Figure 1

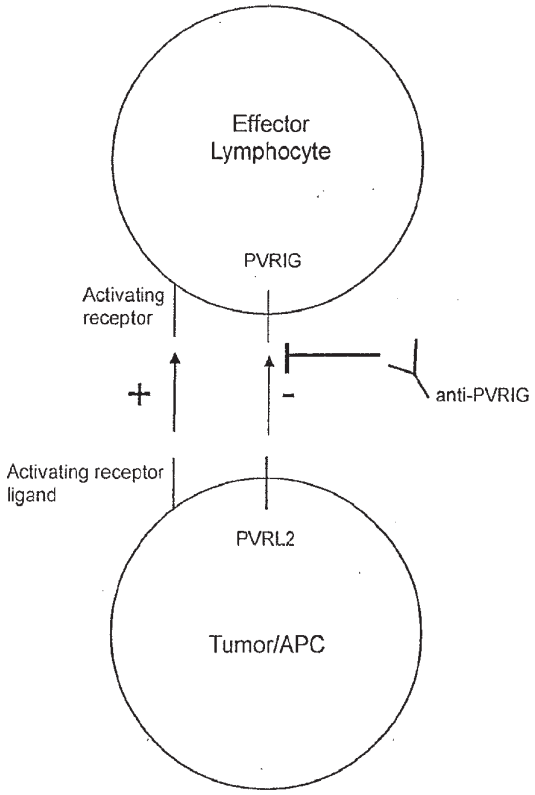

Effector
Lymphocyte
PVRIG
Activating
receptor
+
-
anti-PVRIG
Activating receptor
ligand
PVRL2
Tumor/APC

Figure 2.

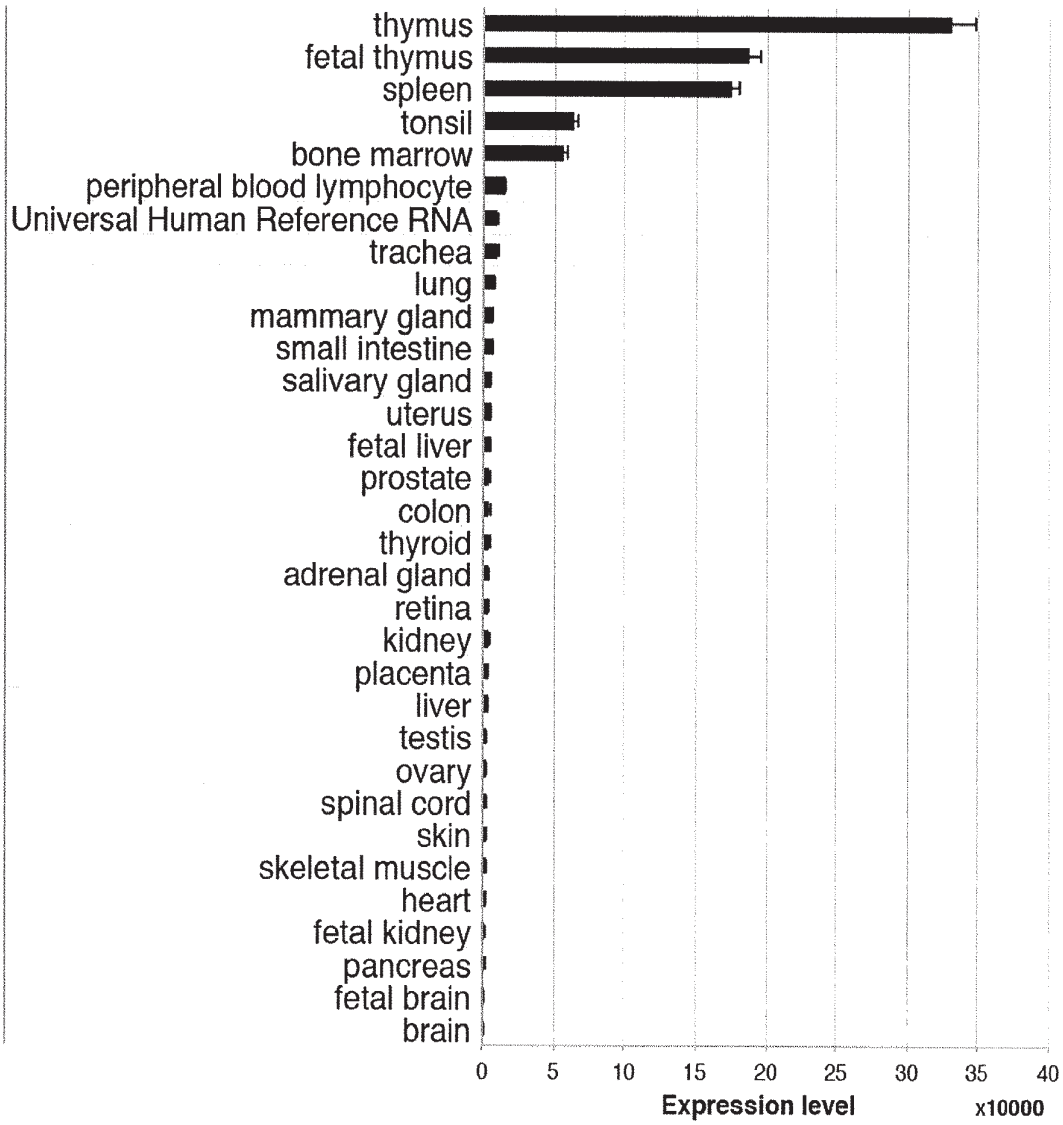

thymus
fetal thymus
spleen
tonsil
bone marrow
peripheral blood lymphocyte
Universal Human Reference RNA
trachea
lung
mammary gland
small intestine
salivary gland
uterus
fetal liver
prostate
colon
thyroid
adrenal gland
retina
kidney
placenta
liver
testis
ovary
spinal cord
skin
skeletal muscle
heart
fetal kidney
pancreas
fetal brain
brain
0
5
10
15
20
25
30
35
40
Expression level
x10000

Figure 3:

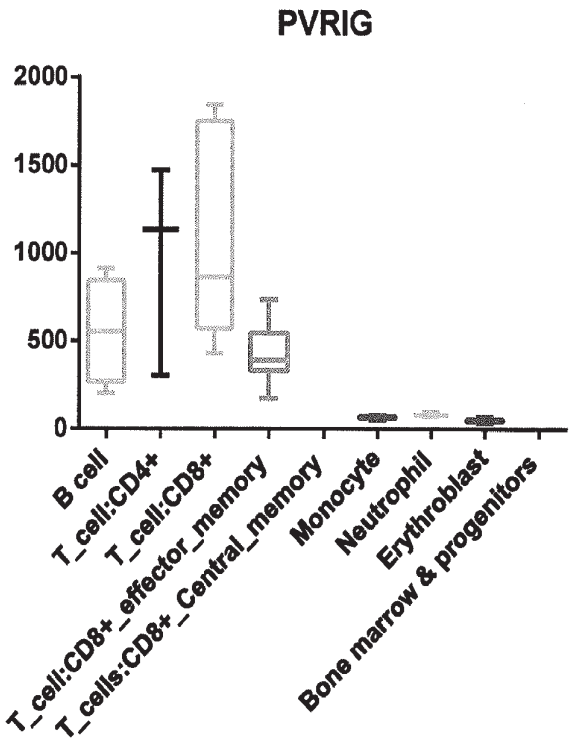

PVRIG
2000
1500
1000
500
0
B cell
T_cell:CD4+
T_cell:CD8+
T_cell:CD8+_effector_memory
T_cells:CD8+_Central_memory
Monocyte
Neutrophil
Erythroblast
Bone marrow & progenitors

Figure 4

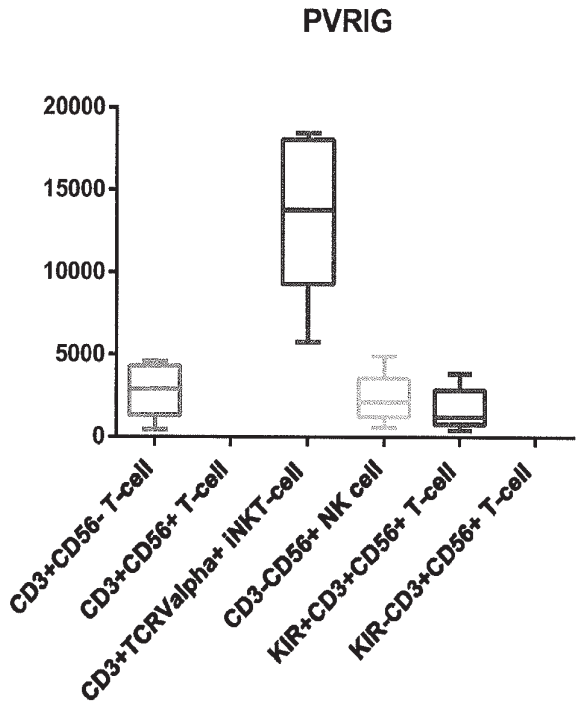

PVRIG
20000
15000
10000
5000
0
CD3+CD56- T-cell
CD3+CD56+ T-cell
CD3+TCRValpha+ iNKT-cell
CD3-CD56+ NK cell
KIR+CD3+CD56+ T-cell
KIR-CD3+CD56+ T-cell

Figure 5a:

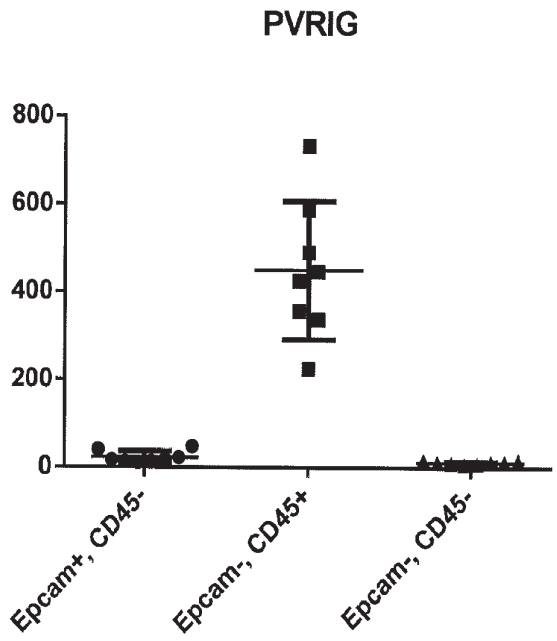


Figure 5b:

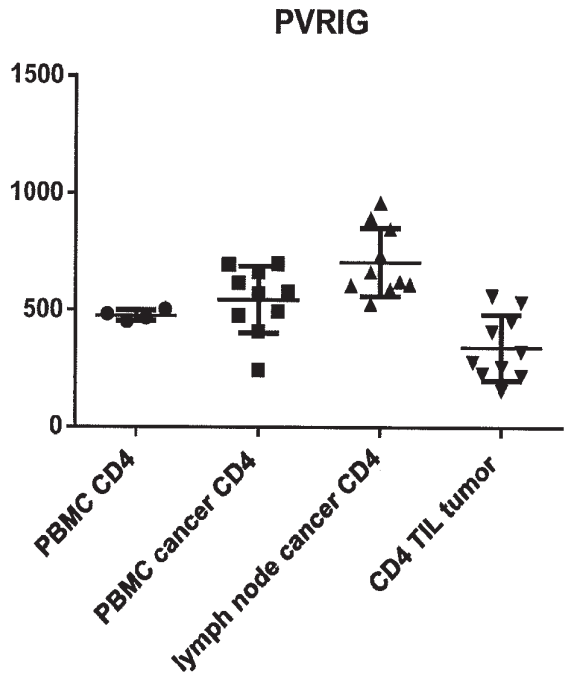

PVRIG
1500
1000
500
0
PBMC CD4
PBMC cancer CD4
lymph node cancer CD4
CD4 TIL tumor

Figure 5c:

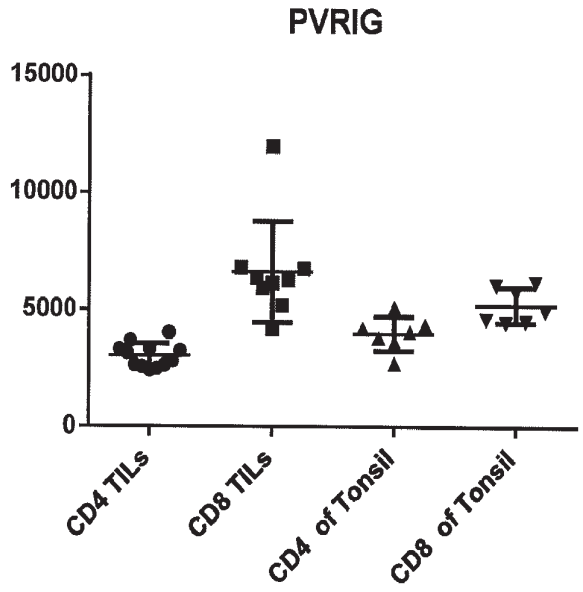

PVRIG
15000
10000
5000
0
CD4 TILs
CD8 TILs
CD4 of Tonsil
CD8 of Tonsil

Figure 6

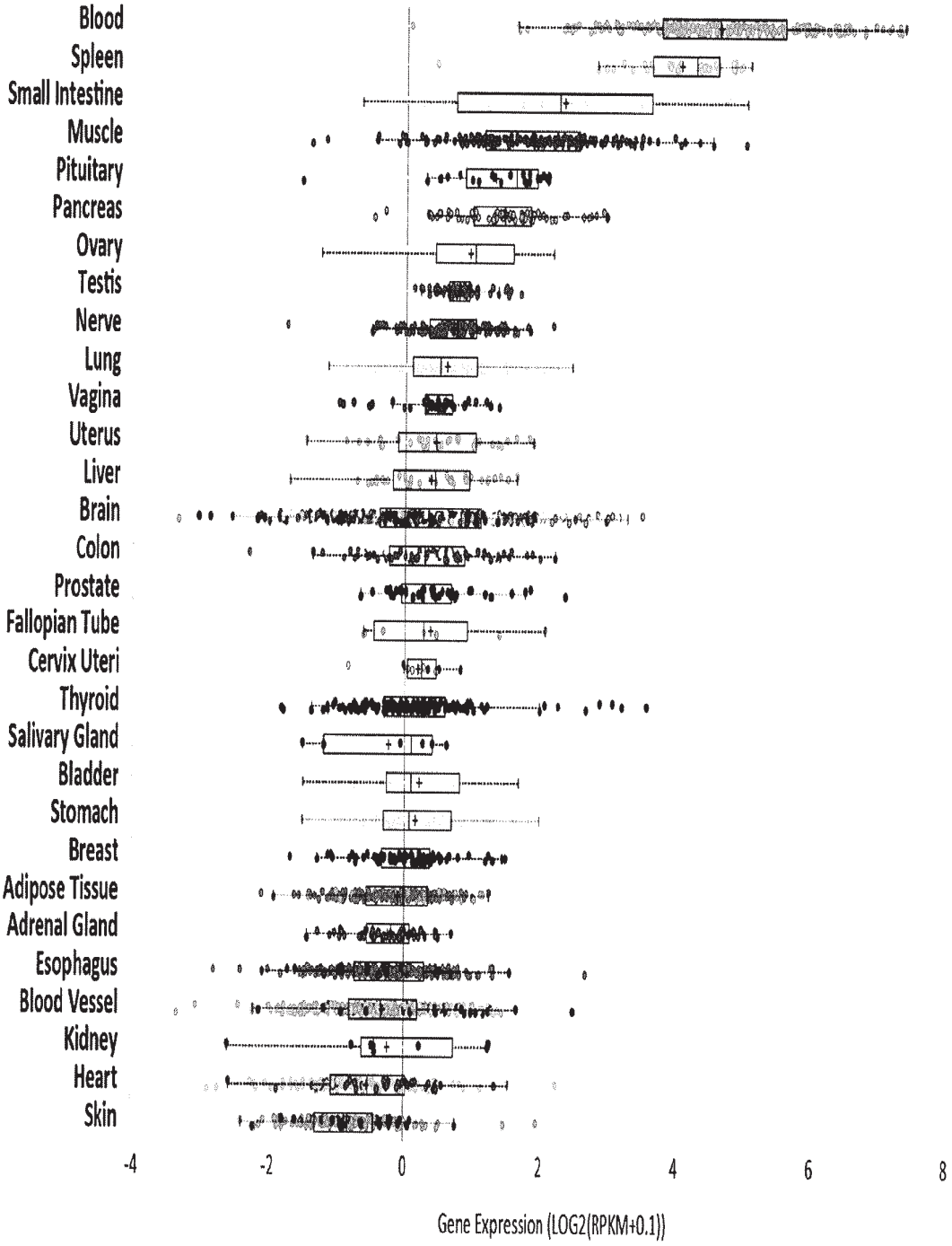

Blood
Spleen
Small Intestine
Muscle
Pituitary
Pancreas
Ovary
Testis
Nerve
Lung
Vagina
Uterus
Liver
Brain
Colon
Prostate
Fallopian Tube
Cervix Uteri
Thyroid
Salivary Gland
Bladder
Stomach
Breast
Adipose Tissue
Adrenal Gland
Esophagus
Blood Vessel
Kidney
Heart
Skin
-4
-2
0
2
4
6
8
Gene Expression (LOG2(RPKM+0.1))

Figure 7

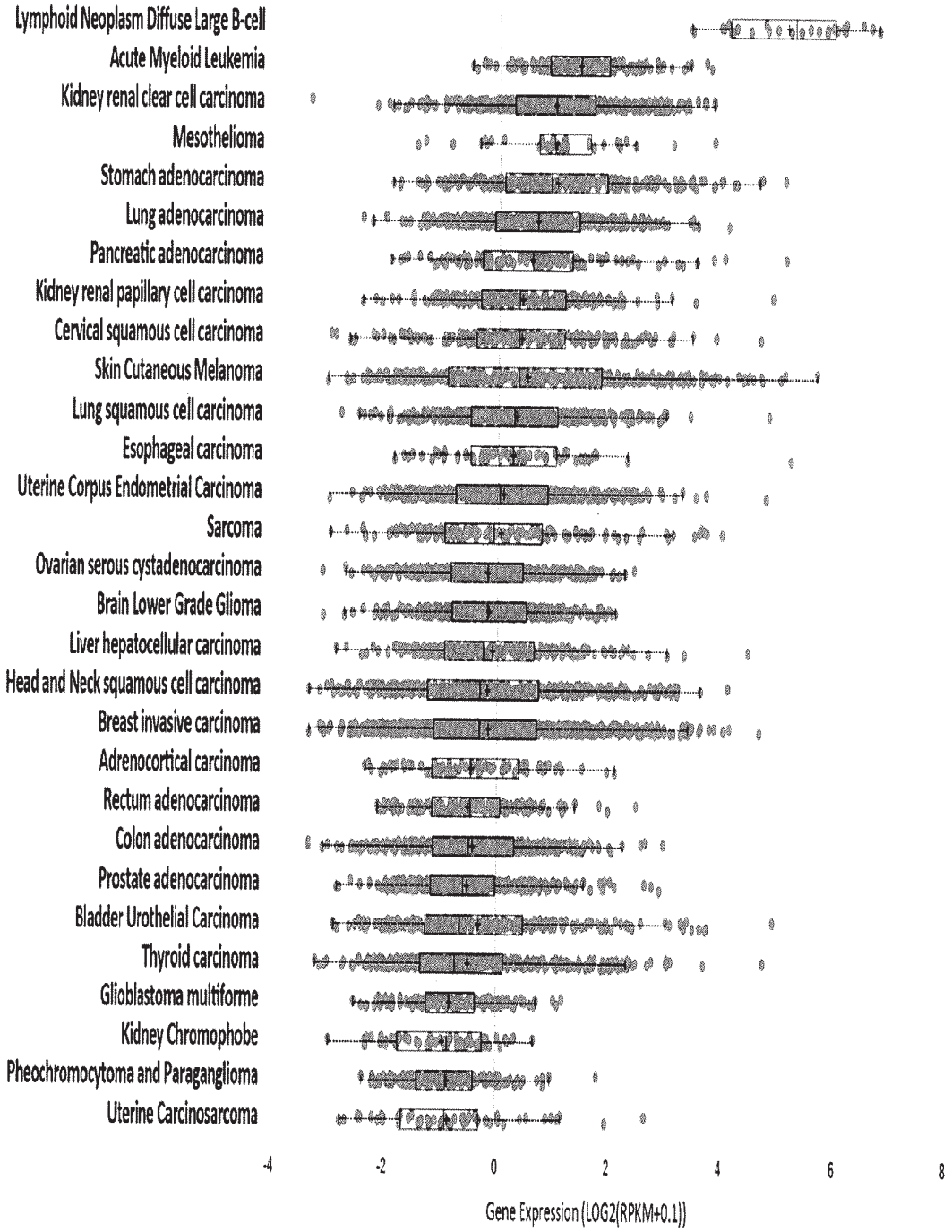
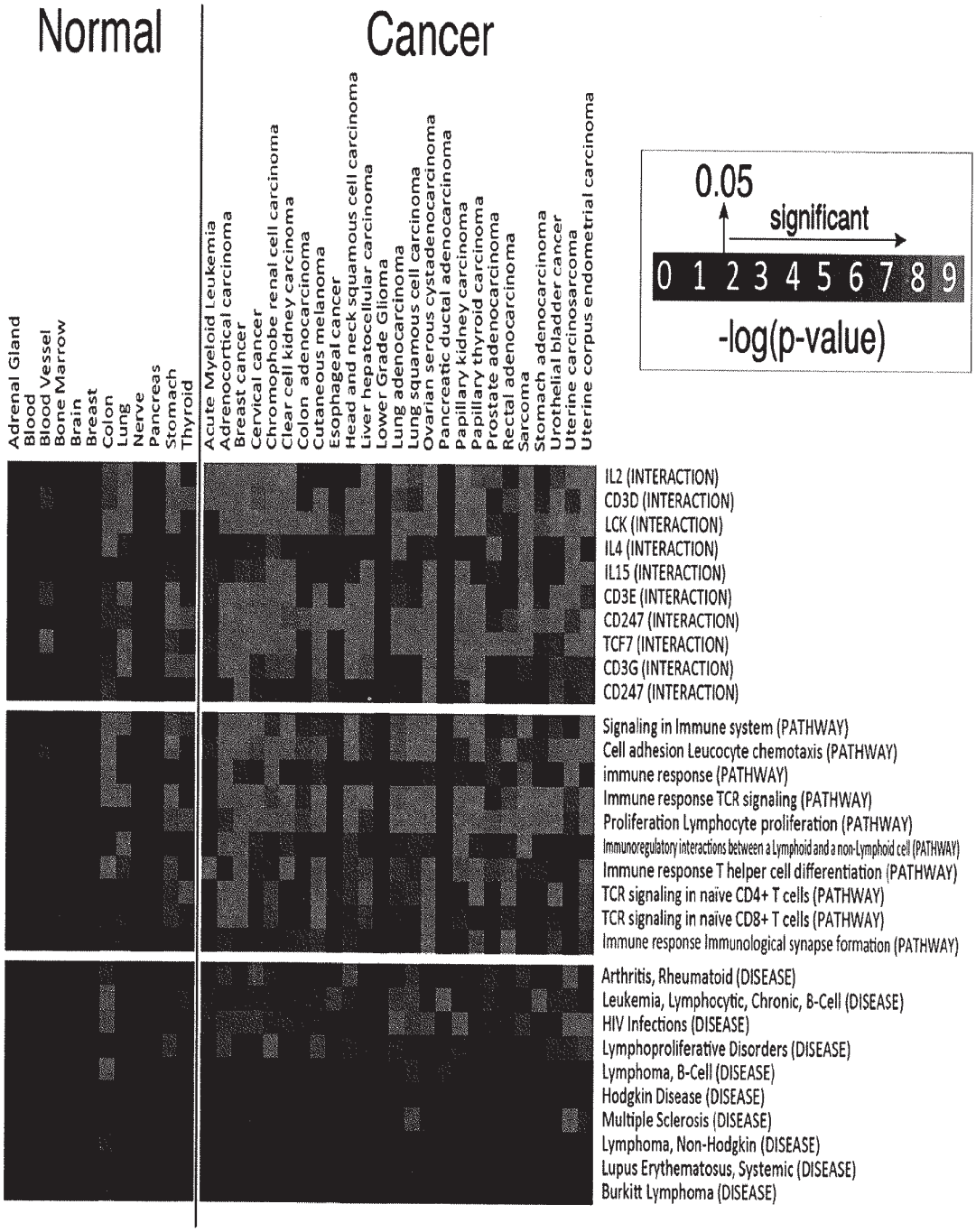

Lymphoid Neoplasm Diffuse Large B-cell
Acute Myeloid Leukemia
Kidney renal clear cell carcinoma
Mesothelioma
Stomach adenocarcinoma
Lung adenocarcinoma
Pancreatic adenocarcinoma
Kidney renal papillary cell carcinoma
Cervical squamous cell carcinoma
Skin Cutaneous Melanoma
Lung squamous cell carcinoma
Esophageal carcinoma
Uterine Corpus Endometrial Carcinoma
Sarcoma
Ovarian serous cystadenocarcinoma
Brain Lower Grade Glioma
Liver hepatocellular carcinoma
Head and Neck squamous cell carcinoma
Breast invasive carcinoma
Adrenocortical carcinoma
Rectum adenocarcinoma
Colon adenocarcinoma
Prostate adenocarcinoma
Bladder Urothelial Carcinoma
Thyroid carcinoma
Glioblastoma multiforme
Kidney Chromophobe
Pheochromocytoma and Paraganglioma
Uterine Carcinosarcoma
-4
-2
0
2
4
6
8
Gene Expression (LOG2(RPKM+0.1))

Figure 8


Normal
Cancer
Adrenal Gland
Blood
Blood Vessel
Bone Marrow
Brain
Breast
Colon
Lung
Nerve
Pancreas
Stomach
Thyroid
Acute Myeloid Leukemia
Adrenocortical carcinoma
Breast cancer
Cervical cancer
Chromophobe renal cell carcinoma
Clear cell kidney carcinoma
Colon adenocarcinoma
Cutaneous melanoma
Esophageal cancer
Head and neck squamous cell carcinoma
Liver hepatocellular carcinoma
Lower Grade Glioma
Lung adenocarcinoma
Lung squamous cell carcinoma
Ovarian serous cystadenocarcinoma
Pancreatic ductal adenocarcinoma
Papillary kidney carcinoma
Papillary thyroid carcinoma
Prostate adenocarcinoma
Rectal adenocarcinoma
Sarcoma
Stomach adenocarcinoma
Urothelial bladder cancer
Uterine carcinosarcoma
Uterine corpus endometrial carcinoma
0.05
significant
0 1 2 3 4 5 6 7 8 9
-log(p-value)
IL2 (INTERACTION)
CD3D (INTERACTION)
LCK (INTERACTION)
IL4 (INTERACTION)
IL15 (INTERACTION)
CD3E (INTERACTION)
CD247 (INTERACTION)
TCF7 (INTERACTION)
CD3G (INTERACTION)
CD247 (INTERACTION)
Signaling in Immune system (PATHWAY)
Cell adhesion Leucocyte chemotaxis (PATHWAY)
immune response (PATHWAY)
Immune response TCR signaling (PATHWAY)
Proliferation Lymphocyte proliferation (PATHWAY)
Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell (PATHWAY)
Immune response T helper cell differentiation (PATHWAY)
TCR signaling in naïve CD4+ T cells (PATHWAY)
TCR signaling in naïve CD8+ T cells (PATHWAY)
Immune response Immunological synapse formation (PATHWAY)
Arthritis, Rheumatoid (DISEASE)
Leukemia, Lymphocytic, Chronic, B-Cell (DISEASE)
HIV Infections (DISEASE)
Lymphoproliferative Disorders (DISEASE)
Lymphoma, B-Cell (DISEASE)
Hodgkin Disease (DISEASE)
Multiple Sclerosis (DISEASE)
Lymphoma, Non-Hodgkin (DISEASE)
Lupus Erythematosus, Systemic (DISEASE)
Burkitt Lymphoma (DISEASE)

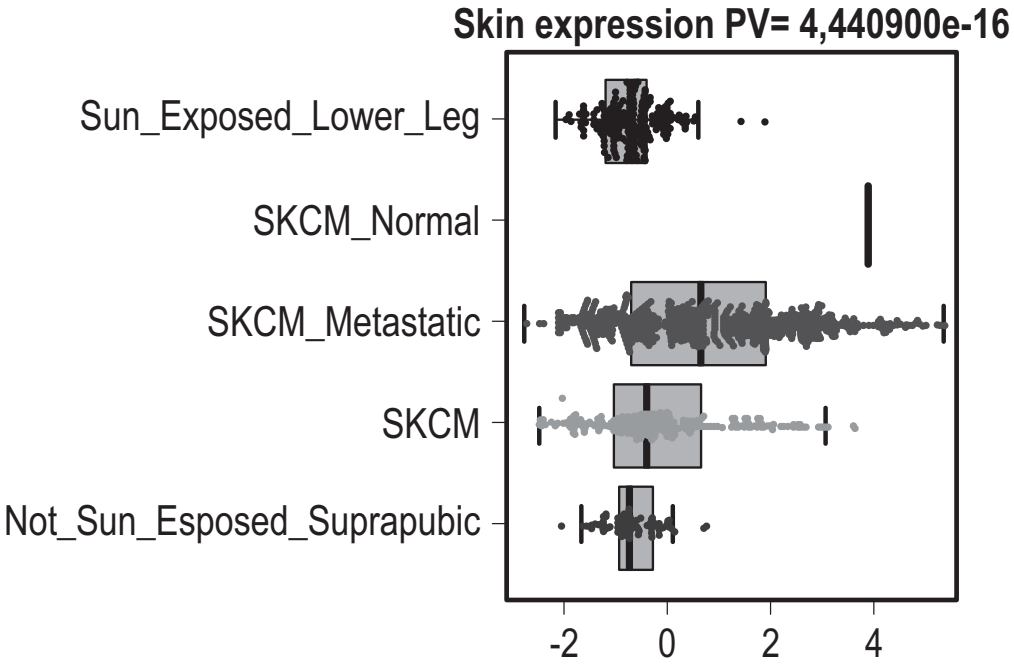


Figure 9

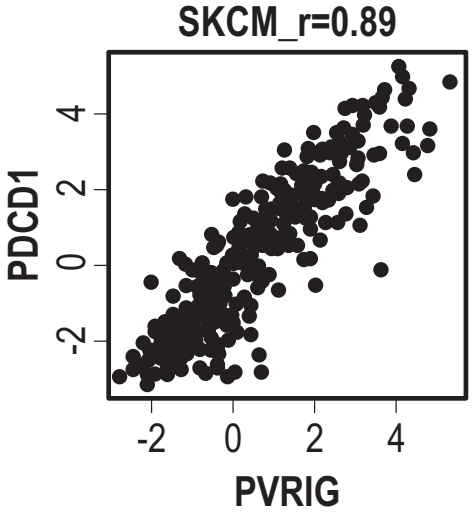


Figure 10

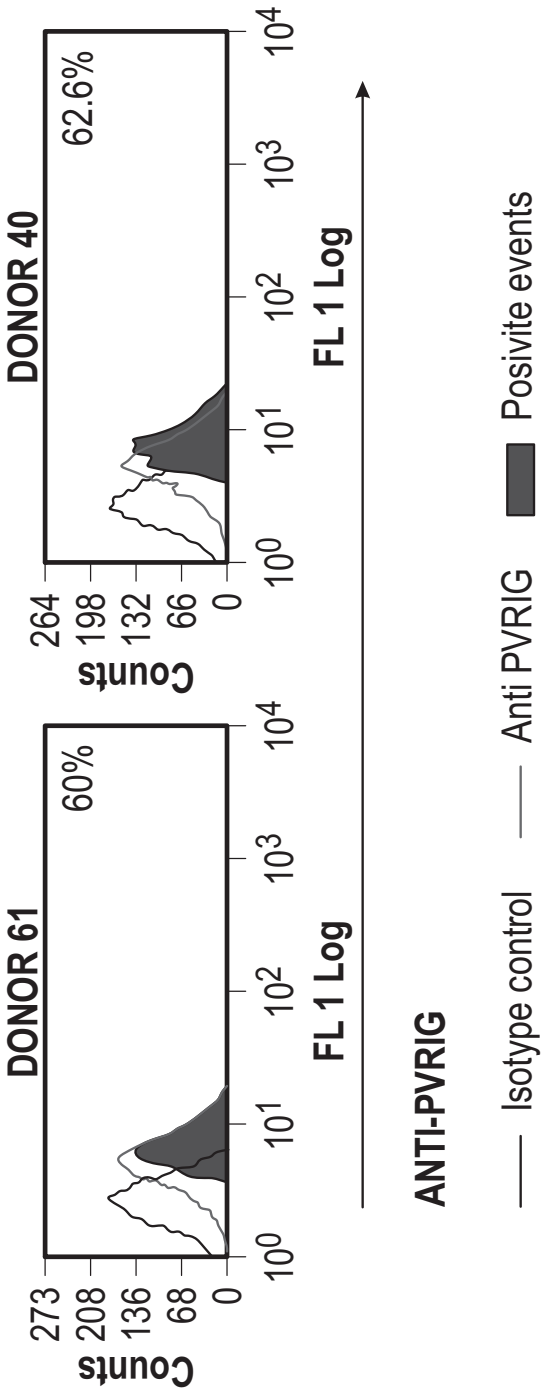

DONOR 61
60%
Counts
273
208
136
68
0
10^0
10^1
10^2
10^3
10^4
FL 1 Log
DONOR 40
62.6%
Counts
264
198
132
66
0
10^0
10^1
10^2
10^3
10^4
FL 1 Log
ANTI-PVRIG
Isotype control
Anti PVRIG
Posivite events

Figure 11

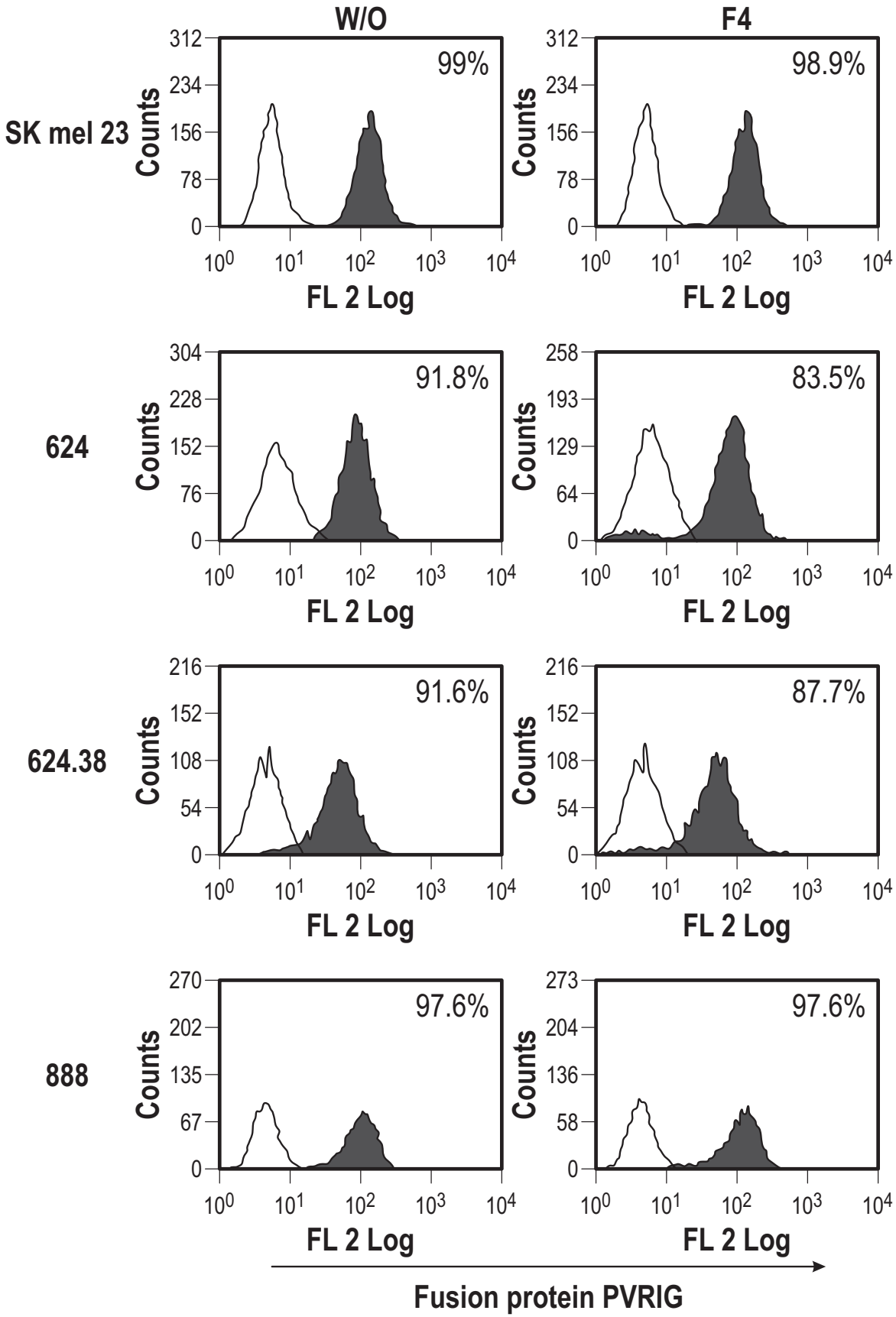

W/O
F4
SK mel 23
624
624.38
888
99%
98.9%
91.8%
83.5%
91.6%
87.7%
97.6%
97.6%
Counts
FL 2 Log
Fusion protein PVRIG

Figure 12

Figure 13

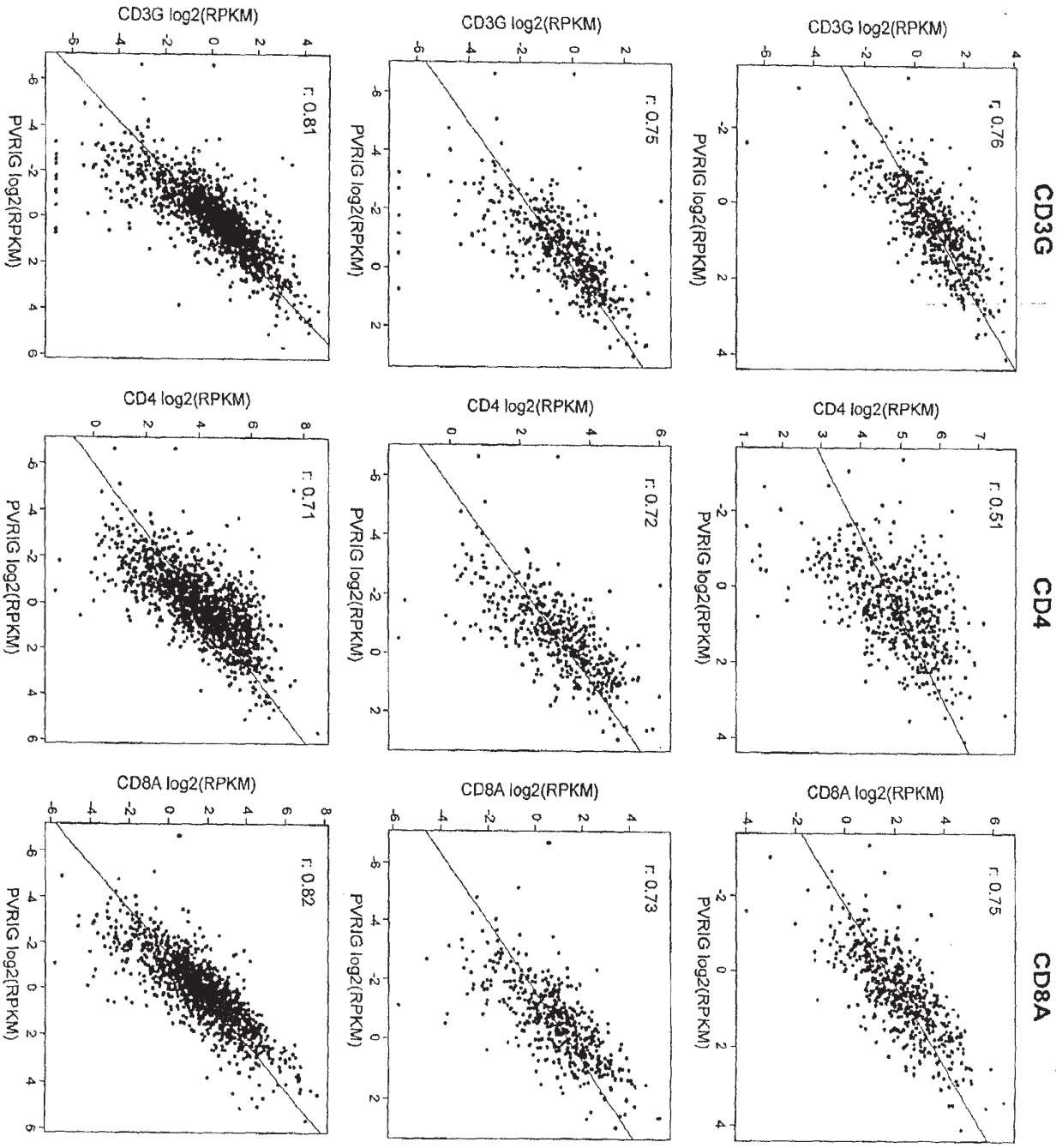
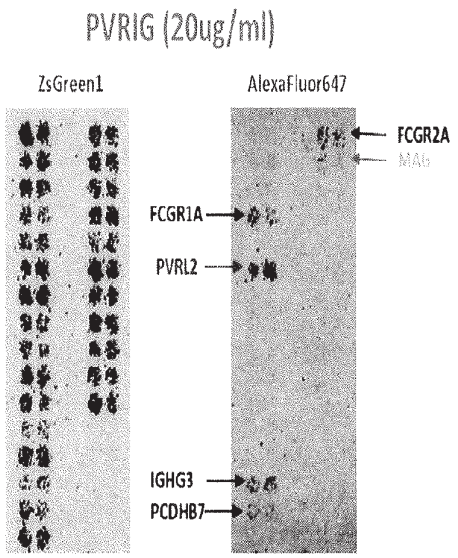
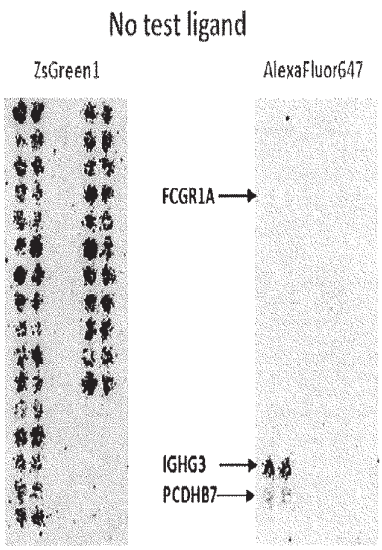

Lung Adenocarcinoma
Colon Adenocarcinoma
Skin cutanous melanoma
CD3G
CD4
CD8A
CD3G log2(RPKM)
CD4 log2(RPKM)
CD8A log2(RPKM)
PVRIG log2(RPKM)
r: 0.76
r: 0.75
r: 0.81
r: 0.51
r: 0.72
r: 0.71
r: 0.75
r: 0.73
r: 0.82

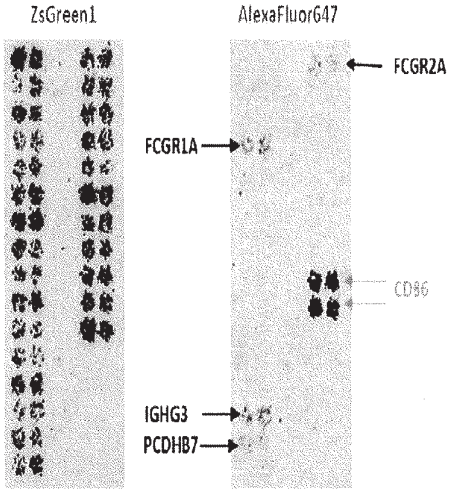
Figure 14:

Spotting pattern

Position	Gene Id	Position	Gene Id
1	ARHGEF2	17	FCGR2A
2	FASLG	18	MAG
3	GPR65	19	KCNJ15
4	FCGR1A	20	C21orf63
5	GNB5	21	MRGPRD
6	PVRL2	22	BAIAP2
7	HBEGF	23	QSOX1
8	PIP5K1C	24	TNFRSF25
9	MRGPRD	25	CD86
10	SHANK2	26	CD86
11	APOM	27	EGFR
12	SLC34A1		
13	STX4		
14	IGHG3		
15	PCDHB7		
16	LY6G6C		







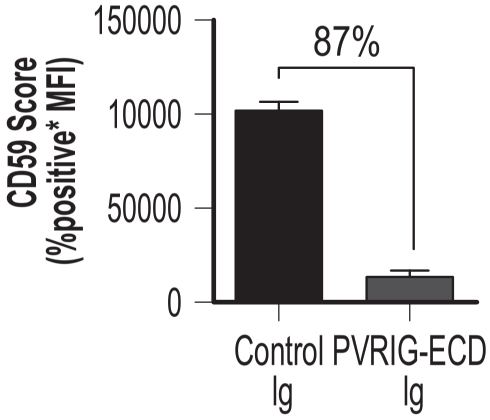


Figure 15A

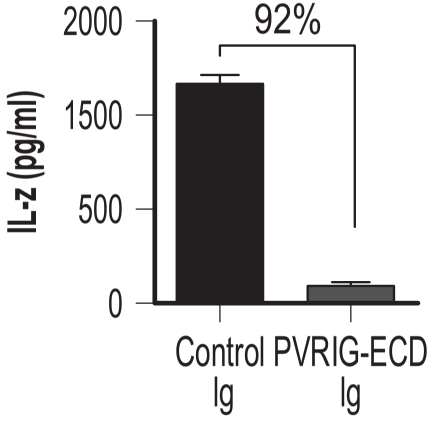


Figure 15B

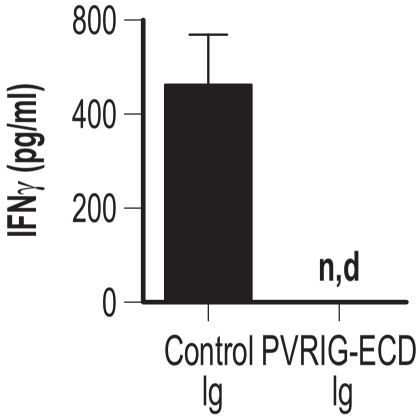


Figure 15C

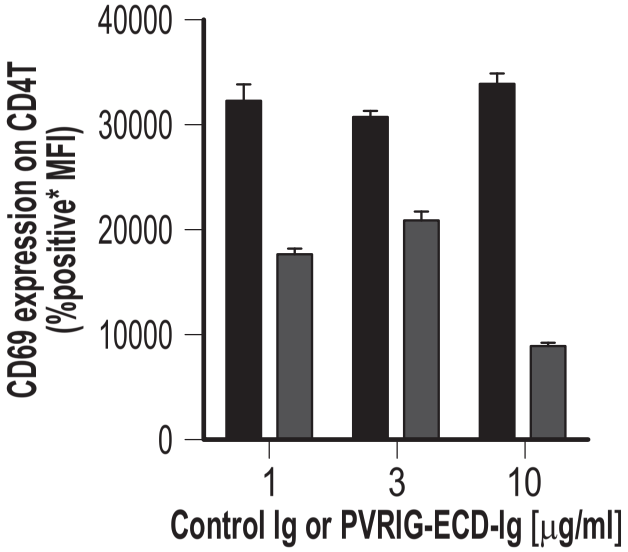


Figure 15D

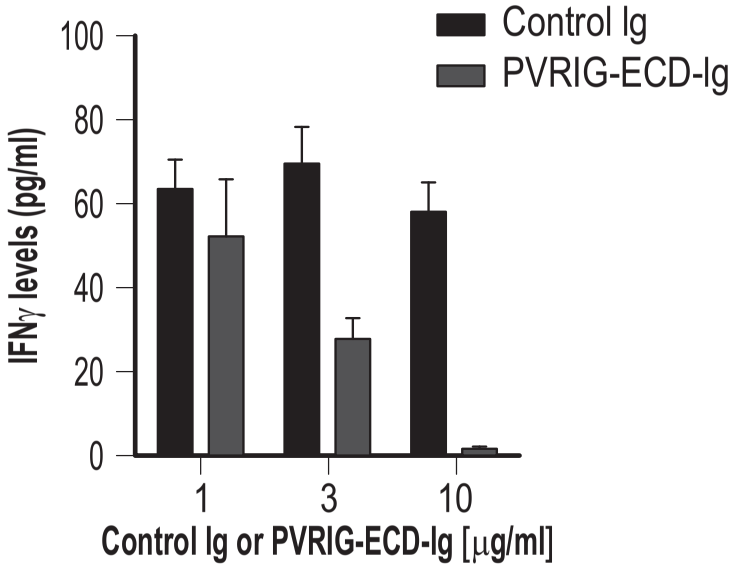


Figure 15E

Figure 16

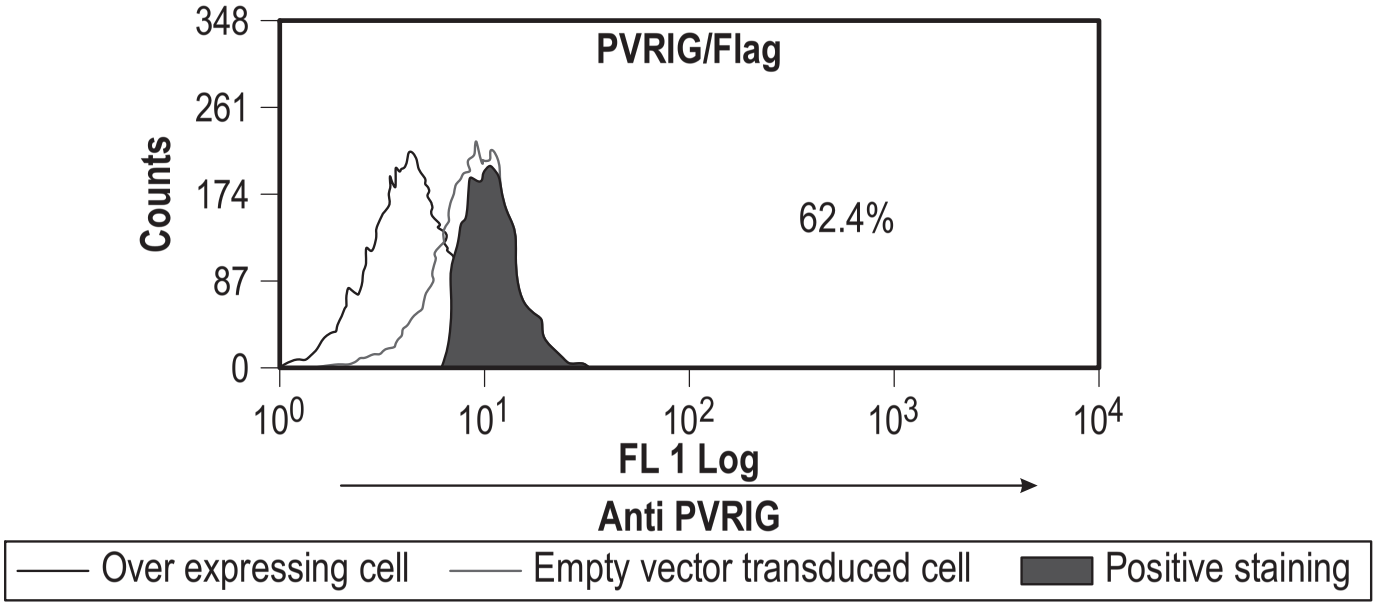
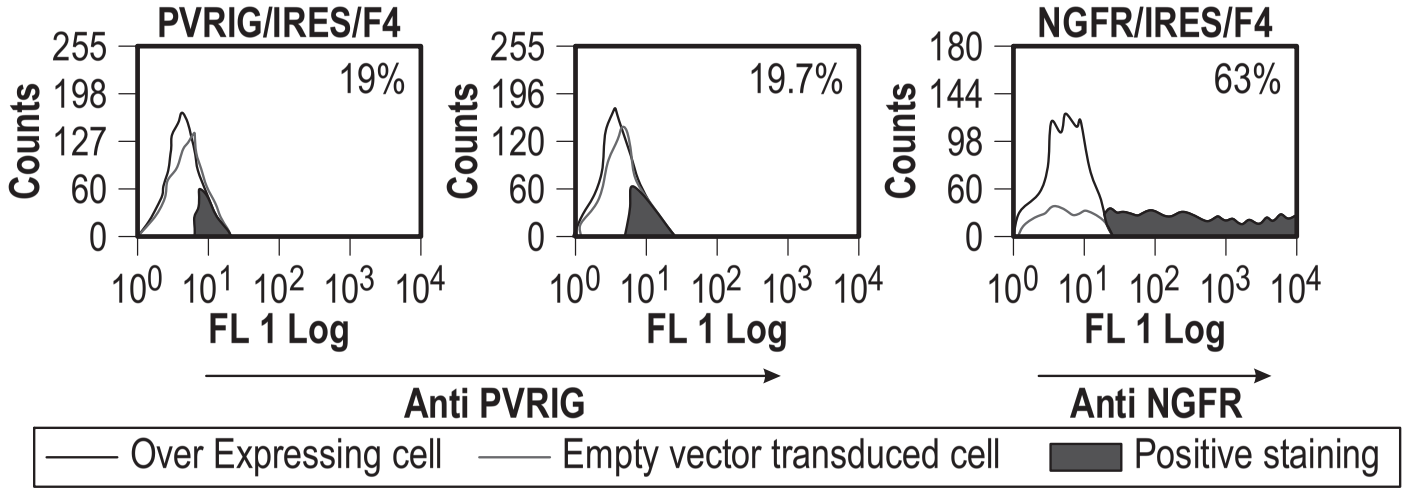


