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Records: 24 (1-24 of 24)
Export type: Family Export

Search History

Step	Search	Results
1	Detection	3,307,323
2	mutation	54,579
3	PTPN11 OR SHP2	628
4	1 AND 2	10,951
5	4 AND 3	46
6	Detection near "mutatio*"	3,708
7	6 AND 3	24

1. Family 81524998 (US2022220564 AA)

[View in PatBase](#)

Title

[EN] IMPROVED METHODS FOR THE EARLY DIAGNOSIS OF UTERINE LEIOMYOMAS AND LEIOMYOSARCOMAS

Abstract

[EN] The present disclosure provides a method for differentiating myometrial tumors/uterine neoplasms such as LM, LMS and IMT. Further, the disclosure provides a method for treating a uterine leiomyoma in a subject, comprising: (a) performing a genotyping assay on a biological sample from the subject to determine whether the subject has a uterine leiomyosarcoma genotype, and (b) surgically removing the uterine leiomyoma if the subject does not have a uterine leiomyosarcoma genotype.

International Class: C12Q1/6886; C12Q1/68; C12Q1/6813; C12Q1/686; C12Q1/6869; A61B17/32

Cooperative Patent Class: A61B17/32002; A61B2017/320024; A61K38/00; C12Q1/6886; C12Q2600/156; C12Q2600/158; C12Q2600/172

Family Information

Patent Number	Publication Date	Application Number	Application Date
BR112021020779 A2	20220104	BR20211120779	20200417
BR112021020779 A8	20220125	BR20211120779	20200417
CN114051537 A	20220215	CN202080044317	20200417
EP3956476 A1	20220223	EP20200723999	20200417
HK40067899 A1	20220909	HK20226057156	20220722
JP2022529294 T2	20220620	JP20210562178T	20200417
US2022220564 AA	20220714	US20210604316	20200417
WO20212580 A1	20201022	WO2020EP60878	20200417

Priority Numbers: EP20190382307 [20190417]; EP20190382322 [20190429]; WO2020EP60878 [20200417]

Probable Patent Assignee: IGENOMIX S L

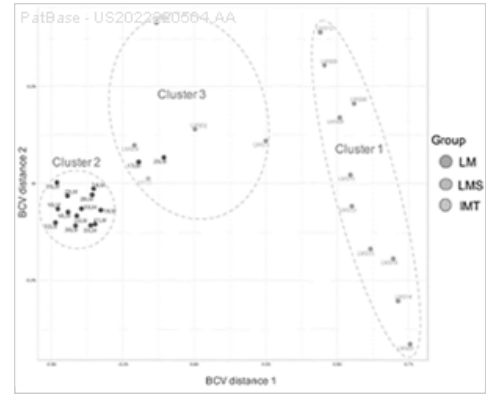
Assignees: IGENOMIX S L

Non Std Assignees: IGENOMIX SL

Inventors: AYMARA MAS PERUCHO; ROBERTO ALONSO VALERO; CARLOS SIMON VALLES; MAS PERUCHO AYMARA; ALONSO VALERO ROBERTO; SIMON VALLES CARLOS

Agent(s): ABG INTELLECTUAL PROPERTY LAW SL; UNITALEN ATTORNEYS AT LAW LTD; HOFFMANN EITLE SLU

Designated States: AL; AT; BA; BE; BG; CH; CY; CZ; DE; DK; EE; ES; FI; FR; GB; GR; HR; HU; IE; IS; IT; LI; LT; LU; LV; MC; ME; MK; MT; NL; NO; PL; PT; RO; RS; SE; SI; SK; SM; TR; AE; AG; AM; AO; AU; AZ; BB; BF; BH; BJ; BN; BR; BW; BY; BZ; CA; CF; CG; CI; CL; CM; CN; CO; CR; CU; DJ; DM; DO; DZ; EC; EG; GA; GD; GE; GH; GM; GN; GQ; GT; GW; HN; ID; IL; IN; IR; JO; JP; KE; KG; KH; KM; KN; KP; KR; KW; KZ; LA; LC; LK; LR; LS; LY; MA; MD; MG; ML; MN; MR; MW; MX; MY; MZ; NA; NE; NG; NI; NZ; OM; PA; PE; PG; PH; QA; RU; RW; SA; SC; SD; SG; SL; SN; ST; SV; SY; SZ; TD; TG; TH; TJ; TM; TN; TT; TZ; UA; UG; US; UZ; VC; VN; WS; ZA; ZM; ZW



2. Family 80646821 (CN111575375 A)

[View in PatBase](#)

Title

[EN] MULTIPLE MYELOMA GENE MUTATION DETECTION KIT AND DETECTION METHOD

Abstract

[EN] The invention discloses a multiple myeloma gene mutation detection kit. The kit comprises multiple imbricated oligonucleotide probes corresponding to detection genes respectively and the probes are used for acquiring variation information of hotspot mutation areas of the detection genes; and 48 detection genes are included. The invention also discloses a method for detection with the adoption of immunomagnetic bead sorted cells and in combination with a high-throughput sequencing technology. With the method, the detection rate of multiple myeloma gene mutation can be increased, the mutation missing detection condition of genes of multiple myeloma at a low-frequency ratio can be effectively avoided, and the method has broad clinical value in diagnosis and treatment of the multiple myeloma and MRD (minimal residual disease) monitoring application.



International Class: C12N15/11; C12N5/09; C12Q1/6806; C12Q1/6869; C12Q1/6886

Cooperative Patent Class: C12N2509/00; C12N5/0693; C12Q1/6806; C12Q1/6869; C12Q1/6886; C12Q2600/156

Family Information

Patent Number	Publication Date	Application Number	Application Date
CN111575375 A	20200825	CN202010384608	20200508

Priority Numbers: CN202010384608 [20200508]

Probable Patent Assignee: NANJING PRACTICE MEDICINE EXAMINATION CO LTD

Assignees: NANJING PRACTICE MEDICINE EXAMINATION CO LTD

Non Std Assignees: NANJING PRACTICE MEDICINE EXAMINATION CO; NANJING MEDICAL PRACTICE TEST CO LTD

Inventors: TANG CHUNHUA; ZHANG PENG; XING KUAN; HE ZHIJIAN; XIE ZHEN; XIA TONGQIAN; YUAN MING; HE GUILUN; AN XUERU; LI PING

3. Family 65108750 (CN106480205 A)

[View in PatBase](#)

Title

[EN] PROBE AND SEQUENCE COMBINATION FOR SIMULTANEOUS DETECTION OF VARIOUS MUTATION TYPES

Abstract

[EN] The invention discloses a probe and a sequence combination for simultaneous detection of various mutation types and particularly provides a kit, a method, a gene chip, a probe and a sequence combination which are high in sensitivity and specificity and used for simultaneous detection of point mutation, short segment insertion and deletion, copy number variation and fusion genes of 57 tumor driver genes listed in a detection list. The invention further discloses a sequence combination and probe associated gene chip and kit and a method for simultaneous detection of various mutation types. By detection of body fluid including blood, hydrothorax, abdominal dropsy and the like and tumor frozen tissues or paraffin sections, comprehensive tumor driver gene mutation information can be acquired, sensitivity and accuracy in tumor gene detection are improved, and accordingly clinicians can be assisted in making of individualized medication schemes to achieve best accurate treatment effects.

