

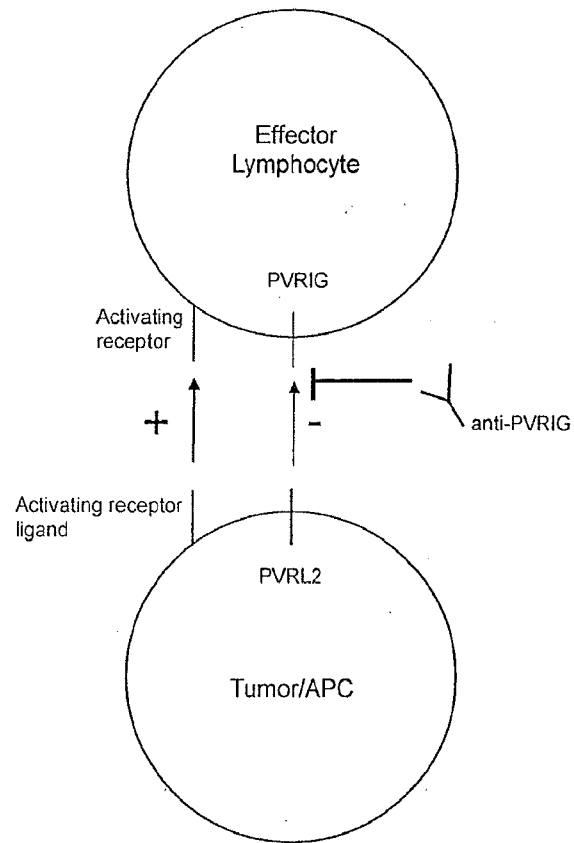
Figure 1

Figure 2.

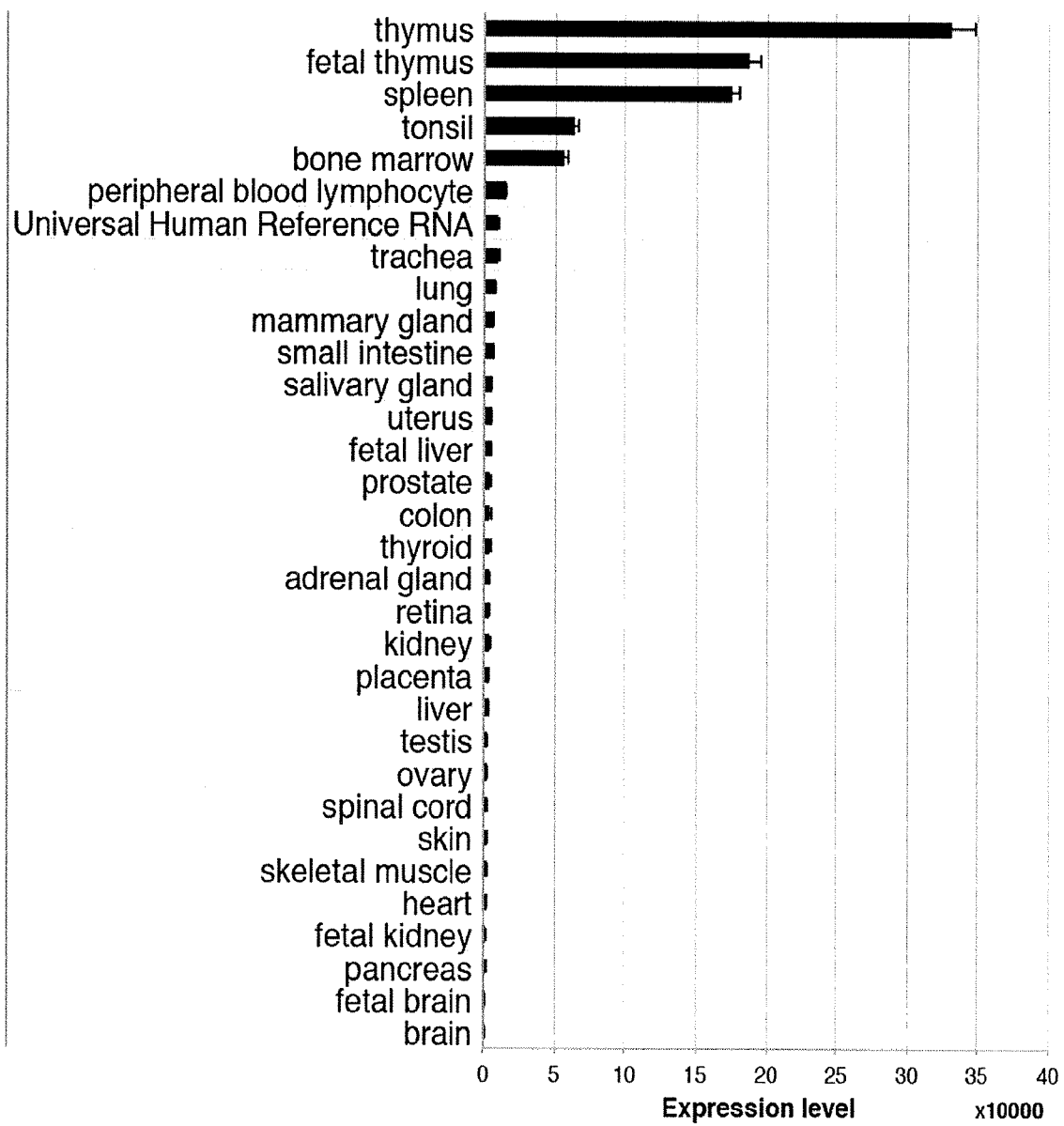


Figure 3:

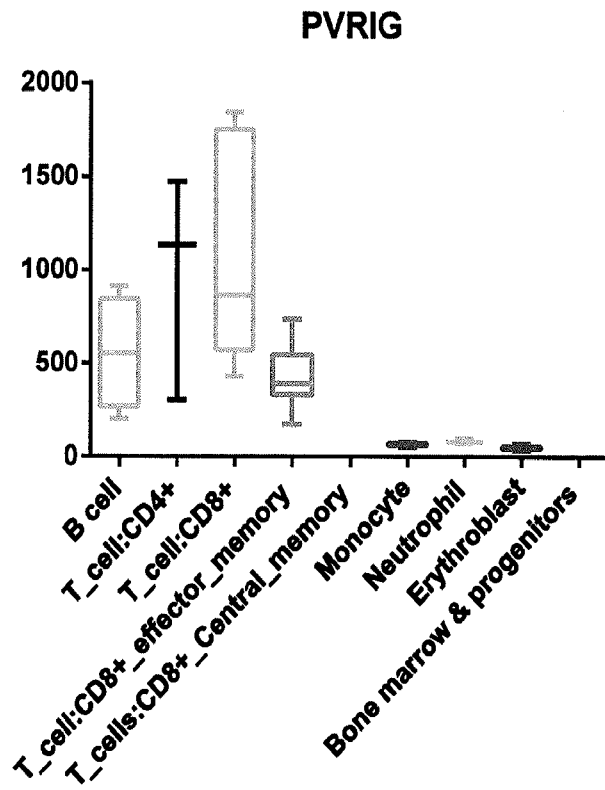


Figure 4

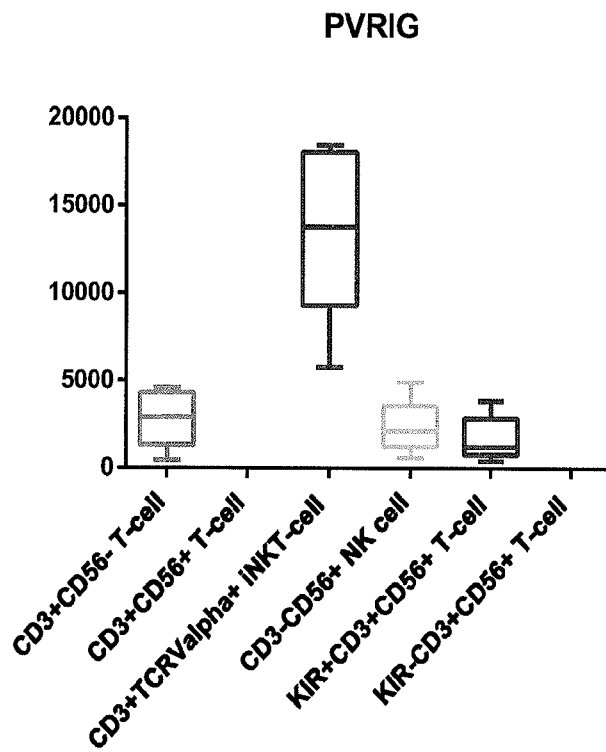


Figure 5a:

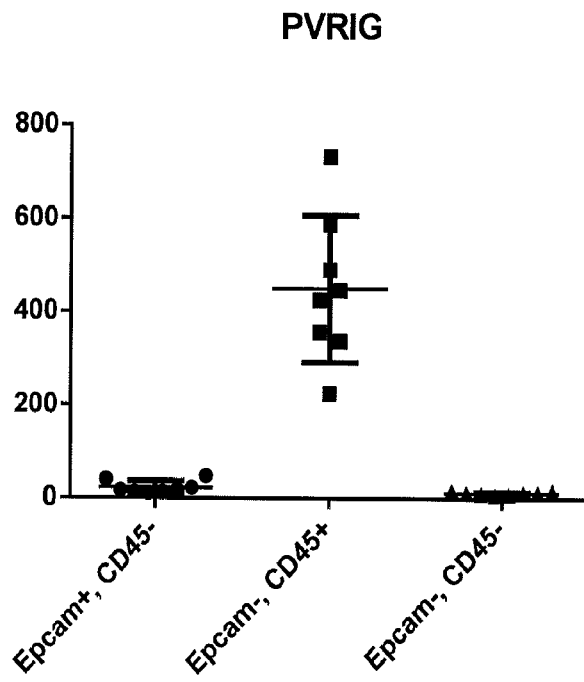


Figure 5b:

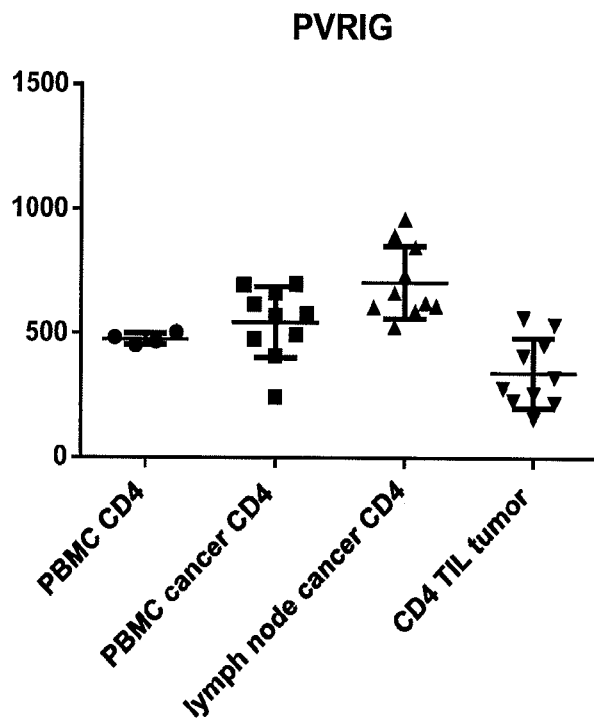


Figure 5c:

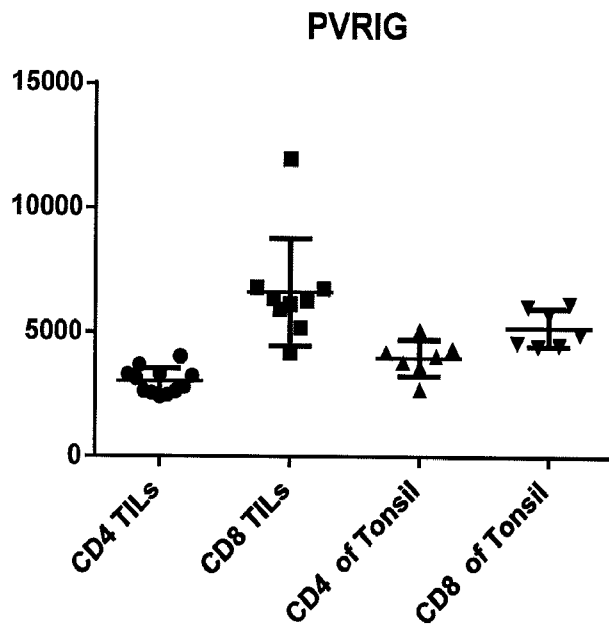


Figure 6



Figure 7

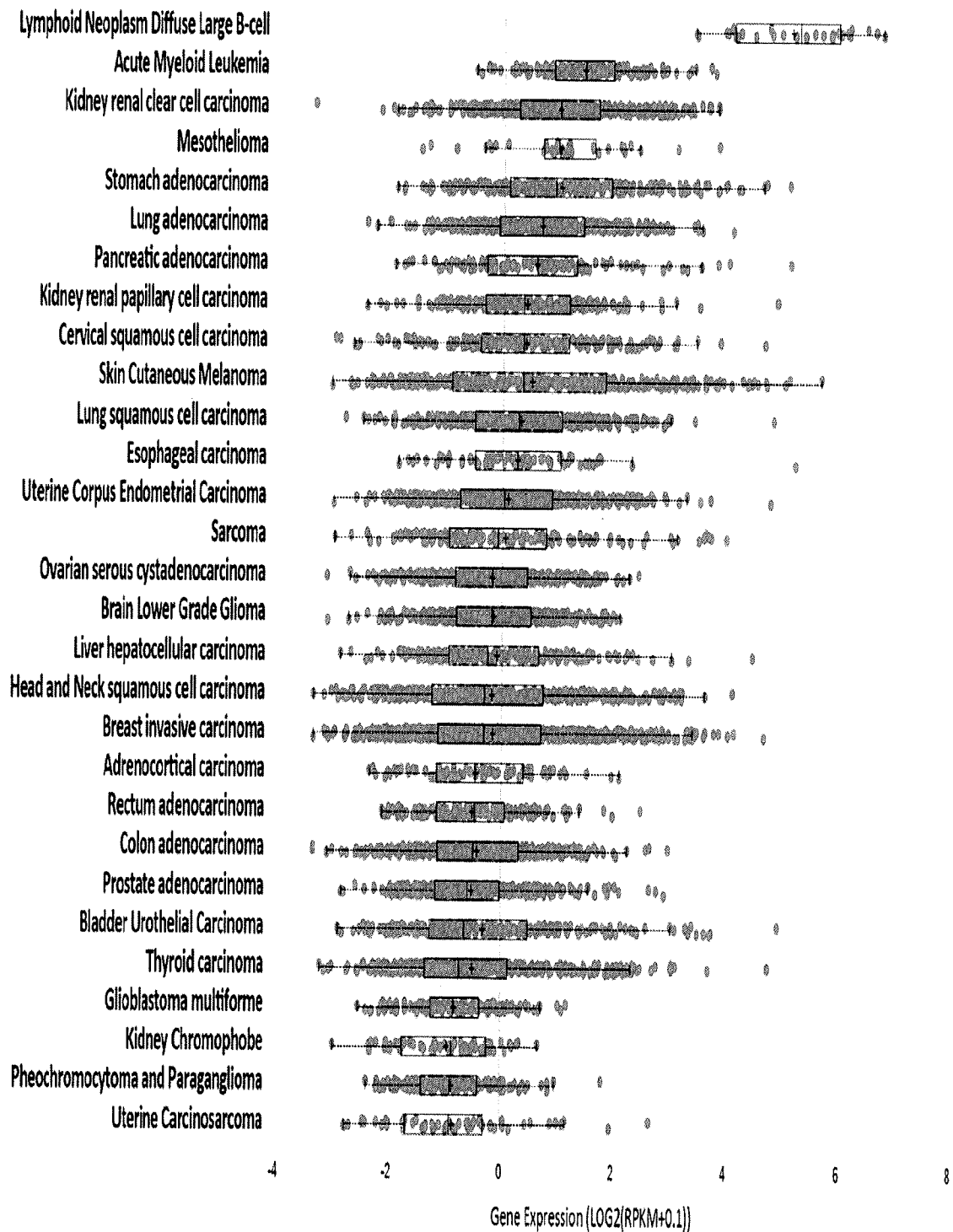


Figure 8

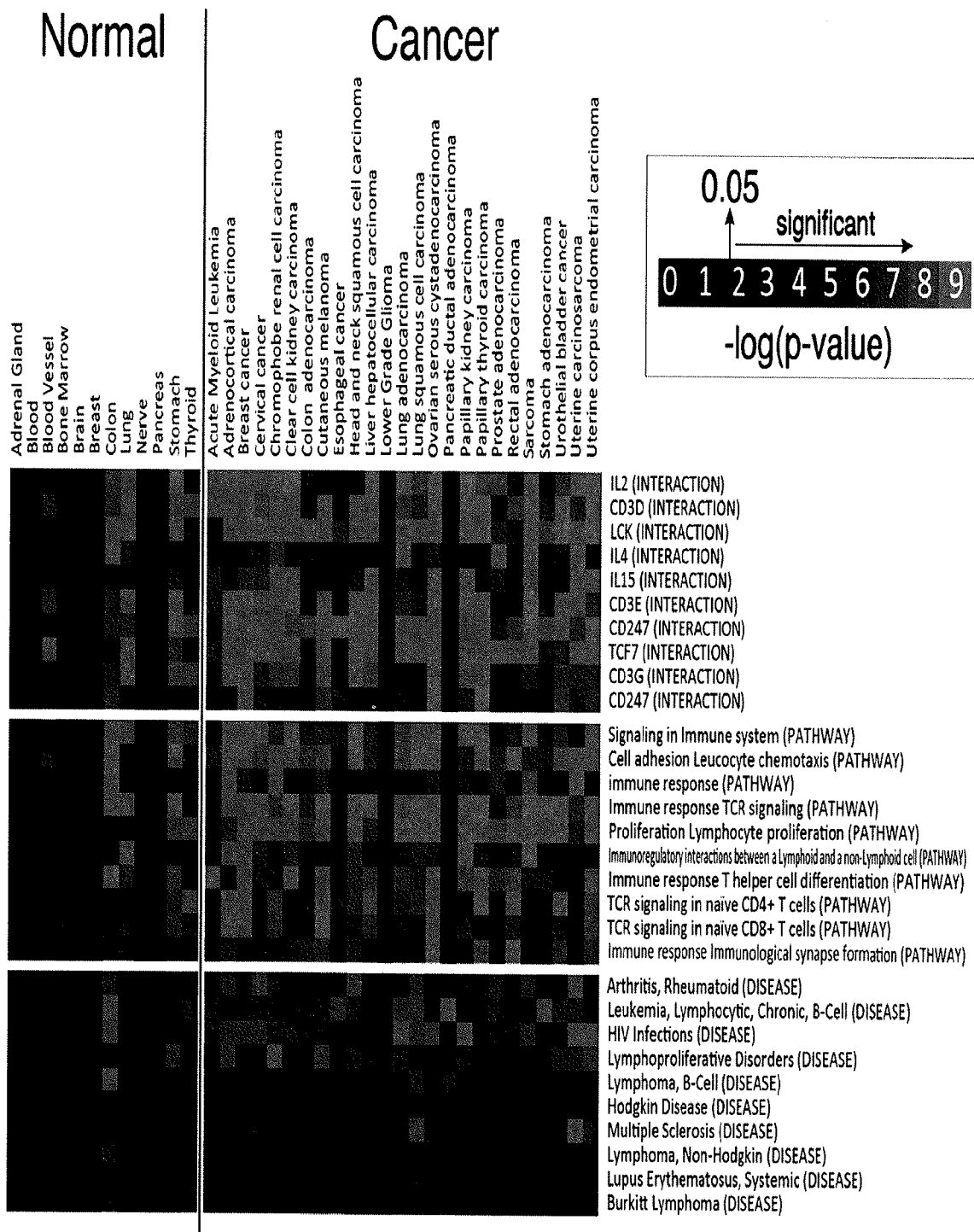


Figure 9

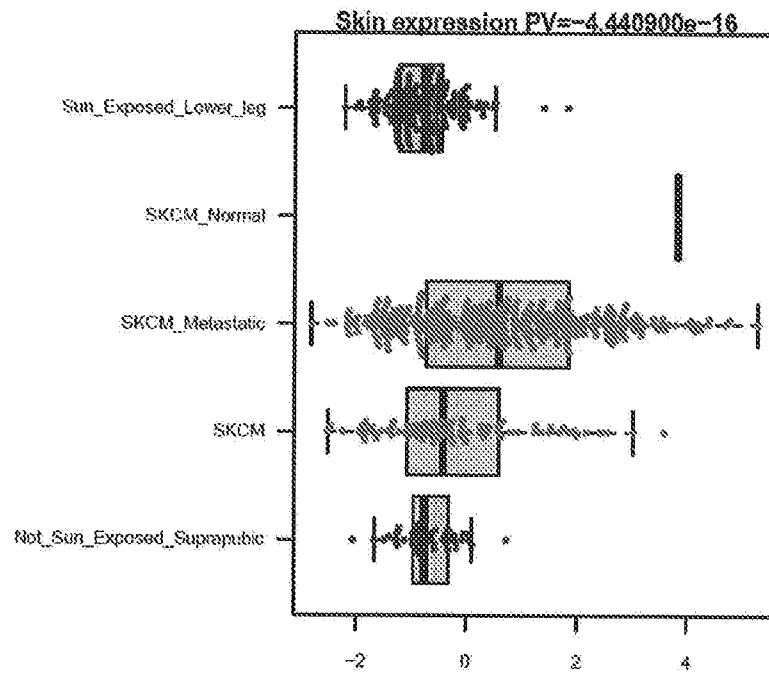


Figure 10

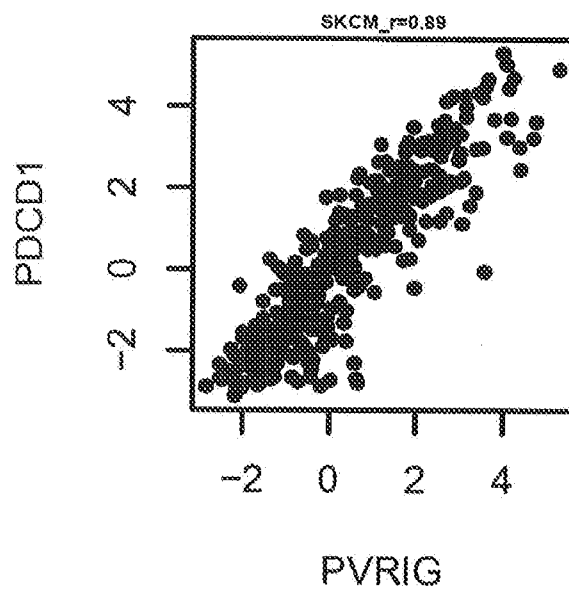


Figure 11

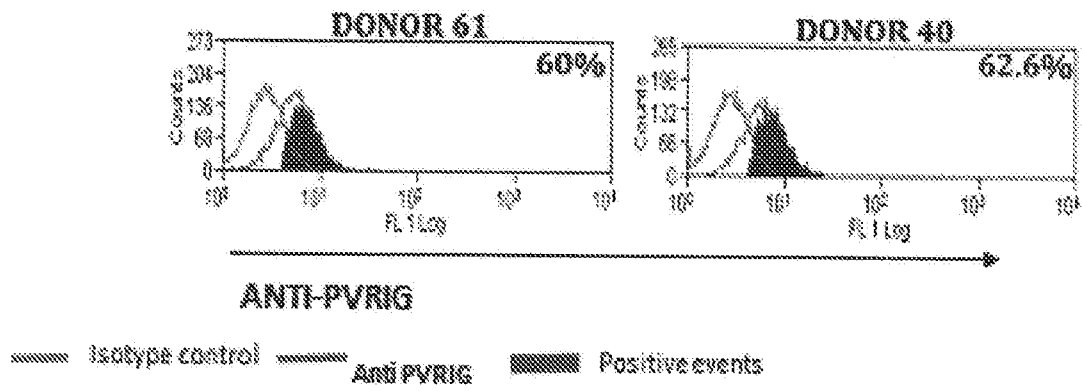


Figure 12

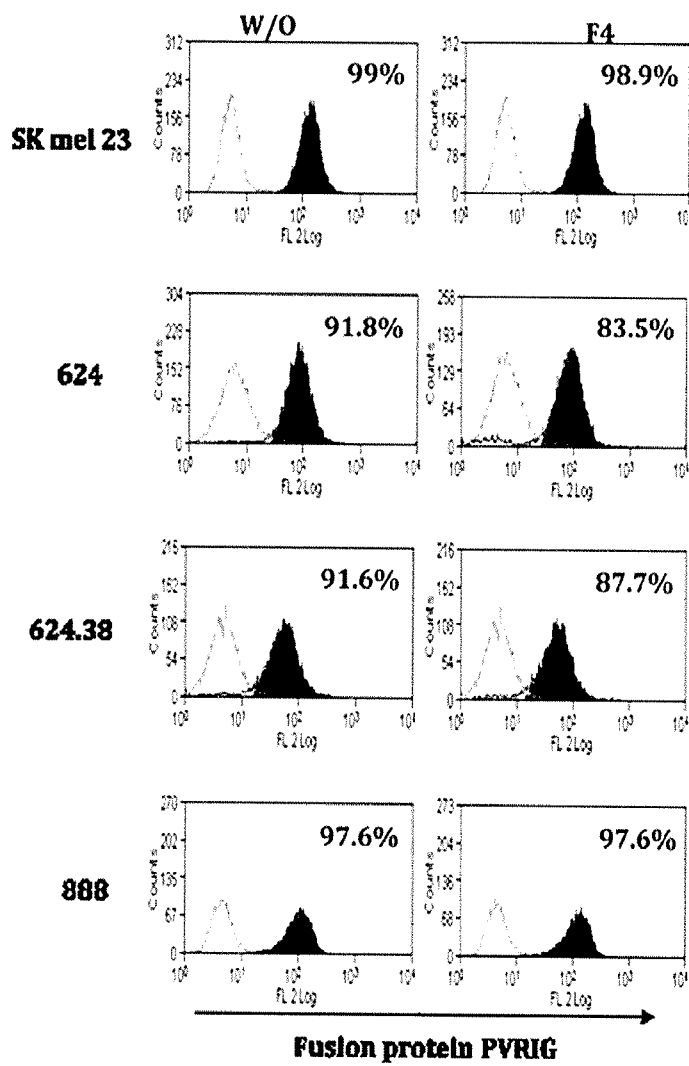


Figure 13

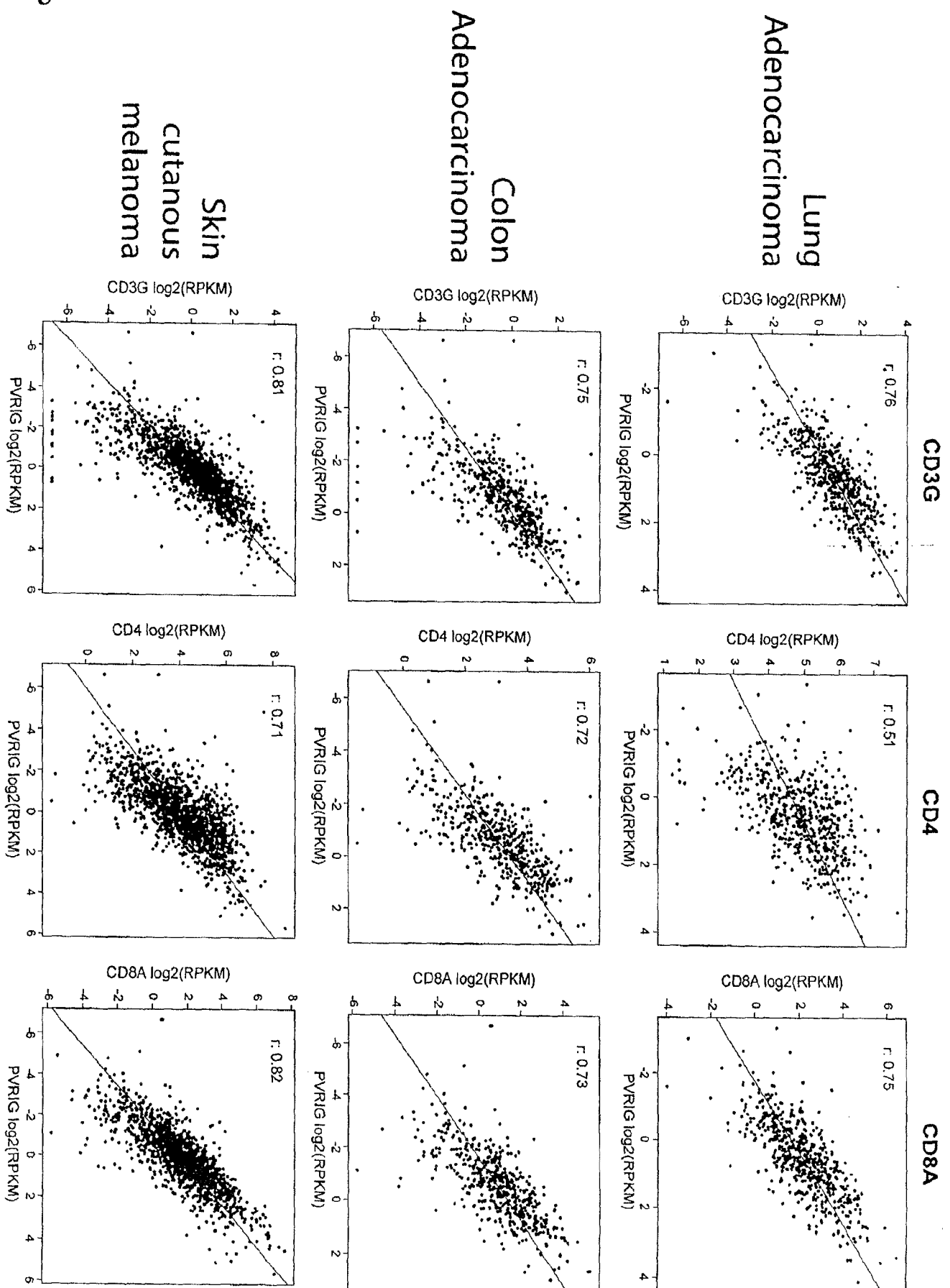


Figure 14:

