

Figura 1A

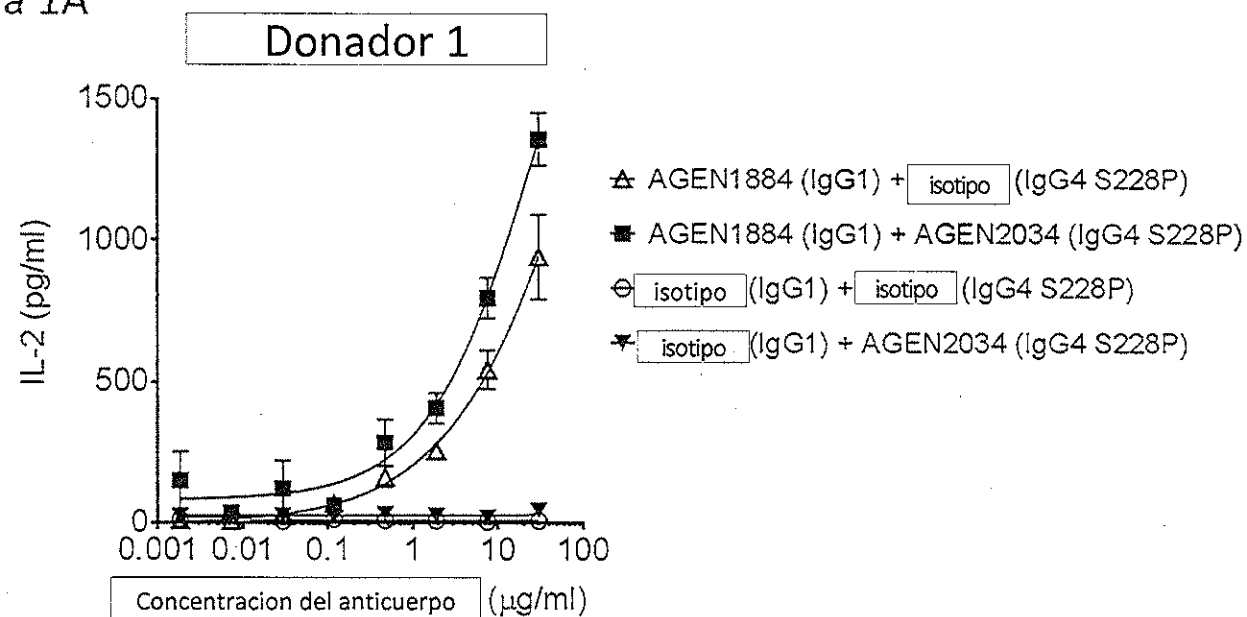


Figura 1B

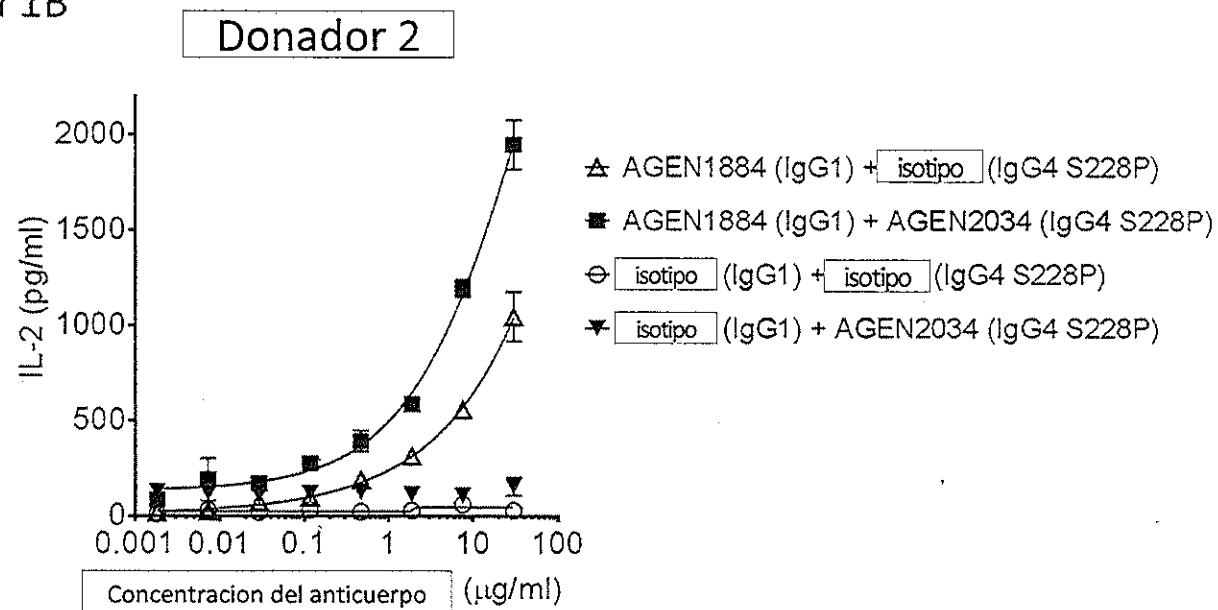
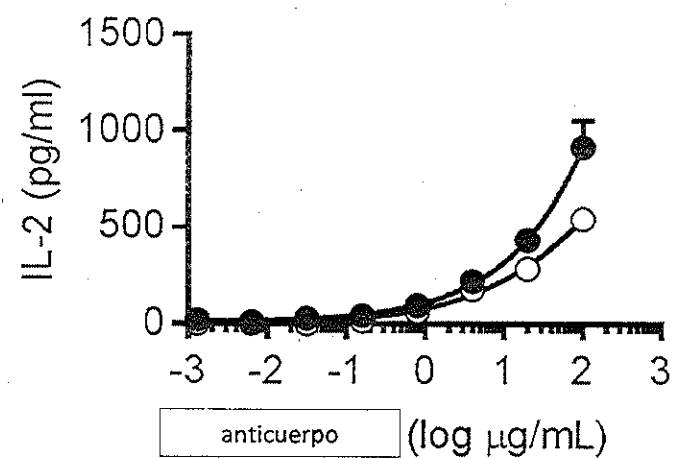


