

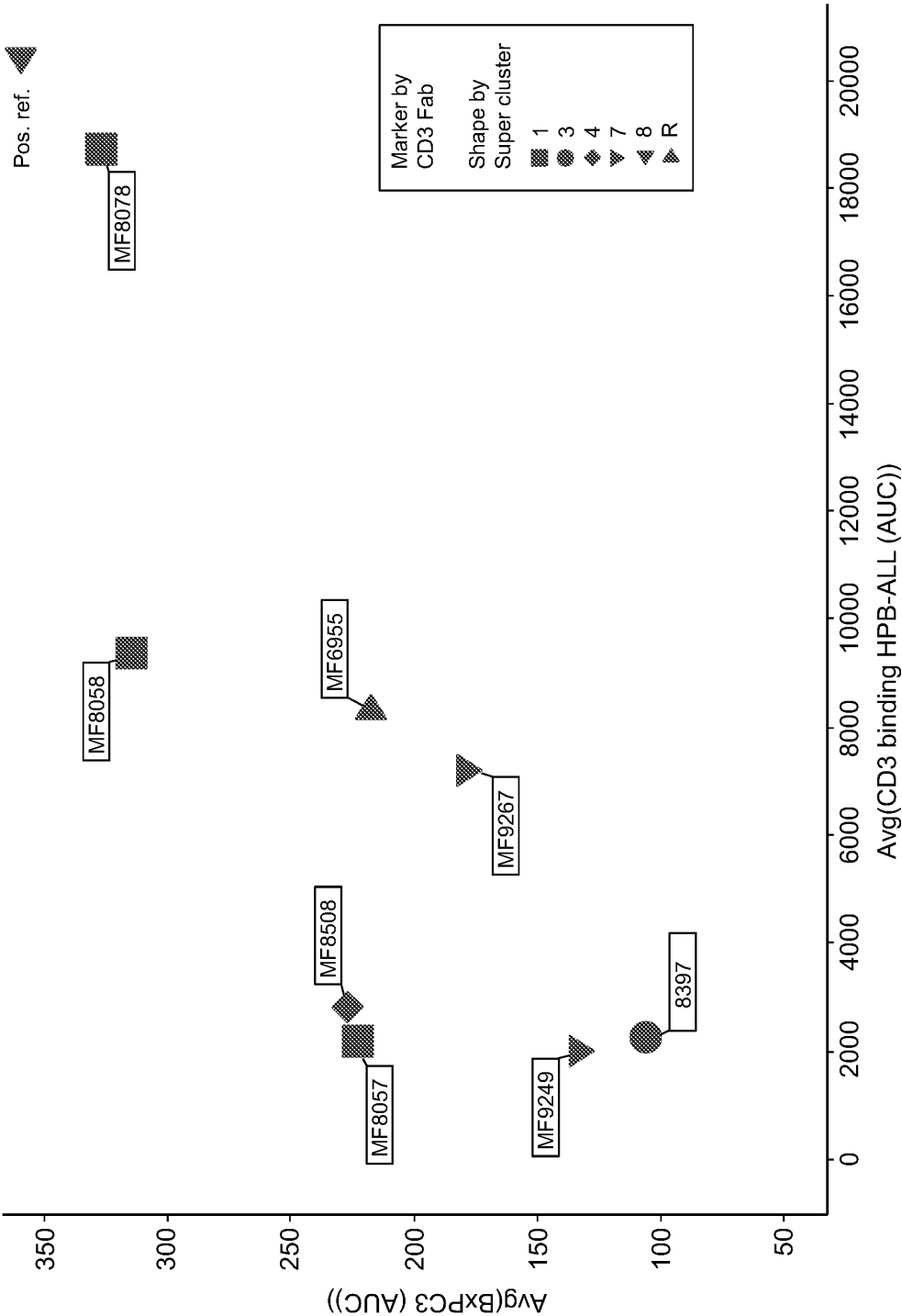


Fig. 1

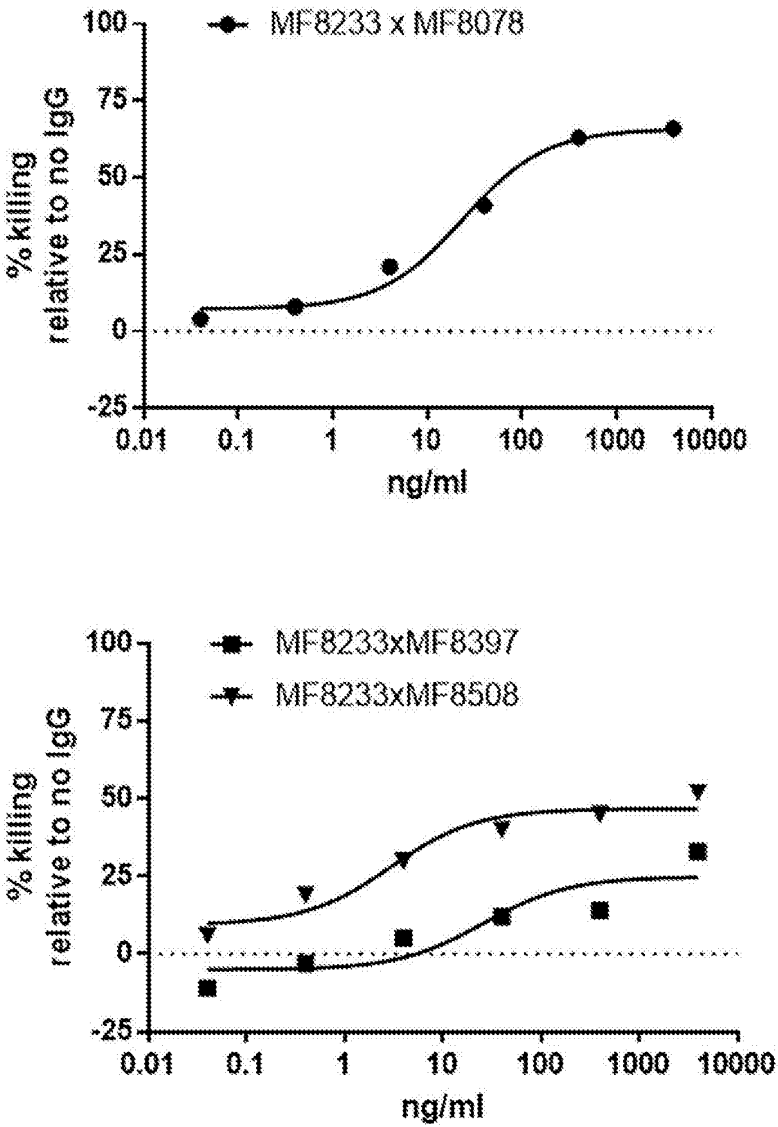


Fig. 2

CD3 Fab	super cluster	CD3 binding (AUC)	lysis % max. (n=1)	BxPC3 lysis (AUC) n=1	lysis EC50 (n=1)	lysis % max. (n=2)	BxPC3 lysis (AUC) n=2	lysis EC50 (n=2)
MF8057	1	2171	64.7	209.3	26.81	58.6	236.0	23.9
MF8058	1	9362	68.3	315.5	4.204	72.3	314.0	2.5
MF8078	1	18723	nd	nd	nd	69.0	327.0	1.9
MF8397	3	2264	22.6	97.5	48.0	33.0	114.0	25.9
MF8508	4	2818	47.1	216.5	2.2	52.5	238.0	3.0
MF9249	7	1994	26.0	115.5	nd	28.8	148.0	1.9
MF9267	7	7220	26.8	162.5	0.3	39.7	192.5	1.5
Pos. ref.	8	20368	72.5	350.5	2.6	79.8	369.0	1.2
MF6955	R	8383	40.7	211.0	1.1	61.9	224.5	7.6

Fig. 3

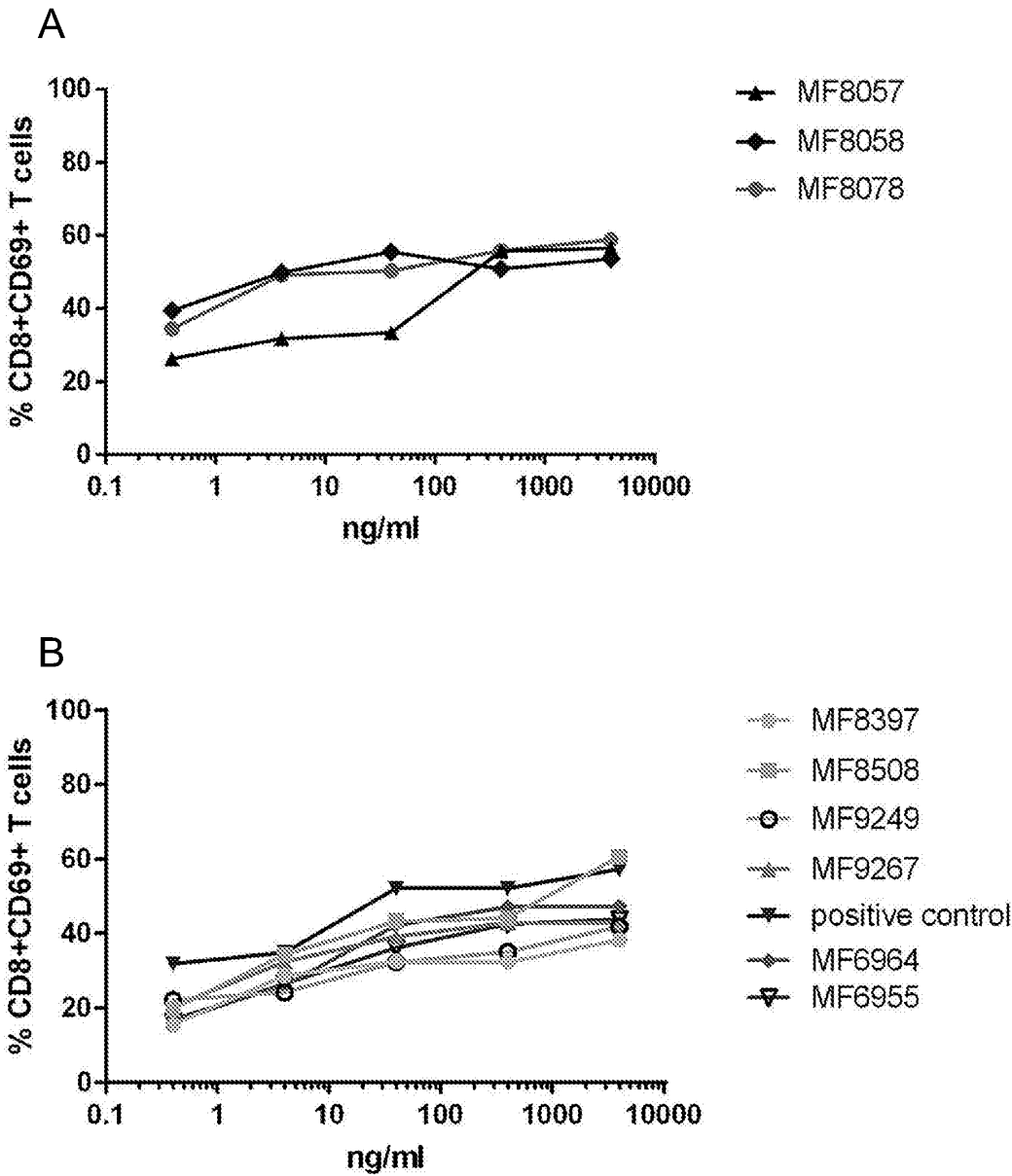


Fig. 4

MF nr.	super cluster	CD3 affinity (AUC HPB-ALL)	CD4+CD69+ (AUC)	CD4+CD25+ (AUC)	CD8+CD69+ (AUC)	CD8+CD25+ (AUC)
MF8057	1	2171	131	66.9	162.4	98.74
MF8058	1	9362	197.8	108.7	202.8	189
MF8078	1	18723	211.5	138.4	202.2	189
MF8397	3	2264	48.75	17.26	120.5	21.4
MF8508	4	2818	171.2	70.39	162.3	91.85
MF9249	7	1994	80.28	29.19	123.6	33.44
MF9267	7	7220	125.5	42.36	146.5	42.1
Pos. ref.	8	20368	225.7	148.6	183.8	186
MF6955	R	8383	186.3	98.82	174.5	114.6