Figure 17



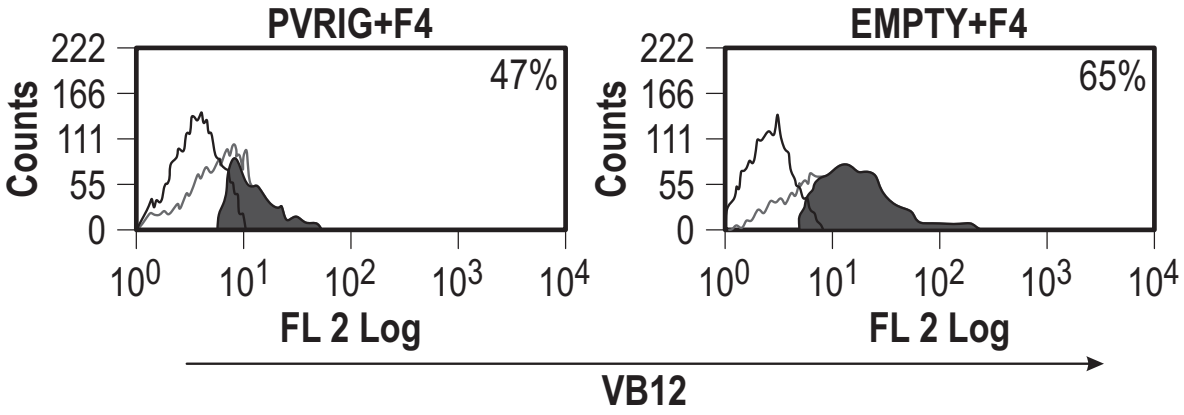


Figure 18A

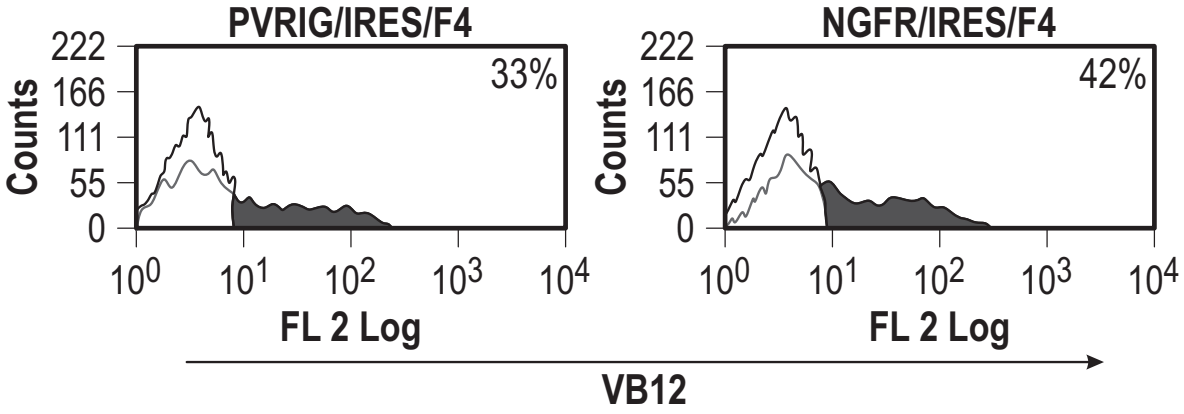


Figure 18B

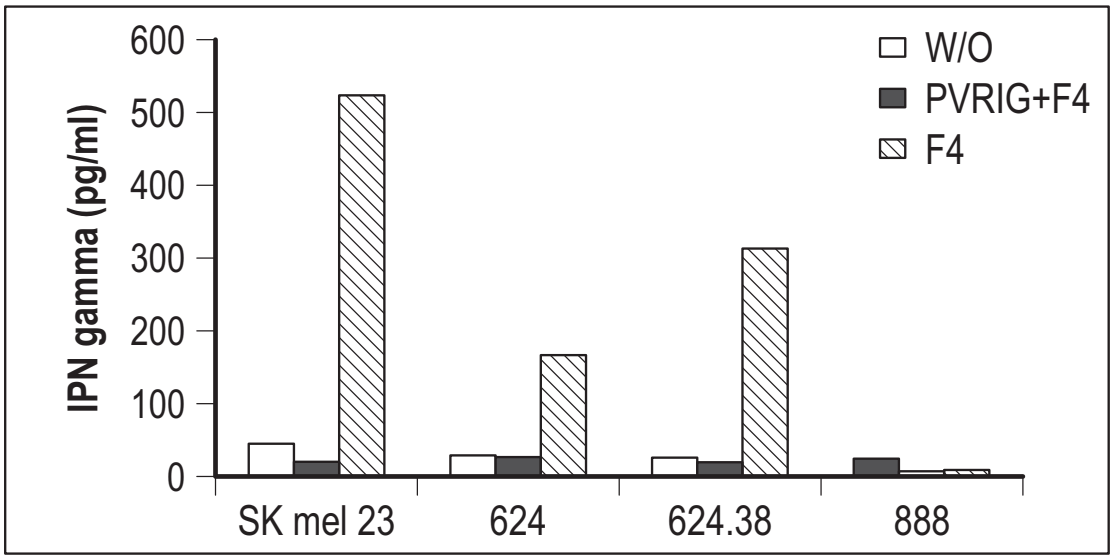


Figure 19

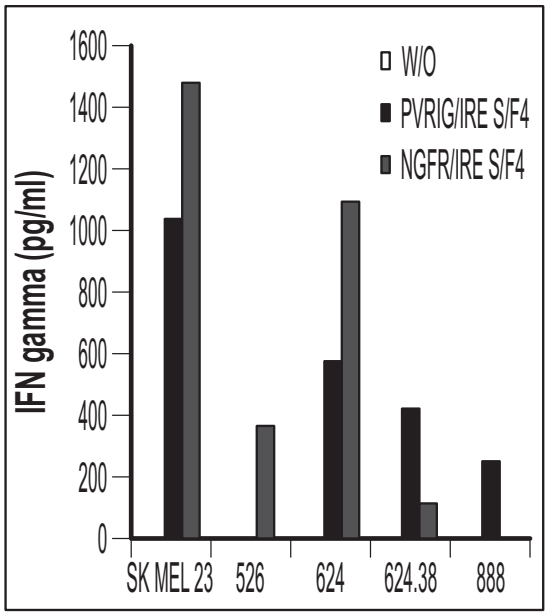


Figure 20A

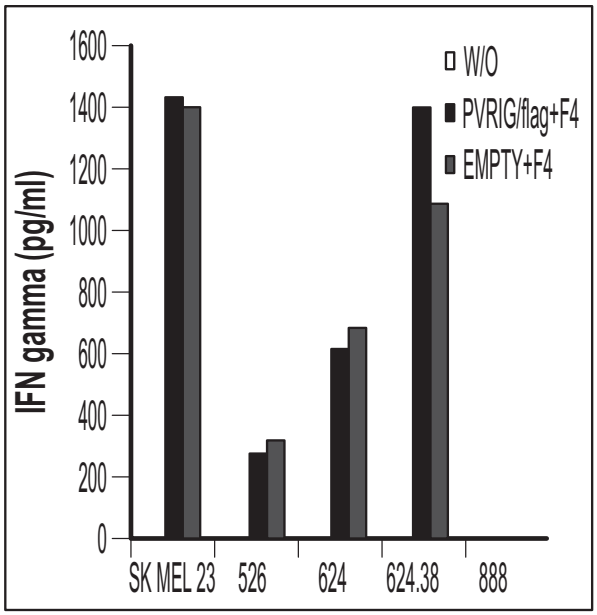


Figure 20B

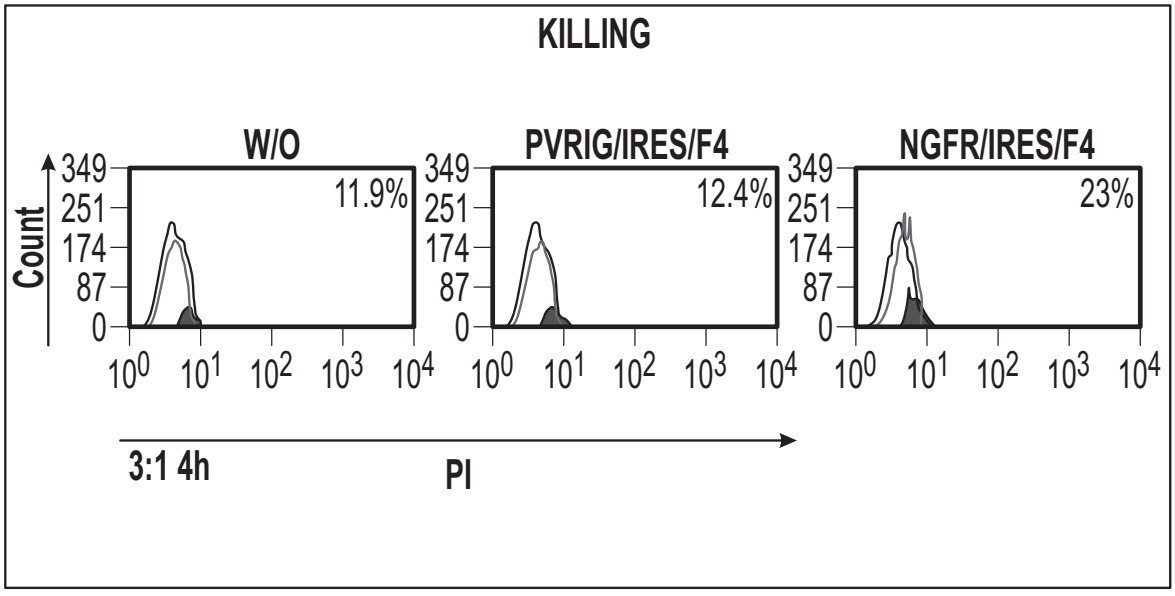


Figure 21

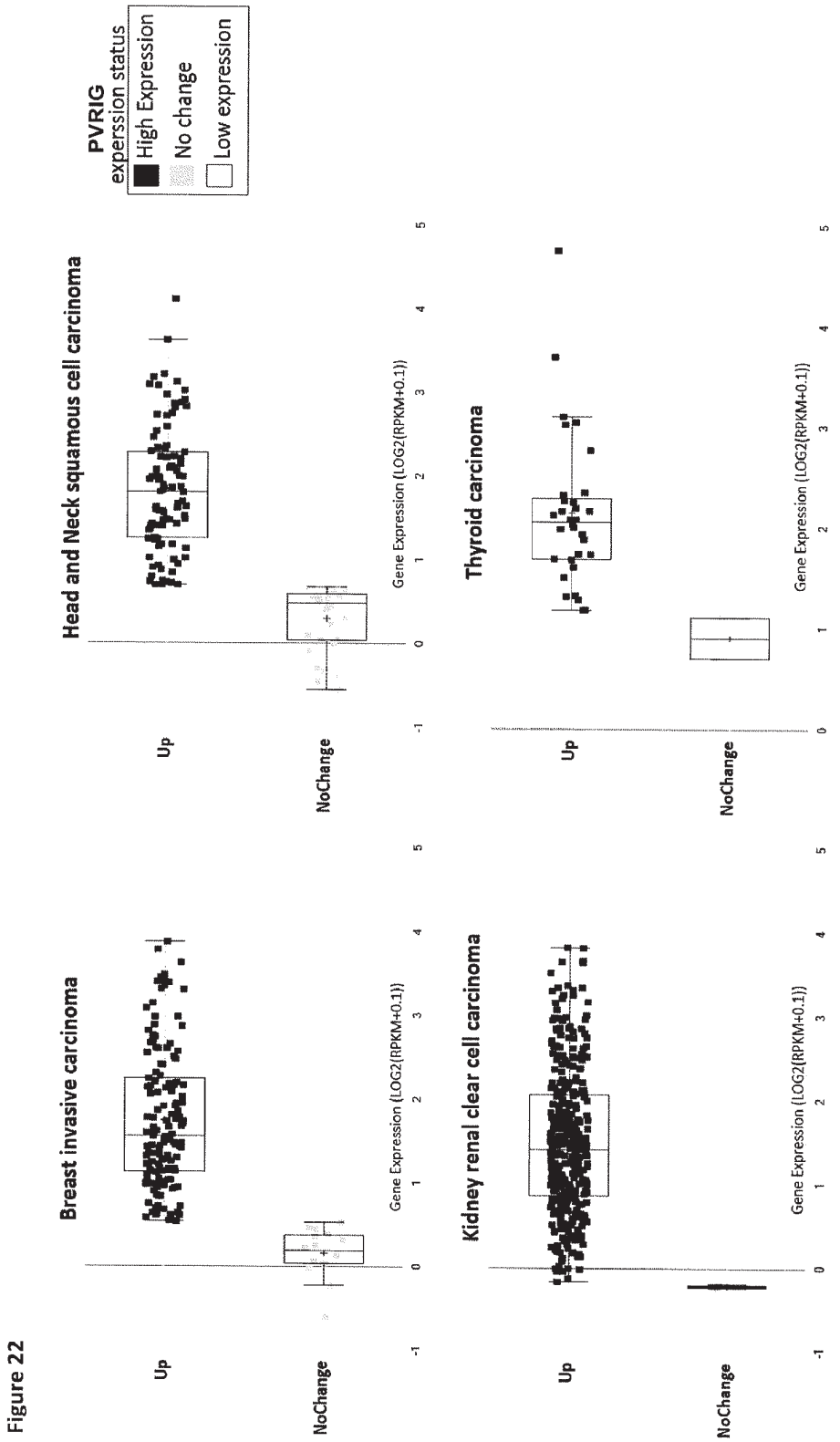
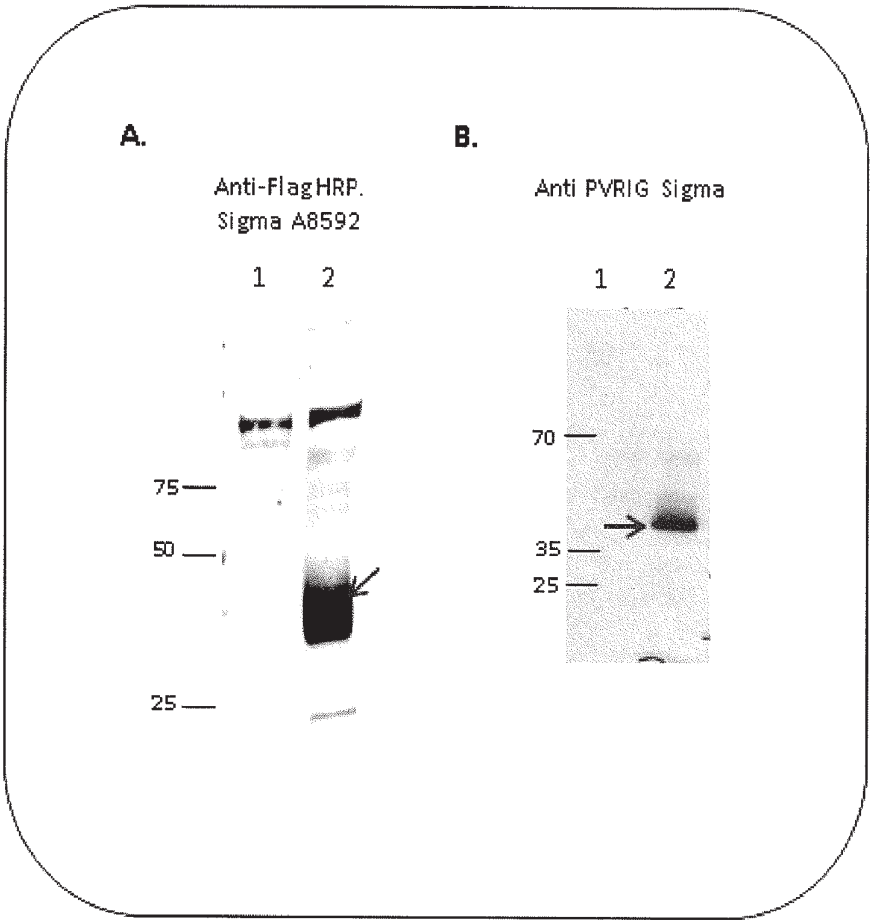

PVRIG
expression status
High Expression
No change
Low expression
Head and Neck squamous cell carcinoma
Thyroid carcinoma
Breast invasive carcinoma
Kidney renal clear cell carcinoma
Up
NoChange
Gene Expression (LOG2(RPKM+0.1))

Figure 22

Fiure 23A

Figure 23B



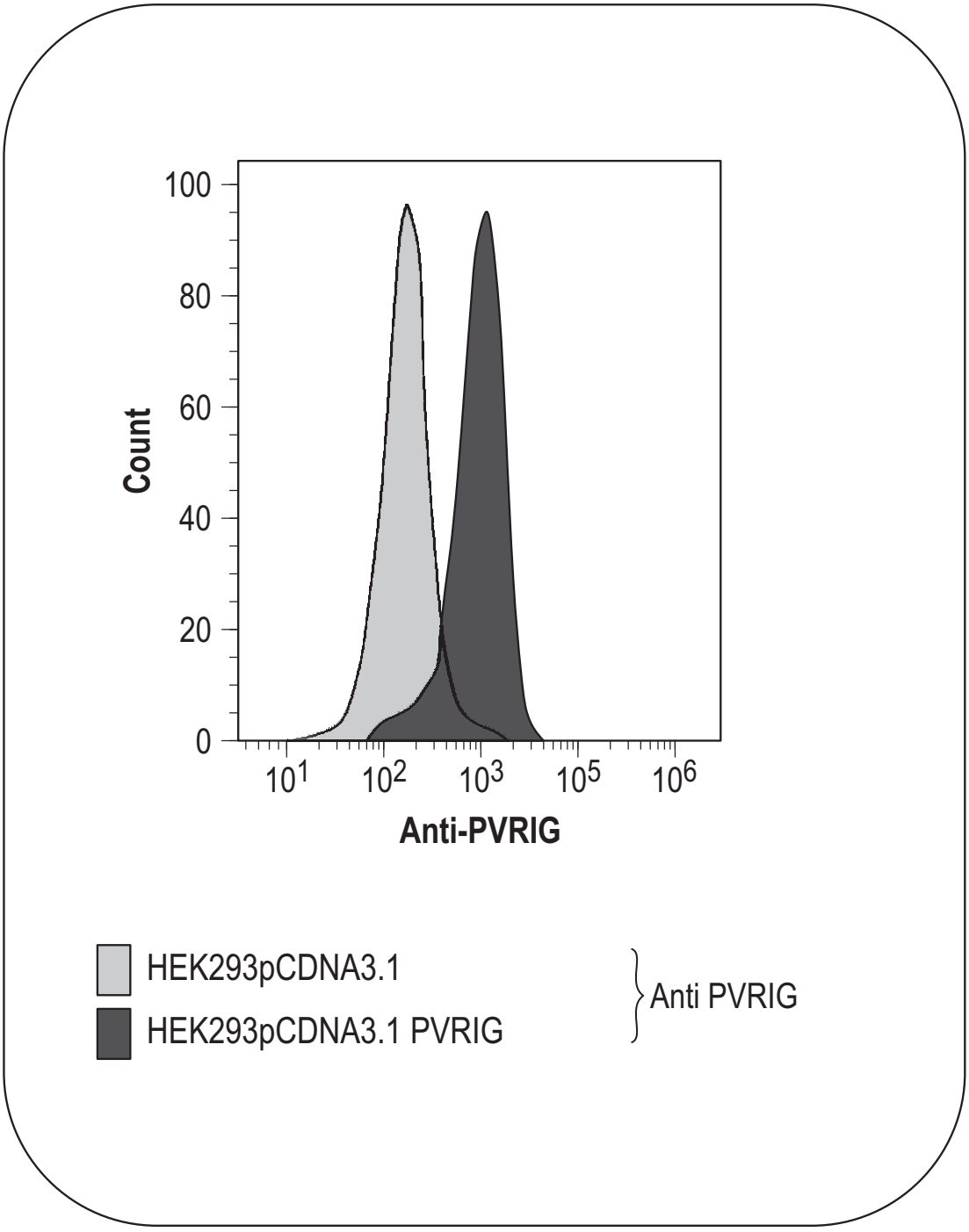

100
80
60
40
20
0
Count
10^1
10^2
10^3
10^5
10^6
Anti-PVRIG
HEK293pCDNA3.1
HEK293pCDNA3.1 PVRIG
Anti PVRIG

Figure 24

Figure 25

Human PVRIG WT Full length

Human PVRIG sequence starting from position 21 - alternative methionine

MGHRTLVLPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIR QWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGSLPPSSDPGLSAPPTPAPILRADLAGILGV SGVLLFGCVYLLHLLRRHKHRPAPRLQPSRTSPQAPRARAWAPSQASQAALHVPYATINTSCRPATLDTAHPHGGPSW WASLPTHAAHRPQGPAAWASTPIPARGSFVSVENGLYAQAGERPPHTGPGLTLFPDPRGPRAMEGPLGVR (SEQ ID NO:8)

Human PVRIG sequence starting from position 1 methionine

MRTEAQVPALQPPEPGLEGAMGHRTLVLPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWG 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 (MGWSCIILFLVATATGVHS (`(SEQ ID NO:10)` + CGEN-PVRIG (41-171 of PVRIG_HUMAN) + Human IgG1 Fc mutated at C220S, C226S, C229S of hinge

MGWSCIILFLVATATGVHSTPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQW APARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGSLPPSSDPGLSAPPTPAPILRADEPKSSDKTHT SPPSPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:11)

Figure 26

Human PVLR2 alpha isoform

>gi|5360210|ref|NP_002847.1| nectin-2 isoform alpha precursor [Homo sapiens]

MARAAALLPSRSPPTPLLWPLLLLLLLETGAQDVRVQVLPEVRGQLGGTVELPCHLLPPVPGLYISLVTW

QRPDAPANHQNVAAFHPKMGPSFPSPKPGSERLSFVSAKQSTGQDTEAELQDATLALHGLTVEDEGNYTC

EFATFPKGSVRGMTWLRVIAKPKNQAEAQKVTFSQDPTTVALCISKEGRPPARISWLSSLDWEAKETQVS

GTLAGTVTVTSRFTLVPSGRADGVTVTCKVEHESFEEPALIPVTLSVRYPPEVSISGYDDNWYLGRTDAT

LSCDVRSNPEPTGYDWSTTSGTFPTSAVAQGSQLVIHAVDSLFNTTFVCTVTNAVGMGRAEQVIFVRETP

RASPRDVGPLVWGAVGGTLLVLLLLAGGSLAFILLRVRRRRKSPGGAGGGASGDGGFYDPKAQVLGNGDP

VFWTPVVPGPMEPDGKDEEEEEEEEKAEKGLMLPPPPALEDDMESQLDGSLISRRAVYV (SEQ ID NO: 12)

Human PVLR2 delta isoform
>gi|112789532|ref|NP_001036189.1| nectin-2 isoform delta precursor [Homo sapiens]
MARAAALLPSRSPPTPLLWPLLLLLLLETGAQDVRVQVLPEVRGQLGGTVELPCHLLPPVPGLYISLVTW
QRPDAPANHQNVAAFHPKMGPSFPSPKPGSERLSFVSAKQSTGQDTEAELQDATLALHGLTVEDEGNYTC
EFATFPKGSVRGMTWLRVIAKPKNQAEAQKVTFSQDPTTVALCISKEGRPPARISWLSSLDWEAKETQVS
GTLAGTVTVTSRFTLVPSGRADGVTVTCKVEHESFEEPALIPVTLSVRYPPEVSISGYDDNWYLGRTDAT
LSCDVRSNPEPTGYDWSTTSGTFPTSAVAQGSQLVIHAVDSLFNTTFVCTVTNAVGMGRAEQVIFVRETP
NTAGAGATGGIIGGIIAAIIATAVAATGILICRQQRKEQTLQGAEEDEDLEGPPSYKPPTPKAKLEAQEM
PSQLFTLGASEHSPLKTPYFDAGASCTEQEMPRYHELPTLEERSGPLHPGATSLGSPIPVPPGPPAVEDV
SLDLEDEEGEEEEEYLDKINPIYDALSY (SEQ ID NO: 13)

Figure 27

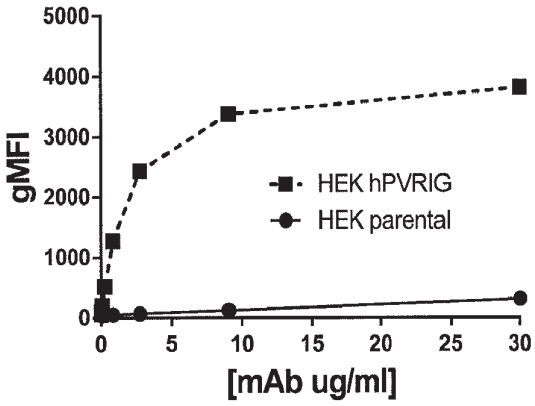


Figure 28

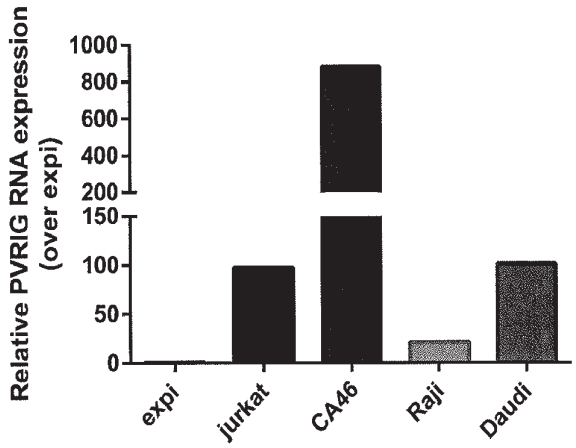


Figure 29

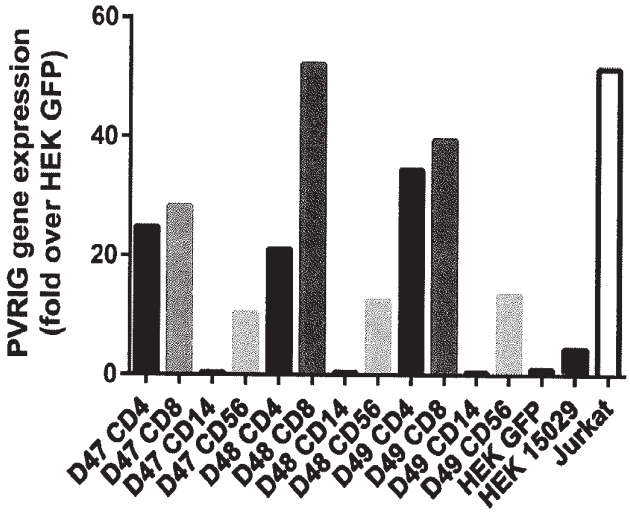

PVRIG gene expression
(fold over HEK GFP)
60
40
20
0
D47 CD4
D47 CD8
D47 CD14
D47 CD56
D48 CD4
D48 CD8
D48 CD14
D48 CD56
D49 CD4
D49 CD8
D49 CD14
D49 CD56
HEK GFP
HEK 15029
Jurkat

Figure 30A

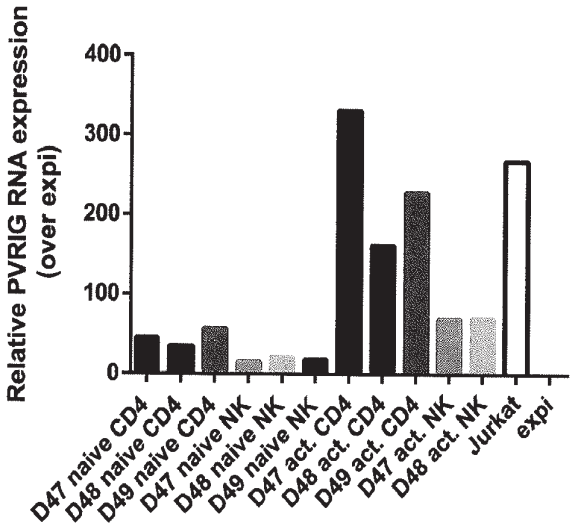


Figure 30B

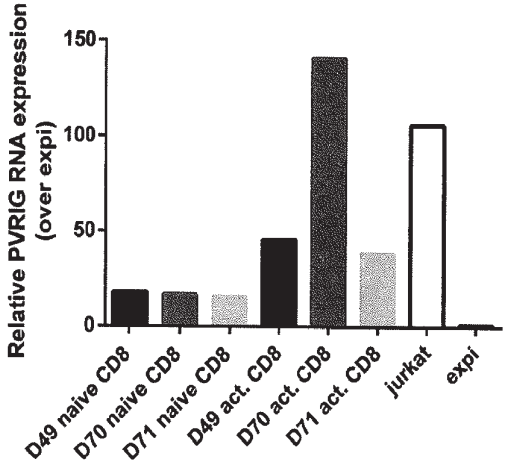


Figure 31A

Antibody (hIgG1)	EC_{50} (HEK OE, nM)	HEK OE/par (5ug/ml, gMFIr)	Jurkat (5ug/ml, gMFIr)	CA46 (5ug/ml, gMFIr)
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 (hIgG1)	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

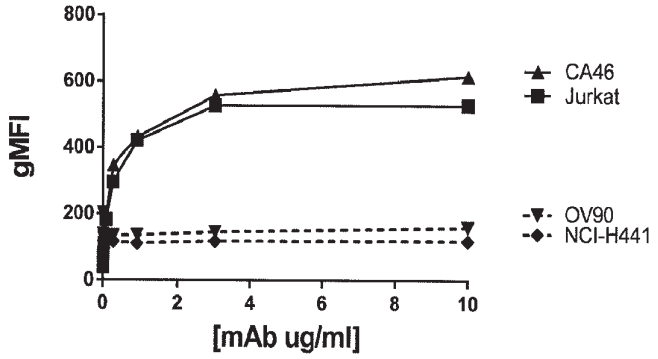
Figure 32A

Antibody (hIgG1)	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.7.002	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

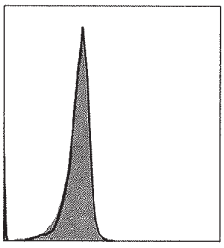
Figure 32B

Antibody (hIgG1)	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


800
600
400
200
0
gMFI
0
2
4
6
8
10
[mAb ug/ml]
CA46
Jurkat
OV90
NCI-H441

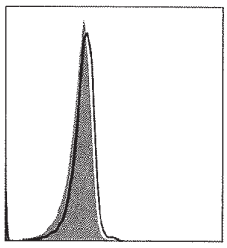
a



expi parental

Figure 34A

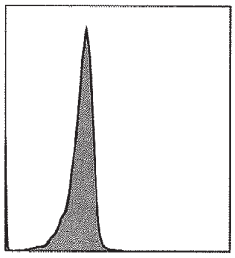
b



cPVRIG transient

Figure 34B

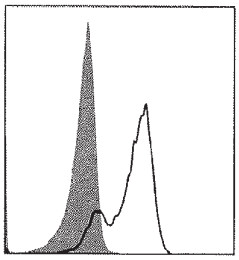
c



expi parental

Figure 34C

d



cPVRIG transient

Figure 34D

Figure 35

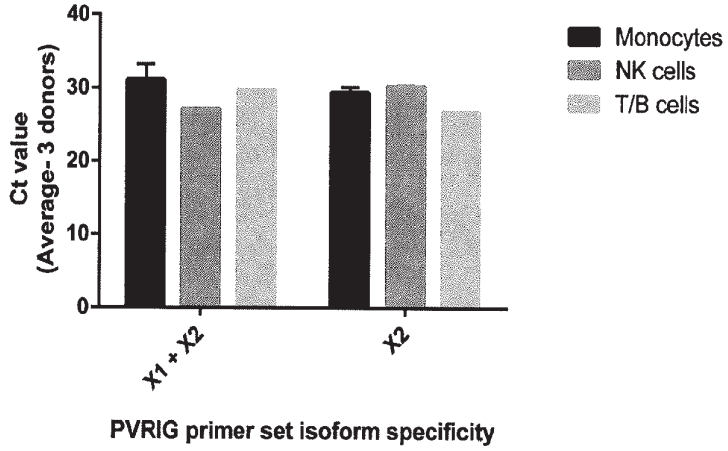

40
30
20
10
0
Ct value
(Average- 3 donors)
X1 + X2
X2
Monocytes
NK cells
T/B cells
PVRIG primer set isoform specificity

Figure 36A

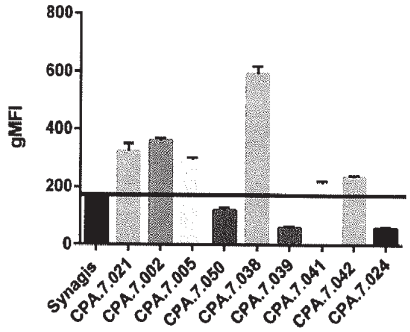


Figure 36B

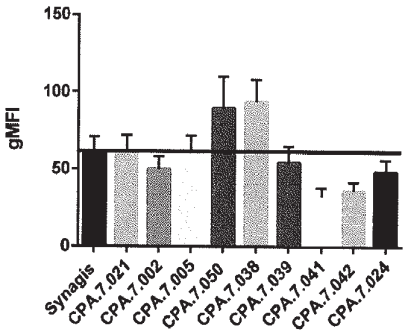


Figure 36C

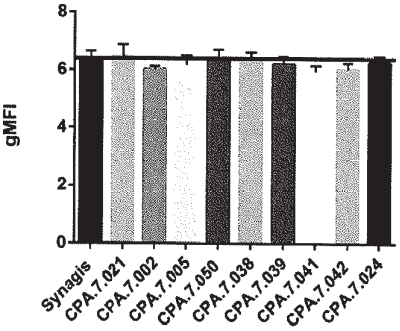


Figure 37A

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	IIPIFGTA	15	AREEVSSPYGMDV	16	TGAVTSGHY	17	DTG	18	LLSYSGASWV	19
CPA.7.003	GFSLSHFS	20	FDPEEGGT	21	ATGIWYSSGWPVDY	22	QSLLDSSGYNY	23	LGS	24	MQALQTPIT	25
CPA.7.004	GYTLTELS	26	FDPEDGET	27	ATVSRVRGVINYYYYMDV	28	QSLLYRNGNNY	29	LGS	30	MQALQTPPT	31
CPA.7.006	GGTFGTYA	32	ITPISATI	33	ARGFEYSDGLLDD	34	QSLFYSDDGNTY	35	RLS	36	MQHMEFPLT	37
CPA.7.008	SGSISSTNW	38	IYHSGST	39	ARVGPAAIYY	40	SNNVGYEG	41	RNN	42	SAWDSSLNAVV	43
CPA.7.009	GYTLTELS	44	FDPEDGET	45	ATAKPGIAVAGQNYYYYYMDV	46	QSLLYRNGNNY	47	LGS	48	MQALQTPPT	49
CPA.7.010	GFTFSSYA	50	ISYDGSNK	51	ASSPIGYSYGYWGGMDV	52	SGIDVRTNK	53	FQSDSDK	54	LIWHTSGWV	55
CPA.7.011	GYTLTELS	56	FDPEDGET	57	ATGPAAAGVGYYYYMDV	58	QSLLYRNGYNY	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	FDPEDGET	69	ATGGYSSGFNYYYYYMDV	70	QSLLYRNGNNY	71	LGS	72	MQALQTPPT	73
CPA.7.014	GYTLTELS	74	FDPEDGET	75	ATGVTTYYYYGMDV	76	QSLLYSNGNNF	77	LGS	78	MQALQTPPT	79
CPA.7.015	GFTFSSYG	80	IRYDGSNK	81	ARDLFDFWWDGMDV	82	QSVSSMY	83	GAS	84	QQYVSSPMYT	85
CPA.7.017	GGTFNNYG	86	IIPLFGTT	87	ARDRMAADGMAVFDY	88	SSNIGRHF	89	KND	90	SSWDAALNGVV	91
CPA.7.018	GYTLTELS	92	FDPEDGET	93	ATEVPMVRGARRYYYYMDV	94	QTLLYINENNY	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	GGSISNSNYY	98	IYYSGST	99	ARGAWELSLGDWFDP	100	SSNIGAGYD	101	GNN	102	QSYDSSLSVYVV	103
CPA.7.021	GFTFGTSS	104	ISFDGTEI	105	AKGSGNIYFYSGMDV	106	QSISGW	107	ETS	108	QQYYSYPLT	109
CPA.7.022	GYTLTELS	110	FDPEDGET	111	ATGVPAAIGVYYYYYMDV	112	QSLLYSNGYNY	113	LGS	114	MQALQSPVT	115
CPA.7.023	GYTLTELS	116	FDPEDGET	117	ATDSRDGPAARGGYYYYMDV	118	QSLLYINGYNY	119	LGS	120	MQALQTPPT	121
CPA.7.024	GGTFSSYA	122	IIPIFGTA	123	ARDAYYYDSSGYYNPDAFDI	124	QSLLHSNGYNY	125	LGS	126	MQGLQTPRT	127
CPA.7.033	GGTFSSSA	128	IIPIYGIT	129	ARDDTARRVRGVPYYYYYAMDV	130	QDIDDD	131	EAS	132	LQHDNLPLT	133
CPA.7.034	GYTLTELS	134	FDPEDGET	135	ATEDPGPVAGPYYYYGMDV	136	QSLLYINGYHY	137	LGS	138	MQALQTPPT	139
CPA.7.036	GGTFSSSA	140	IIPIYGIT	141	ARDDTARRVRGVPYYYYYAMDV	142	QSLLDSDDGNTY	143	TLS	144	MQRLQFPLT	145
CPA.7.040	GYTLTELS	146	FDPEDGET	147	ATGVPAAIGVYYYYYMDV	148	QSLLYRNGYNY	149	WGS	150	MQAVQNPPT	151
CPA.7.046	GGTFSSSA	152	IIPIYGIT	153	ARDDTARRVRGVPYYYYYAMDV	154	QTMNNY	155	DAS	156	QQYGDWLPIT	157
CPA.7.047	GYTLTELS	158	FDPEDGET	159	ATAFPEATISYYYYMDV	160	QSLLYRNGYNY	161	WGS	162	MQAVQNPPT	163
CPA.7.049	GGTFSSSA	164	IIPIYGIT	165	ARDDTARRVRGVPYYYYYAMDV	166	RSLLDSDDGNTH	167	SLS	168	MQRKEFPLT	169
CPA.7.050	GGTFSSYA	170	IIPIFGTA	171	ARGPWYYDSSGYSSYAYYMDV	172	QSLLHSDGYNY	173	LGS	174	MQALHTPGVT	175

Figure 38A

CPA.7.001

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QMQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCAREEVSSPYGMDVWGQGTTVTVSS	176
vhCDR1	GGTFSSYA	177
vhCDR2	IIPIFGTA	178
vhCDR3	AREEVSSPYGMDV	179
Full length HC	QMQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCAREEVSSPYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	180
Variable light (vl) domain	QAVVTQEPSLTVSPGGTVTLTCGTSTGAVTSGHYPYWFQQKPGQAPKTLIYDTGNKHSWTPARFSGSLLGGKAALTLSGAQPE DEADYYCLLSYSGASWVFGGGTKLTVLG	181
vlCDR1	TGAVTSGHY	182
vlCDR2	DTG	183
vlCDR3	LLSYSGASWV	184
Full length light chain	QAVVTQEPSLTVSPGGTVTLTCGTSTGAVTSGHYPYWFQQKPGQAPKTLIYDTGNKHSWTPARFSGSLLGGKAALTLSGAQPE DEADYYCLLSYSGASWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTT PSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	185

Figure 38B
CPA.7.003

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKVSGFSLSHFSMHWVRQVPGKGLEWLGGFDPEEGGTIPAQKFQGRLTMTEDTST ETAYMELSSLRSEDTAVYYCATGIWYSSGWPVDYWGPGTLVTVSS	186
vhCDR1	GFSLSHFS	187
vhCDR2	FDPEEGGT	188
vhCDR3	ATGIWYSSGWPVDY	189
Full length HC	EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADKSTST AYMELSSLRSEDTAVYYCARGPWYYDSSGYSSYAYYMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	190
Variable light (vl) domain	DVVMTQSPLSLPVTPGGPASISCRSSQSLLDSSGYNYVDWYLQKPGQSPQLLISLGSDRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGIYYCMQALQTPITFGQGTRLEIKR	191
vlCDR1	QSLLDSSGYNY	192
vlCDR2	LGS	193
vlCDR3	MQALQTPIT	194
Full length light chain	DVVMTQSPLSLPVTPGGPASISCRSSQSLLDSSGYNYVDWYLQKPGQSPQLLISLGSDRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGIYYCMQALQTPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	195

Figure 38C
CPA.7.004

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATVSRVRGVINYYYYMDV WGKGTTVTVSS	196
vhCDR1	GYTLTELS	197
vhCDR2	FDPEDGET	198
vhCDR3	ATVSRVRGVINYYYYMDV	199
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATVSRVRGVINYYYYMDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	200
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGGGTKLEIKR	201
vlCDR1	QSLLYRNGNNY	202
vlCDR2	LGS	203
vlCDR3	MQALQTPPT	204
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	205

Figure 38D
CPA.7.006

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVRRPGSSVRVSCKPSGGTFGTYAFTWVRQAPGQGLEWMGGITPISATINRAQNLQDRLTITADESTT TVHMDLTSLRSEDTAVYYCARGFEYSDGLLDDWGQGTLVTVSS	206
vhCDR1	GGTFGTYA	207
vhCDR2	ITPISATI	208
vhCDR3	ARGFEYSDGLLDD	209
Full length HC	QVQLVQSGAEVRRPGSSVRVSCKPSGGTFGTYAFTWVRQAPGQGLEWMGGITPISATINRAQNLQDRLTITADESTT TVHMDLTSLRSEDTAVYYCARGFEYSDGLLDDWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	210
Variable light (vl) domain	DIVMTQTPLSLPVIPGEPASISCRSSQSLFYSDDGNTYLDWYLQKPGQSPQLLIYRLSHRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQHMEFPLTFGGGTKVEIKR	211
vlCDR1	QSLFYSDDGNTY	212
vlCDR2	RLS	213
vlCDR3	MQHMEFPLT	214
Full length light chain	DIVMTQTPLSLPVIPGEPASISCRSSQSLFYSDDGNTYLDWYLQKPGQSPQLLIYRLSHRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQHMEFPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	215

Figure 38E
CPA.7.008

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSGTLSLTCVVSGSISSTNWWTWVRQPPGKGLEWIGEIYHSGSTSYNSSLKSRVTISEDKSKNQIS LRLSSVTAADTAVYYCARVGPAAIYYWGQGTLVTVSS	216
vhCDR1	SGSISSTNW	217
vhCDR2	IYHSGST	218
vhCDR3	ARVGPAAIYY	219
Full length HC	QVQLQESGPGLVKPSGTLSLTCVVSGSISSTNWWTWVRQPPGKGLEWIGEIYHSGSTSYNSSLKSRVTISEDKSKNQIS LRLSSVTAADTAVYYCARVGPAAIYYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	220
Variable light (vl) domain	QAGLTQPPSVSKGLRQTATLTCTGNSNNVGYEGAAWLQQHQGHAPKLLLYRNNNRPSGISKRFSASRSGNTASLTITG LQPEDEADYYCSAWDSSLNAVVFGGGTQLTVLG	221
vlCDR1	SNNVGYEG	222
vlCDR2	RNN	223
vlCDR3	SAWDSSLNAVV	224
Full length light chain	QAGLTQPPSVSKGLRQTATLTCTGNSNNVGYEGAAWLQQHQGHAPKLLLYRNNNRPSGISKRFSASRSGNTASLTITG LQPEDEADYYCSAWDSSLNAVVFGGGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADS SPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	225

Figure 38F
CPA.7.009

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATAKPGIAVAGQNYYYYYMDVWGKGTTVTVSS	226
vhCDR1	GYTLTELS	227
vhCDR2	FDPEDGET	228
vhCDR3	ATAKPGIAVAGQNYYYYYMDV	229
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATAKPGIAVAGQNYYYYYMDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	230
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGGGTKLEIKR	231
vlCDR1	QSLLYRNGNNY	232
vlCDR2	LGS	233
vlCDR3	MQALQTPPT	234
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	235

Figure 38G
CPA.7.010

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCASSPIGYSYGYWGGMDVWGQGTTVTVSS	236
vhCDR1	GFTFSSYA	237
vhCDR2	ISYDGSNK	238
vhCDR3	ASSPIGYSYGYWGGMDV	239
Full length HC	EVQLVESGGGLVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCASSPIGYSYGYWGGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	240
Variable light (vl) domain	QAVLTQPASLSASPGASASLTCTLRSGIDVRTNKIFWYQVKPGSPPQHLLTFQSDSDKQQGSGVPSRFSGSKDASANA GILIISGLQSEDEADYYCLIWHTSGWVFGGGTQLTVLG	241
vlCDR1	SGIDVRTNK	242
vlCDR2	FQSDSDK	243
vlCDR3	LIWHTSGWV	244
Full length light chain	QAVLTQPASLSASPGASASLTCTLRSGIDVRTNKIFWYQVKPGSPPQHLLTFQSDSDKQQGSGVPSRFSGSKDASANA GILIISGLQSEDEADYYCLIWHTSGWVFGGGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWK ADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	245

Figure 38H
CPA.7.011

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGPAAAGVGYYYYMDV WGKGTTVTVSS	246
vhCDR1	GYTLTELS	247
vhCDR2	FDPEDGET	248
vhCDR3	ATGPAAAGVGYYYYMDV	249
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGPAAAGVGYYYYMDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	250
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGQGTKVEIKR	251
vlCDR1	QSLLYRNGYNY	252
vlCDR2	LGS	253
vlCDR3	MQALQTPPT	254
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	255

Figure 38I
CPA7.012

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVETGGGLIQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNT LYLQMNSLRAEDTAVYYCARDVMVYCSSTSCYFYGMDVWGQGTTVTVSS	256
vhCDR1	GFTFSSYA	257
vhCDR2	ISYDGSNK	258
vhCDR3	ARDVMVYCSSTSCYFYGMDV	259
Full length HC	EVQLVETGGGLIQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNT LYLQMNSLRAEDTAVYYCARDVMVYCSSTSCYFYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	260
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTVTCQASQDIRDYLNWYQKKPGKAPKLLIYDASNLEAGVPSRFSGSGSGTDFTFTISGLQ PEDVATYYCQQFENLPITFGQGTRLEIKR	261
vlCDR1	QDIRDY	262
vlCDR2	DAS	263
vlCDR3	QQFENLPIT	264
Full length light chain	DIQMTQSPSSLSASVGDRVTVTCQASQDIRDYLNWYQKKPGKAPKLLIYDASNLEAGVPSRFSGSGSGTDFTFTISGLQ PEDVATYYCQQFENLPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	265

Figure 38J
CPA.7.013

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGGYSSGFNYYYYYMDV WGKGTTVTVSS	266
vhCDR1	GYTLTELS	267
vhCDR2	FDPEDGET	268
vhCDR3	ATGGYSSGFNYYYYYMDV	269
Full length HC	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGGYSSGFNYYYYYMDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	270
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGGGTKLEIKR	271
vlCDR1	QSLLYRNGNNY	272
vlCDR2	LGS	273
vlCDR3	MQALQTPPT	274
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	275

Figure 38K
CPA.7.014

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGVTTYYYGMDVWGQGTTVTVSS	276
vhCDR1	GYTLTELS	277
vhCDR2	FDPEDGET	278
vhCDR3	ATGVTTYYYGMDV	279
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGVTTYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	280
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYSNGNNFLDWYLQKPGQSPRLLISLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGIYYCMQALQTPPTFGQGTKVEIKR	281
vlCDR1	QSLLYSNGNNF	282
vlCDR2	LGS	283
vlCDR3	MQALQTPPT	284
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYSNGNNFLDWYLQKPGQSPRLLISLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGIYYCMQALQTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	285

Figure 38L
CPA.7.015

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QITLKESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDLFDFWWDGMDVWGQGTTVTVSS	286
vhCDR1	GFTFSSYG	287
vhCDR2	IRYDGSNK	288
vhCDR3	ARDLFDFWWDGMDV	289
Full length HC	QITLKESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDLFDFWWDGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	290
Variable light (vl) domain	EIVLTQSPGTLSLSPGEKATLSCRVSQSVSSMYLAWYQQKPGQAPRLLIYGASYRATGIPDRFSGSGSGTDFNLTISRLEP EDFAVYYCQQYVSSPMYTFGLGTKLEIKR	291
vlCDR1	QSVSSMY	292
vlCDR2	GAS	293
vlCDR3	QQYVSSPMYT	294
Full length light chain	EIVLTQSPGTLSLSPGEKATLSCRVSQSVSSMYLAWYQQKPGQAPRLLIYGASYRATGIPDRFSGSGSGTDFNLTISRLEP EDFAVYYCQQYVSSPMYTFGLGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	295

Figure 38M
CPA.7.017

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFNNYGISWVRQAPGKGLEWMGQIIPLFGTTKYAQKFQGRVTIAADEPTS TAYMELGSLRSEDTAIYYCARDRMAADGMAVFDYWGQGTLVTVSS	296
vhCDR1	GGTFNNYG	297
vhCDR2	IIPLFGTT	298
vhCDR3	ARDRMAADGMAVFDY	299
Full length HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFNNYGISWVRQAPGKGLEWMGQIIPLFGTTKYAQKFQGRVTIAADEPTS TAYMELGSLRSEDTAIYYCARDRMAADGMAVFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	300
Variable light (vl) domain	QSVLTQPPSVSGTPGQKVIISCSGSSSNIGRHFVFWYQQLPGTAPKLLIYKNDERPSGVPDRFSGSKSGTSASLAVSGLRS EDEADYYCSSWDAALNGVVFGGGTKLTVLG	301
vlCDR1	SSNIGRHF	302
vlCDR2	KND	303
vlCDR3	SSWDAALNGVV	304
Full length light chain	QSVLTQPPSVSGTPGQKVIISCSGSSSNIGRHFVFWYQQLPGTAPKLLIYKNDERPSGVPDRFSGSKSGTSASLAVSGLRS EDEADYYCSSWDAALNGVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV KAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	305

Figure 38N
CPA.7.018

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATEVPMVRGARRYYYYMDVWGKGTTVTVSS	306
vhCDR1	GYTLTELS	307
vhCDR2	FDPEDGET	308
vhCDR3	ATEVPMVRGARRYYYYMDV	309
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATEVPMVRGARRYYYYMDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	310
Variable light (vl) domain	DVVMTQSPLFLAVTPGEPASISCRSSQTLLYINENNYLDWYVQKPGQSPQLLIYLGSTRASGVPDRFSGGGSGTDFTLTI SRVEAEDVGLYYCMQGLQTPPTFGQGTRLEIKR	311
vlCDR1	QTLLYINENNY	312
vlCDR2	LGS	313
vlCDR3	MQGLQTPPT	314
Full length light chain	DVVMTQSPLFLAVTPGEPASISCRSSQTLLYINENNYLDWYVQKPGQSPQLLIYLGSTRASGVPDRFSGGGSGTDFTLTI SRVEAEDVGLYYCMQGLQTPPTFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	315

Figure 38O
CPA.7.019

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKSSETLSLTCSVSGGSISNSNYYWGWIRQPPGKGLEWIGGIYYSGSTYYNPSLESRVTISEDTSKNQIS LKLSSVTAADTAVYYCARGAWELSLGDWFDPWGPGTLVTVSS	316
vhCDR1	GGSISNSNYY	317
vhCDR2	IYYSGST	318
vhCDR3	ARGAWELSLGDWFDP	319
Full length HC	QVQLQESGPGLVKSSETLSLTCSVSGGSISNSNYYWGWIRQPPGKGLEWIGGIYYSGSTYYNPSLESRVTISEDTSKNQIS LKLSSVTAADTAVYYCARGAWELSLGDWFDPWGPGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	320
Variable light (vl) domain	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDIQWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSRSGTSASLAITGL QAEDEADYYCQSYDSSLSVYVVFGGGTQLTVLG	321
vlCDR1	SSNIGAGYD	322
vlCDR2	GNN	323
vlCDR3	QSYDSSLSVYVV	324
Full length light chain	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDIQWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSRSGTSASLAITGL QAEDEADYYCQSYDSSLSVYVVFGGGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	325

Figure 38P
CPA.7.021

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGVVKPGGSLRLSCAASGFTFGTSSMNWVRQAPGKGLEWVAVISFDGTEIHYADSVKGRFTISRDNSKST VFLQMNSLRPDDTALYYCAKGSGNIYFYSGMDVWGQGTTVTVSS	326
vhCDR1	GFTFGTSS	327
vhCDR2	ISFDGTEI	328
vhCDR3	AKGSGNIYFYSGMDV	329
Full length HC	EVQLVESGGGVVKPGGSLRLSCAASGFTFGTSSMNWVRQAPGKGLEWVAVISFDGTEIHYADSVKGRFTISRDNSKST VFLQMNSLRPDDTALYYCAKGSGNIYFYSGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	330
Variable light (vl) domain	DIQMTQSPSTLSASVGDRVTITCRAGQSISGWLAWFQQKPGKAPNLLIYETSTLESGVPSRFSGSGSGTEYTLTISSLQP DDFATYYCQQYYSYPLTFGQGTKVEIKR	331
vlCDR1	QSISGW	332
vlCDR2	ETS	333
vlCDR3	QQYYSYPLT	334
Full length light chain	DIQMTQSPSTLSASVGDRVTITCRAGQSISGWLAWFQQKPGKAPNLLIYETSTLESGVPSRFSGSGSGTEYTLTISSLQP DDFATYYCQQYYSYPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	335

Figure 38Q
CAP.7.022

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGVPAAIGVYYYYYYMDVWGKGTTVTVSS	336
vhCDR1	GYTLTELS	337
vhCDR2	FDPEDGET	338
vhCDR3	ATGVPAAIGVYYYYYYMDV	339
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGVPAAIGVYYYYYYMDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	340
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYSNGYNYLDWYLQKPGQSPQLLISLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQSPVTFGGGTKVEIKR	341
vlCDR1	QSLLYSNGYNY	342
vlCDR2	LGS	343
vlCDR3	MQALQSPVT	344
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYSNGYNYLDWYLQKPGQSPQLLISLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQSPVTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	345

Figure 38R
CPA.7.023

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATDSRDGPAARGGYYYYMDVWGQGTTVTVSS	346
vhCDR1	GYTLTELS	347
vhCDR2	FDPEDGET	348
vhCDR3	ATDSRDGPAARGGYYYYMDV	349
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATDSRDGPAARGGYYYYMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	350
Variable light (vl) domain	DVVMTQSPLSLPVTLGQPASISCRSSQSLLYINGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGQGTKVEIKR	351
vlCDR1	QSLLYINGYNY	352
vlCDR2	LGS	353
vlCDR3	MQALQTPPT	354
Full length light chain	DVVMTQSPLSLPVTLGQPASISCRSSQSLLYINGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	355

Figure 38S
CPA.7.024

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTST AYMELSSLRSEDTAVYYCARDAYYYDSSGYYNPDAFDIWGQGTMVTVSS	356
vhCDR1	GGTFSSYA	357
vhCDR2	IIPIFGTA	358
vhCDR3	ARDAYYYDSSGYYNPDAFDI	359
Full length HC	EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTST AYMELSSLRSEDTAVYYCARDAYYYDSSGYYNPDAFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	360
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSSRASGVPDRFSGSVSGTDFTLKI SRVEAEDVGVYYCMQGLQTPRTFGRGTKLEIKR	361
vlCDR1	QSLLHSNGYNY	362
vlCDR2	LGS	363
vlCDR3	MQGLQTPRT	364
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSSRASGVPDRFSGSVSGTDFTLKI SRVEAEDVGVYYCMQGLQTPRTFGRGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	365

Figure 38T

CPA.7.033

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSS	366
vhCDR1	GGTFSSSA	367
vhCDR2	IIPIYGIT	368
vhCDR3	ARDDTARRVRGVPYYYYYAMDV	369
Full length HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	370
Variable light (vl) domain	ETTLTQSPAFMSATPGDEVNISCKASQDIDDDVSWYQQKPGGAPIFLIQEASTLVPGIPPRFSGSGFGTDFTLTIKNMES EDAAYYFCLQHDNLPLTFGGGTKVDIKR	371
vlCDR1	QDIDDD	372
vlCDR2	EAS	373
vlCDR3	LQHDNLPLT	374
Full length light chain	ETTLTQSPAFMSATPGDEVNISCKASQDIDDDVSWYQQKPGGAPIFLIQEASTLVPGIPPRFSGSGFGTDFTLTIKNMES EDAAYYFCLQHDNLPLTFGGGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	375

