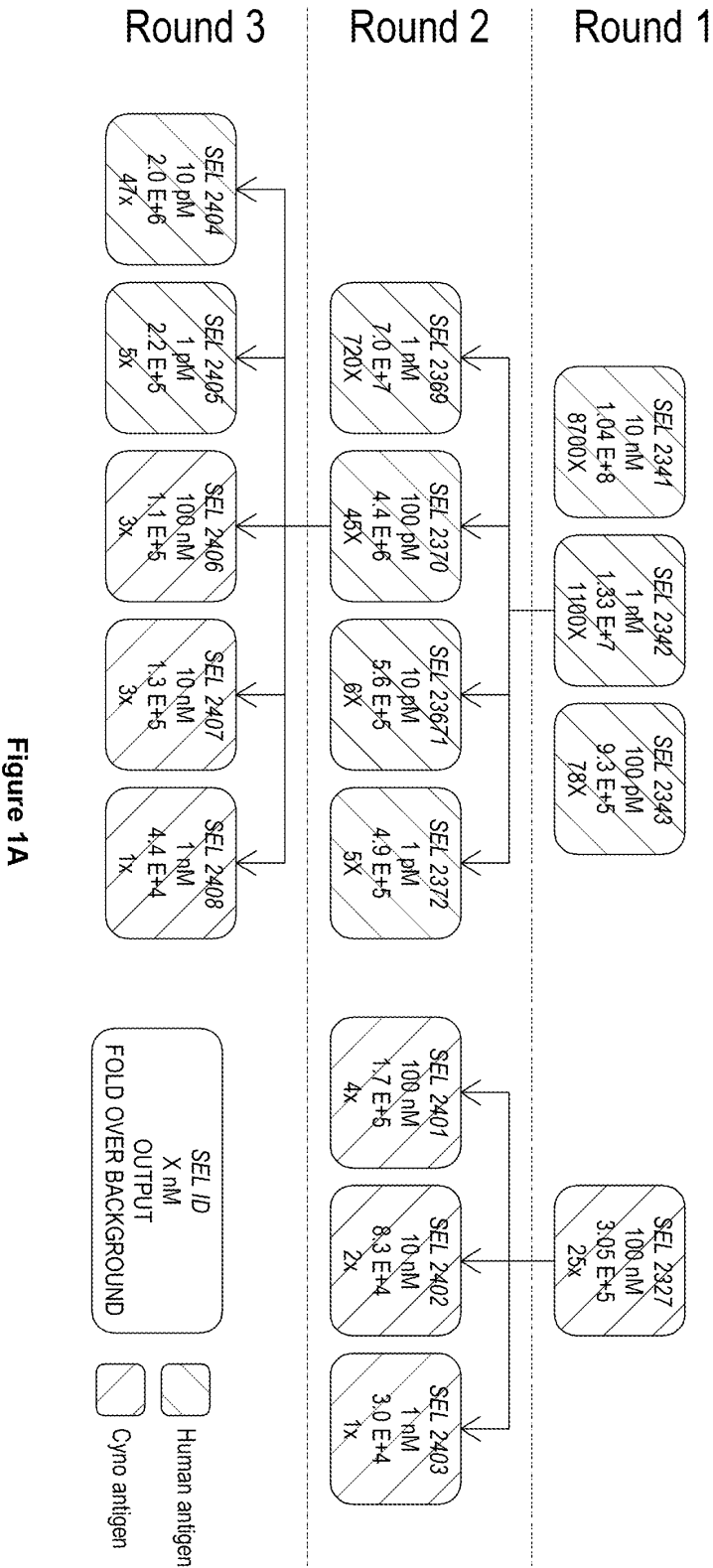




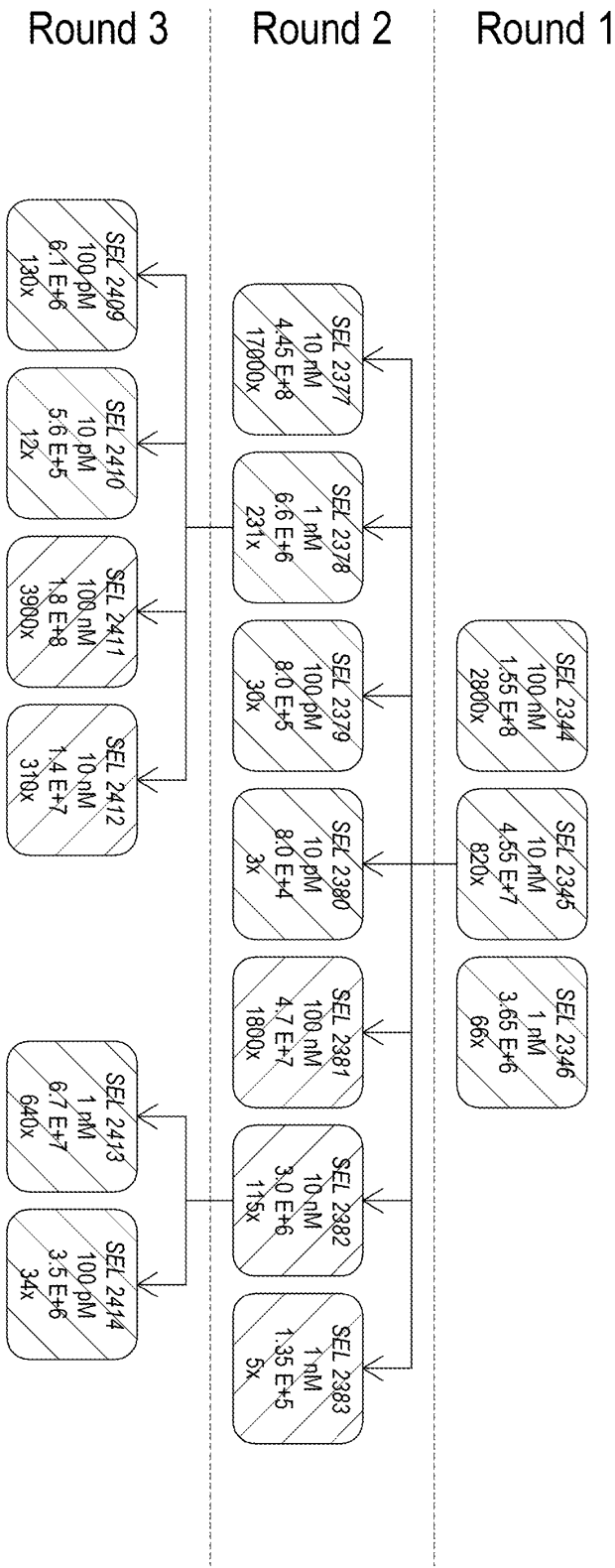


Figure 1B

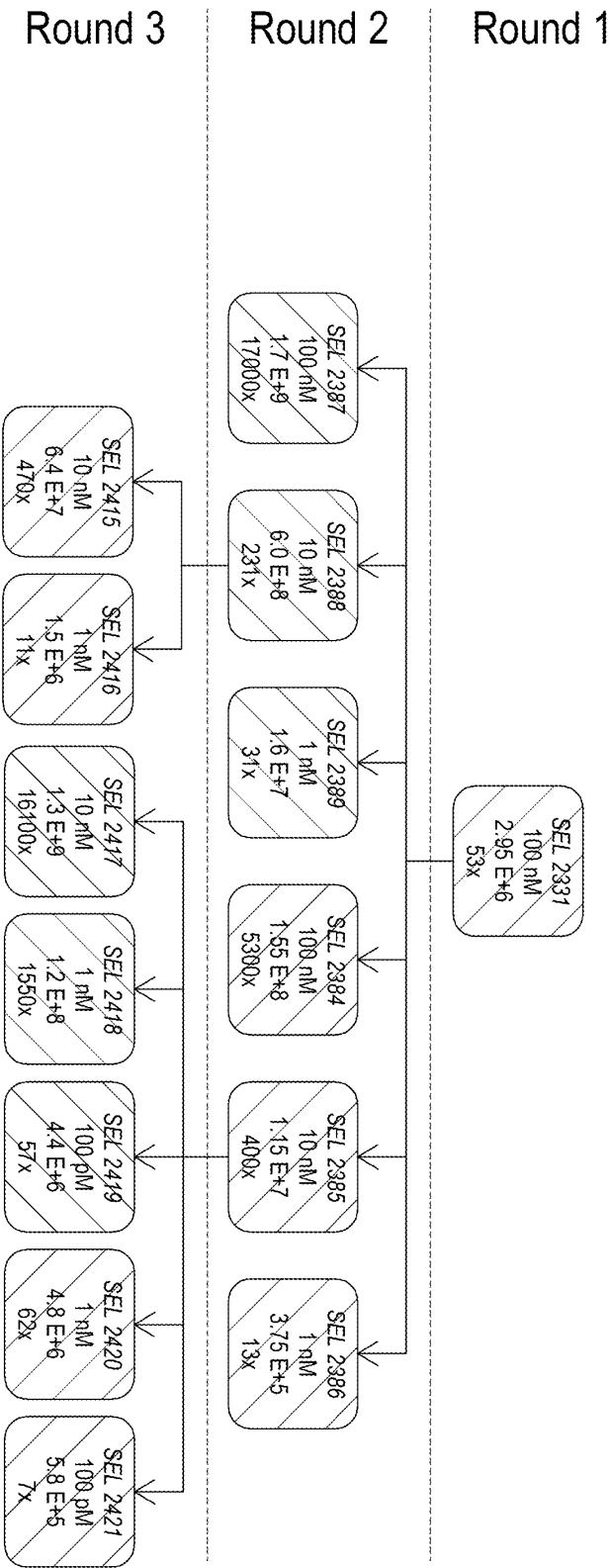


Figure 1C

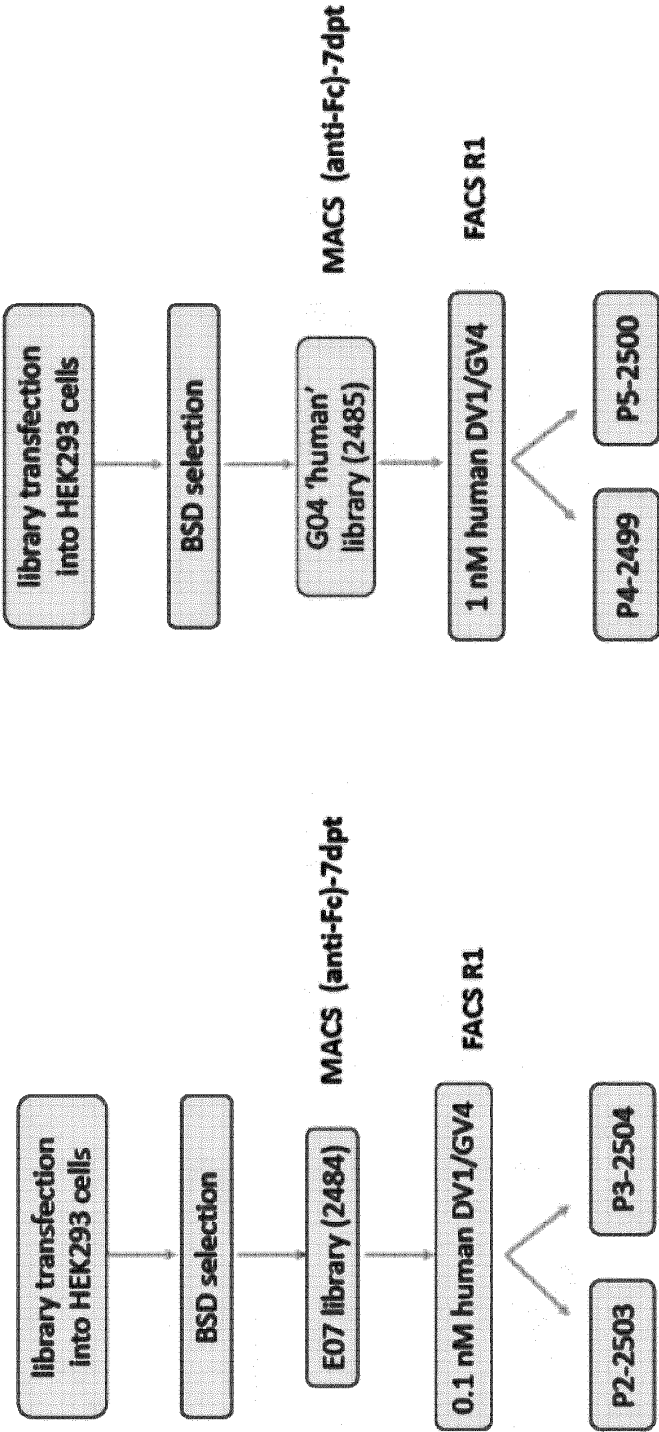


Figure 2A

Figure 2B

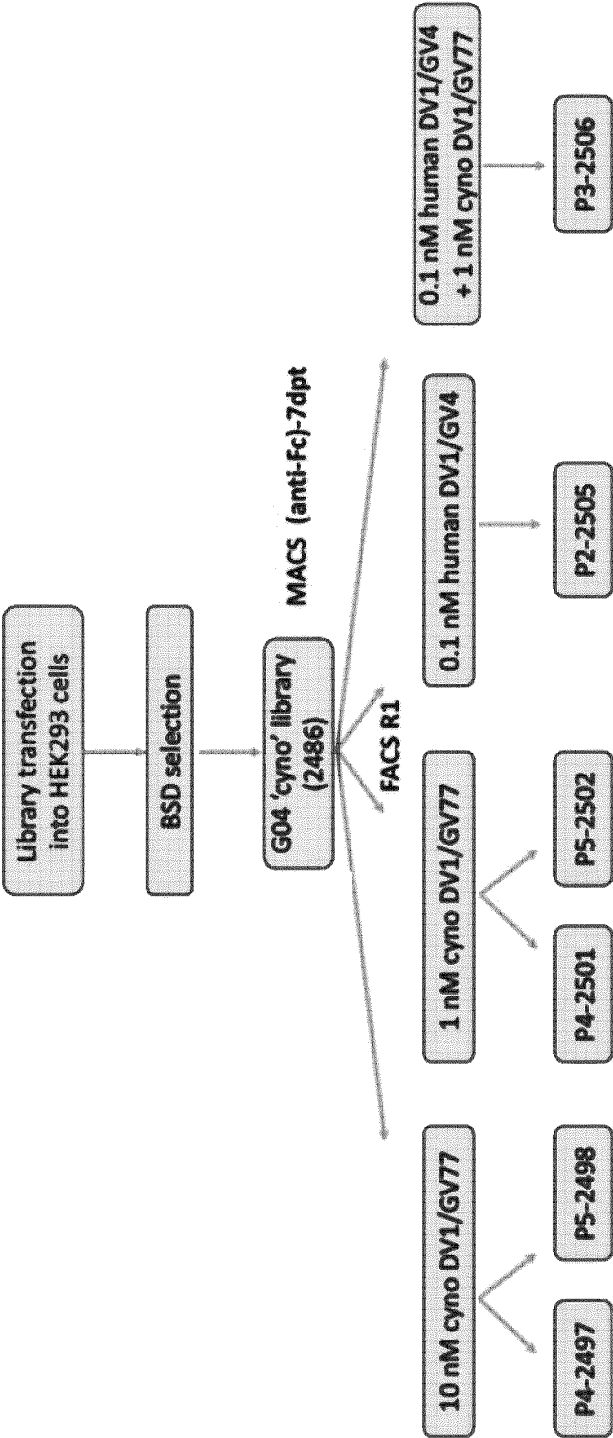


Figure 2C

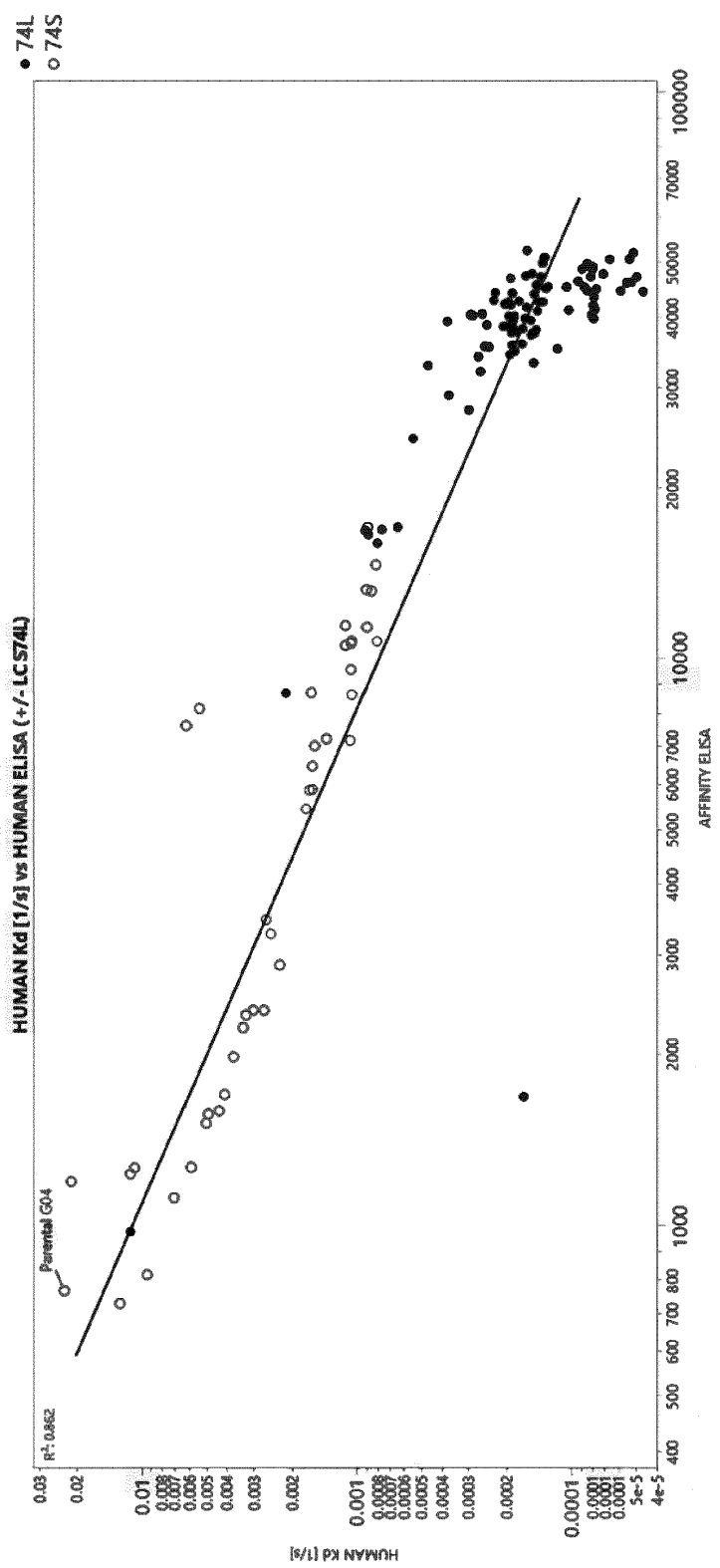


Figure 3A

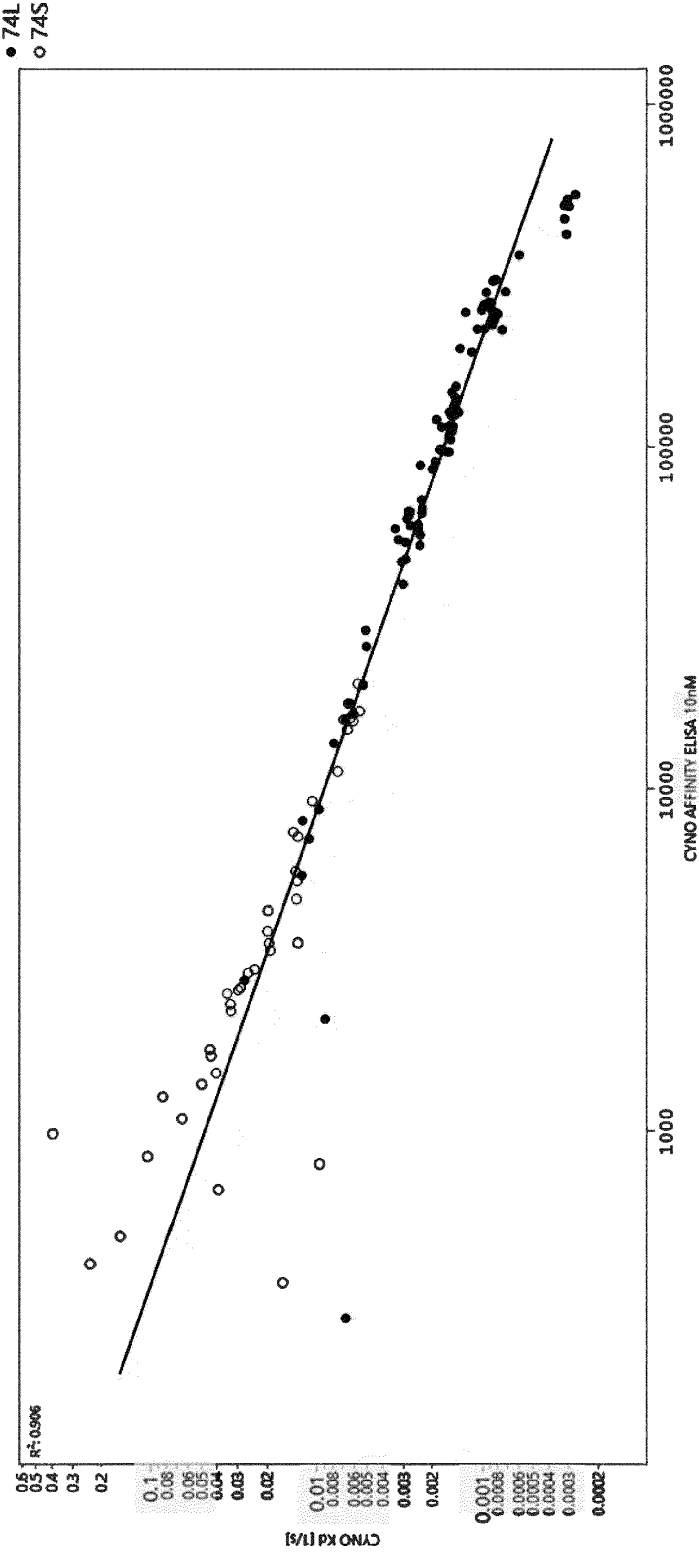


Figure 3B

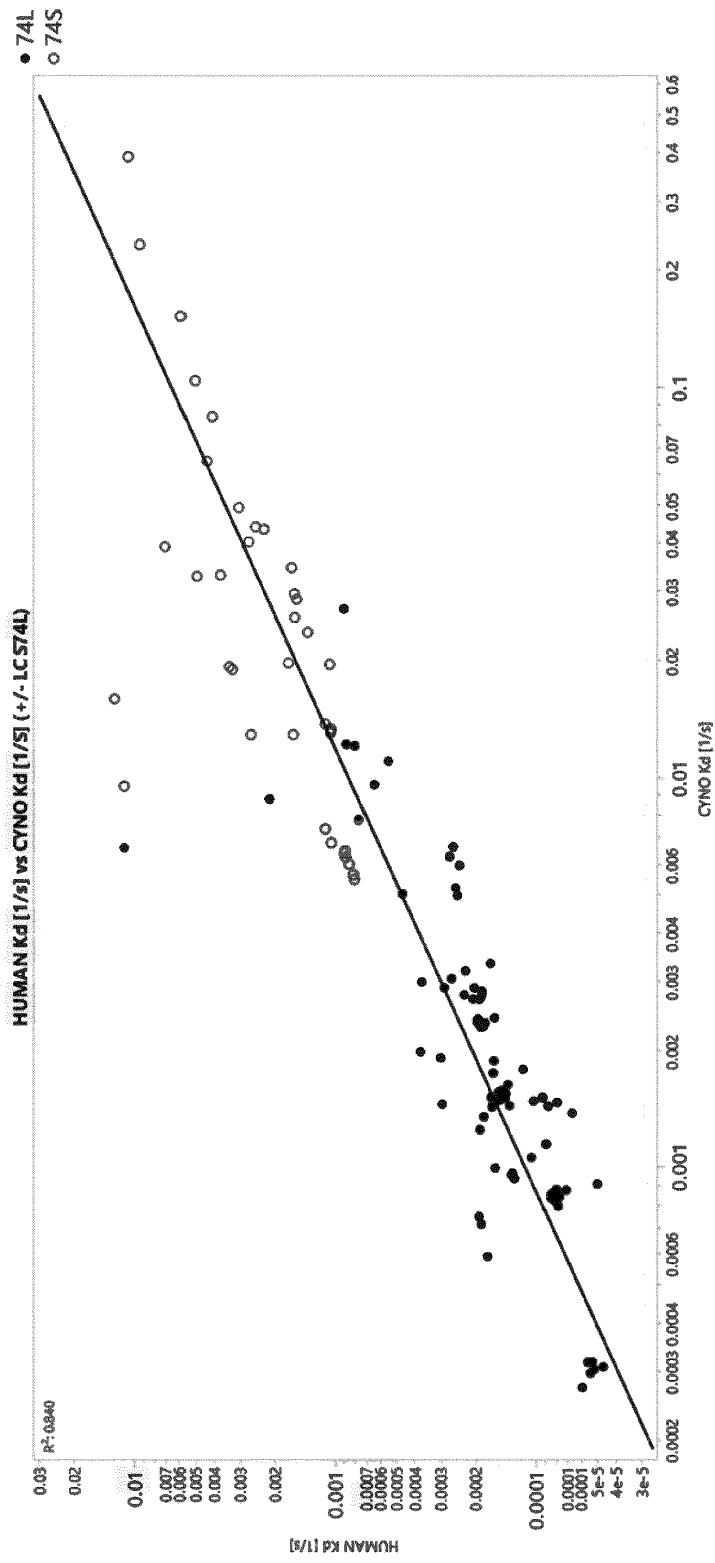


Figure 3C





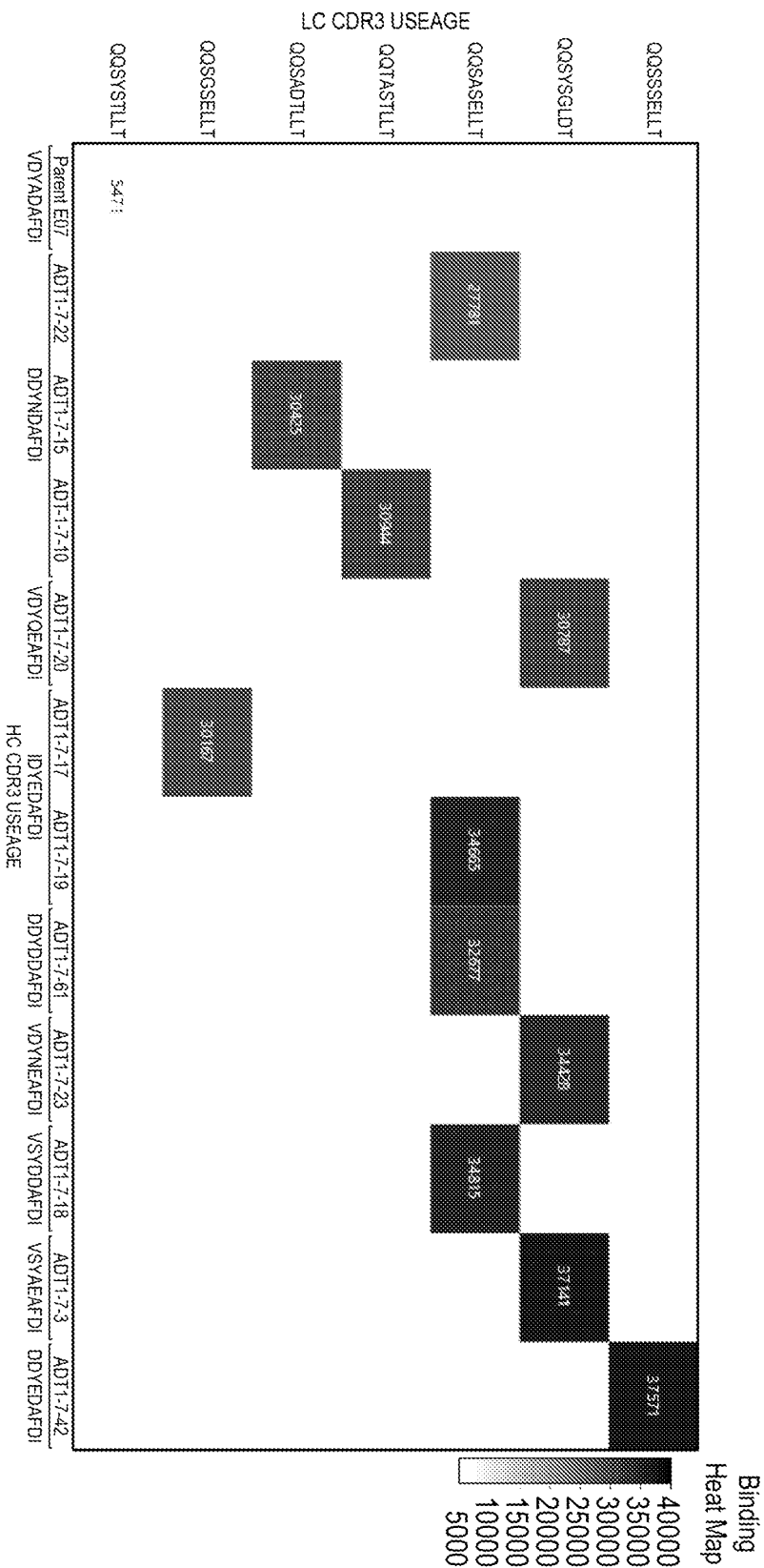
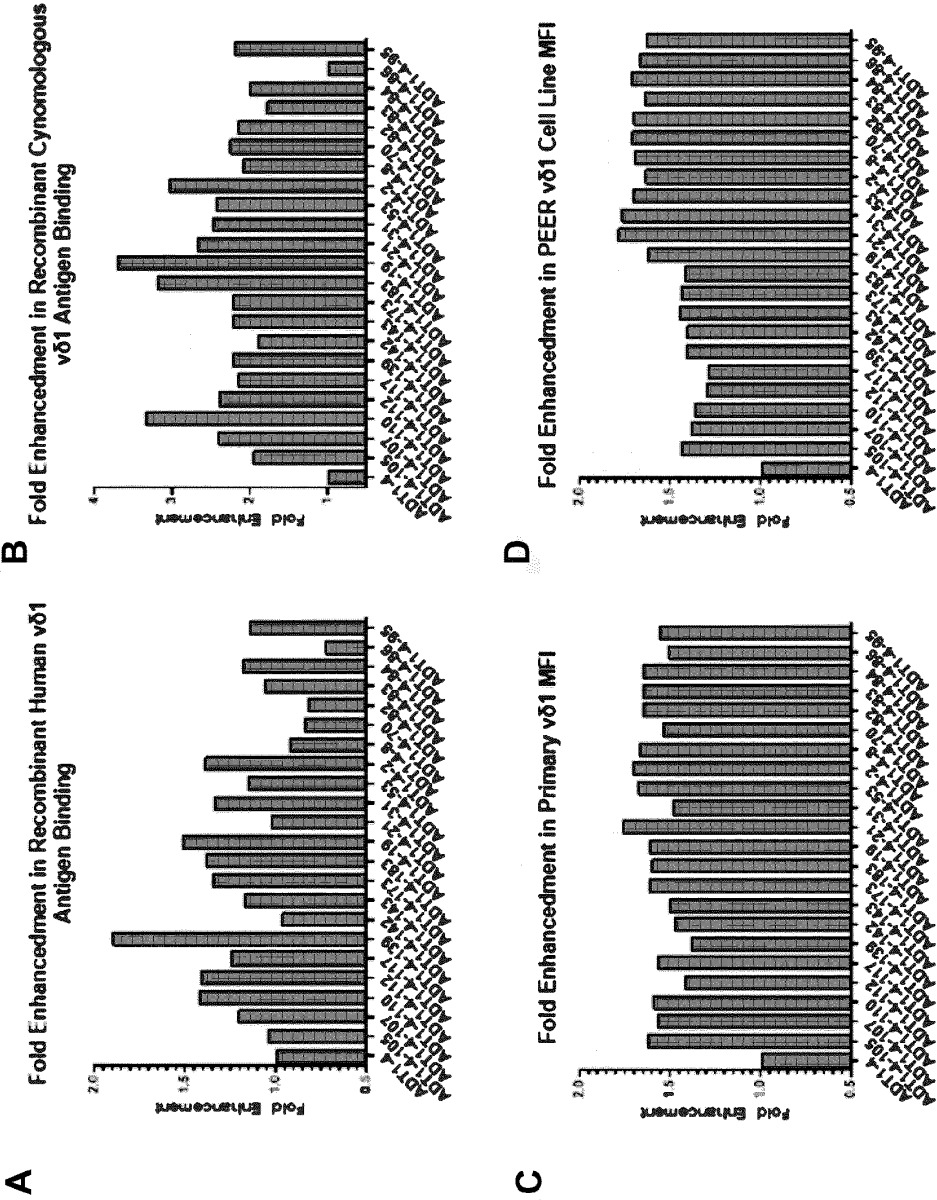