Fig. 5

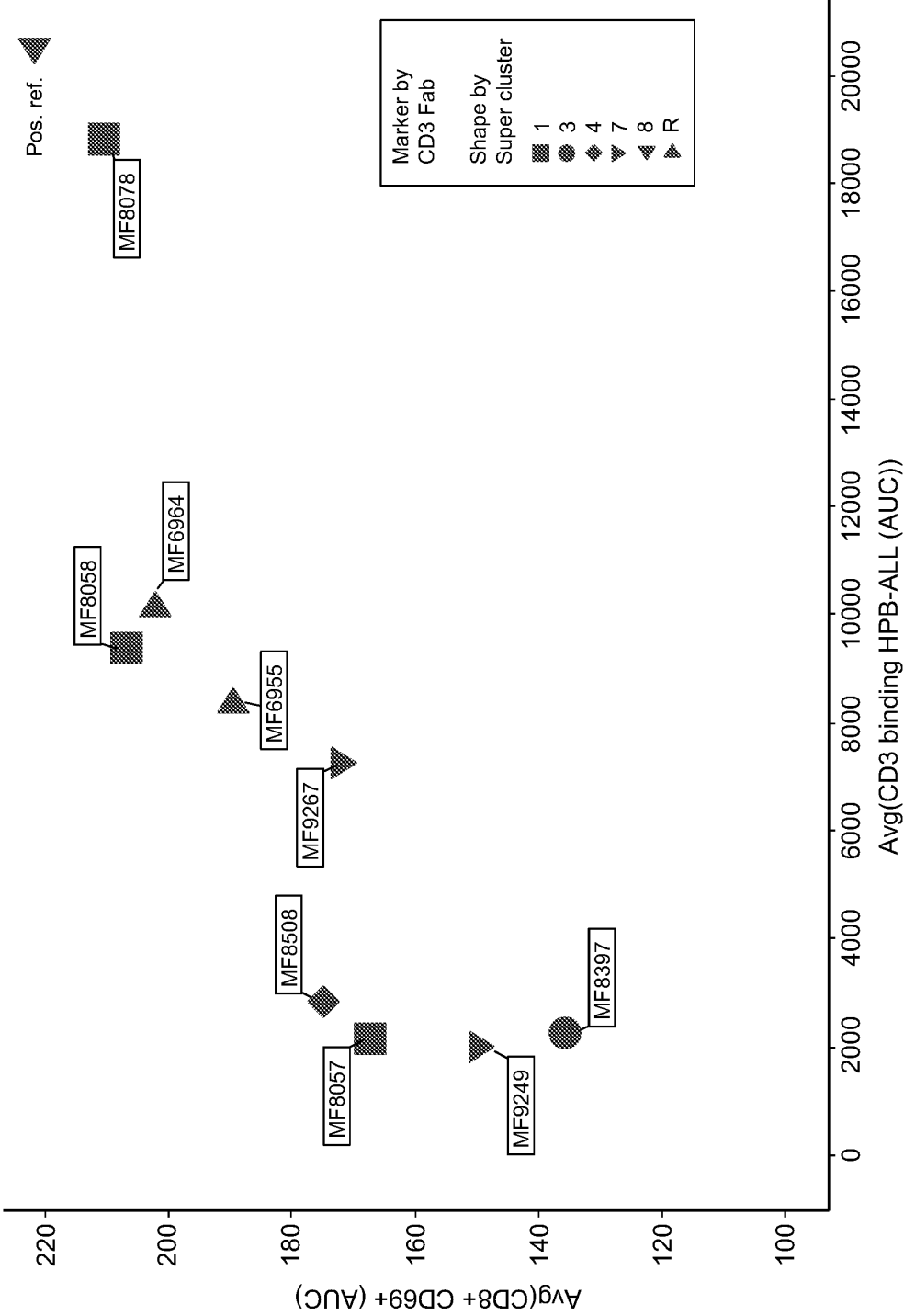


Fig. 6

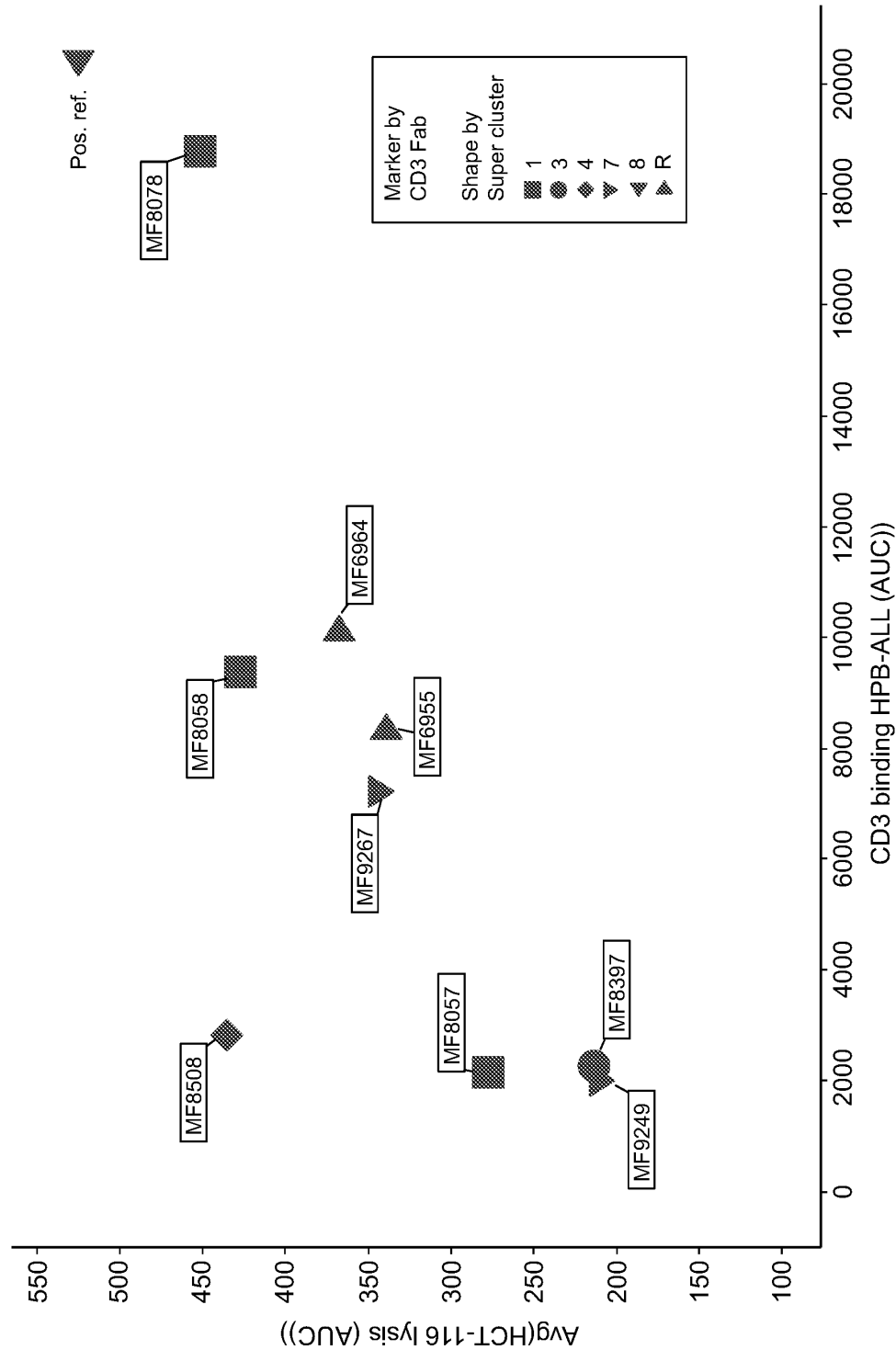
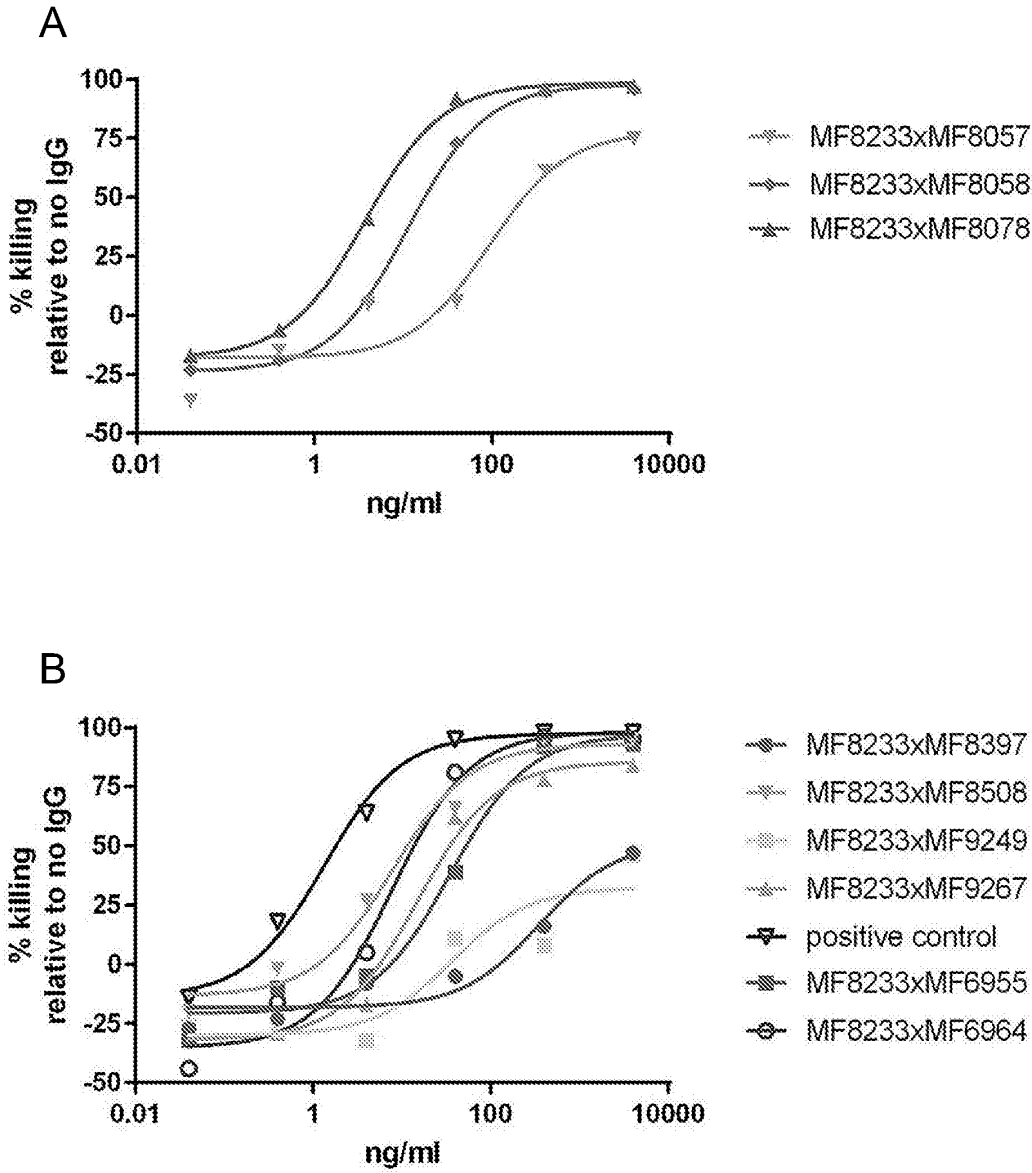


Fig. 7



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Super cluster	CD3 Fab	CD3 binding HPB-ALL (AUC)	HCT-116 lysis (AUC)	lysis EC50
1	MF8057	2171	306.5	93.94
1	MF8058	9362	421.5	11.34
1	MF8078	18723	493	3.729
3	MF8397	2264	220	354.1
4	MF8508	2818	453.5	7.845
7	MF9249	1994	199	36.34
7	MF9267	7220	353	15.09
8	Pos. ref.	20368	547	1.34
R	MF6955	8383	376.5	35.23
R	MF6964	10151	421.5	7.761
ref	MF5196	1578	158	1223