Figure 38U

CPA.7.034

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATEDPGPVAGPYYYYGMDVWGQGTTVTVSS	376
vhCDR1	GYTLTELS	377
vhCDR2	FDPEDGET	378
vhCDR3	ATEDPGPVAGPYYYYGMDV	379
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATEDPGPVAGPYYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	380
Variable light (vl) domain	DVVMTQSPLVLPVTPGEPASISCRSSQSLLYINGYHYLDWYVQRPGQSPQLLIFLGSTRASGVPDRFSGSGSGTDFTLEIS KVEAEDVGIYFCMQALQTPPTFGGGTKVEIKR	381
vlCDR1	QSLLYINGYHY	382
vlCDR2	LGS	383
vlCDR3	MQALQTPPT	384
Full length light chain	DVVMTQSPLVLPVTPGEPASISCRSSQSLLYINGYHYLDWYVQRPGQSPQLLIFLGSTRASGVPDRFSGSGSGTDFTLEIS KVEAEDVGIYFCMQALQTPPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	385

Figure 38V

CPA.7.036

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSS	386
vhCDR1	GGTFSSSA	387
vhCDR2	IIPIYGIT	388
vhCDR3	ARDDTARRVRGVPYYYYYAMDV	389
Full length HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	390
Variable light (vl) domain	DIVMTQTPLSLPVTPGEPASISCRPSQSLLDSDDGNTYLDWYLQKPGQSPQLLIHTLSYRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQRLQFPLTFGGGTKVEIKR	391
vlCDR1	QSLLDSDDGNTY	392
vlCDR2	TLS	393
vlCDR3	MQRLQFPLT	394
Full length light chain	DIVMTQTPLSLPVTPGEPASISCRPSQSLLDSDDGNTYLDWYLQKPGQSPQLLIHTLSYRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQRLQFPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	395

Figure 38W

CPA.7.040

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGVPAAIGVYYYYYYMDVWGKGTTVTVSS	396
vhCDR1	GYTLTELS	397
vhCDR2	FDPEDGET	398
vhCDR3	ATGVPAAIGVYYYYYYMDV	399
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATGVPAAIGVYYYYYYMDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	400
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYWGSYRASGVPDRFSGSGSGTDFTLK ISRVEAEDVGVYYCMQAVQNPPTFGQGTKVDIKR	401
vlCDR1	QSLLYRNGYNY	402
vlCDR2	WGS	403
vlCDR3	MQAVQNPPT	404
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYWGSYRASGVPDRFSGSGSGTDFTLK ISRVEAEDVGVYYCMQAVQNPPTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	405

Figure 38X

CPA.7.046

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSS	406
vhCDR1	GGTFSSSA	407
vhCDR2	IIPIYGIT	408
vhCDR3	ARDDTARRVRGVPYYYYYAMDV	409
Full length HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	410
Variable light (vl) domain	DVVMTQSPAFLSVTPGERVTLSCKASQTMNNYLAWYQQKPGQAPRLLIYDASTRATDTPPRFSGSGSGTEFTLTISSV QSEDFALYYCQQYGDWLPITFGQGTRLEIKR	411
vlCDR1	QTMNNY	412
vlCDR2	DAS	413
vlCDR3	QQYGDWLPIT	414
Full length light chain	DVVMTQSPAFLSVTPGERVTLSCKASQTMNNYLAWYQQKPGQAPRLLIYDASTRATDTPPRFSGSGSGTEFTLTISSV QSEDFALYYCQQYGDWLPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	415

Figure 38Y

CPA.7.047

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATAFPEATISYYYYMDVWGKGTTVTVSS	416
vhCDR1	GYTLTELS	417
vhCDR2	FDPEDGET	418
vhCDR3	ATAFPEATISYYYYMDV	419
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATAFPEATISYYYYMDVWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	420
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYWGSYRASGVPDRFSGSGSGTDFTLK ISRVEAEDVGVYYCMQAVQNPPTFGQGTKVEIKR	421
vlCDR1	QSLLYRNGYNY	422
vlCDR2	WGS	423
vlCDR3	MQAVQNPPT	424
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGYNYLDWYLQKPGQSPQLLIYWGSYRASGVPDRFSGSGSGTDFTLK ISRVEAEDVGVYYCMQAVQNPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	425

Figure 38Z

CPA.7.049

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QMQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYYAMDVWGQGTTVTVSS	426
vhCDR1	GGTFSSSA	427
vhCDR2	IIPIYGIT	428
vhCDR3	ARDDTARRVRGVPYYYYYYAMDV	429
Full length HC	QMQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYYAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	430
Variable light (vl) domain	DIVMTQTPLSLPVTPGEPASMSCRSSRSLLDSDDGNTHLDWYLQKPGQSPQLLIQSLSYRASGVPDRFSGSGSGTDFTL EISRVEAEDVGIYYCMQRKEFPLTFGGGTKVEIKR	431
vlCDR1	RSLLDSDDGNTH	432
vlCDR2	SLS	433
vlCDR3	MQRKEFPLT	434
Full length light chain	DIVMTQTPLSLPVTPGEPASMSCRSSRSLLDSDDGNTHLDWYLQKPGQSPQLLIQSLSYRASGVPDRFSGSGSGTDFTL EISRVEAEDVGIYYCMQRKEFPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	435

Figure 38AA

CPA.7.050

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADKSTST AYMELSSLRSEDTAVYYCARGPWYYDSSGYSSYAYYMDVWGQGTTVTVSS	436
vhCDR1	GGTFSSYA	437
vhCDR2	IIPIFGTA	438
vhCDR3	ARGPWYYDSSGYSSYAYYMDV	439
Full length HC	EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADKSTST AYMELSSLRSEDTAVYYCARGPWYYDSSGYSSYAYYMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	440
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLHSDGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALHTPGVTFGGGTKVEIKR	441
vlCDR1	QSLLHSDGYNY	442
vlCDR2	LGS	443
vlCDR3	MQALHTPGVT	444
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLHSDGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALHTPGVTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	445

Figure 39A
CPA.7.028

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QLQLQESGPGLVKPSETLSLTCTVTGGSISSSSYYWAWIRQPPGKGLEWIGGIYYSGSTYYNVSLESRVTISQDTSKNQFS LKLTSVTAADTAVYYCARGAWELRLGDWFDPWGQGTLVTVSS	446
vhCDR1	GGSISSSSYY	447
vhCDR2	IYYSGST	448
vhCDR3	ARGAWELRLGDWFDP	449
Full length HC	QLQLQESGPGLVKPSETLSLTCTVTGGSISSSSYYWAWIRQPPGKGLEWIGGIYYSGSTYYNVSLESRVTISQDTSKNQFS LKLTSVTAADTAVYYCARGAWELRLGDWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	450
Variable light (vl) domain	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDIQWYQQLPGTAPKLLIYGYSNRPSGVPDRFSGSKSGTSASLAITGL QAEDEADYYCQSYDSSLSVYVVFGGGTQLTVLGQPKAA	451
vlCDR1	SSNIGAGYD	452
vlCDR2	GYS	453
vlCDR3	QSYDSSLSVYVV	454
Full length light chain	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDIQWYQQLPGTAPKLLIYGYSNRPSGVPDRFSGSKSGTSASLAITGL QAEDEADYYCQSYDSSLSVYVVFGGGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	455

Figure 39B
CPA.7.030

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGGGVVQPGGSLRLSCAASRFTFEDYAMHWVRQPPGKGLEWVSGISWKSGGINYADSVKGRFTISRDNAQ NSLYLQMNSLRAEDTALYYCVKDPTLVATDRAFNIWGQGTMVTVSS	456
vhCDR1	RFTFEDYA	457
vhCDR2	ISWKSGGI	458
vhCDR3	VKDPTLVATDRAFNI	459
Full length HC	QVQLQESGGGVVQPGGSLRLSCAASRFTFEDYAMHWVRQPPGKGLEWVSGISWKSGGINYADSVKGRFTISRDNAQ NSLYLQMNSLRAEDTALYYCVKDPTLVATDRAFNIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	460
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQYLQTPDTFGQGTKLEIKRAAPS	461
vlCDR1	QSLLHSNGYNY	462
vlCDR2	LGS	463
vlCDR3	MQYLQTPDT	464
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQYLQTPDTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	465

Figure 39C
CPA.7.041

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYYAMDVWGQGTTVTVSS	466
vhCDR1	GGTFSSSA	467
vhCDR2	IIPIYGIT	468
vhCDR3	ARDDTARRVRGVPYYYYYYAMDV	469
Full length HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYYAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	470
Variable light (vl) domain	EIVLTQSPDFQSVTPKEKVTITCRASQNIDSSLHWYQQKPGQSPKLLINYASQSFSGVPSRFSGSGSGTDFTLTIDSLEPE DAATYFCHQSSSLPLTFGGGTKVEIRRTVAAPS	471
vlCDR1	QNIDSS	472
vlCDR2	YAS	473
vlCDR3	HQSSSLPLT	474
Full length light chain	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDIQWYQQLPGTAPKLLIYGYSNRPSGVPDRFSGSKSGTSASLAITGL QAEDEADYYCQSYDSSLSVVVVFGGGTQLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSS PVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	475

Figure 39D
CPA.7.016

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGSSVKVSCKTSGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTSTA YMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYYAMDVWGQGTTVTVSS	476
vhCDR1	GGTFSSSA	477
vhCDR2	IIPIYGIT	478
vhCDR3	ARDDTARRVRGVPYYYYYYAMDV	479
Full length HC	EVQLVQSGAEVKKPGSSVKVSCKTSGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTSTA YMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYYAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	480
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLQSE DFAVYYCQQYDDWPQTFGQGTRLEIKRTVAAPS	481
vlCDR1	QSVSSY	482
vlCDR2	DAS	483
vlCDR3	QQYDDWPQT	484
Full length light chain	EIVLTQSPGTLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLQSE DFAVYYCQQYDDWPQTFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	485

Figure 39E
CPA.7.020

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QMQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDES TSTAYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYYAMDVWGQGTTVTVSS	486
vhCDR1	GGTFSSSA	487
vhCDR2	IIPIYGIT	488
vhCDR3	ARDDTARRVRGVPYYYYYYAMDV	489
Full length HC	QMQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDES TSTAYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYYAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK	490
Variable light (vl) domain	EIVMTQSPATLSLSTGERATLFCRTSQNVYGEVAWYQQKPGQAPRLLIYDTFERAAGIPAKFSGSGSGTDFTLTISR VEPEDFAVYYCQQRRDWPITFGQGTRLEIKRTVAAPS	491
vlCDR1	QNVYGE	492
vlCDR2	DTF	493
vlCDR3	QQRRDWPIT	494
Full length light chain	EIVMTQSPATLSLSTGERATLFCRTSQNVYGEVAWYQQKPGQAPRLLIYDTFERAAGIPAKFSGSGSGTDFTLTISR VEPEDFAVYYCQQRRDWPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	495

Figure 39F
CPA.7.038

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSS	496
vhCDR1	GGTFSSSA	497
vhCDR2	IIPIYGIT	498
vhCDR3	ARDDTARRVRGVPYYYYYAMDV	499
Full length HC	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	500
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCQASRDISDSLSWYQQKPGKAPKLLIFDASNLKTGVSSRFSGSGSGTDFTFTISSLQPE DIATYYCHQYDNLPLTFGGGTKVEIKRTVAAPS	501
vlCDR1	RDISDS	502
vlCDR2	DAS	503
vlCDR3	HQYDNLPLT	504
Full length light chain	DIQMTQSPSSLSASVGDRVTITCQASRDISDSLSWYQQKPGKAPKLLIFDASNLKTGVSSRFSGSGSGTDFTFTISSLQPE DIATYYCHQYDNLPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	505

Figure 39G
CPA.7.044

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QMQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSS	506
vhCDR1	GGTFSSSA	507
vhCDR2	IIPIYGIT	508
vhCDR3	ARDDTARRVRGVPYYYYYAMDV	509
Full length HC	QMQLVQSGAEVKKPGSSVKVSCKASGGTFSSSAISWVRQAPGQGFEWMGGIIPIYGITDYAQKFQGRVTITTDESTST AYMELSSLTSEDTAVYYCARDDTARRVRGVPYYYYYAMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	510
Variable light (vl) domain	EIVMTQSPATLSLSPGERATLSCRASESVTTFLAWYQQKPGQAPRLLITDASNRATGIPGRFSGSGSGTDFTLTISSLEPE DFAVYYCHQHTNWPLTFGGGTKLEIKRTVAAPS	511
vlCDR1	ESVTTF	512
vlCDR2	DAS	513
vlCDR3	HQHTNWPLT	514
Full length light chain	EIVMTQSPATLSLSPGERATLSCRASESVTTFLAWYQQKPGQAPRLLITDASNRATGIPGRFSGSGSGTDFTLTISSLEPE DFAVYYCHQHTNWPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	515

Figure 39H
CPA.7.045

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATEVGYCSGGSCYISYYYGMDVWGQGTTVTVSS	516
vhCDR1	GYTLTELS	517
vhCDR2	FDPEDGET	518
vhCDR3	ATEVGYCSGGSCYISYYYGMDV	519
Full length HC	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGETIYAQKFQGRVTMTEDTS TDTAYMELSSLRSEDTAVYYCATEVGYCSGGSCYISYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	520
Variable light (vl) domain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGHNFLDWYVQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGQGTKLEIKRTVAAPS	521
vlCDR1	QSLLYRNGHNF	522
vlCDR2	LGS	523
vlCDR3	MQALQTPPT	524
Full length light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLLYRNGHNFLDWYVQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	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	IIPIFGTA	527	AREEVSSPYGMDV	528	TGAVTSGHY	529	DTG	530	LLSYSGASWV	531
CPA.7.002	GGTFSSSA	532	IIPIYGIT	533	ARDDTARRVRGVPYYYYYAMDV	534	QGIGNY	535	SAS	536	QQLKDYPIT	537
CPA.7.003	GFSLSHFS	538	FDPEEGGT	539	ATGIWYSSGWPVDY	540	QSLLDSSGYNY	541	LGS	542	MQALQTPIT	543
CPA.7.004	GYTLTELS	544	FDPEDGET	545	ATVSRVRGVINYYYYMDV	546	QSLLYRNGNNY	547	LGS	548	MQALQTPPT	549
CPA.7.005	GGTFSSSA	550	IIPIYGIT	551	ARDDTARRVRGVPYYYYYAMDV	552	QSVDSS	553	DAS	554	QQYKDWPFT	555
CPA.7.006	GGTFGTYA	556	ITPISATI	557	ARGFEYSDGLLDD	558	QSLFYSDDGNTY	559	RLS	560	MQHMEFPLT	561
CPA.7.007	GGSISSSSYY	562	IYYSGST	563	ARGAWELRLGDWFDP	564	SSNIGAGYD	565	GNN	566	QSYDSSLSIVV	567
CPA.7.008	SGSISSTNW	568	IYHSGST	569	ARVGPAAIYY	570	SNNVGYEG	571	RNN	572	SAWDSSLNAVV	573
CPA.7.009	GYTLTELS	574	FDPEDGET	575	ATAKPGIAVAGQNYYYYYMDV	576	QSLLYRNGNNY	577	LGS	578	MQALQTPPT	579
CPA.7.010	GFTFSSYA	580	ISYDGSNK	581	ASSPIGYSYGYWGGMDV	582	SGIDVRTNK	583	FQSDSDK	584	LIWHTSGWV	585
CPA.7.011	GYTLTELS	586	FDPEDGET	587	ATGPAAAGVGYYYYMDV	588	QSLLYRNGYNY	589	LGS	590	MQALQTPPT	591
CPA.7.012	GFTFSSYA	592	ISYDGSNK	593	ARDVMVYCSSTSCYFYGMDV	594	QDIRDY	595	DAS	596	QQFENLPIT	597
CPA.7.013	GYTLTELS	598	FDPEDGET	599	ATGGYSSGFNYYYYYMDV	600	QSLLYRNGNNY	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	QSLLYSNGNNF	607	LGS	608	MQALQTPPT	609
CPA.7.015	GFTFSSYG	610	IRYDGSNK	611	ARDLFDFWWDGMDV	612	QSVSSMY	613	GAS	614	QQYVSSPMYT	615
CPA.7.016	GGTFSSSA	616	IIPIYGIT	617	ARDDTARRVRGVPYYYYYAMDV	618	QSVSSY	619	DAS	620	QQYDDWPQT	621
CPA.7.017	GGTFNNYG	622	IIPLFGTT	623	ARDRMAADGMAVFDY	624	SSNIGRHF	625	KND	626	SSWDAALNGVV	627
CPA.7.018	GYTLTELS	628	FDPEDGET	629	ATEVPMVRGARRYYYYMDV	630	QTLLYINENNY	631	LGS	632	MQGLQTPPT	633
CPA.7.019	GGSISNSNYY	634	IYYSGST	635	ARGAWELSLGDWFDP	636	SSNIGAGYD	637	GNN	638	QSYDSSLSVYVV	639
CPA.7.020	GGTFSSSA	640	IIPIYGIT	641	ARDDTARRVRGVPYYYYYAMDV	642	QNVYGE	643	DTF	644	QQRRDWPIT	645
CPA.7.021	GFTFGTSS	646	ISFDGTEI	647	AKGSGNIYFYSGMDV	648	QSISGW	649	ETS	650	QQYYSYPLT	651
CPA.7.022	GYTLTELS	652	FDPEDGET	653	ATGVPAAIGVYYYYYYMDV	654	QSLLYSNGYNY	655	LGS	656	MQALQSPVT	657
CPA.7.023	GYTLTELS	658	FDPEDGET	659	ATDSRDGPAARGGYYYYMDV	660	QSLLYINGYNY	661	LGS	662	MQALQTPPT	663
CPA.7.024	GGTFSSYA	664	IIPIFGTA	665	ARDAYYYDSSGYYNPDAFDI	666	QSLLHSNGYNY	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	ARDGAFYYGSENYYNAGWFDP	678	QSLLSGNGYNY	679	LGS	680	MQALKSPLT	681
CPA.7.027	GYTFTNYY	682	INPSGGIT	683	ARAGLGYNWNYAPSGMDV	684	SSDVGGYNY	685	EVS	686	SSYAGSNNLV	687
CPA.7.028	GGSISSSSYY	688	IYYSGST	689	ARGAWELRLGDWFDP	690	SSNIGAGYD	691	GYS	692	QSYDSSLSVYVV	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	GFTFDDYA	694	ISWNSGSI	695	AKDVNRILVAGMVDY	696	QSLLHSNGYNY	697	LGS	698	MQGLQTPIT	699
CPA.7.030	RFTFEDYA	700	ISWKSGGI	701	VKDPTLVATDRAFNI	702	QSLLHSNGYNY	703	LGS	704	MQYLQTPDT	705
CPA.7.031	GGTFSSSA	706	IIPIYGIT	707	ARDDTARRVRGVPYYYYAMDV	708	QSLLDSDDGNIH	709	TLS	710	MQRKEFPLT	711
CPA.7.032	GFTFSSYG	712	ISYDGSNK	713	AKEDRLRFLEWLFYGMDV	714	HDIYTY	715	DAS	716	QQYDNHPPEVT	717
CPA.7.033	GGTFSSSA	718	IIPIYGIT	719	ARDDTARRVRGVPYYYYAMDV	720	QDIDDD	721	EAS	722	LQHDNLPLT	723
CPA.7.034	GYTLTELS	724	FDPEDGET	725	ATEDPGPVAGPYYYYGMDV	726	QSLLYINGYHY	727	LGS	728	MQALQTPPT	729
CPA.7.035	GYMFTNYP	730	INAGTGNT	731	AREGMFYYGLESYYKGGWFDP	732	QSLLHRNGYNY	733	LAS	734	MQALQTPLT	735
CPA.7.036	GGTFSSSA	736	IIPIYGIT	737	ARDDTARRVRGVPYYYYAMDV	738	QSLLDSDDGNTY	739	TLS	740	MQRLQFPLT	741
CPA.7.037	TYTFTTYY	742	IYPSGGNT	743	VRDQNYYYSAMDV	744	QDIRNY	745	DAS	746	QQFENLPIT	747
CPA.7.038	GGTFSSSA	748	IIPIYGIT	749	ARDDTARRVRGVPYYYYAMDV	750	RDISDS	751	DAS	752	HQYDNLPLT	753
CPA.7.039	GFNFRGYA	754	ISGSGGTT	755	AQSYAQIGYGGHIDH	756	SGIDVATYM	757	YKSDSDK	758	LIWHGSHYV	759
CPA.7.040	GYTLTELS	760	FDPEDGET	761	ATGVPAAIGVYYYYYYMDV	762	QSLLYRNGYNY	763	WGS	764	MQAVQNPPT	765
CPA.7.041	GGTFSSSA	766	IIPIYGIT	767	ARDDTARRVRGVPYYYYAMDV	768	QNIDSS	769	YAS	770	HQSSSLPLT	771
CPA.7.042	GGTFSSSA	772	IIPIYGIT	773	ARDDTARRVRGVPYYYYAMDV	774	QSVYNNY	775	DAS	776	QQYNSWPPYT	777
CPA.7.043	GGTFSSYA	778	IIPIFGTA	779	ARDAYYDSSGYYNPDAFDI	780	QSLLYSNGYNY	781	LGS	782	MQARQTPYT	783

Figure 40D

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.7.044	GGTFSSSA	784	IIPIYGIT	785	ARDDTARRVRGVPYYYYYAMDV	786	ESVTTF	787	DAS	788	HQHTNWPLT	789
CPA.7.045	GYTLTELS	790	FDPEDGET	791	ATEVGYCSGGSCYISYYYGMDV	792	QSLLYRNGHNF	793	LGS	794	MQALQTPPT	795
CPA.7.046	GGTFSSSA	796	IIPIYGIT	797	ARDDTARRVRGVPYYYYYAMDV	798	QTMNNY	799	DAS	800	QQYGDWLPIT	801
CPA.7.047	GYTLTELS	802	FDPEDGET	803	ATAFPEATISYYYYMDV	804	QSLLYRNGYNY	805	WGS	806	MQAVQNPPT	807
CPA.7.049	GGTFSSSA	808	IIPIYGIT	809	ARDDTARRVRGVPYYYYYAMDV	810	RSLLDSDDGNTH	811	SLS	812	MQRKEFPLT	813
CPA.7.050	GGTFSSYA	814	IIPIFGTA	815	ARGPWYYDSSGYSSYAYYMDV	816	QSLLHSDGYNY	817	LGS	818	MQALHTPGVT	819

Figure 41A

CHA.7.502

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

Figure 41B

CHA.7.503

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGAELAKPGASVKMSCKASGYTFTSNWMHWVKQRPGQGLEWIGYINPSNGYTECNQKFRDKATLSADKSSSTAYMQLNSLTSADSAVYYCALMISAWLPYWGQGTLVTVSA	828
vhCDR1	GYTFTSNW	829
vhCDR2	INPSNGYT	830
vhCDR3	ALMISAWLPY	831
Variable light (vl) domain	DIVLTQSPASLAISLGQRATISCRASQSVSASSYSYVHWYQQKPGQPPKLLIKYASSLESGVPARFSGSGSGTDFTLNIHPVEEEDTATYYCLHTWEIPYTFGGGTKLEIK	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	QIVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASG 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	DIQMTQSPASLSVSVGETVTITCRASENIFSNLAWYQQKQGKSPQLLVYGEANLAD GVPSRFSGSGSGTQYSLKINSLQSEDFGNYYCQHFWGTPYTFGGGTTLEIK	848
vlCDR1	ENIFSN	849
vlCDR2	GEA	850
vlCDR3	QHFWGTPYT	851

Figure 41E

CHA.7.510

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVTLKESGPGILQPSQTLSLTCSFSGFSLNTSGTGVGWIRQPSGKGLEWLTHIWWN DNKFYNTFLKSRLTISKETSNNQVFLKIASVDTADAATYYCARMAYGNLWFVNWGQ GTLVAVST	852
vhCDR1	GFSLNTSGTG	853
vhCDR2	IWWNDNK	854
vhCDR3	ARMAYGNLWFVN	855
Variable light (vl) domain	DIVLTQSPASLAVSLGQRASISCRASRSVTISGYSYMYWYQQKPGQPPRLLFYLASNL ASGVPARFSGSGSGTDFTLNIHPVEEEDAAIYYCQHSRELPYTFGGGTKLEIK	856
vlCDR1	RSVTISGYSY	857
vlCDR2	LAS	858
vlCDR3	QHSRELPYT	859

Figure 41F

CHA.7.512

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

Figure 41G

CHA.7.514

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLRQSGADLVKPGASVKLSCTASGFNIKDTYIDWVKQRPEQGLDWIGRIDPANG NTKYDPKFQGKATIITDTSSNTAYLQLSNLTSEDTAVYYCARYGSYPYFDYWGRGTTL AVSS	868
vhCDR1	GFNIKDTY	869
vhCDR2	IDPANGNT	870
vhCDR3	ARYGSYPYFDY	871
Variable light (vl) domain	SIVMTQTPKFLLISAGDRVTITCKASQSVRNDVAWYQQKPGQSPKLLMYYASNRYT GVPDRFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYSSPPTFGGGTKLEIK	872
vlCDR1	QSVRND	873
vlCDR2	YAS	874
vlCDR3	QQDYSSPPT	875

Figure 41H

CHA.7.516

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGPELVRPGVSVKISCKVSGYTFTDYVMHWVKQSHAKSLEWIGIISPYSG NTNYNQNFKGKATMTVDKSSSTAYMALARLTSEDSAIYYCAREGDLPMFAYWGQG TLVTVSA	876
vhCDR1	GYTFTDYV	877
vhCDR2	ISPYSGNT	878
vhCDR3	AREGDLPMFAY	879
Variable light (vl) domain	QIVLTQSPTIMSASPGEKVTMTCSASSSVSYIYWYQQNPGSSPRLLIYDTSILASGVPF RFSGSGSGTSYSLTISRMEAEDAATYYCQQWTSYPLTFGSGTKLELK	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 GYNQKFKSKATLSADNPSSTAYMELRSLTSEDSAVYYCAREDKTARNAMDYWGQG TPVTVSS	884
vhCDR1	GYTFTDYN	885
vhCDR2	IYPYIGGS	886
vhCDR3	AREDKTARNAMDY	887
Variable light (vl) domain	DIQMTQSPASLSVSVGETVTIICRVSENIYSNLAWYQQKQGKSPQLLVYEATNLAEG VPSRFSGSGSGTQYSLKINSLQSEDFGSYYCQHFWGTPYTFGGGTKLEIK	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	DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISYSGSTSYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCARHYRYPPYAMDYWGQGTSVTVSS	892
vhCDR1	GYSITSDYA	893
vhCDR2	ISYSGST	894
vhCDR3	ARHYRYPPYAMDY	895
Variable light (vl) domain	DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSSNQKNYLAWYQQKPGQSPKLLVYFASTRESGVPDRFIGSGSGTDFTLTITSVQAEDLADYFCQQHYSTPFTFGSGTKLEIK	896
vlCDR1	QSLLNSSNQKNY	897
vlCDR2	FAS	898
vlCDR3	QQHYSTPFT	899

Figure 41K

CHA.7.520_2

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKQSGPGLVQPSQSLSITCTVSGFSLTSFGVHWVRQSPGKGLEWLGVIWSGGT TVYDAAFISRLSISKDNSKSQVFFKMNSLQTNDTAIYYCARKRGNFYVMDYWGQGT SVTVSS	900
vhCDR1	GFSLTSFG	901
vhCDR2	IWSGGTT	902
vhCDR3	ARKRGNFYVMDY	903
Variable light (vl) domain	DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSSNQKNYLAWYQQKPGQSPKLLVY FASTRESGVPDRFIGSGSGTDFTLTITSVQAEDLADYFCQQHYSTPFTFGSGTKLEIK	904
vlCDR1	QSLLNSSNQKNY	905
vlCDR2	FAS	906
vlCDR3	QQHYSTPFT	907

Figure 41L

CHA.7.522

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQPGSELVRPGTSVKLSCKASGYTFTSYWVHWVRQRHGQGLEWIGNVYPGSGSTNYDEKFKSKGTLTVDTSSSTAYMHLSSLTSEDSAVYYCTRGVLRFPLDYWGQGTTLTVSS	908
vhCDR1	GYTFTSYW	909
vhCDR2	VYPGSGST	910
vhCDR3	TRGVLRFPLDY	911
Variable light (vl) domain	DIVMTQAAPSVPVTPGESVSISCRSSKSLLHSNGNTYLYWFLQRPGQSPHLLIYRMSNLASGVPDRFSGSGSGTAFTLRISRVEAEDVGVYYCMQHLEYPLTFGAGTKLELK	912
vlCDR1	KSLLHSNGNTY	913
vlCDR2	RMS	914
vlCDR3	MQHLEYPLT	915

Figure 41M

CHA.7.524

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGPEVVRPGVSVKISCKGSGYKFPDYVMHWVKQSHAKSLEWIGIISIYSG NTNYNQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCAREGDLPMFAYWGQG TLVTVSA	916
vhCDR1	GYKFPDYV	917
vhCDR2	ISIYSGNT	918
vhCDR3	AREGDLPMFAY	919
Variable light (vl) domain	QIVLTQSPAIMSASPGEKVTMTCNASSSVSYMYWYQQKPISSPRLLIYDTSNLASGV 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	QVQLKESGPGLVAPSQSLSITCTVSGFSLTAYNINWVRQPPGKGLEWLGMIWGDG NTDYNSPLKSRLTISKDNSKSQVFLKMDSLQTDDTARYYCARDLKVRRDSPYTMDY WGQGTSVTVSS	924
vhCDR1	GFSLTAYN	925
vhCDR2	IWGDGNT	926
vhCDR3	ARDLKVRRDSPYTMDY	927
Variable light (vl) domain	NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIY WASNRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCHQYLSSYTFGGGTKLEIK	928
vlCDR1	QSVLYSSNQKNY	929
vlCDR2	WAS	930
vlCDR3	HQYLSSYT	931

Figure 410

CHA.7.527

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	DVQLQESGPGLVKPSQSLSLTCTVTGYSLTSDYAWNWIRQFPGNKLEWMGYITYSGGTTYNPSLKSRISITRDTSKNQFFLQLTSVTTEDTATYYCARRGSGTTVVGDWYFDVWGAGTTVTVSS	932
vhCDR1	GYSLTSDYA	933
vhCDR2	ITYSGGT	934
vhCDR3	ARRGSGTTVVGDWYFDV	935
Variable light (vl) domain	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSFNQKYYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTPTISSVTAEDLAVYYCQQFYTYPYTFGGGTKLEMK	936
vlCDR1	QSLLYSFNQKYY	937
vlCDR2	WAS	938
vlCDR3	QQFYTYPYT	939

Figure 41P

CHA.7.528

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQVQQSGPELVKPGASVKISCKASGYTFTKSNMHWVKQSHGKSLEWIGYIYPYNG GTGYNQNFKSKATLTVDISSSTAYMELRSLTLEDSAVYLCAREADYYGNRGQFDYW GQGTLVTVSA	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	QVQLQQSGAELMRPGTSVKVSCKASGYAFTNHLIEWIKQRPGQGLEWIGVINPGS DSTDYNEKFKDKATLTADKSSSTAYMQLSSLTSDDSAVYFCARSLYYNSWFVYWGQ GTLVTVSA	948
vhCDR1	GYAFTNHL	949
vhCDR2	INPGSDST	950
vhCDR3	ARSLYYNSWFVY	951
Variable light (vl) domain	DIQMTQSPASLSASVGETVTITCRASENIYSYLAWYQQKRGKSPQLLVYNAKTLVEG VPSRFSGSGSGTQFSLKINSLQPEDFGSYYCQHHYGTPYTFGGGTKLEIK	952
vlCDR1	ENIYSY	953
vlCDR2	NAK	954
vlCDR3	QHHYGTPYT	955

Figure 41R

CHA.7.534

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGAELVKPGASVRLSCTASGFSIRDTYIHWVKQRPEQGLDWIGKIDPANGKSEYDPKFQGRATMTTDTSSNTAYLQLSSLTSEDTAVYYCTRYGYYPYFDVWGAGTTVTVFS	956
vhCDR1	GFSIRDTY	957
vhCDR2	IDPANGKS	958
vhCDR3	TRYGYYPYFDV	959
Variable light (vl) domain	SIVMTQTPKFLLVSAGDRVAITCKASQSVRHDVVWYQQKPGQSPKLLIYYASSRYTGVPDRFTGSGYGTDFTFTISTVQAEDLALYFCLQDFSSPWTFGGGTKLEIK	960
vlCDR1	QSVRHD	961
vlCDR2	YAS	962
vlCDR3	LQDFSSPWT	963

Figure 41S

CHA.7.535

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

Figure 41T

CHA.7.537

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPGLVAPSQSLSITCTVSGFSLIGHGVNWIRQPPGKGLEWLGVIWGDGNTDYNSALKSRLSISKDNSKSQVFLKMNSLQTDDTARYFCAVNSAMDYWGQGTAVTVSS	972
vhCDR1	GFSLIGHG	973
vhCDR2	IWGDGNT	974
vhCDR3	AVNSAMDY	975
Variable light (vl) domain	NIVMTQSPKSMSMSVGERVTLNCTASENVASFVSWYQQKPEQSPKLLIYGTSNRYTGVPDRFTGSGSATDFTLTISSVQAEDLGDYHCGQSYNYPFTFGSGTKLEIE	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	QVQLQQSGAELVRPGASVKVSCKTSGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGIYYNDKFKVKTTLTADKSSSTAYMQLSSLTSDDSAVYFCARSETHDTWFAYWGQGTLVTVSA	980
vhCDR1	GYAFTNYL	981
vhCDR2	INPGSGGI	982
vhCDR3	ARSETHDTWFAY	983
Variable light (vl) domain	DIVMTQSQKFISTSVGDRVSITCKASQSVRIAVAWFQQKPGQSPKALIYLASTRHTGVPDRFTGSGSGTDFTLTISNVQSEDLADYFCLQHWNYPYTFGGGTKLEIKR	984
vlCDR1	QSVRIA	985
vlCDR2	LAS	986
vlCDR3	LQHWNYPYT	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	DIVMTQSQKFISTSVGDRVSITCKASQSVRIAVAWFQQKPGQSPKALIYLASTRHTG VPDRFTGSGSGTDFTLTISNVQSEDLADYFCLQHWNYPYTFGGGTKLEIKR	992
vlCDR1	QSVRIA	993
vlCDR2	LAS	994
vlCDR3	LQHWNYPYT	995

Figure 41W

CHA.7.543

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPGLVAPSQSLSITCTVSGFSLSGYGIKWVRQPPGKGLEWLGTIWGDGST DYNSALKSRLSISKDNSKSQVFLKMTSLQTDDTARYYCASDSLGITFGYWGQGTLV 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	QVQLKESGPGLVAPSQSLSITCTVSGFSLTSYAITWVRQPPGKGLEWLGVIWPGGGT NYNSALKSRLSISKDNSKSHLFLKMNSLQTDDTARYYCVRSYDGYLDWYFDVWGTG TTVTVSS	1004
vhCDR1	GFSLTSYA	1005
vhCDR2	IWPGGGT	1006
vhCDR3	VRSYDGYLDWYFDV	1007
Variable light (vl) domain	NIVMTQSPKSMSMSVGERVTLSCKASENVGTYVSWYQQKPDQSPKLLIYGASNRYT GVPDRFTGSGSATDFTLIISSVQAEDLSDYHCGQSYSYPYTFGGGTKLEII	1008
vlCDR1	ENVGTY	1009
vlCDR2	GAS	1010
vlCDR3	GQSYSYPYT	1011

Figure 41Y

CHA.7.545

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

Figure 41Z

CHA.7.546

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

Figure 41AA

CHA.7.547

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QIQLVQSGPDLKKPGETVKISCKASGYTFTTYGMSWVKQAPGRGLKWMGWINTYS GVSTFPDDFKGRFAFSLETSASTAYLQINNLKNEDSATYFCARLGMGSTTGAGYFDV WGTGTTVTVSS	1028
vhCDR1	GYTFTTYG	1029
vhCDR2	INTYSGVS	1030
vhCDR3	ARLGMGSTTGAGYFDV	1031
Variable light (vl) domain	ENVLTQSPAIMSASLGEKVTLSCRASSSVNYMYWYQQKSDASPKLWIYYTSNLAPG VPARFSGSGSGNSYSLTISSVEGEDAATYYCQQFTSSPWTFGGGTKLEIK	1032
vlCDR1	SSVNY	1033
vlCDR2	YTS	1034
vlCDR3	QQFTSSPWT	1035

Figure 41BB

CHA.7.548

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGASVKISCKASGYTFTDYSMNWVKQSHGKSLEWIGDITPNNGSPNYNQKFKDKATLTVDKSSSTVYMELRSLTSEDSAVYYCASLFFDYWGHGTTLTVSS	1036
vhCDR1	GYTFTDYS	1037
vhCDR2	ITPNNGSP	1038
vhCDR3	ASLFFDY	1039
Variable light (vl) domain	DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSGNQKNYLAWYQQKPGQPPKLLIYGASTRDSGVPDRFTGSGSGTDFTLTITSVQAEDLAVYYCQNDHTYPYTFGGGTKLEIK	1040
vlCDR1	QSLLNSGNQKNY	1041
vlCDR2	GAS	1042
vlCDR3	QNDHTYPYT	1043

Figure 41CC

CHA.7.549

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQPGTELVKPGASVKLSCKASGFTFTTHWMHWVRQRPGQGLEWIGNIYPS NGGSNYNEKFKTKATLTVDRSSSTAYMHLSSLTSEDSAVYYCARRVNWDGYYFDYW GQGTTLTVSS	1044
vhCDR1	GFTFTTHW	1045
vhCDR2	IYPSNGGS	1046
vhCDR3	ARRVNWDGYYFDY	1047
Variable light (vl) domain	DIVMTQSQKFMSTSVGDRVSVTCKASQNVGTNVAWYQQKPGQSPKLLIYSASYRY SGVPDRFTGSGSGTDFTLTISNVQSEDLADYFCQQYNSYPLTFGGGTKLEIK	1048
vlCDR1	QNVGTN	1049
vlCDR2	SAS	1050
vlCDR3	QQYNSYPLT	1051

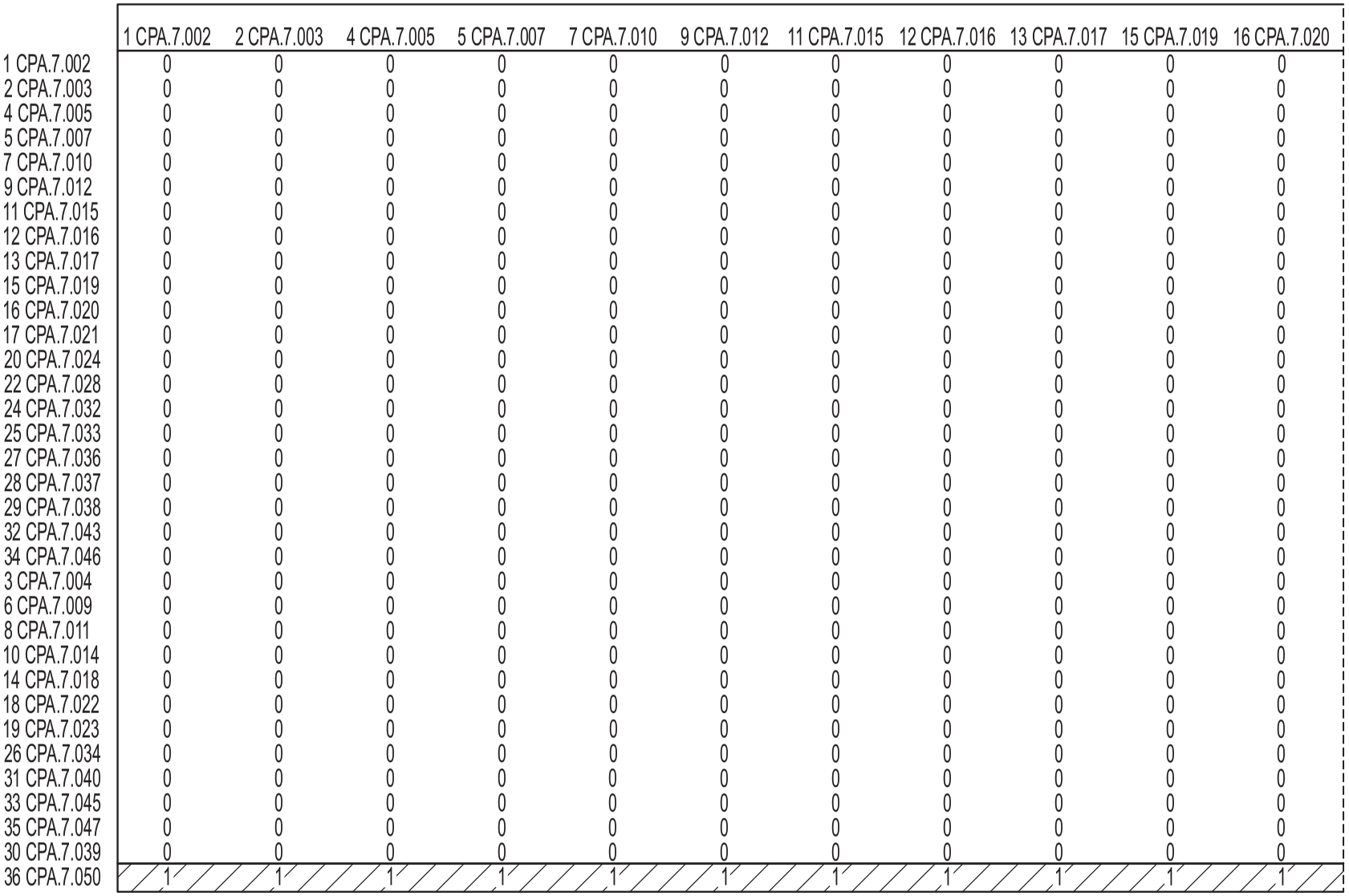
Figure 41DD

CHA.7.550

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGTELVKPGASVKLSCKASGYTFTSYWIHWVKQRPGQGLEWIGNINPSNGGTNYNEKFKSKAALTVDKSSSTAYMQLSSLTSEDSAVYYCARRGLPYFFDYWGQGTTLTVSS	1052
vhCDR1	GYTFTSYW	1053
vhCDR2	INPSNGGT	1054
vhCDR3	ARRGLPYFFDY	1055
Variable light (vl) domain	DIVMTQSQKFMSTSVGDRVSVTCKGSQNVGYNVAWYQQKPGQSPKALVYSASDRHSGVPDRFAGSGSGTDFTLTISNVQSEDLAEYFCQQYNSYPLTFGAGTKLELK	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			



	1 CPA.7.002	2 CPA.7.003	4 CPA.7.005	5 CPA.7.007	7 CPA.7.010	9 CPA.7.012	11 CPA.7.015	12 CPA.7.016	13 CPA.7.017	15 CPA.7.019	16 CPA.7.020
1 CPA.7.002	0	0	0	0	0	0	0	0	0	0	0
2 CPA.7.003	0	0	0	0	0	0	0	0	0	0	0
4 CPA.7.005	0	0	0	0	0	0	0	0	0	0	0
5 CPA.7.007	0	0	0	0	0	0	0	0	0	0	0
7 CPA.7.010	0	0	0	0	0	0	0	0	0	0	0
9 CPA.7.012	0	0	0	0	0	0	0	0	0	0	0
11 CPA.7.015	0	0	0	0	0	0	0	0	0	0	0
12 CPA.7.016	0	0	0	0	0	0	0	0	0	0	0
13 CPA.7.017	0	0	0	0	0	0	0	0	0	0	0
15 CPA.7.019	0	0	0	0	0	0	0	0	0	0	0
16 CPA.7.020	0	0	0	0	0	0	0	0	0	0	0
17 CPA.7.021	0	0	0	0	0	0	0	0	0	0	0
20 CPA.7.024	0	0	0	0	0	0	0	0	0	0	0
22 CPA.7.028	0	0	0	0	0	0	0	0	0	0	0
24 CPA.7.032	0	0	0	0	0	0	0	0	0	0	0
25 CPA.7.033	0	0	0	0	0	0	0	0	0	0	0
27 CPA.7.036	0	0	0	0	0	0	0	0	0	0	0
28 CPA.7.037	0	0	0	0	0	0	0	0	0	0	0
29 CPA.7.038	0	0	0	0	0	0	0	0	0	0	0
32 CPA.7.043	0	0	0	0	0	0	0	0	0	0	0
34 CPA.7.046	0	0	0	0	0	0	0	0	0	0	0
3 CPA.7.004	0	0	0	0	0	0	0	0	0	0	0
6 CPA.7.009	0	0	0	0	0	0	0	0	0	0	0
8 CPA.7.011	0	0	0	0	0	0	0	0	0	0	0
10 CPA.7.014	0	0	0	0	0	0	0	0	0	0	0
14 CPA.7.018	0	0	0	0	0	0	0	0	0	0	0
18 CPA.7.022	0	0	0	0	0	0	0	0	0	0	0
19 CPA.7.023	0	0	0	0	0	0	0	0	0	0	0
26 CPA.7.034	0	0	0	0	0	0	0	0	0	0	0
31 CPA.7.040	0	0	0	0	0	0	0	0	0	0	0
33 CPA.7.045	0	0	0	0	0	0	0	0	0	0	0
35 CPA.7.047	0	0	0	0	0	0	0	0	0	0	0
30 CPA.7.039	0	0	0	0	0	0	0	0	0	0	0
36 CPA.7.050	1	1	1	1	1	1	1	1	1	1	1

Figure 43A

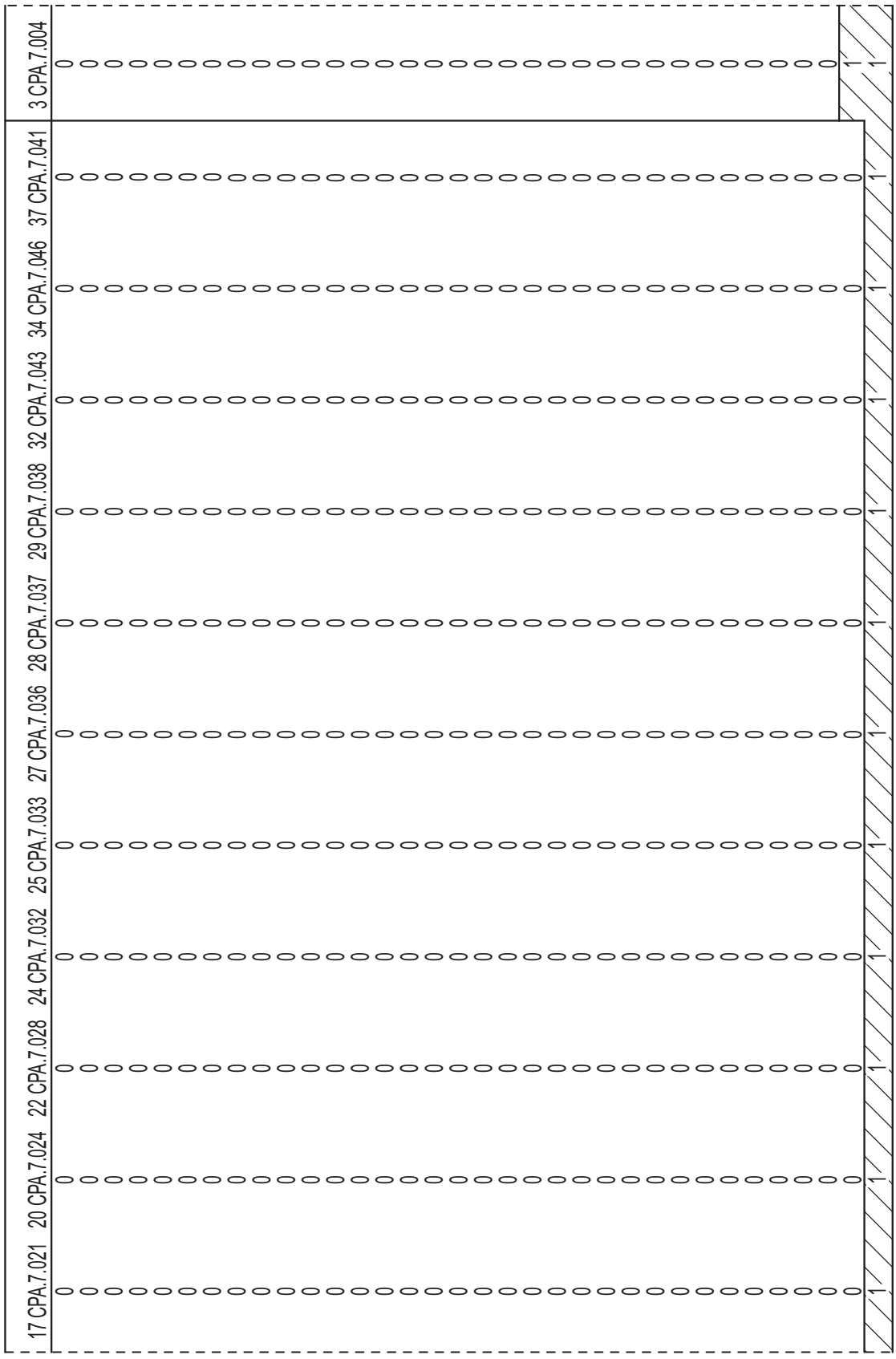

17 CPA.7.021
20 CPA.7.024
22 CPA.7.028
24 CPA.7.032
25 CPA.7.033
27 CPA.7.036
28 CPA.7.037
29 CPA.7.038
32 CPA.7.043
34 CPA.7.046
37 CPA.7.041
3 CPA.7.004

Figure 43B

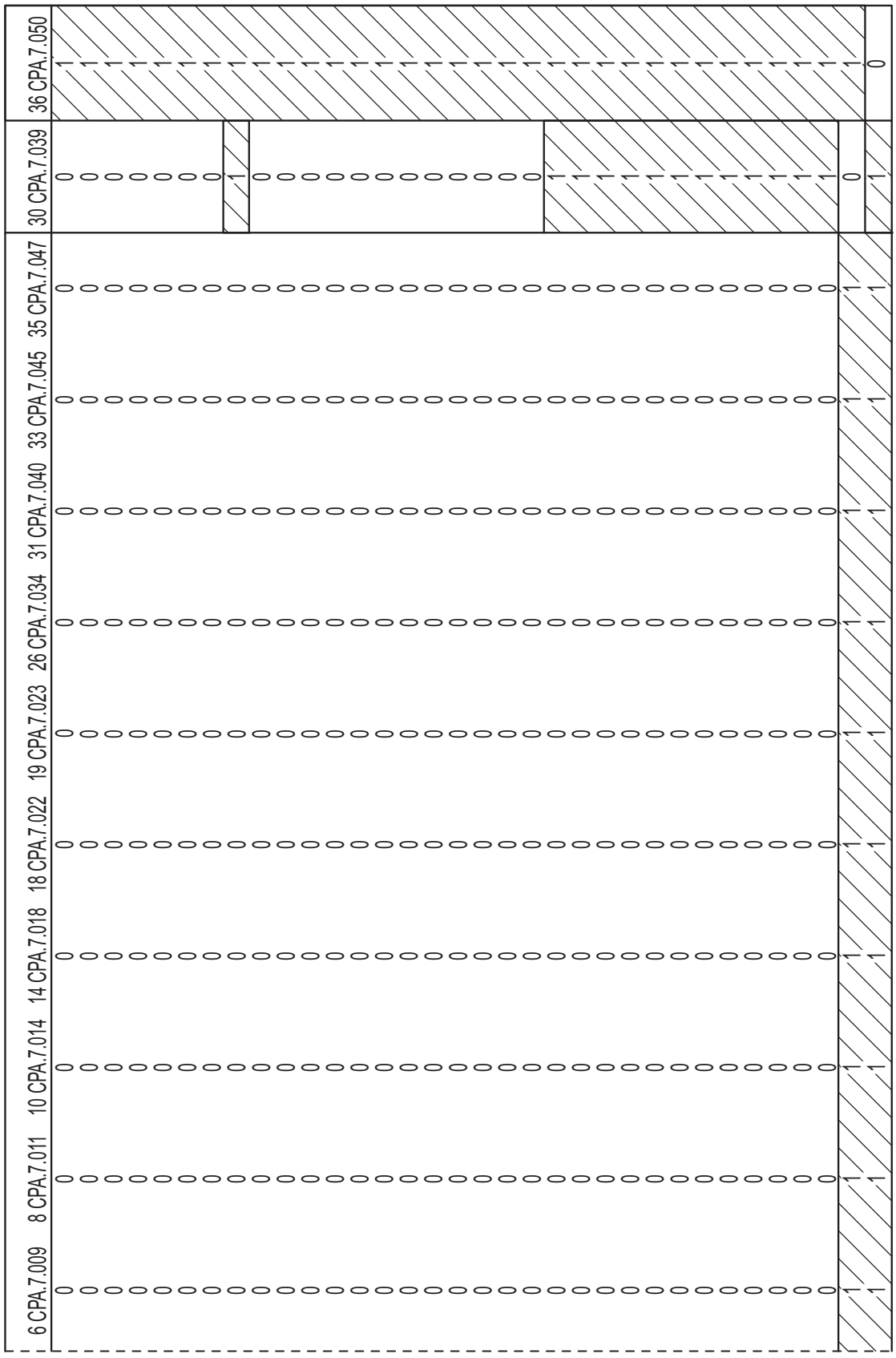

6 CPA.7.009
8 CPA.7.011
10 CPA.7.014
14 CPA.7.018
18 CPA.7.022
19 CPA.7.023
26 CPA.7.034
31 CPA.7.040
33 CPA.7.045
35 CPA.7.047
30 CPA.7.039
36 CPA.7.050