Figure 4C



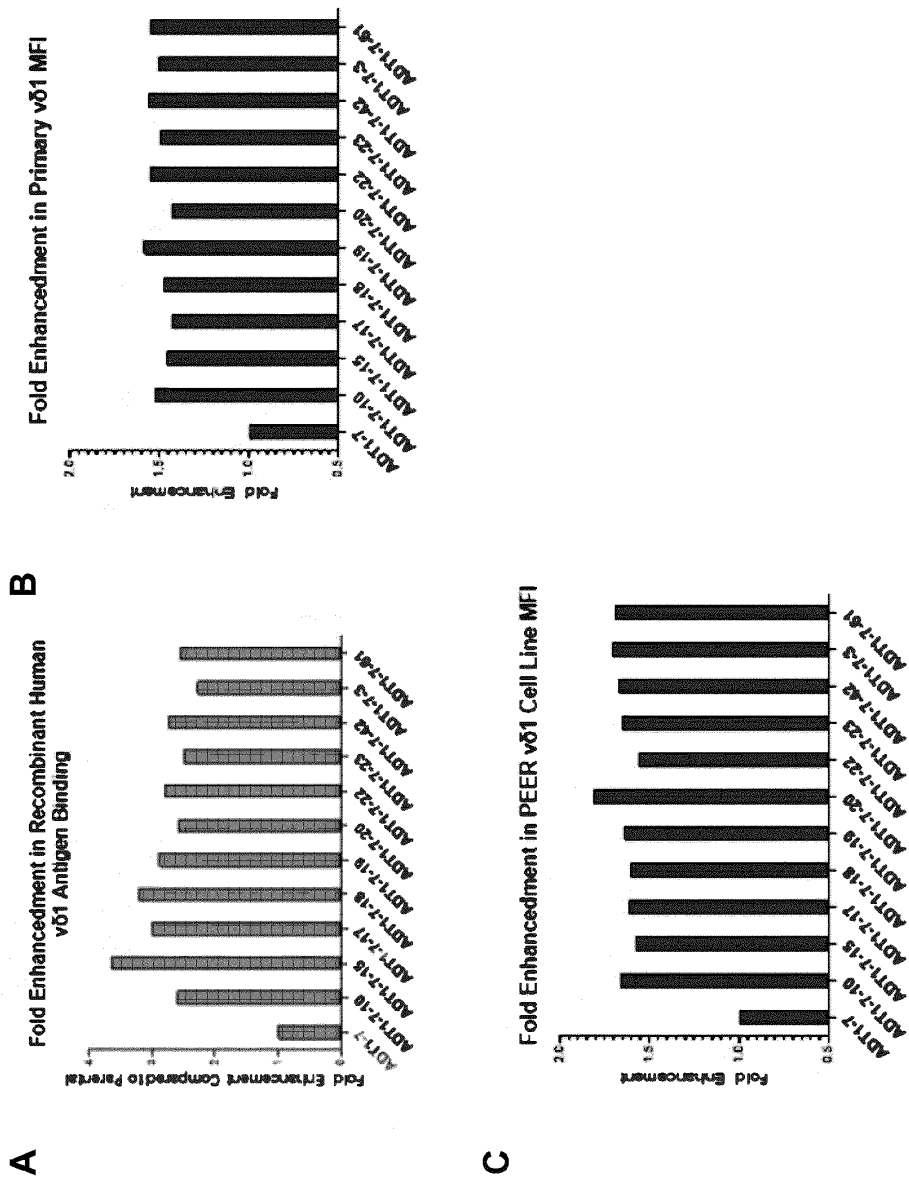


Figure 6

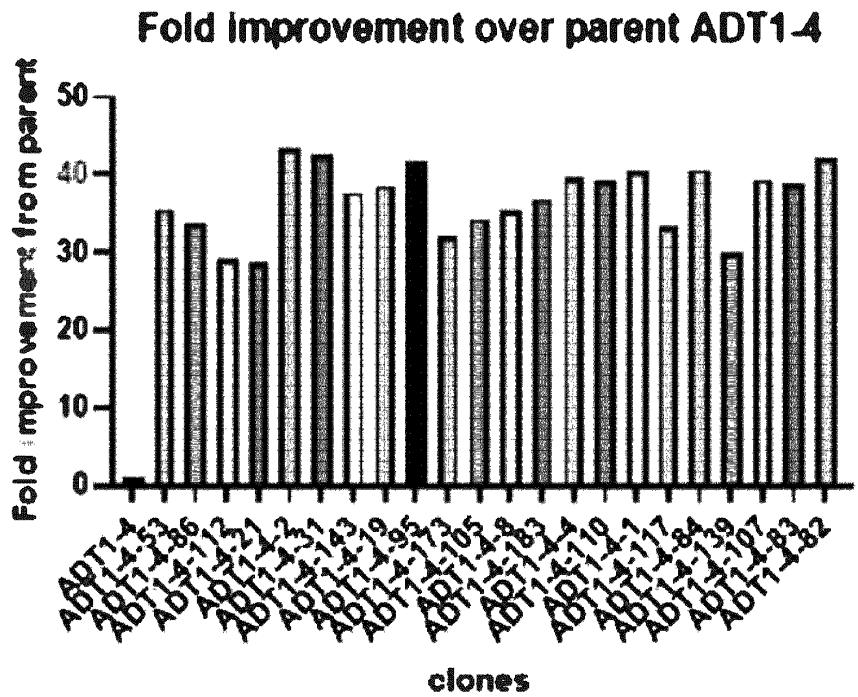


Figure 7A

Fold Improvement from parent ADT1-4 in binding to cyno antigen

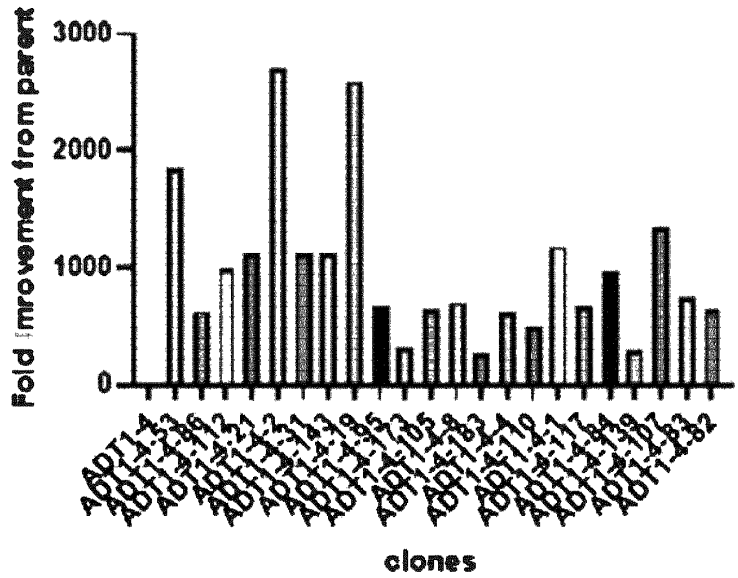
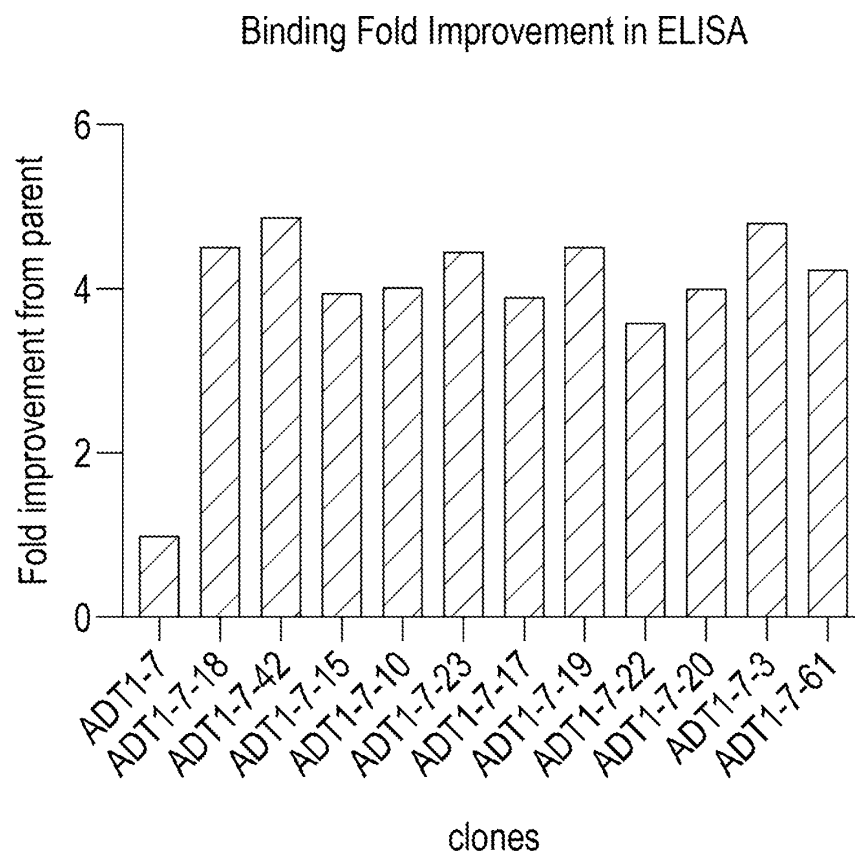


Figure 7B

**Figure 7C**

Human KD

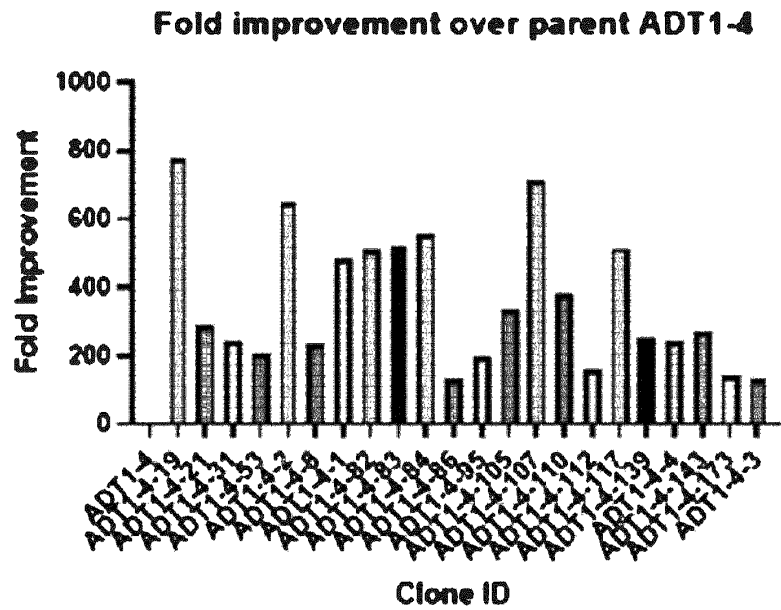


Figure 8A

Cyno KD

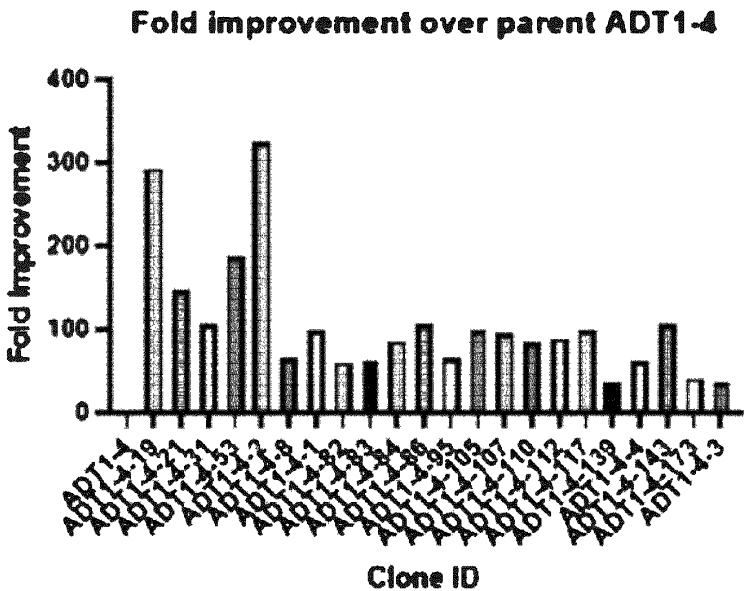


Figure 8B

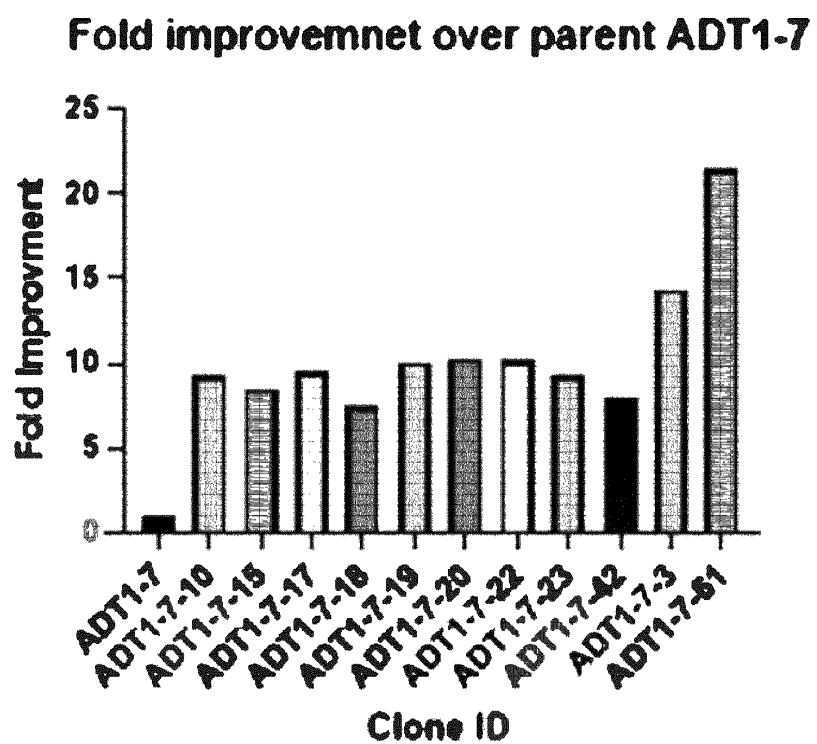


Figure 8C

Clones: ADT1-4-derived Analyte: human VD1

A

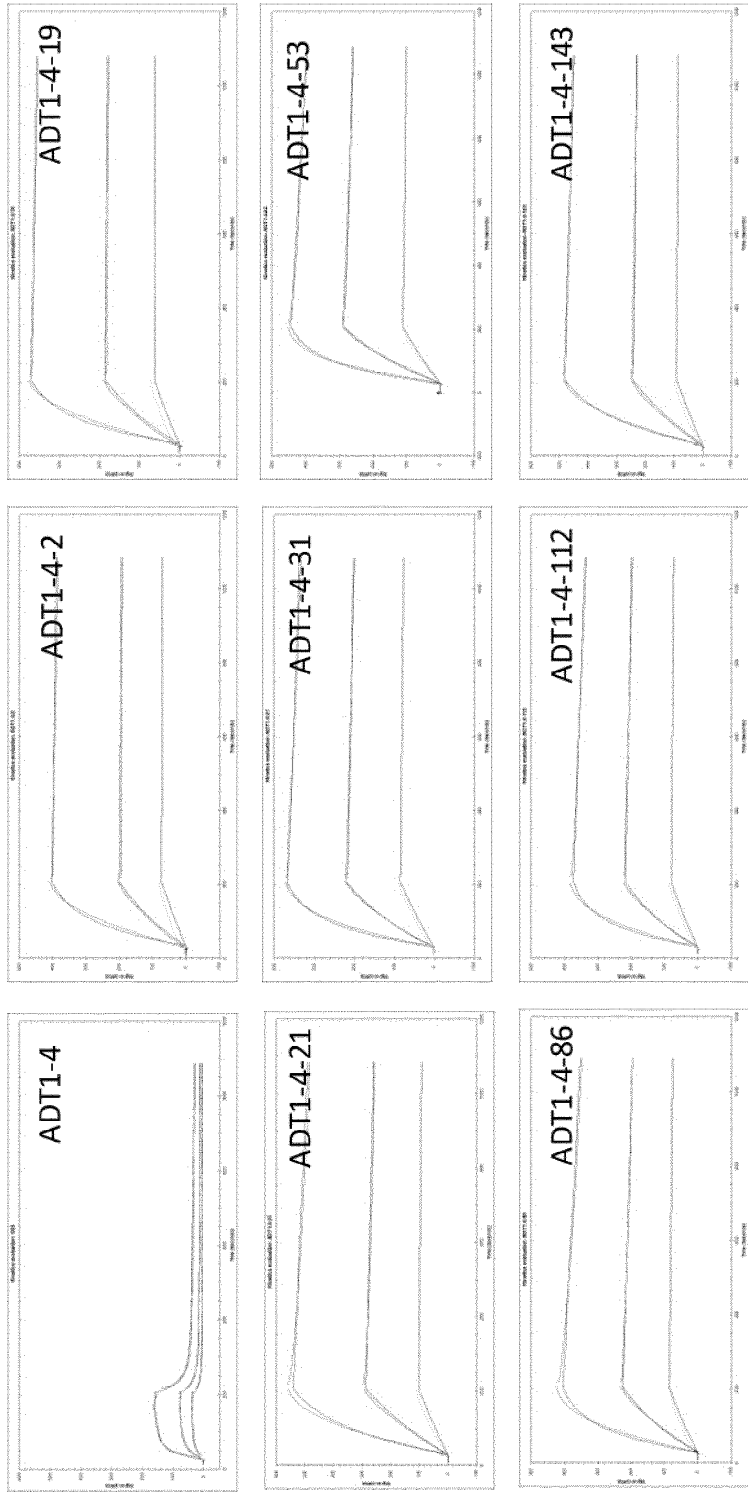


Figure 9A

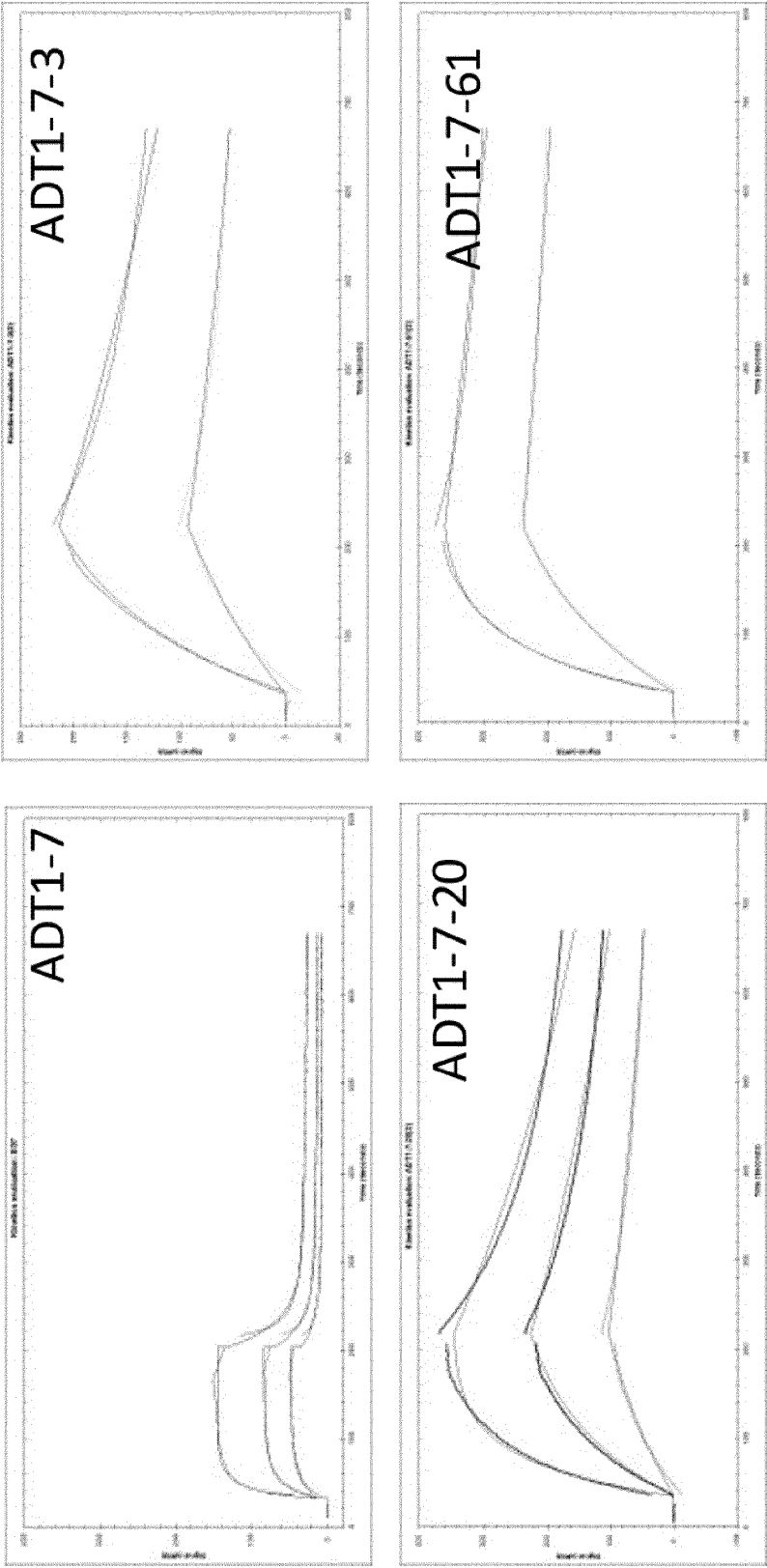


Figure 9B

Clone	Avg KD (M)	Fold-change
ADT1-7	3.81E-08	1.00
ADT1-7-3	3.78E-09	10.07
ADT1-7-20	4.99E-09	7.63
ADT1-7-61	1.04E-09	36.62

Figure 9D

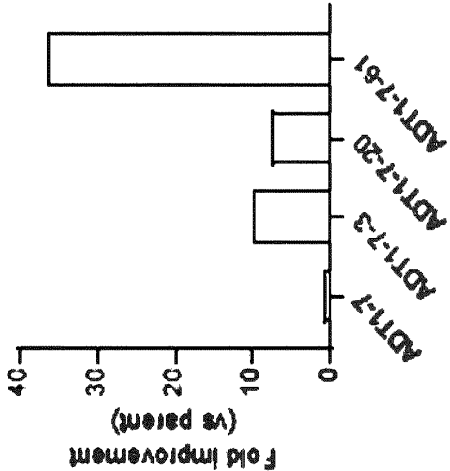


Figure 9F

Clone	Avg KD (M)	Fold-change
ADT1-4	1.49E-07	1.00
ADT1-4-2	1.90E-10	784.21
ADT1-4-19	1.77E-10	841.81
ADT1-4-21	4.74E-10	314.35
ADT1-4-31	4.42E-10	337.49
ADT1-4-53	5.07E-10	294.18
ADT1-4-86	7.16E-10	208.25
ADT1-4-112	5.65E-10	263.95
ADT1-4-143	4.24E-10	351.42

Figure 9C

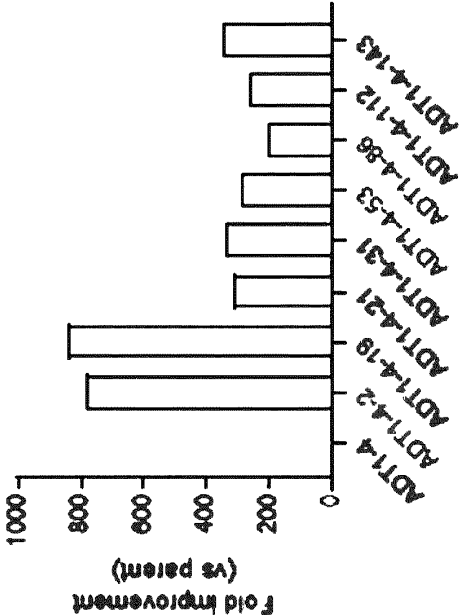
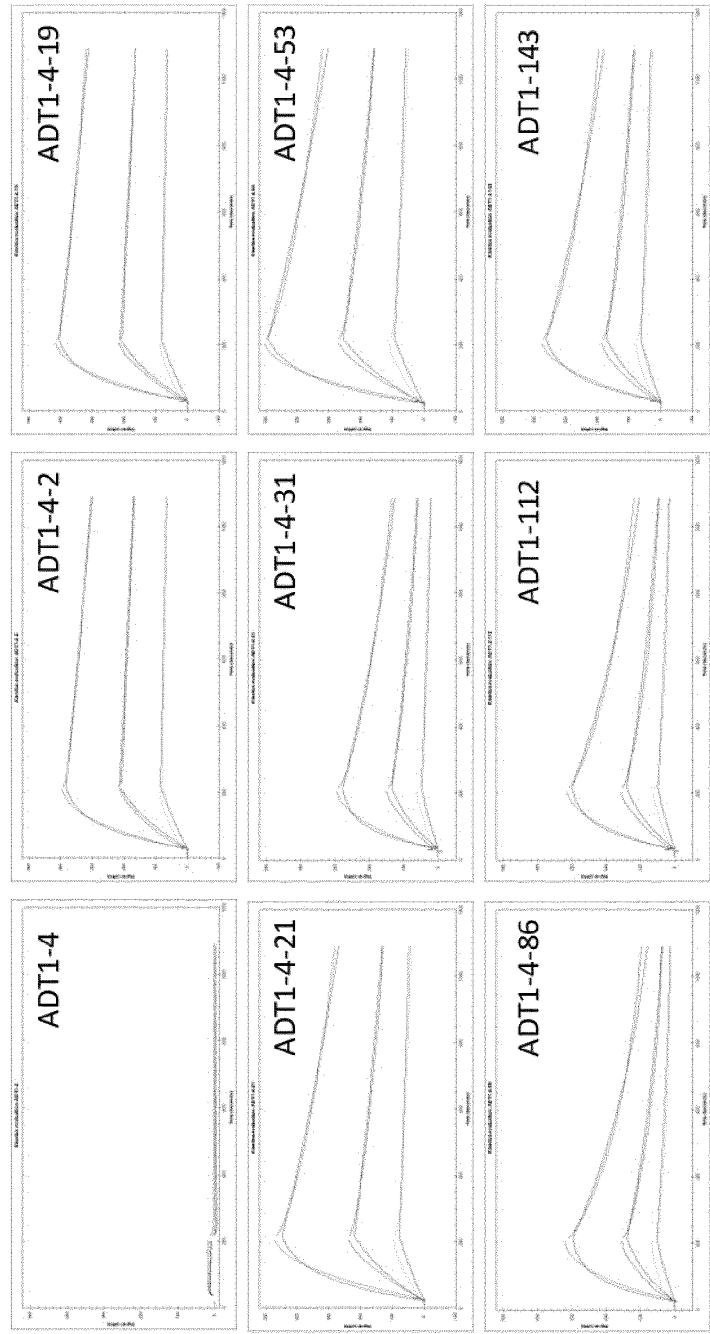