International Class: C12N15/11; C12Q1/68

Cooperative Patent Class: C12Q1/6874; C12Q1/6886; C12Q2600/118; C12Q2600/156; C12Q2600/16

Family Information

Patent Number	Publication Date	Application Number	Application Date
CN106480205 A	20170308	CN201610994059	20161111

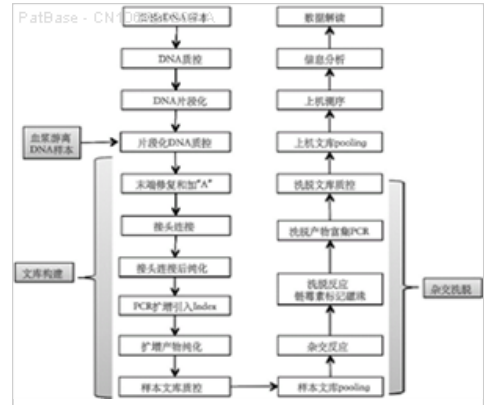
Priority Numbers: CN201610994059 [20161111]

Probable Patent Assignee: BEIJING GENEPLUS TECH CO LTD

Assignees: BEIJING GENEPLUS TECH CO LTD; SUZHOU GENEPLUS BIOMEDICAL ENG CO LTD; BEIJING GENE AND TECHNOLOGY CO LTD

Non Std Assignees: BEIJING GENEPLUS TECHNOLOGY CO; SUZHOU GENEPLUS BIOMEDICAL ENGINEERING CO; XUZHOU KAT INGA BIOMEDICAL ENGINEERING LTD

Inventors: LIU JIUCHENG; YI YUTING; CHEN HAIYAN; GUAN YANFANG; YI XIN; YANG LING



4. Family 77295240 (CN110684848 A)

[View in PatBase](#)

Title

[EN] MULTIPLEX PCR PRIMER GROUP FOR HEREDITARY TUMOR EMBRYONIC SYSTEM MUTATION DETECTION AND KIT

Abstract

[EN] The invention discloses a multiplex PCR primer group for hereditary tumor embryonic system mutation detection and a kit. The multiplex PCR primer group at least comprises primer sequences shown in SEQID NO.: 1-276. Compared with the prior art, the multiple PCR primers are free of interference, multiple PCR can be carried out by mixing the primers at a time, the required multiple genes are amplified, the PCR operation amount is greatly reduced, and then the overall sequencing cost is greatly reduced. In some examples of the invention, all exon regions of 152 core CPG oncogenes inherited by the embryonic system and intron regions in which mutation often occurs can be amplified at one time, including point mutation, small fragment deletion, insertion and other mutation types, which greatly facilitates subsequent high-throughput sequencing operation. Through further interpretation of the high-throughput sequencing data, the tumor onset risk of the to-be-tested person can be evaluated, so that the to-be-tested person is prevented from related unhealthy life styles, the tumor onset risk is reduced, and personalized health management is guided.

International Class: C12N15/11; C12Q1/6858; C12Q1/6886

Cooperative Patent Class: C12Q1/6858; C12Q1/6886; C12Q2600/156; C12Q2600/16

Family Information

Patent Number	Publication Date	Application Number	Application Date
CN110684848 A	20200114	CN201911021454	20191025

Priority Numbers: CN201911021454 [20191025]

Probable Patent Assignee: GUANGZHOU MENDEL GENS MEDICAL TECH CO LTD

Assignees: GUANGZHOU MENDEL GENS MEDICAL TECH CO LTD

Non Std Assignees: GUANGZHOU MENDEL GENS MEDICAL TECHNOLOGY CO; GUANGZHOU WONDER GENETIC MEDICINE TECHNOLOGY CO LTD

Inventors: CHEN MENGLIN; HUANG KAILING; ZHANG NAN; LUO YINGYUN; LIU YANHUI; CHEN ZHUONA; ZHENG ZHOUXIA

5. Family 73174922 (US2020370104 AA)

[View in PatBase](#)

Title

[EN] METHOD FOR DETECTING VARIATION IN NUCLEOTIDE SEQUENCE ON BASIS OF GENE PANEL AND DEVICE FOR DETECTING VARIATION IN NUCLEOTIDE SEQUENCE USING SAME

Abstract

[EN] The present invention provides a method for detection of a mutation in a nucleotide sequence, the method comprising the steps of: obtaining a plurality of target genes for one subject sample by using a gene panel including probes for the plurality of target genes; collecting multiple replicates of nucleotide sequences including nucleotide sequences being identical or non-identical with each of the plurality of target genes by sequencing each of the plurality of target genes in multiple rounds through next generation sequencing (NGS); matching the multiple replicates of nucleotide sequences with reference nucleotide sequences; determining nucleotide sequences unmatched with the reference nucleotide sequences for the plurality of target genes among the multiple replicates of nucleotide sequences; and determining candidates of nucleotide sequence mutations for the plurality of target genes in the subject sample, based on a probability of mutation for a discordant gene locus with the unmatched nucleotide sequences, the probability of mutation being calculated by a computational method according to statistical analysis of unmatched nucleotide sequences.

International Class: C12Q1/6834; G16B20/00; G16B40/00; G16B20/20; C12M1/00; C12Q1/6827; C40B50/06; G06F17/18

Cooperative Patent Class: C12Q1/6834; C12Q2600/156; G06F17/18; G16B20/20; G16B40/00

Family Information

Patent Number	Publication Date	Application Number	Application Date
AU2018315982 AA	20200227	AU20180315982	20180806
AU2018315982 BB	20211104	AU20180315982	20180806
CA3072052 AA	20200204	CA20183072052	20180806
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JP2020529851 T2	20201015	JP20200506731T	20180806
JP6983307 B2	20211217	JP20200506731T	20180806
KR102035615 B1	20191023	KR20170099822	20170807
KR20190015957 A	20190215	KR20170099822	20170807
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WO19031785 A2	20190214	WO2018KR08891	20180806
WO19031785 A3	20190523	WO2018KR08891	20180806
WO19031785 A9	20190711	WO2018KR08891	20180806

Priority Numbers: KR20170099822 [20170807]; WO2018KR08891 [20180806]

Probable Patent Assignee: UNIV YONSEI IACF

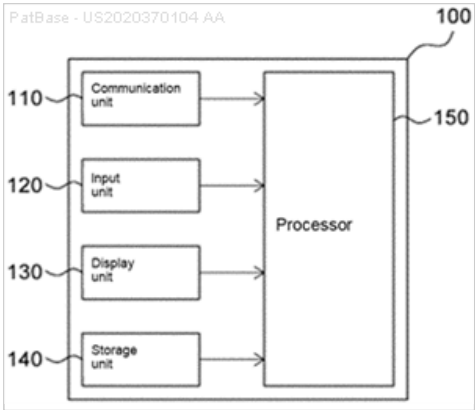
Assignees: YONSEI UNIV UNIVERSITY IND FOUNDATION UIF; YONSEI UNIV UNIV IND FOUNDATION UIF; UNIV YONSEI IACF

Non Std Assignees: KIM SANGWOO; KIM JUNHO; ACADEMIC COOPERATION FOUNDATION YONSEI UNIV IND; INDUSTRY ACADEMIC COOPERATION FOUNDATION YONSEI UNIVERSITY

Inventors: KIM JUNHO; KIM SANGWOO; KIM JUN HO; KIM SANG WOO

Agent(s): SPRUSON AND FERGUSON; NORTON ROSE FULBRIGHT CANADA LLP SENCRL SRL; GRUENECKER PATENT U RECHTSANWAELTE PARTG MBB; INVENTUS INTELLECTUAL PROPERTY GROUP

Designated States: AL; AT; BA; BE; BG; CH; CY; CZ; DE; DK; EE; ES; FI; FR; GB; GR; HR; HU; IE; IS; IT; LI; LT; LU; LV; MC; ME; MK; MT; NL; NO; PL; PT; RO; RS; SE; SI; SK; SM; TR; AE; AG; AM; AO; AU; AZ; BB; BF; BH; BJ; BN; BR; BW; BY; BZ; CA; CF; CG; CI; CL; CM; CN; CO; CR; CU; DJ; DM; DO; DZ; EC; EG; GA; GD; GE; GH; GM; GN; GQ; GT; GW; HN; ID; IL; IN; IR; JO; JP; KE; KG; KH; KM; KN; KP; KW; KZ; LA; LC; LK; LR; LS; LY; MA; MD; MG; ML; MN; MR; MW; MX; MY; MZ; NA; NE; NG; NI; NZ; OM; PA; PE; PG; PH; QA; RU; RW; SA; SC; SD; SG; SL; SN; ST; SV; SY; SZ; TD; TG; TH; TJ; TM; TN; TT; TZ; UA; UG; US; UZ; VC; VN; ZA; ZM; ZW



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[EN] PTPN11 GENE MUTATION DETECTION SPECIFICITY PRIMER AND LIQUID CHIP THEREOF

[EN] The invention discloses a PTPN11 gene mutation detection specificity primer and a liquid chip thereof. The liquid chip mainly comprises: an ASPE primer composed of a 5'-terminal tag sequence and 3'-terminal specificity primer sequences focused on target gene mutation sites, wherein the specificity primer sequences comprise SEQ ID NO.24 and SEQ ID NO.25 focused on a G60V site, SEQ ID NO.26, SEQ ID NO.27 and SEQ ID NO.28 focused on a D61Y/V site, SEQ ID NO.29 and SEQ ID NO.30 focused on an E69K site, SEQ ID NO.31, SEQ ID NO.32 and SEQ ID NO.33 focused on an A72T/D site, SEQ ID NO.34 and SEQ ID NO.35 focused on a T73I site, SEQ ID NO.36, SEQ ID NO.37, SEQ ID NO.38, SEQ ID NO.39, SEQ ID NO.40 and SEQ ID NO.41 focused on an E76K/Q/A/G/V site, SEQ ID NO.42 and SEQ ID NO.43 focused on an S502P site, and/or SEQ ID NO.44, SEQ ID NO.45 and SEQ ID NO.46 focused on a G503A/V site; a microsphere coated by an anti-tag sequence; and an amplimer. The consistency between the detection result of the detection liquid chip provided by the invention and the detection result of a sequencing method is high to 100 percent, and the wild-type and mutant parallel detection of a plurality of mutation sites is realized.