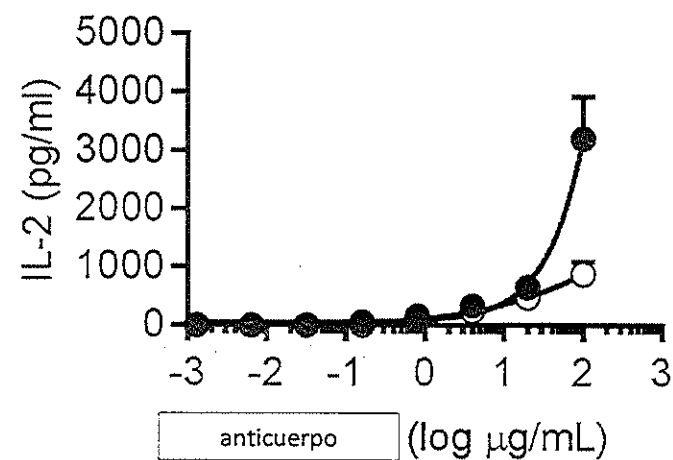
Figura 2A



Donador 3

● AGEN2034 + AGEN1884
○ Controle isotipo + AGEN1884

Figura 2B



Donador 4

● AGEN2034 + AGEN1884
○ Controle isotipo + AGEN1884

Figura 3