Figure 9E

Clone	Avg KD (M)
ADT1-4	No binding
ADT1-4-2	1.92E-09
ADT1-4-19	2.25E-09
ADT1-4-21	4.38E-09
ADT1-4-31	6.45E-09
ADT1-4-53	4.01E-09
ADT1-4-86	9.22E-09
ADT1-4-112	8.27E-09
ADT1-4-143	7.61E-09

B



A

Figure 10

A

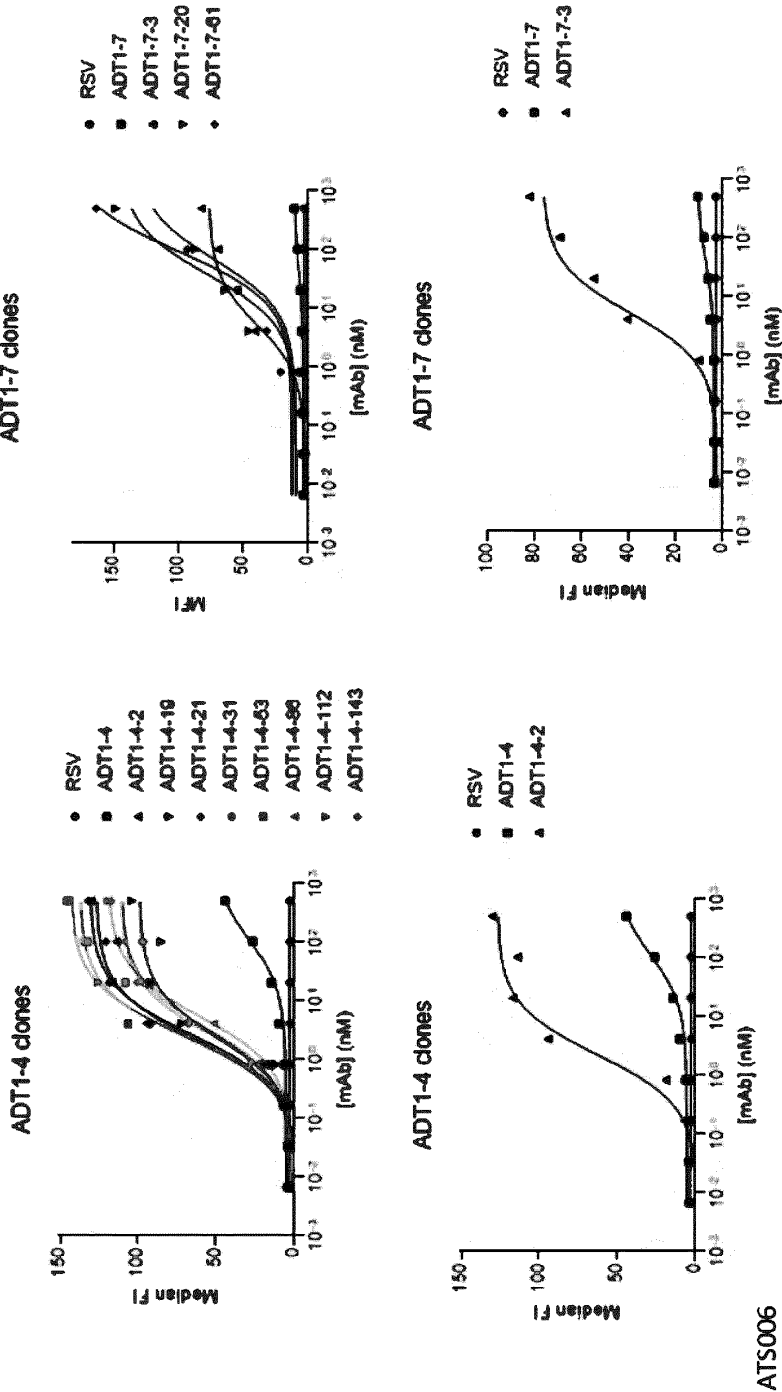


Figure 11A

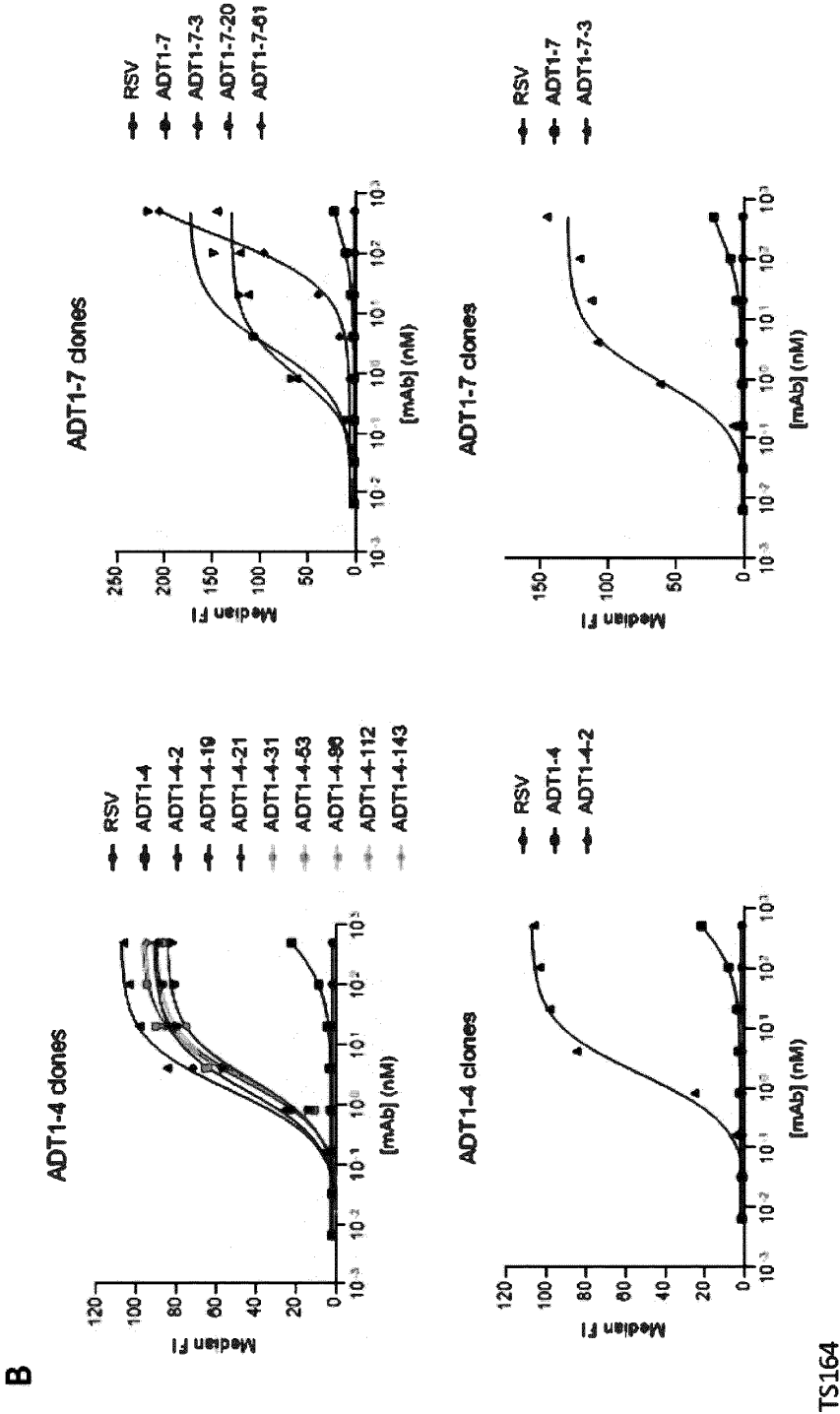


Figure 11B

ATS006			TS164		
mAb	IC50	% improvement in IC50	IC50	% improvement in IC50	
ADT1-4	107.7	0.00	575.9	0.00	
ADT1-4-2	2.164	4876.89	1.703	33716.79	
ADT1-4-19	2.375	4434.74	2.456	23348.70	
ADT1-4-21	2.536	4146.85	1.675	34282.09	
ADT1-4-31	3.33	3134.23	2.63	21797.34	
ADT1-4-53	2.228	4733.93	2.456	23348.70	
ADT1-4-86	5.357	1910.45	2.34	24511.11	
ADT1-4-112	2.621	4009.12	2.436	23541.22	
ADT1-4-143	2.819	3720.50	3.066	18683.43	

ATS006			TS164		
	IC50	% improvement in IC50	IC50	% improvement in IC50	
ADT1-7	>100	0.00	225.6	0.00	
ADT1-7-3	5.153	N/A	0.9517	23604.95	
ADT1-7-20	37.22	N/A	2.684	8305.37	
ADT1-7-61	93.01	N/A	195.7	15.28	

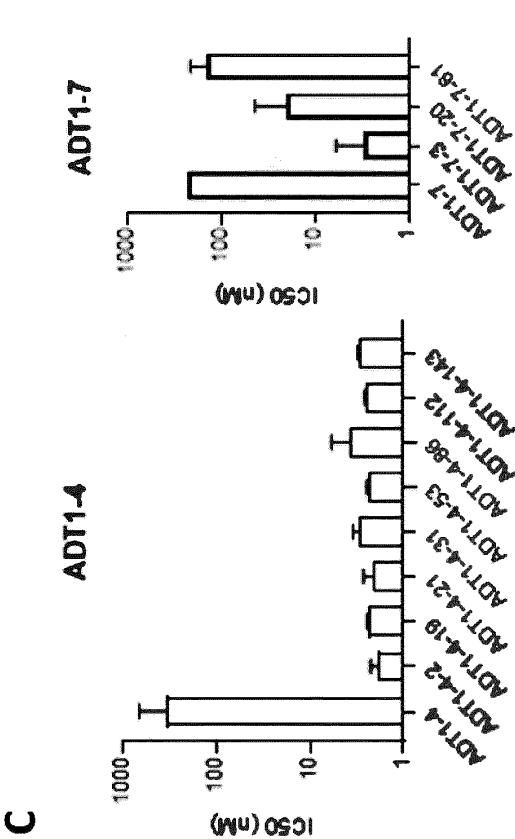


Figure 11C

IC50 (nM)									
mAb	Donor 1 (ATS006)	Donor 2 (TS164)	HEK293T	Raji	CD8 (PBMC)	CD4 (PBMC)	CD56 (PBMC)	CD19 (PBMC)	CD14 (PBMC)
ADT1-4	107.7	575.9	No binding	No binding	No binding	No binding	No binding	No binding	No binding
ADT1-4-2	2.164	1.703	No binding	No binding	No binding	No binding	No binding	No binding	No binding
ADT1-4-19	2.375	2.456	No binding	No binding	No binding	No binding	No binding	No binding	No binding
ADT1-4-21	2.536	1.675	No binding	No binding	No binding	No binding	No binding	No binding	No binding
ADT1-4-31	3.33	2.63	No binding	No binding	No binding	No binding	No binding	No binding	No binding
ADT1-4-53	2.228	2.456	No binding	No binding	No binding	No binding	No binding	No binding	No binding
ADT1-4-86	5.357	2.34	No binding	No binding	No binding	No binding	No binding	No binding	No binding
ADT1-4-112	2.621	2.436	No binding	No binding	No binding	No binding	No binding	No binding	No binding
ADT1-4-143	2.819	3.066	No binding	No binding	No binding	No binding	No binding	No binding	No binding

IC50 (nM)									
mAb	Donor 1 (ATS006)	Donor 2 (TS164)	HEK293T	Raji	CD8 (PBMC)	CD4 (PBMC)	CD56 (PBMC)	CD19 (PBMC)	CD14 (PBMC)
ADT1-7	>100	225.6	No binding	No binding	No binding	No binding	No binding	No binding	No binding
ADT1-7-3	5.153	0.9517	No binding	No binding	No binding	No binding	No binding	No binding	No binding
ADT1-7-20	37.22	2.684	No binding	No binding	No binding	No binding	No binding	No binding	No binding
ADT1-7-61	93.01	195.7	No binding	No binding	No binding	No binding	No binding	No binding	No binding

IC50 (nM)					
mAb	Donor 1 (ATS006)	CD8 (PBMC)	CD4 (PBMC)	CD56 (PBMC)	CD14 (PBMC)
OKT3	2.889	0.252	0.1906	No binding	No binding
RSV (IgG control)	No binding	No binding	No binding	No binding	No binding

Figure 11D

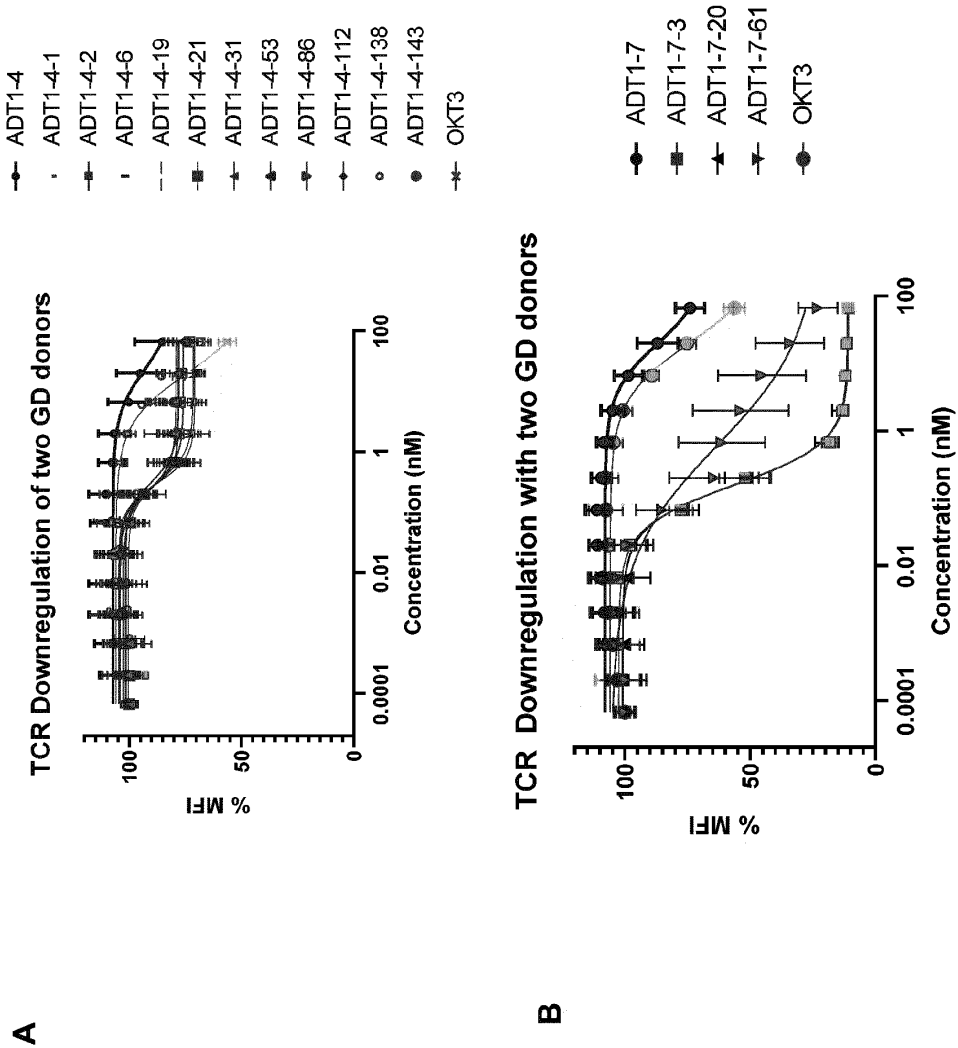


Figure 12

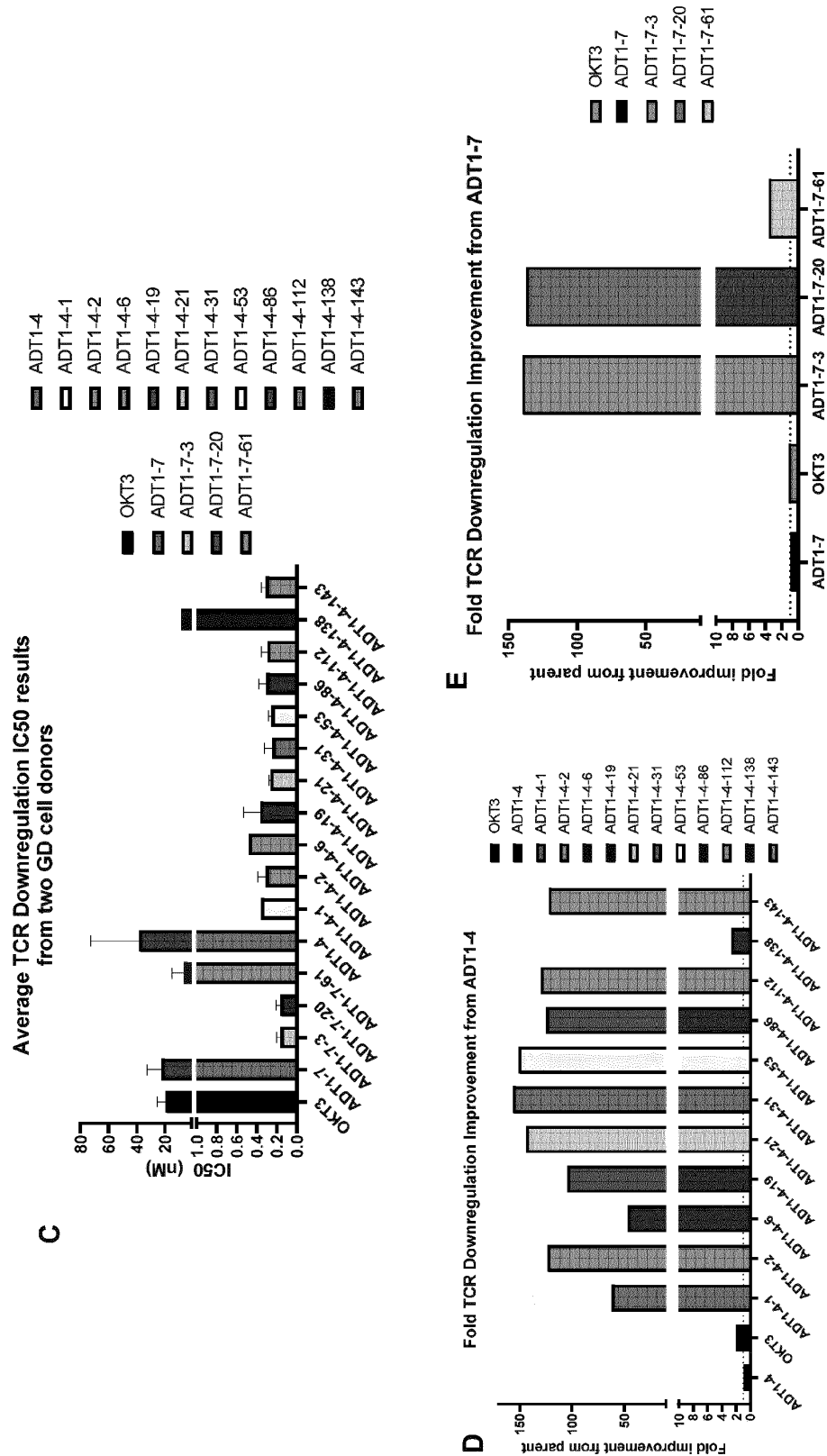


Figure 12 cont.

G

	IC50	% improvement in IC50
ADT1-4	38.28	100
OKT3	19.43	197
ADT1-4-2	0.31	12348
ADT1-4-31	0.24	15630
ADT1-4-21	0.27	14372
ADT1-4-86	0.31	12472
ADT1-4-143	0.31	12219
ADT1-4-19	0.37	10420
ADT1-4-53	0.25	15090
ADT1-4-112	0.30	12964
ADT1-4-1	0.36	6185
ADT1-4-6	0.48	4648
ADT1-4-138	8.38	266

	IC50	Fold improvement in IC50
ADT1-4	38.28	1
OKT3	19.43	2
ADT1-4-1	0.36	62
ADT1-4-2	0.31	123
ADT1-4-6	0.48	46
ADT1-4-19	0.37	104
ADT1-4-21	0.27	144
ADT1-4-31	0.24	156
ADT1-4-53	0.25	151
ADT1-4-86	0.31	125
ADT1-4-112	0.30	130
ADT1-4-138	8.38	3
ADT1-4-143	0.31	122

F

	IC50	% improvement in IC50
ADT1-7	22.42	100
OKT3	19.43	115
ADT1-7-3	0.16	13968
ADT1-7-20	0.16	13697
ADT1-7-61	6.26	358

	IC50	Fold improvement in IC50
ADT1-7	22.42	1
OKT3	19.43	1
ADT1-7-3	0.16	140
ADT1-7-20	0.16	137
ADT1-7-61	6.26	4

Figure 12 cont

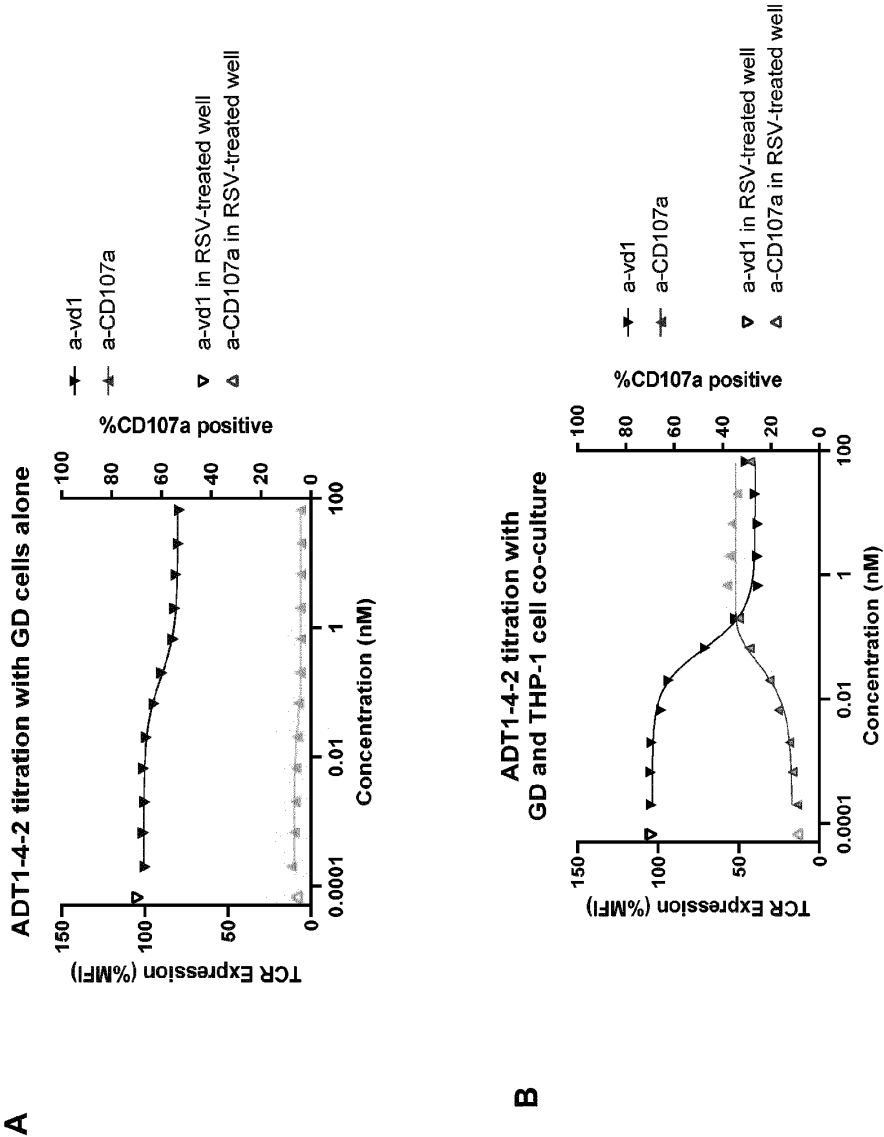
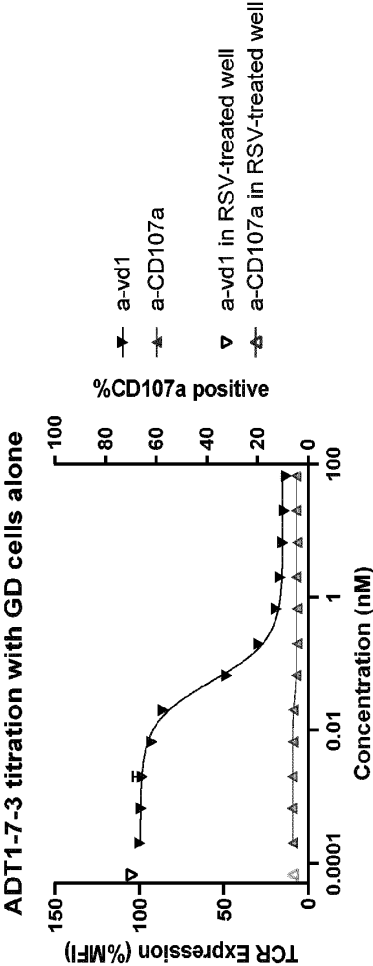


Figure 13

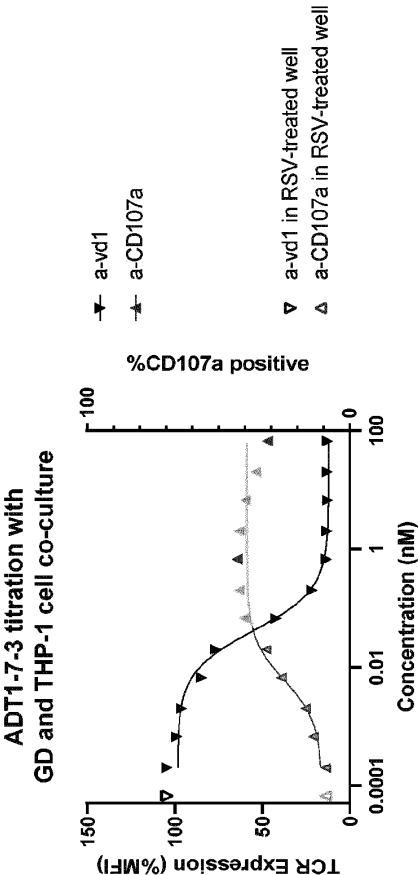
C



E

	% increase in CD107a positive cells
ADT1-4-2	24.705
ADT1-7-3	26.7

F



D

Condition	mAb	% maximum increase in CD107a positive cells
GD	ADT1-4-2	-3.73
GD	ADT1-7-3	-1.28
GD + THP-1	ADT1-4-2	19.53
GD + THP-1	ADT1-7-3	22.3

Figures 13 cont.