Figure 43C

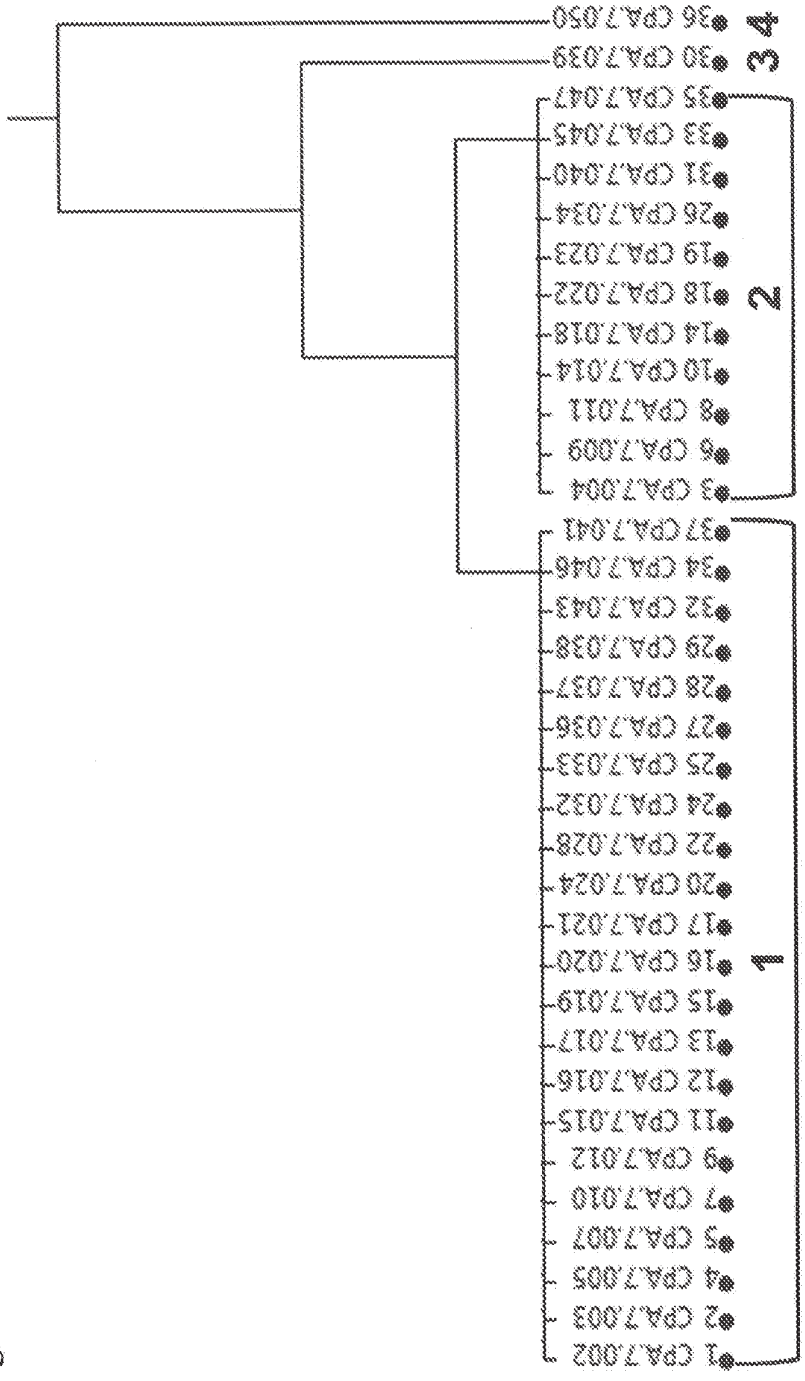

36 CPA.7.050
30 CPA.7.039
35 CPA.7.047
33 CPA.7.045
31 CPA.7.040
26 CPA.7.034
19 CPA.7.023
18 CPA.7.022
14 CPA.7.018
10 CPA.7.014
8 CPA.7.011
6 CPA.7.009
3 CPA.7.004
37 CPA.7.041
34 CPA.7.046
32 CPA.7.043
29 CPA.7.038
28 CPA.7.037
27 CPA.7.036
25 CPA.7.033
24 CPA.7.032
22 CPA.7.028
20 CPA.7.024
17 CPA.7.021
16 CPA.7.020
15 CPA.7.019
13 CPA.7.017
12 CPA.7.016
11 CPA.7.015
9 CPA.7.012
7 CPA.7.010
5 CPA.7.007
4 CPA.7.005
2 CPA.7.003
1 CPA.7.002
4
3
2
1

Figure 44

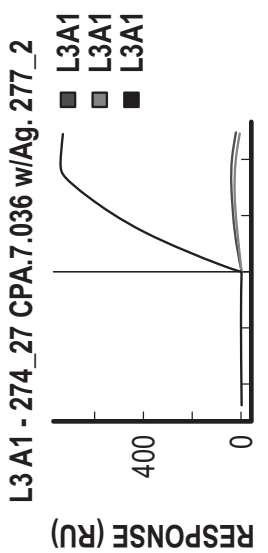


Figure 45A

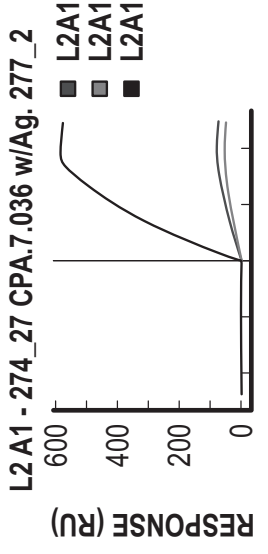


Figure 45B

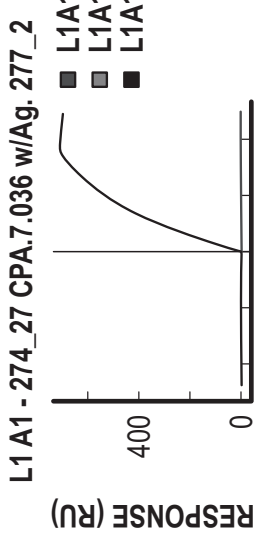


Figure 45C

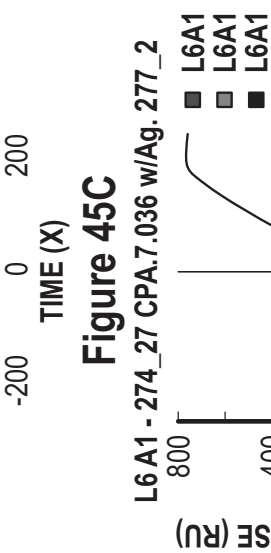


Figure 45D

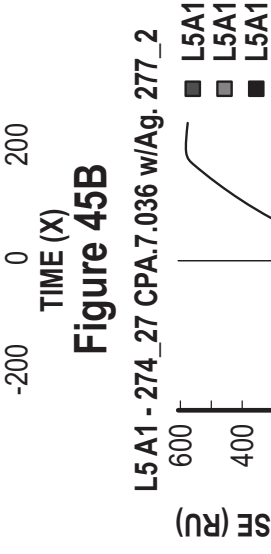


Figure 45E

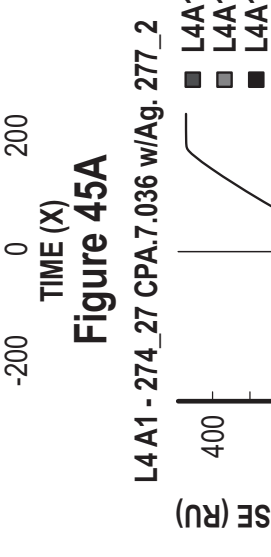


Figure 45F

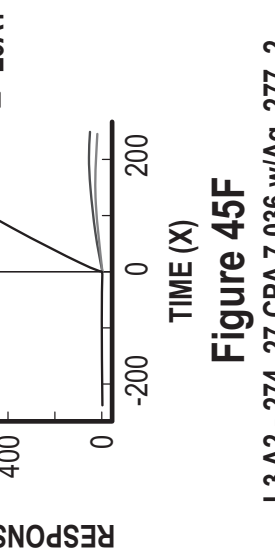


Figure 45G

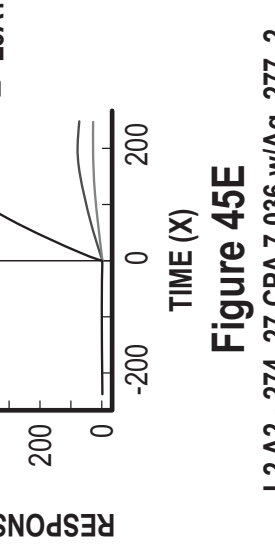


Figure 45H

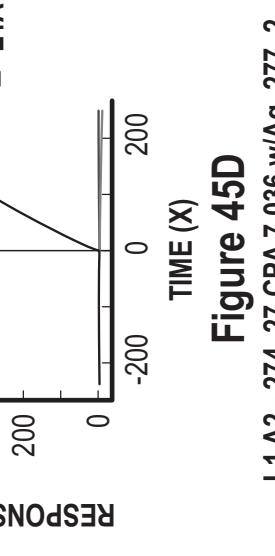


Figure 45I

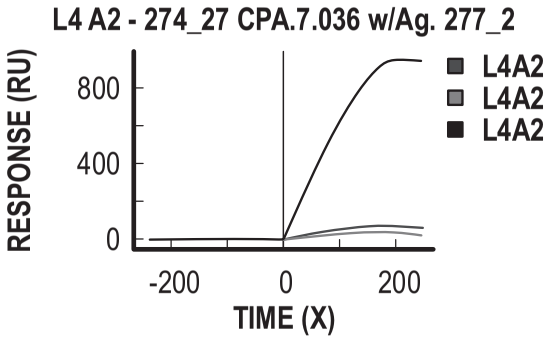


Figure 45J

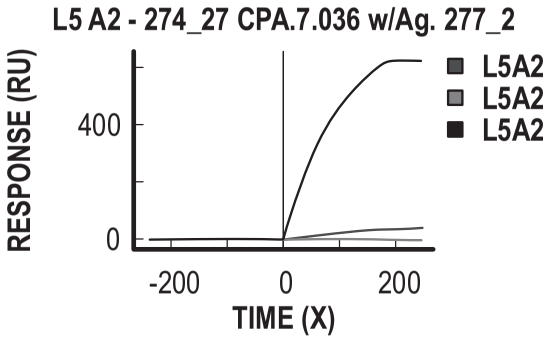


Figure 45K

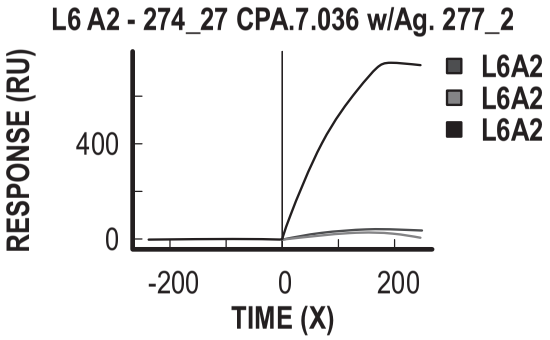


Figure 45L

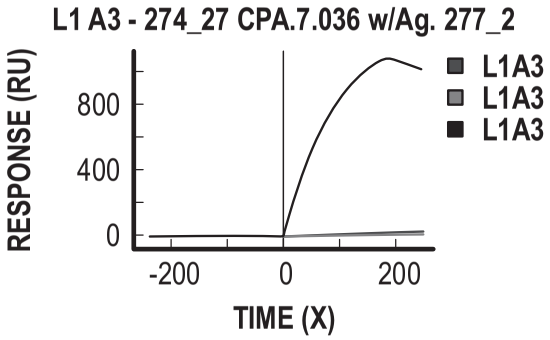


Figure 45M

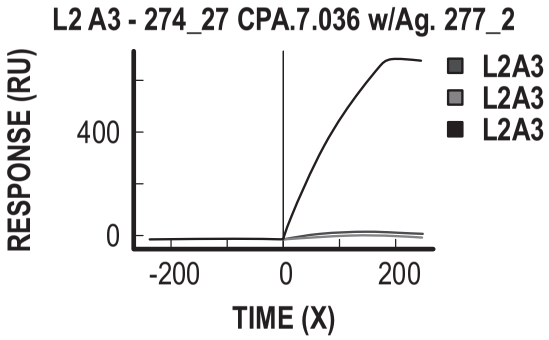


Figure 45N

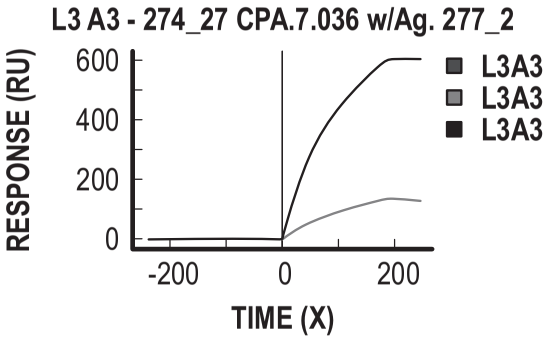


Figure 45O

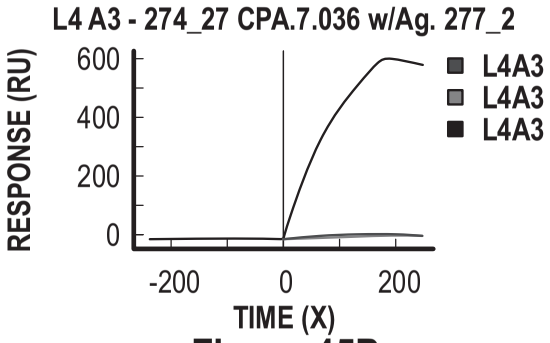


Figure 45P

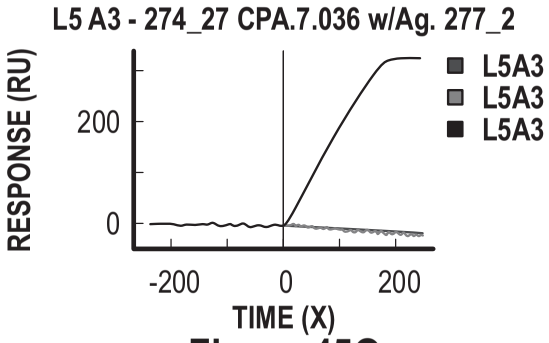


Figure 45Q

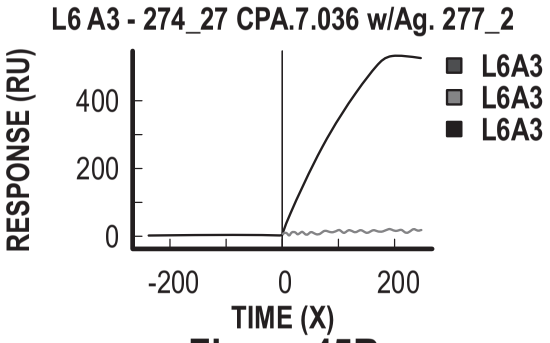


Figure 45R

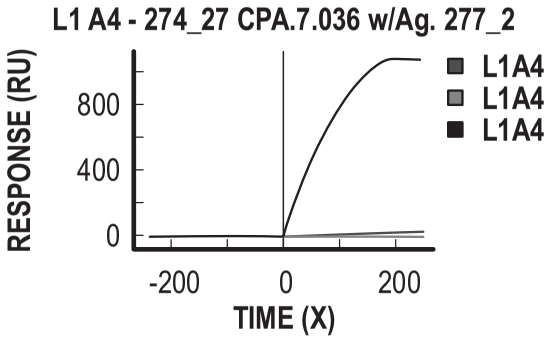


Figure 45S

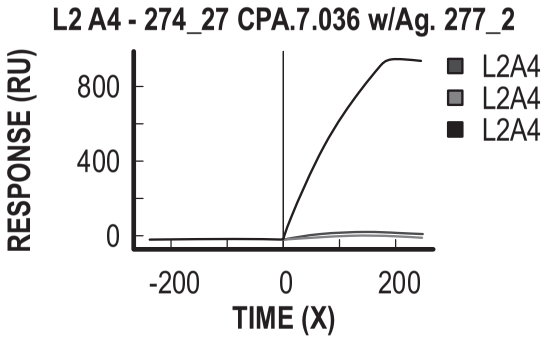


Figure 45T

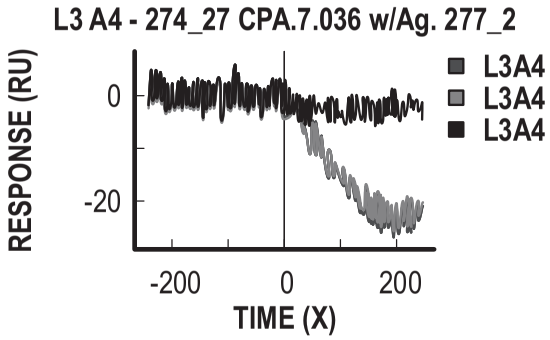


Figure 45U

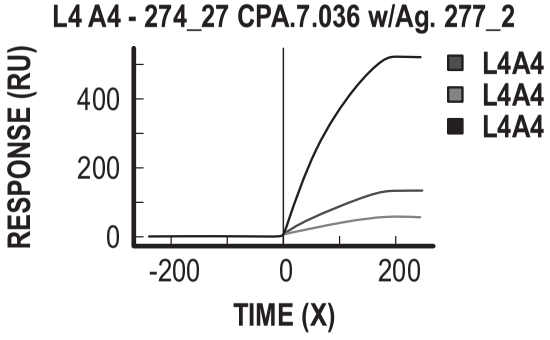


Figure 45V

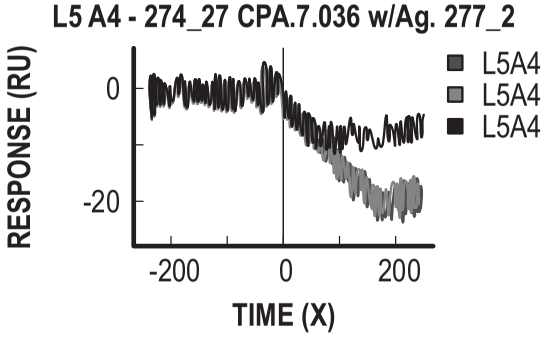


Figure 45W

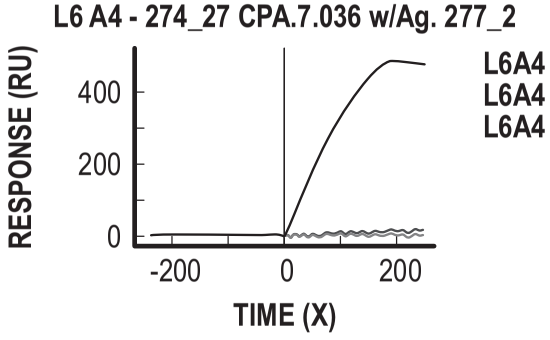


Figure 45X

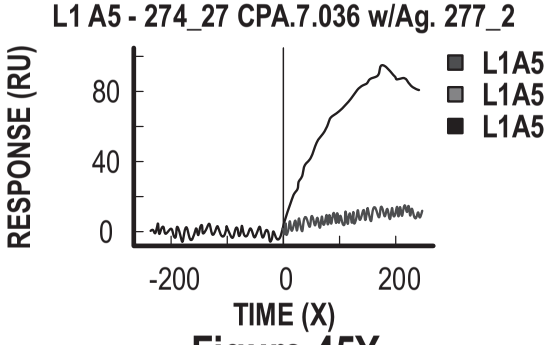


Figure 45Y

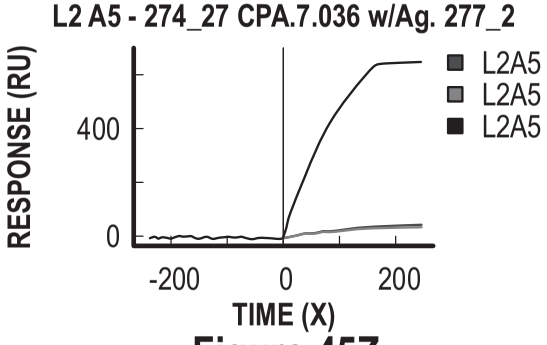


Figure 45Z

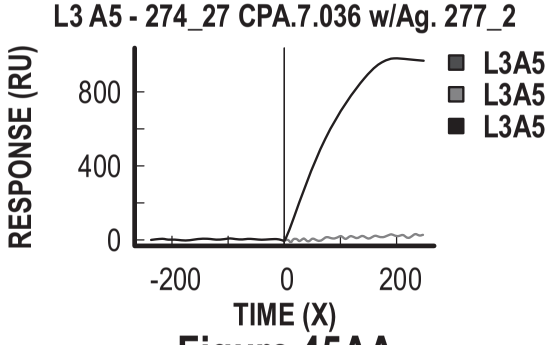


Figure 45AA

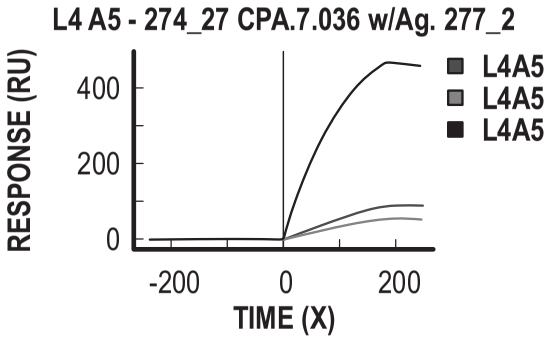


Figure 45BB

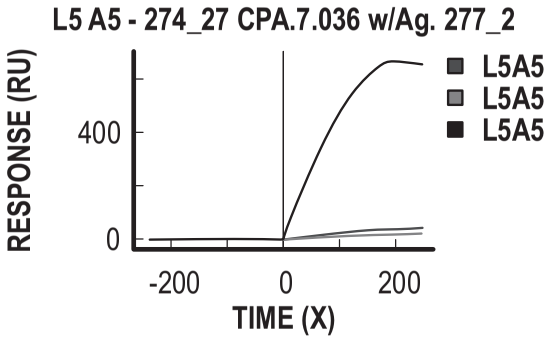


Figure 45CC

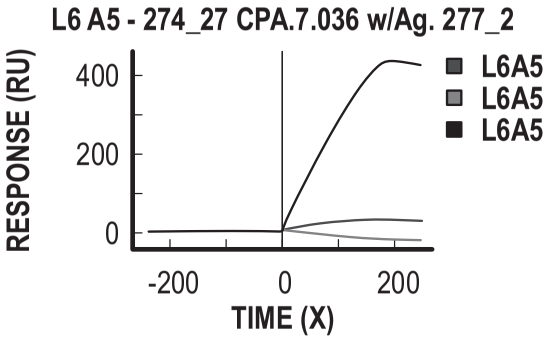


Figure 45DD

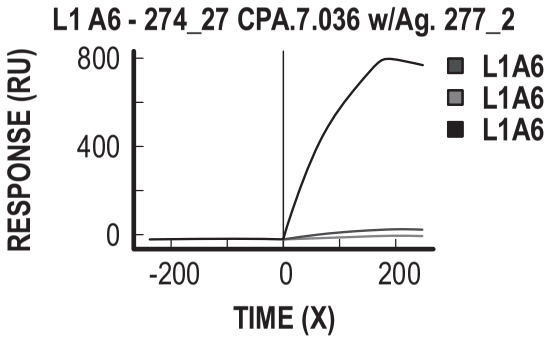


Figure 45EE

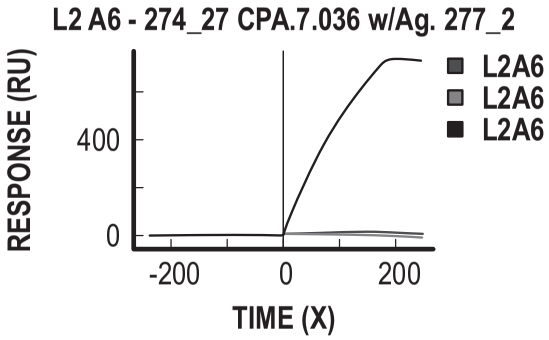


Figure 45FF

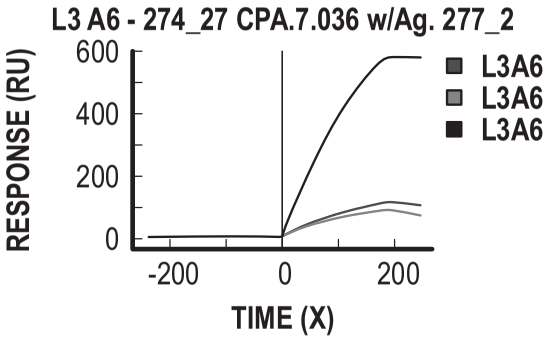


Figure 45GG

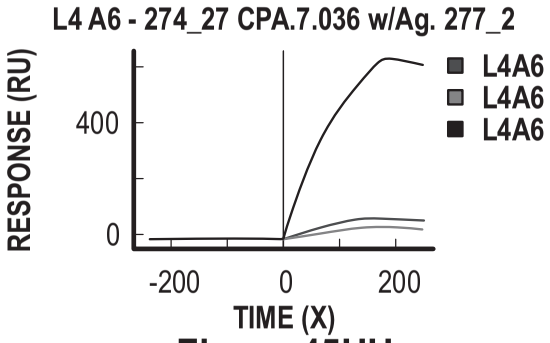


Figure 45HH

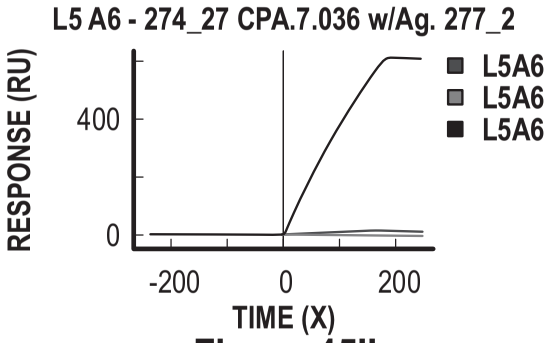


Figure 45II

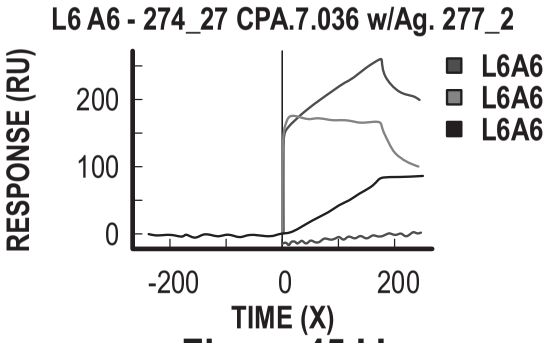


Figure 45JJ

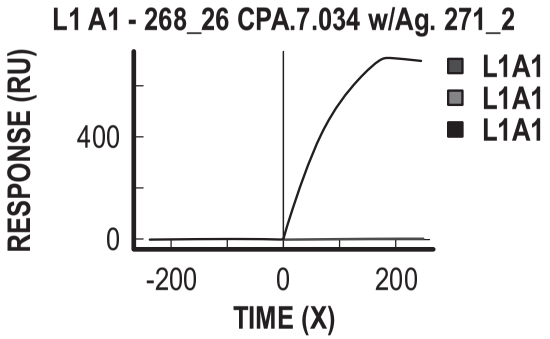


Figure 46A

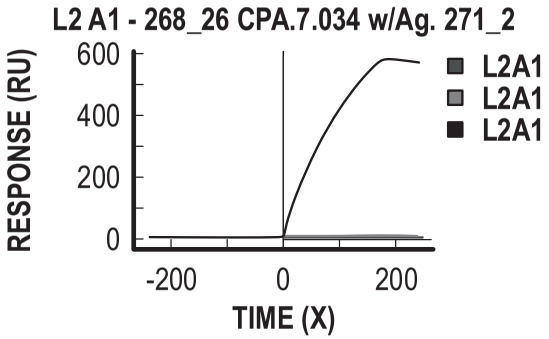


Figure 46B

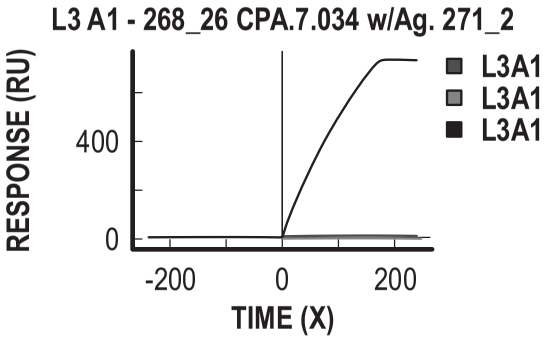


Figure 46C

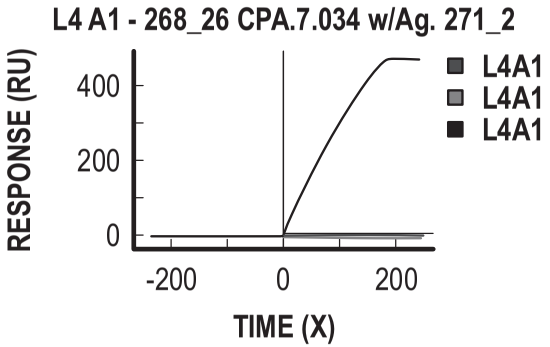


Figure 46D

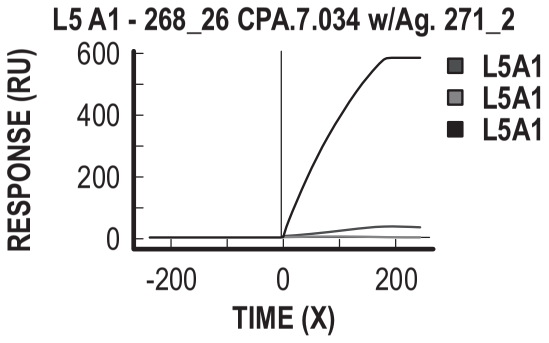


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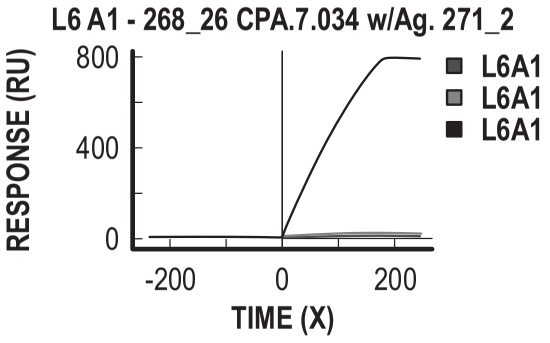


Figure 46F

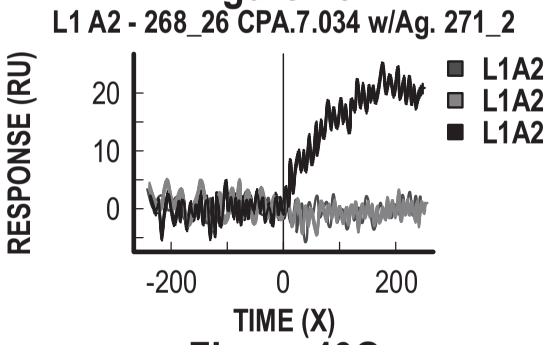


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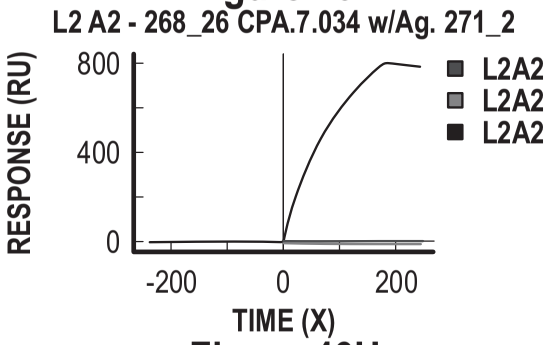


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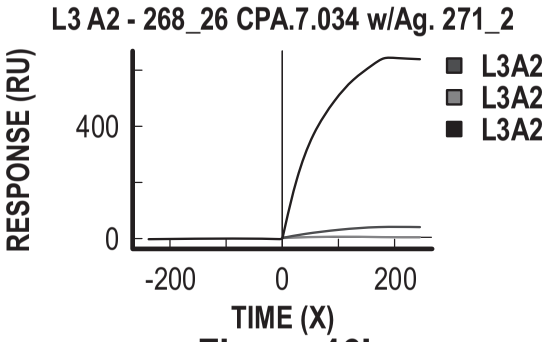


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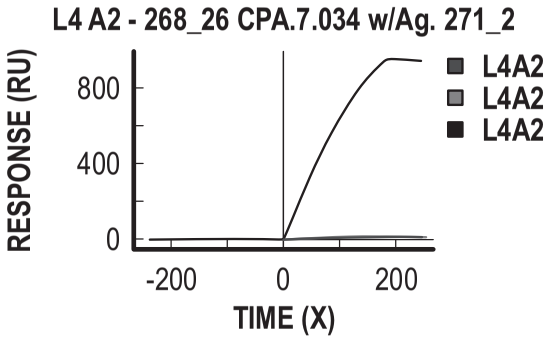


Figure 46J

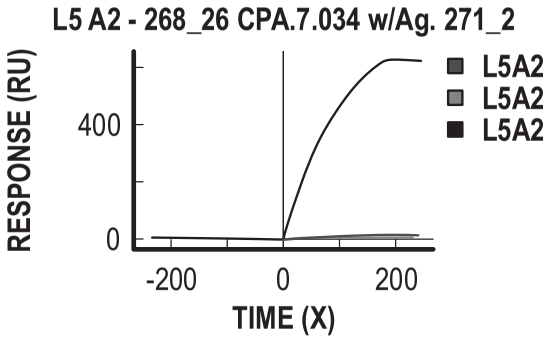


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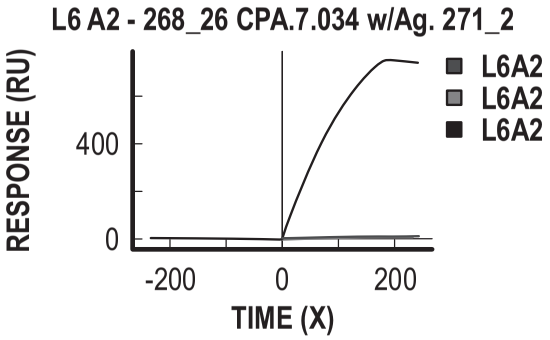


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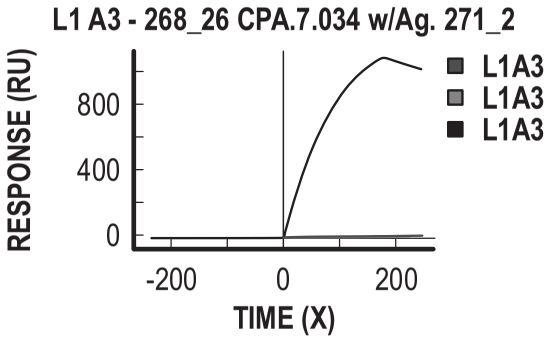


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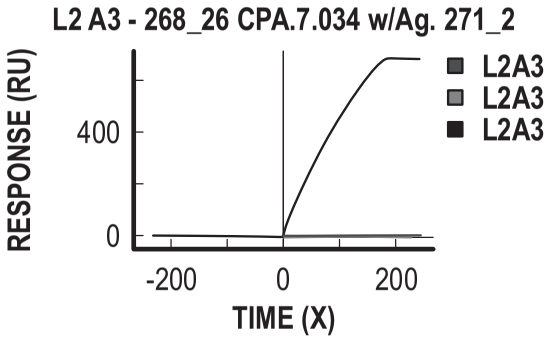


Figure 46N

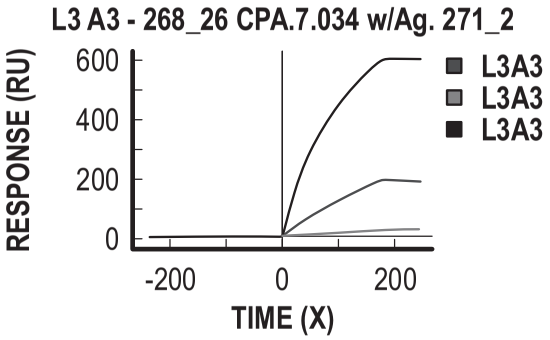


Figure 46O

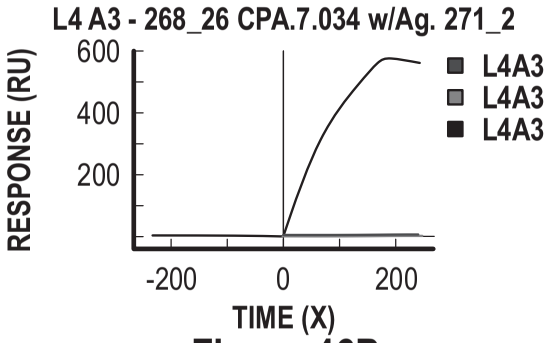


Figure 46P

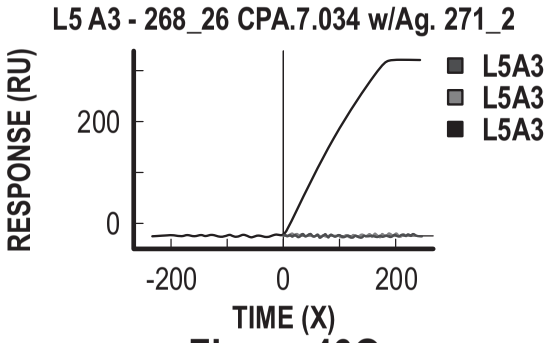


Figure 46Q

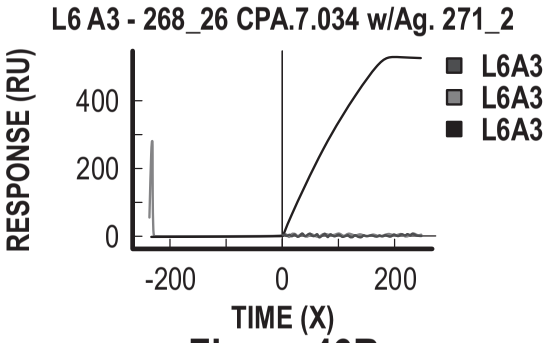


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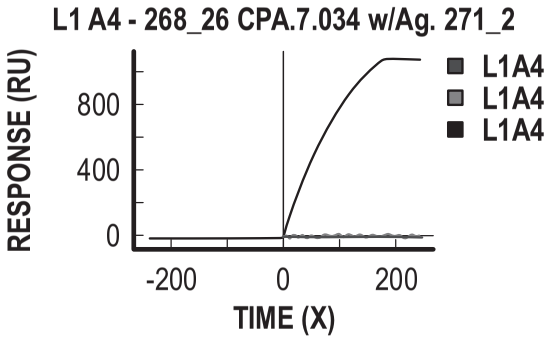


Figure 46S

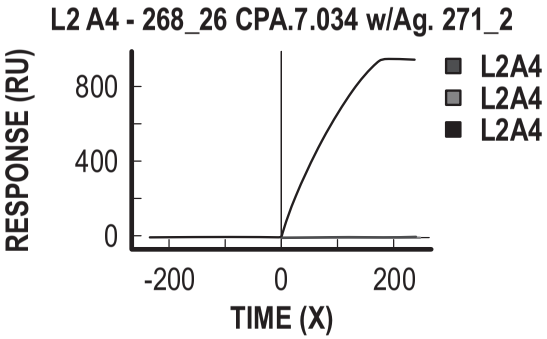


Figure 46T

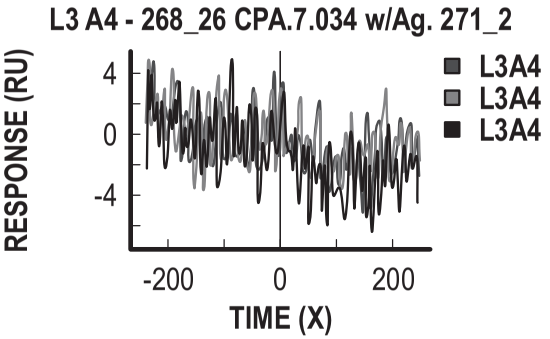


Figure 46U

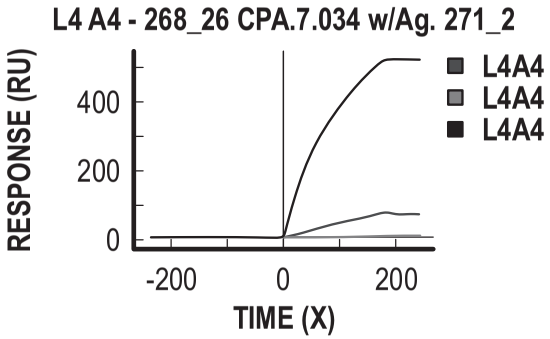


Figure 46V

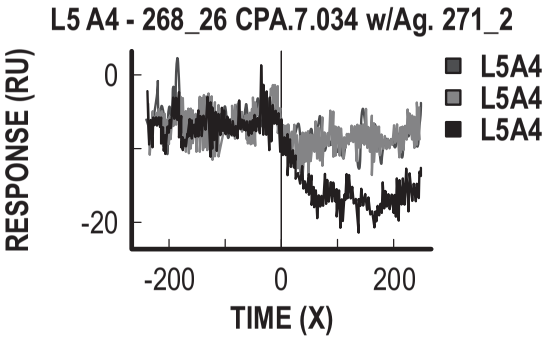


Figure 46W

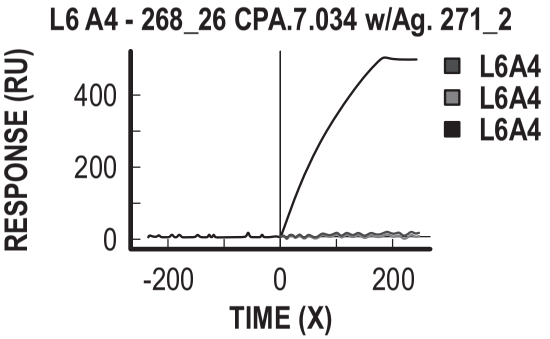


Figure 46X

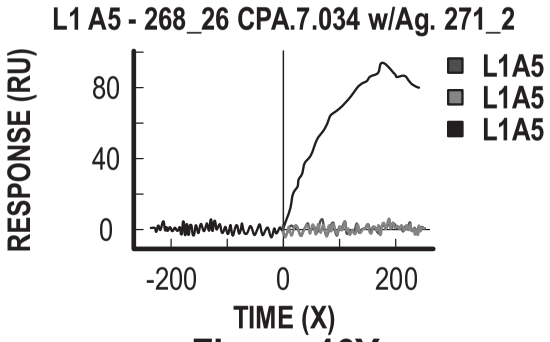


Figure 46Y

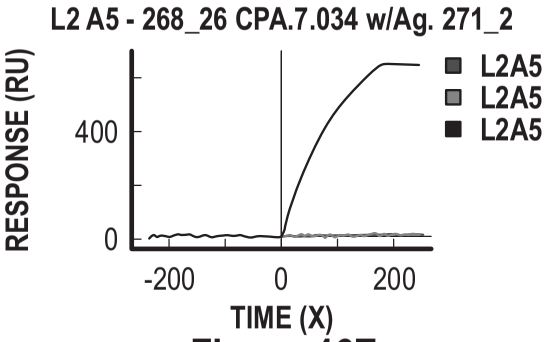


Figure 46Z

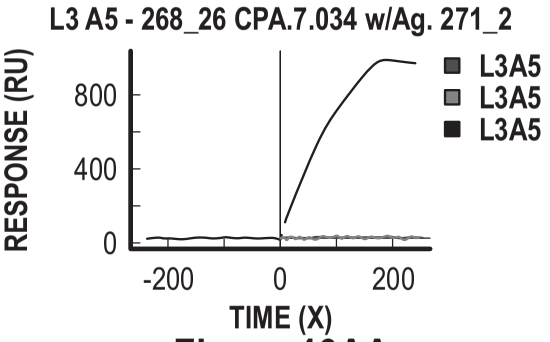


Figure 46AA

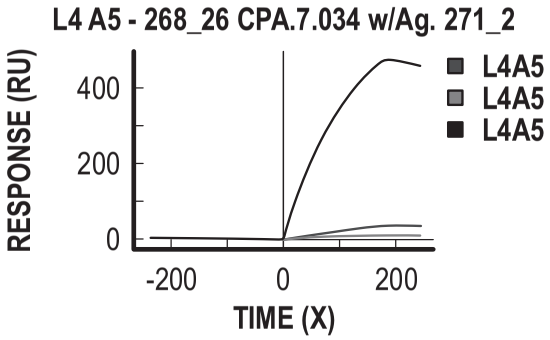


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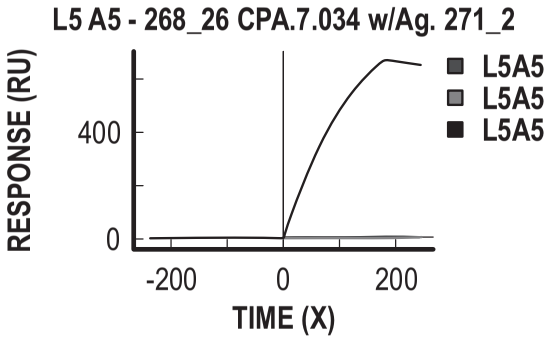


Figure 46CC

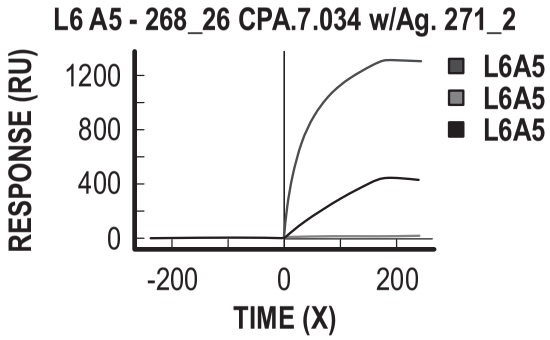


Figure 46DD

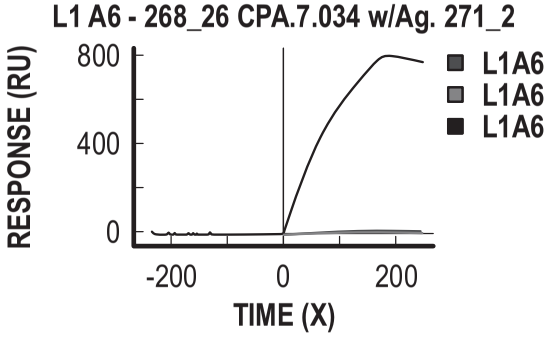


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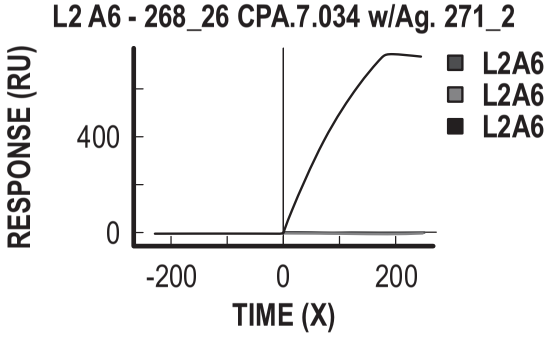