PatBase - CN102994621.B	序 列 表	3.14.16
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Patent Number	Publication Date	Application Number	Application Date
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CN102994621 B	20141210	CN201110269795	20110913

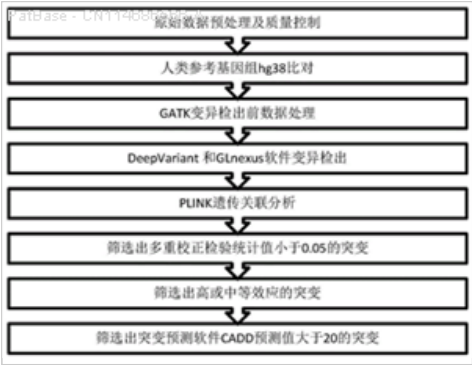
Inventors: XU JIASSEN; HE JIAYING

7. Family 92163187 (CN114686566 A)

[View in PatBase](#)

Title
[EN] GENETIC RISK FACTOR SCREENING METHOD AND APPLICATION THEREOF

Abstract
[EN] The invention discloses a genetic risk factor screening method, which comprises the following steps: carrying out high-throughput gene sequencing, simultaneously carrying out targeted capture on disease-related genes, taking genome healthy person data of thousands of persons as a contrast, carrying out genetic association analysis by using a DeepVariant + GLneux mutation detection combination and PLINK software, and screening out genetic risk factors of related diseases. According to the present invention, the bioinformatics analysis is optimized and innovated, the traditional GATK Best Practice analysis process is not used, the DeepVariant + GLneux combination is adopted to carry out mutation detection, and the PLINK software is adopted to carry out the genetic association analysis; the method can be used as an efficient and accurate genetic risk factor detection and screening method, is particularly suitable for Chinese NS-CHD children, and can be applied to efficient and accurate screening of other genetic disease gene risk factors.



International Class: C12Q1/6809; G06N3/04; G16B20/20; G16B20/30; G16B40/00

Cooperative Patent Class: C12Q1/6809; G06N3/0454; G16B20/20; G16B20/30; G16B40/00

Family Information

Patent Number	Publication Date	Application Number	Application Date
CN114686566 A	20220701	CN202011618060	20201231

Priority Numbers: CN202011618060 [20201231]

Probable Patent Assignee: SUZHOU ARK BIOTECHNOLOGY LTD CO

Assignees: SUZHOU ARK BIOTECHNOLOGY LTD CO

Non Std Assignees: SUZHOU ARK BIOTECHNOLOGY CO LTD; SUZHOU ARK BIOLOGICAL TECHNOLOGY CO LTD

Inventors: CHEN XIAO; JIANG YONGPING; CHEN YING; GU HONGCANG

8. Family 80931748 (CN111647648 A)

[View in PatBase](#)

Title

[EN] GENE PANEL USED FOR DETECTING BREAST CANCER GENE MUTATION, DETECTION METHOD USED FOR DETECTING BREAST CANCER GENE MUTATION AND APPLICATION OF GENE PANEL

Abstract

[EN] The invention relates to a gene panel used for detecting breast cancer gene mutation, and a detection method and application of the gene panel. The panel disclosed by the invention comprises 54419 pieces of targeted DNA (deoxyribonucleic acid) probes. The targeted DNA comprises the exon regions of 445 pieces of genes on the human genomes, 2573 pieces of MSI (microsatellite instability) sites and 566 position intervals used for detecting gene fusion. The detection method in the invention can be used for detecting SNV (single nucleotide variation), Indel (Insertion and Deletion), CNV (Copy Number Variation), Fusion, MSI, TMB (Tumor Mutational Burden), HLA (human leucocyte antigen) parting and the like of a tumor somatic cell multi-site DNA mutation. An optimal individual treatment medicine and scheme can be conveniently selected according to the genome features of patients in a breast cancer immunotherapy process.

International Class: C12N15/11; C12Q1/6858; C12Q1/6886; G16B30/10

Cooperative Patent Class: C12Q1/6858; C12Q1/6886; C12Q2600/156; G16B30/10

Family Information

Patent Number	Publication Date	Application Number	Application Date
CN111647648 A	20200911	CN202010437090	20200521

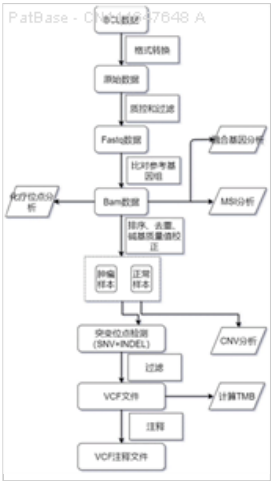
Priority Numbers: CN202010437090 [20200521]

Probable Patent Assignee: BEIDOU LIFE SCIENCE GUANGZHOU CO LTD

Assignees: BEIDOU LIFE SCIENCE GUANGZHOU CO LTD; QIAN ZHIRONG

Non Std Assignees: BEIDOU LIFE SCIENCE GUANGZHOU CO; BEIDOU LIFE SCIENCES GUANGZHOU CO LTD; MONEY ZHIRONG

Inventors: QIAN ZHIRONG; SHI JIANTAO; LI WENBIN; YE HUI



9. Family 82319129 (CN112029865 A)

[View in PatBase](#)

Title

[EN] PROBE GROUP AND GENE CHIP FOR SIMULTANEOUSLY DETECTING MULTIPLE GENE MUTATION TYPES AND APPLICATION OF PROBE GROUP AND GENE CHIP

Abstract

[EN] The invention belongs to the technical field of gene detection, and particularly relates to a probe group for simultaneously detecting multiple gene mutation types. According to the probe group, mutation detection can be carried out on up to 102 genes at one time, so that known and/or unknown mutations can be found; 14 # exon skipping mutation of the MET gene, a BCL2L11 (BIM) 2 # intron deletion polymorphism related region and NTRK1/2/3 hotspot fusion mutation of related rare hotspot variation can be detected at one time; and known hotspot fusion variation and unknown fusion variation of the six genes -ALK, ROS1, RET, NTRK1, NTRK2 and NTRK3 of specific fusion breakpoint regions can be detected more sensitively (0.5 percent).