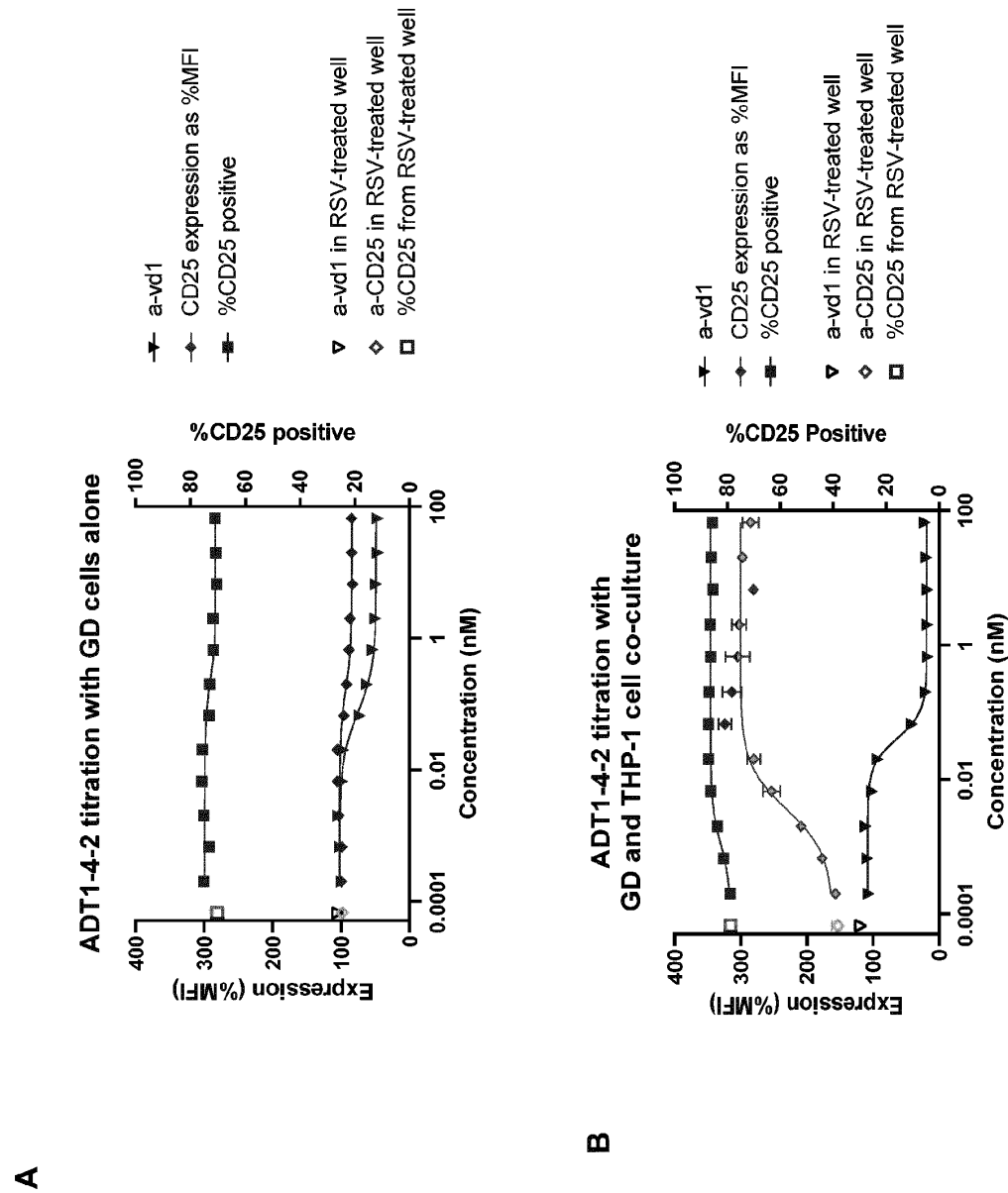
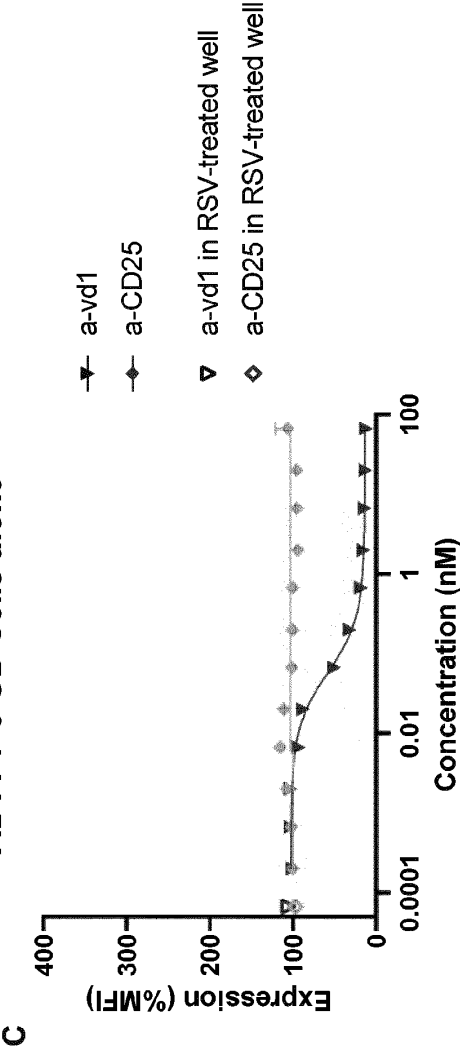


Figure 14

ADT1-7-3 GD Cells alone



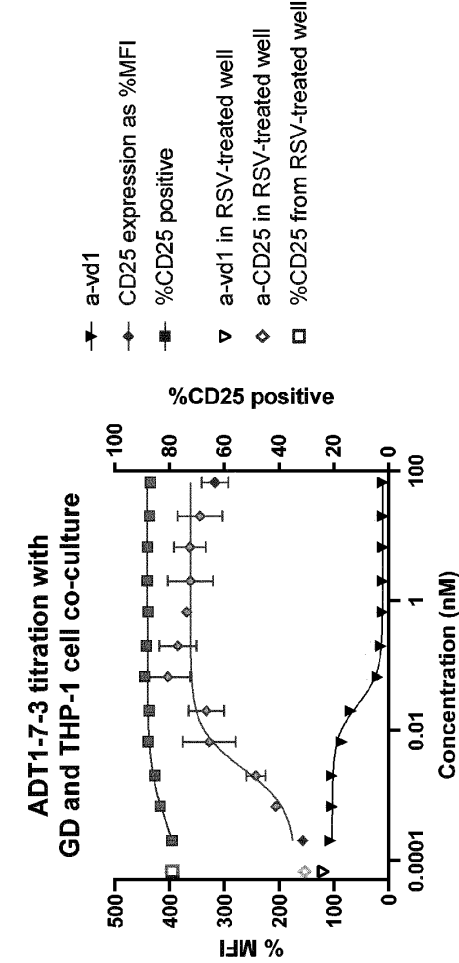
E

	% increase in CD25 expression
ADT1-4-2	170.1
ADT1-7-3	220.9

F

Condition	mAb	% maximum increase in CD25 expression
GD	ADT1-4-2	-15.23
GD + THP-1	ADT1-4-2	116.8
GD	ADT1-7-3	3.84
GD + THP-1	ADT1-7-3	162.2

D



Figures 14 cont.

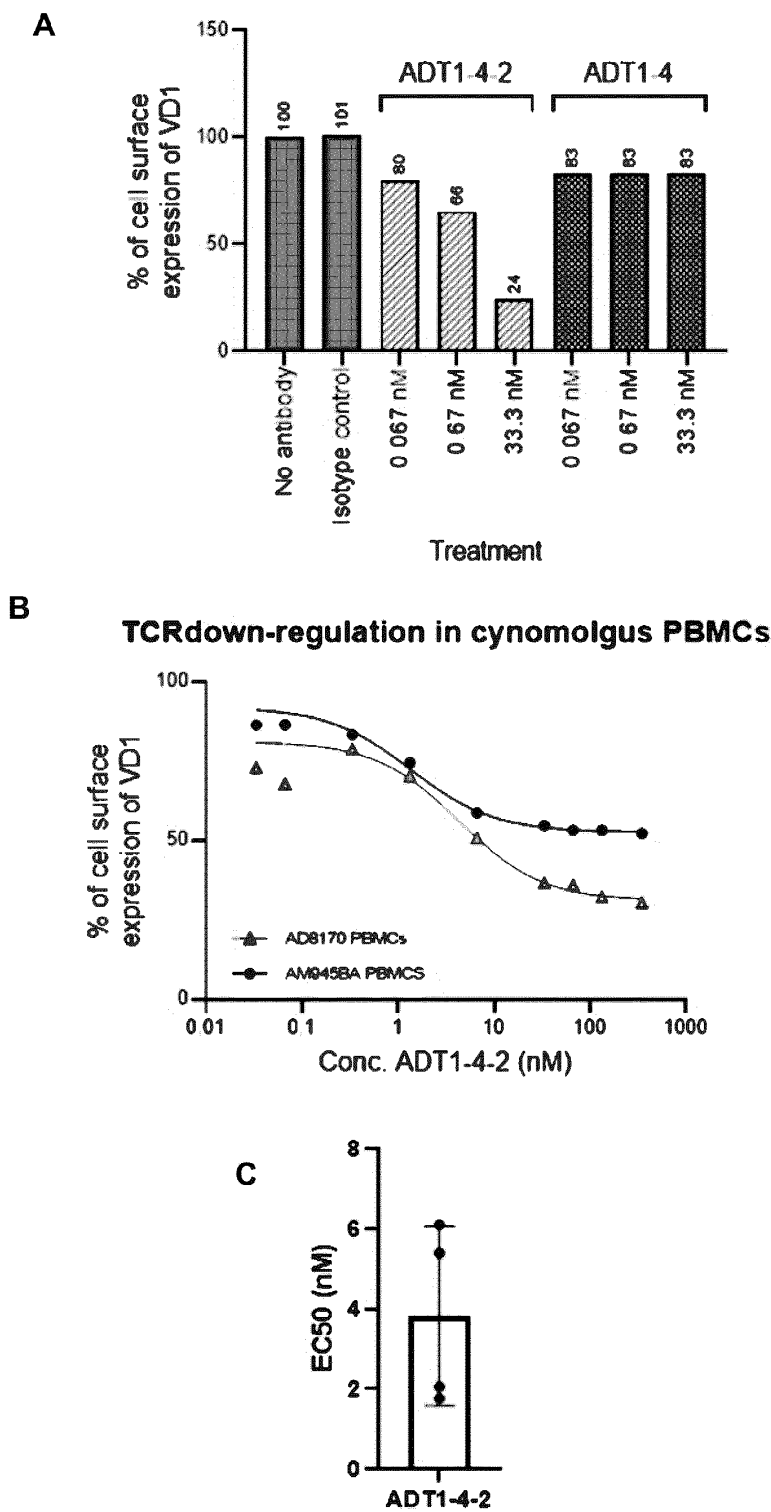


Figure 15

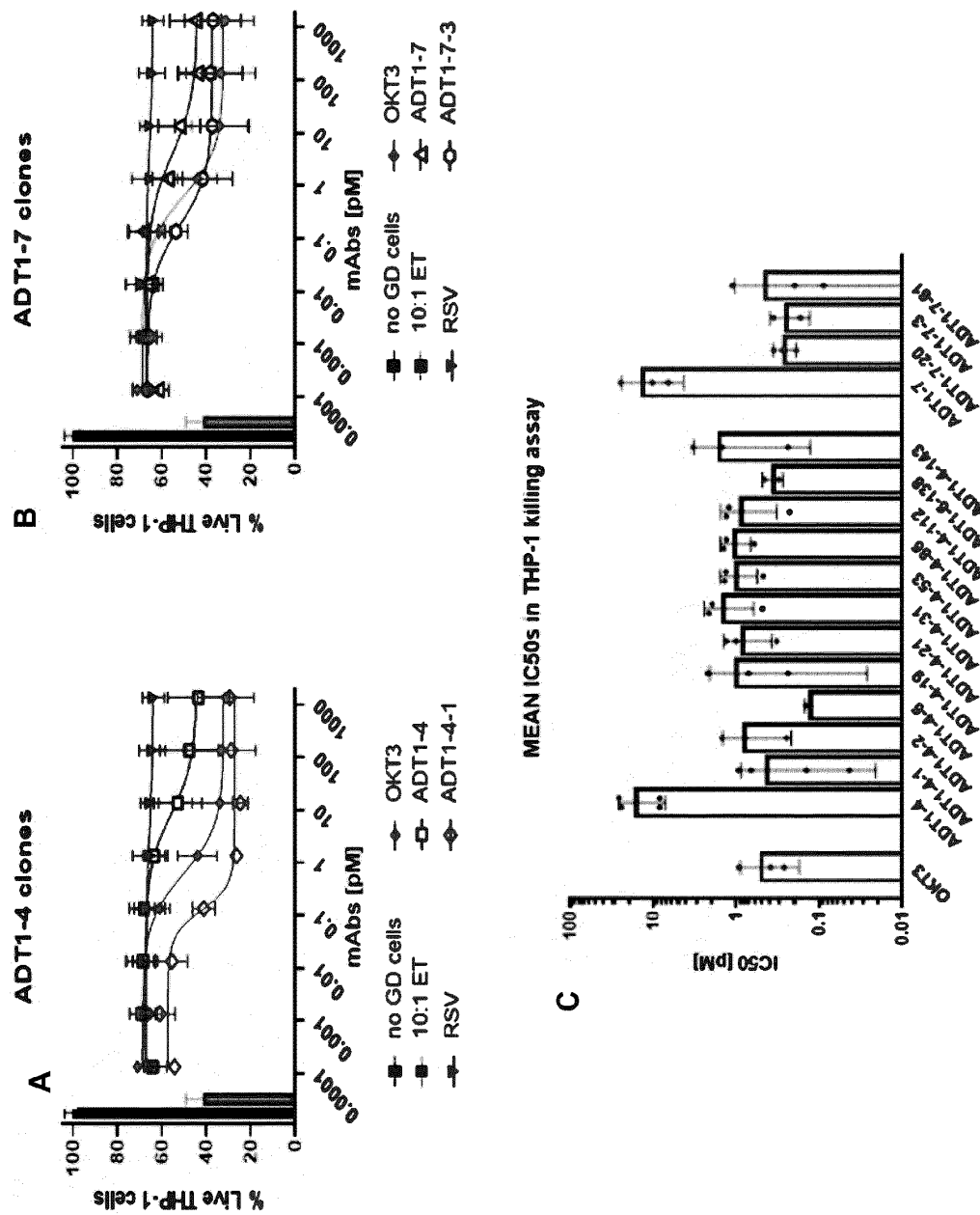


Figure 16

Clone ID	THP-1 killing assay EC50 [pM] (average of ≥3 donors)	Standard deviation	Fold improvement	% improvement over parent
OKT3 _(anti CD3)	3.53	2.40		
ADT1-4	121.47	136.80	1.0	100%
ADT1-4-1	3.00	2.87	40.5	4049%
ADT1-4-2	6.33	3.67	19.2	1918%
ADT1-4-6	0.93	0.07	130.1	13014%
ADT1-4-19	8.33	6.13	14.6	1458%
ADT1-4-21	6.13	2.93	19.8	1980%
ADT1-4-31	10.93	4.73	11.1	1111%
ADT1-4-53	7.40	3.13	16.4	1641%
ADT1-4-86	7.60	2.87	16.0	1598%
ADT1-4-112	6.47	3.53	18.8	1878%
ADT1-6-138	2.53	0.73	47.9	4795%
ADT1-4-143	13.07	9.27	9.3	930%
ADT1-7	65.20	54.80	1.0	100%
ADT1-7-20	1.87	0.53	34.9	3493%
ADT1-7-3	1.33	0.87	48.9	4890%
ADT1-7-61	3.60	3.60	18.1	1811%

Figure 16 cont.

D

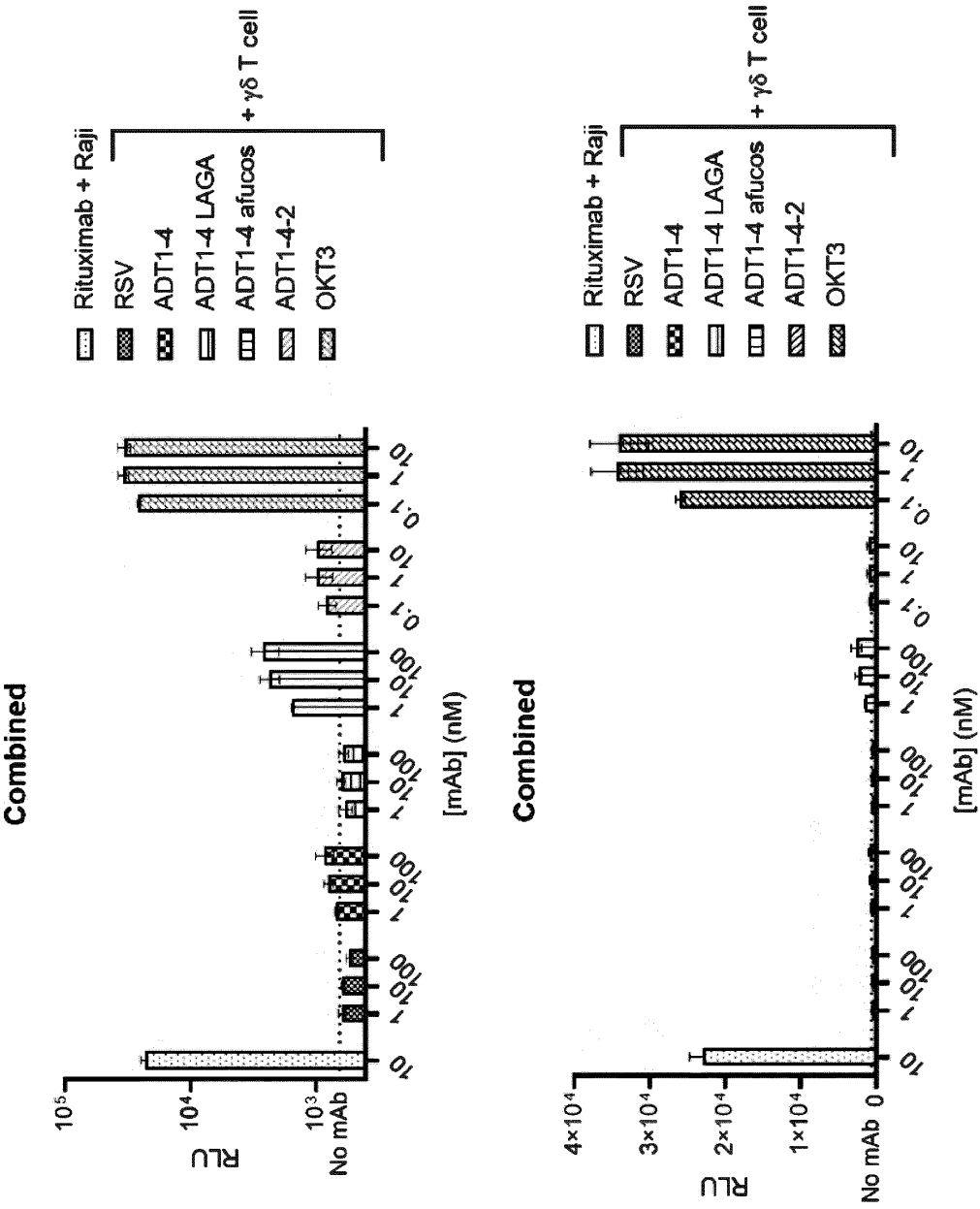


Figure 17

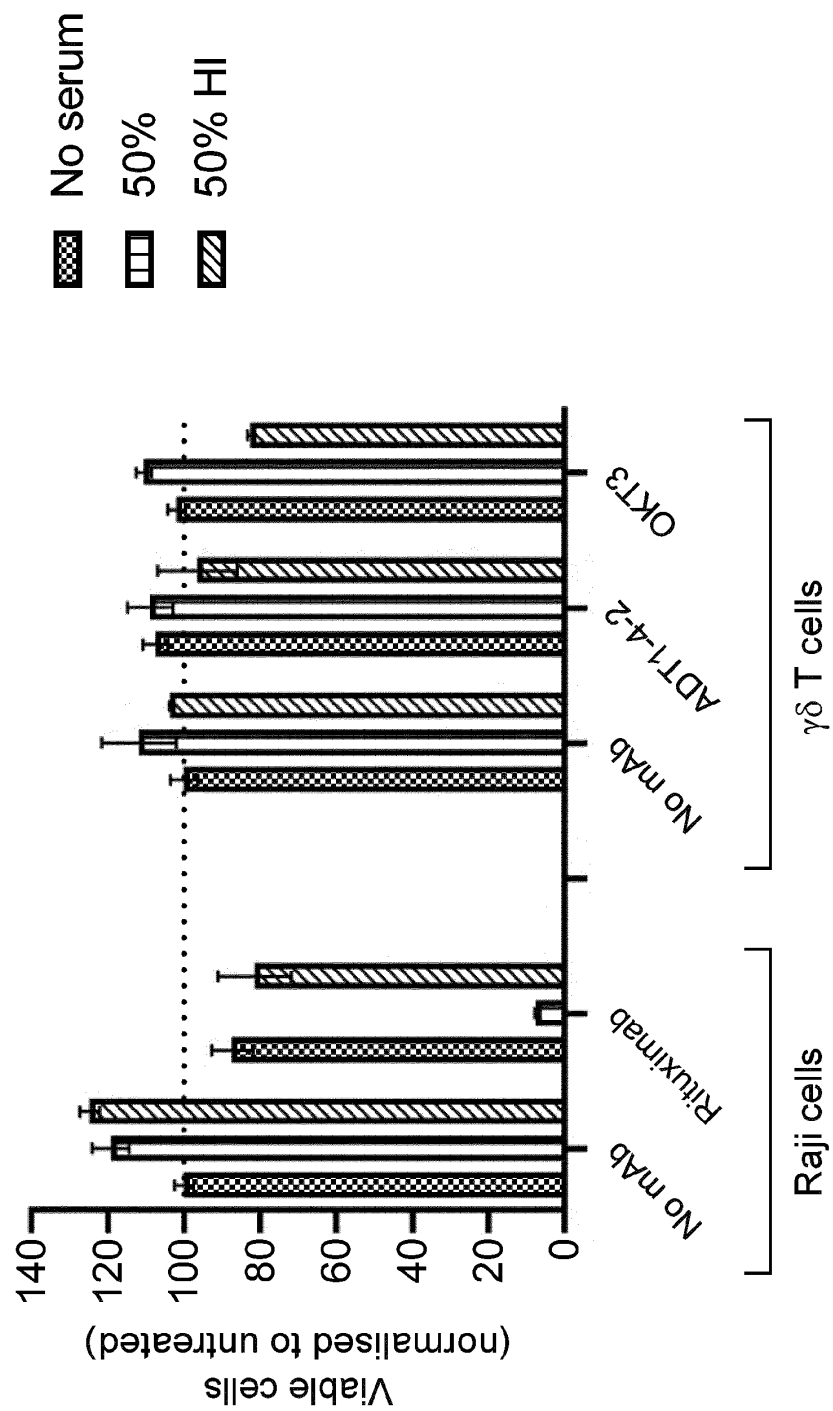


Figure 18

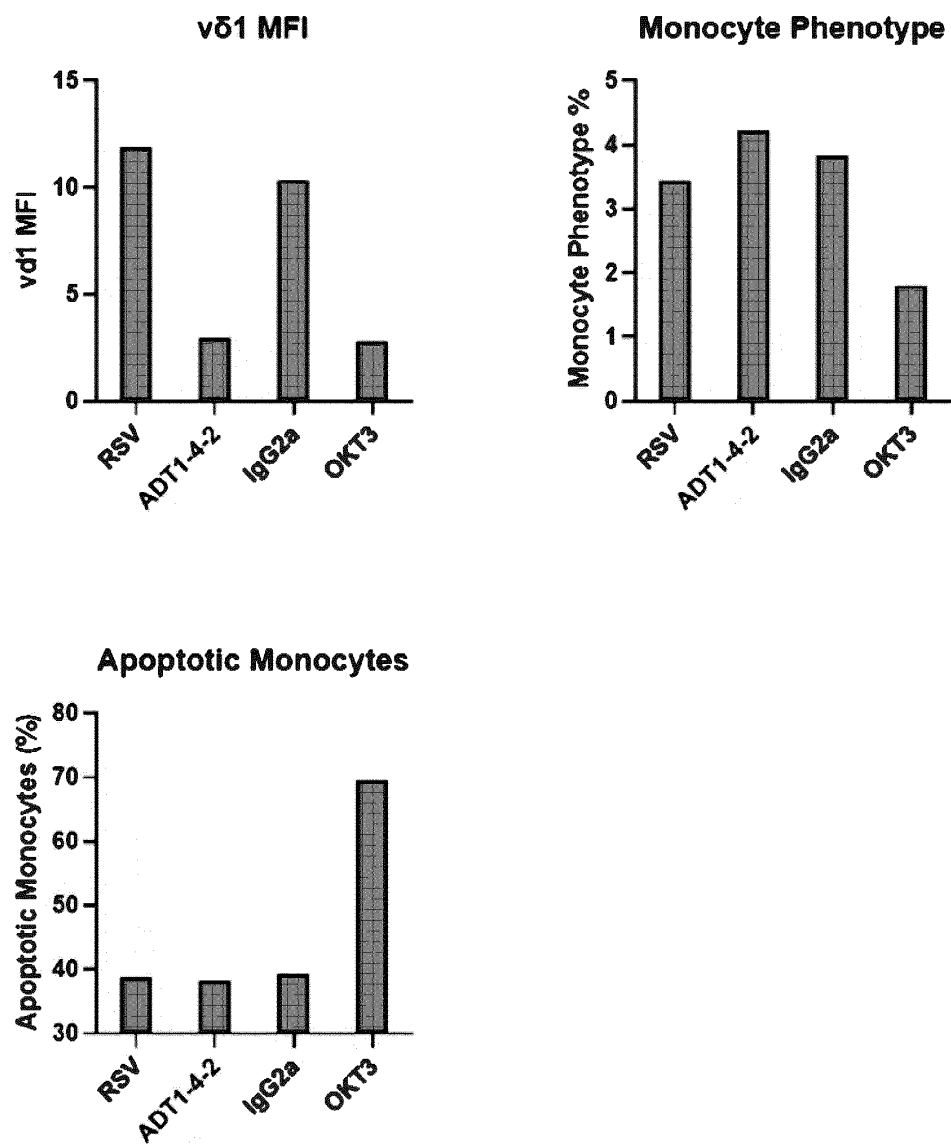


Figure 19

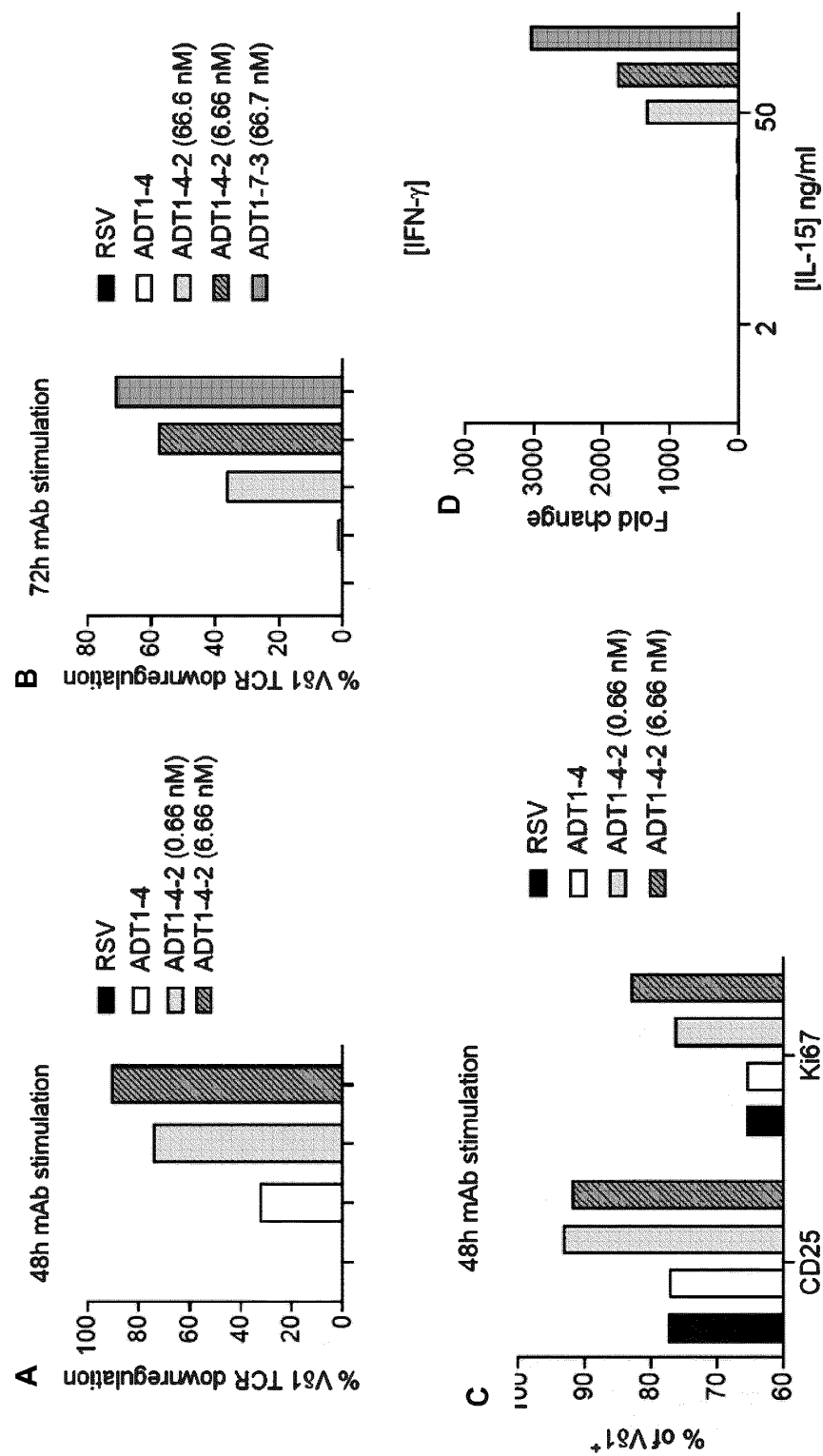


Figure 20

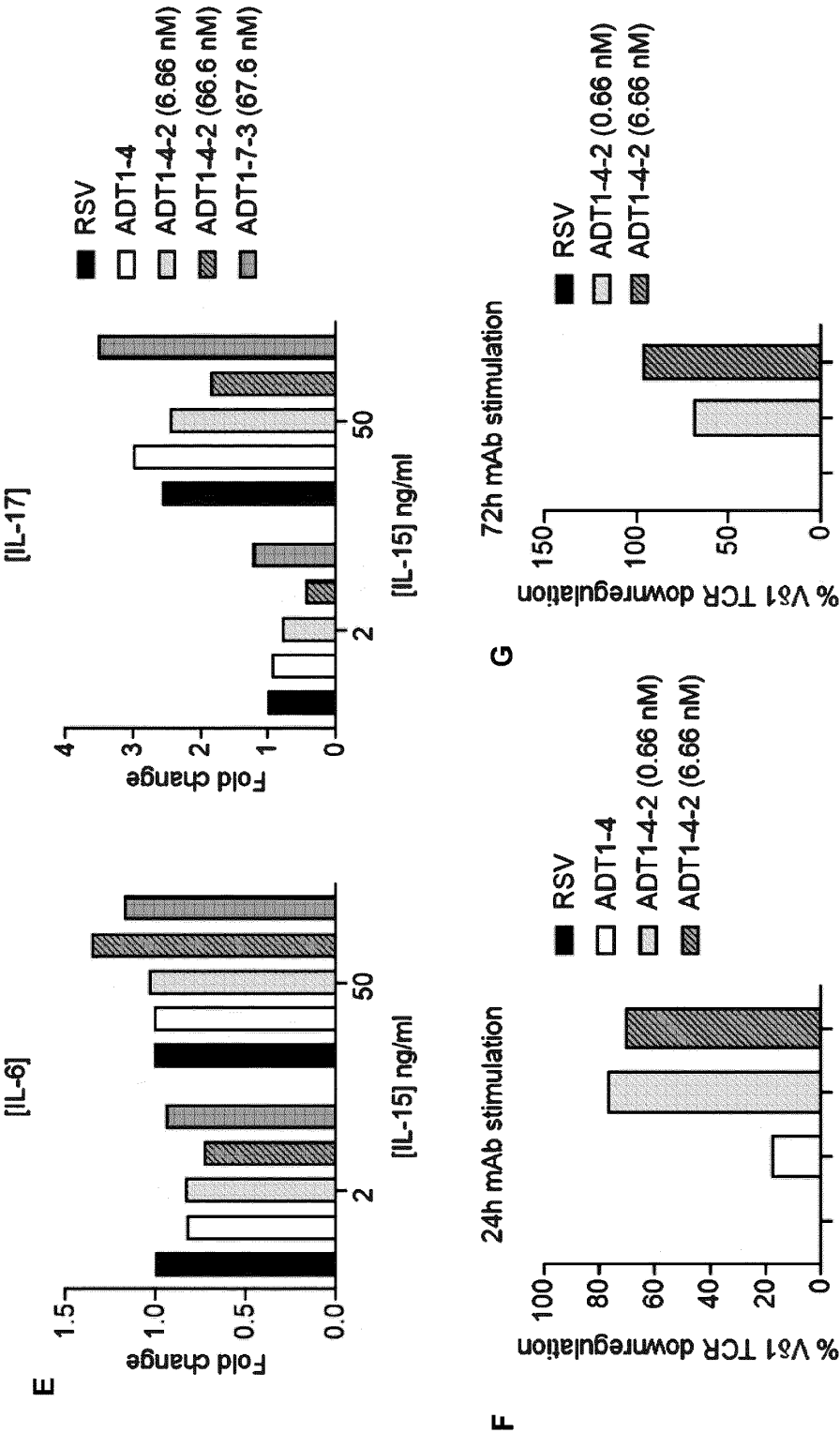


Figure 20 cont.