Figure 46FF

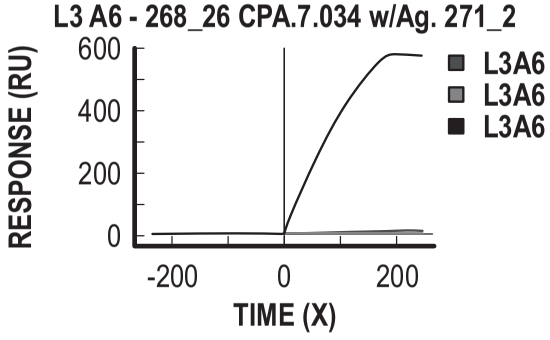


Figure 46GG

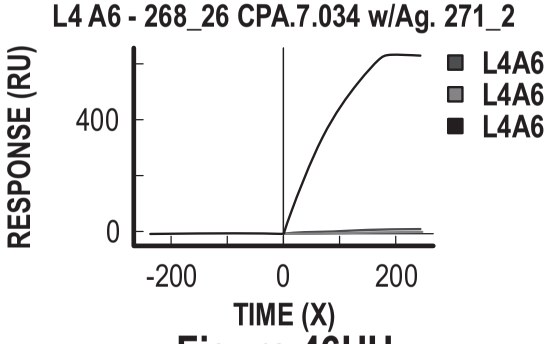


Figure 46HH

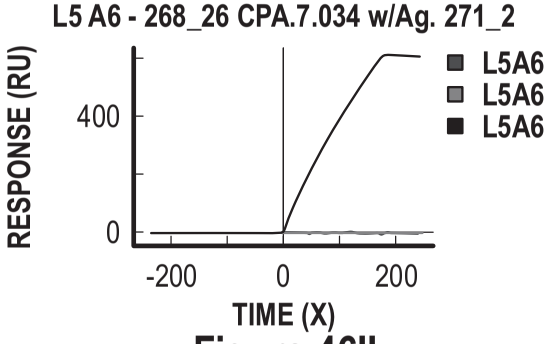


Figure 46II

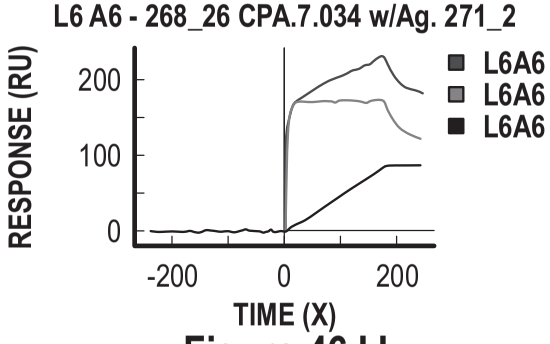


Figure 46JJ

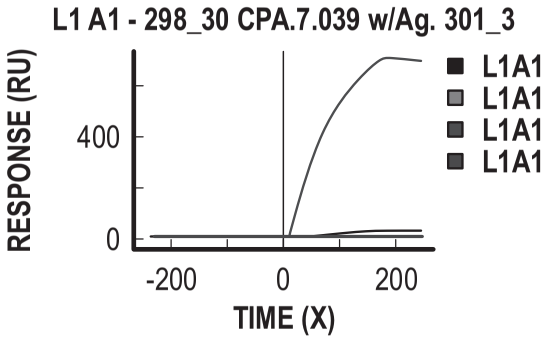


Figure 47A

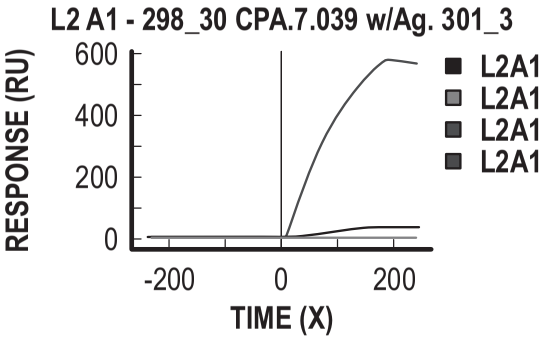


Figure 47B

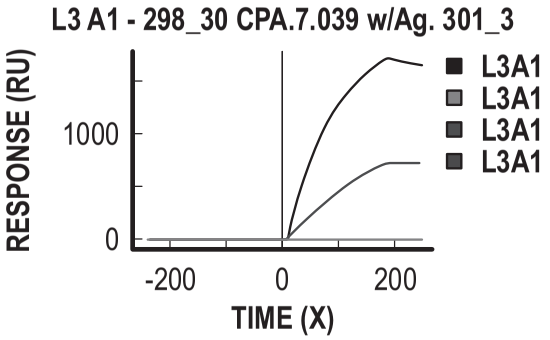


Figure 47C

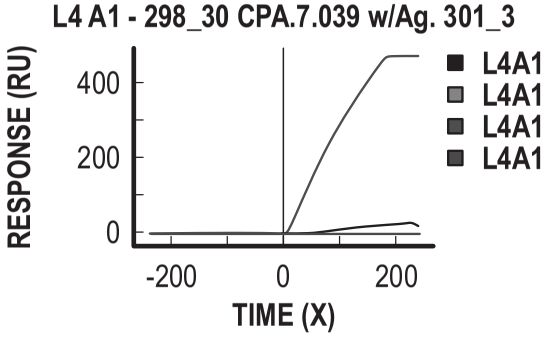


Figure 47D

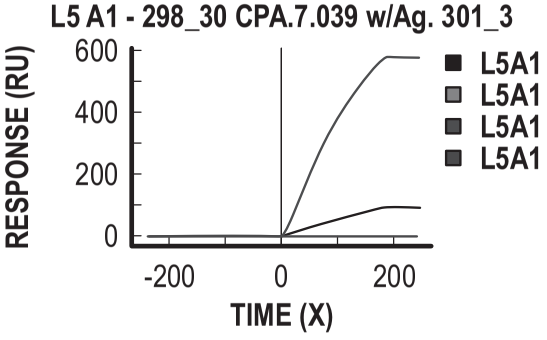


Figure 47E

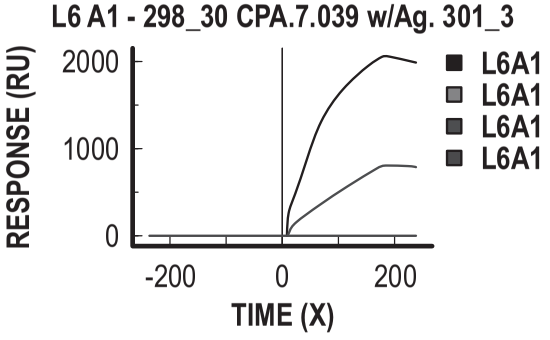


Figure 47F

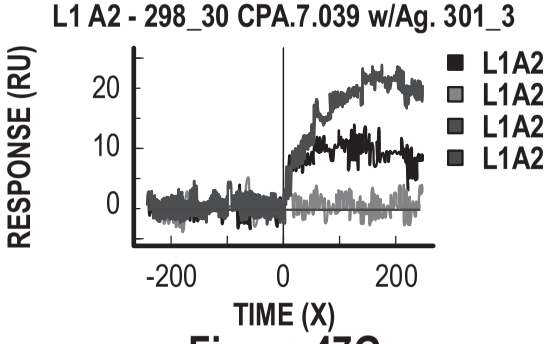


Figure 47G

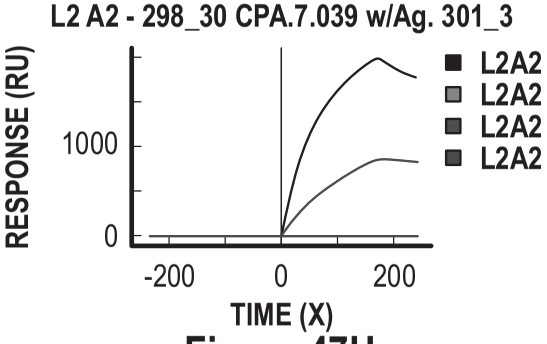


Figure 47H

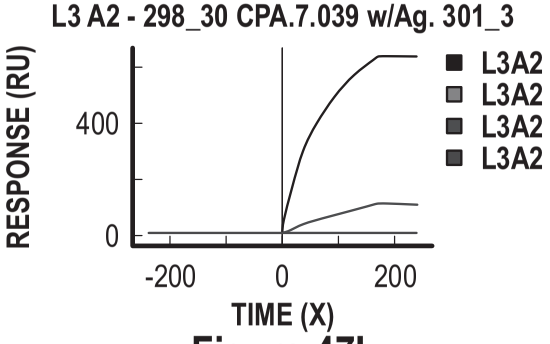


Figure 47I

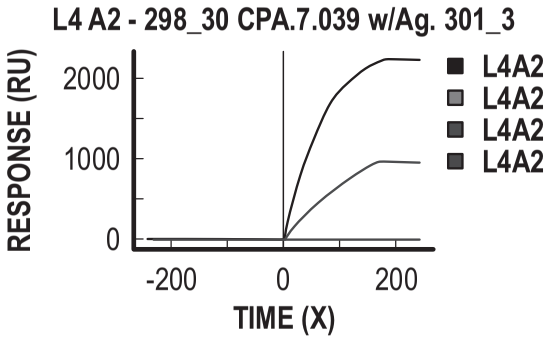


Figure 47J

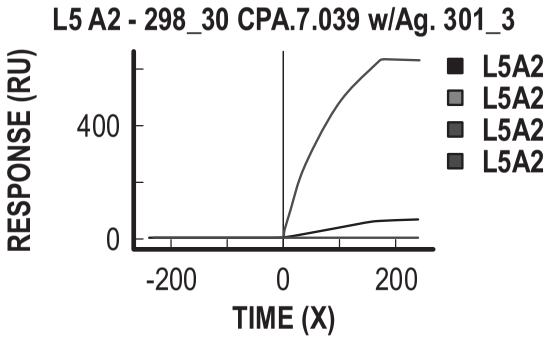


Figure 47K

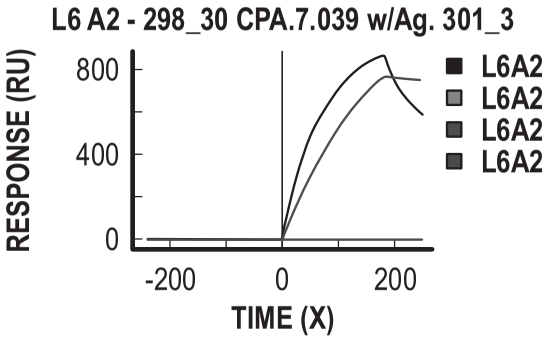


Figure 47L

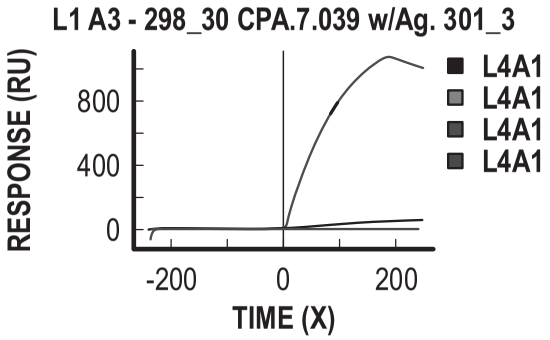


Figure 47M

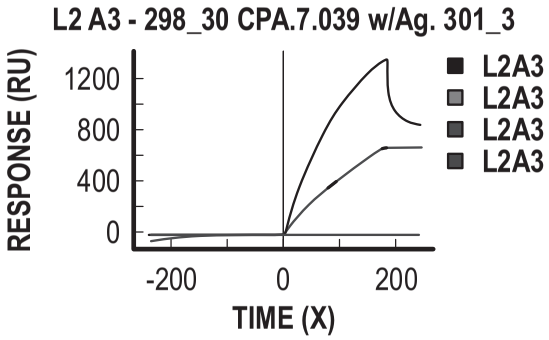


Figure 47N

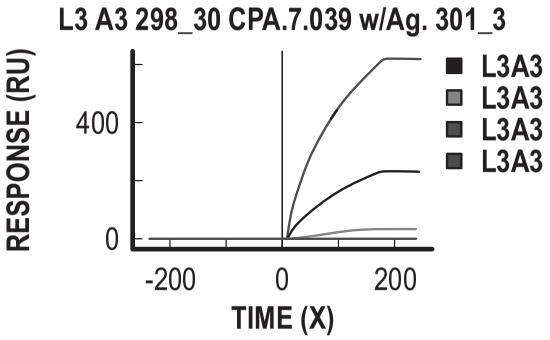


Figure 47O

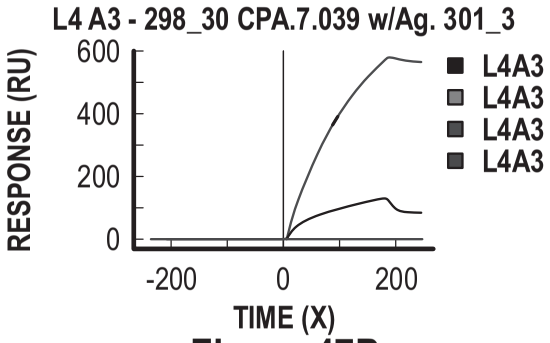


Figure 47P

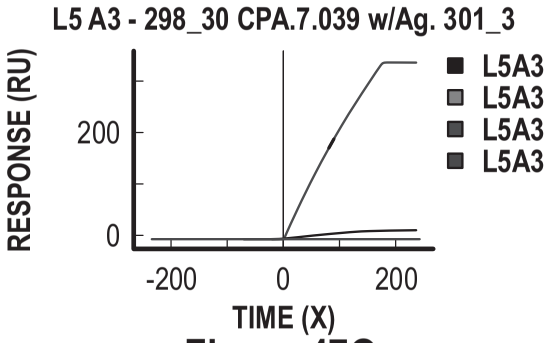


Figure 47Q

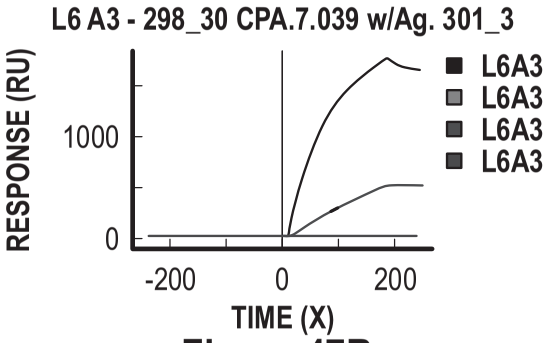


Figure 47R

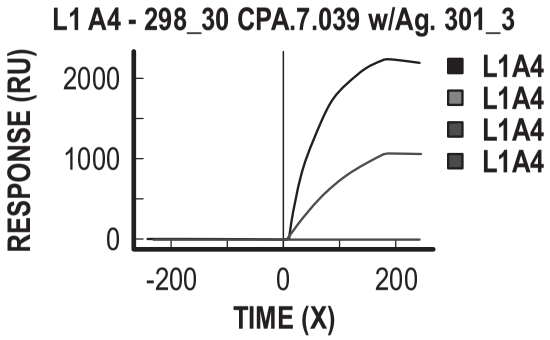


Figure 47S

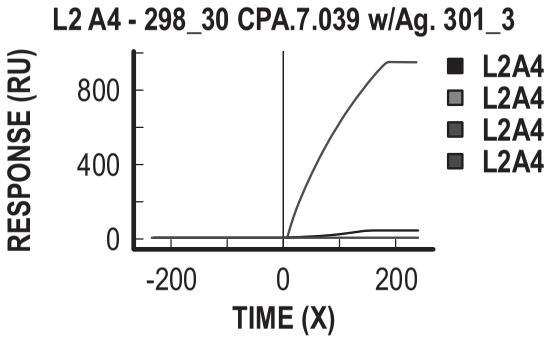


Figure 47T

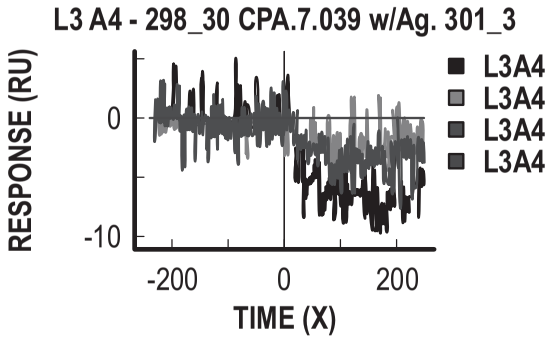


Figure 47U

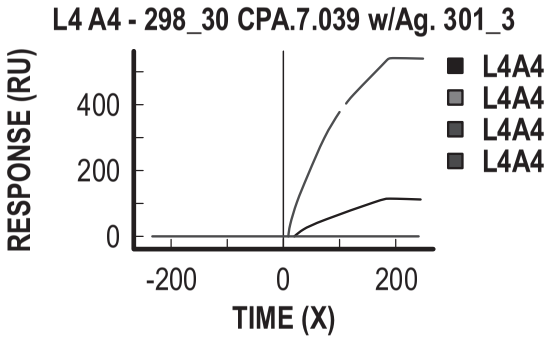


Figure 47V

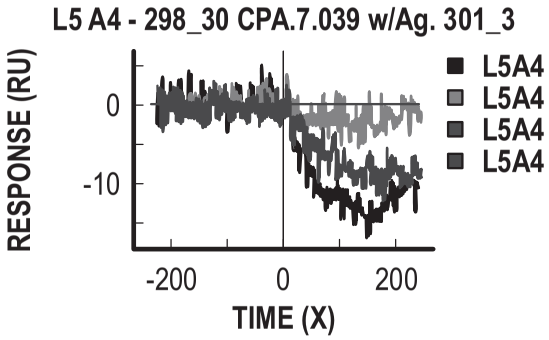


Figure 47W

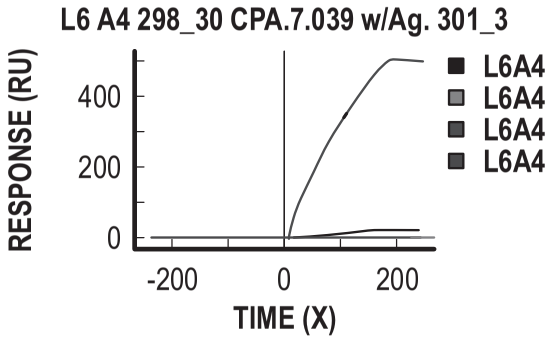


Figure 47X

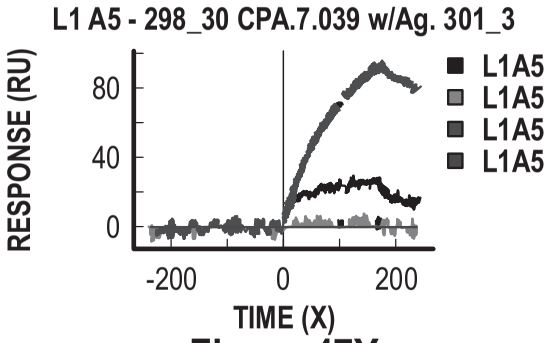


Figure 47Y

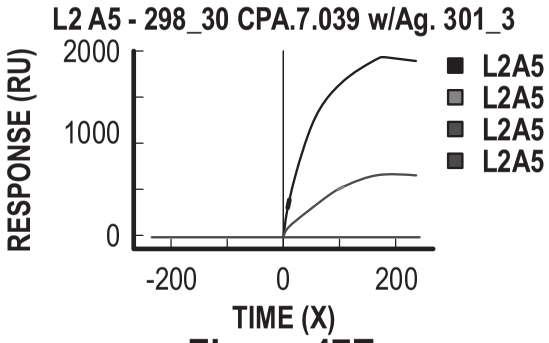


Figure 47Z

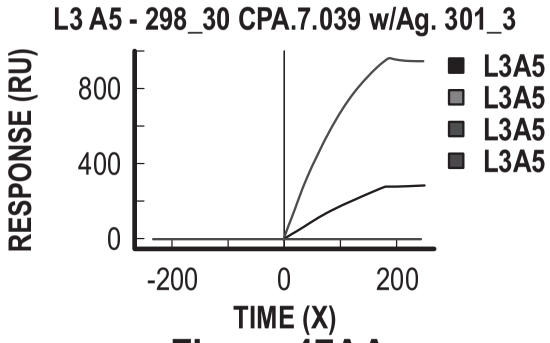


Figure 47AA

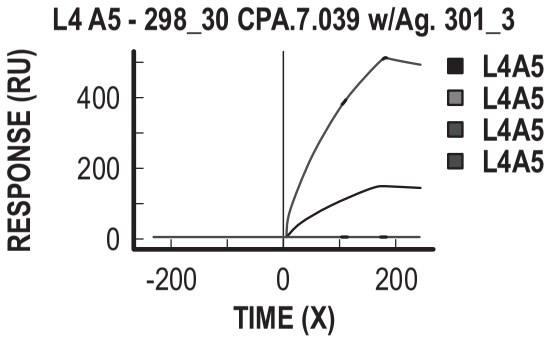


Figure 47BB

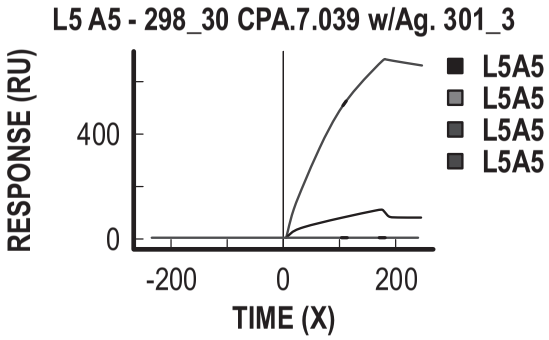


Figure 47CC

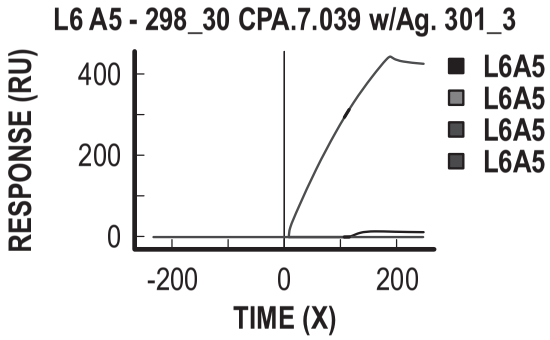


Figure 47DD

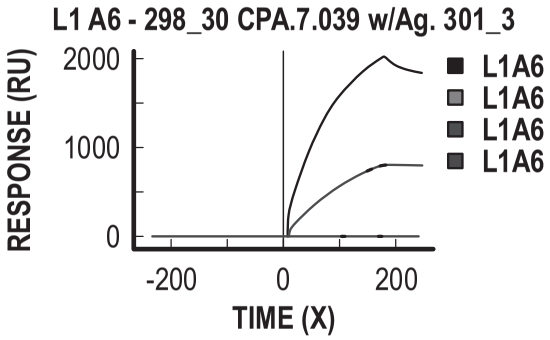


Figure 47EE

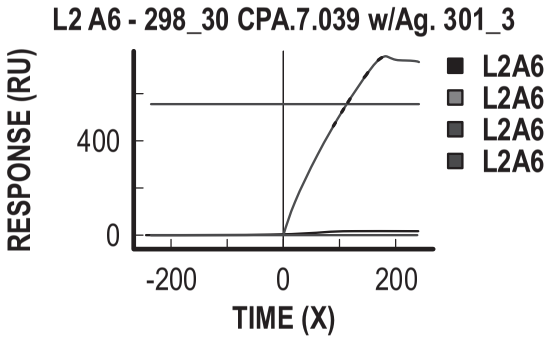


Figure 47FF

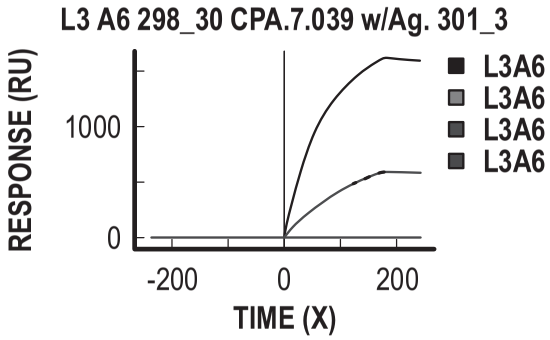


Figure 47GG

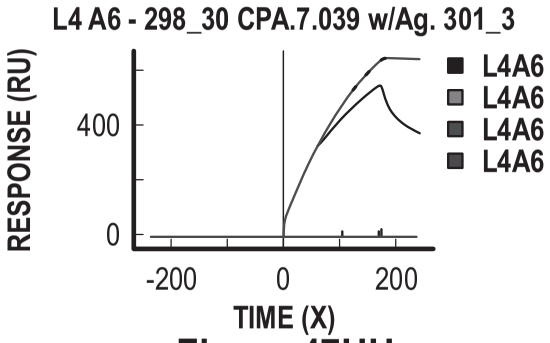


Figure 47HH

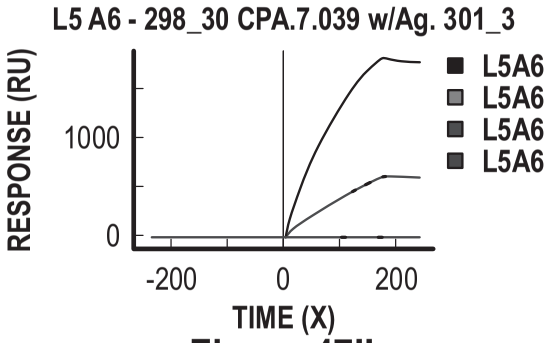


Figure 47II

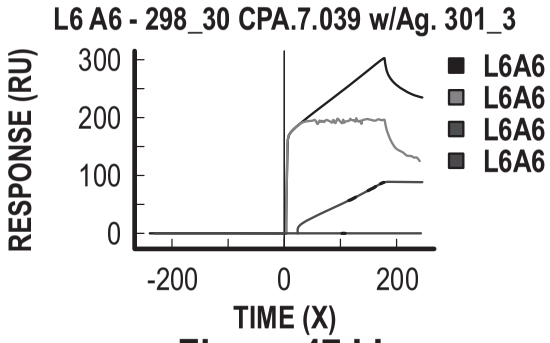


Figure 47JJ

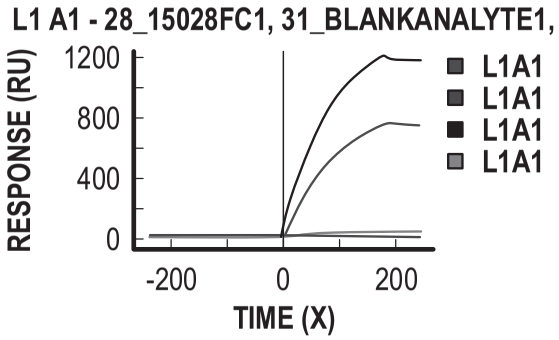


Figure 48A

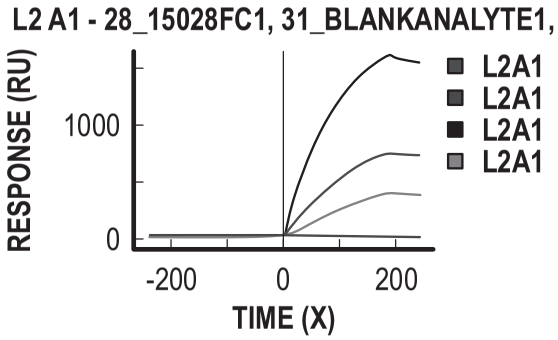


Figure 48B

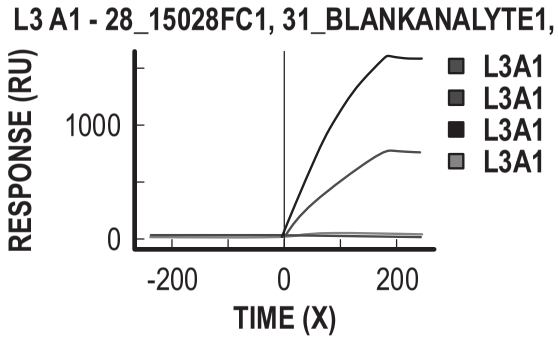


Figure 48C

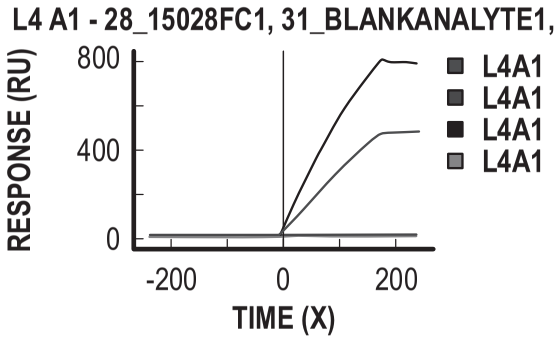


Figure 48D

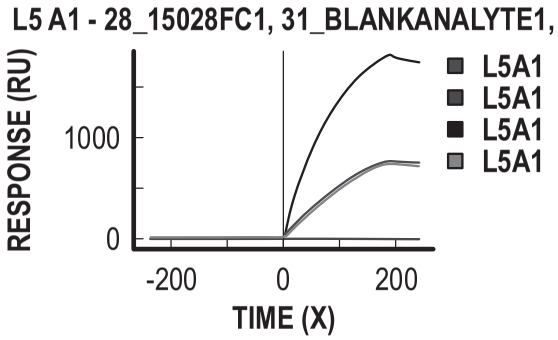


Figure 48E

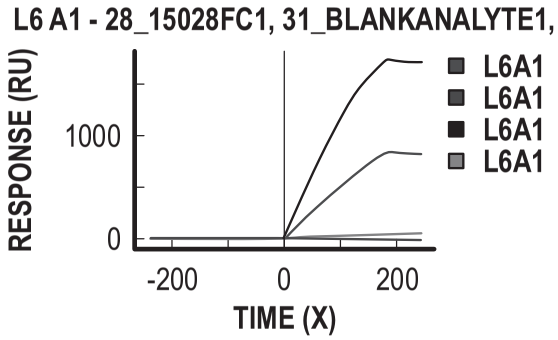


Figure 48F

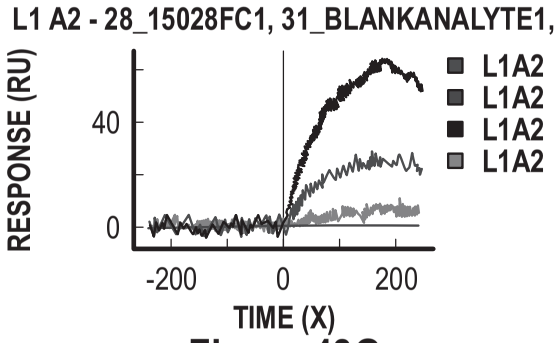


Figure 48G

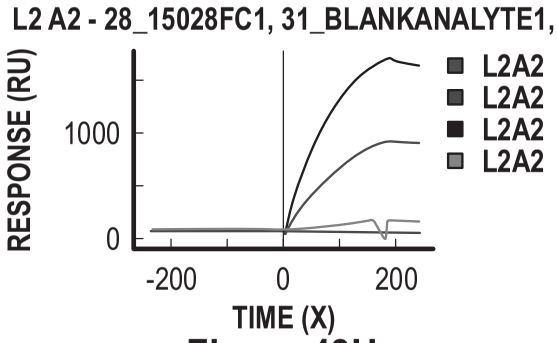


Figure 48H

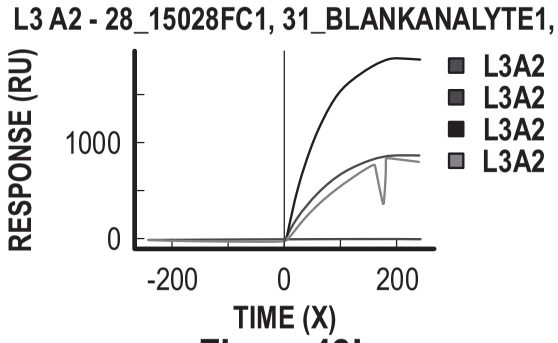


Figure48I

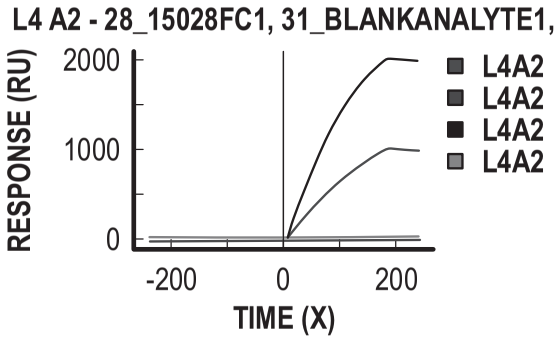


Figure 48J

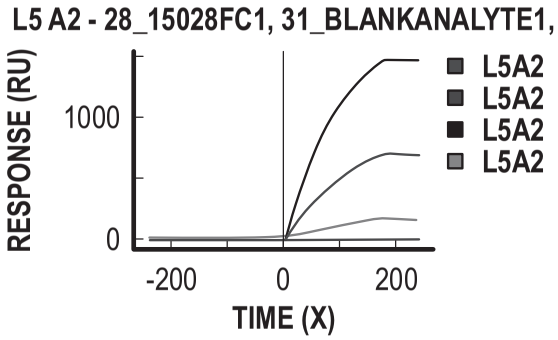


Figure 48K

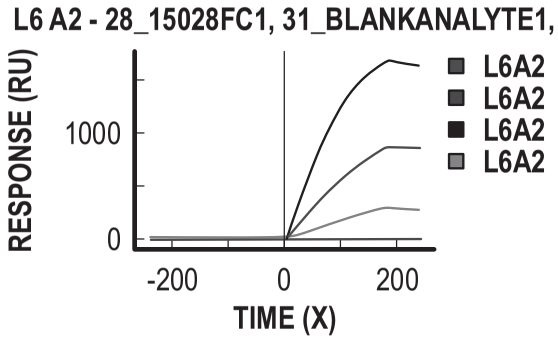


Figure 48L

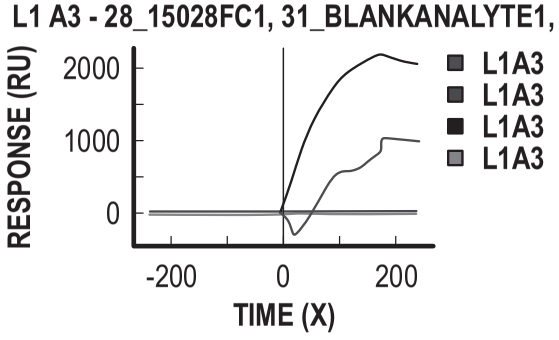


Figure 48M

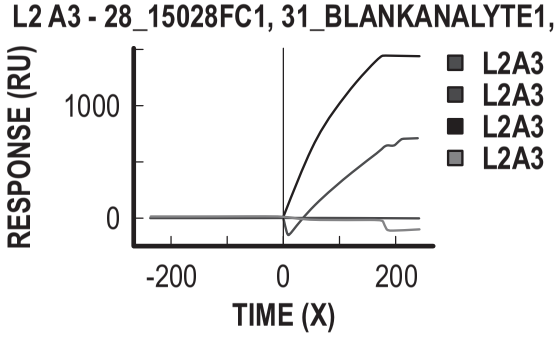


Figure 48N

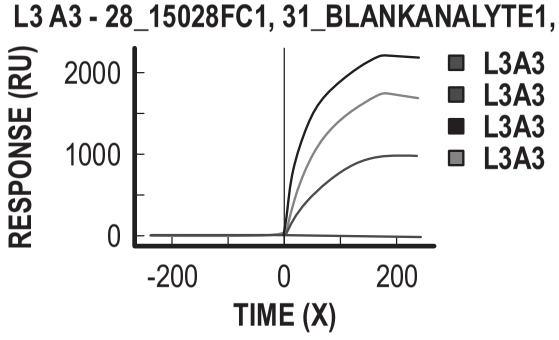


Figure 48O

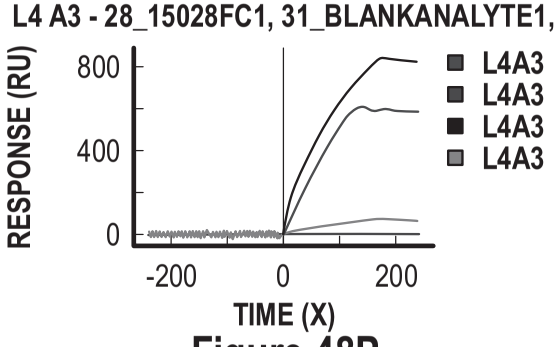


Figure 48P

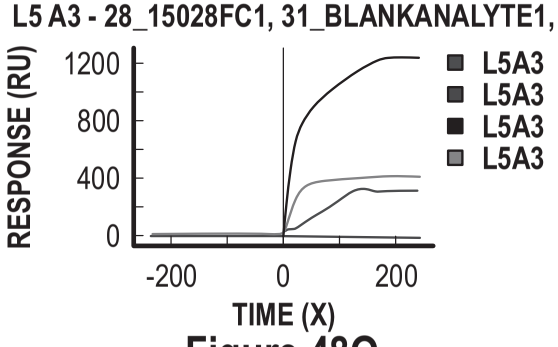


Figure 48Q

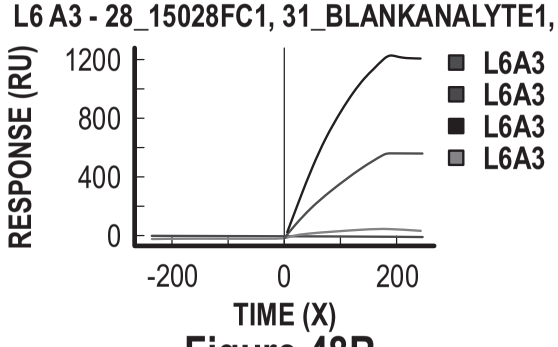


Figure 48R

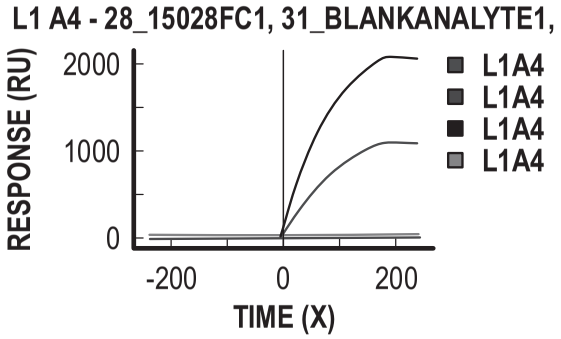


Figure 48S

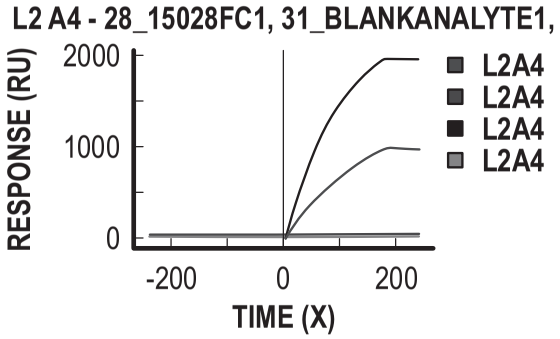


Figure 48T

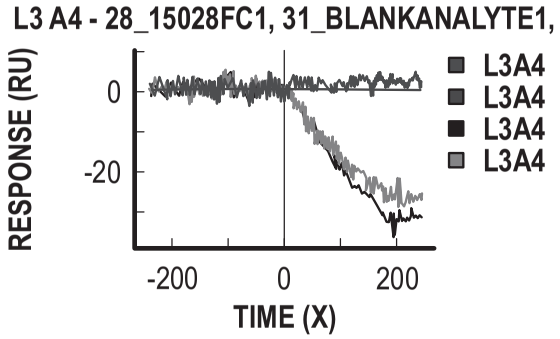


Figure 48U

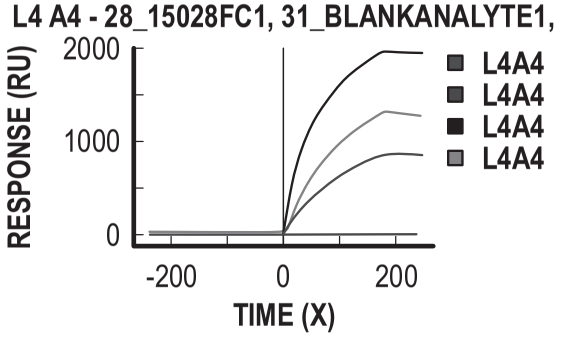


Figure 48V

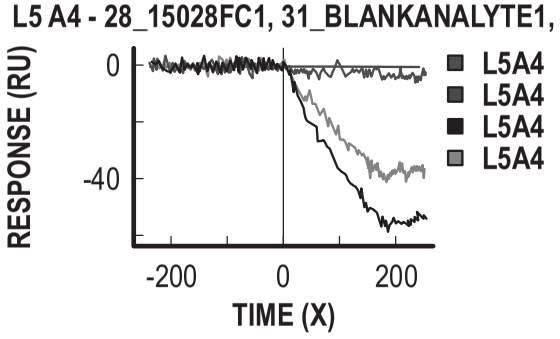


Figure 48W

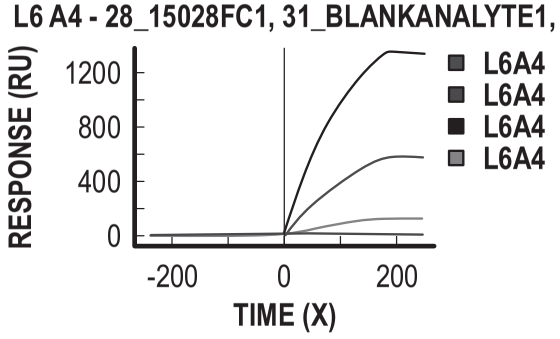


Figure 48X

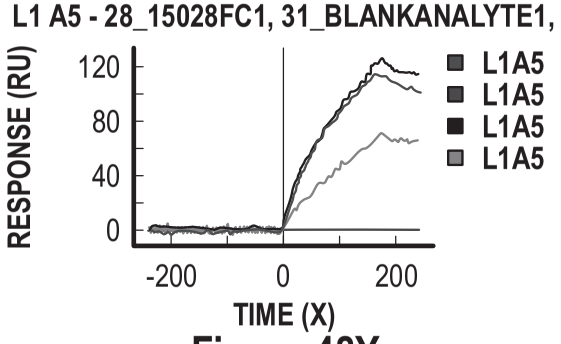


Figure 48Y

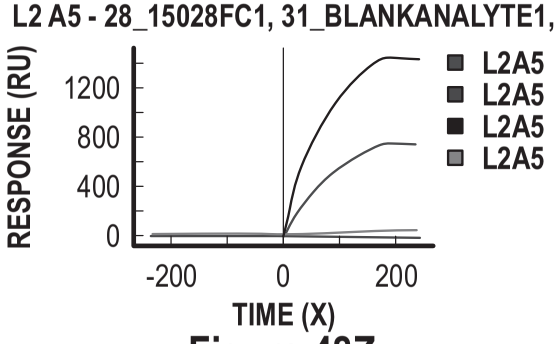


Figure 48Z

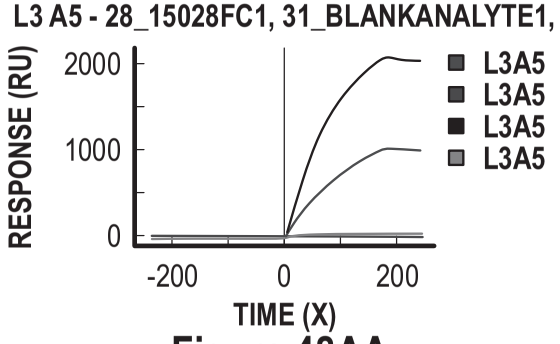


Figure 48AA

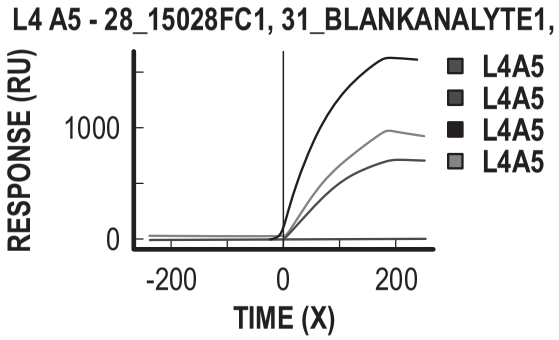


Figure 48BB

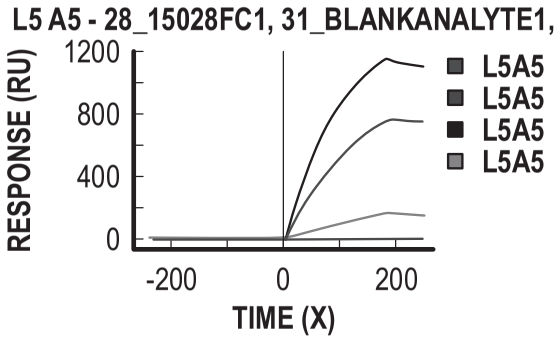


Figure 4CC

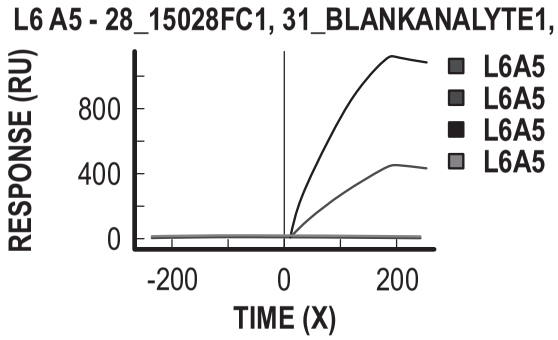


Figure 48DD

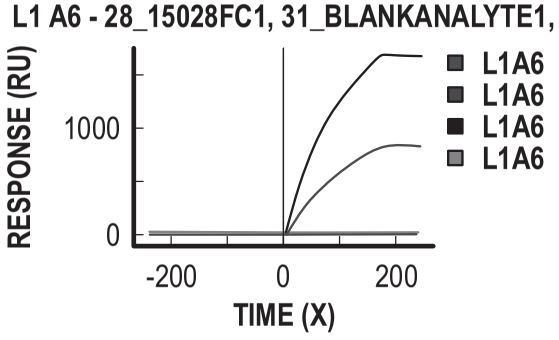


Figure 48EE

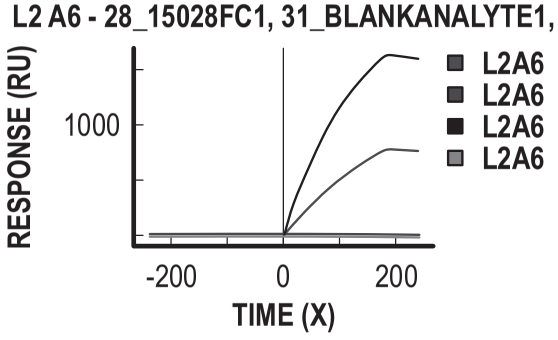


Figure 48FF

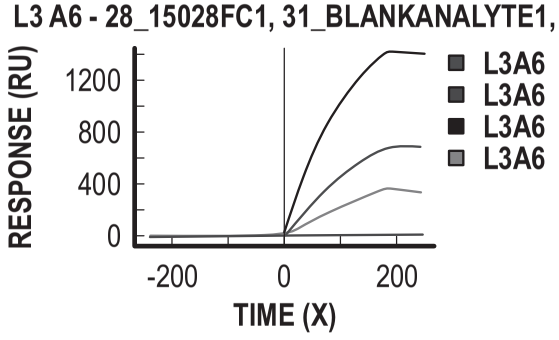


Figure 48GG

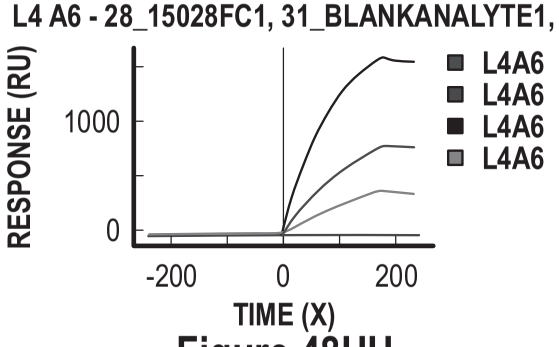


Figure 48HH

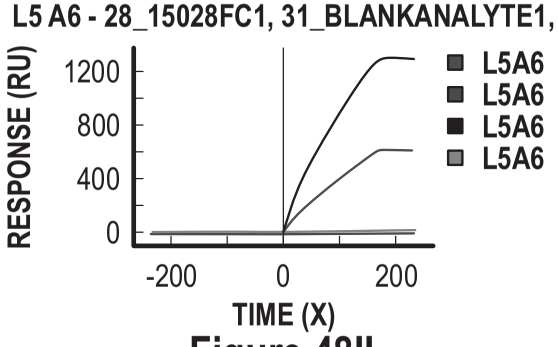


Figure 48II

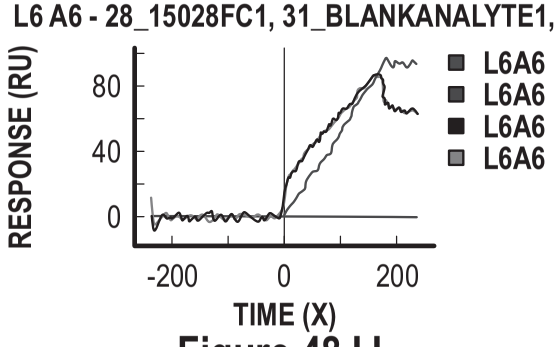


Figure 48JJ

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

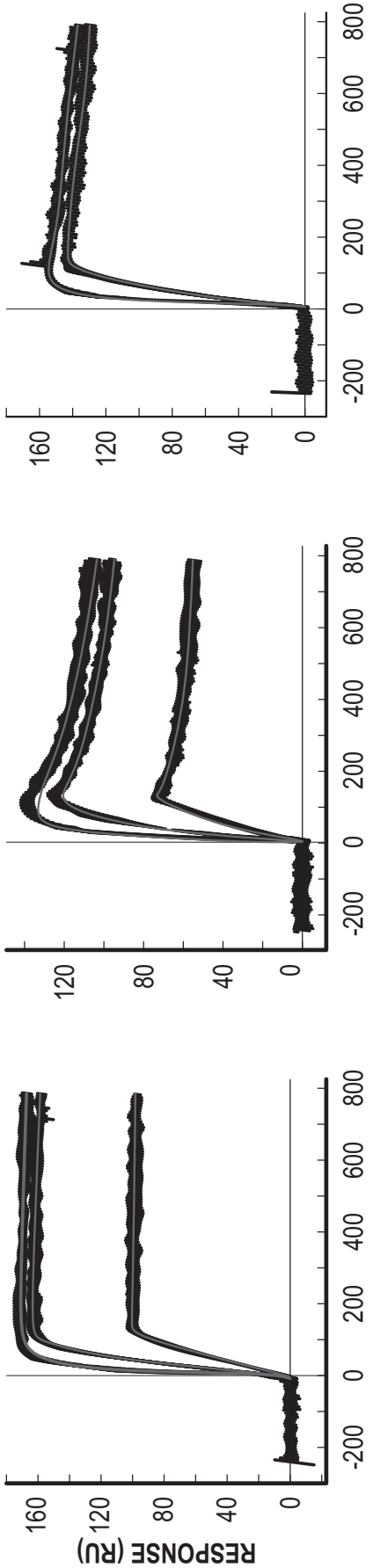


Figure 50A

Figure 50B

Figure 50C

Figure 50D

Figure 50E

Figure 50F

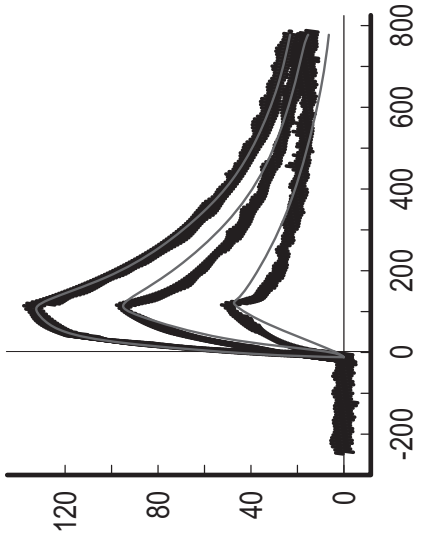


Figure 50G

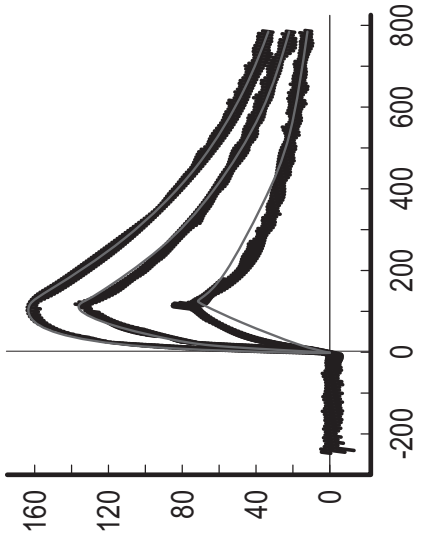


Figure 50H

Figure 50I

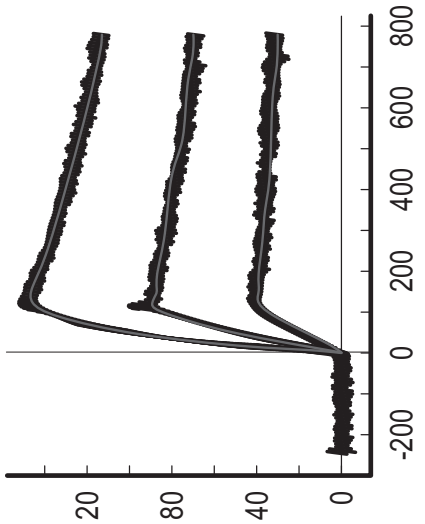


Figure 50J

Figure 50K

Figure 50L

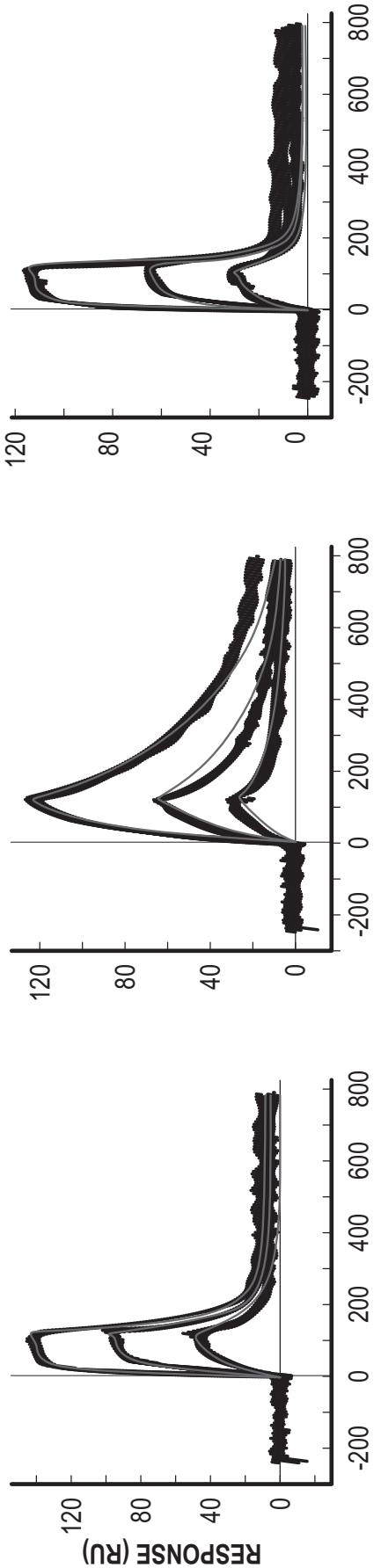


Figure 50M

Figure 50N

Figure 50O

Figure 50P

Figure 50Q

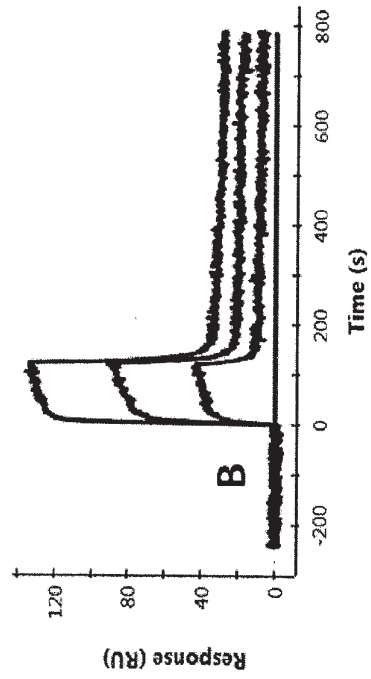


FIGURE 51B

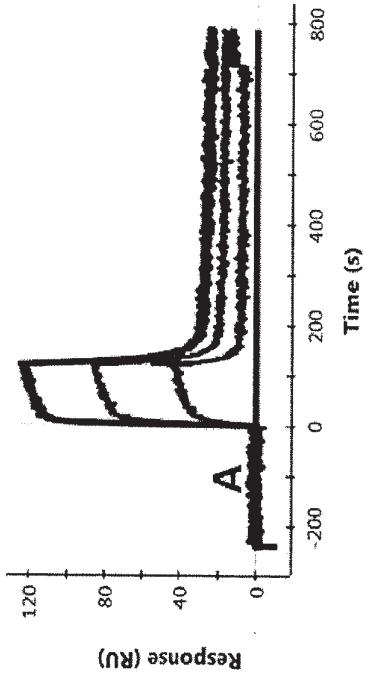


FIGURE 51A

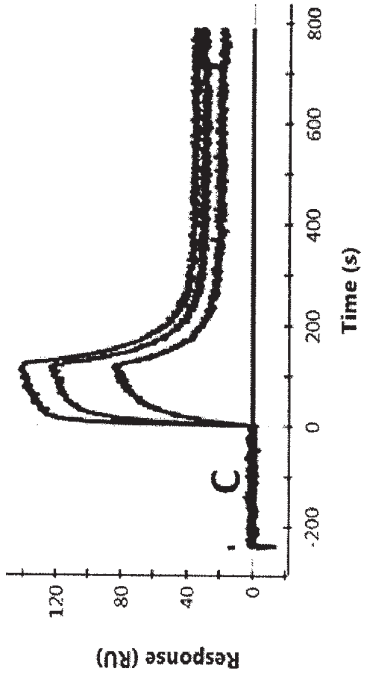


FIGURE 51C

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

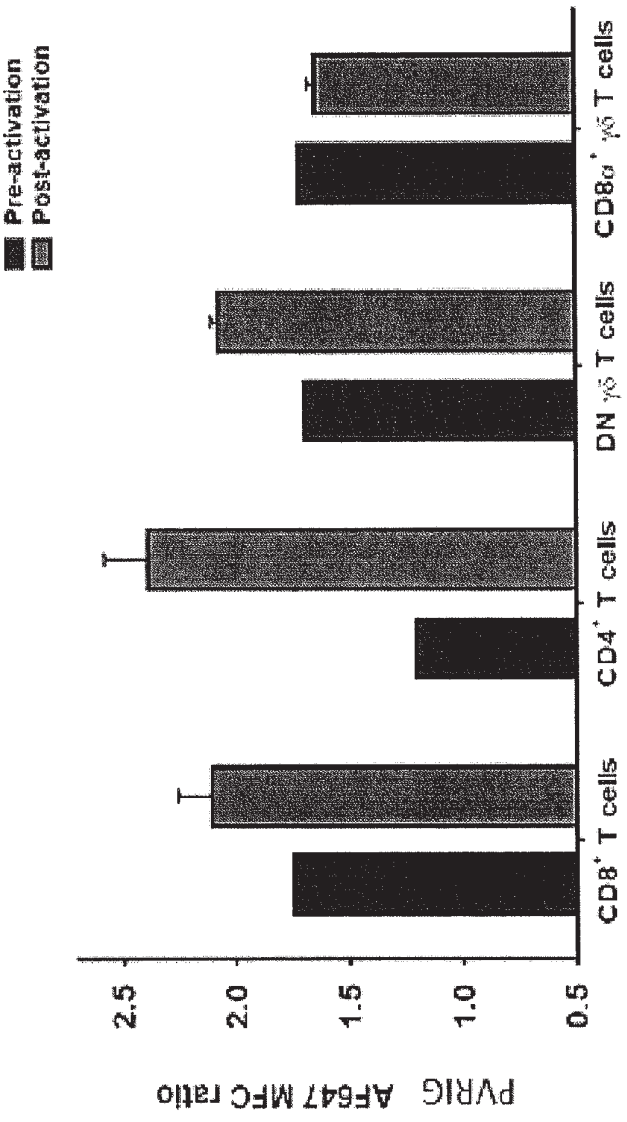

Pre-activation
Post-activation
PVRIG AF647 MFC ratio
2.5
2.0
1.5
1.0
0.5
CD8+ T cells
CD4+ T cells
DN γδ T cells
CD8α+ γδ T cells

Figure 53

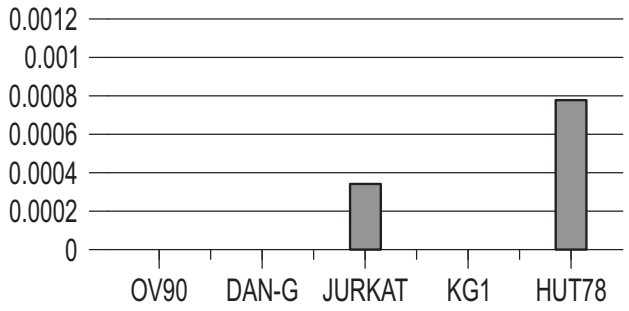
Cell line	ATCC No./CLS /ECACC No.	Morphology	Source
HL-60	ATCC, CCL-240	Leukemia	Blood
THP1	ATCC, TIB-202	Monocyte	Blood
KG-1	ATCC, CCL-246	Macrophage	Bone marrow
Jurkat	ATCC, TIB-152	T Cell	Blood
RPMI8226	ATCC, CCL-155	B lymphocyte	Blood
DAN-G	CLS, 300162	Epithelial	Pancreas
OV90	ATCC, CRL-11732	Epithelial	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 54

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 murine leukemia virus-induced tumor
P388D1	CCL-46	Macrophage	Lymphoblast
KLN205	CRL-1453	Epithelial	Lung
CT26	CRL-2638	Fibroblast	Colon
Renca	CRL-2947	Epithelial	Kidney

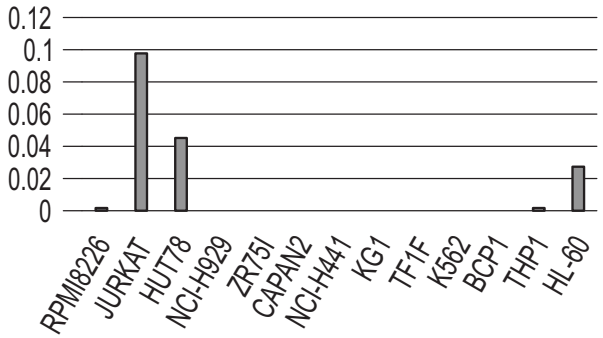
A.



HUMAN CELL LINE	CT VALUE	
	HUMAN PVRIG	HRPL19
OV90	UNDETERMINED	24.582
DAN-G	UNDETERMINED	23.184
JURKAT	31.552	24.107
KG1	UNDETERMINED	23.197
HUT78	29.626	23.192

Figure 56A

B.



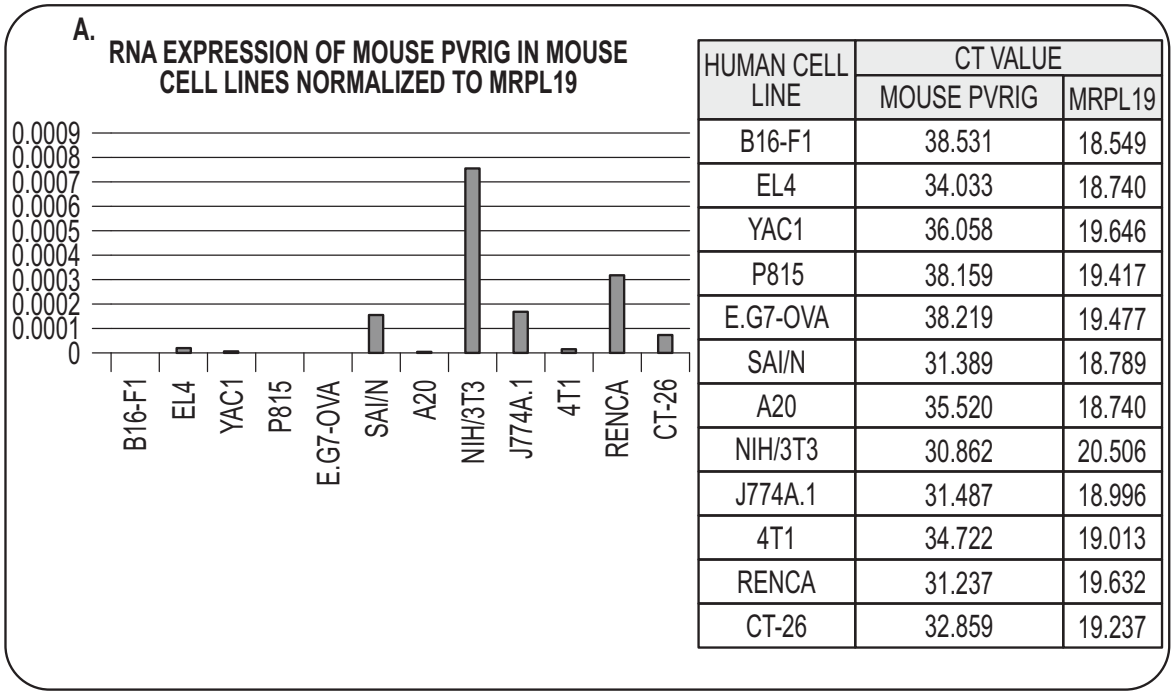
HUMAN CELL LINE	CT VALUE	
	HUMAN PVRIG	
RPMI8226	33.995	24.887
JURKAT	30.591	27.235
HUT78	29.688	25.225
NCI-H929	UNDETERMINED	25.228
ZR75I	UNDETERMINED	23.889
CAPAN2	UNDETERMINED	28.714
NCI-H441	UNDETERMINED	24.886
KG1	UNDETERMINED	25.835
TF1F	38.133	25.988
K562	36.400	26.160
BCP1	UNDETERMINED	25.860
THP1	34.678	24.615
HL-60	31.133	25.955

Figure 56B

C.