International Class: C12N15/11; C12Q1/6886

Cooperative Patent Class: C12Q1/6886; C12Q2600/106; C12Q2600/156

Family Information

Patent Number	Publication Date	Application Number	Application Date
CN112029865 A	20201204	CN202010991893	20200918

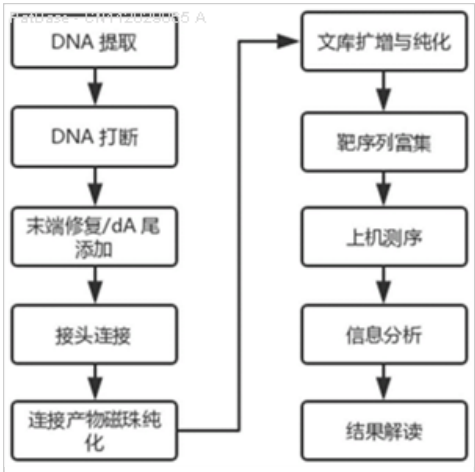
Priority Numbers: CN202010991893 [20200918]

Probable Patent Assignee: WUHAN HONGKANGJIAN GENE DIAGNOSIS TECH CO LTD

Assignees: WUHAN HONGKANGJIAN GENE DIAGNOSIS TECH CO LTD

Non Std Assignees: WUHAN HONGKANGJIAN GENE DIAGNOSIS TECHNOLOGY CO; WUHAN 156 HEALTHY GENE DIAGNOSIS TECHNOLOGY CO LTD

Inventors: LYU XIAOXING; ZHANG JIAN; YUAN MENG; WU WEIKANG; LYU XINGXING



10. Family 76349377 (EP3561075 A1)

[View in PatBase](#)

Extended Family Number: 48164370

Title

[EN] DETECTING MUTATIONS IN TUMOUR BIOPSIES AND CELL-FREE SAMPLES

Abstract

[EN] The invention provides a method for detecting one or more mutations or genetic variations in a blood, serum, or plasma sample of a subject having cancer or suspected of having cancer, the method comprising: identifying a plurality of mutations or genetic variations in a tumor sample of the subject by whole exome sequencing; collecting a blood, serum, or plasma sample from the subject, and isolating cell-free DNA from the blood, serum, plasma, or tumor sample; amplifying a plurality of loci corresponding to the mutations or genetic variations from the cell-free DNA to obtain amplicons; sequencing the amplicons to obtain sequence reads; and detecting one or more of the mutations or genetic variations present in the cell-free DNA from the sequence reads; optionally wherein the cell-free DNA comprises circulating tumor DNA.

International Class: C12Q1/6869; C12Q1/6886; G16B20/10; G16H50/20; G16B20/20

Cooperative Patent Class: C12Q1/6806; C12Q1/6869; C12Q1/6886; C12Q2539/10; C12Q2600/156; C12Q2600/158; C12Q2600/16; C12Q2600/172; G06N20/00; G06N7/005; G16B15/00; G16B20/00; G16B20/10; G16B20/20; G16B25/00; G16B25/20; G16B40/00; G16B40/20; G16H10/40; G16H50/20; G16Z99/00

Family Information

Patent Number	Publication Date	Application Number	Application Date
DE602015057663 D1	20200910	DE201560057663T	20150421
EP3561075 A1	20191030	EP20190159999	20150421

Priority Numbers: US20140982245P [20140421]; US20140987407P [20140501]; EP20150718754 [20150421]; US20150148173P [20150415]; US20140994791P [20140516]; US20150147377P [20150414]; US20140066514P [20141021]; US20150146188P [20150410]; WO2015US26957 [20150421]

Probable Patent Assignee: NATERA INC

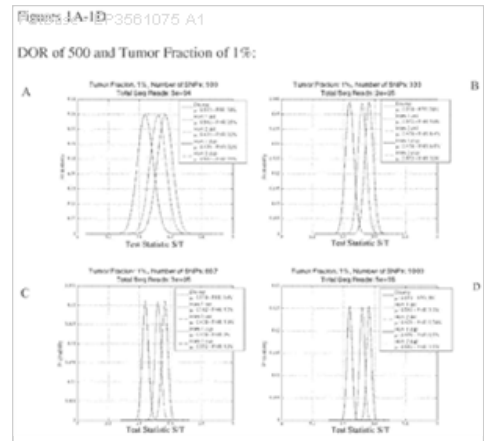
Assignees: NATERA INC

Inventors: BABIARZ JOSHUA; CONSTANTIN TUDOR POMPILIU; GEMELOS GEORGE; HILL MATTHEW MICAH; KIRKIZLAR HUSEYIN ESER; RABINOWITZ MATTHEW; SAKARYA ONUR; ZIMMERMAN BERNHARD; EUBANK LANE; SIGURJONSSON STYRMIR

Non Std Inventors: EUBANK LANE A; SIGURJONSSON STYRMIR

Agent(s): GIBBS RICHARD; MARKS AND CLERK LLP

Designated States: AL; AT; BE; BG; CH; CY; CZ; DE; DK; EE; ES; FI; FR; GB; GR; HR; HU; IE; IS; IT; LI; LT; LU; LV; MC; MK; MT; NL; NO; PL; PT; RO; RS; SE; SI; SK; SM; TR



11. Family 77002219 (CN110592213 A)

[View in PatBase](#)

Title
[EN] GENE PANEL FOR PREDICTING NEW ANTIGEN LOAD AND DETECTING GENOME MUTATION

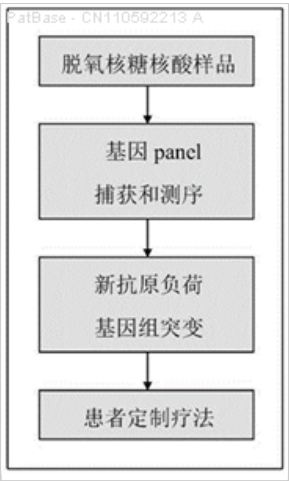
Abstract
[EN] The invention relates to the fields of biotechnology, DNA mutation detection technology and bioinformatics, in particular to a gene panel for predicting a new antigen load and detecting genome mutation. Specifically, the invention relates to the gene panel which combines 839 genes and integrates 511 gene fusion events. The gene panel provided by the invention can rapidly, efficiently and accurately predict a new antigen load, and can also detect DNA mutation of multiple sites at one time, so that an optimal individualized treatment drug and scheme can be selected according to genomic characteristics of a patient in a cancer immunotherapy process. In addition, the gene panel provided by the invention can also be used for measuring various types of biomarkers such as SNV, Indel, CNV, gene fusion, MSI, TMB and HLA.

International Class: C12N15/11; C12Q1/6886
Cooperative Patent Class: C12Q1/6886; C12Q2600/106; C12Q2600/156

Family Information

Patent Number	Publication Date	Application Number	Application Date
CN110592213 A	20191220	CN201910824393	20190902

Priority Numbers: CN201910824393 [20190902]
Probable Patent Assignee: SHENZHEN NEOCURA BIOLOGICAL MEDICAL TECH CO LTD
Assignees: SHENZHEN NEOCURA BIOLOGICAL MEDICAL TECH CO LTD; SHENZHEN XINHE BIOMEDICAL TECHNOLOGY CO LTD
Non Std Assignees: SHENZHEN NEOCURA BIOLOGICAL MEDICAL TECHNOLOGY CO
Inventors: JIN TAIQING; WAN JI; PAN XIAOXIN; WANG ZHIQIANG; CAI XUE ER; WANG YIXING; YU TAO; GUAN JIANHONG; SONG QI



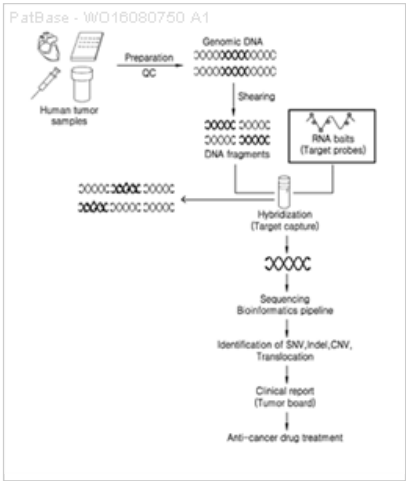
12. Family 62470143 (WO16080750 A1)

[View in PatBase](#)

Title
[EN] GENE PANEL FOR DETECTING CANCER GENOME MUTANT

Abstract
[EN] The present invention relates to a composition for detecting the mutation of cancer cell genomic DNA and a method for detecting the mutation of cancer cell genomic DNA. The composition, according to one aspect of the present invention, may be used for analyzing, at once with high sensitivity and accuracy, various gene mutations from a sample comprising a cancer cell genome, and on the basis of the results of such analysis, a patient-tailored cancer therapeutic agent may be efficiently explored.