Fig. 9

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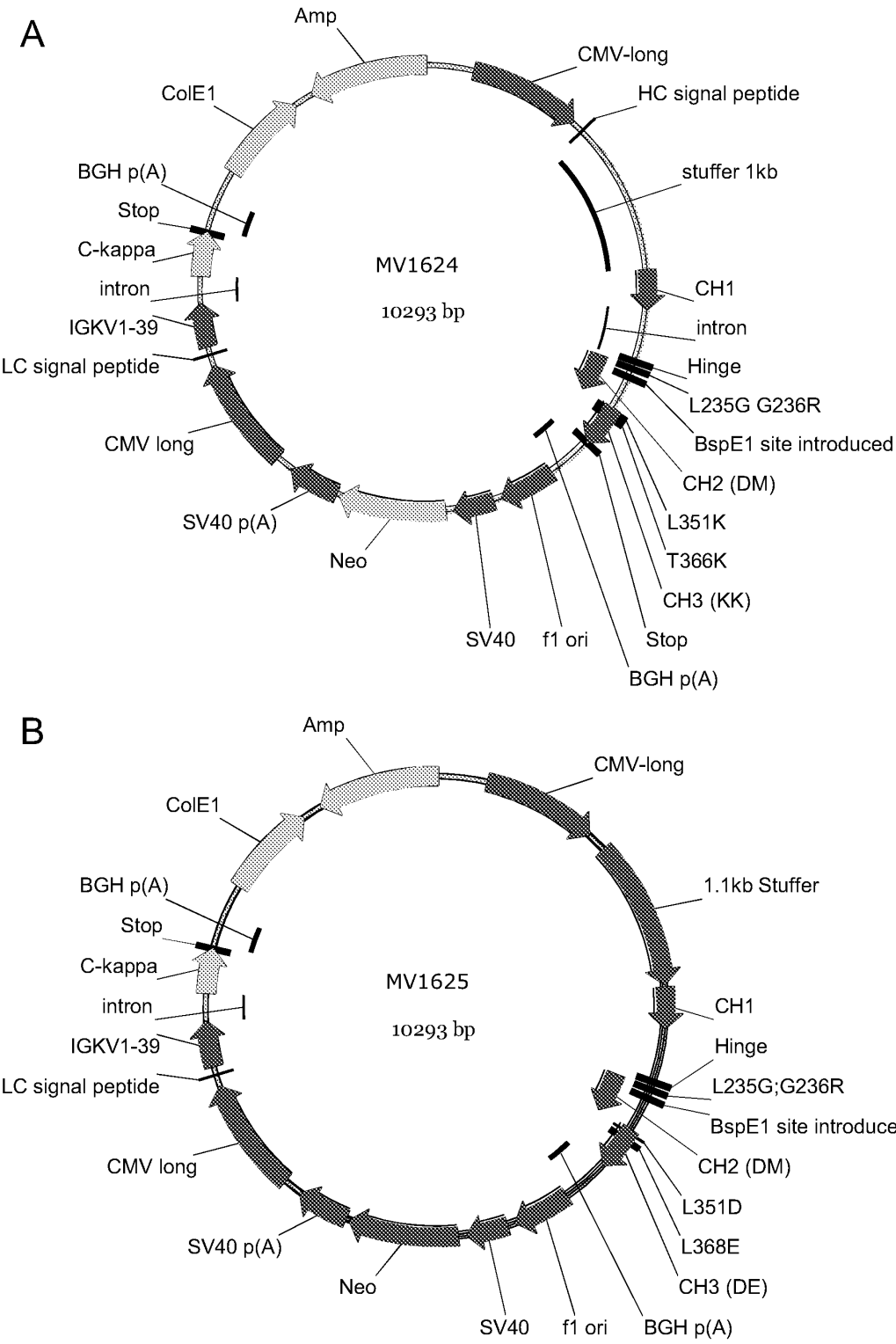


Fig. 10

Figure 11

Figure 11A:

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQQSYSTPPTFGQGTKVEIK
RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTLTLSKA
DYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 11B:

gacatccagatgacccagtcctccatcctccctgtctgcatctgtaggagacagagtcacc
D I Q M T Q S P S S L S A S V G D R V T
atcacttgccgggcaagtcagagcattagcagctacttaaattggtatcagcagaaacca
I T C R A S Q S I S S Y L N W Y Q Q K P
gggaaagccctaaagtcctgatctatgctgcatccagtttgcaaagtgggtcccatca
G K A P K L L I Y A A S S L Q S G V P S
aggttcagtggcagtggtatctgggacagatttcactctcaccatcagcagtcgtcaacct
R F S G S G S G T D F T L T I S S L Q P
gaagatgttgcaacttactactgtcaacagagttacagtacccctccaacgttcggccaa
E D F A T Y Y C Q Q S Y S T P P T F G Q
gggaccaaggtggagatcaaa
G T K V E I K

Figure 11C:

cgaactgtggctgcaccatctgtcttcacatcttcccggccatctgatgagcagttgaaatct
R T V A A P S V F I F P P S D E Q L K S
ggaactgcctctgttggtgctgctgaataacttctatcccagagaggccaaagtacag
G T A S V V C L L N N F Y P R E A K V Q
tggaaggtggataacgccctccaatcgggtaactcccaggagagtggtcacagagcaggac
W K V D N A L Q S G N S Q E S V T E Q D
agcaaggacagcacctacagcctcagcagcaccctgacgctgagcaaagcagactacgag
S K D S T Y S L S S T L T L S K A D Y E
aaacacaaaagtcctacgcctgcgaagtcacccatcagggcctgagctcgcccgtcacaaag
K H K V Y A C E V T H Q G L S S P V T K
agcttcaacaggggagagtgtag
S F N R G E C -

Figure 11D

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQQSYSTPPTFGQTRLEIK

Figure 11E

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQQSYSTP

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Figure 11F

CDR1 : QSISSY,
CDR2 : AAS,
CDR3 : QQSYSTP.

Figure 12

Figure 12A

CH1:

gctagcaccaaggggcccatcggtcttccccctggcacccctcctccaagagcacctctggg
A S T K G P S V F P L A P S S K S T S G
ggcacagcgccctgggctgcttggtcaaggactacttccccgaaccggtgacggtgtcg
G T A A L G C L V K D Y F P E P V T V S
tggaactcaggcgccctgaccagcggtgcacaccttcccggtgtcctacagtctctca
W N S G A L T S G V H T F P A V L Q S S
ggactctactccctcagcagcgctgacggtgccctccagcagcttgggcacccagacc
G L Y S L S S V V T V P S S S L G T Q T
tacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagtt
Y I C N V N H K P S N T K V D K R V

Figure 12B

Hinge:

gagcccaaatcttgtgacaaaactcacacatgccaccggtgccca
E P K S C D K T H T C P P C P

Figure 12C

CH2:

gcacctgaactcctggggggacggtcagttcttcttccccccaaaaccaaggacacc
A P E L L G G P S V F L F P P K P K D T
ctcatgatctcccgacccctgaggtcacatgcgtgggtgggacgtgagccacgaagac
L M I S R T P E V T C V V V D V S H E D
cctgaggtcaagttcaactggtacgtggacggcggtggaggtgcataatgccaagacaaag
P E V K F N W Y V D G V E V H N A K T K
ccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcac
P R E E Q Y N S T Y R V V S V L T V L H
caggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcc
Q D W L N G K E Y K C K V S N K A L P A
cccatcgagaaaaccatctccaaagccaaa
P I E K T I S K A K

Figure 12D

CH2 containing L235G and G236R silencing substitutions:

gcacctgaactcggcaggggaccgtcagttcttcttccccccaaaacccaaggacacc
 A P E L G R G P S V F L F P P K P K D T
 ctcatgatctcccgaccctgaggtcacatgcgtggtggtggacgtgagccacgaagac
 L M I S R T P E V T C V V V D V S H E D
 cctgaggtcaagttcaactgggtacgtggacggcgtggaggtgcataatgccaagacaaaag
 P E V K F N W Y V D G V E V H N A K T K
 ccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcac
 P R E E Q Y N S T Y R V V S V L T V L H
 caggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcc
 Q D W L N G K E Y K C K V S N K A L P A
 cccatcgagaaaaccatctccaaagccaaa
 P I E K T I S K A K

Figure 12E

CH3: KK of DEKK

gggcagccccgagaaccacaggtgtacaccaagcccccatccccggaggagatgaccaag
 G Q P R E P Q V Y T K P P S R E E M T K
 aaccaggtcagcctgaagtgcctgggtcaaaggcttctatcccagcgacatcgccgtggag
 N Q V S L K C L V K G F Y P S D I A V E
 tgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactcc
 W E S N G Q P E N N Y K T T P P V L D S
 gacggctccttcttctctatagcaagctcaccgtggacaagagcaggtggcagcagggg
 D G S F F L Y S K L T V D K S R W Q Q G
 aacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagc
 N V F S C S V M H E A L H N H Y T Q K S
 ctctccctgtctccgggttga
 L S L S P G -

Figure 12F

CH3: DE of DEKK

gggcagccccgagaaccacaggtgtacaccgaccccccatccccggaggagatgaccaag
 G Q P R E P Q V Y T D P P S R E E M T K
 aaccaggtcagcctgacctgcgaggtcaaaggcttctatcccagcgacatcgccgtggag
 N Q V S L T C E V K G F Y P S D I A V E
 tgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactcc
 W E S N G Q P E N N Y K T T P P V L D S
 gacggctccttcttctctatagcaagctcaccgtggacaagagcaggtggcagcagggg
 D G S F F L Y S K L T V D K S R W Q Q G
 aacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagc
 N V F S C S V M H E A L H N H Y T Q K S
 ctctccctgtctccgggttga
 L S L S P G -

Figure 13

- Supercluster 1:

- o MF8057,

- DNA

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1  ggcccagccg gccatggccg aggtgcagct ggtgcagtct ggagctgagg tgaagaagcc
61  tgggtcctcg gtgaaggtct cctgcaaggc ttctggaggc accttccgca gctttggtat
121 cagttgggtg cgacaggccc ctggacaagg acttgagtgg atgggaggat tcatccctgt
181 ccttggtaca gcaaaactac cacagaaatt ccagggcaga gtgacgatta tcgcggacaa
241 atccacgaac acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta
301 ttactgtgcg cgaaggggta actggaaccc gttcgacccc tggggccagg gaaccctggt
361 caccgtctcg agt

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- AA

FW1	>MF8057.cep_FW1 -1AA in FW4 EVQLVQSGAEVKKPGSSVKVSKASGGTFR
FW2	>MF8057.cep_FW2 -1AA in FW4 WVRQAPGQGLEWMG
FW3	>MF8057.cep_FW3 -1AA in FW4 RVTIIADKSTNTAYMELSSLRSEDVAVYYCAR
FW4	>MF8057.cep_FW4 -1AA in FW4 WGQGTILVTVSS
CDR1	>MF8057.cep_CDR1 -1AA in FW4 SFGIS
CDR2	>MF8057.cep_CDR2 -1AA in FW4 GFIPVLGTANYAQKFQG
CDR3	>MF8057.cep_CDR3 -1AA in FW4 RGNWNPFD
VH	>MF8057.cep_VH -1AA in FW4 EVQLVQSGAEVKKPGSSVKVSKASGGTFRSFGISWVRQAPGQGLEWMGGFIPVLGTANYAQKFQGRVTI IADKSTNTAYMELSSLRSEDVAVYYCARRGNWNPFDPWGQGTILVTVSS

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o MF8058,

▪ DNA

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1  ggcccagccg gccatggccc aggtgcagct ggtgcagtct ggggctgagg tgaagaagcc
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121 tactatcagc tgggtgcgac aggcccttgg acaggggctt gagtggctgg gggggatcat
181 ccctcttttt ggtacaatta cctacgcaca gaagttccag ggcagagtca cgattaccgc
241 ggacaaatcc acgaacactg ccttcattga actgagcagc ctgagatctg aggacacggc
301 catgtattat tgtacgcgac gggggaactg gaacccttc gacccttggg gccagggaac
361 cctggtcacc gtctcgagt