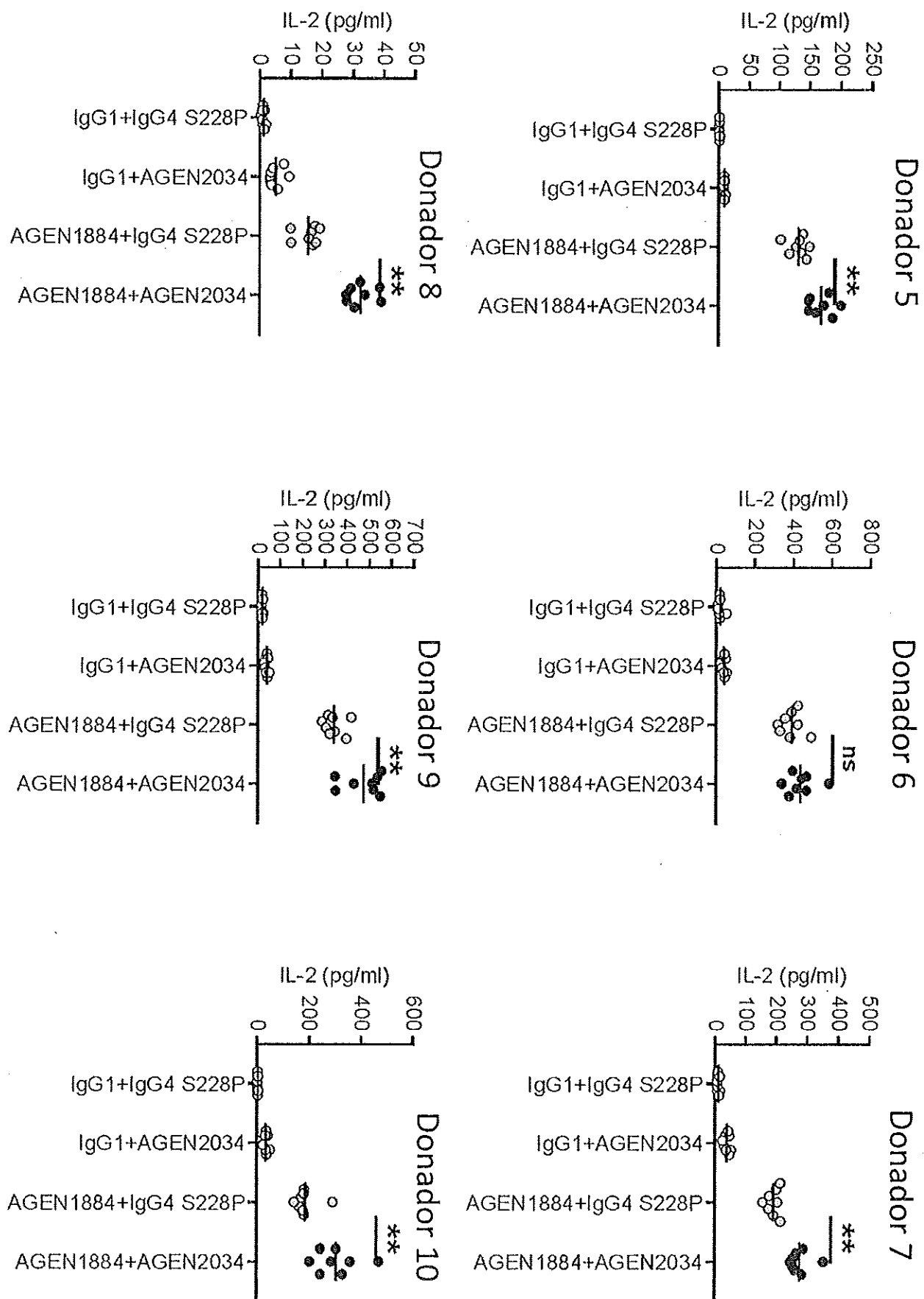
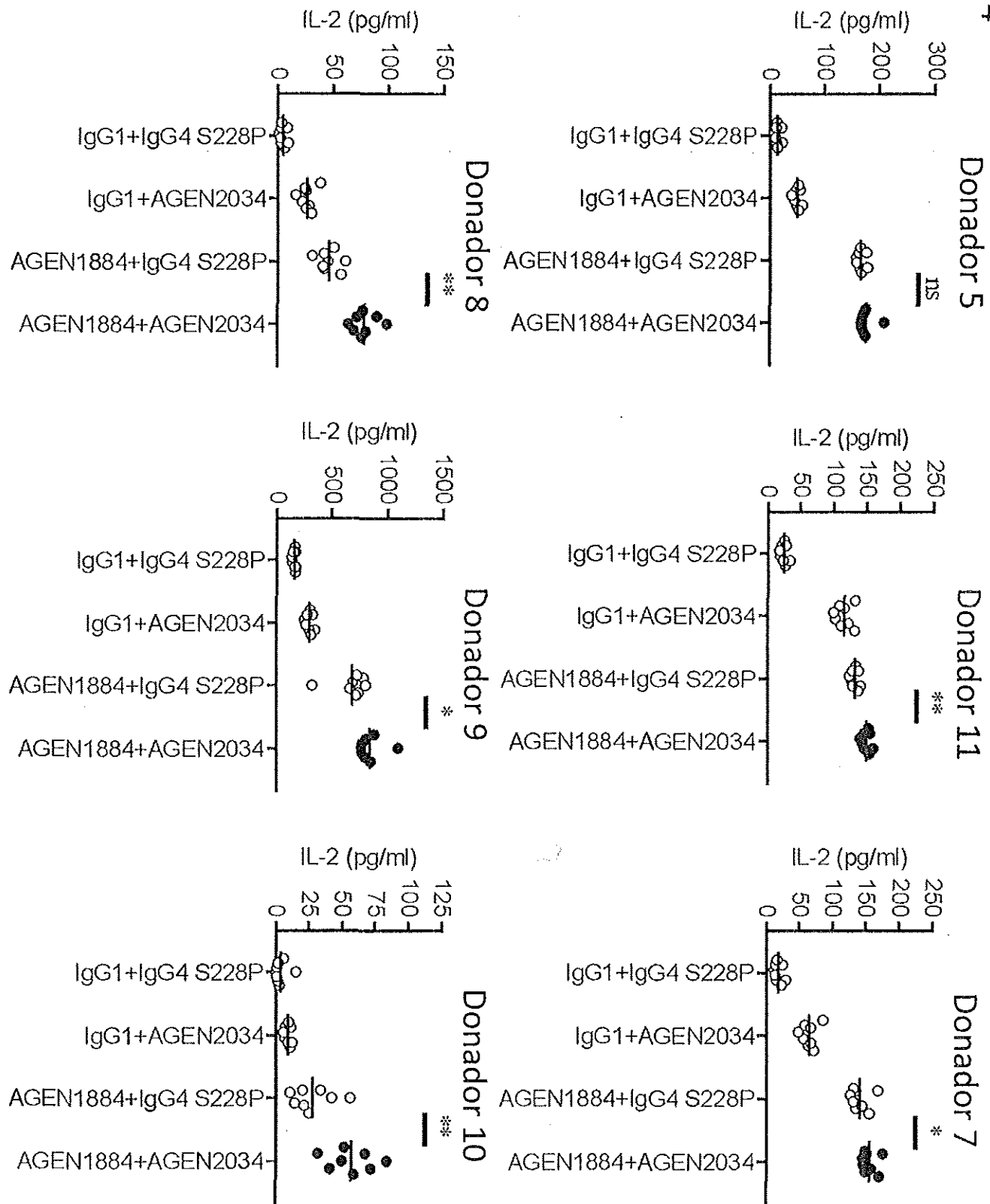
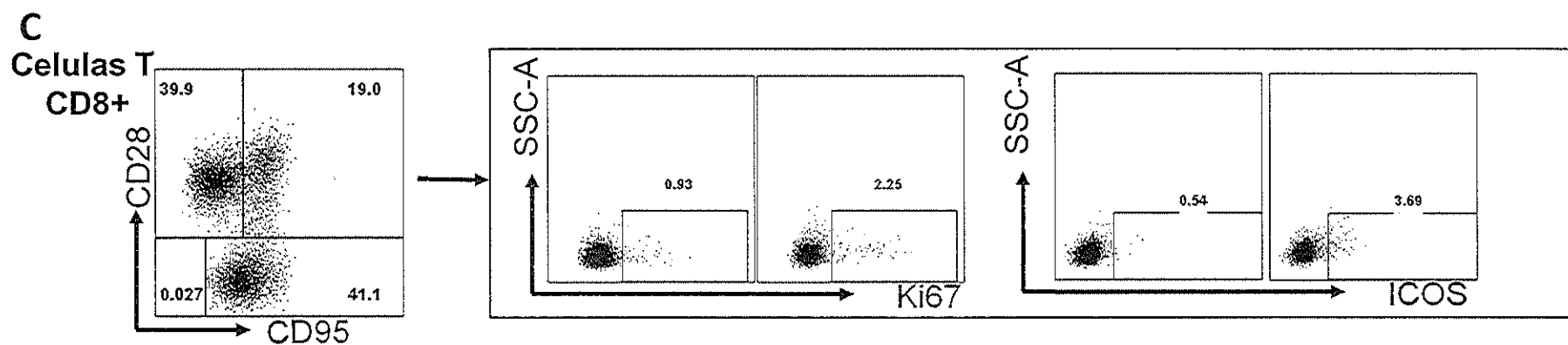