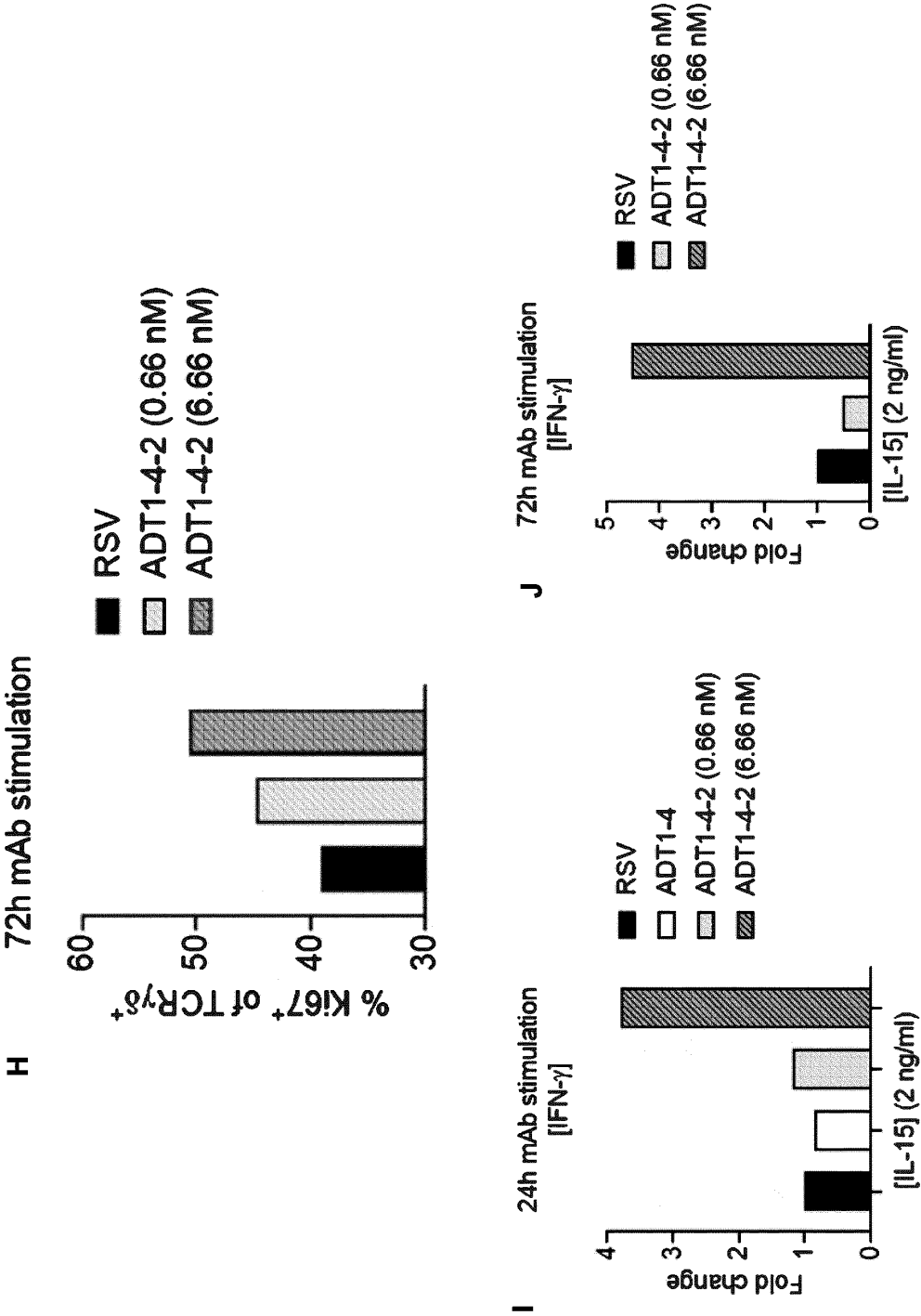


Figure 20 cont.

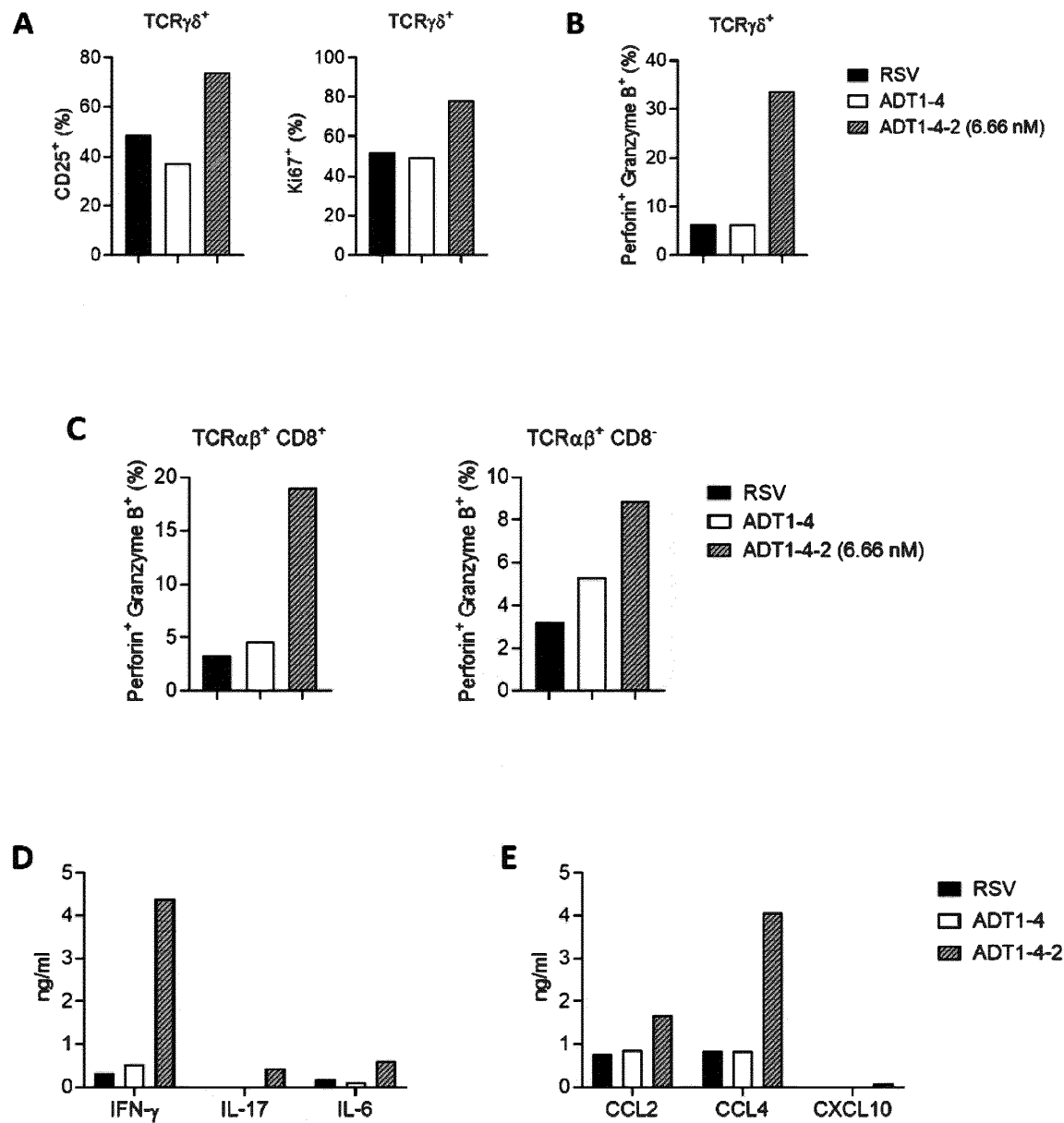


Figure 21

ADT1-4-105 2499_01_D07
 DIQMTQSPALASVGDRVTITCRASQD INDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGSGTEFTLTATISSLPDDFATYYCQQRKYSTPQITFGQGRLEIK
 ADT1-4-107 2499_01_F07
 DIQMTQSPALASVGDRVTITCRASQD INDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGSGTEFTLTATISSLPDDFATYYCQQRKYSTPQITFGQGRLEIK
 ADT1-4-110 2499_02_A02
 DIQMTQSPALASVGDRVTITCRASQD INDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGSGTEFTLTATISSLPDDFATYYCQQRKYSTPQITFGQGRLEIK
 ADT1-4-112 2499_02_B04
 DIQMTQSPALASVGDRVTITCRASQD INDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGSGTEFTLTATISSLPDDFATYYCQQRKYSTPQITFGQGRLEIK
 ADT1-4-117 2499_02_F12
 DIQMTQSPALASVGDRVTITCRASQD INDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGSGTEFTLTATISSLPDDFATYYCQQRKYSTPQITFGQGRLEIK
 ADT1-4-119 2501_01_H01
 DIQMTQSPALASVGDRVTITCRASQD INDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGSGTEFTLTATISSLPDDFATYYCQQRKYSTPQITFGQGRLEIK
 ADT1-4-21 2501_02_A05
 DIQMTQSPALASVGDRVTITCRASQD INDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGSGTEFTLTATISSLPDDFATYYCQQRKYSTPQITFGQGRLEIK
 ADT1-4-31 2501_02_G09
 DIQMTQSPALASVGDRVTITCRASQD INDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGSGTEFTLTATISSLPDDFATYYCQQRKYSTPQITFGQGRLEIK
 ADT1-4-139 2502_01_C07
 DIQMTQSPALASVGDRVTITCRASQD INDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGSGTEFTLTATISSLPDDFATYYCQQRKYSTPQITFGQGRLEIK
 ADT1-4-4 2502_01_E01
 DIQMTQSPALASVGDRVTITCRASQD INDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGSGTEFTLTATISSLPDDFATYYCQQRKYSTPQITFGQGRLEIK
 ADT1-4-143 2502_01_E05
 DIQMTQSPALASVGDRVTITCRASQD INDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGSGTEFTLTATISSLPDDFATYYCQQRKYSTPQITFGQGRLEIK
 ADT1-4-53 2505_02_E12
 DIQMTQSPALASVGDRVTITCRASQD INDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGSGTEFTLTATISSLPDDFATYYCQQRKYSTPQITFGQGRLEIK

Figure 22

ADT1-4-173 2505_02_g11
 DIQMTQSPFALSASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK

ADT1-4-2 2506_01_B10
 DIQMTQSPFALSASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK

ADT1-4-8 2506_01_B11
 DIQMTQSPFALSASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK

ADT1-4-82 2506_02_B09
 DIQMTQSPFALSASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK

ADT1-4-83 2506_02_B10
 DIQMTQSPFALSASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK

ADT1-4-3 2506_02_C01
 DIQMTQSPFALSASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK

ADT1-4-84 2506_02_C02
 DIQMTQSPFALSASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK

ADT1-4-86 2506_02_C12
 DIQMTQSPFALSASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK

ADT1-4-95 2506_02_H04
 DIQMTQSPFALSASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK

ADT1-4-1 2501_01_C09
 DIQMTQSPFALSASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK

ADT1-4-6 2506_1_B06
 DIQMTQSPFALSASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK

ADT1-4-138 2502_01_B03
 DIQMTQSPFALSASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK

Figure 22 cont.

ADT1-4-105 2499_01_D07
EVQLQQSGPGLVKPSQTLTSLTCAISGDSVSSKSAAWNNWIRQSPSRGLEWLGETYRSKWSTDYAAASVKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGGGTLTVTSS

ADT1-4-107 2499_01_F07
EVQLQQSGPGLVKPSQTLTSLTCAISGDSVSSKSAAWNNWIRQSPSRGLEWLGETYRSKWSTDYAAASVKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGGGTLTVTSS

ADT1-4-110 2499_02_A02
EVQLQQSGPGLVKPSQTLTSLTCAISGDSVSSKSAAWNNWIRQSPSRGLEWLGETYRSKWSTDYAAASVKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVEYVDVWGGGTLTVTSS

ADT1-4-112 2499_02_B04
EVQLQQSGPGLVKPSQTLTSLTCAISGDSVSSKSAAWNNWIRQSPSRGLEWLGETYRSKWSTDYAAASVKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGGGTLTVTSS

ADT1-4-117 2499_02_F12
EVQLQQSGPGLVKPSQTLTSLTCAISGDSVSSKSAAWNNWIRQSPSRGLEWLGETYRSKWSTDYAAASVKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGGGTLTVTSS

ADT1-4-119 2501_01_H01
EVQLQQSGPGLVKPSQTLTSLTCAISGDSVSSKSAAWNNWIRQSPSRGLEWLGETYRSKWSTDYAAASVKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGGGTLTVTSS

ADT1-4-21 2501_02_A05
EVQLQQSGPGLVKPSQTLTSLTCAISGDSVSSKSAAWNNWIRQSPSRGLEWLGETYRSKWSTDYAAASVKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWADYVDVWGGGTLTVTSS

ADT1-4-31 2501_02_G09
EVQLQQSGPGLVKPSQTLTSLTCAISGDSVSSKSAAWNNWIRQSPSRGLEWLGETYRSKWSTDYAAASVKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGGGTLTVTSS

ADT1-4-139 2502_01_C07
EVQLQQSGPGLVKPSQTLTSLTCAISGDSVSSKSAAWNNWIRQSPSRGLEWLGETYRSKWSTDYAAASVKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGGGTLTVTSS

ADT1-4-4 2502_01_E01
EVQLQQSGPGLVKPSQTLTSLTCAISGDSVSSKSAAWNNWIRQSPSRGLEWLGETYRSKWSTDYAAASVKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGGGTLTVTSS

ADT1-4-143 2502_01_E05
EVQLQQSGPGLVKPSQTLTSLTCAISGDSVSSKSAAWNNWIRQSPSRGLEWLGETYRSKWSTDYAAASVKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGGGTLTVTSS

ADT1-4-53 2505_02_E12
EVQLQQSGPGLVKPSQTLTSLTCAISGDSVSSKSAAWNNWIRQSPSRGLEWLGETYRSKWSTDYAAASVKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWADYVDVWGGGTLTVTSS

Figure 23

ADT1-4-173 2505_02_G11
EVQLQSGPGLVKPSQTLSTCAISGDVSYSKSAANNWIRQSPSRGLEWLGRTYYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWAGYVDVWGQGLVTVSS
ADT1-4-2 2506_01_B10
EVQLQSGPGLVKPSQTLSTCAISGDVSYSKSAANNWIRQSPSRGLEWLGRTYYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWVGYVDVWGQGLVTVSS
ADT1-4-8 2506_01_B11
EVQLQSGPGLVKPSQTLSTCAISGDVSYSKSAANNWIRQSPSRGLEWLGRTYYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWVGYADVWGQGLVTVSS
ADT1-4-82 2506_02_B09
EVQLQSGPGLVKPSQTLSTCAISGDVSYSKSAANNWIRQSPSRGLEWLGRTYYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWVGYADVWGQGLVTVSS
ADT1-4-83 2506_02_B10
EVQLQSGPGLVKPSQTLSTCAISGDVSYSKSAANNWIRQSPSRGLEWLGRTYYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARSWVGYSVDVWGQGLVTVSS
ADT1-4-3 2506_02_C01
EVQLQSGPGLVKPSQTLSTCAISGDVSYSKSAANNWIRQSPSRGLEWLGRTYYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARSWVGYSVDVWGQGLVTVSS
ADT1-4-84 2506_02_C02
EVQLQSGPGLVKPSQTLSTCAISGDVSYSKSAANNWIRQSPSRGLEWLGRTYYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWADYVDVWGQGLVTVSS
ADT1-4-86 2506_02_C12
EVQLQSGPGLVKPSQTLSTCAISGDVSYSKSAANNWIRQSPSRGLEWLGRTYYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWVGYADVWGQGLVTVSS
ADT1-4-95 2506_02_H04
EVQLQSGPGLVKPSQTLSTCAISGDVSYSKSAANNWIRQSPSRGLEWLGRTYYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWVGYADVWGQGLVTVSS
ADT1-4-1 2501_01_C09
EVQLQSGPGLVKPSQTLSTCAISGDVSYSKSAANNWIRQSPSRGLEWLGRTYYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWVGYADVWGQGLVTVSS
ADT1-4-6 2506_1_B06
EVQLQSGPGLVKPSQTLSTCAISGDVSYSKSAANNWIRQSPSRGLEWLGRTYYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWAGYPDVWGQGLVTVSS
ADT1-4-138 2502_01_B03
EVQLQSGPGLVKPSQTLSTCAISGDVSYSKSAANNWIRQSPSRGLEWLGRTYYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWADYVDVWGQGLVTVSS

Figure 23 cont.

ADT1-7-10 2503_1_C12
DIQMTQSPSSLSASVGDRVTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLSQSGVPSRFSGSGSGTEFTLTISISLQPEDFATYYCQQTASTLLTFGRTKVEIK
ADT1-7-15 2503_1_F01
DIQMTQSPSSLSASVGDRVTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLSQSGVPSRFSGSGSGTEFTLTISISLQPEDFATYYCQQSADTLLTFGRTKVEIK
ADT1-7-17 2503_1_G05
DIQMTQSPSSLSASVGDRVTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLSQSGVPSRFSGSGSGTEFTLTISISLQPEDFATYYCQQSGSEILLTFGRTKVEIK
ADT1-7-18 2503_1_G06
DIQMTQSPSSLSASVGDRVTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLSQSGVPSRFSGSGSGTEFTLTISISLQPEDFATYYCQQSASELLTFGRTKVEIK
ADT1-7-19 2503_1_G10
DIQMTQSPSSLSASVGDRVTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLSQSGVPSRFSGSGSGTEFTLTISISLQPEDFATYYCQQSYSGLDLTFGRTKVEIK
ADT1-7-20 2503_1_H02
DIQMTQSPSSLSASVGDRVTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLSQSGVPSRFSGSGSGTEFTLTISISLQPEDFATYYCQQSASELLTFGRTKVEIK
ADT1-7-22 2503_2_A02
DIQMTQSPSSLSASVGDRVTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLSQSGVPSRFSGSGSGTEFTLTISISLQPEDFATYYCQQSASELLTFGRTKVEIK
ADT1-7-23 2503_2_A07
DIQMTQSPSSLSASVGDRVTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLSQSGVPSRFSGSGSGTEFTLTISISLQPEDFATYYCQQSYSGLDLTFGRTKVEIK
ADT1-7-42 2503_2_H06
DIQMTQSPSSLSASVGDRVTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLSQSGVPSRFSGSGSGTEFTLTISISLQPEDFATYYCQQSSSEILLTFGRTKVEIK
ADT1-7-3 2504_1_A01
DIQMTQSPSSLSASVGDRVTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLSQSGVPSRFSGSGSGTEFTLTISISLQPEDFATYYCQQSYSGLDLTFGRTKVEIK
ADT1-7-61 2504_1_F02
DIQMTQSPSSLSASVGDRVTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLSQSGVPSRFSGSGSGTEFTLTISISLQPEDFATYYCQQSASELLTFGRTKVEIK

Figure 24

ADT1-7-10 2503_1_C12
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDDYNDADFIMGQGLVTVSS

ADT1-7-15 2503_1_F01
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDDYNDADFIMGQGLVTVSS

ADT1-7-17 2503_1_G05
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARIDYEDADFIMGQGLVTVSS

ADT1-7-18 2503_1_G06
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARIDSYEDADFIMGQGLVTVSS

ADT1-7-19 2503_1_G10
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARIDYEDADFIMGQGLVTVSS

ADT1-7-20 2503_1_H02
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARVDYQEAADFIMGQGLVTVSS

ADT1-7-22 2503_2_A02
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDDYNDADFIMGQGLVTVSS

ADT1-7-23 2503_2_A07
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARVDYNEADFIMGQGLVTVSS

ADT1-7-42 2503_2_H06
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDDYEDADFIMGQGLVTVSS

ADT1-7-3 2504_1_A01
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARVSYAEADFIMGQGLVTVSS

ADT1-7-61 2504_1_F02
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDDYDDADFIMGQGLVTVSS

