_145197 NM_145198 NM_145199	51601	-0,77	1,12E-03
ZCWCC3	213000_at	AP000693	NM_015358	23515	-0,77	1,90E-03
CLCN3	201735_s_at	NM_001829	NM_001829 NM_173872	1182	-0,77	8,06E-03
FLJ32370	226483_at	AI890761	NM_152417	137695	-0,76	2,24E-03
FYCO1	218204_s_at	NM_024513	NM_024513	79443	-0,76	1,16E-07
NEIL2	226585_at	BE466620	NM_145043	252969	-0,76	5,49E-04
KCNH2	205262_at	NM_000238	NM_000238 NM_172056 NM_172057	3757	-0,76	9,14E-06
BF966015	226787_at	BF966015	---	---	-0,76	3,80E-06
BBP	213882_at	AA012917	NM_032027	83941	-0,76	1,89E-03
GSTZ1	209531_at	BC001453	NM_001513 NM_145870 NM_145871	2954	-0,76	3,56E-03
EIF2C1	228120_at	AW136032	NM_012199	26523	-0,76	6,17E-03
PCTK2	206474_at	NM_002595	NM_002595	5128	-0,76	4,76E-03
C13orf21	243094_at	BF509416	NM_001010897	387923	-0,76	5,57E-03
MAPRE3	214270_s_at	AI885178	NM_012326	22924	-0,76	3,88E-03

BG017239	1558045_a_at	BG017239	---	---	-0,75	3,87E-03
COL27A1	225288_at	AI949136	NM_032888	85301	-0,75	9,38E-04
AI672159	226550_at	AI672159	---	---	-0,75	1,09E-04
MBNL1	201152_s_at	N31913	NM_021038 NM_207292 NM_207293 NM_207294 NM_207295 NM_207296 NM_207297	4154	-0,75	1,55E-04
TBN	1556178_x_at	BU618741	NM_138572	129685	-0,75	9,97E-03
TMAP1	227326_at	BE966768	NM_001008528 NM_001008529 NM_198530	439921	-0,75	4,09E-04
TNFRSF21	218856_at	NM_016629	NM_014452	27242	-0,75	6,87E-03
CHMP1.5	218177_at	AA293502	NM_020412	57132	-0,75	5,52E-05
SHFM3	221519_at	AF281859	NM_022039	6468	-0,75	1,33E-03
AU151635	232111_at	AU151635	---	---	-0,75	1,40E-07
PTK9L	202009_at	NM_007284	NM_007284	11344	-0,75	8,11E-03
PAM	214620_x_at	BF038548	NM_000919 NM_138766 NM_138821 NM_138822	5066	-0,75	3,40E-03
WDFY3	212606_at	AL536319	NM_014991 NM_178583 NM_178585	23001	-0,75	1,05E-03
KIAA1277	221885_at	AI131051	NM_015689	27147	-0,75	5,98E-03
DIRAS2	219619_at	NM_017594	NM_017594	54769	-0,74	6,42E-03
EXT2	202012_s_at	AA196245	NM_000401 NM_207122	2132	-0,74	5,88E-04
C18orf17	238480_at	AI871745	NM_153211	125488	-0,74	4,89E-04
SLC9A1	209453_at	M81768	NM_003047	6548	-0,74	5,21E-06
PCBD1	203557_s_at	NM_000281	NM_000281 NM_001001939	5092	-0,74	2,72E-04
C6orf83	225850_at	BF975327	NM_145169	113402	-0,74	6,67E-03
PIGV	219238_at	NM_017837	NM_017837	55650	-0,74	4,79E-04
KIAA0276	243691_at	AA150455	NM_015115	23142	-0,74	7,85E-03
PAM	212958_x_at	AI022882	NM_000919 NM_138766 NM_138821 NM_138822	5066	-0,74	9,54E-03
NM_152909	1553719_s_at	NM_152909	---	---	-0,74	1,13E-03
PKD1	216949_s_at	L39891	NM_000296 NM_001009944	5310	-0,74	1,43E-03
AI768895	231069_at	AI768895	---	---	-0,74	7,25E-03

MTMR7	228024_at	AW028100	NM_004686	9108	-0,74	3,76E-05
BRUNOL4	223653_x_at	AW593887	NM_020180	56853	-0,74	9,74E-03
LOH12CR1	227723_at	BF439234	NM_058169	118426	-0,74	7,19E-03
PTN	209465_x_at	AL565812	NM_002825	5764	-0,73	7,19E-03
RPL4	226556_at	BF431260	NM_000968	6124	-0,73	4,08E-03
MTRF1	219822_at	NM_004294	NM_004294	9617	-0,73	1,42E-04
PCCA	203860_at	NM_000282	NM_000282	5095	-0,73	9,56E-03
RPS4Y1	201909_at	NM_001008	NM_001008	6192	-0,73	2,03E-03
FLJ11273	222787_s_at	AV705186	NM_018374	54664	-0,73	7,27E-04
CSE-C	224391_s_at	AF303378	NM_170601	54414	-0,73	3,37E-03
KIAA0323	212356_at	AB002321	NM_015299	23351	-0,73	8,63E-03
AI061377	235232_at	AI061377	---	---	-0,73	9,74E-03
SH3YL1	204019_s_at	NM_015677	NM_015677	26751	-0,73	2,48E-03
LOC255458	1556180_at	BE646146	---	255458	-0,73	6,08E-05
JAGN1	223104_at	AF212230	NM_032492	84522	-0,73	2,17E-05
FLJ10038	205511_at	NM_017976	---	55056	-0,73	5,36E-03
FLJ13984	220007_at	NM_024770	NM_024770	79828	-0,73	6,13E-03
TMEM34	219074_at	NM_018241	NM_018241	55751	-0,73	8,00E-03
ARRDC1	226405_s_at	AK001822	NM_152285	92714	-0,72	2,87E-03
BF056746	228425_at	BF056746	---	---	-0,72	4,99E-04
P15RS	222559_s_at	T79568	NM_018170	55197	-0,72	1,36E-05
FLJ23560	219487_at	NM_024685	NM_024685	79738	-0,72	9,23E-03
ANKH	223093_at	T99215	NM_054027	56172	-0,72	3,35E-03
VAPA	225198_at	AL571942	NM_003574 NM_194434	9218	-0,72	2,38E-03
CCDC2	219174_at	NM_025103	NM_025103	80173	-0,72	2,41E-03
AA709148	243751_at	AA709148	---	---	-0,72	2,28E-04
GART	217445_s_at	AF008655	NM_000819 NM_175085	2618	-0,72	1,27E-03
LOC389906 LOC389910 LOC401625	1558046_x_at	BC017239	XM_372273 XM_374343 XM_377076	389906 389910 401625	-0,72	1,71E-03
SAV1	222573_s_at	AI679398	NM_021818	60485	-0,72	5,04E-04
BBS2	223227_at	AF342736	NM_031885	583	-0,72	2,39E-03
FLJ10726	218314_s_at	NM_018195	NM_018195	55216	-0,72	9,03E-04
AK055769	1558801_at	AK055769	---	---	-0,71	5,90E-03
R53065	240430_at	R53065	---	---	-0,71	6,12E-03
WDFY3	212602_at	AI806395	NM_014991 NM_178583 NM_178585	23001	-0,71	1,21E-03
CSNK2A2	203575_at	NM_001896	NM_001896	1459	-0,71	5,96E-03
KIAA0992	200907_s_at	AU157932	NM_016081	23022	-0,71	2,15E-03
LMNA	212086_x_at	AK026584	NM_005572 NM_170707 NM_170708	4000	-0,71	6,61E-03
BE502930	235124_at	BE502930	---	---	-0,71	3,16E-04
AI765014	224649_x_at	AI765014	---	---	-0,71	2,78E-03
TTC13	219481_at	NM_024525	NM_024525	79573	-0,71	1,48E-03
GAS5	224841_x_at	BF316352	---	60674	-0,71	6,06E-03

AI652899	228812_at	AI652899	---	---	-0,71	5,25E-05
PLCB1	213222_at	AL049593	NM_015192 NM_182734	23236	-0,71	7,21E-04
DET1	219641_at	NM_017996	NM_017996	55070	-0,71	1,63E-03
ACSL3	201660_at	AL525796	NM_004457 NM_203372	2181	-0,71	3,90E-04
MGC2749	200076_s_at	BC006479	NM_024069	79036	-0,71	6,49E-03
QPCT	205174_s_at	NM_012413	NM_012413	25797	-0,71	6,07E-03
PML	209640_at	M79462	NM_002675 NM_033238 NM_033239 NM_033240 NM_033242 NM_033244 NM_033245 NM_033246 NM_033247 NM_033249 NM_033250	5371	-0,70	3,55E-03
LRRC27	1558483_at	AK098652	NM_030626	80313	-0,70	3,75E-03
STK16	209622_at	AB020739	NM_001008910 NM_003691	8576	-0,70	2,64E-04
CRYZL1	219767_s_at	NM_005111	NM_005111 NM_145311 NM_145858	9946	-0,70	2,94E-03
TMEM43	217795_s_at	W74580	NM_024334	79188	-0,70	3,09E-03
DFFA	203277_at	NM_004401	NM_004401 NM_213566	1676	-0,70	4,51E-03
BF062875	230072_at	BF062875	---	---	-0,70	7,79E-04
AW974666	222365_at	AW974666	---	---	-0,70	3,83E-03
AA827878	223577_x_at	AA827878	---	---	-0,70	8,67E-03
TMEM43	222418_s_at	AA115485	NM_024334	79188	-0,70	3,97E-03
C14orf118	219720_s_at	NM_017972	NM_017926 NM_017972	55668	-0,70	1,92E-03
LOC285550	227270_at	BF593037	XM_209656	285550	-0,70	1,40E-03
LRRC28	227423_at	AI655972	NM_144598	123355	-0,70	6,98E-04
PFN2	237116_at	AI262277	NM_002628 NM_053024	5217	-0,70	2,39E-03
JMY	226352_at	BF447037	NM_152405	133746	-0,70	9,37E-04
TLOC1	225352_at	AI763287	NM_003262	7095	-0,69	2,60E-04
PPID	204186_s_at	AI014573	NM_005038	5481	-0,69	1,10E-03
FLJ38968	226383_at	AI652452	NM_152316	120534	-0,69	1,37E-03
KIAA0992	200897_s_at	NM_016081	NM_016081	23022	-0,69	1,00E-03
SLC30A5	232432_s_at	AK022818	NM_022902 NM_024055	64924	-0,69	2,34E-03
AIG1	230520_at	T78402	NM_016108	51390	-0,69	7,09E-05
FKBP9	212169_at	AL050187	NM_007270	11328	-0,69	3,13E-03
T1	56829_at	H61826	NM_031466	83696	-0,69	4,28E-03

AA813998	235837_at	AA813998	---	---	-0,69	7,10E-03
SNAP91	204953_at	NM_014841	NM_014841	9892	-0,69	8,76E-03
PLD3	201050_at	NM_012268	NM_012268	23646	-0,69	2,09E-03
CGI-41	218914_at	NM_015997	NM_015997	51093	-0,69	6,72E-03
RARA	226037_at	AA404273	NM_000964	5914	-0,69	9,78E-04
MYO9A	219027_s_at	NM_006901	NM_006901	4649	-0,68	3,06E-03
RDH13	1559190_s_at	AL833150	NM_138412	112724	-0,68	6,77E-03
RGS14	204280_at	NM_006480	NM_006480	10636	-0,68	1,43E-04
FLJ34222	235717_at	AA180985	XM_371175	284350	-0,68	3,45E-05
BF434383	235473_at	BF434383	---	---	-0,68	8,03E-04
CDKL3	219831_at	NM_016508	NM_016508	51265	-0,68	4,12E-05
FRBZ1	226962_at	AW299558	NM_194314	360023	-0,68	3,75E-03
FLJ37953	241825_at	AI265967	NM_152382	129450	-0,68	8,57E-04
TRIM4	223384_s_at	BE501464	NM_033017 NM_033091	89122	-0,68	2,58E-03
SF3B3	200688_at	D13642	NM_012426	23450	-0,68	4,67E-03
PHF10	219126_at	NM_018288	NM_018288 NM_133325	55274	-0,68	2,92E-03
IL17RB	235531_at	AA928257	NM_018725 NM_172234	55540	-0,68	2,10E-03
BCL2L13	224035_s_at	AF183411	NM_015367	23786	-0,68	7,08E-04
MAN1A2	217922_at	AL157902	NM_006699	10905	-0,68	3,21E-03
ZNF232	236075_s_at	AI693543	NM_014519	7775	-0,68	6,78E-03
BC024246	1556301_at	BC024246	---	---	-0,68	2,06E-04
ZRANB1	225130_at	AW003734	NM_017580	54764	-0,67	1,84E-04
PP1665	32502_at	AL041124	NM_030792	81544	-0,67	9,49E-04
CAB39	224311_s_at	AF151824	NM_016289	51719	-0,67	2,14E-03
KRTAP4-7	225225_at	BF791544	NM_033061	85287	-0,67	8,80E-03
SLC30A5	218989_x_at	NM_022902	NM_022902 NM_024055	64924	-0,67	6,75E-03
RNF41	201961_s_at	AL583171	NM_005785 NM_194358 NM_194359	10193	-0,67	8,95E-03
C6orf168	232067_at	BC004869	NM_032511	84553	-0,67	2,42E-03
TNIP2	232160_s_at	AL137262	NM_024309	79155	-0,67	1,56E-03
DKFZP564D172	212936_at	AI927701	NM_032042	83989	-0,67	5,18E-04
LOC439962	1560047_s_at	AA127813	XM_498479	439962	-0,67	3,91E-03
MCM3APAS	220459_at	NM_018118	---	114044	-0,67	2,26E-03
SLC35E1	229410_at	AI659219	NM_024881	79939	-0,67	5,75E-03
FBXW7	229419_at	BF222826	NM_018315 NM_033632	55294	-0,67	9,92E-04
C10orf22	212500_at	AL049319	NM_032804	84890	-0,67	3,49E-04
SURF2	205224_at	NM_017503	NM_017503	6835	-0,67	3,01E-04
MGC12966	224452_s_at	BC006110	NM_032706	84792	-0,67	4,02E-04
FLJ20195	223833_at	BC002482	NM_017706	54853	-0,67	5,69E-03
FLJ20542	233625_x_at	AK021939	NM_017871 NM_032179	54973	-0,67	8,46E-04

LRCH2	227688_at	AK022128	NM_020871	57631	-0,67	2,21E-04
SLC22A17	218675_at	NM_020372	NM_016609 NM_020372	51310	-0,67	3,50E-03
ARNT2	202986_at	NM_014862	NM_014862	9915	-0,67	1,18E-03
LOC440118	AFFX-M27830_M_at	AFFX-M27830_M	XM_498554	440118	-0,67	5,77E-03
FLJ23518	223300_s_at	AI286012	NM_024725	79780	-0,66	7,90E-04
PROSC	209384_at	AA176833	NM_007198	11212	-0,66	1,14E-03
P15RS	222558_at	T79568	NM_018170	55197	-0,66	1,67E-04
PPP2R5C	201877_s_at	NM_002719	NM_002719 NM_178586 NM_178587 NM_178588	5527	-0,66	3,07E-06
SGNE1	203889_at	NM_003020	NM_003020	6447	-0,66	1,31E-04
CNOT6L	1553267_a_at	NM_144571	NM_144571	246175	-0,66	5,11E-03
TTLL1	205652_s_at	NM_012263	NM_001008572 NM_012263	25809	-0,66	3,38E-04
AD023	223411_at	AF225422	NM_020679	57409	-0,66	7,26E-06
KIF3C	203389_at	AF035621	NM_002254	3797	-0,66	2,70E-04
AI598222	235679_at	AI598222	---	---	-0,65	7,93E-03
PPP3CA	202457_s_at	AA911231	NM_000944	5530	-0,65	9,97E-03
RPIP8	213439_x_at	AI197670	NM_006695	10900	-0,65	1,69E-03
NSMCE1	224666_at	AF161451	NM_145080	197370	-0,65	3,16E-04
BACE1	222462_s_at	AI653425	NM_012104 NM_138971 NM_138972 NM_138973	23621	-0,65	3,25E-03
MPI	202472_at	NM_002435	NM_002435	4351	-0,65	8,59E-04
FBXW7	222729_at	BE551877	NM_018315 NM_033632	55294	-0,65	2,52E-03
NELF	221214_s_at	NM_015537	NM_015537	26012	-0,65	7,98E-04
HLA-A	215313_x_at	AA573862	NM_002116	3105	-0,65	7,23E-03
FGF2	204422_s_at	NM_002006	NM_002006	2247	-0,65	4,86E-07
P15RS	225953_at	AI684281	NM_018170	55197	-0,65	3,76E-04
GAS5	224741_x_at	BG329175	---	60674	-0,65	8,18E-03
IPO8	205701_at	NM_006390	NM_006390	10526	-0,65	7,25E-04
ECE2	230706_s_at	AI084921	NM_014693	9718	-0,65	4,71E-04
ZCSL3	213853_at	AL050199	NM_181706	120526	-0,65	6,76E-03
PSEN1	226577_at	N49844	NM_000021 NM_007318 NM_007319	5663	-0,65	3,44E-03
LOC284018	226901_at	AI214996	NM_181655 NM_181656	284018	-0,64	5,00E-04
FLJ32384	238547_at	AI972367	NM_144608	124790	-0,64	3,77E-03
LOC284106	230727_at	BE348515	XM_375449	284106	-0,64	7,65E-03
WDR32	219001_s_at	NM_024345	NM_024345	79269	-0,64	1,25E-04

RNF13	201779_s_at	AF070558	NM_007282 NM_183381 NM_183382 NM_183383 NM_183384	11342	-0,64	1,26E-04
VPS33B	218415_at	NM_018668	NM_018668	26276	-0,64	7,92E-03
SPTBN2	231311_at	AA725246	NM_006946	6712	-0,64	1,71E-03
LOC389906	1569629_x_at	BC017231	XM_372273	389906	-0,64	4,97E-04
C22orf9	227144_at	AA476916	NM_001009880 NM_015264	23313	-0,64	3,58E-03
PHKA1	205450_at	NM_002637	NM_002637	5255	-0,64	3,01E-03
COPS7A	209029_at	AF193844	NM_016319	50813	-0,64	6,55E-05
EIF2S3	205321_at	NM_001415	NM_001415	1968	-0,64	8,39E-03
TM6SF1	1558102_at	AK055438	NM_023003	53346	-0,64	2,18E-04
ATCAY	227365_at	AL566774	NM_033064	85300	-0,64	8,51E-03
CGI-119	223892_s_at	AF182414	NM_016056	51643	-0,64	1,66E-04
APG7L	224025_s_at	BC000091	NM_006395	10533	-0,64	4,74E-03
CIRBP	230142_s_at	AW088030	NM_001280	1153	-0,64	2,64E-03
C21orf127	220311_at	NM_013240	NM_013240 NM_182749	29104	-0,64	2,93E-03
DKFZP566D1346	238597_at	BG028770	NM_030816	81573	-0,63	9,05E-03
WNT3	229103_at	AA463626	NM_030753	7473	-0,63	1,82E-03
C10orf88	219240_s_at	NM_024942	NM_024942	80007	-0,63	2,53E-03
KCNMB3	235980_at	AA767763	NM_014407 NM_171828 NM_171829 NM_171830	27094	-0,63	9,48E-04
LOC440360	236838_at	H11609	XM_498641	440360	-0,63	4,34E-03
AA868380	230569_at	AA868380	---	---	-0,63	7,44E-03
C3orf6	235051_at	BF696931	NM_174908 NM_178335	152137	-0,63	9,04E-03
BLP2	1552426_a_at	NM_078474	NM_025141 NM_078474	80213	-0,63	9,66E-03
PPID	204185_x_at	NM_005038	NM_005038	5481	-0,63	3,34E-03
CXorf12	204340_at	NM_003492	NM_003492	8269	-0,63	4,03E-03
PLCB1	211925_s_at	AY004175	NM_015192 NM_182734	23236	-0,63	8,12E-05
MYO7A	208189_s_at	NM_000260	NM_000260	4647	-0,63	1,17E-04
UBE2D3	229355_at	AU150386	NM_003340 NM_181886 NM_181887 NM_181888 NM_181889 NM_181890 NM_181891 NM_181892 NM_181893	7323	-0,63	6,20E-03
CYP2U1	226393_at	AW055161	NM_183075	113612	-0,63	7,35E-03

PFDN5	207132_x_at	NM_002624	NM_002624 NM_145896 NM_145897	5204	-0,63	9,53E-04
WSB1	201294_s_at	N24643	NM_015626 NM_134264 NM_134265	26118	-0,63	2,39E-03
MGC45386	227008_at	AI393309	NM_198527	374659	-0,63	9,40E-03
PROSC	214545_s_at	NM_007198	NM_007198	11212	-0,62	3,15E-04
SELM	226051_at	BF973568	NM_080430	140606	-0,62	4,03E-03
FLJ21919	202809_s_at	NM_023015	NM_023015	65123	-0,62	7,33E-03
MGC5356	220426_at	NM_024059	NM_024059	79025	-0,62	6,04E-03
KIAA1671	225525_at	AB051458	XM_371461	85379	-0,62	1,04E-03
SNX6	217789_at	NM_021249	NM_021249 NM_152233	58533	-0,62	4,75E-03
MPPE1	213727_x_at	AI743654	NM_023075 NM_138608	65258	-0,62	7,16E-04
ST6GALNAC6	222571_at	AK023900	NM_013443	30815	-0,62	2,17E-03
MGC5391	226639_at	AI304320	NM_032740	84826	-0,62	3,40E-03
MAP7	215471_s_at	AJ242502	NM_003980	9053	-0,62	3,97E-04
FLJ11273	226529_at	BF513060	NM_018374	54664	-0,62	7,53E-03
ADCK2	44120_at	AI879381	NM_052853	90956	-0,62	3,67E-03
TST	209605_at	D87292	NM_003312	7263	-0,62	8,01E-03
NUDT2	218609_s_at	NM_001161	NM_001161 NM_147172 NM_147173	318	-0,62	7,23E-03
AI632010	244687_at	AI632010	---	---	-0,62	3,57E-04
PHC1	225958_at	AI554106	NM_004426	1911	-0,62	8,62E-05
PIK3CB	212688_at	BC003393	NM_006219	5291	-0,62	6,77E-04
LOC401466	1555241_at	BC032347	XM_376783	401466	-0,61	2,14E-03
KIAA1458	224843_at	AB040891	XM_044434	57606	-0,61	4,73E-04
AV756131	224915_x_at	AV756131	XM_497769	441951	-0,61	3,59E-03
APRT	213892_s_at	AA927724	NM_000485	353	-0,61	6,05E-04
WDR41	218055_s_at	NM_018268	NM_018268	55255	-0,61	5,04E-03
LOC143458	234985_at	AW043782	NM_174902	143458	-0,61	1,09E-04
MGC15429	224821_at	AL520200	NM_032750	84836	-0,61	1,73E-03
LOC387593	239715_at	AI374756	---	387593	-0,61	7,41E-03
MGC2494	219709_x_at	NM_023933	NM_023933	65990	-0,61	7,21E-03
SBF2	226169_at	AW276572	NM_030962	81846	-0,61	2,63E-03
CGI-119	222845_x_at	AF161526	NM_016056	51643	-0,61	6,18E-04
UBE2D3	200669_s_at	NM_003340	NM_003340 NM_181886 NM_181887 NM_181888 NM_181889 NM_181890 NM_181891 NM_181892 NM_181893	7323	-0,61	7,57E-04
NPC1L1	220166_at	NM_013389	NM_013389	29881	-0,61	9,81E-04