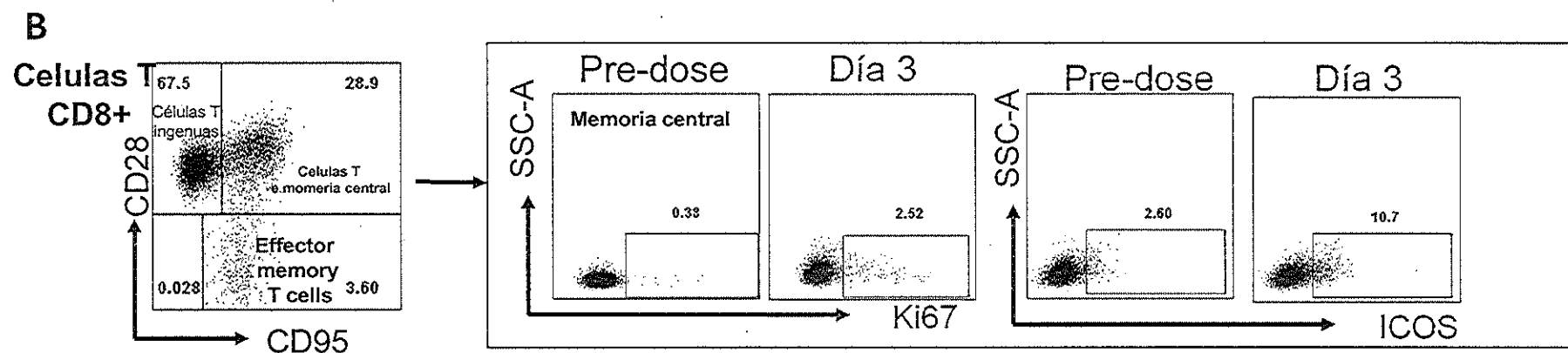
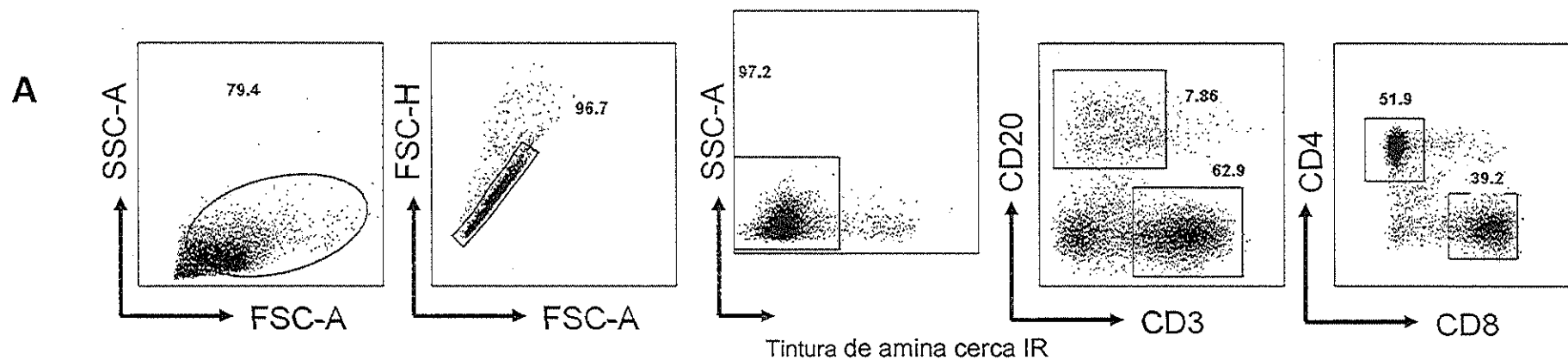