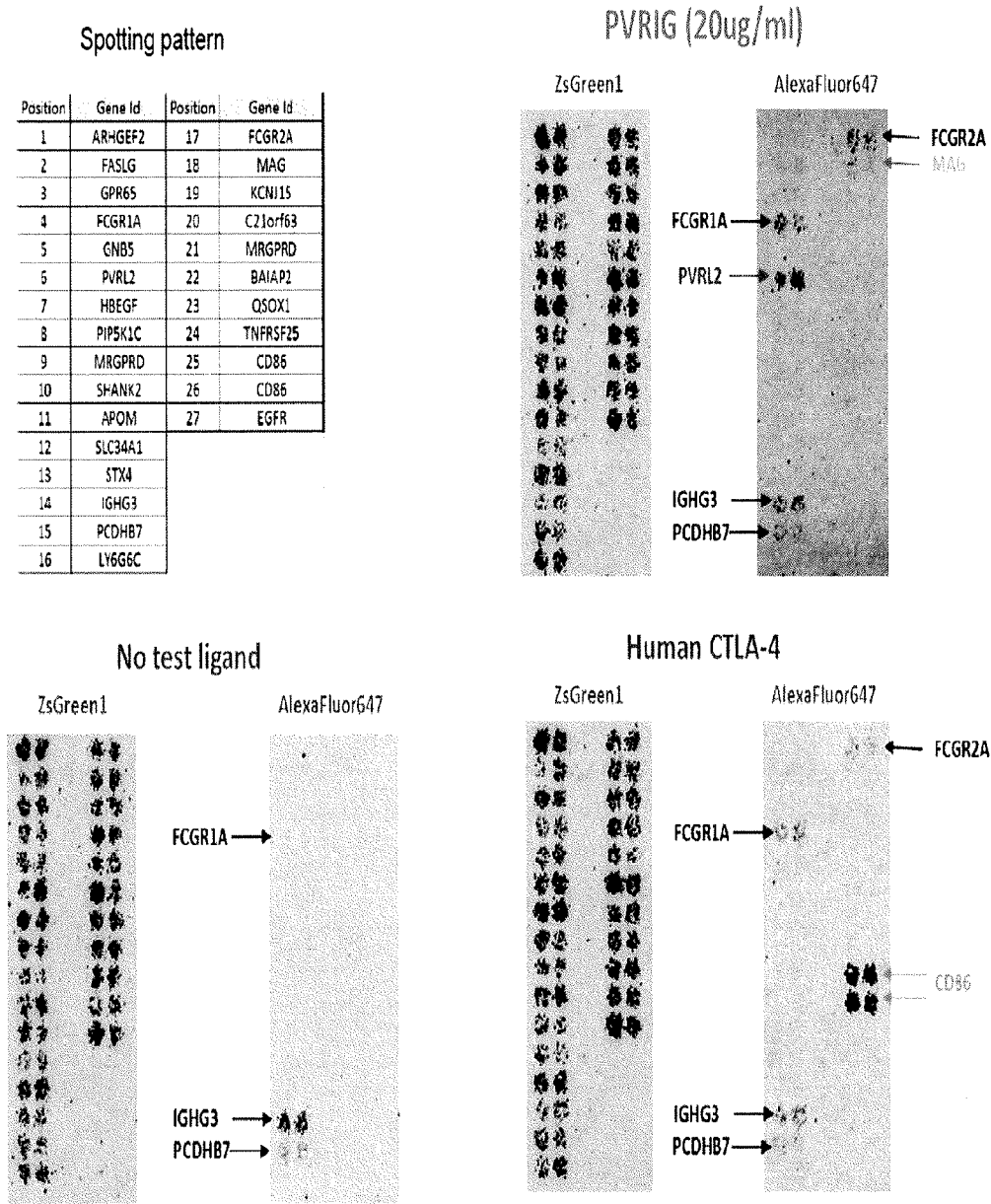


FIG. 15A

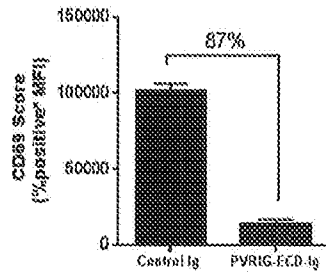


FIG. 15B

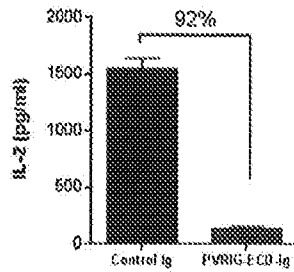


FIG. 15C

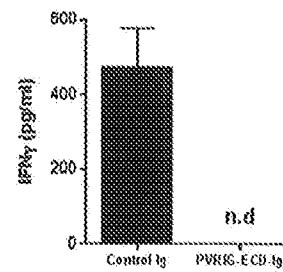


FIG. 15D

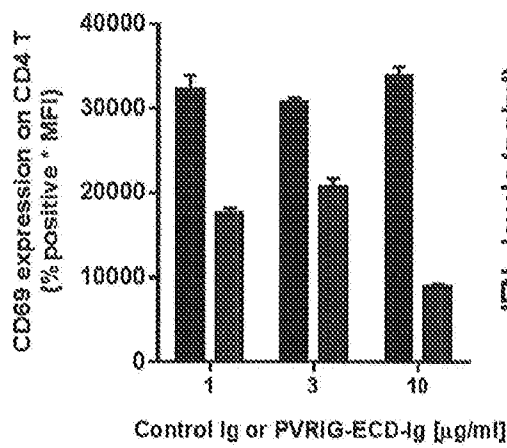


FIG. 15E

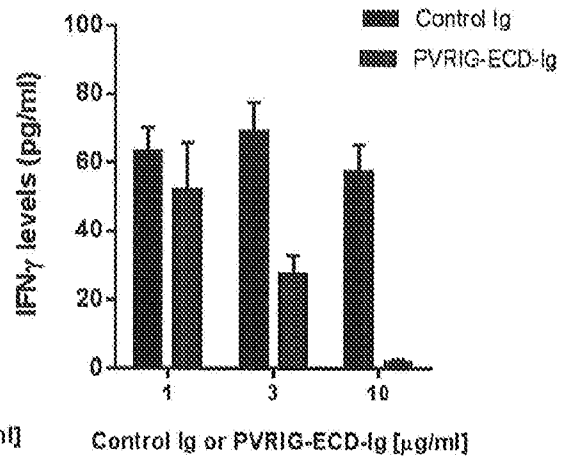


Figure 16

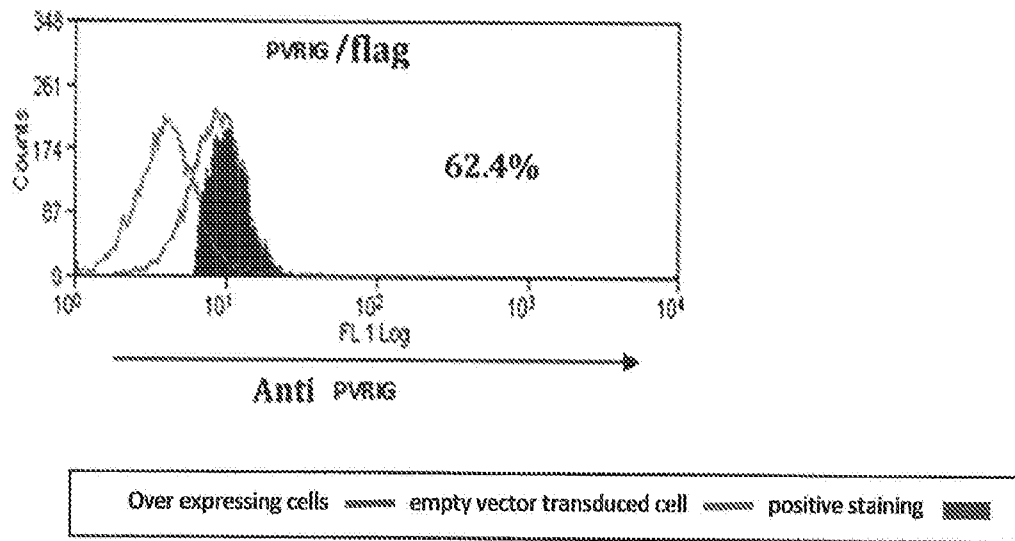


Figure 17

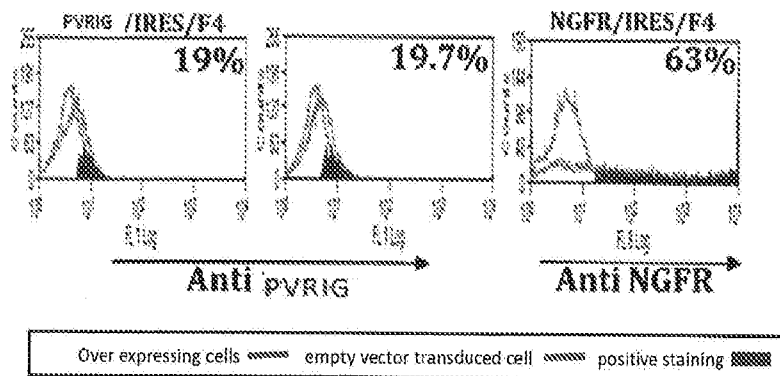


Figure 18A

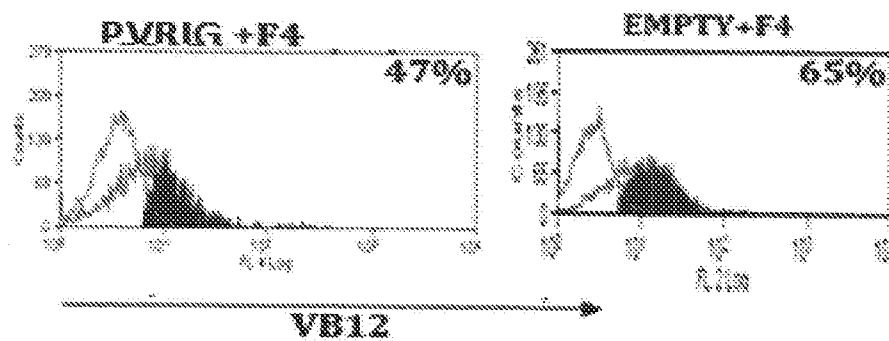


Figure 18B

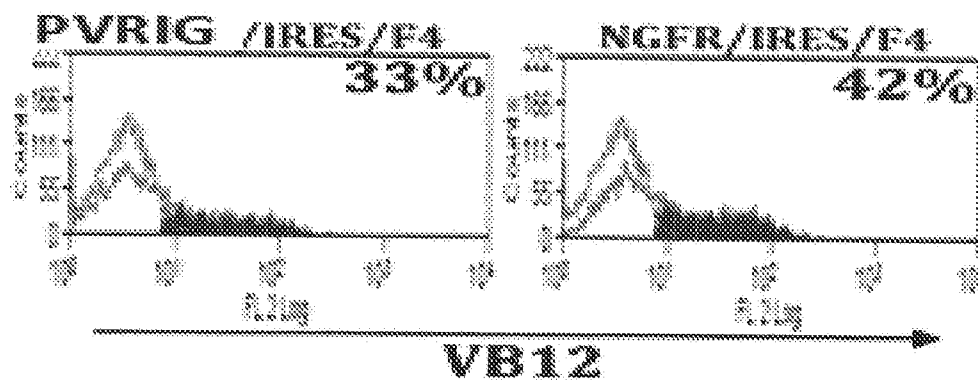


Figure 19

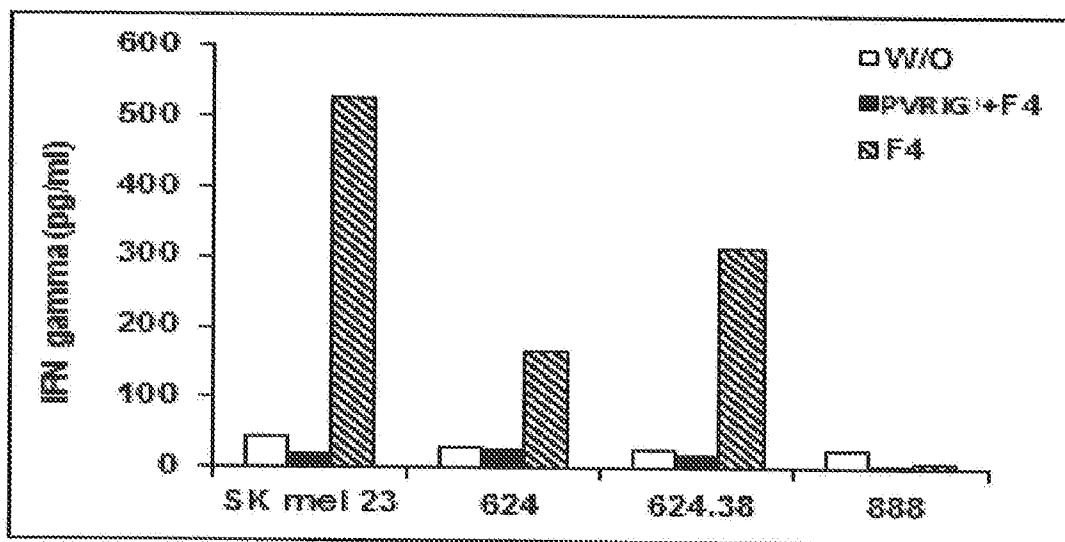


Figure 20A

A

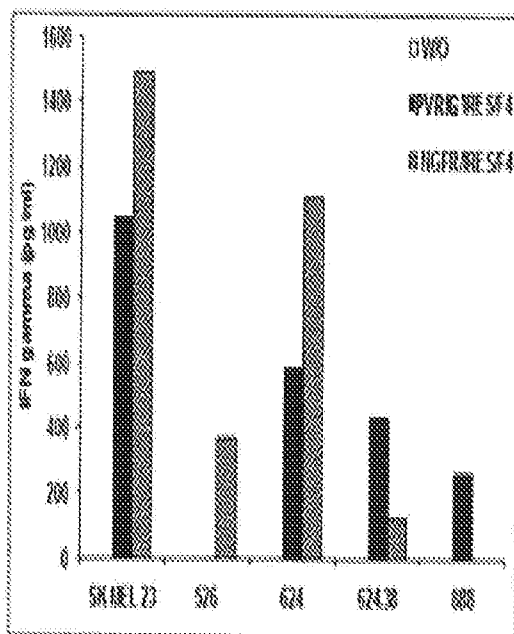


Figure 20B

B

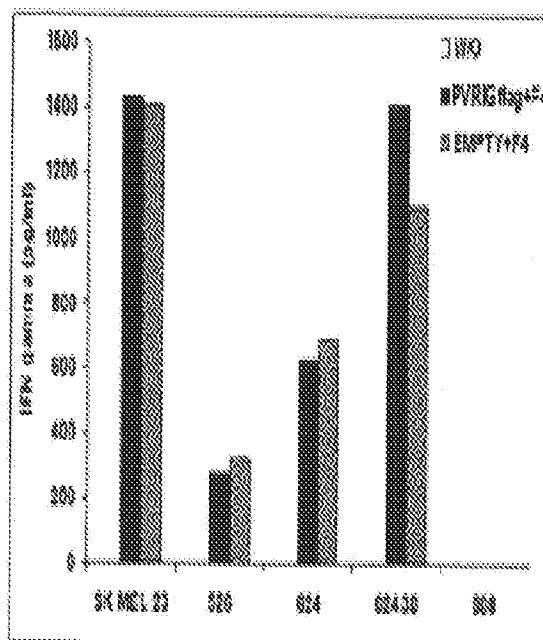


Figure 21

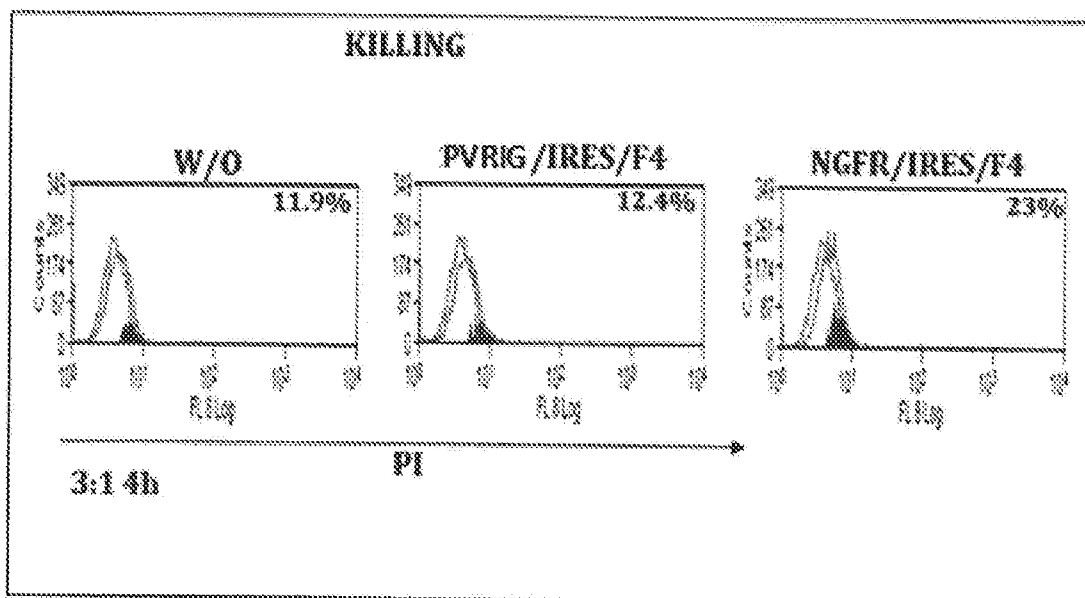


Figure 22

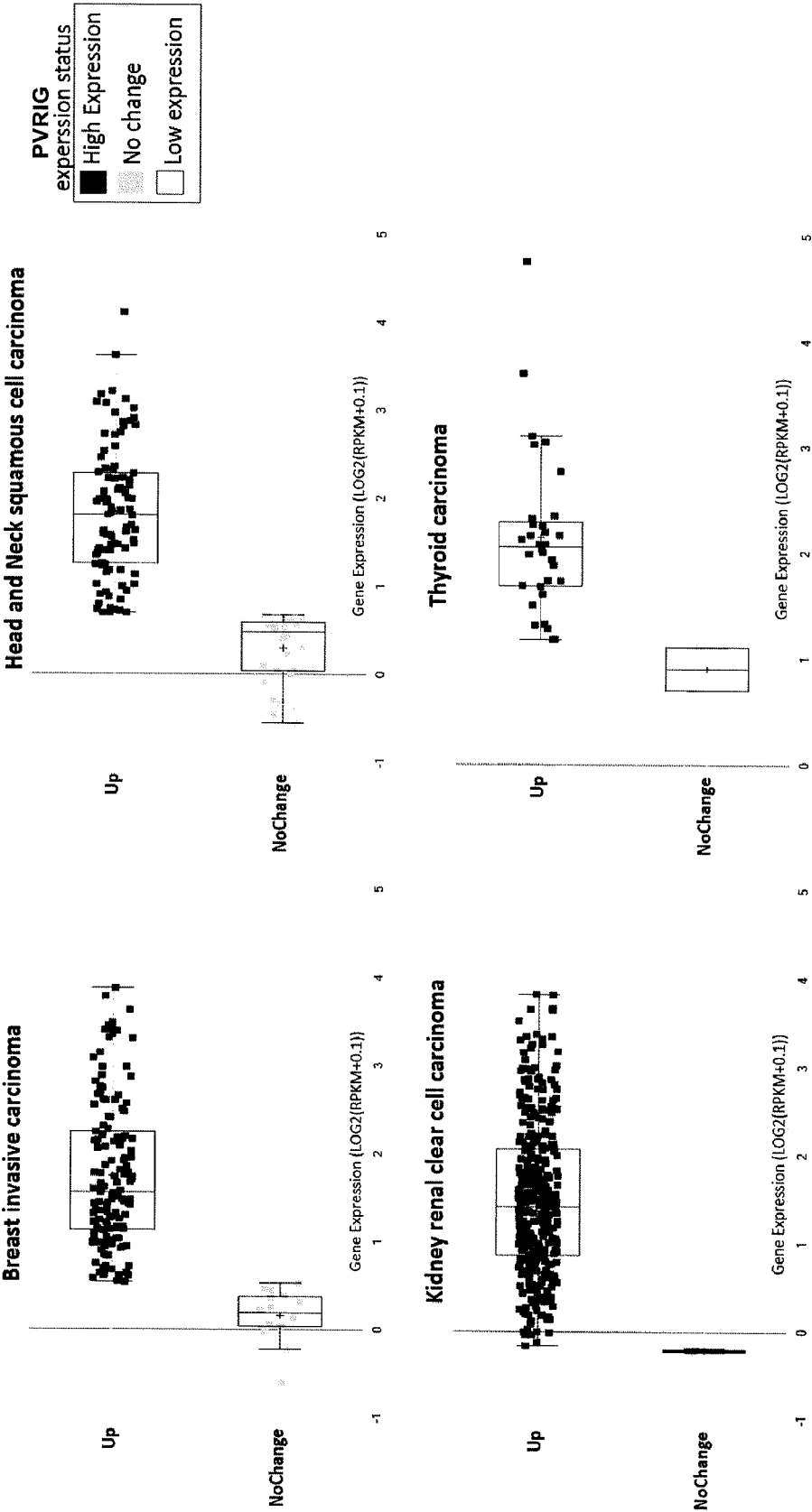


Figure 23A

Figure 23B

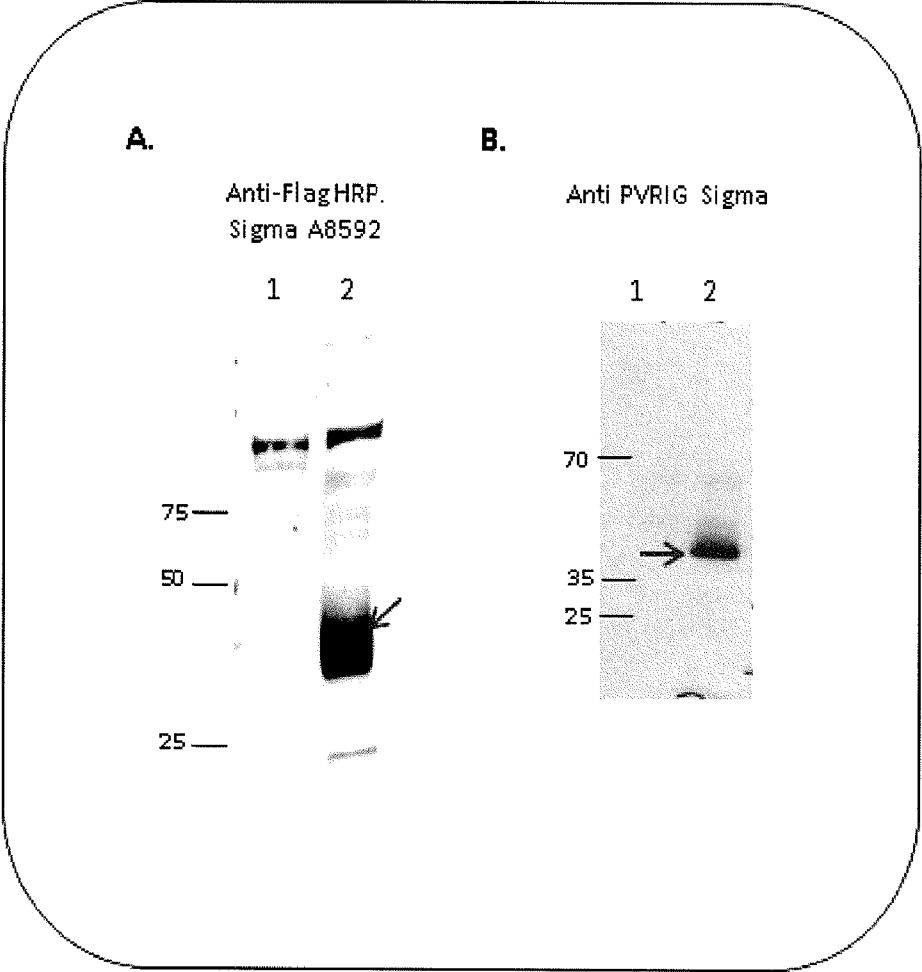


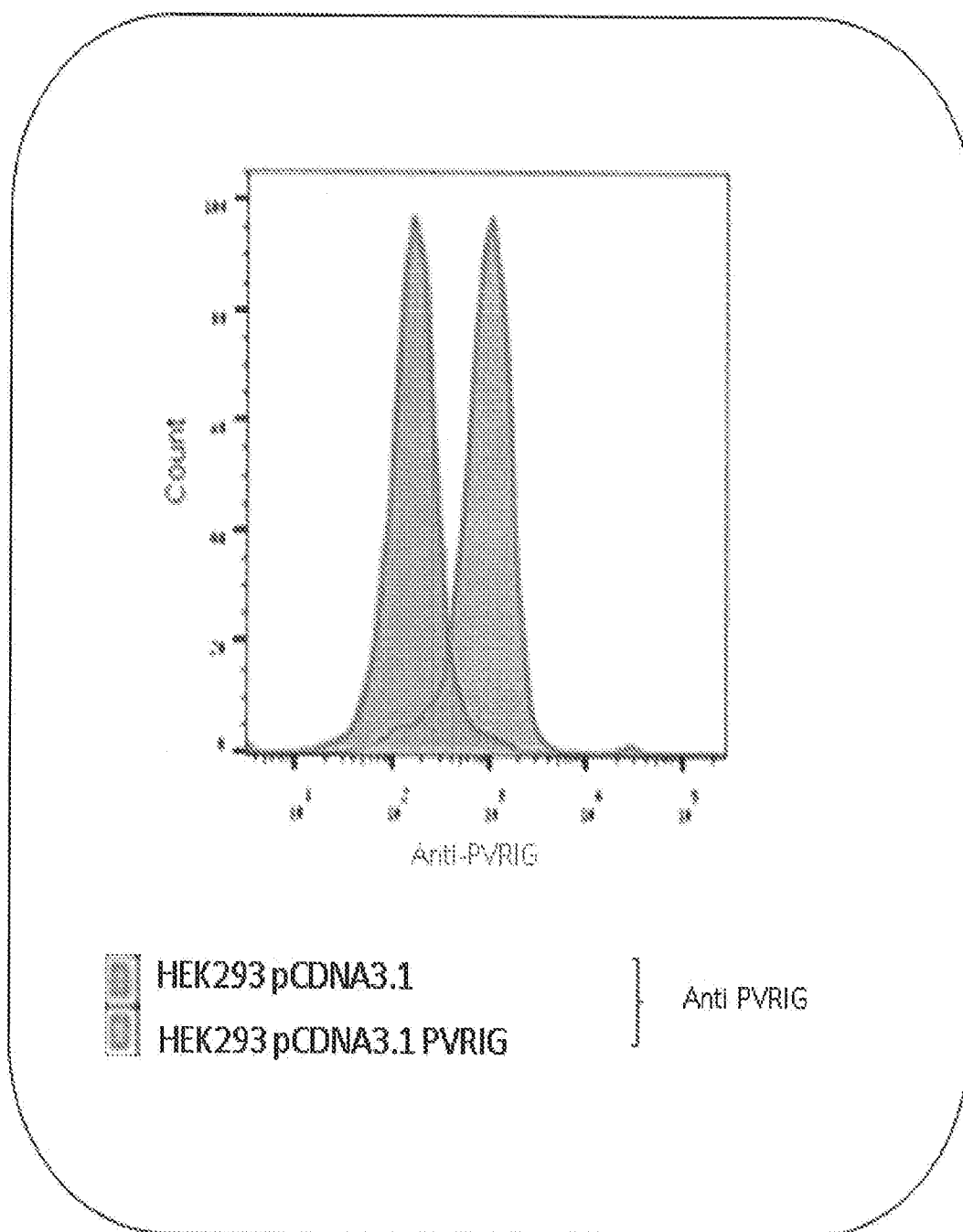
Figure 24

Figure 25

Human PVRIG WT Full length

Human PVRIG sequence starting from position 21 - alternative methionine

MGHRTLVLPPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGFLGSGSISLTVSWGGPNGAGGTTLAVLHPERGIR
QWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGSLPPSSDPGLSAPPTPAPILRADLAGILGV
 SGVLLFGCVYLLHLLRRHKHRPAPRLQPSRTSPQAPRARAWAPSQASQAALHVPYATINTSCRPATLDTAHPHGGPSW
 WASLPTHAAHRPQGPAAWASTPIPARGSFVSVENGLYAQAGERPPHTGPGLTLFPDPRGPRAmegPLGVR (SEQ ID
 NO:8)

Human PVRIG sequence starting from position 1 methionine

MRTEAQVPALQPPEPGLEGAMGHRTLVLPPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGFLGSGSISLTVSWG
GPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGSLPPSSDPG
LSAPPTPAPILRADLAGILGVSGVLLFGCVYLLHLLRRHKHRPAPRLQPSRTSPQAPRARAWAPSQASQAALHVPYATIN
 TSCRPATLDTAHPHGGPSWWASLPTHAAHRPQGPAAWASTPIPARGSFVSVENGLYAQAGERPPHTGPGLTLFPDPR
 GPRAmegPLGVR (SEQ ID NO:9)

Alternative signal P with three C to S Mutations at the Fc domain

CGEN-PVRIGHH-2 Alternative SP (MGWSCILFLVATATGVHS ((SEQ ID NO:10) + CGEN-PVRIG (41-171
 of PVRIG_HUMAN) + Human IgG1 Fc mutated at C220S, C226S, C229S of hinge

MGWSCILFLVATATGVHSTPEVWVQVRMEATELSSFTIRCGFLGSGSISLTVSWGGPNGAGGTTLAVLHPERGIROW
APARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGSLPPSSDPGLSAPPTPAPILRADEPKSSDKTHT
SPPSPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHODWLNQKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN
GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:11)

Figure 26

Human PVLR2 alpha isoform

>gi|5360210|ref|NP_002847.1| nectin-2 isoform alpha precursor [Homo sapiens]
MARAAALLPSRSPPTPLWPLLLLLLLETGAQDVRVQVLPEVRGQLGGTVELPCHLLPPVPGLYISLVTW
QRPDAPANHQNVAAAFHPKMGPSFSPKPGSERLSFVSAKQSTGQDTEAELQDATLALHGLTVEDEGNYTC
EFATFPKGSVRGMTWLRVIAKPKNQAEAQKVTFSDPTTVALCISKEGRPPARISWLSSLDWEAKETQVS
GTLAGTVTVTSRFTLVPSGRADGVTVTCKVEHESFEEDPALIPVTLVRYPPPEVSISGYDDNWYLGRTDAT
LSCDVRNPEPTGYDWSTTSGTFPTSAVAQGSQQLVIHAVDSLNTTFVCTVTNAVGMGRAEQVIFVRETP
RASPRDVGPLVWGAVGGTLLVLLLLAGGSLAFILLRVRRRRKSPGGAGGGASGDGGFYDPKAQVLGNGDP
VFWTPVVPGPMEPDGKDEEEEEEEKAEGMLMLPPPPALEDDMESQLDGSLISRRAVYV (SEQ ID NO: 12)

Human PVLR2 delta isoform

>gi|112789532|ref|NP_001036189.1| nectin-2 isoform delta precursor [Homo sapiens]
MARAAALLPSRSPPTPLWPLLLLLLLETGAQDVRVQVLPEVRGQLGGTVELPCHLLPPVPGLYISLVTW
QRPDAPANHQNVAAAFHPKMGPSFSPKPGSERLSFVSAKQSTGQDTEAELQDATLALHGLTVEDEGNYTC
EFATFPKGSVRGMTWLRVIAKPKNQAEAQKVTFSDPTTVALCISKEGRPPARISWLSSLDWEAKETQVS
GTLAGTVTVTSRFTLVPSGRADGVTVTCKVEHESFEEDPALIPVTLVRYPPPEVSISGYDDNWYLGRTDAT
LSCDVRNPEPTGYDWSTTSGTFPTSAVAQGSQQLVIHAVDSLNTTFVCTVTNAVGMGRAEQVIFVRETP
NTAGAGATGGIIGGIIAAIIATAVAATGILICRQQRKEQTLQGAEEDEDELEGPPSYKPPTPKAKLEAQEM
PSQFRTLGAESHPLKTPYFDAGASCTEQEMPRYHELPTLEERSGPLHPGATSLGSPPIVPPGPPAVEDV
SLDLEDEEGEEEEYLDKINPIYDALSY (SEQ ID NO: 13)

Figure 27

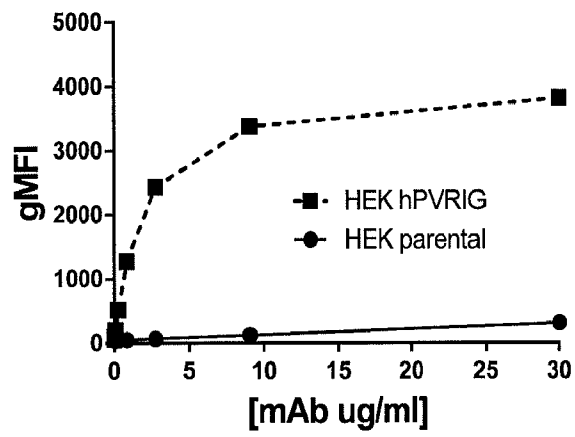


Figure 28

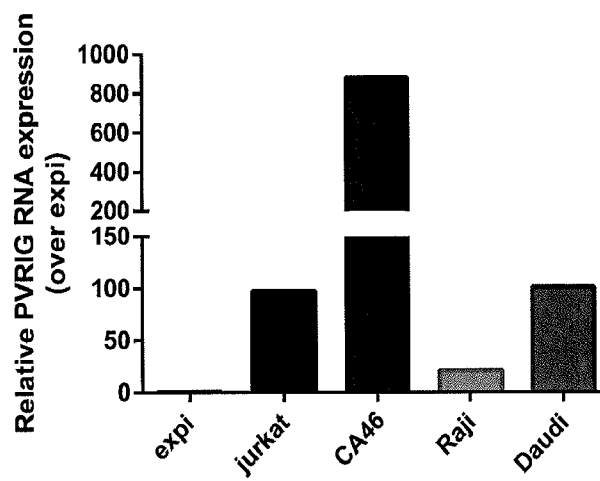


Figure 29

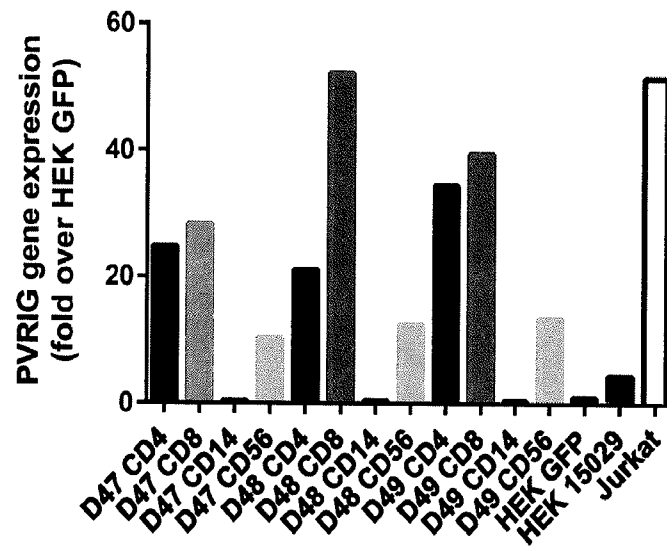


Figure 30A

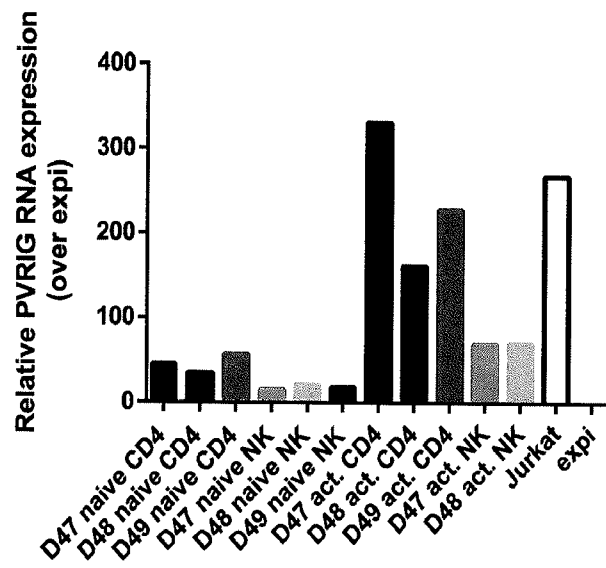


Figure 30B

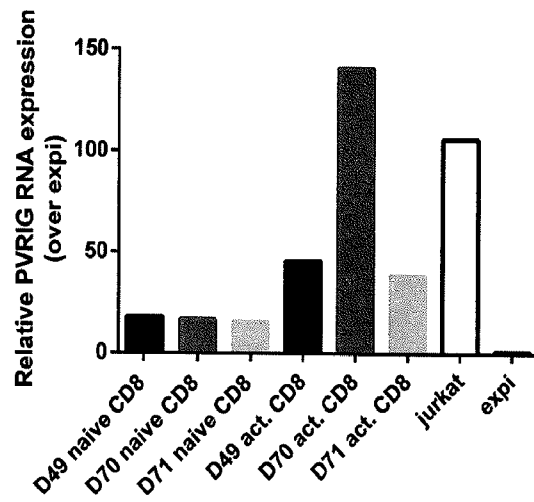


Figure 31A

Antibody (hlgG1)	EC ₅₀ (HEK OE, nM)	HEK OE/par (5ug/ml, gMFlr)	Jurkat (5ug/ml, gMFlr)	CA46 (5ug/ml, gMFlr)
CPA.7.002	53.47	11.97	1.25	1.16
CPA.7.003	7.12	1.28	3.85	6.71
CPA.7.004	43.74	25.18	1.03	1.16
CPA.7.005	125.50	15.77	0.93	1.02
CPA.7.007	0.99	2.90	4.42	9.82
CPA.7.008	Not tested	Not tested	Not tested	Not tested
CPA.7.009	67.30	8.35	0.93	0.99
CPA.7.010	30.00	18.76	1.08	1.01
CPA.7.011	128.80	10.86	0.93	0.96
CPA.7.012	0.40	2.01	4.89	8.23
CPA.7.014	19.66	5.90	1.14	0.92
CPA.7.015	1.74	6.64	4.3	7.33
CPA.7.016	28.38	2.20	1.11	1.04
CPA.7.017	2.62	4.56	0.99	1.49
CPA.7.018	20.38	2.06	1.05	0.96
CPA.7.019	2.11	1.94	4.66	9.23
CPA.7.020	108.30	1.37	1.64	1.45
CPA.7.021	12.41	30.59	4.47	7.96
CPA.7.022	7.73	4.60	1.01	1.24
CPA.7.023	10.90	20.31	0.9	1.01
CPA.7.024	22.91	9.92	1.14	1.25
CPA.7.025	No binding	No binding	Not tested	Not tested
CPA.7.026	8.169	1.16	1.00	0.99
CPA.7.027	No binding	No binding	Not tested	Not tested
CPA.7.028	21.5	2.34	9.57	3.16
CPA.7.029	3.87	1.24	1.17	0.85
CPA.7.031	No binding	No binding	Not tested	Not tested
CPA.7.032	49.62	4.50	1.81	1.64
CPA.7.033	221	1.8221999	1.94	1.17
CPA.7.034	55.69	4.12	1.25	1.01
CPA.7.035	No binding	No binding	Not tested	Not tested
CPA.7.036	14.19	5.68	1.69	1.46
CPA.7.037	Not reliable fit	4.56	1.78	1.28

Figure 31B

Antibody (hlgG1)	EC ₅₀ (HEK OE, nM)	HEK OE/par (5ug/ml, gMFir)	Jurkat (5ug/ml, gMFir)	CA46 (5ug/ml, gMFir)
CPA.7.038	2436	4.36	Not tested	Not tested
CPA.7.039	2.99	6.52	1.55	1.40
CPA.7.040	0.84	7.91	1.78	1.59
CPA.7.041	14.35	3.25	Not tested	Not tested
CPA.7.042	5.42	4.20	1.57	1.28
CPA.7.043	7.63	5.47	1.20	1.08
CPA.7.044	43.64	3.24	1.03	0.97
CPA.7.045	5.17	4.04	1.68	1.05
CPA.7.046	Not reliable fit	Not tested	Not tested	Not tested
CPA.7.047	4.61	5.89	0.81	0.92
CPA.7.049	1.94	2.56	Not tested	Not tested
CPA.7.050	121.5	4.29	2.72	2.02

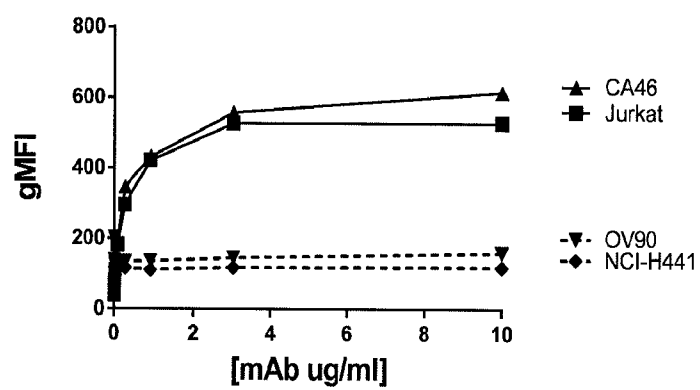
Figure 32A

Antibody (hlgG1)	Human CD56 int. NK (gMFlr, 5ug/ml)	Human CD8+ T cells (gMFlr, 5ug/ml)	Expi cyno OE/par (gMFlr, 5ug/ml)	Cyno NK cells (gMFlr, 5ug/ml)	Cyno CD3+ T cells (gMFlr, 5ug/ml)
CPA.7.002	3.21	1.01	1.16	2.24	1.01
CPA.7.003	16.21	1.41	1.36	Not tested	Not tested
CPA.7.004	1.30	0.98	1.1	Not tested	Not tested
CPA.7.005	2.35	1.07	1.21	1.12	0.99
CPA.7.007	5.31	1.32	1.11	Not tested	Not tested
CPA.7.008	Not tested	Not tested	Not tested	Not tested	Not tested
CPA.7.009	1.34	0.98	1.08	Not tested	Not tested
CPA.7.010	2.09	1.06	1.41	Not tested	Not tested
CPA.7.011	1.19	1.02	1.06	Not tested	Not tested
CPA.7.012	1.62	1.18	1.98	Not tested	Not tested
CPA.7.014	1.57	0.98	1.06	Not tested	Not tested
CPA.7.015	2.82	1.14	1.11	Not tested	Not tested
CPA.7.016	2.39	1.05	1.43	Not tested	Not tested
CPA.7.017	1.73	0.86	1.30	Not tested	Not tested
CPA.7.018	1.62	1.04	1.06	Not tested	Not tested
CPA.7.019	4.23	1.36	1.23	Not tested	Not tested
CPA.7.020	3.12	1.07	3.10	Not tested	Not tested
CPA.7.021	3.74	1.23	1.08	1.91	1.01
CPA.7.022	1.27	0.87	Not tested	Not tested	Not tested
CPA.7.023	1.11	0.99	1.08	Not tested	Not tested
CPA.7.024	1.20	1.02	5.67	0.30	1.06
CPA.7.025	Not tested	Not tested	1.41	Not tested	Not tested
CPA.7.026	1.72	0.92	1.31	Not tested	Not tested
CPA.7.027	Not tested	Not tested	1.45	Not tested	Not tested
CPA.7.028	21.42	1.40	1.34	Not tested	Not tested
CPA.7.029	1.24	0.90	1.29	Not tested	Not tested
CPA.7.031	Not tested	Not tested	1.47	Not tested	Not tested
CPA.7.032	10.43	0.93	1.46	Not tested	Not tested
CPA.7.033	2.46	0.93	1.39	Not tested	Not tested
CPA.7.034	1.05	0.89	1.33	Not tested	Not tested
CPA.7.035	Not tested	Not tested	1.24	Not tested	Not tested
CPA.7.036	4.17	0.87	1.24	Not tested	Not tested
CPA.7.037	1.64	1.01	1.40	Not tested	Not tested
CPA.7.038	18.08	1.03	7.88	3.35	1.01
CPA.7.039	1.43	0.92	7.53	0.31	1.01

Figure 32B

Antibody (hlgG1)	Human CD56 int. NK (gMFir, 5ug/ml)	Human CD8+ T cells (gMFir, 5ug/ml)	Expi cyno OE/par (gMFir, 5ug/ml)	Cyno NK cells (gMFir, 5ug/ml)	Cyno CD3+ T cells (gMFir, 5ug/ml)
CPA.7.040	1.73	0.88	1.32	Not tested	Not tested
CPA.7.041	6.15	1.01	3.31	1.26	0.98
CPA.7.042	6.10	0.92	3.71	1.38	0.99
CPA.7.043	1.10	0.83	1.50	Not tested	Not tested
CPA.7.044	8.79	0.88	1.31	Not tested	Not tested
CPA.7.045	1.28	0.84	1.43	Not tested	Not tested
CPA.7.046	Not tested	Not tested	4.42	Not tested	Not tested
CPA.7.047	0.99	0.90	1.29	Not tested	Not tested
CPA.7.049	Not tested	Not tested	1.37	Not tested	Not tested
CPA.7.050	4.98	1.23	1.47	0.64	1.03

Figure 33



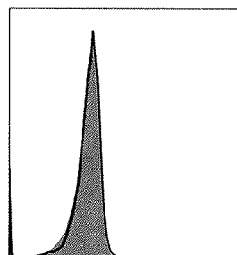
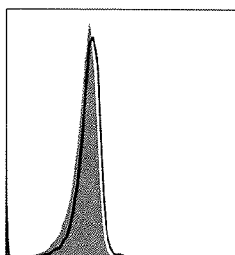
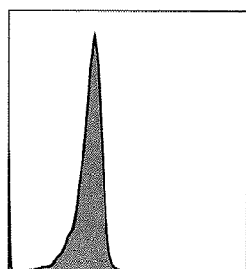
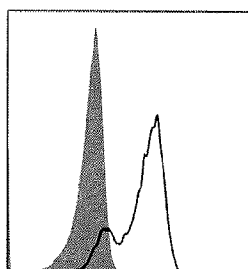
a**expi parental****Figure 34A****b****cPVRIG transient****Figure 34B****c****expi parental****Figure 34C****d****cPVRIG transient****Figure 34D**

Figure 35

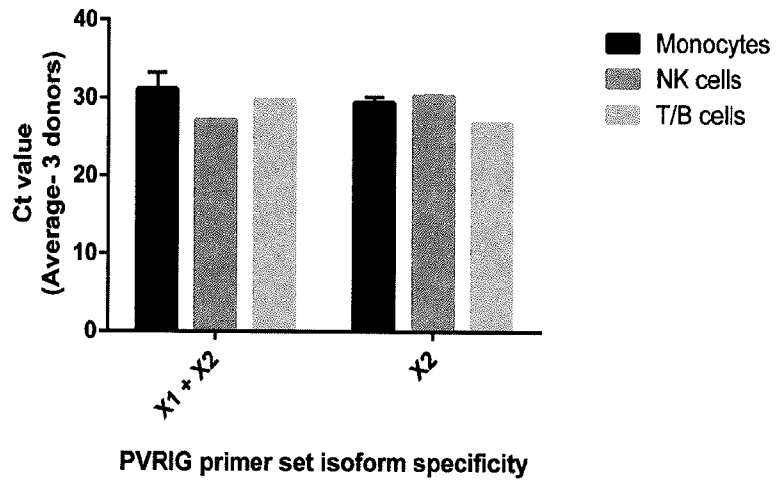


Figure 36A

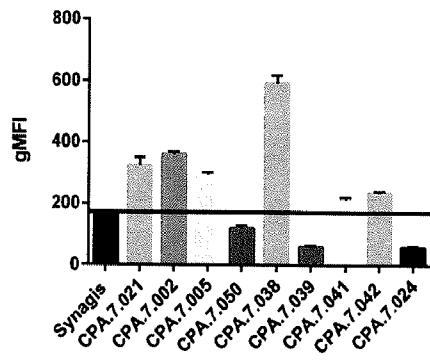


Figure 36B

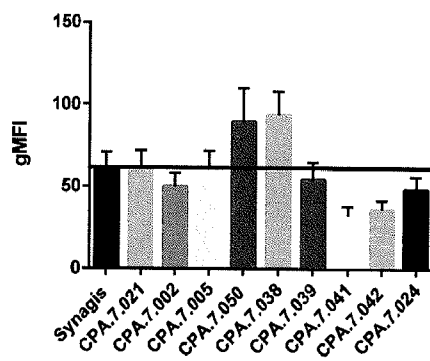


Figure 36C

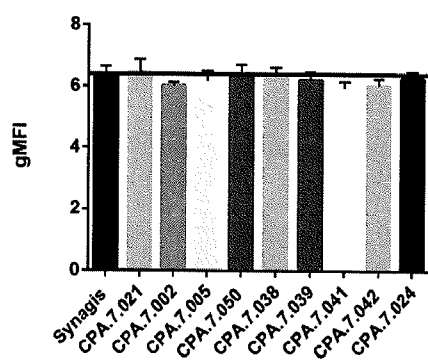


Figure 37A

Name	Hcdr1	SEQ ID NO:	Hcdr2	SEQ ID NO:	Hcdr3	SEQ ID NO:	Lcdr1	SEQ ID NO:	Lcdr2	SEQ ID NO:	Lcdr3	SEQ ID NO:
CPA.7.001	GGTFSSYA	14	IPIFGTA	15	AREEVSSPYGMDV	16	TGAVTSGHY	17	DTG	18	LLSYSGASWV	19
CPA.7.003	GFSLSHFS	20	FDPEEGGT	21	ATGIWYSSGWPPVDY	22	QSLDSSGYN	23	LGS	24	MQALQTPIT	25
CPA.7.004	GYTLTELS	26	FPEDGET	27	ATVSRVRGVINYYYYMDV	28	QSLLYRNGN	29	LGS	30	MQALQTPPT	31
CPA.7.006	GGTFGTYA	32	ITPISATI	33	ARGFEYSDGLLDD	34	QSLFYSDDGNTY	35	RLS	36	MQHMEFFLT	37
CPA.7.008	SGSISSTNW	38	IYHSGST	39	ARVGPAAIYY	40	SNNVGYEG	41	RNN	42	SAWDSSLNAV	43
CPA.7.009	GYTLTELS	44	FPEDGET	45	ATAKPGIAGVAGQNYYYYYMDV	46	QSLLYRNGN	47	LGS	48	MQALQTPPT	49
CPA.7.010	GFTFSSYA	50	ISYDGSNK	51	ASSPIGYSGYWGGMDV	52	SGIDVRTNK	53	FQSDSK	54	LIWHTSGWV	55
CPA.7.011	GYTLTELS	56	FPEDGET	57	ATGPAAAGVGYYYYMDV	58	QSLLYRNGYN	59	LGS	60	MQALQTPPT	61
CPA.7.012	GFTFSSYA	62	ISYDGSNK	63	ARDVMVYCSSTSCYFYGMDV	64	QDIRDY	65	DAS	66	QQFENLPIT	67
CPA.7.013	GYTLTELS	68	FPEDGET	69	ATGGYSSGFNYYYYMDV	70	QSLLYRNGN	71	LGS	72	MQALQTPPT	73
CPA.7.014	GYTLTELS	74	FPEDGET	75	ATGVTTYYYGMDV	76	QSLLYSNGN	77	LGS	78	MQALQTPPT	79
CPA.7.015	GFTFSSYG	80	IRYDGSNK	81	ARDLDFWWDGMDV	82	QSVSSMY	83	GAS	84	QQYVSSPMYT	85
CPA.7.017	GGTFNNYG	86	IIPFLGTT	87	ARDRMAADGMAVFDY	88	SSNIGRHF	89	KND	90	SSWDAALNGV	91
CPA.7.018	GYTLTELS	92	FPEDGET	93	ATEVPMVRGARRYYYYYMDV	94	QTLTYINEN	95	LGS	96	MQGLQTPPT	97

Figure 37B

Name	Hcdr1	SEQ ID NO:	Hcdr2	SEQ ID NO:	Hcdr3	SEQ ID NO:	Lcdr1	SEQ ID NO:	Lcdr2	SEQ ID NO:	Lcdr3	SEQ ID NO:
CPA.7.019	GGISNSNVY	98	IWYSGT	99	ARGAWELSLGDFDP	100	SSNIGAGYD	101	GNN	102	QSYDSSLVYV	103
CPA.7.021	GFTFGTSS	104	ISFDGTEI	105	AKGSGNIYFSGMDV	106	QSIQGW	107	ETS	108	QQYYSYPLT	109
CPA.7.022	GYTLTELS	110	FPEDGET	111	ATGVPAAGVYYYYYMDV	112	QSLLYSNGYNY	113	LGS	114	MQALQSPVT	115
CPA.7.023	GYTLTELS	116	FPEDGET	117	ATDSRDGPAARGGYYYMDV	118	QSLLYINGYNY	119	LGS	120	MQALQTPPT	121
CPA.7.024	GGTFSSYA	122	IIPIFGTA	123	ARDAYYDSSGYNPDAFDI	124	QSLHSHNGYNY	125	LGS	126	MQGLQTPRT	127
CPA.7.033	GGTFSSA	128	IIPIYGIT	129	ARDDTARRVRGVYYYYYAMDV	130	QDIDDD	131	EAS	132	LQHDNLPLT	133
CPA.7.034	GYTLTELS	134	FPEDGET	135	ATEDPGPVAGPYYYGMDV	136	QSLLYINGYHY	137	LGS	138	MQALQTPPT	139
CPA.7.036	GGTFSSA	140	IIPIYGIT	141	ARDDTARRVRGVYYYYYAMDV	142	QSLDSDDGNTY	143	TLS	144	MQRLQFPLT	145
CPA.7.040	GYTLTELS	146	FPEDGET	147	ATGVPAAGVYYYYYMDV	148	QSLLYRNGYNY	149	WGS	150	MQAVQNPPT	151
CPA.7.046	GGTFSSA	152	IIPIYGIT	153	ARDDTARRVRGVYYYYYAMDV	154	QTMNNY	155	DAS	156	QQYGDWLPJT	157
CPA.7.047	GYTLTELS	158	FPEDGET	159	ATAFPEATISYYMYMDV	160	QSLLYRNGYNY	161	WGS	162	MQAVQNPPT	163
CPA.7.049	GGTFSSA	164	IIPIYGIT	165	ARDDTARRVRGVYYYYYAMDV	166	RSLLDSDDGNTY	167	SLS	168	MQRKEFPLT	169
CPA.7.050	GGTFSSYA	170	IIPIFGTA	171	ARGPWYDSSGYSSYAYMYMDV	172	QSLHSHDGNYNY	173	LGS	174	MQALHTPGVT	175

Figure 38A

CPA.7.001

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QMLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTAYME LSSLRSEDTAIVYCAR EEVSSPYGMDV WGQGTTTVTVSS	176
vhCDR1	GGTFSSYA	177
vhCDR2	IIPIFGTA	178
vhCDR3	AREEVSSPYGMDV	179
Full length HC	QMLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTAYME LSSLRSEDTAIVYCAR EEVSSPYGMDV WGQGTTTVTVSSASTKGPSVFPLA SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTV PS SSSLGTQYICNVNHHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVWVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRVSVLT VLHQDWLNGKEYCKVSNKALPAPI EKTISKAKGQPREPQWTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TT PPVLDSDGGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	180
Variable light (vl) domain	QAVVTQEP SLTVSPGGTVTLTCGTSTIGAVTSGHY PYWFQQKPGQAPK TLIYDTGNKHSWTPARFSGSLGGKAALTLSGAQPE DEADYYCLLSYSGASWVFGGGTKLTVLG	181
vlCDR1	TGAVTSGHY	182
vlCDR2	DTG	183
vlCDR3	LLSYSGASWV	184
Full length light chain	QAVVTQEP SLTVSPGGTVTLTCGTSTIGAVTSGHY PYWFQQKPGQAPK TLIYDTGNKHSWTPARFSGSLGGKAALTLSGAQPE DEADYYCLLSYSGASWVFGGGTKLTVLGQPKAAPSV TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTT PSKQSN NKYAA SSVLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	185

Figure 38B
CPA.7.003

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKVSGFSLSHFSMHWWVRQVPGKGLEWLGFGDPEEGGTIPAQKFQGRITMTEDTSTETAYMELSSLRSEDTAVYYCATGIWYSSGWVPVDYWGPGLVTVSS	186
vhCDR1	<u>GFSLSHFS</u>	187
vhCDR2	<u>FDPEEGGT</u>	188
vhCDR3	<u>ATGIWYSSGWVPVDY</u>	189
Full length HC	EVQLVQSGAEVKKPGSSVKVCKASGGTFSSYAISWVRQAPGQGLEWMGGIPIFGTANYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGPWYYDSSGYSSAYYMDVWGQGTITVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK	190
Variable light (vl) domain	DVWMTQSPPLSPVTPGGPASISCRSSQSLDSSGYNVVDWYVLPKPGQSPQLLISLGSDDRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGIYYCMQALQTPITFGQGRLEIKR	191
vlCDR1	<u>QSLDSSGYNV</u>	192
vlCDR2	<u>LGS</u>	193
vlCDR3	<u>MQALQTPIT</u>	194
Full length light chain	DVWMTQSPPLSPVTPGGPASISCRSSQSLDSSGYNVVDWYVLPKPGQSPQLLISLGSDDRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGIYYCMQALQTPITFGQGRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCILNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	195

Figure 38C
CPA.7.004

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVCKVSGYTLIELSMHWRQAPGKGLWMGGFDPEGETIYAQKFQGRVTMTEDTS TDTAYMELSLRSED TAVYCATVSRVRGVINYYMMDV WGKGTTVTVSS	196
vhCDR1	<u>GYTLIELS</u>	197
vhCDR2	<u>FDPEGET</u>	198
vhCDR3	<u>ATVSRVRGVINYYMMDV</u>	199
Full length HC	EVQLVQSGAEVKKPGASVKVCKVSGYTLIELSMHWRQAPGKGLWMGGFDPEGETIYAQKFQGRVTMTEDTS TDTAYMELSLRSED TAVYCATVSRVRGVINYYMMDV WGKGTTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLV KDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHHKPSNTKVDDKKVEPKSCDKHTC PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWVYDGVGVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGGSFFLYSKLTVDKSRWQQGNVFCSMVHEALHNHYTQKSLSLSPGK	200
Variable light (vl) domain	DVVMTQSPSLPVTTPGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGYYVCMQALQTPPTFGGGTKLEIKR	201
vlCDR1	<u>QSLLYRNGNNY</u>	202
vlCDR2	<u>IGS</u>	203
vlCDR3	<u>MQALQTPPT</u>	204
Full length light chain	DVVMTQSPSLPVTTPGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGYYVCMQALQTPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWVKVDNA LQSGNSQESVTEQDSKDSSTLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	205

Figure 38D
CPA.7.006

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVRRPGSSVRVSCKPSGGTFTGYAFTWVRQAPGQGLEWMGGITPISATINRAQNLQDRLTITADESTT TVHMDLTSLRSEDATVYYCARGFEYSDGLDDWGQGTIVTVSS	206
vhCDR1	<u>GGTFTGYA</u>	207
vhCDR2	<u>ITPISATI</u>	208
vhCDR3	<u>ARGEYSDGLDD</u>	209
Full length HC	QVQLVQSGAEVRRPGSSVRVSCKPSGGTFTGYAFTWVRQAPGQGLEWMGGITPISATINRAQNLQDRLTITADESTT TVHMDLTSLRSEDATVYYCARGFEYSDGLDDWGQGTIVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKHTHTCPPCPAP ELGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSMHEALHNNHYTQKSLSPGK	210
Variable light (vl) domain	DIVMTQTPLSLPVIPGEPASISCRSSQSLFYSDDGNTYLDWYVLPKPGQSPQLLIYRLSHRASGVDPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQHMFEPLTFGGGTKEIKR	211
vlCDR1	<u>QSLFYSDDGNTY</u>	212
vlCDR2	<u>RLS</u>	213
vlCDR3	<u>MQHMEFPLT</u>	214
Full length light chain	DIVMTQTPLSLPVIPGEPASISCRSSQSLFYSDDGNTYLDWYVLPKPGQSPQLLIYRLSHRASGVDPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQHMFEPLTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWVKVDN ALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	215

Figure 38E
CPA.7.008

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSGTLSTCVVSSGSISSTNWWTWVRQPPGKGLWIGEIHSGSTSYNSSLSKSRVTISEDKSKNQIS LRLSSVTAADTAVVYCARVGPAAIYYWGQGTILTVSS	216
vhCDR1	<u>SGSISSTNW</u>	217
vhCDR2	<u>IYHSGST</u>	218
vhCDR3	<u>ARVGPAAIYY</u>	219
Full length HC	QVQLQESGPGLVKPSGTLSTCVVSSGSISSTNWWTWVRQPPGKGLWIGEIHSGSTSYNSSLSKSRVTISEDKSKNQIS LRLSSVTAADTAVVYCARVGPAAIYYWGQGTILTVSSASTKGPSVFLPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNITKVDKKVEPKSCDKTHITCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPP VLDSDGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	220
Variable light (vl) domain	QAGLTQPPSVSKGLRQTATLTCTGNSNNVGYEGAAWLQQHQGHAPKLLLYRNNNNRPSGISKRFSASRSGNTASLTITG LQPEDEADYYCSAWDSSLNAVVFGGGTQLTVLG	221
vlCDR1	<u>SNNVGYEG</u>	222
vlCDR2	<u>RNN</u>	223
vlCDR3	<u>SAWDSSLNAV</u>	224
Full length light chain	QAGLTQPPSVSKGLRQTATLTCTGNSNNVGYEGAAWLQQHQGHAPKLLLYRNNNNRPSGISKRFSASRSGNTASLTITG LQPEDEADYYCSAWDSSLNAVVFGGGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADS SPVKAGVETTTTPSKQSNKNKYAASSYLSTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	225

Figure 38F
CPA.7.009

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHWVRQAPGKGLWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATAKPGIAVAGQNYYYMDVWVGKGTTVTVSS	226
vhCDR1	<u>GYTLTELS</u>	227
vhCDR2	<u>FDPEDGET</u>	228
vhCDR3	<u>ATAKPGIAVAGQNYYYMDV</u>	229
Full length HC	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHWVRQAPGKGLWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATAKPGIAVAGQNYYYMDVWVGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHHKPSNTKV/DKKVEPKSCD KTHCTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPETCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST YRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	230
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKI SRVEAEDVGVVYCMQALQTPPTFGGGTKLEIKR	231
vlCDR1	<u>QSLLYRNGNNY</u>	232
vlCDR2	<u>LGS</u>	233
vlCDR3	<u>MQALQTPPT</u>	234
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKI SRVEAEDVGVVYCMQALQTPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKPDSTYLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	235

Figure 38G
CPA.7.010

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGRSLRLSCAASGFTFSSYAMHWVVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCASSPIGYSYGYWGGMDVWGGQTTVTYSS	236
vhCDR1	<u>GFTFSSYA</u>	237
vhCDR2	<u>ISYDGSNK</u>	238
vhCDR3	<u>ASSPIGYSYGYWGGMDV</u>	239
Full length HC	EVQLVESGGGLVQPGRSLRLSCAASGFTFSSYAMHWVVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCASSPIGYSYGYWGGMDVWGGQTTVTYSSASTKGPSVFLAPSSKSTSGGTAALGCLVK DYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVWSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPPVLDSDGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	240
Variable light (vl) domain	QAVLTQPASLSASPGASASLTCTLRSGIDVRTNKIFWYQVKPGSPPPQHLLTFQSDSDKQQGSGVPSRFSGSKDASANA GILISGLQSEDEADYYCLIWHTSGWVFGGGTQLTLVG	241
vlCDR1	<u>SGIDVRTNK</u>	242
vlCDR2	<u>FQSDSDK</u>	243
vlCDR3	<u>LIWHTSGWV</u>	244
Full length light chain	QAVLTQPASLSASPGASASLTCTLRSGIDVRTNKIFWYQVKPGSPPPQHLLTFQSDSDKQQGSGVPSRFSGSKDASANA GILISGLQSEDEADYYCLIWHTSGWVFGGGTQLTLVGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWK ADSSPVKAGVETITTPSKQSNKNYAASSYLSLTPEQWKSHRYSQCQVTHEGSTVEKTVAPTECS	245

Figure 38H
CPA.7.011

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHWVRQAPGKGLWVGDFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGPAAAGVGYYYMDV WGKGTTTVTVSS	246
vhCDR1	<u>GYTLTELS</u>	247
vhCDR2	<u>FDPEDGET</u>	248
vhCDR3	<u>ATGPAAAGVGYYYMDV</u>	249
Full length HC	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHWVRQAPGKGLWVGDFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGPAAAGVGYYYMDVWGKGTTTVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLV KDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSWTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	250
Variable light (vl) domain	DVVMTQSPPLSPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGWYVCMQALQTPPTFGQGTKEIKR	251
vlCDR1	<u>QSLLYRNGYNY</u>	252
vlCDR2	<u>LGS</u>	253
vlCDR3	<u>MQALQTPPT</u>	254
Full length light chain	DVVMTQSPPLSPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGWYVCMQALQTPPTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRPAKVQWVKVDNA LQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	255

Figure 38I
CPA7.012

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLVWVAVISYDGSNKYYADSVKGRFTISRDN SKNT LYLQMNSLRAEDTAVYVCARDVMVYCSSTSCYFYGMDVWGQGTTVTVSS	256
vhCDR1	<u>GFTSSYA</u>	257
vhCDR2	<u>ISYDGSNK</u>	258
vhCDR3	<u>ARDVMVYCSSTSCYFYGMDV</u>	259
Full length HC	EVQLVETGGGLIQGRSLRLSCAASGFTSSYAMHWVRQAPGKGLVWVAVISYDGSNKYYADSVKGRFTISRDN SKNT LYLQMNSLRAEDTAVYVCARDVMVYCSSTSCYFYGMDVWGQGTTVTVSSASTKGPSVFLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	260
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTVTTCQASQDIRDYLNWYQKPKGKAPKLLIYDASNLEAGVPSRFSGGSGGTDFTFTISGLQ PEDVATYCCQQFENLPITFGQGRLEIKR	261
vlCDR1	<u>QDIRDY</u>	262
vlCDR2	<u>DAS</u>	263
vlCDR3	<u>QQFENLPIT</u>	264
Full length light chain	DIQMTQSPSSLSASVGDRVTVTTCQASQDIRDYLNWYQKPKGKAPKLLIYDASNLEAGVPSRFSGGSGGTDFTFTISGLQ PEDVATYCCQQFENLPITFGQGRLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	265

Figure 38J
CPA.7.013

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLMSHWRQAPGKGLEWMGGEDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGGYSSGFNYYYYMDV WGKGTTVTVSS	266
vhCDR1	<u>GYTLTSL</u>	267
vhCDR2	<u>FDPEDGET</u>	268
vhCDR3	<u>ATGGYSSGFNYYYYMDV</u>	269
Full length HC	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLMSHWRQAPGKGLEWMGGEDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGGYSSGFNYYYYMDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFEPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTVPSSSLGTQYICNVNHNKPSNTKVDKKVEPKSCDKTHTC PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVWS VLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	270
Variable light (vl) domain	DVVMTQSPSLPVTTPGEPASICRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKI SRVEAEDVGYYVCMQALQTPPTFGGGTKLEIKR	271
viCDR1	<u>QSLLYRNGNNY</u>	272
viCDR2	<u>LGS</u>	273
viCDR3	<u>MQALQTPPT</u>	274
Full length light chain	DVVMTQSPSLPVTTPGEPASICRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKI SRVEAEDVGYYVCMQALQTPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	275