RNF13	201780_s_at	NM_007282	NM_007282 NM_183381 NM_183382 NM_183383 NM_183384	11342	-0,61	9,87E-04
ARFIP1	214483_s_at	AF124489	NM_014447	27236	-0,60	3,32E-05
AI741365	229757_at	AI741365	---	---	-0,60	4,00E-03
FAM14A	223626_x_at	AF208232	NM_032036	83982	-0,60	4,30E-04
DBT	205369_x_at	J03208	NM_001918	1629	-0,60	2,60E-03
MRPL1	223154_at	AF212225	NM_020236	65008	-0,60	2,59E-03
KIAA1223	225731_at	BF196876	XM_046747	57182	-0,60	4,63E-03
NFATC4	213345_at	AI624015	NM_004554	4776	-0,60	1,80E-03
BF185165	226227_x_at	BF185165	XM_497769	441951	-0,59	3,75E-03
GAL	207466_at	NM_015973	NM_015973	51083	-0,59	6,79E-03
LOC92017	225608_at	H15273	NM_001009607	92017	-0,59	1,54E-05
WDR9	214820_at	AJ002572	NM_001007246 NM_018963 NM_033656	54014	-0,59	4,03E-04
PLEKHA3	223370_at	AF286162	NM_019091	65977	-0,59	4,77E-03
PPM1K	235061_at	AV706522	NM_152542	152926	-0,59	2,94E-03
MTL5	241466_at	AI275776	NM_004923	9633	-0,59	5,56E-04
DHX32	218198_at	NM_018180	NM_018180	55760	-0,59	7,21E-03
DKFZp451M2119	231540_at	BF511274	NM_182565	285023	-0,59	1,28E-03
MTM1	36920_at	U46024	NM_000252	4534	-0,59	4,62E-03
ALKBH	236721_at	AI922200	NM_006020	8846	-0,59	7,70E-03
BC019017	1558128_at	BC019017	---	---	-0,59	1,03E-03
CDC42EP3	209288_s_at	AL136842	NM_006449	10602	-0,59	8,78E-04
FLJ20277	233638_s_at	AK026430	NM_017739	55624	-0,59	4,86E-03
AI766065	224647_at	AI766065	---	---	-0,59	1,11E-03
SETDB2	235339_at	W65369	NM_031915	83852	-0,59	5,43E-03
BE326214	229287_at	BE326214	---	---	-0,59	8,90E-04
HS2ST1	203285_s_at	NM_012262	NM_012262	9653	-0,58	4,84E-04
N51708	213930_at	N51708	XM_499012	441104	-0,58	1,86E-03
GPR56	212070_at	AL554008	NM_005682 NM_201524 NM_201525	9289	-0,58	2,25E-03
LOC119710	228249_at	AA535128	NM_138787	119710	-0,58	7,12E-03
FLJ13576	234726_s_at	AK025482	NM_022484	64418	-0,58	5,50E-03
PFDN5	210908_s_at	AB055804	NM_002624 NM_145896 NM_145897	5204	-0,58	1,71E-03
SIDT2	218765_at	NM_015996	NM_015996	51092	-0,58	4,83E-03
FLJ21168	204666_s_at	NM_025073	NM_025073	80143	-0,58	9,92E-04
KIAA0241	212475_at	AI797458	NM_015060	23080	-0,58	4,82E-05
CHIC1	228345_at	AI745136	XR_000216	53344	-0,58	6,80E-03
BE645776	227288_at	BE645776	XM_068632	133993	-0,58	4,35E-04
CTBS	218923_at	AW304174	NM_004388	1486	-0,58	8,95E-03
TMF1	235566_at	AW591660	NM_007114	7110	-0,58	7,30E-03

PKNOX1	221883_at	AA133342	NM_004571 NM_197976	5316	-0,58	1,27E-03
ACTR1B	202135_s_at	NM_005735	NM_005735	10120	-0,58	2,50E-03
TNFRSF21	214581_x_at	BE568134	NM_014452	27242	-0,58	8,02E-03
PEX7	211033_s_at	BC006268	NM_000288	5191	-0,58	8,93E-03
EIF4E3	225941_at	AI935522	---	317649	-0,58	5,78E-03

Se reivindica lo siguiente:

1. Una línea celular clonal establecida que comprende células susceptibles de intoxicación por una BoNT/A,

donde las células presentan una diferencia de al menos 1.5 veces en los niveles de expresión genética de tres o más genes, en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164 y

donde los niveles de expresión genética se seleccionan del grupo de ADAMTS9, ASCL1, BASP1, DOK5, DPYD, GNB4, GNG11, GTSF1, MAOA, MINA, MSN, PEG3, PLK2, PRSS12, RNF182, SLC44A5, SPARC, TFPI2 y TPTE y

donde la línea celular clonal comprende células susceptibles de intoxicación por BoNT/A en alrededor de 100 pM o menos de una BoNT/A.

2. La línea celular clonal establecida de la Reivindicación 1, donde las células presentan una diferencia de al menos 2.0 veces en los niveles de expresión genética de uno o más genes en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164, una

diferencia de al menos 3.0 veces en los niveles de expresión genética de uno o más genes en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164 o una diferencia de al menos 4.0 veces en los niveles de expresión genética de uno o más genes en comparación con los niveles de expresión de estos genes en células de la línea celular SiMa original DSMZ ACC 164.

3. La línea celular clonal establecida de la Reivindicación 1, donde los niveles de expresión genética se miden antes de la diferenciación de la célula o después de la diferenciación de la célula.

4. La línea celular clonal establecida de la Reivindicación 1, donde la célula de una línea celular clonal presenta alrededor de 100 pM o menos de una BoNT/A en al menos 5 o más pasajes celulares.

RESUMEN DE LA INVENCIÓN

La presente memoria descriptiva describe líneas celulares clonales susceptibles de intoxicación por BoNT/A, métodos para producir tales líneas celulares clonales y métodos para detectar la actividad del serotipo A de la toxina botulínica usando tales líneas celulares clonales.

FIG. 1A.

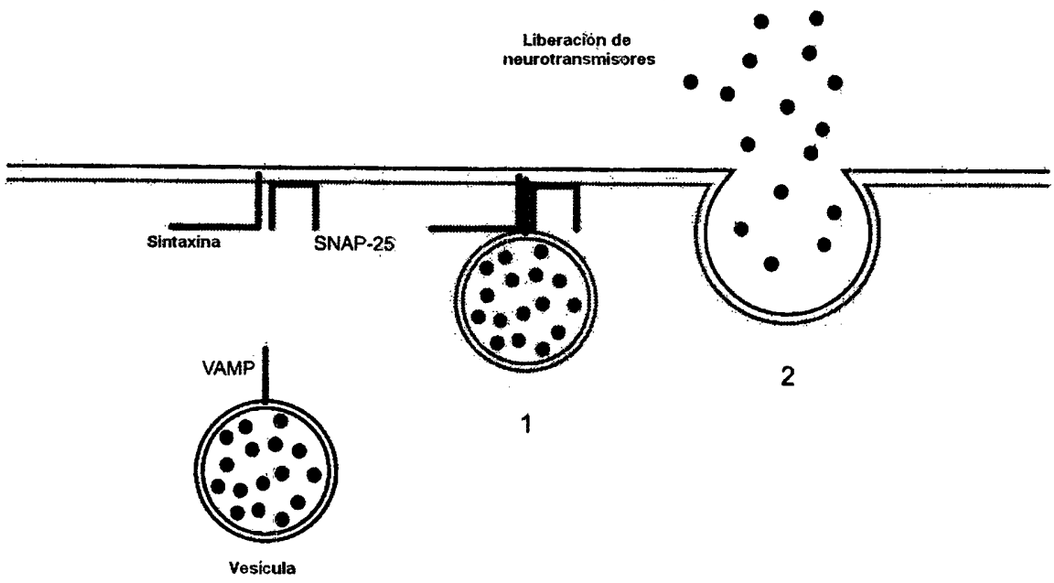

Liberación de
neurotransmisores
Sintaxina
SNAP-25
VAMP
Vesícula
1
2

FIG. 1B.

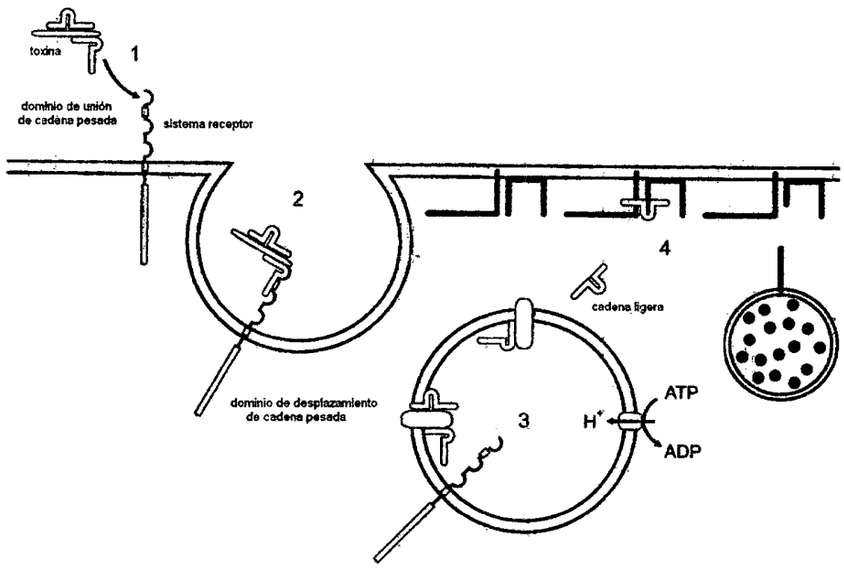

toxina
1
dominio de unión
de cadena pesada
sistema receptor
2
4
cadena ligera
dominio de desplazamiento
de cadena pesada
3
H+
ATP
ADP

FIG. 2A.

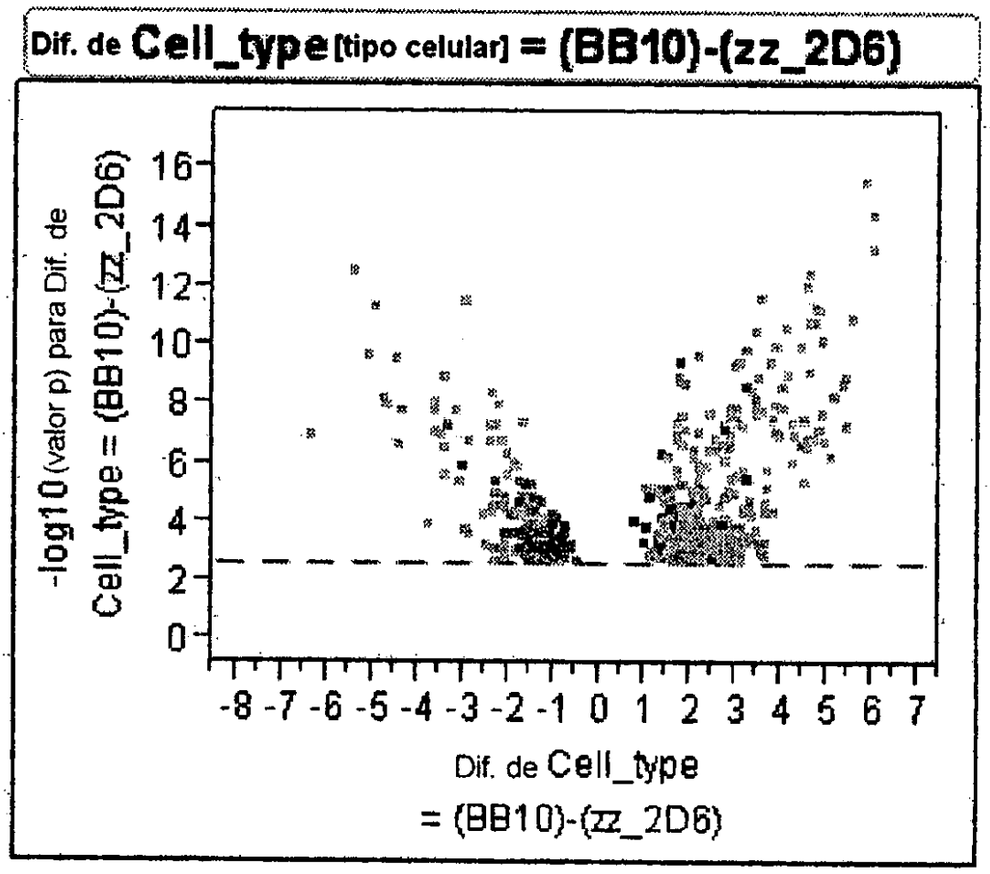

Dif. de Cell_type [tipo celular] = (BB10)-(zz_2D6)
-log10 (valor p) para Dif. de Cell_type = (BB10)-(zz_2D6)
16
14
12
10
8
6
4
2
0
-8 -7 -6 -5 -4 -3 -2 -1 0 1 2 3 4 5 6 7
Dif. de Cell_type
= (BB10)-(zz_2D6)

FIG. 2B.

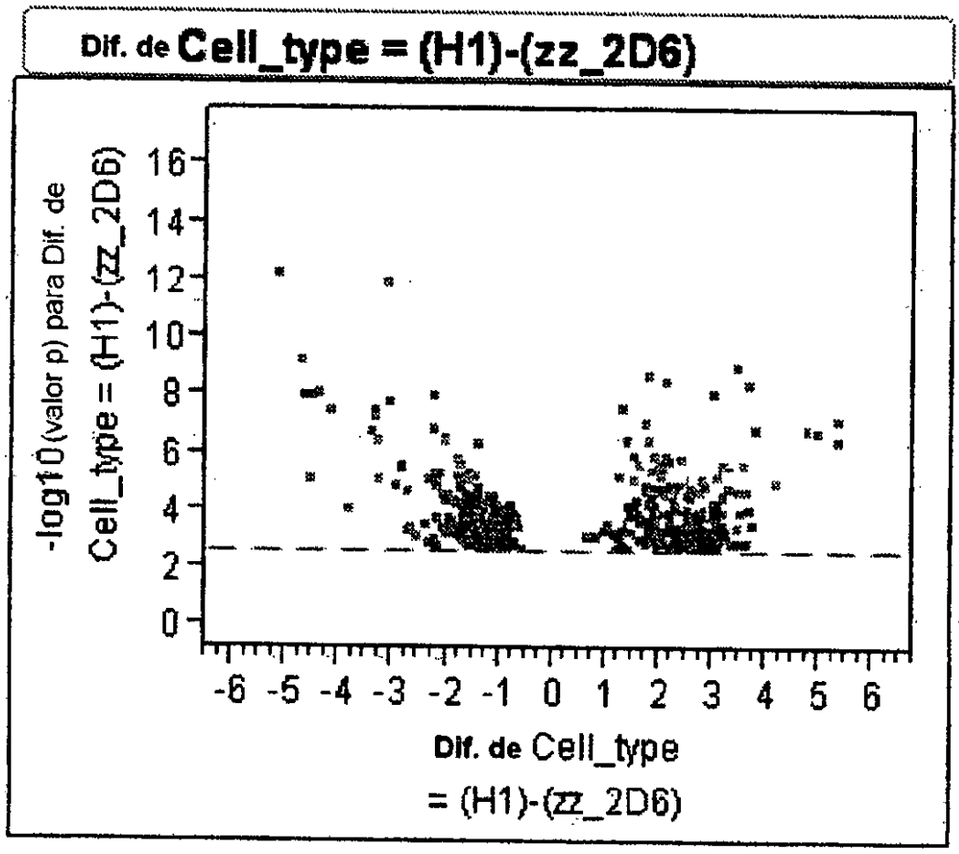

Dif. de Cell_type = (H1)-(zz_2D6)
-log10(valor p) para Dif. de Cell_type = (H1)-(zz_2D6)
16
14
12
10
8
6
4
2
0
-6 -5 -4 -3 -2 -1 0 1 2 3 4 5 6
Dif. de Cell_type = (H1)-(zz_2D6)

FIG. 2C.

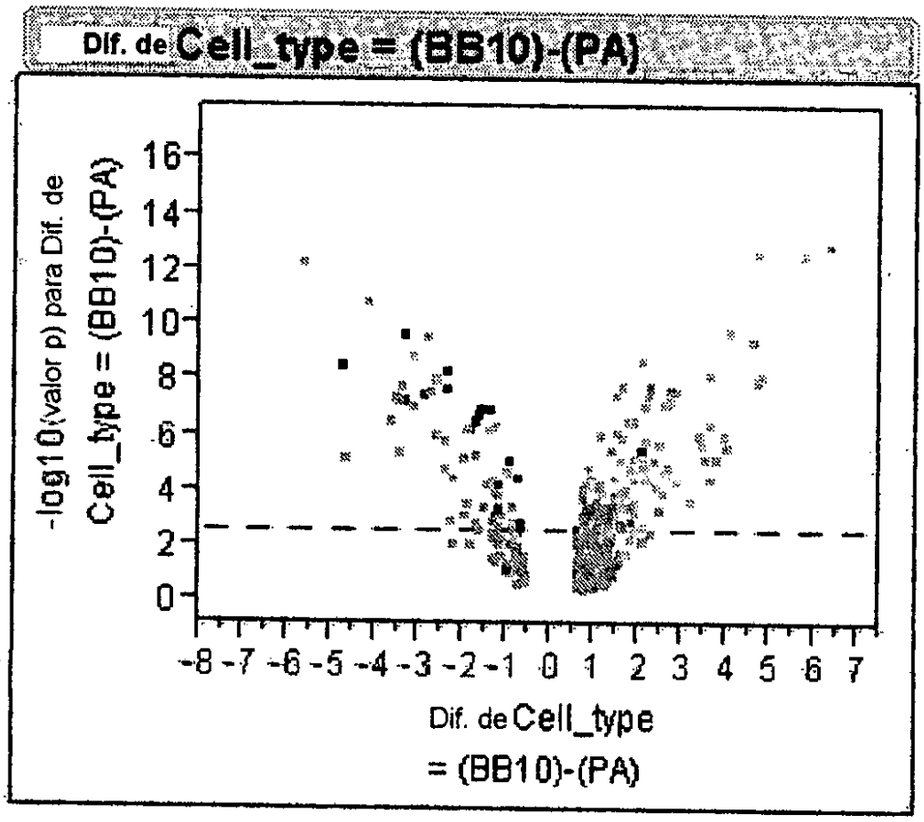

Dif. de Cell_type = (BB10)-(PA)
-log10(valor p) para Dif. de Cell_type = (BB10)-(PA)
16
14
12
10
8
6
4
2
0
-8 -7 -6 -5 -4 -3 -2 -1 0 1 2 3 4 5 6 7
Dif. de Cell_type = (BB10)-(PA)

FIG. 2D.

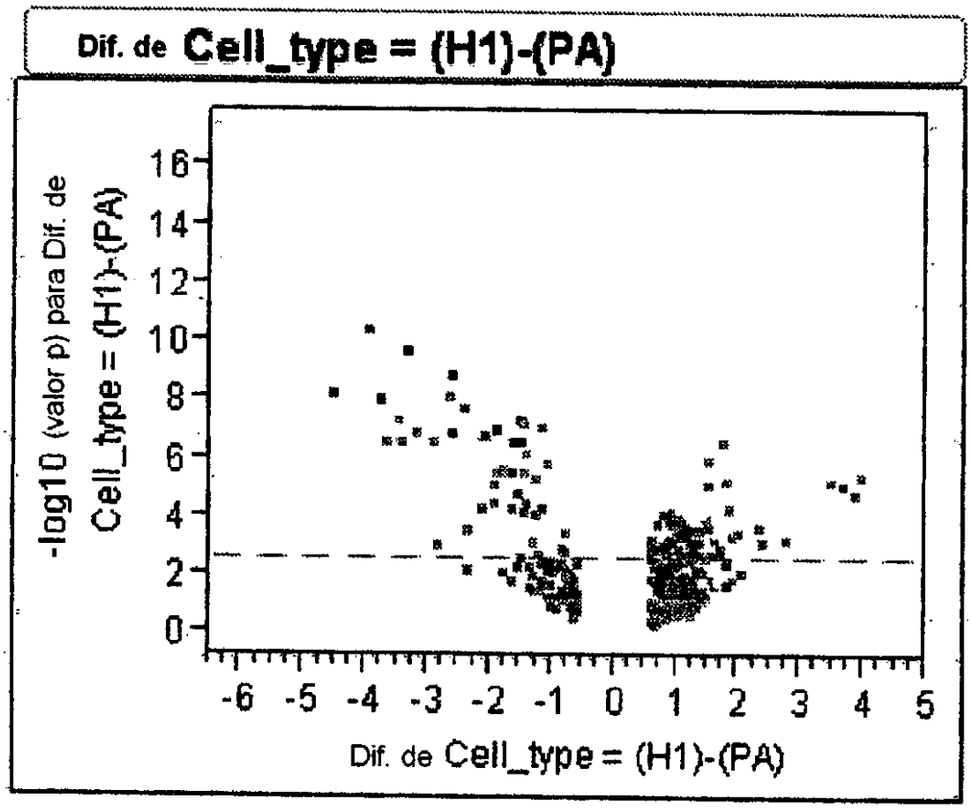

Dif. de Cell_type = (H1)-(PA)
-log10 (valor p) para Dif. de Cell_type = (H1)-(PA)
16
14
12
10
8
6
4
2
0
-6 -5 -4 -3 -2 -1 0 1 2 3 4 5
Dif. de Cell_type = (H1)-(PA)

FIG. 2E.

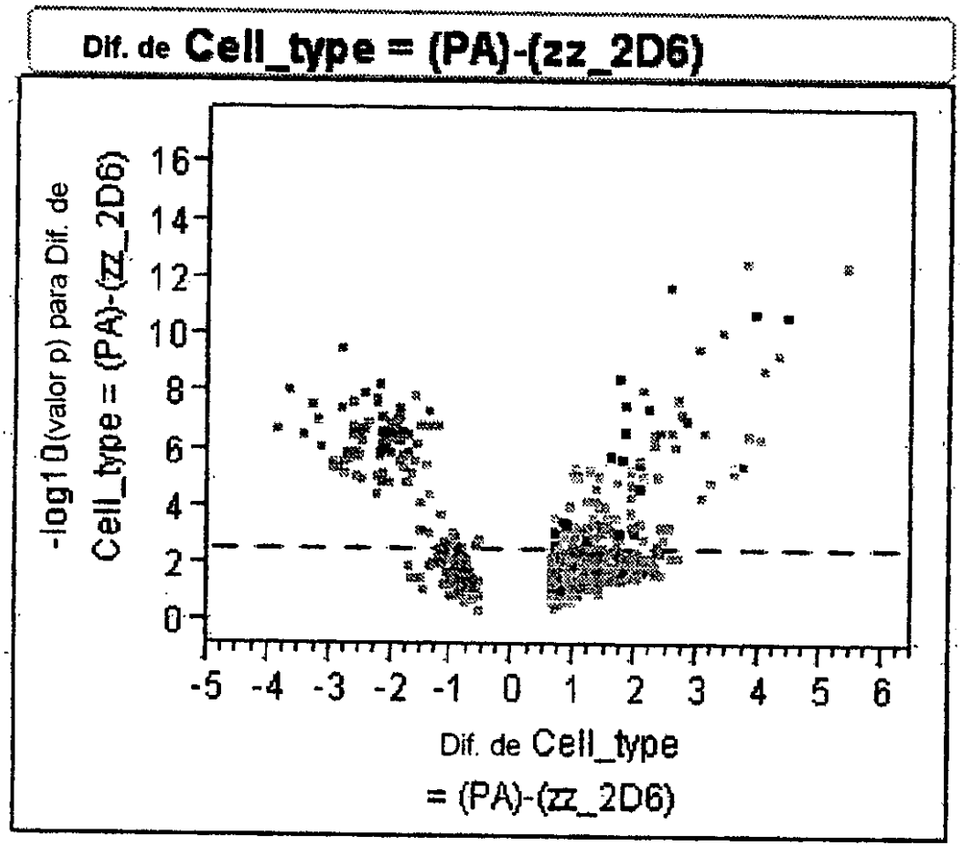
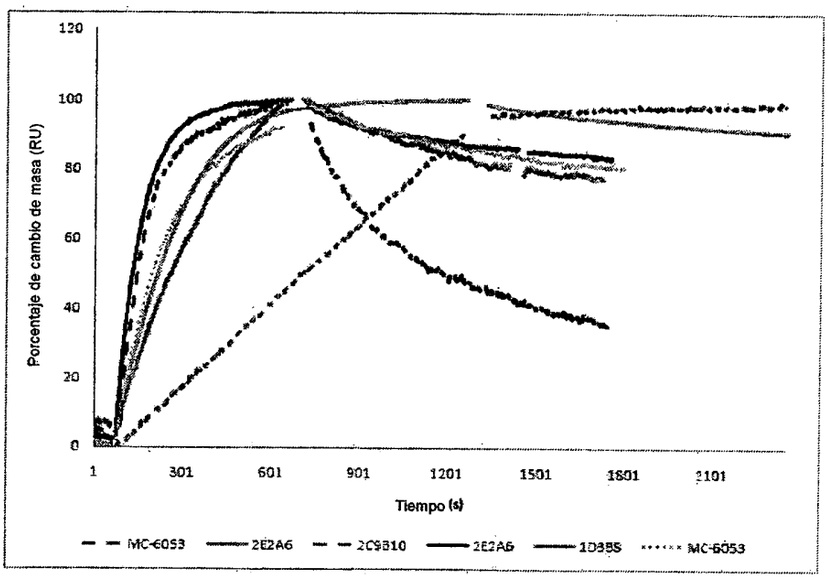
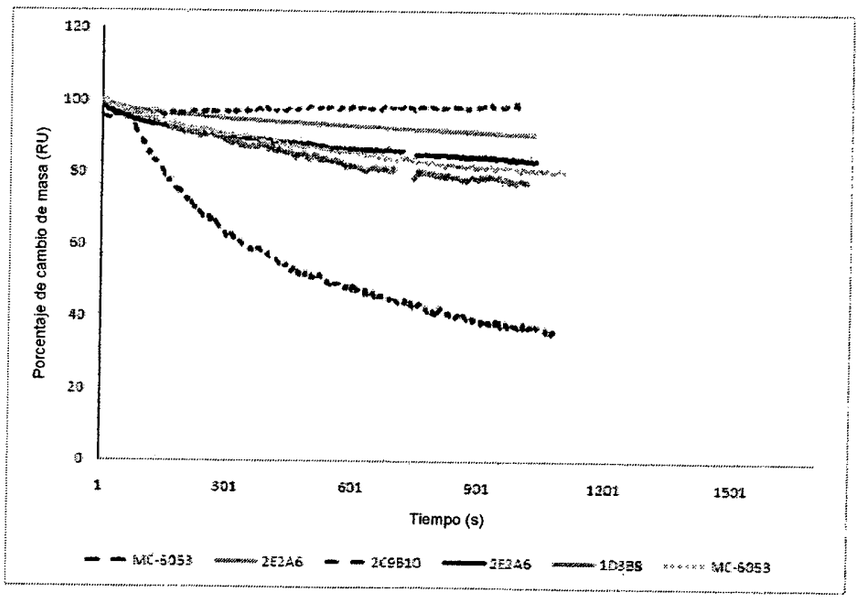

Dif. de Cell_type = (PA)-(zz_2D6)
-log10(valor p) para Dif. de Cell_type = (PA)-(zz_2D6)
16
14
12
10
8
6
4
2
0
-5 -4 -3 -2 -1 0 1 2 3 4 5 6
Dif. de Cell_type = (PA)-(zz_2D6)

FIG. 3A.


