

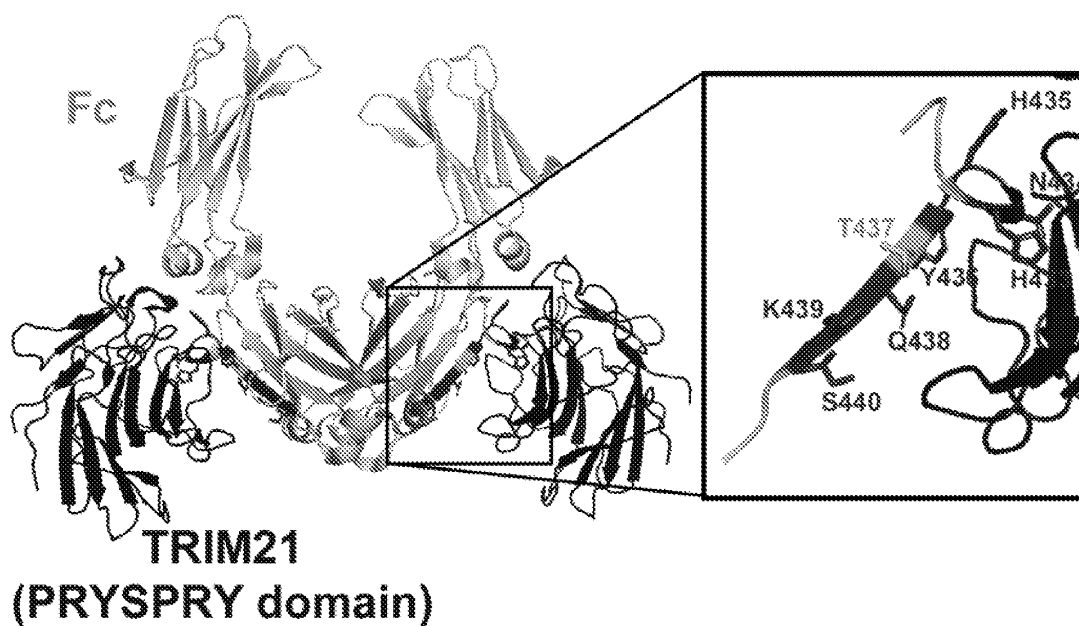


Figure 1A

```

SVFLFPPKPKDTLMISRTPEVTCVVV
DVSHEDPEVKFNWYVDGVEVHNAKTK
PREEQYNSTYRVVSVLTVLHQDWLNG
KEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCL
VKGFYPSDIAVEWESNGQPENNYKTT
PPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPG
K

```

Figure 1B

Sequences of Fc variants from biopanning

	Biopanning of Fc library	
	Round 2	Round 3
Clone #1 (TRHFTQKI)	5 hits	49 hits
Clone #2 (HNHYTQQR)	2 hits	0 hits
Wild type (HNHYTQKS)	10 hits	0 hits
Single hit sequences	18 sequences	1 sequence
Nonsense sequences	15 sequences	2 sequences