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▪ AA

FW2	>MF8058.cep_FW2 -1AA in FW4 WVRQAPQGLEWLG
FW1	>MF8058.cep_FW1 -1AA in FW4 QVQLVQSGAEVKKPGSSVKVSKASGDAFK
FW3	>MF8058.cep_FW3 -1AA in FW4 RVTITADKSTNTAFMELSSLRSEDAMYYCTR
FW4	>MF8058.cep_FW4 -1AA in FW4 WGQGTLLVTVSS
CDR1	>MF8058.cep_CDR1 -1AA in FW4 SKTFTIS
CDR2	>MF8058.cep_CDR2 -1AA in FW4 GIIPLEFGTITYAQKFQG
CDR3	>MF8058.cep_CDR3 -1AA in FW4 RGNWNPFD
VH	>MF8058.cep_VH -1AA in FW4 QVQLVQSGAEVKKPGSSVKVSKASGDAFKSKTFTISWVRQAPQGLEWLGGIIPLEFGTITYAQKFQGRV TITADKSTNTAFMELSSLRSEDAMYYCTRRGNWNPFDWGQGTLLVTVSS

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o MF8078,

▪ DNA

```

1  ggcccagccg gccatggccg aggtgcagct ggtgcagtct gggctctgagt tgaagaagcc
61  tgggtcctcg gtgaaggtct cctgcaaggc ttctggagtc accttcaaca gcagaacctt
121 tactatcagt tgggtgcgac aggcccttgg acaagggctt gagtggctgg ggagtatcat
181 ccctatTTTT ggtacaataa cctacgcaca gaagttccag ggcagagtca cgattaccgc
241 ggacaaatcc acgagcactg ccttcattga actgaccagc ctgagatctg aggacacggc
301 catatattat tgtacgagac gggggaactg gaacccttc gacccttggg gccagggcac
361 cctggtcacc gtctcgagt

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▪ AA

FW1	>MF8078.cep_FW1 -1AA in FW4 EVQLVQSGSELKKPGSSVKVSKASGVTFN
FW2	>MF8078.cep_FW2 -1AA in FW4 WVRQAPGQGLEWLG
FW3	>MF8078.cep_FW3 -1AA in FW4 RVTITADKSTSTAFMELTSLSRSEDTAIYYCTR
FW4	>MF8078.cep_FW4 -1AA in FW4 WGQGTLLVTVSS
CDR1	>MF8078.cep_CDR1 -1AA in FW4 SRTFTIS
CDR2	>MF8078.cep_CDR2 -1AA in FW4 SIIPFGTITYAQKFQG
CDR3	>MF8078.cep_CDR3 -1AA in FW4 RGNWNPFD
VH	>MF8078.cep_VH -1AA in FW4 EVQLVQSGSELKKPGSSVKVSKASGVTFNSRTFTISWVRQAPGQGLEWLGSIIPFGTITYAQKFQGRV TITADKSTSTAFMELTSLSRSEDTAIYYCTRRGNWNPFDWGQGTLLVTVSS

MF8048

FW1	>MF8048.cep_FW1 -1AA in FW4 QVQLVQSGAEVKKPGSSVKVSKASGGTFR
FW2	>MF8048.cep_FW2 -1AA in FW4 WVRQAPGQGLEWVG
FW3	>MF8048.cep_FW3 -1AA in FW4 RVTITADKSATTAYMELSSLRSEDTAIYYCAK
FW4	>MF8048.cep_FW4 -1AA in FW4 WGQGTLLVTVSS
CDR1	>MF8048.cep_CDR1 -1AA in FW4 GSGIS
CDR2	>MF8048.cep_CDR2 -1AA in FW4 GFIPFFGSANYAQKFRD
CDR3	>MF8048.cep_CDR3 -1AA in FW4 RGNWNPLDP
VH	>MF8048.cep_VH -1AA in FW4 QVQLVQSGAEVKKPGSSVKVSKASGGTFRGSGISWVRQAPGQGLEWVGGFIPFFGSANYAQKFRDRVTITADKSATTAYMELSSLRSEDTAIYYCAKRGWNPLDPWGQGTLLVTVSS
FW1	>MF8048.cep_FW1 -1AA in FW4 caggtgcagctggtgcagtcctgggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaagg cttctggaggcaccttcaga
FW2	>MF8048.cep_FW2 -1AA in FW4 tgggtgcgacaggccctggacaagggcttgagtgggtgggc
FW3	>MF8048.cep_FW3 -1AA in FW4 agagtcacgattaccgcgacaaaatccgcgaccacagcctacatggaactgagcagcctgagatctgagg acacggccatatattactgtgcgaaa
FW4	>MF8048.cep_FW4 -1AA in FW4 tggggccagggcaccttggtcaccgtctcgagt
CDR1	>MF8048.cep_CDR1 -1AA in FW4 ggttctggtatcagc
CDR2	>MF8048.cep_CDR2 -1AA in FW4 gggttcacccctttctttggttcagcaaaactacgcacagaagttccgggac
CDR3	>MF8048.cep_CDR3 -1AA in FW4 agaggaaattggaaccgctcgacccc
VH	>MF8048.cep_VH -1AA in FW4 caggtgcagctggtgcagtcctgggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaagg cttctggaggcaccttcagaggttctggtatcagctgggtgcgacaggccctggacaagggcttgagtg ggtgggcgggttcacccctttctttggttcagcaaaactacgcacagaagttccgggacagagtcacgatt accgcgacaaaatccgcgaccacagcctacatggaactgagcagcctgagatctgaggacacggccatat attactgtgcgaaaaagaggaaattggaaccgctcgacccctggggccagggcaccttggtcaccgtctc gagt

MF8101

FW1	>MF8101.cep_FW1 -1AA in FW4 QVQLVQSGAEVKKPGSSVKVSKASGVTFK
FW2	>MF8101.cep_FW2 -1AA in FW4 WVRQAPGQGLEWLG
FW3	>MF8101.cep_FW3 -1AA in FW4 RVSITADKSTNTAYLELNSLRSEDTAIYYCAR
FW4	>MF8101.cep_FW4 -1AA in FW4 WGQGTLLVTVSS
CDR1	>MF8101.cep_CDR1 -1AA in FW4 SKTLTIS
CDR2	>MF8101.cep_CDR2 -1AA in FW4 GIIPIFGSITYAQKFQD
CDR3	>MF8101.cep_CDR3 -1AA in FW4 RGNWNPFD
VH	>MF8101.cep_VH -1AA in FW4 QVQLVQSGAEVKKPGSSVKVSKASGVTFKSKTLTISWVRQAPGQGLEWLGGIIPIFGSITYAQKFQDRV SITADKSTNTAYLELNSLRSEDTAIYYCARRGNWNPFDWPWGQGTLLVTVSS
FW1	>MF8101.cep_FW1 -1AA in FW4 caggtgcagctggtgcagctctgggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaagg cttctggagtcaccttcaaa
FW2	>MF8101.cep_FW2 -1AA in FW4 tgggtgcgacaggccctggacaagggcttgagtggctggga
FW3	>MF8101.cep_FW3 -1AA in FW4 agagtctcgattaccgcgacaaaatccacgaacacagcctacttggaactgaacagcctgaggtctgagg acacggccatttattattgtgcgaga
FW4	>MF8101.cep_FW4 -1AA in FW4 tggggccagggcacctgggtcaccgtctcgagt
CDR1	>MF8101.cep_CDR1 -1AA in FW4 agcaaaaccttaactatcagc
CDR2	>MF8101.cep_CDR2 -1AA in FW4 gggatcatccctatttttggttcaataacctacgcacagaagttccaggac
CDR3	>MF8101.cep_CDR3 -1AA in FW4 cgggggaactggaacccttcgacccc
VH	>MF8101.cep_VH -1AA in FW4 caggtgcagctggtgcagctctgggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaagg cttctggagtcaccttcaaaagcaaaaccttaactatcagctgggtgacagggccctggacaagggct tgagtggctgggagggatcatccctatttttggttcaataacctacgcacagaagttccaggacagagtc tcgattaccgcgacaaaatccacgaacacagcctacttggaactgaacagcctgaggtctgaggacacgg ccatttattattgtgcgagacgggggaactggaacccttcgacccctggggccagggcacctgggtcac cgtctcgagt

MF8056

FW1	>MF8056.cep_FW1 -1AA in FW4 EVQLVQSGAEVKKPGSSVKVSKASGGTFR
FW2	>MF8056.cep_FW2 -1AA in FW4 WVRQAPGQGLEWVG
FW3	>MF8056.cep_FW3 -1AA in FW4 RVTITADKSATTAYMELSSLRSEDTAIYYCAK
FW4	>MF8056.cep_FW4 -1AA in FW4 WGQGTLLVTVSS
CDR1	>MF8056.cep_CDR1 -1AA in FW4 GSGIS
CDR2	>MF8056.cep_CDR2 -1AA in FW4 GFIPFFGSANYAQKFRD
CDR3	>MF8056.cep_CDR3 -1AA in FW4 RGNWNPFDP
VH	>MF8056.cep_VH -1AA in FW4 EVQLVQSGAEVKKPGSSVKVSKASGGTFRGSGISWVRQAPGQGLEWVGGFIPFFGSANYAQKFRDRVTITADKSATTAYMELSSLRSEDTAIYYCAKRGWNPNFDPWGQGTLLVTVSS
FW1	>MF8056.cep_FW1 -1AA in FW4 gaggtgcagctggtgcagctctggagctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaagg cttctggaggcaccttcaga
FW2	>MF8056.cep_FW2 -1AA in FW4 tgggtgcgacaggcccttgacaagggcttgagtgggtgggc
FW3	>MF8056.cep_FW3 -1AA in FW4 agagtcacgattaccgcgacaaaatccgcgaccacagcctacatggaactgagcagcctgagatctgagg acacggccatatattactgtgcaaa
FW4	>MF8056.cep_FW4 -1AA in FW4 tggggccagggcaccttggtcaccgtctcgagt
CDR1	>MF8056.cep_CDR1 -1AA in FW4 ggttctggtatcagc
CDR2	>MF8056.cep_CDR2 -1AA in FW4 gggttcacccctttcttgggttcagcaaaactacgcacagaagttccgggac
CDR3	>MF8056.cep_CDR3 -1AA in FW4 agaggaaattggaaccggttcgacccc
VH	>MF8056.cep_VH -1AA in FW4 gaggtgcagctggtgcagctctggagctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaagg cttctggaggcaccttcagaggttctggtatcagctgggtgcgacaggccctggacaagggcttgagtg ggtgggcgggttcacccctttcttgggttcagcaaaactacgcacagaagttccgggacagagtcacgatt accgcgacaaaatccgcgaccacagcctacatggaactgagcagcctgagatctgaggacacggccatat attactgtgcaaaaagaggaaattggaaccggttcgacccctggggccagggcaccttggtcaccgtctc gagt

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- Supercluster 3:
 - MF8397

- DNA