Figure 38K
CPA.7.014

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVCKVSGYTLT <small>ELSMHWVRQAPGKGL</small> EWMMGGFDPE <small>GETIYAQKFQGRVTMTEDTS</small> TDTAYMELSSLRSEDTAVYCATGVT <small>TYYYGMDVWGQGT</small> TVVSS	276
vhCDR1	<u>GYTLT<small>ELS</small></u>	277
vhCDR2	<u>FDPEDGET</u>	278
vhCDR3	<u>ATGVT<small>TYYYGMDV</small></u>	279
Full length HC	EVQLVQSGAEVKKPGASVKVCKVSGYTLT <small>ELSMHWVRQAPGKGL</small> EWMMGGFDPE <small>GETIYAQKFQGRVTMTEDTS</small> TDTAYMELSSLRSEDTAVYCATGVT <small>TYYYGMDVWGQGT</small> TVVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWVSQVLT LHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFPYSDIAVEWESNGQ PENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	280
Variable light (vl) domain	DVWMTQSPVLSPLPTPGEPASISCRSSQSL <small>LYSNGN</small> NFLDWY <small>LQKPGQSPRL</small> LI <small>SLG</small> SNRASGVPDFSGSGSGTDFTLK <small>I</small> SRVEAEDVGIYYC <small>MQALQTPPTFGQGT</small> KVEIKR	281
vlCDR1	<u>QSL<small>LYSNGN</small>NE</u>	282
vlCDR2	<u>LGS</u>	283
vlCDR3	<u>MQALQTPPT</u>	284
Full length light chain	DVWMTQSPVLSPLPTPGEPASISCRSSQSL <small>LYSNGN</small> NFLDWY <small>LQKPGQSPRL</small> LI <small>SLG</small> SNRASGVPDFSGSGSGTDFTLK <small>I</small> SRVEAEDVGIYYC <small>MQALQTPPTFGQGT</small> KVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	285

Figure 38L
CPA.7.015

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QITLKESGGVWQPGGSLRLSCAASGFTFSSYGIMHWVRQAPGKGLEWVAFIRYDGSNKYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYVCARDLFD FWWDGMDV VWGQGT TVTVSS	286
vhCDR1	<u>GFTFSSYG</u>	287
vhCDR2	<u>IRYDGSNK</u>	288
vhCDR3	<u>ARDLFDFWWDGMDV</u>	289
Full length HC	QITLKESGGVWQPGGSLRLSCAASGFTFSSYGIMHWVRQAPGKGLEWVAFIRYDGSNKYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYVCARDLFD FWWDGMDV VWGQGT TVTVSS ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHITCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPPVLDSDGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	290
Variable light (vl) domain	EIVLTQSPGTLSLSPGEKATLSCRVSSQSVSSMYLAWYQQKPGQAPRLIIYGASYRATGIPDRFSGSGSGTDFNLTISRLEP EDFAVYQCQQWSSPMYTFGLGTLKLEIKR	291
vlCDR1	<u>QSVSSMY</u>	292
vlCDR2	<u>GAS</u>	293
vlCDR3	<u>QQVSSPMYT</u>	294
Full length light chain	EIVLTQSPGTLSLSPGEKATLSCRVSSQSVSSMYLAWYQQKPGQAPRLIIYGASYRATGIPDRFSGSGSGTDFNLTISRLEP EDFAVYQCQQWSSPMYTFGLGTLKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	295

Figure 38M
CPA.7.017

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVCKASGGTFNNYGISWVRQAPGKGLEWMGQIPLFGTTKYAQKFQGRVITIAADEPTS TAYMELGSLRSEDTAIYYCARDRMAADGMMAVFDYWGQGTLLTVSS	296
vhCDR1	<u>GGTFNNYG</u>	297
vhCDR2	<u>IPLFGTT</u>	298
vhCDR3	<u>ARDRMAADGMMAVFDY</u>	299
Full length HC	QVQLVQSGAEVKKPGSSVKVCKASGGTFNNYGISWVRQAPGKGLEWMGQIPLFGTTKYAQKFQGRVITIAADEPTS TAYMELGSLRSEDTAIYYCARDRMAADGMMAVFDYWGQGTLLTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYF PEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPEC APELGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVWSVLTVL HQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	300
Variable light (vl) domain	QSVLTQPPSVSGTPGQKVIISCSGSSNIGRHFVFWYQQLPGTAPKLLIYKNDERPSGVDPDRFSGSKSGTSASLAVSGLRS EDEADYVCSSWDAALNGVWVFGGGTKLTVLG	301
vlCDR1	<u>SSNIGRHF</u>	302
vlCDR2	<u>KND</u>	303
vlCDR3	<u>SSWDAALNGVV</u>	304
Full length light chain	QSVLTQPPSVSGTPGQKVIISCSGSSNIGRHFVFWYQQLPGTAPKLLIYKNDERPSGVDPDRFSGSKSGTSASLAVSGLRS EDEADYVCSSWDAALNGVWVFGGGTKLTVLGPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV KAGVETTTPSKQSNKNKYAASSYLSTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	305

Figure 38N
CPA.7.018

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHVWRQAPGKGLWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYCATVEPVMVRGARRYYYMDVWGKGTITVVS	306
vhCDR1	<u>GYTLTELS</u>	307
vhCDR2	<u>FDPEDGET</u>	308
vhCDR3	<u>ATEVPMVRGARRYYYMDV</u>	309
Full length HC	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHVWRQAPGKGLWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYCATVEPVMVRGARRYYYMDVWGKGTITVVSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCWVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	310
Variable light (vl) domain	DWVMTQSPFLAVTPGEPASISCRSSQTLTYINENNYLDWYVQKPGQSPQLLIYLGSTRASGVDPDRFSGGSGTDFTLTI SRVEAEDVGLYYCMQGLQTPPTFGQGRLEIKR	311
vlCDR1	<u>QTLTYINENNY</u>	312
vlCDR2	<u>LGS</u>	313
vlCDR3	<u>MQGLQTPPTI</u>	314
Full length light chain	DWVMTQSPFLAVTPGEPASISCRSSQTLTYINENNYLDWYVQKPGQSPQLLIYLGSTRASGVDPDRFSGGSGTDFTLTI SRVEAEDVGLYYCMQGLQTPPTFGQGRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	315

Figure 380
CPA.7.019

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKSETLSLTCSVSGGISNSNYWGWIRQPPGKGLEWIGGIYSGSTYYNPSLESRVTISEDTSKNQIS LKLSVTAADTAVVYCARGAWELSLGDFWDPWGPGLTVTVSS	316
vhCDR1	<u>GGISNSNY</u>	317
vhCDR2	<u>IYSGST</u>	318
vhCDR3	<u>ARGAWELSLGDFWDP</u>	319
Full length HC	QVQLQESGPGLVKSETLSLTCSVSGGISNSNYWGWIRQPPGKGLEWIGGIYSGSTYYNPSLESRVTISEDTSKNQIS LKLSVTAADTAVVYCARGAWELSLGDFWDPWGPGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVWSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	320
Variable light (vl) domain	QSVLTQPPSVSGAPGQRVTISCTGSSNIGAGYDIQWYQQLPGTAPKLLIYGNNNRPSGVDPDRFSGSRGTSASLAITGL QAEDEADWYCQSYDSSLSVWVWFGGGTQLTVLG	321
vlCDR1	<u>SSNIGAGYD</u>	322
vlCDR2	<u>GNN</u>	323
vlCDR3	<u>QSYDSSLSVWVW</u>	324
Full length light chain	QSVLTQPPSVSGAPGQRVTISCTGSSNIGAGYDIQWYQQLPGTAPKLLIYGNNNRPSGVDPDRFSGSRGTSASLAITGL QAEDEADWYCQSYDSSLSVWVWFGGGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTTPSKQSNKNKYAASSYLSTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	325

Figure 38P
CPA.7.021

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGVVVKPGGSLRLSCAASGFTFGTSSMNWVRQAPGKGLEWVAVISFDGTEIHAYADSVKGRFTISRDNKST VFLQMNSLRPDDTALYYCAKSGNIIFYSGMDVWGQGTITVTVSS	326
vhCDR1	<u>GFTFGTSS</u>	327
vhCDR2	<u>ISFDGTEI</u>	328
vhCDR3	<u>AKSGNIIFYSGMDV</u>	329
Full length HC	EVQLVESGGGVVVKPGGSLRLSCAASGFTFGTSSMNWVRQAPGKGLEWVAVISFDGTEIHAYADSVKGRFTISRDNKST VFLQMNSLRPDDTALYYCAKSGNIIFYSGMDVWGQGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHTCPPCP APELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPGK	330
Variable light (vl) domain	DIQMTQSPSTLSASVGDRVTITCRAGQSIGSLWLFQKPKGKAPNLLIYETISLTESGVPSRFSGSGTEYTLTISSLQP DDFATYYCQQYYSYPLTFGQGTKEIKR	331
vlCDR1	<u>QSIGSLW</u>	332
vlCDR2	<u>ETS</u>	333
vlCDR3	<u>QQYYSYPLT</u>	334
Full length light chain	DIQMTQSPSTLSASVGDRVTITCRAGQSIGSLWLFQKPKGKAPNLLIYETISLTESGVPSRFSGSGTEYTLTISSLQP DDFATYYCQQYYSYPLTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSYSTSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	335

Figure 38Q
CAP.7.022

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVCKVSGYTLIELSMHWVRQAPGKGLWVGMDVWGKTTTVSS TDTAYMELSSLRSEDTAVYCATGVPAAGVYYYYYMDVWGKTTTVSS	336
vhCDR1	<u>GYTLIELS</u>	337
vhCDR2	<u>FDPEDGET</u>	338
vhCDR3	<u>ATGVPAAGVYYYYYMDV</u>	339
Full length HC	EVQLVQSGAEVKKPGASVKVCKVSGYTLIELSMHWVRQAPGKGLWVGMDVWGKTTTVSSASTKGPSVFLAPSSKSTSGGTAALGCL TDTAYMELSSLRSEDTAVYCATGVPAAGVYYYYYMDVWGKTTTVSSASTKGPSVFLAPSSKSTSGGTAALGCL VKDYFPEPVTYSWNSGALTSVHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLIHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSPGK	340
Variable light (vl) domain	DVVMTQSPPLSPVTPGEPASISCRSSQSLLYSNGYNYLDWYLYQKPGQSPQLLISLGSNRSASGVPDRFSGSGSGTDFTLK SRVEAEDVGVVYCMQALQSPVTFGGGTKEIKR	341
vlCDR1	<u>QSLLYSNGYNY</u>	342
vlCDR2	<u>LGS</u>	343
vlCDR3	<u>MQALQSPVT</u>	344
Full length light chain	DVVMTQSPPLSPVTPGEPASISCRSSQSLLYSNGYNYLDWYLYQKPGQSPQLLISLGSNRSASGVPDRFSGSGSGTDFTLK SRVEAEDVGVVYCMQALQSPVTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	345

Figure 38R
CPA.7.023

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDEGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATDSRDGPAARGGYMDVWVGQGTTVTVSS	346
vhCDR1	<u>GYTLTELS</u>	347
vhCDR2	<u>FDPEDGEI</u>	348
vhCDR3	<u>ATDSRDGPAARGGYMDV</u>	349
Full length HC	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDEGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATDSRDGPAARGGYMDVWVGQGTTVTVSSASTKGPVFLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGPPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALNHYTKQSLSLSPGK	350
Variable light (vl) domain	DWVMTQSPVLSPLPVTLGQPAISICRSSQSLLYINGVNYLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKI SRVEAEDVGWYCMQALQTPPTFGQGTKEIKR	351
vlCDR1	<u>QSLLYINGNY</u>	352
vlCDR2	<u>LGS</u>	353
vlCDR3	<u>MQALQTPPT</u>	354
Full length light chain	DWVMTQSPVLSPLPVTLGQPAISICRSSQSLLYINGVNYLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKI SRVEAEDVGWYCMQALQTPPTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	355

Figure 38S
CPA.7.024

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGSSVKVCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDAYYYDSSGGYNPDADFIDWGQGTMTVTVSS	356
vhCDR1	<u>GGTFSSYA</u>	357
vhCDR2	<u>IIPIFGTA</u>	358
vhCDR3	<u>ARDAYYYDSSGGYNPDADFID</u>	359
Full length HC	EVQLVQSGAEVKKPGSSVKVCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDAYYYDSSGGYNPDADFIDWGQGTMTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGGSFFLYSKLTVDKSRWQQGNVFCFSCVMHEALHNHYTQKSLSLSPGK	360
Variable light (vl) domain	DWVMTQSPVLSPLPTPGEPASISCRSSQSLHHSNGYNLDWYVLPKPGQSPQLLIYLGSSRASGVDPDRFSGSVSGTDFTLKISRVEAEDVGVYYCMQGLQTPRTFGRGTKLEIKR	361
vlCDR1	<u>QSLHHSNGYNY</u>	362
vlCDR2	<u>LGS</u>	363
vlCDR3	<u>MQGLQTPRT</u>	364
Full length light chain	DWVMTQSPVLSPLPTPGEPASISCRSSQSLHHSNGYNLDWYVLPKPGQSPQLLIYLGSSRASGVDPDRFSGSVSGTDFTLKISRVEAEDVGVYYCMQGLQTPRTFGRGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	365

Figure 38T

CPA.7.033

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSSAISWVRQAPGQGEFWMGGIIPIYGITDYAQKFQGRVTITDESTSTAYMELSSLTSED TA VYVCARD DTARRVRGV PPYY YAMD VWGQGT TV TVSS	366
vhCDR1	<u>GGTFSSSA</u>	367
vhCDR2	<u>IIPIYGIT</u>	368
vhCDR3	<u>ARDDTARRVRGVPPYYYAMDV</u>	369
Full length HC	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSSAISWVRQAPGQGEFWMGGIIPIYGITDYAQKFQGRVTITDESTSTAYMELSSLTSED TA VYVCARD DTARRVRGV PPYY YAMD VWGQGT TV TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV PSSSLGTQTYICNVN HKPSN TKVDKK VEPKSCDK TH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKG FPSDIAVEWESNGQPENNYK TT PPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCVMHEALHNHYTQKSLS SPGK	370
Variable light (vl) domain	ETTLTQSPAFMSATPGDEVNISKASQDIDDDVSWYQQKPGGAPIFLIQEASTLVPGIPPRFSGSGFGTDFTLTIKNMES EDAA YFCLQH HDNLPLT FGGGTKVDIKR	371
vlCDR1	<u>QDIDDD</u>	372
vlCDR2	<u>EAS</u>	373
vlCDR3	<u>LQHDNLPLT</u>	374
Full length light chain	ETTLTQSPAFMSATPGDEVNISKASQDIDDDVSWYQQKPGGAPIFLIQEASTLVPGIPPRFSGSGFGTDFTLTIKNMES EDAA YFCLQH HDNLPLT FGGGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCILNNFYFPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	375

Figure 38U

CPA.7.034

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHVWRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATEDPGPVAGPYYYGMDVWGGGTTTVTVSS	376
vhCDR1	<u>GYTLTELS</u>	377
vhCDR2	<u>FDPEDGET</u>	378
vhCDR3	<u>ATEDPGPVAGPYYYGMDV</u>	379
Full length HC	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHVWRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATEDPGPVAGPYYYGMDVWGGGTTTVTVSSASTKGPSVFP LAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTH TCPGPCAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPVLDSDGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	380
Variable light (vl) domain	DVVMTQSPVLVPTPGEPAISCRSSQSLIYINGYHYLDWYVQRPQGSPQLLIFLGSTRASGVPDFRFGSGSGTDFLTLEIS KVEAEDVGIFYFCMQALQTPPTFGGGTKVEIKR	381
vlCDR1	<u>QSLIYINGYHY</u>	382
vlCDR2	<u>LGS</u>	383
vlCDR3	<u>MQALQTPPT</u>	384
Full length light chain	DVVMTQSPVLVPTPGEPAISCRSSQSLIYINGYHYLDWYVQRPQGSPQLLIFLGSTRASGVPDFRFGSGSGTDFLTLEIS KVEAEDVGIFYFCMQALQTPPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKSTYSLSLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	385

Figure 38V

CPA.7.036

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSED AVVYCARD DTARRVRGVPIYYYAMDVWGQGTITVTVSS	386
vhCDR1	<u>GGTFSSA</u>	387
vhCDR2	<u>IIPYGIT</u>	388
vhCDR3	<u>ARDDTARRVRGVPIYYYAMDV</u>	389
Full length HC	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSED AVVYCARD DTARRVRGVPIYYYAMDVWGQGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLT VLHQDWLNGKEY CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK	390
Variable light (vl) domain	DIVMTQTPLSLPVTPGEPASISCRPSQSLDSDDDGNTYLDWY LQKPGQSPQLLIH TL SYRASGV PD RFSGSGSGTDFTLKI SRVEAEDVGVVY CMQRLQFPLT FGGGTKVEIKR	391
vlCDR1	<u>QSLDSDDDGNTY</u>	392
vlCDR2	<u>TL</u>	393
vlCDR3	<u>MQRLQFPLT</u>	394
Full length light chain	DIVMTQTPLSLPVTPGEPASISCRPSQSLDSDDDGNTYLDWY LQKPGQSPQLLIH TL SYRASGV PD RFSGSGSGTDFTLKI SRVEAEDVGVVY CMQRLQFPLT FGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFY P REAKVQWKVDNA LQSGNSQESVTEQDSKDS TYSL ST TL SKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	395

Figure 38W

CPA.7.040

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHWVRQAPGKLEWMGGFDPEGETIYAKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGVPAAGVYYYYYMDVVGKGTITVSS	396
vhCDR1	<u>GYTLTELS</u>	397
vhCDR2	<u>FDPEDGEI</u>	398
vhCDR3	<u>ATGVPAAGVYYYYYMDV</u>	399
Full length HC	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHWVRQAPGKLEWMGGFDPEGETIYAKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGVPAAGVYYYYYMDVVGKGTITVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVWTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGSFELYSKLTVDKSRWQQGNVFCSMHEALHNYHTQKSLSLSPGK	400
Variable light (vl) domain	DVVMTQSPSLPVTGPGEASISCRSSQSLLYRNGYNLDWYLQKPGQSPQLLIYWGSYRASGVDPDRFSGSGSGTDFTLK ISRVEAEDGVVYCMQAVQNPPPTFGQGTKVDIKR	401
viCDR1	<u>QSLLYRNGYNY</u>	402
viCDR2	<u>WGS</u>	403
viCDR3	<u>MQAVQNPPPT</u>	404
Full length light chain	DVVMTQSPSLPVTGPGEASISCRSSQSLLYRNGYNLDWYLQKPGQSPQLLIYWGSYRASGVDPDRFSGSGSGTDFTLK ISRVEAEDGVVYCMQAVQNPPPTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCILLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSSTLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	405

Figure 38X

CPA.7.046

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITDESTST AYMELSSLTSEDYAVYVCARDDTARRVRGVPIYYYAMDVWGQGTITVTVSS	406
vhCDR1	<u>GGTFSSSA</u>	407
vhCDR2	<u>IPIYGIT</u>	408
vhCDR3	<u>ARDDTARRVRGVPIYYYAMDV</u>	409
Full length HC	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITDESTST AYMELSSLTSEDYAVYVCARDDTARRVRGVPIYYYAMDVWGQGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPVLDSDGSFELYSLKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK	410
Variable light (vl) domain	DVVMTQSPAFLSVTPGERVTLSCKASQTMNNYLAWYQQKPGQAPRLIYDASTRATDTPPRFSGSGSGTEFTLTISV QSEDFALYYCCQQYGDWLPIITFGQGTRLEIKR	411
vlCDR1	<u>QTMNNY</u>	412
vlCDR2	<u>DAS</u>	413
vlCDR3	<u>QQYGDWLPIIT</u>	414
Full length light chain	DVVMTQSPAFLSVTPGERVTLSCKASQTMNNYLAWYQQKPGQAPRLIYDASTRATDTPPRFSGSGSGTEFTLTISV QSEDFALYYCCQQYGDWLPIITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYFPREAKVQWKVDNALQS GNSQESVTEQDSKDYSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	415

Figure 38Y

CPA.7.047

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHVWRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVVYCATAFPEATISYYYMDVWGKGTITVVS	416
vhCDR1	<u>GYTLTELS</u>	417
vhCDR2	<u>FDPEDGEI</u>	418
vhCDR3	<u>ATAFPEATISYYYMDV</u>	419
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHVWRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVVYCATAFPEATISYYYMDVWGKGTITVVSASTKGPSVFP LAPSSKSTSGGTAALGCLVKD YFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSWTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRVVSVLT VLIHQDWLNGKEYCKVSNKALPAPIEKTSKAGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK	420
Variable light (vl) domain	DVVMTQSPPLSPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYWGSYRASGVDPDRFSGSGGTFTLK ISRVEAEDVGVVYCMQAVQNPPPTFGQGKTKVEIKR	421
vlCDR1	<u>QSLLYRNGYNY</u>	422
vlCDR2	<u>WGS</u>	423
vlCDR3	<u>MQAVQNPPPT</u>	424
Full length light chain	DVVMTQSPPLSPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYWGSYRASGVDPDRFSGSGGTFTLK ISRVEAEDVGVVYCMQAVQNPPPTFGQGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	425

Figure 38Z

CPA.7.049

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QMQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFEWMGGIPIYGITDYAQKFQGRVTITDESTST AYMELSSLTSED TA VVYCARDDTARRVRGVPPYYYYAMDVWGQGT TV TVSS	426
vhCDR1	<u>GGTFSSA</u>	427
vhCDR2	<u>IPIYGIT</u>	428
vhCDR3	<u>ARDDTARRVRGVPPYYYYAMDV</u>	429
Full length HC	QMQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFEWMGGIPIYGITDYAQKFQGRVTITDESTST AYMELSSLTSED TA VVYCARDDTARRVRGVPPYYYYAMDVWGQGT TV TVSSASTKGPSVFLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRV VSVLT TV LHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK	430
Variable light (vl) domain	DIVMTQTPLSLPVTPGEPASMSCRSSRSLDSDGNT HL DWY L QKPGQSPQLLIQSLSYRASGV PD RFSGSGSGTDFTL EISRVEAEDVGIYYCMQRKEFPLT FG GGTKVEIKR	431
vlCDR1	<u>RSLLDSDDGNTH</u>	432
vlCDR2	<u>SLS</u>	433
vlCDR3	<u>MQRKEFPLT</u>	434
Full length light chain	DIVMTQTPLSLPVTPGEPASMSCRSSRSLDSDGNT HL DWY L QKPGQSPQLLIQSLSYRASGV PD RFSGSGSGTDFTL EISRVEAEDVGIYYCMQRKEFPLT FG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV V CLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	435

Figure 38AA

CPA.7.050

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGSSVKVCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYVCARGPWYDSSGYSSAYYMDVWGQGTITVTVSS	436
vhCDR1	<u>GGTFSSYA</u>	437
vhCDR2	<u>IIPIFGTA</u>	438
vhCDR3	<u>ARGPWYDSSGYSSAYYMDV</u>	439
Full length HC	EVQLVQSGAEVKKPGSSVKVCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYVCARGPWYDSSGYSSAYYMDVWGQGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	440
Variable light (vl) domain	DVVMTQSPISLPVTPGEPASISCRSSQSLHSDGYNLDWYVLPKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALHTPGVTFFGGGTKVEIKR	441
vICDR1	<u>QSLHSDGYN</u>	442
vICDR2	<u>LGS</u>	443
vICDR3	<u>MQALHTPGVT</u>	444
Full length light chain	DVVMTQSPISLPVTPGEPASISCRSSQSLHSDGYNLDWYVLPKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALHTPGVTFFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVWCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSLPTKSFNRGEC	445

Figure 39A
CPA.7.028

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QLQLQESGPGGLVKPSETLSLTCTVTGGSSSSYYWAWIRQPPGKGLEWIGGIYSGSTYYNVSLERSVTISQDTSKNQFS LKLTSVTAADTAIVYVCARGAWELRLGDWFDPPWGQGTLLTVSS	446
vhCDR1	GGSSSSYY	447
vhCDR2	IYSGST	448
vhCDR3	ARGAWELRLGDWFDPP	449
Full length HC	QLQLQESGPGGLVKPSETLSLTCTVTGGSSSSYYWAWIRQPPGKGLEWIGGIYSGSTYYNVSLERSVTISQDTSKNQFS LKLTSVTAADTAIVYVCARGAWELRLGDWFDPPWGQGTLLTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKHTCTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYCKVKSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK	450
Variable light (vl) domain	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDIQWYQQLPQTAPKLLIYGYSNRPSGVDPDRFSGSKSGTSASLAITGL QAEDEADYYCQSYDSSLSVYVWFGGGTQLTVLGQPKAA	451
vlCDR1	SSNIGAGYD	452
vlCDR2	GYS	453
vlCDR3	QSYDSSLSVYVW	454
Full length light chain	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDIQWYQQLPQTAPKLLIYGYSNRPSGVDPDRFSGSKSGTSASLAITGL QAEDEADYYCQSYDSSLSVYVWFGGGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTTPSKQSNKIKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	455

Figure 39B
CPA.7.030

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGGGVVQPGGSLRLSCAASRFTFEDYAMHWVRQPPGKGLVWVSGISWKSGGINYADSVKGRFTISRDNAAQ NSLYLQMNSLRAEDTALYYCVKDPTLVATDRAFNWGGQTMVTVSS	456
vhCDR1	RFTFEDYA	457
vhCDR2	ISWKSGGI	458
vhCDR3	VKDPTLVATDRAFN	459
Full length HC	QVQLQESGGGVVQPGGSLRLSCAASRFTFEDYAMHWVRQPPGKGLVWVSGISWKSGGINYADSVKGRFTISRDNAAQ NSLYLQMNSLRAEDTALYYCVKDPTLVATDRAFNWGGQTMVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDY FPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHHKPSNTKYVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVWVSIVTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSPGK	460
Variable light (vl) domain	DVVMTQSPVLPVTPGEPASISCRSSQSLHSGNYNYLDWYVLPKQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKI SRVEAEDVGVYVCMQYVLPDTPDFTFGQGTKEIKRAAPS	461
vlCDR1	QSLHSGNYNY	462
vlCDR2	LGS	463
vlCDR3	MQYVLPDTPD	464
Full length light chain	DVVMTQSPVLPVTPGEPASISCRSSQSLHSGNYNYLDWYVLPKQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKI SRVEAEDVGVYVCMQYVLPDTPDFTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	465

Figure 39C
CPA.7.041

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFEWMGGIPIYGITDYAQKFQGRVTITTDESTST AYMELSLTSEDYAVYCARDDTARRVRGVPYVYYAMIDVWGQGTITVTVSS	466
vhCDR1	GGTFSSA	467
vhCDR2	IPIYGIT	468
vhCDR3	ARDDTARRVRGVPYVYYAMDV	469
Full length HC	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFEWMGGIPIYGITDYAQKFQGRVTITTDESTST AYMELSLTSEDYAVYCARDDTARRVRGVPYVYYAMIDVWGQGTITVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGC LVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPEAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLIHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFVSMHEALHNHYTQKSLSLSPGK	470
Variable light (vl) domain	EIVLTQSPDFQSVTPKEKVTITCRASQNISSSLHWYQQKPGQSPKLLINYSQSFSGVPSRFSGSGTDFTLTIDSLEPE DAATYFCHQSSSLPLTFGGGKVEIRRTVAAPS	471
viCDR1	QNIDSS	472
viCDR2	YAS	473
viCDR3	HQSSSLPLT	474
Full length light chain	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDIQWYQQLPGTAPKLLIYGYSNRPSGVPDRFSGSKSGTSASIAITGL QAEDEADYYCQSYDSSLVYVVFGGGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVVAWKADSS PVKAGVETITPSKQSNKNKYAASSYLSTLPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	475

Figure 39D
CPA.7.016

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGSSVKVCKTSGGTFSSAISWVRQAPGQGFEWMGGIPIYGITDYAQKFQGRVTITTDESTSTAYMELSSLTSEDITAVYCARDDTARRVRGVPYPPYYAMDVWGQGTITVTVSS	476
vhCDR1	GGTFSSA	477
vhCDR2	IIPYGIT	478
vhCDR3	ARDDTARRVRGVPYPPYYAMDV	479
Full length HC	EVQLVQSGAEVKKPGSSVKVCKTSGGTFSSAISWVRQAPGQGFEWMGGIPIYGITDYAQKFQGRVTITTDESTSTAYMELSSLTSEDITAVYCARDDTARRVRGVPYPPYYAMDVWGQGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKHTCPPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	480
Variable light (vl) domain	EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRRATGIPARFSGSGGTDFLTITSLQSEDFAVYYCCQYDDWPQTGFGQGRLEIKRTVAAPS	481
vlCDR1	QSVSSY	482
vlCDR2	DAS	483
vlCDR3	QQYDDWPQT	484
Full length light chain	EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRRATGIPARFSGSGGTDFLTITSLQSEDFAVYYCCQYDDWPQTGFGQGRLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	485

Figure 39E
CPA.7.020

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QMLVQSGAEVKKPGSSVKVSCKASGGTFSSAISWVRQAPGQGFEWMGGIPIYGITDYAQKFQGRVTITDES TSTAYMELSSLTSEDYAVYCARDDTARRVRGVPYVYYAMDVWGGGTTTVSS	486
vhCDR1	GGTFSSA	487
vhCDR2	IPIYGIT	488
vhCDR3	ARDDTARRVRGVPYVYYAMDV	489
Full length HC	QMLVQSGAEVKKPGSSVKVSCKASGGTFSSAISWVRQAPGQGFEWMGGIPIYGITDYAQKFQGRVTITDES TSTAYMELSSLTSEDYAVYCARDDTARRVRGVPYVYYAMDVWGGGTTTVSSASTKGPSVFLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTLC LVKGFYPDSIAVEWESNGQPENNYKTTTPVLDSDGSEFLYSLKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKSL SLSPGK	490
Variable light (vl) domain	EIVMTQSPATLSLTGERATLFCRTSQNVYGEVAWYQQKPGQAPRLIYDTERAAGIPAKFSGSGSGTDFTLTISR VEPEDFAVYCCQQRRDWPIFGGQGRLEIKRTVAAPS	491
vlCDR1	QNVYGE	492
vlCDR2	DTF	493
vlCDR3	QQRRDWPIIT	494
Full length light chain	EIVMTQSPATLSLTGERATLFCRTSQNVYGEVAWYQQKPGQAPRLIYDTERAAGIPAKFSGSGSGTDFTLTISR VEPEDFAVYCCQQRRDWPIFGGQGRLEIKRTVAAPSVEPDSDEQLKSGTASVCLLNFPYFPAKQVQWVNDN ALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	495

Figure 39F
CPA.7.038

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFQEWMGIIPIYGITDYAQKFQGRVTITIDESTST AYMELSSLTSEDYAVVYCARDTARRVRGVPPYYVYAMDVWGQGTITVTVSS	496
vhCDR1	GGTFSSA	497
vhCDR2	IIPYGIT	498
vhCDR3	ARDDTARRVRGVPPYYVYAMDV	499
Full length HC	QVQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFQEWMGIIPIYGITDYAQKFQGRVTITIDESTST AYMELSSLTSEDYAVVYCARDTARRVRGVPPYYVYAMDVWGQGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRV VSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPYSDIAVEW ESNGQPENNYKTTTPPVLDSDGSEFLYSLKLTVDKSRWQQGNVFSCVMEALHNHYTQKSLSLSPGK	500
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCQASRDIDSLSWYQQKPGKAPKLLIFDASNLKTGVSSRFSGSGGTDFTFITISLQPE DIATYYCHQYDNLPLTFGGGTKEIKRTVAAPS	501
vlCDR1	RDIDS	502
vlCDR2	DAS	503
vlCDR3	HQYDNLPLT	504
Full length light chain	DIQMTQSPSSLSASVGDRVTITCQASRDIDSLSWYQQKPGKAPKLLIFDASNLKTGVSSRFSGSGGTDFTFITISLQPE DIATYYCHQYDNLPLTFGGGTKEIKRTVAAPSVFIPPSDEQLKSGTASWCLLNINFPYREAKVQWKVDNALQSGNSQ ESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	505

Figure 39G
CPA.7.044

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QMQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFQGRVTITTTDESTST AYMELSSLTSEDYAVYCARDDTARRVRGVPIYYYAMDVWGQGTITVTVSS	506
vhCDR1	GGTFSSA	507
vhCDR2	IIPYGIT	508
vhCDR3	ARDDTARRVRGVPIYYYAMDV	509
Full length HC	QMQLVQSGAEVKKPGSSVKVCKASGGTFSSAISWVRQAPGQGFWMGGIPIYGITDYAQKFQGRVTITTTDESTST AYMELSSLTSEDYAVYCARDDTARRVRGVPIYYYAMDVWGQGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKFNWVYDGVGVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPVLDSDGSFELYSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	510
Variable light (vl) domain	EIVMTQSPATLSLSPGERATLSCRASESVTTFWAWYQQKPKGQAPRLITDASNRAATGIPGRFSGSGSGTDFTLTISLEPE DFAVYCHQHTNWPLTFGGGTGLEIKRTVAAPS	511
vlCDR1	ESVTFE	512
vlCDR2	DAS	513
vlCDR3	HQHTNWPLT	514
Full length light chain	EIVMTQSPATLSLSPGERATLSCRASESVTTFWAWYQQKPKGQAPRLITDASNRAATGIPGRFSGSGSGTDFTLTISLEPE DFAVYCHQHTNWPLTFGGGTGLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	515

Figure 39H
CPA.7.045

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSED TAVYCATVGYCSGGSCYISYYGMDVWVGQGT TVVSS	516
vhCDR1	GYTLTELS	517
vhCDR2	FPEDGET	518
vhCDR3	ATEVGYCSGGSCYISYYGMDV	519
Full length HC	EVQLVQSGAEVKKPGASVKVCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSED TAVYCATVGYCSGGSCYISYYGMDVWVGQGT TVVSSASTKGPSVFP LAPSSKSTSGGTAAL GCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPETVTCVAVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYR VWSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK	520
Variable light (vl) domain	DWVMTQSPVLPVTPGEPASISCRSSQSLLYRNHNFLDWVYVQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKI SRVEAEDGVVYCMQALQTPPTFGQGT KLEIKRTVAAPS	521
vlCDR1	QSLLYRNHNF	522
vlCDR2	LGS	523
vlCDR3	MQALQTPPT	524
Full length light chain	DWVMTQSPVLPVTPGEPASISCRSSQSLLYRNHNFLDWVYVQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKI SRVEAEDGVVYCMQALQTPPTFGQGT KLEIKRTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSSTYSLSLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	525

Figure 40A

CDRs

Name	Hcdr1	SEQ ID NO:	Hcdr2	SEQ ID NO:	Hcdr3	SEQ ID NO:	Lcdr1	SEQ ID NO:	Lcdr2	SEQ ID NO:	Lcdr3	SEQ ID NO:
CPA.7.001	GGTFSSYA	526	IPIFGTA	527	AREEVSSPYGMDV	528	TGAVTSGHY	529	DTG	530	LLSYSGASWV	531
CPA.7.002	GGTFSSA	532	IPIYGIT	533	ARDDTARRVRGVPYYYAMDV	534	QGIGNY	535	SAS	536	QQLKDYPT	537
CPA.7.003	GFSLSHFS	538	FDPEEGT	539	ATGIWYSSGWPPVDY	540	QSLDSSGNY	541	LGS	542	MQALQTPIT	543
CPA.7.004	GTYLTLS	544	FPEDGET	545	ATVSRVRGVINYYYMDV	546	QSLYRNGNYY	547	LGS	548	MQALQTPPT	549
CPA.7.005	GGTFSSA	550	IPIYGIT	551	ARDDTARRVRGVPYYYAMDV	552	QSVDS	553	DAS	554	QYKDWPF	555
CPA.7.006	GGTFGYA	556	ITPISATI	557	ARGFEYSDGLLDD	558	QSLFYSDDGNTY	559	RLS	560	MQHMEFPLT	561
CPA.7.007	GGSISSSY	562	IYSGST	563	ARGAWELRLGDWFDP	564	SSNIGAGYD	565	GNN	566	QSYDSSLSIYV	567
CPA.7.008	SGSISSTNW	568	IYHSGST	569	ARVGPAAIY	570	SNNVGYEG	571	RNN	572	SAWDSSSLNAV	573
CPA.7.009	GTYLTLS	574	FPEDGET	575	ATAKPGIAVAGQNYYYMDV	576	QSLYRNGNYY	577	LGS	578	MQALQTPPT	579
CPA.7.010	GFTFSSA	580	ISYDGSNK	581	ASSPIGYSYGYWGGMDV	582	SGIDVRTNK	583	FQSDSDK	584	LIWHTSGWV	585
CPA.7.011	GTYLTLS	586	FPEDGET	587	ATGPAAGVGYYYMDV	588	QSLYRNGNYY	589	LGS	590	MQALQTPPT	591
CPA.7.012	GFTFSSA	592	ISYDGSNK	593	ARDVMVYCSSTCYFYGMDV	594	QDIRDY	595	DAS	596	QQFENLPIT	597
CPA.7.013	GTYLTLS	598	FPEDGET	599	ATGGYSSGFNYYYMDV	600	QSLYRNGNYY	601	LGS	602	MQALQTPPT	603

Figure 40B

Name	Hcdr1	SEQ ID NO:	Hcdr2	SEQ ID NO:	Hcdr3	SEQ ID NO:	Lcdr1	SEQ ID NO:	Lcdr2	SEQ ID NO:	Lcdr3	SEQ ID NO:
CPA.7.014	GYTLTELS	604	FDPEDGET	605	ATGVTTYYYYGMDV	606	QSLLYSNGNMF	607	LGS	608	MQALQTPPT	609
CPA.7.015	GFTFSSYG	610	IRYDGSNK	611	ARDLDFWWDGMDV	612	QSVSSMY	613	GAS	614	QQYVSSPMYT	615
CPA.7.016	GGTFSSSA	616	IPIYGIT	617	ARDDTARRVRGVPPYYYYAMDV	618	QSVSSY	619	DAS	620	QQYDDWVPQT	621
CPA.7.017	GGTFNNYG	622	IPLFGTT	623	ARDRMAADGMAVFDY	624	SSNIGRHF	625	KND	626	SSWDAALNGVV	627
CPA.7.018	GYTLTELS	628	FDPEDGET	629	ATEVPMVRGARRYYYMDV	630	QTLTYINENNY	631	LGS	632	MQGLQTPPT	633
CPA.7.019	GGSISSNNY	634	IYSGST	635	ARGAWELSLGDWFDP	636	SSNIGAGYD	637	GNN	638	QSYDSSLSVVVV	639
CPA.7.020	GGTFSSSA	640	IPIYGIT	641	ARDDTARRVRGVPPYYYYAMDV	642	QNVYGE	643	DTF	644	QQRDDWPIT	645
CPA.7.021	GFTFGTSS	646	ISFDGTEI	647	AKGSGNIIFYSGMDV	648	QSIGSW	649	ETS	650	QQYVSYPLT	651
CPA.7.022	GYTLTELS	652	FDPEDGET	653	ATGVPAAGVYYYYYYMDV	654	QSLLYSNGYNY	655	LGS	656	MQALQSPVT	657
CPA.7.023	GYTLTELS	658	FDPEDGET	659	ATDSRDGPAARGGGYYYYMDV	660	QSLLYINGYNY	661	LGS	662	MQALQTPPT	663
CPA.7.024	GGTFSSYA	664	IPIFGTA	665	ARDAYYYDSSGGYNNPDADF	666	QSLHSHNGYNY	667	LGS	668	MQGLQTPRT	669
CPA.7.025	GFSLTSGGMS	670	IDWNDDK	671	ARIRGMTWGFDS	672	QSVSSSY	673	GAS	674	QQYGTTPFA	675
CPA.7.026	GYTFTAYY	676	INPNSGGT	677	ARDGAFFYGSSENNYAGWFDP	678	QSLLSGNGYNY	679	LGS	680	MQALKSPLT	681
CPA.7.027	GYTFTNNY	682	INPSGGIT	683	ARAGLGYNWNYPAGMDV	684	SSDVGGYNY	685	EVS	686	SSVAGSNNLV	687
CPA.7.028	GGSISSSSYY	688	IYSGST	689	ARGAWELRLGDWFDP	690	SSNIGAGYD	691	GYS	692	QSYDSSLSVVVV	693

Figure 40C

Name	Hcdr1	SEQ ID NO:	Hcdr2	SEQ ID NO:	Hcdr3	SEQ ID NO:	Lcdr1	SEQ ID NO:	Lcdr2	SEQ ID NO:	Lcdr3	SEQ ID NO:
CPA.7.029	GFTDDYA	694	ISWNSGI	695	AKDVNRILVAGMVDY	696	QSLHSHNGYNY	697	LGS	698	MQGLQTPT	699
CPA.7.030	RFTFEDYA	700	ISWKSGL	701	VKDPTLVATDRAFNI	702	QSLHSHNGYNY	703	LGS	704	MQYLQTPDT	705
CPA.7.031	GGTFSSA	706	IPIYGIT	707	ARDDTARRVRGVPPYYYYYAMDV	708	QSLDSDDGNIH	709	TLS	710	MQRKEFPLT	711
CPA.7.032	GFTFSSYG	712	ISYDGSNK	713	AKEDRLRFLFWFYGMVDY	714	HDITYY	715	DAS	716	QQYDNHPPEVT	717
CPA.7.033	GGTFSSA	718	IPIYGIT	719	ARDDTARRVRGVPPYYYYYAMDV	720	QDIDDD	721	EAS	722	LQHDNLPLT	723
CPA.7.034	GTYLTLS	724	FDPEDGET	725	ATEDPGPVAGPYYYYYGMVDY	726	QSLLYINGYHY	727	LGS	728	MQALQTPPT	729
CPA.7.035	GYMFTNYP	730	INAGTGNT	731	AREGMFYGLSYKGGWFDP	732	QSLHSHNGYNY	733	LAS	734	MQALQTPLT	735
CPA.7.036	GGTFSSA	736	IPIYGIT	737	ARDDTARRVRGVPPYYYYYAMDV	738	QSLDSDDGNTY	739	TLS	740	MQRLQFPLT	741
CPA.7.037	TYTFTTY	742	IYPSGGNT	743	VRDQNYYSAMDY	744	QDIRNY	745	DAS	746	QQFENLPIT	747
CPA.7.038	GGTFSSA	748	IPIYGIT	749	ARDDTARRVRGVPPYYYYYAMDV	750	RDSDS	751	DAS	752	HQYDNLPIT	753
CPA.7.039	GFNFRGYA	754	ISGSGGTT	755	AQSYAQIGYGGHIDH	756	SGIDVATYM	757	YKSDSK	758	LIWHGSHVY	759
CPA.7.040	GTYLTLS	760	FDPEDGET	761	ATGVPAAGVYYYYYMDV	762	QSLLYRNGYNY	763	WGS	764	MQAVQNPPT	765
CPA.7.041	GGTFSSA	766	IPIYGIT	767	ARDDTARRVRGVPPYYYYYAMDV	768	QNIDSS	769	YAS	770	HQSSSLPLT	771
CPA.7.042	GGTFSSA	772	IPIYGIT	773	ARDDTARRVRGVPPYYYYYAMDV	774	QSVVNNY	775	DAS	776	QQYNSWPPYT	777
CPA.7.043	GGTFSSA	778	IPIFGTA	779	ARDAYYDSSGYNPDADF	780	QSLLYSNGYNY	781	LGS	782	MQARQTPYT	783

Figure 40D

Name	Hcdr1	SEQ ID			SEQ ID			SEQ ID			SEQ ID			SEQ ID			SEQ ID		
		NO:	Hcdr2	NO:	Hcdr3	NO:	Lcdr1	NO:	Lcdr2	NO:	Lcdr3	NO:	Lcdr4	NO:	Lcdr5	NO:	Lcdr6	NO:	Lcdr7
CPA.7.044	GGTFSSA	784	IPIYGIT	785	ARDDTARRVRGVPPYYYAMDV	786	ESVTF	787	DAS	788	HQHTNWPLT	789							
CPA.7.045	GVTLELS	790	FDPEDGET	791	ATEVGVCSCGYISYYGMDV	792	QSLLYRNGHNF	793	LGS	794	MQALQTPPT	795							
CPA.7.046	GGTFSSA	796	IPIYGIT	797	ARDDTARRVRGVPPYYYAMDV	798	QTMNNY	799	DAS	800	QQYGDWLPIT	801							
CPA.7.047	GVTLELS	802	FDPEDGET	803	ATAFPEATISYYYMDV	804	QSLLYRNGYNY	805	WGS	806	MQAVQNPPT	807							
CPA.7.049	GGTFSSA	808	IPIYGIT	809	ARDDTARRVRGVPPYYYAMDV	810	RSLLDSDDGNTN	811	SLS	812	MQRKEFPLT	813							
CPA.7.050	GGTFSSA	814	IPIFGTA	815	ARGPWYDSSGYSYAYYMDV	816	QSLHSDGYNY	817	LGS	818	MQALHTPGVT	819							

Figure 41A

CHA.7.502

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	DVQLVESGGDLVQPGGSRKLSCTASGFTFSNFGMHWVRQAPEKGLEWVAYISSGSSTIYYADTVKGRFTISRDNPEPTLFLQMTSLRSEDAMYYCTRLDYITNSYSMDHWGQGTSTVTVSS	820
vhCDR1	GFTFSNFG	821
vhCDR2	ISSGSSTI	822
vhCDR3	TRLDYITNSYSMDH	823
Variable light (vl) domain	QIVLTQSPALMSASPGEKVTLTCSASSSLPYIWYQQKPGSSPKPWIYLTSLNLSGVPARFSGSRSGTSYSLTISSVEAEDAATYYCQQWSSNPFTFGSGTKLEIK	824
vlCDR1	SSLPY	825
vlCDR2	LTS	826
vlCDR3	QQWSSNPFT	827

Figure 41B

CHA.7.503

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGAELAKPGASVKMSCKASGYTFTSNWMHWVKQRPGQGLEWIGYINP SNGYTECNQKFRDKATLSADKSSSTAYMQLNSLTADSAVYYCALMISAWLPYWG QGTLVTVSA	828
vhCDR1	GYTFTSNW	829
vhCDR2	INPSNGYT	830
vhCDR3	ALMISAWLPY	831
Variable light (vl) domain	DIVLTQSPASLAISLGQRATISCRASQSVSASSYSYVHWYQQKPGQPPKLLIKYASSLE SGVPARFSGSGSGTDFTLNIHPVEEEDTATYYCLHTWEIPYTFGGGTKLEIK	832
vlCDR1	QSVSASSYSY	833
vlCDR2	YAS	834
vlCDR3	LHTWEIPYT	835

Figure 41C

CHA.7.506

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGAELTRPGASVNLSCKASGYTFTSYWMQWVKQRPGQGLEWIGAIYPG DGDTRFNQKFKGKATLTADESSSTAYMQLSSLASEDSAVYYCATYYRYDDYWGQGT TLTVSS	836
vhCDR1	GYTFTSYW	837
vhCDR2	IYPGDGDT	838
vhCDR3	ATYYRYDDY	839
Variable light (vl) domain	QIVLTQSPAIMASASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASG VPTRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPYTFGGGTKLEIK	840
vlCDR1	SSVSY	841
vlCDR2	DTS	842
vlCDR3	QQWSSNPYT	843

Figure 41D

CHA.7.508

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPDLVKPGASMKISCKASGYTFIDYNIHWVKQSQGKSLDWIGYIYPYNG GTGYNQKFKNKATLTVDSSSSTAYMEVRSLTFEDSAVYFCAREADYYGNRGQFDYW GQGTLVTVSA	844
vhCDR1	GYTFIDYN	845
vhCDR2	IYPYNGGT	846
vhCDR3	AREADYYGNRGQFDY	847
Variable light (vl) domain	DIQMTQSPASLSVSVGETVTITCRASENIFSNLAWYQQKQKSPQLLVYGEANLAD GVPSRFSGSGSGTQYSLKINSLSQSEDFGNYYCQHFWGTPYTFGGGTLEIK	848
vlCDR1	ENIFSN	849
vlCDR2	GEA	850
vlCDR3	QHFWGTPYT	851