Figure 25

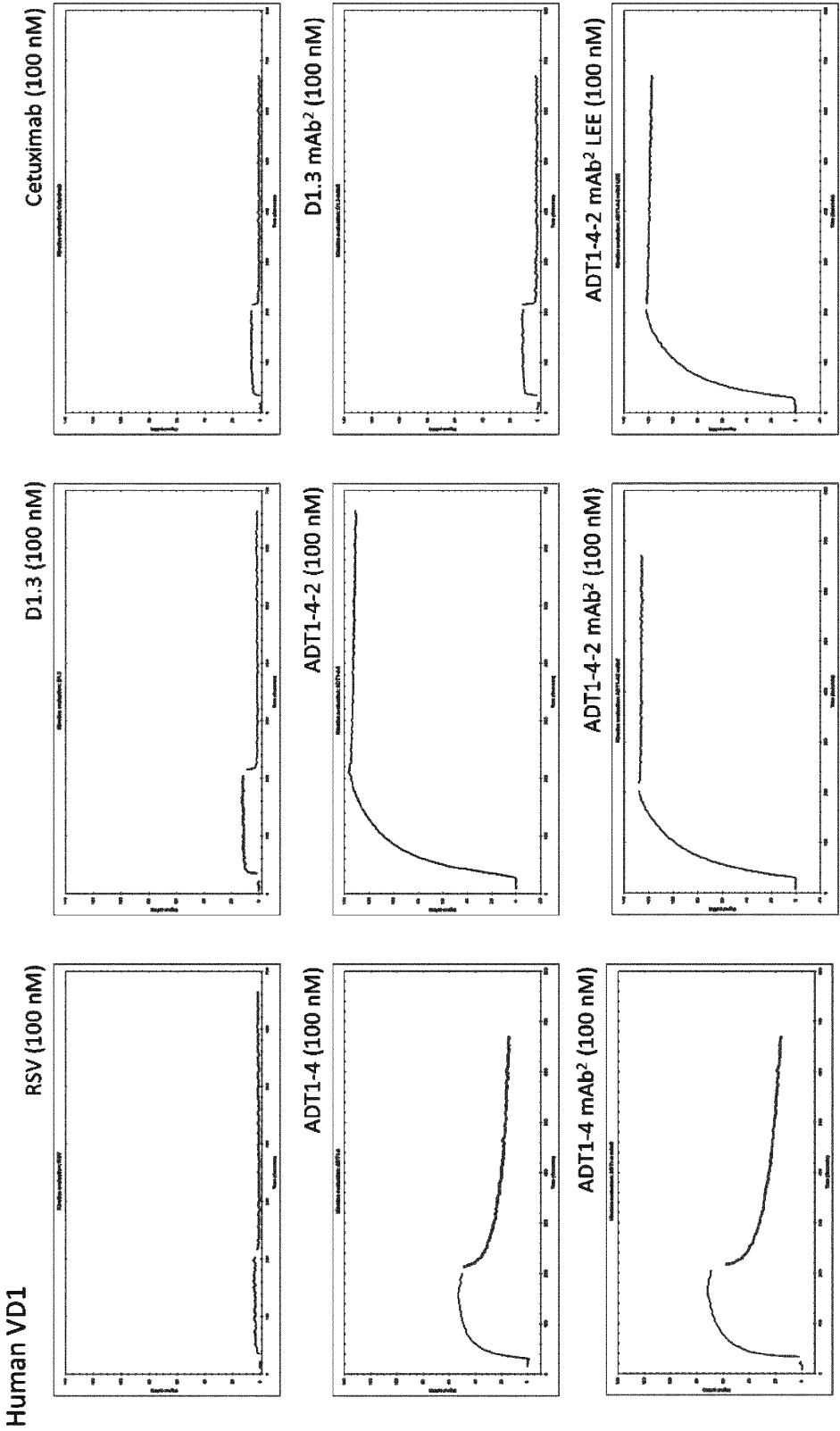


FIG 26A

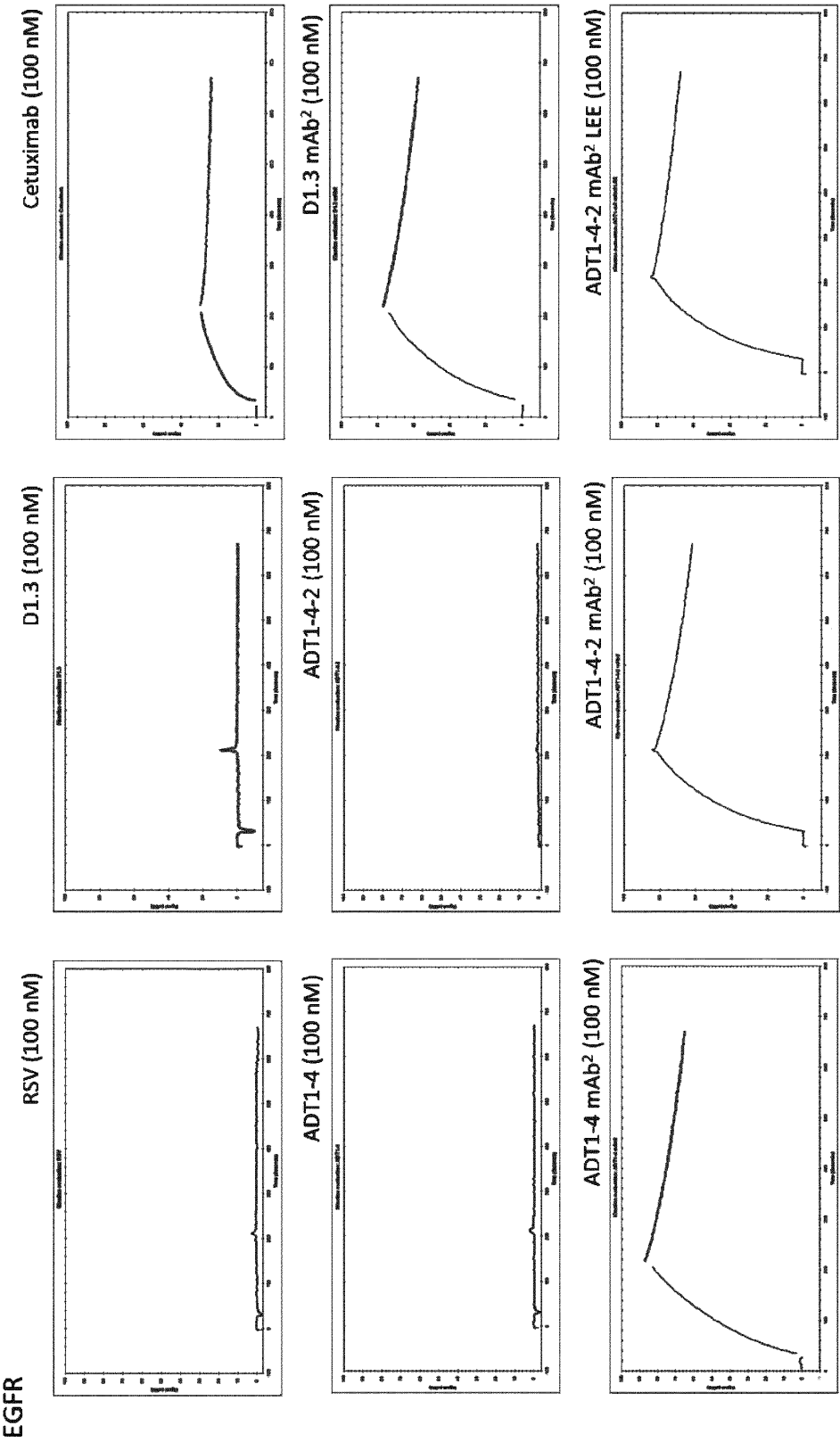


FIG 26B

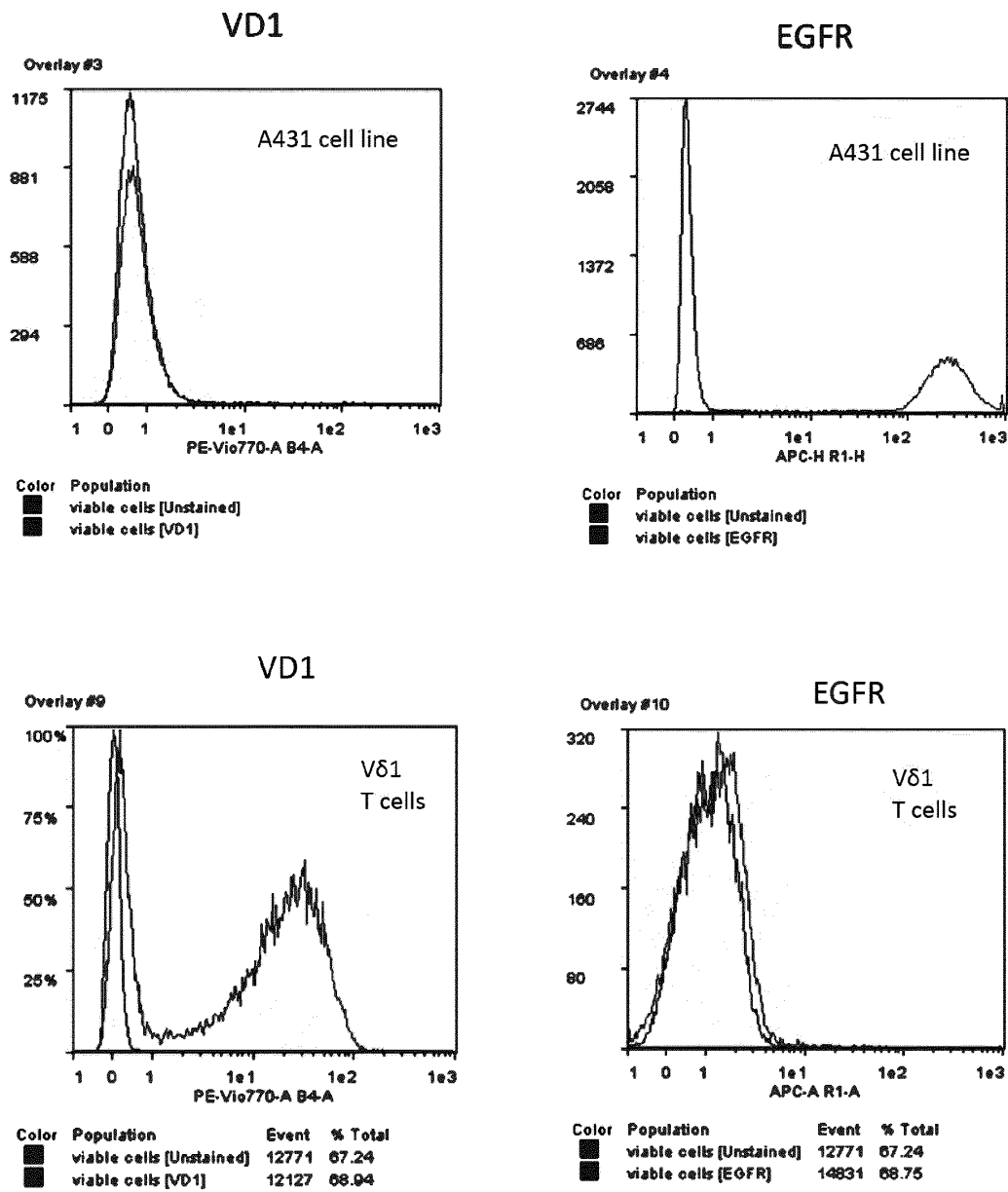


FIG 27A

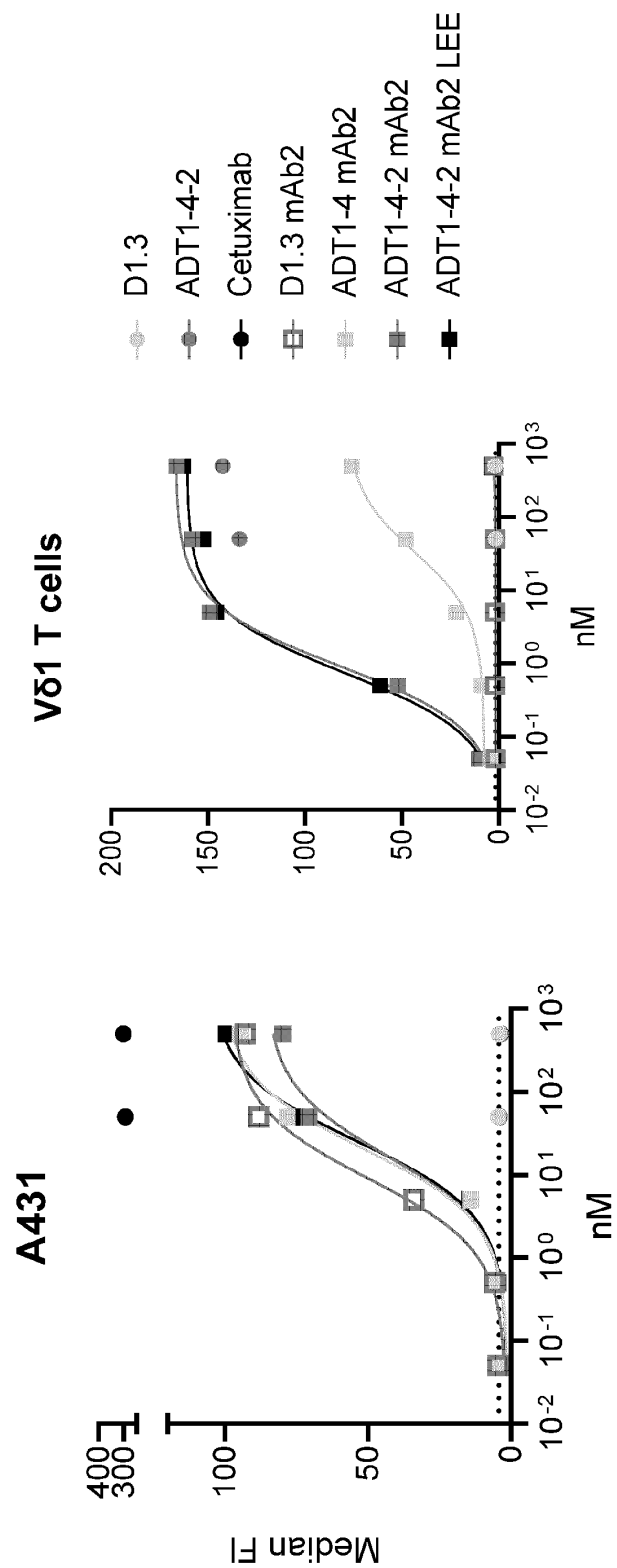


FIG 27B

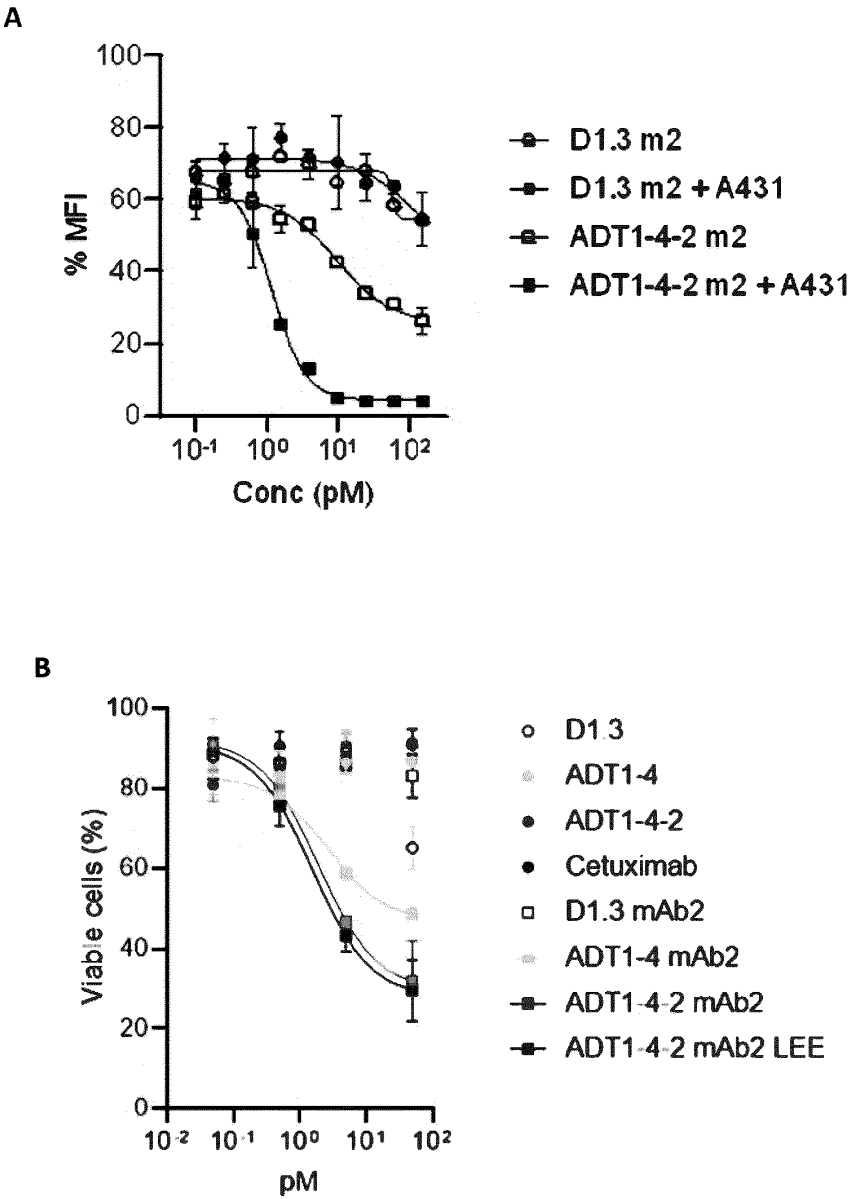


FIG 28

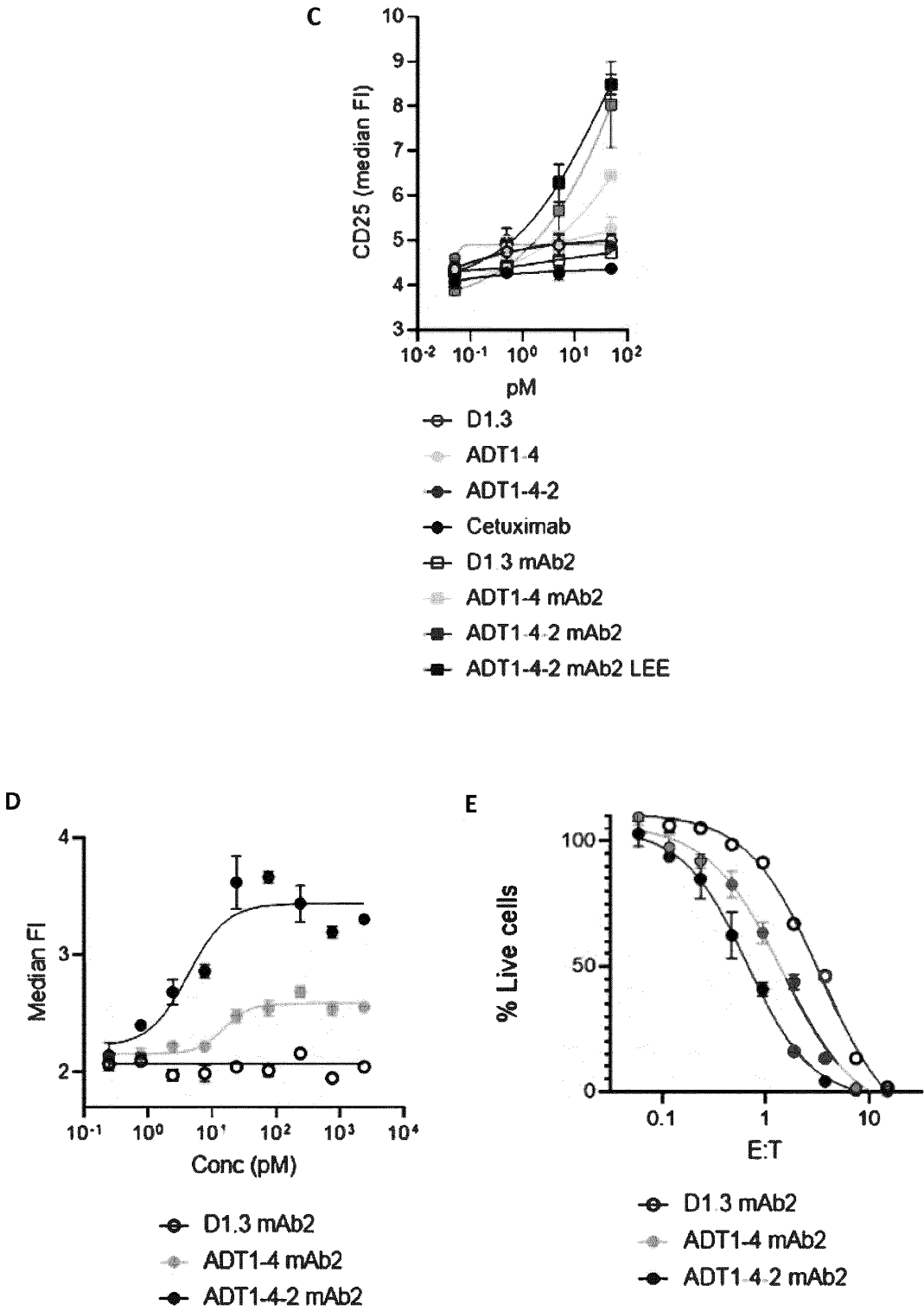


FIG 28 cont.

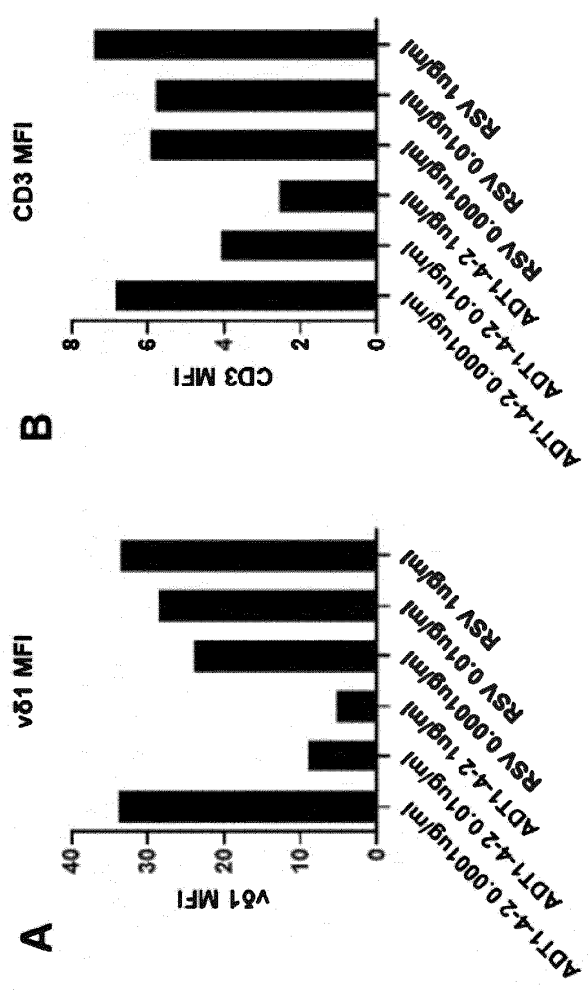


FIG 29

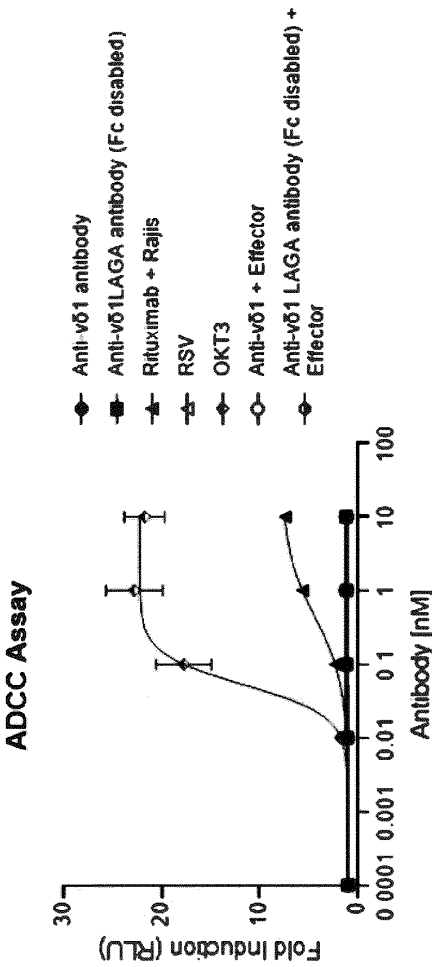


FIG 30

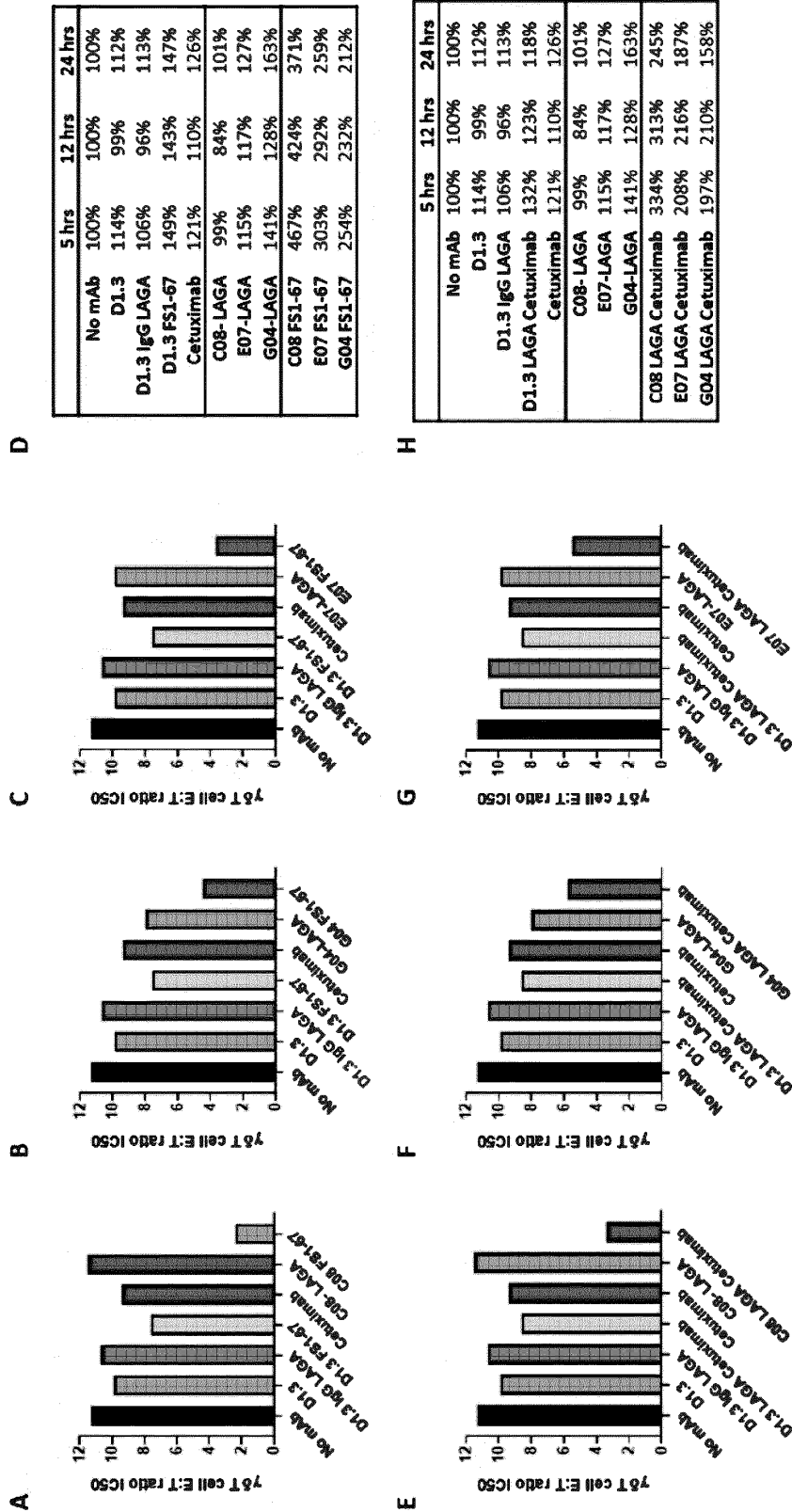


FIGURE 31

EGFR binding domains (IgG1 CH1-CH2-CH3)

FS1-67 (SEQ ID NO: 385)
ASTKGPSVFPLAAPSCKSTSGGTAALGCLIVKDYFPEPVTVSNWSGALTSGVHTFPVLIQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKHTHTCPCPAPELIGGSPVFLFPPKPKDTIMISRTPEVTCV
VVDUSHEDEPKFNNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDELDDEGPPVSLTCLVKGFTYPSDIAVEWESSTYGPNNYKTTTPVLDSDGSFFLY
SKLTVSYRWYKGNVFSCVMHEALHNHYTQKSLSLSPG

LEE (SEQ ID NO: 392)
ASTKGPSVFPLAAPSCKSTSGGTAALGCLIVKDYFPEPVTVSNWSGALTSGVHTFPVLIQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKHTHTCPCPAPELIGGSPVFLFPPKPKDTIMISRTPEVTCV
VVDUSHEDEPKFNNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDELDDEGPPVSLTCLVKGFTYPSDIAVEWESSTYGPNNYKTTTPVLDSDGSFFLY
SKLTVSYRWYKGNVFSCVMHEALHNHYTQKSLSLSPG

LEE1 (SEQ ID NO: 509)
ASTKGPSVFPLAAPSCKSTSGGTAALGCLIVKDYFPEPVTVSNWSGALTSGVHTFPVLIQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKHTHTCPCPAPELIGGSPVFLFPPKPKDTIMISRTPEVTCV
VVDUSHEDEPKFNNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDELDDEGPPVSLTCLVKGFTYPSDIAVEWESSTYGPNNYKTTTPVLDSDGSFFLY
SKLTVSYRWYKGNVFSCVMHEALHNHYTQKSLSLSPG

LEE2 (SEQ ID NO: 521)
ASTKGPSVFPLAAPSCKSTSGGTAALGCLIVKDYFPEPVTVSNWSGALTSGVHTFPVLIQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKHTHTCPCPAPELIGGSPVFLFPPKPKDTIMISRTPEVTCV
VVDUSHEDEPKFNNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDELDDEGPPVSLTCLVKGFTYPSDIAVEWESSTYGPNNYKTTTPVLDSDGSFFLY
SKLTVSYRWYKGNVFSCVMHEALHNHYTQKSLSLSPG

LEE3 (SEQ ID NO: 531)
ASTKGPSVFPLAAPSCKSTSGGTAALGCLIVKDYFPEPVTVSNWSGALTSGVHTFPVLIQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKHTHTCPCPAPELIGGSPVFLFPPKPKDTIMISRTPEVTCV
VVDUSHEDEPKFNNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDELDDEGPPVSLTCLVKGFTYPSDIAVEWESSTYGPNNYKTTTPVLDSDGSFFLY
SKLTVSYRWYKGNVFSCVMHEALHNHYTQKSLSLSPG

FS1-65 (SEQ ID NO: 540)
ASTKGPSVFPLAAPSCKSTSGGTAALGCLIVKDYFPEPVTVSNWSGALTSGVHTFPVLIQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKHTHTCPCPAPELIGGSPVFLFPPKPKDTIMISRTPEVTCV
VVDUSHEDEPKFNNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDELDDEGPPVSLTCLVKGFTYPSDIAVEWESSTYGPNNYKTTTPVLDSDGSFFLY
YSKLTVSYRWYKGNVFSCVMHEALHNHYTQKSLSLSPG

747 (SEQ ID NO: 551)
ASTKGPSVFPLAAPSCKSTSGGTAALGCLIVKDYFPEPVTVSNWSGALTSGVHTFPVLIQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKHTHTCPCPAPELIGGSPVFLFPPKPKDTIMISRTPEVTCV
VVDUSHEDEPKFNNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDELDDEGPPVSLTCLVKGFTYPSDIAVEWESSTYGPNNYKTTTPVLDSDGSFFLY
SKLTVSYRWYKGNVFSCVMHEALHNHYTQKSLSLSPG

FIGURE 32

[illegible]

	AB LOOP	CD LOOP	EF LOOP
F81-67	L358T.T359D.K360D.N361G.Q362P	N384T.G385Y.Q386G	D413S.K414Y.S415W.Q418Y.Q419K
LEE	T359E.K360E.N361G.Q362P	N384T.G385Y.Q386G	D413S.K414Y.S415W.Q418Y.Q419K
LEE1		N384T.G385Y.Q386G	D413S.K414Y.S415W.Q418Y.Q419K
LEE2	T359E.K360E.N361G.Q362P		D413S.K414Y.S415W.Q418Y.Q419K
LEE3	T359E.K360E.N361G.Q362P	N384T.G385Y.Q386G	D413S.K414Y.S415W
777	L358T.T359E.K360S.N361G.Q362P	A378V	D413S.K414N.S415L.Q418T.Q419K.N421H
F81-65	T359D.K360E.N361G.361-1G.Q362P	N384K.G385F.Q386G	D413S.K414Y.S415W.Q418V.Q419K

FIGURE 32 cont.

Human CH3 numbering convention (with cross-reference to IGHG1*01 wild-type)				
CH3 Human Sequence IGHG1 amino acid translation J00228 (J00228 corresponds to the IGHG1*01 allele)	IMGT unique numbering for C-DOMAIN	IMGT CH3 exon numbering – see IMGT.Org (also for source of this adapted Table)	Eu numbering – see Edelman, G.M. et al., Proc. Natl. Acad. USA, 63, 78-85 (1969).	Kabat numbering – see Kabat, E.A. et al., NIH publication n° 91-3242, pp 662,680,689 (1991).
G	1.4	1	341	361
Q	1.3	2	342	363
P	1.2	3	343	364
R	1.1	4	344	365
E	1	5	345	366
P	2	6	346	367
Q	3	7	347	368
V	4	8	348	369
Y	5	9	349	370
T	6	10	350	371
L	7	11	351	372
P	8	12	352	373
P	9	13	353	374
S	10	14	354	375
R	11	15	355	376
D	12	16	356	377
E	13	17	357	378
L	14	18	358	381
T	15	19	359	382
K	16	20	360	383
N	17	21	361	384
(extra insert found in one example construct)	17.1	21.1	361.1	384.1
Q	18	22	362	385
V	19	23	363	386
S	20	24	364	387
L	21	25	365	388
T	22	26	366	389
C	23	27	367	390
L	24	28	368	391
V	25	29	369	392
K	26	30	370	393
G	27	31	371	394
F	28	32	372	395
Y	29	33	373	396
P	30	34	374	397
S	35	35	375	398
D	36	36	376	399
I	37	37	377	400
A	38	38	378	401

FIGURE 33 cont.

V	39	39	379	402
E	40	40	380	405
W	41	41	381	406
E	42	42	382	407
S	43	43	383	408
N	44	44	384	410
G	45	45	385	411
Q	45.1	46	386	414
P	45.2	47	387	415
E	45.3	48	388	416
N	45.4	49	389	417
N	77	50	390	418
Y	78	51	391	419
K	79	52	392	420
T	80	53	393	421
T	81	54	394	422
P	82	55	395	423
P	83	56	396	424
V	84	57	397	425
L	84.1	58	398	426
D	84.2	59	399	427
S	84.3	60	400	428
D	84.4	61	401	430
G	85.4	62	402	433
S	85.3	63	403	434
F	85.2	64	404	435
F	85.1	65	405	436
L	85	66	406	437
Y	86	67	407	438
S	87	68	408	439
K	88	69	409	440
L	89	70	410	441
T	90	71	411	442
V	91	72	412	443
D	92	73	413	444
K	93	74	414	445
S	94	75	415	446
R	95	76	416	447
W	96	77	417	448
Q	97	78	418	449
Q	98	79	419	450
G	99	80	420	451
N	100	81	421	452
V	101	82	422	453
F	102	83	423	454
S	103	84	424	455

FIGURE 33 cont.