120
100
80
60
40
20
0
Porcentaje de cambio de masa (RU)
1
301
601
901
1201
1501
1801
2101
Tiempo (s)
MC-6053
2E2A6
2C9B10
2E2A6
1D3B5
MC-6053

0621

FIG. 3B.


120
100
80
60
40
20
0
Porcentaje de cambio de masa (RU)
1
301
601
901
1201
1501
Tiempo (s)
MC-6053
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1D3B5
MC-6053

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<110> Birgitte Jacky
Wang, Joanne
Zhu, Hong
Hodges, D. Dianne
Fernandez-Salas, Ester

<120> Células útiles para ensayos de actividad de serotipo A de toxina botulínica basados en inmunoensayos

<130> 18495 (BOT)

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Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
        35                  40                  45
Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
    50                  55                  60
Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65                  70                  75                  80
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
                85                  90                  95
Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
            100                 105                 110
Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
        115                 120                 125
Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
    130                 135                 140
Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile
145                 150                 155                 160
Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr
                165                 170                 175
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
            180                 185                 190
Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
        195                 200                 205
Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
    210                 215                 220
Leu Ile His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225                 230                 235                 240
Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
                245                 250                 255
Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
            260                 265                 270
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Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
275 280 285
Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
290 295 300
Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305 310 315 320
Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
325 330 335
Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
340 345 350
Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn
355 360 365
Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr
370 375 380
Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
385 390 395 400
Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu
405 410 415
Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
420 425 430
Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Asp Lys Gly Tyr Asn Lys
435 440 445
Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
450 455 460
Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu
465 470 475 480
Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
485 490 495
Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro
500 505 510
Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
515 520 525
Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
530 535 540
Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu
545 550 555 560
His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu
565 570 575
Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys
580 585 590
Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu
595 600 605
Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr
610 615 620
Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala
625 630 635 640
Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu
645 650 655
Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala
660 665 670
Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys
675 680 685
Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu
690 695 700
Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys
705 710 715 720
Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu
725 730 735
Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn
740 745 750
Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp

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        755                 760                 765
Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile
    770                 775                 780
Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met
785                 790                 795                 800
Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys
                805                 810                 815
Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly
            820                 825                 830
Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp
        835                 840                 845
Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser
    850                 855                 860
Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn
865                 870                 875                 880
Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser
                885                 890                 895
Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn
            900                 905                 910
Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu
        915                 920                 925
Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser
    930                 935                 940
Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn
945                 950                 955                 960
Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val
                965                 970                 975
Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu
            980                 985                 990
Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser
        995                 1000                1005
Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu
    1010                1015                1020
Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro
1025                1030                1035                1040
Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys
                1045                1050                1055
Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe
            1060                1065                1070
Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr
        1075                1080                1085
Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr
    1090                1095                1100
Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn
1105                1110                1115                1120
Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu
                1125                1130                1135
Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser
            1140                1145                1150
Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly
        1155                1160                1165
Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val
    1170                1175                1180
Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala
1185                1190                1195                1200
Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn
                1205                1210                1215
Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr
            1220                1225                1230
Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
        1235                1240                1245
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Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser
1250 1255 1260
Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys
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Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu
1285 1290 1295

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Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
35 40 45
Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
50 55 60
Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65 70 75 80
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
85 90 95
Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
100 105 110
Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
115 120 125
Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
130 135 140
Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile
145 150 155 160
Ile Gln Phe Glu Cys Lys Ser Phe Gly His Asp Val Leu Asn Leu Thr
165 170 175
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
180 185 190
Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
195 200 205
Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
210 215 220
Leu Ile His Ala Glu His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225 230 235 240
Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
245 250 255
Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
260 265 270
Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
275 280 285
Lys Phe Lys Asp Val Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Ile
290 295 300
Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305 310 315 320
Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
325 330 335
Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
340 345 350
Asn Phe Val Asn Phe Phe Lys Val Ile Asn Arg Lys Thr Tyr Leu Asn
355 360 365
Phe Asp Lys Ala Val Phe Arg Ile Asn Ile Val Pro Asp Glu Asn Tyr

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    370                 375                 380
Thr Ile Lys Asp Gly Phe Asn Leu Lys Gly Ala Asn Leu Ser Thr Asn
385                 390                 395                 400
Phe Asn Gly Gln Asn Thr Glu Ile Asn Ser Arg Asn Phe Thr Arg Leu
                405                 410                 415
Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
            420                 425                 430
Gly Ile Ile Pro Phe Lys Thr Lys Ser Leu Asp Glu Gly Tyr Asn Lys
        435                 440                 445
Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
    450                 455                 460
Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asp Lys Val Glu Glu
465                 470                 475                 480
Ile Thr Ala Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
                485                 490                 495
Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asp Phe Asp Asn Glu Pro
            500                 505                 510
Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
        515                 520                 525
Glu Pro Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
    530                 535                 540
Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu
545                 550                 555                 560
His Gly Asp Ser Arg Ile Ile Leu Thr Asn Ser Ala Glu Glu Ala Leu
                565                 570                 575
Leu Lys Pro Asn Val Ala Tyr Thr Phe Phe Ser Ser Lys Tyr Val Lys
            580                 585                 590
Lys Ile Asn Lys Ala Val Glu Ala Phe Met Phe Leu Asn Trp Ala Glu
        595                 600                 605
Glu Leu Val Tyr Asp Phe Thr Asp Glu Thr Asn Glu Val Thr Thr Met
    610                 615                 620
Asp Lys Ile Ala Asp Ile Thr Ile Ile Val Pro Tyr Ile Gly Pro Ala
625                 630                 635                 640
Leu Asn Ile Gly Asn Met Leu Ser Lys Gly Glu Phe Val Glu Ala Ile
                645                 650                 655
Ile Phe Thr Gly Val Val Ala Met Leu Glu Phe Ile Pro Glu Tyr Ala
            660                 665                 670
Leu Pro Val Phe Gly Thr Phe Ala Ile Val Ser Tyr Ile Ala Asn Lys
        675                 680                 685
Val Leu Thr Val Gln Thr Ile Asn Asn Ala Leu Ser Lys Arg Asn Glu
    690                 695                 700
Lys Trp Asp Glu Val Tyr Lys Tyr Thr Val Thr Asn Trp Leu Ala Lys
705                 710                 715                 720
Val Asn Thr Gln Ile Asp Leu Ile Arg Glu Lys Met Lys Lys Ala Leu
                725                 730                 735
Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn
            740                 745                 750
Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp
        755                 760                 765
Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Ser Ala Met Ile Asn Ile
    770                 775                 780
Asn Lys Phe Leu Asp Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met
785                 790                 795                 800
Ile Pro Tyr Ala Val Lys Arg Leu Lys Asp Phe Asp Ala Ser Val Arg
                805                 810                 815
Asp Val Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Val Leu
            820                 825                 830
Gln Val Asp Arg Leu Lys Asp Glu Val Asn Asn Thr Leu Ser Ala Asp
        835                 840                 845
Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Lys Lys Leu Leu Ser
    850                 855                 860
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Thr Phe Thr Glu Tyr Ile Lys Asn Ile Val Asn Thr Ser Ile Leu Ser
865                 870                 875                 880
Ile Val Tyr Lys Lys Asp Asp Leu Ile Asp Leu Ser Arg Tyr Gly Ala
                885                 890                 895
Lys Ile Asn Ile Gly Asp Arg Val Tyr Tyr Asp Ser Ile Asp Lys Asn
            900                 905                 910
Gln Ile Lys Leu Ile Asn Leu Glu Ser Ser Thr Ile Glu Val Ile Leu
        915                 920                 925
Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser
    930                 935                 940
Phe Trp Ile Lys Ile Pro Lys Tyr Phe Ser Lys Ile Asn Leu Asn Asn
945                 950                 955                 960
Glu Tyr Thr Ile Ile Asn Cys Ile Glu Asn Asn Ser Gly Trp Lys Val
                965                 970                 975
Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Asn Lys Gln
            980                 985                 990
Asn Ile Gln Arg Val Val Phe Lys Tyr Ser Gln Met Val Asn Ile Ser
        995                 1000                1005
Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu
    1010                1015                1020
Thr Lys Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro
1025                1030                1035                1040
Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Lys Ile Met Phe Lys
                1045                1050                1055
Leu Asp Gly Cys Arg Asp Pro Arg Arg Tyr Ile Met Ile Lys Tyr Phe
            1060                1065                1070
Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr
        1075                1080                1085
Asp Ser Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asn Tyr
    1090                1095                1100
Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Phe Asp Pro Asn
1105                1110                1115                1120
Lys Tyr Val Asp Val Asn Asn Ile Gly Ile Arg Gly Tyr Met Tyr Leu
                1125                1130                1135
Lys Gly Pro Arg Gly Ser Val Val Thr Thr Asn Ile Tyr Leu Asn Ser
            1140                1145                1150
Thr Leu Tyr Glu Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly
        1155                1160                1165
Asn Glu Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val
    1170                1175                1180
Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala
1185                1190                1195                1200
Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn
                1205                1210                1215
Leu Ser Gln Val Val Val Met Lys Ser Lys Asp Asp Gln Gly Ile Arg
            1220                1225                1230
Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
        1235                1240                1245
Phe Ile Gly Phe His Leu Tyr Asp Asn Ile Ala Lys Leu Val Ala Ser
    1250                1255                1260
Asn Trp Tyr Asn Arg Gln Val Gly Lys Ala Ser Arg Thr Phe Gly Cys
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Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Ser Ser Leu
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            20                  25                  30
Val Lys Ala Phe Lys Ile His Glu Gly Val Trp Val Ile Pro Glu Arg
        35                  40                  45
Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
    50                  55                  60
Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65                  70                  75                  80
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Ile Lys Leu Phe Asp
                85                  90                  95
Arg Ile Tyr Ser Thr Gly Leu Gly Arg Met Leu Leu Ser Phe Ile Val
            100                 105                 110
Lys Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
        115                 120                 125
Val Ile Asp Thr Asn Cys Ile Asn Val Ile Glu Pro Gly Gly Ser Tyr
    130                 135                 140
Arg Ser Glu Glu Leu Asn Leu Val Ile Thr Gly Pro Ser Ala Asp Ile
145                 150                 155                 160
Ile Gln Phe Glu Cys Lys Ser Phe Gly His Asp Val Phe Asn Leu Thr
                165                 170                 175
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
            180                 185                 190
Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
        195                 200                 205
Gly Ala Gly Thr Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
    210                 215                 220
Leu Ile His Ala Ala His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225                 230                 235                 240
Arg Val Leu Lys Val Lys Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
                245                 250                 255
Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly Asn Asp Thr Asn
            260                 265                 270
Phe Ile Asp Ser Leu Trp Gln Lys Lys Phe Ser Arg Asp Ala Tyr Asp
        275                 280                 285
Asn Leu Gln Asn Ile Ala Arg Ile Leu Asn Glu Ala Lys Thr Ile Val
    290                 295                 300
Gly Thr Thr Thr Pro Leu Gln Tyr Met Lys Asn Ile Phe Ile Arg Lys
305                 310                 315                 320
Tyr Phe Leu Ser Glu Asp Ala Ser Gly Lys Ile Ser Val Asn Lys Ala
                325                 330                 335
Ala Phe Lys Glu Phe Tyr Arg Val Leu Thr Arg Gly Phe Thr Glu Leu
            340                 345                 350
Glu Phe Val Asn Pro Phe Lys Val Ile Asn Arg Lys Thr Tyr Leu Asn
        355                 360                 365
Phe Asp Lys Ala Val Phe Arg Ile Asn Ile Val Pro Asp Glu Asn Tyr
    370                 375                 380
Thr Ile Asn Glu Gly Phe Asn Leu Glu Gly Ala Asn Ser Asn Gly Gln
385                 390                 395                 400
Asn Thr Glu Ile Asn Ser Arg Asn Phe Thr Arg Leu Lys Asn Phe Thr
                405                 410                 415
Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg Gly Ile Ile Pro
            420                 425                 430
Phe Lys Thr Lys Ser Leu Asp Glu Gly Tyr Asn Lys Ala Leu Asn Tyr
        435                 440                 445
Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu
    450                 455                 460
Asp Asn Phe Thr Asn Asp Leu Asp Lys Val Glu Glu Ile Thr Ala Asp
465                 470                 475                 480
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Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Ser Asp Leu Ile Gln
485 490 495
Gln Tyr Tyr Leu Thr Phe Asp Phe Asp Asn Glu Pro Glu Asn Ile Ser
500 505 510
Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu Glu Pro Met Pro
515 520 525
Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu Leu Asp Lys Tyr
530 535 540
Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu His Gly Asp Ser
545 550 555 560
Arg Ile Ile Leu Thr Asn Ser Ala Glu Glu Ala Leu Leu Lys Pro Asn
565 570 575
Val Ala Tyr Thr Phe Phe Ser Ser Lys Tyr Val Lys Lys Ile Asn Lys
580 585 590
Ala Val Glu Ala Val Ile Phe Leu Ser Trp Ala Glu Glu Leu Val Tyr
595 600 605
Asp Phe Thr Asp Glu Thr Asn Glu Val Thr Thr Met Asp Lys Ile Ala
610 615 620
Asp Ile Thr Ile Ile Val Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly
625 630 635 640
Asn Met Val Ser Lys Gly Glu Phe Val Glu Ala Ile Leu Phe Thr Gly
645 650 655
Val Val Ala Leu Leu Glu Phe Ile Pro Glu Tyr Ser Leu Pro Val Phe
660 665 670
Gly Thr Phe Ala Ile Val Ser Tyr Ile Ala Asn Lys Val Leu Thr Val
675 680 685
Gln Thr Ile Asn Asn Ala Leu Ser Lys Arg Asn Glu Lys Trp Asp Glu
690 695 700
Val Tyr Lys Tyr Thr Val Thr Asn Trp Leu Ala Lys Val Asn Thr Gln
705 710 715 720
Ile Asp Leu Ile Arg Glu Lys Met Lys Lys Ala Leu Glu Asn Gln Ala
725 730 735
Glu Ala Thr Arg Ala Ile Ile Asn Tyr Gln Tyr Asn Gln Tyr Thr Glu
740 745 750
Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp Leu Ser Ser Lys
755 760 765
Leu Asn Arg Ser Ile Asn Arg Ala Met Ile Asn Ile Asn Lys Phe Leu
770 775 780
Asp Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile Pro Tyr Ala
785 790 795 800
Val Lys Arg Leu Lys Asp Phe Asp Ala Ser Val Arg Asp Val Leu Leu
805 810 815
Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Leu Gln Val Asp Arg
820 825 830
Leu Lys Asp Glu Val Asn Asn Thr Leu Ser Ala Asp Ile Pro Phe Gln
835 840 845
Leu Ser Lys Tyr Val Asn Asp Lys Lys Leu Leu Ser Thr Phe Thr Glu
850 855 860
Tyr Ile Lys Asn Ile Val Asn Thr Ser Ile Leu Ser Ile Val Tyr Lys
865 870 875 880
Lys Asp Asp Leu Ile Asp Leu Ser Arg Tyr Gly Ala Lys Ile Asn Ile
885 890 895
Gly Asp Arg Val Tyr Tyr Asp Ser Ile Asp Lys Asn Gln Ile Lys Leu
900 905 910
Ile Asn Leu Glu Ser Ser Thr Ile Glu Val Ile Leu Lys Asn Ala Ile
915 920 925
Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Lys
930 935 940
Ile Pro Lys Tyr Phe Ser Lys Ile Asn Leu Asn Asn Glu Tyr Thr Ile
945 950 955 960
Ile Asn Cys Ile Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr

965 970 975
Gly Glu Ile Ile Trp Thr Leu Gln Asp Asn Lys Gln Asn Ile Gln Arg
980 985 990
Val Val Phe Lys Tyr Ser Gln Met Val Asn Ile Ser Asp Tyr Ile Asn
995 1000 1005
Arg Trp Met Phe Val Thr Ile Thr Asn Asn Arg Leu Thr Lys Ser Lys
1010 1015 1020
Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu
1025 1030 1035 1040
Gly Asn Ile His Ala Ser Asn Lys Ile Met Phe Lys Leu Asp Gly Cys
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Arg Asp Pro Arg Arg Tyr Ile Met Ile Lys Tyr Phe Asn Leu Phe Asp
1060 1065 1070
Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp Ser Gln Ser
1075 1080 1085
Asn Pro Gly Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Gln Tyr Asp
1090 1095 1100
Lys Pro Tyr Tyr Met Leu Asn Leu Phe Asp Pro Asn Lys Tyr Val Asp
1105 1110 1115 1120
Val Asn Asn Ile Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg
1125 1130 1135
Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Thr Leu Tyr Met
1140 1145 1150
Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Glu Asp Asn
1155 1160 1165
Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn
1170 1175 1180
Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys
1185 1190 1195 1200
Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val
1205 1210 1215
Val Val Met Lys Ser Lys Asp Asp Gln Gly Ile Arg Asn Lys Cys Lys
1220 1225 1230
Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly Phe Val Gly Phe
1235 1240 1245
His Leu Tyr Asp Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn
1250 1255 1260
Arg Gln Val Gly Lys Ala Ser Arg Thr Phe Gly Cys Ser Trp Glu Phe
1265 1270 1275 1280
Ile Pro Val Asp Asp Gly Trp Gly Glu Ser Ser Leu
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Met Pro Leu Val Asn Gln Gln Ile Asn Tyr Tyr Asp Pro Val Asn Gly
1 5 10 15
Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Ala Gly Lys Met Gln Pro
20 25 30
Val Lys Ala Phe Lys Ile His Asn Lys Val Trp Val Ile Pro Glu Arg
35 40 45
Asp Ile Phe Thr Asn Pro Glu Glu Val Asp Leu Asn Pro Pro Pro Glu
50 55 60
Ala Lys Gln Val Pro Ile Ser Tyr Tyr Asp Ser Ala Tyr Leu Ser Thr
65 70 75 80
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Ile Lys Leu Phe Glu
85 90 95

```
Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Ile Ser Ile Val
            100                 105                 110
Arg Gly Ile Pro Phe Trp Gly Gly Gly Lys Ile Asp Thr Glu Leu Lys
        115                 120                 125
Val Ile Asp Thr Asn Cys Ile Asn Ile Ile Gln Leu Asp Asp Ser Tyr
    130                 135                 140
Arg Ser Glu Glu Leu Asn Leu Ala Ile Ile Gly Pro Ser Ala Asn Ile
145                 150                 155                 160
Ile Glu Ser Gln Cys Ser Ser Phe Arg Asp Asp Val Leu Asn Leu Thr
                165                 170                 175
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
            180                 185                 190
Thr Val Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
        195                 200                 205
Gly Ala Gly Lys Phe Ala Gln Asp Pro Ala Val Ala Leu Ala His Glu
    210                 215                 220
Leu Ile His Ala Glu His Arg Leu Tyr Gly Ile Ala Ile Asn Thr Asn
225                 230                 235                 240
Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ala Gly Leu
                245                 250                 255
Glu Val Ser Leu Glu Glu Leu Ile Thr Phe Gly Gly Asn Asp Ala Lys
            260                 265                 270
Phe Ile Asp Ser Leu Gln Lys Lys Glu Phe Ser Leu Tyr Tyr Tyr Asn
        275                 280                 285
Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
    290                 295                 300
Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305                 310                 315                 320
Tyr Leu Leu Ser Glu Asp Ala Thr Gly Lys Phe Leu Val Asp Arg Leu
                325                 330                 335
Lys Phe Asp Glu Leu Tyr Lys Leu Leu Thr Glu Ile Tyr Thr Glu Asp
            340                 345                 350
Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn
        355                 360                 365
Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Asp Val Asn Tyr
    370                 375                 380
Thr Ile His Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
385                 390                 395                 400
Phe Asn Gly Gln Asn Ile Glu Ile Asn Asn Lys Asn Phe Asp Lys Leu
                405                 410                 415
Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
            420                 425                 430
Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Asp Glu Gly Tyr Asn Lys
        435                 440                 445
Ala Leu Asn Glu Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
    450                 455                 460
Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asp Lys Val Glu Glu
465                 470                 475                 480
Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
                485                 490                 495
Asp Leu Ile Gln Gln Tyr Tyr Leu Asn Phe Asn Phe Asp Asn Glu Pro
            500                 505                 510
Glu Asn Thr Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
        515                 520                 525
Glu Pro Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
    530                 535                 540
Leu Asn Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Lys
545                 550                 555                 560
His Ser Asn Ser Arg Ile Ile Leu Thr Asn Ser Ala Lys Glu Ala Leu
                565                 570                 575
Leu Lys Pro Asn Ile Val Tyr Thr Phe Phe Ser Ser Lys Tyr Ile Lys
```

```
          580                 585                 590
Ala Ile Asn Lys Ala Val Glu Ala Val Thr Phe Val Asn Trp Ile Glu
      595                 600                 605
Asn Leu Val Tyr Asp Phe Thr Asp Glu Thr Asn Glu Val Ser Thr Met
  610                 615                 620
Asp Lys Ile Ala Asp Ile Thr Ile Val Ile Pro Tyr Ile Gly Pro Ala
625                 630                 635                 640
Leu Asn Ile Gly Asn Met Ile Tyr Lys Gly Glu Phe Val Glu Ala Ile
                645                 650                 655
Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Ile Val Pro Glu Ile Ala
            660                 665                 670
Leu Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Val Ser Asn Lys
        675                 680                 685
Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu
    690                 695                 700
Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Ile
705                 710                 715                 720
Val Asn Thr Gln Ile Asn Leu Ile Arg Glu Lys Met Lys Lys Ala Leu
                725                 730                 735
Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn
            740                 745                 750
Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp
        755                 760                 765
Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Ser Ala Met Ile Asn Ile
    770                 775                 780
Asn Lys Phe Leu Asp Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met
785                 790                 795                 800
Ile Pro Tyr Ala Val Lys Arg Leu Lys Asp Phe Asp Ala Ser Val Arg
                805                 810                 815
Asp Val Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly
            820                 825                 830
Gln Val Asn Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Ala Asp
        835                 840                 845
Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Lys Lys Leu Leu Ser
    850                 855                 860
Thr Phe Thr Glu Tyr Ile Lys Asn Ile Thr Asn Ala Ser Ile Leu Ser
865                 870                 875                 880
Ile Val Tyr Lys Asp Asp Asp Leu Ile Asp Leu Ser Arg Tyr Gly Ala
                885                 890                 895
Glu Ile Tyr Asn Gly Asp Lys Val Tyr Tyr Asn Ser Ile Asp Lys Asn
            900                 905                 910
Gln Ile Arg Leu Ile Asn Leu Glu Ser Ser Thr Ile Glu Val Ile Leu
        915                 920                 925
Lys Lys Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser
    930                 935                 940
Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn
945                 950                 955                 960
Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val
                965                 970                 975
Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Phe Gln Asp Thr Gln Glu
            980                 985                 990
Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser
        995                 1000                1005
Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Ile
    1010                1015                1020
Thr Lys Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro
1025                1030                1035                1040
Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Lys Ile Met Phe Lys
                1045                1050                1055
Leu Asp Gly Cys Arg Asp Pro His Arg Tyr Ile Val Ile Lys Tyr Phe
            1060                1065                1070
```

```
Asn Leu Phe Asp Lys Glu Leu Ser Glu Lys Glu Ile Lys Asp Leu Tyr
        1075                1080                1085
Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr
    1090                1095                1100
Leu Gln Tyr Asp Lys Ser Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn
1105                1110                1115                1120
Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu
                1125                1130                1135
Lys Gly Pro Arg Asp Asn Val Met Thr Thr Asn Ile Tyr Leu Asn Ser
            1140                1145                1150
Ser Leu Tyr Met Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly
        1155                1160                1165
Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val
    1170                1175                1180
Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala
1185                1190                1195                1200
Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn
                1205                1210                1215
Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr
            1220                1225                1230
Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
        1235                1240                1245
Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser
    1250                1255                1260
Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys
1265                1270                1275                1280
Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Arg Glu Arg Pro Leu
                1285                1290                1295
```