Figura 4



Figuras 5A-5C



Figuras 6A-6D

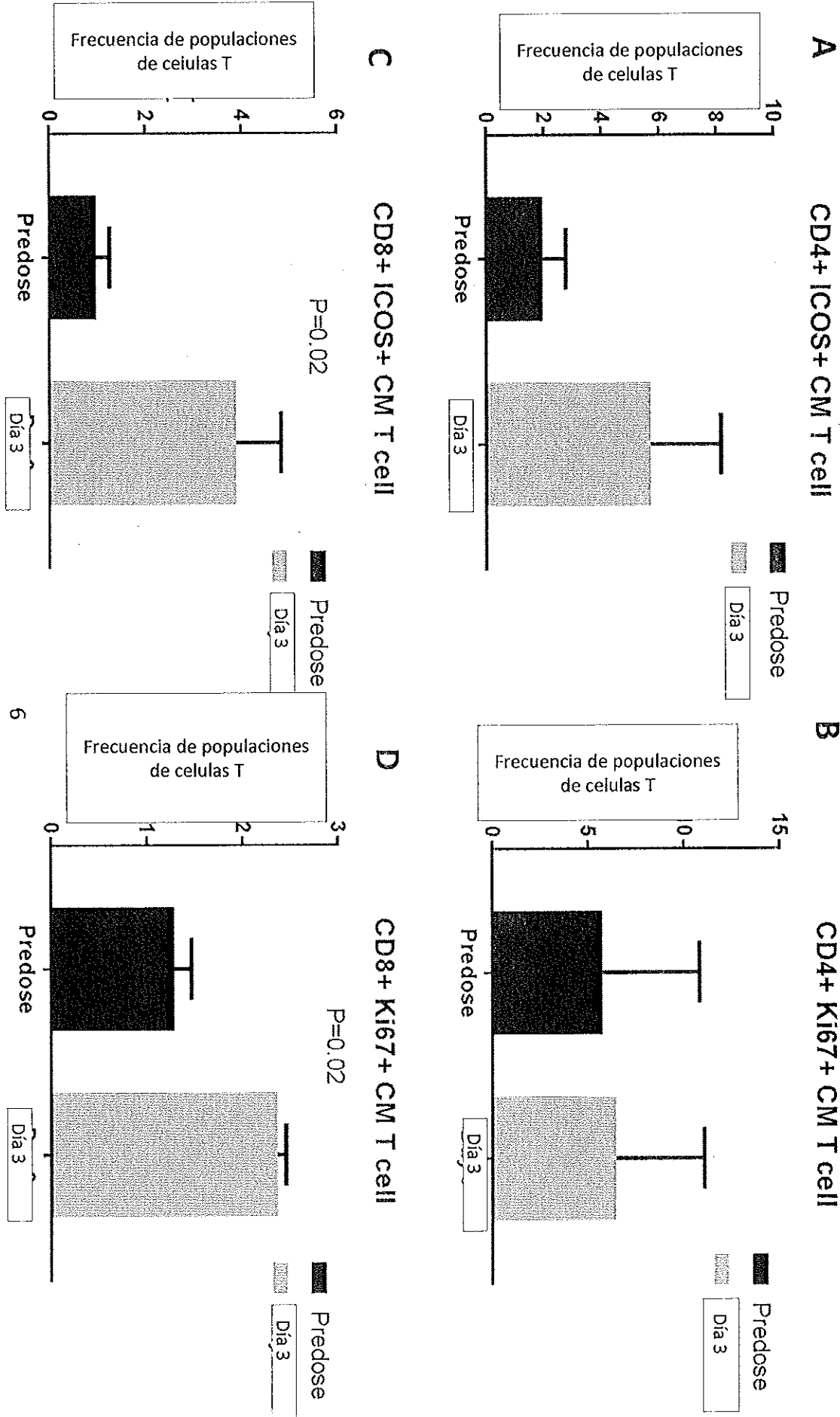


Figure 7A

P16410	CTLA4_HUMAN	1	MACLGFRHKAQLNLATRTWPCTLLFLLFIPVFCKAMHVAQPAVVLASSRGIASFVCEY	60
G7PL88	CTLA4_MACFA	1	R.....R.Y....S.....S.....N.....	60
P09793	CTLA4_MOUSE	1	LR.Y....Q.PS....FVA.LT.....SE.IQ.T..S.....H.V...P...	60
Q62859	CTLA4_RAT	1	L..Y.TH.Q.PS....FGV.LS.....I.SE.IQ.T..S.....H.V...P...	60
			*****::*:*:*:*: * * * : *****:*.::*:*:*:*****.*:*.*** **	
P16410	CTLA4_HUMAN	61	ASPGKATEVRVTVLRLQADSQVTEVCAATYMMGNELTFLDDSICTGTSSGNQVNLTIQGLR	120
G7PL88	CTLA4_MACFA	61		120
P09793	CTLA4_MOUSE	61	SPSHNTD.....TND.M.....T.FTEK.TVG...YPF.S..FNESR.....	120
Q62859	CTLA4_RAT	61	..SHNTD.....TND.....T.FTVK.T.G....PF.S..FNESR.....	120
			: :: *****:*.::*****:~ * : *** :*:~ . :*****	
P16410	CTLA4_HUMAN	121	AMDTGLYICKVELMYPYPPYLGIGNGTQIYVIDPEPCPDSDFLWILAAVSSGLFFYSFL	180
G7PL88	CTLA4_MACFA	121	M.....	180
P09793	CTLA4_MOUSE	121	.V.....L.....FV.M.....V...L.....	180
Q62859	CTLA4_RAT	121	.A.....F.....FV.M.....	180
			* *****:*****:~*:*****:*****.*** *****	
P16410	CTLA4_HUMAN	181	LTAVSLSKMLKKRSPLTTGVYVKMPTEPECEKQFQPYFIPIN	223
G7PL88	CTLA4_MACFA	181		223
P09793	CTLA4_MOUSE	181	VS.....	223
Q62859	CTLA4_RAT	181	V.....NRT.....	223
			:*****.~ *****:*****:*****	

Figure 7B

SP	P16410	CTLA4_HUMAN	MACLGFRHKAQLNLATRTWPCTLLFFLLFIP--VFC-----KAMHVAQPAVVLA---	48