C	104	85	425	456
S	105	86	426	457
V	106	87	427	458
M	107	88	428	459
H	108	89	429	460
E	109	90	430	461
A	110	91	431	462
L	112	92	432	463
H	113	93	433	464
N	114	94	434	465
H	115	95	435	466
Y	116	96	436	467
T	117	97	437	468
Q	118	98	438	469
K	119	99	439	470
S	120	100	440	471
L	121	101	441	472
S	122	102	442	473
L	123	103	443	474
S	124	104	444	475
P	125	105	445	476
G	129	CHS 106	446	477
K	130	CHS 107	447	478

FIGURE 33 cont

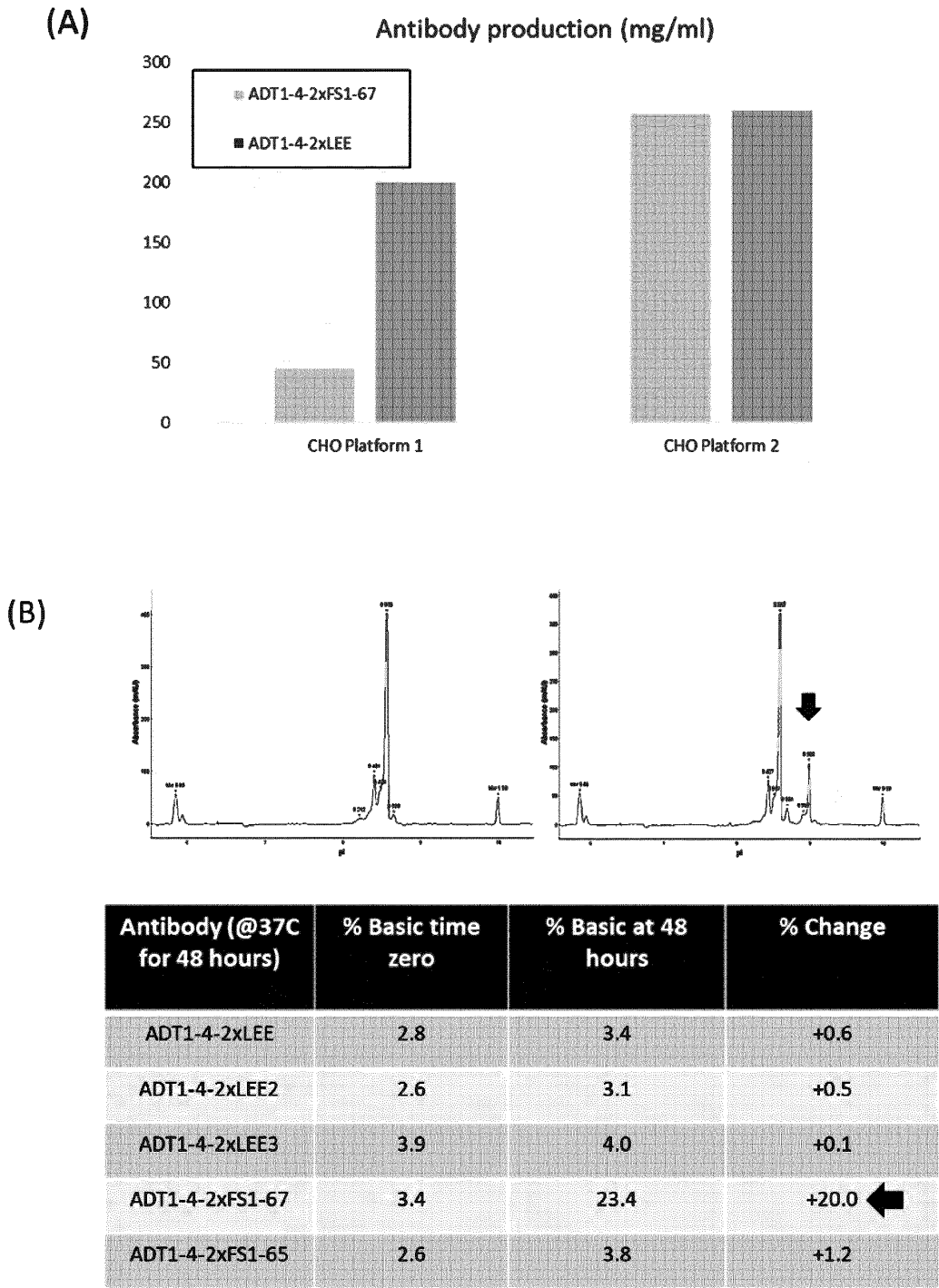
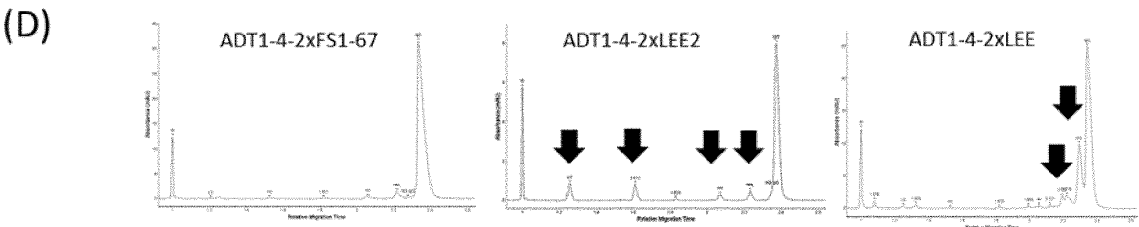


FIGURE 34

(C)

Antibody	Tm onset (°C)	Tagg onset (°C)	Delta(°C)
ADT1-4-2xLEE	63.8	63.8	0
ADT1-4-2xLEE2	67.7	64.2	-3.5
ADT1-4-2xLEE3	67.8	64.4	-3.4
ADT1-4-2xFS1-67	68.9	65.7	-3.2
ADT1-4-2xFS1-65	74	57.6	-16.4



Antibody @ 5mg/ml	% Monomer (time zero)	% Monomer (18 days, 37°C)	% change over 18-days
ADT1-4-2xLEE	98.0	60.6	-37.4
ADT1-4-2xLEE2	97.7	74.0	-23.7
ADT1-4-2xLEE3	97.5	68.3	-29.2
ADT1-4-2xFS1-67	95.6	94.0	-1.6
ADT1-4-2xFS1-65	96.8	72.7	-24.1

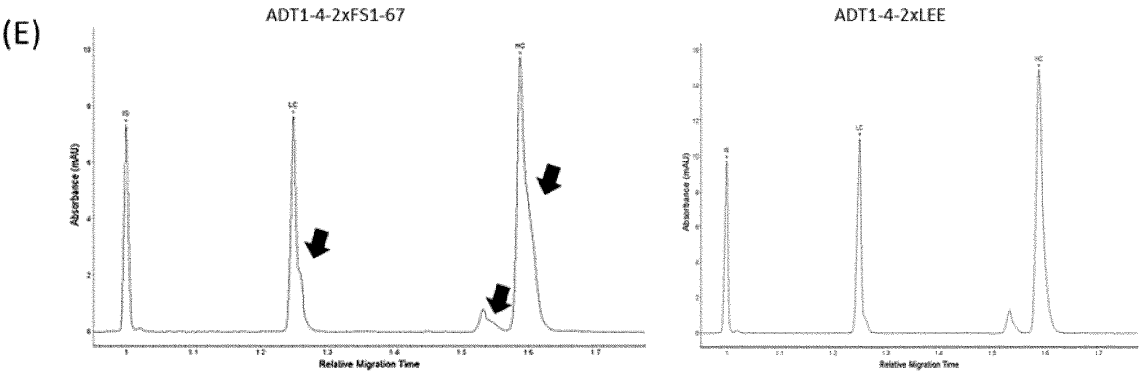


FIGURE 34 cont.
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(F)

Antibody	Yield	Stable Charge at 37C	Favorable Tm/Tagg delta	%Monomer 5mg/ml, 18d @ 37C (non-reduced)	Typical HC + LC profile at 5mg/ml 18 d @ 37C (reduced)	Total Score	AB loop modifications	BC loop modifications	EF loop modifications	No. of changes (and % identity) relative P343 to G446 (EU numbering)
ADT1-4-2xLEE	++	+++	+++	+	++	11	T359E.K360E.N361G.Q362P	N384T.G385Y.Q386G	D413S.K414Y.S415W.Q418Y.Q419K	12 (88%)
ADT1-4-2xLEE2	++	+++	++	++	++	11	T359E.K360E.N361G.Q362P	No changes from wild-type	D413S.K414Y.S415W.Q418Y.Q419K	9 (91%)
ADT1-4-2xLEE3	++	+++	++	++	++	11	T359E.K360E.N361G.Q362P	N384T.G385Y.Q386G	D413S.K414Y.S415W	10 (90%)
ADT1-4-2xFS1-67	+	+	++	+++	-	7	L358T.T359D.K360D.N361G.Q362P	N384T.G385Y.Q386G	D413S.K414Y.S415W.Q418Y.Q419K	13 (88%)
ADT1-4-2xFS1-65	++	+++	-	++	++	9	T359D.K360D.N361G.Q362P	N384T.G385Y.Q386G	D413S.K414Y.S415W.Q418Y.Q419K	13 (88%)

FIGURE 34 cont.

Antibody	EC50 (pM)	EC95 (pM)	MFI (at saturation)
EGFR control	N/A	N/A	~ 0.4950
ADT1-4-2xADT3-2	275.9	2698	101.1
ADT1-4-6xADT3-2	279.2	2766	87.56
ADT1-4-138xADT3-2	208.8	2254	46.31

c)

Antibody	Affinity to Vδ1 (nM)
ADT1-4-2/ADT3-2	0.24
ADT1-4-6/ADT3-2	1.26
ADT1-4-138/ADT3-2	18.3

Note: EGFR affinity similar for all
Approx. 1 nM

A)

B)

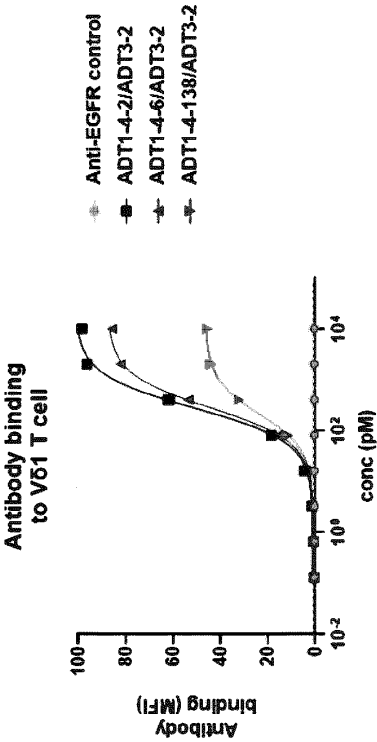
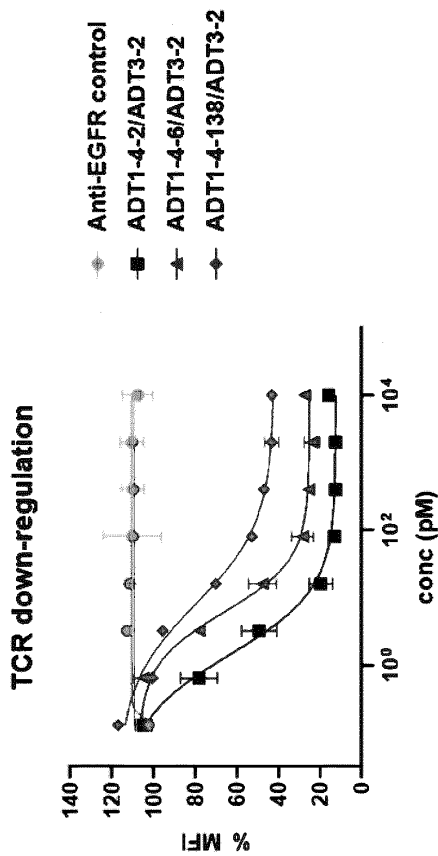


FIGURE 35

E)

Antibody	EC50 (pM)	EC95 (pM)	% change (at saturation)
EGFR control	N/A	N/A	-
ADT1-4-2xADT3-2	1.422	37.85	101.9
ADT1-4-6xADT3-2	6.056	83.63	81.94
ADT1-4-138xADT3-2	7.981	495.6	75.34

D)



G)

Antibody	% inc CD107a-pos (at saturation)
EGFR control	-
ADT1-4-2xADT3-2	34.86
ADT1-4-6xADT3-2	28.09
ADT1-4-138xADT3-2	12.04

F)

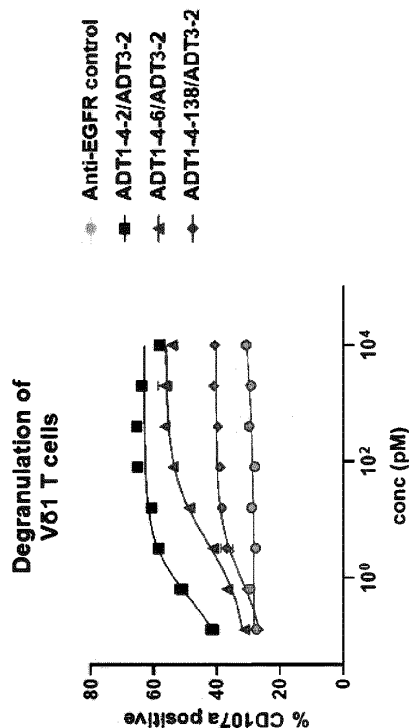


FIGURE 35 cont.

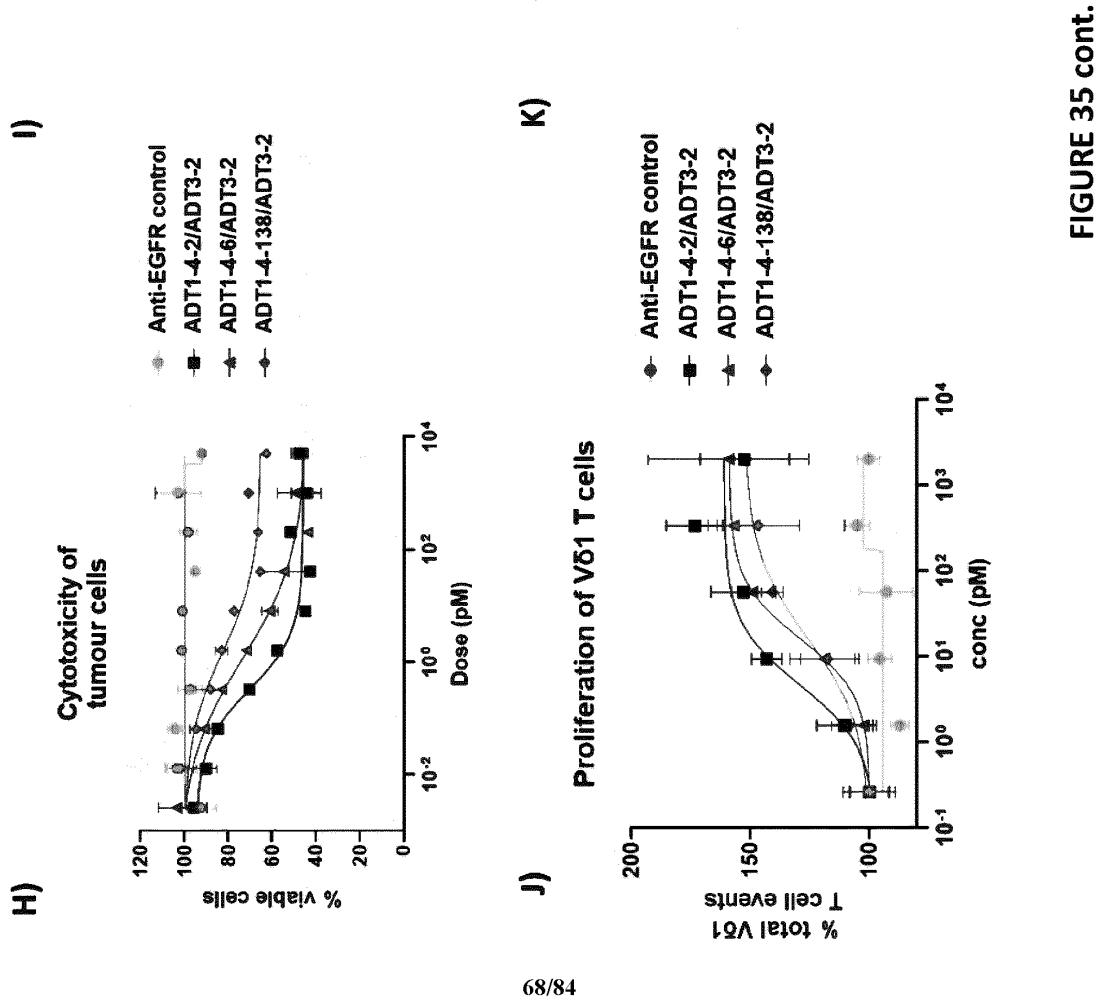
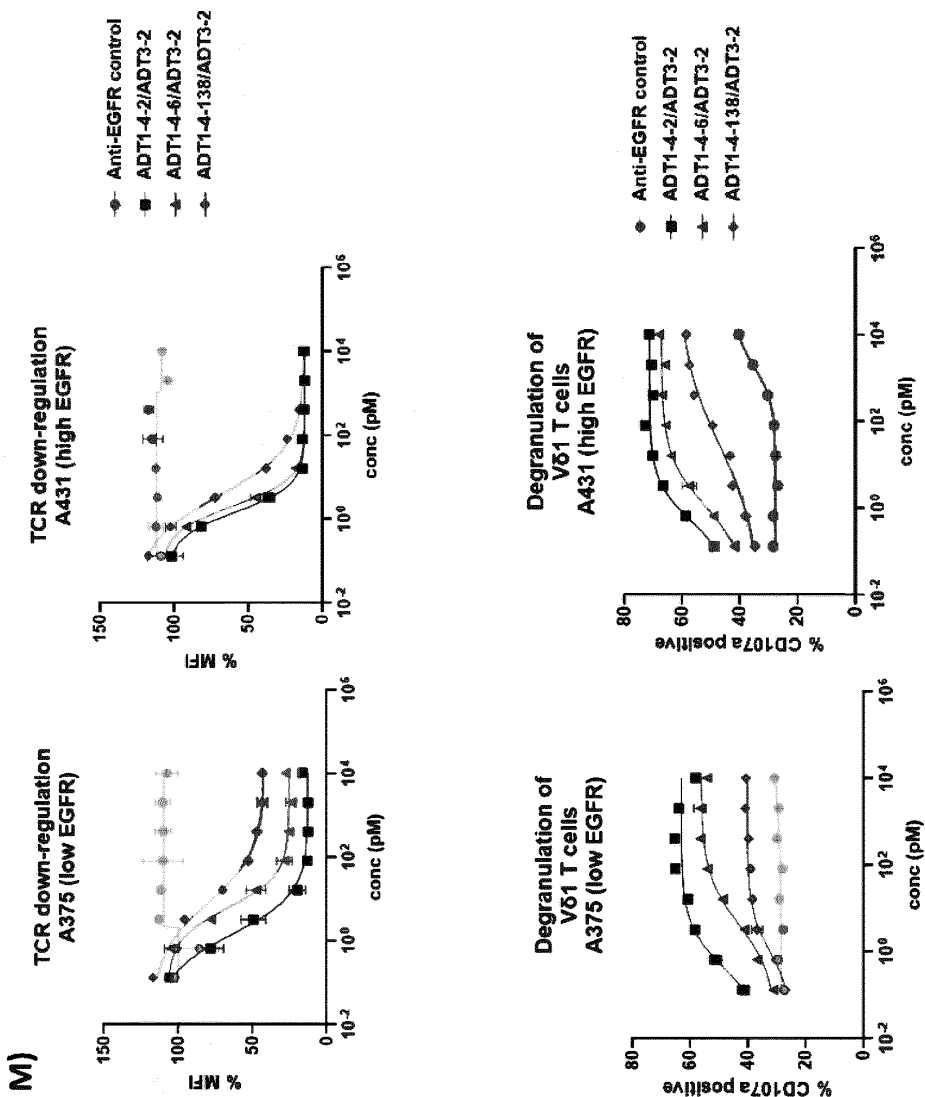


FIGURE 35 cont.

L)

Technical effect conferred on primary tissue-derived V61+ by anti-V61 TCR antibodies of this invention	Is this effect further enhanced by increasing the affinity of the antibody to less than 10nM ?	Can the diminished effect conferred by lower affinity molecules be compensated for by increasing conc. 100-fold or more ?
Binding (MFI)	YES	NO
V61 TCR downregulation	YES	NO
CD107A upregulation	YES	NO
Cytotoxicity	YES	NO
Proliferation	YES	YES

FIGURE 35 cont.



Antibody	TCR Downregulation % change (at saturation)	
	A375 (low EGFR)	A431 (high EGFR)
EGFR control	-	-
ADT1-4-2xADT3-2	101.9	99
ADT1-4-6xADT3-2	81.94	99.15
ADT1-4-138xADT3-2	75.34	98.73

Antibody	Degranulation % change (at saturation)	
	A375 (low EGFR)	A431 (high EGFR)
EGFR control	-	-
ADT1-4-2xADT3-2	34.86	42.92
ADT1-4-6xADT3-2	28.09	38.77
ADT1-4-138xADT3-2	12.04	33.13

FIGURE 35 cont.

(A)

Antibody	Alias (if any)	Affinity to EGFR (nM)	No of changes vs wild-type immunoglobulin sequence		
			AB loop	CD loop	EF loop
ADT1-4-2	-	-	0	0	0
ADT1-4-2xADT3-1	ADT1-4-2xFS1-67	1.37	5	3	5
ADT1-4-2xADT3-2	ADT1-4-2xLEE	1.49	4	3	5
ADT1-4-2xADT3-3	ADT1-4-2xFS1-65	1.35	6	3	5
ADT1-4-2xADT3-4	ADT1-4-2x747	2.35	5(+1)	3	6
ADT1-4-2xADT3-5	ADT1-4-2xLEE1	142	0	3	5
ADT1-4-2xADT3-6	ADT1-4-2xLEE2	19.2	4	0	5
ADT1-4-2xADT3-7	ADT1-4-2xLEE3	8.63	4	3	3

(B)

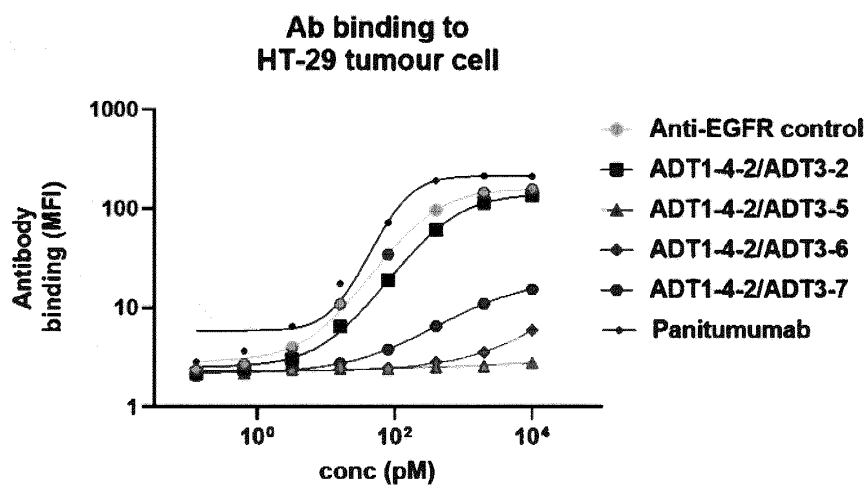
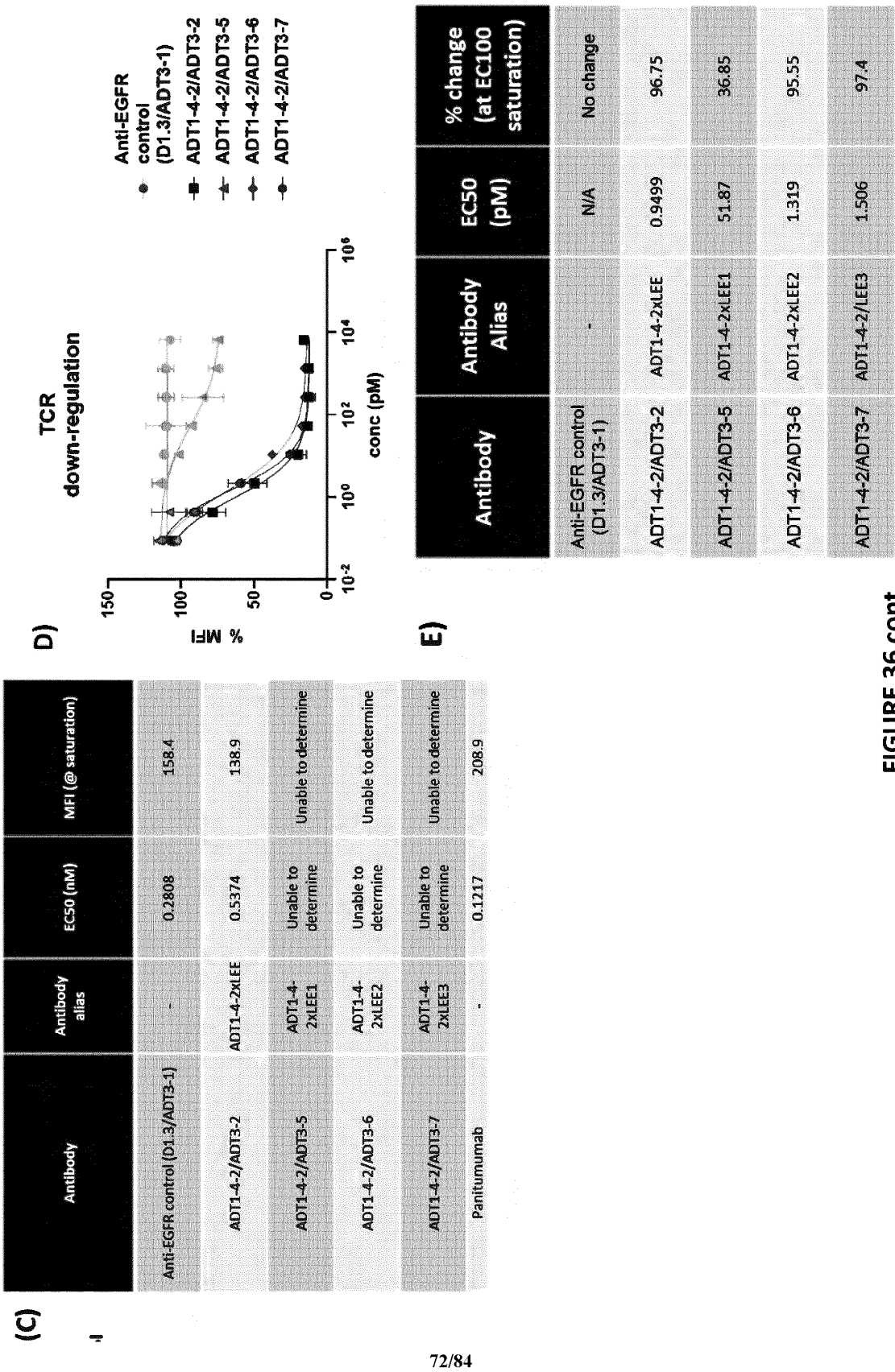
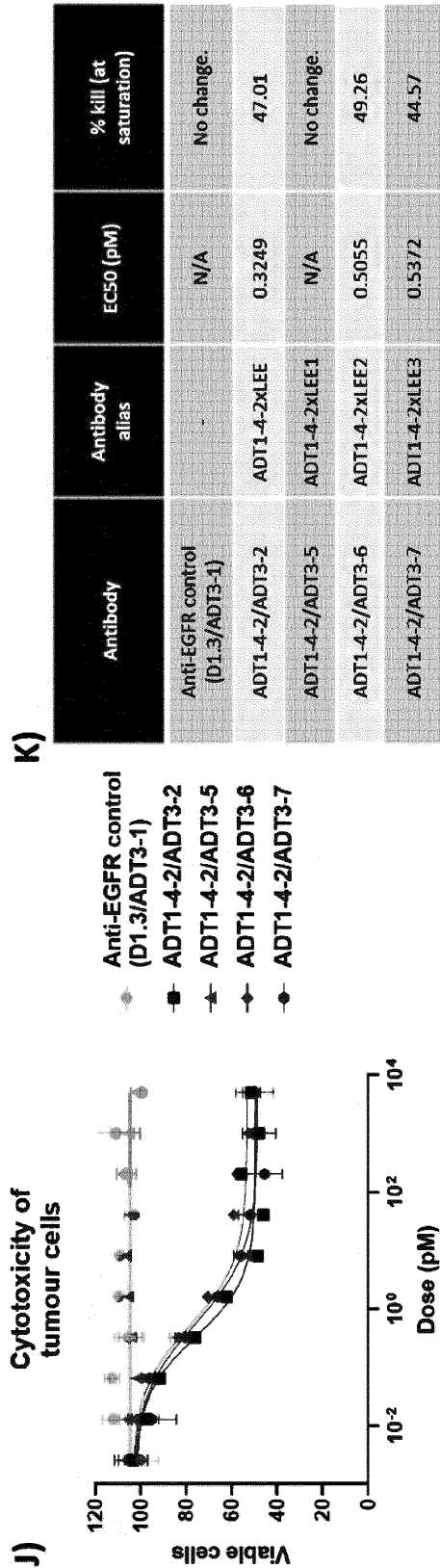


FIGURE 36





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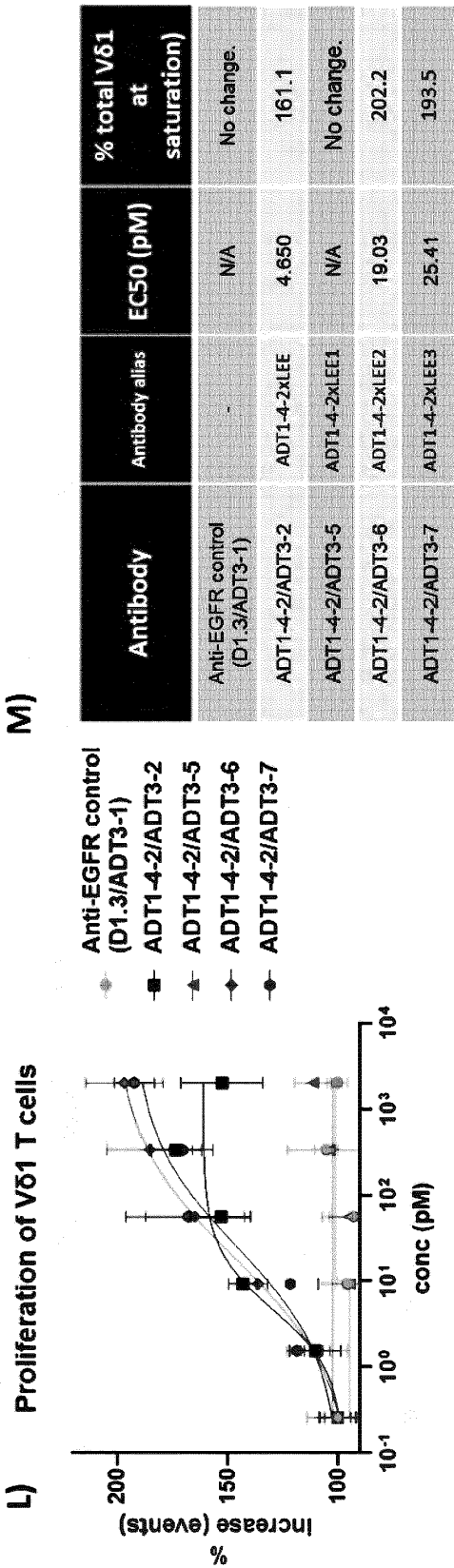


FIGURE 36 cont.