Figure 1C

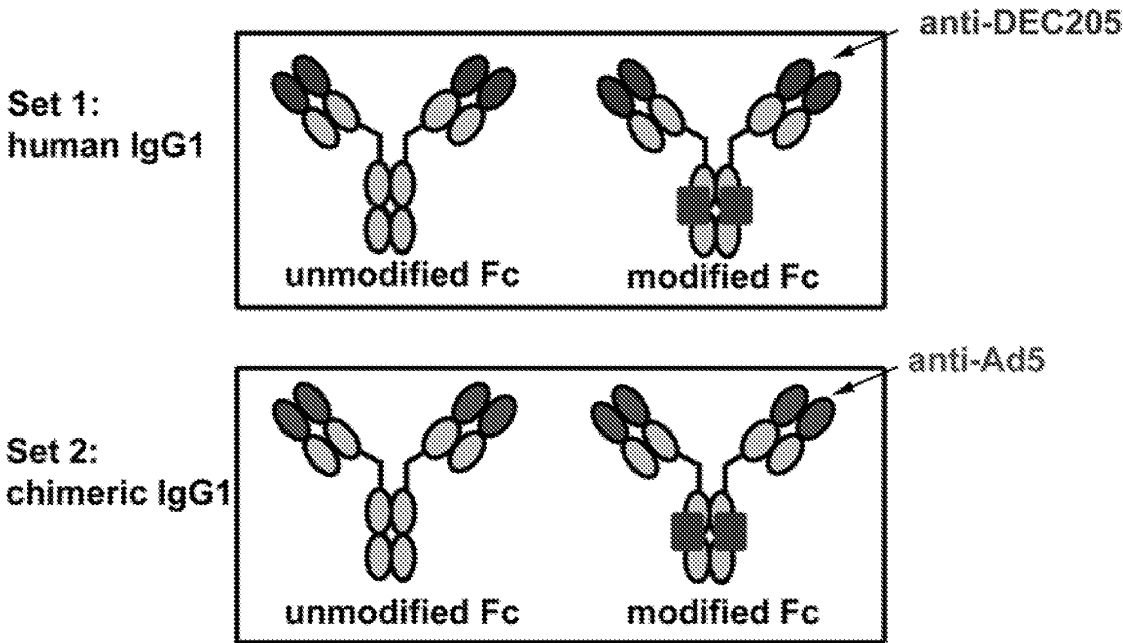


Figure 1D

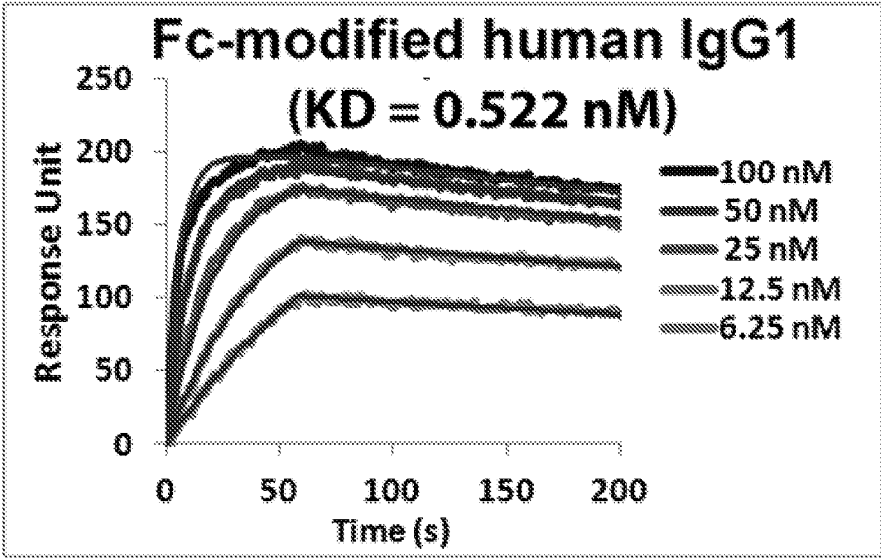


Figure 1E

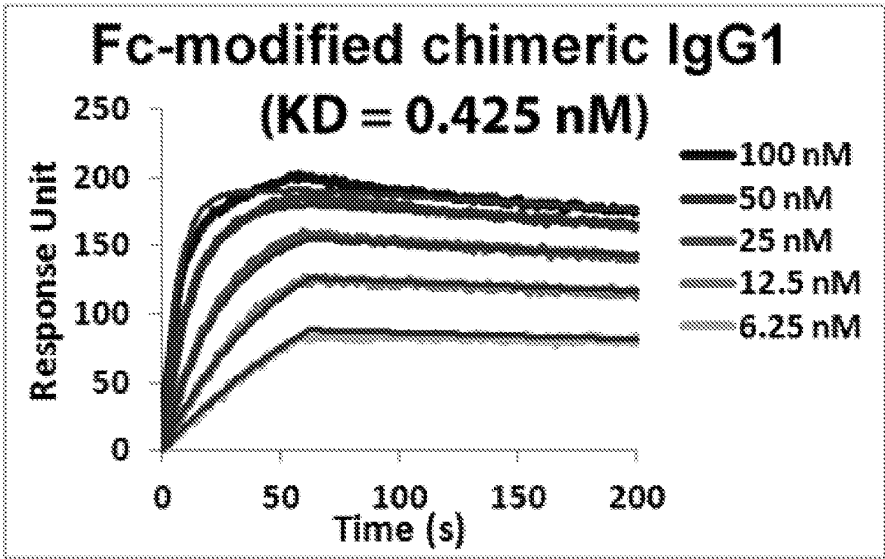


Figure 1F

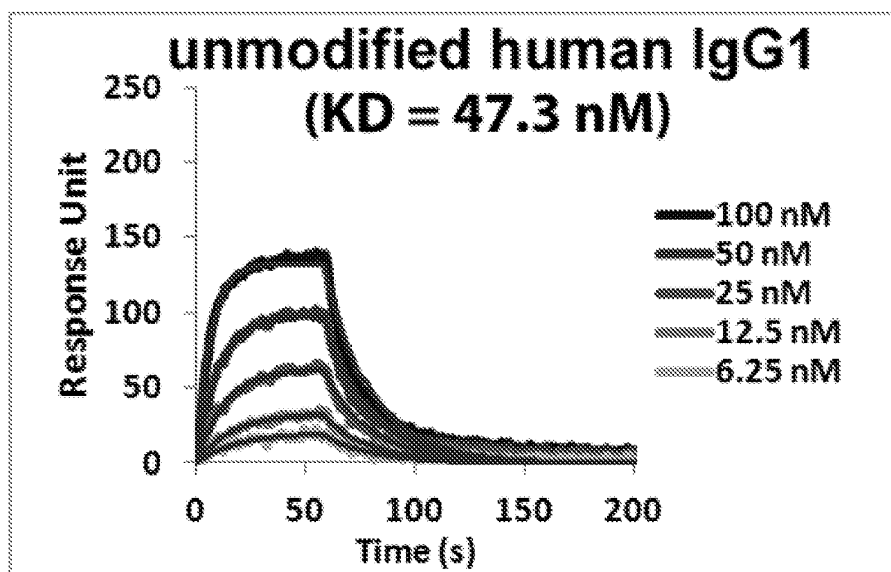


Figure 1G

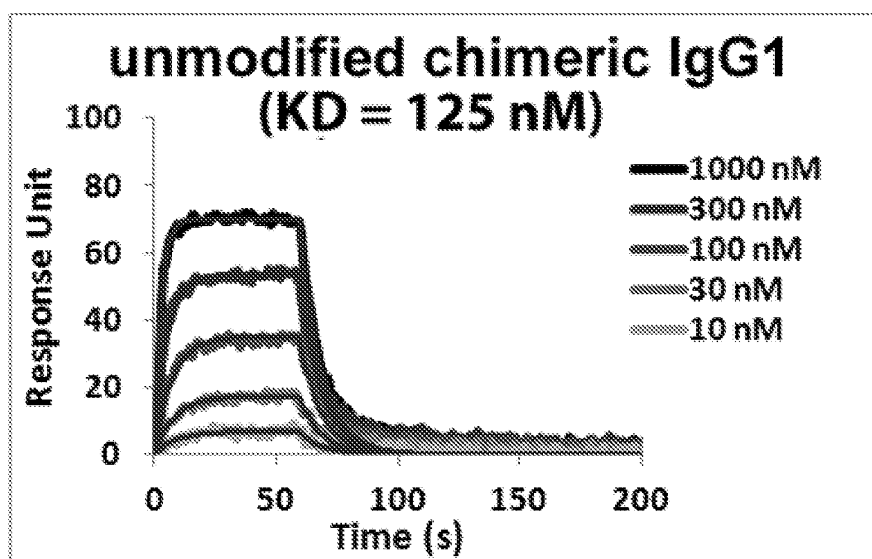


Figure 1H

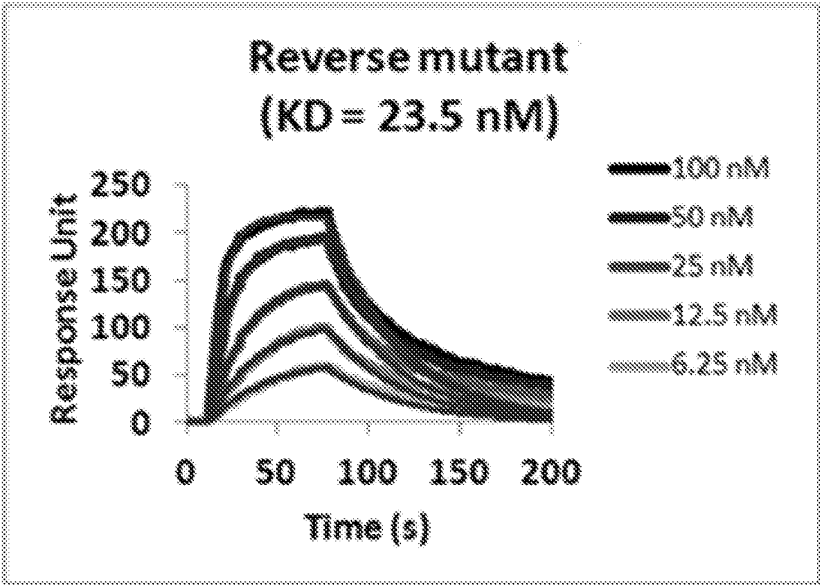


Figure 1l

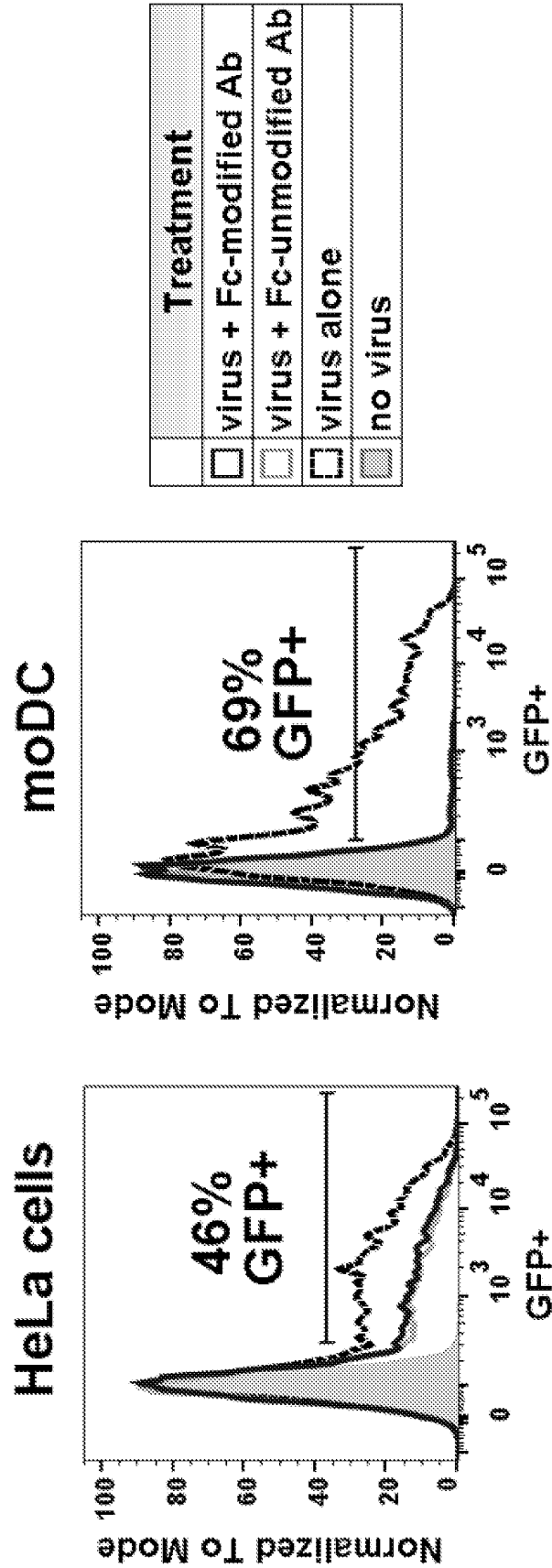


Figure 2A

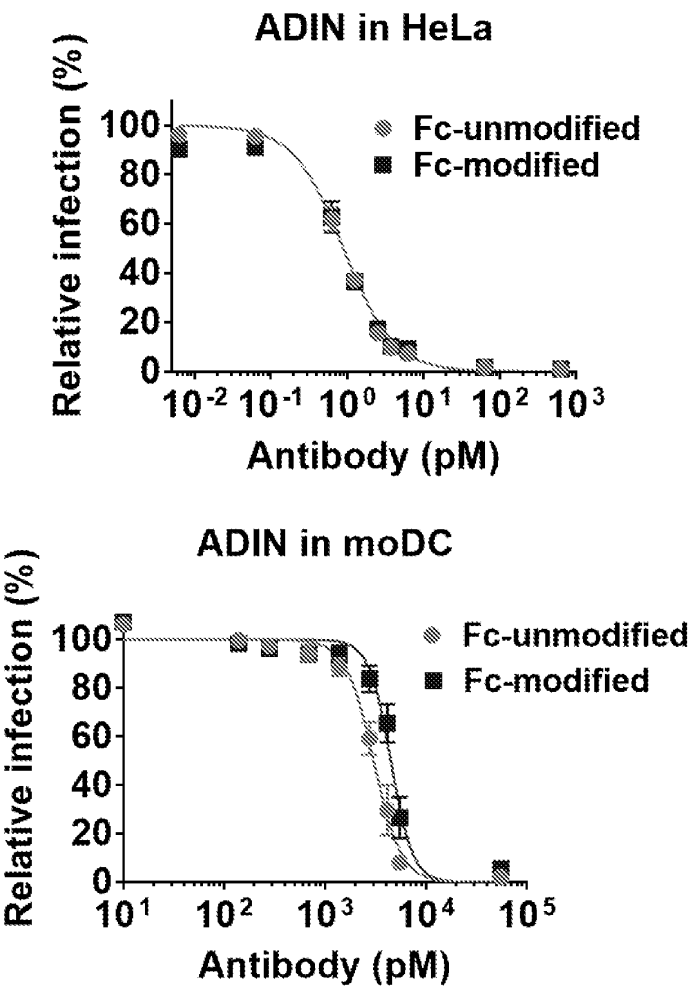


Figure 2B

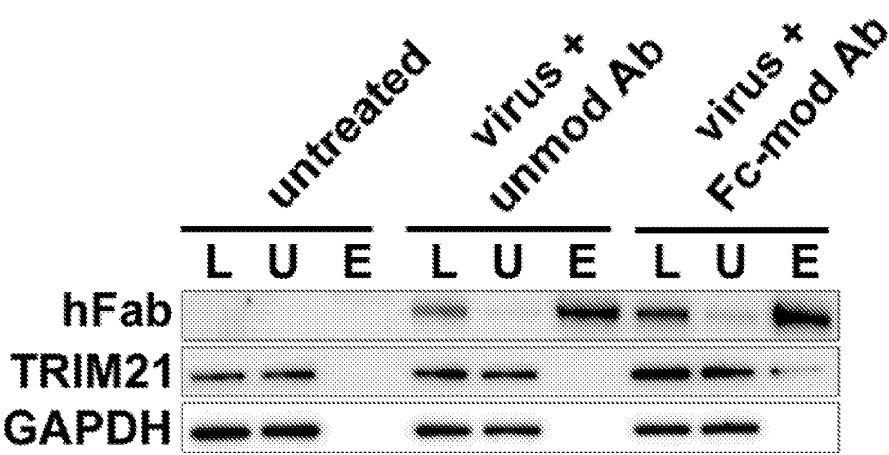


Figure 2C

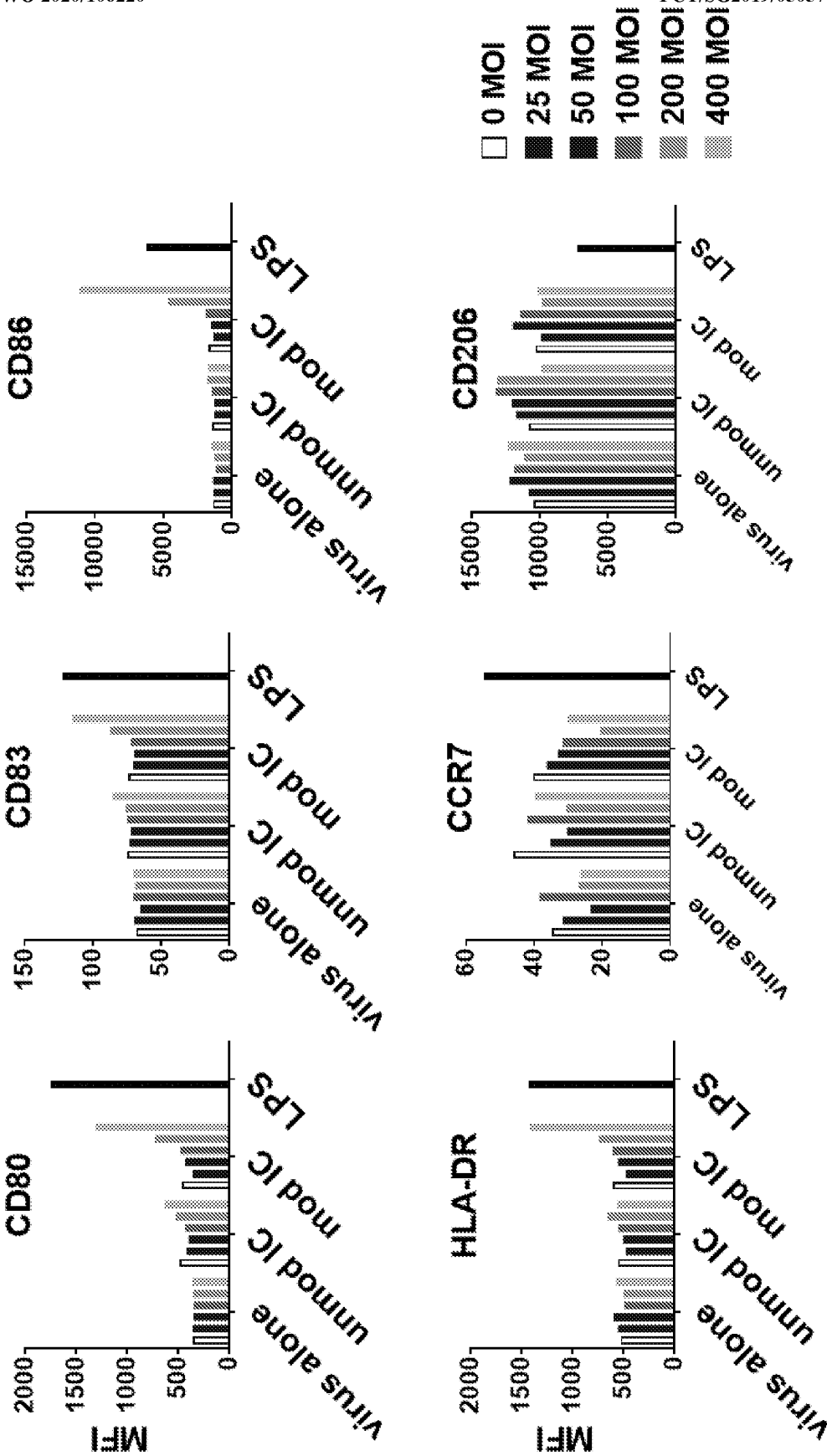


Figure 3A

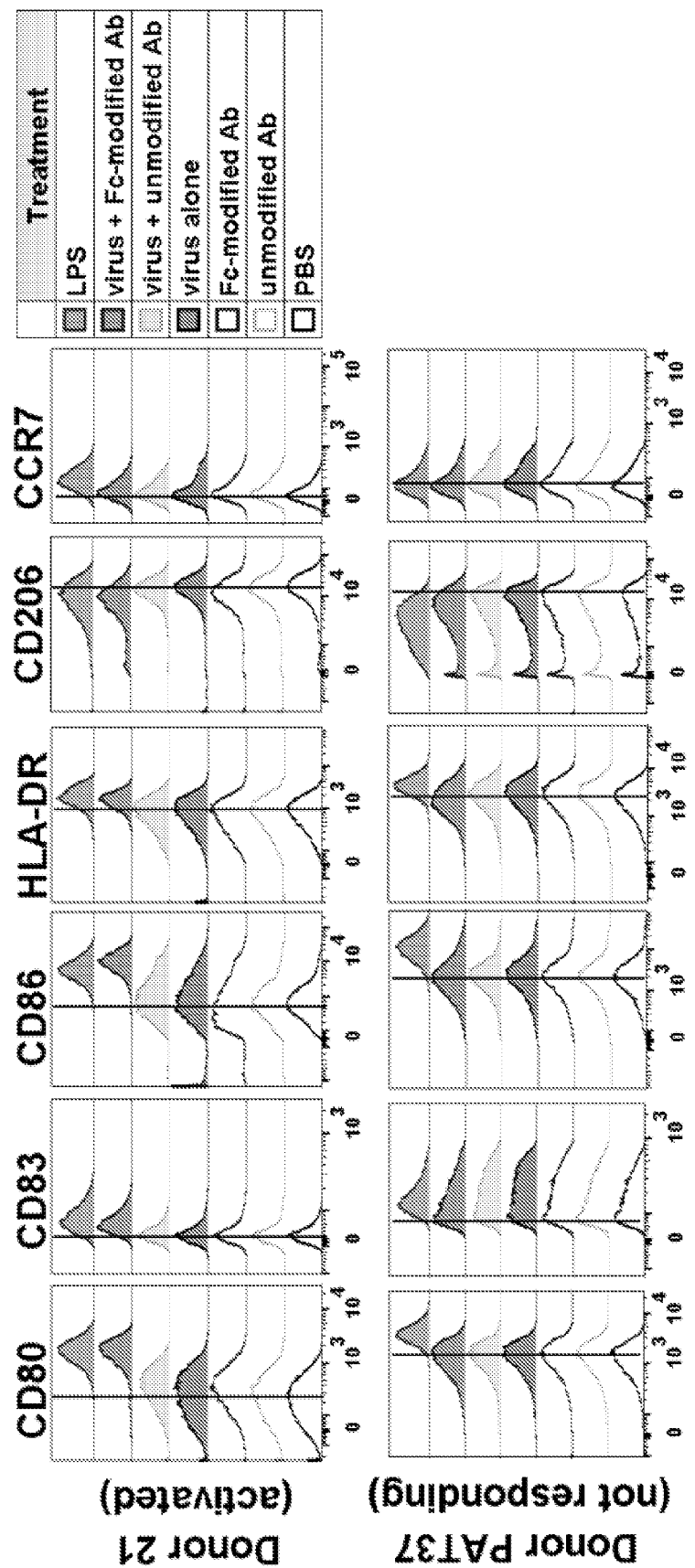


Figure 3B

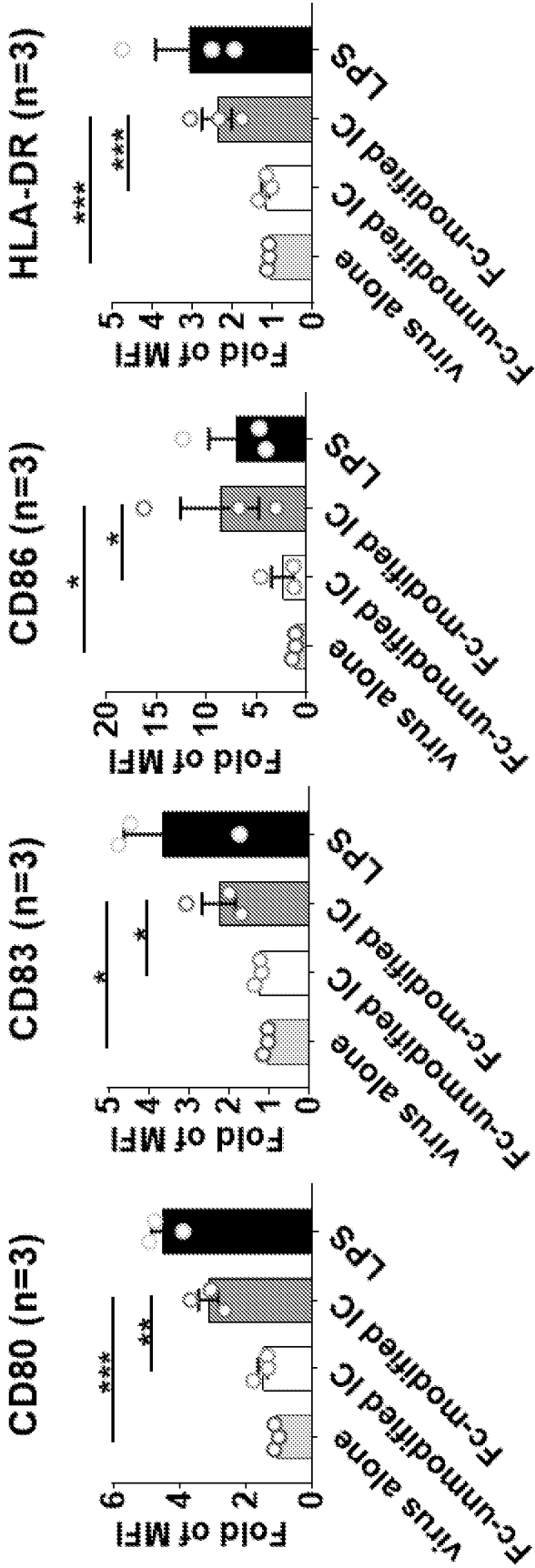


Figure 3C

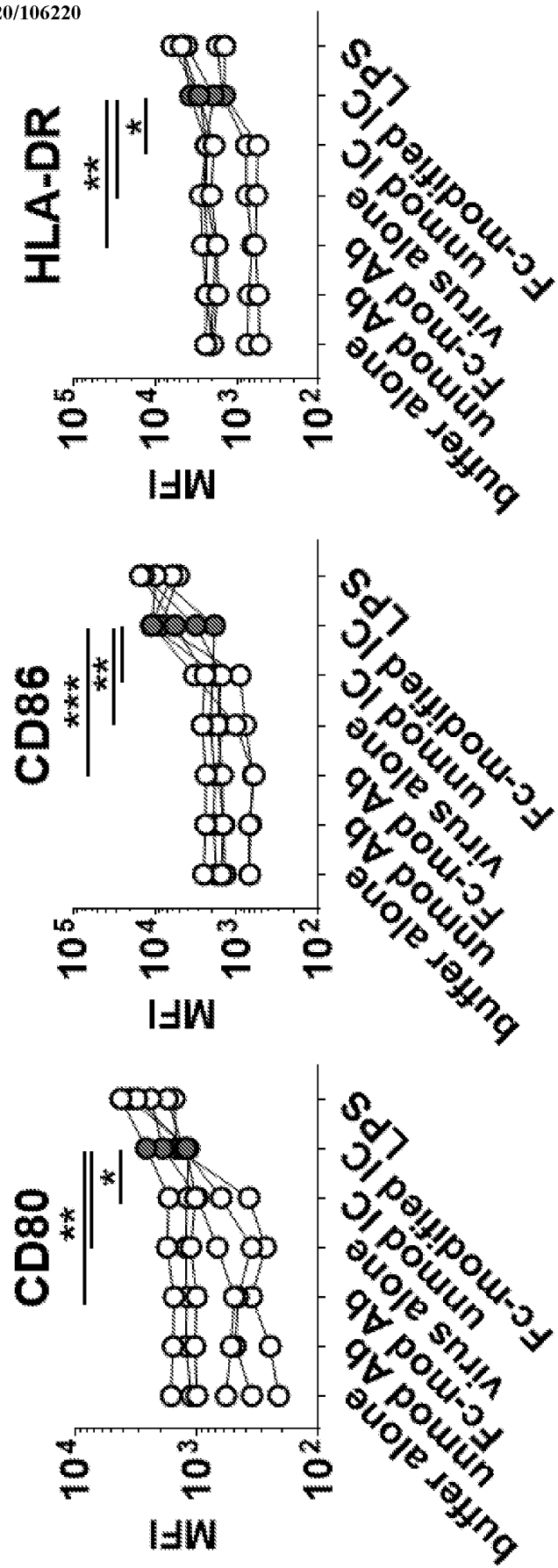


Figure 3D

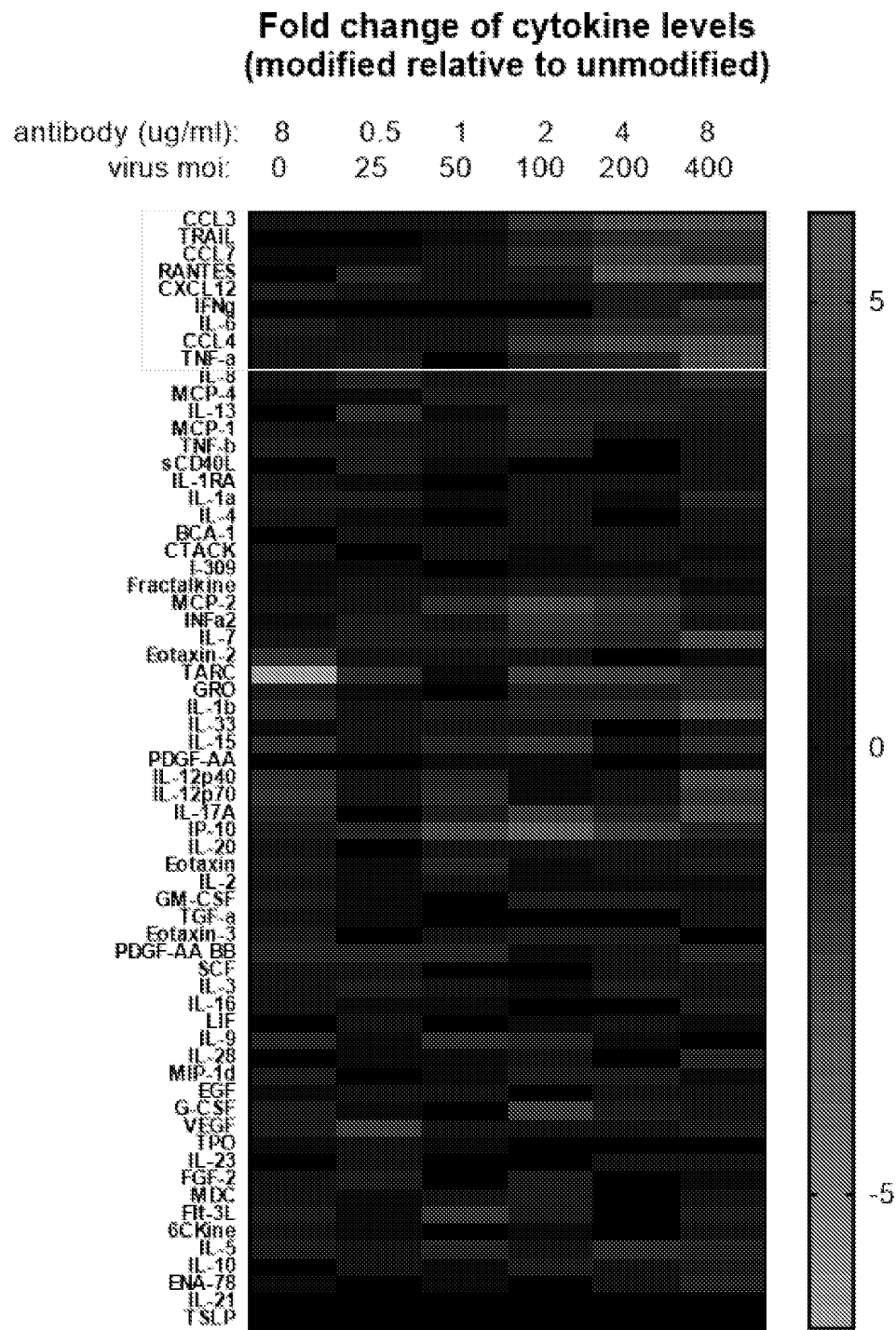


Figure 4A

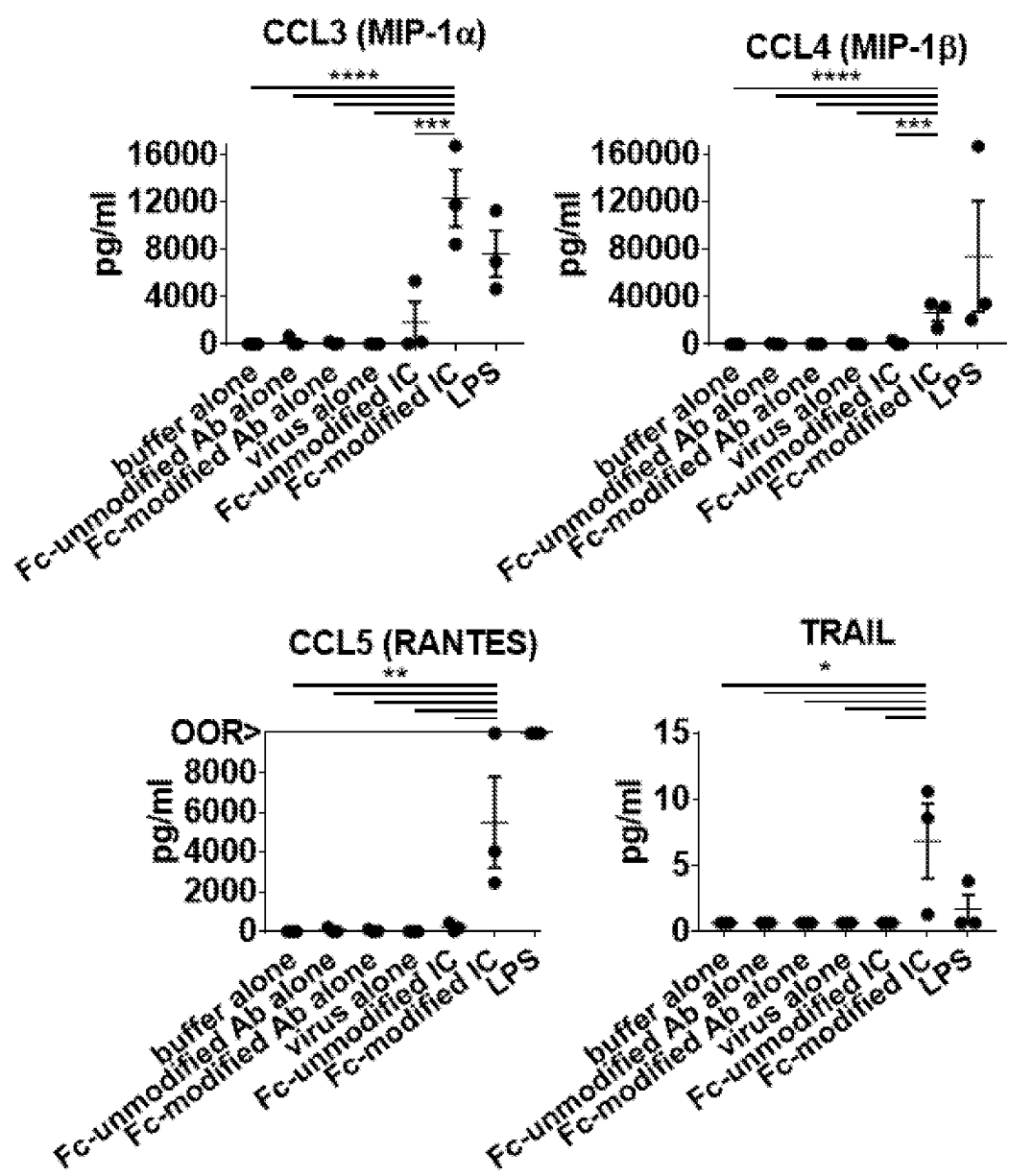


Figure 4B

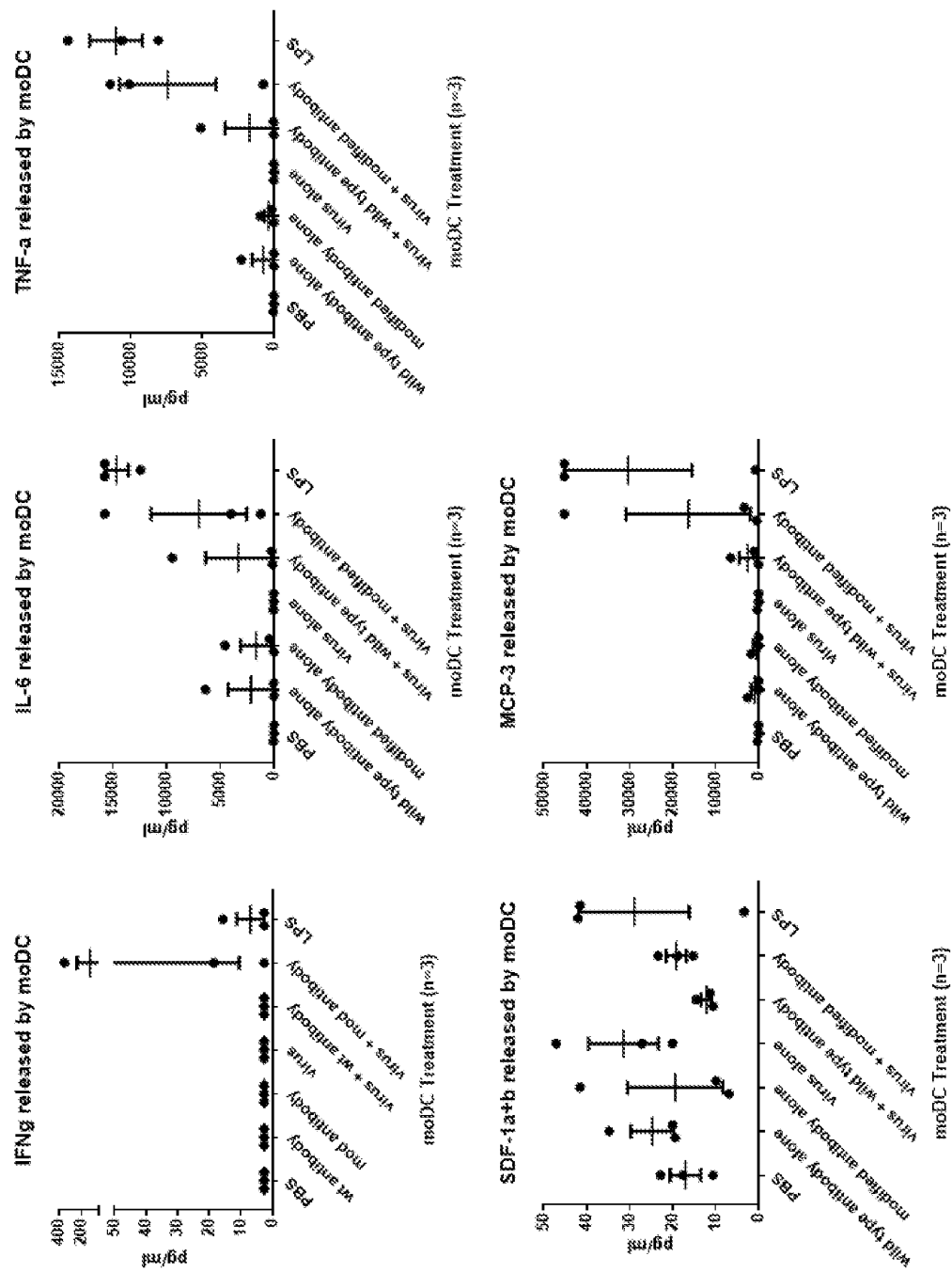


Figure 4C

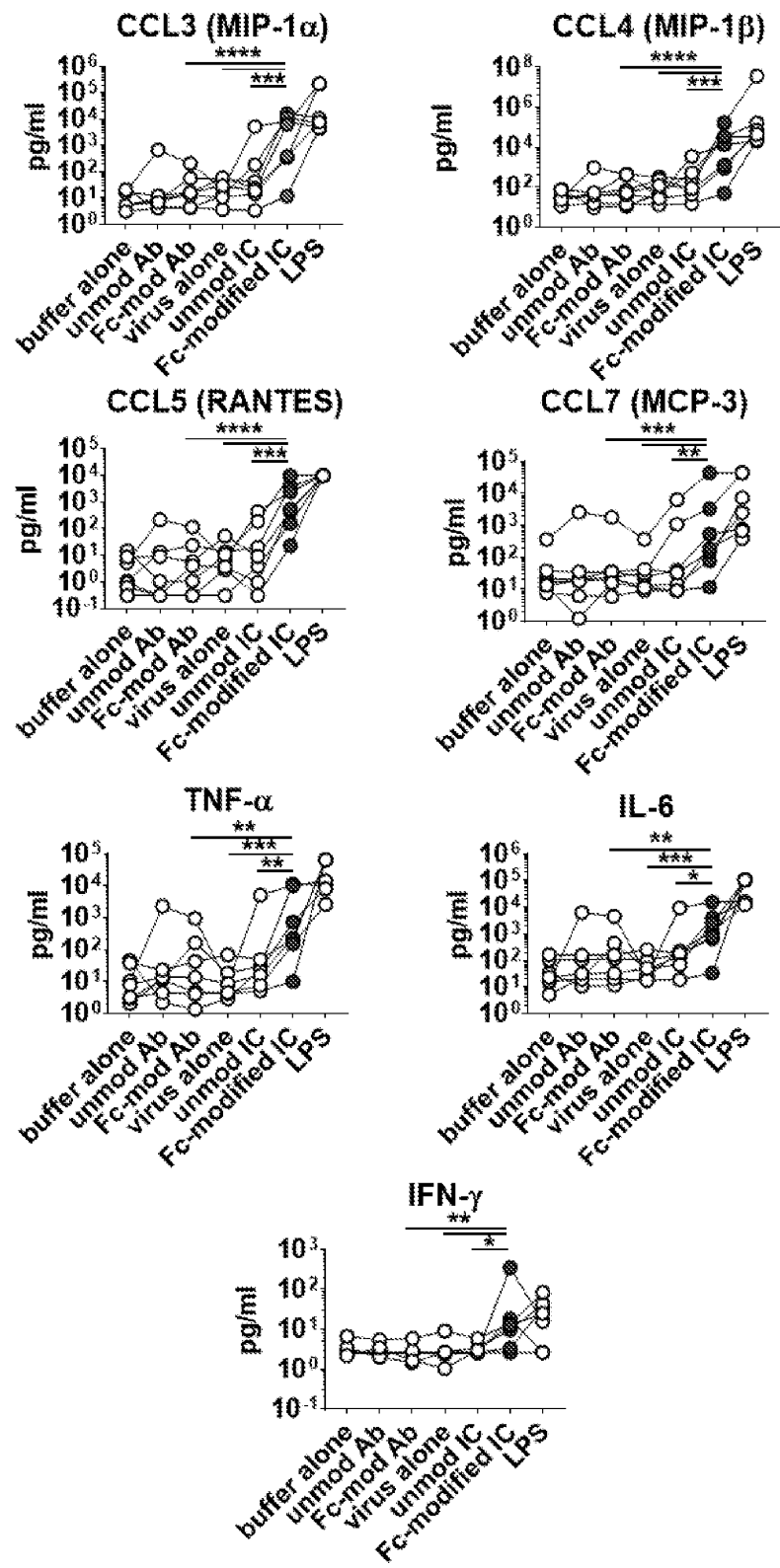


Figure 4D

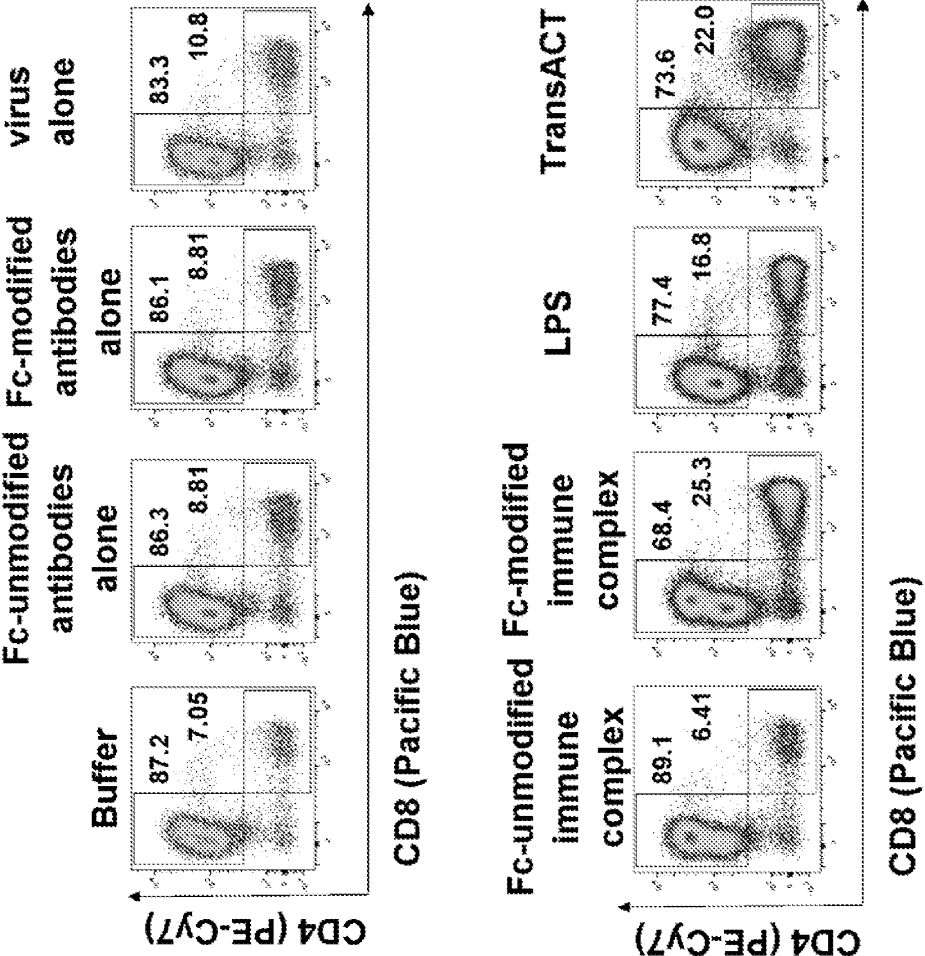


Figure 5A

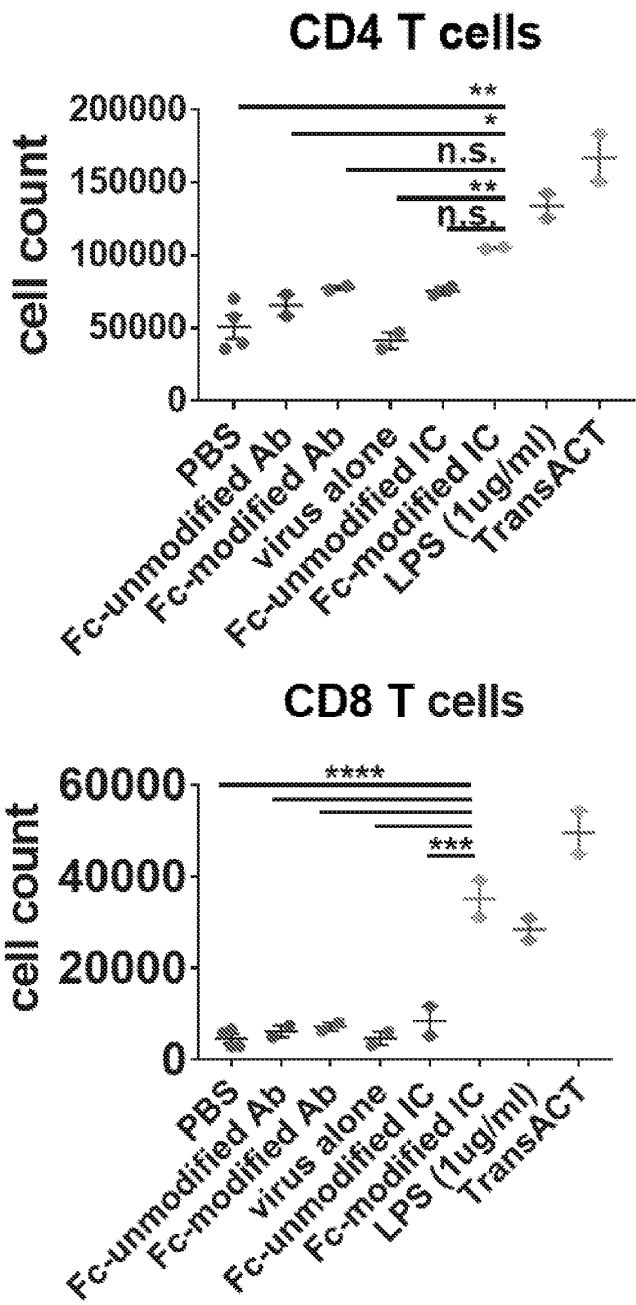


Figure 5B

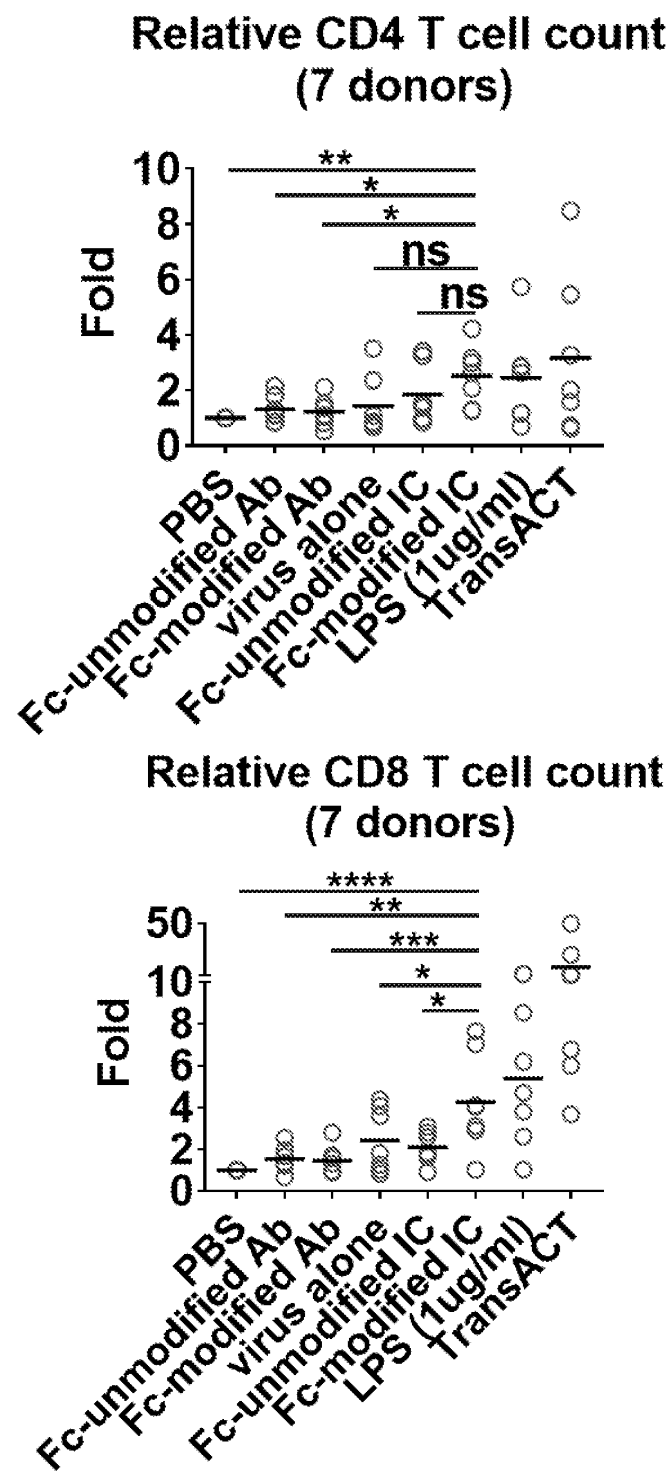


Figure 5C

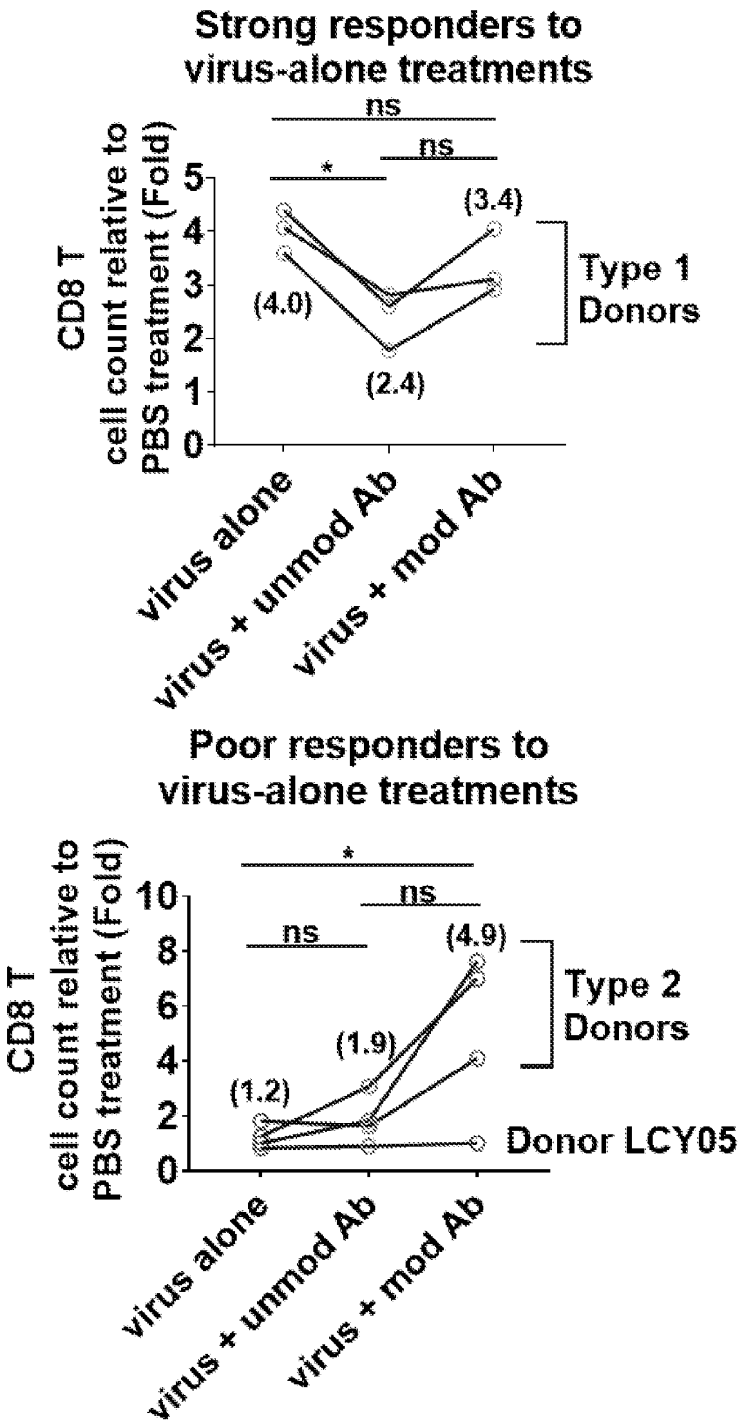


Figure 5D

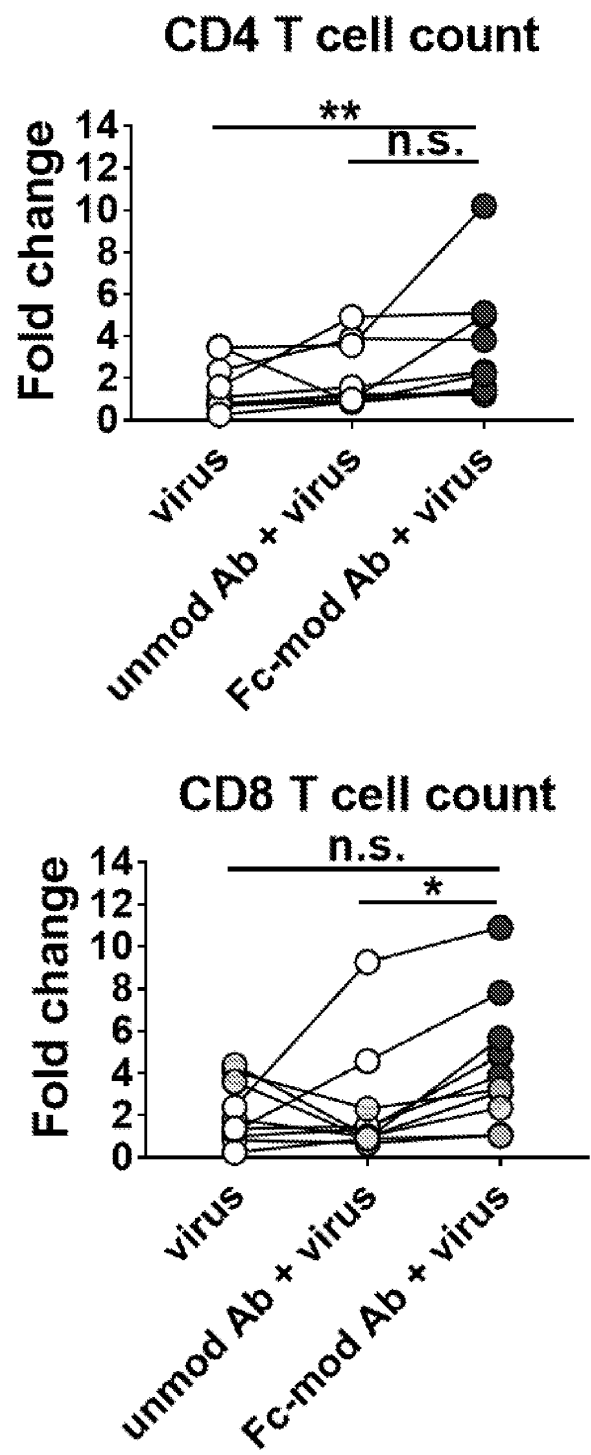


Figure 5E

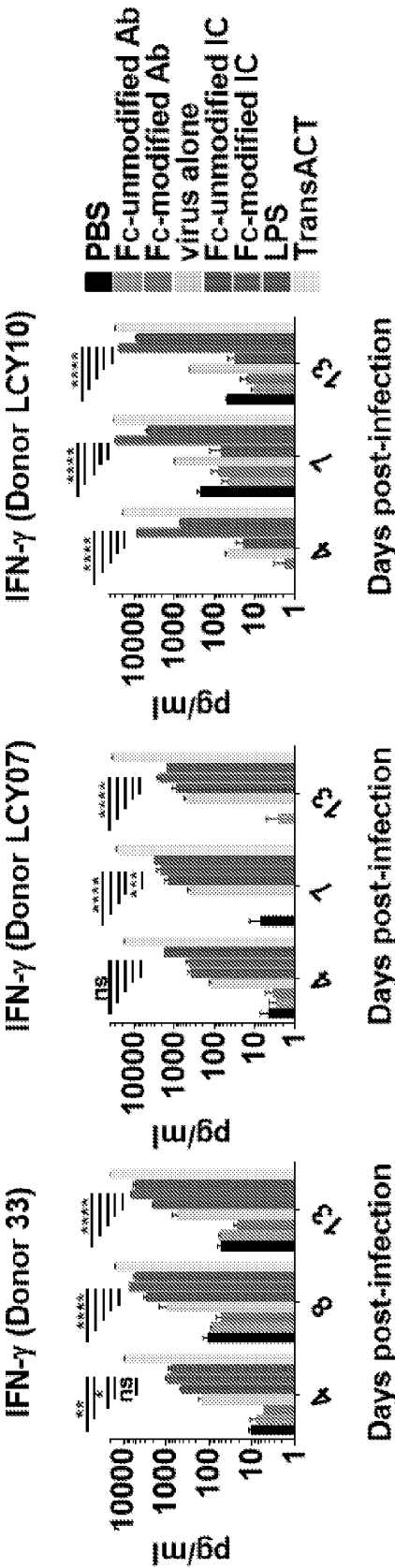


Figure 6A

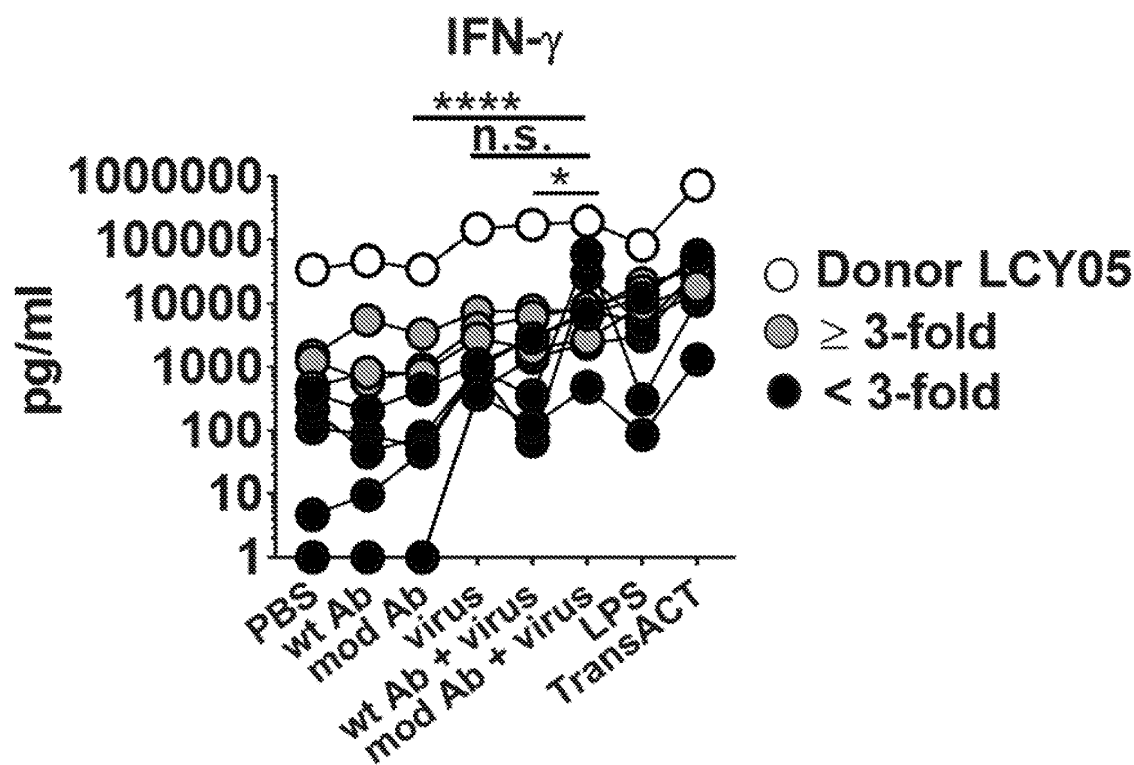


Figure 6B

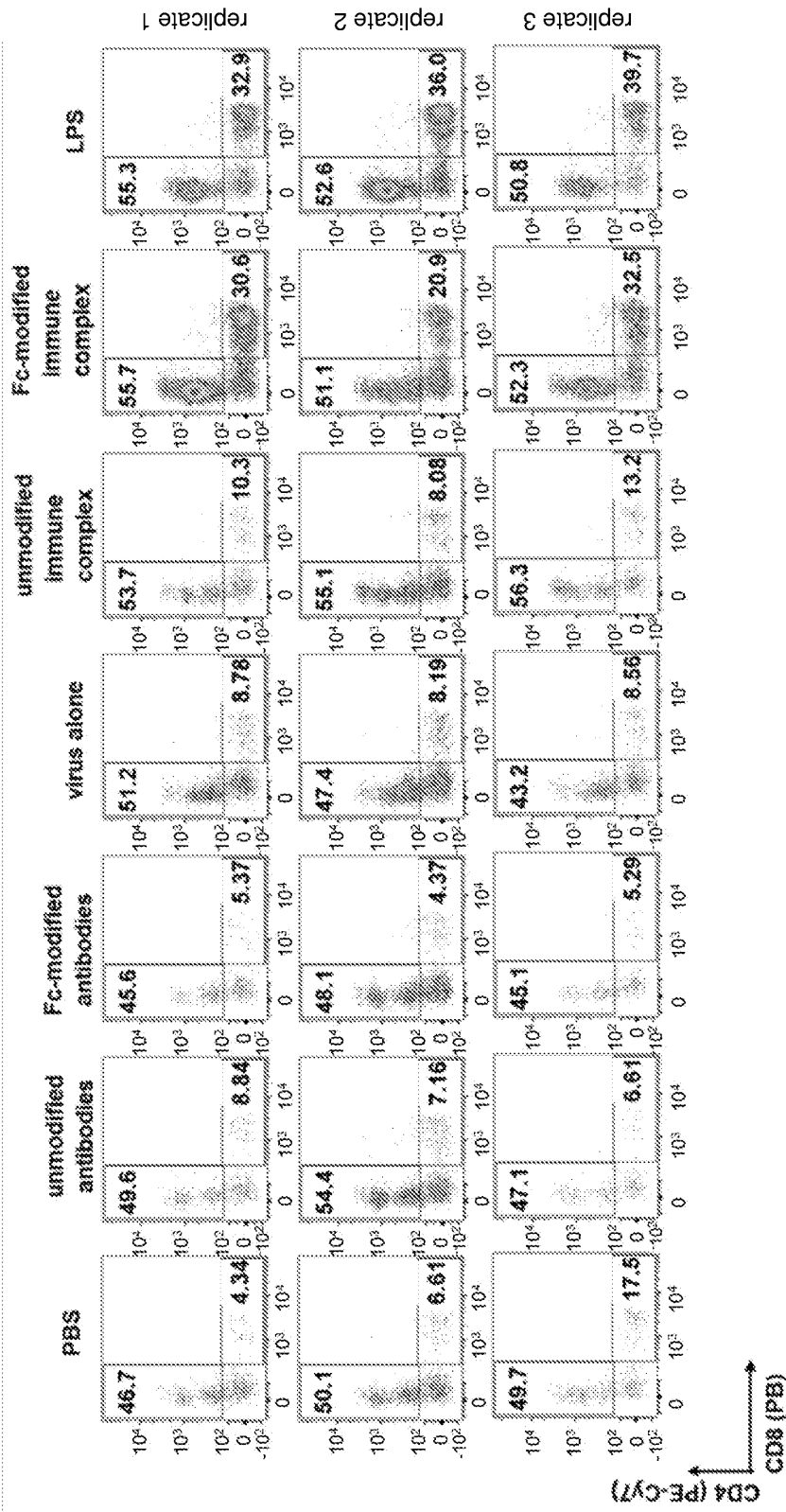


Figure 7

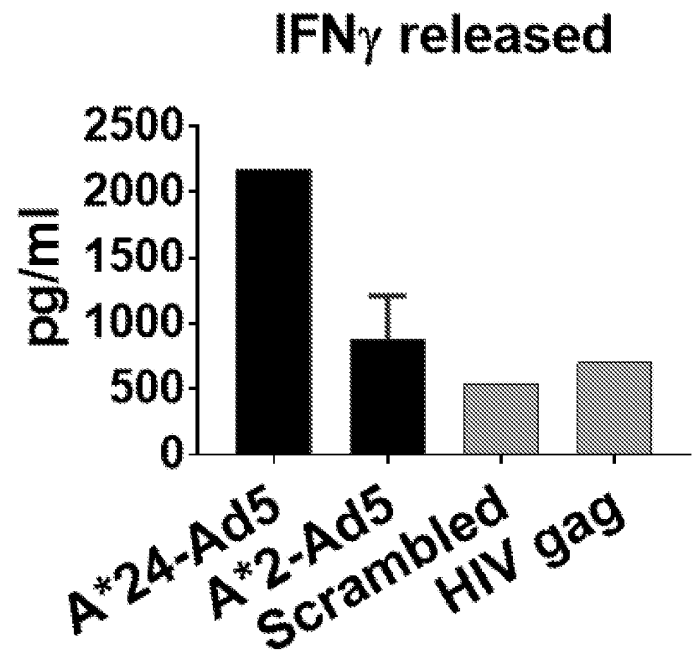


Figure 8A

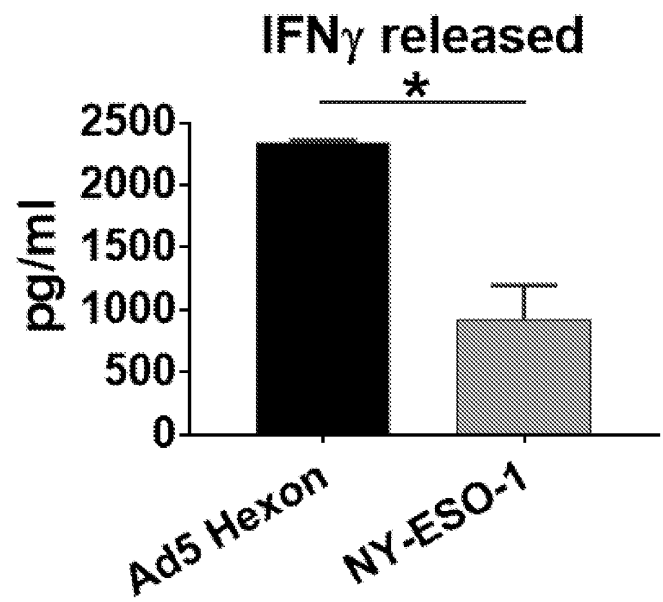


Figure 8B

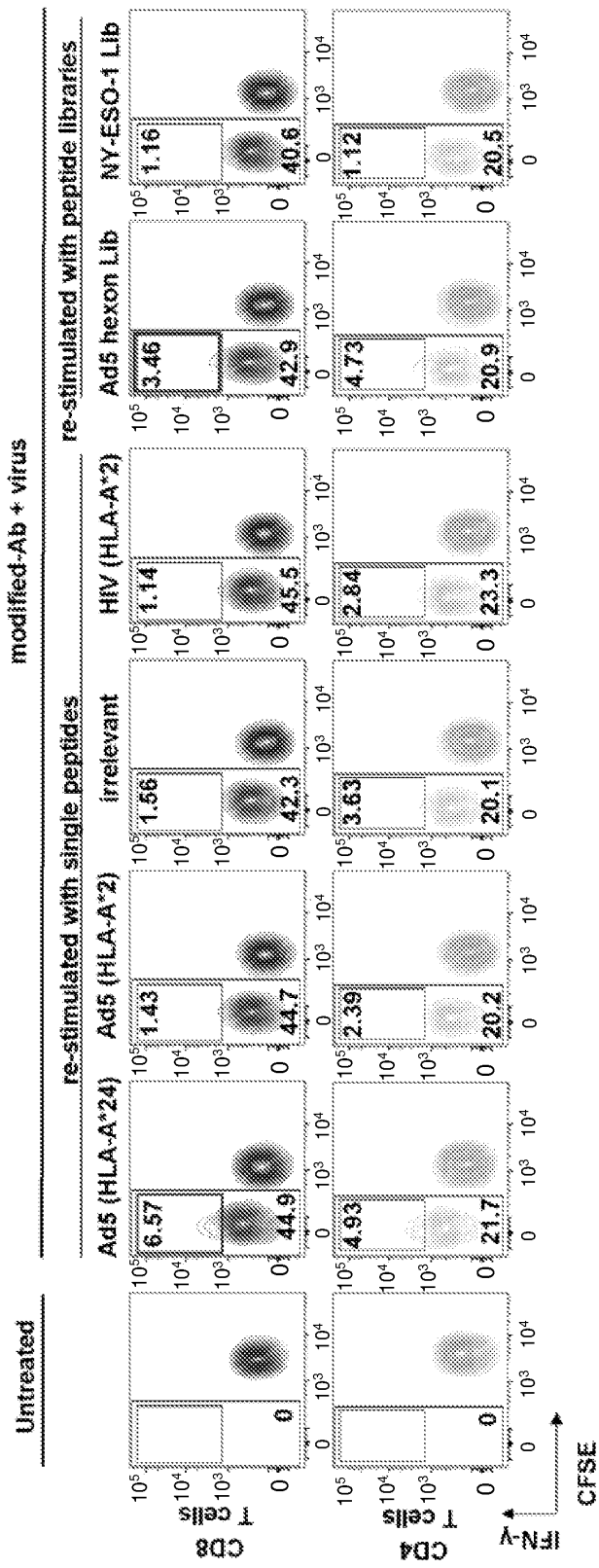


Figure 8C

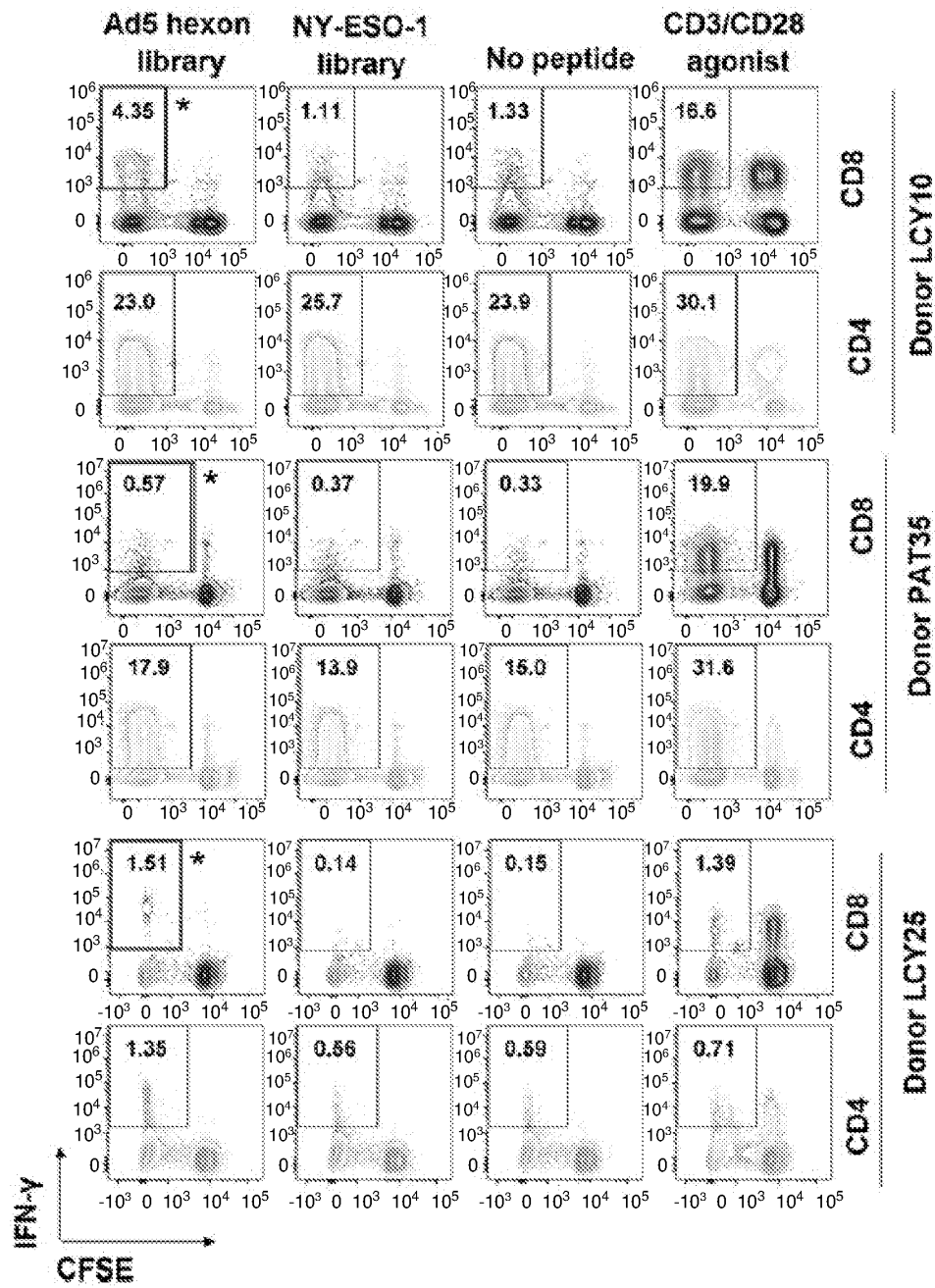


Figure 8D

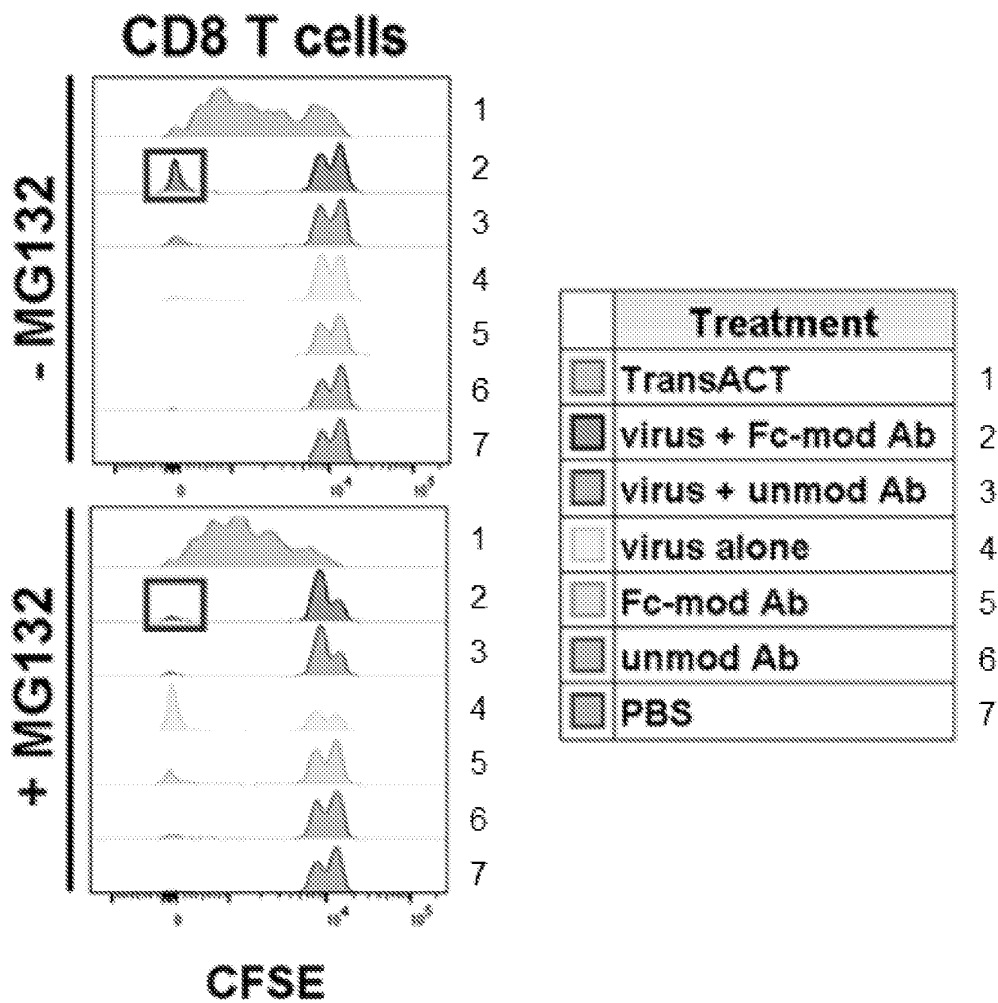


Figure 8E