<210> 5
<211> 206
<212> PRT
<213> Homo sapiens

<400> 5

```
Met Ala Glu Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg
 1                5                  10                  15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
        35                  40                  45
Met Leu Asp Glu Gln Gly Glu Gln Leu Asp Arg Val Glu Glu Gly Met
    50                  55                  60
Asn His Ile Asn Gln Asp Met Lys Glu Ala Glu Lys Asn Leu Lys Asp
65                  70                  75                  80
Leu Gly Lys Cys Cys Gly Leu Phe Ile Cys Pro Cys Asn Lys Leu Lys
                85                  90                  95
Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
            100                 105                 110
Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
        115                 120                 125
Ile Ser Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn
    130                 135                 140
Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu
145                 150                 155                 160
Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
                165                 170                 175
Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile
            180                 185                 190
Asp Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
```

195 200 205

<210> 6
<211> 206
<212> PRT
<213> Homo sapiens

<400> 6
Met Ala Glu Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg
1 5 10 15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
20 25 30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
35 40 45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
50 55 60
Asp Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp
65 70 75 80
Leu Gly Lys Phe Cys Gly Leu Cys Val Cys Pro Cys Asn Lys Leu Lys
85 90 95
Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
100 105 110
Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
115 120 125
Ile Ser Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn
130 135 140
Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu
145 150 155 160
Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
165 170 175
Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile
180 185 190
Asp Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
195 200 205

<210> 7
<211> 206
<212> PRT
<213> Macaca mulatta

<400> 7
Met Ala Glu Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg
1 5 10 15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
20 25 30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
35 40 45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
50 55 60
Asp Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp
65 70 75 80
Leu Gly Lys Phe Cys Gly Leu Cys Val Cys Pro Cys Asn Lys Leu Lys
85 90 95
Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
100 105 110
Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
115 120 125
Ile Ser Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn
130 135 140

```
Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu
145                 150                 155                 160
Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
                165                 170                 175
Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile
            180                 185                 190
Asp Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
        195                 200                 205


<210> 8
<211> 206
<212> PRT
<213> Rattus norvegicus

<400> 8
Met Ala Glu Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg
 1                5                  10                  15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
        35                  40                  45
Met Leu Asp Glu Gln Gly Glu Gln Leu Asp Arg Val Glu Glu Gly Met
    50                  55                  60
Asn His Ile Asn Gln Asp Met Lys Glu Ala Glu Lys Asn Leu Lys Asp
65                  70                  75                  80
Leu Gly Lys Cys Cys Gly Leu Phe Ile Cys Pro Cys Asn Lys Leu Lys
                85                  90                  95
Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
            100                 105                 110
Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
        115                 120                 125
Ile Ser Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn
    130                 135                 140
Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu
145                 150                 155                 160
Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
                165                 170                 175
Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile
            180                 185                 190
Asp Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
        195                 200                 205


<210> 9
<211> 206
<212> PRT
<213> Rattus norvegicus

<400> 9
Met Ala Glu Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg
 1                5                  10                  15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
        35                  40                  45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
    50                  55                  60
Asp Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp
65                  70                  75                  80
Leu Gly Lys Phe Cys Gly Leu Cys Val Cys Pro Cys Asn Lys Leu Lys
```

```
                85                  90                  95
Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
            100                 105                 110
Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
        115                 120                 125
Ile Ser Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn
    130                 135                 140
Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu
145                 150                 155                 160
Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
                165                 170                 175
Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile
            180                 185                 190
Asp Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
        195                 200                 205
```

<210> 10
<211> 206
<212> PRT
<213> Mus musculus

<400> 10

```
Met Ala Glu Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg
 1               5                  10                  15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
        35                  40                  45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
    50                  55                  60
Asp Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp
65                  70                  75                  80
Leu Gly Lys Phe Cys Gly Leu Cys Val Cys Pro Cys Asn Lys Leu Lys
                85                  90                  95
Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
            100                 105                 110
Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
        115                 120                 125
Ile Ser Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn
    130                 135                 140
Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu
145                 150                 155                 160
Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
                165                 170                 175
Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile
            180                 185                 190
Asp Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
        195                 200                 205
```

<210> 11
<211> 206
<212> PRT
<213> Gallus gallus

<400> 11

```
Met Ala Glu Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg
 1               5                  10                  15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30
```

```
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
        35                  40                  45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
    50                  55                  60
Asp Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp
65                  70                  75                  80
Leu Gly Lys Phe Cys Gly Leu Cys Val Cys Pro Cys Asn Lys Leu Lys
                85                  90                  95
Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
            100                 105                 110
Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
        115                 120                 125
Ile Ser Gly Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn
    130                 135                 140
Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile Gly Asn Leu
145                 150                 155                 160
Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
                165                 170                 175
Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile
            180                 185                 190
Asp Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
        195                 200                 205
```

<210> 12
<211> 204
<212> PRT
<213> Carassius auratus

<400> 12

```
Met Ala Glu Asp Ala Asp Met Arg Asn Glu Leu Ser Asp Met Gln Gln
 1                  5                  10                  15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
        35                  40                  45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
    50                  55                  60
Asp Gln Ile Asn Lys Asp Met Lys Asp Ala Glu Lys Asn Leu Asn Asp
65                  70                  75                  80
Leu Gly Lys Phe Cys Gly Leu Cys Ser Cys Pro Cys Asn Lys Met Lys
                85                  90                  95
Ser Gly Gly Ser Lys Ala Trp Gly Asn Asn Gln Asp Gly Val Val Ala
            100                 105                 110
Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala Ile Ser
        115                 120                 125
Gly Gly Phe Ile Arg Arg Val Thr Asp Asp Ala Arg Glu Asn Glu Met
    130                 135                 140
Asp Glu Asn Leu Glu Gln Val Gly Gly Ile Ile Gly Asn Leu Arg His
145                 150                 155                 160
Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg Gln Ile
                165                 170                 175
Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile Asp Glu
            180                 185                 190
Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
        195                 200
```

<210> 13
<211> 203
<212> PRT

<213> Carassius auratus

<400> 13

```
Met Ala Asp Glu Ala Asp Met Arg Asn Glu Leu Thr Asp Met Gln Ala
 1               5                  10                  15
Arg Ala Asp Gln Leu Gly Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
        35                  40                  45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
    50                  55                  60
Asp Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp
65                  70                  75                  80
Leu Gly Asn Leu Cys Gly Leu Cys Pro Cys Pro Cys Asn Lys Leu Lys
                85                  90                  95
Gly Gly Gly Gln Ser Trp Gly Asn Asn Gln Asp Gly Val Val Ser Ser
            100                 105                 110
Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala Ile Ser Gly
        115                 120                 125
Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn Glu Met Asp
    130                 135                 140
Glu Asn Leu Glu Gln Val Gly Ser Ile Ile Gly Asn Leu Arg His Met
145                 150                 155                 160
Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg Gln Ile Asp
                165                 170                 175
Arg Ile Met Asp Met Ala Asp Ser Asn Lys Thr Arg Ile Asp Glu Ala
            180                 185                 190
Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
        195                 200
```

<210> 14
<211> 204
<212> PRT
<213> Danio rerio

<400> 14

```
Met Ala Glu Asp Ser Asp Met Arg Asn Glu Leu Ala Asp Met Gln Gln
 1               5                  10                  15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
        35                  40                  45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
    50                  55                  60
Asp Gln Ile Asn Lys Asp Met Lys Asp Ala Glu Lys Asn Leu Asn Asp
65                  70                  75                  80
Leu Gly Lys Phe Cys Gly Leu Cys Ser Cys Pro Cys Asn Lys Met Lys
                85                  90                  95
Ser Gly Ala Ser Lys Ala Trp Gly Asn Asn Gln Asp Gly Val Val Ala
            100                 105                 110
Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala Ile Ser
        115                 120                 125
Gly Gly Phe Ile Arg Arg Val Thr Asp Asp Ala Arg Glu Asn Glu Met
    130                 135                 140
Asp Glu Asn Leu Glu Gln Val Gly Gly Ile Ile Gly Asn Leu Arg His
145                 150                 155                 160
Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg Gln Ile
                165                 170                 175
Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Thr Arg Ile Asp Glu
            180                 185                 190
```

Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
195 200

<210> 15
<211> 203
<212> PRT
<213> Danio rerio

<400> 15
Met Ala Asp Glu Ser Asp Met Arg Asn Glu Leu Asn Asp Met Gln Ala
1 5 10 15
Arg Ala Asp Gln Leu Gly Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
20 25 30
Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
35 40 45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
50 55 60
Asp Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp
65 70 75 80
Leu Gly Asn Leu Cys Gly Leu Cys Pro Cys Pro Cys Asn Lys Leu Lys
85 90 95
Gly Gly Gly Gln Ser Trp Gly Asn Asn Gln Asp Gly Val Val Ser Ser
100 105 110
Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala Ile Ser Gly
115 120 125
Gly Phe Ile Arg Arg Val Thr Asn Asp Ala Arg Glu Asn Glu Met Asp
130 135 140
Glu Asn Leu Glu Gln Val Gly Ser Ile Ile Gly Asn Leu Arg His Met
145 150 155 160
Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg Gln Ile Asp
165 170 175
Arg Ile Met Asp Met Ala Asp Ser Asn Lys Thr Arg Ile Asp Glu Ala
180 185 190
Asn Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
195 200

<210> 16
<211> 210
<212> PRT
<213> Torpedo marmorata

<400> 16
Met Glu Asn Ser Val Glu Asn Ser Met Asp Pro Arg Ser Glu Gln Glu
1 5 10 15
Glu Met Gln Arg Cys Ala Asp Gln Ile Thr Asp Glu Ser Leu Glu Ser
20 25 30
Thr Arg Arg Met Leu Gln Leu Val Glu Glu Ser Lys Asp Ala Gly Ile
35 40 45
Arg Thr Leu Val Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile
50 55 60
Glu Glu Gly Met Asp Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys
65 70 75 80
Asn Leu Ser Asp Leu Gly Lys Cys Cys Gly Leu Cys Ser Cys Pro Cys
85 90 95
Asn Lys Leu Lys Asn Phe Glu Ala Gly Gly Ala Tyr Lys Lys Val Trp
100 105 110
Gly Asn Asn Gln Asp Gly Val Val Ala Ser Gln Pro Ala Arg Val Met
115 120 125
Asp Asp Arg Glu Gln Met Ala Met Ser Gly Gly Tyr Ile Arg Arg Ile

```
    130                 135                 140
Thr Asp Asp Ala Arg Glu Asn Glu Met Glu Glu Asn Leu Asp Gln Val
145                 150                 155                 160
Gly Ser Ile Ile Gly Asn Leu Arg His Met Ala Leu Asp Met Ser Asn
                165                 170                 175
Glu Ile Gly Ser Gln Asn Ala Gln Ile Asp Arg Ile Val Val Lys Gly
            180                 185                 190
Asp Met Asn Lys Ala Arg Ile Asp Glu Ala Asn Lys His Ala Thr Lys
        195                 200                 205
Met Leu
    210
```

<210> 17
<211> 206
<212> PRT
<213> Xenopus laevis

<400> 17

```
Met Ala Asp Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg
 1               5                  10                  15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30
Leu Gln Tyr Val Glu Gly Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
        35                  40                  45
Met Leu Asp Glu Gln Gly Glu Gln Leu Asp Arg Val Glu Glu Gly Met
    50                  55                  60
Asn His Ile Asn Gln Asp Met Lys Glu Ala Glu Lys Asn Leu Lys Asp
65                  70                  75                  80
Leu Gly Lys Cys Cys Gly Leu Phe Ile Cys Pro Cys Asn Lys Leu Lys
                85                  90                  95
Ser Ser Gly Ala Tyr Asn Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
            100                 105                 110
Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
        115                 120                 125
Ile Ser Gly Gly Phe Val Arg Arg Val Thr Asn Asp Ala Arg Glu Thr
    130                 135                 140
Glu Met Asp Glu Asn Leu Glu Gln Val Gly Gly Ile Ile Gly Asn Leu
145                 150                 155                 160
Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
                165                 170                 175
Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Ala Arg Ile
            180                 185                 190
Asp Glu Ala Asn Lys His Ala Thr Lys Met Leu Gly Ser Gly
        195                 200                 205
```

<210> 18
<211> 206
<212> PRT
<213> Xenopus laevis

<400> 18

```
Met Ala Asp Asp Ala Asp Met Arg Asn Glu Leu Glu Glu Met Gln Arg
 1               5                  10                  15
Arg Ala Asp Gln Leu Ala Asp Glu Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30
Leu Gln Tyr Val Glu Gly Ser Lys Asp Ala Gly Ile Arg Thr Leu Val
        35                  40                  45
Met Leu Asp Glu Gln Gly Glu Gln Leu Glu Arg Ile Glu Glu Gly Met
    50                  55                  60
```

```
Glu Gln Ile Asn Lys Asp Met Lys Glu Ala Glu Lys Asn Leu Thr Asp
65                  70                  75                  80
Leu Gly Lys Phe Cys Gly Leu Cys Val Cys Pro Cys Asn Lys Leu Lys
                85                  90                  95
Ser Ser Asp Ala Tyr Lys Lys Ala Trp Gly Asn Asn Gln Asp Gly Val
            100                 105                 110
Val Ala Ser Gln Pro Ala Arg Val Val Asp Glu Arg Glu Gln Met Ala
        115                 120                 125
Ile Ser Gly Gly Phe Val Arg Arg Val Thr Asn Asp Ala Arg Glu Thr
    130                 135                 140
Glu Met Asp Glu Asn Leu Glu Gln Val Gly Gly Ile Ile Gly Asn Leu
145                 150                 155                 160
Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr Gln Asn Arg
                165                 170                 175
Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys Ala Arg Ile
            180                 185                 190
Asp Glu Ala Asn Lys His Ala Thr Lys Met Leu Gly Ser Gly
        195                 200                 205
```

<210> 19
<211> 212
<212> PRT
<213> Strongylocentrotus purpuratus

<400> 19

```
Met Glu Asp Gln Asn Asp Met Asn Met Arg Ser Glu Leu Glu Glu Ile
 1               5                  10                  15
Gln Met Gln Ser Asn Met Gln Thr Asp Glu Ser Leu Glu Ser Thr Arg
            20                  25                  30
Arg Met Leu Gln Met Ala Glu Glu Ser Gln Asp Met Gly Ile Lys Thr
        35                  40                  45
Leu Val Met Leu Asp Glu Gln Gly Glu Gln Leu Asp Arg Ile Glu Glu
    50                  55                  60
Gly Met Asp Gln Ile Asn Thr Asp Met Arg Glu Ala Glu Lys Asn Leu
65                  70                  75                  80
Thr Gly Leu Glu Lys Cys Cys Gly Ile Cys Val Cys Pro Trp Lys Lys
                85                  90                  95
Leu Gly Asn Phe Glu Lys Gly Asp Asp Tyr Lys Lys Thr Trp Lys Gly
            100                 105                 110
Asn Asp Asp Gly Lys Val Asn Ser His Gln Pro Met Arg Met Glu Asp
        115                 120                 125
Asp Arg Asp Gly Cys Gly Gly Asn Ala Ser Met Ile Thr Arg Ile Thr
    130                 135                 140
Asn Asp Ala Arg Glu Asp Glu Met Asp Glu Asn Leu Thr Gln Val Ser
145                 150                 155                 160
Ser Ile Val Gly Asn Leu Arg His Met Ala Ile Asp Met Gln Ser Glu
                165                 170                 175
Ile Gly Ala Gln Asn Ser Gln Val Gly Arg Ile Thr Ser Lys Ala Glu
            180                 185                 190
Ser Asn Glu Gly Arg Ile Asn Ser Ala Asp Lys Arg Ala Lys Asn Ile
        195                 200                 205
Leu Arg Asn Lys
    210
```

<210> 20
<211> 212
<212> PRT
<213> Drosophila melanogaster

<400> 20
Met Pro Ala Asp Pro Ser Glu Glu Val Ala Pro Gln Val Pro Lys Thr
1 5 10 15
Glu Leu Glu Glu Leu Gln Ile Asn Ala Gln Gly Val Ala Asp Glu Ser
20 25 30
Leu Glu Ser Thr Arg Arg Met Leu Ala Leu Cys Glu Glu Ser Lys Glu
35 40 45
Ala Gly Ile Arg Thr Leu Val Ala Leu Asp Asp Gln Gly Glu Gln Leu
50 55 60
Asp Arg Ile Glu Glu Gly Met Asp Gln Ile Asn Ala Asp Met Arg Glu
65 70 75 80
Ala Glu Lys Asn Leu Ser Gly Met Glu Lys Cys Cys Gly Ile Cys Val
85 90 95
Leu Pro Cys Asn Lys Ser Gln Ser Phe Lys Glu Asp Asp Gly Thr Trp
100 105 110
Lys Gly Asn Asp Asp Gly Lys Val Val Asn Asn Gln Pro Gln Arg Val
115 120 125
Met Asp Asp Arg Asn Gly Met Met Ala Gln Ala Gly Tyr Ile Gly Arg
130 135 140
Ile Thr Asn Asp Ala Arg Glu Asp Glu Met Glu Glu Asn Met Gly Gln
145 150 155 160
Val Asn Thr Met Ile Gly Asn Leu Arg Asn Met Ala Leu Asp Met Gly
165 170 175
Ser Glu Leu Glu Asn Gln Asn Arg Gln Ile Asp Arg Ile Asn Arg Lys
180 185 190
Gly Glu Ser Asn Glu Ala Arg Ile Ala Val Ala Asn Gln Arg Ala His
195 200 205
Gln Leu Leu Lys
210

<210> 21
<211> 212
<212> PRT
<213> Hirudo medicinalis

<400> 21
Met Ala Lys Asp Ile Lys Pro Lys Pro Ala Asn Gly Arg Asp Ser Pro
1 5 10 15
Thr Asp Leu Gln Glu Ile Gln Leu Gln Met Asn Ala Ile Thr Asp Asp
20 25 30
Ser Leu Glu Ser Thr Arg Arg Met Leu Ala Met Cys Glu Glu Ser Lys
35 40 45
Asp Ala Gly Ile Arg Thr Leu Val Met Leu Asp Glu Gln Gly Glu Gln
50 55 60
Leu Asp Arg Ile Glu Glu Gly Met Asp Gln Ile Asn Gln Asp Met Arg
65 70 75 80
Asp Ala Glu Lys Asn Leu Glu Gly Met Glu Lys Cys Cys Gly Leu Cys
85 90 95
Ile Leu Pro Trp Lys Arg Thr Lys Asn Phe Asp Lys Gly Ala Glu Trp
100 105 110
Asn Lys Gly Asp Glu Gly Lys Val Asn Thr Asp Gly Pro Arg Leu Val
115 120 125
Val Gly Asp Gly Asn Met Gly Pro Ser Gly Gly Phe Ile Thr Lys Ile
130 135 140
Thr Asn Asp Ala Arg Glu Glu Glu Met Glu Gln Asn Met Gly Glu Val
145 150 155 160
Ser Asn Met Ile Ser Asn Leu Arg Asn Met Ala Val Asp Met Gly Ser
165 170 175
Glu Ile Asp Ser Gln Asn Arg Gln Val Asp Arg Ile Asn Asn Lys Met
180 185 190

```
Thr Ser Asn Gln Leu Arg Ile Ser Asp Ala Asn Lys Arg Ala Ser Lys
        195                 200                 205
Leu Leu Lys Glu
    210
```

<210> 22
<211> 212
<212> PRT
<213> Loligo pealei

<400> 22

```
Met Ser Ala Asn Gly Glu Val Glu Val Pro Lys Thr Glu Leu Glu Glu
 1               5                  10                  15
Ile Gln Gln Gln Cys Asn Gln Val Thr Asp Asp Ser Leu Glu Ser Thr
            20                  25                  30
Arg Arg Met Leu Asn Met Cys Glu Glu Ser Lys Glu Ala Gly Ile Arg
        35                  40                  45
Thr Leu Val Met Leu Asp Glu Gln Gly Glu Gln Leu Asp Arg Ile Glu
    50                  55                  60
Glu Gly Leu Asp Gln Ile Asn Gln Asp Met Lys Asp Ala Glu Lys Asn
65                  70                  75                  80
Leu Glu Gly Met Glu Lys Cys Cys Gly Leu Cys Val Leu Pro Trp Lys
                85                  90                  95
Arg Gly Lys Ser Phe Glu Lys Ser Gly Asp Tyr Ala Asn Thr Trp Lys
            100                 105                 110
Lys Asp Asp Asp Gly Pro Thr Asn Thr Asn Gly Pro Arg Val Thr Val
        115                 120                 125
Gly Asp Gln Asn Gly Met Gly Pro Ser Ser Gly Tyr Val Thr Arg Ile
    130                 135                 140
Thr Asn Asp Ala Arg Glu Asp Asp Met Glu Asn Asn Met Lys Glu Val
145                 150                 155                 160
Ser Ser Met Ile Gly Asn Leu Arg Asn Met Ala Ile Asp Met Gly Asn
                165                 170                 175
Glu Ile Gly Ser Gln Asn Arg Gln Val Asp Arg Ile Gln Gln Lys Ala
            180                 185                 190
Glu Ser Asn Glu Ser Arg Ile Asp Glu Ala Asn Lys Lys Ala Thr Lys
        195                 200                 205
Leu Leu Lys Asn
    210
```

<210> 23
<211> 220
<212> PRT
<213> Lymnaea stagnalis

<400> 23

```
Met Thr Thr Asn Gly Glu Ile Leu Pro Val Gly Glu Glu Glu Glu Glu
 1               5                  10                  15
Glu Leu Gly Glu Asp Ala Leu Leu Arg Lys Gln Ile Asp Cys Asn Thr
            20                  25                  30
Asn Glu Ser Leu Glu Ser Thr Arg Arg Met Leu Ser Leu Cys Glu Glu
        35                  40                  45
Ser Lys Glu Ala Gly Ile Lys Thr Leu Val Met Leu Asp Glu Gln Gly
    50                  55                  60
Glu Gln Leu Asp Arg Ile Glu Glu Gly Met Gly Gln Ile Asn Gln Asp
65                  70                  75                  80
Met Arg Asp Ala Glu Lys Asn Leu Glu Gly Leu Glu Lys Cys Cys Gly
                85                  90                  95
Leu Cys Val Leu Pro Trp Lys Arg Ser Lys Asn Phe Glu Lys Gly Ser
```

```
            100                 105                 110
Asp Tyr Asn Lys Thr Trp Lys Ala Ser Glu Asp Gly Lys Ile Asn Thr
        115                 120                 125
Asn Gly Pro Arg Leu Val Val Asp Gln Gly Asn Gly Ser Gly Pro Thr
    130                 135                 140
Gly Gly Tyr Ile Thr Arg Ile Thr Asn Asp Ala Arg Glu Asp Glu Met
145                 150                 155                 160
Glu Gln Asn Ile Gly Glu Val Ala Gly Met Val Ser Asn Leu Arg Asn
                165                 170                 175
Met Ala Val Asp Met Gly Asn Glu Ile Glu Ser Gln Asn Lys Gln Leu
            180                 185                 190
Asp Arg Ile Asn Gln Lys Gly Gly Ser Leu Asn Val Arg Val Asp Glu
        195                 200                 205
Ala Asn Lys Arg Ala Asn Arg Ile Leu Arg Lys Gln
    210                 215                 220
```