International Class: C12Q1/68
Cooperative Patent Class: C12Q1/6806; C12Q1/6886; C12Q2600/136; C12Q2600/158; C12Q1/68



Family Information

Patent Number	Publication Date	Application Number	Application Date
KR20160059446 A	20160526	KR20150161608	20151118
WO16080750 A1	20160526	WO2015KR12384	20151118

Priority Numbers: KR20140161093 [20141118]; KR20150161608 [20151118]
Probable Patent Assignee: SAMSUNG LIFE PUBLIC WELFARE FOUNDATION
Assignees: SAMSUNG LIFE PUBLIC WELFARE FOUNDATION
Inventors: BAE JOON SEOL; KIM NA YOUNG; PARK WOONG YANG
Agent(s): YPLEE MOCK AND PARTNERS

Designated States: AE; AG; AL; AM; AO; AT; AU; AZ; BA; BB; BE; BF; BG; BH; BJ; BN; BR; BW; BY; BZ; CA; CF; CG; CH; CI; CL; CM; CN; CO; CR; CU; CY; CZ; DE; DK; DM; DO; DZ; EC; EE; EG; ES; FI; FR; GA; GB; GD; GE; GH; GM; GN; GQ; GR; GT; GW; HN; HR; HU; ID; IE; IL; IN; IR; IS; IT; JP; KE; KG; KM; KN; KP; KZ; LA; LC; LK; LR; LS; LT; LU; LV; LY; MA; MC; MD; ME; MG; MK; ML; MN; MR; MT; MW; MX; MY; MZ; NA; NE; NG; NI; NL; NO; NZ; OM; PA; PE; PG; PH; PL; PT; QA; RO; RS; RU; RW; SA; SC; SD; SE; SG; SI; SK; SL; SM; SN; ST; SV; SY; SZ; TD; TG; TH; TJ; TM; TN; TR; TT; TZ; UA; UG; US; UZ; VC; VN; ZA; ZM; ZW

13. Family 52327910 (US2012295819 AA)

[View in PatBase](#)

Title

[EN] METHODS AND COMPOSITIONS FOR MULTIPLEX PCR

Abstract

[EN] The present invention provides methods, compositions, kits, systems and apparatus that are useful for multiplex PCR of one or more nucleic acids present in a sample. In particular, various target-specific primers are provided that allow for the selective amplification of one or more target sequences. In one aspect, the invention relates to target-specific primers useful for the selective amplification of one or more target sequences associated with cancer or inherited disease. In some aspects, amplified target sequences obtained using the disclosed methods, kits, systems and apparatuses can be used in various downstream processes including nucleic acid sequencing and used to detect the presence of genetic variants.

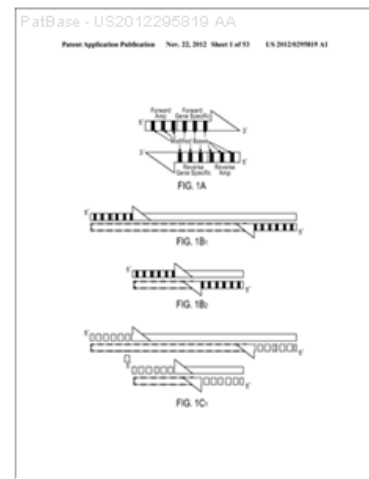
International Class: C12Q1/68; C12Q1/6874; C12Q1/6886; C07H21/02; C07H21/04; C12N15/10; C12Q1/6806; C12Q1/6855; C12Q1/686; C12Q1/6879; C12Q1/6883; C40B50/06; C12P19/34; C40B20/00; G06T13/00; G06T13/80

Cooperative Patent Class: C12Q1/6855; C12Q1/6858; C12N15/1065; C12Q1/6806; C12Q1/686; C12Q1/6874; C12Q1/6886; C12Q2600/16; C12Q1/6846; C12Q2521/307; C12Q2525/101; C12Q2525/191; C12Q2537/143; C12Q1/6879; C12Q1/6883; C12Q2537/16; C12Q1/6853; C12Q2600/156; G06T13/80

US Class: 1/1; 435/6.1; 435/6.12; 435/91.2; 435/91.52; 506/16; 506/2; 506/26; 506/4; 506/9; 536/23.1; 536/24.3

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Patent Number	Publication Date	Application Number	Application Date
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Patent Number	Publication Date	Application Number	Application Date
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Priority Numbers: US20110564763P [20111129]; US20110578192P [20111220]; US20120594160P [20120202]; US20120598881P [20120214]; US20120598892P [20120214]; US20120625596P [20120417]; WO2012US62494 [20121029]; US20120639017P [20120426]; WO2012US35612 [20120427]; US20120458739 [20120427]; US20120619178 [20120914]; US20120619815 [20120914]; US20120618805 [20120914]; US20110479952P [20110428]; US20110531574P [20110906]; US20110531583P [20110906]; US20110538079P [20110922]; US20140037575P [20140814]; US20140046845P [20140905]; WO2015US45209 [20150814]; EP20120781556 [20121029]; EP20120719880 [20120427]; EP20150170140 [20121029]; EP20150200283 [20120427]; EP20180194509 [20120427]; EP20150200283 [20151215]; US20140518904 [20141020]; US20120663334 [20121029]; US20150795826 [20150709]; US20120583574P [20121015]; US20120679706 [20121116]; US20150796400 [20150710]; US20180965595 [20180427]; US20180965650 [20180427]; US20140518857 [20141020]; US20140518885 [20141020]; US20150796696 [20150710]; US20150795774 [20150709]; US20150826385 [20150814]; US20160068466 [20160311]; US20200949159 [20201015]; US20130735561 [20130107]

Probable Patent Assignee: LIFE TECHNOLOGIES CORP

Assignees: LIFE TECHNOLOGIES CORP; LIFE TECH CORP; LEAMON JOHN; ANDERSEN MARK; THORNTON MICHAEL; GOOGLE INC

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Inventors: LEAMON JOHN; ANDERSEN MARK; THORNTON MICHAEL; BRAMLETT KELLI; GUY ROMAIN P; HAASE CHET

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Designated States: AL; AT; BE; BG; CH; CY; CZ; DE; DK; EE; ES; FI; FR; GB; GR; HR; HU; IE; IS; IT; LI; LT; LU; LV; MC; MK; MT; NL; NO; PL; PT; RO; RS; SE; SI; SK; SM; TR; BA; ME; AE; AG; AM; AO; AU; AZ; BB; BF; BH; BJ; BR; BW; BY; BZ; CA; CF; CG; CI; CL; CM; CN; CO; CR; CU; DM; DO; DZ; EC; EG; GA; GD; GE; GH; GM; GN; GQ; GT; GW; HN; ID; IL; IN; JP; KE; KG; KM; KN; KP; KR; KZ; LA; LC; LK; LR; LS; LY; MA; MD; MG; ML; MN; MR; MW; MX; MY; MZ; NA; NE; NG; NI; NZ; OM; PE; PG; PH; QA; RU; RW; SC; SD; SG; SL; SN; ST; SV; SY; SZ; TD; TG; TH; TJ; TM; TN; TT; TZ; UA; UG; US; UZ; VC; VN; ZA; ZM; ZW; BN; PA; IR; SA

14. Family 65240384 (CN106521012 A)

[View in PatBase](#)

Title

[EN] DETECTION REAGENT KIT FOR DETECTING MDS (MYELODYSPLASTIC SYNDROME)-RELATED GENE GROUP

Abstract

[EN] The invention discloses a groups of sequencing reagent kits for screening MDS (myelodysplastic syndrome)-related gene mutation and subsequence medical interpretation databases. The MDS-related gene group includes 16 genes of U2AF1, TP53 and the like. The sequencing reagent kits comprise multiple PCR (polymerase chain reaction) primers for amplifying all exons of the 16 MDS-related genes. The sequencing reagent kits and the medical interpretation databases have the advantages that the reagent kits for screening the MDS gene mutation are high in detection efficiency and detection rate and wide in mutant gene coverage; given medical interpretation reports are accurate and authoritative, and the like.