Figure 41E

CHA.7.510

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVTLKESGPGILQPSQTLSTCSFSGFSLNTSGTGVGWIRQPSGKGLEWLTHIWWN DNKFYNTFLKSRLTISKETSNNQVFLKIASVDTADAATYYCARMAYGNLWVFNWGQ GTLVAVST	852
vhCDR1	GFSLNTSGTG	853
vhCDR2	IWWNDNK	854
vhCDR3	ARMAYGNLWVFN	855
Variable light (vl) domain	DIVLTQSPASLAVSLGQRASISCRASRSVTISGYSYMYWYQQKPGQPPRLLFYLASNL ASGVPARFSGSGSGTDFTLNHPVEEEDAAIYYCQHSRELPTYFGGGTKLEIK	856
vlCDR1	RSVTISGYSY	857
vlCDR2	LAS	858
vlCDR3	QHSRELPTY	859

Figure 41F

CHA.7.512

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QIQLVQSGPELKPPRETVKISCKASGYTFTDYSMHWVKQAPGKGLKWMGWINTETGEPTYADDFKGRFAFSLEASASSAYLQINILKDEDTATYFCARSRGGYYEDYYALDYWGQGTSVTVSS	860
vhCDR1	GYTFTDYS	861
vhCDR2	INTETGEP	862
vhCDR3	ARSRGGYYEDYYALDY	863
Variable light (vl) domain	DIQMTQSPASLSASVGESVTITCRASGNIHYLLAWYQQKQKGKSPQLLVYNAKNLADGVPSRFSGSGSGTQFSLKINSIQPEDFGSYQCQHFWISPPTFGGGTKLEIK	864
vlCDR1	GNIHY	865
vlCDR2	NAK	866
vlCDR3	QHFWISPPT	867

Figure 41G

CHA.7.514

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLRQSGADLVKPGASVKLSCTASG FN IKDTYIDWVKQRPEQGLDWIGRIDPANG NTKYDPKFQGGKATIIITDTSSNTAYLQLSNLTSED AV YYC ARYGSYPYFDY WGRGTTL AVSS	868
vhCDR1	GFNIKDTY	869
vhCDR2	IDPANGNT	870
vhCDR3	ARYGSYPYFDY	871
Variable light (vl) domain	SIVMTQTPKFLLISAGDRVITITCKASQ SV RNDVAWYQQKPGQSPKLLMY YAS NRYT GVPDRFTGSGYGTDFTFTISTVQAEDLAVYFC QQDYSSPPT FGGGTKLEIK	872
vlCDR1	QSVRND	873
vlCDR2	YAS	874
vlCDR3	QQDYSSPPT	875

Figure 41H

CHA.7.516

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGPELVRPGVSVKISCKVSGYTFTDYV/MHWVKQSHAKSLEWIGIISPYSG <u>NTNYNQNFKGKATMTVDKSSSTAYMALARLTSEDSAIYYCAREGDLPMFAY</u> WGQG TLVTVSA	876
vhCDR1	GYTFTDYV	877
vhCDR2	ISPYSGNT	878
vhCDR3	AREGDLPMFAY	879
Variable light (vl) domain	QIVLTQSPTIMSASPGEKVTMTCSASSSVSYIYWYQQNPGSSPRLLIYD <u>TS</u> SILASGVPF RFGSGSGTSYSLTISRMEAEDAATYYC <u>QQWTSYPLT</u> FGSGTKLELK	880
vlCDR1	SSVSY	881
vlCDR2	DTS	882
vlCDR3	QQWTSYPLT	883

Figure 41I

CHA.7.518

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGASVKISCKASGYTFTDYNINWVKQSHGKSLEWIGYIYPYIGGS GYNQKF K SKATLSADNPSS T AYMELRSLTSEDSAVYYCAREDKTARNAMDYWGQG TPVTVSS	884
vhCDR1	GYTFTDYN	885
vhCDR2	IYPYIGGS	886
vhCDR3	AREDKTARNAMDY	887
Variable light (vl) domain	DIQMTQSPASLSVSVGETVTIICRVSENIYSNLA W YQQKQKGKSPQLLVYEATNLAEG VPSRFGSGSGTQYSLKINSLQSEDFGSYYCQHFWGTPYTFGGG T KLEIK	888
vlCDR1	ENIYSN	889
vlCDR2	EAT	890
vlCDR3	QHFWGTPYT	891

Figure 41J

CHA.7.520_1

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	DVQLQESGPGLVKPSQSLTCTVT <u>GYSITSDYA</u> WNWIRQFPGNKLEWMGYISYSG <u>STSYNPSLKS</u> RISITRDTSKNQFFLQLNSVTTEDTATYYC <u>ARHYRYPPYAMDY</u> WGQGTSVTVSS	892
vhCDR1	GYSITSDYA	893
vhCDR2	ISYSGST	894
vhCDR3	ARHYRYPPYAMDY	895
Variable light (vl) domain	DIVMTQSPSSLAMSVGQKVTMSCKSSQSLN <u>SSNQKNY</u> LAWYQQKPGQSPKLLVY <u>FAS</u> TRESGVPDRFIGSGSGTDFTLTITSVQAEDLADYFC <u>QQHYSTPFT</u> FGSGTKLEIK	896
vlCDR1	QSLN <u>SSNQKNY</u>	897
vlCDR2	FAS	898
vlCDR3	QQHYSTPFT	899

Figure 41K

CHA.7.520_2

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKQSGPGLVQPSSLSITCTVSGFSLTSFGVHWVRQSPGKGLEWLGV <u>IWSGGT</u> TVYDAAFISRLSISKDNSKSQVFFKMNSLQTNDTAIYYCARKRGNFYVMDYWGQGT SVTVSS	900
vhCDR1	GFSLTSG	901
vhCDR2	IWSGGT	902
vhCDR3	ARKRGNFYVMDY	903
Variable light (vl) domain	DIVMTQSPSSLAMSVGQKVTMSCKSSQSLNSSNQKNYLAWYQQKPGQSPKLLVY <u>FASTRESGVPDRFIGSGSGTDFTLTITSVQAEDLADYFCQQHYSTPFT</u> FGSGTKLEIK	904
vlCDR1	QSLNSSNQKNY	905
vlCDR2	FAS	906
vlCDR3	QQHYSTPFT	907

Figure 41L

CHA.7.522

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQPGSELVRPGTSVKLSCKASGYTFTSYWVHWVRQRHGQGLEWIGNVYPG SGSTNYDEKFKSKGTLTVDTSSTAYMHLSSLTSEDSAVYYCTRGVLRFLDYWGQG TTLTVSS	908
vhCDR1	GYTFTSYW	909
vhCDR2	VYPGSGST	910
vhCDR3	TRGVLRFLDY	911
Variable light (vl) domain	DIVMTQAAPSPVPTPGESVSISCRSSKSLLSNGNTYLYWFLQRPQGSPHLLIYRMS NLASGVDPDRFSGSGSGTAFTLRISRVEAEDVGVYYCMQHLEYPLTFGAGTKLELK	912
vlCDR1	KSLLSNGNTY	913
vlCDR2	RMS	914
vlCDR3	MQHLEYPLT	915

Figure 41M

CHA.7.524

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGPEVVRPGVSVKISCKGSGYKFPDYVMHWVKQSHAKSLEWIGIISIYSG <u>NTNYNQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCAREGDLPMFAYWGQG</u> TLVTVSA	916
vhCDR1	GYKFPDYV	917
vhCDR2	ISIYSGNT	918
vhCDR3	AREGDLPMFAY	919
Variable light (vl) domain	QIVLTQSPAIMASAPGEKVTMTCNASSSVSYMYWYQQKPISSPRLLIYDTSNLAGSV PVRFSGSGSGTSYSLTIGRMEAEDAATYYCQQWSSYPLTFGAGTKVEVK	920
vlCDR1	SSVSY	921
vlCDR2	DTS	922
vlCDR3	QQWSSYPLT	923

Figure 41N

CHA.7.526

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPGLVAPSQSL SITCTVSGFSLTAYNINWVRQPPGKGLEWLGMIWGDG NTDYN SPLKSRLTISKDNSKSQVFLKMDSLQTD TARYYCARDLKVRRDSPYTMDY WGQGTSVTVSS	924
vhCDR1	GFSLTAYN	925
vhCDR2	IWGDGNT	926
vhCDR3	ARDLKVRRDSPYTMDY	927
Variable light (vl) domain	NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIY WASNRESGVPDRFTGSGSGTDFTLTIS SVQAEDLAVYYCHQYLSSYTFGGGTKLEIK	928
vlCDR1	QSVLYSSNQKNY	929
vlCDR2	WAS	930
vlCDR3	HQYLSSYT	931

Figure 410

CHA.7.527

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	DVQLQESGPGLVKPSQSLTCTVT <u>GYSLTSDY</u> AWNWRQFPGNKLEWMGYITYSG <u>GTTYNPSLKS</u> RISITRDTSKNQFFLQLTSVTTEDTATYYC <u>ARRGSGTTVVDWYFDV</u> WGAGTTTVSS	932
vhCDR1	GYSLTSDYA	933
vhCDR2	ITYSGGT	934
vhCDR3	ARRGSGTTVVDWYFDV	935
Variable light (vl) domain	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSFNQKY Y LAWYQQKPGQSPKLLIYW <u>A</u> STRESGVPDRFTGSGSGTDFTPTISSVTAEDLAVYYC <u>QQFYTPYT</u> FGGGTKLEMK	936
vlCDR1	QSLLYSFNQKY	937
vlCDR2	WAS	938
vlCDR3	QQFYTPYT	939

Figure 41P

CHA.7.528

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQVQQSGPELVKPGASVKISCKASGYTFTKSNMHWVKQSHGKSLEWIGYIYPYNG GTGYNQNFKSKATLTVDISSSTAYMELRSLTLEDSAVYLCAREADYYGNRGQFDYW GQGT LVT VSA	940
vhCDR1	GYTFTKSN	941
vhCDR2	IYPYNGGT	942
vhCDR3	AREADYYGNRGQFDY	943
Variable light (vl) domain	DIQMTQSPASLSVSVGETVTITCRASDNIFSNLAWYHQKQGKSPHLLVYGATNLAD GVPSRFSGSGSGTQYSLKINSLQSEDFGDYYCQHFWGTPYTFGGGTKLEIK	944
vlCDR1	DNIFSN	945
vlCDR2	GAT	946
vlCDR3	QHFWGTPYT	947

Figure 41Q

CHA.7.530

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGAELMRPGTSVKVSCKASGYAFTNHLIEWIKQRPQGQLEWIGVINPGSDSTDYNEKFKDKATLTADKSSSTAYMQLSSLTSDDSAVYFCARSLYYNSWVFYWGQGTLLTVSA	948
vhCDR1	GYAFTNHL	949
vhCDR2	INPGSDST	950
vhCDR3	ARSLYYNSWVFY	951
Variable light (vl) domain	DIQMTQSPASLSASVGETVTITCRASENIYSYLAWYQQKRGKSPQLLVYNAKTLVEGVPSRFSGSGSGTQFSLKINSIQPEDFGSYQCQHHYGTPYTFGGGTKLEIK	952
vlCDR1	ENIYSY	953
vlCDR2	NAK	954
vlCDR3	QHHYGTPYT	955

Figure 41R

CHA.7.534

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGAELVKPGASVRLSCTAS <u>GFSIRDTY</u> IHWVKQRPEQGLDWIGKIDPANG <u>KSEYDPKFQGRATMTTDTSSNTAYLQLSSLTSEDTAVYYCTRYGYYPYFDV</u> WGAGTT VTVFS	956
vhCDR1	GFSIRDTY	957
vhCDR2	IDPANGKS	958
vhCDR3	TRYGYYPYFDV	959
Variable light (vl) domain	SIVMTQTPKFLVLSAGDRVAITCKASQSVRHDVWWYQQKPGQSPKLLIYYA <u>SSRYTG</u> VPDRFTGSGYGTDFTFTISTVQAEDLALYFCLQDFSSPWTFGGGTKLEIK	960
vlCDR1	QSVRHD	961
vlCDR2	YAS	962
vlCDR3	LQDFSSPWT	963

Figure 41S

CHA.7.535

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGASVKISCKTSGYTFTKNTMHWVRQSHGKSLEWIGGINPNSG GASFNQKFMGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARDGYDGDWFFDVWG AGTTVTVSS	964
vhCDR1	GYTFTKNT	965
vhCDR2	INPNSGGA	966
vhCDR3	ARDGYDGDWFFDV	967
Variable light (vl) domain	DIQMNQSPFSLASLGDTVTITCHASQNIYVWLSWYQQKPGNIPKLLIYKASDLHTG VPSRFGSGSGTDFTLNISSLQPEDIATYYCQQGQSYPRTFGGGTKLEIK	968
vlCDR1	QNIYVW	969
vlCDR2	KAS	970
vlCDR3	QQGQSYPRT	971

Figure 41T

CHA.7.537

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPGLVAPSQSL SITCTVSGFSLIGHGVNWIRQPPGKGLEWLGVIWGDGN TDYNSALKSRLSISKDNSKSQVFLKMNSLQTDDTARYFC <u>AVNSAMDY</u> WGQGTAVT VSS	972
vhCDR1	GFSLIGHG	973
vhCDR2	IWGDGNT	974
vhCDR3	AVNSAMDY	975
Variable light (vl) domain	NIVMTQSPKSMMSVGERVT LNCTASENVASFVSWYQQKPEQSPKLLIY <u>GTS</u> NRYT GVPDRFTGSGSATDFTLT ISSVQAEDLG DYHCGQSYNYPFTFGSGTKLEIE	976
vlCDR1	ENVASF	977
vlCDR2	GTS	978
vlCDR3	GQSYNYPFT	979

Figure 41U

CHA.7.538_1

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGAELVRPGASVKVCKTSGYAFTNYLIEWVKQRPQGQLEWIGVINPGSG GIYYNDKFKVKTTLTADKSSSTAYMQLSSLTSDDSAVYFCARSETHDTWFAYWGQG TLVTVSA	980
vhCDR1	GYAFTNYL	981
vhCDR2	INPGSGGI	982
vhCDR3	ARSETHDTWFAY	983
Variable light (vl) domain	DIVMTQSQKFISTSVGDRVSITCKASQSVRIAVAWFQQKPGQSPKALIYLASTRHTG VPDRFTGSGSGTDFTLTISNVQSEDLADYFCLQHWNPYPYTFGGGTKLEIKR	984
vlCDR1	QSVRIA	985
vlCDR2	LAS	986
vlCDR3	LQHWNPYPY	987

Figure 41V

CHA.7.538_2

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGAELVRPGTSVKMSCKAAGYTFTNYWIGWVKQRPGHGLEWIGDIYPG GGYTNYNEKFKGKATLTADTSSSTAYMQLSSLTSEDSAIYYCASPYYGSSYGFAFWG QGTLVTVSA	988
vhCDR1	GYTFTNYW	989
vhCDR2	IYPGGGYT	990
vhCDR3	ASPYYGSSYGFAF	991
Variable light (vl) domain	DIVMTQSQKFISTSVGDRVSITCKASQSVRIAVAWFQQKPGQSPKALIYLA ¹ STRHTG VPDRFTGSGSGTDFLTISNVQSEDLADYFC ² LQHWNPYT ³ FGGGTKLEIKR	992
vlCDR1	QSVRIA	993
vlCDR2	LAS	994
vlCDR3	LQHWNPYT	995

Figure 41W

CHA.7.543

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPGLVAPSQSL SITCTVSGFSLSGYG I K W V R Q P P G K G L E W L G T I W G D G S T D Y N S A L K S R L S I S K D N S K S Q V F L K M T S L Q T D D T A R Y Y C A S D S L G I T F G Y W G Q G T L V TVSA	996
vhCDR1	GFSLSGYG	997
vhCDR2	IWGDGST	998
vhCDR3	ASDSLGITFGY	999
Variable light (vl) domain	DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGV PSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPLTFGAGTKLELK	1000
vlCDR1	QDISNY	1001
vlCDR2	YTS	1002
vlCDR3	QQGNTLPLT	1003

Figure 41X

CHA.7.544

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPGLVAPSQSL SITCTVSG <u>GFSLT</u> SYAITWVRQPPGKGLEWLGVIWPGGGT NYNSALKSRLSISKDNSKSHLFLKMNSLQTDDTARYYC <u>VRSYDGYLDWYFDV</u> WGTG TTVTVSS	1004
vhCDR1	GFSLTSYA	1005
vhCDR2	IWPGGGT	1006
vhCDR3	VRSYDGYLDWYFDV	1007
Variable light (vl) domain	NIVMTQSPKSMMSVGERVTLSCKASE <u>ENVGTY</u> VSWYQQKPDQSPKLLIYG <u>GAS</u> NRYT GVPDRFTGSGSATDFTLISSVQAEDLSDYHCG <u>QSYSYPYT</u> FGGGTKLEII	1008
vlCDR1	ENVGTY	1009
vlCDR2	GAS	1010
vlCDR3	GQSYSYPYT	1011

Figure 41Y

CHA.7.545

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QIQLVQSGPDLKPKGETVKISCKASGYTFTTYGMSWVKQAPGRGLKWMGWINTYS GVSTFPDDFKGRFAFSLETSASTAYLQINNLIKNEFSATYFCARLGMGSTTGAGYFDV WGTGTTVTVSS	1012
vhCDR1	GYTFTTYG	1013
vhCDR2	INTYSGVS	1014
vhCDR3	ARLGMGSTTGAGYFDV	1015
Variable light (vl) domain	DIVLTQSPAIMASAPGEKVTMTCSASSVSSWYLHWYQQKSGASPKLWIYGTSNLA SGVPARFSGSGSGTSYSLTISSVEAEDAATYYCQQYRSDPYTFGSGTKLEIK	1016
vlCDR1	SSVSSWY	1017
vlCDR2	GTS	1018
vlCDR3	QQYRSDPYT	1019

Figure 41Z

CHA.7.546

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QIQLVQSGPELKKPGETVKISCKASGYTFTTYGMSWVKQAPGKGLKWMGWINTYS GVSTYADDFEGRFAFSLETSVSTAYLQINNLIKNETATYFCARLGRGSTTGAGYLDV WGTGTTVTVSS	1020
vhCDR1	GYTFTTYG	1021
vhCDR2	INTYSGVS	1022
vhCDR3	ARLGRGSTTGAGYLDV	1023
Variable light (vl) domain	DIVLTQSPAIMASAPGEKVSMTCSASSSVSSWYLHWYQQKSGASPKLWIYGTSLA SGVPARFSGSGSGTSYSLTISVVEAEDAATYYCQQYHSDPYTFGSGTKLEIK	1024
vlCDR1	SSVSSWY	1025
vlCDR2	GTS	1026
vlCDR3	QQYHSDPYT	1027

Figure 41AA

CHA.7.547

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QIQLVQSGPDLKPKGETVKISCKASGYTFTTYGMSWVKQAPGRGLKWMGWINTYS GVSTFPDDFKGRFAFSLETSASTAYLQINNLIKNEFSATYFCARLGMGSTTGAGYFDV WGTGTTVTSS	1028
vhCDR1	GYTFTTYG	1029
vhCDR2	INTYSGVS	1030
vhCDR3	ARLGMGSTTGAGYFDV	1031
Variable light (vl) domain	ENVLTQSPAIMSASLGEKVTLSKRASSSVNYMYWYQQKSDASPKLWIYYTSLAPG VPARFSGSGSGNSYSLTISVVEGEDAATYYCQQFTSSPWTFGGGTKLEIK	1032
vlCDR1	SSVNY	1033
vlCDR2	YTS	1034
vlCDR3	QQFTSSPWT	1035

Figure 41BB

CHA.7.548

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGASVKISCKASGYTFTDYSMNWVKQSHGKSLEWIGDITPNNG SPNYNQKF K DATLTVDKSSSTVYME L RLTSEDSAVVYCASLFFDYWGHGTTLTVSS	1036
vhCDR1	GYTFTDYS	1037
vhCDR2	ITPNNGSP	1038
vhCDR3	ASLFFDY	1039
Variable light (vl) domain	DIVMTQSPSSLSVSAGEKVTMSCKSSQSLN S GNQKNYLAWYQQKPGQPPKLLIYG ASTRDSGVPDRFTGSGSGTDFTLTITSVQAEDLAVVYQCNDHTYPYT F GGG T KLEIK	1040
vlCDR1	QSLN S GNQKNY	1041
vlCDR2	GAS	1042
vlCDR3	QNDHTYPYT	1043

Figure 41CC

CHA.7.549

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQPGTELVKPGASVKLSCKAS <u>GFTFTTH</u> WMHWVRQRPQGQGLEWIGNIYPS <u>NGGS</u> NYNEKF K ATLTVD R SS T AYMHLSSLTSEDSAVYYCARRVNWDGY F DYW GQGTTLTVSS	1044
vhCDR1	GFTFTTHW	1045
vhCDR2	IYPSNGGS	1046
vhCDR3	ARRVNWDGYFDY	1047
Variable light (vl) domain	DIVMTQSQKFMSTSVGDRVSVTCKASQNVGTNVAWYQQKPGQSPKLLIY <u>S</u> ASYRY SGVPDRFTGSGSGTDFLTISNVQSEDLADYFC <u>QQYNSYPLT</u> FGGGTKLEIK	1048
vlCDR1	QNVGTN	1049
vlCDR2	SAS	1050
vlCDR3	QQYNSYPLT	1051

Figure 41DD

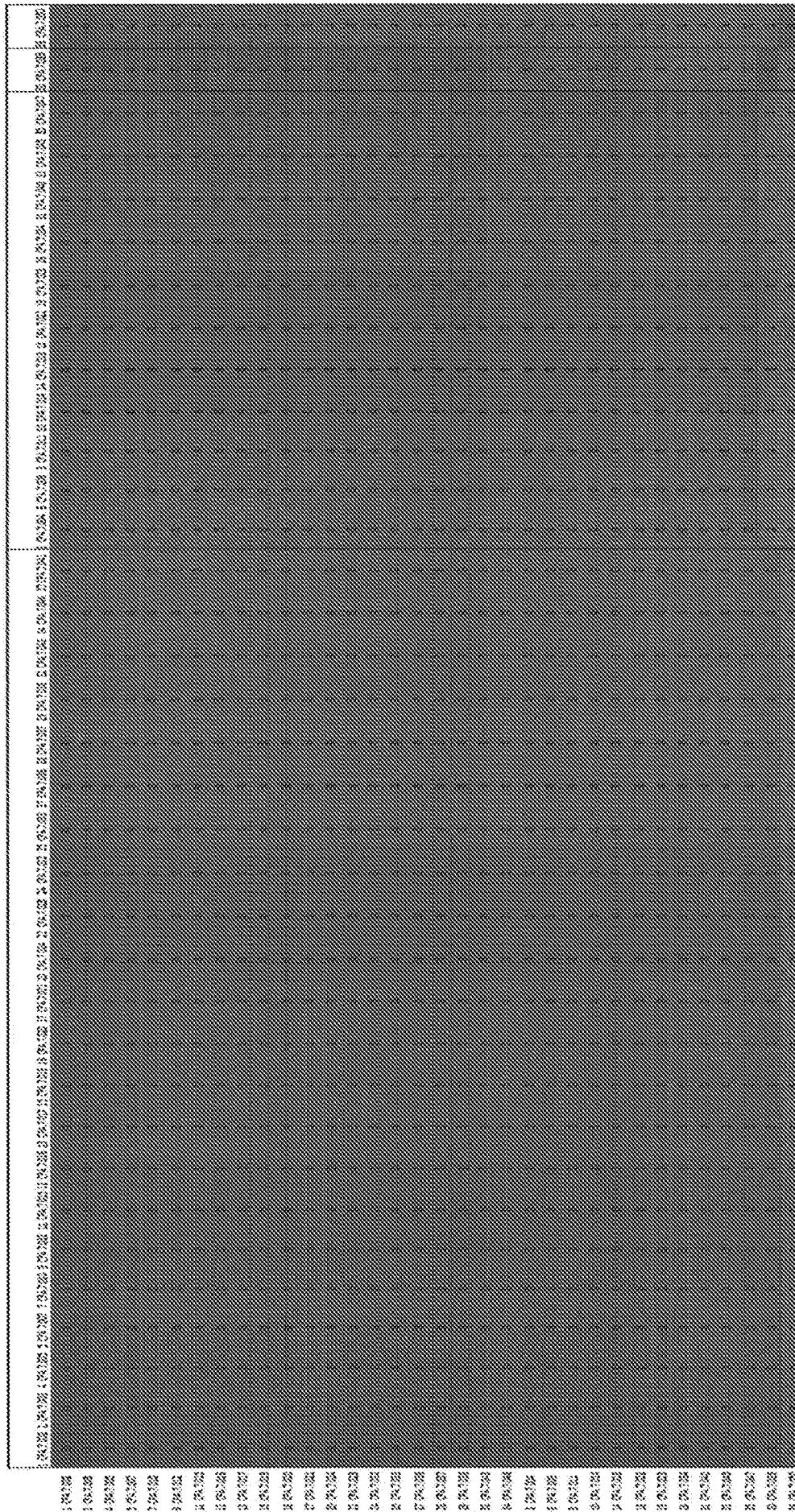
CHA.7.550

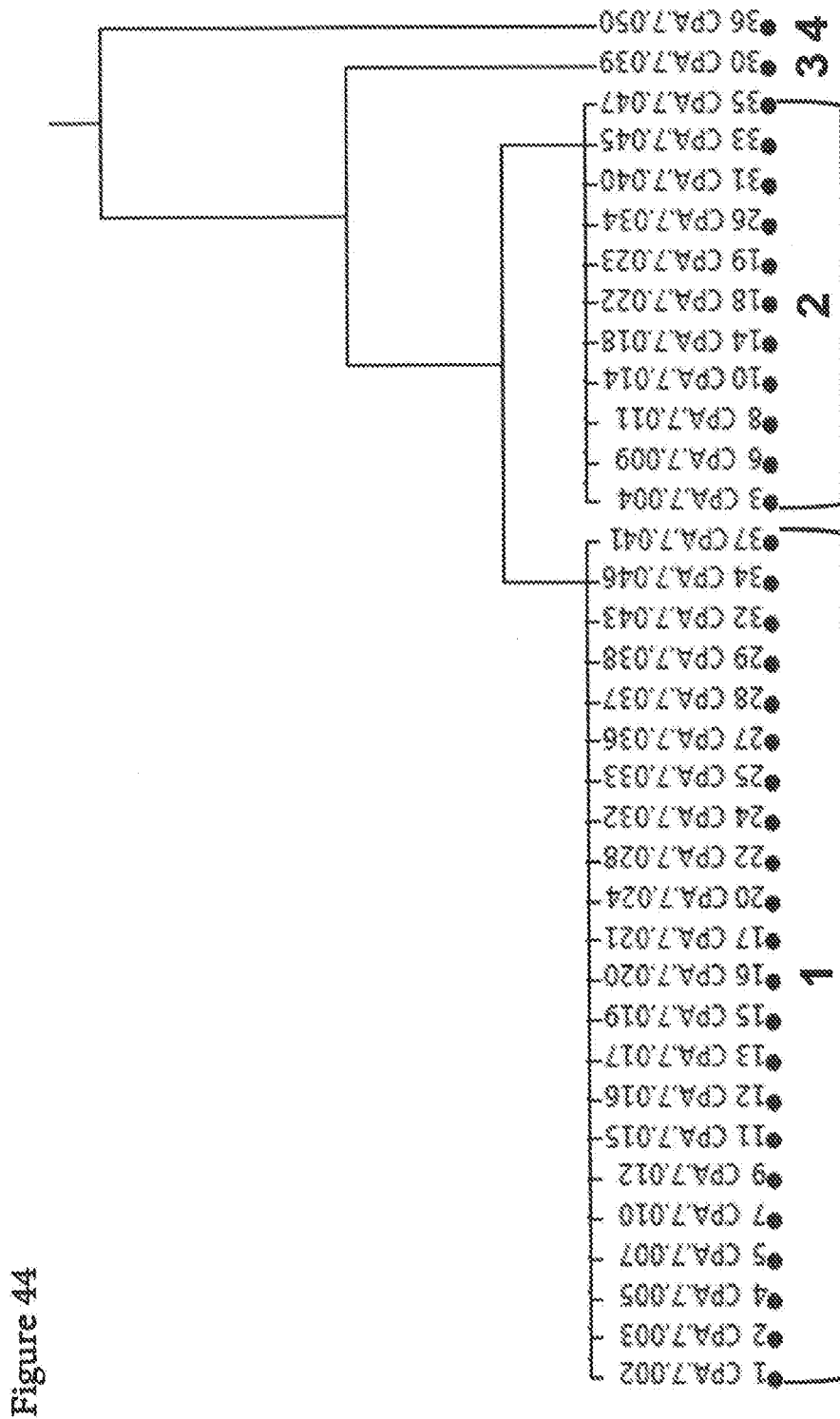
What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGTELVKPGASVKLSCKASGYTFTSYWIHWVKQRPGQGLEWIGNINPSN GGTINYNKFKSKAALTVDKSSSTAYMQLSSLTSEDSAVVYCARRGLPYFFDYWGQG TTLTVSS	1052
vhCDR1	GYTFTSYW	1053
vhCDR2	INPSNGGT	1054
vhCDR3	ARRGLPYFFDY	1055
Variable light (vl) domain	DIVMTQSQKFMSTSVGDRVSVTCKGSQNVGYNVAWYQQKPGQSPKALVYSASDR HSGVPDRFAGSGSGTDFTLTISNVQSEDLAEYFCQQYNSYPLTFGAGTKLELK	1056
vlCDR1	QNVGYN	1057
vlCDR2	SAS	1058
vlCDR3	QQYNSYPLT	1059

Figure 42

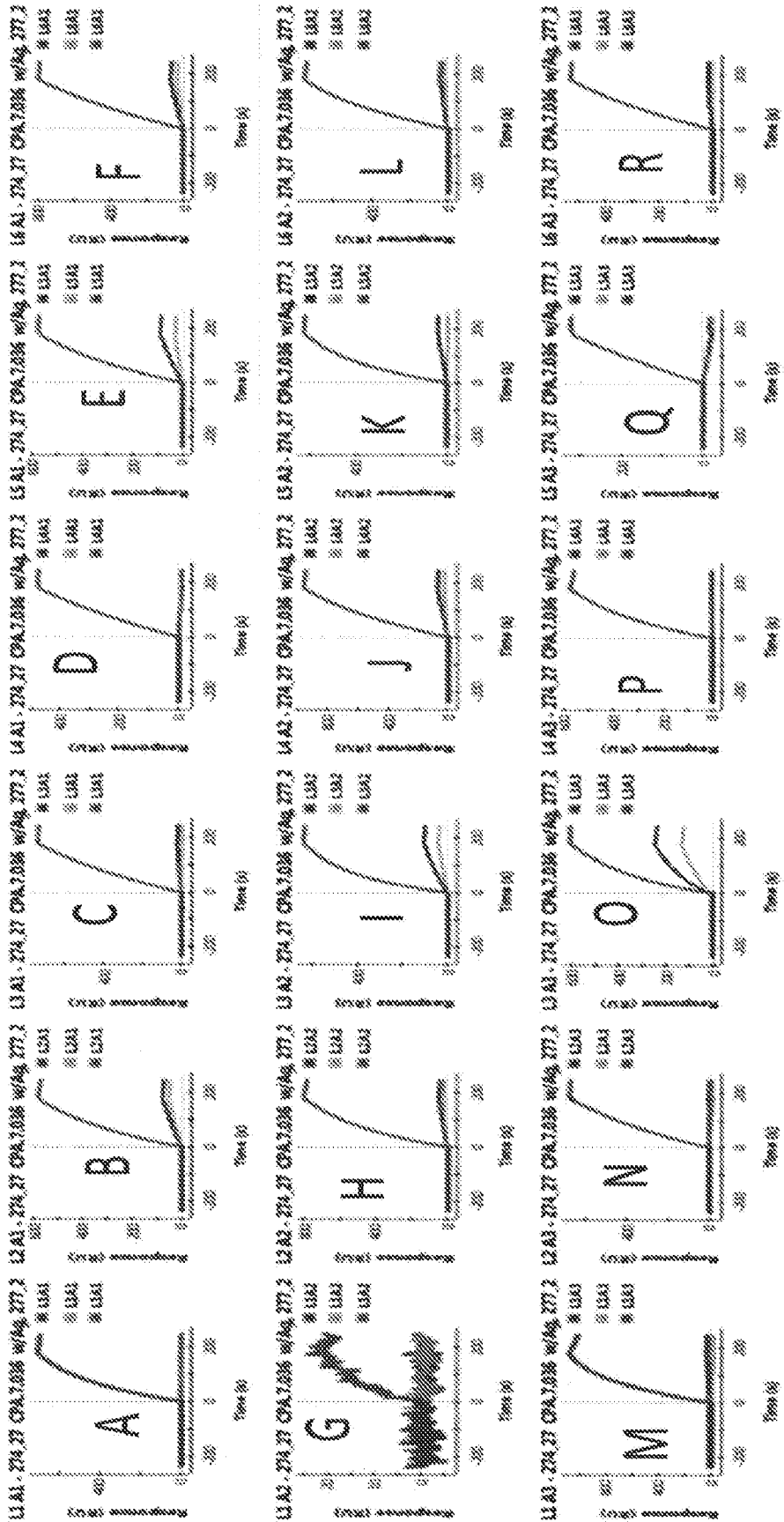
1	2	3	4
CPA.7.002	CPA.7.004	CPA.7.039	CPA.7.050
CPA.7.003	CPA.7.009		
CPA.7.005	CPA.7.011		
CPA.7.007	CPA.7.014		
CPA.7.010	CPA.7.018		
CPA.7.012	CPA.7.022		
CPA.7.015	CPA.7.023		
CPA.7.016	CPA.7.034		
CPA.7.017	CPA.7.040		
CPA.7.019	CPA.7.045		
CPA.7.020	CPA.7.047		
CPA.7.021			
CPA.7.024			
CPA.7.028			
CPA.7.032			
CPA.7.033			
CPA.7.036			
CPA.7.037			
CPA.7.038			
CPA.7.043			
CPA.7.046			
CPA.7.041			

Figure 43

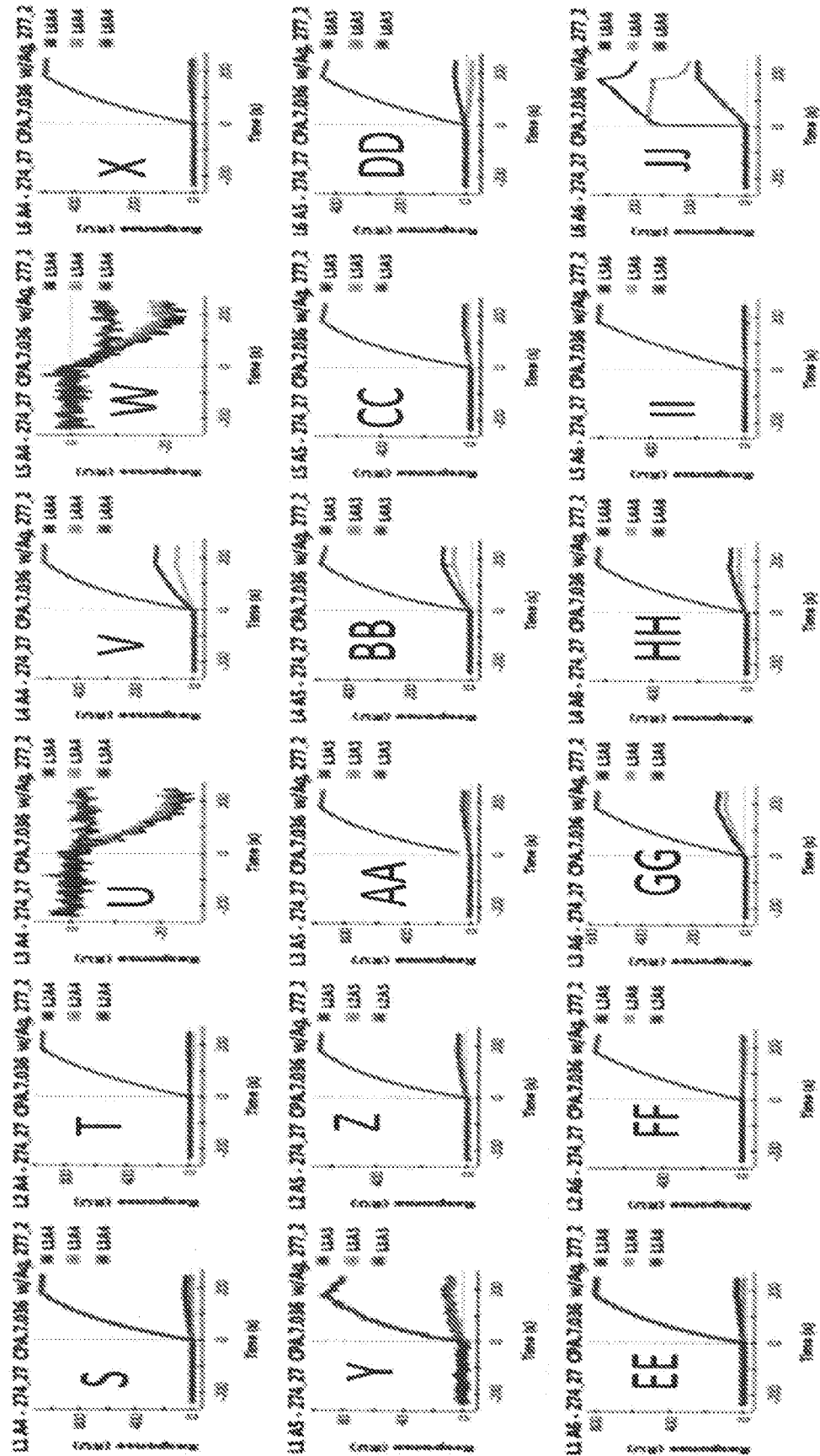




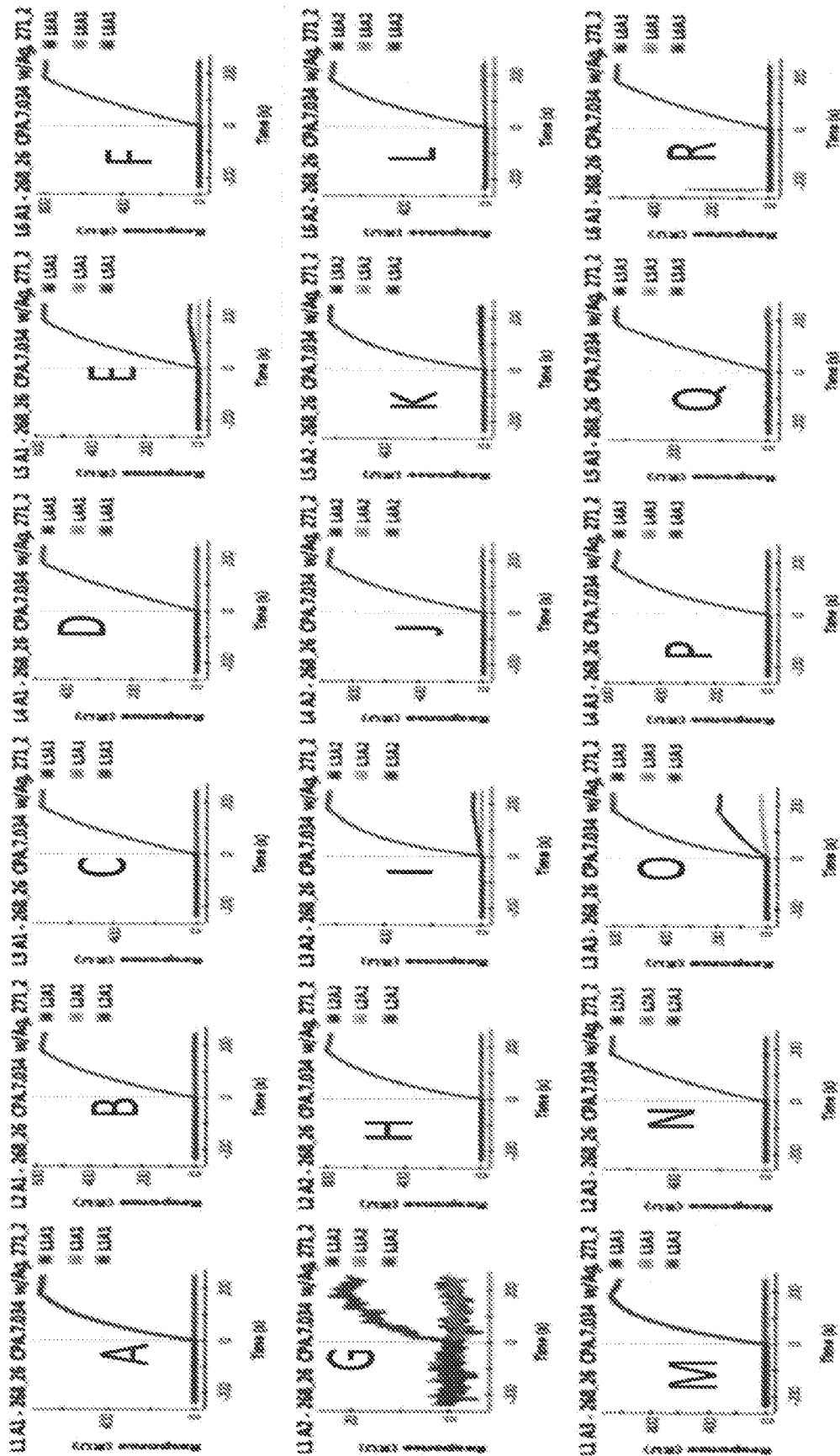
Figures 45A - 45R



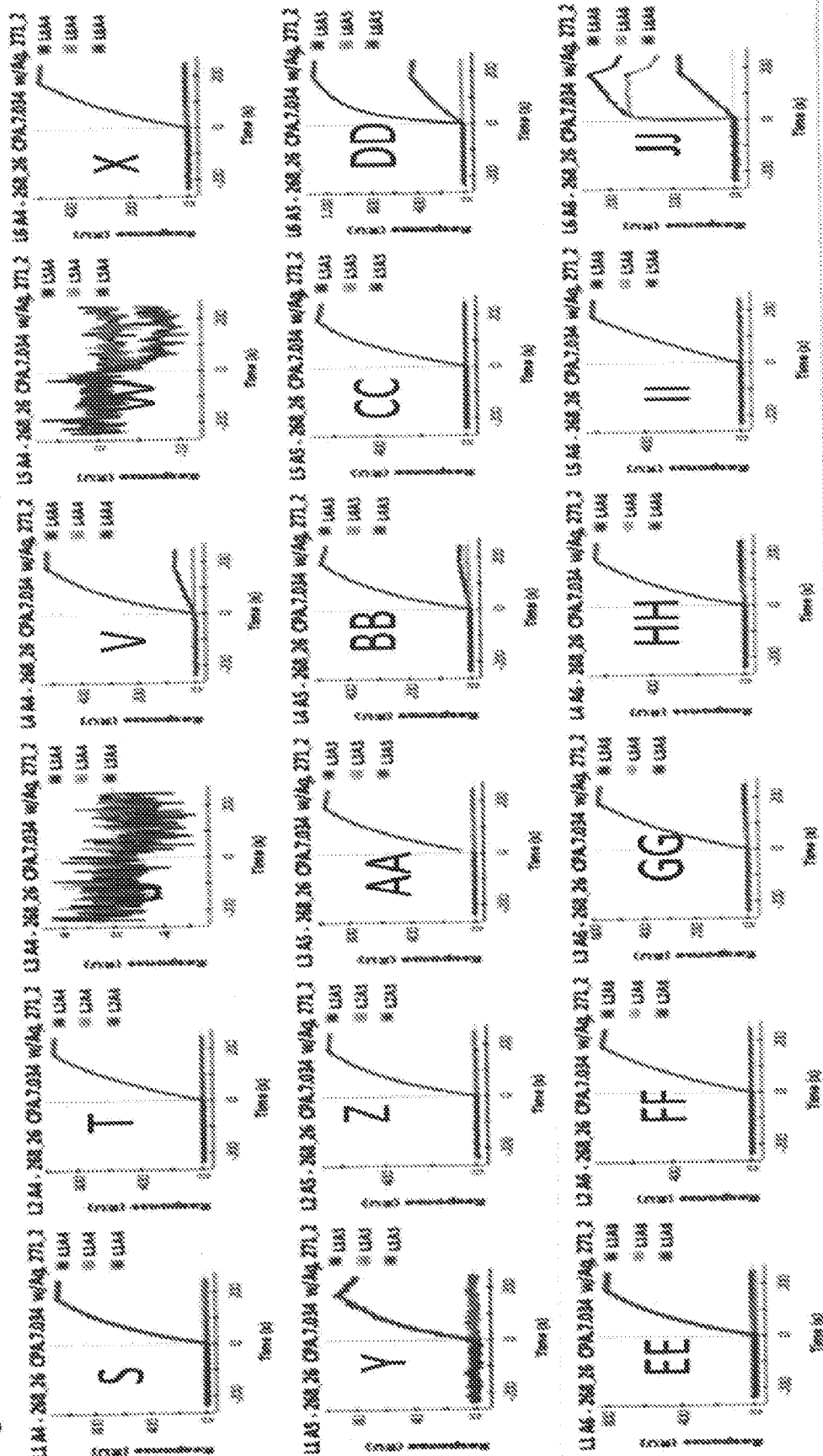
Figures 45S - 45JJ



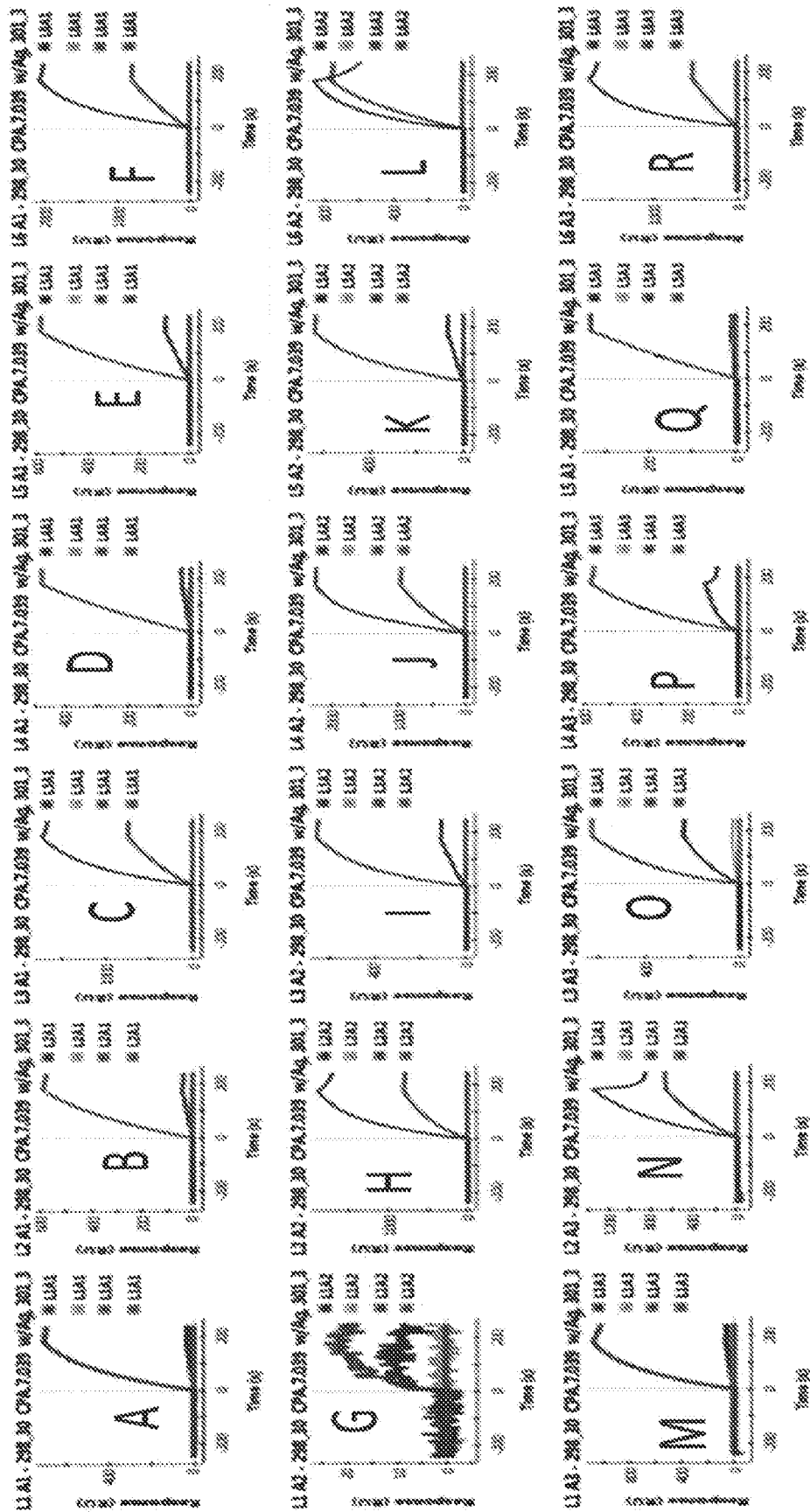
Figures 46A - 46R



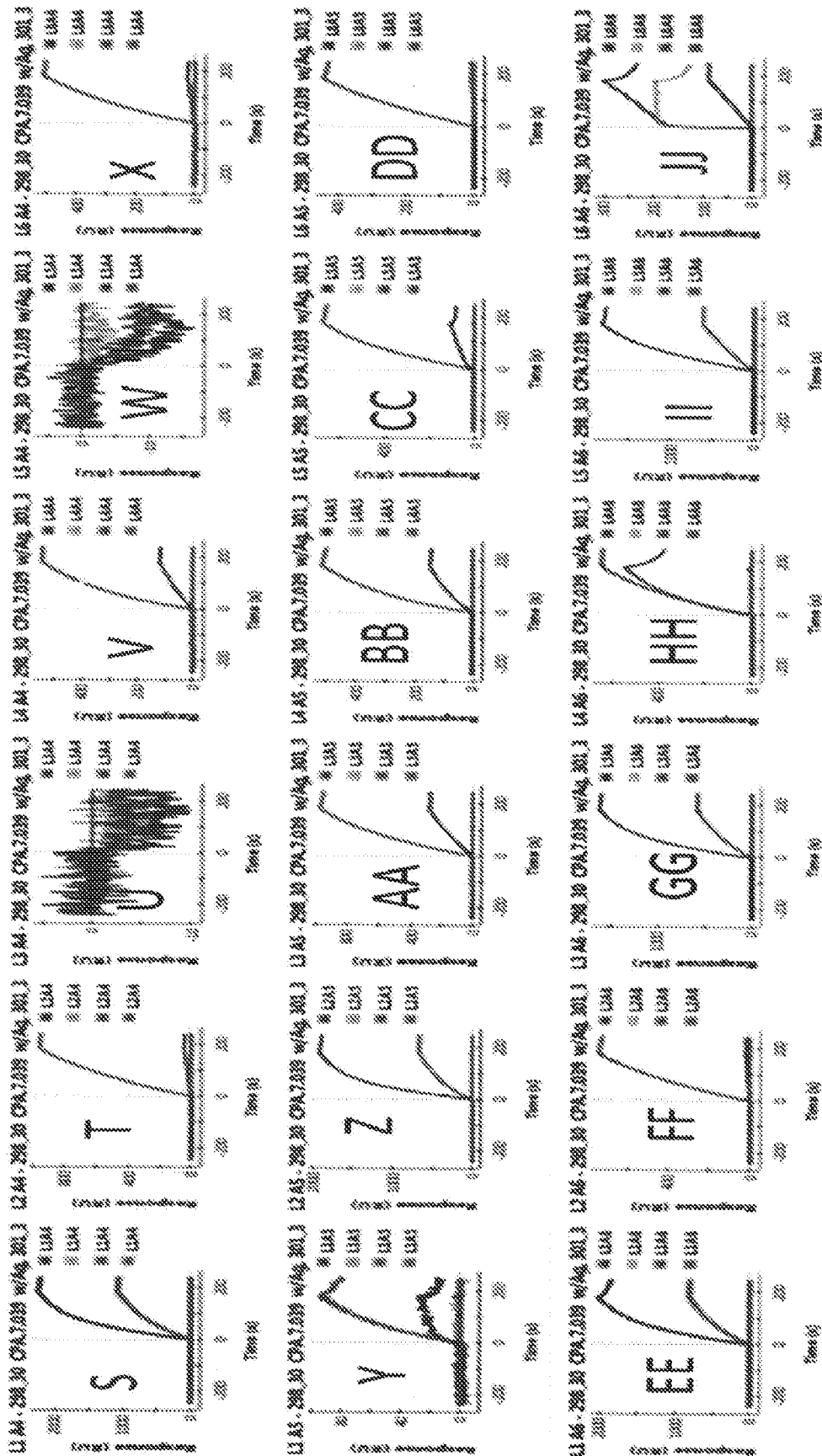
Figures 46S - 46J]