<210> 24
<211> 207
<212> PRT
<213> Caenorhabditis elegans

<400> 24

```
Met Ser Gly Asp Asp Asp Ile Pro Glu Gly Leu Glu Ala Ile Asn Leu
 1               5                  10                  15
Lys Met Asn Ala Thr Thr Asp Asp Ser Leu Glu Ser Thr Arg Arg Met
            20                  25                  30
Leu Ala Leu Cys Glu Glu Ser Lys Glu Ala Gly Ile Lys Thr Leu Val
        35                  40                  45
Met Leu Asp Asp Gln Gly Glu Gln Leu Glu Arg Cys Glu Gly Ala Leu
    50                  55                  60
Asp Thr Ile Asn Gln Asp Met Lys Glu Ala Glu Asp His Leu Lys Gly
65                  70                  75                  80
Met Glu Lys Cys Cys Gly Leu Cys Val Leu Pro Trp Asn Lys Thr Asp
                85                  90                  95
Asp Phe Glu Lys Thr Glu Phe Ala Lys Ala Trp Lys Lys Asp Asp Asp
            100                 105                 110
Gly Gly Val Ile Ser Asp Gln Pro Arg Ile Thr Val Gly Asp Ser Ser
        115                 120                 125
Met Gly Pro Gln Gly Gly Tyr Ile Thr Lys Ile Thr Asn Asp Ala Arg
    130                 135                 140
Glu Asp Glu Met Asp Glu Asn Val Gln Gln Val Ser Thr Met Val Gly
145                 150                 155                 160
Asn Leu Arg Asn Met Ala Ile Asp Met Ser Thr Glu Val Ser Asn Gln
                165                 170                 175
Asn Arg Gln Leu Asp Arg Ile His Asp Lys Ala Gln Ser Asn Glu Val
            180                 185                 190
Arg Val Glu Ser Ala Asn Lys Arg Ala Lys Asn Leu Ile Thr Lys
        195                 200                 205
```

<210> 25
<211> 808
<212> PRT
<213> Homo sapiens

<400> 25

```
Met Gly Ala Pro Ala Cys Ala Leu Ala Leu Cys Val Ala Val Ala Ile
 1               5                  10                  15
Val Ala Gly Ala Ser Ser Glu Ser Leu Gly Thr Glu Gln Arg Val Val
            20                  25                  30
```

```
Gly Arg Ala Ala Glu Val Pro Gly Pro Glu Pro Gly Gln Gln Glu Gln
          35                  40                  45
Leu Val Phe Gly Ser Gly Asp Ala Val Glu Leu Ser Cys Pro Pro Pro
      50                  55                  60
Gly Gly Gly Pro Met Gly Pro Thr Val Trp Val Lys Asp Gly Thr Gly
65                  70                  75                  80
Leu Val Pro Ser Glu Arg Val Leu Val Gly Pro Gln Arg Leu Gln Val
                85                  90                  95
Leu Asn Ala Ser His Glu Asp Ser Gly Ala Tyr Ser Cys Arg Gln Arg
            100                 105                 110
Leu Thr Gln Arg Val Leu Cys His Phe Ser Val Arg Val Thr Asp Ala
        115                 120                 125
Pro Ser Ser Gly Asp Asp Glu Asp Gly Glu Asp Glu Ala Glu Asp Thr
    130                 135                 140
Gly Val Asp Thr Gly Ala Pro Tyr Trp Thr Arg Pro Glu Arg Met Asp
145                 150                 155                 160
Lys Lys Leu Leu Ala Val Pro Ala Ala Asn Thr Val Arg Phe Arg Cys
                165                 170                 175
Pro Ala Ala Gly Asn Pro Thr Pro Ser Ile Ser Trp Leu Lys Asn Gly
            180                 185                 190
Arg Glu Phe Arg Gly Glu His Arg Ile Gly Gly Ile Lys Leu Arg His
        195                 200                 205
Gln Gln Trp Ser Leu Val Met Glu Ser Val Val Pro Ser Asp Arg Gly
    210                 215                 220
Asn Tyr Thr Cys Val Val Glu Asn Lys Phe Gly Ser Ile Arg Gln Thr
225                 230                 235                 240
Tyr Thr Leu Asp Val Leu Glu Arg Ser Pro His Arg Pro Ile Leu Gln
                245                 250                 255
Ala Gly Leu Pro Ala Asn Gln Thr Ala Val Leu Gly Ser Asp Val Glu
            260                 265                 270
Phe His Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Leu
        275                 280                 285
Lys His Val Glu Val Asn Gly Ser Lys Val Gly Pro Asp Gly Thr Pro
    290                 295                 300
Tyr Val Thr Val Leu Lys Ser Trp Ile Ser Glu Ser Val Glu Ala Asp
305                 310                 315                 320
Val Arg Leu Arg Leu Ala Asn Val Ser Glu Arg Asp Gly Gly Glu Tyr
                325                 330                 335
Leu Cys Arg Ala Thr Asn Phe Ile Gly Val Ala Glu Lys Ala Phe Trp
            340                 345                 350
Leu Ser Val His Gly Pro Arg Ala Ala Glu Glu Glu Leu Val Glu Ala
        355                 360                 365
Asp Glu Ala Gly Ser Val Tyr Ala Gly Ile Leu Ser Tyr Gly Val Gly
    370                 375                 380
Phe Phe Leu Phe Ile Leu Val Val Ala Ala Val Thr Leu Cys Arg Leu
385                 390                 395                 400
Arg Ser Pro Pro Lys Lys Gly Leu Gly Ser Pro Thr Val His Lys Ile
                405                 410                 415
Ser Arg Phe Pro Leu Lys Arg Gln Val Ser Leu Glu Ser Asn Ala Ser
            420                 425                 430
Met Ser Ser Asn Thr Pro Leu Val Arg Ile Ala Arg Leu Ser Ser Gly
        435                 440                 445
Glu Gly Pro Thr Leu Ala Asn Val Ser Glu Leu Glu Leu Pro Ala Asp
    450                 455                 460
Pro Lys Trp Glu Leu Ser Arg Ala Arg Leu Thr Leu Gly Lys Pro Leu
465                 470                 475                 480
Gly Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Ile Gly Ile
                485                 490                 495
Asp Lys Asp Arg Ala Ala Lys Pro Val Thr Val Ala Val Lys Met Leu
            500                 505                 510
Lys Asp Asp Ala Thr Asp Lys Asp Leu Ser Asp Leu Val Ser Glu Met
```

```
        515                 520                 525
Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu
    530                 535                 540
Gly Ala Cys Thr Gln Gly Gly Pro Leu Tyr Val Leu Val Glu Tyr Ala
545                 550                 555                 560
Ala Lys Gly Asn Leu Arg Glu Phe Leu Arg Ala Arg Arg Pro Pro Gly
                565                 570                 575
Leu Asp Tyr Ser Phe Asp Thr Cys Lys Pro Pro Glu Glu Gln Leu Thr
            580                 585                 590
Phe Lys Asp Leu Val Ser Cys Ala Tyr Gln Val Ala Arg Gly Met Glu
        595                 600                 605
Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn
    610                 615                 620
Val Leu Val Thr Glu Asp Asn Val Met Lys Ile Ala Asp Phe Gly Leu
625                 630                 635                 640
Ala Arg Asp Val His Asn Leu Asp Tyr Tyr Lys Lys Thr Thr Asn Gly
                645                 650                 655
Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val
            660                 665                 670
Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu
        675                 680                 685
Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val Glu Glu
    690                 695                 700
Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn
705                 710                 715                 720
Cys Thr His Asp Leu Tyr Met Ile Met Arg Glu Cys Trp His Ala Ala
                725                 730                 735
Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg
            740                 745                 750
Val Leu Thr Val Thr Ser Thr Asp Glu Tyr Leu Asp Leu Ser Ala Pro
        755                 760                 765
Phe Glu Gln Tyr Ser Pro Gly Gly Gln Asp Thr Pro Ser Ser Ser Ser
    770                 775                 780
Ser Gly Asp Asp Ser Val Phe Ala His Asp Leu Leu Pro Pro Ala Pro
785                 790                 795                 800
Pro Ser Ser Gly Gly Ser Arg Thr
                805
```

<210> 26
<211> 806
<212> PRT
<213> Homo sapiens

<400> 26

```
Met Gly Ala Pro Ala Cys Ala Leu Ala Leu Cys Val Ala Val Ala Ile
 1               5                  10                  15
Val Ala Gly Ala Ser Ser Glu Ser Leu Gly Thr Glu Gln Arg Val Val
            20                  25                  30
Gly Arg Ala Ala Glu Val Pro Gly Pro Glu Pro Gly Gln Gln Glu Gln
        35                  40                  45
Leu Val Phe Gly Ser Gly Asp Ala Val Glu Leu Ser Cys Pro Pro Pro
    50                  55                  60
Gly Gly Gly Pro Met Gly Pro Thr Val Trp Val Lys Asp Gly Thr Gly
65                  70                  75                  80
Leu Val Pro Ser Glu Arg Val Leu Val Gly Pro Gln Arg Leu Gln Val
                85                  90                  95
Leu Asn Ala Ser His Glu Asp Ser Gly Ala Tyr Ser Cys Arg Gln Arg
            100                 105                 110
Leu Thr Gln Arg Val Leu Cys His Phe Ser Val Arg Val Thr Asp Ala
        115                 120                 125
```

```
Pro Ser Ser Gly Asp Asp Glu Asp Gly Glu Asp Glu Ala Glu Asp Thr
    130                 135                 140
Gly Val Asp Thr Gly Ala Pro Tyr Trp Thr Arg Pro Glu Arg Met Asp
145                 150                 155                 160
Lys Lys Leu Leu Ala Val Pro Ala Ala Asn Thr Val Arg Phe Arg Cys
                165                 170                 175
Pro Ala Ala Gly Asn Pro Thr Pro Ser Ile Ser Trp Leu Lys Asn Gly
            180                 185                 190
Arg Glu Phe Arg Gly Glu His Arg Ile Gly Gly Ile Lys Leu Arg His
        195                 200                 205
Gln Gln Trp Ser Leu Val Met Glu Ser Val Val Pro Ser Asp Arg Gly
    210                 215                 220
Asn Tyr Thr Cys Val Val Glu Asn Lys Phe Gly Ser Ile Arg Gln Thr
225                 230                 235                 240
Tyr Thr Leu Asp Val Leu Glu Arg Ser Pro His Arg Pro Ile Leu Gln
                245                 250                 255
Ala Gly Leu Pro Ala Asn Gln Thr Ala Val Leu Gly Ser Asp Val Glu
            260                 265                 270
Phe His Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Leu
        275                 280                 285
Lys His Val Glu Val Asn Gly Ser Lys Val Gly Pro Asp Gly Thr Pro
    290                 295                 300
Tyr Val Thr Val Leu Lys Thr Ala Gly Ala Asn Thr Thr Asp Lys Glu
305                 310                 315                 320
Leu Glu Val Leu Ser Leu His Asn Val Thr Phe Glu Asp Ala Gly Glu
                325                 330                 335
Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Phe Ser His His Ser Ala
            340                 345                 350
Trp Leu Val Val Leu Pro Ala Glu Glu Glu Leu Val Glu Ala Asp Glu
        355                 360                 365
Ala Gly Ser Val Tyr Ala Gly Ile Leu Ser Tyr Gly Val Gly Phe Phe
    370                 375                 380
Leu Phe Ile Leu Val Val Ala Ala Val Thr Leu Cys Arg Leu Arg Ser
385                 390                 395                 400
Pro Pro Lys Lys Gly Leu Gly Ser Pro Thr Val His Lys Ile Ser Arg
                405                 410                 415
Phe Pro Leu Lys Arg Gln Val Ser Leu Glu Ser Asn Ala Ser Met Ser
            420                 425                 430
Ser Asn Thr Pro Leu Val Arg Ile Ala Arg Leu Ser Ser Gly Glu Gly
        435                 440                 445
Pro Thr Leu Ala Asn Val Ser Glu Leu Glu Leu Pro Ala Asp Pro Lys
    450                 455                 460
Trp Glu Leu Ser Arg Ala Arg Leu Thr Leu Gly Lys Pro Leu Gly Glu
465                 470                 475                 480
Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Ile Gly Ile Asp Lys
                485                 490                 495
Asp Arg Ala Ala Lys Pro Val Thr Val Ala Val Lys Met Leu Lys Asp
            500                 505                 510
Asp Ala Thr Asp Lys Asp Leu Ser Asp Leu Val Ser Glu Met Glu Met
        515                 520                 525
Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gly Ala
    530                 535                 540
Cys Thr Gln Gly Gly Pro Leu Tyr Val Leu Val Glu Tyr Ala Ala Lys
545                 550                 555                 560
Gly Asn Leu Arg Glu Phe Leu Arg Ala Arg Arg Pro Pro Gly Leu Asp
                565                 570                 575
Tyr Ser Phe Asp Thr Cys Lys Pro Pro Glu Glu Gln Leu Thr Phe Lys
            580                 585                 590
Asp Leu Val Ser Cys Ala Tyr Gln Val Ala Arg Gly Met Glu Tyr Leu
        595                 600                 605
Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu
```

```
    610                 615                 620
Val Thr Glu Asp Asn Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg
625                 630                 635                 640
Asp Val His Asn Leu Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu
                645                 650                 655
Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr
            660                 665                 670
His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe
        675                 680                 685
Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe
    690                 695                 700
Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn Cys Thr
705                 710                 715                 720
His Asp Leu Tyr Met Ile Met Arg Glu Cys Trp His Ala Ala Pro Ser
                725                 730                 735
Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg Val Leu
            740                 745                 750
Thr Val Thr Ser Thr Asp Glu Tyr Leu Asp Leu Ser Ala Pro Phe Glu
        755                 760                 765
Gln Tyr Ser Pro Gly Gly Gln Asp Thr Pro Ser Ser Ser Ser Ser Gly
    770                 775                 780
Asp Asp Ser Val Phe Ala His Asp Leu Leu Pro Pro Ala Pro Pro Ser
785                 790                 795                 800
Ser Gly Gly Ser Arg Thr
                805
```

<210> 27
<211> 694
<212> PRT
<213> Homo sapiens

<400> 27

```
Met Gly Ala Pro Ala Cys Ala Leu Ala Leu Cys Val Ala Val Ala Ile
 1                5                  10                  15
Val Ala Gly Ala Ser Ser Glu Ser Leu Gly Thr Glu Gln Arg Val Val
            20                  25                  30
Gly Arg Ala Ala Glu Val Pro Gly Pro Glu Pro Gly Gln Gln Glu Gln
        35                  40                  45
Leu Val Phe Gly Ser Gly Asp Ala Val Glu Leu Ser Cys Pro Pro Pro
    50                  55                  60
Gly Gly Gly Pro Met Gly Pro Thr Val Trp Val Lys Asp Gly Thr Gly
65                  70                  75                  80
Leu Val Pro Ser Glu Arg Val Leu Val Gly Pro Gln Arg Leu Gln Val
                85                  90                  95
Leu Asn Ala Ser His Glu Asp Ser Gly Ala Tyr Ser Cys Arg Gln Arg
            100                 105                 110
Leu Thr Gln Arg Val Leu Cys His Phe Ser Val Arg Val Thr Asp Ala
        115                 120                 125
Pro Ser Ser Gly Asp Asp Glu Asp Gly Glu Asp Glu Ala Glu Asp Thr
    130                 135                 140
Gly Val Asp Thr Gly Ala Pro Tyr Trp Thr Arg Pro Glu Arg Met Asp
145                 150                 155                 160
Lys Lys Leu Leu Ala Val Pro Ala Ala Asn Thr Val Arg Phe Arg Cys
                165                 170                 175
Pro Ala Ala Gly Asn Pro Thr Pro Ser Ile Ser Trp Leu Lys Asn Gly
            180                 185                 190
Arg Glu Phe Arg Gly Glu His Arg Ile Gly Gly Ile Lys Leu Arg His
        195                 200                 205
Gln Gln Trp Ser Leu Val Met Glu Ser Val Val Pro Ser Asp Arg Gly
    210                 215                 220
```

```
Asn Tyr Thr Cys Val Val Glu Asn Lys Phe Gly Ser Ile Arg Gln Thr
225                 230                 235                 240
Tyr Thr Leu Asp Val Leu Glu Arg Ser Pro His Arg Pro Ile Leu Gln
                245                 250                 255
Ala Gly Leu Pro Ala Asn Gln Thr Ala Val Leu Gly Ser Asp Val Glu
            260                 265                 270
Phe His Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Leu
        275                 280                 285
Lys His Val Glu Val Asn Gly Ser Lys Val Gly Pro Asp Gly Thr Pro
    290                 295                 300
Tyr Val Thr Val Leu Lys Val Ser Leu Glu Ser Asn Ala Ser Met Ser
305                 310                 315                 320
Ser Asn Thr Pro Leu Val Arg Ile Ala Arg Leu Ser Ser Gly Glu Gly
                325                 330                 335
Pro Thr Leu Ala Asn Val Ser Glu Leu Glu Leu Pro Ala Asp Pro Lys
            340                 345                 350
Trp Glu Leu Ser Arg Ala Arg Leu Thr Leu Gly Lys Pro Leu Gly Glu
        355                 360                 365
Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Ile Gly Ile Asp Lys
    370                 375                 380
Asp Arg Ala Ala Lys Pro Val Thr Val Ala Val Lys Met Leu Lys Asp
385                 390                 395                 400
Asp Ala Thr Asp Lys Asp Leu Ser Asp Leu Val Ser Glu Met Glu Met
                405                 410                 415
Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gly Ala
            420                 425                 430
Cys Thr Gln Gly Gly Pro Leu Tyr Val Leu Val Glu Tyr Ala Ala Lys
        435                 440                 445
Gly Asn Leu Arg Glu Phe Leu Arg Ala Arg Arg Pro Pro Gly Leu Asp
    450                 455                 460
Tyr Ser Phe Asp Thr Cys Lys Pro Pro Glu Glu Gln Leu Thr Phe Lys
465                 470                 475                 480
Asp Leu Val Ser Cys Ala Tyr Gln Val Ala Arg Gly Met Glu Tyr Leu
                485                 490                 495
Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu
            500                 505                 510
Val Thr Glu Asp Asn Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg
        515                 520                 525
Asp Val His Asn Leu Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu
    530                 535                 540
Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr
545                 550                 555                 560
His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe
                565                 570                 575
Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe
            580                 585                 590
Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn Cys Thr
        595                 600                 605
His Asp Leu Tyr Met Ile Met Arg Glu Cys Trp His Ala Ala Pro Ser
    610                 615                 620
Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg Val Leu
625                 630                 635                 640
Thr Val Thr Ser Thr Asp Glu Tyr Leu Asp Leu Ser Ala Pro Phe Glu
                645                 650                 655
Gln Tyr Ser Pro Gly Gly Gln Asp Thr Pro Ser Ser Ser Ser Ser Gly
            660                 665                 670
Asp Asp Ser Val Phe Ala His Asp Leu Leu Pro Pro Ala Pro Pro Ser
        675                 680                 685
Ser Gly Gly Ser Arg Thr
    690
```

<210> 28
<211> 604
<212> PRT
<213> Homo sapiens

<400> 28
Ala Gln Arg Arg Lys Glu Arg Glu Glu Leu Ala Gln Gln Tyr Glu Ala
1 5 10 15
Ile Leu Arg Glu Cys Gly His Gly Arg Phe Gln Trp Thr Leu Tyr Phe
20 25 30
Val Leu Gly Leu Ala Leu Met Ala Asp Gly Val Glu Val Phe Val Val
35 40 45
Gly Phe Val Leu Pro Ser Ala Glu Lys Asp Met Cys Leu Ser Asp Ser
50 55 60
Asn Lys Gly Met Leu Gly Leu Ile Val Tyr Leu Gly Met Met Val Gly
65 70 75 80
Ala Phe Leu Trp Gly Gly Leu Ala Asp Arg Leu Gly Arg Arg Gln Cys
85 90 95
Leu Leu Ile Ser Leu Ser Val Asn Ser Val Phe Ala Phe Phe Ser Ser
100 105 110
Phe Val Gln Gly Tyr Gly Thr Phe Leu Phe Cys Arg Leu Leu Ser Gly
115 120 125
Val Gly Ile Gly Gly Ser Ile Pro Ile Val Phe Ser Tyr Phe Ser Glu
130 135 140
Phe Leu Ala Gln Glu Lys Arg Gly Glu His Leu Ser Trp Leu Cys Met
145 150 155 160
Phe Trp Met Ile Gly Gly Val Tyr Ala Ala Ala Met Ala Trp Ala Ile
165 170 175
Ile Pro His Tyr Gly Trp Ser Phe Gln Met Gly Ser Ala Tyr Gln Phe
180 185 190
His Ser Trp Arg Val Phe Val Leu Val Cys Ala Phe Pro Ser Val Phe
195 200 205
Ala Ile Gly Ala Leu Thr Thr Gln Pro Glu Ser Pro Arg Phe Phe Leu
210 215 220
Glu Asn Gly Lys His Asp Glu Ala Trp Met Val Leu Lys Gln Val His
225 230 235 240
Asp Thr Asn Met Arg Ala Lys Gly His Pro Glu Arg Val Phe Ser Val
245 250 255
Thr His Ile Lys Thr Ile His Gln Glu Asp Glu Leu Ile Glu Ile Gln
260 265 270
Ser Asp Thr Gly Thr Trp Tyr Gln Arg Trp Gly Val Arg Ala Leu Ser
275 280 285
Leu Gly Gly Gln Val Trp Gly Asn Phe Leu Ser Cys Phe Gly Pro Glu
290 295 300
Tyr Arg Arg Ile Thr Leu Met Met Met Gly Val Trp Phe Thr Met Ser
305 310 315 320
Phe Ser Tyr Tyr Gly Leu Thr Val Trp Phe Pro Asp Met Ile Arg His
325 330 335
Leu Gln Ala Val Asp Tyr Ala Ser Arg Thr Lys Val Phe Pro Gly Glu
340 345 350
Arg Val Glu His Val Thr Phe Asn Phe Thr Leu Glu Asn Gln Ile His
355 360 365
Arg Gly Gly Gln Tyr Phe Asn Asp Lys Phe Ile Gly Leu Arg Leu Lys
370 375 380
Ser Val Ser Phe Glu Asp Ser Leu Phe Glu Glu Cys Tyr Phe Glu Asp
385 390 395 400
Val Thr Ser Ser Asn Thr Phe Phe Arg Asn Cys Thr Phe Ile Asn Thr
405 410 415
Val Phe Tyr Asn Thr Asp Leu Phe Glu Tyr Lys Phe Val Asn Ser Arg
420 425 430

```
Leu Ile Asn Ser Thr Phe Leu His Asn Lys Glu Gly Cys Pro Leu Asp
        435                 440                 445
Val Thr Gly Thr Gly Glu Gly Ala Tyr Met Val Tyr Phe Val Ser Phe
    450                 455                 460
Leu Gly Thr Leu Ala Val Leu Pro Gly Asn Ile Val Ser Ala Leu Leu
465                 470                 475                 480
Met Asp Lys Ile Gly Arg Leu Arg Met Leu Ala Gly Ser Ser Val Met
                485                 490                 495
Ser Cys Val Ser Cys Phe Phe Leu Ser Phe Gly Asn Ser Glu Ser Ala
            500                 505                 510
Met Ile Ala Leu Leu Cys Leu Phe Gly Gly Val Ser Ile Ala Ser Trp
        515                 520                 525
Asn Ala Leu Asp Val Leu Thr Val Glu Leu Tyr Pro Ser Asp Lys Arg
    530                 535                 540
Thr Thr Ala Phe Gly Phe Leu Asn Ala Leu Cys Lys Leu Ala Ala Val
545                 550                 555                 560
Leu Gly Ile Ser Ile Phe Thr Ser Phe Val Gly Ile Thr Lys Ala Ala
                565                 570                 575
Pro Ile Leu Phe Ala Ser Ala Ala Leu Ala Leu Gly Ser Ser Leu Ala
            580                 585                 590
Leu Lys Leu Pro Glu Thr Arg Gly Gln Val Leu Gln
        595                 600
```