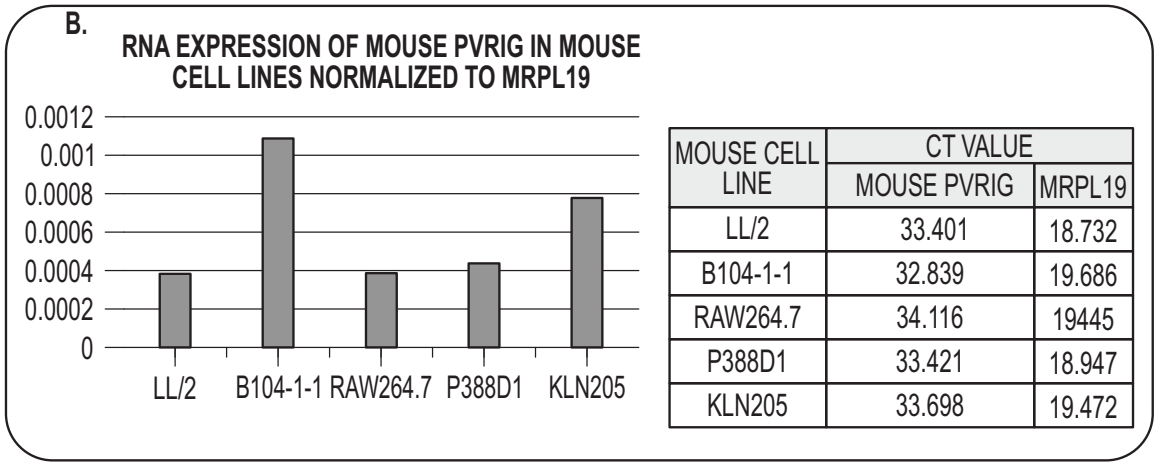
HUMAN CELL LINE	CT VALUE					
	HUMAN PVRIG	HTATA BOX	HRPL19	HPBGD	HSDHA	HHPRT1
DAN-G	39.92	30.14	27.4	27.4	26.59	27.99
NCI-H441	39.46	28.34	26.71	26.71	26.2	27.36
KG1	38.95	28.39	26.74	28.28	26.39	26.39
TF1F	39.22	29.25	27.61	33.74	36.25	36.25

Figure 56C



HUMAN CELL LINE	CT VALUE	
	MOUSE PVRIG	MRPL19
B16-F1	38.531	18.549
EL4	34.033	18.740
YAC1	36.058	19.646
P815	38.159	19.417
E.G7-OVA	38.219	19.477
SAI/N	31.389	18.789
A20	35.520	18.740
NIH/3T3	30.862	20.506
J774A.1	31.487	18.996
4T1	34.722	19.013
RENCA	31.237	19.632
CT-26	32.859	19.237

Figure 57A



MOUSE CELL LINE	CT VALUE	
	MOUSE PVRIG	MRPL19
LL/2	33.401	18.732
B104-1-1	32.839	19.686
RAW264.7	34.116	19445
P388D1	33.421	18.947
KLN205	33.698	19.472

Figure 57B

Figure 58

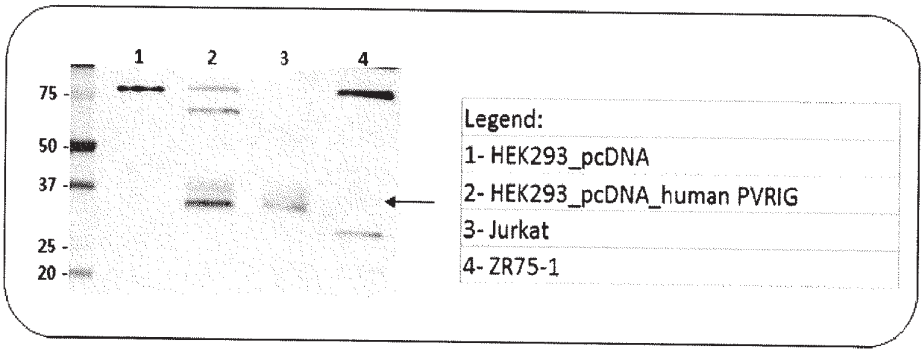
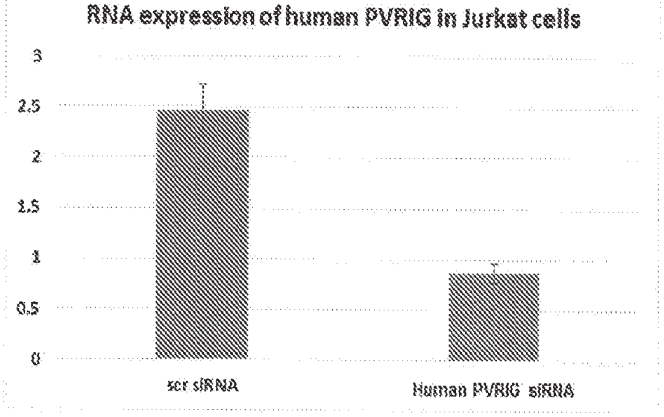

1
2
3
4
75 -
50 -
37 -
25 -
20 -
Legend:
1- HEK293_pcDNA
2- HEK293_pcDNA_human PVRIG
3- Jurkat
4- ZR75-1

Figure 59



Sample Name	Ct value		
	Human PVRIG	hHPRT1	hRPL19
Scr siRNA#1	30.622	21.608	21.924
Scr siRNA#2	30.526	21.953	21.915
Scr siRNA#3	30.820	22.327	22.156
hPVRIG siRNA#1	32.923	22.658	22.462
hPVRIG siRNA#2	32.678	22.859	22.542
hPVRIG siRNA#3	32.927	22.598	22.779

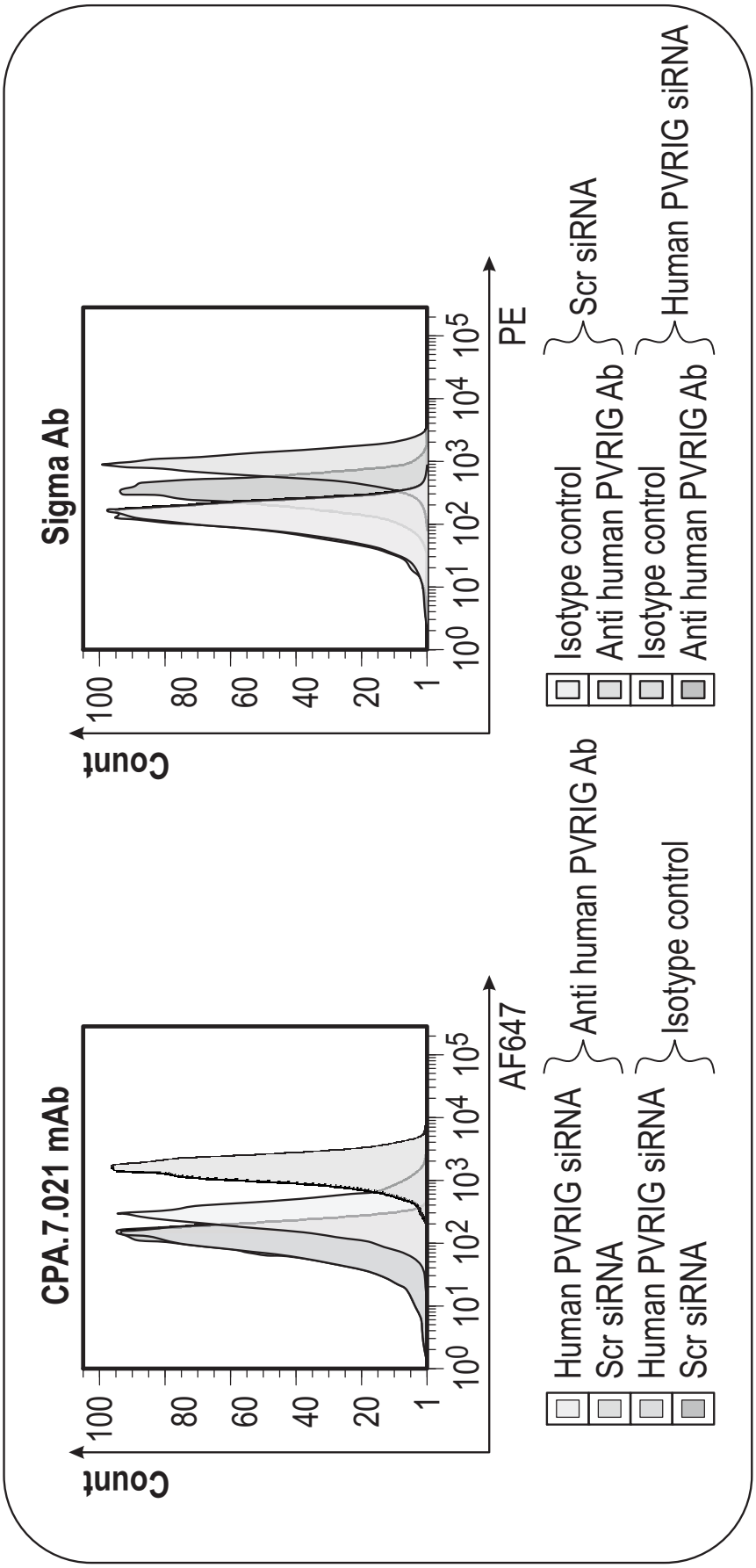

CPA.7.021 mAb
Sigma Ab
Count
AF647
PE
Human PVRIG siRNA
Scr siRNA
Human PVRIG siRNA
Scr siRNA
Anti human PVRIG Ab
Isotype control
Isotype control
Anti human PVRIG Ab
Scr siRNA
Human PVRIG siRNA

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	IIPIFGTA	1061	AREEVSSPYGMDV	1062	TGAVTSGHY	1063	DTG	1064	LLSYSGASWV	1065
CPA.7.002	GGTFSSSA	1066	IIPIYGIT	1067	ARDDTARRVRGVPYYYYA MDV	1068	QGIGNY	1069	SAS	1070	QQLKDYPIT	1071
CPA.7.003	GFSLSHFS	1072	FDPEEGGT	1073	ATGIWYSSGWPVDY	1074	QSLLDSSGYNY	1075	LGS	1076	MQALQTPIT	1077
CPA.7.004	GYTLTELS	1078	FDPEDGET	1079	ATVSRVRGVINYYYYMDV	1080	QSLLYRNGNNY	1081	LGS	1082	MQALQTPPT	1083
CPA.7.005	GGTFSSSA	1084	IIPIYGIT	1085	ARDDTARRVRGVPYYYYA MDV	1086	QSVDSS	1087	DAS	1088	QQYKDWPFT	1089
CPA.7.006	GGTFGTYA	1090	ITPISATI	1091	ARGFEYSDGLLDD	1092	QSLFYSDDGNTY	1093	RLS	1094	MQHMEFPLT	1095
CPA.7.007	GGSISSSSYY	1096	IYYSGST	1097	ARGAWELRLGDWFDP	1098	SSNIGAGYD	1099	GNN	1100	QSYDSSLSIVVV	1101
CPA.7.008	SGSISSTNW	1102	IYHSGST	1103	ARVGPAAIYY	1104	SNNVGYEG	1105	RNN	1106	SAWDSSLNAVV	1107
CPA.7.009	GYTLTELS	1108	FDPEDGET	1109	ATAKPGIAVAGQNYYYYM DV	1110	QSLLYRNGNNY	1111	LGS	1112	MQALQTPPT	1113
CPA.7.010	GFTFSSYA	1114	ISYDGSNK	1115	ASSPIGYSYGYWGGMDV	1116	SGIDVRTNK	1117	FQSDSDK	1118	LIWHTSGWV	1119
CPA.7.011	GYTLTELS	1120	FDPEDGET	1121	ATGPAAAGVGYYYMDV	1122	QSLLYRNGYNY	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	ATGGYSSGFNYYYYYMDV	1134	QSLLYRNGNNY	1135	LGS	1136	MQALQTPPT	1137
CPA.7.014	GYTLTELS	1138	FDPEDGET	1139	ATGVTTYYYYGMDV	1140	QSLLYSNGNNF	1141	LGS	1142	MQALQTPPT	1143
CPA.7.015	GFTFSSYG	1144	IRYDGSNK	1145	ARDLFDFWWDGMDV	1146	QSVSSMY	1147	GAS	1148	QQYVSSPMYT	1149

Figure 63B

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.7.016	GGTFSSSA	1150	IIPIYGIT	1151	ARDDTARRVRGVPYYYYYAMDV	1152	QSVSSY	1153	DAS	1154	QQYDDWPQT	1155
CPA.7.017	GGTFNNYG	1156	IIPLFGTT	1157	ARDRMAADGMAVFDY	1158	SSNIGRHF	1159	KND	1160	SSWDAALNGVV	1161
CPA.7.018	GYTLTELS	1162	FDPEDGET	1163	ATEVPMVRGARRYYYMDV	1164	QTLLYINENNY	1165	LGS	1166	MQGLQTPPT	1167
CPA.7.019	GGSISNSNYY	1168	IYYSGST	1169	ARGAWELSLGDWFDP	1170	SSNIGAGYD	1171	GNN	1172	QSYDSSLSVYVV	1173
CPA.7.020	GGTFSSSA	1174	IIPIYGIT	1175	ARDDTARRVRGVPYYYYYAMDV	1176	QNVYGE	1177	DTF	1178	QQRRDWPIT	1179
CPA.7.021	GFTFGTSS	1180	ISFDGTEI	1181	AKGSGNIYFYSGMDV	1182	QSISGW	1183	ETS	1184	QQYYSYPLT	1185
CPA.7.022	GYTLTELS	1186	FDPEDGET	1187	ATGVPAAIGVYYYYYYMDV	1188	QSLLYSNGYNY	1189	LGS	1190	MQALQSPVT	1191
CPA.7.023	GYTLTELS	1192	FDPEDGET	1193	ATDSRDGPAARGGYYYYMDV	1194	QSLLYINGYNY	1195	LGS	1196	MQALQTPPT	1197
CPA.7.024	GGTFSSYA	1198	IIPIFGTA	1199	ARDAYYYDSSGYYNPDAFDI	1200	QSLLHSNGYNY	1201	LGS	1202	MQGLQTPRT	1203
CPA.7.025	GFSLTSGGMS	1204	IDWNDDK	1205	ARIRGMTWGFDS	1206	QSVSSSY	1207	GAS	1208	QQYGTTPFA	1209
CPA.7.026	GYTFTAYY	1210	INPNSGGT	1211	ARDGAFYYGSENYYNAGWFDP	1212	QSLLSGNGYNY	1213	LGS	1214	MQALKSPLT	1215
CPA.7.027	GYTFTNYY	1216	INPSGGIT	1217	ARAGLGYNWNYAPSGMDV	1218	SSDVGGYNY	1219	EVS	1220	SSYAGSNNLV	1221
CPA.7.028	GGSISSSSYY	1222	IYYSGST	1223	ARGAWELRLGDWFDP	1224	SSNIGAGYD	1225	GYS	1226	QSYDSSLSVYVV	1227
CPA.7.029	GFTFDDYA	1228	ISWNSGSI	1229	AKDVNRILVAGMVDY	1230	QSLLHSNGYNY	1231	LGS	1232	MQGLQTPIT	1233
CPA.7.030	RFTFEDYA	1234	ISWKSGGI	1235	VKDPTLVATDRAFNI	1236	QSLLHSNGYNY	1237	LGS	1238	MQYLQTPDT	1239

Figure 63C

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	GGTFSSSA	1240	IIPIYGIT	1241	ARDDTARRVRGVPYYYYYAMDV	1242	QSLLDSDDGNIH	1243	TLS	1244	MQRKEFPLT	1245
CPA.7.032	GFTFSSYG	1246	ISYDGSNK	1247	AKEDRLRFLEWLFYGMDV	1248	HDIYTY	1249	DAS	1250	QQYDNHPPEVT	1251
CPA.7.033	GGTFSSSA	1252	IIPIYGIT	1253	ARDDTARRVRGVPYYYYYAMDV	1254	QDIDDD	1255	EAS	1256	LQHDNLPLT	1257
CPA.7.034	GYTLTELS	1258	FDPEDGET	1259	ATEDPGPVAGPYYYYGMDV	1260	QSLLYINGYHY	1261	LGS	1262	MQALQTPPT	1263
CPA.7.035	GYMFTNYP	1264	INAGTGNT	1265	AREGMFYYGLESYYKGGWFDP	1266	QSLLHRNGYNY	1267	LAS	1268	MQALQTPLT	1269
CPA.7.036	GGTFSSSA	1270	IIPIYGIT	1271	ARDDTARRVRGVPYYYYYAMDV	1272	QSLLDSDDGNTY	1273	TLS	1274	MQRLQFPLT	1275
CPA.7.037	TYTFTTYY	1276	IYPSGGNT	1277	VRDQNYYYSAMDV	1278	QDIRNY	1279	DAS	1280	QQFENLPIT	1281
CPA.7.038	GGTFSSSA	1282	IIPIYGIT	1283	ARDDTARRVRGVPYYYYYAMDV	1284	RDISDS	1285	DAS	1286	HQYDNLPLT	1287
CPA.7.039	GFNFRGYA	1288	ISGSGGTT	1289	AQSYAQIGYGGHIDH	1290	SGIDVATYM	1291	YKSDSDK	1292	LIWHGSHYV	1293
CPA.7.040	GYTLTELS	1294	FDPEDGET	1295	ATGVPAAIGVYYYYYYMDV	1296	QSLLYRNGYNY	1297	WGS	1298	MQAVQNPPT	1299
CPA.7.041	GGTFSSSA	1300	IIPIYGIT	1301	ARDDTARRVRGVPYYYYYAMDV	1302	QNIDSS	1303	YAS	1304	HQSSSLPLT	1305
CPA.7.042	GGTFSSSA	1306	IIPIYGIT	1307	ARDDTARRVRGVPYYYYYAMDV	1308	QSVYNNY	1309	DAS	1310	QQYNSWPPYT	1311
CPA.7.043	GGTFSSYA	1312	IIPIFGTA	1313	ARDAYYYDSSGYYNPDAFDI	1314	QSLLYSNGYNY	1315	LGS	1316	MQARQTPYT	1317
CPA.7.044	GGTFSSSA	1318	IIPIYGIT	1319	ARDDTARRVRGVPYYYYYAMDV	1320	ESVTTF	1321	DAS	1322	HQHTNWPLT	1323
CPA.7.045	GYTLTELS	1324	FDPEDGET	1325	ATEVGYCSGGSCYISYYYGMDV	1326	QSLLYRNGHNF	1327	LGS	1328	MQALQTPPT	1329
CPA.7.046	GGTFSSSA	1330	IIPIYGIT	1331	ARDDTARRVRGVPYYYYYAMDV	1332	QTMNNY	1333	DAS	1334	QQYGDWLPIT	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	IIPIYGIT	1343	ARDDTARRVRGVPYYYYAMDV	1344	RSLLDSDDGNTH	1345	SLS	1346	MQRKEFPLT	1347
CPA.7.050	GGTFSSYA	1348	IIPIFGTA	1349	ARGPWYYDSSGYSSYAYYMDV	1350	QSLLHSDGYNY	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

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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

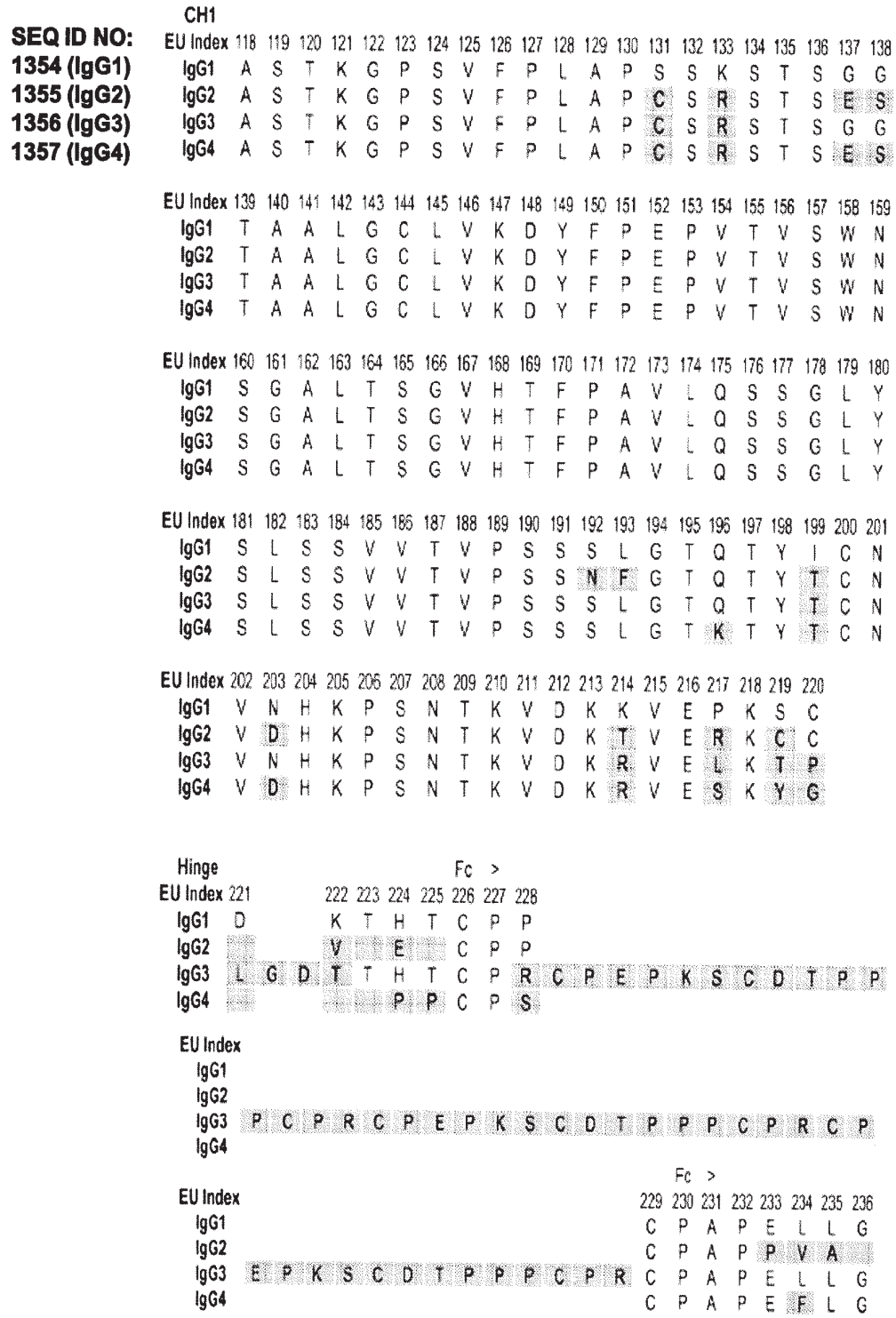

SEQ ID NO:
1354 (IgG1)
1355 (IgG2)
1356 (IgG3)
1357 (IgG4)
CH1
EU Index 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138
IgG1 A S T K G P S V F P L A P S S K S T S G G
IgG2 A S T K G P S V F P L A P C S R S T S E S
IgG3 A S T K G P S V F P L A P C S R S T S G G
IgG4 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
Fc >
EU Index 221 222 223 224 225 226 227 228
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 P
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
Fc >
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 E P K S C D T P P P C P R 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 EVWVQVRMEATELSSFTIRCGF (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

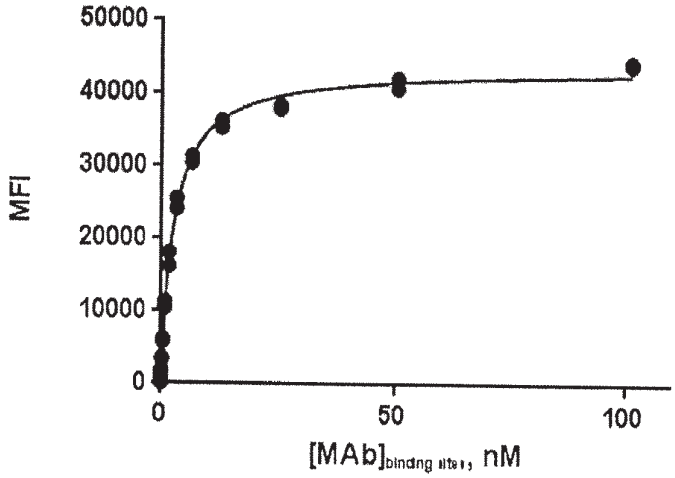

50000
40000
30000
20000
10000
0
MFI
0
50
100
[MAb]binding site, nM

Figure 69A

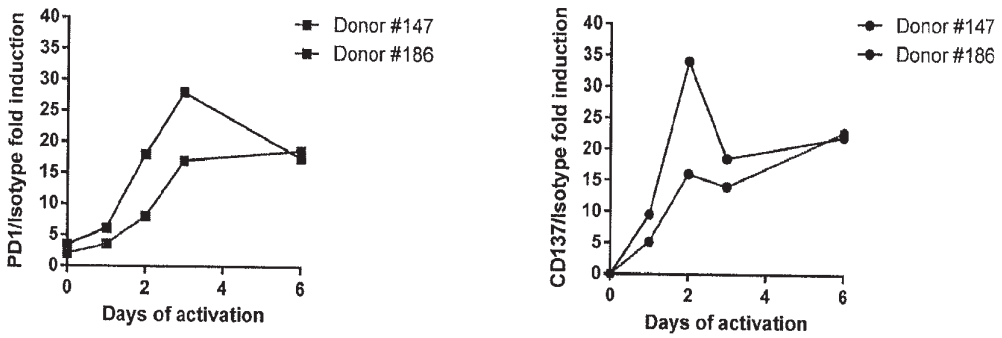


Figure 69B

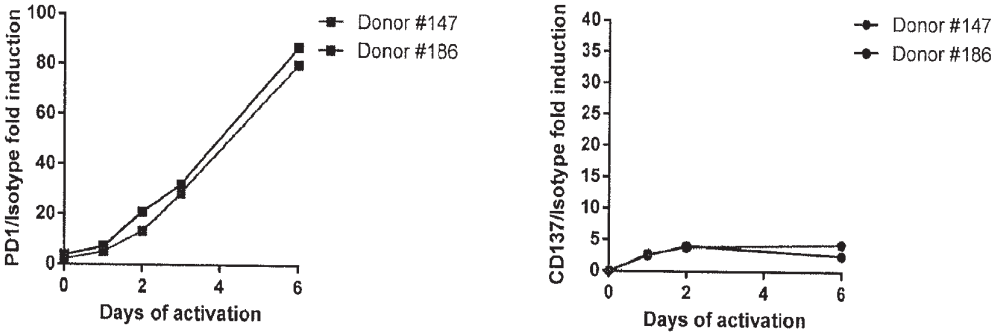
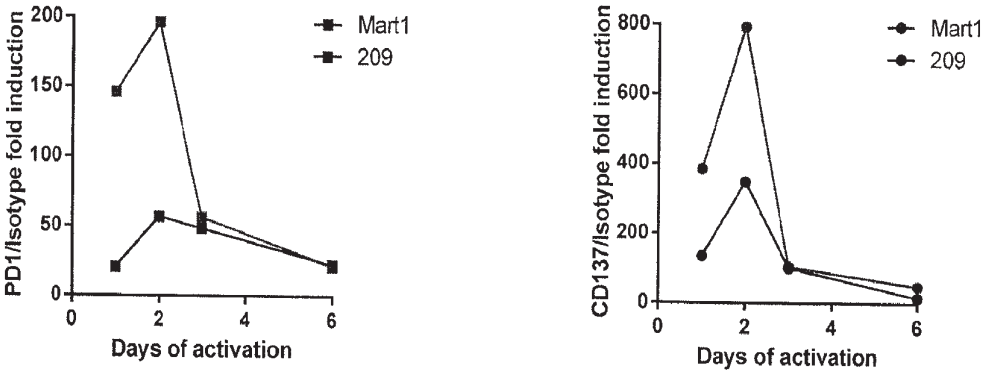


Figure 69C



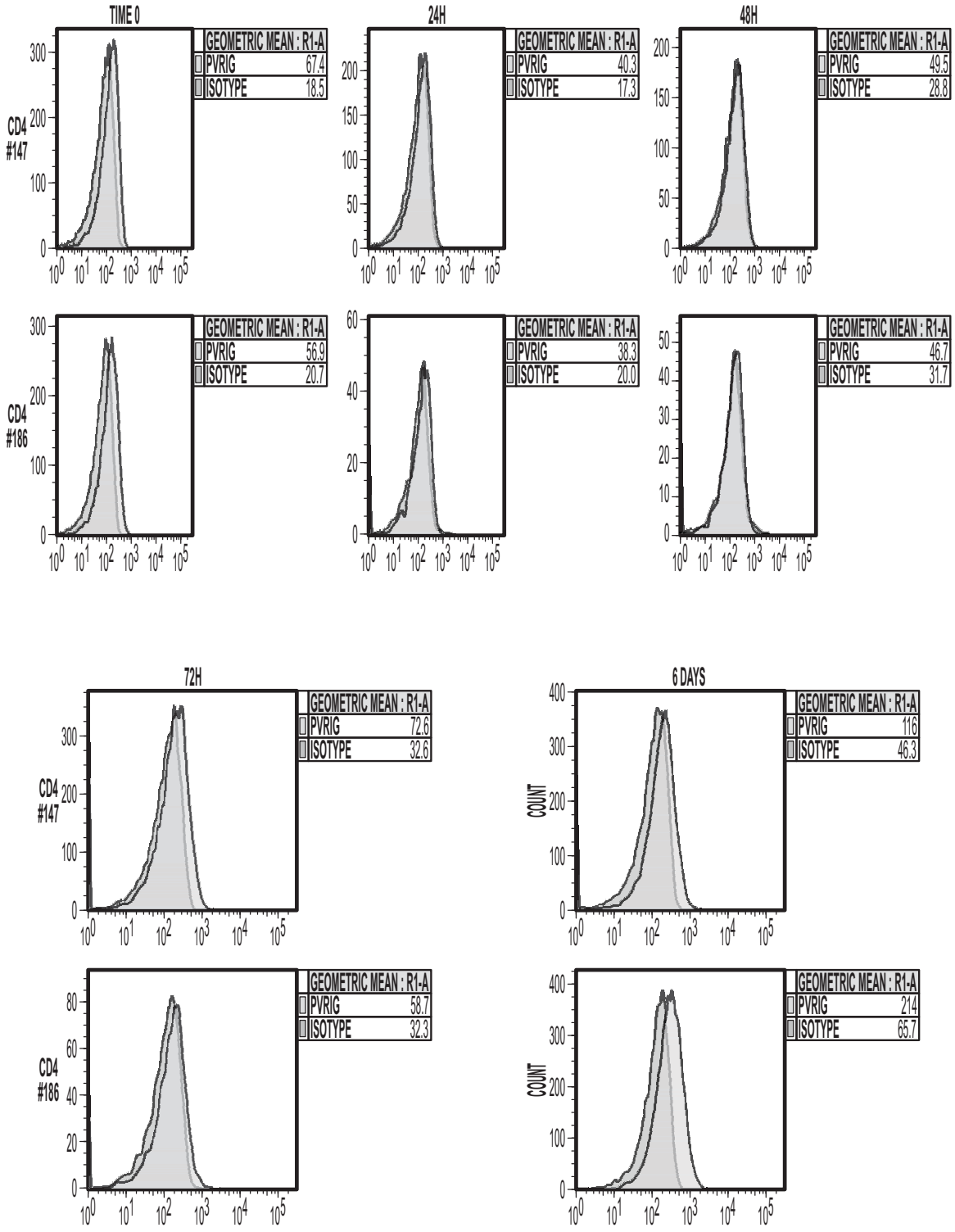

TIME 0
24H
48H
72H
6 DAYS
CD4 #147
CD4 #186
COUNT
GEOMETRIC MEAN : R1-A
PVRIG 67.4
ISOTYPE 18.5
PVRIG 40.3
ISOTYPE 17.3
PVRIG 49.5
ISOTYPE 28.8
PVRIG 56.9
ISOTYPE 20.7
PVRIG 38.3
ISOTYPE 20.0
PVRIG 46.7
ISOTYPE 31.7
PVRIG 72.6
ISOTYPE 32.6
PVRIG 116
ISOTYPE 46.3
PVRIG 58.7
ISOTYPE 32.3
PVRIG 214
ISOTYPE 65.7

FIG. 70A

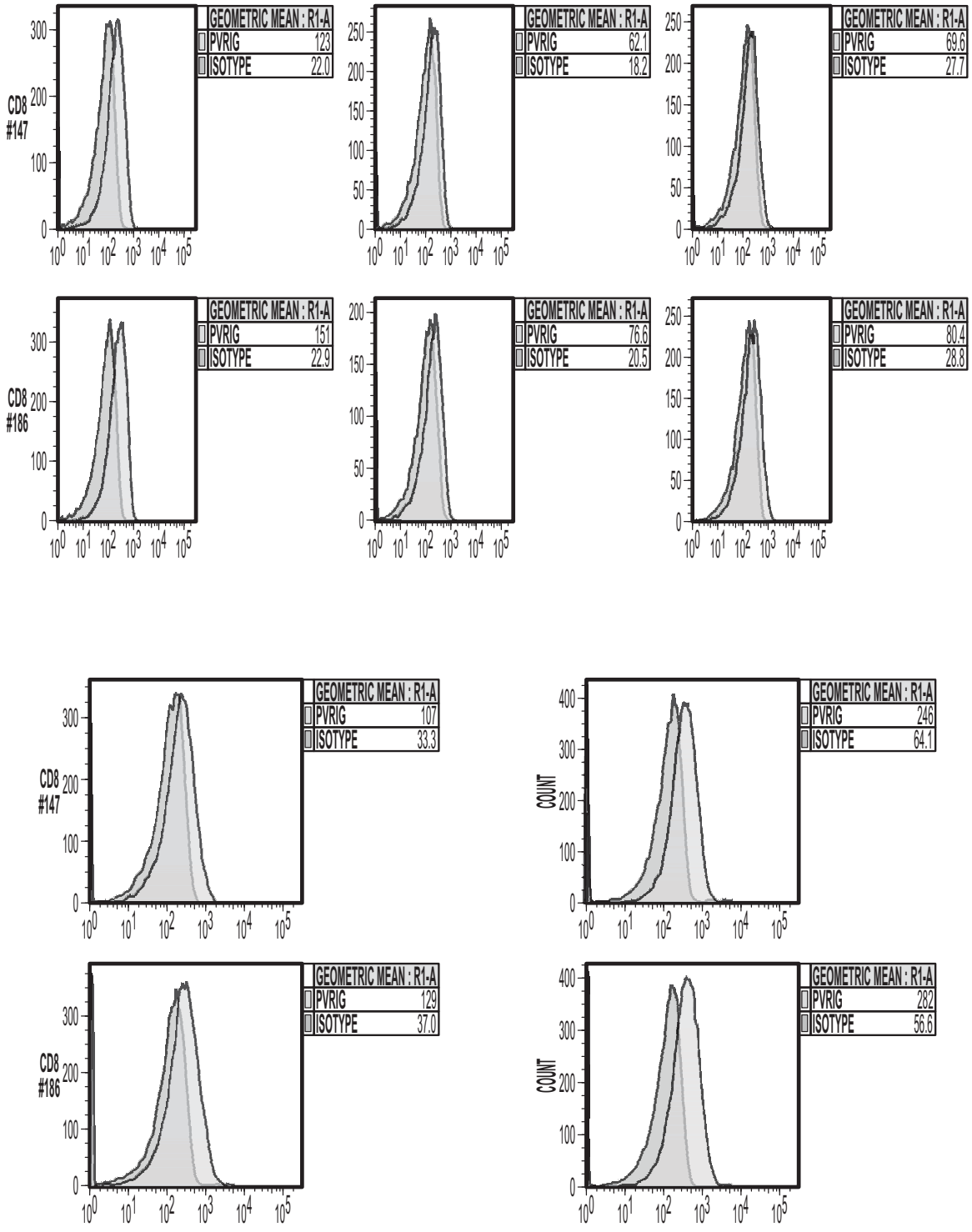
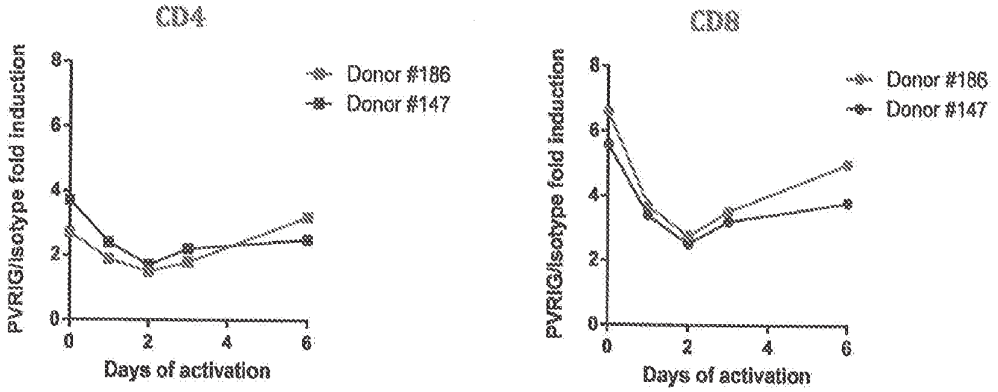

CD8 #147
CD8 #186
COUNT
GEOMETRIC MEAN : R1-A
PVRIG 123
ISOTYPE 22.0
PVRIG 62.1
ISOTYPE 18.2
PVRIG 69.6
ISOTYPE 27.7
PVRIG 151
ISOTYPE 22.9
PVRIG 76.6
ISOTYPE 20.5
PVRIG 80.4
ISOTYPE 28.8
PVRIG 107
ISOTYPE 33.3
PVRIG 246
ISOTYPE 64.1
PVRIG 129
ISOTYPE 37.0
PVRIG 282
ISOTYPE 56.6

FIG. 70B

Figure 70C


CD4
PVRIG/isotype fold induction
Days of activation
Donor #186
Donor #147
CD8
PVRIG/isotype fold induction
Days of activation
Donor #186
Donor #147

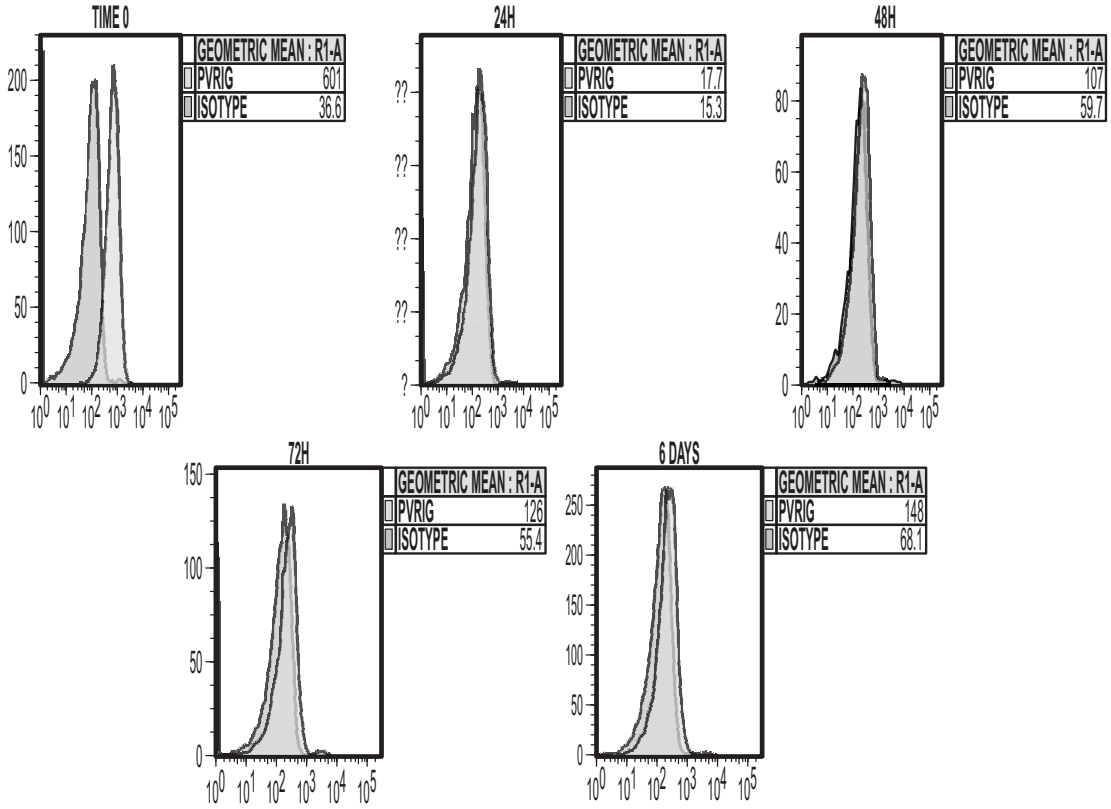


FIG. 71A

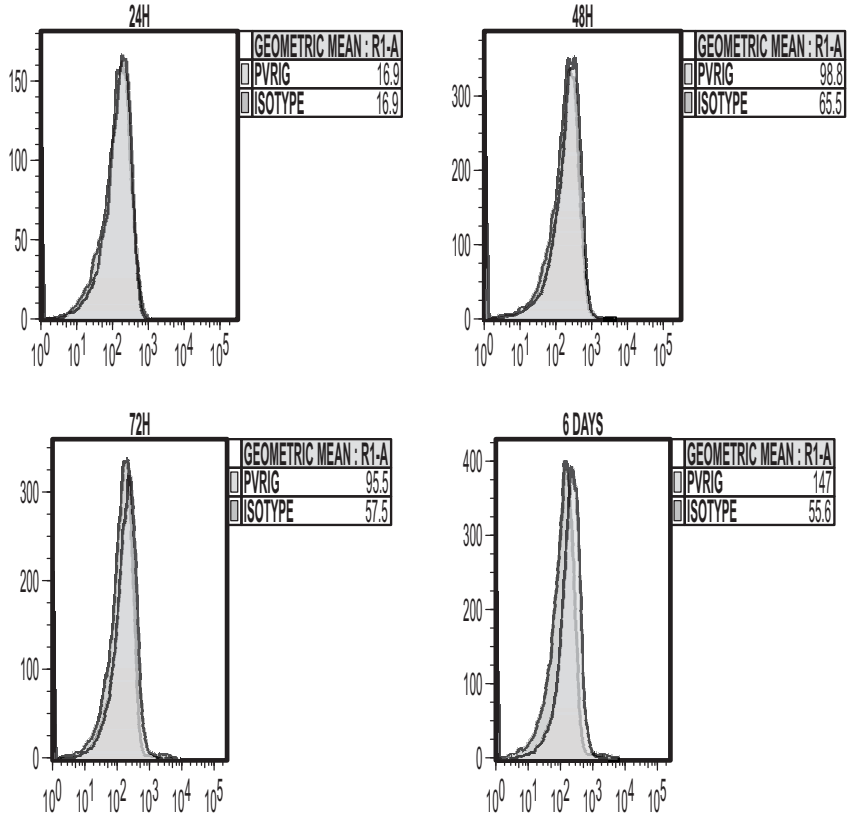


FIG. 71B

Figure 71C

C

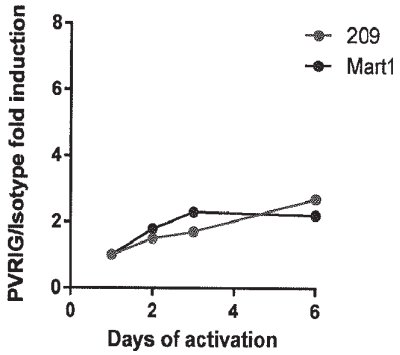
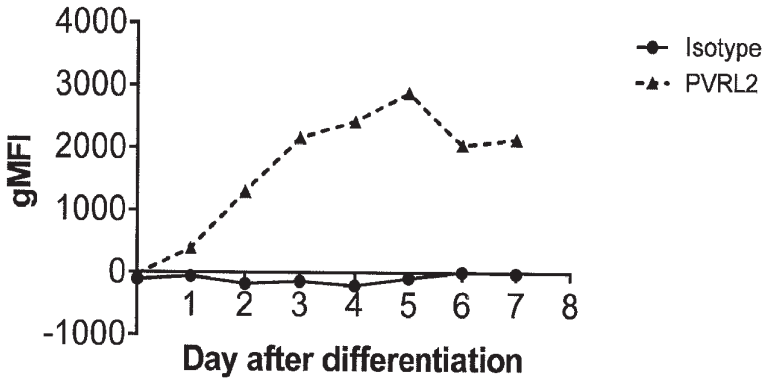

PVRIG/Isotype fold induction
8
6
4
2
0
0
2
4
6
Days of activation
209
Mart1

Figure 72


4000
3000
2000
1000
0
-1000
gMFI
1 2 3 4 5 6 7 8
Day after differentiation
Isotype
PVRL2

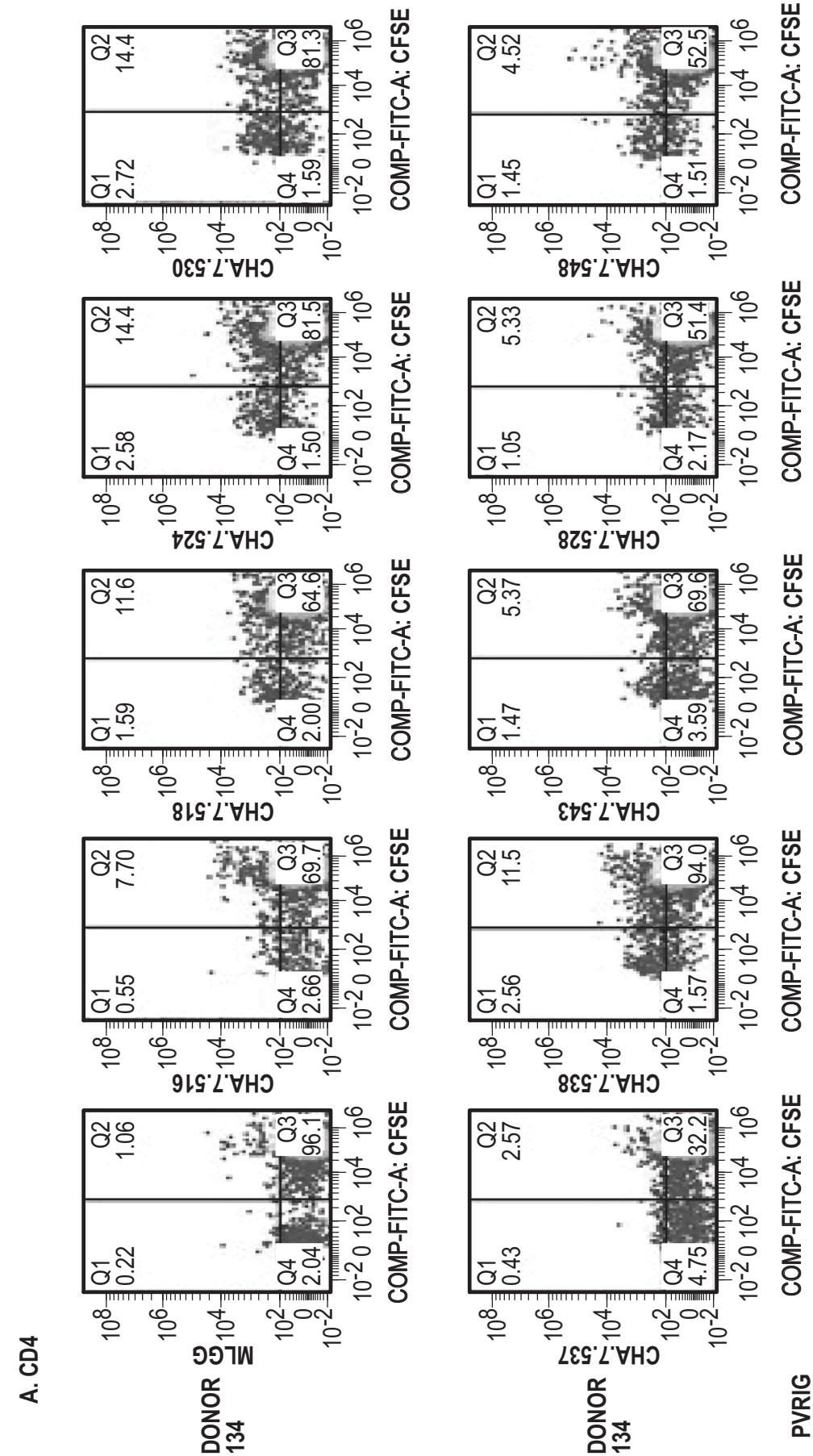

A. CD4
DONOR 134
MLGG
CHA.7.516
CHA.7.518
CHA.7.524
CHA.7.530
DONOR 134
CHA.7.537
CHA.7.538
CHA.7.543
CHA.7.548
CHA.7.528
Q1 0.22
Q2 1.06
Q4 2.04
Q3 96.1
Q1 0.55
Q2 7.70
Q4 2.66
Q3 69.7
Q1 1.59
Q2 11.6
Q4 2.00
Q3 64.6
Q1 2.58
Q2 14.4
Q4 1.50
Q3 81.5
Q1 2.72
Q2 14.4
Q4 1.59
Q3 81.3
Q1 0.43
Q2 2.57
Q4 4.75
Q3 32.2
Q1 2.56
Q2 11.5
Q4 1.57
Q3 94.0
Q1 1.47
Q2 5.37
Q4 3.59
Q3 69.6
Q1 1.05
Q2 5.33
Q4 2.17
Q3 51.4
Q1 1.45
Q2 4.52
Q4 1.51
Q3 52.5
COMP-FITC-A: CFSE
PVRIG
CFSE

Figure 73A-1

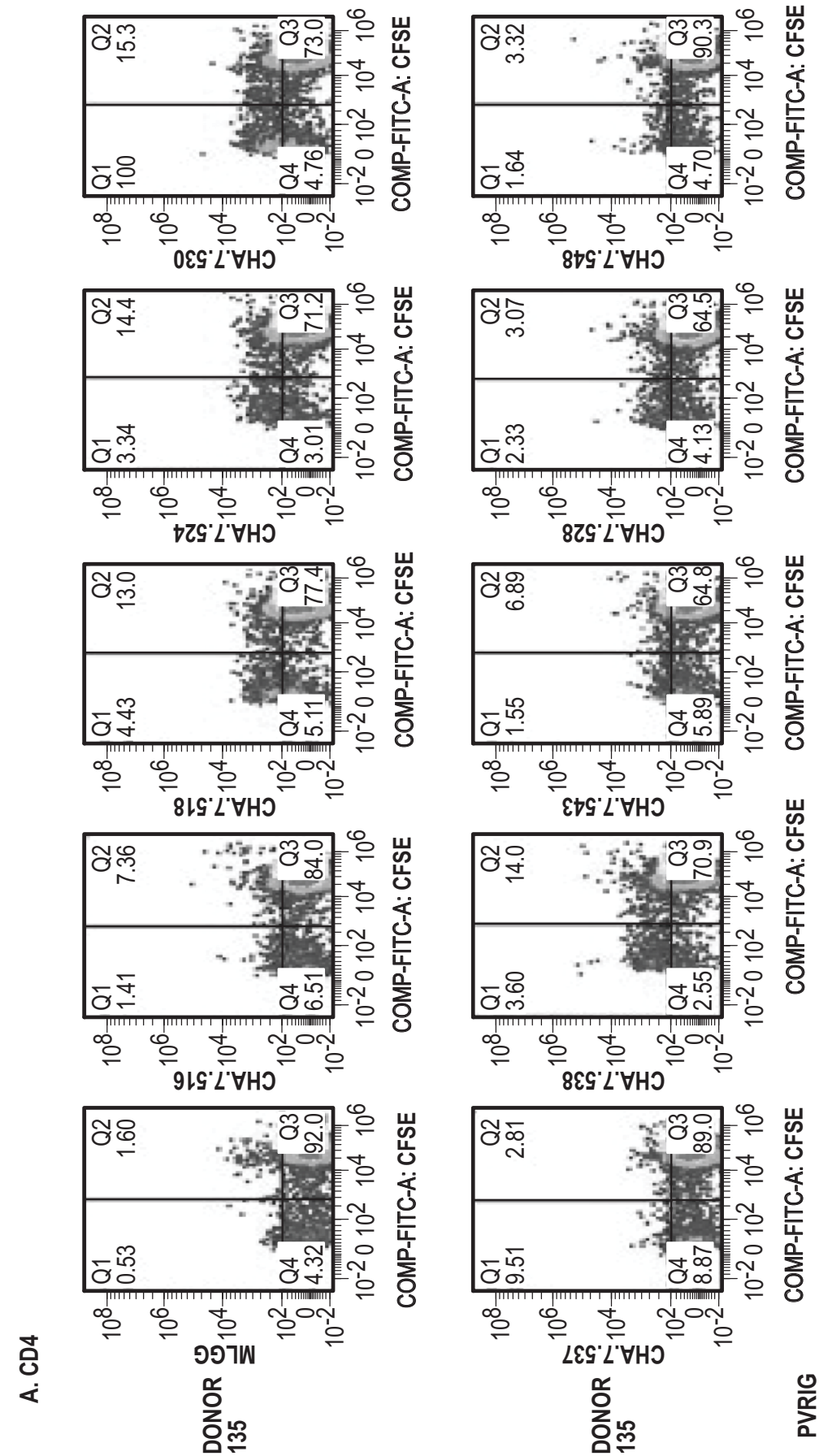

A. CD4
DONOR 135
MLGG
CHA.7.537
CHA.7.538
CHA.7.543
CHA.7.548
CHA.7.516
CHA.7.518
CHA.7.524
CHA.7.528
CHA.7.530
Q1 0.53
Q2 1.60
Q4 4.32
Q3 92.0
Q1 9.51
Q2 2.81
Q4 8.87
Q3 89.0
Q1 1.41
Q2 7.36
Q4 6.51
Q3 84.0
Q1 3.60
Q2 14.0
Q4 2.55
Q3 70.9
Q1 4.43
Q2 13.0
Q4 5.11
Q3 77.4
Q1 1.55
Q2 6.89
Q4 5.89
Q3 64.8
Q1 3.34
Q2 14.4
Q4 3.01
Q3 71.2
Q1 2.33
Q2 3.07
Q4 4.13
Q3 64.5
Q1 100
Q2 15.3
Q4 4.76
Q3 73.0
Q1 1.64
Q2 3.32
Q4 4.70
Q3 90.3
COMP-FITC-A: CFSE
PVRIG
CFSE