```

1  caggtgcagc tgggtgcagtc tgggggaggc ctggtacagc ctgggggggc cctgagactc
61  tcctgtgcaa cctctggatt caaattcagt agctatgcc tgagctgggt ccgccaggca
121 ccaggaagg gactggagtg ggtctcaggt attagtggta gtggtcgcac cacatggtat
181 gcagactccg tgaagggccg gtccaccatc tccagagaca attccaagaa cacgctgtat
241 ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gagagacggc
301 ggatacagct atggccctta ctggtacttc gatctctggg gccgtggaac cctggtcacc
361 cctggtcaccg tctccagt

```

- AA

FW1	>MF8397.cep_FW1 QVQLVQSGGGLVQPGGSLRLSCATSGFKFS
FW2	>MF8397.cep_FW2 WVRQAPGKGLEWVS
FW3	>MF8397.cep_FW3 RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR
FW4	>MF8397.cep_FW4 WGRGTLVTVSS
CDR1	>MF8397.cep_CDR1 SYALS
CDR2	>MF8397.cep_CDR2 GISGSGRTTWYADSVKG
CDR3	>MF8397.cep_CDR3 DGGYSYGPYWF DL
VH	>MF8397.cep_VH QVQLVQSGGGLVQPGGSLRLSCATSGFKFSYALSWVRQAPGKGLEWVSGISGSGRTTWYADSVKGRFTI SRDN SKNTLYLQMNSLRAEDTAVYYCARDGGYSYGPYWF DLWGRGTLVTVSS

21/57

MF8562

FW1	>MF8562.cep_FW1 QVQLVESGGGLVQPGGSLRLSCATSGFTFI
FW2	>MF8562.cep_FW2 WVRQAPGKGLEWVS
FW3	>MF8562.cep_FW3 RFTISRDNKNTLFLQMNSLRAEDTAVYYCAR
FW4	>MF8562.cep_FW4 WGRGTLVTVSS
CDR1	>MF8562.cep_CDR1 SYALS
CDR2	>MF8562.cep_CDR2 AISGSGRTTWYADSVKG
CDR3	>MF8562.cep_CDR3 DGGYTYGPYWYFDL
VH	>MF8562.cep_VH QVQLVESGGGLVQPGGSLRLSCATSGFTFISYALSWVRQAPGKGLEWVSAISGSGRTTWYADSVKGRFTI SRDNKNTLFLQMNSLRAEDTAVYYCARDGGYTYGPYWYFDLWGRGTLVTVSS
FW1	>MF8562.cep_FW1 caggtgcagctggtggagtcctgggggaggcctggtacagcctggggggtccctgagactctcctgtgcaa cctctggattcacctttatc
FW2	>MF8562.cep_FW2 tgggtccgccaggtccagggaaggggctggaatgggtctca
FW3	>MF8562.cep_FW3 cggttcaccatctccagagacaattccaagaacacgctgtttctgcaaatgaacagcctgagagccgagg acacggccgtatattactgtgcgaga
FW4	>MF8562.cep_FW4 tggggccgtggcaccctggtcaccgtctcgagt
CDR1	>MF8562.cep_CDR1 agctatgccctgagc
CDR2	>MF8562.cep_CDR2 gctattagtggtagtggtcgtaccacatggtacgcagactccgtgaagggc
CDR3	>MF8562.cep_CDR3 gacggtggatacacctatggcccttactggtacttcgatctc
VH	>MF8562.cep_VH caggtgcagctggtggagtcctgggggaggcctggtacagcctggggggtccctgagactctcctgtgcaa cctctggattcacctttatcagctatgccctgagctgggtccgccaggtccagggaaggggctggaatg ggctcagctattagtggtagtggtcgtaccacatggtacgcagactccgtgaagggccggttcaccatc tccagagacaattccaagaacacgctgtttctgcaaatgaacagcctgagagccgaggacacggccgtat attactgtgcgagagacggtggatacacctatggcccttactggtacttcgatctctggggccgtggcac cctggtcaccgtctcgagt

22/57

- Supercluster 4:
 - MF8508

- DNA

```

1  ggcccagccg gccatggccg aggtgcagct ggtggagtct gggggaggat tggtagagcc
61  tggcagggtcc ctgagactct cctgtgcaac ctctggattc aactttgatg attataccat
121  gcaactgggtc cggcaagctc caggggaagg cctggagtgg gtctcagata ttagttggag
181  tagtggttagc ataggctatg cggactctgt gaagggccga ttcaccatct ccagagacaa
241  cgccaagaac tccctgtggc tgcaaatgaa cagtctgaga actgaggaca cggccttgta
301  tttctgtgca aaagatcata gggggtacgg tgactacgag ggtggtggct ttgactactg
361  gggccaggga accctggtca ccgtctccag t

```

- AA

FW1	>MF8508.cep_FW1 EVQLVESGGGLVQPGRSLRLSCATSGFNFD
FW2	>MF8508.cep_FW2 WVRQAPGKGLEWVS
FW3	>MF8508.cep_FW3 RFTISRDNAKNSLWLQMNSLRTEDTALYFCAK
FW4	>MF8508.cep_FW4 WGQGTILVTVSS
CDR1	>MF8508.cep_CDR1 DYTMH
CDR2	>MF8508.cep_CDR2 DISWSSGSIGYADSVKG
CDR3	>MF8508.cep_CDR3 DHRGYGDYEGGGFDY
VH	>MF8508.cep_VH EVQLVESGGGLVQPGRSLRLSCATSGFNFD DYTMHWVRQAPGKGLEWVSDISWSSGSIGYADSVKGRFTI SRDNAKNSLWLQMNSLRTEDTALYFCAKDHRGYGDYEGGGFDYWGQGTILVTVSS

MF8998

FW1	>MF8998.cep_FW1 EVQLVESGGGLVQPGRSLRLSCATSGFTFD
FW2	>MF8998.cep_FW2 WVRQAPGKGLEWVS
FW3	>MF8998.cep_FW3 RFTISRDNAKNSLYLQMNSLRAEDTALYFCAK
FW4	>MF8998.cep_FW4 WGQGTLVTVSS
CDR1	>MF8998.cep_CDR1 DYTEMH
CDR2	>MF8998.cep_CDR2 DISWSSGSIGYADSVKG
CDR3	>MF8998.cep_CDR3 DHRGYGDYEGGGFDH
VH	>MF8998.cep_VH EVQLVESGGGLVQPGRSLRLSCATSGFTFDDYTMHWVRQAPGKGLEWVSDISWSSGSIGYADSVKGRFTI SRDNAKNSLYLQMNSLRAEDTALYFCAKDHRGYGDYEGGGFDHWGQGTLVTVSS
FW1	>MF8998.cep_FW1 gaggtgcagctggtggagctctgggggaggccttggtacagcctggcaggtccctgagactctcctgtgcaa cctctggattcacctttgat
FW2	>MF8998.cep_FW2 tggttcggaagctccagggaaggcctggagtggtctca
FW3	>MF8998.cep_FW3 cgattcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaacagtctgagagctgagg acacggccttgattttctgtgcaaaa
FW4	>MF8998.cep_FW4 tggttcggaagccttggtcaccgtctccagt
CDR1	>MF8998.cep_CDR1 gattataccatgcac
CDR2	>MF8998.cep_CDR2 gatattagttggagtagtggttagcataggctatgaggactctgtgaagggc
CDR3	>MF8998.cep_CDR3 gatcataggggtacggtgactacgaggggtggtggcctttgaccac
VH	>MF8998.cep_VH gaggtgcagctggtggagctctgggggaggccttggtacagcctggcaggtccctgagactctcctgtgcaa cctctggattcacctttgatgattataccatgcactgggtccggcaagctccagggaaggcctggagtg ggtctcagatattagttggagtagtggttagcataggctatgaggactctgtgaagggccgattcaccatc tcagagacaacgccaagaactccctgtatctgcaaatgaacagtctgagagctgaggacacggccttggt atttctgtgcaaaagatcataggggtacggtgactacgaggggtggtggcctttgaccactggggccaggg aaccttggtcaccgtctccagt

MF10401

FW1	>MF10401_FW1 EVQLVESGGVTVVQPGGSLRLSCAASGFTFD
FW2	>MF10401_FW2 WVRQAPGKGLEWVS
FW3	>MF10401_FW3 RFTISRDNKNSLYLQMNSLRTEDTALYYCAK
FW4	>MF10401_FW4 WGRGTLVTVSS
CDR1	>MF10401_CDR1 DYTMH
CDR2	>MF10401_CDR2 DISWSSGSIYYADSVKG
CDR3	>MF10401_CDR3 DHRGYGDYEGGGFDY
VH	>MF10401_VH EVQLVESGGVTVVQPGGSLRLSCAASGFTFDDYTMHWVRQAPGKGLEWVSDISWSSGSIYYADSVKGRFTI SRDNKNSLYLQMNSLRTEDTALYYCAKDHRGYGDYEGGGFDYWGRGTLVTVSS
FW1	>MF10401_FW1 gaggtgcagctggtggagagcgcgcgctggtggtgagcccgcgcgagcctgagactgagctgcgccc ccagcggttcaccttcgac
FW2	>MF10401_FW2 tgggtgagacaggcccccggaaggcgctggagtgggtgagc
FW3	>MF10401_FW3 agattcaccatcagcagagacaacagcaagaacagcctgtacctgcagatgaacagcctgagaaccgagg acaccgacctgtactactgcgccaag
FW4	>MF10401_FW4 tggggcagaggcaccctgggtaccgtctcagac
CDR1	>MF10401_CDR1 gactacaccatgcac
CDR2	>MF10401_CDR2 gacatcagctggagcgcgcgagcatctactacgcccagagcgtgaagggc
CDR3	>MF10401_CDR3 gaccacagaggctacggcgactacgagggcgcggttcgactac
VH	>MF10401_VH gaggtgcagctggtggagagcgcgcgctggtggtgagcccgcgcgagcctgagactgagctgcgccc ccagcggttcaccttcgacgactacaccatgcactgggtgagacaggcccccggaaggcgctggagt ggtgagcgacatcagctggagcgcgcgagcatctactacgcccagagcgtgaagggcagattcaccatc agcagagacaacagcaagaacagcctgtacctgcagatgaacagcctgagaaccgaggacaccgacctgt actactgcgccaaggaccacagaggtacggcgactacgagggcgcggttcgactactggggcagagg caccctgggtaccgtctcagac

MF10428

FW1	>MF10428_FW1 EVQLVESGGGLVQPGRSLRLSCVTSGFTFD
FW2	>MF10428_FW2 WVRQAPGKGLEWVS
FW3	>MF10428_FW3 RFTISRDNKDSLQYLMNSLRTEDTALYYCAK
FW4	>MF10428_FW4 WGQGTLVTVSS
CDR1	>MF10428_CDR1 DYTMH
CDR2	>MF10428_CDR2 DISWSSGTTGYADSVKG
CDR3	>MF10428_CDR3 DHMGYGDYEGGGFDY
VH	>MF10428_VH EVQLVESGGGLVQPGRSLRLSCVTSGFTFDDYTMHWVRQAPGKGLEWVSDISWSSGTTGYADSVKGRFTI SRDNKDSLQYLMNSLRTEDTALYYCAKDHMGYGDYEGGGFDYWGQGTLVTVSS
FW1	>MF10428_FW1 gaagtgcagctggtggagctctgggggaggcttggtacagcctggcaggtccctgagactctcctgtgtaa cctctggattcacctttgat
FW2	>MF10428_FW2 tgggtccggcaagctccggggaagggcctggagtggtctca
FW3	>MF10428_FW3 cgattcaccatctccagagacaatgccaggactccctgtatctgcaaatgaacagtctgagaactgagg acacggccttgattactgtgcaaaa
FW4	>MF10428_FW4 tggggccagggaaccctgggtaccgtctcgagc
CDR1	>MF10428_CDR1 gattataccatgcac
CDR2	>MF10428_CDR2 gatattagttggagtagtgccaccactggctatgaggactctgtgaagggc
CDR3	>MF10428_CDR3 gatcatatggggtacggtgactacgaggggtgggtgctttgactac
VH	>MF10428_VH gaagtgcagctggtggagctctgggggaggcttggtacagcctggcaggtccctgagactctcctgtgtaa cctctggattcacctttgatgattataccatgcactgggtccggcaagctccggggaagggcctggagtg ggtctcagatattagttggagtagtgccaccactggctatgaggactctgtgaagggccgattcaccatc tccagagacaatgccaggactccctgtatctgcaaatgaacagtctgagaactgaggacacggccttgt attactgtgcaaaaagatcatatggggtacggtgactacgaggggtgggtgctttgactactggggccaggg aacctgggtaccgtctcgagc

- Supercluster 7:
 - MF9249
 - DNA

```

1  ggcccagccg gccatggccg aggtgcagct ggtgcagtct ggagcagaag tgaaaaagcc
61  cggggagctct ctgaagatct cctgtaaggg ttctggatac agttttacta ggttttggat
121 cggtctgggtg cgccagatgc ccgggaaagg cctggagtgg atggggatca tctatcctgg
181 tgactctgat accagataca gcccgtcctt ccaaggccag gtcaccatct cagccgacaa
241 gtccaccagt accgcctacc tgcagtggag cagcctgaag gcctcggaca ccggcatgta
301 ttattgtgtg agacatatac gatattttga ctggtcggaa gactaccact attacctgga
361 cgtctggggc aaagggacca cggtcaccgt ctccagt

```

- AA

FW1	>MF9249.cep_FW1 EVQLVQSGAEVKKPGESLKISCKGSGYSFT
FW2	>MF9249.cep_FW2 WVRQMPGKGLEWMG
FW3	>MF9249.cep_FW3 QVTISADKSTSTAYLQWSSLKASDTGMYYCVR
FW4	>MF9249.cep_FW4 WGKGTTTVTVSS
CDR1	>MF9249.cep_CDR1 RFWIG
CDR2	>MF9249.cep_CDR2 IIYPGDS DTRYSPSFQG
CDR3	>MF9249.cep_CDR3 HIRYFDWSE DYHYYLDV
VH	>MF9249.cep_VH EVQLVQSGAEVKKPGESLKISCKGSGYSFTRFWIGWVRQMPGKGLEWMGIIYPGDS DTRYSPSFQGQVTI SADKSTSTAYLQWSSLKASDTGMYYCVRHIRYFDWSE DYHYYLDVWGKGTTTVTVSS

- Supercluster 7:

- MF9267

- DNA