```

IGHG1  ASTKGPSVFPLAPSSKSTS--GGTAAAGCLVKDYFPEP-VTVSWNSGALT--SGVHTFPA 55
IGHG2  ASTKGPSVFPLAPCSRSTS--ESTAAAGCLVKDYFPEP-VTVSWNSGALT--SGVHTFPA 55
IGHG3  ASTKGPSVFPLAPCSRSTS--GGTAAAGCLVKDYFPEP-VTVSWNSGALT--SGVHTFPA 55
IGHG4  ASTKGPSVFPLAPCSRSTS--ESTAAAGCLVKDYFPEP-VTVSWNSGALT--SGVHTFPA 55
IGHA1  ASPTSPKVPLSLCST-QPDG--NVVIACLWQGFPPQEPLSVTWSESGQG--VTARNFPP 55
IGHA2  ASPTSPKVPLSLDST-PQDG--NVVACLWQGFPPQEPLSVTWSESGQN--VTARNFPP 55
IGHD   APTKAPUVFPIISGCR-HPKONSFVVLACLITGYHPTS-VIVTWYMGTS--QPQRIFPE 56
IGHE   ASTQSPSVFPLTROCKNIESNATSVILGCLATGYFPEP-VMVITWDTGSLN--GTIMILFA 57
IGHM   GSASAPTLFPLVSCEN-SFSDTSSVAVGCLAQDFLPDS-ITFSWKYKONSDDISSTRGFPS 58
      .  . * : ** :      . . : . **  . : *   : . : *      : *

IGHG1  V-LQSSGLYSLSSVVTVPSSSLGT---QTYTCNVNHHKPSNTKVDKWE----- 99
IGHG2  V-LQSSGLYSLSSVVTVPSSNFGT---QTYTCNVNHHKPSNTKVDKVERK----- 101
IGHG3  V-LQSSGLYSLSSVVTVPSSSLGT---QTYTCNVNHHKPSNTKVDKVELKTPFGDTHTC 111
IGHG4  V-LQSSGLYSLSSVVTVPSSSLGT---KTYTCNVNHHKPSNTKVDKRVESK----- 101
IGHA1  SQDASGDLYTTSSQLTLPA----- 74
IGHA2  SQDASGDLYTTSSQLTLPA----- 74
IGHD   I-QRRDSYMTSSQLSTPLQWRQ---GEYKCVVQHTASKSKKEIF----- 98
IGHE   TILTLSGHYATISLLTV-SGANAK---QMFTCRVAHTPSSTDWVDNKTFVCSRDFTFPPT 113
IGHM   V--LRGGKYAATSQVLLPSKVMKQGTDEHVVCVKVQHPNGNKEK--N--VPLPVIAELPPK 112
      . . *   *   :

IGHG1  ----- 99
IGHG2  ----- 101
IGHG3  PRCPEPKSCDTPPPCPR-----CPE-----P-----K----- 133
IGHG4  ----- 101
IGHA1  ----- 74
IGHA2  ----- 74
IGHD   -----RWPESPKQASSVPTAQPOAEGSLA 123
IGHE   VK-ILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGE-- 170
IGHM   VS-VFVPPRDGFFGNPRKSKLICQATGFSRQIQVSWLREGKQVSGSVTTDQVQAEAKES 171

IGHG1  -----PKSCDKTHICPPCPAPELL----- 118