TR	G7PL88	G7PL88_MACFA	MACLGFRHKAQLNLATRTWPCTLLFFLLFIP--VFS-----KAMHVAQPAVVLA---	48
SP	P10747	CD28_HUMAN	-----MLRLLLALN--LFPS-IQVTGNKILVKQSP-MLV---	30
SP	Q9Y6W8	ICOS_HUMAN	-----MKSGLWY-----FF--LFCLRIKVLGTGEINGSANYEMFI---	32
SP	Q7Z6A9	BTLA_HUMAN	-----MKTLPAMLGTGKLFV--FFFLIPYLDIWNHNGKESCDVQLYIK	41
SP	Q15116	PDCD1_HUMAN	-----MQIPQAPWPVWAVLQLGWRPGWFLDSPD-RPWNPTTFSPALLVV---	44
			*	:
SP	P16410	CTLA4_HUMAN	-----SSRGIASFVCEYASPGKA---TEVRVTVLRQADSQVTEVCAATYMMGNE--LT	96
TR	G7PL88	G7PL88_MACFA	-----NSRGIASFVCEYASPGKA---TEVRVTVLRQADSQVTEVCAATYMMGNE--LT	96
SP	P10747	CD28_HUMAN	-----AYDNAVNLSCKYSYNLFS---REFRASLHKGLDSA-VEVCVYGNYSQQQLQVY	79
SP	Q9Y6W8	ICOS_HUMAN	-----FHNGGVQILCKYPD--IV---QQFKMQLLKGGQ----ILCDLTCTKSGSGNTVS	76
SP	Q7Z6A9	BTLA_HUMAN	RQSEHSILAGDPFELECPVKYCANRPHVTWCKLN---GT-----TCVKLEDRQ-----	86
SP	Q15116	PDCD1_HUMAN	-----TEGDNATFTCSFSNTSESFVLNWYRMSPSNQTDK----LAAFPEDR-----	86
			:	*
SP	P16410	CTLA4_HUMAN	FLDDSICT---GTSSGNQVNLTII---QGLRAMDTGLYICKVELMYPPPYLGIG-----	144
TR	G7PL88	G7PL88_MACFA	FLDDSICT---GTSSGNQVNLTII---QGLRAMDTGLYICKVELMYPPPYMGIG-----	144
SP	P10747	CD28_HUMAN	SKTGFNCD---GKLGNESVTFYL---QNLVYNQTDIYFCKIEVMYPPPYLDNEK-----	127
SP	Q9Y6W8	ICOS_HUMAN	IKSLKFCH---SQLSNNSVSFFL---YNLDHSHANYFYFCNLSIFDPPPFKVTILT-----	124
SP	Q7Z6A9	BTLA_HUMAN	-----TSWKEEKNISFFILHFEPVLPNDNGSYRCSANFQSNL---IE-----	125
SP	Q15116	PDCD1_HUMAN	SQPGQDCRFRVTQLPNGRDFHMSV---VRARRNDSGTYLCGAISLAPKAQIKESLRAELR	143