```

1 gaggtgcagc tgggtggagtc tggggcagag gtgaaaaagc ccggggagtc tctgaagatc
61 tcttgtaagg gttctggata cagttttact aggtattgga tcggctgggt gcgccagatg
121 cccgggaaag gcctggagtg gatggggatc atctatcctg gtgactctga taccagatac
181 agcccgctct tccaaggcca ggtcaccatc tcagccgaca agtccatcag tactgcctac
241 ctgcagtgga gcagcctgaa ggctcggac accgccatgt attattgtgt gagaaatata
301 cgatattttg tctggtcgga ggactaccac tactacatgg acgtctgggg caaagggacc
361 acggtcaccgt ctccagt

```

- AA

FW1	>MF9267.cep_FW1 EVQLVESGAIEVKKPGESLKISCKGSGYSFT
FW2	>MF9267.cep_FW2 WVRQMPGKGLEWMG
FW3	>MF9267.cep_FW3 QVTISADKSISTAYLQWSSLKASDTAMYYCVR
FW4	>MF9267.cep_FW4 WGKGTTTVTVSS
CDR1	>MF9267.cep_CDR1 RYWIG
CDR2	>MF9267.cep_CDR2 IIYPGDS DTRYSPSFQG
CDR3	>MF9267.cep_CDR3 NIRYFVWSE DYHYMDV
VH	>MF9267.cep_VH EVQLVESGAIEVKKPGESLKISCKGSGYSFTRYWIGWVRQMPGKGLEWMGIIYPGDS DTRYSPSFQGQVTI SADKSISTAYLQWSSLKASDTAMYYCVRNIRYFVWSE DYHYMDVWGKGTTTVTVSS

28/57

PDL1 MFsMF5377

DNA

```

1 gaggtgcagct ggtgcagtct ggagctgagg tgaagaagcc
61 tgggtcctcg gtgaaggctc cctgcaaggc ttctggaggc atcttcagca cctatgctat
121 cagctgggtg cgacaggccc ctggacaagg gcttgagtgg atgggaggga tcatccctat
181 ctttgataca ccaaactacg cacagaagtt ccagggcaga gtcacgatta ccgcggacaa
241 atccacgagc acagcctaca tggacctgag cagcctgaga tctgaggaca cggccgtata
301 ttactgtgcg aaaaacgtgc gtggatatag tgcctacgac cttgactact ggggccaggg
361 caccctggtc accgtctcca gt

```

AA

FW1	FW1 EVQLVQSGAEVKKPGSSVKVSKASGGIFS
FW2	FW2 WVRQAPGQGLEWMG
FW3	FW3 RVTITADKSTSTAYMDLSSLRSED TAVYYCAK
FW4	FW4 WGQGTLVTVSS
CDR1	CDR1 TYAIS
CDR2	CDR2 GIIPFDTPNYAQKFQG
CDR3	CDR3 NVRGYSAYDL DY
VH	VH EVQLVQSGAEVKKPGSSVKVSKASGGIFSTYAI SWVRQAPGQGLEWM GGIIPFDTPNYAQKFQGRVTITADKSTSTAYMDLSSLRSED TAVYYCAKNVRGYSAYDL DYWGQGTLVTVSS

29/57

MF5444

DNA

c aggtgcagct ggtgcaatct gggctctgagt tgaagaagcc

61 tggggcctca gtgaagggtt cctgcaaggc ttctggatac accttcacta gctattctat

121 gaattgggtg cgacaggccc ctggacaagg gcttgagtgg atgggatgga tcaacaccaa

181 cactgggaac ccaacgtatg ccagggcctt cacaggacgg ttgtcttct ccttgacac

241 ctctgtcagc acggcatatc tgcagatcag cagcctaaag gctgaggaca ctgccgtgta

301 ttactgtgcg agagatcacg attttcggac tgggagggct ttgatattct ggggccaaag

361 gaccacgggc accgtctcca gt

AA

FW1	FW1 QVQLVQSGSELKKPGASVKVSCKASGYTFT
FW2	FW2 WVRQAPGQGLEWMG
FW3	FW3 RFVFSLDTSVSTAYLQISSLKAEDTAVYYCAR
FW4	FW4 WGQGTITVTVSS
CDR1	CDR1 SYSMN
CDR2	CDR2 WINTNTGNPTYAQGFTG
CDR3	CDR3 DHDFRTGRAFDI
VH	VH QVQLVQSGSELKKPGASVKVSCKASGYTFTSYSMNWVRQAPGQGLEWM GWINTNTGNPTYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARDHDFRTGRAFDIWGQGTITVTVSS

30/57

MF5380

DNA

g aggtgcagct ggtggagtct gggggagacg tgggtccagcc
 61 tgggaggtcc ctgagactct cctgtgcagc ctctggattc accttcagta gctatggcat
 121 gcactgggtc cgccaggctc caggcaaggg gctggagtgg gtggcagtta tatcatatga
 181 tggaaagtaat aaatactatg cagactccgt gaagggccga ttcaccatct ccagagacaa
 241 ctccaagagc acgctgtttc tgcaaataaa cagcctgaga gctgaggaca cggctgtgta
 301 tttctgtgtg agaggcctcc ccataactat ggttcgggga gcgtactcct ttgactactg
 361 gggccagggc accctggtea ccgtctccag t

AA

FW1	FW1 EVQLVESGGDVVQPGKSLRLSCAASGFTFS
FW2	FW2 WVRQAPGKGLEWVA
FW3	FW3 RFTISRDNKSTLFLQMNSLRAEDTAVYFCVR
FW4	FW4 WGQGTILTVSS
CDR1	CDR1 SYGMH
CDR2	CDR2 VISYDGSNKYYADSVKG
CDR3	CDR3 GLPITMVRGAYSFDY
VH	VH EVQLVESGGDVVQPGKSLRLSCAASGFTFSYGMHWVRQAPGKLEWV AVISYDGSNKYYADSVKGRFTISRDNKSTLFLQMNSLRAEDTAVYFCVRGLPITMVRGAYSFDYWGQGTILTVSS

EGFR MFsMF8233

DNA