IGHG2  -----CCVECPPCPAEFV----- 114
IGHG3  -----SCDTPPPCPRCPEPKSCDTPPPCPRCPAPELL----- 165
IGHG4  -----YGPPCPSCPAEFL----- 115
IGHA1  -----TQCLAGKSVTCHVKHYINP--SQDVTVPVCPVSTPTPTSPSTFPPT 117
IGHA2  -----TQCPDGKSVTCHVKHYTNS--SQDVTVPVCPVFP----- 105
IGHD   KATTAPATTNT-----GRGGEEMKK--EKEKEEQEEREITKTPECPSTHT----- 165
IGHE   ---LASTQSELTLSQKHWSLDRITYTCQVTYQGHT--FEDSTKWCAD-SNP----- 214
IGHM   GPTTYKVTSTLTIKESDNLGQSMFTCRVDHRLT--FQQNASSMCVEDQ----- 218

IGHG1  -----GGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN-AKT 172
IGHG2  -----AGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN-AKT 168
IGHG3  -----GGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN-AKT 219
IGHG4  -----GGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN-AKT 169
IGHA1  PSPSCCHPRLSLHRP-ALEDLLLGSEANLTCTLTGLRDAS-GVTFTWTPSSGKSAV-QGP 174
IGHA2  -PPFCCHPRLSLHRP-ALEDLLLGSEANLTCTLTGLRDAS-GATFTWTPSSGKSAV-QGP 161
IGHD   ---QPLGVYLLTP-AVQDLWLRDKATFTCFVVGSDLDK--AHLTIWEVAGKVPTGGVEE 217
IGHE   -----RGVSAYLSRPSEF-DLFIRKSPTITCLVVDLAPSKGTVMNLWSRASGKPVN-HST 267
IGHM   ----DTAIRVFAIPP-SFASIFLTSTKTLTCLVTDLTYYD-SVTISWTRONGEAVK-THT 271
      *       : :      . **  . . . . . : . *   .

```

Figure 9A

IGHG1	KFREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ--PREPQV	231
IGHG2	KFREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKAKGQ--PREPQV	227
IGHG3	KFREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ--PREPQV	278
IGHG4	KFREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQ--PREPQV	228
IGHA1	---PERDLGCGYSVSSVLPGCAEFWNHGKFTTCTAAYPESKTPLTATLSKS--GNTFRPEV	230
IGHA2	---PERDLGCGYSVSSVLPGCAQFWNHGKFTTCTAAHPELKTPLTANITKS--GNTFRPEV	217