Figures 47A - 47R



Figures 47S - 47JJ



Figures 48A - 48R

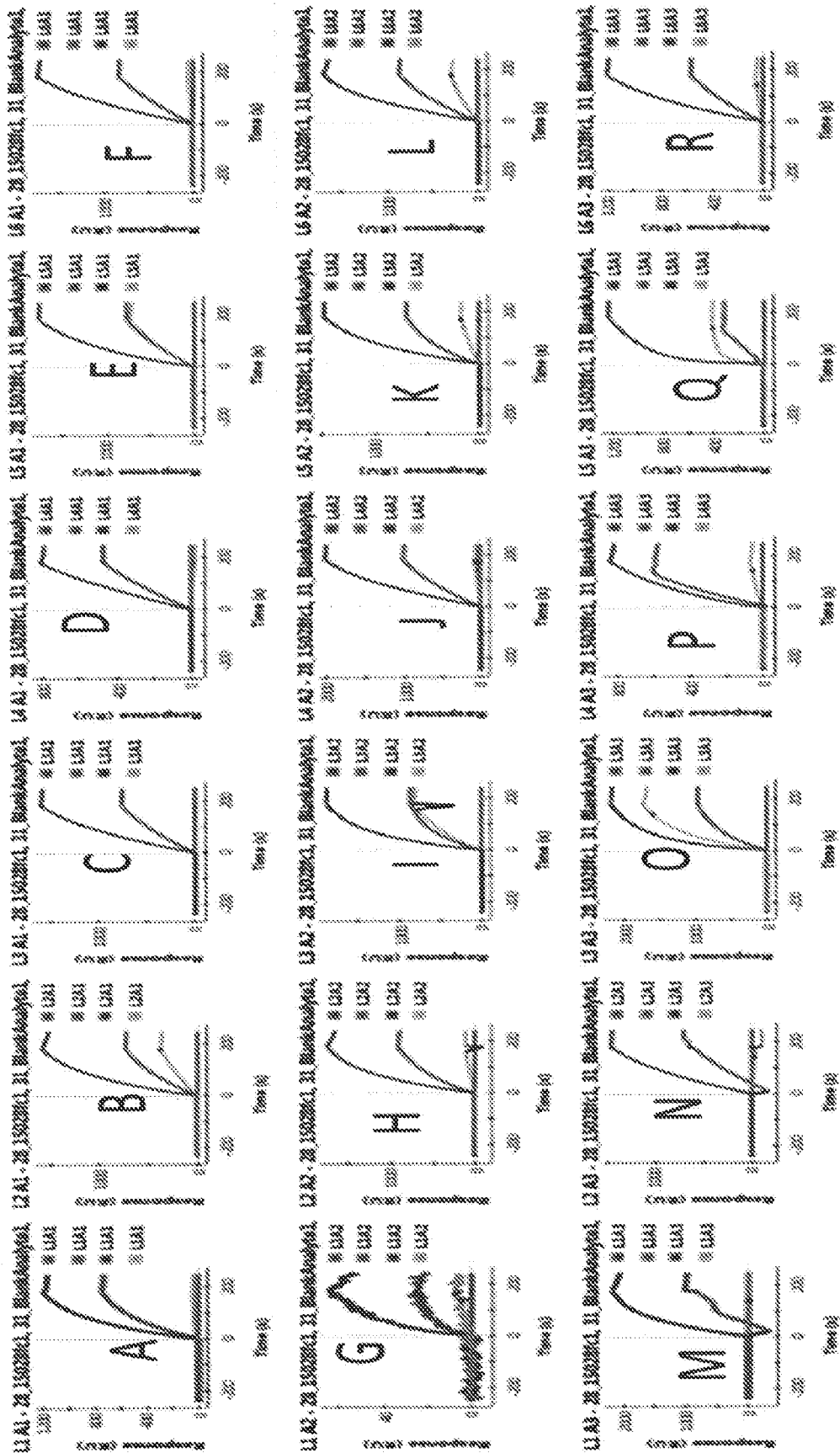


Figure 49

Table 1

		k_a	k_d	K_D
Fab Clone	Figure	1/M-s	1/s	M
CPA.7.021	50A	2.20E+05	2.90E-05	1.32E-10
CPA.7.028	50B	3.08E+06	4.33E-04	1.41E-10
CPA.7.019	50C	8.59E+05	1.87E-04	2.18E-10
CPA.7.012	50D	1.51E+06	9.54E-04	6.32E-10
CPA.7.007	50E	3.24E+05	4.55E-04	1.41E-09
CPA.7.015	50F	3.13E+05	1.11E-03	3.55E-09
CPA.7.050	50G	7.08E+04	4.00E-04	5.65E-09
CPA.7.048	50H	1.35E+05	2.57E-03	1.90E-08
CPA.7.049	50I	1.51E+05	3.67E-03	2.44E-08
CPA.7.040	50J	1.33E+05	3.69E-03	2.77E-08
CPA.7.020	50K	1.34E+05	3.86E-03	2.88E-08
CPA.7.002	50L	4.59E+04	2.83E-03	6.16E-08
CPA.7.022	50M	3.55E+06	2.96E-01	8.33E-08
CPA.7.005	50N	5.22E+04	4.39E-03	8.41E-08
CPA.7.004	50O	2.12E+06	4.00E-01	1.89E-07
CPA.7.010	50P	9.06E+04	1.72E-02	1.89E-07
CPA.7.008	50Q	2.46E+04	2.03E-02	8.23E-07

Figure 50A-50Q

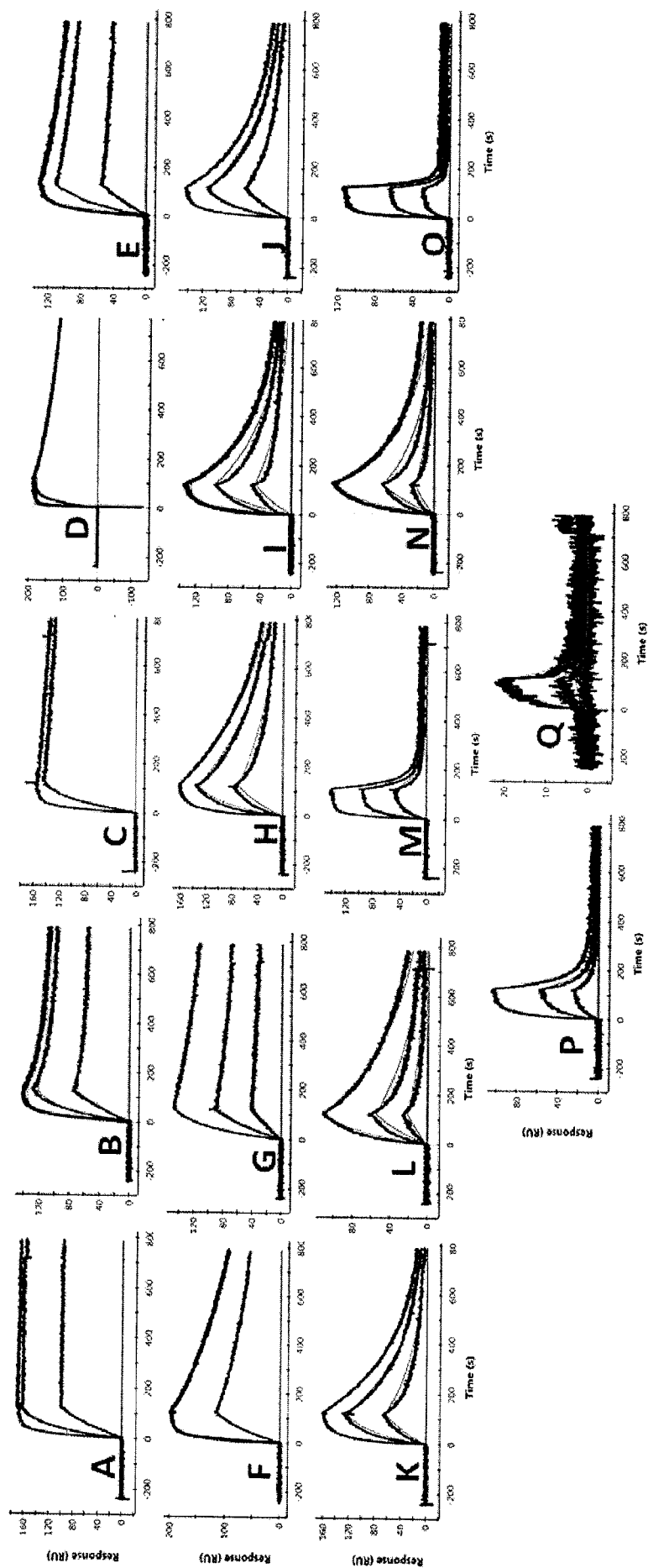


FIGURE 51A

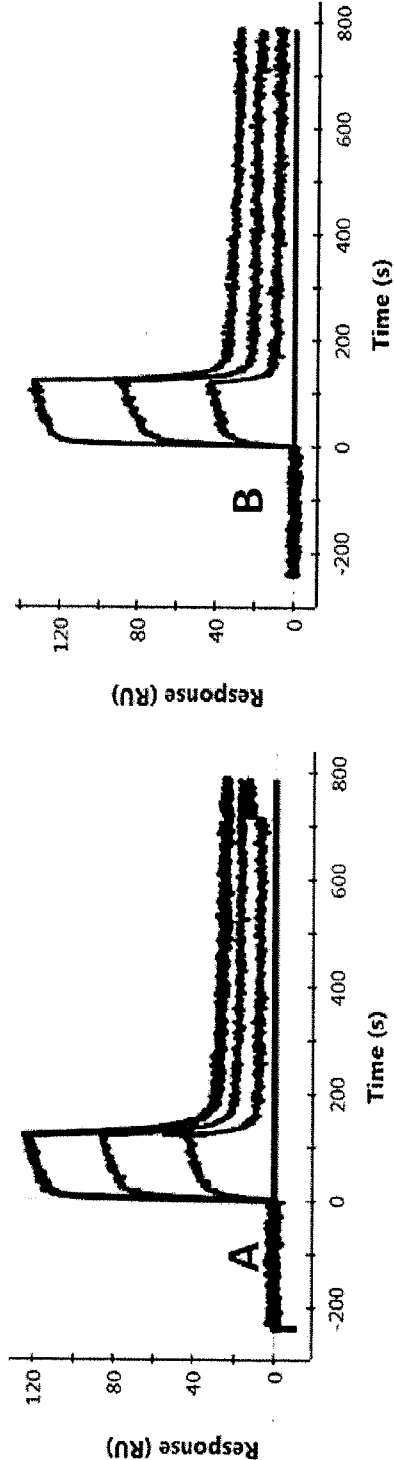


FIGURE 51B

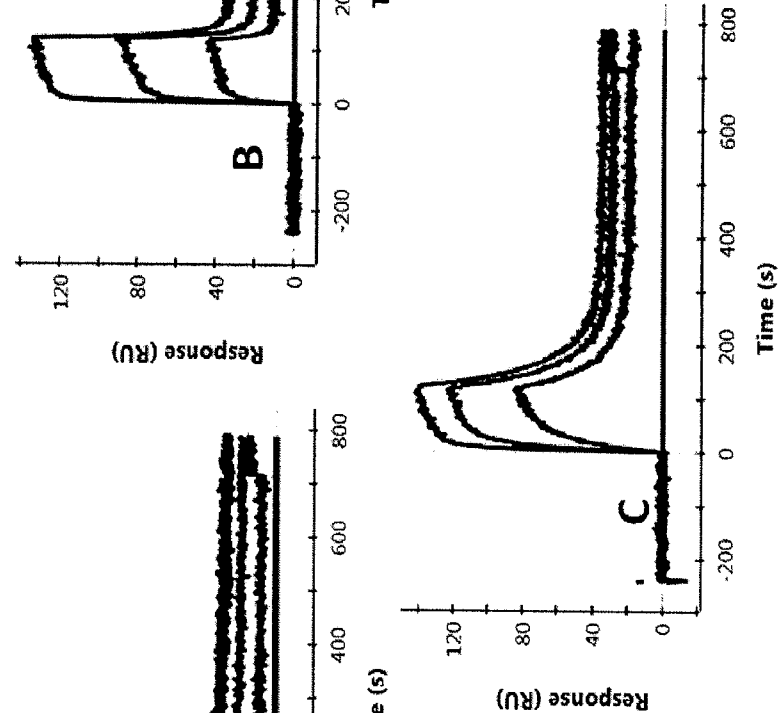


FIGURE 51C

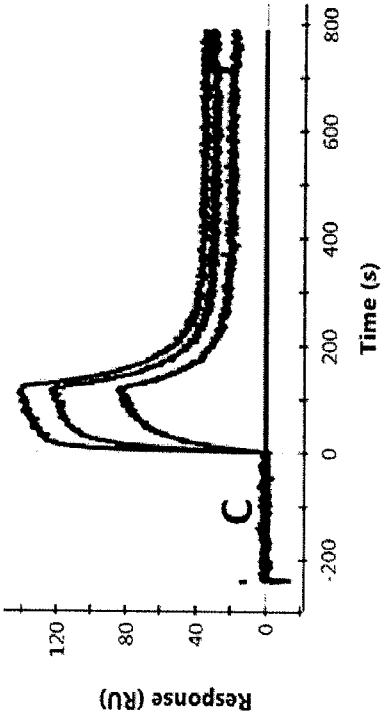


Figure 52A

Antibody	ELISA Signal	% Blocking	> 80% blocking
No mab control	1.376	0	NO
CPA.7.001	0.099	93	YES
CPA.7.002	0.558	59	NO
CPA.7.003	0.153	89	YES
CPA.7.004	0.166	88	YES
CPA.7.005	1.551	-13	NO
CPA.7.006	0.134	90	YES
CPA.7.007	0.529	62	NO
CPA.7.008	0.281	80	YES
CPA.7.009	0.05	96	YES
CPA.7.010	0.141	90	YES
CPA.7.011	0.067	95	YES
CPA.7.012	0.045	97	YES
CPA.7.013	0.045	97	YES
CPA.7.014	0.044	97	YES
CPA.7.015	0.142	90	YES
CPA.7.016	1.553	-13	NO
CPA.7.017	0.197	86	YES
CPA.7.018	0.156	89	YES
CPA.7.019	0.146	89	YES
CPA.7.020	0.728	47	NO
CPA.7.021	0.122	91	YES
CPA.7.022	0.081	94	YES
CPA.7.023	0.047	97	YES
CPA.7.024	0.048	97	YES
CPA.7.025	1.159	16	NO
CPA.7.026	1.12	19	NO
CPA.7.027	1.181	14	NO
CPA.7.028	0.702	49	NO
CPA.7.029	1.272	8	NO
CPA.7.030	1.176	15	NO
CPA.7.031	0.673	51	NO
CPA.7.032	0.427	69	NO
CPA.7.033	0.186	86	YES

Figure 52B

Antibody	ELISA Signal	% Blocking	> 80% blocking
CPA.7.034	0.26	81	YES
CPA.7.035	1.16	16	NO
CPA.7.036	0.184	87	YES
CPA.7.037	0.915	34	NO
CPA.7.038	0.301	78	NO
CPA.7.039	0.541	61	NO
CPA.7.040	0.048	97	YES
CPA.7.041	0.356	74	NO
CPA.7.042	0.307	78	NO
CPA.7.043	0.773	44	NO
CPA.7.044	1.025	26	NO
CPA.7.045	0.93	32	NO
CPA.7.046	0.104	92	YES
CPA.7.047	0.223	84	YES
CPA.7.049	0.077	94	YES
CPA.7.050	0.174	87	YES

Figure 53

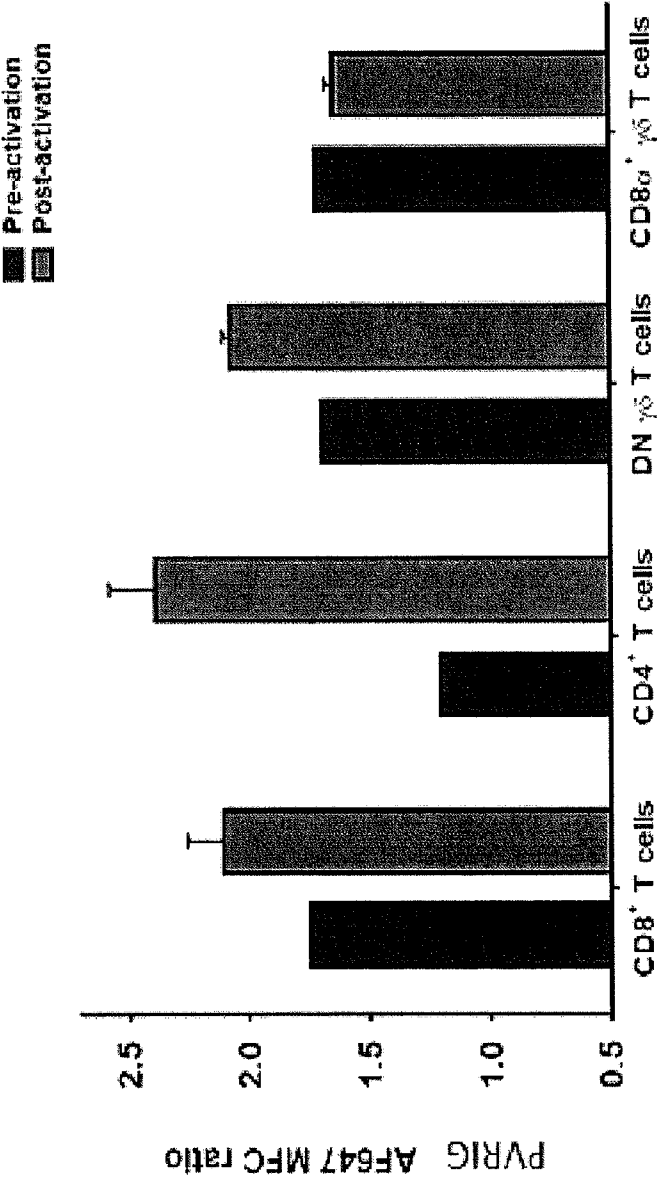


Figure 54

Cell line	ATCC No./CLS /ECACC No.	Morphology	Source
HL-60	ATCC, CCL-240	Leukemia	Blood
THP1	ATCC, TIB-202	Monocyte	Blood
KG-1	ATCC, CCL-246	Macrophage	Bone marrow
Jurkat	ATCC, TIB-152	T Cell	Blood
RPMI8226	ATCC, CCL-155	B lymphocyte	Blood
DAN-G	CLS, 300162	Epithelial	Pancreas
OV90	ATCC, CRL-11732	Epithelial	Ovary
NCI-H441	ATCC, CRL-174	Epithelial	Lung
TF1	ATCC, CRL-2003	Erythroblast	Bone Marrow
Capan2	ATCC, HTB-80	polygonal	Pancreas
ZR75-1	ATCC, CRL-1500	Epithelial	Mammary gland
Karpas299	ECACC, 06072604-1VL	Lymphoma	Blood
NK-YTS	ATCC, CL-273	Lymphoblast	Blood
H9	ATCC, HTB-176	Lymphoblast	Blood
K562	ATCC, CCL-243	Lymphoblast	Bone Marrow
NCI-H929	ATCC, CRL-9068	Lymphoblast	B Lymphocytes
BCP1	ATCC, CRL-2294	Lymphoblast	B Lymphoblast
HUT78	ATCC, TIB-161	Lymphoblast	Blood
HEK293	ATCC, CRL-3216	Epithelial	Kidney

Figure 55

Cell line	ATCC No.	Morphology	Source
4T1	CRL-2539	Epithelial	Mammary gland
B16-F1	CRL-6323	Spindle-shaped+epithelial-like cells	Skin
EL4	TIB-39	T-lymphoblast	blood
E.G7-OVA	CRL-2113	T-lymphoblast	blood
YAC-1	TIB-160	T-lymphoblast	blood
A20	TIB-208	B-lymphoblast	blood
P815	TIB-64	Mast cells	blood
NIH/3T3	CRL-1658	fibroblast	embryo
Sal/N	CRL-2544	fibroblast	fibrosarcoma
J774A.1	TIB-67	Macrophage	blood
LL/2	CRL-1642	Epithelial	Lung
B104-1-1	CRL-1887	Fibroblast	Glioblastoma
RAW264.7	TIB-71	Macrophage	Abelson leukemia virus-induced tumor
P388D1	CCL-46	Macrophage	Lymphoblast
KLN205	CRL-1453	Epithelial	Lung
CT26	CRL-2638	Fibroblast	Colon
Renca	CRL-2947	Epithelial	Kidney

Figure 56A

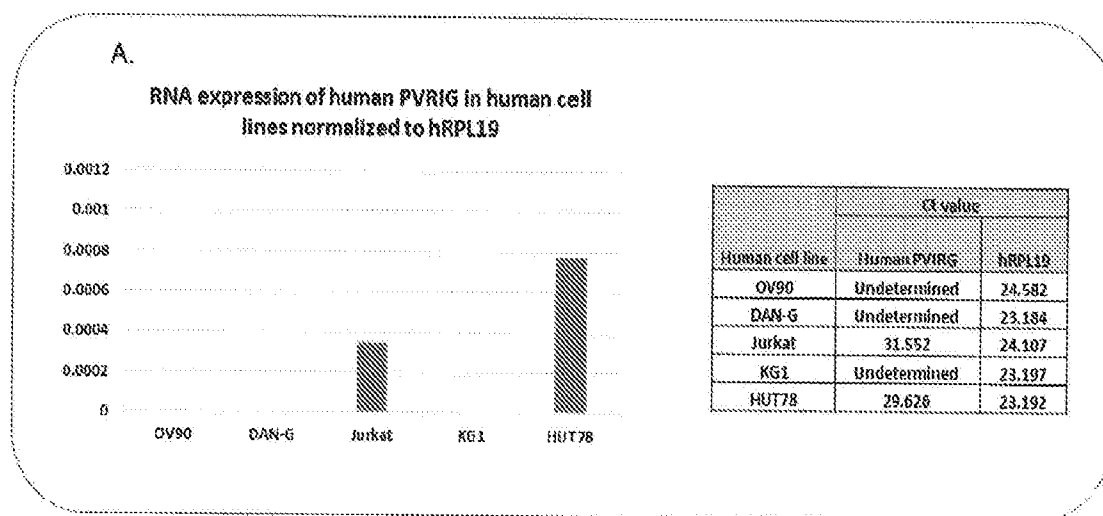


Figure 56B

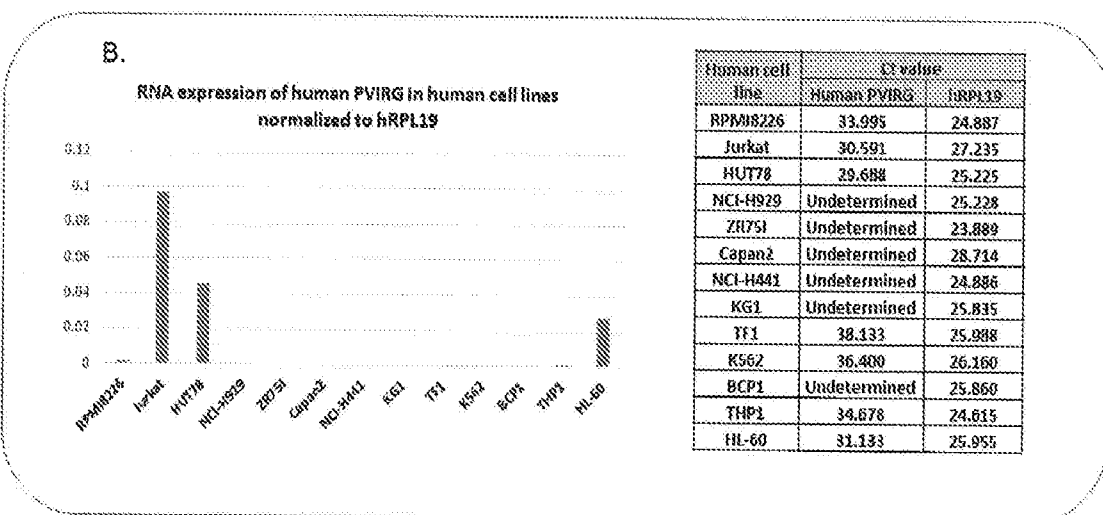


Figure 56C

C.

Human cell line	Ct value					
	Human PVIRG	hTATA box	hRPL19	hPBGD	hSDHA	hHPRT1
DAN-G	39.92	30.14	27.4	27.4	26.59	27.99
NCI-H441	35.46	28.34	26.71	26.71	26.2	27.36
KG1	38.95	28.39	26.74	28.28	26.39	26.39
TF1	39.22	29.25	27.61	33.74	36.25	36.25

Figure 57A

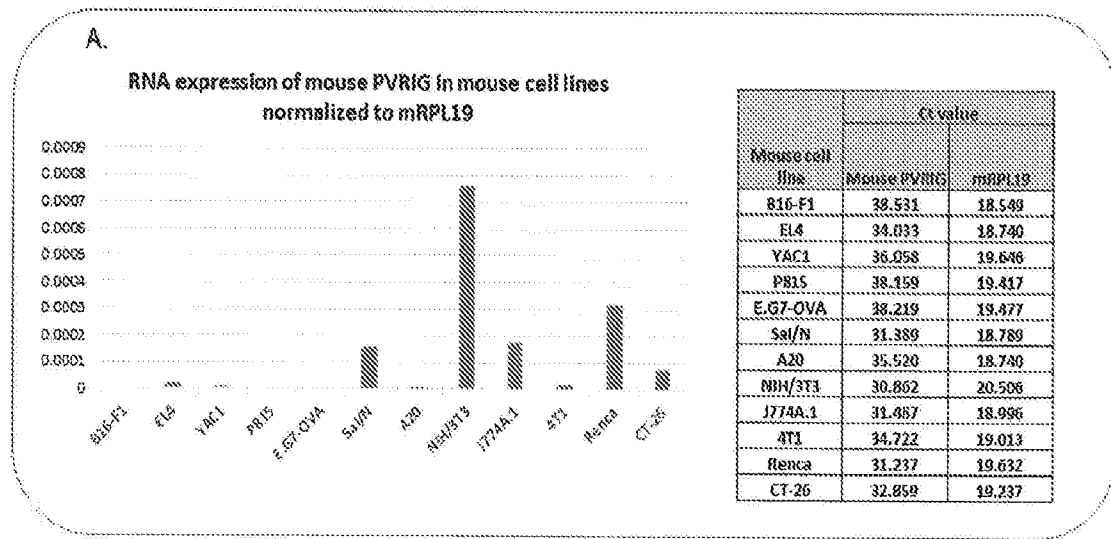


Figure 57B

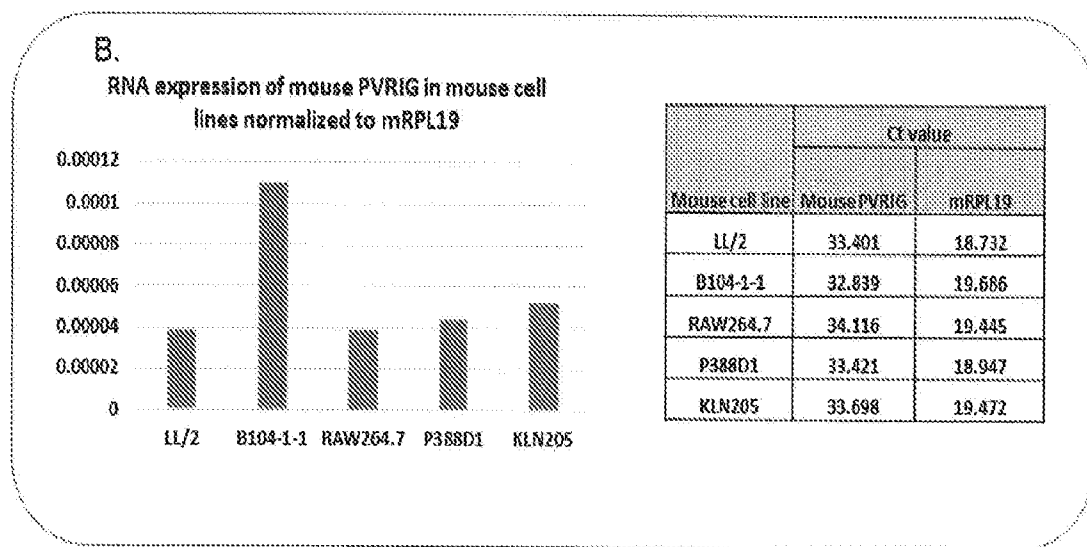


Figure 58

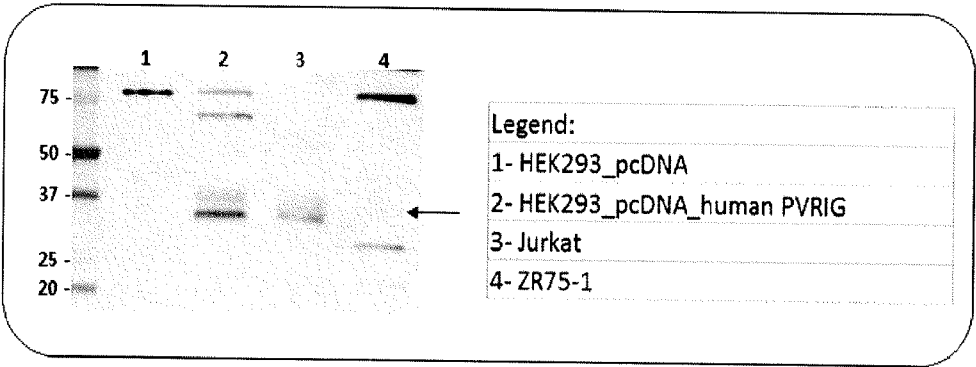


Figure 59

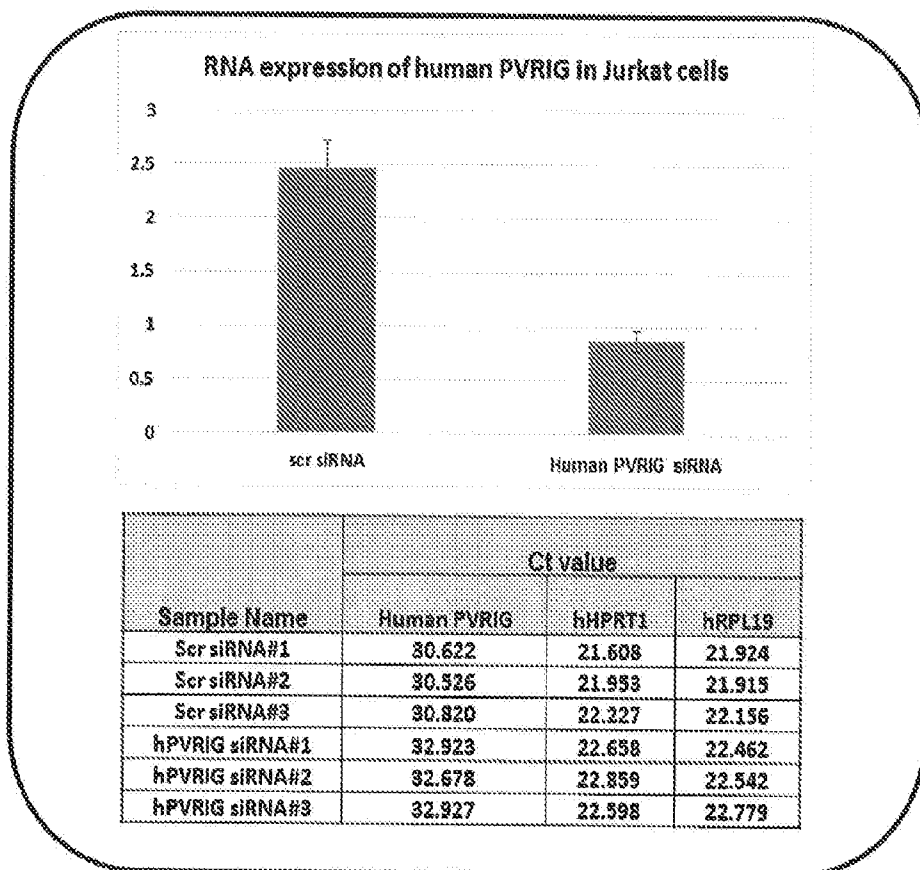


Figure 60

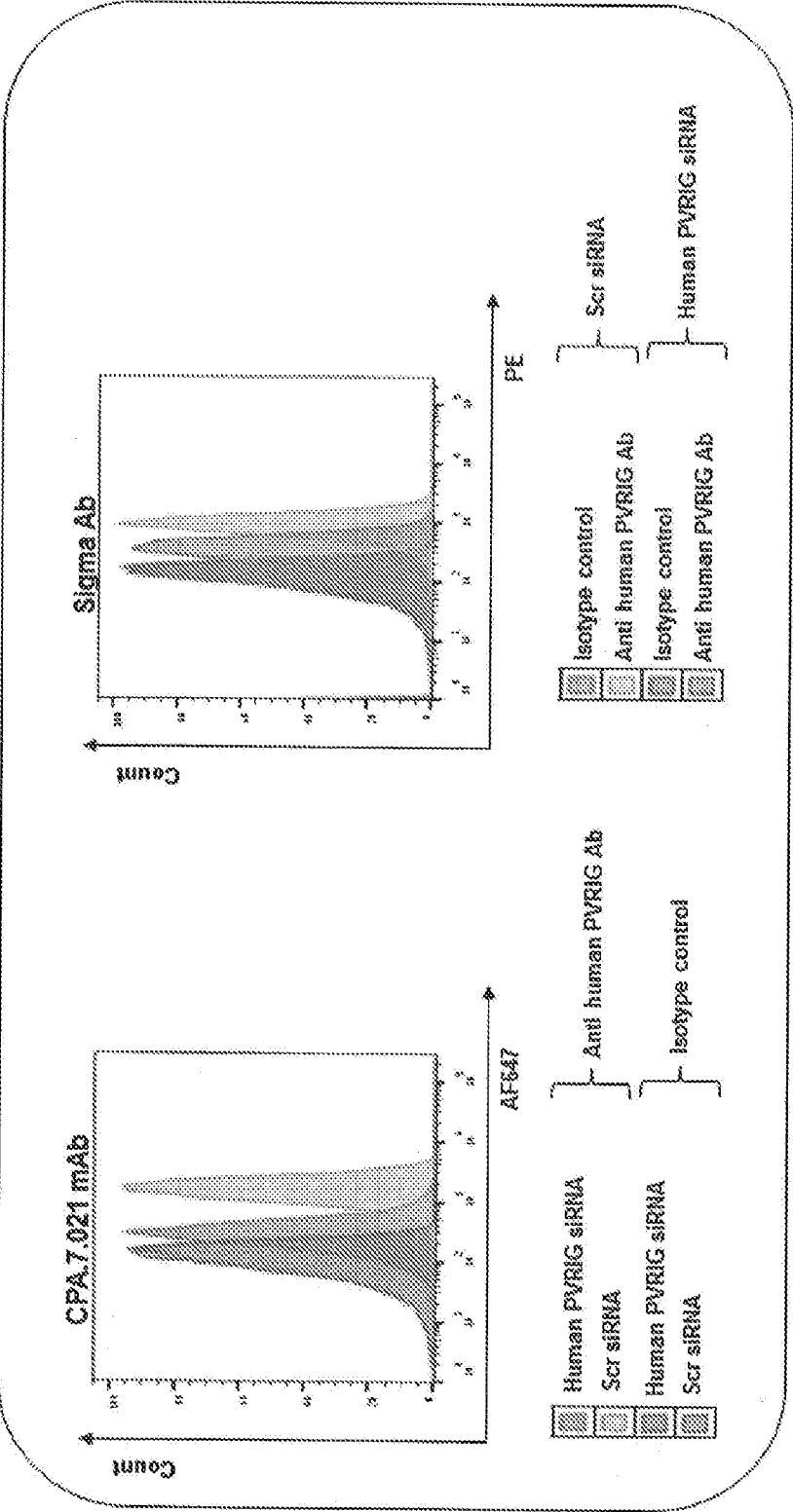


Figure 61

Cell line	qRT-PCR	FACS	WB	%KD-RNA	%KD-FACS
	(PVRIG Ct / HSKG Ct)	(fold change from isotype)			
OV90	Undetermined/24.582	NT	NT		
DAN-G	Undetermined/23.184	NT	NT		
Jurkat	31.552/24.107	14	+	65	82
KG1	Undetermined/23.197	NT	NT		
HUT78	29.626/23.192	X	NT		
RPMI8226	33.995/24.887	NT	NT		
NCI-H929	Undetermined/25.228	NT	NT		
ZR75-1	Undetermined/23.889	X	X		
Capan2	Undetermined/28.714	X	NT		
NCI-H441	Undetermined/24.886	NT	NT		
TF1	38.133/25.988	NT	NT		
K562	36.400/26.160	NT	NT		
BCP1	Undetermined/25.860	NT	NT		
THP1	34.678/24.615	NT	NT		
HL60	31.133/25.955	NT	NT		
Karpas299	NT	X	NT		
NK-YTS	NT	X	NT		

Figure 62

Cell line	qRT-PCR (PVRIG Ct / HSKG Ct)	FACS (fold change from isotype)	WB	%KD- RNA	%KD- FACS
4T1	34.722/19.013	NT	NT		
B16-F1	38.531/18.549	NT	NT		
EL4	34.033/18.740	NT	NT		
YAC-1	36.058/19.646	NT	NT		
P815	38.159/19.417	NT	NT		
E.G7-OVA	38.219/19.477	NT	NT		
NIH3T3	29.94 / 21.25	X	NT		
SAI/N	31.389/18.789	X	NT		
J774A.1	31.487/18.996	X	NT		
A20	35.520/18.740	NT	NT		
LL/2	33.401/18.732	NT	NT		
B104-1-1	32.839/19.686	NT	NT		
RAW264.7	34.116/19.445	NT	NT		
P388D1	33.421/18.947	NT	NT		
KLN205	33.698/19.472	NT	NT		
Renca	31.237/19.632	X	NT		

Figure 63A

Name	Hcdr1	SEQ ID NO:	Hcdr2	SEQ ID NO:	Hcdr3	SEQ ID NO:	Lcdr1	SEQ ID NO:	Lcdr2	SEQ ID NO:	Lcdr3	SEQ ID NO:
CPA.7.001	GGTFSSYA	1060	IPIFGTA	1061	AREEVSSPYGMDV	1062	TGAVTSGHY	1063	DTG	1064	LLSYSGASWV	1065
CPA.7.002	GGTFSSA	1066	IPIYGIT	1067	ARDDTARRVRGVPYVYYA MDV	1068	QGIGNY	1069	SAS	1070	QQLKDYPIT	1071
CPA.7.003	GFSLSHFS	1072	FDPEEGT	1073	ATGIWYSSGWVVDY	1074	QSLDSSGNY	1075	LGS	1076	MQALQTPIT	1077
CPA.7.004	GYTLTELS	1078	FDPEDGET	1079	ATVSRVRGVINWYVYMDV	1080	QSLYRNGNYY	1081	LGS	1082	MQALQTPPT	1083
CPA.7.005	GGTFSSA	1084	IPIYGIT	1085	ARDDTARRVRGVPYVYYA MDV	1086	QSVDS	1087	DAS	1088	QQYKDWPF	1089
CPA.7.006	GGTFGTYA	1090	ITPISATI	1091	ARGFEYSDGILLDD	1092	QSLFYSDDGNTY	1093	RLS	1094	MQHMEFPLT	1095
CPA.7.007	GGSISSSY	1096	IYSGST	1097	ARGAWELRLGDWFD	1098	SSNIGAGVD	1099	GNN	1100	QSYDSSLSIVV	1101
CPA.7.008	SGSISSTNW	1102	IYHSGST	1103	ARVGPAIY	1104	SNNVGYEG	1105	RNN	1106	SAWDSSSLNAV	1107
CPA.7.009	GYTLTELS	1108	FDPEDGET	1109	ATAKPGIAVAGQNYVYVYM DV	1110	QSLYRNGNYY	1111	LGS	1112	MQALQTPPT	1113
CPA.7.010	GFTFSSYA	1114	ISYDGSNK	1115	ASSPIGYSYGYWGGMDV	1116	SGIDVRTNK	1117	FQSDSK	1118	LIWHTSGWV	1119
CPA.7.011	GYTLTELS	1120	FDPEDGET	1121	ATGPAAAGVGYVYVYMDV	1122	QSLYRNGNYY	1123	LGS	1124	MQALQTPPT	1125
CPA.7.012	GFTFSSYA	1126	ISYDGSNK	1127	ARDVMVYCSSTSCYFYGM DV	1128	QDIRDY	1129	DAS	1130	QQFENLPIT	1131
CPA.7.013	GYTLTELS	1132	FDPEDGET	1133	ATGGYSSGFNYVYVYMDV	1134	QSLYRNGNYY	1135	LGS	1136	MQALQTPPT	1137
CPA.7.014	GYTLTELS	1138	FDPEDGET	1139	ATGVTITYVYVYVYMDV	1140	QSLYRNGNYY	1141	LGS	1142	MQALQTPPT	1143
CPA.7.015	GFTFSSYG	1144	IRYDGSNK	1145	ARDLDFFWWDGMDV	1146	QSVSSMY	1147	GAS	1148	QQYVSSPMYT	1149

Name		Hcdr1		SEQ ID NO:	Hcdr2	SEQ ID NO:	Hcdr3		SEQ ID NO:	Lcdr1	SEQ ID NO:	Lcdr2	SEQ ID NO:	Lcdr3	SEQ ID NO:
CPA.7.031	GGTFSSA	1240	IPIYGIT	1241	ARDDTARRVRGVPPYYYYAMDV	1242	QSLDSDDDGNIH	1243	TLS	1244	MQRKEFPLT	1245			
CPA.7.032	GFTFSSYG	1246	ISYDGSNK	1247	AKEDRLRFLEWLFYGM DV	1248	HDIYTY	1249	DAS	1250	QQYDNHPPEVT	1251			
CPA.7.033	GGTFSSA	1252	IPIYGIT	1253	ARDDTARRVRGVPPYYYYAMDV	1254	QDIDDD	1255	EAS	1256	LQHDNLPLT	1257			
CPA.7.034	GYLTELS	1258	FDPEDGET	1259	ATEDPGPVAGPPYYYYGMDV	1260	QSLLYINGVHY	1261	LGS	1262	MQALQTPTT	1263			
CPA.7.035	GYMFTNYP	1264	INAGTGNT	1265	AREGMFYGLESYKGGWFDP	1266	QSLLRNGYNY	1267	LAS	1268	MQALQTPLT	1269			
CPA.7.036	GGTFSSA	1270	IPIYGIT	1271	ARDDTARRVRGVPPYYYYAMDV	1272	QSLDSDDDGNTY	1273	TLS	1274	MQRLOQFPLT	1275			
CPA.7.037	TYTFTTVY	1276	YPSGGNT	1277	VRDQNYYSAMDV	1278	QDIRNY	1279	DAS	1280	QQFENLPIT	1281			
CPA.7.038	GGTFSSA	1282	IPIYGIT	1283	ARDDTARRVRGVPPYYYYAMDV	1284	RDISDS	1285	DAS	1286	HQYDNLPLT	1287			
CPA.7.039	GFNFRGYA	1288	ISGSGGTT	1289	AQSYAQIGYGGHIDH	1290	SGIDVATYM	1291	YKSDSDK	1292	LIW/HGSHYV	1293			
CPA.7.040	GYLTELS	1294	FDPEDGET	1295	ATGVPAAGVYYYYYMDV	1296	QSLLYRNGYNY	1297	WGS	1298	MQAVQNPPT	1299			
CPA.7.041	GGTFSSA	1300	IPIYGIT	1301	ARDDTARRVRGVPPYYYYAMDV	1302	QNIDSS	1303	YAS	1304	HQSSSLPLT	1305			
CPA.7.042	GGTFSSA	1306	IPIYGIT	1307	ARDDTARRVRGVPPYYYYAMDV	1308	QSVYNNY	1309	DAS	1310	QQYNSWPPYT	1311			
CPA.7.043	GGTFSSYA	1312	IPIFGTA	1313	ARDAYYDSSGYNPDAFDI	1314	QSLLYSNGYNY	1315	LGS	1316	MQARQTPYT	1317			
CPA.7.044	GGTFSSA	1318	IPIYGIT	1319	ARDDTARRVRGVPPYYYYAMDV	1320	ESVTTF	1321	DAS	1322	HQHTNWPLT	1323			
CPA.7.045	GYLTELS	1324	FDPEDGET	1325	ATEVGYCSGGSCYISYYGMDV	1326	QSLLYRNGHNF	1327	LGS	1328	MQALQTPTT	1329			
CPA.7.046	GGTFSSA	1330	IPIYGIT	1331	ARDDTARRVRGVPPYYYYAMDV	1332	QTMNNY	1333	DAS	1334	QQYGDWLPIIT	1335			