Figure 73A-2

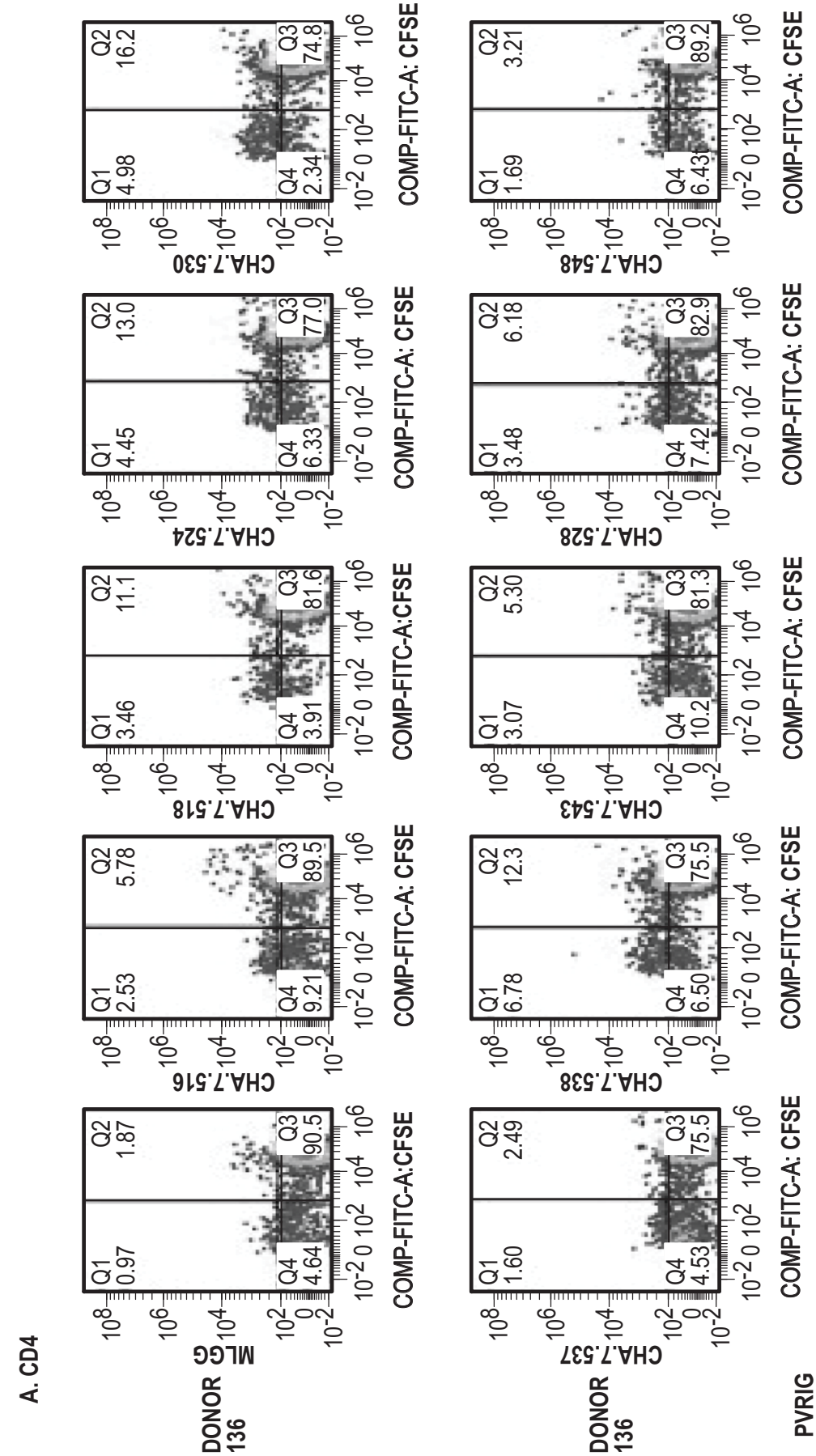

A. CD4
DONOR 136
MLGG
CHA.7.516
CHA.7.518
CHA.7.524
CHA.7.530
DONOR 136
CHA.7.537
CHA.7.538
CHA.7.543
CHA.7.528
CHA.7.548
Q1 0.97
Q2 1.87
Q4 4.64
Q3 90.5
Q1 2.53
Q2 5.78
Q4 9.21
Q3 89.5
Q1 3.46
Q2 11.1
Q4 3.91
Q3 81.6
Q1 4.45
Q2 13.0
Q4 6.33
Q3 77.0
Q1 4.98
Q2 16.2
Q4 2.34
Q3 74.8
Q1 1.60
Q2 2.49
Q4 4.53
Q3 75.5
Q1 6.78
Q2 12.3
Q4 6.50
Q3 75.5
Q1 3.07
Q2 5.30
Q4 10.2
Q3 81.3
Q1 3.48
Q2 6.18
Q4 7.42
Q3 82.9
Q1 1.69
Q2 3.21
Q4 6.43
Q3 89.2
COMP-FITC-A:CFSE
COMP-FITC-A: CFSE
PVRIG
CFSE

Figure 73A-3

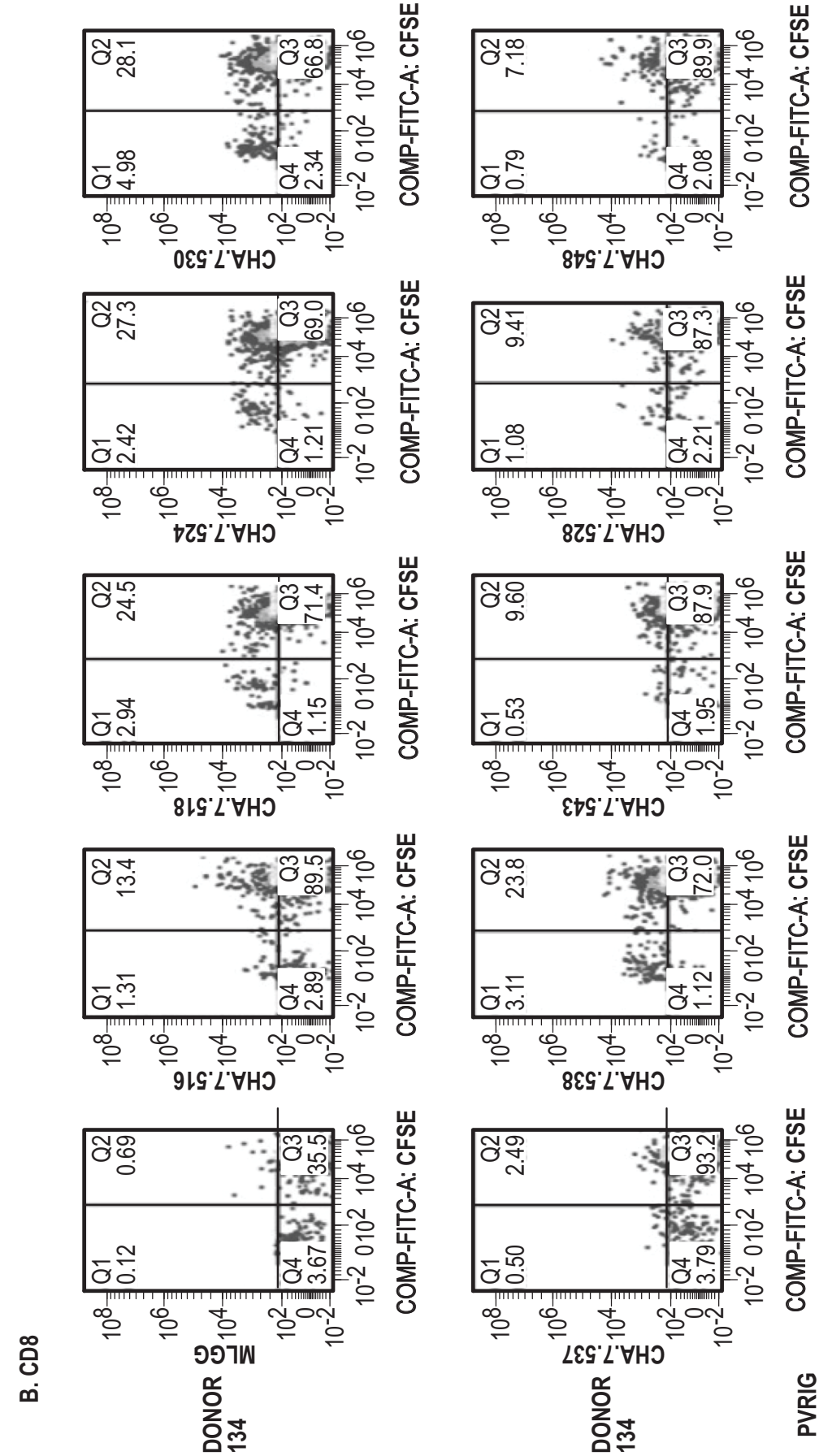

B. CD8
DONOR 134
MLGG
CHA.7.516
CHA.7.518
CHA.7.524
CHA.7.530
DONOR 134
CHA.7.537
CHA.7.538
CHA.7.543
CHA.7.528
CHA.7.548
Q1 0.12
Q2 0.69
Q4 3.67
Q3 35.5
Q1 1.31
Q2 13.4
Q4 2.89
Q3 89.5
Q1 2.94
Q2 24.5
Q4 1.15
Q3 71.4
Q1 2.42
Q2 27.3
Q4 1.21
Q3 69.0
Q1 4.98
Q2 28.1
Q4 2.34
Q3 66.8
Q1 0.50
Q2 2.49
Q4 3.79
Q3 93.2
Q1 3.11
Q2 23.8
Q4 1.12
Q3 72.0
Q1 0.53
Q2 9.60
Q4 1.95
Q3 87.9
Q1 1.08
Q2 9.41
Q4 2.21
Q3 87.3
Q1 0.79
Q2 7.18
Q4 2.08
Q3 89.9
COMP-FITC-A: CFSE
PVRIG
CFSE

Figure 73B-1

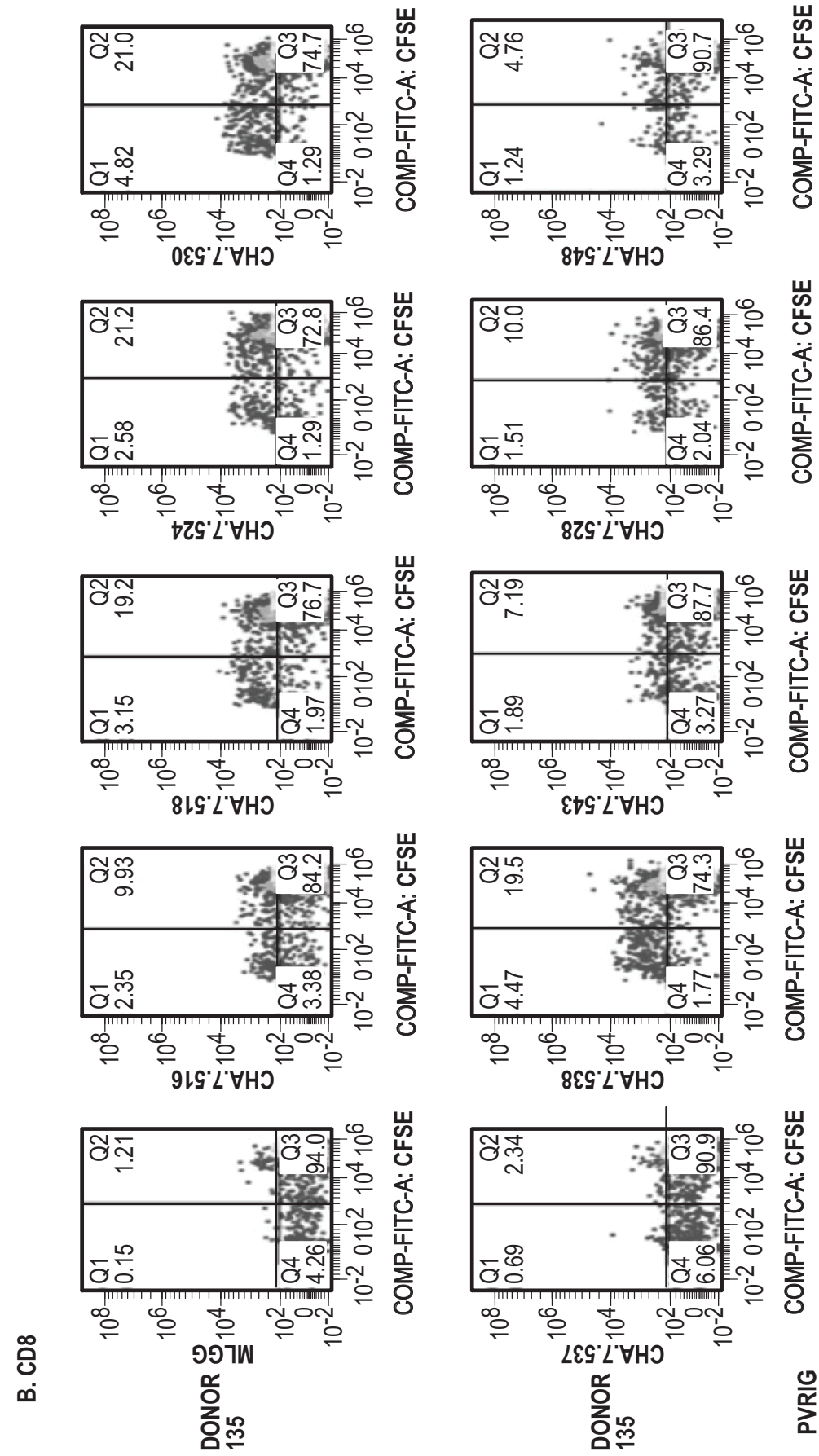

B. CD8
DONOR 135
MLGG
CHA.7.516
CHA.7.518
CHA.7.524
CHA.7.530
DONOR 135
CHA.7.537
CHA.7.538
CHA.7.543
CHA.7.548
CHA.7.528
Q1 0.15
Q2 1.21
Q4 4.26
Q3 94.0
Q1 2.35
Q2 9.93
Q4 3.38
Q3 84.2
Q1 3.15
Q2 19.2
Q4 1.97
Q3 76.7
Q1 2.58
Q2 21.2
Q4 1.29
Q3 72.8
Q1 4.82
Q2 21.0
Q4 1.29
Q3 74.7
Q1 0.69
Q2 2.34
Q4 6.06
Q3 90.9
Q1 4.47
Q2 19.5
Q4 1.77
Q3 74.3
Q1 1.89
Q2 7.19
Q4 3.27
Q3 87.7
Q1 1.51
Q2 10.0
Q4 2.04
Q3 86.4
Q1 1.24
Q2 4.76
Q4 3.29
Q3 90.7
COMP-FITC-A: CFSE
PVRIG
CFSE

Figure 73B-2

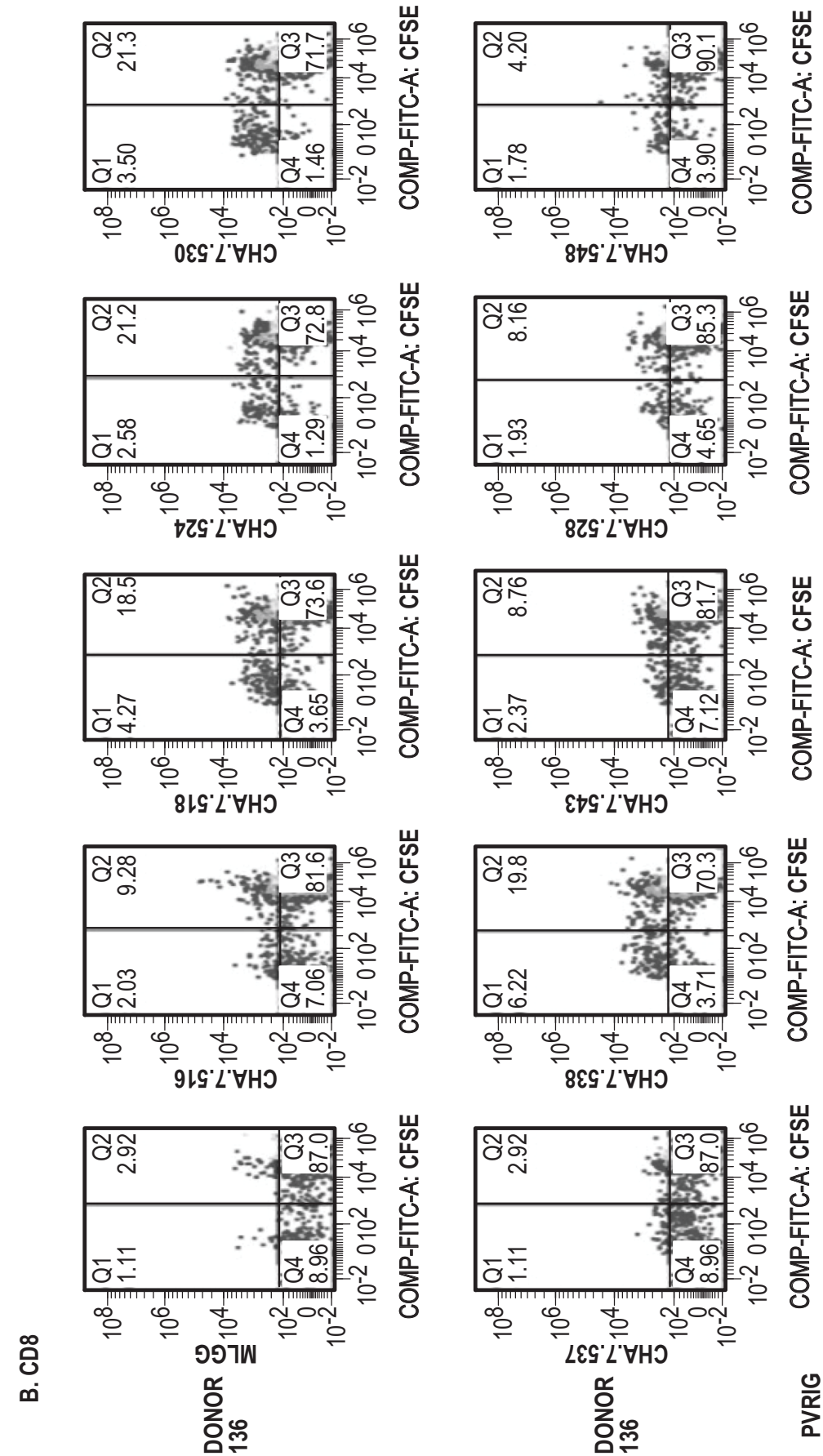

B. CD8
DONOR 136
MLGG
CHA.7.516
CHA.7.518
CHA.7.524
CHA.7.530
DONOR 136
CHA.7.537
CHA.7.538
CHA.7.543
CHA.7.528
CHA.7.548
Q1 1.11
Q2 2.92
Q4 8.96
Q3 87.0
Q1 2.03
Q2 9.28
Q4 7.06
Q3 81.6
Q1 4.27
Q2 18.5
Q4 3.65
Q3 73.6
Q1 2.58
Q2 21.2
Q4 1.29
Q3 72.8
Q1 3.50
Q2 21.3
Q4 1.46
Q3 71.7
Q1 1.11
Q2 2.92
Q4 8.96
Q3 87.0
Q1 6.22
Q2 19.8
Q4 3.71
Q3 70.3
Q1 2.37
Q2 8.76
Q4 7.12
Q3 81.7
Q1 1.93
Q2 8.16
Q4 4.65
Q3 85.3
Q1 1.78
Q2 4.20
Q4 3.90
Q3 90.1
COMP-FITC-A: CFSE
PVRIG
CFSE

Figure 73B-3

Figure 74A

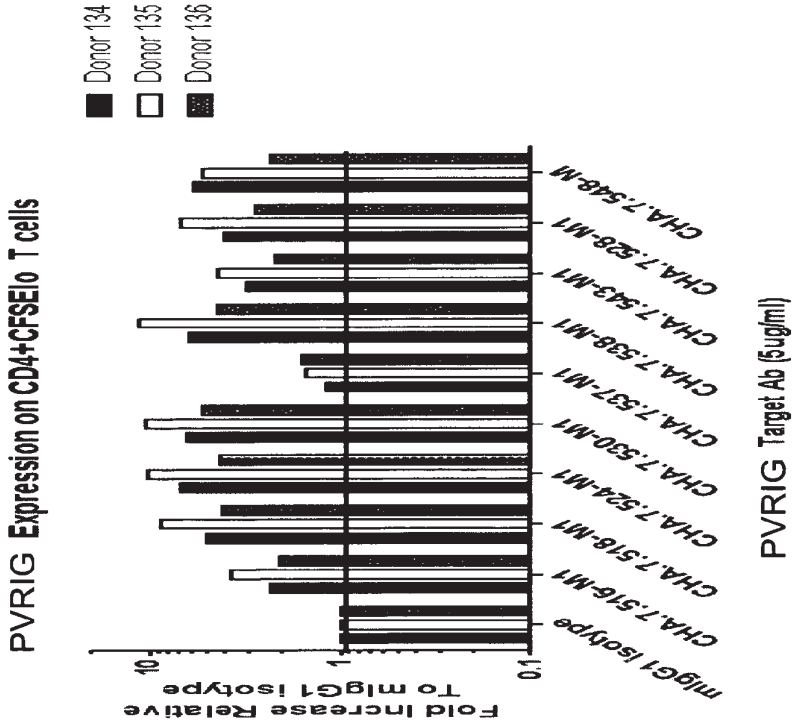


Figure 74B

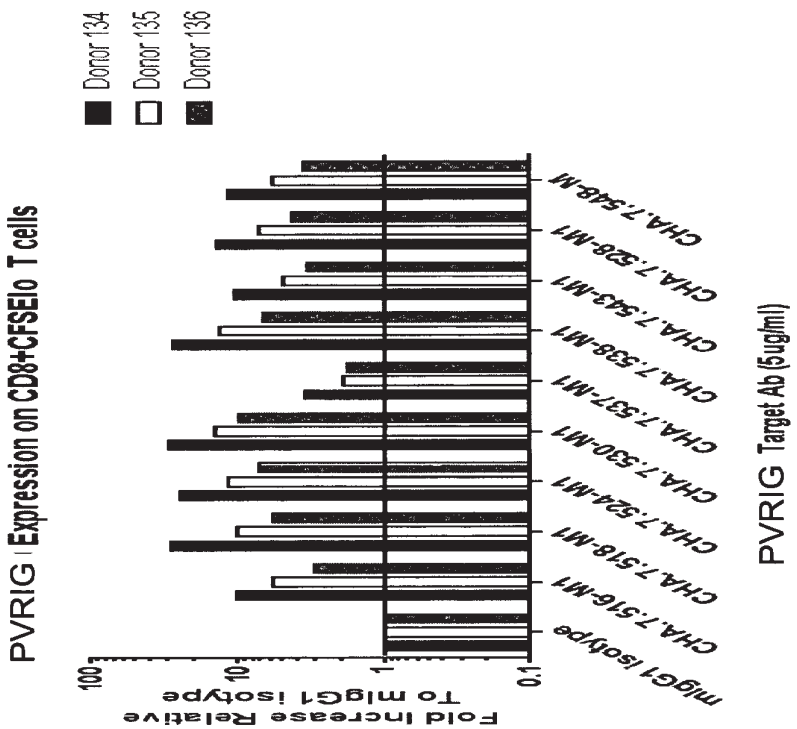


Figure 75B

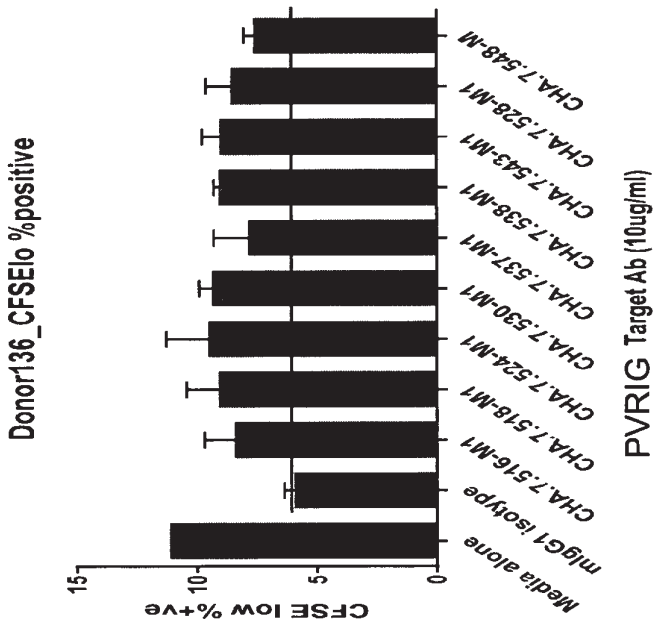


Figure 75A

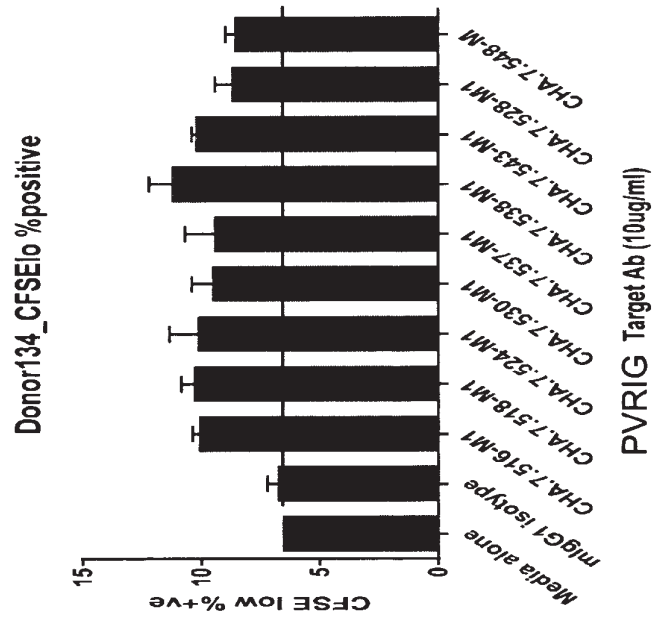


Figure 76

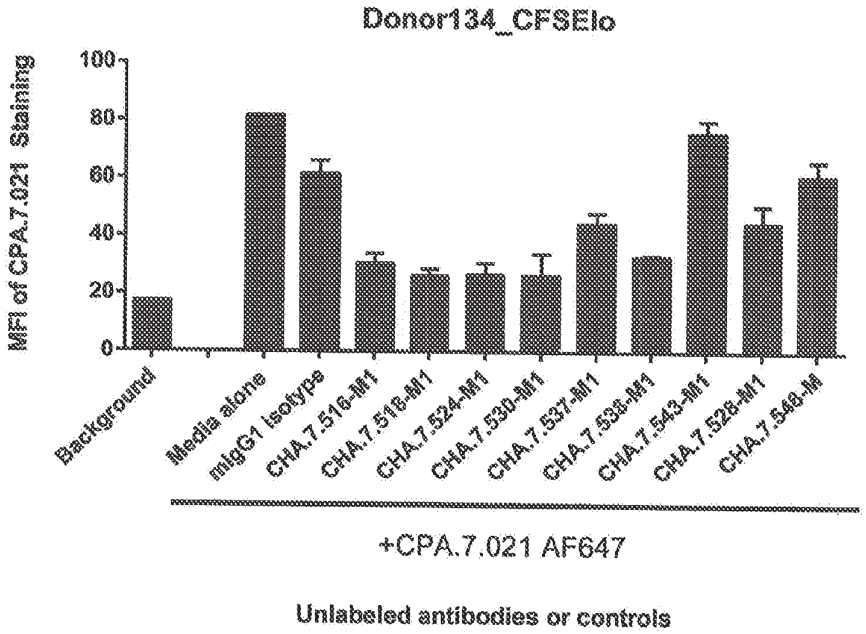

Donor134_CFSElo
MFI of CPA.7.021 Staining
100
80
60
40
20
0
Background
Media alone
mIgG1 isotype
CHA.7.516-M1
CHA.7.518-M1
CHA.7.524-M1
CHA.7.530-M1
CHA.7.537-M1
CHA.7.538-M1
CHA.7.543-M1
CHA.7.525-M1
CHA.7.546-M
+CPA.7.021 AF647
Unlabeled antibodies or controls

Figure 77

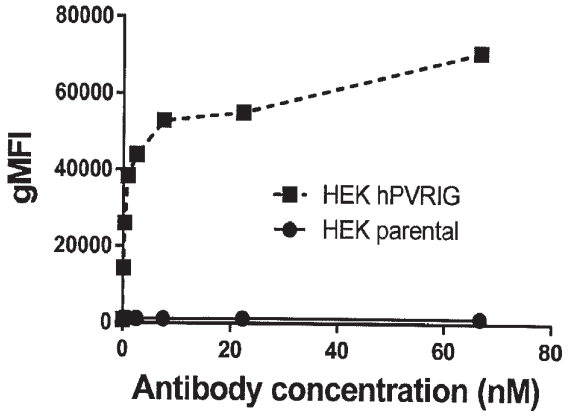

80000
60000
40000
20000
0
gMFI
HEK hPVRIG
HEK parental
0
20
40
60
80
Antibody concentration (nM)

Figure 78

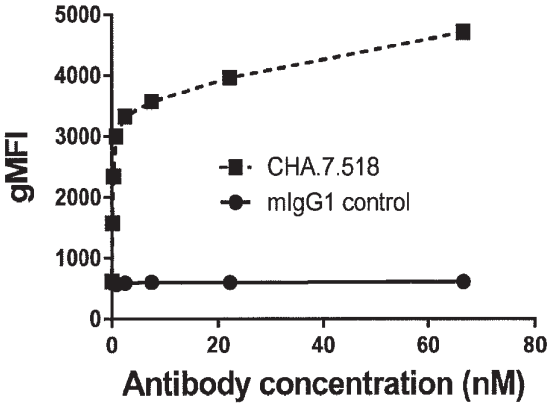

5000
4000
3000
2000
1000
0
gMFI
CHA.7.518
mIgG1 control
0
20
40
60
80
Antibody concentration (nM)

Figure 79A

Antibody (mIgG)	EC_{50} (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)	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}

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

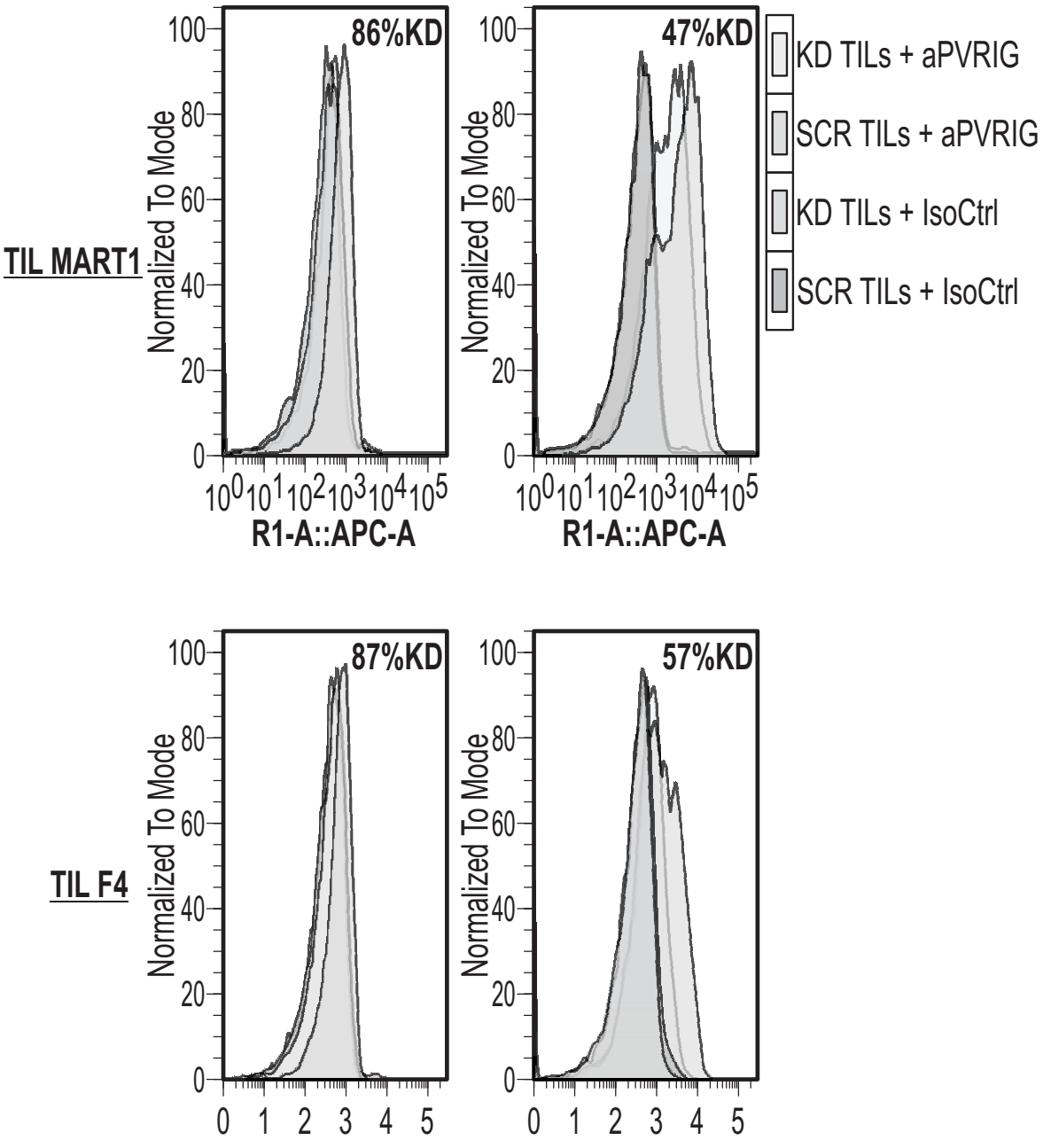

TIL MART1
TIL F4
86%KD
47%KD
87%KD
57%KD
Normalized To Mode
R1-A::APC-A
KD TILs + aPVRIG
SCR TILs + aPVRIG
KD TILs + IsoCtrl
SCR TILs + IsoCtrl

FIG. 82

FIGURE 83A

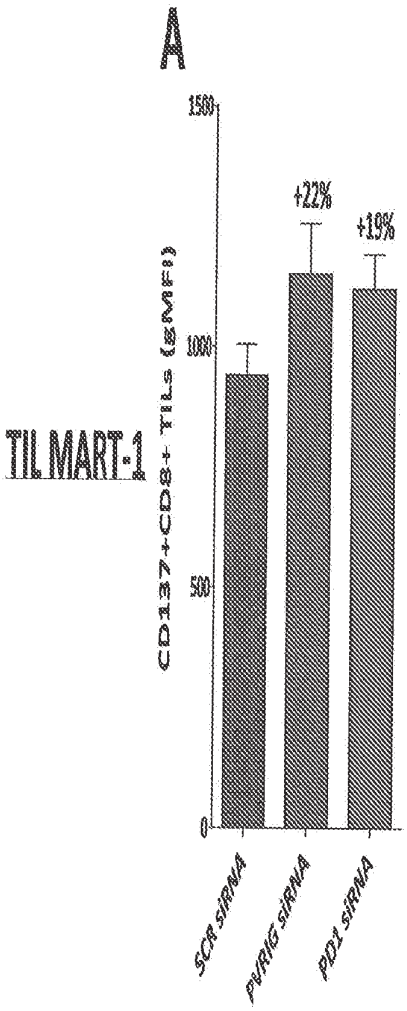


FIGURE 83B

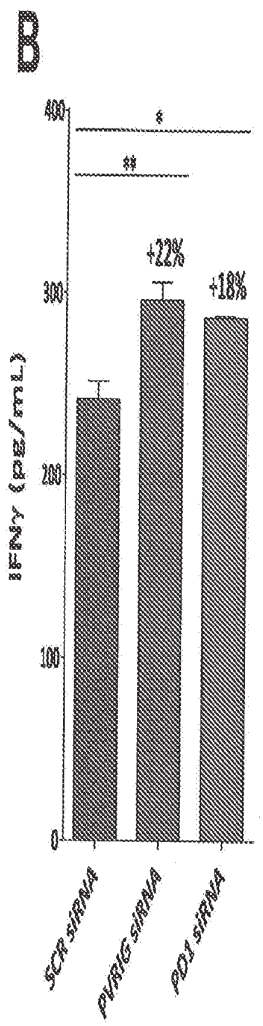
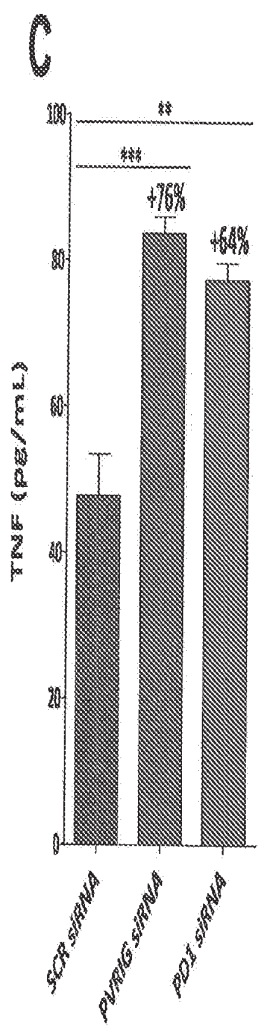


FIGURE 83C



TIL F4

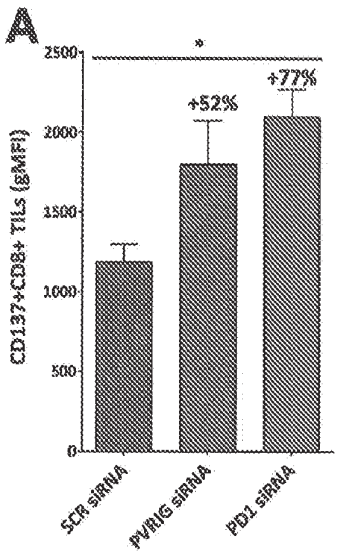


FIGURE 84A

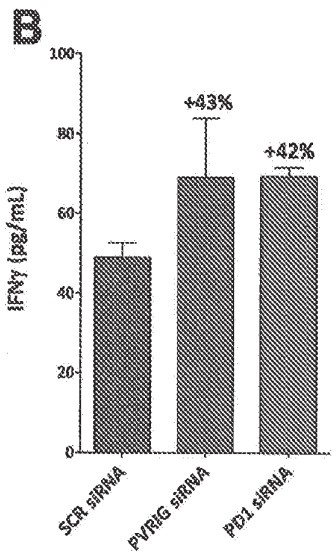


FIGURE 84B

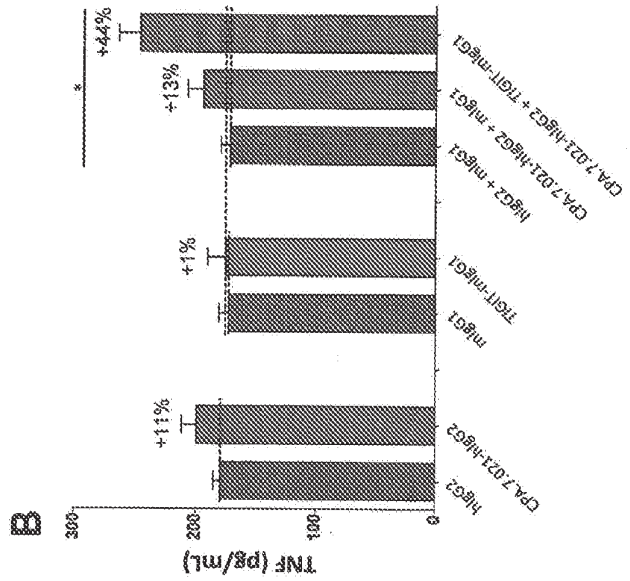


FIGURE 85B

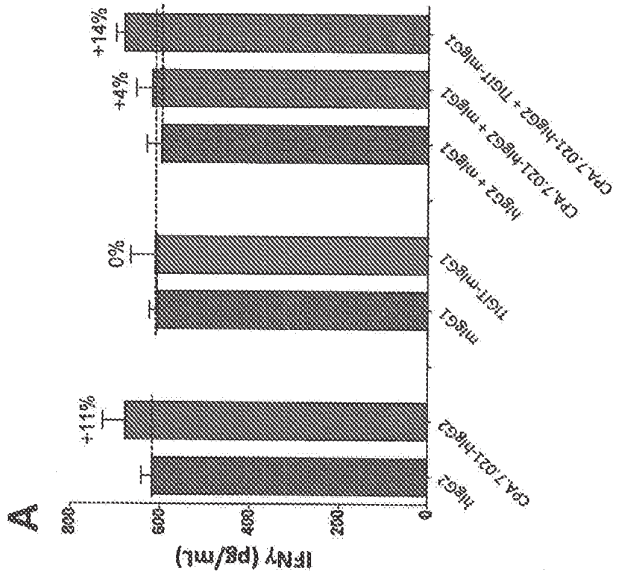


FIGURE 85A

TIL 209

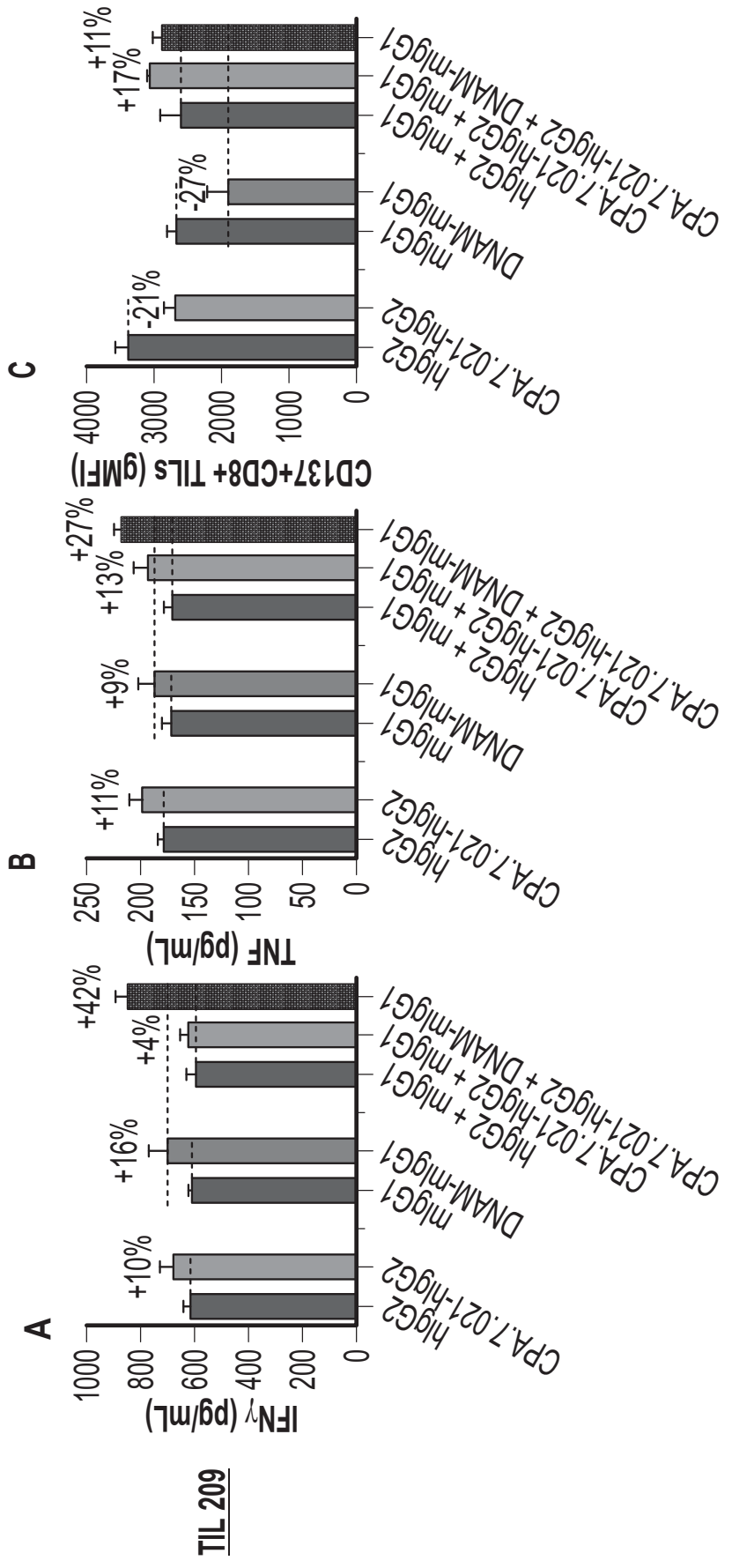


Figure 86A

Figure 86B

Figure 86C

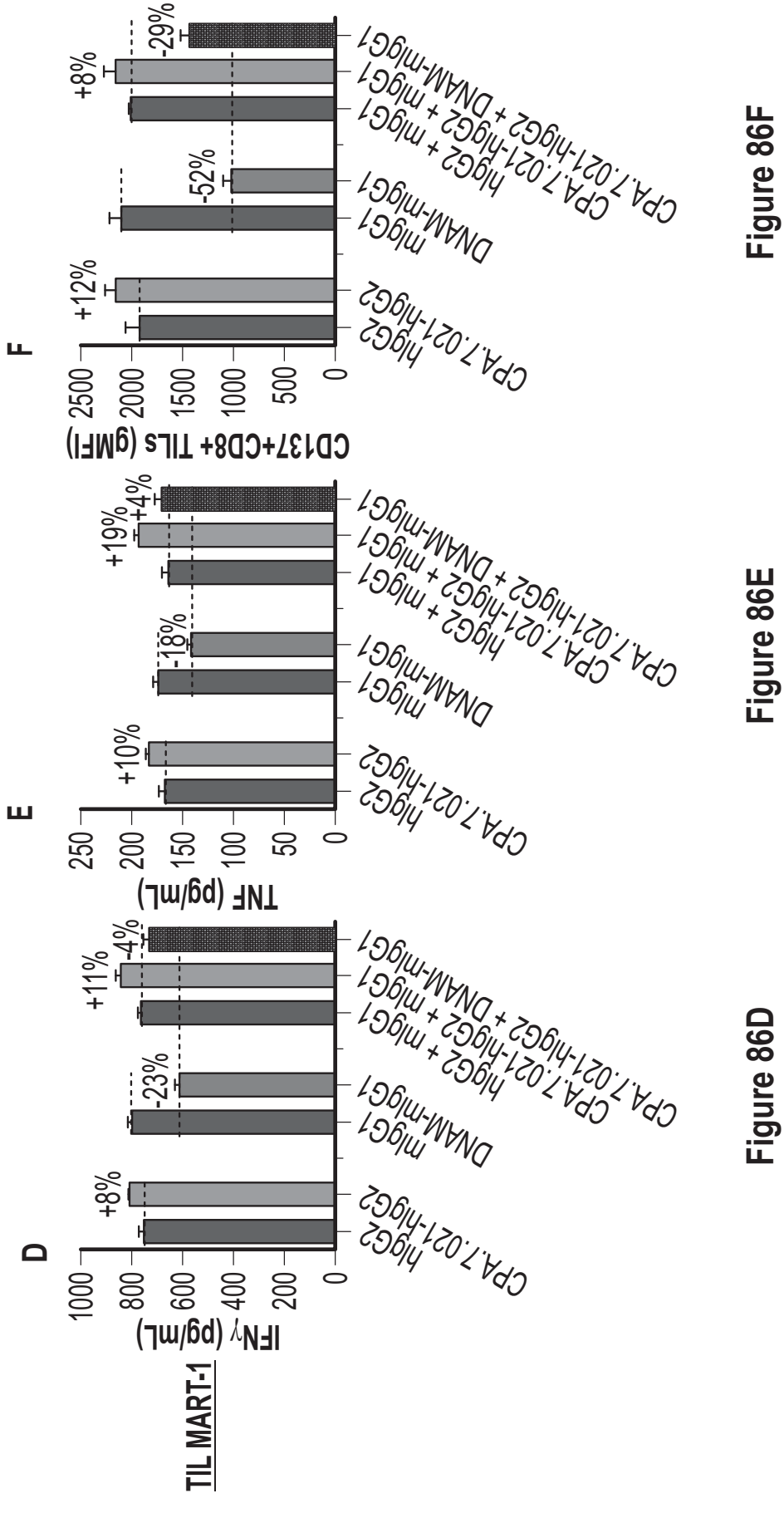


Figure 86D

Figure 86E

Figure 86F

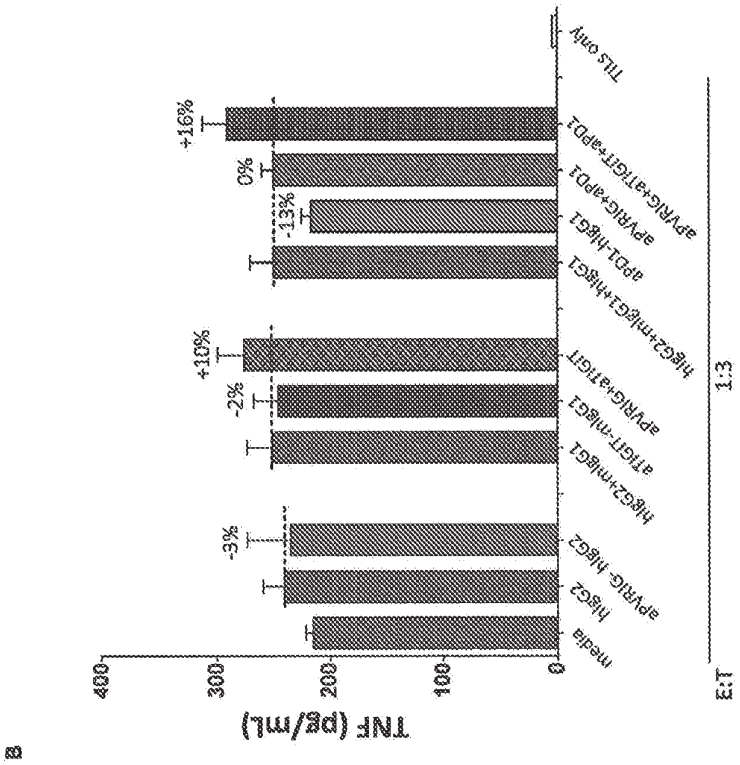


FIGURE 87B

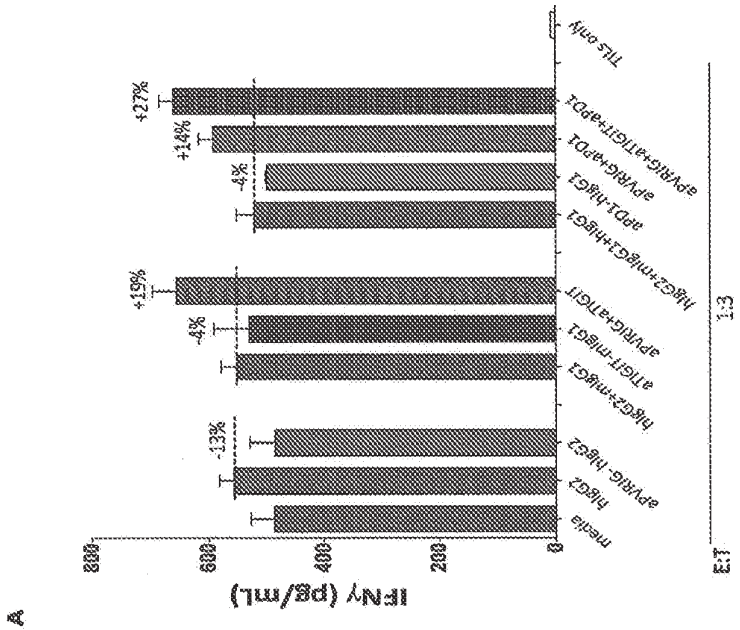


FIGURE 87A

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 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
(SEQ ID NO: 1368)

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

```
seq              10        20        30        40        50        60        70        80        90
AbM              10        20        30        40        50  a     60        70        80  abc   90
          b b b     p     p b b b   b b    b  bi i     i ibb  b          i  b   b b b x    b b b  b     bibibb
518       EVQLQQSGPELVKPGASVKISCKAS GYTFTDYNIN WVKQSHGKSLEWIG YIYPYIGGSG YNQKFKSKATLSADNPSSTAYMELRSLTSEDSAVYYCAR
          *   *   * **      *                   * ** **   *                *    **** *** ***  *     *  *   *
1-46*01   QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYYMH WVRQAPGQGLEWMG IINPSGGSTS YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h518H1    QVQLVQSGAEVKKPGASVKVSCKAS GYTFTDYNIN WVRQAPGQGLEWMG YIYPYIGGSG YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h518H2    QVQLVQSGAEVKKPGASVKVSCKAS GYTFTDYNIN WVRQAPGQGLEWIG YIYPYIGGSG YAQKFQGRVTMTADTSTSTVYMELSSLRSEDTAVYYCAR
h518H3    QVQLVQSGAEVKKPGASVKISCKAS GYTFTDYNIN WVRQAPGQGLEWIG YIYPYIGGSG YAQKFQGRATLTADTSTSTAYMELSSLRSEDTAVYYCAR
h518H4    QVQLVQSGAEVKKPGASVKISCKAS GYTFTDYNIN WVRQAPGQGLEWIG YIYPYIGGSG YAQKFQGRATLTADNSTSTAYMELSSLRSEDTAVYYCAR
                    V                   #                                 N
```

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

deamidation substitutions: Q/S/A

SUBSTITUTE SHEET (RULE 26)

Figure 88B
Humanized sequences of CHA.7.518 antibody VL

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

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

Joining region IMGT J00242|IGKJ2*01|YTFGQGTKLEIK (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   bi bi i     ii ibbi      i   b   b     b b b  b    ib bib
518      DIQMTQSPASLSVSVGETVTITIC RVSENTYSNLA WYQQKQGKSPQLLVY EATNLAE GVPSRFSGSGSGTQYSLKINSLQSEDFGSYYC
             *   *   **   *                   *  * *  *                    *** * *  *   **
IGKV1-39 DIQMTQSPSSLSASVGDRVTITC RASQSISSYLN WYQQKPGKAPKLLIY AASSLQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
h518L1   DIQMTQSPSSLSASVGDRVTITC RVSENTYSNLA WYQQKPGKAPKLLIY EATNLAE GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
h518L2   DIQMTQSPSSLSASVGDRVTITC RVSENIYSNLA WYQQKPGKAPKLLIY EATNLAE GVPSRFSGSGSGTDYTLTISSLQPEDFATYYC
h518L3   DIQMTQSPSSLSASVGDRVTITC RVSENTYSNLA WYQQKPGKAPKLLVY EATNLAE GVPSRFSGSGSGTDYTLTISSLQPEDFGTYYC
                                  V                  #  #                 S                 #

seq          90        100
AbM          90        100
             ibi  iib  i   b b b
518      QHFWGTPYT FGGGTKLEIK (SEQ ID NO: 1378)
                      *
IGKV1-39 QQSYSTPP (SEQ ID NO: 1379)
h518L1   QHFWGTPYT FGQGTKLEIK (SEQ ID NO: 1380)
h518L2   QHFWGTPYT FGQGTKLEIK (SEQ ID NO: 1381)
h518L3   QHFWGTPYT FGQGTKLEIK (SEQ ID NO: 1382)
            @