IGHD	GLLERHSHSGSQSHSRLTLPRSLWNAGTSVTCTLNHESLPPQRLMALREPAQAQFVKLSL	277
IGHE	RKEEKQRNGTLTVTSTLPVGTIRDWIEGETYQCRVTHPHLPRAIMRSTTKTSGP--RAAPEV	326
IGHM	NISESHPNATFSAVGEASICEEDWNSGERFTCTVTHTDLPSPPLWQTISRPKGVALHRPDV	331
	* * * *	:
IGHG1	YTLPPSRDELT-KNQVSLTCLVKGIFYPSDIAVEWESNGQ--PENNYKTPFPVLDSG---G	285
IGHG2	YTLPPSREEMT-KNQVSLTCLVKGIFYPSDISVEWESNGQ--PENNYKTPFPMLDSG---G	281
IGHG3	YTLPPSREEMT-KNQVSLTCLVKGIFYPSDIAVEWESSGQ--PENNYNTTPFPMLDSG---G	332
IGHG4	YTLPPSQEEMT-KNQVSLTCLVKGIFYPSDIAVEWESNGQ--PENNYKTPFPVLDSG---G	282
IGHA1	HLLPPPSEELALNELVTLTCLARGFSFKDVLVRWLQGSQELPREKYLWASRQEPSQGT	290
IGHA2	HLLPPPSEELALNELVTLTCLARGFSFKDVLVRWLQGSQELPREKYLWASRQEPSQGT	277
IGHD	NLLASDPP---EAASWLLCEVSGFSPFNILLMWLEDQREVNTSGFAPARPP--PQPRST	332
IGHE	YAFATPEWPGS-RDKRTLACLIQNEMPEDISVQWLHNEVQLPDARHSTTQPRKTKG---S	382
IGHM	YLLPPAREQLNLRESATITCLVTGFSPADVTVQMMQRGQPLSPEKYVTSAPMPFEPQAP-G	390
	: . : * . * * : : *	.
IGHG1	SFFLYSKLTVDKSRWQQGNVFSCSVMHREALHN-HYTQKSLSLSPGK-----	330
IGHG2	SFFLYSKLTVDKSRWQQGNVFSCSVMHREALHN-HYTQKSLSLSPGK-----	326
IGHG3	SFFLYSKLTVDKSRWQQGNIFSCSVMHREALHN-RFTQKSLSLSPGK-----	377
IGHG4	SFFLYSKLTVDKSRWQEGNVFSCSVMHREALHN-HYTQKSLSLSLGK-----	327
IGHA1	TFAVTSILRVAAEDWKKGDTFSCMVGHEALPL-AFTQKTIDRLAGKPTHVNVSVVMAEVD	349
IGHA2	TYAVTSILEVAAEDWKKGETFSCMVGHEALPL-AFTQKTIDRMAGKPTHINVSVMMAEAD	336
IGHD	TFWANSVLVPPAPSPQPATIYTCVVSHEDSRTLLNASRSLEVSIVT-----DH--	380
IGHE	GFFVFSRLLEVTRAWEQKQDEFICRAVHEAASFSQTVQRAVSVNPGK-----	428
IGHM	RYFAHSILTVSEEEWNTGETYTCVVAHEALPN-RVTERTVDKSTGKPTLYNVSLVMSDTA	449
	: * * * : * . **	.
IGHG1	-----	330
IGHG2	-----	326
IGHG3	-----	377
IGHG4	-----	327
IGHA1	GTCY	353
IGHA2	GTCY	340
IGHD	GPMK	384
IGHE	-----	428
IGHM	GTCY	453