International Class: C12N15/11; C12Q1/68

Cooperative Patent Class: C12Q1/686; C12Q1/6869; C12Q1/6886; C12Q2600/106; C12Q2600/118; C12Q2600/156; C12Q2600/16

Family Information

Patent Number	Publication Date	Application Number	Application Date
CN106521012 A	20170322	CN201611241375	20161229

Priority Numbers: CN201611241375 [20161229]

Probable Patent Assignee: TIANJIN SINO US DIAGNOSTICS MEDICAL DIAGNOSIS TECH CO LTD

Assignees: TIANJIN SINO US DIAGNOSTICS MEDICAL DIAGNOSIS TECH CO LTD

Non Std Assignees: TIANJIN SINO US DIAGNOSTICS MEDICAL DIAGNOSIS TECHNOLOGY CO; TIANJIN CONCORD GORGEOUS MEDICAL DIAGNOSTIC TECHNOLOGIES LTD

Inventors: KOU KUNYUAN; LI JING; JIA YUJIAO; ZHANG DONGLEI

15. Family 86513281 (CN113249483 A)

[View in PatBase](#)

Title

[EN] GENE COMBINATION AND SYSTEM FOR DETECTING TUMOR MUTATION BURDEN AND APPLICATION

Abstract

[EN] The invention discloses gene combination and system for detecting tumor mutation burden and application. The tumor mutation burden detection gene combination disclosed by the invention comprises 824 gene combinations, and the system comprises a tumor mutation burden calculation module based on the 824 gene combinations and a reagent for detecting each gene mutation in the 824 gene combinations and/or a module or software for analyzing a high-throughput sequencing result. The calculation module is used for calculating the tumor mutation burden (TMB), wherein $TMB = s/n$, s is the total number of variation sites, meeting a screening threshold value, in an exon coding region in the 824 gene combinations, and n is the base mega number of the coding region covered by the 824 gene combinations. The TMB based on 824 gene combinations and TMB results of whole exon sequencing (WES) are highly consistent, and the gene combination has a relatively ideal clinical prediction effect in the real world and has a very good application prospect.

International Class: C12N15/12; C12Q1/6858; C12Q1/6886; G16B20/50

Cooperative Patent Class: C12Q1/6858; C12Q1/6886; C12Q2600/106; C12Q2600/156; G16B20/50

Family Information

Patent Number	Publication Date	Application Number	Application Date
CN113249483 A	20210813	CN202110645065	20210610
CN113249483 B	20211008	CN202110645065	20210610

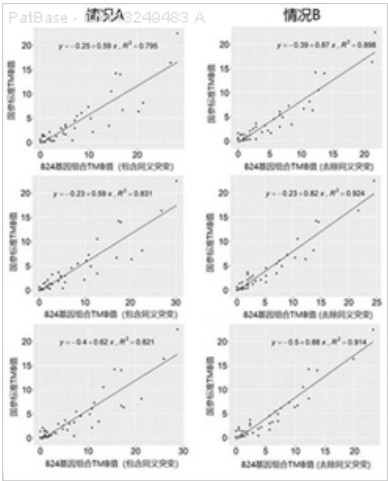
Priority Numbers: CN202110645065 [20210610]

Probable Patent Assignee: GENETRON HEALTH TECH INC

Assignees: GENETRON HEALTH TECH INC; GENETRON HEALTH BEIJING CO LTD

Non Std Assignees: GENETRON HEALTH TECHNOLOGIES INC

Inventors: CHENG XIAOLEI; ZHAO XIAOFEI; HUANG XIN; GUO JINGYU; ZHENG QIAOSONG; WANG SIZHEN



16. Family 70353540 (CN108251525 A)

[View in PatBase](#)

Title

[EN] DETECTION KITS USED FOR DETECTING ALL RELATED GENES

Abstract

[EN] The invention discloses a group of sequencing kits which are used for screening ALL related gene mutation, and a subsequent medical science decoding database. The ALL related genes comprise 16 genes including FAT1 and KRAS. The sequencing kits comprise multiple PCR primers which are used for amplification of all the exons of the 16 ALL related genes. The detection kits used for screening ALL genemutation are high in detection efficiency, wide in mutation gene coverage, and high in detection rate; and obtained medical science decoding reports are accurate and authoritative.

International Class: C12Q1/6886

Cooperative Patent Class: C12Q1/6886; C12Q2600/106; C12Q2600/118; C12Q2600/156

Family Information

Patent Number	Publication Date	Application Number	Application Date
CN108251525 A	20180706	CN201711053097	20171031

Priority Numbers: CN201711053097 [20171031]

Probable Patent Assignee: TIANJIN SINO US DIAGNOSTICS MEDICAL DIAGNOSIS TECH CO LTD

Assignees: TIANJIN SINO US DIAGNOSTICS MEDICAL DIAGNOSIS TECH CO LTD

Non Std Assignees: TIANJIN SINO US DIAGNOSTICS MEDICAL DIAGNOSIS TECHNOLOGY CO; TIANJIN CONCORD GORGEOUS MEDICAL DIAGNOSTIC TECHNOLOGIES LTD

Inventors: LIN YANI; KUN RU; JIA YUJIAO

17. Family 73940984 (CN109609647 A)

[View in PatBase](#)

Title

[EN] NEXT GENERATION SEQUENCING-BASED DETECTION PANEL AND DETECTION KIT FOR PAN-CANCER TARGETING, CHEMOTHERAPY AND IMMUNE DRUGS AND APPLICATION THEREOF

Abstract

[EN] The invention discloses a next generation sequencing-based detection panel and detection kit for pan-cancer targeting, chemotherapy and immune drugs and application thereof. The detection panel includes gene mutations related to pan-cancer type, treatment and prognosis, tumor mutation load calculation related exon regions and microsatellite instability sites. According the technical solution of the present invention, the detection panel includes the gene mutations related to pan-cancer type, treatment and prognosis, the tumor mutation load calculation related exon regions and the microsatellite instability sites, and the gene information included is comprehensive; a variety of tumor mutations can be jointly detected; and the detection panel and detection kit can be used for the concomitant diagnosis of targeted drugs, chemotherapeutics or immune drugs to obtain accurate results.

International Class: C12Q1/6886

Cooperative Patent Class: C12Q1/6886; C12Q2600/106; C12Q2600/112; C12Q2600/118; C12Q2600/156

Family Information

Patent Number	Publication Date	Application Number	Application Date
CN109609647 A	20190412	CN201910074640	20190125
CN109609647 B	20220823	CN201910074640	20190125

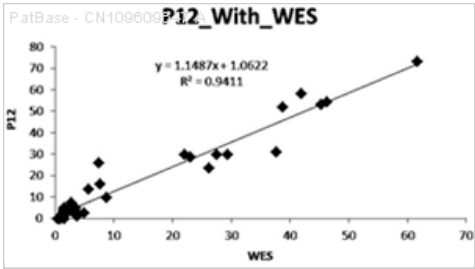
Priority Numbers: CN201910074640 [20190125]

Probable Patent Assignee: ZHENYUE BIOTECHNOLOGY JIANGSU CO LTD

Assignees: ZHENYUE BIOTECHNOLOGY JIANGSU CO LTD

Non Std Assignees: ZHENYUE BIOTECHNOLOGY JIANGSU CO; ZHEN WYATT BIOLOGICAL TECHNOLOGY CO LTD JIANGSU

Inventors: ZHU WEI; ZENG XUEXIA; HE JI; SONG XIAOFENG; YAN LINLIN; DU BO; HONG YUANYUAN; XIA YAN; CHEN WEIZHI; GUO XIANCHAO; YAN HUITING; ZHAO LILI



18. Family 90392111 (WO22056021 A1)

[View in PatBase](#)

Title

[EN] METHODS OF DETECTING AN INACTIVATING MUTATION OF PBRM1 IN MENINGIOMA

Abstract

[EN] Provided herein are methods for detecting an inactivating mutation of polybromo 1 (PBRM1) in an individual having meningioma, as well as methods of diagnosis, prognosis and treatment of meningioma related thereto.

International Class: G01N33/574

Cooperative Patent Class: C12Q1/68; G01N33/57407

Family Information

Patent Number	Publication Date	Application Number	Application Date
WO22056021 A1	20220317	WO2021US49495	20210908

Priority Numbers: US20200076191P [20200909]

Probable Patent Assignee: FOUND MEDICINE INC

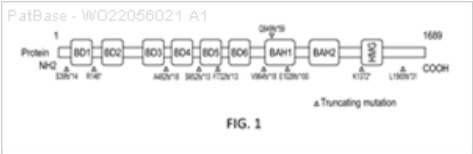
Assignees: FOUND MEDICINE INC

Non Std Assignees: FOUNDATION MEDICINE INC

Inventors: WILLIAMS ERIK

Agent(s): QI YAN; MORRISON AND FOERSTER LLP

Designated States: AE; AG; AL; AM; AO; AT; AU; AZ; BA; BB; BE; BF; BG; BH; BJ; BN; BR; BW; BY; BZ; CA; CF; CG; CH; CI; CL; CM; CN; CO; CR; CU; CY; CZ; DE; DJ; DK; DM; DO; DZ; EC; EE; EG; ES; FI; FR; GA; GB; GD; GE; GH; GM; GN; GQ; GR; GT; GW; HN; HR; HU; ID; IE; IL; IN; IR; IS; IT; JO; JP; KE; KG; KH; KM; KN; KP; KR; KW; KZ; LA; LC; LK; LR; LS; LT; LU; LV; LY; MA; MC; MD; ME; MG; MK; ML; MN; MR; MT; MW; MX; MY; MZ; NA; NE; NG; NI; NL; NO; NZ; OM; PA; PE; PG; PH; PL; PT; QA; RO; RS; RU; RW; SA; SC; SD; SE; SG; SI; SK; SL; SM; SN; ST; SV; SY; SZ; TD; TG; TH; TJ; TM; TN; TR; TT; TZ; UA; UG; US; UZ; VC; VN; WS; ZA; ZM; ZW