<210> 29
<211> 683
<212> PRT
<213> Homo sapiens

<400> 29

```
Met Asp Asp Tyr Lys Tyr Gln Asp Asn Tyr Gly Gly Tyr Ala Pro Ser
 1               5                  10                  15
Asp Gly Tyr Tyr Arg Gly Asn Glu Ser Asn Pro Glu Glu Asp Ala Gln
            20                  25                  30
Ser Asp Val Thr Glu Gly His Asp Glu Glu Asp Glu Ile Tyr Glu Gly
        35                  40                  45
Glu Tyr Gln Gly Ile Pro His Pro Asp Asp Val Lys Ala Lys Gln Ala
    50                  55                  60
Lys Met Ala Pro Ser Arg Met Asp Ser Leu Arg Gly Gln Thr Asp Leu
65                  70                  75                  80
Met Ala Glu Arg Leu Glu Asp Glu Glu Gln Leu Ala His Gln Tyr Glu
                85                  90                  95
Thr Ile Met Asp Glu Cys Gly His Gly Arg Phe Gln Trp Ile Leu Phe
            100                 105                 110
Phe Val Leu Gly Leu Ala Leu Met Ala Asp Gly Val Glu Val Phe Val
        115                 120                 125
Val Ser Phe Ala Leu Pro Ser Ala Glu Lys Asp Met Cys Leu Ser Ser
    130                 135                 140
Ser Lys Lys Gly Met Leu Gly Met Ile Val Tyr Leu Gly Met Met Ala
145                 150                 155                 160
Gly Ala Phe Ile Leu Gly Gly Leu Ala Asp Lys Leu Gly Arg Lys Arg
                165                 170                 175
Val Leu Ser Met Ser Leu Ala Val Asn Ala Ser Phe Ala Ser Leu Ser
            180                 185                 190
Ser Phe Val Gln Gly Tyr Gly Ala Phe Leu Phe Cys Arg Leu Ile Ser
        195                 200                 205
Gly Ile Gly Ile Gly Gly Ala Leu Pro Ile Val Phe Ala Tyr Phe Ser
    210                 215                 220
Glu Phe Leu Ser Arg Glu Lys Arg Gly Glu His Leu Ser Trp Leu Gly
225                 230                 235                 240
Ile Phe Trp Met Thr Gly Gly Leu Tyr Ala Ser Ala Met Ala Trp Ser
```

```
                245                 250                 255
Ile Ile Pro His Tyr Gly Trp Gly Phe Ser Met Gly Thr Asn Tyr His
            260                 265                 270
Phe His Ser Trp Arg Val Phe Val Ile Val Cys Ala Leu Pro Cys Thr
        275                 280                 285
Val Ser Met Val Ala Leu Lys Phe Met Pro Glu Ser Pro Arg Phe Leu
    290                 295                 300
Leu Glu Met Gly Lys His Asp Glu Ala Trp Met Ile Leu Lys Gln Val
305                 310                 315                 320
His Asp Thr Asn Met Arg Ala Lys Gly Thr Pro Glu Lys Val Phe Thr
                325                 330                 335
Val Ser Asn Ile Lys Thr Pro Lys Gln Met Asp Glu Phe Ile Glu Ile
            340                 345                 350
Gln Ser Ser Thr Gly Thr Trp Tyr Gln Arg Trp Leu Val Arg Phe Lys
        355                 360                 365
Thr Ile Phe Lys Gln Val Trp Asp Asn Ala Leu Tyr Cys Val Met Gly
    370                 375                 380
Pro Tyr Arg Met Asn Thr Leu Ile Leu Ala Val Val Trp Phe Ala Met
385                 390                 395                 400
Ala Phe Ser Tyr Tyr Gly Leu Thr Val Trp Phe Pro Asp Met Ile Arg
                405                 410                 415
Tyr Phe Gln Asp Glu Glu Tyr Lys Ser Lys Met Lys Val Phe Phe Gly
            420                 425                 430
Glu His Val Tyr Gly Ala Thr Ile Asn Phe Thr Met Glu Asn Gln Ile
        435                 440                 445
His Gln His Gly Lys Leu Val Asn Asp Lys Phe Thr Arg Met Tyr Phe
    450                 455                 460
Lys His Val Leu Phe Glu Asp Thr Phe Phe Asp Glu Cys Tyr Phe Glu
465                 470                 475                 480
Asp Val Thr Ser Thr Asp Thr Tyr Phe Lys Asn Cys Thr Ile Glu Ser
                485                 490                 495
Thr Ile Phe Tyr Asn Thr Asp Leu Tyr Glu His Lys Phe Ile Asn Cys
            500                 505                 510
Arg Phe Ile Asn Ser Thr Phe Leu Glu Gln Lys Glu Gly Cys His Met
        515                 520                 525
Asp Leu Glu Gln Asp Asn Asp Phe Leu Ile Tyr Leu Val Ser Phe Leu
    530                 535                 540
Gly Ser Leu Ser Val Leu Pro Gly Asn Ile Ile Ser Ala Leu Leu Met
545                 550                 555                 560
Asp Arg Ile Gly Arg Leu Lys Met Ile Gly Gly Ser Met Leu Ile Ser
                565                 570                 575
Ala Val Cys Cys Phe Phe Leu Phe Phe Gly Asn Ser Glu Ser Ala Met
            580                 585                 590
Ile Gly Trp Gln Cys Leu Phe Cys Gly Thr Ser Ile Ala Ala Trp Asn
        595                 600                 605
Ala Leu Asp Val Ile Thr Val Glu Leu Tyr Pro Thr Asn Gln Arg Ala
    610                 615                 620
Thr Ala Phe Gly Ile Leu Asn Gly Leu Cys Lys Phe Gly Ala Ile Leu
625                 630                 635                 640
Gly Asn Thr Ile Phe Ala Ser Phe Val Gly Ile Thr Lys Val Val Pro
                645                 650                 655
Ile Leu Leu Ala Ala Ala Ser Leu Val Gly Gly Gly Leu Ile Ala Leu
            660                 665                 670
Arg Leu Pro Glu Thr Arg Glu Gln Val Leu Ile
        675                 680
```

<210> 30
<211> 727
<212> PRT
<213> Homo sapiens

<400> 30

```
Met Glu Asp Ser Tyr Lys Asp Arg Thr Ser Leu Met Lys Gly Ala Lys
 1               5                  10                  15
Asp Ile Ala Arg Glu Val Lys Lys Gln Thr Val Lys Lys Val Asn Gln
            20                  25                  30
Ala Val Asp Arg Ala Gln Asp Glu Tyr Thr Gln Arg Ser Tyr Ser Arg
        35                  40                  45
Phe Gln Asp Glu Glu Asp Asp Asp Asp Tyr Tyr Pro Ala Gly Glu Thr
    50                  55                  60
Tyr Asn Gly Glu Ala Asn Asp Asp Glu Gly Ser Ser Glu Ala Thr Glu
65                  70                  75                  80
Gly His Asp Glu Asp Asp Glu Ile Tyr Glu Gly Glu Tyr Gln Gly Ile
                85                  90                  95
Pro Ser Met Asn Gln Ala Lys Asp Ser Ile Val Ser Val Gly Gln Pro
            100                 105                 110
Lys Gly Asp Glu Tyr Lys Asp Arg Arg Glu Leu Glu Ser Glu Arg Arg
        115                 120                 125
Ala Asp Glu Glu Glu Leu Ala Gln Gln Tyr Glu Leu Ile Ile Gln Glu
    130                 135                 140
Cys Gly His Gly Arg Phe Gln Trp Ala Leu Phe Phe Val Leu Gly Met
145                 150                 155                 160
Ala Leu Met Ala Asp Gly Val Glu Val Phe Val Val Gly Phe Val Leu
                165                 170                 175
Pro Ser Ala Glu Thr Asp Leu Cys Ile Pro Asn Ser Gly Ser Gly Trp
            180                 185                 190
Leu Gly Ser Ile Val Tyr Leu Gly Met Met Val Gly Ala Phe Phe Trp
        195                 200                 205
Gly Gly Leu Ala Asp Lys Val Gly Arg Lys Gln Ser Leu Leu Ile Cys
    210                 215                 220
Met Ser Val Asn Gly Phe Phe Ala Phe Leu Ser Ser Phe Val Gln Gly
225                 230                 235                 240
Tyr Gly Phe Phe Leu Phe Cys Arg Leu Leu Ser Gly Phe Gly Ile Gly
                245                 250                 255
Gly Ala Ile Pro Thr Val Phe Ser Tyr Phe Ala Glu Val Leu Ala Arg
            260                 265                 270
Glu Lys Arg Gly Glu His Leu Ser Trp Leu Cys Met Phe Trp Met Ile
        275                 280                 285
Gly Gly Ile Tyr Ala Ser Ala Met Ala Trp Ala Ile Ile Pro His Tyr
    290                 295                 300
Gly Trp Ser Phe Ser Met Gly Ser Ala Tyr Gln Phe His Ser Trp Arg
305                 310                 315                 320
Val Phe Val Ile Val Cys Ala Leu Pro Cys Val Ser Ser Val Val Ala
                325                 330                 335
Leu Thr Phe Met Pro Glu Ser Pro Arg Phe Leu Leu Glu Val Gly Lys
            340                 345                 350
His Asp Glu Ala Trp Met Ile Leu Lys Leu Ile His Asp Thr Asn Met
        355                 360                 365
Arg Ala Arg Gly Gln Pro Glu Lys Val Phe Thr Val Asn Lys Ile Lys
    370                 375                 380
Thr Pro Lys Gln Ile Asp Glu Leu Ile Glu Ile Glu Ser Asp Thr Gly
385                 390                 395                 400
Thr Trp Tyr Arg Arg Cys Phe Val Arg Ile Arg Thr Glu Leu Tyr Gly
                405                 410                 415
Ile Trp Leu Thr Phe Met Arg Cys Phe Asn Tyr Pro Val Arg Asp Asn
            420                 425                 430
Thr Ile Lys Leu Thr Ile Val Trp Phe Thr Leu Ser Phe Gly Tyr Tyr
        435                 440                 445
Gly Leu Ser Val Trp Phe Pro Asp Val Ile Lys Pro Leu Gln Ser Asp
    450                 455                 460
Glu Tyr Ala Leu Leu Thr Arg Asn Val Glu Arg Asp Lys Tyr Ala Asn
```

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465                 470                 475                 480
Phe Thr Ile Asn Phe Thr Met Glu Asn Gln Ile His Thr Gly Met Glu
                485                 490                 495
Tyr Asp Asn Gly Arg Phe Ile Gly Val Lys Phe Lys Ser Val Thr Phe
            500                 505                 510
Lys Asp Ser Val Phe Lys Ser Cys Thr Phe Glu Asp Val Thr Ser Val
        515                 520                 525
Asn Thr Tyr Phe Lys Asn Cys Thr Phe Ile Asp Thr Val Phe Asp Asn
    530                 535                 540
Thr Asp Phe Glu Pro Tyr Lys Phe Ile Asp Ser Glu Phe Lys Asn Cys
545                 550                 555                 560
Ser Phe Phe His Asn Lys Thr Gly Cys Gln Ile Thr Phe Asp Asp Asp
                565                 570                 575
Tyr Ser Ala Tyr Trp Ile Tyr Phe Val Asn Phe Leu Gly Thr Leu Ala
            580                 585                 590
Val Leu Pro Gly Asn Ile Val Ser Ala Leu Leu Met Asp Arg Ile Gly
        595                 600                 605
Arg Leu Thr Met Leu Gly Gly Ser Met Val Leu Ser Gly Ile Ser Cys
    610                 615                 620
Phe Phe Leu Trp Phe Gly Thr Ser Glu Ser Met Met Ile Gly Met Leu
625                 630                 635                 640
Cys Leu Tyr Asn Gly Leu Thr Ile Ser Ala Trp Asn Ser Leu Asp Val
                645                 650                 655
Val Thr Val Glu Leu Tyr Pro Thr Asp Arg Arg Ala Thr Gly Phe Gly
            660                 665                 670
Phe Leu Asn Ala Leu Cys Lys Ala Ala Ala Val Leu Gly Asn Leu Ile
        675                 680                 685
Phe Gly Ser Leu Val Ser Ile Thr Lys Ser Ile Pro Ile Leu Leu Ala
    690                 695                 700
Ser Thr Val Leu Val Cys Gly Gly Leu Val Gly Leu Cys Leu Pro Asp
705                 710                 715                 720
Thr Arg Thr Gln Val Leu Met
                725
```

<210> 31
<211> 742
<212> PRT
<213> Homo sapiens

<400> 31

```
Met Glu Glu Gly Phe Arg Asp Arg Ala Ala Phe Ile Arg Gly Ala Lys
 1               5                  10                  15
Asp Ile Ala Lys Glu Val Lys Lys His Ala Ala Lys Lys Val Val Lys
            20                  25                  30
Gly Leu Asp Arg Val Gln Asp Glu Tyr Ser Arg Arg Ser Tyr Ser Arg
        35                  40                  45
Phe Glu Glu Glu Asp Asp Asp Asp Asp Phe Pro Ala Pro Ser Asp Gly
    50                  55                  60
Tyr Tyr Arg Gly Glu Gly Thr Gln Asp Glu Glu Glu Gly Gly Ala Ser
65                  70                  75                  80
Ser Asp Ala Thr Glu Gly His Asp Glu Asp Asp Glu Ile Tyr Glu Gly
                85                  90                  95
Glu Tyr Gln Asp Ile Pro Arg Ala Glu Ser Gly Gly Lys Gly Glu Arg
            100                 105                 110
Met Ala Asp Gly Ala Pro Leu Ala Gly Val Arg Gly Gly Leu Ser Asp
        115                 120                 125
Gly Glu Gly Pro Pro Gly Gly Arg Gly Glu Ala Gln Arg Arg Lys Glu
    130                 135                 140
Arg Glu Glu Leu Ala Gln Gln Tyr Glu Ala Ile Leu Arg Glu Cys Gly
145                 150                 155                 160
```

```
His Gly Arg Phe Gln Trp Thr Leu Tyr Phe Val Leu Gly Leu Ala Leu
                165                 170                 175
Met Ala Asp Gly Val Glu Val Phe Val Val Gly Phe Val Leu Pro Ser
            180                 185                 190
Ala Glu Lys Asp Met Cys Leu Ser Asp Ser Asn Lys Gly Met Leu Gly
        195                 200                 205
Leu Ile Val Tyr Leu Gly Met Met Val Gly Ala Phe Leu Trp Gly Gly
    210                 215                 220
Leu Ala Asp Arg Leu Gly Arg Arg Gln Cys Leu Leu Ile Ser Leu Ser
225                 230                 235                 240
Val Asn Ser Val Phe Ala Phe Phe Ser Ser Phe Val Gln Gly Tyr Gly
                245                 250                 255
Thr Phe Leu Phe Cys Arg Leu Leu Ser Gly Val Gly Ile Gly Gly Ser
            260                 265                 270
Ile Pro Ile Val Phe Ser Tyr Phe Ser Glu Phe Leu Ala Gln Glu Lys
        275                 280                 285
Arg Gly Glu His Leu Ser Trp Leu Cys Met Phe Trp Met Ile Gly Gly
    290                 295                 300
Val Tyr Ala Ala Ala Met Ala Trp Ala Ile Ile Pro His Tyr Gly Trp
305                 310                 315                 320
Ser Phe Gln Met Gly Ser Ala Tyr Gln Phe His Ser Trp Arg Val Phe
                325                 330                 335
Val Leu Val Cys Ala Phe Pro Ser Val Phe Ala Ile Gly Ala Leu Thr
            340                 345                 350
Thr Gln Pro Glu Ser Pro Arg Phe Phe Leu Glu Asn Gly Lys His Asp
        355                 360                 365
Glu Ala Trp Met Val Leu Lys Gln Val His Asp Thr Asn Met Arg Ala
    370                 375                 380
Lys Gly His Pro Glu Arg Val Phe Ser Val Thr His Ile Lys Thr Ile
385                 390                 395                 400
His Gln Glu Asp Glu Leu Ile Glu Ile Gln Ser Asp Thr Gly Thr Trp
                405                 410                 415
Tyr Gln Arg Trp Gly Val Arg Ala Leu Ser Leu Gly Gly Gln Val Trp
            420                 425                 430
Gly Asn Phe Leu Ser Cys Phe Gly Pro Glu Tyr Arg Arg Ile Thr Leu
        435                 440                 445
Met Met Met Gly Val Trp Phe Thr Met Ser Phe Ser Tyr Tyr Gly Leu
    450                 455                 460
Thr Val Trp Phe Pro Asp Met Ile Arg His Leu Gln Ala Val Asp Tyr
465                 470                 475                 480
Ala Ser Arg Thr Lys Val Phe Pro Gly Glu Arg Val Gly His Val Thr
                485                 490                 495
Phe Asn Phe Thr Leu Glu Asn Gln Ile His Arg Gly Gly Gln Tyr Phe
            500                 505                 510
Asn Asp Lys Phe Ile Gly Leu Arg Leu Lys Ser Val Ser Phe Glu Asp
        515                 520                 525
Ser Leu Phe Glu Glu Cys Tyr Phe Glu Asp Val Thr Ser Ser Asn Thr
    530                 535                 540
Phe Phe Arg Asn Cys Thr Phe Ile Asn Thr Val Phe Tyr Asn Thr Asp
545                 550                 555                 560
Leu Phe Glu Tyr Lys Phe Val Asn Ser Arg Leu Ile Asn Ser Thr Phe
                565                 570                 575
Leu His Asn Lys Glu Gly Cys Pro Leu Asp Val Thr Gly Thr Gly Glu
            580                 585                 590
Gly Ala Tyr Met Val Tyr Phe Val Ser Phe Leu Gly Thr Leu Ala Val
        595                 600                 605
Leu Pro Gly Asn Ile Val Ser Ala Leu Leu Met Asp Lys Ile Gly Arg
    610                 615                 620
Leu Arg Met Leu Ala Gly Ser Ser Val Met Ser Cys Val Ser Cys Phe
625                 630                 635                 640
Phe Leu Ser Phe Gly Asn Ser Glu Ser Ala Met Ile Ala Leu Leu Cys
```

```
                645                 650                 655
Leu Phe Gly Gly Val Ser Ile Ala Ser Trp Asn Ala Leu Asp Val Leu
            660                 665                 670
Thr Val Glu Leu Tyr Pro Ser Asp Lys Arg Thr Thr Ala Phe Gly Phe
        675                 680                 685
Leu Asn Ala Leu Cys Lys Leu Ala Ala Val Leu Gly Ile Ser Ile Phe
    690                 695                 700
Thr Ser Phe Val Gly Ile Thr Lys Ala Ala Pro Ile Leu Phe Ala Ser
705                 710                 715                 720
Ala Ala Leu Ala Leu Gly Ser Ser Leu Ala Leu Lys Leu Pro Glu Thr
                725                 730                 735
Arg Gly Gln Val Leu Gln
            740
```

<210> 32
<211> 7
<212> PRT
<213> Secuencia artificial

<220>
<223> antígeno de SNAP-25 que tiene un extremo carboxiterminal libre en el residuo P1 del enlace de escisil del sitio de escisión de la BoNT/A

<400> 32
Arg Ile Asp Glu Ala Asn Gln
1 5

<210> 33
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> antígeno de SNAP-25 que tiene un extremo carboxiterminal libre en el residuo P1 del enlace de escisil del sitio de escisión de la BoNT/A

<400> 33
Thr Arg Ile Asp Glu Ala Asn Gln
1 5

<210> 34
<211> 9
<212> PRT
<213> Secuencia artificial

<220>
<223> antígeno de SNAP-25 que tiene un extremo carboxiterminal libre en el residuo P1 del enlace de escisil del sitio de escisión de la BoNT/A

<400> 34
Lys Thr Arg Ile Asp Glu Ala Asn Gln
1 5

<210> 35
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> antígeno de SNAP-25 que tiene un extremo carboxiterminal libre en el residuo P1 del enlace de escísil del sitio de escisión de la BoNT/A

<400> 35
Asn Lys Thr Arg Ile Asp Glu Ala Asn Gln
1 5 10

<210> 36
<211> 11
<212> PRT
<213> Secuencia artificial

<220>
<223> antígeno de SNAP-25 que tiene un extremo carboxiterminal libre en el residuo P1 del enlace de escísil del sitio de escisión de la BoNT/A

<400> 36
Ser Asn Lys Thr Arg Ile Asp Glu Ala Asn Gln
1 5 10

<210> 37
<211> 12
<212> PRT
<213> Secuencia artificial

<220>
<223> antígeno de SNAP-25 que tiene un extremo carboxiterminal libre en el residuo P1 del enlace de escísil del sitio de escisión de la BoNT/A

<400> 37
Asp Ser Asn Lys Thr Arg Ile Asp Glu Ala Asn Gln
1 5 10

<210> 38
<211> 13
<212> PRT
<213> Secuencia artificial

<220>
<223> antígeno de SNAP-25 que tiene un extremo carboxiterminal carboxilado libre en el residuo P1 del enlace de escísil del sitio de escisión de la BoNT/A

<221> SITIO
<222> (13)...(13)
<223> glutamina carboxilada

<400> 38

Cys Asp Ser Asn Lys Thr Arg Ile Asp Glu Ala Asn Gln
1 5 10

<210> 39
<211> 7
<212> PRT
<213> Secuencia artificial

<220>
<223> antígeno de SNAP-25 que tiene un extremo carboxiterminal libre en el residuo P1 del enlace de escísil del sitio de escisión de la BoNT/A

<400> 39
Arg Ile Asp Glu Ala Asn Lys
1 5

<210> 40
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> antígeno de SNAP-25 que tiene un extremo carboxiterminal libre en el residuo P1 del enlace de escísil del sitio de escisión de la BoNT/A

<400> 40
Ala Arg Ile Asp Glu Ala Asn Lys
1 5

<210> 41
<211> 9
<212> PRT
<213> Secuencia artificial

<220>
<223> antígeno de SNAP-25 que tiene un extremo carboxiterminal libre en el residuo P1 del enlace de escísil del sitio de escisión de la BoNT/A

<400> 41
Lys Ala Arg Ile Asp Glu Ala Asn Lys
1 5

<210> 42
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> antígeno de SNAP-25 que tiene un extremo carboxiterminal libre en el residuo P1 del enlace de escísil del sitio de escisión de la BoNT/A

<400> 42
Asn Lys Ala Arg Ile Asp Glu Ala Asn Lys

1 5 10

<210> 43
<211> 11
<212> PRT
<213> Secuencia artificial

<220>
<223> antígeno de SNAP-25 que tiene un extremo carboxiterminal libre en el residuo P1 del enlace de escísil del sitio de escisión de la BoNT/A

<400> 43
Met Asn Lys Ala Arg Ile Asp Glu Ala Asn Lys
1 5 10

<210> 44
<211> 12
<212> PRT
<213> Secuencia artificial

<220>
<223> antígeno de SNAP-25 que tiene un extremo carboxiterminal libre en el residuo P1 del enlace de escísil del sitio de escisión de la BoNT/A

<400> 44
Asp Met Asn Lys Ala Arg Ile Asp Glu Ala Asn Lys
1 5 10

<210> 45
<211> 13
<212> PRT
<213> Secuencia artificial

<220>
<223> antígeno de SNAP-25 que tiene un extremo carboxiterminal carboxilado libre en el residuo P1 del enlace de escísil del sitio de escisión de la BoNT/A

<221> SITE
<222> (13)...(13)
<223> Lisina carboxilada

<400> 45
Cys Asp Met Asn Lys Ala Arg Ile Asp Glu Ala Asn Lys
1 5 10

<210> 46
<211> 11
<212> PRT
<213> Secuencia artificial

<220>
<223> antígeno de SNAP-25

<400> 46

Cys Gly Gly Gly Arg Ile Asp Glu Ala Asn Gln
1 5 10

<210> 47
<211> 11
<212> PRT
<213> Secuencia artificial

<220>
<223> antígeno de SNAP-25

<400> 47
Cys Gly Gly Gly Arg Ile Asp Glu Ala Asn Lys
1 5 10

<210> 48
<211> 88
<212> PRT
<213> Secuencia artificial

<220>
<223> BirA-HisTag?-SNAP-25-134-197

<400> 48
Met Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp
1 5 10 15
His His His His His His His Ile Arg Arg Val Thr Asn Asp Ala
20 25 30
Arg Glu Asn Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile
35 40 45
Gly Asn Leu Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr
50 55 60
Gln Asn Arg Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys
65 70 75 80
Thr Arg Ile Asp Glu Ala Asn Gln
85

<210> 49
<211> 97
<212> PRT
<213> Secuencia artificial

<220>
<223> BirA-HisTag?-SNAP-25-134-206

<400> 49
Met Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp
1 5 10 15
His His His His His His His Ile Arg Arg Val Thr Asn Asp Ala
20 25 30
Arg Glu Asn Glu Met Asp Glu Asn Leu Glu Gln Val Ser Gly Ile Ile
35 40 45
Gly Asn Leu Arg His Met Ala Leu Asp Met Gly Asn Glu Ile Asp Thr
50 55 60
Gln Asn Arg Gln Ile Asp Arg Ile Met Glu Lys Ala Asp Ser Asn Lys
65 70 75 80
Thr Arg Ile Asp Glu Ala Asn Gln Arg Ala Thr Lys Met Leu Gly Ser
85 90 95

Gly

<210> 50
<211> 16
<212> PRT
<213> Secuencia artificial

<220>
<223> péptido BirA

<400> 50
Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His
1 5 10 15

<210> 51
<211> 7570
<212> ADN
<213> Secuencia artificial

<220>
<223> construcción de expresión pQBI-25/GFP-BoNT/A-LC.

<400> 51
gacggatcgg gagatctccc gatcccctat ggtcgactct cagtacaatc tgctctgatg 60
ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
ttagggttag gcgttttgcg ctgcttcgcc tcgaggcctg gccattgcat acgttgtatc 240
catatcataa tatgtacatt tatattggct catgtccaac attaccgcca tgttgacatt 300
gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 360
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 420
cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 480
attgacgtca atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt 540
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 600
atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca 660
tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg 720
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 780
aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg 840
gtaggcgtgt acggtgggag gtctatataa gcagagctcg tttagtgaac cgtcagatcg 900
cctggagacg ccatccacgc tgttttgacc tccatagaag acaccgggac cgatccagcc 960
tccgcgggcc accatggagg gcccggttac cggtaccgga tccagatatc tgggcggccg 1020
ctcagcaagc ttcgcgaatt cgggaggcgg aggtggagct agcaaaggag aagaactctt 1080
cactggagtt gtcccaattc ttgttgaatt agatggtgat gttaacggcc acaagttctc 1140
tgtcagtgga gagggtgaag gtgatgcaac atacggaaaa cttaccctga agttcatctg 1200
cactactggc aaactgcctg ttccatggcc aacactagtc actactctgt gctatggtgt 1260
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gcctaactac ggctacacta gaaggacagt atttggtatc tgcgctctgc tgaagccagt 4980
taccttcgga aaaagagttg gtagctcttg atccggcaaa caaaccaccg ctggtagcgg 5040
tggtttttt gtttgcaagc agcagattac gcgcagaaaa aaaggatctc aagaagatcc 5100
tttgatcttt tctacggggt ctgacgctca gtggaacgaa aactcacgtt aagggatttt 5160
ggtcatgaga ttatcaaaaa ggatcttcac ctagatcctt ttaaattaaa aatgaagttt 5220
taaatcaatc taaagtatat atgagtaaac ttggtctgac agttaccaat gcttaatcag 5280
tgaggcacct atctcagcga tctgtctatt tcgttcatcc atagttgcct gactccccgt 5340
cgtgtagata actacgatac gggagggctt accatctggc cccagtgctg caatgatacc 5400
gcgagaccca cgctcaccgg ctccagattt atcagcaata aaccagccag ccggaagggc 5460
cgagcgcaga agtggtcctg caactttatc cgcctccatc cagtctatta attgttgccg 5520
ggaagctaga gtaagtagtt cgccagttaa tagtttgcgc aacgttgttg ccattgctac 5580
aggcatcgtg gtgtcacgct cgtcgtttgg tatggcttca ttcagctccg gttcccaacg 5640
atcaaggcga gttacatgat cccccatgtt gtgcaaaaaa gcggttagct ccttcggtcc 5700
tccgatcgtt gtcagaagta agttggccgc agtgttatca ctcatggtta tggcagcact 5760
gcataattct cttactgtca tgccatccgt aagatgcttt tctgtgactg gtgagtactc 5820
aaccaagtca ttctgagaat agtgtatgcg gcgaccgagt tgctcttgcc cggcgtcaat 5880
acgggataat accgcgccac atagcagaac tttaaaagtg ctcatcattg gaaaacgttc 5940
ttcggggcga aaactctcaa ggatcttacc gctgttgaga tccagttcga tgtaacccac 6000
tcgtgcaccc aactgatctt cagcatcttt tactttcacc agcgtttctg ggtgagcaaa 6060
aacaggaagg caaaatgccg caaaaaaggg aataagggcg acacggaaat gttgaatact 6120
catactcttc ctttttcaat attattgaag catttatcag ggttattgtc tcatgagcgg 6180
atacatattt gaatgtattt agaaaaataa acaaataggg gttccgcgca catttccccg 6240

aaaagtgcca cctgacgtc 6259

<210> 54
<211> 245
<212> PRT
<213> Secuencia artificial

<220>
<223> secuencia de aminoácidos GFP.

<400> 54

Ala	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val
1				5				10						15	
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu
			20					25					30		
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys
		35					40					45			
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu
	50					55					60				
Cys	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg
65					70					75					80
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg
				85					90					95	
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val
			100					105					110		
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile
		115					120					125			
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn
	130					135					140				
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly
145					150					155					160
Ile	Lys	Val	Asn	Phe	Lys	Thr	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val
				165					170					175	
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro
			180					185					190		
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser
		195					200					205			
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val
	210					215					220				
Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Asn	Ile	Asp
225					230					235					240
Gly	Gly	Gly	Gly	Gly											
				245											

<210> 55
<211> 4
<212> PRT
<213> Secuencia artificial

<220>
<223> espaciador flexible espaciador G

<400> 55

Gly	Gly	Gly	Gly
1			

<210> 56

<211> 5
<212> PRT
<213> Secuencia artificial

<220>
<223> espaciador flexible espaciador G

<400> 56
Gly Gly Gly Gly Ser
1 5

<210> 57
<211> 4
<212> PRT
<213> Secuencia artificial

<220>
<223> espaciador flexible espaciador A

<400> 57
Ala Ala Ala Ala
1

<210> 58
<211> 5
<212> PRT
<213> Secuencia artificial

<220>
<223> espaciador flexible espaciador A

<400> 58
Ala Ala Ala Ala Val
1 5

<210> 59
<211> 821
<212> PRT
<213> Homo sapiens

<400> 59
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
1 5 10 15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
20 25 30
Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
35 40 45
Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
50 55 60
Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65 70 75 80
Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
85 90 95
Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
100 105 110
Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
115 120 125
Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val