Figure 9B

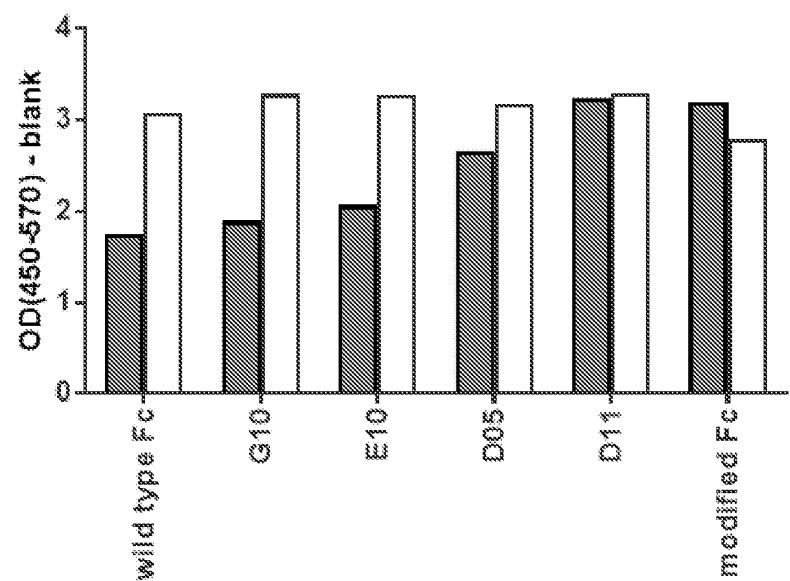


Figure 10

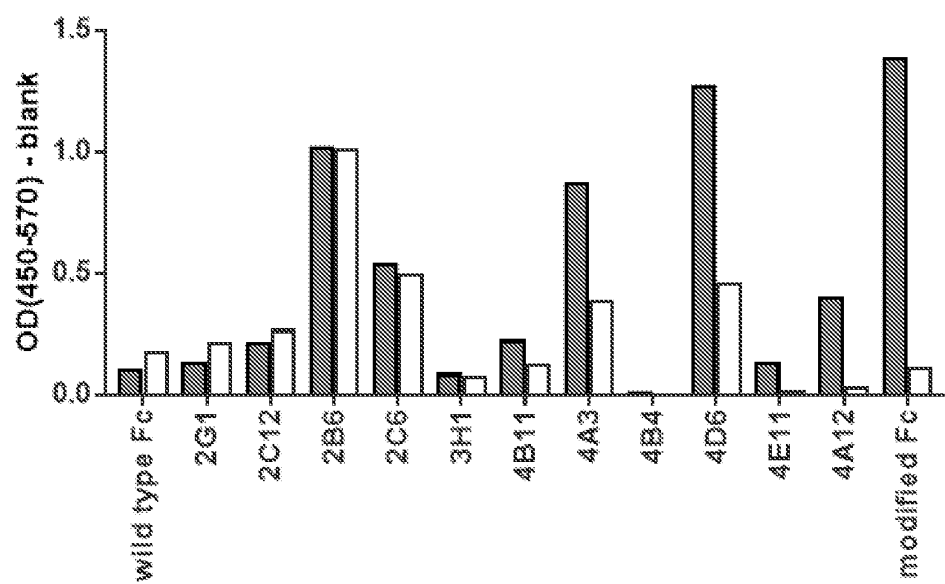


Figure 11

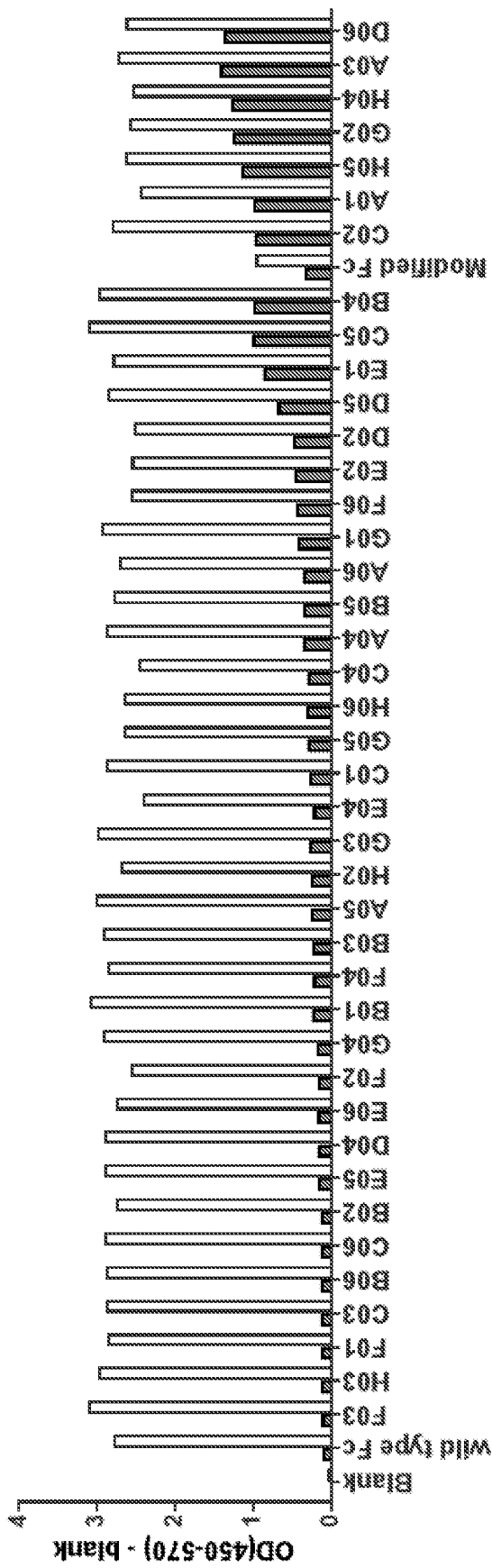


Figure 12A

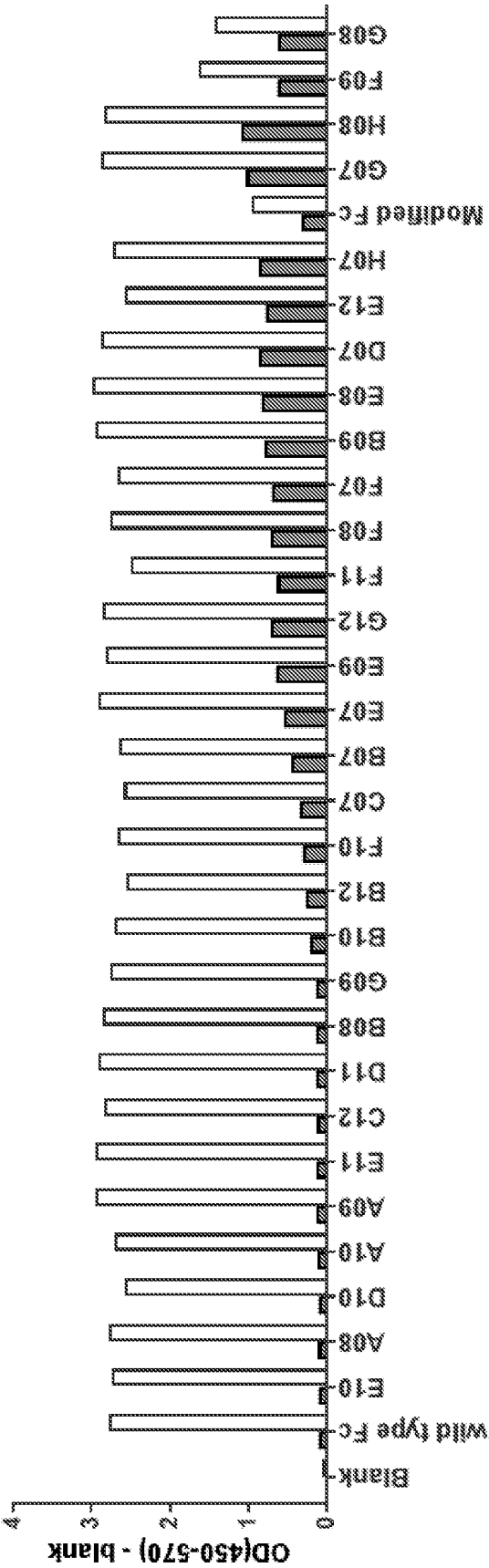


Figure 12B

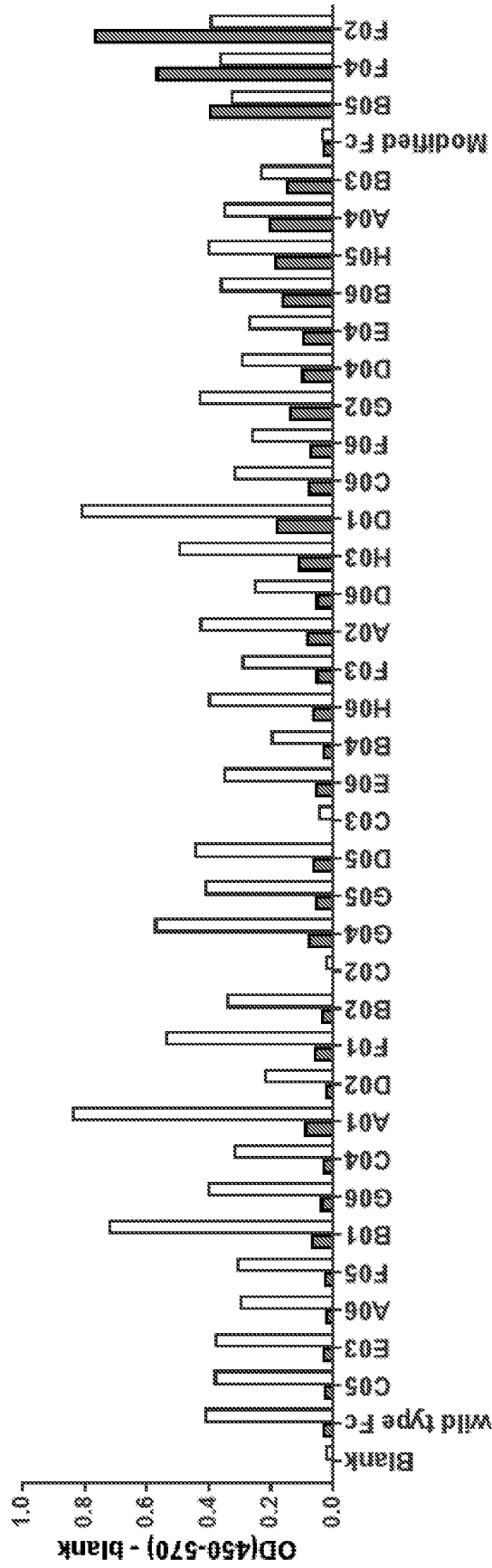


Figure 12C

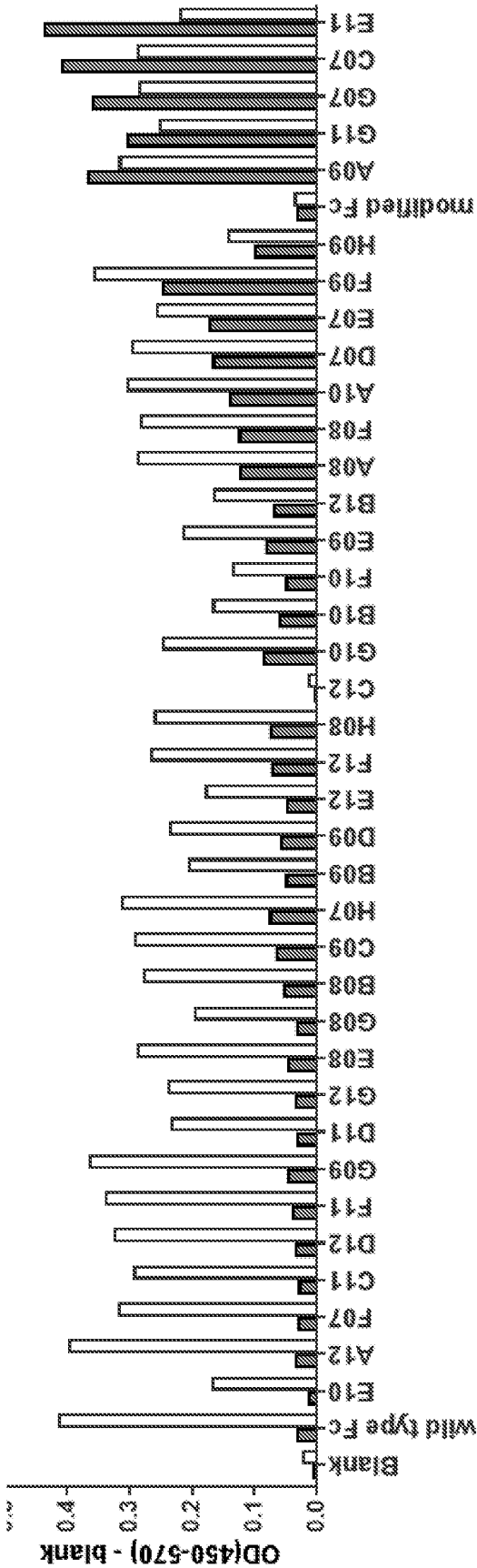


Figure 12D

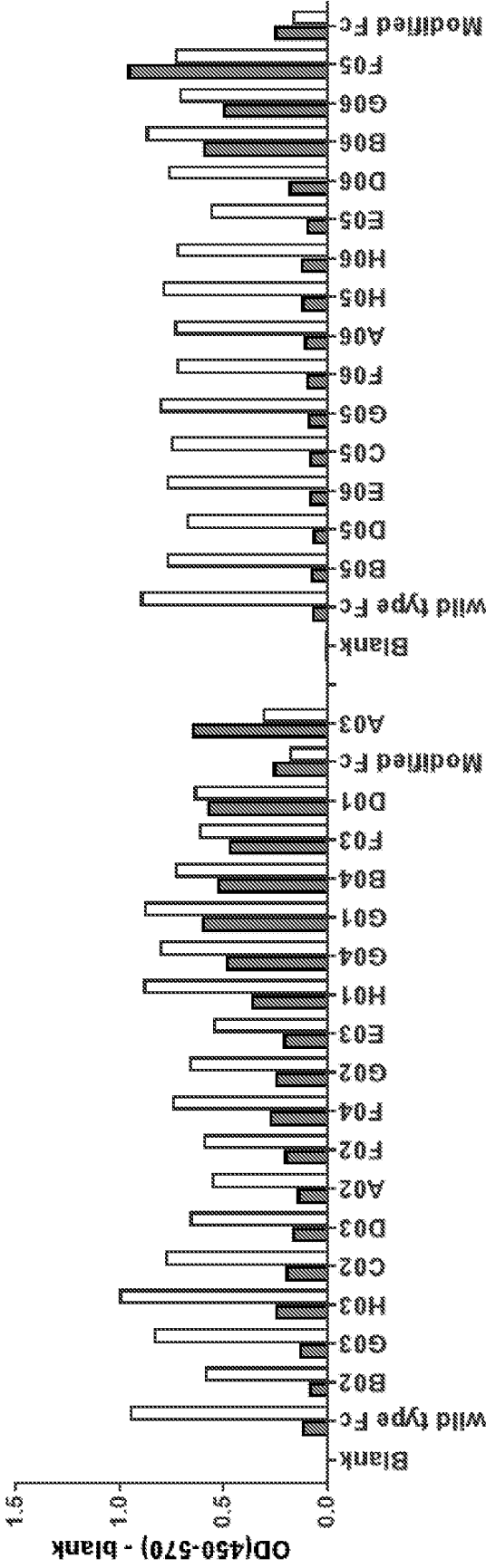


Figure 12E

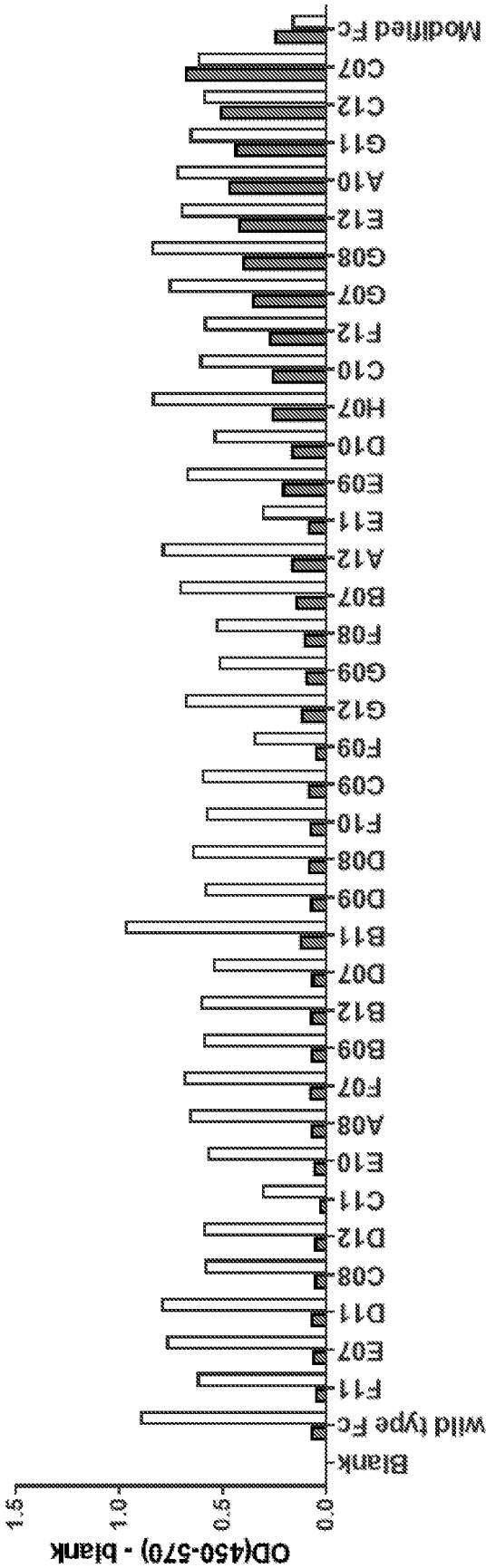


Figure 12F

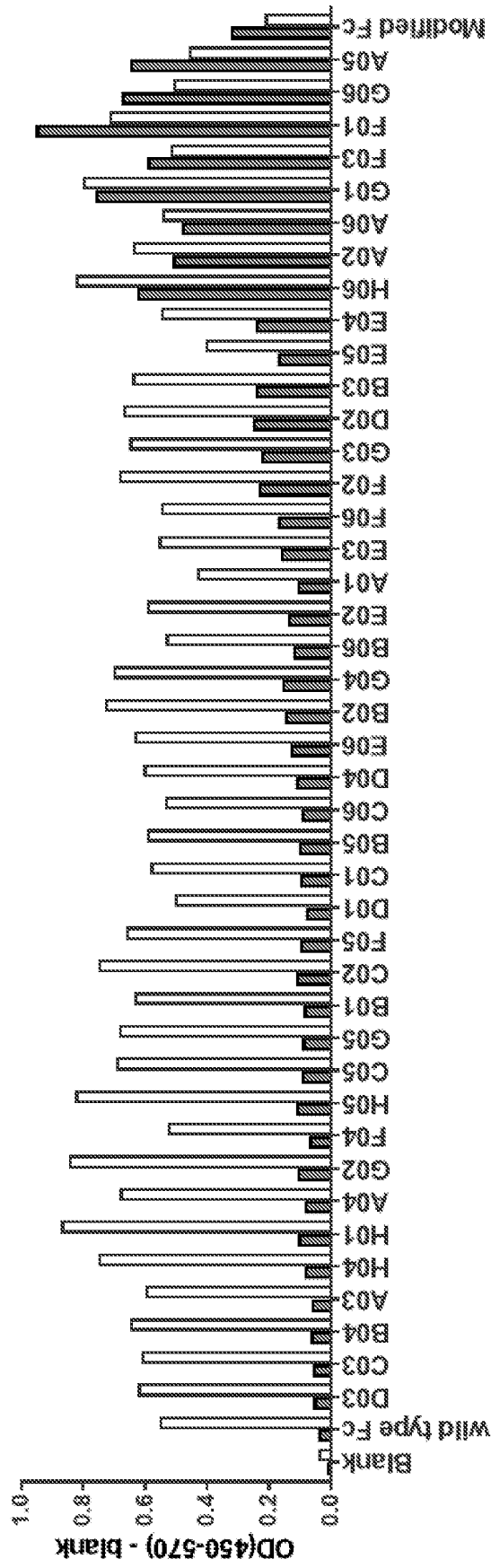


Figure 12G

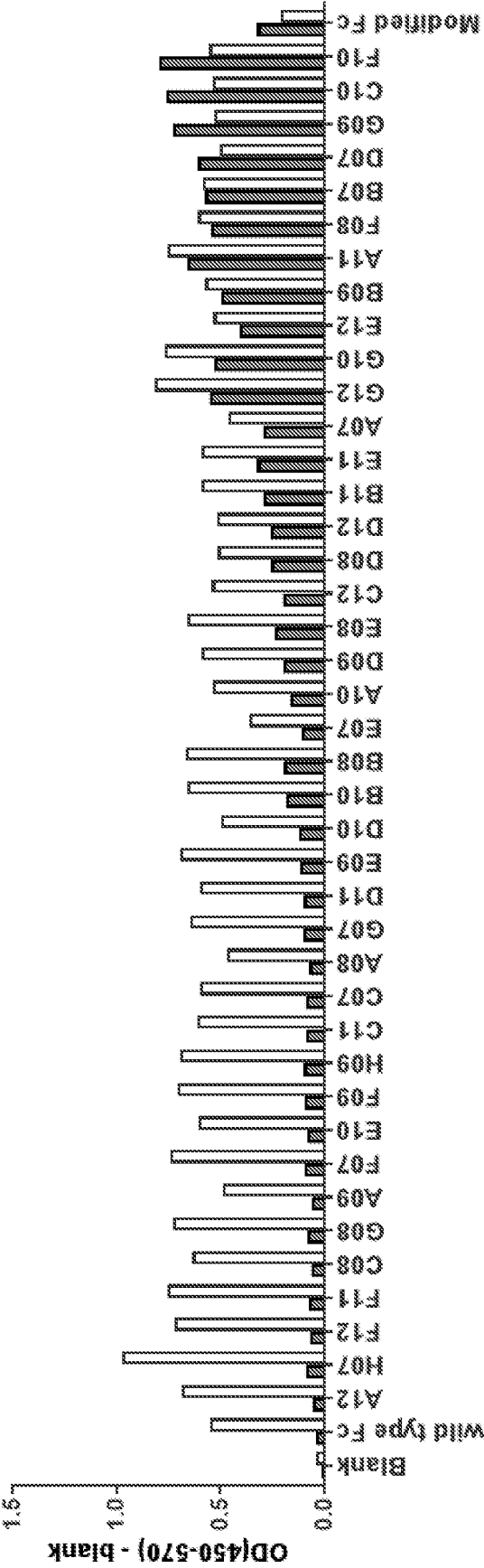


Figure 12H

SN	GROUP	CH2 REGION		CH3 REGION				ELISA ID IN EXPT #1	ELISA ID IN EXPT #2	ELISA ID IN EXPT #3	No of clones in Expt#3	KD (M)	mAbC maturation Assay	
		T253*	T256	H433	N434	H435*	Y436							S440
1	Group 1 (PSH)	:	P	S	H	H	Y	G			2H9, 4B9	2	5.50E-11	
2		:	P	S	H	H	Y	S	4B4, 4A12	1E8, 1H7, 2B5, 2G11, 3F5, 3G1, 3G11, 4A2, 4F5, 4F8, 4H6, 4G10	12	1.56E-10		
3		:	P	S	H	H	Y	I			105, 4E12	2		
4		:	P	S	H	H	Y	R			1E9	1		
5		:	P	S	H	L	Y	Y			1F8	1		
6		:	P	S	H	H	F	S			3B4, 4G1	2		
7		:	A	S	H	H	Y	S			4D9	1		
8		:	S	S	H	H	Y	N			3C8	1		
9	Group 2 (FVH)	:	P	V	H	H	Y	S			not found in panning	1	9.57E-11	
10		:	P	V	H	H	Y	R			2E7, 3G4	2	8.92E-10	
11		:	P	V	H	H	F	S			2A9	1		
12		:	P	V	H	H	Y	V			3E12	1		
13		:	A	V	H	H	Y	G			3G12	1		
14		:	T	V	H	H	F	S			3D5	1		
15	Group 3 (PH)	:	P	H	H	H	Y	S			2E4, 2F5	2	2.11E-08	
16		:	P	H	H	H	Y	R			2H6, 3H6	2		
17		:	P	H	H	H	Y	I			3A2	1		
18		:	P	H	H	H	T	N			3H7	1		
19		:	P	H	H	H	Y	T			4B10	1		
20		:	P	A	H	H	Y	T			3G7	1		
21		:	P	D	H	H	Y	R			1A2	1		
22		:	P	D	H	H	Y	S			3C2	1		
23		:	P	D	H	H	F	S			4E11	1		
24		:	P	P	H	H	Y	S			1A6	1		
25		:	P	Q	H	H	Y	S			4E3	1		
26		:	P	T	H	H	Y	S			1B4, 3G8	2		
27		:	A	H	H	H	Y	S			3D11	1		
28		:	A	Q	H	H	F	S			4E10	1		
29		:	A	T	H	H	Y	S			4G2	1		
30		:	T	T	H	H	F	S			2G12	1		
31		:	T	T	H	H	Y	S			4D9	1		
32	Group 4 (PTR)	:	P	T	R	H	Y	S			1E1, 3G6	2	4.98E-10	
33		:	P	T	R	H	F	S			2F4, 4D7	2		
34		:	P	T	R	H	L	S			4A11	1		
35		:	P	T	R	H	Y	I			2G7, 4B7	2		
36		:	P	T	R	H	F	G			3A10	1		
37		:	T	T	R	H	F	S			1B3, 2C2	2		
38		:	T	T	R	H	Y	S			1E6, 2B8	2		
39		:	T	T	R	H	Y	S			3C10	1		
40		:	P	T	R	H	F	I			PN04-90		4.25E-10	Yes
41		:	T	T	R	H	F	I			V5		2.85E-08	
42		:	P	H	R	H	F	I			V1		1.08E-08	Yes
43		:	P	T	N	H	F	I			V2		1.62E-06	
44	Group 5 (FVR)	:	P	T	R	H	Y	I			V3		2.11E-10	
45		:	P	T	R	H	F	S			V4		2.75E-10	
46		:	P	V	R	H	Y	S			1A1, 1F9, 1G8, 1H5, 2E11, 4C10, 5C7	7	1.69E-10	
47		:	P	V	R	H	F	S			1A3, 1D6, 2C7, 2F2, 4F1, 3F5	6		
48		:	P	V	R	H	Y	G			1G2, 4C9	2		
49		:	P	V	R	H	L	S			1H4	1		
50		:	P	V	R	H	F	R			3A3	1		
51		:	P	V	R	H	Y	R			4A5, 4G5	2		
52		:	P	V	R	H	Y	P			4F10	1		
53		:	A	V	R	H	T	N			3C12	1		
54		:	A	V	R	H	Y	I			3F12	1		
55		:	T	V	R	H	T	R			1C4	1		
56	Group 6 (FVR)	:	T	V	R	H	Y	I			1E4	1		
57		:	T	V	R	H	T	S			1G3	1		
58		:	T	V	R	H	Y	V			2B4	1		
59		:	T	V	R	H	Y	S			2C4, 3F8, 4A1	3		