```
c aggttcagct ggtgcagctct ggagctgagg tgaagaagcc
      61 tggggcctca gtgaaggctct cctgcaaggc ttctggttac acctttacca gctatggtat
     121 cagctgggtg cgacaggccc ctggacaagg gcttgagtgg atgggatgga tcagcgctta
     181 caatgccaac acaaactatg cacagaagct ccagggcaga gtcaccatga ccacagacac
     241 atccacgagc acagcctaca tggagctgag gagcctgaga tctgacgaca cggctgtgta
     301 ttactgtgca aaagatcgtc attggcattg gtggctggac gcctttgatt attggggcca
     361 aggtaccctg gtcaccgtct ccagt
```

AA

FW1: QVQLVQSGAEVKKPGASVKVSCKASGYTFT

FW2: WVRQAPGQGLEWMG

FW3: RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAK

FW4: WGQGTILVTVSS

CDR1: SYGIS

CDR2: WISAYNANTNYAQKLQG

CDR3: DRHWHWWLDAFDY

VH: QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWM

GWISAYNANTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAKDRHWHWWLDAFDYWGQGTILVTVSS

32/57

MF9891

DNA

c aggttcagct ggtgcagctct ggagctgagg tgaagaagcc

61 tggggcctca gtgaaggtct cctgcaaggc ttctggttac acctttacca gctatggtat

121 cagctgggtg cgacaggccc ctggacaagg gcttgagtgg atgggatgga tcagcgctta

181 caatgccaac aaaaactatg cacagaagct ccagggcaga gtcaccatga ccacagacac

241 atccacgagc acagcctaca tggagctgag gagcctgaga tctgacgaca cggctgtgta

301 ttactgtgca aaagatctgt acggtcattg gtggctggat gcctttgatt attggggcca

361 aggtaccctg gtcaccgtct ccagt

AA

FW1	FW1 QVQLVQSGAEVKKPGASVKVSCKASGYTFT
FW2	FW2 WVRQAPGQGLEWMG
FW3	FW3 RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAK
FW4	FW4 WGQGLTVTVSS
CDR1 1	CDR1 SYGIS
CDR2 2	CDR2 WISAYNANTNYAQKLQG
CDR3 3	CDR3 DLYGHWLDAFDY
VH	VH QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWM GWISAYNANTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAKDLYGHWLDAFDYWGQGLTVTVSS

MF9886

DNA

c aggttcagct ggtgcagctct ggagctgagg tgaagaagcc

61 tggggcctca gtgaaggtct cctgcaaggc ttctggttac acctttacca gctatggtat

121 cagctgggtg cgacaggccc ctggacaagg gcttgagtgg atgggatgga tcagcgctta

181 caatgccaac acaaactatg cacagaagct ccagggcaga gtcaccatga ccacagacac

241 atccacgagc acagcctaca tggagctgag gagcctgaga tctgacgaca cggctgtgta

301 ttactgtgca aaaggtccag gttctcattg gtggctggat gcctttgatt attggggcca

361 aggtaccctg gtcaccgtct ccagt

AA

FW1	FW1 QVQLVQSGAEVKKPGASVKVSCKASGYTFT
FW2	FW2 WVRQAPGQGLEWMG
FW3	FW3 RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAK
FW4	FW4 WGQGLTVTVSS
CDR1 1	CDR1 SYGIS
CDR2 2	CDR2 WISAYNANTNYAQKLQG
CDR3 3	CDR3 GPGSHWWLDAFDY
VH	VH QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWM GWISAYNANTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAKGPGSHWWLDAFDYWGQGLTVTVSS

MF9873

DNA

c aggttcagct ggtgcagctct ggagctgagg tgaagaagcc

61 tggggcctca gtgaaggtct cctgcaaggc ttctggttac acctttacca gctatggtat

121 cagctgggtg cgacaggccc ctggacaagg gcttgagtgg atgggatgga tcagcgctta

181 caatgccaac acaaactatg cacagaagct ccagggcaga gtcaccatga ccacagacac

241 atccacgagc acagcctaca tggagctgag gagcctgaga tctgacgaca cggctgtgta

301 ttactgtgca aaagatagag gttggcattg gtggctggat gcctttgatt attggggcca

361 aggtaccctg gtcaccgtct ccagt

AA

FW1	FW1 QVQLVQSGAEVKKPGASVKVSCKASGYTFT
FW2	FW2 WVRQAPGQGLEWMG