```
    130                 135                 140
Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145                 150                 155                 160
Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
                165                 170                 175
Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
            180                 185                 190
Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
        195                 200                 205
Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
    210                 215                 220
Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225                 230                 235                 240
Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
                245                 250                 255
Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
            260                 265                 270
Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
        275                 280                 285
Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
    290                 295                 300
Gly Leu Pro Tyr Leu Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr
305                 310                 315                 320
Asp Lys Glu Ile Glu Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp
                325                 330                 335
Ala Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe
            340                 345                 350
His Ser Ala Trp Leu Thr Val Leu Pro Ala Pro Gly Arg Glu Lys Glu
        355                 360                 365
Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly
    370                 375                 380
Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met
385                 390                 395                 400
Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His
                405                 410                 415
Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala
            420                 425                 430
Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr
        435                 440                 445
Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser
    450                 455                 460
Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys
465                 470                 475                 480
Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val
                485                 490                 495
Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val
            500                 505                 510
Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu
        515                 520                 525
Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His
    530                 535                 540
Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu
545                 550                 555                 560
Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu
                565                 570                 575
Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg
            580                 585                 590
Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr
        595                 600                 605
Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His
    610                 615                 620
```

Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met
625 630 635 640
Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr
645 650 655
Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro
660 665 670
Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser
675 680 685
Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr
690 695 700
Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His
705 710 715 720
Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met
725 730 735
Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln
740 745 750
Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu
755 760 765
Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro
770 775 780
Asp Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro
785 790 795 800
Asp Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn
805 810 815
Gly Ser Val Lys Thr
820

<210> 60
<211> 822
<212> PRT
<213> Homo sapiens

<400> 60
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
1 5 10 15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
20 25 30
Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
35 40 45
Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
50 55 60
Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65 70 75 80
Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
85 90 95
Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
100 105 110
Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
115 120 125
Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
130 135 140
Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145 150 155 160
Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
165 170 175
Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
180 185 190
Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
195 200 205
Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser

```
    210                 215                 220
Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225                 230                 235                 240
Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
                245                 250                 255
Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
            260                 265                 270
Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
        275                 280                 285
Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
    290                 295                 300
Gly Leu Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser
305                 310                 315                 320
Asn Ala Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly
                325                 330                 335
Glu Tyr Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser
            340                 345                 350
Ala Trp Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys
        355                 360                 365
Glu Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile
    370                 375                 380
Gly Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg
385                 390                 395                 400
Met Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val
                405                 410                 415
His Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser
            420                 425                 430
Ala Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile
        435                 440                 445
Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val
    450                 455                 460
Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp
465                 470                 475                 480
Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val
                485                 490                 495
Val Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala
            500                 505                 510
Val Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp
        515                 520                 525
Leu Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys
    530                 535                 540
His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro
545                 550                 555                 560
Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr
                565                 570                 575
Leu Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn
            580                 585                 590
Arg Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr
        595                 600                 605
Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile
    610                 615                 620
His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val
625                 630                 635                 640
Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp
                645                 650                 655
Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala
            660                 665                 670
Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp
        675                 680                 685
Ser Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro
    690                 695                 700
```

```
Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly
705                 710                 715                 720
His Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met
                725                 730                 735
Met Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys
            740                 745                 750
Gln Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu
        755                 760                 765
Glu Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr
    770                 775                 780
Pro Asp Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser
785                 790                 795                 800
Pro Asp Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile
                805                 810                 815
Asn Gly Ser Val Lys Thr
            820
```

<210> 61
<211> 769
<212> PRT
<213> Homo sapiens

<400> 61

```
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1               5                  10                  15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
            20                  25                  30
Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
        35                  40                  45
Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
    50                  55                  60
Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65                  70                  75                  80
Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
                85                  90                  95
Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
            100                 105                 110
Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
        115                 120                 125
Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
    130                 135                 140
Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145                 150                 155                 160
Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
                165                 170                 175
Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
            180                 185                 190
Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
        195                 200                 205
Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
    210                 215                 220
Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225                 230                 235                 240
Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
                245                 250                 255
Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
            260                 265                 270
Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
        275                 280                 285
Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
```

```
    290                 295                 300
Gly Leu Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser
305                 310                 315                 320
Asn Ala Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly
                325                 330                 335
Glu Tyr Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser
            340                 345                 350
Ala Trp Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys
        355                 360                 365
Glu Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile
    370                 375                 380
Gly Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg
385                 390                 395                 400
Met Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val
                405                 410                 415
His Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser
            420                 425                 430
Ala Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile
        435                 440                 445
Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val
    450                 455                 460
Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp
465                 470                 475                 480
Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val
                485                 490                 495
Val Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala
            500                 505                 510
Val Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp
        515                 520                 525
Leu Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys
    530                 535                 540
His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro
545                 550                 555                 560
Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr
                565                 570                 575
Leu Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn
            580                 585                 590
Arg Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr
        595                 600                 605
Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile
    610                 615                 620
His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val
625                 630                 635                 640
Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp
                645                 650                 655
Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala
            660                 665                 670
Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp
        675                 680                 685
Ser Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro
    690                 695                 700
Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly
705                 710                 715                 720
His Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met
                725                 730                 735
Met Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys
            740                 745                 750
Gln Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu
        755                 760                 765
Ile
```

<210> 62
<211> 709
<212> PRT
<213> Homo sapiens

<400> 62

```
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1               5                  10                  15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
            20                  25                  30
Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
        35                  40                  45
Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
    50                  55                  60
Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65                  70                  75                  80
Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
                85                  90                  95
Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
            100                 105                 110
Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
        115                 120                 125
Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
    130                 135                 140
Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145                 150                 155                 160
Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
                165                 170                 175
Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
            180                 185                 190
Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
        195                 200                 205
Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
    210                 215                 220
Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225                 230                 235                 240
Asn His Thr Tyr His Leu Asp Val Val Ala Pro Gly Arg Glu Lys Glu
                245                 250                 255
Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly
            260                 265                 270
Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met
        275                 280                 285
Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His
    290                 295                 300
Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala
305                 310                 315                 320
Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr
                325                 330                 335
Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser
            340                 345                 350
Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys
        355                 360                 365
Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val
    370                 375                 380
Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val
385                 390                 395                 400
Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu
                405                 410                 415
Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His
```

```
            420                 425                 430
Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu
        435                 440                 445
Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu
    450                 455                 460
Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg
465                 470                 475                 480
Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr
                485                 490                 495
Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His
            500                 505                 510
Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met
        515                 520                 525
Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr
    530                 535                 540
Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro
545                 550                 555                 560
Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser
                565                 570                 575
Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr
            580                 585                 590
Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His
        595                 600                 605
Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met
    610                 615                 620
Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln
625                 630                 635                 640
Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu
                645                 650                 655
Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro
            660                 665                 670
Asp Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro
        675                 680                 685
Asp Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn
    690                 695                 700
Gly Ser Val Lys Thr
705
```

<210> 63
<211> 707
<212> PRT
<213> Homo sapiens

<400> 63

```
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1               5                  10                  15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
            20                  25                  30
Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu Asp Asp Thr
        35                  40                  45
Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn Lys Arg Ala
    50                  55                  60
Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg Leu His Ala Val
65                  70                  75                  80
Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala Gly Gly Asn Pro
                85                  90                  95
Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu Phe Lys Gln Glu
            100                 105                 110
His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His Trp Ser Leu Ile
        115                 120                 125
```

```
Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr Thr Cys Val Val
    130                 135                 140
Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His Leu Asp Val Val
145                 150                 155                 160
Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly Leu Pro Ala Asn
                165                 170                 175
Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val Cys Lys Val Tyr
            180                 185                 190
Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His Val Glu Lys Asn
        195                 200                 205
Gly Ser Lys Tyr Gly Pro Asp Gly Leu Pro Tyr Leu Lys Val Leu Lys
    210                 215                 220
Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu Val Leu Tyr Ile
225                 230                 235                 240
Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr Cys Leu Ala Gly
                245                 250                 255
Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu Thr Val Leu Pro
            260                 265                 270
Ala Pro Gly Arg Glu Lys Glu Ile Thr Ala Ser Pro Asp Tyr Leu Glu
        275                 280                 285
Ile Ala Ile Tyr Cys Ile Gly Val Phe Leu Ile Ala Cys Met Val Val
    290                 295                 300
Thr Val Ile Leu Cys Arg Met Lys Asn Thr Thr Lys Lys Pro Asp Phe
305                 310                 315                 320
Ser Ser Gln Pro Ala Val His Lys Leu Thr Lys Arg Ile Pro Leu Arg
                325                 330                 335
Arg Gln Val Thr Val Ser Ala Glu Ser Ser Ser Ser Met Asn Ser Asn
            340                 345                 350
Thr Pro Leu Val Arg Ile Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr
        355                 360                 365
Pro Met Leu Ala Gly Val Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys
    370                 375                 380
Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu
385                 390                 395                 400
Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Val Gly Ile Asp Lys
                405                 410                 415
Asp Lys Pro Lys Glu Ala Val Thr Val Ala Val Lys Met Leu Lys Asp
            420                 425                 430
Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val Ser Glu Met Glu Met
        435                 440                 445
Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gly Ala
    450                 455                 460
Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys
465                 470                 475                 480
Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Arg Pro Pro Gly Met Glu
                485                 490                 495
Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu Glu Gln Met Thr Phe Lys
            500                 505                 510
Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu
        515                 520                 525
Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu
    530                 535                 540
Val Thr Glu Asn Asn Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg
545                 550                 555                 560
Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu
                565                 570                 575
Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr
            580                 585                 590
His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Met Trp Glu Ile Phe
        595                 600                 605
Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe
```

```
    610                 615                 620
Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn Cys Thr
625                 630                 635                 640
Asn Glu Leu Tyr Met Met Met Arg Asp Cys Trp His Ala Val Pro Ser
                645                 650                 655
Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg Ile Leu
            660                 665                 670
Thr Leu Thr Thr Asn Glu Glu Glu Lys Lys Val Ser Gly Ala Val Asp
        675                 680                 685
Cys His Lys Pro Pro Cys Asn Pro Ser His Leu Pro Cys Val Leu Ala
    690                 695                 700
Val Asp Gln
705
```

<210> 64
<211> 706
<212> PRT
<213> Homo sapiens

<400> 64

```
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1               5                  10                  15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
            20                  25                  30
Leu Glu Pro Glu Gly Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu
        35                  40                  45
Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys
    50                  55                  60
Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly
65                  70                  75                  80
Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn
                85                  90                  95
Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly
            100                 105                 110
Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr
        115                 120                 125
Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln
    130                 135                 140
Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu
145                 150                 155                 160
Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile
                165                 170                 175
Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp Gly Leu Pro
            180                 185                 190
Tyr Leu Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu
        195                 200                 205
Ile Glu Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu
    210                 215                 220
Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala
225                 230                 235                 240
Trp Leu Thr Val Leu Pro Ala Pro Gly Arg Glu Lys Glu Ile Thr Ala
                245                 250                 255
Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly Val Phe Leu
            260                 265                 270
Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met Lys Asn Thr
        275                 280                 285
Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His Lys Leu Thr
    290                 295                 300
Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Glu Ser Ser
305                 310                 315                 320
```

```
Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr Thr Arg Leu
                325                 330                 335
Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu
            340                 345                 350
Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu
        355                 360                 365
Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu
    370                 375                 380
Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val Thr Val Ala
385                 390                 395                 400
Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu
                405                 410                 415
Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile
            420                 425                 430
Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile
        435                 440                 445
Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg
    450                 455                 460
Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu
465                 470                 475                 480
Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala
                485                 490                 495
Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu
            500                 505                 510
Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met Lys Ile Ala
        515                 520                 525
Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys
    530                 535                 540
Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu
545                 550                 555                 560
Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val
                565                 570                 575
Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile
            580                 585                 590
Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp
        595                 600                 605
Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys
    610                 615                 620
Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu
625                 630                 635                 640
Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu Tyr Leu Asp
                645                 650                 655
Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp Thr Arg
            660                 665                 670
Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro Asp Pro Met
        675                 680                 685
Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn Gly Ser Val
    690                 695                 700
Lys Thr
705
```

<210> 65
<211> 705
<212> PRT
<213> Homo sapiens

<400> 65

```
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1               5                  10                  15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
```

```
            20                  25                  30
Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
        35                  40                  45
Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
    50                  55                  60
Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65                  70                  75                  80
Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
                85                  90                  95
Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
            100                 105                 110
Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
        115                 120                 125
Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
    130                 135                 140
Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145                 150                 155                 160
Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
                165                 170                 175
Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
            180                 185                 190
Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
        195                 200                 205
Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
    210                 215                 220
Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225                 230                 235                 240
Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
                245                 250                 255
Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
            260                 265                 270
Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
        275                 280                 285
Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
    290                 295                 300
Gly Leu Pro Tyr Leu Lys Val Leu Lys Val Ser Ala Glu Ser Ser Ser
305                 310                 315                 320
Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr Thr Arg Leu Ser
                325                 330                 335
Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu Leu
            340                 345                 350
Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu Gly
        355                 360                 365
Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala
    370                 375                 380
Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val Thr Val Ala Val
385                 390                 395                 400
Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val
                405                 410                 415
Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile Ile
            420                 425                 430
Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val
        435                 440                 445
Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Arg
    450                 455                 460
Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu Glu
465                 470                 475                 480
Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala Arg
                485                 490                 495
Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala
            500                 505                 510
```

```
Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met Lys Ile Ala Asp
        515                 520                 525
Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys Thr
    530                 535                 540
Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe
545                 550                 555                 560
Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val Leu
                565                 570                 575
Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro
            580                 585                 590
Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys
        595                 600                 605
Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys Trp
    610                 615                 620
His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp
625                 630                 635                 640
Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu Tyr Leu Asp Leu
                645                 650                 655
Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp Thr Arg Ser
            660                 665                 670
Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro Asp Pro Met Pro
        675                 680                 685
Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn Gly Ser Val Lys
    690                 695                 700
Thr
705
```

<210> 66
<211> 704
<212> PRT
<213> Homo sapiens

<400> 66

```
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1               5                  10                  15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
            20                  25                  30
Leu Glu Pro Glu Gly Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu
        35                  40                  45
Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys
    50                  55                  60
Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly
65                  70                  75                  80
Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn
                85                  90                  95
Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly
            100                 105                 110
Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr
        115                 120                 125
Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln
    130                 135                 140
Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu
145                 150                 155                 160
Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile
                165                 170                 175
Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp Gly Leu Pro
            180                 185                 190
Tyr Leu Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu
        195                 200                 205
Ile Glu Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu
```

```
    210                 215                 220
Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala
225                 230                 235                 240
Trp Leu Thr Val Leu Pro Ala Pro Gly Arg Glu Lys Glu Ile Thr Ala
                245                 250                 255
Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly Val Phe Leu
            260                 265                 270
Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met Lys Asn Thr
        275                 280                 285
Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His Lys Leu Thr
    290                 295                 300
Lys Arg Ile Pro Leu Arg Arg Gln Val Ser Ala Glu Ser Ser Ser Ser
305                 310                 315                 320
Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr Thr Arg Leu Ser Ser
                325                 330                 335
Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu Leu Pro
            340                 345                 350
Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu Gly Lys
        355                 360                 365
Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Val
    370                 375                 380
Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val Thr Val Ala Val Lys
385                 390                 395                 400
Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val Ser
                405                 410                 415
Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn
            420                 425                 430
Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val Glu
        435                 440                 445
Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Arg Pro
    450                 455                 460
Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu Glu Gln
465                 470                 475                 480
Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala Arg Gly
                485                 490                 495
Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala
            500                 505                 510
Arg Asn Val Leu Val Thr Glu Asn Asn Val Met Lys Ile Ala Asp Phe
        515                 520                 525
Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys Thr Thr
    530                 535                 540
Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp
545                 550                 555                 560
Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Met
                565                 570                 575
Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val
            580                 585                 590
Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro
        595                 600                 605
Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys Trp His
    610                 615                 620
Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu
625                 630                 635                 640
Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu Tyr Leu Asp Leu Ser
                645                 650                 655
Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp Thr Arg Ser Ser
            660                 665                 670
Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro Asp Pro Met Pro Tyr
        675                 680                 685
Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn Gly Ser Val Lys Thr
    690                 695                 700
```

<210> 67
<211> 680
<212> PRT
<213> Homo sapiens

<400> 67

```
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1               5                  10                  15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
            20                  25                  30
Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu Asp Asp Thr
        35                  40                  45
Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn Lys Arg Ala
    50                  55                  60
Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg Leu His Ala Val
65                  70                  75                  80
Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala Gly Gly Asn Pro
                85                  90                  95
Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu Phe Lys Gln Glu
            100                 105                 110
His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His Trp Ser Leu Ile
        115                 120                 125
Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr Thr Cys Val Val
    130                 135                 140
Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His Leu Asp Val Val
145                 150                 155                 160
Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly Leu Pro Ala Asn
                165                 170                 175
Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val Cys Lys Val Tyr
            180                 185                 190
Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His Val Glu Lys Asn
        195                 200                 205
Gly Ser Lys Tyr Gly Pro Asp Gly Leu Pro Tyr Leu Lys Val Leu Lys
    210                 215                 220
His Ser Gly Ile Asn Ser Ser Asn Ala Glu Val Leu Ala Leu Phe Asn
225                 230                 235                 240
Val Thr Glu Ala Asp Ala Gly Glu Tyr Ile Cys Lys Val Ser Asn Tyr
                245                 250                 255
Ile Gly Gln Ala Asn Gln Ser Ala Trp Leu Thr Val Leu Pro Lys Gln
            260                 265                 270
Gln Ala Pro Gly Arg Glu Lys Glu Ile Thr Ala Ser Pro Asp Tyr Leu
        275                 280                 285
Glu Ile Ala Ile Tyr Cys Ile Gly Val Phe Leu Ile Ala Cys Met Val
    290                 295                 300
Val Thr Val Ile Leu Cys Arg Met Lys Asn Thr Thr Lys Lys Pro Asp
305                 310                 315                 320
Phe Ser Ser Gln Pro Ala Val His Lys Leu Thr Lys Arg Ile Pro Leu
                325                 330                 335
Arg Arg Gln Val Thr Val Ser Ala Glu Ser Ser Ser Ser Met Asn Ser
            340                 345                 350
Asn Thr Pro Leu Val Arg Ile Thr Thr Arg Leu Ser Ser Thr Ala Asp
        355                 360                 365
Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu Leu Pro Glu Asp Pro
    370                 375                 380
Lys Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu Gly Lys Pro Leu Gly
385                 390                 395                 400
Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Val Gly Ile Asp
                405                 410                 415
Lys Asp Lys Pro Lys Glu Ala Val Thr Val Ala Val Lys Met Leu Lys
```