60		:	T	V	R	L	Y	S			2E9	1		
61		:	T	V	R	H	Y	R			3E5, 3G9, 4E7, 4B5	4		
62		:	P	I	R	H	F	S			1E2	1		
63		:	P	I	R	H	Y	S			2H7	1		

Figure 13A

SN	GROUP	CH2 REGION		CH3 REGION				ELISA ID IN EXPT #1	ELISA ID IN EXPT #2	ELISA ID IN EXPT #3	No of clones in Expt#3	KD (M)	mODC evaluation Assay
		T25*	T256	H33	H334	H35*	Y436	S440					
54	Group 6 (F)	Y	P	H	N	H	F	R		1B5	1		
55		Y	P	H	N	H	F	T		1B7	1		
56		Y	P	H	N	H	T	R		1B9, 4A6	2		
67		Y	P	H	N	H	Y	S		1B12, 1C7, 1F7, 1F10, 1G5, 1H6, 2B3, 2D1, 2G4, 2E12, 3F10, 2G1, 2G10, 2H3, 2H8, 3D10, 3C3, 3E9, 3F2, 3F9, 3H1, 3H8, 4C12, 4D2, 4D8, 4E8, 5E2	27		
68		Y	P	H	N	H	T	S		1C2, 1D7, 4G12, 3B6	4		
69		Y	P	H	N	H	T	T		1C5	1		
70		Y	P	H	N	H	Y	D		1F6, 4A7	2		
71		Y	P	H	N	H	S	W		1G1	1		
72		Y	P	H	N	H	T	M		1G7	1		
73		Y	P	H	N	H	T	A		1G12	1		
74		Y	P	H	N	H	T	D		1H8	1		
75		Y	P	H	N	H	Y	R	2B6	3A1, 2C12, 3B7, 4G2, 4F2	5		
76		Y	P	H	N	H	Y	A		2A8, 4B8	2		
77		Y	P	H	N	H	L	S		2A10	1		
78		Y	P	H	N	H	F	S	2C12	2B5, 2F8	2		
79		Y	P	H	N	H	Y	T		2C5, 2D7, 4B3, 3G2	4		
80		Y	P	H	N	H	F	I		2F12	1		
81		Y	P	H	N	H	T	R		3D1	1		
82		Y	P	H	N	H	Y	R		3D3	1		
83		Y	P	H	N	H	S	S		3H5	1		
84		Y	P	H	I	H	Y	S		3F11	1		
85		Y	P	H	I	H	F	M		3E11	1		
86		Y	P	H	L	H	T	S		2H5, 4B11	2		
87		Y	P	H	L	H	V	S		4D12	1		
88		Y	P	H	M	H	T	R		1D2	1		
89		Y	P	H	M	H	Y	S		2D9	1		
90		Y	P	H	N	H	L	N	2G1		0		
91		Y	P	H	N	H	T	Y	D11		0		
92	Group 7 (A)	Y	A	H	N	H	F	M	D5	4D5, 2C6	0	5.68E-09	
93		Y	A	H	N	H	F	S		1H2, 3D6, 2C9	3		
94		Y	A	H	N	H	T	S		2A2, 1G4	2		
95		Y	A	H	N	H	T	F		2A4	1		
96		Y	A	H	N	H	Y	S		1B1, 4E2, 3A12	3		
97		Y	A	H	N	H	Y	I		1F4	1		
98		Y	A	H	N	H	Y	G		2B8	1		
99		Y	A	H	N	H	Y	D		4A10	1		
100		Y	A	H	N	H	Y	N		4B2	1		
101		Y	A	H	M	H	Y	S		4F5	1		
102	Group 8 (others)	Y	T	H	N	H	Y	A		1C3	1		
103		Y	T	H	N	H	Y	I		1D10, 4A9, 3F11	3		
104		Y	T	H	N	H	Y	T		1E5, 3C9, 4H9, 4F11	4		
105		Y	T	H	N	H	Y	A		1E7	1		
106		Y	T	H	N	H	Y	R		2F5, 4C3	2		
107		Y	T	H	N	H	Y	S		2F9	1		
108		Y	T	H	N	H	Y	E		2G9	1		
109		Y	T	H	N	H	Y	C		3F9	1		
110		Y	T	H	N	H	Y	Y		4C1	1		
111		Y	T	H	N	H	Y	D		4E5	1		
112		Y	T	H	N	H	F	S	4A3	1C12, 1F2, 1G9, 2C11, 2E6, 2F3, 2F11, 2G5, 3A6, 4D9, 3B2	11		
113		Y	T	H	N	H	F	C		3C11	1		
114		Y	T	H	N	H	F	Y		3D7	1		
115		Y	T	H	N	H	F	N		3G3	1		
116		Y	T	H	N	H	F	R		4B4	1		
117		Y	T	H	N	H	T	S	3H1	2D5	1		
118		Y	T	H	L	H	F	S	4B11	1B10, 2B1, 2B2, 4G7, 4D10	5		
119		Y	T	H	L	H	Y	S		3A6, 2B9, 2B10, 2D6, 2F1, 2F7, 2G8, 3B9, 3B12, 4H5, 3E10	11		
120		Y	T	H	L	H	Y	R		2B12, 4F4	2		
121		Y	T	H	L	H	F	R		2D2	1		
122		Y	T	H	L	L	Y	G		2E10	1		
123		Y	T	H	L	H	Y	T		3D12	1		
124		Y	T	H	L	H	Y	V		4A8	1		
125		Y	T	H	M	H	Y	S		1B2, 4C3,	2		
126		Y	V	H	N	H	Y	R		4A2	1		
127		Y	G	H	N	H	Y	M		1H5	1		
128		Y	I	H	N	H	Y	N		3F7	1		
129		Y	K	H	N	H	F	S		1G4	1		
130		Y	N	H	N	H	T	N		3B1	1		
131		Y	N	H	N	H	Y	S		3E7, 4A4, 4H7, 4D4	4		
132		Y	N	H	N	H	Y	R		4A12	1		
133		Y	S	H	N	H	Y	S		1D4, 4E6, 1D11	3		
134		Y	S	H	N	H	S	S		3E12	1		
135		Y	S	H	N	H	Y	A		4F12	1		