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

Figure 88C
Humanized sequences of CHA.7.524 antibody VH

Potential humanized sequence based on IMGT IGHV1-46*01 acceptor framework
IGHV1-46*01
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR (SEQ ID NO: 1383)
Joining region IMGT J00256|IGHJ4*01|YFDYWGQGTLVTVSS (SEQ ID NO: 1384)

```
seq          10        20        30        40        50        60        70        80        90
AbM          10        20        30        40        50  a     60        70        80  abc   90
          b b b     p     p b b b   b b   b  bi i     i ibb  b        i  b   b b b x   b b b  b     bibibb
524    QVQLQQSGPEVVRPGVSVKISCKGS GYKFPDYVMH WVKQSHAKSLEWIG IISIYSGNTN YNQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCAR
          *   *  **  *   *   *              * ***** *       IISIYSGNTN  *  **   * * *  *    ** *   * *
1-46*01 QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYYMH WVRQAPGQGLEWMG IINPSGGSTS YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h524H1 QVQLVQSGAEVKKPGASVKVSCKAS GYKFPDYVMH WVRQAPGQGLEWMG IISIYSGNTN YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h524H2 QVQLVQSGAEVKKPGASVKVSCKAS GYKFPDYVMH WVRQAPGQGLEWIG IISIYSGNTN YAQKFQGRVTMTVDTSTSTVYMELSSLRSEDTAVYYCAR
h524H3 QVQLVQSGAEVKKPGASVKISCKGS GYKFPDYVMH WVRQAPGQGLEWIG IISIYSGNTN YAQKFQGRATMTVDTSTSTAYMELSSLRSEDTAVYYCAR
h524H4 QVQLVQSGAEVKKPGASVKISCKGS GYKFPDYVMH WVRQAPGQGLEWIG IISIYSGNTN YAQKFQGRATMTVDKSTSTAYMELSSLRSEDTAVYYCAR
                                                          # #  N                                    I
                                  V
```

```
seq          100       110
AbM                 i    b b b
524    EGDLPMFAY WGQGTLVTVSA (SEQ ID NO: 1385)
                           * (1-46*01 disclosed as SEQ ID NO: 1386)
h524H1 EGDLPMFAY WGQGTLVTVSS (SEQ ID NO: 1387)
h524H2 EGDLPMFAY WGQGTLVTVSS (SEQ ID NO: 1388)
h524H3 EGDLPMFAY WGQGTLVTVSS (SEQ ID NO: 1389)
h524H4 EGDLPMFAY WGQGTLVTVSS (SEQ ID NO: 1390)
               @
```

deamidation substitutions: Q/S/A
@ methionine oxidation substitutions: L/F/A

Figure 88D
humanized sequences of CHA.7.524 antibody VL

Potential humanized sequence based on IMGT IGKV3-11*01 acceptor framework
IGKV3-11*01
EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPP (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
          b b b   p p     b b b  b   b  bi bi i    ii ibbi     i   b   b     b b b  b    ib bib
524       QIVLTQSPAIMSASPGEKVTMTC NASSSVS-YMY WYQQKPISSPRLLIY DTSNLAS GVPVRFSGSGSGTSYSLTIGRMEAEDAATYYC
          *         ** *   ** **              ***                * *     ***    ***  *   * *
IGKV3-11  EIVLTQSPATLSLSPGERATLSC RASQSVSSYLA WYQQKPGQAPRLLIY DASNRAT GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC
h524L1    EIVLTQSPATLSLSPGERATLSC NASSSVS-YMY WYQQKPGQAPRLLIY DTSNLAS GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC
h524L2    EIVLTQSPATLSLSPGERATLSC NASSSVS-YMY WYQQKPGQAPRLLIY DTSNLAS GIPARFSGSGSGTDYTLTISSLEPEDFAVYYC
h524L3    EIVLTQSPATLSLSPGERVTMSC NASSSVS-YMY WYQQKPGQAPRLLIY DTSNLAS GVPARFSGSGSGTDYTLTISSMEPEDFAVYYC
                          M A                 #         S         #                    A

seq          90        100
AbM          90        100
          ibi  iib  i   b b b
524       QQWSSYPLT FGAGTKVEVK (SEQ ID NO: 1393)
                    *   * *
IGKV3-11  QQRSNWPP (SEQ ID NO: 1394)
h524L1    QQWSSYPLT FGQGTKLEIK (SEQ ID NO: 1395)
h524L2    QQWSSYPLT FGQGTKLEIK (SEQ ID NO: 1396)
h524L3    QQWSSYPLT FGQGTKVEIK (SEQ ID NO: 1397)
             @          V
```

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
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR (SEQ ID NO: 1398)
Joining region IMGT J00256|IGHJ4*01|YFDYWGQGTLVTVSS (SEQ ID NO: 1399)

```
seq              10        20        30        40        50        60        70        80        90
AbM              10        20        30        40        50  a     60        70        80  abc   90
          b b b     p     p b b b   b b    b  bi i     i ibb  b         i  b   b b b x    b b b  b     bibibb
530       QVQLQQSGAELMRPGTSVKVSCKAS GYAFTNHLIE WIKQRPGQGLEWIG VINPGSDSTD YNEKFKDKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR
            *     ***  *                        ** *       *                 **  **** * * * *  *  *    * * *   *
1-46*01   QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYYMH WVRQAPGQGLEWMG IINPSGGSTS YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h530H1    QVQLVQSGAEVKKPGASVKVSCKAS GYAFTNHLIE WVRQAPGQGLEWMG VINPGSDSTD YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h530H2    QVQLVQSGAEVKKPGASVKVSCKAS GYAFTNHLIE WVRQAPGQGLEWIG VINPGSDSTD YAQKFQGRVTMTADTSTSTVYMELSSLRSEDTAVYYCAR
h530H3    QVQLVQSGAEVKKPGASVKVSCKAS GYAFTNHLIE WIRQAPGQGLEWIG VINPGSDSTD YAQKFQGRATLTADTSTSTAYMELSSLRSEDTAVYYCAR
h530H4    QVQLVQSGAEVKKPGASVKVSCKAS GYAFTNHLIE WIRQAPGQGLEWIG VINPGSDSTD YAQKFQGRATLTADKSTSTAYMELSSLRSEDTAVYYCAR
                    M                   #                   #         N                                       F

seq     100       110
AbM               110
                i   b b b
530       SLYYNSWFVY WGQGTLVTVSA (SEQ ID NO: 1400)
                               * (1-46*01 disclosed as SEQ ID NO: 1401)
h530H1    SLYYNSWFVY WGQGTLVTVSS (SEQ ID NO: 1402)
h530H2    SLYYNSWFVY WGQGTLVTVSS (SEQ ID NO: 1403)
h530H3    SLYYNSWFVY WGQGTLVTVSS (SEQ ID NO: 1404)
h530H4    SLYYNSWFVY WGQGTLVTVSS (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
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPP (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   bi bi i    ii ibbi     i   b   b     b b b  b    ib bib
530  DIQMTQSPASLSASVGETVTITC RASENIYSYLA WYQQKRGKSPQLLVY NAKTLVE GVPSRFSGSGSGTQFSLKINSLQPEDFGSYYC
                  *     **                  *   * *                 * * * *          **
IGKV1-39 DIQMTQSPSSLSASVGDRVTITC RASQSISSYLN WYQQKPGKAPKLLIY AASSLQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
h530L1   DIQMTQSPSSLSASVGDRVTITC RASENIYSYLA WYQQKPGKAPKLLIY NAKTLVE GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
h530L2   DIQMTQSPSSLSASVGDRVTITC RASENIYSYLA WYQQKPGKAPKLLVY NAKTLVE GVPSRFSGSGSGTDFTLTISSLQPEDFGTYYC
                                          #                   S         #

seq          90        100
AbM          90        100
             ibi  iib  i   b b b
530  QHHYGTPYT FGGGTKLEIK (SEQ ID NO: 1408)
                  *
IGKV1-39 QQSYSTPP (SEQ ID NO: 1409)
h530L1   QHHYGTPYT FGQGTKLEIK (SEQ ID NO: 1410)
h530L2   QHHYGTPYT FGQGTKLEIK (SEQ ID NO: 1411)

# deamidation substitutions: Q/S/A/D
```

Figure 88G
Humanized sequences of CHA.7.538_1 antibody VH

Potential humanized sequence based on IMGT IGHV1-46*01 acceptor framework
IGHV1-46*01
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR (SEQ ID NO: 1412)
Joining region IMGT J00256|IGHJ4*01|YFDYWGQGTLVTVSS (SEQ ID NO: 1413)

```
seq             10        20        30        40        50        60        70        80        90
AbM             10        20        30        40        50  a     60        70        80  abc   90
         b b b     p     p b b b   b b    b  bi i     i ibb  b          i  b   b b b x    b b b  b     bibibb
538_1    QVQLQQSGAELVRPGASVKVSCKTS GYAFTNYLIE WVKQRPGQGLEWIG VINPGSGGIY YNDKFKVKTTLTADKSSSTAYMQLSSLTSDDSAVYFCAR
           *     ***          *                * *       *                **  **** * * * *  *  *    * * *   *
1-46*01  QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYYMH WVRQAPGQGLEWMG IINPSGGSTS YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h5381H1  QVQLVQSGAEVKKPGASVKVSCKAS GYAFTNYLIE WVRQAPGQGLEWMG VINPGSGGIY YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h5381H2  QVQLVQSGAEVKKPGASVKVSCKAS GYAFTNYLIE WVRQAPGQGLEWIG VINPGSGGIY YAQKFQGRVTMTADTSTSTVYMELSSLRSEDTAVYYCAR
h5381H3  QVQLVQSGAEVKKPGASVKVSCKTS GYAFTNYLIE WVRQAPGQGLEWIG VINPGSGGIY YAQKFQGRVTLTADTSTSTAYMELSSLRSEDTAVYYCAR
h5381H4  QVQLVQSGAEVKKPGASVKVSCKTS GYAFTNYLIE WVRQAPGQGLEWIG VINPGSGGIY YAQKFQGRVTLTADKSTSTAYMELSSLRSEDTAVYYCAR
                  V                   #                   #         N      T                                 F

seq    100        110
AbM                110
                    i   b b b
538_1    SETHDTWFAY WGQGTLVTVSA (SEQ ID NO: 1414)
                           * (1-46*01 disclosed as SEQ ID NO: 1415)
h5381H1  SETHDTWFAY WGQGTLVTVSS (SEQ ID NO: 1416)
h5381H2  SETHDTWFAY WGQGTLVTVSS (SEQ ID NO: 1417)
h5381H3  SETHDTWFAY WGQGTLVTVSS (SEQ ID NO: 1418)
h5381H4  SETHDTWFAY WGQGTLVTVSS (SEQ ID NO: 1419)
              @
```

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 IGKV1-39*01 acceptor framework
IGKV1-39*01
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPP (SEQ ID NO: 1420)

Joining region IMGT J00242|IGKJ2*01|YTFGQGTKLEIK (SEQ ID NO: 1421)

IGKV1-17*02
DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISNLQPEDFATYYCLQHNSYPP (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   b   bi bi i    ii ibbi     i   b   b     b b b  b    ib bib
538      DIVMTQSQKFISTSVGDRVSITC KASQSVRIAVA WFQQKPGQSPKALIY LASTRHT GVPDRFTGSGSGTDFTLTISNVQSEDLADYFC
           *    **** *     *      *     **  *                 *  *          ** *  * * *
IGKV1-39 DIQMTQSPSSLSASVGDRVTITC RASQSISSYLN WYQQKPGKAPKLLIY AASSLQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
h538L1   DIQMTQSPSSLSASVGDRVTITC KASQSVRIAVA WYQQKPGKAPKLLIY LASTRHT GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
h538L2   DIQMTQSPSSLSASVGDRVTITC KASQSVRIAVA WFQQKPGKAPKALIY LASTRHT GVPSRFSGSGSGTDFTLTISSVQPEDFATYYC
                   I T                        S                                          L   F

seq          90        100
AbM          90        100
             ibi iib   i   b b b
538      LQHWNYPYT FGGGTKLEIK (SEQ ID NO: 1423)
                   *
IGKV1-39 QQSYSTPP (SEQ ID NO: 1424)
h538L1   LQHWNYPYT FGQGTKLEIK (SEQ ID NO: 1425)
h538L2   LQHWNYPYT FGQGTKLEIK (SEQ ID NO: 1426)
             @#

# 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
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR (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  a     60        70        80  abc   90
                 b b b       p       p b b b   b b     b  bi i     i ibb  b           i  b   b b b x   b b b  b     bibibb
538_2    QVQLQQSGAELVRPGTSVKMSCKAA GYTFTNYWIG WVKQRPGHGLEWIG DIYPGGGYTN YNEKFKGKATLTADTSSSTAYMQLSSLTSEDSAIYYCAS
             *     ***  *   *   *              * *  *    *                **  * **  *  *  *   *  *  *    * *  *
1-46*01  QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYYMH WVRQAPGQGLEWMG IINPSGGSTS YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h5382H1  QVQLVQSGAEVKKPGASVKVSCKAS GYTFTNYWIG WVRQAPGQGLEWMG DIYPGGGYTN YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h5382H2  QVQLVQSGAEVKKPGASVKVSCKAS GYTFTNYWIG WVRQAPGQGLEWMG DIYPGGGYTN YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
h5382H3  QVQLVQSGAEVKKPGASVKVSCKAS GYTFTNYWIG WVRQAPGQGLEWIG DIYPGGGYTN YAQKFQGRATLTADTSTSTAYMELSSLRSEDTAVYYCAS
                                    V                   # @                 #  N                                  I

seq      100       110       110
Abm                 i   b b b
538_2    FYTGSSTGFAF WGQGTLVTVSA (SEQ ID NO: 1429)
                             * (1-46*01 disclosed as SEQ ID NO: 1430)
h5382H1  FYTGSSYGFAF WGQGTLVTVSS (SEQ ID NO: 1431)
h5382H2  FYTGSSYGFAF WGQGTLVTVSS (SEQ ID NO: 1432)
h5382H3  FYTGSSYGFAF WGQGTLVTVSS (SEQ ID NO: 1433)

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

Figure 89A

humanized CHA.7.518 VH

h518HH1

QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYNINWVRQAPGQGLEWMGYIYPYIGGSGYAQKFQGRVTMTRDTSTSTVY
MELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLVTVSS (SEQ ID NO: 1434)

h518HH2

QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYNINWVRQAPGQGLEWIGYIYPYIGGSGYAQKFQGRVTMTADTSTSTVY
MELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLVTVSS (SEQ ID NO: 1435)

h518HH3

QVQLVQSGAEVKKPGASVKISCKASGYTFTDYNINWVRQAPGQGLEWIGYIYPYIGGSGYAQKFQGRATLTADTSTSTAYM
ELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLVTVSS (SEQ ID NO: 1436)

h518HH4

QVQLVQSGAEVKKPGASVKISCKASGYTFTDYNINWVRQAPGQGLEWIGYIYPYIGGSGYAQKFQGRATLTADNSTSTAYM
ELSSLRSEDTAVYYCAREDKTARNAMDYWGQGTLVTVSS (SEQ ID NO: 1437)

humanized CHA.7.524 VH

h524HH1

QVQLVQSGAEVKKPGASVKVSCKASGYKFPDYVMHWVRQAPGQGLEWMGIISIYSGNTNYAQKFQGRVTMTRDTSTSTV
YMELSSLRSEDTAVYYCAREGDLPMFAYWGQGTLVTVSS (SEQ ID NO: 1438)

h524HH2

QVQLVQSGAEVKKPGASVKVSCKASGYKFPDYVMHWVRQAPGQGLEWIGIISIYSGNTNYAQKFQGRVTMTVDTSTSTVY
MELSSLRSEDTAVYYCAREGDLPMFAYWGQGTLVTVSS (SEQ ID NO: 1439)

h524HH3

QVQLVQSGAEVKKPGASVKISCKGSGYKFPDYVMHWVRQAPGQGLEWIGIISIYSGNTNYAQKFQGRATMTVDTSTSTAY
MELSSLRSEDTAVYYCAREGDLPMFAYWGQGTLVTVSS (SEQ ID NO: 1440)

Figure 89B
h524HH4
QVQLVQSGAEVKKPGASVKISCKGSGYKFPDYVMHWVRQAPGQGLEWIGIISIYSGNTNYAQKFQGRATMTVDKSTSTAY
MELSSLRSEDTAVYYCAREGDLPMFAYWGQGTLVTVSS (SEQ ID NO: 1441)

humanized CHA.7.530 VH
h530HH1
QVQLVQSGAEVKKPGASVKVSCKASGYAFTNHLIEWVRQAPGQGLEWMGVINPGSDSTDYAQKFQGRVTMTRDTSTSTVY
MELSSLRSEDTAVYYCARSLYYNSWFVYWGQGTLVTVSS (SEQ ID NO: 1442)

h530HH2
QVQLVQSGAEVKKPGASVKVSCKASGYAFTNHLIEWVRQAPGQGLEWIGVINPGSDSTDYAQKFQGRVTMTADTSTSTVY
MELSSLRSEDTAVYYCARSLYYNSWFVYWGQGTLVTVSS (SEQ ID NO: 1443)

h530HH3
QVQLVQSGAEVKKPGASVKVSCKASGYAFTNHLIEWIRQAPGQGLEWIGVINPGSDSTDYAQKFQGRATLTADTSTSTAYM
ELSSLRSEDTAVYYCARSLYYNSWFVYWGQGTLVTVSS (SEQ ID NO: 1444)

h530HH4
QVQLVQSGAEVKKPGASVKVSCKASGYAFTNHLIEWIRQAPGQGLEWIGVINPGSDSTDYAQKFQGRATLTADKSTSTAYM
ELSSLRSEDTAVYYCARSLYYNSWFVYWGQGTLVTVSS (SEQ ID NO: 1445)

humanized CHA.7.538_1 VH
h5381HH1
QVQLVQSGAEVKKPGASVKVSCKASGYAFTNYLIEWVRQAPGQGLEWMGVINPGSGGIYYAQKFQGRVTMTRDTSTSTVY
MELSSLRSEDTAVYYCARSETHDTWFAYWGQGTLVTVSS (SEQ ID NO: 1446)

h5381HH2
QVQLVQSGAEVKKPGASVKVSCKASGYAFTNYLIEWVRQAPGQGLEWIGVINPGSGGIYYAQKFQGRVTMTADTSTSTVY
MELSSLRSEDTAVYYCARSETHDTWFAYWGQGTLVTVSS (SEQ ID NO: 1447)

Figure 89C
h5381HH3
QVQLVQSGAEVKKPGASVKVSCKTSGYAFTNYLIEWVRQAPGQGLEWIGVINPGSGGIYYAQKFQGRVTLTADTSTSTAYM
ELSSLRSEDTAVYYCARSETHDTWFAYWGQGTLVTVSS (SEQ ID NO: 1448)

h5381HH4
QVQLVQSGAEVKKPGASVKVSCKTSGYAFTNYLIEWVRQAPGQGLEWIGVINPGSGGIYYAQKFQGRVTLTADKSTSTAYM
ELSSLRSEDTAVYYCARSETHDTWFAYWGQGTLVTVSS (SEQ ID NO: 1449)

humanized CHA.7.538_2 VH
h5382HH1
QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWIGWVRQAPGQGLEWMGDIYPGGGYTNYAQKFQGRVTMTRDTSTSTV
YMELSSLRSEDTAVYYCARPYYGSSYGFAFWGQGTLVTVSS (SEQ ID NO: 1450)

h5382HH2
QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWIGWVRQAPGQGLEWIGDIYPGGGYTNYAQKFQGRVTMTADTSTSTV
YMELSSLRSEDTAVYYCASPYYGSSYGFAFWGQGTLVTVSS (SEQ ID NO: 1451)

h5382HH3
QVQLVQSGAEVKKPGASVKMSCKASGYTFTNYWIGWVRQAPGQGLEWIGDIYPGGGYTNYAQKFQGRATLTADTSTSTA
YMELSSLRSEDTAVYYCASPYYGSSYGFAFWGQGTLVTVSS (SEQ ID NO: 1452)

humanized CHA.7.518 VL
h518HL1
DIQMTQSPSSLSASVGDRVTITCRVSENIYSNLAWYQQKPGKAPKLLIYEATNLAEGVPSRFSGSGSGTDFTLTISSLQPEDFA
TYYCQHFWGTPYTFGQGTKLEIK (SEQ ID NO: 1453)

h518HL2
DIQMTQSPSSLSASVGDRVTITCRVSENIYSNLAWYQQKPGKAPKLLIYEATNLAEGVPSRFSGSGSGTDYTLTISSLQPEDFA
TYYCQHFWGTPYTFGQGTKLEIK (SEQ ID NO: 1454)

Figure 89D
h518HL3
DIQMTQSPSSLSASVGDRVTITCRVSENIYSNLAWYQQKPGKAPKLLVYEATNLAEGVPSRFSGSGSGTDYTLTISSLQPEDF
GTYYCQHFWGTPYTFGQGTKLEIK (SEQ ID NO: 1455)

humanized CHA.7.524 VL
h524HL1
EIVLTQSPATLSLSPGERATLSCNASSSVSYMYWYQQKPGQAPRLLIYDTSNLASGIPARFSGSGSGTDFTLTISSLEPEDFAVY
YCQQWSSYPLTFGQGTKLEIK (SEQ ID NO: 1456)

h524HL2
EIVLTQSPATLSLSPGERATLSCNASSSVSYMYWYQQKPGQAPRLLIYDTSNLASGIPARFSGSGSGTDYTLTISSLEPEDFAVY
YCQQWSSYPLTFGQGTKLEIK (SEQ ID NO: 1457)

h524HL2
EIVLTQSPATLSLSPGERVTMSCNASSSVSYMYWYQQKPGQAPRLLIYDTSNLASGVPARFSGSGSGTDYTLTISSMEPEDFA
VYYCQQWSSYPLTFGQGTKVEIK (SEQ ID NO: 1458)

humanized CHA.7.530 VL
h530HL1
DIQMTQSPSSLSASVGDRVTITCRASENIYSYLAWYQQKPGKAPKLLIYNAKTLVEGVPSRFSGSGSGTDFTLTISSLQPEDFA
TYYCQHHYGTPYTFGQGTKLEIK (SEQ ID NO: 1459)

h530HL2
DIQMTQSPSSLSASVGDRVTITCRASENIYSYLAWYQQKPGKAPKLLVYNAKTLVEGVPSRFSGSGSGTDFTLTISSLQPEDFG
TYYCQHHYGTPYTFGQGTKLEIK (SEQ ID NO: 1460)

humanized CHA.7.538_1/538_2 VL
h538HL1
DIQMTQSPSSLSASVGDRVTITCKASQSVRIAVAWYQQKPGKAPKLLIYLASTRHTGVPSRFSGSGSGTDFTLTISSLQPEDFA
TYYCLQHWNYPYTFGQGTKLEIK (SEQ ID NO: 1461)

Figure 89E
h538HL2
DIQMTQSPSSLSASVGDRVTITCKASQSVRIAVAWFQQKPGKAPKALIYLASTRHTGVPSRFSGSGSGTDFTLTISSVQPEDFA
TYYCLQHWNYPYTFGQGTKLEIK (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 (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
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

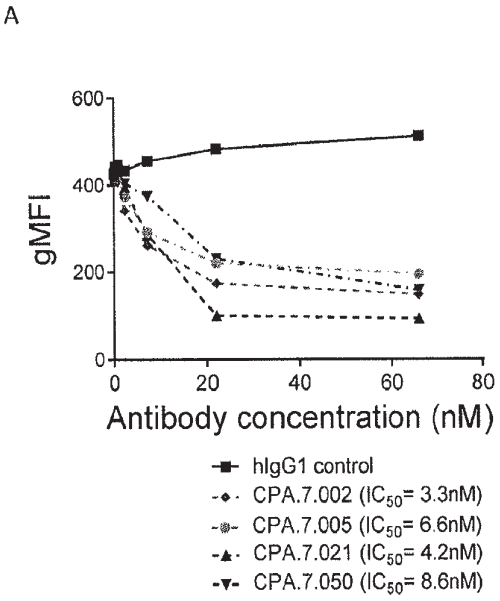
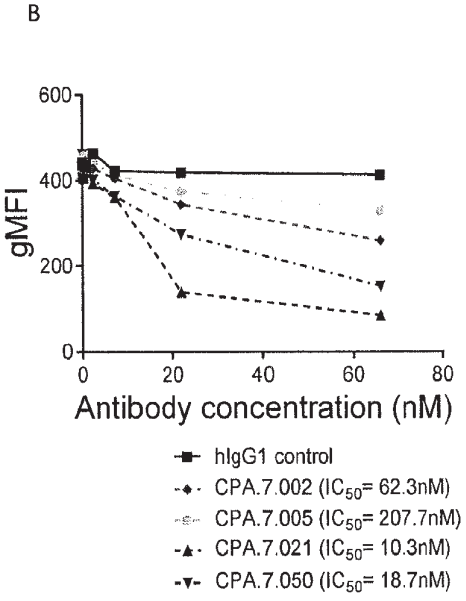


FIGURE 93B



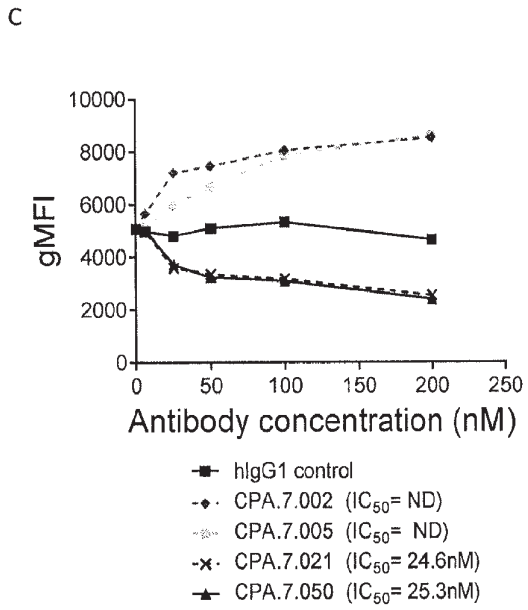
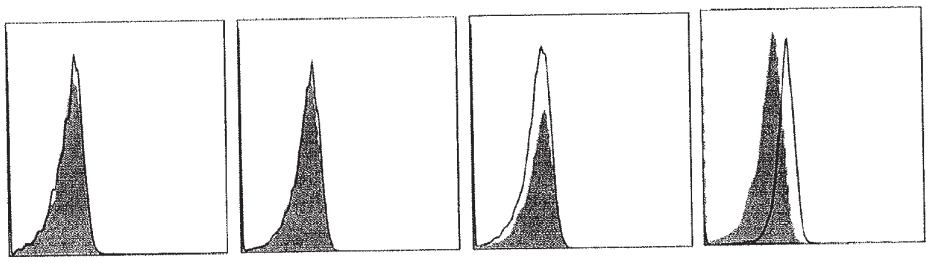


FIGURE 93C

FIG. 94A FIG. 94B FIG. 94C FIG. 94D

a b c d



e f g h

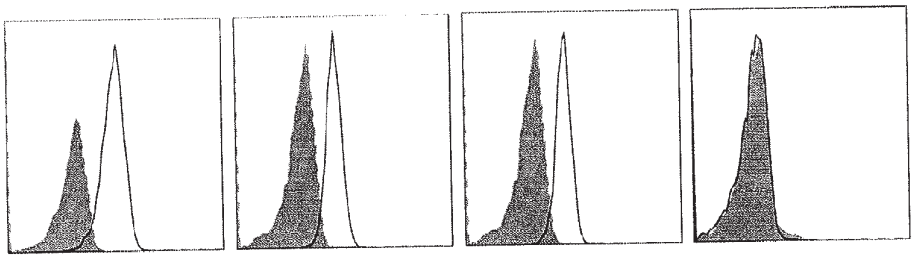


FIG. 94E FIG. 94F FIG. 94G FIG. 94H

FIG. 95A

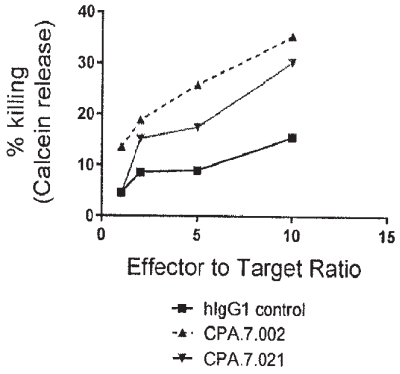


FIG. 95B

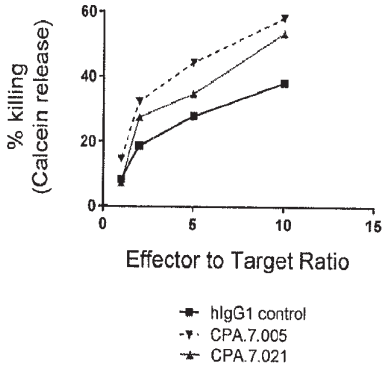


FIG. 95C

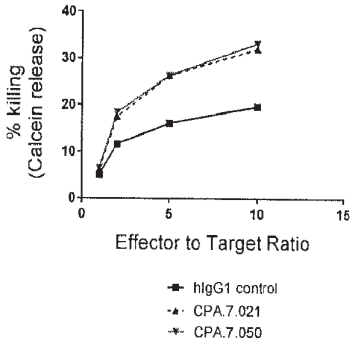


FIG. 95D

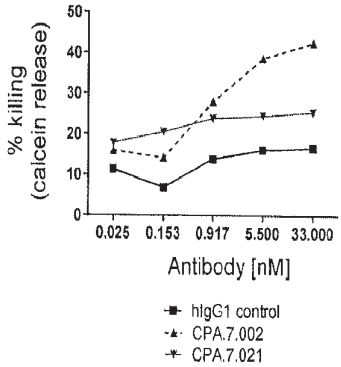


FIG. 95E

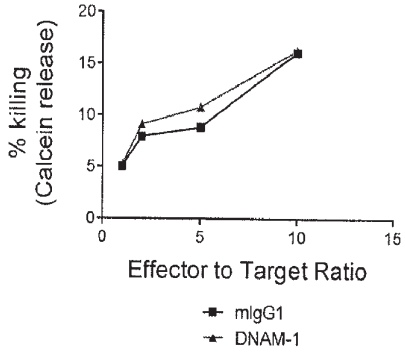


FIG. 95F

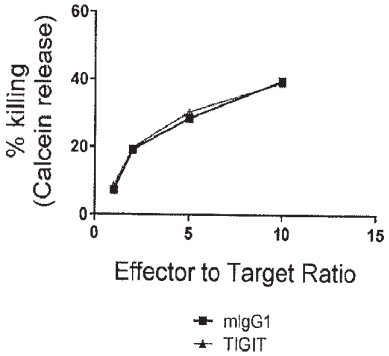
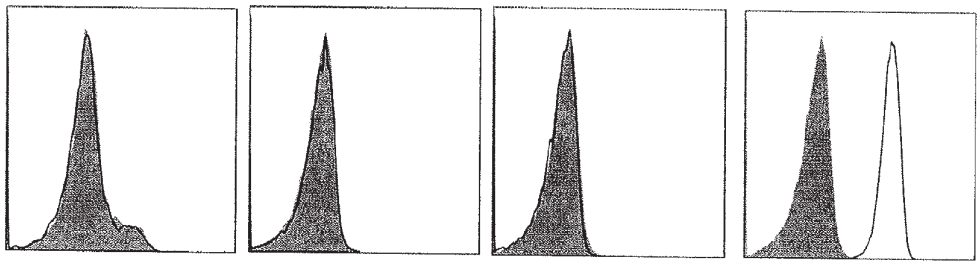


FIG. 96A FIG. 96B FIG. 96C FIG. 96D

a b c d



e f g h

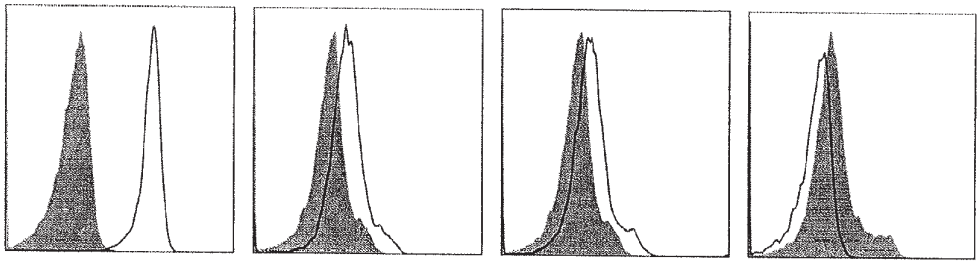
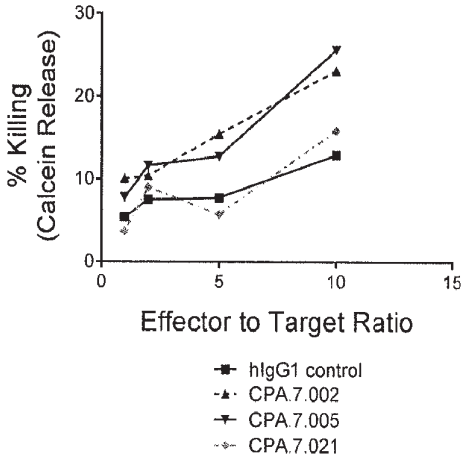


FIG. 96E FIG. 96F FIG. 96G FIG. 96H

A

FIGURE 97A



B

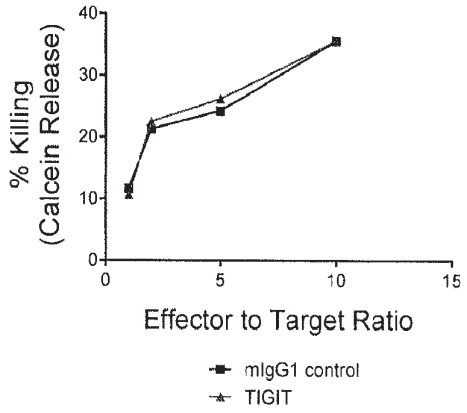


FIGURE 97B

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

Figure 100

```
NP_076975.2-Homosapiens                 TPEVWVQVKMEATELSSFTIKCGFLGSGSISLVTVSWGGPSGAGGTSLAVLHPEGSPQW
XP_005549281.1-Macacafascicularis       TPEVWVQVQMEATELSSFTVKCGFLGSGSISLVTVSWGGPSGAGGTSLAVLHPELGSPQW
XP_003732227.1-Callithrixjacchus        TPEVWVQVQMKATELSSFIVKCGFLGSGSISLVTVSWGGPSGAGGTSLAVLHPELGSPQW
XP_001103603.1-Macacamulatta            TPEVWVQVQMEATELSSFTVKCGFLGSGSISLVTVSWGGPSGAGGTSLAVLHPELGSPQW
                                        ********:*:******** ::****** ************:****** ******* * ***

NP_076975.2-Homosapiens                 APARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGSLPPSSDPGLSA
XP_005549281.1-Macacafascicularis       APARQARWETQSSISLALEDSGASSPFANTTFCCKFASFPEGSWESCGSLPPSSDPGLSA
XP_003732227.1-Callithrixjacchus        APAHQARWETQSSISLVLEEPGASSPSANTTFCCKFASFPEGSWEACGSLPPSSDPGLSA
XP_001103603.1-Macacamulatta            APARQARWETQSSISLGLEDSGASSPFANTTFCCKFASFPEGSWESCGSLPPSSDPGLSA
                                        ***:************** ***** ********************:**************

NP_076975.2-Homosapiens                 PPTFAPILRAD
XP_005549281.1-Macacafascicularis       PPTFVPILRAD
XP_003732227.1-Callithrixjacchus        PIL-------RAD
XP_001103603.1-Macacamulatta            PPTFVPILRAD
                                        *      ***
```

SEQ ID NOS 1463-1466, respectively, in order of appearance

Figure 101

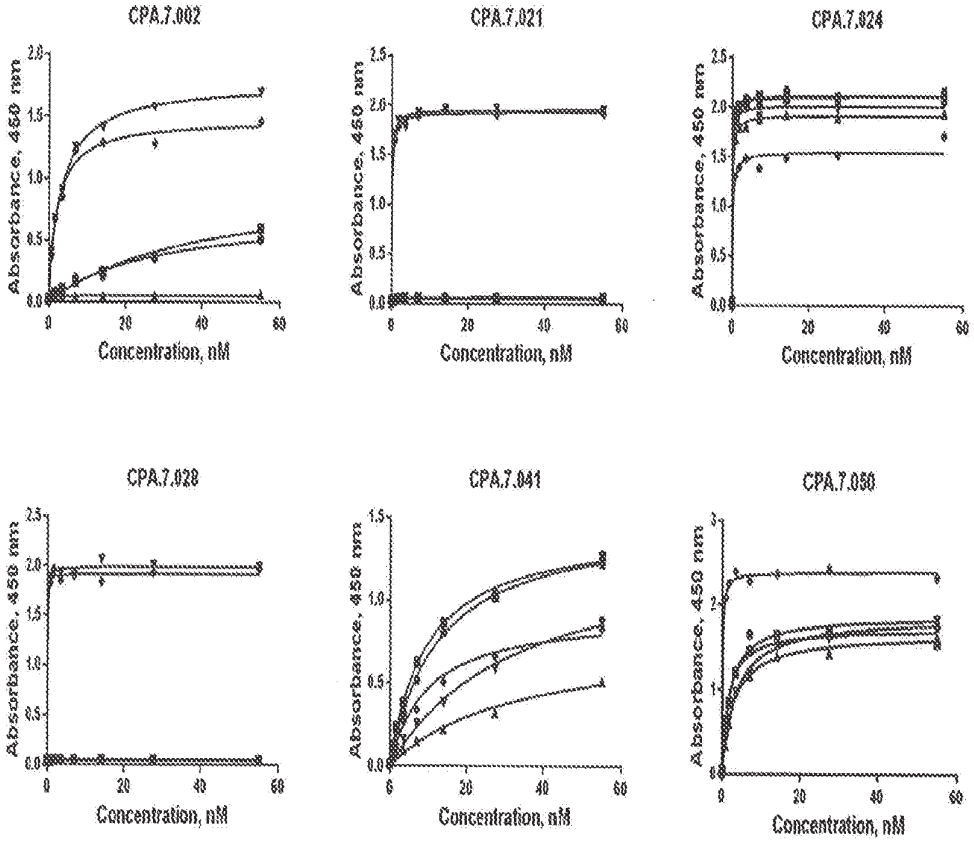


Figure 102

mAb	Cyno cross-reactivity	Epitope bin	Epitope group
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

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGS
LPPSSDPGLSAPPTPAPILRAD

Figure 103B

>PVRIG_NP_076975_from_21_to_171_Sequence_of_Human_WT_ECD_(with_SP) SEQ ID NO: 1468

MGHRTLVLPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCA
NTTFCCKFASFPEGSWEACGSLPPSSDPGLSAPPTPAPILRAD

Figure 103C

>PVRIG_NP_076975_from_43_to_146_Sequence_of_Ig_Domain SEQ ID NO: 1469

EVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEA

Figure 103D

>PVRIG_Splice_Variant_P6 SEQ ID NO: 1470

MGHRTLVLPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCA
NTTFCCKFASFPEGSWEACGSLPPSSDPGLSAPPTPAPILRADLAGILGVSGVLLFGCVYLLHLLRRHKHR

Figure 103E

>PVRIG_Splice_Variant_P8 SEQ ID NO: 1471

MGHRTLVLPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCA
NTTFCCKFASFPEGSWEACGSLPPSSDPGLSVPPTPAPILRADLAGILGVSGVLLFDCGYLLHLLCRQKHRPAPRLQPSHTSS

Figure 103F

>PVRIG_Splice_Variant_P4 SEQ ID NO: 1472

MGHRTLVLPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRWLSAPPTPAPILRADLAGILGVSGVLLFGCVYLLHLLRRHKHRPAPRLQPSRTSPQAPRARAWAPSQA
SQAALHVPYATINTSCRPATLDTAHPHGGPSWWASLPTHAAHRPQGPAAWASTPIPARGSFVSVENGLYAQAGERPPHTGPGLTLFPDPRGPRAMEGPLGVR

Figure 103G

>PVRIG_Splice_Variant_P7 SEQ ID NO: 1473

MGHRTLVLPWVLLTLCVTAGLSAPPTPAPILRADLAGILGVSGVLLFGCVYLLHLLRRHKHRPAPRLQPSRTSPQAPRARAWAPSQASQAALHVPYATINTSCRPATLDT
AHPHGGPSWWASLPTHAAHRPQGPAAWASTPIPARGSFVSVENGLYAQAGERPPHTGPGLTLFPDPRGPRAMEGPLGVR

Figure 103H

>PVRIG_Splice_Variant_P14 SEQ ID NO: 1474

MGHRTLVLPWVLLTLCVTAGLSVPPTPAPILRADLAGILGVSGVLLFDCGYLLHLLCRQKHRPAPRLQPSHTSS

Figure 103I

>PVRIG_Splice_Variant_P3 SEQ ID NO: 1475

MGHRTLVLPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCA
NTTFCCKFASFPEGSWEACGSLPPSSDPGGAGARGPGGQGGARELATHLILVSVPRALCPADSCPHSAGRPGRDLGGLRSPPLWLCLPPSSAAPT

Figure 103J

>PVRIG_Splice_Variant_P10 SEQ ID NO: 1476

MGHRTLVLPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGAQISPRGPKIGGPPCPRPGPAGKPRAASLSSW
KALGPAAPAPTPPSAASLRPSQAALHVPYATINTSCRPATLDTAHPHGGPSWWASLPTHAAHRPQGPAAWASTPIPARGSFVSVENGLYAQAGERPPHTGPGLTLFPD
PRGPRAMEGPLGVR

Figure 103K

>PVRIG_Splice_Variant_P13 SEQ ID NO: 1477

MGHRTLVLPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCA
NTTFCCKFASFPGCSSRPLCHYQHQLPPSYFGHSSPPWGAVLVGVTPHPRCTPAPGPCRLGLHTHPCTWQLCLC

Figure 103L

>PVRIG_Splice_Variant_P3_ECD SEQ ID NO: 1478

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGS
LPPSSDPGGAGARGPGGQGGARELATHLILVSVPRALCPADSCPHSAGRPGRDLGGLRSPPLWLCLPPSSAAPT

Figure 103M

>PVRIG_Splice_Variant_P10_ECD SEQ ID NO: 1479

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGAQISPRGPKIGGPPCPRPGPAGKPRAASLSSWKALGPAAPAPTPPSAASLRPS
QAALHVPYATINTSCRPATLDTAHPHGGPSWWASLPTHAAHRPQGPAAWASTPIPARGSFVSVENGLYAQAGERPPHTGPGLTLFPDPRGPRAMEGPLGVR

Figure 103N

>PVRIG_Splice_Variant_P13_ECD SEQ ID NO: 1480

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPGCSSRPLCHY
QHQLPPSYFGHSSPPWGAVLVGVTPHPRCTPAPGPCRLGLHTHPCTWQLCLC

Figure 103O

>PVRIG_Splice_Variant_P3_ECD_Unique SEQ ID NO: 1481

GAGARGPGGQGGARELATHLILVSVPRALCPADSCPHSAGRPGRDLGGLRSPPLWLCLPPSSAAPT

Figure 103P

>PVRIG_Splice_Variant_P10_ECD_All_Unique SEQ ID NO: 1482

AQISPRGPKIGGPPCPRPGPAGKPRAASLSSWKALGPAAPAPTPPSAASLRPSQAALHVPYATINTSCRPATLDTAHPHGGPSWWASLPTHAAHRPQGPAAWASTPIP
ARGSFVSVENGLYAQAGERPPHTGPGLTLFPDPRGPRAMEGPLGVR

Figure 103Q

>PVRIG_Splice_Variant_P10_ECD_Unique_without_intracellular SEQ ID NO: 1483

AQISPRGPKIGGPPCPRPGPAGKPRAASLSSWKALGPAAPAPTPPSAASLRP

Figure 103R

>PVRIG_Splice_Variant_P13_ECD_Unique SEQ ID NO: 1484

GCSSRPLCHYQHQLPPSYFGHSSPPWGAVLVGVTPHPRCTPAPGPCRLGLHTHPCTWQLCLC

Figure 103S

>PVRIG_NP_076975_from_41_to_169_variation_of_ECD_(without_SP) SEQ ID NO: 1485

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGS
LPPSSDPGLSAPPTPAPILR

Figure 103T

>PVRIG_NP_076975_from_41_to_170_variation_of_ECD_(without_SP) SEQ ID NO: 1486

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGS
LPPSSDPGLSAPPTPAPILRA

Figure 103U

>PVRIG_NP_076975_from_41_to_172_variation_of_ECD_(without_SP) SEQ ID NO: 1487

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGS
LPPSSDPGLSAPPTPAPILRADL

Figure 103V

>PVRIG_NP_076975_from_41_to_173_variation_of_ECD_(without_SP) SEQ ID NO: 1488

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGS
LPPSSDPGLSAPPTPAPILRADLA

Figure 103W

>PVRIG_NP_076975_from_41_to_144_variation_of_Ig_Domain SEQ ID NO: 1489

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSW

Figure 103X

>PVRIG_NP_076975_from_41_to_145_variation_of_Ig_Domain SEQ ID NO: 1490

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWE

Figure 103Y

>PVRIG_NP_076975_from_41_to_146_variation_of_Ig_Domain SEQ ID NO: 1491

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEA

Figure 103Z

>PVRIG_NP_076975_from_41_to_147_variation_of_Ig_Domain SEQ ID NO: 1492

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEAC

Figure 103AA

>PVRIG_NP_076975_from_41_to_148_variation_of_Ig_Domain SEQ ID NO: 1493

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACG

Figure 103AB

>PVRIG_NP_076975_from_42_to_144_variation_of_Ig_Domain SEQ ID NO: 1494

PEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSW

Figure 103AC

>PVRIG_NP_076975_from_42_to_145_variation_of_Ig_Domain SEQ ID NO: 1495

PEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWE

Figure 103AD

>PVRIG_NP_076975_from_42_to_146_variation_of_Ig_Domain SEQ ID NO: 1496

PEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEA

Figure 103AE

>PVRIG_NP_076975_from_42_to_147_variation_of_Ig_Domain SEQ ID NO: 1497

PEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEAC

Figure 103AF

>PVRIG_NP_076975_from_42_to_148_variation_of_Ig_Domain SEQ ID NO: 1498

PEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACG

Figure 103AG

>PVRIG_NP_076975_from_43_to_144_variation_of_Ig_Domain SEQ ID NO: 1499

EVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSW

Figure 103AH

>PVRIG_NP_076975_from_43_to_145_variation_of_Ig_Domain SEQ ID NO: 1500

EVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWE

Figure 103AI

>PVRIG_NP_076975_from_43_to_147_variation_of_Ig_Domain SEQ ID NO: 1501

EVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEAC

Figure 103AJ

>PVRIG_NP_076975_from_43_to_148_variation_of_Ig_Domain SEQ ID NO: 1502

EVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACG

Figure 103AK

>PVRIG_NP_076975_from_44_to_144_variation_of_Ig_Domain SEQ ID NO: 1503

VWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSW

Figure 103AL

>PVRIG_NP_076975_from_44_to_145_variation_of_Ig_Domain SEQ ID NO: 1504

VWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWE

Figure 103AM

>PVRIG_NP_076975_from_44_to_146_variation_of_Ig_Domain SEQ ID NO: 1505

VWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEA

Figure 103AN

>PVRIG_NP_076975_from_44_to_147_variation_of_Ig_Domain SEQ ID NO: 1506

VWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEAC

Figure 103AO

>PVRIG_NP_076975_from_44_to_148_variation_of_Ig_Domain SEQ ID NO: 1507

VWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACG

Figure 103AP

>PVRIG_NP_076975_from_45_to_144_variation_of_Ig_Domain SEQ ID NO: 1508

WVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSW

Figure 103AQ

>PVRIG_NP_076975_from_45_to_145_variation_of_Ig_Domain SEQ ID NO: 1509

WVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWE

Figure 103AR

>PVRIG_NP_076975_from_45_to_146_variation_of_Ig_Domain SEQ ID NO: 1510

WVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEA

Figure 103AS

>PVRIG_NP_076975_from_45_to_147_variation_of_Ig_Domain SEQ ID NO: 1511

WVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEAC

Figure 103AT

>PVRIG_NP_076975_from_45_to_148_variation_of_Ig_Domain SEQ ID NO: 1512

WVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACG

Figure 103AU

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

MRTGNTQAAHATNMGQMQTLVLFSTLLTLCVSEASPEVWVQVQMEATNLSSFSVHCGVLGYSLISLVTVSCEGFVDAGRTKLAVLHPEFGTQQWAPARQAHWETP
NSVSVTLTMGQSKARSSLANTTFCCEFVTFPHGSRVACRDLHRSDPGLSAPTPALNLQADLVRILGTSGVFLFGFIFILCLRWQQRHWCLSKSQPSLTSTQAQVETQPPHL
ASTHSSFISMENGLYALA

Figure 103AV

>PVRIG_2nd_Met_Mouse_WT SEQ ID NO: 1514

MGQMQTLVLFSTLLTLCVSEASPEVWVQVQMEATNLSSFSVHCGVLGYSLISLVTVSCEGFVDAGRTKLAVLHPEFGTQQWAPARQAHWETPNSVSVTLTMGQSKA
RSSLANTTFCCEFVTFPHGSRVACRDLHRSDPGLSAPTPALNLQADLVRILGTSGVFLFGFIFILCLRWQQRHWCLSKSQPSLTSTQAQVETQPPHLASTHSSFISMENGLY
ALA

Figure 103AW

>PVRIG_Mouse_WT_ECD_(without_SP) SEQ ID NO: 1515

SPEVWVQVQMEATNLSSFSVHCGVLGYSLISLVTVSCEGFVDAGRTKLAVLHPEFGTQQWAPARQAHWETPNSVSVTLTMGQSKARSSLANTTFCCEFVTFPHGSRV
ACRDLHRSDPGLSAPTPALNLQAD

Figure 103AX

>PVRIG_Mouse_WT_ECD_(with_SP) SEQ ID NO: 1516

MGQMQTLVLFSTLLTLCVSEASPEVWVQVQMEATNLSSFSVHCGVLGYSLISLVTVSCEGFVDAGRTKLAVLHPEFGTQQWAPARQAHWETPNSVSVTLTMGQSKA
RSSLANTTFCCEFVTFPHGSRVACRDLHRSDPGLSAPTPALNLQAD

Figure 103AY

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

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGS
LPPSSDPGLSAPPTPAPILRADEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

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

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPFANTTFCCKFASFPEGSWEASGSL
PPSSDPGLSAPPTPAPILRADEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 103BA

>PVRIG_HH-2_(Human_ECD_+_Human_IgG1_Fc_mutated_at_C220S,_C226S,_C229S_of_hinge)_-_without_SP SEQ ID NO: 1519

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGS
LPPSSDPGLSAPPTPAPILRADEPKSSDKTHTSPPSPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 103BB

>PVRIG_HH-2-1-
1_(Human_ECD_with_C127F_mutation_+_Human_IgG1_Fc_mutated_at_C220S,_C226S,_C229S_of_hinge,_encoded_by_natural_codons_instea
d_of_codons_optimized_for_CHO_cells)_-_without_SP SEQ ID NO: 1520

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPFANTTFCCKFASFPEGSWEACGSL
PPSSDPGLSAPPTPAPILRADEPKSSDKTHTSPPSPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 103BC

>PVRIG_MM-1_(Mouse_ECD_+_mouse_IgG2a_Fc)_-_without_SP SEQ ID NO: 1521

SPEVWVQVQMEATNLSSFSVHCGVLGYSLISLVTVSCEGFVDAGRTKLAVLHPEFGTQQWAPARQAHWETPNSVSVTLTMGQSKARSSLANTTFCCEFVTFPHGSRV
ACRDLHRSDPGLSAPTPALNLQADEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTLR
VVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSK
LRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK

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

SPEVWVQVQMEATNLSSFSVHCGVLGYSLISLVTVSCEGFVDAGRTKLAVLHPEFGTQQWAPARQAHWETPNSVSVTLTMGQSKARSSLANTTFCCEFVTFPHGSRV
ACRDLHRSDPGLSAPTPALNLQADEPRGPTIKPSPPSKSPAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTLR
VVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSK
LRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK

Figure 103BE

>Human_Fc_(IgG1) SEQ ID NO: 1523

EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
HYTQKSLSLSPGK

Figure 103BF

>Human_Fc_(IgG1)_C220S SEQ ID NO: 1524

EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
HYTQKSLSLSPGK

Figure 103BG

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

EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVS
NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
HYTQKSLSLSPGK

Figure 103BH

>Human_Fc_(IgG1)_without_hinge SEQ ID NO: 1526

APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 103BI

>Mouse_Fc_(IgG2a) SEQ ID NO: 1527

EPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVN
NKDLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLH
NHHTTKSFSRTPGK

Figure 103BJ

>Mouse_Fc_(IgG2a)_Fc_with_the_N297A_mutation SEQ ID NO: 1528

EPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYASTLRVVSALPIQHQDWMSGKEFKCKVN
NKDLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLH
NHHTTKSFSRTPGK

Figure 103BK

>Mouse_Fc_(IgG2a)_without_hinge SEQ ID NO: 1529

APNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPK
GSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK

Figure 103BL

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

EPKSSDKTHTSPPSPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
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

CACAGGCTGCCCATGCAAC

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

MGHRTLVLPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCA
NTTFCCKFASFPEGSWEACGSLPPSSDPGLSAPPTPAPILRADLAGILGVSGVLLFGCVYLLHLLRRHKHRPAPRLQPSRTSPQAPRARAWAPSQASQAALHVPYATINTS
CRPATLDTAHPHGGPSWWASLPTHAAHRPQGPAAWASTPIPARGSFVSVENGLYAQAGERPPHTGPGLTLFPDPRGPRAMEGPLGVRDYKDDDDK

Figure 103BV

>PVRIG_Mouse_First_Methionine_signal_peptide-Flag-ECD SEQ ID NO: 1540

MRTGNTQAAHATNMGQMQTLVLFSTLLTLCVSEADYKDDDDKSPEVWVQVQMEATNLSSFSVHCGVLGYSLISLVTVSCEGFVDAGRTKLAVLHPEFGTQQWAPAR
QAHWETPNSVSVTLTMGQSKARSSLANTTFCCEFVTFPHGSRVACRDLHRSDPGLSAPTPALNLQADLVRILGTSGVFLFGFIFILCLRWQQRHWCLSKSQPSLTSTQAQ
VETQPPHLASTHSSFISMENGLYALA

Figure 103BW

>PVRIG_Mouse_Third_Methionine_untagged SEQ ID NO: 1541

MQTLVLFSTLLTLCVSEASPEVWVQVQMEATNLSSFSVHCGVLGYSLISLVTVSCEGFVDAGRTKLAVLHPEFGTQQWAPARQAHWETPNSVSVTLTMGQSKARSSLA
NTTFCCEFVTFPHGSRVACRDLHRSDPGLSAPTPALNLQADLVRILGTSGVFLFGFIFILCLRWQQRHWCLSKSQPSLTSTQAQVETQPPHLASTHSSFISMENGLYALA

Figure 103BX

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

MQTLVLFSTLLTLCVSEADYKDDDDKSPEVWVQVQMEATNLSSFSVHCGVLGYSLISLVTVSCEGFVDAGRTKLAVLHPEFGTQQWAPARQAHWETPNSVSVTLTMG
QSKARSSLANTTFCCEFVTFPHGSRVACRDLHRSDPGLSAPTPALNLQADLVRILGTSGVFLFGFIFILCLRWQQRHWCLSKSQPSLTSTQAQVETQPPHLASTHSSFISME
NGLYALA