FW3	FW3 RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAK
FW4	FW4 WGQGLTVTVSS
CDR1 1	CDR1 SYGIS
CDR2 2	CDR2 WISAYNANTNYAQKLQG
CDR3 3	CDR3 DRGWHWWLDAFDY
VH	VH QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWM GWISAYNANTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAKDRGWHWWLDAFDYWGQGLTVTVSS

MF9988

DNA

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AA

FW1	FW1 QVQLVQSGAEVKKPGASVKVSCKASGYTFT
FW2	FW2 WVRQAPGQGLEWMG
FW3	FW3 RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAK
FW4	FW4 WGQGTLLTVSS
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MF6744 anti-CD137 antibody sequence:

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AA

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FW2: WVRQMPGKGLEWMG

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CDR1: SYWIG

CDR2: IIFPDDSDTRYSPSFQG

CDR3: LGGYSGYAEDFVDF

VH: EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWM

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H1H7232B (1129) VH - MF6955 in combination with common light chain

VH gene: IGHV3-9

DNA:

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Protein:

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37/57

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VH gene: IGHV3-9

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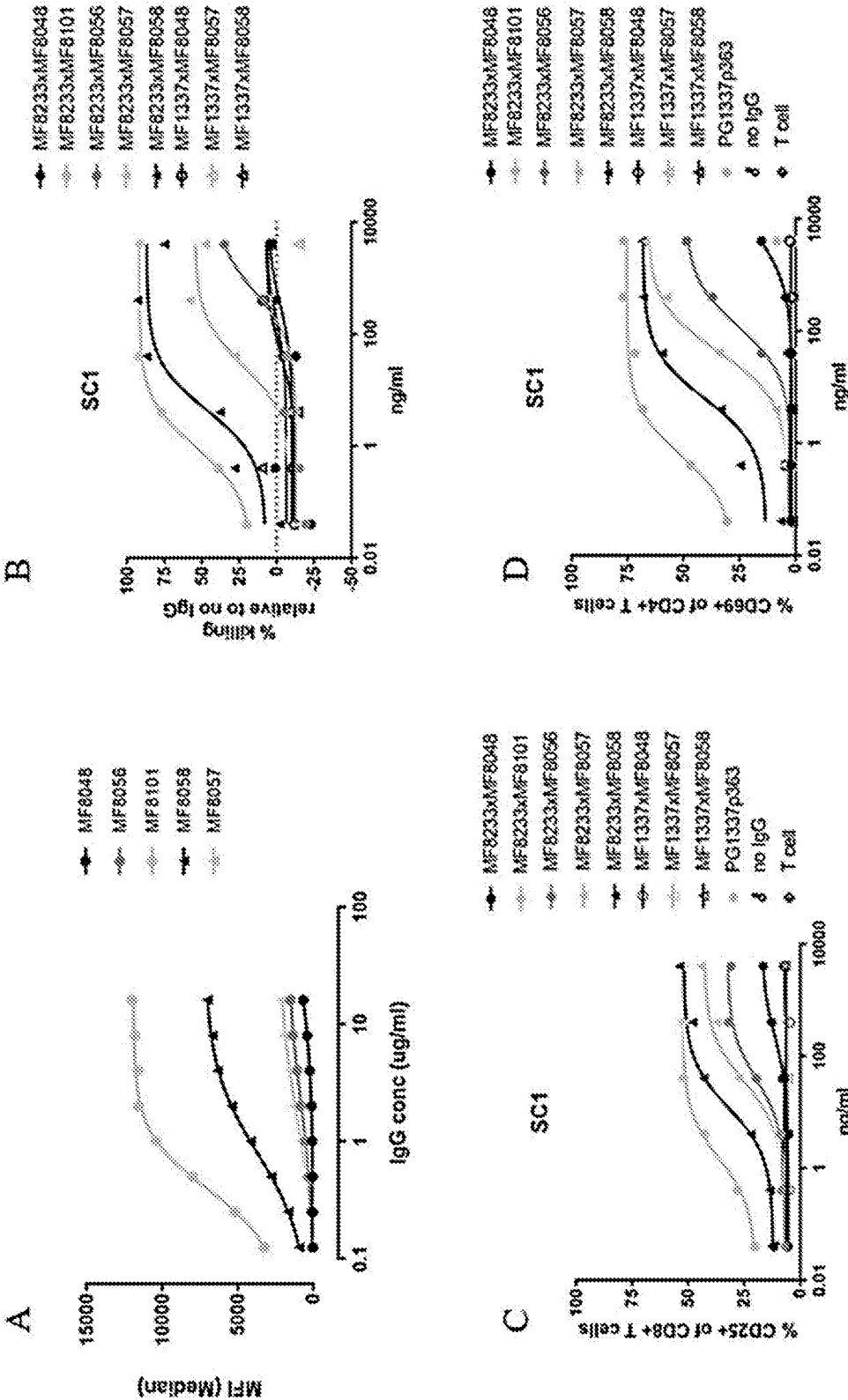


Fig. 14 (A-B-C-D)

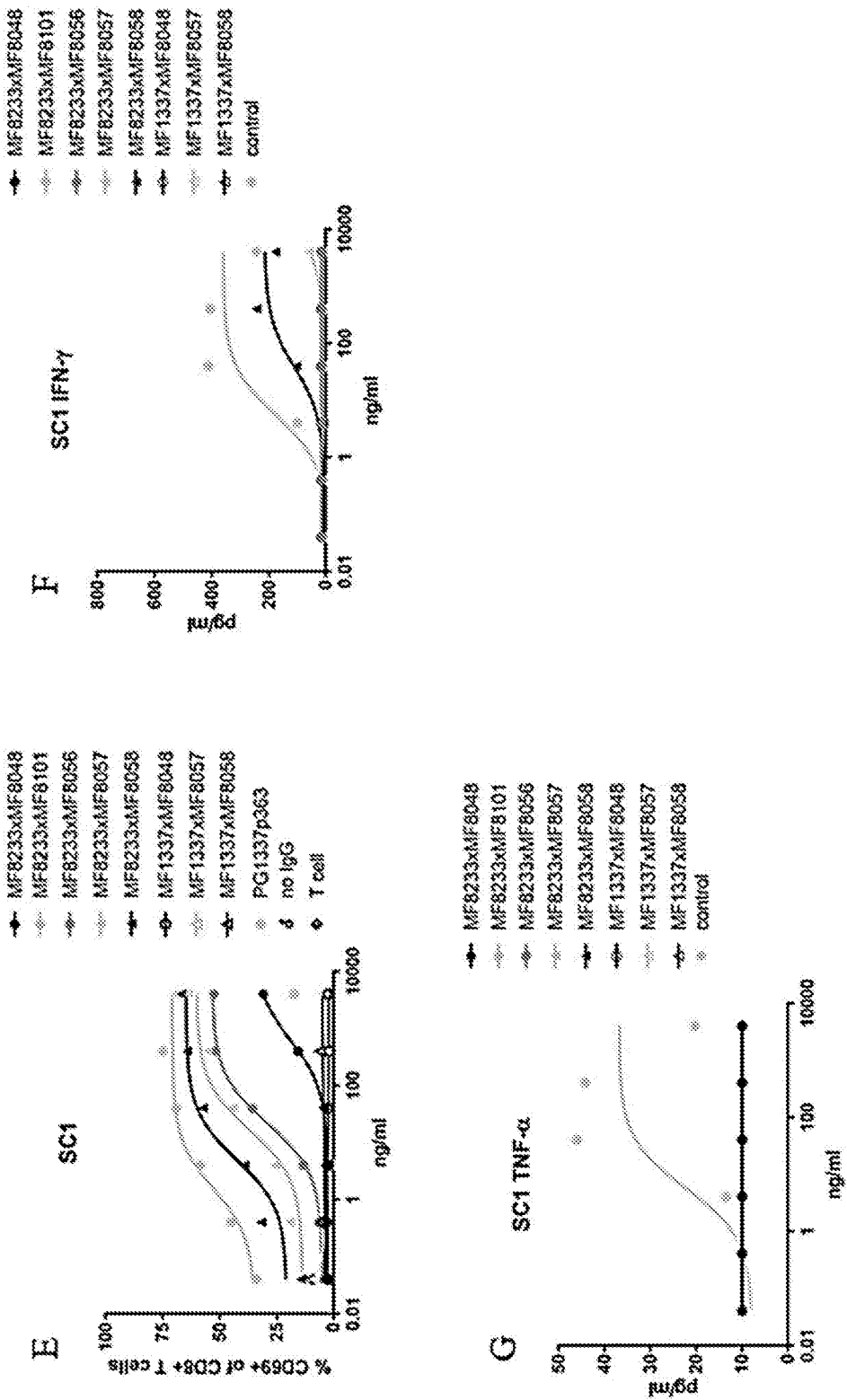


Fig. 14 (E-F-G)

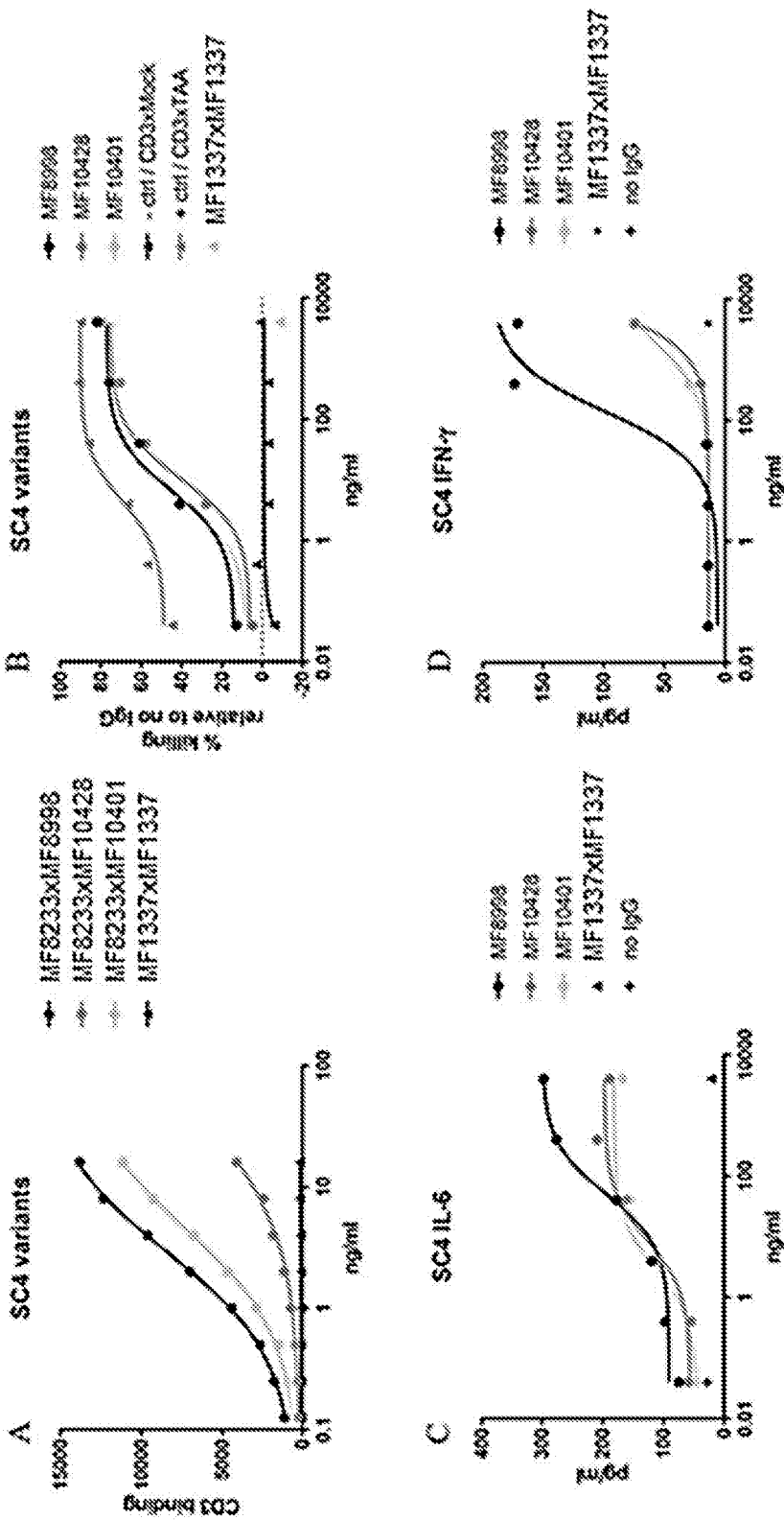


Fig. 15 (A-B-C-D)

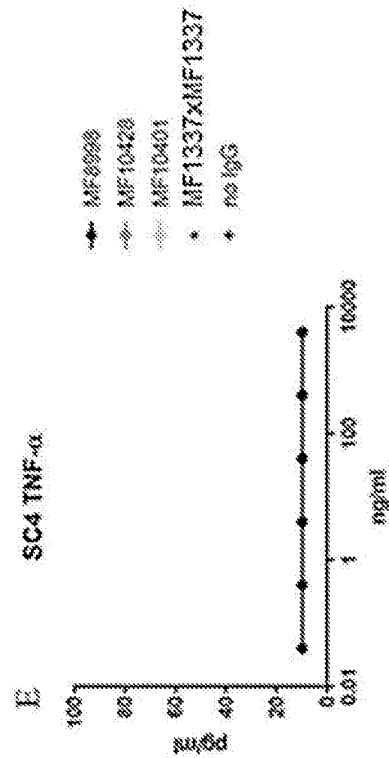


Fig. 15E

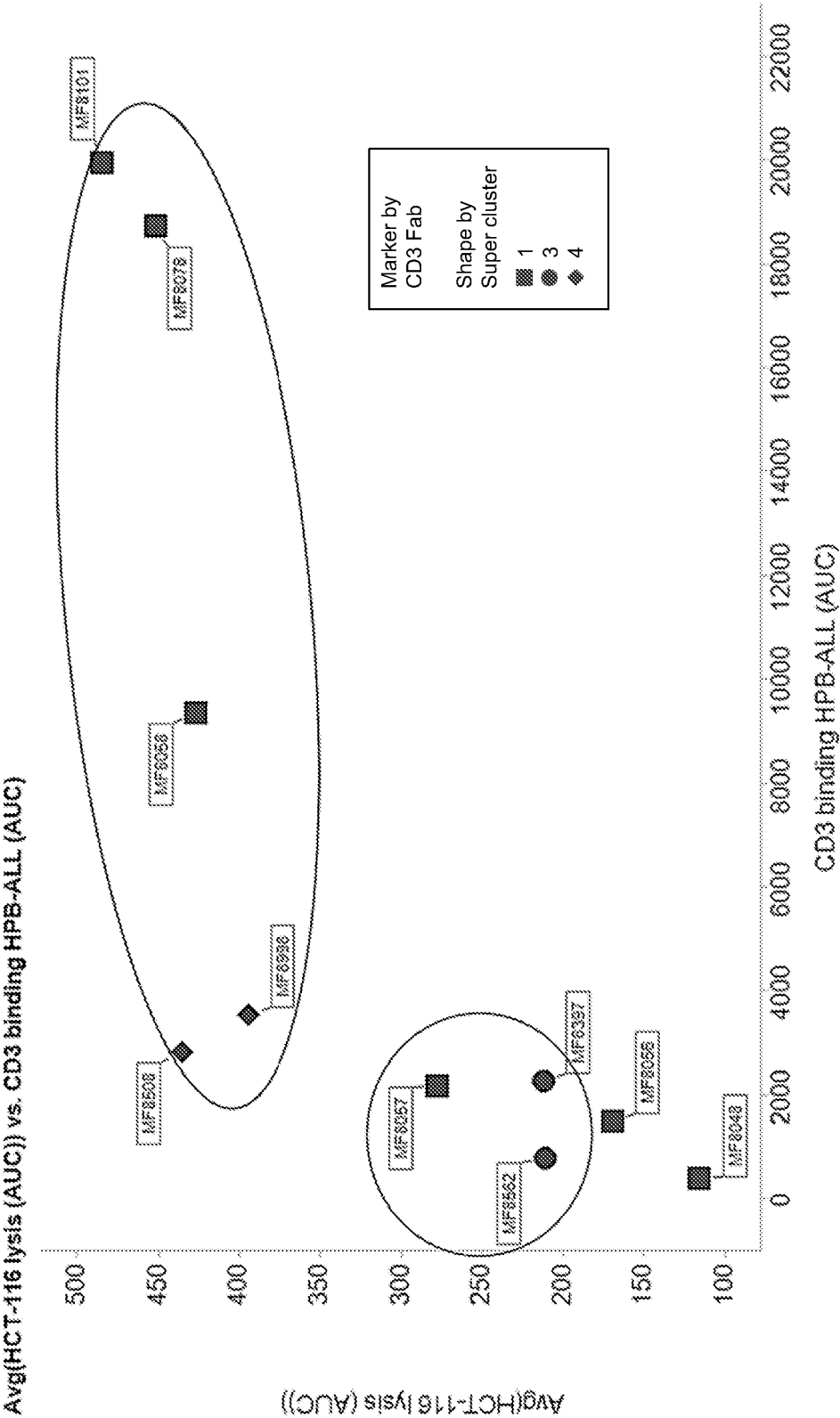


Fig. 16A

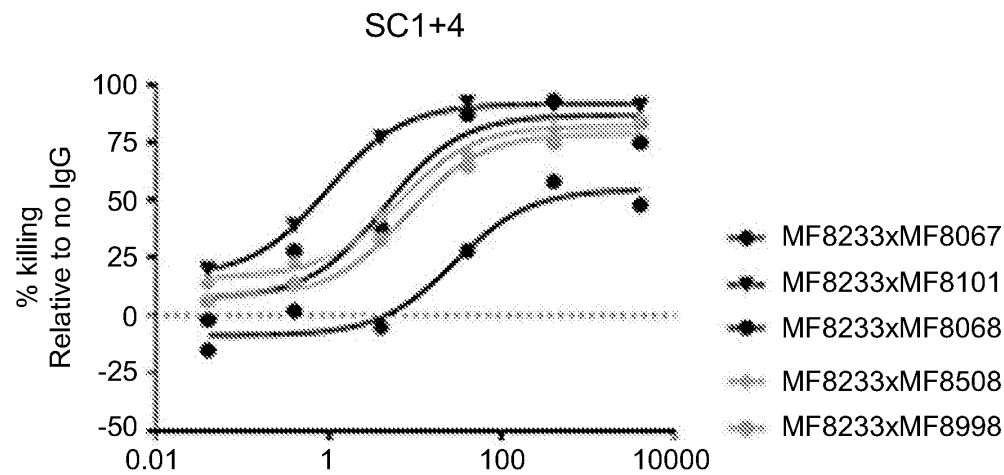


Fig. 16B

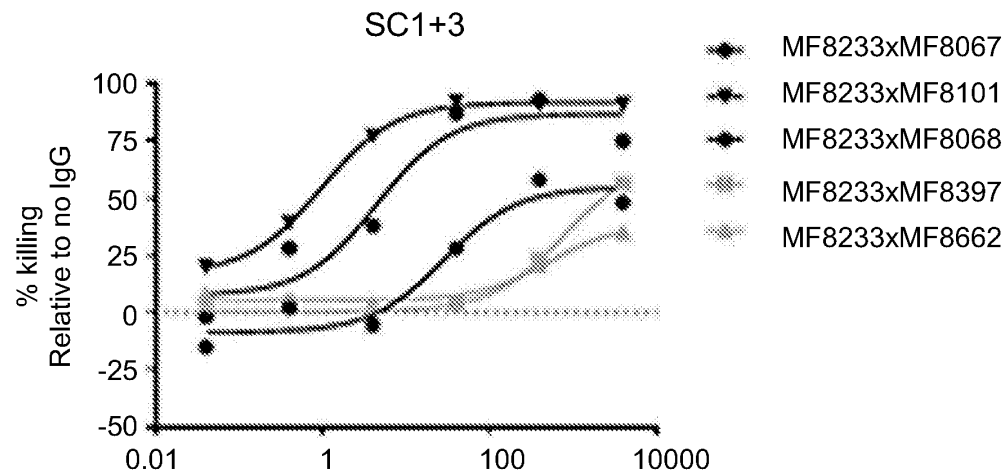


Fig. 16C

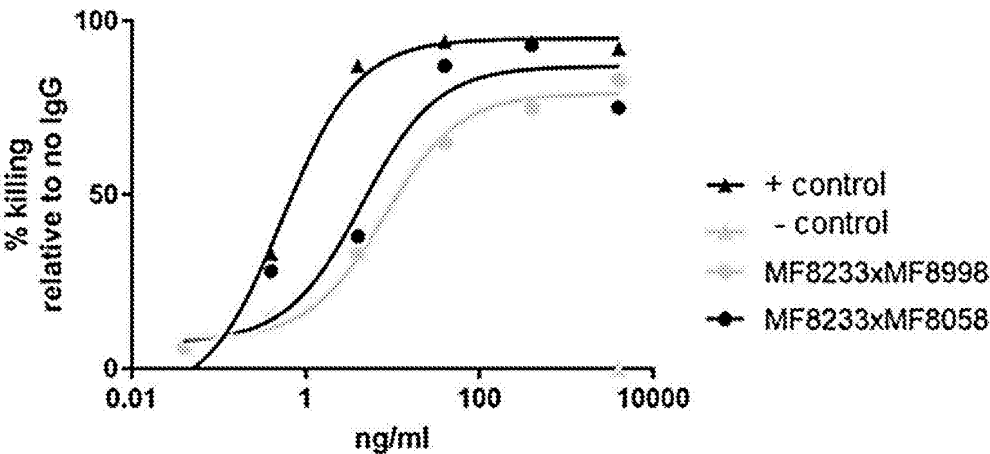


Fig. 17

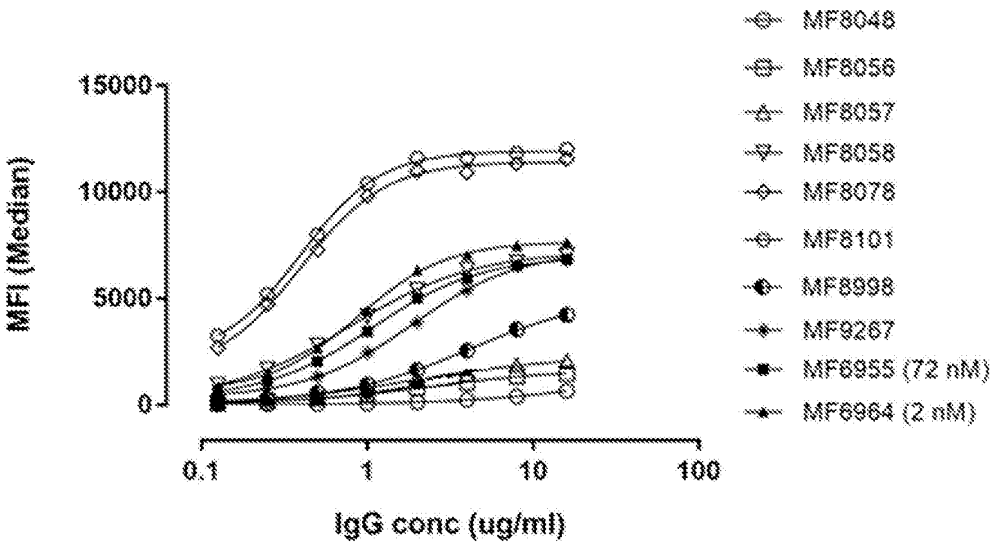


Fig. 18

Figure 19

CLEC12A (SEQ ID NO: 1)

>NC_000012.12:9951268-9995209 Homo sapiens chromosome 12, GRCh38.p13 Primary Assembly

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Figure 20

CD3 γ chain (SEQ ID NO: 2)

MEQGRGLAVL	ILAIILLQGT	LAQSIKGNHL	VKVYDYQEDG	SVLLTCDAEA	KNITWFKDGK	60
MIGFLTEDKK	KWNLGSNAKD	PRGMYQCKGS	QNKSKPLQVY	YRMCQNCIEL	NAATISGFLF	120
AEIVSIFVLA	VGVIYFIAGQD	GVRQSRASDK	QTLLPNDQLY	QPLKDREDDQ	YSHLQGNQLR	180
RN						182

CD3 δ chain (SEQ ID NO: 3)

MEHSTFLSGL	VLATLLSQVS	PFKIPIEELE	DRVFNVCNTS	ITWVEGTVGT	LLSDITRLDL	60
GKRILDPRGI	YRCNGTDIYK	DKESTVQVHY	RMCQSCVELD	PATVAGIIVT	DVIATLLLLAL	120
GVFCFAGHET	GRLSGAADTQ	ALLRNDQVYQ	PLRDRDDAQY	SHLGGNWARN	K	171

CD3 ϵ chain (SEQ ID NO: 4)

MQSGTHWRVL	GLCLLSVGW	GQDGNEEMGG	ITQTPYKVS	SGTTVILTCP	QYPGSEILWQ	60
HNDKNIGGDE	DDKNIGSDED	HLSLKEFSEL	EQSGYYVCYP	RGSKPEDANF	YLYLRARVCE	120
NCMEMDVMSV	ATIVIVDICI	TGGLLLLVIY	WSKNRKAKAK	PVTRGAGAGG	RQRGQNKERP	180
PPVPNPDIYEP	IRKGQRDLYS	GLNQRR				207

CD3 ζ chain (SEQ ID NO: 5)

MKWKALFTAA	ILQAQLPITE	AQSFGLLDPK	LCYLLDGILF	IYGVILTALF	LRVKFSRSAD	60
APAYQQGQNG	LYNELNLGRR	EEYDVLDKRR	GRDPEMGGKP	QRRKNPQEG	YNELQKDKMA	120
EAYSEIGMKG	ERRRGKGHDG	LYQGLSTATK	DTYDALHMQA	LPPR		164