Figure 13B

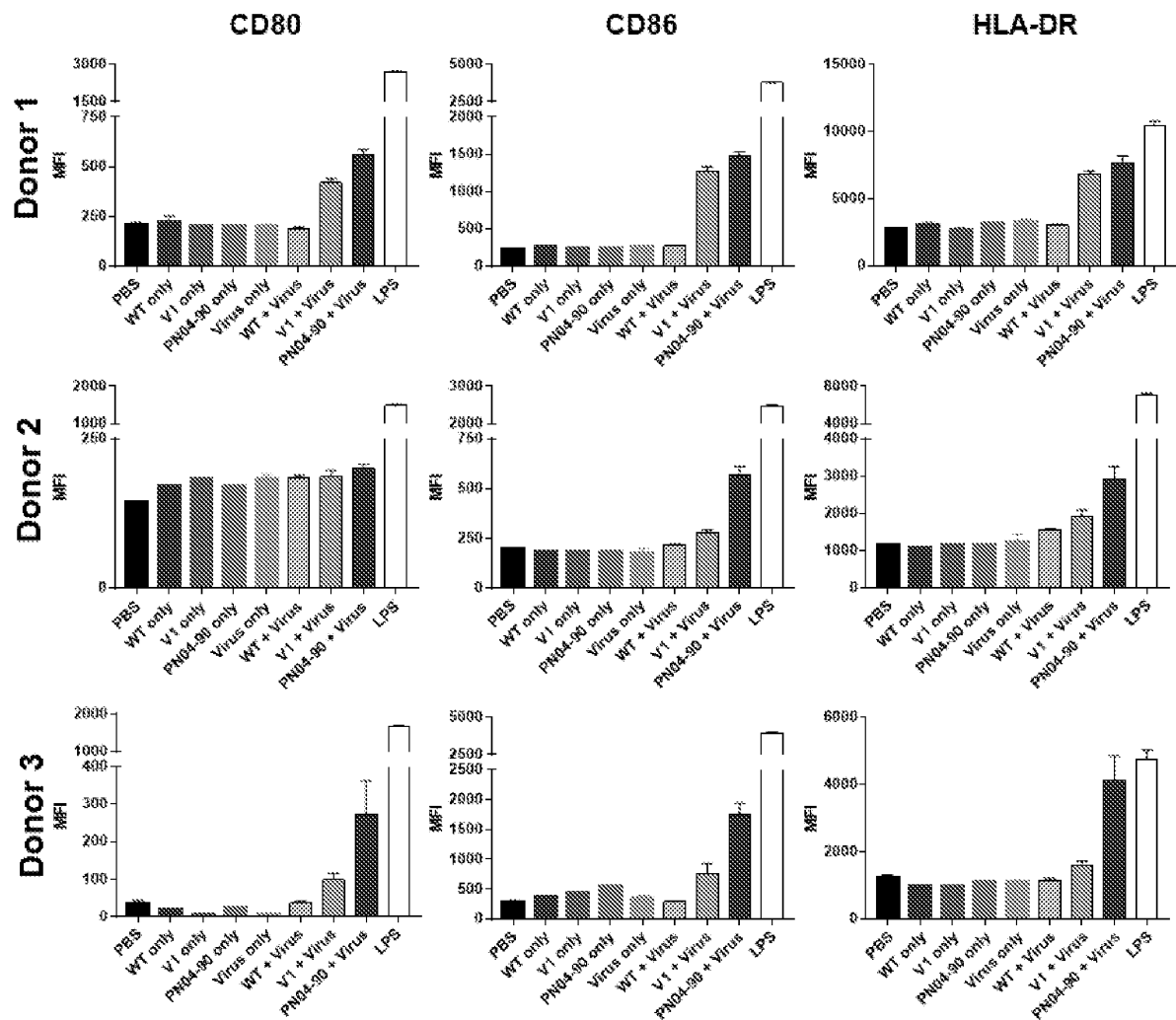


Figure 14

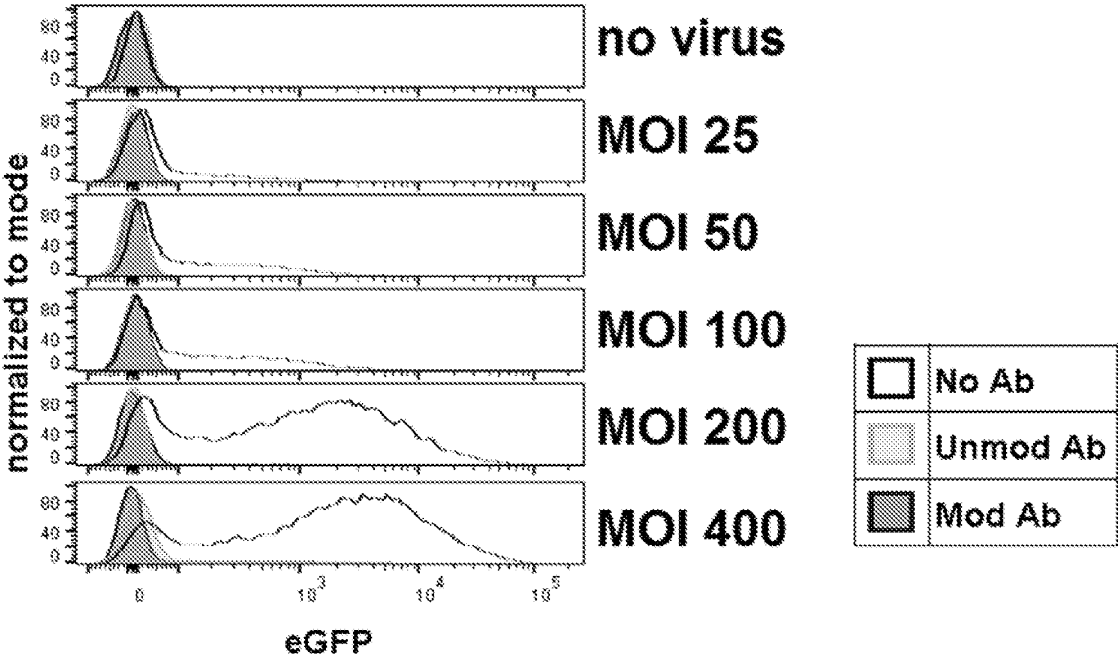


Figure 15A

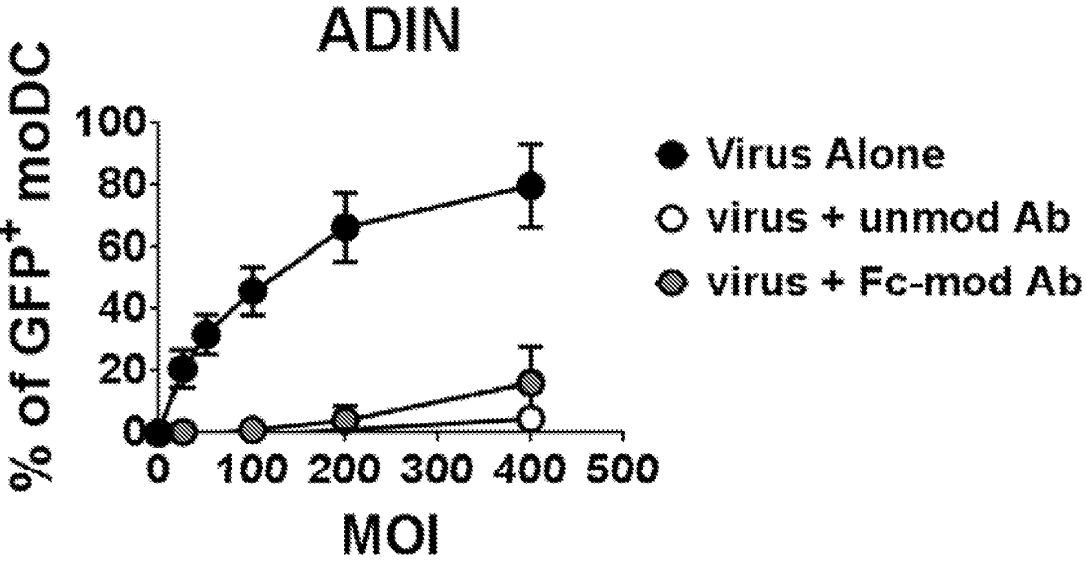


Figure 15B

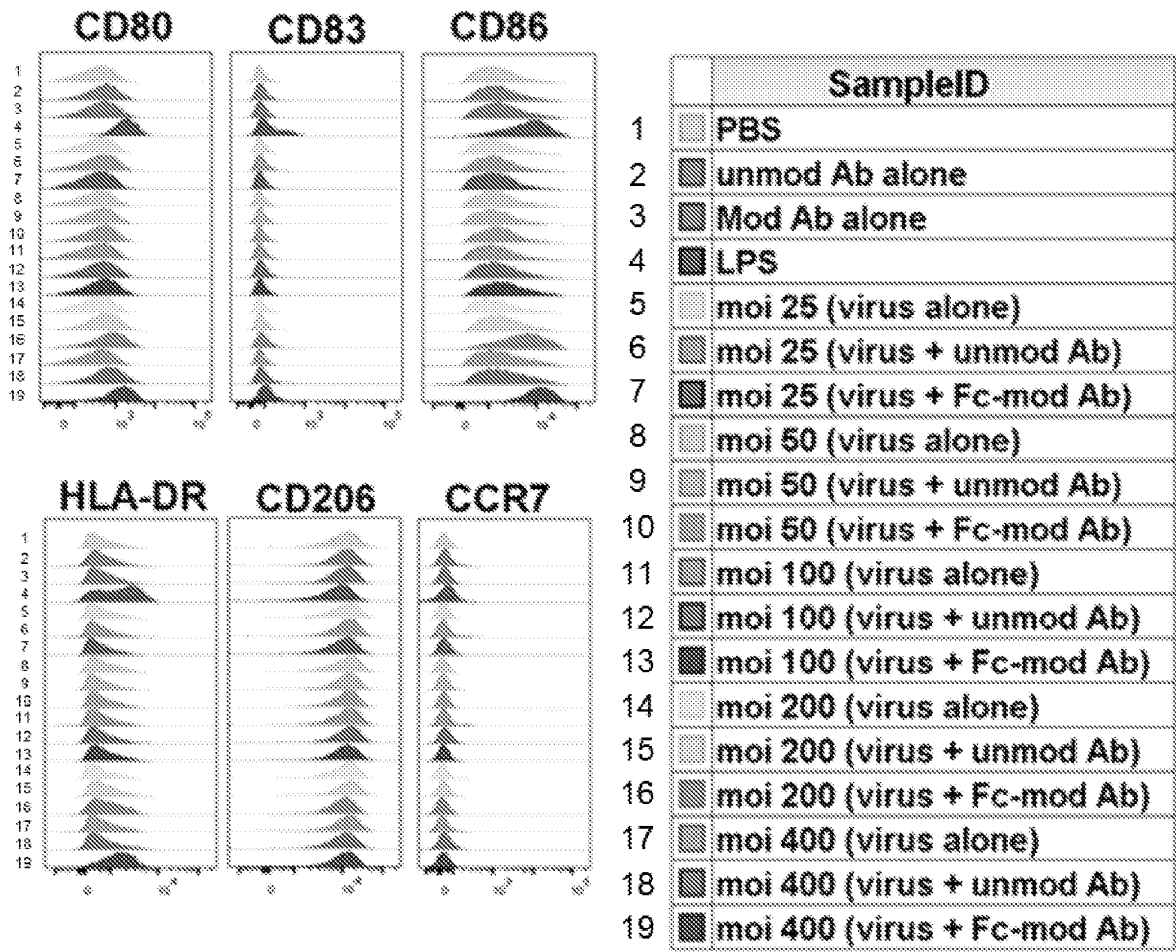


Figure 16A

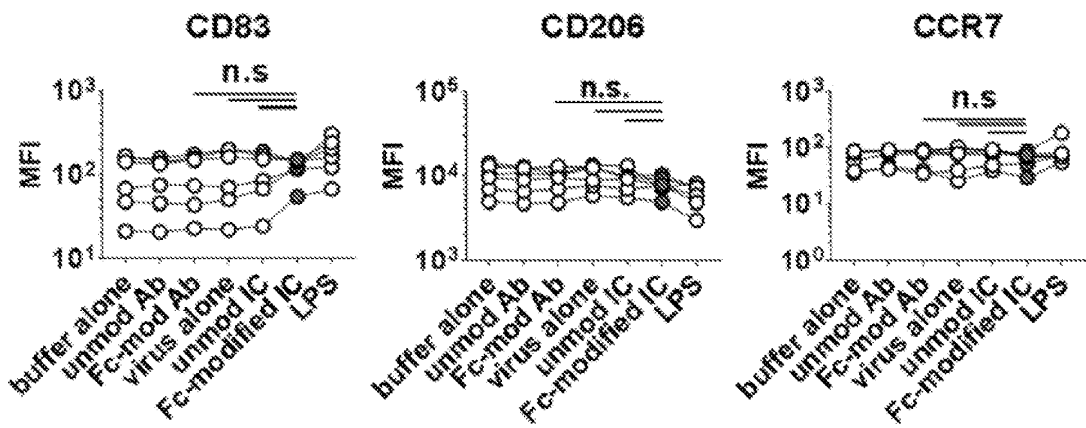


Figure 16B

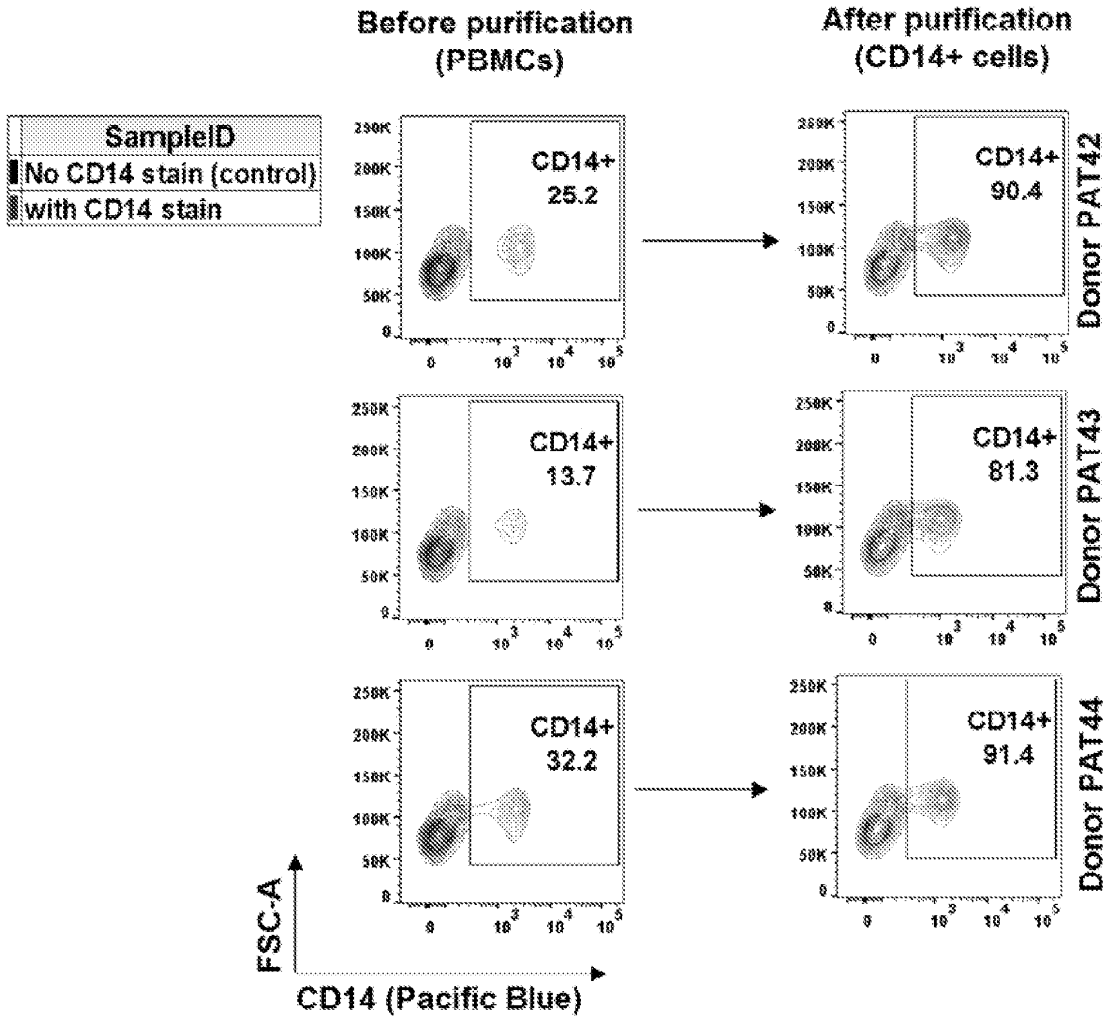


Figure 16C

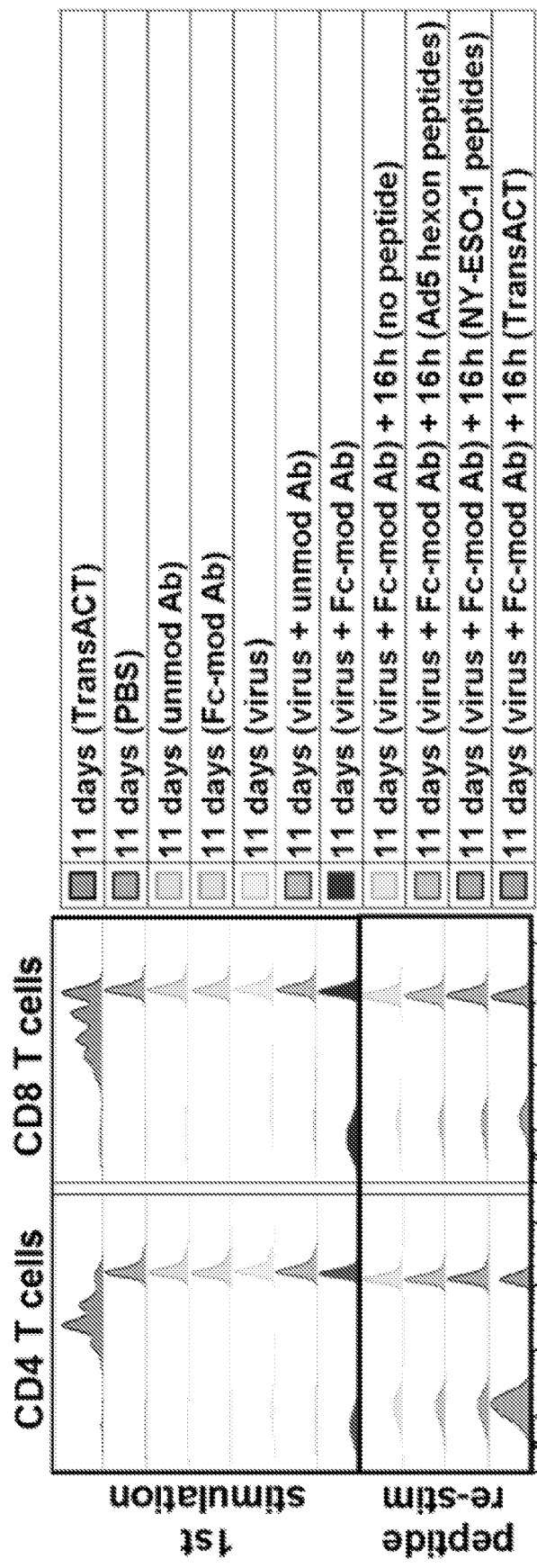


Figure 17A

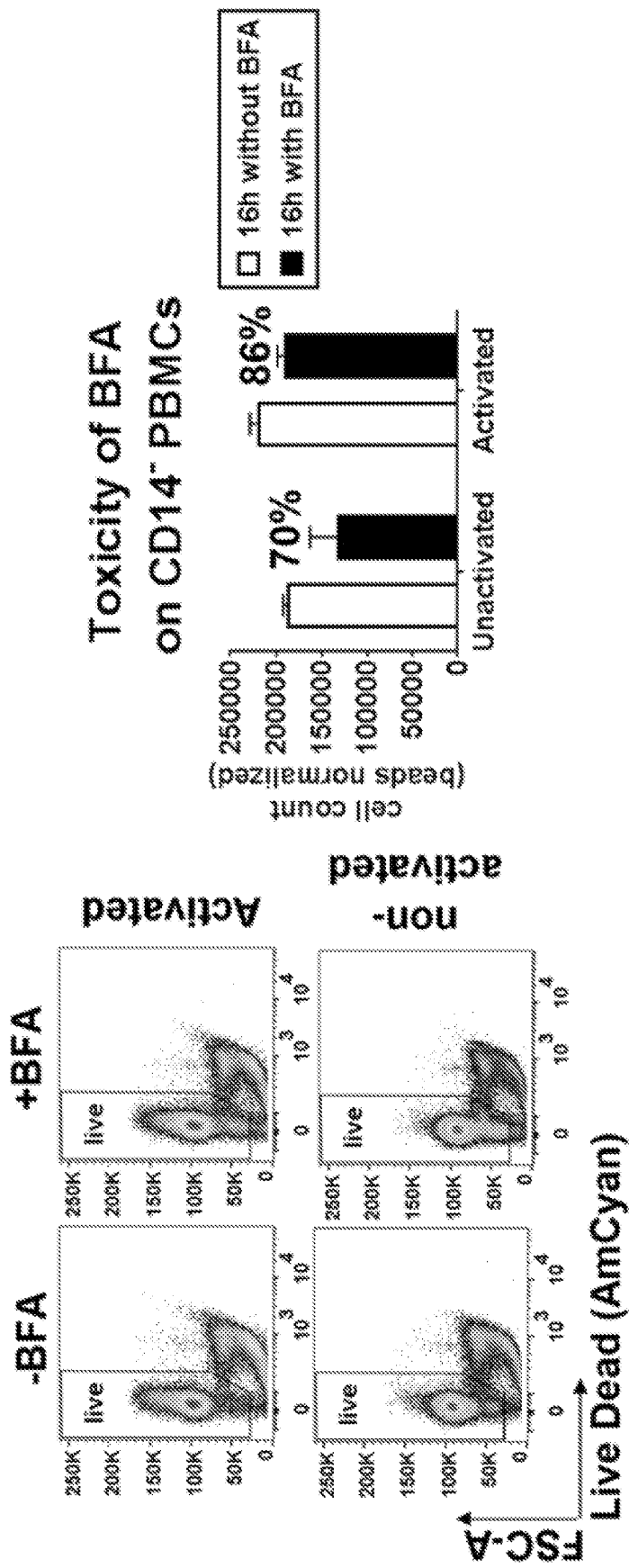
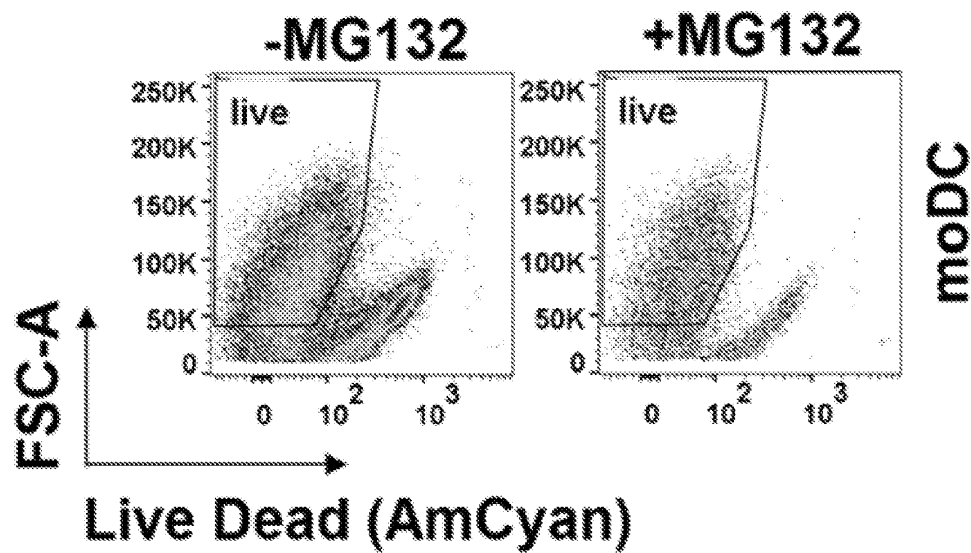


Figure 17B



Toxicity of MG132 on moDC

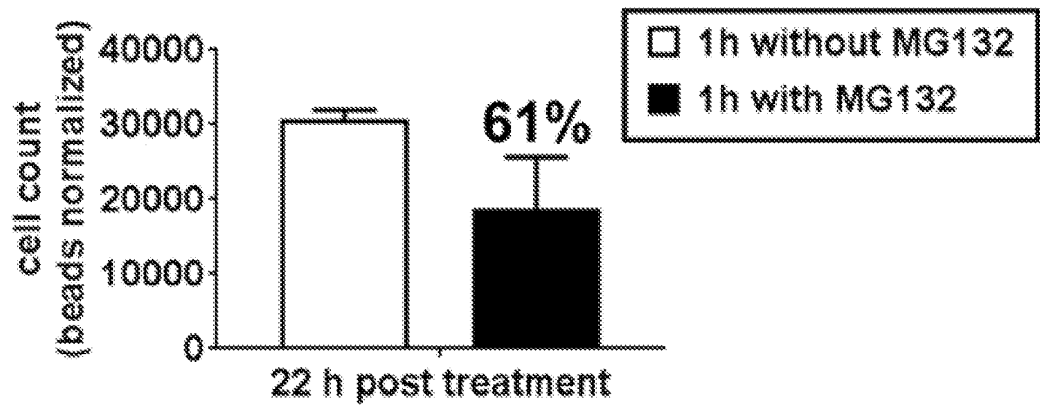


Figure 17C