19. Family 66519480 (US2020140957 AA)

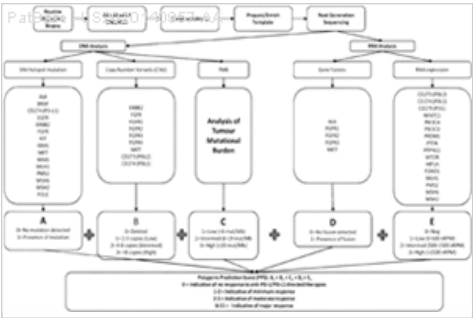
[View in PatBase](#)

Title

[EN] METHOD FOR DETERMINING THE SUSCEPTIBILITY OF A PATIENT SUFFERING FROM PROLIFERATIVE DISEASE TO TREATMENT USING AN AGENT WHICH TARGETS A COMPONENT OF THE PD 1/PD-L1 PATHWAY

Abstract

[EN] A method for determining the susceptibility of a patient suffering from proliferative disease to treatment using an agent which targets a component of the PD1/PD-L1 pathway, said method comprising determining in a tumour sample from said patient at least three biomarkers selected from list including those directly related to the PD-1/PD-L1 pathway as well as other oncogenic biomarkers and the tumour mutational burden, and relating the presence of more than one of said biomarkers as an indicator susceptibility to said agent. Methods for making the determinations and algorithms for dealing with the results are also described and claimed.



International Class: C12Q1/6886; G16H20/10; G16H50/20; C12Q; C12Q1/6869; G01N33/53

Cooperative Patent Class: C12Q1/6886; C12Q2600/106; C12Q2600/156; C12Q2600/158; G01N2800/52; G16H20/10; G16H50/20; Y02A90/10

Family Information

Patent Number	Publication Date	Application Number	Application Date
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WO18229487 A1	20181220	WO2018GB51624	20180613

Priority Numbers: GB20170009360 [20170613]; GB20170017512 [20171025]; WO2018GB51624 [20180613]

Probable Patent Assignee: ONCOLOGICA UK LTD

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Non Std Assignees: LODDO MARCO; WILLIAMS GARETH; SNELSON KEEDA

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Designated States: AL; AT; BA; BE; BG; CH; CY; CZ; DE; DK; EE; ES; FI; FR; GB; GR; HR; HU; IE; IS; IT; LI; LT; LU; LV; MC; ME; MK; MT; NL; NO; PL; PT; RO; RS; SE; SI; SK; SM; TR; AE; AG; AM; AO; AU; AZ; BB; BF; BH; BJ; BN; BR; BW; BY; BZ; CA; CF; CG; CI; CL; CM; CN; CO; CR; CU; DJ; DM; DO; DZ; EC; EG; GA; GD; GE; GH; GM; GN; GQ; GT; GW; HN; ID; IL; IN; IR; JO; JP; KE; KG; KH; KM; KN; KP; KR; KW; KZ; LA; LC; LK; LR; LS; LY; MA; MD; MG; ML; MN; MR; MW; MX; MY; MZ; NA; NE; NG; NI; NZ; OM; PA; PE; PG; PH; QA; RU; RW; SA; SC; SD; SG; SL; SN; ST; SV; SY; SZ; TD; TG; TH; TJ; TM; TN; TT; TZ; UA; UG; US; UZ; VC; VN; ZA; ZM; ZW

20. Family 77979534 (WO21114422 A1)

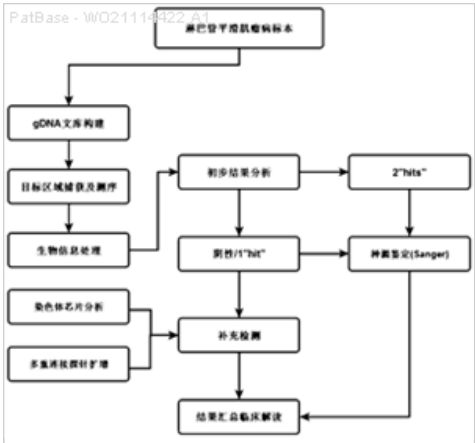
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Title

[EN] JOINT LYMPHANGIOLEIOMYOMATOSIS DETECTION METHOD AND USE THEREOF

Abstract

[EN] Disclosed is a joint lymphangioleiomyomatosis (LAM) detection method and the use thereof, which fall within the technical field of gene detection. The method comprising the following steps: carrying out liquid phase capture targeting sequencing, which involves: designing a Panel for TSC1 and TSC2 gene whole exon coding regions, which are heavily related to LAM, and mutant genes, which are closely related to solid tumors, constructing a gDNA library, carrying out hybrid capture, and sequencing on a machine; carrying out sorting, which involves: analyzing the above-mentioned sequencing data by means of bioinformatics processing, wherein if the TSC1 and TSC2 genes are negative, carrying out supplementary detection by using a chromosome chip analysis method; if a single strike site is detected, performing supplementary detection by using multiplex ligation-dependent probe amplification; and if sites having no clear sources of a somatic mutation and an embryonic system mutation are detected, carrying out supplementary detection by using Sanger detection. The method improves the positive variation detection ratio of LAM patients.



International Class: C12Q1/6858; C12Q1/6886; C12N15/11; C12Q1/6869

Cooperative Patent Class: C12Q1/6858; C12Q1/6886; C12Q2600/156; C12Q2600/16

Family Information

Patent Number	Publication Date	Application Number	Application Date
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CN110885879 B	20201113	CN201911281998	20191213
WO21114422 A1	20210617	WO2019CN129173	20191227

Priority Numbers: CN201911281998 [20191213]

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Designated States: AE; AG; AL; AM; AO; AT; AU; AZ; BA; BB; BE; BF; BG; BH; BJ; BN; BR; BW; BY; BZ; CA; CF; CG; CH; CI; CL; CM; CN; CO; CR; CU; CY; CZ; DE; DJ; DK; DM; DO; DZ; EC; EE; EG; ES; FI; FR; GA; GB; GD; GE; GH; GM; GN; GQ; GR; GT; GW; HN; HR; HU; ID; IE; IL; IN; IR; IS; IT; JO; JP; KE; KG; KH; KM; KN; KP; KR; KW; KZ; LA; LC; LK; LR; LS; LT; LU; LV; LY; MA; MC; MD; ME; MG; MK; ML; MN; MR; MT; MW; MX; MY; MZ; NA; NE; NG; NI; NL; NO; NZ; OM; PA; PE; PG; PH; PL; PT; QA; RO; RS; RU; RW; SA; SC; SD; SE; SG; SI; SK; SL; SM; SN; ST; SV; SY; SZ; TD; TG; TH; TJ; TM; TN; TR; TT; TZ; UA; UG; US; UZ; VC; VN; ZA; ZM; ZW

21. Family 34404632 (US2008274469 AA)

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Title

[EN] C-KIT ONCOGENE MUTATIONS IN MELANOMA

Abstract

[EN] The present invention provides methods of detecting c-KIT-dependent-melanoma for diagnostic and prognostic purposes. The invention further provides methods of treating such melanoma by inhibiting c-KIT.