Figure 63D

Name	Hcdr1	SEQ ID NO:	Hcdr2	SEQ ID NO:	Hcdr3	SEQ ID NO:	Lcdr1	SEQ ID NO:	Lcdr2	SEQ ID NO:	Lcdr3	SEQ ID NO:
CPA.7.047	GYTLTELS	1336	FDPEDGET	1337	ATAFPEATISYYYMDV	1338	QSLLYRNGYNY	1339	WGS	1340	MQAVQNPPT	1341
CPA.7.049	GGTFSSSA	1342	IPIYGIT	1343	ARDDTARRVRGVPYYYVYMDV	1344	RSLLDSDDGNTNTH	1345	SLS	1346	MQRKEFPLT	1347
CPA.7.050	GGTFSSYA	1348	IPIFGTA	1349	ARGPWYDSSGYSSAYYMDV	1350	QSLHSDGYNY	1351	LGS	1352	MQALHTPGVT	1353

Figure 64A

Disease	CD8A	CD4	CD3G	PD-1
Kidney renal clear cell carcinoma	0.89	0.75	0.83	0.9
Sarcoma	0.87	0.64	0.88	0.82
Liver hepatocellular carcinoma	0.86	0.6	0.78	0.63
Skin Cutaneous Melanoma	0.86	0.77	0.87	0.89
Head and Neck squamous cell carcinoma	0.85	0.72	0.82	0.86
Breast invasive carcinoma	0.84	0.67	0.81	0.85
Testicular Germ Cell Tumors	0.84	0.66	0.88	0.84
Stomach adenocarcinoma	0.8	0.66	0.78	0.78
Mesothelioma	0.79	0.63	0.8	0.67
Thyroid carcinoma	0.79	0.72	0.87	0.83
Lung squamous cell carcinoma	0.78	0.65	0.77	0.81
Kidney Chromophobe	0.77	0.6	0.7	0.71
Pancreatic adenocarcinoma	0.77	0.57	0.76	0.8
Rectum adenocarcinoma	0.77	0.69	0.68	0.72
Uterine Corpus Endometrial Carcinoma	0.77	0.68	0.75	0.7

Figure 64B

Bladder Urothelial Carcinoma	0.76	0.68	0.81	0.82
Lung adenocarcinoma	0.76	0.52	0.74	0.77
Prostate adenocarcinoma	0.76	0.73	0.72	0.76
Cervical squamous cell carcinoma and endocervical adenocarcinoma	0.74	0.64	0.76	0.7
Colon adenocarcinoma	0.74	0.71	0.75	0.67
Kidney renal papillary cell carcinoma	0.69	0.51	0.66	0.61
Uterine Carcinosarcoma	0.69	0.4	0.59	0.58
Ovarian serous cystadenocarcinoma	0.67	0.64	0.66	0.6
Esophageal carcinoma	0.63	0.57	0.66	0.65
Acute Myeloid Leukemia	0.58	-0.15	0.56	0.29
Pheochromocytoma and Paraganglioma	0.57	0.33	0.42	0.49
Adrenocortical carcinoma	0.55	0.49	0.66	0.64

Figure 65

Antibodies	Isotype	Conjugated to	Manufacturer	Catalog number	concentration (ug/ul)	Staining concentration
Anti-human PVRIG - CPA.7.021	Human IgG2	AF-647	Compugen	CPA.7.021	0.2	7.5 ug/ml
Human IgG2 isotype control	Human IgG2	AF-647	Compugen		0.2	7.5 ug/ml
Anti-CD4	mIgG1	FITC	Biolegend	300506	0.4	4 ug/ml
Anti-CD8	mIgG1	FITC	Biolegend	300906	0.15	1.5 ug/ml
Anti-CD137	mIgG1	PE	Biolegend	309804	0.2	2 ug/ml
Anti-PD1	mIgG1	APC-cy7	Biolegend	329922	0.2	4 ug/ml
isotype control	mIgG1	PE	Biolegend	400112	0.4	2 ug/ml
isotype control	mIgG1	APC-cy7	Biolegend	400128	0.2	4 ug/ml

Figure 66A

		CH1																				
SEQ ID NO:	EU Index	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138
1354 (IgG1)	IgG1	A	S	T	K	G	P	S	V	F	P	L	A	P	S	S	K	S	T	S	G	G
1355 (IgG2)	IgG2	A	S	T	K	G	P	S	V	F	P	L	A	P	C	S	R	S	T	S	E	S
1356 (IgG3)	IgG3	A	S	T	K	G	P	S	V	F	P	L	A	P	C	S	R	S	T	S	G	G
1357 (IgG4)	IgG4	A	S	T	K	G	P	S	V	F	P	L	A	P	C	S	R	S	T	S	E	S
	EU Index	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159
	IgG1	T	A	A	L	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N
	IgG2	T	A	A	L	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N
	IgG3	T	A	A	L	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N
	IgG4	T	A	A	L	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N
	EU Index	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
	IgG1	S	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G	L	Y
	IgG2	S	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G	L	Y
	IgG3	S	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G	L	Y
	IgG4	S	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G	L	Y
	EU Index	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201
	IgG1	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q	T	Y	I	C	N
	IgG2	S	L	S	S	V	V	T	V	P	S	S	N	F	G	T	Q	T	Y	T	C	N
	IgG3	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q	T	Y	T	C	N
	IgG4	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	K	T	Y	T	C	N
	EU Index	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220		
	IgG1	V	N	H	K	P	S	N	T	K	V	D	K	K	V	E	P	K	S	C		
	IgG2	V	D	H	K	P	S	N	T	K	V	D	K	T	V	E	R	K	C	C		
	IgG3	V	N	H	K	P	S	N	T	K	V	D	K	R	V	E	L	K	T	P		
	IgG4	V	D	H	K	P	S	N	T	K	V	D	K	R	V	E	S	K	Y	G		
		Hinge																				
	EU Index	221		222	223	224	225	226	227	228	Fc >											
	IgG1	D			K	T	H	T	C	P	P											
	IgG2				V		E		C	P	P											
	IgG3	L	G	D	T	T	H	T	C	P	R	C	P	E	P	K	S	C	D	T	P	P
	IgG4						P	P	C	P	S											
	EU Index																					
	IgG1																					
	IgG2																					
	IgG3	P	C	P	R	C	P	E	P	K	S	C	D	T	P	P	P	C	P	R	C	P
	IgG4																					
	EU Index														229	230	231	232	233	234	235	236
	IgG1														C	P	A	P	E	L	L	G
	IgG2														C	P	A	P	P	V	A	
	IgG3														C	P	A	P	E	L	L	G
	IgG4														C	P	A	P	E	F	L	G

Figure 66B

		CH2																											
SEQ ID NO:	EU Index	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257							
1354 (IgG1)	IgG1	G	P	S	V	F	L	F	P	P	K	P	K	D	T	L	M	I	S	R	T	P							
1355 (IgG2)	IgG2	G	P	S	V	F	L	F	P	P	K	P	K	D	T	L	M	I	S	R	T	P							
1356 (IgG3)	IgG3	G	P	S	V	F	L	F	P	P	K	P	K	D	T	L	M	I	S	R	T	P							
1357 (IgG4)	IgG4	G	P	S	V	F	L	F	P	P	K	P	K	D	T	L	M	I	S	R	T	P							
EU Index		258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278							
	IgG1	E	V	T	C	V	V	V	D	V	S	H	E	D	P	E	V	K	F	N	W	Y							
	IgG2	E	V	T	C	V	V	V	D	V	S	H	E	D	P	E	V	Q	F	N	W	Y							
	IgG3	E	V	T	C	V	V	V	D	V	S	H	E	D	P	E	V	Q	F	K	W	Y							
	IgG4	E	V	T	C	V	V	V	D	V	S	Q	E	D	P	E	V	Q	F	N	W	Y							
EU Index		279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299							
	IgG1	V	D	G	V	E	V	H	N	A	K	T	K	P	R	E	E	Q	Y	N	S	T							
	IgG2	V	D	G	V	E	V	H	N	A	K	T	K	P	R	E	E	Q	F	N	S	T							
	IgG3	V	D	G	V	E	V	H	N	A	K	T	K	P	R	E	E	Q	Y	N	S	T							
	IgG4	V	D	G	V	E	V	H	N	A	K	T	K	P	R	E	E	Q	F	N	S	T							
EU Index		300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320							
	IgG1	Y	R	V	V	S	V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K							
	IgG2	F	R	V	V	S	V	L	T	V	V	H	Q	D	W	L	N	G	K	E	Y	K							
	IgG3	F	R	V	V	S	V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K							
	IgG4	Y	R	V	V	S	V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K							
EU Index		321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340								
	IgG1	C	K	V	S	N	K	A	L	P	A	P	I	E	K	T	I	S	K	A	K								
	IgG2	C	K	V	S	N	K	G	L	P	A	P	I	E	K	T	I	S	K	T	K								
	IgG3	C	K	V	S	N	K	A	L	P	A	P	I	E	K	T	I	S	K	T	K								
	IgG4	C	K	V	S	N	K	G	L	P	S	S	I	E	K	T	I	S	K	A	K								
		CH3																											
EU Index		341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361							
	IgG1	G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	D	E	L	T	K	N							
	IgG2	G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	E	E	M	T	K	N							
	IgG3	G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	E	E	M	T	K	N							
	IgG4	G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	Q	E	E	M	T	K	N							
EU Index		362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382							
	IgG1	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D	I	A	V	E	W	E							
	IgG2	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D	I	A	V	E	W	E							
	IgG3	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D	I	A	V	E	W	E							
	IgG4	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D	I	A	V	E	W	E							
EU Index		383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403							
	IgG1	S	N	G	Q	P	E	N	N	Y	K	T	T	P	P	V	L	D	S	D	G	S							
	IgG2	S	N	G	Q	P	E	N	N	Y	K	T	T	P	P	M	L	D	S	D	G	S							
	IgG3	S	S	G	Q	P	E	N	N	Y	N	T	T	P	P	M	L	D	S	D	G	S							
	IgG4	S	N	G	Q	P	E	N	N	Y	K	T	T	P	P	V	L	D	S	D	G	S							

Figure 66C

SEQ ID NO:	EU Index	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424
1354 (IgG1)	IgG1	F	F	L	Y	S	K	L	T	V	D	K	S	R	W	Q	Q	G	N	V	F	S
1355 (IgG2)	IgG2	F	F	L	Y	S	K	L	T	V	D	K	S	R	W	Q	Q	G	N	V	F	S
1356 (IgG3)	IgG3	F	F	L	Y	S	K	L	T	V	D	K	S	R	W	Q	Q	G	N	I	F	S
1357 (IgG4)	IgG4	F	F	L	Y	S	R	L	T	V	D	K	S	R	W	Q	E	G	N	V	F	S

EU Index	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445
IgG1	C	S	V	M	H	E	A	L	H	N	H	Y	T	Q	K	S	L	S	L	S	P
IgG2	C	S	V	M	H	E	A	L	H	N	H	Y	T	Q	K	S	L	S	L	S	P
IgG3	C	S	V	M	H	E	A	L	H	N	R	F	T	Q	K	S	L	S	L	S	P
IgG4	C	S	V	M	H	E	A	L	H	N	H	Y	T	Q	K	S	L	S	L	S	L

EU Index	446	447
IgG1	G	K
IgG2	G	K
IgG3	G	K
IgG4	G	K

Figure 67

PVRIG ECD Fragment A TTLAVLHPERGIRQWAPARQA (SEQ ID NO: 1358)

PVRIG ECD Fragment B TTLAVLHPERGIRQWAPARQARWETQSSISLILE (SEQ ID NO: 1359)

PVRIG ECD Fragment C ARQARWETQSSISLILE (SEQ ID NO: 1360)

PVRIG ECD Fragment D TFCCKFASFPEGSWEA (SEQ ID NO: 1361)

PVRIG ECD Fragment E TFCCKFASFPEGSWEACGSLPPSS (SEQ ID NO: 1362)

PVRIG ECD Fragment F EATELSSFTIRCGFL (SEQ ID NO: 1363)

PVRIG ECD Fragment G EVVVQVRMEATELSSFTIRCGF (SEQ ID NO: 1364)

PVRIG ECD Fragment H FTIRCGFLGSGSISLVTVS (SEQ ID NO: 1365)

PVRIG ECD Fragment I SISLVTVSWGGPNGAGGTTLAVLH (SEQ ID NO: 1366)

PVRIG ECD Fragment J SISLILEGSGASSPCANTTFCCKFAS (SEQ ID NO: 1367)

Figure 68

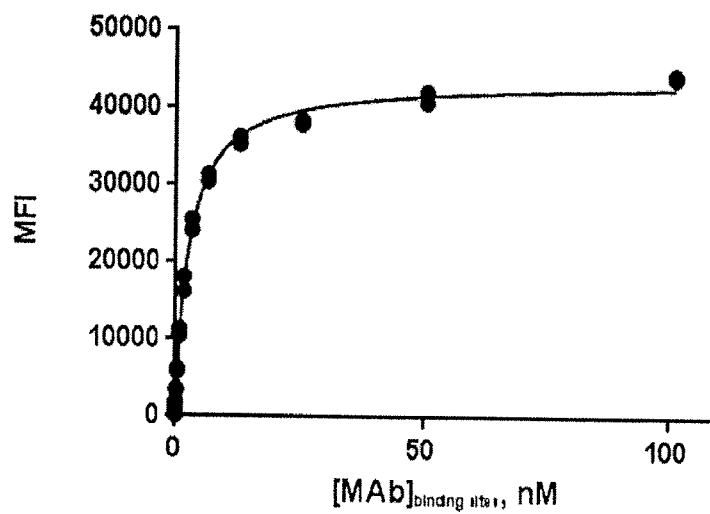


Figure 69A

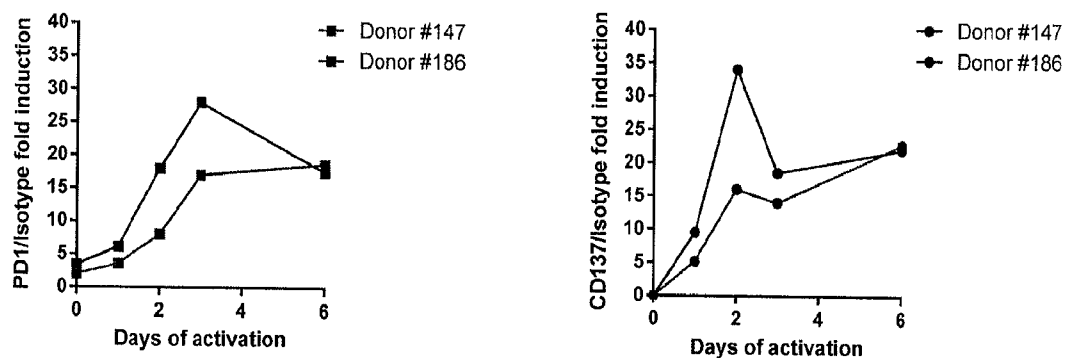


Figure 69B

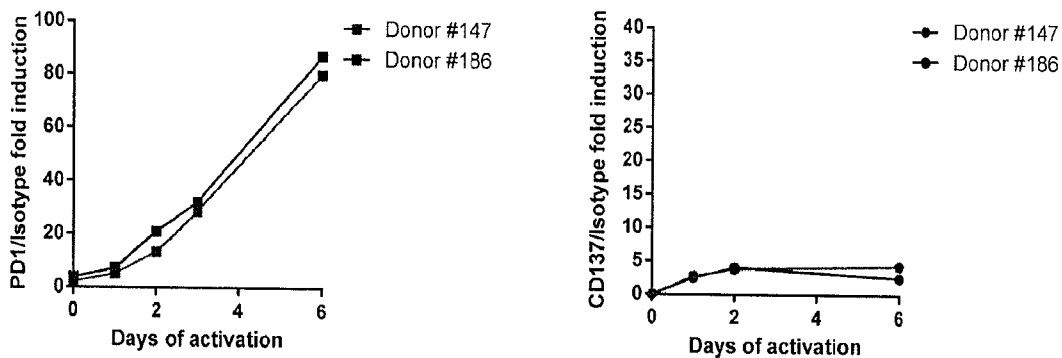


Figure 69C

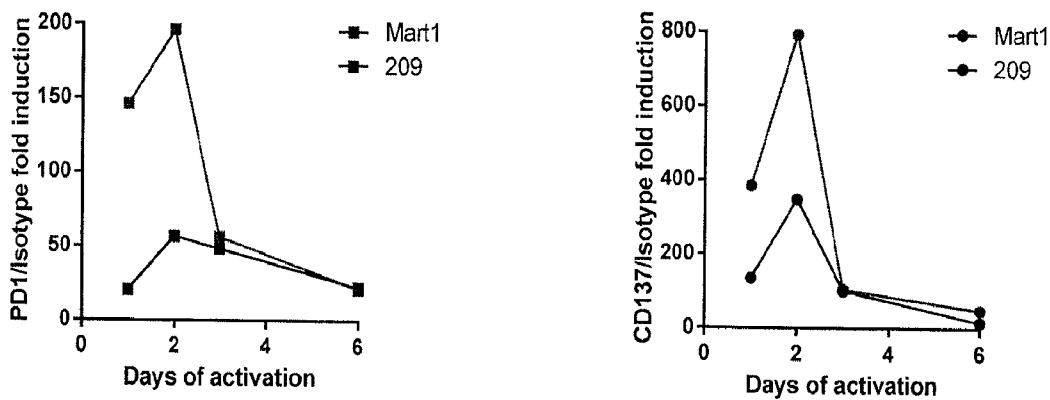


Figure 70A

A

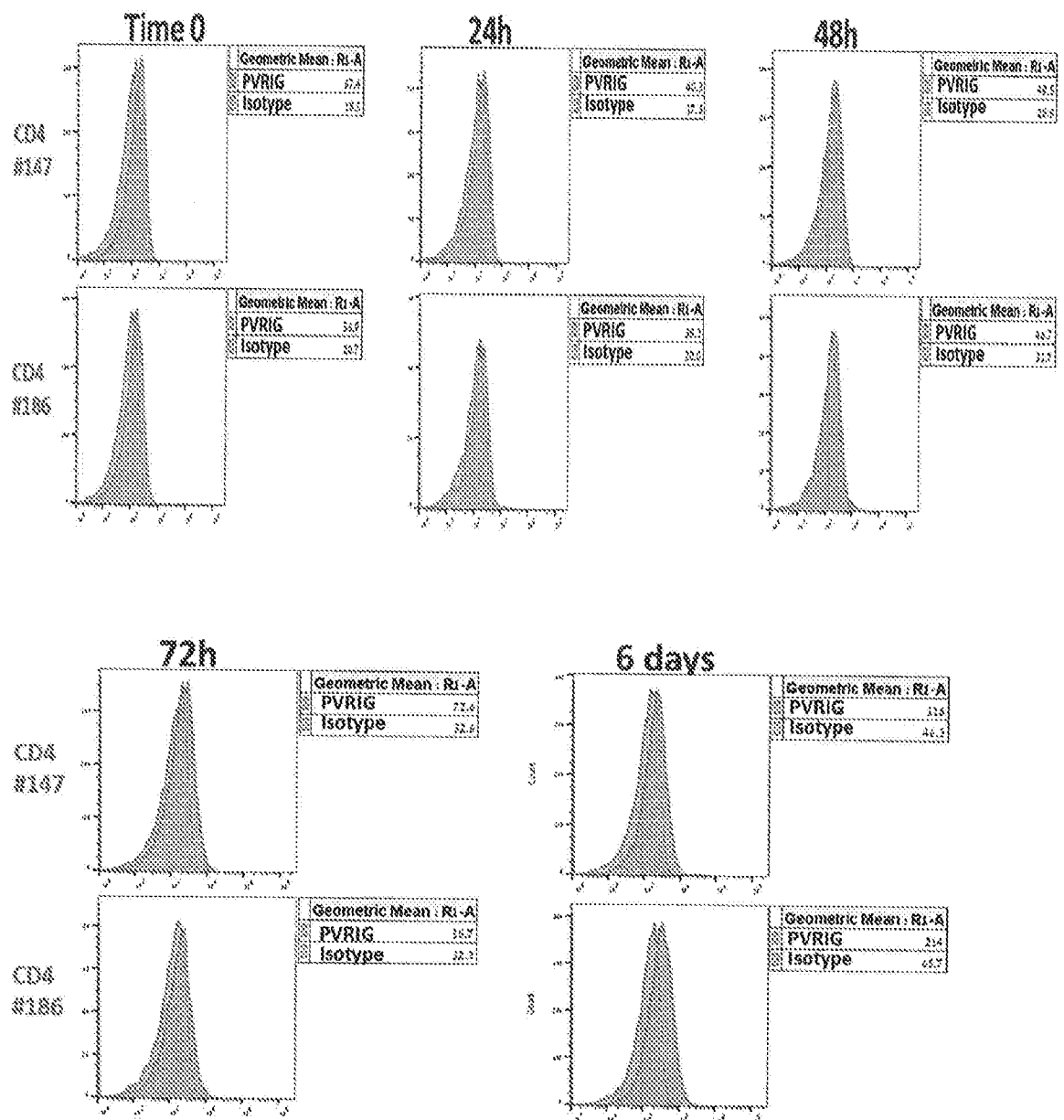


Figure 708

B

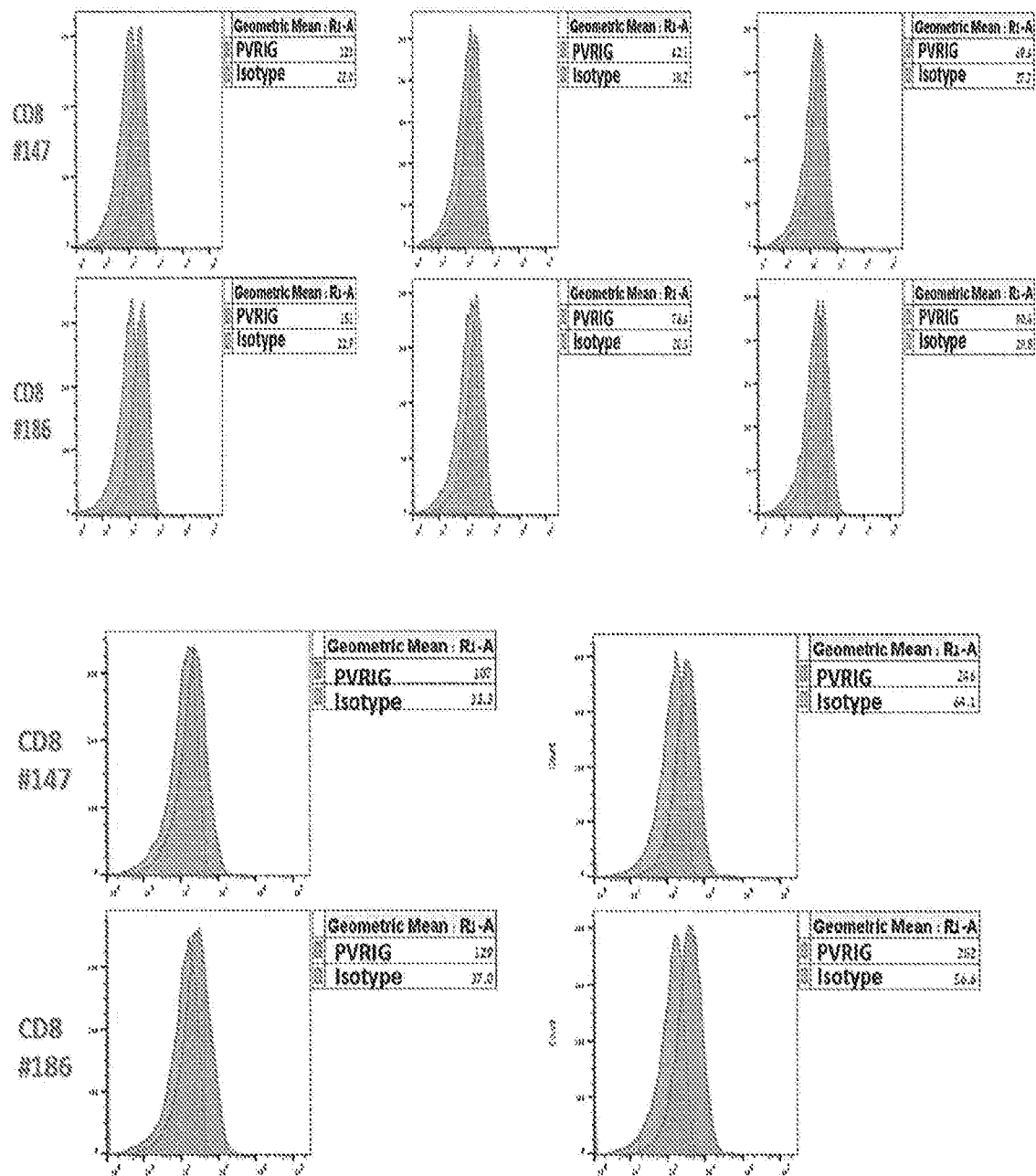


Figure 70C

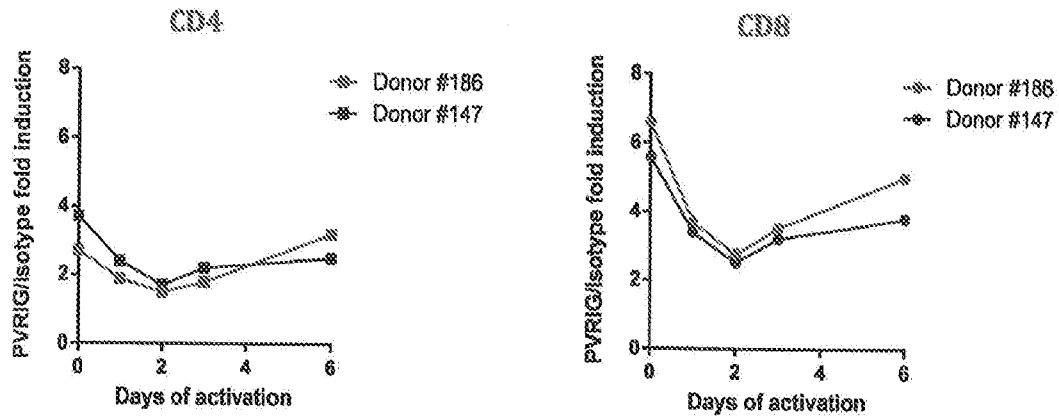


Figure 71A

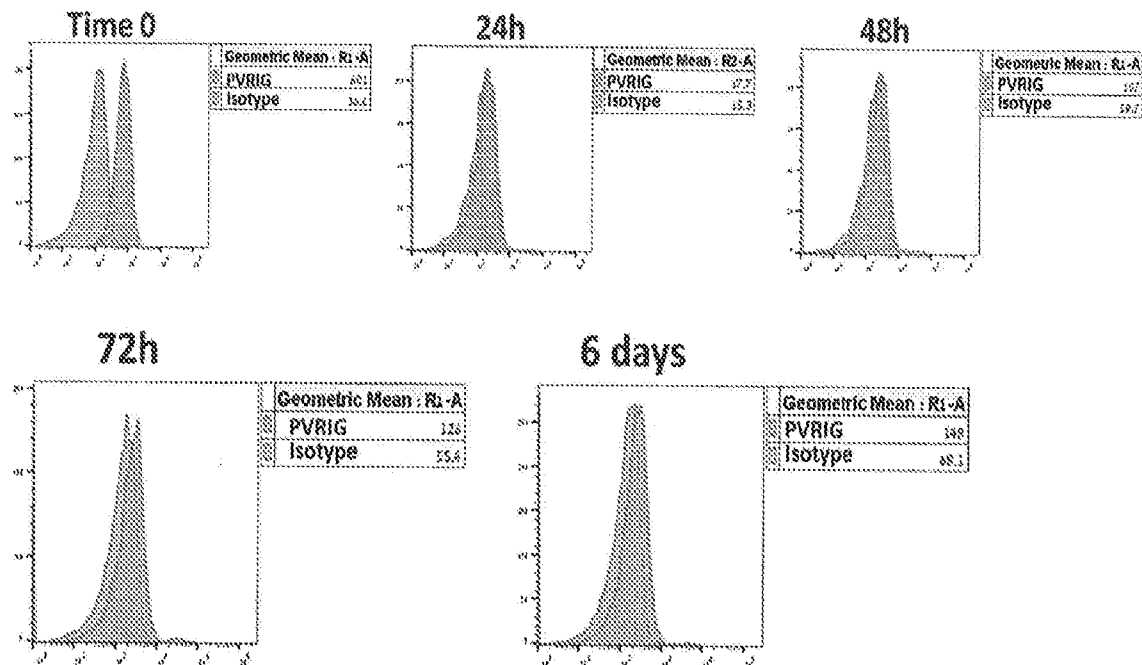


Figure 71B

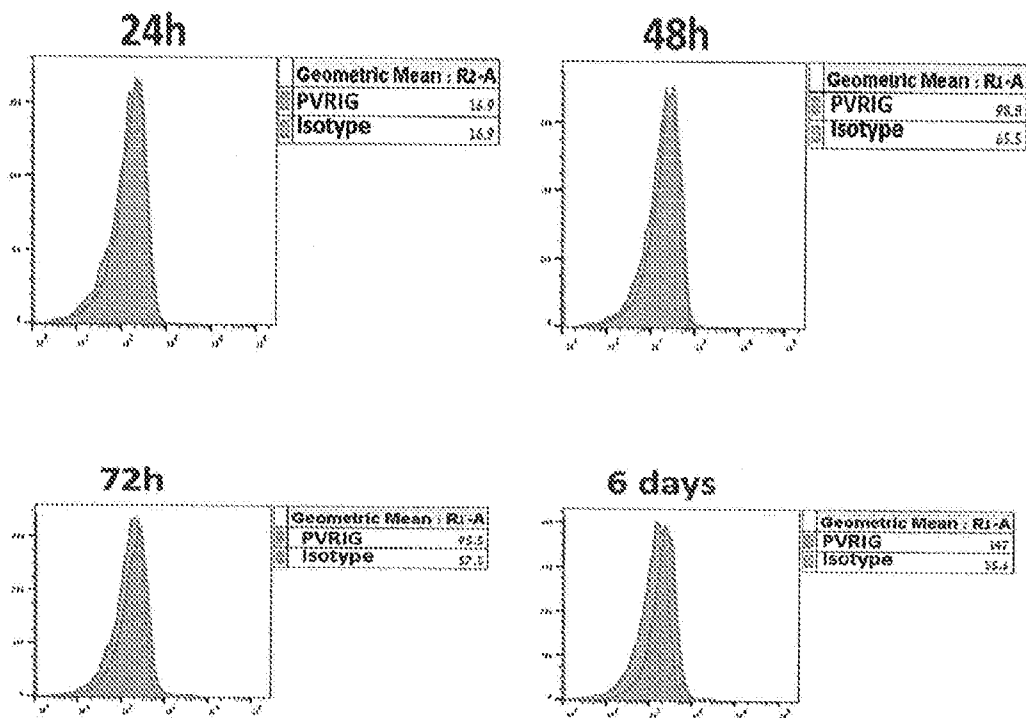


Figure 71C

C

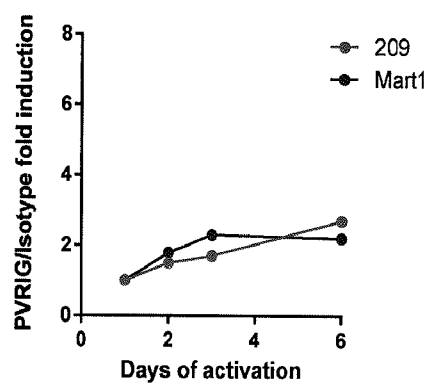


Figure 72

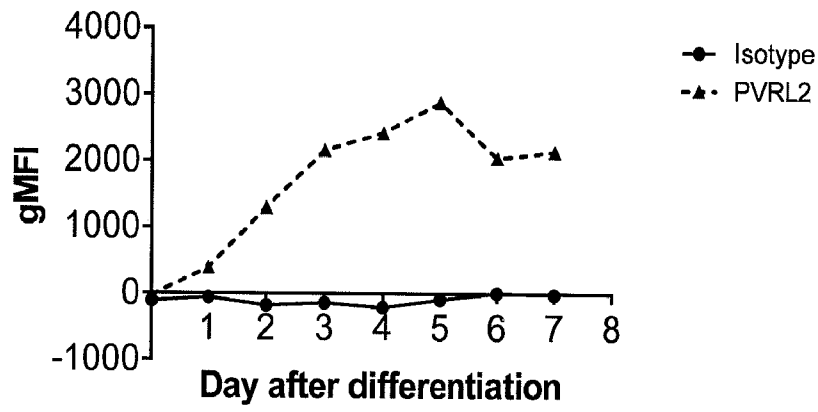


Figure 73A

A. CD4

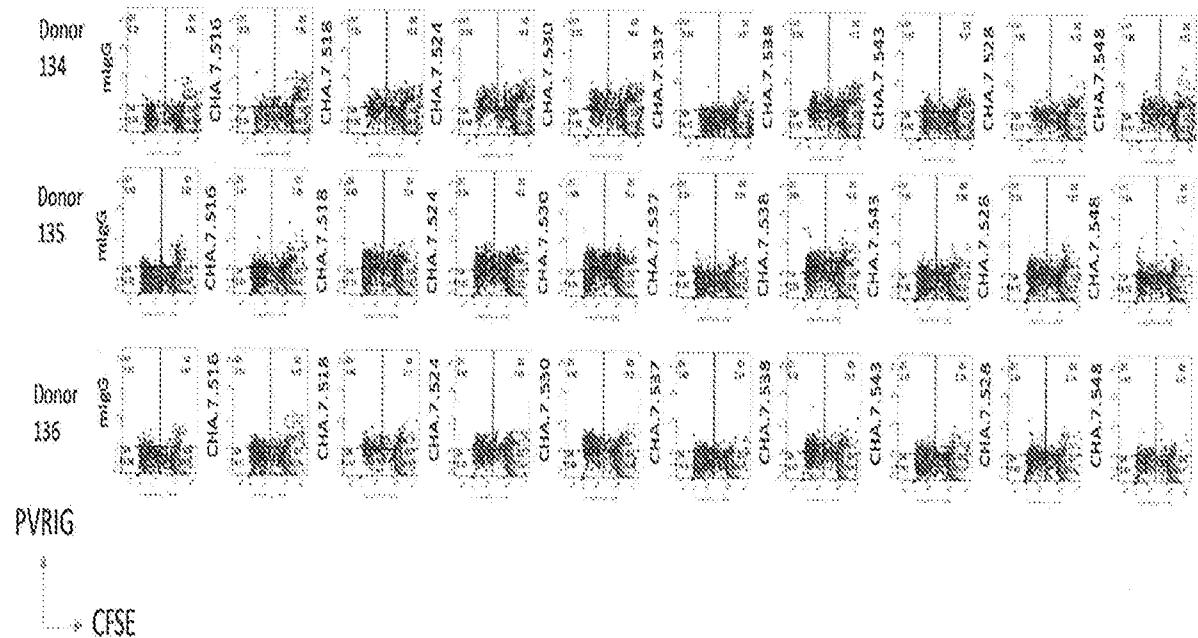


Figure 73B

B. CD8

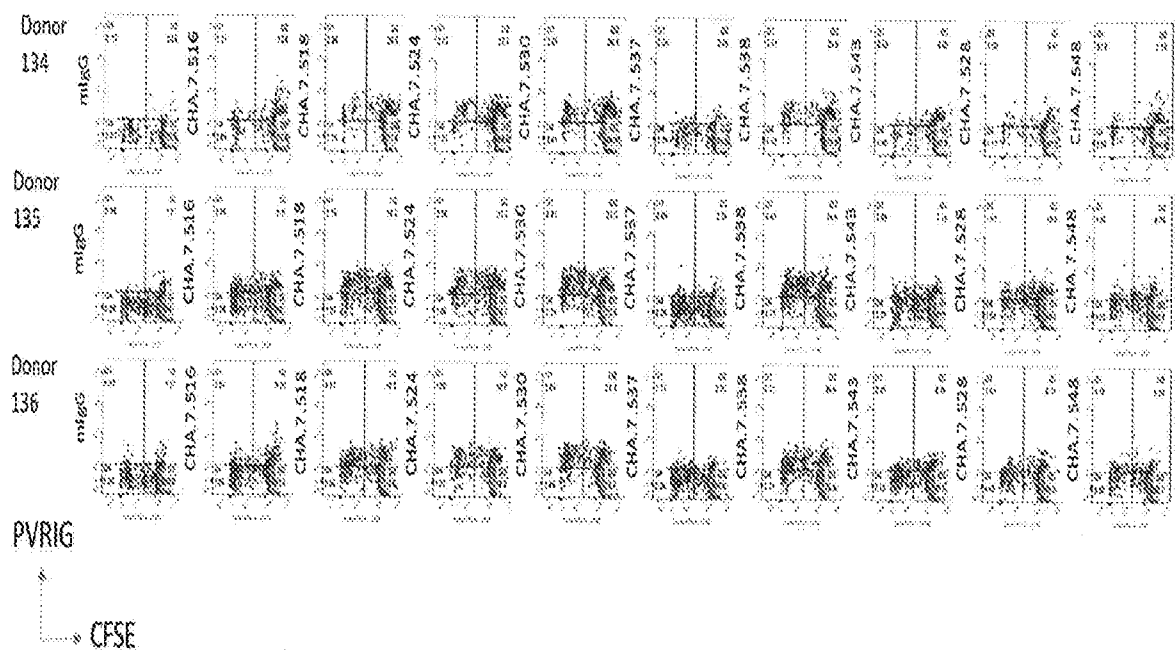


Figure 74A

PVRIG Expression on CD4+CFSE10 T cells

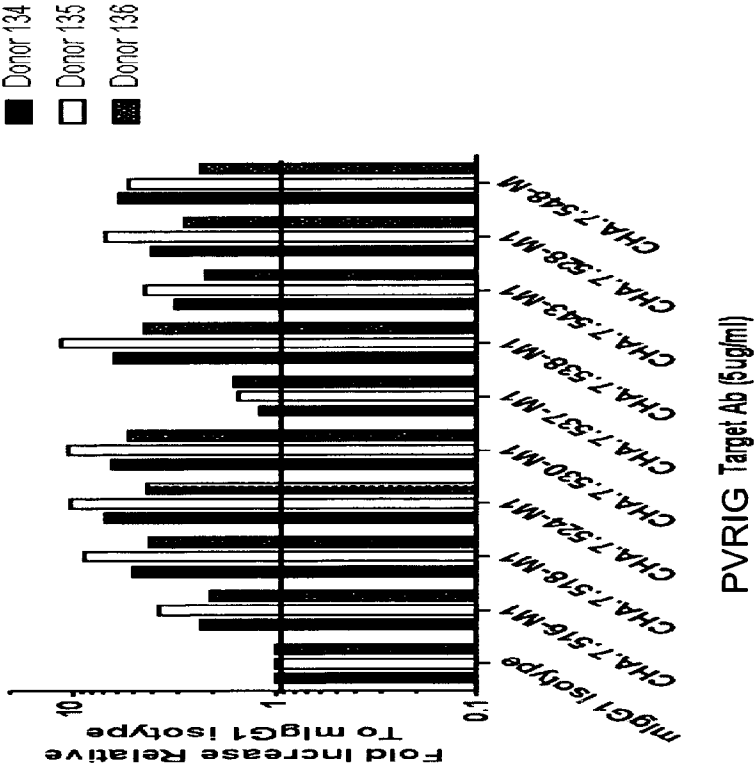


Figure 74B

PVRIG Expression on CD8+CFSE10 T cells

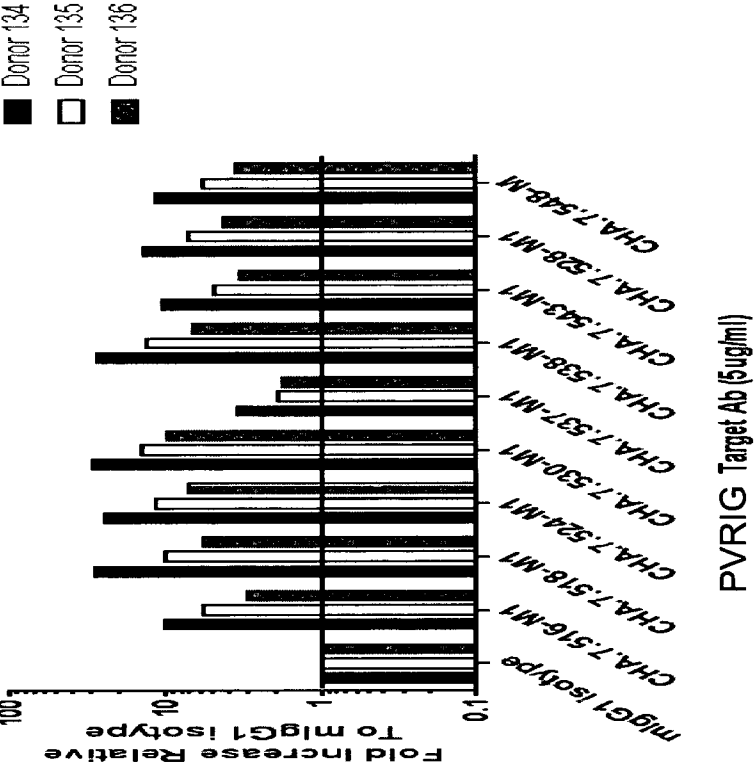


Figure 75A

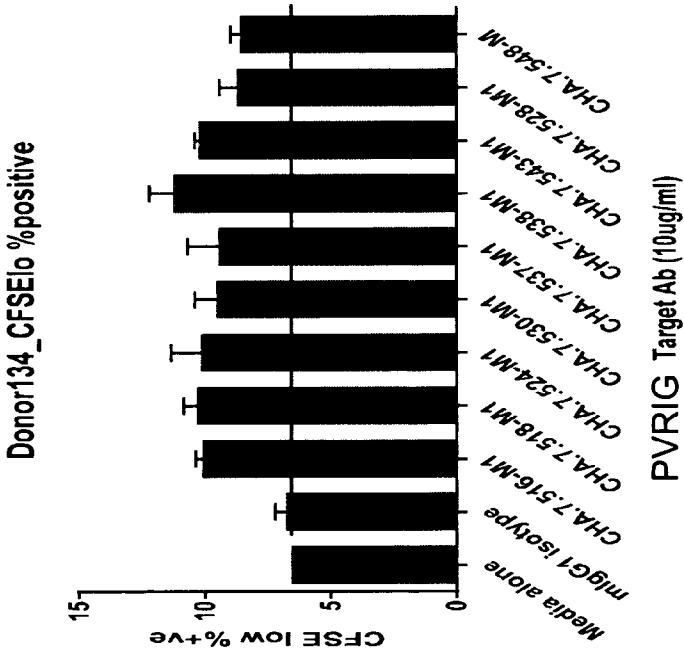


Figure 75B

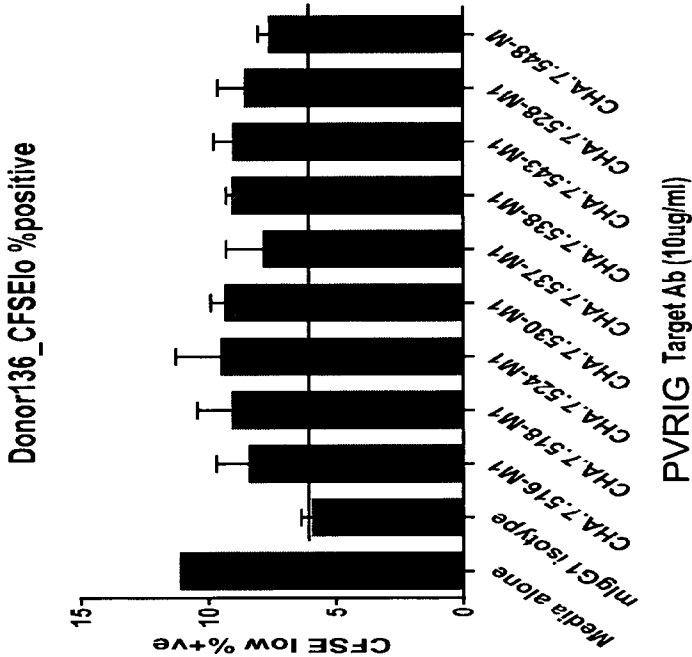


Figure 76

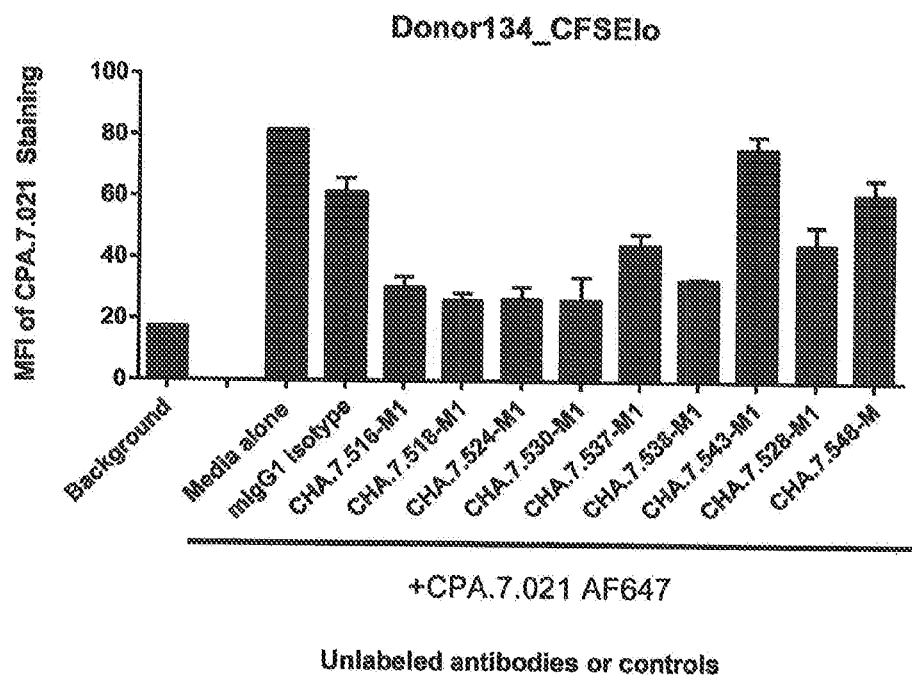


Figure 77

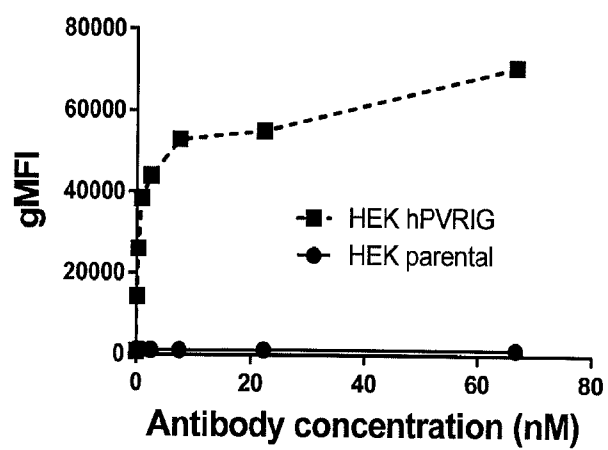


Figure 78

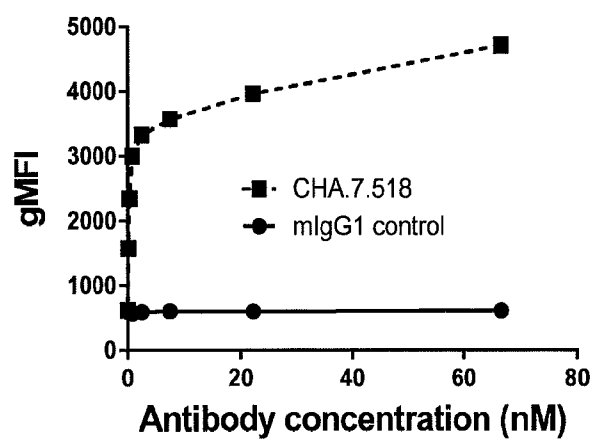


Figure 79A

Antibody (mIgG)	EC₅₀ (HEK OE, nM)	HEK OE/par (3.3ug/ml, gMFir)	Jurkat (3.3ug/ml, gMFir)
CHA.7.502	40.18	71.99	6.21
CHA.7.503	1.05	260.98	23.59
CHA.7.506	No binding	0.76	No binding
CHA.7.508	3.30	45.86	6.50
CHA.7.510	92.81	16.32	4.19
CHA.7.512	52.99	5.12	1.47
CHA.7.514	5.31	49.82	7.67
CHA.7.516	0.79	37.90	5.73
CHA.7.518	0.36	42.24	6.58
CHA.7.520	No binding	1.01	No binding
CHA.7.522	91.44	10.12	2.99
CHA.7.524	0.46	48.33	7.87
CHA.7.525	3.05	41.86	4.30
CHA.7.526	2.99	47.28	3.98
CHA.7.527	No binding	0.98	No binding
CHA.7.528	7.31	44.88	6.17
CHA.7.530	0.33	51.14	8.04
CHA.7.534	1.87	43.72	5.05
CHA.7.535	3.67	40.44	2.79
CHA.7.537	2.47	36.61	5.53