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Figure 7C

SP	P16410	CTLA4_HUMAN	-NGTQIIYVIDP-----EPCPDS-----DFLLWILAAVSSGLFFYSFLLTAVSL--S-KML	190
TR	G7PL88	G7PL88_MACFA	-NGTQIIYVIDP-----EPCPDS-----DFLLWILAAVSSGLFFYSFLLTAVSL--S-KML	190
SP	P10747	CD28_HUMAN	SNGTIIHVKGK-----HLCPSPLFPGPSKPFWVLVVVGVLACYSLLVTVAFI--IFWVR	180
SP	Q9Y6W8	ICOS_HUMAN	--GGYLHIYES-----QLCCQL-----KFWLPIGCAA---FVVVCILGCIL--ICWLT	165
SP	Q7Z6A9	BTLA_HUMAN	SHSTTLYVTDVKSASERPSKDEMASR-PWLLYRLLPLGG---LPLLITTCFCLFCCLRR	180
SP	Q15116	PDCD1_HUMAN	VTERRAEVPTA-----HPSPSPRPAG-QFQTLVVGVVGGLLGSLVLLVWVLAV--ICSRA	195
			:	
SP	P16410	CTLA4_HUMAN	KKRSP---LTTGVYVKMPPT-----PEC-EKQFQPYFIPIN-----	223
TR	G7PL88	G7PL88_MACFA	KKRSP---LTTGVYVKMPPT-----PEC-EKQFQPYFIPIN-----	223
SP	P10747	CD28_HUMAN	SKRSR---LLHSDYMNMTPRR-----PGPTRKHYQPYAPPRD--FAAYRS-----	220
SP	Q9Y6W8	ICOS_HUMAN	KKKYSSSVHDPNGEYMFMRVN-----TAKKSRLTDVTL-----	199
SP	Q7Z6A9	BTLA_HUMAN	HQGKQNELSDTAGREINLVD AHLKSEQTEASTRQNSQVLLSETGIYDNDPDLCFRMQEGS	240
SP	Q15116	PDCD1_HUMAN	ARG-----TIG-----ARR-----TGQP-LKEDPSAVPVF--SVDYGELDFQWREKT	234
			:	
SP	P16410	CTLA4_HUMAN	-----	
TR	G7PL88	G7PL88_MACFA	-----	
SP	P10747	CD28_HUMAN	-----	
SP	Q9Y6W8	ICOS_HUMAN	-----	
SP	Q7Z6A9	BTLA_HUMAN	EVYSNPCLEENKP--GIVYASLNH SVIGPNSRLARNVKEAPTEYASI-----CVRS-	289
SP	Q15116	PDCD1_HUMAN	PEPPVPCVPEQTEYATIVFP---SGMGTSSPARRGSADGPRSAQPLRPEDGHCSWPL	288