International Class: C07H21/00; C07H21/02; C07H21/04; C07K14/435; C12P19/00; C12P19/34; C12Q1/68; G01N33/53; C12Q1/6886; A61K39/395; A61K45/00; A61P35/00; C12N15/09

Cooperative Patent Class: A61P35/00; C12Q1/6886; C12Q2600/106; C12Q2600/118; C12Q2600/156

US Class: 435/6; 435/6.11; 435/6.14; 435/6.140P; 435/6P

Family Information

Patent Number	Publication Date	Application Number	Application Date
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Priority Numbers: US20050729171P [20051021]; WO2006US41510 [20061023]; EP20060836496 [20061023]; EP20160150667 [20061023]; NZ20060568385 [20061023]; US20130055752 [20131016]; US20080090855 [20080418]; US20060090855 [20061023]

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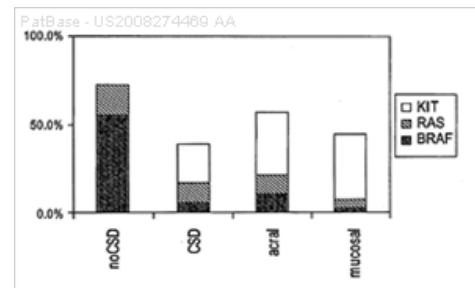
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MD; MG; MK; ML; MN; MR; MW; MX; MY; MZ; NA; NE; NG; NI; NO; NZ; OM; PG; PH; RS; RU; SC; SD; SG; SL; SM; SN; SV; SY; SZ; TD; TG; TJ; TM; TN; TT; TZ; UA; UG; US; UZ; VC; VN; ZA; ZM; ZW

22. Family 75456487 (US2022213555 AA)

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Title

[EN] NEXT GENERATION SEQUENCING-BASED DETECTION PANEL FOR GLIOMA, DETECTION KIT, DETECTION METHOD AND APPLICATION THEREOF

Abstract

[EN] Disclosed are a next generation sequencing-based detection panel for glioma, a detection kit, a detection method and an application thereof. The detection panel contains glioma-related genes and loci, wherein the glioma-related genes and loci contain SNP locus on chromosome 1, SNP locus on chromosome 19, MGMT, ATRX, H3F3A, ACVR1, CTC, HIST1H3B, MLH1, PLCG1, SMO, AKT1, CTNNB1, HIST1H3C, MSH2, PMS2, TERT, ATRX, DAXX, HRAS, MSH6, PPMID, TP53, BCOR, DDX3X, IDH1, MYC, PTCH1 and the like.

International Class: C12M1/00; C12M1/34; C12Q1/6858; C12Q1/6886; G16B20/20; G16B20/30; C12Q1/6869

Cooperative Patent Class: C12Q1/6858; C12Q2600/118; C12Q1/6886; C12Q2600/112; C12Q2600/136; C12Q2600/154; C12Q2600/156; G16B20/30; C12M1/00; C12M1/34; C12Q1/6869

Family Information

Patent Number	Publication Date	Application Number	Application Date
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WO20224159 A1	20201112	WO2019CN106606	20190919

Priority Numbers: CN201910373158 [20190506]; CN201910372726 [20190506]; CN201910373154 [20190506]; WO2019CN106606 [20190919]

Probable Patent Assignee: ZHENHE PREC MEDICAL SCIENCE EXAMINATION LABORATORY WUXI CO LTD

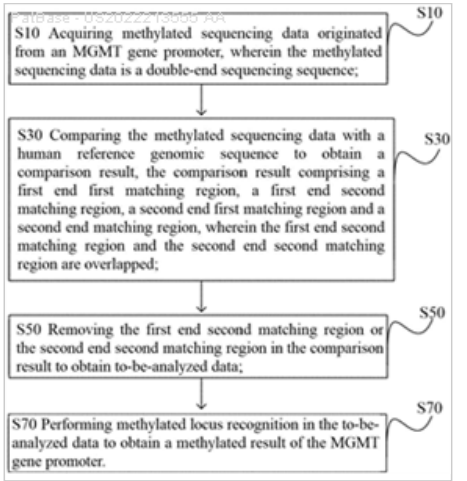
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23. Family 28448972 (US2003125289 AA)

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Title
[EN] NOONAN SYNDROME GENE

Abstract
[EN] Diagnostic and therapeutic applications for Noonan Syndrome are described. The diagnostic and therapeutic applications are based on certain mutations in the protein tyrosine phosphatase gene PTPN11 and its expression product, PTPN11, as well as mutations in other components in a PTPN11 signal transduction pathway promoting an increased signaling flux. Also described are nucleotide sequences, amino acid sequences, probes, and primers related to PTPN11 and PTPN11 variants, and cells expressing such variants.

International Class: A61K31/7088; A61K38/00; A61K39/00; C12N9/16; C12Q1/68; C12Q1/6883; G01N33/573; G01N33/68; C12N15/55; C12Q1/42; C07H21/02; C07H21/04; A61K38/17; A61K48/00; C12N; C12P19/34; G01N33/53; G01N33/567

Cooperative Patent Class: A61K2039/505; A61K38/00; C12N9/16; C12Q1/6883; C12Q2600/156; C12Q2600/158; C12Q2600/172

US Class: 435/6; 435/6.11; 435/6.110S; 435/6.12; 435/6.120S; 435/6S; 435/7.2; 435/7.200S; 514/12; 514/16.4; 514/16.400S; 514/44; 514/44.00AP; 514/44A; 514/7.5; 514/7.500S; 536/23.1; 536/23.5; 536/24.31

Family Information

Patent Number	Publication Date	Application Number	Application Date
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CA2495529 AA	20050207	CA20022495529	20021001
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WO03029422 A2	20030410	WO2002US31290	20021001
WO03029422 A3	20031211	WO2002US31290	20021001

Priority Numbers: US20010326532P [20011001]; WO2002US31290 [20021001]; US20020262552 [20021001]

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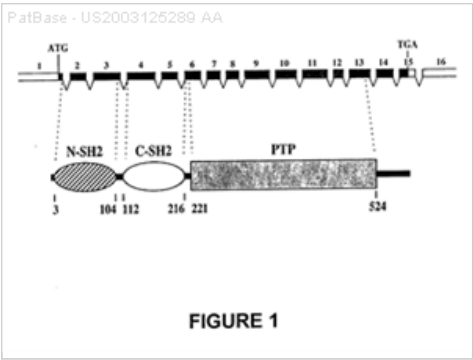
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[EN] METHOD FOR DETERMINING THE PRESENCE OR ABSENCE OF MINIMAL RESIDUAL DISEASE (MRD) IN A SUBJECT WHO HAS BEEN TREATED FOR A DISEASE

[EN] The present invention is focused on a method, kit and system for determining the presence or absence of minimal residual disease in a subject who has been treated for a proliferative disease wherein said method, kit and system comprise: (A) amplifying and sequencing at least one nucleotide sequence comprised in genomic DNA from a biological sample obtained from said subject prior to treatment for said disease, to obtain a first list of characters reading from left to right; (B) amplifying and sequencing at least one nucleotide sequence comprised in genomic DNA from a biological sample obtained from said subject after treatment for said disease, to obtain a second list of characters reading from left to right, wherein when a nucleotide sequence is mutated it is a genetic marker for said proliferative disease; (C) determining, for each second list of characters obtained in step (B), the degree of similarity, DS, with each first list of characters obtained in step (A); (D) selecting, for each second list of characters obtained in step (B), the DS of highest value, DSHV; (E) adding up the number of second lists of characters which have a DSHV that is greater than a threshold value, T, to obtain Lc, (F) adding up the total number of second lists of characters, Lt; (G) calculating the level of minimal residual disease, MRD, according to any of the following formulae: $MRD = (Lc \times k) / (Lt \times D)$ or $MRD = Lc / Lt$ or $MRD = g \times Lc \times (D / k) / Lt$; (H) determining (i) the minimum variant read frequency, minVRF, of said genetic marker, (ii) the limit of detection, D-limit, of said genetic marker (iii) the average mutation noise, avMut and (iv) the average position noise, avPos; (I) determining the experimental sensitivity, ES, from the greater of the minVRF, D-limit, avMut and avPos or from the greater of minVRF and D-limit; (J) determining the presence or absence of minimal residual disease in said subject by comparing the value of the level of minimal residual disease with the value of ES, the values of minVRF, D-limit, avMut and avPos, or the values of minVRF and D-limit; wherein when said level of minimal residual disease is equal to or greater than said ES, minVRF, D-limit, avMut or avPos values, minimal residual disease is present in said subject.

Cooperative Patent Class: C12Q1/6851; C12Q1/6858; C12Q1/6886; C12Q2600/118; C12Q2600/156; G16B20/00; G16B25/20; G16B30/10

Patent Number	Publication Date	Application Number	Application Date
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