Figure 79B

CHA.7.538	0.52	35.80	7.37
CHA.7.543	0.52	49.81	6.73
CHA.7.544	0.76	42.60	5.68
CHA.7.545	0.76	44.31	6.53
CHA.7.546	0.61	43.14	6.42
CHA.7.547	14.37	10.94	1.02
CHA.7.548	0.27	45.26	7.37
CHA.7.549	2.60	29.71	2.23
CHA.7.550	1.34	27.72	2.10

Figure 80A

Antibody (mIgG)	Human CD56 int. NK (gMFir, 10ug/ml)	Human CD8+ T cells (gMFir, 10ug/ml)	Expi cyno OE/par (gMFir, 3.3ug/ml)	Cyno NK cells (gMFir, 10ug/ml)	Cyno CD8+ T cells (gMFir, 10ug/ml)
CHA.7.502	1.97	1.41	60.49	Not tested	Not tested
CHA.7.503	3.15	1.96	106.3	Not tested	Not tested
CHA.7.506	Not tested	Not tested	0.77	Not tested	Not tested
CHA.7.508	3.6	4.09	41.49	Not tested	Not tested
CHA.7.510	3.13	2.73	38.21	Not tested	Not tested
CHA.7.512	1.30	1.15	8.96	Not tested	Not tested
CHA.7.514	4.16	5.15	65.20	Not tested	Not tested
CHA.7.516	4.22	4.09	60.05	1.76	2.09
CHA.7.518	5.08	6.69	83.51	1.92	2.09
CHA.7.520	1.13	1.04	Not tested	Not tested	Not tested
CHA.7.522	2.06	1.90	27.24	Not tested	Not tested

Figure 80B

CHA.7.524	5.50	6.12	66.32	1.78	2.02
CHA.7.525	1.98	1.76	0.85	Not tested	Not tested
CHA.7.526	2.08	1.71	0.79	Not tested	Not tested
CHA.7.527	1.16	0.99	Not tested	Not tested	Not tested
CHA.7.528	3.08	3.63	12.2	1.21	1.18
CHA.7.530	6.04	6.47	60.80	1.73	1.89
CHA.7.534	2.60	1.96	46.27	Not tested	Not tested
CHA.7.535	2.24	1.28	0.82	Not tested	Not tested
CHA.7.537	3.90	3.41	1.55	1.18	1.19
CHA.7.538	6.49	6.17	15.16	1.36	1.45
CHA.7.543	4.48	4.33	0.83	1.35	1.39
CHA.7.544	2.36	2.54	61.09	Not tested	Not tested
CHA.7.545	2.54	2.82	0.91	Not tested	Not tested
CHA.7.546	2.75	2.95	0.85	Not tested	Not tested
CHA.7.547	2.21	1.13	26.65	Not tested	Not tested
CHA.7.548	3.15	3.35	4.25	1.18	1.09
CHA.7.549	3.05	1.42	1.00	Not tested	Not tested
CHA.7.550	1.60	1.29	0.90	Not tested	Not tested

Figure 81A

Antibody (mIgG)	IC₅₀ (nM)
CHA.7.502	39.90
CHA.7.503	No IC ₅₀
CHA.7.506	31.65
CHA.7.508	37.88
CHA.7.510	55.00
CHA.7.512	839.6
CHA.7.514	38.88
CHA.7.516	33.11
CHA.7.518	23.15
CHA.7.520	619.3
CHA.7.522	50.48
CHA.7.524	30.20
CHA.7.525	85.52
CHA.7.526	58.88
CHA.7.527	No IC ₅₀
CHA.7.528	28.88
CHA.7.530	34.56
CHA.7.534	181.4
CHA.7.535	821.1
CHA.7.537	38.95
CHA.7.538	51.87
CHA.7.543	No IC ₅₀

Figure 81B

CHA.7.544	No IC ₅₀
CHA.7.545	96.06
CHA.7.546	92.05
CHA.7.547	27.94
CHA.7.548	18.98
CHA.7.549	36.12
CHA.7.550	58.34

Figure 82

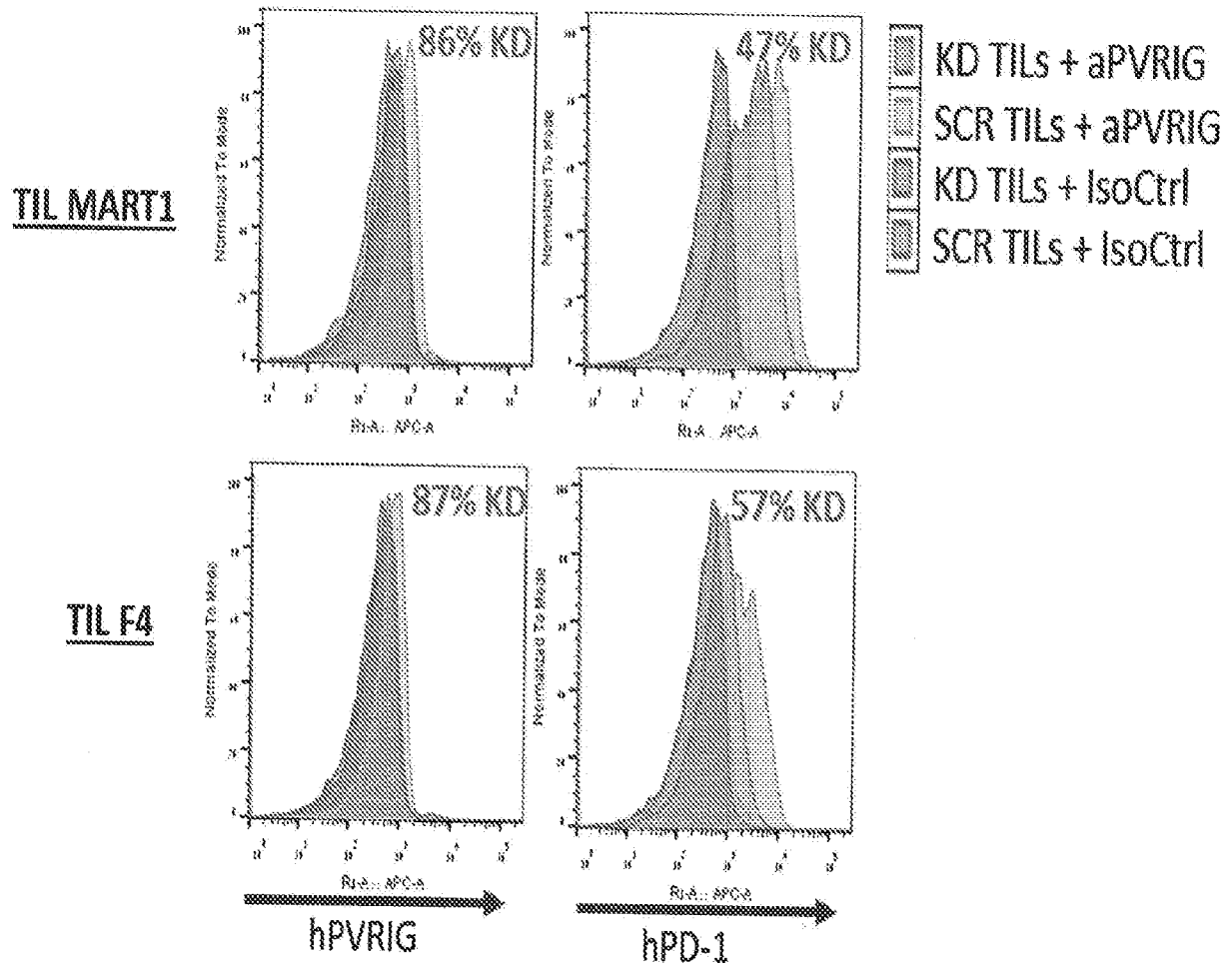


FIGURE 83A

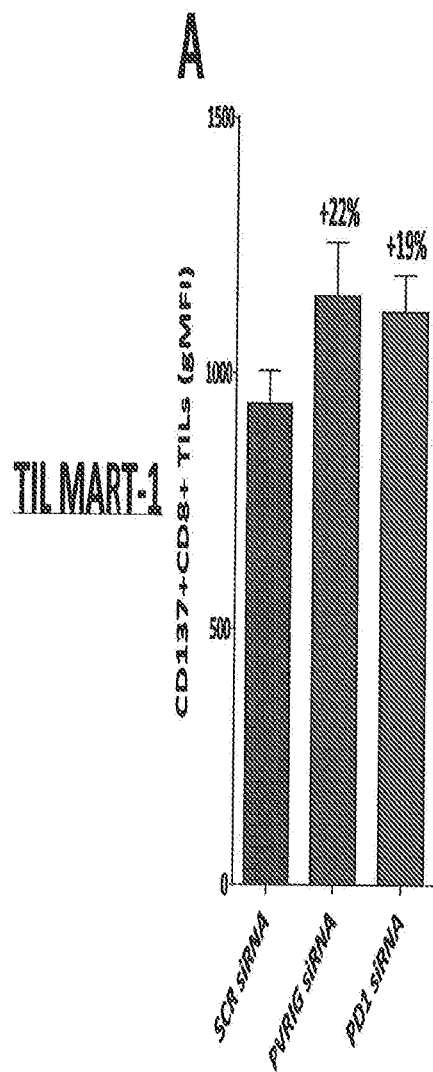


FIGURE 83B

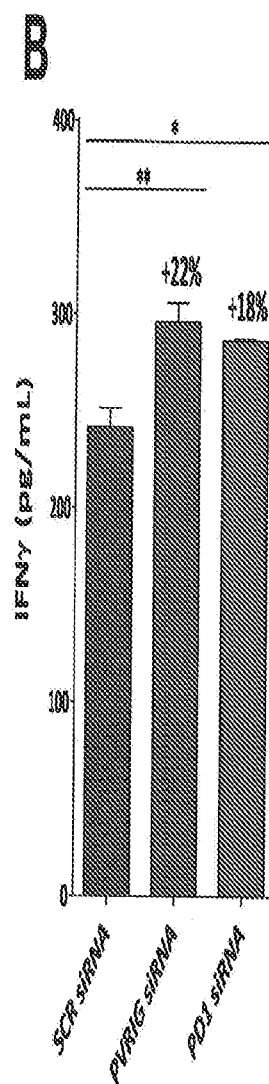
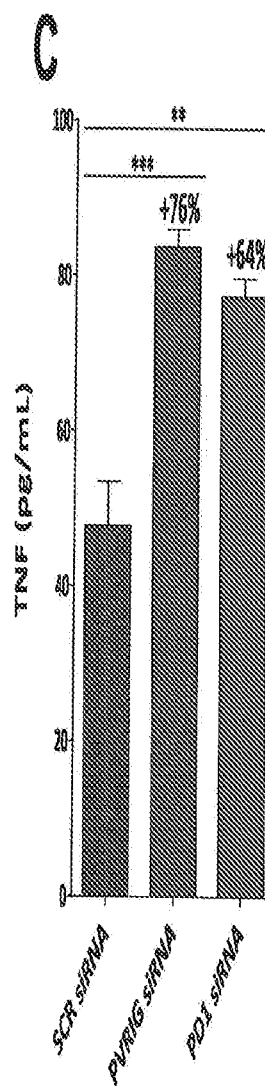


FIGURE 83C



TIL F4

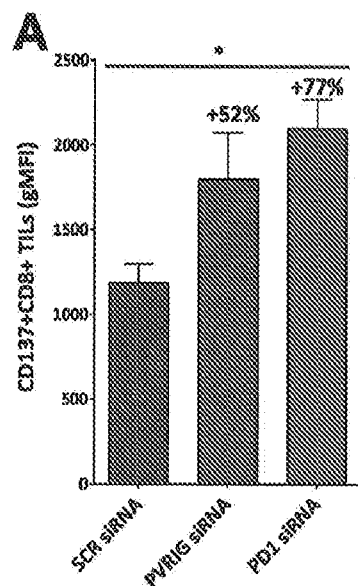


FIGURE 84A

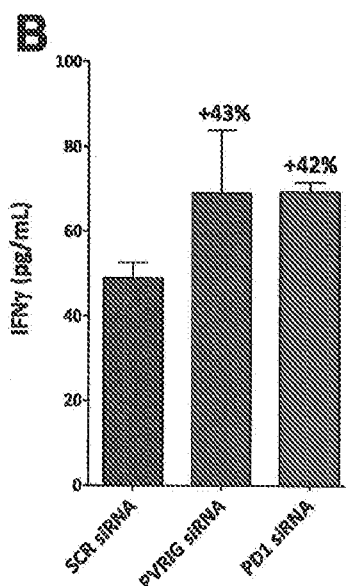


FIGURE 84B

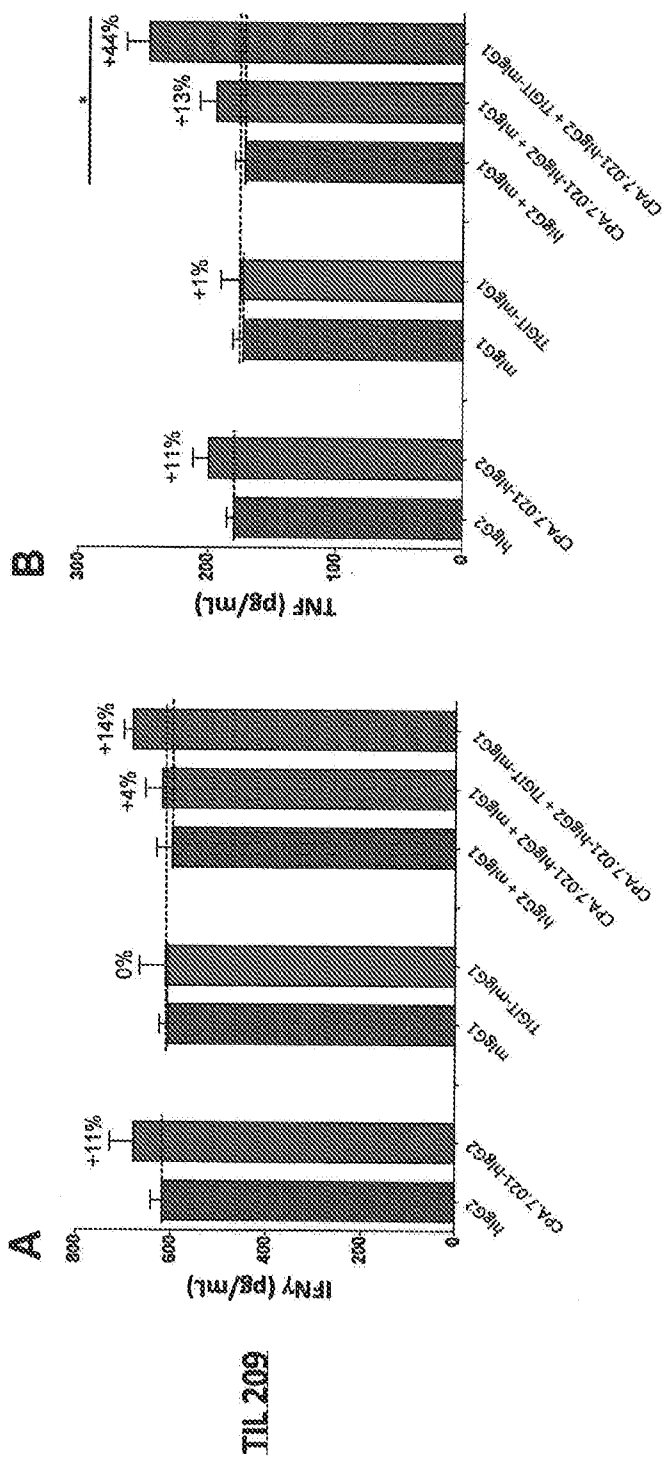
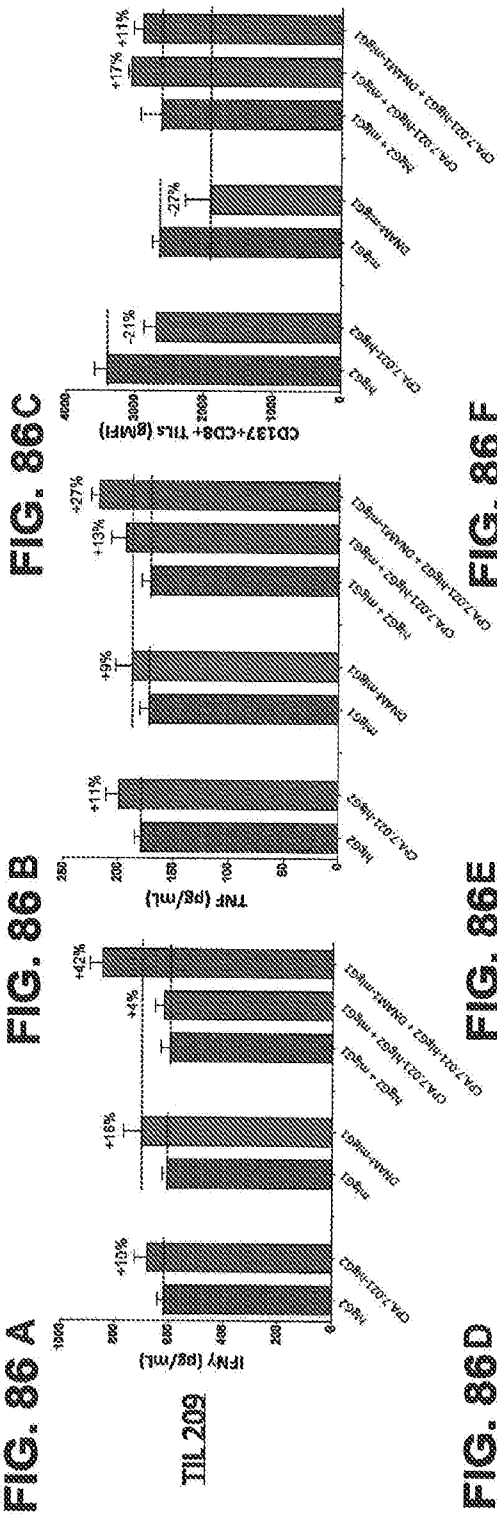
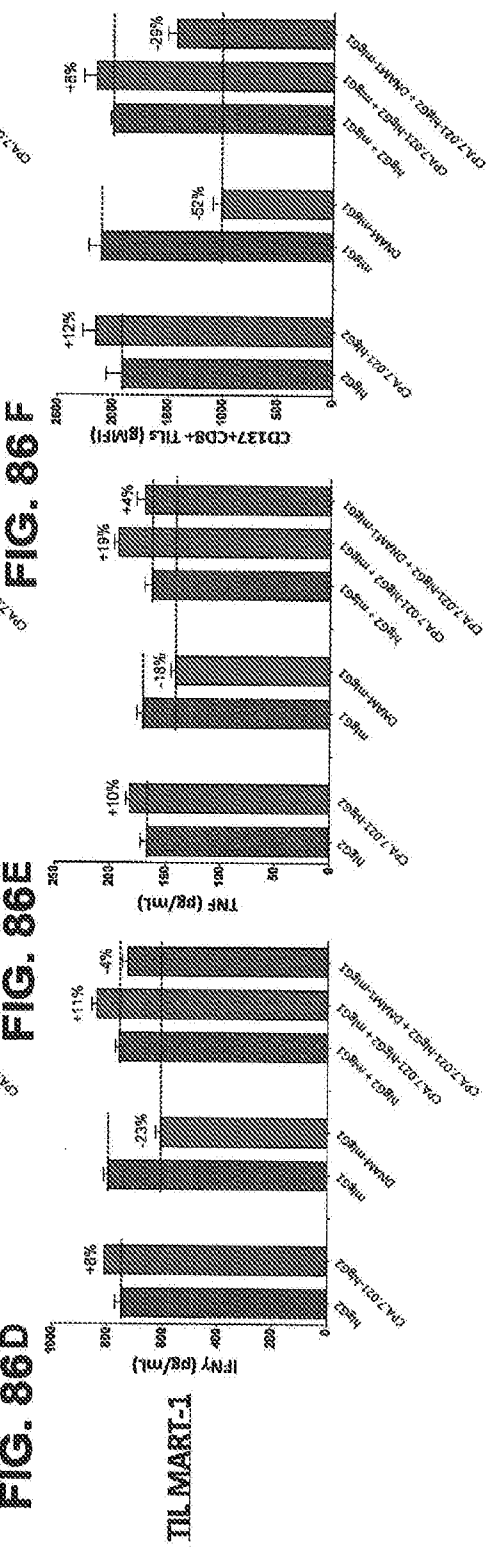
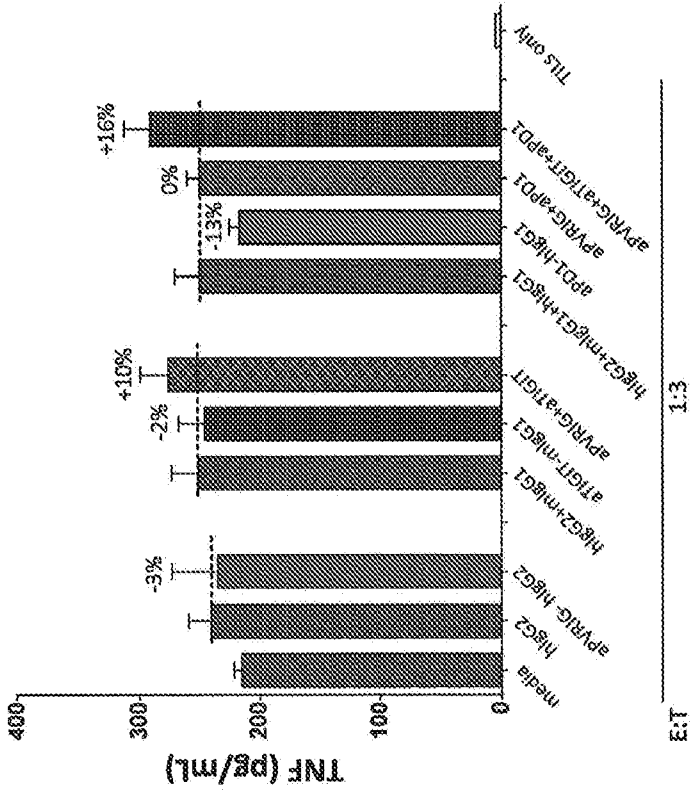


FIGURE 85B

FIGURE 85A



B



A

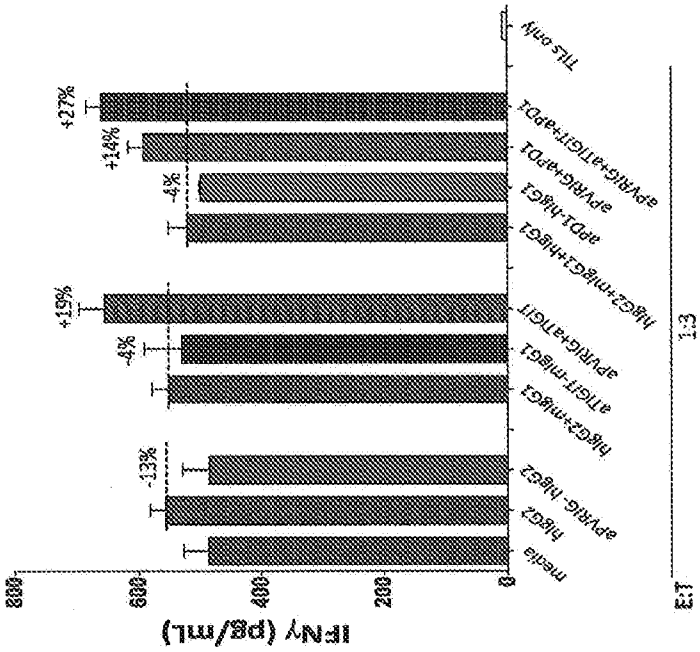


FIGURE 87A

FIGURE 87B

Figure 88A
Humanized sequences of CHA.7.518 antibody VH

Potential humanized sequence based on IMGT IGHV1-46*01 acceptor framework (AbM CDR definition)

IGHV1-46*01 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYMHVWRQAPGQGLEWMGIIINPSGGSTSYAQKFQGRVTMTTRDTSTSTVYMELSSLSRSEDSTAVYYCAR
 (SEQ ID NO: 1368)

Joining region IMGT J00256|IGHJ4*01|YFDYWGQGLTVTVSS (SEQ ID NO: 1369)

seq	10	20	30	40	50	60	70	80	90
AbM	10	20	30	40	50	60	70	80	90
	b b b	p b b b	b b b	b i i	i i b b	b	b b b x	b b b	b b b b b
518	EVQLQQSGPELVKPGASVKISCKAS	GYTFTDYNIN	WVKQSHGKSLEWIG	YIYPYIGGSG	YNQKFQGRVTMTTRDTSTSTVYMELSSLSRSEDSTAVYYCAR				
	* * *	* * *	* * *	* * *	* * *				
1-46*01	QVQLVQSGAEVKKPGASVKVCKAS	GYTFTSYMH	WVRQAPGQGLEWMG	IINPSGGSTS	YAQKFQGRVTMTTRDTSTSTVYMELSSLSRSEDSTAVYYCAR				
h518H1	QVQLVQSGAEVKKPGASVKVCKAS	GYTFTDYNIN	WVRQAPGQGLEWMG	YIYPYIGGSG	YNQKFQGRVTMTTRDTSTSTVYMELSSLSRSEDSTAVYYCAR				
h518H2	QVQLVQSGAEVKKPGASVKVCKAS	GYTFTDYNIN	WVRQAPGQGLEWMG	YIYPYIGGSG	YNQKFQGRVTMTTRDTSTSTVYMELSSLSRSEDSTAVYYCAR				
h518H3	QVQLVQSGAEVKKPGASVKISCKAS	GYTFTDYNIN	WVRQAPGQGLEWMG	YIYPYIGGSG	YNQKFQGRVTMTTRDTSTSTVYMELSSLSRSEDSTAVYYCAR				
h518H4	QVQLVQSGAEVKKPGASVKISCKAS	GYTFTDYNIN	WVRQAPGQGLEWMG	YIYPYIGGSG	YNQKFQGRVTMTTRDTSTSTVYMELSSLSRSEDSTAVYYCAR				

seq	100	110	120
AbM		i b b b	
518	EDKTARNANDY	WGQGITLVTVSS	(SEQ ID NO: 1370)
	*		(1-46*01 disclosed as SEQ ID NO: 1371)
h518H1	EDKTARNANDY	WGQGITLVTVSS	(SEQ ID NO: 1372)
h518H2	EDKTARNANDY	WGQGITLVTVSS	(SEQ ID NO: 1373)
h518H3	EDKTARNANDY	WGQGITLVTVSS	(SEQ ID NO: 1374)
h518H4	EDKTARNANDY	WGQGITLVTVSS	(SEQ ID NO: 1375)

deamidation substitutions: Q/S/A

Figure 88B
Humanized sequences of CHA.7.518 antibody VL

Potential humanized sequence based on IMGT IGKV1-39*01 acceptor framework

IGKV1-39*01
 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRFGSGSGTDFTLTISLQPEDFATYYCQQSYSTPP (SEQ ID NO: 1376)

Joining region IMGT J00242|IGKJ2*01|YTFGGTKLEIK (SEQ ID NO: 1377)

seq	10	20	30	40	50	60	70	80
AbM	10	20	30	40	50	60	70	80
	b b b	p p p	b b b	b b b	i i i	b b b	b b b	ib bib
518	DIQMTQSPASLSVSGEVTIIC	RVSENIYSNLA	WYQQKQKSPQLLVY	EATNLAE	GVPSRFGSGSGTDYTLTISSLQSEDFGSYYC	***	*	*
	*	*	*	*	*	*	*	*
IGKV1-39	DIQMTQSPSSLSASVGDRVTITC	RASQSISSYL	WYQQKPGKAPKLLIY	AASSLQ	GVPSRFGSGSGTDFTLTISLQPEDFATYYC			
h518L1	DIQMTQSPSSLSASVGDRVTITC	RVSENIYSNLA	WYQQKPGKAPKLLIY	EATNLAE	GVPSRFGSGSGTDFTLTISLQPEDFATYYC			
h518L2	DIQMTQSPSSLSASVGDRVTITC	RVSENIYSNLA	WYQQKPGKAPKLLIY	EATNLAE	GVPSRFGSGSGTDYTLTISSLQPEDFATYYC			
h518L3	DIQMTQSPSSLSASVGDRVTITC	RVSENIYSNLA	WYQQKPGKAPKLLIY	EATNLAE	GVPSRFGSGSGTDYTLTISSLQPEDFATYYC			

seq 90 100
AbM 90 100
 ibi iib i b b b
 518 QHFWGTPYT FGGTKLEIK (SEQ ID NO: 1378)

IGKV1-39 QQSYSTPP (SEQ ID NO: 1379)
 h518L1 QHFWGTPYT FGGTKLEIK (SEQ ID NO: 1380)
 h518L2 QHFWGTPYT FGGTKLEIK (SEQ ID NO: 1381)
 h518L3 QHFWGTPYT FGGTKLEIK (SEQ ID NO: 1382)

deamidation substitutions: Q/S/A/D
 @ tryptophan oxidation substitutions: Y/F/H

Figure 88D

humanized sequences of CHA.7.524 antibody VL

Potential humanized sequence based on IMGT IGKV3-11*01 acceptor framework

IGKV3-11*01
 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIIYDASNRAFGIPARFSGSGGTDTLTITSSLEPEDFAVYYCQQRSNWPP (SEQ ID NO: 1391)
 Joining region IMGT J00242|IGKJ2*01|YTFGQGTKLEIK (SEQ ID NO: 1392)

seq	10	20	30	40	50	60	70	80
AbM	10	20	30	40	50	60	70	80
524	b b b	p p	b b b	b b b	i i	b b	b b b	ib bib
	QIVLTQSPALMSASPGEKVTWTC	NASSSVS-YMY	WYQQKPGQAPRLIIY	DTSNLLAS	GVVPRFSGSGGTDTLTITSSLEPEDFAVYYC	***	***	***
	*	***	***	***	***	***	***	***
IGKV3-11	EIVLTQSPATLSLSPGERATLSC	RASQSVSSYLA	WYQQKPGQAPRLIIY	DASNRA	GIPARFSGSGGTDTLTITSSLEPEDFAVYYC	***	***	***
h524L1	EIVLTQSPATLSLSPGERATLSC	NASSSVS-YMY	WYQQKPGQAPRLIIY	DTSNLLAS	GIPARFSGSGGTDTLTITSSLEPEDFAVYYC	***	***	***
h524L2	EIVLTQSPATLSLSPGERATLSC	NASSSVS-YMY	WYQQKPGQAPRLIIY	DTSNLLAS	GIPARFSGSGGTDTLTITSSLEPEDFAVYYC	***	***	***
h524L3	EIVLTQSPATLSLSPGERATLSC	NASSSVS-YMY	WYQQKPGQAPRLIIY	DTSNLLAS	GIPARFSGSGGTDTLTITSSLEPEDFAVYYC	***	***	***

seq	90	100
AbM	90	100
524	ibi iib i	b b b
	QQWSSYPLT	FGAGTKVEIK
	*	*
IGKV3-11	QQRSNWPP	(SEQ ID NO: 1394)
h524L1	QQWSSYPLT	FGQGTKLEIK
h524L2	QQWSSYPLT	FGQGTKLEIK
h524L3	QQWSSYPLT	FGQGTKLEIK

deamidation substitutions: Q/S/A/D
 @ tryptophan oxidation substitutions: Y/F/H

Figure 88E
Humanized sequences of CHA.7.530 antibody VH

Potential humanized sequence based on IMGT IGHV1-46*01 acceptor framework

IGHV1-46*01

QVQLVQSGAEVKKPGASVKVCKASGYFTTSYMHVVRQAPGQGLEWMGIINPSSGGSTSYAQKFQGRVTMTDSTSTVYMESSLRSEDTAIVYCAR (SEQ ID NO: 1398)

Joining region IMGT J00256|IGHJ4*01|YFDYWGQGLTVTVSS (SEQ ID NO: 1399)

seq	10	20	30	40	50	60	70	80	90
AbM	10	20	30	40	50	60	70	80	90
	b b b	p b b b	b b b	b b i i	i i b b b	i b b b x	b b b b	b b b b	b i b b b
530	QVQLVQSGAEVKKPGASVKVCKAS	GYFTTSYMH	WVRQAPGQGLEWMG	IINPSSGGST	SYAQKFQGRVTMTDSTSTVYMESSLRSEDTAIVYCAR	YNEKFKDKATLTADKSSSTAYMQLSLTSDDSAIVYFCAR	***	***	***
1-46*01	QVQLVQSGAEVKKPGASVKVCKAS	GYFTTSYMH	WVRQAPGQGLEWMG	IINPSSGGST	SYAQKFQGRVTMTDSTSTVYMESSLRSEDTAIVYCAR	YNEKFKDKATLTADKSSSTAYMQLSLTSDDSAIVYFCAR	***	***	***
h530H1	QVQLVQSGAEVKKPGASVKVCKAS	GYFTTSYMH	WVRQAPGQGLEWMG	IINPSSGGST	SYAQKFQGRVTMTDSTSTVYMESSLRSEDTAIVYCAR	YNEKFKDKATLTADKSSSTAYMQLSLTSDDSAIVYFCAR	***	***	***
h530H2	QVQLVQSGAEVKKPGASVKVCKAS	GYFTTSYMH	WVRQAPGQGLEWMG	IINPSSGGST	SYAQKFQGRVTMTDSTSTVYMESSLRSEDTAIVYCAR	YNEKFKDKATLTADKSSSTAYMQLSLTSDDSAIVYFCAR	***	***	***
h530H3	QVQLVQSGAEVKKPGASVKVCKAS	GYFTTSYMH	WVRQAPGQGLEWMG	IINPSSGGST	SYAQKFQGRVTMTDSTSTVYMESSLRSEDTAIVYCAR	YNEKFKDKATLTADKSSSTAYMQLSLTSDDSAIVYFCAR	***	***	***
h530H4	QVQLVQSGAEVKKPGASVKVCKAS	GYFTTSYMH	WVRQAPGQGLEWMG	IINPSSGGST	SYAQKFQGRVTMTDSTSTVYMESSLRSEDTAIVYCAR	YNEKFKDKATLTADKSSSTAYMQLSLTSDDSAIVYFCAR	***	***	***

seq	100	110	110
AbM	100	110	110
	i b b b	i b b b	i b b b
530	SLYVNSWVFVY	WGQGLTVTVSS	(SEQ ID NO: 1400)
h530H1	SLYVNSWVFVY	WGQGLTVTVSS	(SEQ ID NO: 1402)
h530H2	SLYVNSWVFVY	WGQGLTVTVSS	(SEQ ID NO: 1403)
h530H3	SLYVNSWVFVY	WGQGLTVTVSS	(SEQ ID NO: 1404)
h530H4	SLYVNSWVFVY	WGQGLTVTVSS	(SEQ ID NO: 1405)

deamidation substitutions: Q/S/A

@ tryptophan oxidation substitutions: Y/F/H

Figure 88F

Humanized sequences of CHA.7.530 antibody VL

Potential humanized sequence based on IMGT IGKV1-39*01 acceptor framework (AbM CDR definition)
 IGKV1-39*01

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRFGSGSGTDFTLTISSLPEDFATYYCQQSYSTPP (SEQ ID NO: 1406)

Joining region IMGT J00242|IGKJ2*01|YTFGQGTKLEIK (SEQ ID NO: 1407)

seq	10	20	30	40	50	60	70	80
AbM	10	20	30	40	50	60	70	80
	b b b	p p p	b b b	b i b i	i i i b b i	i b b	b b b b	b b b b
530	DIQMTQSPASLSASVGETVTITC	**	RASENIYSYLA	WYQKPGKSPQLLIVY	NAKTLVE	GVPSRFGSGSGTQFSLKINSIQPEDFGSYVC		
	*			*	*	*	*	*
IGKV1-39	DIQMTQSPSSLSASVGDRVTITC	RASQSISSYLN	WYQKPGKAPKLLIY	AASSLQ	GVPSRFGSGSGTDFTLTISSLPEDFATYYC			
h530L1	DIQMTQSPSSLSASVGDRVTITC	RASENIYSYLA	WYQKPGKAPKLLIY	NAKTLVE	GVPSRFGSGSGTDFTLTISSLPEDFATYYC			
h530L2	DIQMTQSPSSLSASVGDRVTITC	RASENIYSYLA	WYQKPGKAPKLLIY	NAKTLVE	GVPSRFGSGSGTDFTLTISSLPEDFATYYC			
		#	S	#				

seq	90	100
AbM	90	100
	i b i	i b b b
530	QHVGTPYT	FGGGTKLEIK
	*	
IGKV1-39	QQSYSTPP	(SEQ ID NO: 1409)
h530L1	QHVGTPYT	FGGGTKLEIK
h530L2	QHVGTPYT	FGGGTKLEIK

deamidation substitutions: Q/S/A/D

Figure 88G**Humanized sequences of CEA.7.538_1 antibody VH**

Potential humanized sequence based on IMGT IGHV1-46*01 acceptor framework

IGHV1-46*01

QVQLVQSGAEVKKPGASVKVCKASGYFTFSYMHVWRQAPGQGLEWMGIINPSGGSTSYAQKFQGRVTMTTRDTSTSTVYMELSSLRSEDTAIVYCAR (SEQ ID NO: 1412)

Joining region IMGT J00256|IGHJ4*01|YFDYWGQGLVTVSS (SEQ ID NO: 1413)

seq	10	20	30	40	50	60	70	80	90
AbM	10	20	30	40	50	60	70	80	90
	b b b	p b b	b b b	b b i	i b b	b	a	b	b
538_1	QVQLQSGAEVLRPGASVKVCKTS	GYAFTNYLIE	WVKQRPQGQLEWIG	VINP	GGGIY	YNDKFKVKITLTADKSSSTAYNQSLTSDSDSAVYFCAR			
	*	***	*	*	*	***	*	*	*
1-46*01	QVQLVQSGAEVKKPGASVKVCKAS	GYFTFSYMH	WVRQAPGQGLEWMG	IINP	SGGSTS	YAQKFQGRVTMTTRDTSTSTVYMELSSLRSEDTAIVYCAR			
h5381H1	QVQLVQSGAEVKKPGASVKVCKAS	GYAFTNYLIE	WVRQAPGQGLEWMG	VINP	SGGGIY	YAQKFQGRVTMTTRDTSTSTVYMELSSLRSEDTAIVYCAR			
h5381H2	QVQLVQSGAEVKKPGASVKVCKAS	GYAFTNYLIE	WVRQAPGQGLEWMG	VINP	SGGGIY	YAQKFQGRVTMTTRDTSTSTVYMELSSLRSEDTAIVYCAR			
h5381H3	QVQLVQSGAEVKKPGASVKVCKTS	GYAFTNYLIE	WVRQAPGQGLEWIG	VINP	SGGGIY	YAQKFQGRVTMTTRDTSTSTVYMELSSLRSEDTAIVYCAR			
h5381H4	QVQLVQSGAEVKKPGASVKVCKTS	GYAFTNYLIE	WVRQAPGQGLEWIG	VINP	SGGGIY	YAQKFQGRVTMTTRDTSTSTVYMELSSLRSEDTAIVYCAR			

seq	100	110
AbM	i	b b b
538_1	SETHDTWFAY	WGQGLVTVSSA
	*	(1-46*01 disclosed as SEQ ID NO: 1415)
h5381H1	SETHDTWFAY	WGQGLVTVSS
h5381H2	SETHDTWFAY	WGQGLVTVSS
h5381H3	SETHDTWFAY	WGQGLVTVSS
h5381H4	SETHDTWFAY	WGQGLVTVSS

deamidation substitutions: Q/S/A

@ tryptophan oxidation substitutions: Y/F/H

Figure 88H
humanized sequences of CHA.7.538_1 antibody VL
 Potential humanized sequence based on IMGT IGV1-39*01 acceptor framework
 IGV1-39*01
 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSIQGVPSRFSGSGTDFTLTITSSLOPEDFATYYCQQSYSTPP (SEQ ID NO: 1420)

Joining region IMGT J00242|IGKJ2*01|YTFGGGTKLEIK (SEQ ID NO: 1421)
 IGV1-17*02
 DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLWYQQKPGKAPKRLIYAASSIQGVPSRFSGSGTDFTLTITSSLOPEDFATYYCLOHNSYPP (SEQ ID NO: 1422)

seq	10	20	30	40	50	60	70	80
AbM	10	20	30	40	50	60	70	80
	b b b	p p p	b b b	bi bi i	ii ibbi	i b b	b b b	ib bib
538	DIQMTQSPSSLSASVGDRVTITC	KASQSVRIAVA	WFOQKPGQSPKALII	LASTRHT	GVPSRFSGSGTDFTLTITSSLOPEDFATYYC	QQSYSTPP	FGGGTKLEIK	YTFGGGTKLEIK
	*	****	*	*	*	*	*	*
IGKV1-39	DIQMTQSPSSLSASVGDRVTITC	RASQSISSYL	WYQQKPGKAPKLLI	AASSLQS	GVPSRFSGSGTDFTLTITSSLOPEDFATYYC	QQSYSTPP	FGGGTKLEIK	YTFGGGTKLEIK
h538L1	DIQMTQSPSSLSASVGDRVTITC	KASQSVRIAVA	WYQQKPGKAPKLLI	LASTRHT	GVPSRFSGSGTDFTLTITSSLOPEDFATYYC	QQSYSTPP	FGGGTKLEIK	YTFGGGTKLEIK
h538L2	DIQMTQSPSSLSASVGDRVTITC	KASQSVRIAVA	WYQQKPGKAPKLLI	LASTRHT	GVPSRFSGSGTDFTLTITSSLOPEDFATYYC	QQSYSTPP	FGGGTKLEIK	YTFGGGTKLEIK
	I	T	S					L F

seq	90	100
AbM	90	100
	ibi iib i	b b b
538	LQHMNYPYT	FGGGTKLEIK
	*	
IGKV1-39	QQSYSTPP	(SEQ ID NO: 1424)
h538L1	LQHMNYPYT	FGGGTKLEIK
h538L2	LQHMNYPYT	FGGGTKLEIK
	@##	

deamidation substitutions: Q/S/A/D
 @ tryptophan oxidation substitutions: Y/F/H

Figure 88I

humanized sequences of CEA.7.538_2 antibody VH

Potential humanized sequence based on IMGT IGHV1-46*01 acceptor framework

IGHV1-46*01

QVQLVQSGAEVKPGASVKVSCKASGYTFTSYMHVVRQAPGQGLEWMGIINPSSGTSVAQKFQGRVTMTDSTSTVYMEISSLRSEDTAVYYCAR (SEQ ID NO: 1427)

Joining region

IMGT J00256|IGHJ4*01|YFDYWGQGTLVTVSS (SEQ ID NO: 1428)

seq	10	20	30	40	50	60	70	80	90
AbM	10	20	30	40	50	60	70	80	90
538_2	b b b	p b b b	b b b	b i i	i i b b	b	b b x	b b b	b b i b i b b
1-46*01	QVQLVQSGAEVKPGASVKVSCKAS	GYTFTSYMH	VVRQAPGQGLEWMGI	INPSSGTS	VAQKFQGRVTMTDSTSTVYMEISSLRSEDTAVYYCAR				
h5382H1	QVQLVQSGAEVKPGASVKVSCKAS	GYTFTSYMH	VVRQAPGQGLEWMGI	INPSSGTS	VAQKFQGRVTMTDSTSTVYMEISSLRSEDTAVYYCAR				
h5382H2	QVQLVQSGAEVKPGASVKVSCKAS	GYTFTSYMH	VVRQAPGQGLEWMGI	INPSSGTS	VAQKFQGRVTMTDSTSTVYMEISSLRSEDTAVYYCAR				
h5382H3	QVQLVQSGAEVKPGASVKVSCKAS	GYTFTSYMH	VVRQAPGQGLEWMGI	INPSSGTS	VAQKFQGRVTMTDSTSTVYMEISSLRSEDTAVYYCAR				

seq	100	110
AbM	100	110
538_2	PTGSSYGAF	WGQGLTVTSA
h5382H1	PTGSSYGAF	WGQGLTVTSA
h5382H2	PTGSSYGAF	WGQGLTVTSA
h5382H3	PTGSSYGAF	WGQGLTVTSA

deamidation substitutions: Q/S/A

@ tryptophan oxidation substitutions: Y/F/H

Figure 89A

humanized CHA.7.518 VH	
h518HH1	QVQLVQSGAEVKKPGASVKVCKASGYTFTDYNINWVRQAPGQGLEWMGYIYPYIGGSGYAQKFQGRVTMTTRDTSTSTVY MELSSLRSEDTAVYYCAREDKTARNAMDYWGQGLVTVSS (SEQ ID NO: 1434)
h518HH2	QVQLVQSGAEVKKPGASVKVCKASGYTFTDYNINWVRQAPGQGLEWIGYIYPYIGGSGYAQKFQGRVTMTADTSTSTVY MELSSLRSEDTAVYYCAREDKTARNAMDYWGQGLVTVSS (SEQ ID NO: 1435)
h518HH3	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYNINWVRQAPGQGLEWIGYIYPYIGGSGYAQKFQGRATLTADTSTSTAYM ELSSLRSEDTAVYYCAREDKTARNAMDYWGQGLVTVSS (SEQ ID NO: 1436)
h518HH4	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYNINWVRQAPGQGLEWIGYIYPYIGGSGYAQKFQGRATLTADNSTSTAYM ELSSLRSEDTAVYYCAREDKTARNAMDYWGQGLVTVSS (SEQ ID NO: 1437)
humanized CHA.7.524 VH	
h524HH1	QVQLVQSGAEVKKPGASVKVCKASGYKFPDYYVMHWWVRQAPGQGLEWMGIISIYSGNTNYAQKFQGRVTMTTRDTSTSTV YMELSSLRSEDTAVYYCAREGDLPMFAYWGQGLVTVSS (SEQ ID NO: 1438)
h524HH2	QVQLVQSGAEVKKPGASVKVCKASGYKFPDYYVMHWWVRQAPGQGLEWIGIISIYSGNTNYAQKFQGRVTMTVDTSTSTVY MELSSLRSEDTAVYYCAREGDLPMFAYWGQGLVTVSS (SEQ ID NO: 1439)
h524HH3	QVQLVQSGAEVKKPGASVKISCKGSGYKFPDYYVMHWWVRQAPGQGLEWIGIISIYSGNTNYAQKFQGRATMTVDTSTSTAY MELSSLRSEDTAVYYCAREGDLPMFAYWGQGLVTVSS (SEQ ID NO: 1440)

Figure 89B

h524HH4
QVQLVQSGAEVKKPGASVKISKCKSGYKFPDYYVMHWVRQAPGQGLEWIGIHSYSGNTNYAQKFQGRATMTVDKSTSTAY
MELSSLRSEDTA VYYCAREGDLPMFAYWGQGLVTVSS (SEQ ID NO: 1441)

humanized CHA.7.530 VH

h530HH1
QVQLVQSGAEVKKPGASVKVSCKASGYAFTNHLIEWVRQAPGQGLEWMGVNPGSDSDTDY AQKFQGRVTMTTRDTSTSTVY
MELSSLRSEDTA VYYCARSLYYNSWVFVYWGQGLVTVSS (SEQ ID NO: 1442)

h530HH2
QVQLVQSGAEVKKPGASVKVSCKASGYAFTNHLIEWVRQAPGQGLEWIGVINPGSDSDTDY AQKFQGRVTMTADTSTSTVY
MELSSLRSEDTA VYYCARSLYYNSWVFVYWGQGLVTVSS (SEQ ID NO: 1443)

h530HH3
QVQLVQSGAEVKKPGASVKVSCKASGYAFTNHLIEWIRQAPGQGLEWIGVINPGSDSDTDY AQKFQGRATLTADTSTSTAYM
ELSSLRSEDTA VYYCARSLYYNSWVFVYWGQGLVTVSS (SEQ ID NO: 1444)

h530HH4
QVQLVQSGAEVKKPGASVKVSCKASGYAFTNHLIEWIRQAPGQGLEWIGVINPGSDSDTDY AQKFQGRATLTADKSTSTAYM
ELSSLRSEDTA VYYCARSLYYNSWVFVYWGQGLVTVSS (SEQ ID NO: 1445)

humanized CHA.7.538_1 VH

h5381HH1
QVQLVQSGAEVKKPGASVKVSCKASGYAFTNYLIEWVRQAPGQGLEWMGVNPGSGGIYYAQKFQGRVTMTTRDTSTSTVY
MELSSLRSEDTA VYYCARSETHDTWFAYWGQGLVTVSS (SEQ ID NO: 1446)

h5381HH2
QVQLVQSGAEVKKPGASVKVSCKASGYAFTNYLIEWVRQAPGQGLEWIGVINPGSGGIYYAQKFQGRVTMTADTSTSTVY
MELSSLRSEDTA VYYCARSETHDTWFAYWGQGLVTVSS (SEQ ID NO: 1447)