```
            420                 425                 430
Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val Ser Glu Met Glu
        435                 440                 445
Met Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gly
    450                 455                 460
Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val Glu Tyr Ala Ser
465                 470                 475                 480
Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Arg Pro Pro Gly Met
                485                 490                 495
Glu Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu Glu Gln Met Thr Phe
            500                 505                 510
Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala Arg Gly Met Glu Tyr
        515                 520                 525
Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Val
    530                 535                 540
Leu Val Thr Glu Asn Asn Val Met Lys Ile Ala Asp Phe Gly Leu Ala
545                 550                 555                 560
Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg
                565                 570                 575
Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr
            580                 585                 590
Thr His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Met Trp Glu Ile
        595                 600                 605
Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val Glu Glu Leu
    610                 615                 620
Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn Cys
625                 630                 635                 640
Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys Trp His Ala Val Pro
                645                 650                 655
Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg Ile
            660                 665                 670
Leu Thr Leu Thr Thr Asn Glu Ile
        675                 680
```

<210> 68
<211> 396
<212> PRT
<213> Homo sapiens

<400> 68

```
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1               5                  10                  15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
            20                  25                  30
Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
        35                  40                  45
Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
    50                  55                  60
Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65                  70                  75                  80
Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
                85                  90                  95
Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
            100                 105                 110
Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
        115                 120                 125
Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
    130                 135                 140
Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145                 150                 155                 160
```

```
Lys Thr Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
                165                 170                 175
Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
            180                 185                 190
Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
        195                 200                 205
Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
    210                 215                 220
Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225                 230                 235                 240
Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
                245                 250                 255
Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
            260                 265                 270
Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
        275                 280                 285
Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
    290                 295                 300
Gly Leu Pro Tyr Leu Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr
305                 310                 315                 320
Asp Lys Glu Ile Glu Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp
                325                 330                 335
Ala Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe
            340                 345                 350
His Ser Ala Trp Leu Thr Val Leu Pro Gly Ile Tyr Cys Ser Phe Ser
        355                 360                 365
Leu Gly Phe Phe Pro Phe Ser Trp Leu Thr Ala Ile Lys Leu Thr Gln
    370                 375                 380
Leu Leu Leu Ser Glu Met Ala Pro Phe Ile Leu Ala
385                 390                 395
```

<210> 69
<211> 317
<212> PRT
<213> Homo sapiens

<400> 69

```
Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1               5                  10                  15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
            20                  25                  30
Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
        35                  40                  45
Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
    50                  55                  60
Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65                  70                  75                  80
Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
                85                  90                  95
Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
            100                 105                 110
Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
        115                 120                 125
Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
    130                 135                 140
Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145                 150                 155                 160
Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
                165                 170                 175
Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
```

```
            180                 185                 190
Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
        195                 200                 205
Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
    210                 215                 220
Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225                 230                 235                 240
Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
                245                 250                 255
Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
            260                 265                 270
Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
        275                 280                 285
Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
    290                 295                 300
Gly Leu Pro Tyr Leu Lys Val Leu Lys Val Arg Thr Phe
305                 310                 315
```

<210> 70
<211> 266
<212> PRT
<213> Homo sapiens

<400> 70

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Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1               5                  10                  15
Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
            20                  25                  30
Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
        35                  40                  45
Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
    50                  55                  60
Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65                  70                  75                  80
Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
                85                  90                  95
Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
            100                 105                 110
Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
        115                 120                 125
Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
    130                 135                 140
Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145                 150                 155                 160
Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
                165                 170                 175
Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
            180                 185                 190
Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
        195                 200                 205
Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
    210                 215                 220
Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225                 230                 235                 240
Asn His Thr Tyr His Leu Asp Val Val Gly Glu Ser Ala Ser Pro Arg
                245                 250                 255
Val Ala Ala Ala Tyr Gln Pro Ile Leu Ala
            260                 265
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<210> 71
<211> 336
<212> DNA
<213> Mus musculus

<400> 71
caggtgaagc tgcaggagtc tggcgctgag ttggtgaaac ctggggcttc agtgaagata 60
tcctgcaagg cttctggcta catcttcact gaccatgctc ttcactgggt gaggcagaag 120
cctgaacagg gcctggaatg gattgggtat atttttcccg gaaatggtaa tattgagtac 180
aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag tactgcctac 240
atgcagctca acagcctgac atctggagat tctgcaatgt atttctgtaa aaagatggac 300
tactggggcc aagggaccac ggtcaccgtc tcctca 336

<210> 72
<211> 112
<212> PRT
<213> Mus musculus

<400> 72
Gln Val Lys Leu Gln Glu Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp His
20 25 30
Ala Leu His Trp Val Arg Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Phe Pro Gly Asn Gly Asn Ile Glu Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Asn Ser Leu Thr Ser Gly Asp Ser Ala Met Tyr Phe Cys
85 90 95
Lys Lys Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
100 105 110

<210> 73
<211> 336
<212> ADN
<213> Mus musculus

<400> 73
caggtgaagc tgcaggagtc tggcgctgag ttggtgaaac ctggggcttc agtgaagatc 60
tcctgcaagg cttctggtta caccttcact gaccattcta ttcactgggt gaagcagaag 120
cctggacagg gcctagaatg gattggatat ctttttcccg gaaatggtaa ttttgaatat 180
aatgagaaat tcaagggcaa ggccacactg actgcagaca aatcctccag cactgcctac 240
atgcacctca acagcctgac atctgaggat tctgcagtgt atttctgtaa aaagatggac 300
tactggggcc aagggaccac ggtcaccgtc tcctca 336

<210> 74
<211> 112
<212> PRT
<213> Mus musculus

<400> 74
Gln Val Lys Leu Gln Glu Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30
Ser Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Leu Phe Pro Gly Asn Gly Asn Phe Glu Tyr Asn Glu Lys Phe

```
    50                  55                  60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95
Lys Lys Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
            100                 105                 110
```

<210> 75
<211> 336
<212> ADN
<213> Mus musculus

<400> 75
caggttcagc tgcagcagtc cgacgctgag ttggtgaaac ctggggcttc agtgaagata 60
tcctgcaggg cttctggcta caccttcact gaccattcta ttcactgggt gaagcagcag 120
cctggccagg gcctggaatg gatcggatat atttttcccg gaaatggaaa tattgaatac 180
aatgacaaat tcaagggcaa ggccacactg actgcagaca aatcctccgg cactgcctac 240
atgcagctca acagcctgac atctgaggat tctgcagtgt atttctgtaa aaggatgggg 300
tactggggtc aaggaacctc agtcaccgtc tcctca 336

<210> 76
<211> 112
<212> PRT
<213> Mus musculus

<400> 76
```
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Ile Ser Cys Arg Ala Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30
Ser Ile His Trp Val Lys Gln Gln Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Phe Pro Gly Asn Gly Asn Ile Glu Tyr Asn Asp Lys Phe
    50                  55                  60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Gly Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95
Lys Arg Met Gly Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
            100                 105                 110
```

<210> 77
<211> 336
<212> ADN
<213> Mus musculus

<400> 77
caggtcaagc tgcaggagtc tggcgctgag ttggtgaaac ctggggcttc agtgaagatc 60
tcctgcaagg cttctggcta caccttcact gaccattcta ttcactgggt gaagcagaag 120
cctggacagg gcctagaatg gattggatat ctttttcccg gaaatggtaa ttttgagtac 180
aatgaaaaat tcaagggcaa ggccacactg actgcagaca aatcctccag cactgtctac 240
atgtacctca acagcctgac atctgaggat tctgcagtgt atttctgtaa aaggatgggg 300
tactggggcc aagggaccac ggtcaccgtc tcctca 336

<210> 78
<211> 112
<212> PRT

<213> Mus musculus

<400> 78

```
Gln Val Lys Leu Gln Glu Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30
Ser Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Leu Phe Pro Gly Asn Gly Asn Phe Glu Tyr Asn Glu Lys Phe
    50                  55                  60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Val Tyr
65                  70                  75                  80
Met Tyr Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95
Lys Arg Met Gly Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
            100                 105                 110
```

<210> 79
<211> 336
<212> ADN
<213> Mus musculus

<400> 79

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caggtcaagc tgcaggagtc tggacctgaa ctggtaaagc ctggggcttc agtgaagatg 60
tcctgcaagg cttctggata cacattcact aactatgtta tacactgggt gaagcaaaag 120
cctgggcagg gccttgagtg gattggatat attaatcctt acaatgatgg ctctaagtac 180
aatgagaagt tcaaaggcaa ggcctcactg acttcagaca aatcctccag cacagcctac 240
atggagctca gcagcctgac ctctgaggac tctgcggtct attactgtgc aagaatggac 300
tactggggcc aagggaccac ggtcaccgtc tcctca                           336
```

<210> 80
<211> 112
<212> PRT
<213> Mus musculus

<400> 80

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
            20                  25                  30
Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Asn Glu Lys Phe
    50                  55                  60
Lys Gly Lys Ala Ser Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Met Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
            100                 105                 110
```

<210> 81
<211> 336
<212> ADN
<213> Mus musculus

<400> 81

caggtcaagc tgcaggagtc tggacctgaa ctggtaaagc ctggggcttc agtgaagatg 60
tcctgcaagg cttctggata cacattcact aactatgtta tacactgggt gaagcaaaag 120
cctgggcagg gccttgagtg gattggatat attaatcctt acaatgatgg ctctaagtac 180
aatgagaagt tcaaaggcaa ggcctcactg acttcagaca aatcctccag cacagcctac 240
atggagctca gcagcctgac ctctgaggac tctgcggtct attactgtgc aagaatgggg 300
tactggggcc aagggaccac ggtcaccgtc tcctca 336

<210> 82
<211> 112
<212> PRT
<213> Mus musculus

<400> 82
Gln Val Gln Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30
Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Lys Ala Ser Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Met Gly Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
100 105 110

<210> 83
<211> 342
<212> ADN
<213> Mus musculus

<400> 83
gatgttttga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60
atctcttgca gatctagtca gagcattgta catagtaatg gaaacaccta tttagaatgg 120
tacctgcaga aaccaggcca gtctccaaag ctcctgatct acaaagtttc caaccgattt 180
tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
agcagagtgg aggctgagga tctgggagtt tattactgct ttcaaggttc acatgttcct 300
cctacgttcg gtgctgggac caagctggag ctgaaacggg ct 342

<210> 84
<211> 113
<212> PRT
<213> Mus musculus

<400> 84
Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15
Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30
Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Ser His Val Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110
Arg

<210> 85
<211> 324
<212> ADN
<213> Mus musculus

<400> 85
gacatccaga tgactcagtc tccagcctcc ctatctgcat ctgtgggaga aactgtcacc 60
atcacatgtc gaacaactga aaatatttac agttattttg tatggtctca gcagagacag 120
ggaaaatctc ctcagctccg ggtctataat gcaaaatcct tagcagaagg tgtgccatca 180
agtttcaatg tcagtgtatc aggcacacag ttttctctga agatcaatag cctgcagcct 240
gaagattttg ggacttatca ctgtcaacac cattatggta ctccgtacac gttcggaggg 300
gggaccaggc tggaaataag acgg 324

<210> 86
<211> 108
<212> PRT
<213> Mus musculus

<400> 86
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Glu Thr Val Thr Ile Thr Cys Arg Thr Thr Glu Asn Ile Tyr Ser Tyr
20 25 30
Phe Val Trp Ser Gln Gln Arg Gln Gly Lys Ser Pro Gln Leu Arg Val
35 40 45
Tyr Asn Ala Lys Ser Leu Ala Glu Gly Val Pro Ser Ser Phe Asn Val
50 55 60
Ser Val Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Gly Thr Tyr His Cys Gln His His Tyr Gly Thr Pro Tyr
85 90 95
Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Arg Arg
100 105

<210> 87
<211> 339
<212> ADN
<213> Mus musculus

<400> 87
gatgttttg atgacccaaac tccactcact ttgtcggtta ccattggaca accagcttcc 60
atctcttgc aagtccagtca gagcctctta tatactaatg gaaaaaccta tttgacttgg 120
ttattccag aggccaggcca gtctccaaaa cgcctaatct atctggtgtc tgaattggac 180
tctggagtc cctgacaggtt cagtggcagt ggttcaggga cagatttcac actggaaatc 240
accagagtg gaggctgagga tttgggagtt tattactgct tgcagagtgc acattttcca 300
ttcacgttc ggctcgggcac caagctggaa atcaaacgg 339

<210> 88
<211> 113
<212> PRT
<213> Mus musculus

<400> 88
Asp Val Leu Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly

```
 1               5                  10                  15
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Thr
            20                  25                  30
Asn Gly Lys Thr Tyr Leu Thr Trp Leu Phe Gln Arg Pro Gly Gln Ser
        35                  40                  45
Pro Lys Arg Leu Ile Tyr Leu Val Ser Glu Leu Asp Ser Gly Val Pro
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile
65                  70                  75                  80
Thr Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Leu Gln Ser
                85                  90                  95
Ala His Phe Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
Arg
```

<210> 89
<211> 339
<212> ADN
<213> Mus musculus

<400> 89
gatgttgtga tgacccaaac tccactcact ctgtcggtga ccattggaca accagcgttc 60
atctcttgca agtccagtca gagcctcttt aacactaatg gcaaaaccta tttgacttgg 120
ttaattcaga ggccaggcca gtctccacag cgcctgatct atctggtgtc caaattggac 180
tctggcgtcc cggacaggtt cagtggcagt ggctcaggga cagatttcac actgaaaatc 240
agcagagtgg aggctgagga tctgggagtt tattactgcc tgcagagtag ccattttccg 300
tttacgttcg gctcgggcac caagctggaa atcaaacgg   339

<210> 90
<211> 113
<212> PRT
<213> Mus musculus

<400> 90
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Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
 1               5                  10                  15
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Thr
            20                  25                  30
Asn Gly Lys Thr Tyr Leu Thr Trp Leu Ile Gln Arg Pro Gly Gln Ser
        35                  40                  45
Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80
Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Leu Gln Ser
                85                  90                  95
Ser His Phe Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
Arg
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<210> 91
<211> 327
<212> ADN
<213> Mus musculus

<400> 91
gatgttgtgc taactcagtc tcctgccacc ctgtctgtga ctccaggaga tagagtcagt 60
ctttcctgca gggccagcca aaatattggc aactacctac actggtatca acagaaatca 120

catgagtctc caaggcttct catcaagtat gcttcccagt ccatctctgg gatcccctcc 180
aggttcagtg gcagtggatc agtcacagat ttcactctca atatcaacag tgtggagact 240
gaagattttg gaatgtattt ctgtcaacag agtgacacct ggcctctcac gttcggtgct 300
gggaccaagc tggagctgaa acgggct 327

<210> 92
<211> 108
<212> PRT
<213> Mus musculus

<400> 92
Asp Val Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1 5 10 15
Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Asn Ile Gly Asn Tyr
20 25 30
Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
35 40 45
Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Val Thr Asp Phe Thr Leu Asn Ile Asn Ser Val Glu Thr
65 70 75 80
Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asp Thr Trp Pro Leu
85 90 95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
100 105

<210> 93
<211> 8
<212> PRT
<213> Mus musculus

<400> 93
Thr Phe Thr Asp His Ser Ile His
1 5

<210> 94
<211> 8
<212> PRT
<213> Mus musculus

<400> 94
Thr Phe Thr Asn Tyr Val Ile His
1 5

<210> 95
<211> 8
<212> PRT
<213> Mus musculus

<400> 95
Ile Phe Thr Asp His Ala Leu His
1 5

<210> 96
<211> 17
<212> PRT
<213> Mus musculus

<400> 96
Tyr Ile Phe Pro Gly Asn Gly Asn Ile Glu Tyr Asn Asp Lys Phe Lys
1 5 10 15
Gly

<210> 97
<211> 17
<212> PRT
<213> Mus musculus

<400> 97
Tyr Leu Phe Pro Gly Asn Gly Asn Phe Glu Tyr Asn Glu Lys Phe Lys
1 5 10 15
Gly

<210> 98
<211> 17
<212> PRT
<213> Mus musculus

<400> 98
Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15
Gly

<210> 99
<211> 17
<212> PRT
<213> Mus musculus

<400> 99
Tyr Ile Phe Pro Gly Asn Gly Asn Ile Glu Tyr Asn Glu Lys Phe Lys
1 5 10 15
Gly

<210> 100
<211> 5
<212> PRT
<213> Mus musculus

<400> 100
Lys Arg Met Gly Tyr
1 5

<210> 101
<211> 5
<212> PRT
<213> Mus musculus

<400> 101
Lys Lys Met Asp Tyr

1 5

<210> 102
<211> 5
<212> PRT
<213> Mus musculus

<400> 102
Ala Arg Met Asp Tyr
1 5

<210> 103
<211> 16
<212> PRT
<213> Mus musculus

<400> 103
Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 104
<211> 11
<212> PRT
<213> Mus musculus

<400> 104
Arg Thr Thr Glu Asn Ile Tyr Ser Tyr Phe Val
1 5 10

<210> 105
<211> 16
<212> PRT
<213> Mus musculus

<400> 105
Lys Ser Ser Gln Ser Leu Leu Tyr Thr Asn Gly Lys Thr Tyr Leu Thr
1 5 10 15

<210> 106
<211> 16
<212> PRT
<213> Mus musculus

<400> 106
Lys Ser Ser Gln Ser Leu Leu Asn Thr Asn Gly Lys Thr Tyr Leu Thr
1 5 10 15

<210> 107
<211> 11
<212> PRT
<213> Mus musculus

<400> 107
Arg Ala Ser Gln Asn Ile Gly Asn Tyr Leu His
1 5 10

<210> 108
<211> 7
<212> PRT
<213> Mus musculus

<400> 108
Lys Val Ser Asn Arg Phe Ser
1 5

<210> 109
<211> 7
<212> PRT
<213> Mus musculus

<400> 109
Asn Ala Lys Ser Leu Ala Glu
1 5

<210> 110
<211> 7
<212> PRT
<213> Mus musculus

<400> 110
Leu Val Ser Glu Leu Asp Ser
1 5

<210> 111
<211> 7
<212> PRT
<213> Mus musculus

<400> 111
Leu Val Ser Lys Leu Asp Ser
1 5

<210> 112
<211> 7
<212> PRT
<213> Mus musculus

<400> 112
Tyr Ala Ser Gln Ser Ile Ser
1 5

<210> 113
<211> 9
<212> PRT
<213> Mus musculus

<400> 113
Phe Gln Gly Ser His Val Pro Pro Thr
1 5

<210> 114
<211> 9
<212> PRT
<213> Mus musculus

<400> 114
Gln His His Tyr Gly Thr Pro Tyr Thr
1 5

<210> 115
<211> 9
<212> PRT
<213> Mus musculus

<400> 115
Leu Gln Ser Ala His Phe Pro Phe Thr
1 5

<210> 116
<211> 9
<212> PRT
<213> Mus musculus

<400> 116
Leu Gln Ser Ser His Phe Pro Phe Thr
1 5

<210> 117
<211> 9
<212> PRT
<213> Mus musculus

<400> 117
Gln Gln Ser Asp Thr Trp Pro Leu Thr
1 5

<210> 118
<211> 5
<212> PRT
<213> Mus musculus

<400> 118
Asp His Ala Leu His
1 5

<210> 119
<211> 5
<212> PRT
<213> Mus musculus

<400> 119
Asp His Ser Ile His
1 5

<210> 120
<211> 5
<212> PRT
<213> Mus musculus

<400> 120
Asn Tyr Val Ile His
1 5

<210> 121
<211> 9
<212> PRT
<213> Mus musculus

<400> 121
Ile Phe Pro Gly Asn Gly Asn Ile Glu
1 5

<210> 122
<211> 9
<212> PRT
<213> Mus musculus

<400> 122
Leu Phe Pro Gly Asn Gly Asn Phe Glu
1 5

<210> 123
<211> 9
<212> PRT
<213> Mus musculus

<400> 123
Ile Asn Pro Tyr Asn Asp Gly Ser Lys
1 5

<210> 124
<211> 11
<212> PRT
<213> Mus musculus

<400> 124
His Leu Ala Asn Thr Tyr Tyr Tyr Phe Asp Tyr
1 5 10

<210> 125
<211> 5
<212> PRT
<213> Mus musculus

<400> 125
Ser Asn Gly Asn Thr
1 5

<210> 126

<211> 5
<212> PRT
<213> Mus musculus

<400> 126
Glu Asn Ile Tyr Ser
 1   5

<210> 127
<211> 5
<212> PRT
<213> Mus musculus

<400> 127
Thr Ser Gly Tyr Ser
 1   5

<210> 128
<211> 5
<212> PRT
<213> Mus musculus

<400> 128
Gln Asp Ile Lys Ser
 1   5

<210> 129
<211> 5
<212> PRT
<213> Mus musculus

<400> 129
Gln Asn Ile Gly Asn
 1   5

<210> 130
<211> 4654
<212> ADN
<213> Homo sapiens

<400> 130
ggcggcggct ggaggagagc gcggtggaga gccgagcggg cgggcggcgg gtgcggagcg 60
ggcgagggag cgcgcgcggc cgccacaaag ctcgggcgcc gcggggctgc atgcggcgta 120
cctggcccgg cgcggcgact gctctccggg ctggcggggg ccggccgcga gccccggggg 180
ccccgaggcc gcagcttgcc tgcgcgctct gagccttcgc aactcgcgag caaagtttgg 240
tggaggcaac gccaagcctg agtcctttct tcctctcgtt ccccaaatcc gagggcagcc 300
cgcgggcgtc atgcccgcgc tcctccgcag cctggggtac gcgtgaagcc cgggaggctt 360
ggcgccggcg aagacccaag gaccactctt ctgcgtttgg agttgctccc cgcaaccccg 420
ggctcgtcgc tttctccatc ccgacccacg cggggcgcgg ggacaacaca ggtcgcggag 480
gagcgttgcc attcaagtga ctgcagcagc agcggcagcg cctcggttcc tgagcccacc 540
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1389

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO
NIT : 800.176.089-2
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Industria y Comercio
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RECIBO DE CAJA

No. 11 - 0099034

Bogotá D.C., Octubre 07 de 2011 - 15:59:30

RECIBIDO DE : CASTILLO PINEDA & ASOCIADOS NI 800.253.423

*** Soporte del Pago ***

TIPO PAGO	BANCO	CUENTA	No. PAGO	FECHA PAGO	VR PAGO
CONSIGNACION	BANCO DE BOGOTA	062754387	425029640	07/10/2011	1.142.000.00

*** Conceptos Pagados ***

CANT.	RENTISTICO	CONCEPTO	Vr UNDITARIO	Vr CONCEPTO
1	50005-01-01 SOLICITUDES	1 TRAMITES DE SOL. DE PATENTE DE INVENCION	571.000.00	571.000.00
				$571.000.00

SON: **QUINIENTOS SETENTA Y UN MIL PESOS MONEDA CORRIENTE***

Responsable: _____
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Recibo de Caja Aplicado al Expediente No. _____

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO
No. 11-133166- -00000-0000
Fecha: 2011-10-07 16:09:48 Dep. 2020 DIR.NUEVASCR
Tra. 11 PATENTEIYII Eve: 379 FASENACIONALII
Act. 411 PRESENTACION Folios: 1389

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SUPERINTENDENCIA

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No. 11-133166- -00000-0000

Fecha: 2011-10-07 16:09:48 Dep. 2020 DIR.NUEVASCR
Tra. 11 PATENTEIYII Eve: 379 FASENACIONALII
Act. 411 PRESENTACION Folios: 1389

PATENTE DE INVENCIÓN ☐ MODELO

- ☐ Indicación que se solicita una patente.
- ☐ Datos de identificación del solicitante o de la persona que presenta la solicitud
- ☐ Descripción de la invención
- ☐ Dibujos de ser estos pertinentes
- ☐ Comprobante de pago de las tasas establecidas (De ser el caso formato de descuento)

Completa ☐ Incompleta ☐

PATENTE DE INVENCIÓN PCT ☑ MODELO DE UTILIDAD PCT ☐ Art.33 Decisión 486/00, Circular Única

- ☑ Indicación que se solicita una PCT
- ☑ Copia de la solicitud en español, tal como fue presentada inicialmente (capítulo descriptivo, reivindicatorio, resumen)
- ☑ Dibujos de ser estos pertinentes
- ☑ Comprobante de pago de las tasas establecidas (de ser el caso formato de descuento)

Completa ☑ Incompleta ☐

DISEÑO INDUSTRIAL ☐ (Art. 119 Decisión 486/00)

- ☐ Indicación que se solicita Diseño industrial
- ☐ Datos de identificación del solicitante o de la persona que presenta la solicitud
- ☐ Representación gráfica y fotográfica del Diseño industrial o muestra del material que incorpora el diseño
- ☐ Comprobante de pago de las tasas establecidas

Completa ☐ Incompleta ☐

ESQUEMA DE TRAZADO ☐ (Art. 92 Decisión 486/00)

- ☐ Indicación que se solicita un esquema de trazado
- ☐ Datos de identificación del solicitante o de la persona que presenta la solicitud
- ☐ Representación gráfica de un esquema de trazado
- ☐ Comprobante de pago de las tasas establecidas

Completa ☐ Incompleta ☐