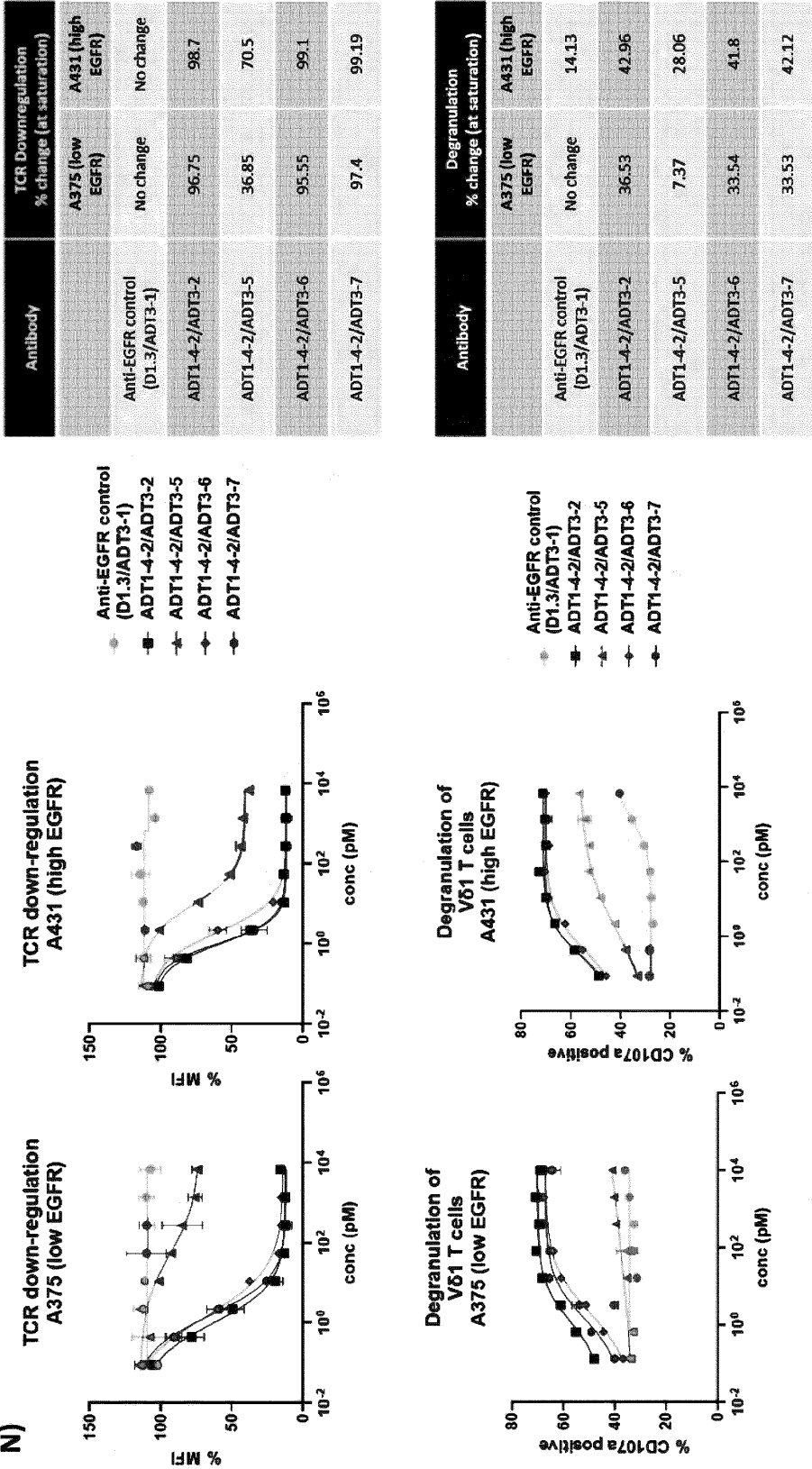


FIGURE 36 cont.

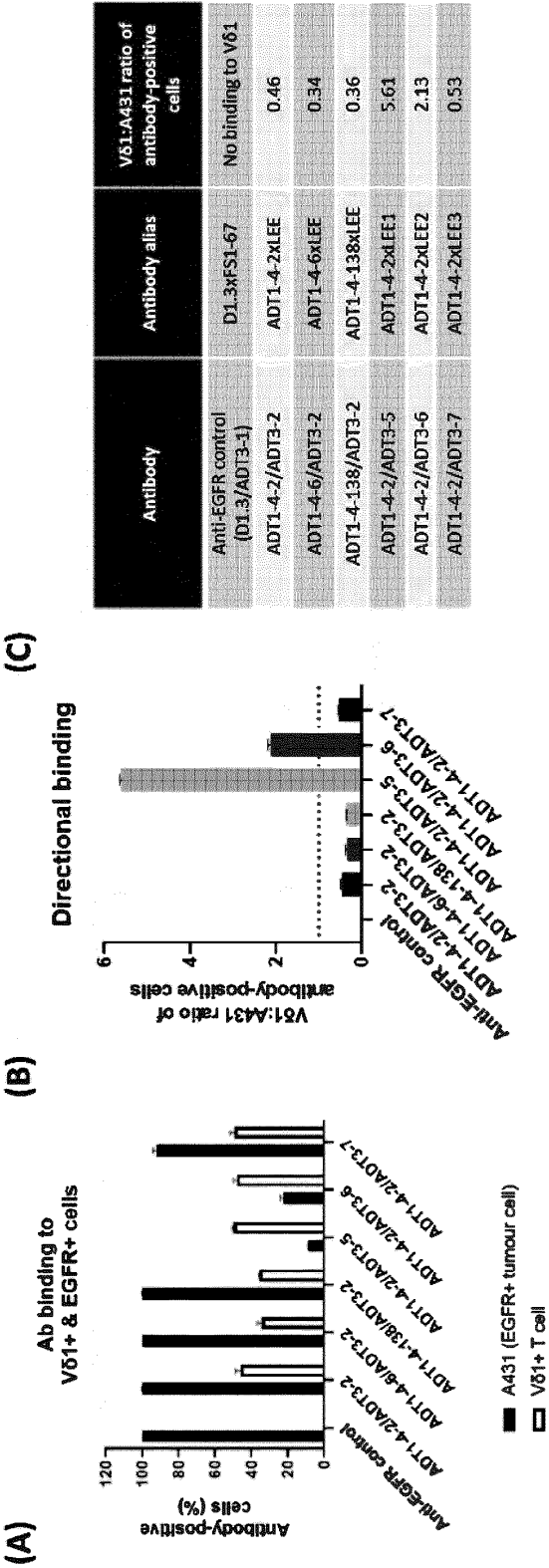
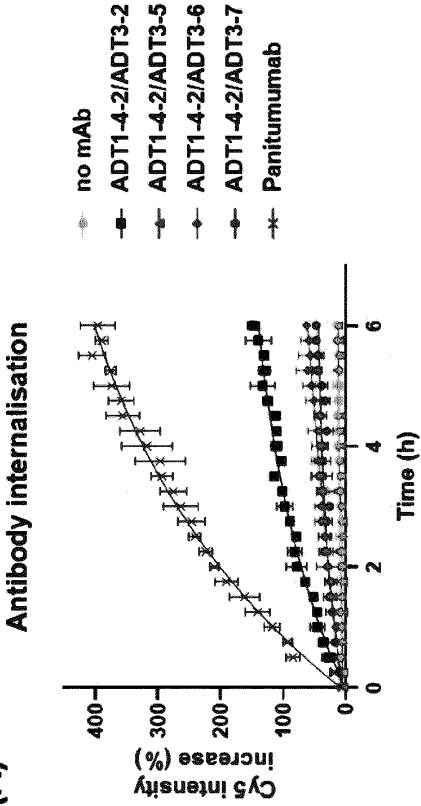


FIGURE 37

(B)

Antibody	Antibody alias	% intracellular increase Cys5 signal at 8.5 h
No mAb	N/A	13.1
ADT1-4-2/ADT3-2	ADT1-4-2xLEE	147.8
ADT1-4-2/ADT3-5	ADT1-4-2xLEE1	11.6
ADT1-4-2/ADT3-6	ADT1-4-2xLEE2	63.7
ADT1-4-2/ADT3-7	ADT1-4-2xLEE3	50.8
Panitumumab	N/A	396.2

(A)



(D)

Antibody	Antibody alias	Fold-change reduction in antibody concentration
IgG control	N/A	0.86
ADT1-4-2/ADT3-2	ADT1-4-2xLEE	18.07
ADT1-4-2/ADT3-5	ADT1-4-2xLEE1	1.08
ADT1-4-2/ADT3-6	ADT1-4-2xLEE2	1.56
ADT1-4-2/ADT3-7	ADT1-4-2xLEE3	3.02

(C)

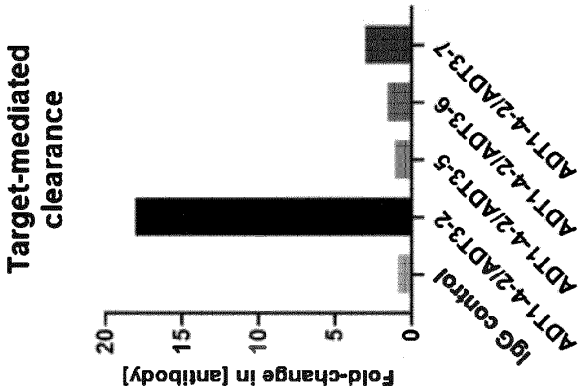


FIGURE 38

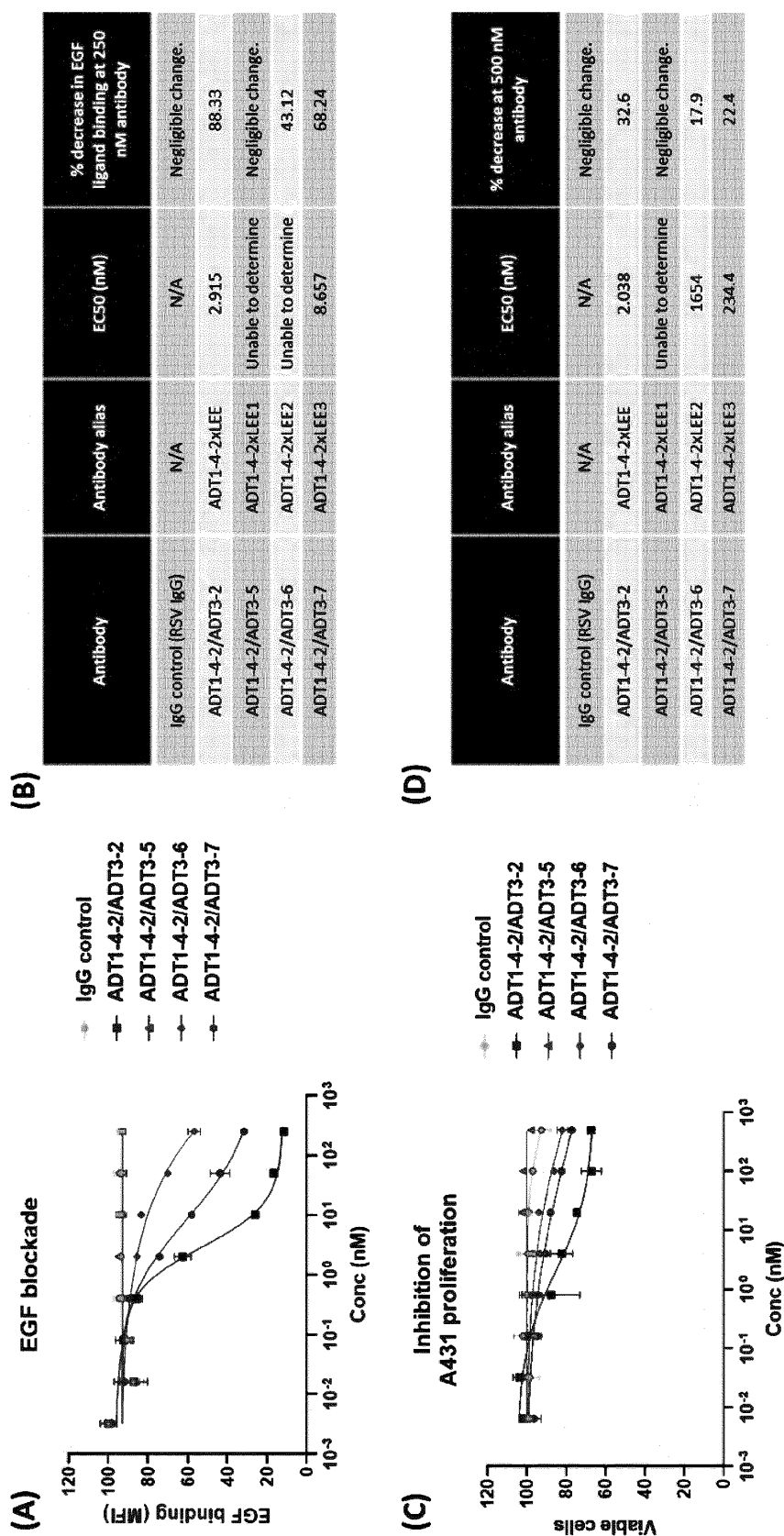
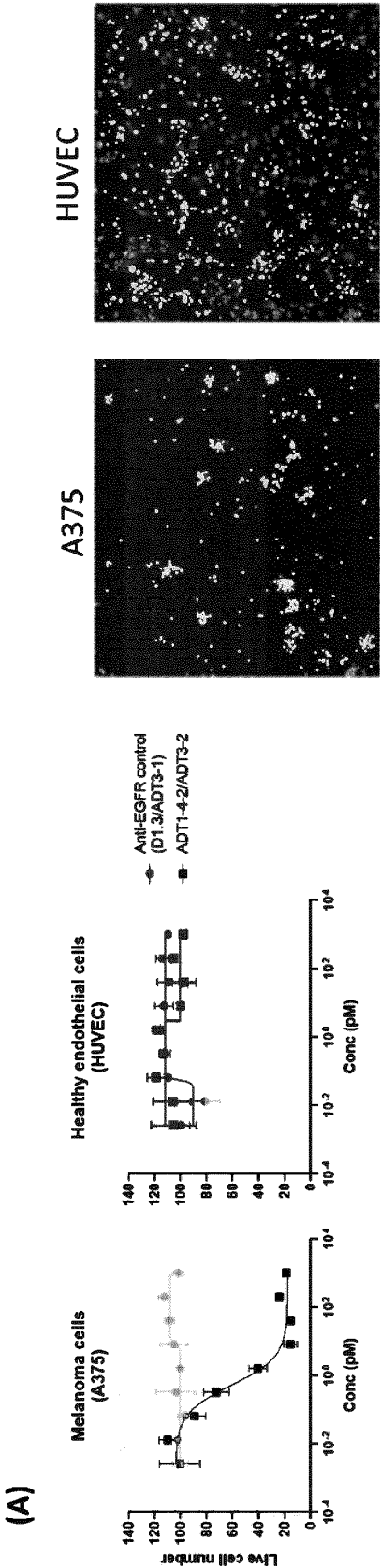
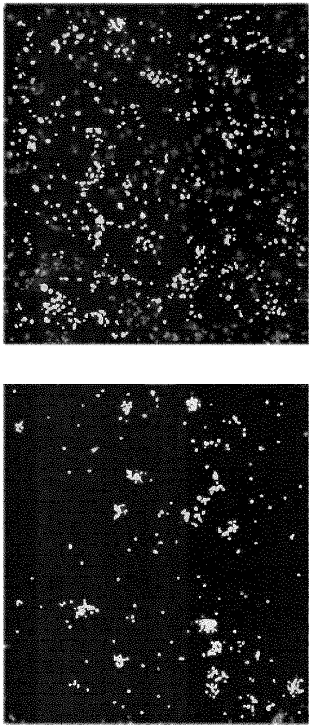


FIGURE 39



HUVEC

A375



(C)

Antibody	EC50 (pM)	% kill (at saturation)
A375	0.5091	86.2
HUVEC	N/A	No change.

FIGURE 40

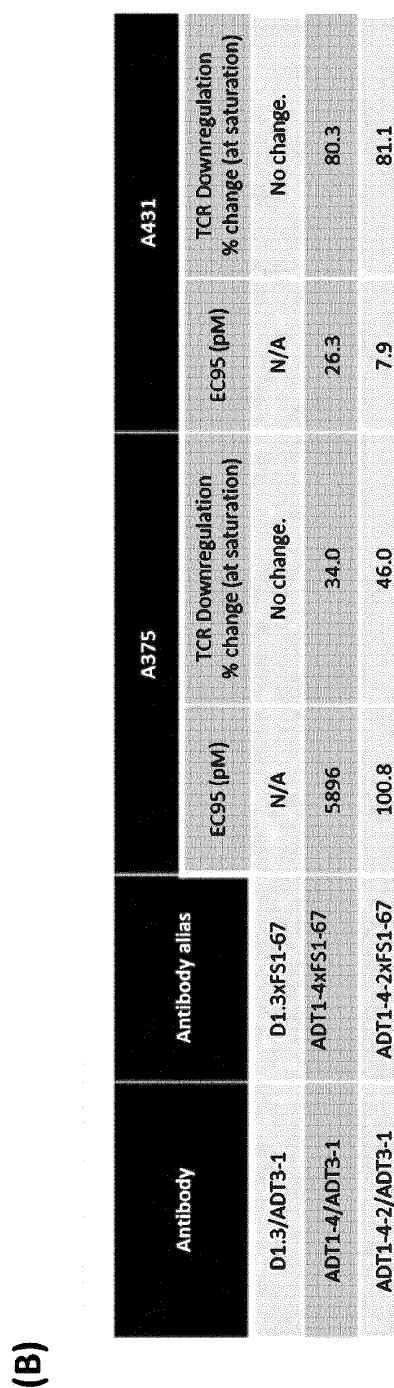
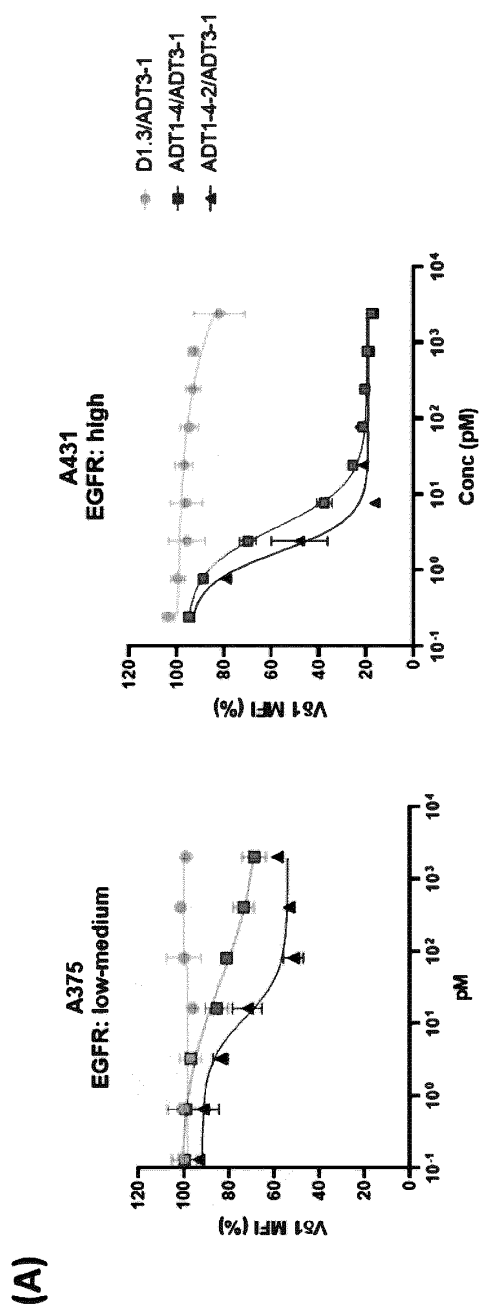


FIGURE 41

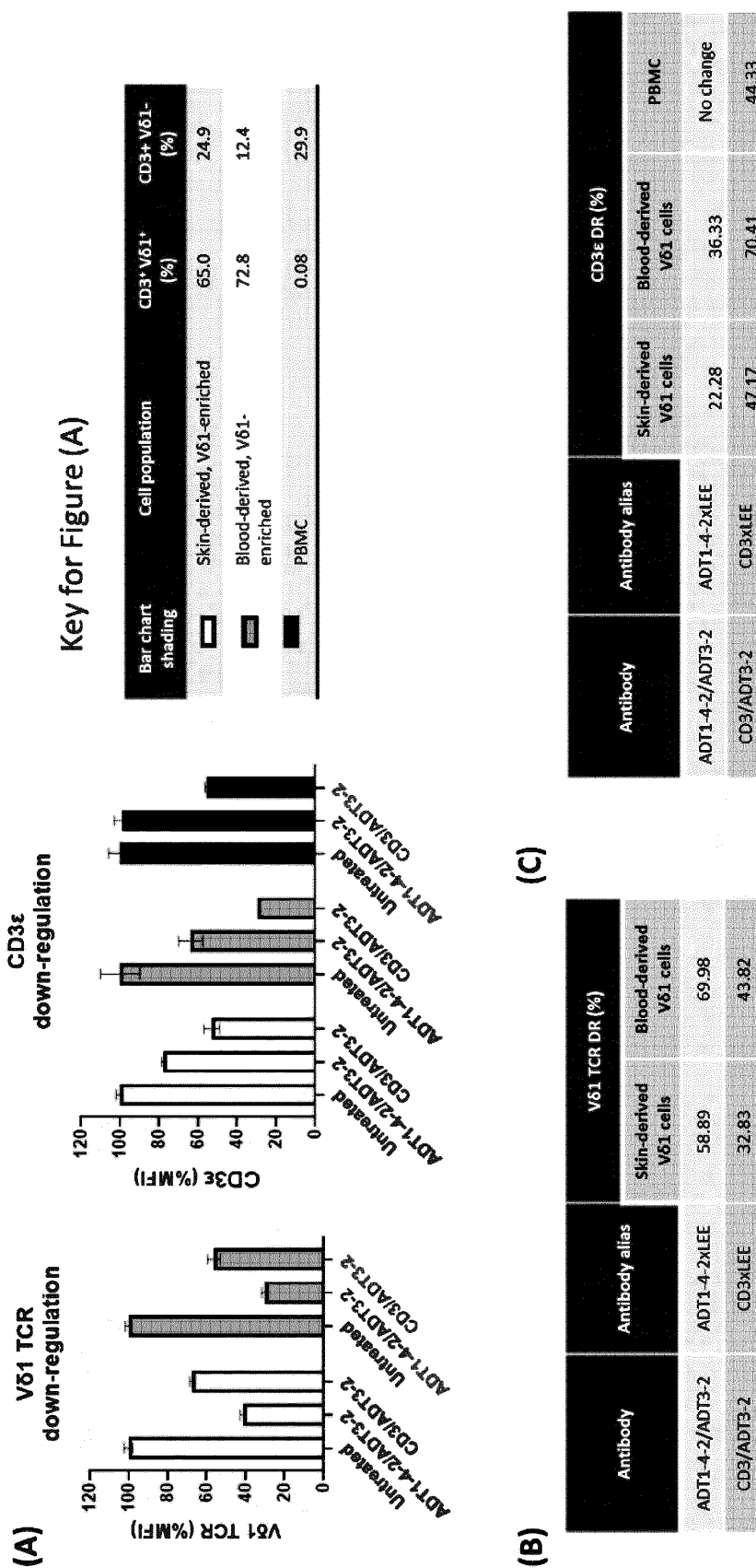
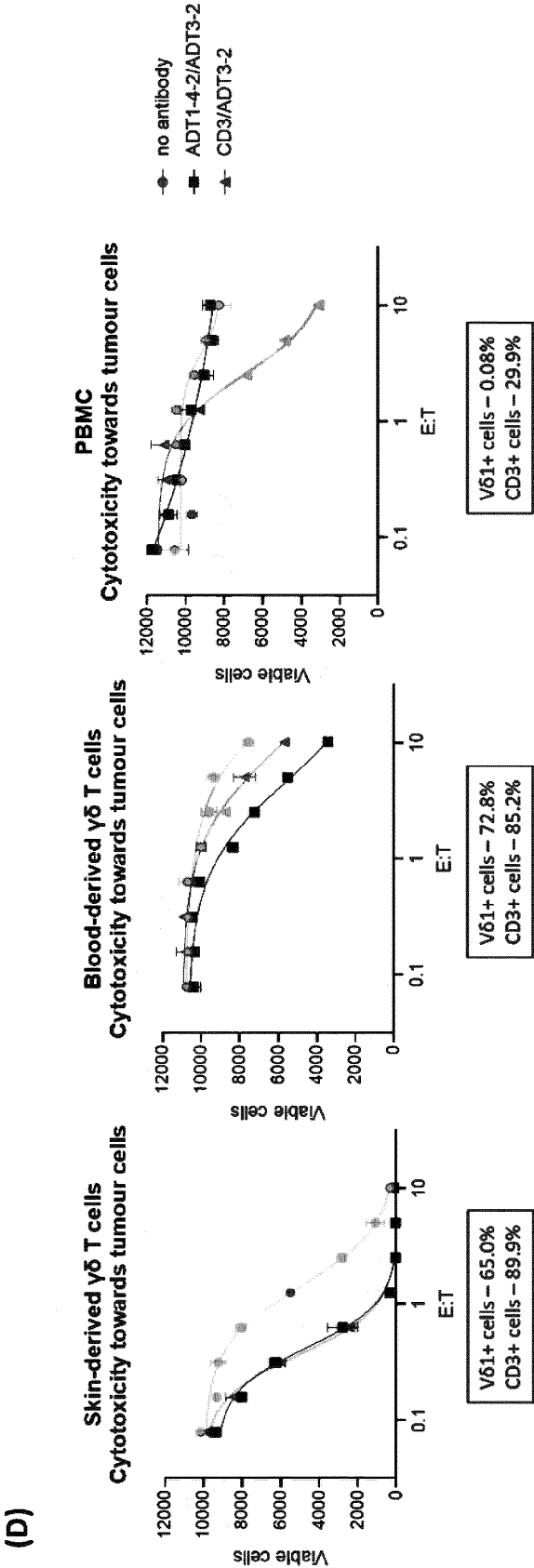


FIGURE 42



(E)

Antibody	Antibody alias	Targeted subset	Tumour cytotoxicity score		
			Skin-derived $\gamma\delta$ T cells	Blood-derived $\gamma\delta$ T cells	PBMC
ADT1-4-2/ADT3-2	ADT1-4-2xLEE	V61+	++	++	-
CD3/ADT3-2	CD3xLEE	CD3+	++	+	++

FIGURE 42 cont.

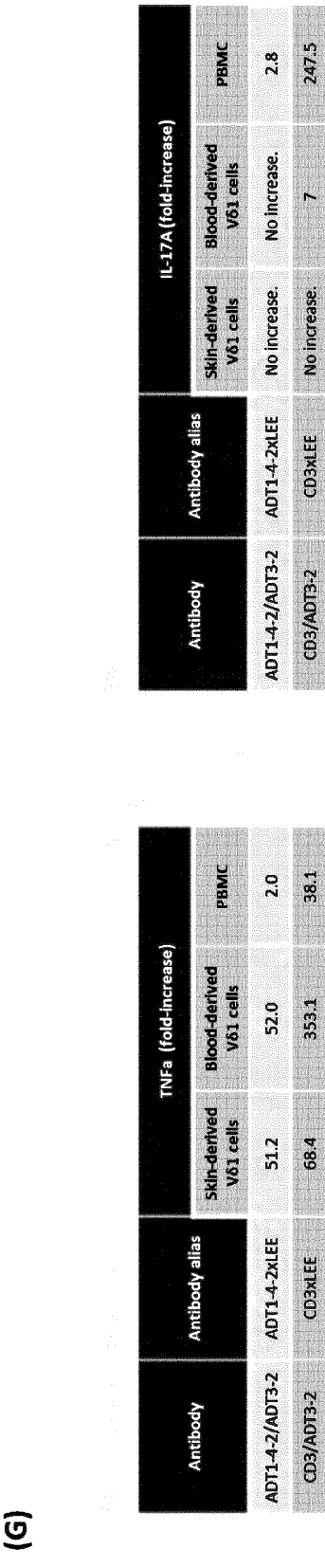
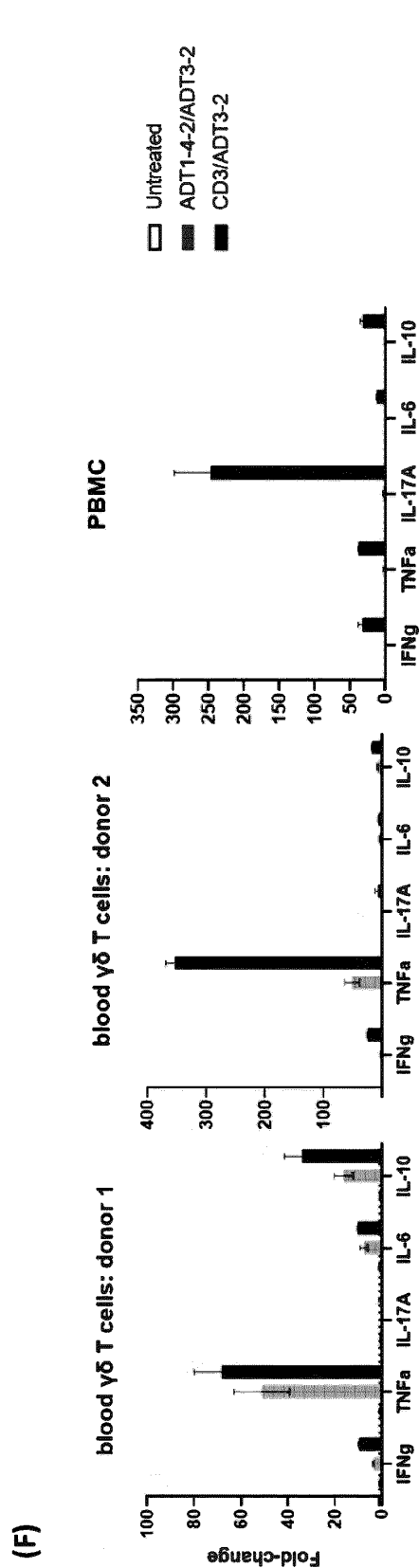


FIGURE 42 cont.

(I)

Antibody	Antibody alias	EC50 (pM)	% total Vδ1 at saturation
Anti-EGFR control (D1.3/ADT3-1)	-	N/A	No change.
ADT1-4-2/ADT3-2	ADT1-4-2xLEE	4.65	161.1
CD3/ADT3-2	CD3xLEE	38.98	143.7

(H)

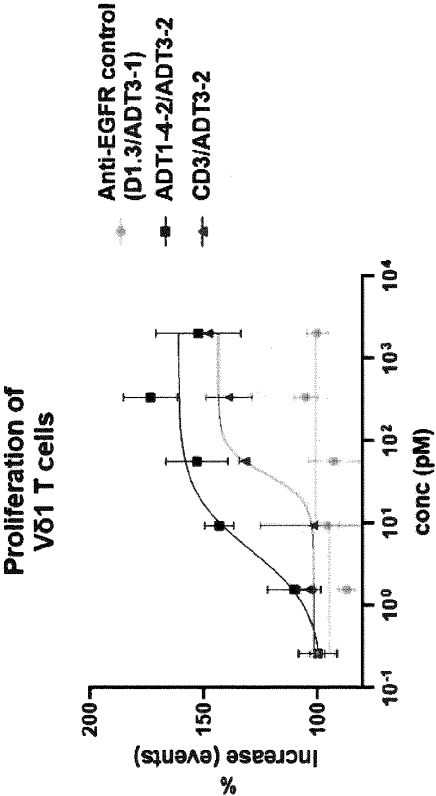


FIGURE 42 cont.