Figure 89C

h5381HH3

QVQLVQSGAEVKKPGASVKVSCKTSGYAFTNLYIEWVRQAPGQGLEWIGVINPGSGGIYYAQKFQGRVTLTADTSTSTAYM
ELSSLRSEDTAVYYCARSETHDTWFAYWGQGLVTVSS (SEQ ID NO: 1448)

h5381HH4

QVQLVQSGAEVKKPGASVKVSCKTSGYAFTNLYIEWVRQAPGQGLEWIGVINPGSGGIYYAQKFQGRVTLTADKSTSTAYM
ELSSLRSEDTAVYYCARSETHDTWFAYWGQGLVTVSS (SEQ ID NO: 1449)

humanized CHA.7.538_2 VH

h5382HH1

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYWIGWVRQAPGQGLEWMGDIYPGGYTNYAQKFQGRVTMTTRDTSTSTV
YMESSLRSEDTAVYYCARPYYGSSYGFAFWGQGLVTVSS (SEQ ID NO: 1450)

h5382HH2

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYWIGWVRQAPGQGLEWIGDIYPGGYTNYAQKFQGRVTMTADTSTSTV
YMESSLRSEDTAVYYCASPYYGSSYGFAFWGQGLVTVSS (SEQ ID NO: 1451)

h5382HH3

QVQLVQSGAEVKKPGASVKMSCKASGYTFTNYYWIGWVRQAPGQGLEWIGDIYPGGYTNYAQKFQGRATLTADTSTSTA
YMESSLRSEDTAVYYCASPYYGSSYGFAFWGQGLVTVSS (SEQ ID NO: 1452)

humanized CHA.7.518 VL

h518HL1

DIQMTQSPSSLSASVGDRVTITCRVSENIYSNLAWYQQKPGKAPKLLIYEATNLAEGVPSRFSGSGGTDFTLTISSLQPEDFA
TYYCQHFHWGTPYTFGQGQTKLEIK (SEQ ID NO: 1453)

h518HL2

DIQMTQSPSSLSASVGDRVTITCRVSENIYSNLAWYQQKPGKAPKLLIYEATNLAEGVPSRFSGSGGTDYTLTISSSLQPEDFA
TYYCQHFHWGTPYTFGQGQTKLEIK (SEQ ID NO: 1454)

Figure 89D
h518HL3

DIQMTQSPSSLSASVGDRVTITCRVSENIYSNLAWYQQKPGKAPKLLVYEATNLAEGVPSRFSGSGSGTDYTLTISSLQPEDF
GTYQCQHFHFGTPYTFGGQGTKLEIK (SEQ ID NO: 1455)

humanized CHA.7.524 VL

h524HL1

EIVLTQSPATLSLSPGERATLSCNASSSVSYMYWYQQKPGQAPRLIYDTSNLA SGIPARFSGSGSGTDFTLTISSELPEDFAVY
YCQQWSSYPPLTFGGQGTKLEIK (SEQ ID NO: 1456)

h524HL2

EIVLTQSPATLSLSPGERATLSCNASSSVSYMYWYQQKPGQAPRLIYDTSNLA SGIPARFSGSGSGTDYTLTISSLEPEDFAVY
YCQQWSSYPPLTFGGQGTKLEIK (SEQ ID NO: 1457)

h524HL2

EIVLTQSPATLSLSPGERVTMSCNASSSVSYMYWYQQKPGQAPRLIYDTSNLA SGVPARFSGSGSGTDYTLTISSMEPEDFA
VYYCQQWSSYPPLTFGGQGTKVEIK (SEQ ID NO: 1458)

humanized CHA.7.530 VL

h530HL1

DIQMTQSPSSLSASVGDRVTITCRASENIYSYLAWYQQKPGKAPKLLIYN AKTLVEGVPSRFSGSGSGTDFTLTISSLQPEDFA
TYYCQH HYGTPYTFGGQGTKLEIK (SEQ ID NO: 1459)

h530HL2

DIQMTQSPSSLSASVGDRVTITCRASENIYSYLAWYQQKPGKAPKLLVYN AKTLVEGVPSRFSGSGSGTDFTLTISSLQPEDFG
TYYCQH HYGTPYTFGGQGTKLEIK (SEQ ID NO: 1460)

humanized CHA.7.538_1/538_2 VL

h538HL1

DIQMTQSPSSLSASVGDRVTITCKASQSVRIAVA WYQQKPGKAPKLLIYL ASTRHTGVPSRFSGSGSGTDFTLTISSLQPEDFA
TYYCLQHWNYPTFGGQGTKLEIK (SEQ ID NO: 1461)

Figure 89E

h538HL2

DIQMTQSPSSLASVGDRTTITCKASQSVRIAVAFQKPGKAPKALIYLASTRHTGVPSRFSGSGGTDFTLTISVVQPEDFA
TYCYCLQHWNPYPYTFGGQGTKLEIK (SEQ ID NO: 1462)

Figure 90: humanized CHA.7 VH-VL Pairs

Antibody CHA.7.518

	VH	VL
ch518	chimVH	chimVL
h518-1	h518HH1	h518HL1 (optional)
h518-2	h518HH2	h518HL2
h518-3	h518HH3	h518HL2
h518-4	h518HH3	h518HL3
h518-5	h518HH4	h518HL3

Antibody CHA.7.524

	VH	VL
ch524	chimVH	chimVL
h524-1	h524HH1	h524HL1 (optional)
h524-2	h524HH2	h524HL2
h524-3	h524HH3	h524HL3
h524-4	h524HH4	h524HL3

Antibody CHA.7.530

	VH	VL
ch530	chimVH	chimVL
h530-1	h530HH1	h530HL1 (optional)
h530-2	h530HH2	h530HL2
h530-3	h530HH3	h530HL1
h530-4	h530HH3	h530HL2
h530-5	h530HH4	h530HL2

Antibody CHA.7.538_1

	VH	VL
ch538.1	chimVH	chimVL
h538.1-1	h538.1HH1	h538.1HL1 (optional)
h538.1-2	h538.1HH2	h538.1HL2
h538.1-3	h538.1HH3	h538.1HL2
h538.1-4	h538.1HH4	h538.1HL2

Antibody CHA.7.538_2

	VH	VL
ch538.2	chimVH	chimVL
h538.2-1	h538.2HH1	h538.1HL1 (optional)
h538.2-2	h538.2HH2	h538.1HL2
h538.2-3	h538.2HH3	h538.1HL2

Figure 91

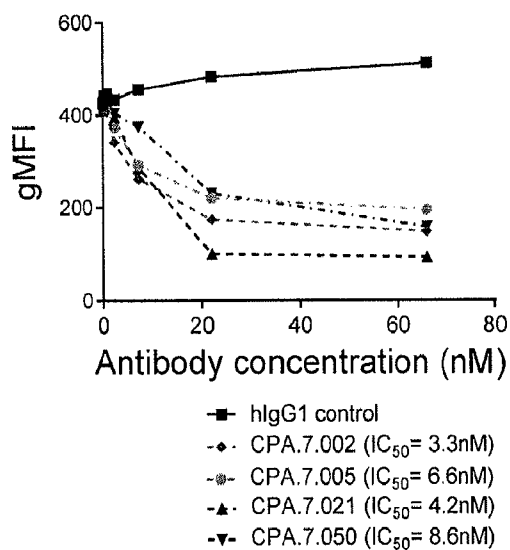
Antibody (mIgG)	Human CD56 int. NK (gMFlr, 10ug/ml)	Human CD8+ T cells (gMFlr, 10ug/ml)	Expi cyno OE/par (gMFlr, 3.3ug/ml)	Cyno NK cells (gMFlr, 10ug/ml)	Cyno CD8+ T cells (gMFlr, 10ug/ml)
CHA.7.502	1.97	1.41	60.49	Not tested	Not tested
CHA.7.503	3.15	1.96	106.3	Not tested	Not tested
CHA.7.506	Not tested	Not tested	0.77	Not tested	Not tested
CHA.7.508	3.6	4.09	41.49	Not tested	Not tested
CHA.7.510	3.13	2.73	38.21	Not tested	Not tested
CHA.7.512	1.30	1.15	8.96	Not tested	Not tested
CHA.7.514	4.16	5.15	65.20	Not tested	Not tested
CHA.7.516	4.22	4.09	60.05	1.76	2.09
CHA.7.518	5.08	6.69	83.51	1.92	2.09
CHA.7.520	1.13	1.04	Not tested	Not tested	Not tested
CHA.7.522	2.06	1.90	27.24	Not tested	Not tested
CHA.7.524	5.50	6.12	66.32	1.78	2.02
CHA.7.525	1.98	1.76	0.85	Not tested	Not tested
CHA.7.526	2.08	1.71	0.79	Not tested	Not tested
CHA.7.527	1.16	0.99	Not tested	Not tested	Not tested
CHA.7.528	3.08	3.63	12.2	1.21	1.18
CHA.7.530	6.04	6.47	60.80	1.73	1.89
CHA.7.534	2.60	1.96	46.27	Not tested	Not tested
CHA.7.535	2.24	1.28	0.82	Not tested	Not tested
CHA.7.537	3.90	3.41	1.55	1.18	1.19
CHA.7.538	6.49	6.17	15.16	1.36	1.45
CHA.7.543	4.48	4.33	0.83	1.35	1.39
CHA.7.544	2.36	2.54	61.09	Not tested	Not tested
CHA.7.545	2.54	2.82	0.91	Not tested	Not tested
CHA.7.546	2.75	2.95	0.85	Not tested	Not tested
CHA.7.547	2.21	1.13	26.65	Not tested	Not tested
CHA.7.548	3.15	3.35	4.25	1.18	1.09
CHA.7.549	3.05	1.42	1.00	Not tested	Not tested
CHA.7.550	1.60	1.29	0.90	Not tested	Not tested

Figure 92

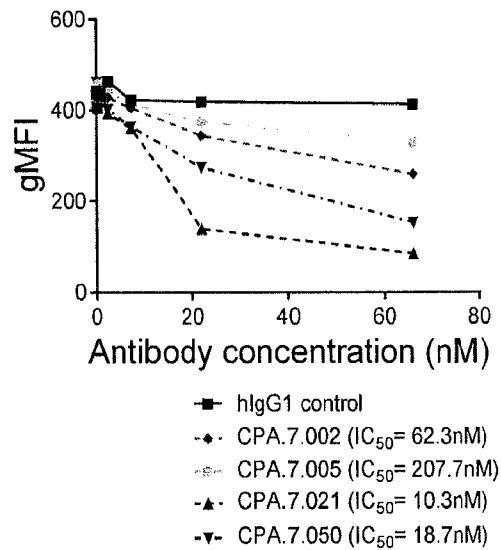
Antibody (mIgG)	IC ₅₀ (nM)
CHA.7.502	39.90
CHA.7.503	No IC ₅₀
CHA.7.506	31.65
CHA.7.508	37.88
CHA.7.510	55.00
CHA.7.512	839.6
CHA.7.514	38.88
CHA.7.516	33.11
CHA.7.518	23.15
CHA.7.520	619.3
CHA.7.522	50.48
CHA.7.524	30.20
CHA.7.525	85.52
CHA.7.526	58.88
CHA.7.527	No IC ₅₀
CHA.7.528	28.88
CHA.7.530	34.56
CHA.7.534	181.4
CHA.7.535	821.1
CHA.7.537	38.95
CHA.7.538	51.87
CHA.7.543	No IC ₅₀
CHA.7.544	No IC ₅₀
CHA.7.545	96.06
CHA.7.546	92.05
CHA.7.547	27.94
CHA.7.548	18.98
CHA.7.549	36.12
CHA.7.550	58.34

FIGURE 93A

A

**FIGURE 93B**

B



C

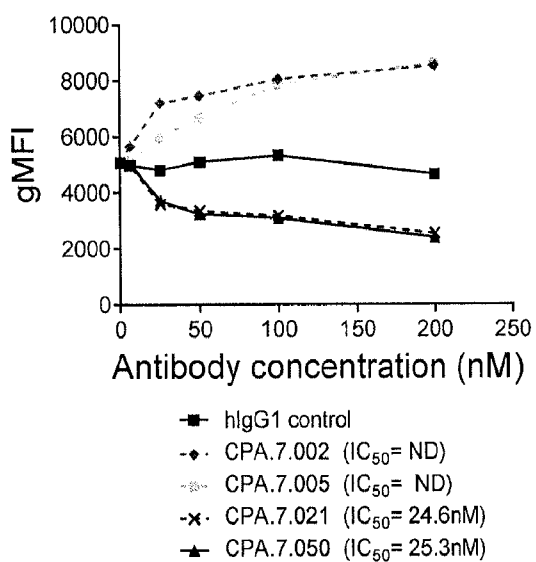
**FIGURE 93C**

FIG. 94A

a

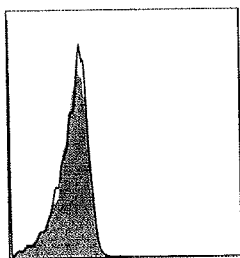


FIG. 94B

b

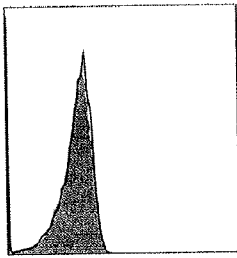


FIG. 94C

c

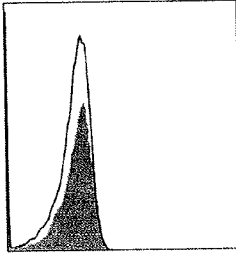
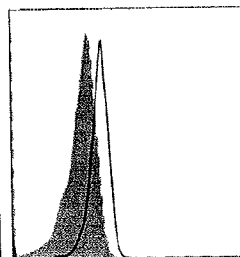
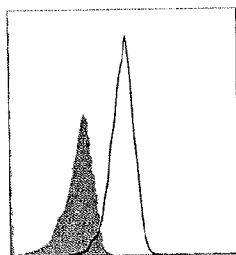


FIG. 94D

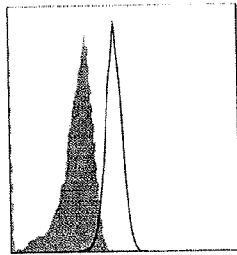
d



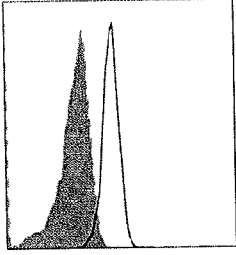
e



f



g



h

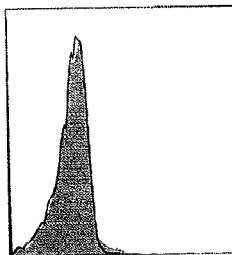


FIG. 94E

FIG. 94F

FIG. 94G

FIG. 94H

FIG. 95A

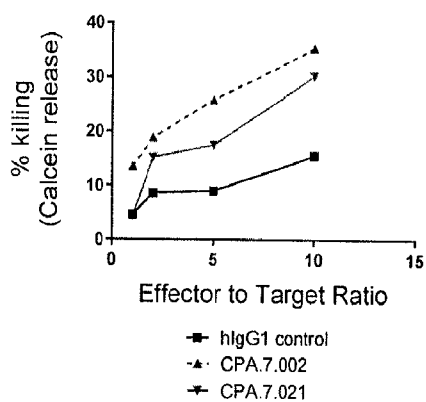


FIG. 95B

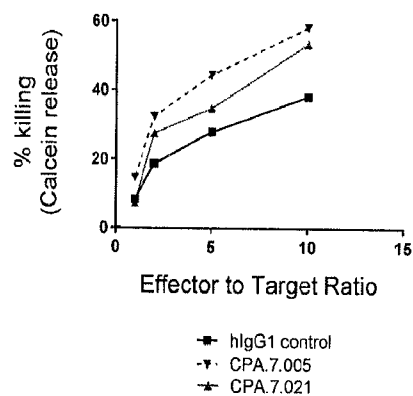


FIG. 95C

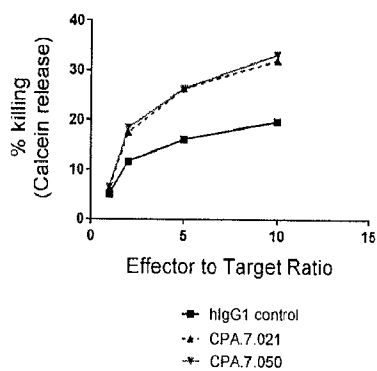


FIG. 95D

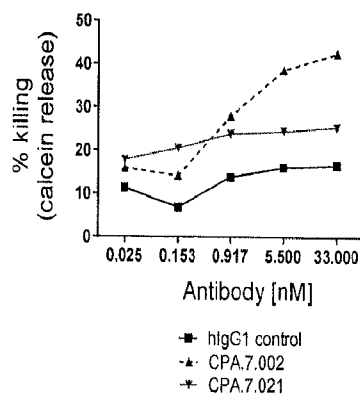


FIG. 95E

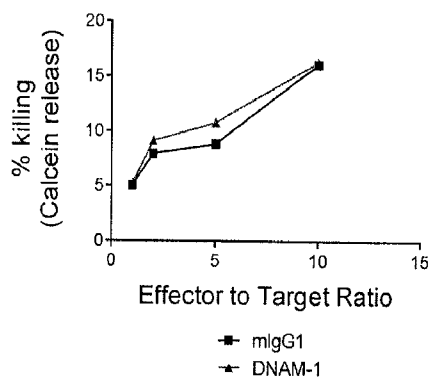


FIG. 95F

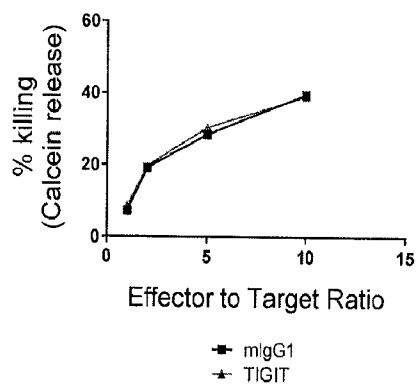
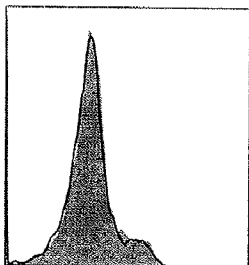
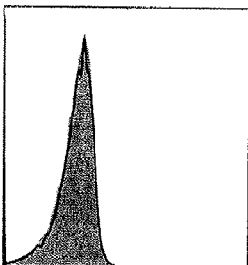
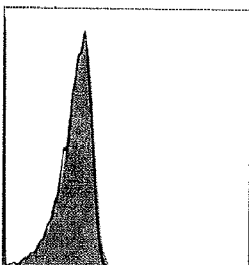
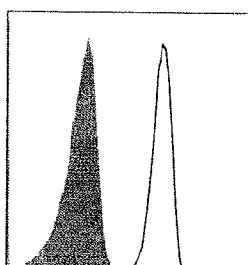
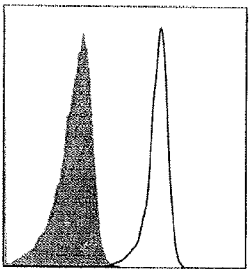
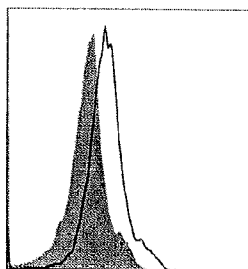
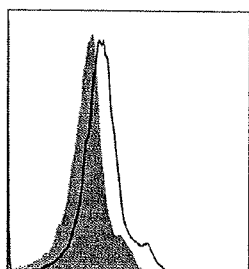
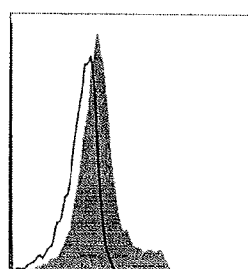
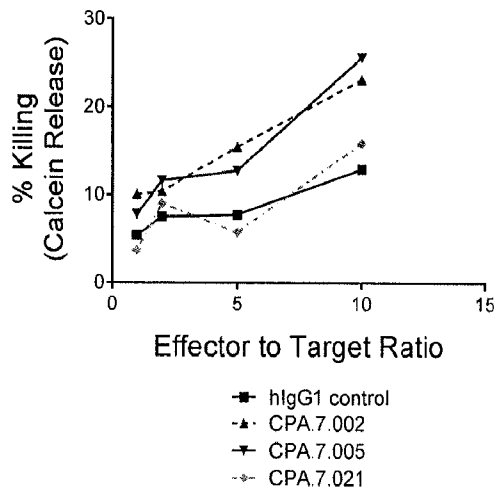


FIG. 96A**a****FIG. 96B****b****FIG. 96C****c****FIG. 96D****d****e****f****g****h****FIG. 96E****FIG. 96F****FIG. 96G****FIG. 96H**

A

FIGURE 97A

B

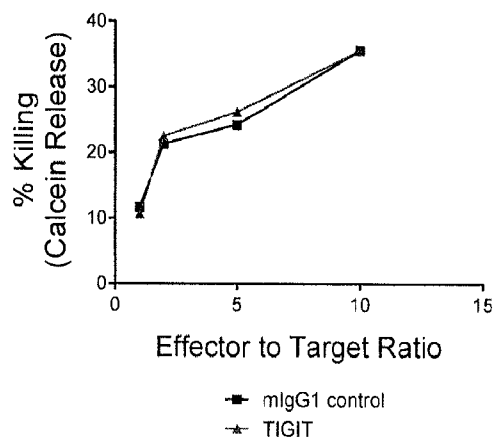
**FIGURE 97B**

Figure 98

Antibody (hIgG1)	Assay permutation and orientation	IC ₅₀ (nM)
CPA.7.002	HEK + PVRIG Fc (P)	3.3
	HEK + PVRIG Fc (NP)	62.3
	HEK hPVRIG + PVRL2 Fc	Increased binding
CPA.7.005	HEK + PVRIG Fc (P)	6.6
	HEK + PVRIG Fc (NP)	207.7
	HEK hPVRIG + PVRL2 Fc	Increased binding
CPA.7.021	HEK + PVRIG Fc (P)	4.2
	HEK + PVRIG Fc (NP)	10.3
	HEK hPVRIG + PVRL2 Fc	24.6
CPA.7.036	HEK + PVRIG Fc (P)	6.9
	HEK + PVRIG Fc (NP)	10.9
CPA.7.037	HEK + PVRIG Fc (P)	6.5
	HEK + PVRIG Fc (NP)	19.1
CPA.7.038	HEK + PVRIG Fc (P)	3.5
	HEK + PVRIG Fc (NP)	6.7
CPA.7.039	HEK + PVRIG Fc (P)	14.0
	HEK + PVRIG Fc (NP)	32.7
CPA.7.041	HEK + PVRIG Fc (P)	5.8
	HEK + PVRIG Fc (NP)	16.2
CPA.7.042	HEK + PVRIG Fc (P)	3.6
	HEK + PVRIG Fc (NP)	8.3
CPA.7.050	HEK + PVRIG Fc (P)	8.6
	HEK + PVRIG Fc (NP)	18.7
	HEKhPVRIG + PVRL2 Fc	25.3

Figure 99

Antibody (hIgG1)	Target Cell line	Fold change in cytotoxicity relative to control
CPA.7.002	Reh	2.9
	MOLM-13	1.9
CPA.7.005	Reh	1.6
	MOLM-13	1.6
CPA.7.021	Reh	1.9
	MOLM-13	0.7
CPA.7.036	Reh	0.9
CPA.7.037	Reh	1.1
CPA.7.038	Reh	0.8
CPA.7.041	Reh	0.7
CPA.7.042	Reh	0.7
CPA.7.050	Reh	1.6
TIGIT	Reh	1.1
	MOLM-13	1.1
DNAM-1	Reh	1.2

```

NP_076975.2-Homo sapiens
XP_005549281.1-Macaca fascicularis
XP_003732227.1-Callithrix jacchus
XP_001103603.1-Macaca mulatta

TPEVVVQVQVMEATELSSTFTYHCGFLGSGSISLVTVSNGGPDGAGGTTLAVLHPELCITROW
TPEVVVQVQVQVMEATELSSTFTYHCGFLGSGSISLVTVSNGGPDGAGGTTLAVLHPELCITROW
TPEVVVQVQVQVMEATELSSTFTYHCGFLGSGSISLVTVSNGGPDGAGGTTLAVLHPELCITROW
TPEVVVQVQVQVMEATELSSTFTYHCGFLGSGSISLVTVSNGGPDGAGGTTLAVLHPELCITROW
*****:***** 22*****

NP_076975.2-Homo sapiens
XP_005549281.1-Macaca fascicularis
XP_003732227.1-Callithrix jacchus
XP_001103603.1-Macaca mulatta

APARQARWETQSSISLLEEGSGASSPANTTFOCKFASFPEGSWESCGSLPSSSDPGLSA
APARQARWETQSSISLLEEGSGASSPANTTFOCKFASFPEGSWESCGSLPSSSDPGLSA
APARQARWETQSSISLLEEGSGASSPANTTFOCKFASFPEGSWESCGSLPSSSDPGLSA
APARQARWETQSSISLLEEGSGASSPANTTFOCKFASFPEGSWESCGSLPSSSDPGLSA
*****,*****:*****

NP_076975.2-Homo sapiens
XP_005549281.1-Macaca fascicularis
XP_003732227.1-Callithrix jacchus
XP_001103603.1-Macaca mulatta

EPTFPILRAD
PPTFPILRAD
FIL-----RAD
EPTFPILRAD
*      ***

```

SEQ ID NOS 1453-1466, respectively, in order of appearance

Figure 102

mAb	Cyno	Epitope bin	Epitope group
	cross-reactivity		
CPA.7.002	+	1	2
CPA.7.021	-	1	1
CPA.7.024	+++	1	3
CPA.7.028	-	1	1
CPA.7.041	++	1	2
CPA.7.050	+++	4	3

Figure 103A

>PVRIG_NP_076975_from_41_to_171_Sequence_of_Human_WT_ECD_(without_SP) SEQ ID NO: 1467

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTWSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGS
LPPSSDPGLSAPPTPAPILRAD

Figure 103B

>PVRIG_NP_076975_from_21_to_171_Sequence_of_Human_WT_ECD_(with_SP) SEQ ID NO: 1468

MGHRTLVPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTWSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCA
NTTFCCKFASFPEGSWEACGS LPPSSDPGLSAPPTPAPILRAD

Figure 103C

>PVRIG_NP_076975_from_43_to_146_Sequence_of_Ig_Domain SEQ ID NO: 1469

EVWVQVRMEATELSSFTIRCGFLGSGSISLVTWSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEA

Figure 103D

>PVRIG_Splice_Variant_P6 SEQ ID NO: 1470

MGHRTLVPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTWSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCA
NTTFCCKFASFPEGSWEACGS LPPSSDPGLSAPPTPAPILRADLAGILGVSGVLLFGCVLLHLLRRHKHR

Figure 103E

>PVRIG_Splice_Variant_P8 SEQ ID NO: 1471

MGHRTLVPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTWSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCA
NTTFCCKFASFPEGSWEACGS LPPSSDPGLSVPPTPAPILRADLAGILGVSGVLLFDCGYLLHLLCRQKHRPAPRLQPSHTSS

Figure 103F

>PVRIG_Splice_Variant_P4 SEQ ID NO: 1472
 MGHRTLVPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRWLSAPPTPAPILRADLAGILVSGVLLFGCVYLLHLLRRHKHRPAPRLQPSRTSPQAPRARAWAPSQASQAALHVPYATINTSCRPATLDTAHPHGGPSWWASLPTHAHRPQGPAAWASTPIPARGSFVSVENGLYQAQAGERPPHTGPGTLTFDPDRGPRAMEGPLGVR

Figure 103G

>PVRIG_Splice_Variant_P7 SEQ ID NO: 1473
 MGHRTLVPWVLLTLCVTAGLSAPPTPAPILRADLAGILVSGVLLFGCVYLLHLLRRHKHRPAPRLQPSRTSPQAPRARAWAPSQASQAALHVPYATINTSCRPATLDTAHPHGGPSWWASLPTHAHRPQGPAAWASTPIPARGSFVSVENGLYQAQAGERPPHTGPGTLTFDPDRGPRAMEGPLGVR

Figure 103H

>PVRIG_Splice_Variant_P14 SEQ ID NO: 1474
 MGHRTLVPWVLLTLCVTAGLSVPPTPAPILRADLAGILVSGVLLFDCGYLLHLLCRQKHRPAPRLQPSHTSS

Figure 103I

>PVRIG_Splice_Variant_P3 SEQ ID NO: 1475
 MGHRTLVPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGFLGSGISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCA
 NTTFCCKFASFPEGWEACGSLPPSSDPGGAGARGPGGGQGGARELATHLILVSVPRALCPADSCPHSAGRGRDLGGLRSPPLWLCLPPSSAAPT

Figure 103J

>PVRIG_Splice_Variant_P10 SEQ ID NO: 1476
 MGHRTLVPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGFLGSGISLVTVSWGPNAGAGGTTLAVLHPERGAQISPRGPKIGGPPCPRPGPAGKPRAASSLSSW
 KALGPAAPAPTPPSAASLRPSQAALHVPYATINTSCRPATLDTAHPHGGPSWWASLPTHAHRPQGPAAWASTPIPARGSFVSVENGLYQAQAGERPPHTGPGTLTFPD
 PRGPRAMEGPLGVR

Figure 103K

>PVRIG_Splice_Variant_P13 SEQ ID NO: 1477

MGHRTLVLPPWLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGFLGSGSISLTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCA
NTTFCCKFASFPGCSSRPLCHYQHQLPPSYFGHSSPPWGAVLVGVTTPHPRCTPAPGPCRLGLHHPCTWQLCLC

Figure 103L

>PVRIG_Splice_Variant_P3_ECD SEQ ID NO: 1478

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGWEACGS
LPPSSDPGGAGARGPGGGGGARELATHLILVSVPRALCPADSCPHSAGRPRDLGGLRSPPLWLCLPPSSAAPT

Figure 103M

>PVRIG_Splice_Variant_P10_ECD SEQ ID NO: 1479

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLTVSWGGPNGAGGTTLAVLHPERGAQISPRGPKIGGPPCPRPAGKPRAASSLWKALGPAAPAPTPPSAASLRPS
QAALHVPYATINTSCRPATLDTAHPHGGGPSWWASLPTHAHRPQQGPAAWASTPIPARGSFVSVENGLYAQAGERPPHTGPGTLTLPDPRGRPRAMEGPLGVR

Figure 103N

>PVRIG_Splice_Variant_P13_ECD SEQ ID NO: 1480

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPGCSSRPLCHY
QHQLPPSYFGHSSPPWGAVLVGVTTPHPRCTPAPGPCRLGLHHPCTWQLCLC

Figure 103O

>PVRIG_Splice_Variant_P3_ECD_Unique SEQ ID NO: 1481

GAGARGPGGGGGARELATHLILVSVPRALCPADSCPHSAGRPRDLGGLRSPPLWLCLPPSSAAPT

Figure 103P

>PVRIG_Splice_Variant_P10_ECD_All_Unique SEQ ID NO: 1482
AQISPRGPKIGGPPCPRPGAGKPRAASSLSSWKALGPAAPAPTPPSAASLRPSQAALHVPYATINTSCRPATLDTAHPHGGPSWWASLPTHAAHRPQGPAAWASTPIP
ARGSFVSVENGLYAQAGERPPHTGPGLTLFPDPRGRAMEGPLGVR

Figure 103Q

>PVRIG_Splice_Variant_P10_ECD_Unique_without_intracellular SEQ ID NO: 1483
AQISPRGPKIGGPPCPRPGAGKPRAASSLSSWKALGPAAPAPTPPSAASLRP

Figure 103R

>PVRIG_Splice_Variant_P13_ECD_Unique SEQ ID NO: 1484
GCSSRPLCHYQHQLPPSYFGHSSPPWGAVLVGVTPHPRCTPAPGPCRLGLHHPCTWQLCLC

Figure 103S

>PVRIG_NP_076975_from_41_to_169_variation_of_ECD_(without_SP) SEQ ID NO: 1485
TPEVWVQVRMEATELSSFTIRCGLGSGISLVTVSWGGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGS
LPPSSDPGLSAPPTPAPILR

Figure 103T

>PVRIG_NP_076975_from_41_to_170_variation_of_ECD_(without_SP) SEQ ID NO: 1486
TPEVWVQVRMEATELSSFTIRCGLGSGISLVTVSWGGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGS
LPPSSDPGLSAPPTPAPILRA

Figure 103U

>PVRIG_NP_076975_from_41_to_172_variation_of_ECD_(without_SP) SEQ ID NO: 1487
 TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSGWEACGS
 LPSSDPGLSAPPTAPILRADL

Figure 103V

>PVRIG_NP_076975_from_41_to_173_variation_of_ECD_(without_SP) SEQ ID NO: 1488
 TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSGWEACGS
 LPSSDPGLSAPPTAPILRADLA

Figure 103W

>PVRIG_NP_076975_from_41_to_144_variation_of_lg_Domain SEQ ID NO: 1489
 TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSW

Figure 103X

>PVRIG_NP_076975_from_41_to_145_variation_of_lg_Domain SEQ ID NO: 1490
 TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSGWE

Figure 103Y

>PVRIG_NP_076975_from_41_to_146_variation_of_lg_Domain SEQ ID NO: 1491
 TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSGWEA

Figure 103Z

>PVRIG_NP_076975_from_41_to_147_variation_of_Ig_Domain SEQ ID NO: 1492
TPEVWVQVRMEATELSSFTIRCGLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGWEAC

Figure 103AA

>PVRIG_NP_076975_from_41_to_148_variation_of_Ig_Domain SEQ ID NO: 1493
TPEVWVQVRMEATELSSFTIRCGLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGWEACG

Figure 103AB

>PVRIG_NP_076975_from_42_to_144_variation_of_Ig_Domain SEQ ID NO: 1494
PEVWVQVRMEATELSSFTIRCGLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSW

Figure 103AC

>PVRIG_NP_076975_from_42_to_145_variation_of_Ig_Domain SEQ ID NO: 1495
PEVWVQVRMEATELSSFTIRCGLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGWE

Figure 103AD

>PVRIG_NP_076975_from_42_to_146_variation_of_Ig_Domain SEQ ID NO: 1496
PEVWVQVRMEATELSSFTIRCGLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGWEA

Figure 103AE

>PVRIG_NP_076975_from_42_to_147_variation_of_Ig_Domain SEQ ID NO: 1497
PEVWVQVRMEATELSSFTIRCGLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGWEAC

Figure 103AF

>PVRIG_NP_076975_from_42_to_148_variation_of_Ig_Domain SEQ ID NO: 1498
PEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSGWEACG

Figure 103AG

>PVRIG_NP_076975_from_43_to_144_variation_of_Ig_Domain SEQ ID NO: 1499
EVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSGW

Figure 103AH

>PVRIG_NP_076975_from_43_to_145_variation_of_Ig_Domain SEQ ID NO: 1500
EVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSGWE

Figure 103AI

>PVRIG_NP_076975_from_43_to_147_variation_of_Ig_Domain SEQ ID NO: 1501
EVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSGWEAC

Figure 103AJ

>PVRIG_NP_076975_from_43_to_148_variation_of_Ig_Domain SEQ ID NO: 1502
EVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSGWEACG

Figure 103AK

>PVRIG_NP_076975_from_44_to_144_variation_of_Ig_Domain SEQ ID NO: 1503
VWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSGW

Figure 103AL

>PVRIG_NP_076975_from_44_to_145_variation_of_Ig_Domain SEQ ID NO: 1504
 VVWQVRMEATELSSFTIRCGFLGSGISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSGWE

Figure 103AM

>PVRIG_NP_076975_from_44_to_146_variation_of_Ig_Domain SEQ ID NO: 1505
 VVWQVRMEATELSSFTIRCGFLGSGISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSGWEA

Figure 103AN

>PVRIG_NP_076975_from_44_to_147_variation_of_Ig_Domain SEQ ID NO: 1506
 VVWQVRMEATELSSFTIRCGFLGSGISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSGWEAC

Figure 103AO

>PVRIG_NP_076975_from_44_to_148_variation_of_Ig_Domain SEQ ID NO: 1507
 VVWQVRMEATELSSFTIRCGFLGSGISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSGWEACG

Figure 103AP

>PVRIG_NP_076975_from_45_to_144_variation_of_Ig_Domain SEQ ID NO: 1508
 VVWQVRMEATELSSFTIRCGFLGSGISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSGW

Figure 103AQ

>PVRIG_NP_076975_from_45_to_145_variation_of_Ig_Domain SEQ ID NO: 1509
 VVWQVRMEATELSSFTIRCGFLGSGISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSGWE

Figure 103AR

>PVRIG_NP_076975_from_45_to_146_variation_of_lg_Domain SEQ ID NO: 1510
WVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEA

Figure 103AS

>PVRIG_NP_076975_from_45_to_147_variation_of_lg_Domain SEQ ID NO: 1511
WVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEAC

Figure 103AT

>PVRIG_NP_076975_from_45_to_148_variation_of_lg_Domain SEQ ID NO: 1512
WVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACG

Figure 103AU

>PVRIG_XP_006544085_PREDICTED_transmembrane_protein_PVRIG-like_isoform_X2_[Mus_musculus] SEQ ID NO: 1513
MRTGNTQAAAHATNMGQMQLVLFSTLLTLCVSEASPEVWVQVQMEATNLSSFSVHCGVLGYSLSISLVTVSCGEFVDAGRTKLAVLHPEFGTQQWAPARQAHWETP
NSVSVTLTMGQSKARSSLANTTFCCEFVTFPHGSRVACRDLHRSDPGLSAPTPALNLQADLVRLGTSGVFLFGFIFILCLRWQQRHWCLSKSQPSLTSTQAQVETQPPHL
ASTHSSFISMENGLYALA

Figure 103AV

>PVRIG_2nd_Met_Mouse_WT SEQ ID NO: 1514
MGQMQLVLFSTLLTLCVSEASPEVWVQVQMEATNLSSFSVHCGVLGYSLSISLVTVSCGEFVDAGRTKLAVLHPEFGTQQWAPARQAHWETPNSVSVTLTMGQSKA
RSSLANTTFCCEFVTFPHGSRVACRDLHRSDPGLSAPTPALNLQADLVRLGTSGVFLFGFIFILCLRWQQRHWCLSKSQPSLTSTQAQVETQPPHLASTHSSFISMENGLY
ALA

Figure 103AW

>PVRIG_Mouse_WT_ECD_(without_SP) SEQ ID NO: 1515
SPEVWVQVQMEATNLSFSVHCGVLGYSLISLVTVSCEGFVDAGRTKLAVLHPEFGTQQWAPARQAHWETPNSVSVTLTMGQSKARSSLANTTCCEFTFPHGSRV
ACRDLHRSDPGLSAPTPALNLOAD

Figure 103AX

>PVRIG_Mouse_WT_ECD_(with_SP) SEQ ID NO: 1516
MGQMQLTLVLFSTLLTLCVSEASPEVWVQVQMEATNLSFSVHCGVLGYSLISLVTVSCEGFVDAGRTKLAVLHPEFGTQQWAPARQAHWETPNSVSVTLTMGQSKA
RSSLANTTFCCEFTFPHGSRVACRDLHRSDPGLSAPTPALNLOAD

Figure 103AY

>PVRIG_HH-1_(Human_ECD_+_human_IgG1_Fc_mutated_C220S_at_hinge)_-_without_SP SEQ ID NO: 1517
TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGWEACGS
LPSSDPGLSAPPTPAPILRADEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVWS
VLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKKS
RWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

Figure 103AZ

>PVRIG_HH-1-1_(Human_ECD_with_C127F_and_C147S_mutations_+_human_IgG1_Fc_mutated_C220S_at_hinge)_-_without_SP SEQ ID NO:
1518
TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGWEASGSL
PPSSDPGLSAPPTPAPILRADEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR
WQQGNVFSCSVMEALHNHYTQKSLSLSPGK

Figure 103BA

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>PVRIG_HH-2_(Human_ECD_+_Human_IgG1_Fc_mutated_at_C220S,_C226S,_C229S_of_hinge)_-_without_SP SEQ ID NO: 1519
TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWAEACGS
LPSSDPGLSAPPTAPILRADEPKSSDKTHTSPSPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVVS
VLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNNYKTTTPVLDSDGGSFFLYSKLTVDKKS
RWQGNVFCSCVMHEALHNHYTQKSLSLSPGK
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Figure 103BB

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>PVRIG_HH-2-1-
1_(Human_ECD_with_C127F_mutation_+_Human_IgG1_Fc_mutated_at_C220S,_C226S,_C229S_of_hinge,_encoded_by_natural_codons_instead_of_codons_optimized_for_CHO_cells)_-_without_SP SEQ ID NO: 1520
TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGPNAGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWAEACGS
LPSSDPGLSAPPTAPILRADEPKSSDKTHTSPSPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVVS
VLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNNYKTTTPVLDSDGGSFFLYSKLTVDKSR
WQGNVFCSCVMHEALHNHYTQKSLSLSPGK
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Figure 103BC

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>PVRIG_MM-1_(Mouse_ECD_+_mouse_IgG2a_Fc)_-_without_SP SEQ ID NO: 1521
SPEVWVQVRMEATNLSSFSVHCGVLGYSLSLVTVSCGEFVDAGRTKLAVLHPEFGTQQWAPARQAHWETPNVSVVTLTMGQSKARSSLANTTFCCEFTFPHGSRV
ACRDLHRSDPGLSAPTPALNLQADEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMSISLPIVTCVVVDVSEDDPDVQISWTFVNNVEVHTAQQTQTHREDYNSTLR
VVSALPIQHQQDWMMSGKEFKCKVNNKDLPAPIERTISKPKGSRAPQVYVLPPEEEMTKKQVTLTCMVTDMPEDIVVEWTNNGKTELNYKNTEPVLDSDGGSFFLYSKLTVDKSR
LRVEKKNWVERNSYSCSVVHEGLHNHHTTKFSRTPGK
```

Figure 103BD

>PVRIG_MM-1-1_(Mouse_ECD_+_mouse_IgG2a_Fc_with_3_C_mutated_to_S_at_hinge)_-_without_SP_SEQ_ID NO: 1522

SPEVWVQVQMEATNLSSFVHCGVLGYSLISLVTVSCEGFVDAGRTKLAVLHPEFGTQQWAPARQAHWETPNSVSVTLTMGQSKARSSLANTTFCCEFTVTFPHGSRV
ACRDLHRSDPGLSAPTPALNLQADEPRGPTIKPSPSPAPNLLGGPSVFIFPPKIDVLMISLSPIVTCVVDVSEDDPDVQISWFMNNEVHTAQQTTHREDYNSTLR
VVSALPIQHQQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSRAPQVYVLPPEEEMTKKQVLTLCMVTDMPEDIWVEWTNNGKTELNYKNTEPVLDSDSGSYFMYSK
LRVEKKNWVERNSYSCSWHEGLHNHHTTKSFSRTPGK

Figure 103BE

>Human_Fc_(IgG1) SEQ ID NO: 1523

EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVVS
NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHN
HYTQKSLSLSPGK

Figure 103BF

>Human_Fc_(IgG1)_C220S SEQ ID NO: 1524

EPKSSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVVS
NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHN
HYTQKSLSLSPGK

Figure 103BG

>Human_Fc_(IgG1)_with_the_C220S_(at_hinge)_and_N297A_mutations SEQ ID NO: 1525

EPKSSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVVS
NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHN
HYTQKSLSLSPGK

Figure 103BH

>Human_Fc_(IgG1)_without_hinge SEQ ID NO: 1526

APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVHQDWLNGKEYCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK

Figure 103BI

>Mouse_Fc_(IgG2a) SEQ ID NO: 1527

EPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMSISPIVTCVVDVSEDDPDVQISWVFNNEVHTAQQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVN
NKDLPAPIERTISKPKGSRAPQVYVLPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNYSYSCSVVHEGLH
NHHTTKSFSRTPGK

Figure 103BJ

>Mouse_Fc_(IgG2a)_Fc_with_the_N297A_mutation SEQ ID NO: 1528

EPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMSISPIVTCVVDVSEDDPDVQISWVFNNEVHTAQQTQTHREDYASTLRVVSALPIQHQDWMSGKEFKCKVN
NKDLPAPIERTISKPKGSRAPQVYVLPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNYSYSCSVVHEGLH
NHHTTKSFSRTPGK

Figure 103BK

>Mouse_Fc_(IgG2a)_without_hinge SEQ ID NO: 1529

APNLLGGPSVFIFPPKIKDVLMSISPIVTCVVDVSEDDPDVQISWVFNNEVHTAQQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPK
GSRAPQVYVLPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNYSYSCSVVHEGLHNNHHTTKSFSRTPGK

Figure 103BL

>Human_Fc_(IgG1)_with_the_C220S_C226S_C229S_mutations_(at_hinge) SEQ ID NO: 1530
EPKSSDKTHTSPSPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYCKKVS
NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVCMHEALHN
HYTQKSLSLSPGK

Figure 103BM

>PVRIG_PRIMER_200-554_m15029_F SEQ ID NO: 1531
CCACCAACCTCTCGTCTTTC

Figure 103BN

>PVRIG_PRIMER_200-553_m15029_R SEQ ID NO: 1532
TCATGCCAGAGCATACAG

Figure 103BO

>PVRIG_PRIMER_200-571_m15029_F SEQ ID NO: 1533
CAGTGCCTCTAACTGCTGAC

Figure 103BP

>PVRIG_PRIMER_200-572_m15029_R SEQ ID NO: 1534
TCACTGTTACCAGGGAGATGAG

Figure 103BQ

>PVRIG_PRIMER_200-549_m15029_F SEQ ID NO: 1535

CACAGGCTGCCCCATGCAAC

Figure 103BR

>PVRIG_PRIMER_200-551_m15029_R SEQ ID NO: 1536

TGCCTGGGTGCTAGTGAGAG

Figure 103BS

>PVRIG_PRIMER_200-554_m15029_F SEQ ID NO: 1537

CCACCAACCTCTCGTCTTTC

Figure 103BT

>PVRIG_PRIMER_200-546_m15029_R SEQ ID NO: 1538

GACCCTGTTACCTGTCATTG

Figure 103BU

>PVRIG_flag_protein SEQ ID NO: 1539

MGHRTLVPWVLLTLCVTAGTPEVWQVRMEATELSSFTIRCGFLGSGSISLVTVSWGPNAGAGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCA
NTTFCKFASFPEGSWEACGSLPPSSDPGLSAPPTPAPILRADLAGILGVSGVLLFGCVYLLHLLRRHKHRPAPRLQPSRTSPQAPRARAWAPSQASQAALHVPYATINTS
CRPATLDTAHPHGGPSWWASLPTHAHRPQGPAAWASTPIPARGSFVSVENGLYAQAAGERPPHTGPGLTLFPDPRGPRAMEGPLGVRDYKDDDDK

Figure 103BV

>PVRIG_Mouse_First_Methionine_signal_peptide-Flag-ECD SEQ ID NO: 1540

MRTGNTQAAHATNMGMQTLVLFSTLLTLCVSEADYKDDDDKSPVWVQVQMEATNLSFSVHCGVLGYSLISLVTVSCEGFVDAGRTKLAVLHPEFGTQQWAPAR
QAHWETPNVSVTLTMGQSKARSSLANTTFCCEFTFPHGSRVACRDLHRSDPGLSAPTPALNLQADLVRILGTSGVFLFGFIFILCLRWQQRHWCLSKSQPSLTSTQAQ
VETQPPHLASTHSSFISMENGLYALA

Figure 103BW

>PVRIG_Mouse_Third_Methionine_untagged SEQ ID NO: 1541

MQTLVLFSTLLTLCVSEASPEVWVQVQMEATNLSFSVHCGVLGYSLISLVTVSCEGFVDAGRTKLAVLHPEFGTQQWAPARQAHWETPNVSVTLTMGQSKARSSLA
NTTFCCEFTFPHGSRVACRDLHRSDPGLSAPTPALNLQADLVRILGTSGVFLFGFIFILCLRWQQRHWCLSKSQPSLTSTQAQVETQPPHLASTHSSFISMENGLYALA

Figure 103BX

>PVRIG_Mouse_Third_Methionine_signal peptide-Flag-ECD SEQ ID NO: 1542

MQTLVLFSTLLTLCVSEADYKDDDDKSPVWVQVQMEATNLSFSVHCGVLGYSLISLVTVSCEGFVDAGRTKLAVLHPEFGTQQWAPARQAHWETPNVSVTLTMG
QSKARSSLANTTFCCEFTFPHGSRVACRDLHRSDPGLSAPTPALNLQADLVRILGTSGVFLFGFIFILCLRWQQRHWCLSKSQPSLTSTQAQVETQPPHLASTHSSFISME
NGLYALA