

Fig. 1A

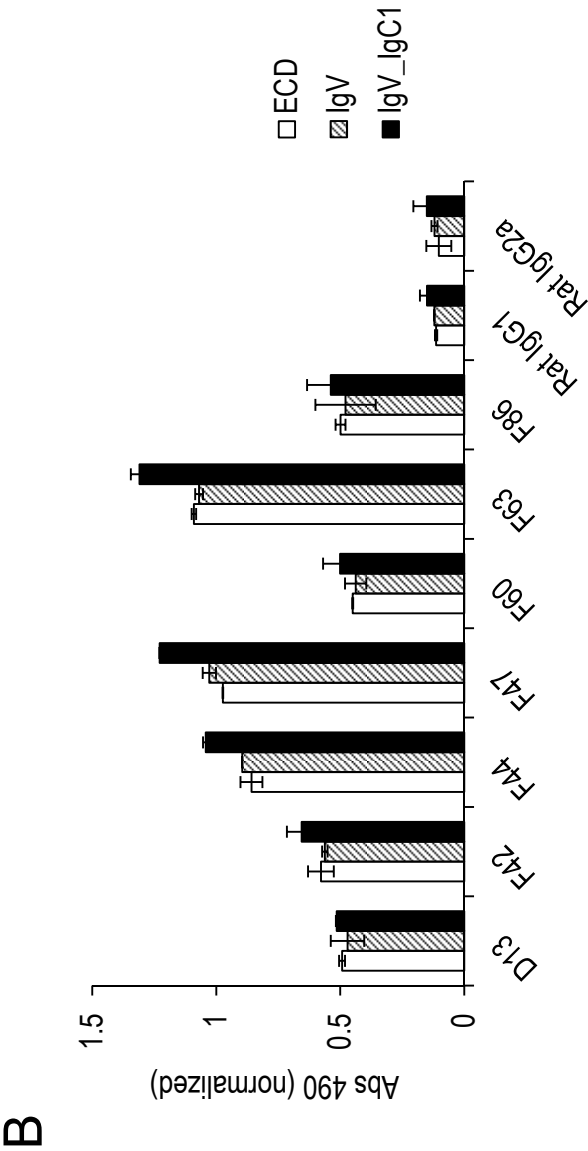
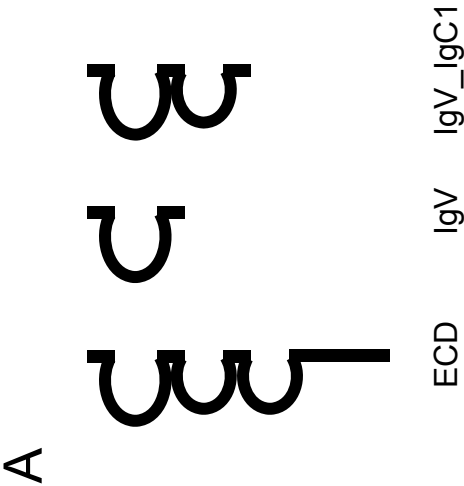


Fig. 1B

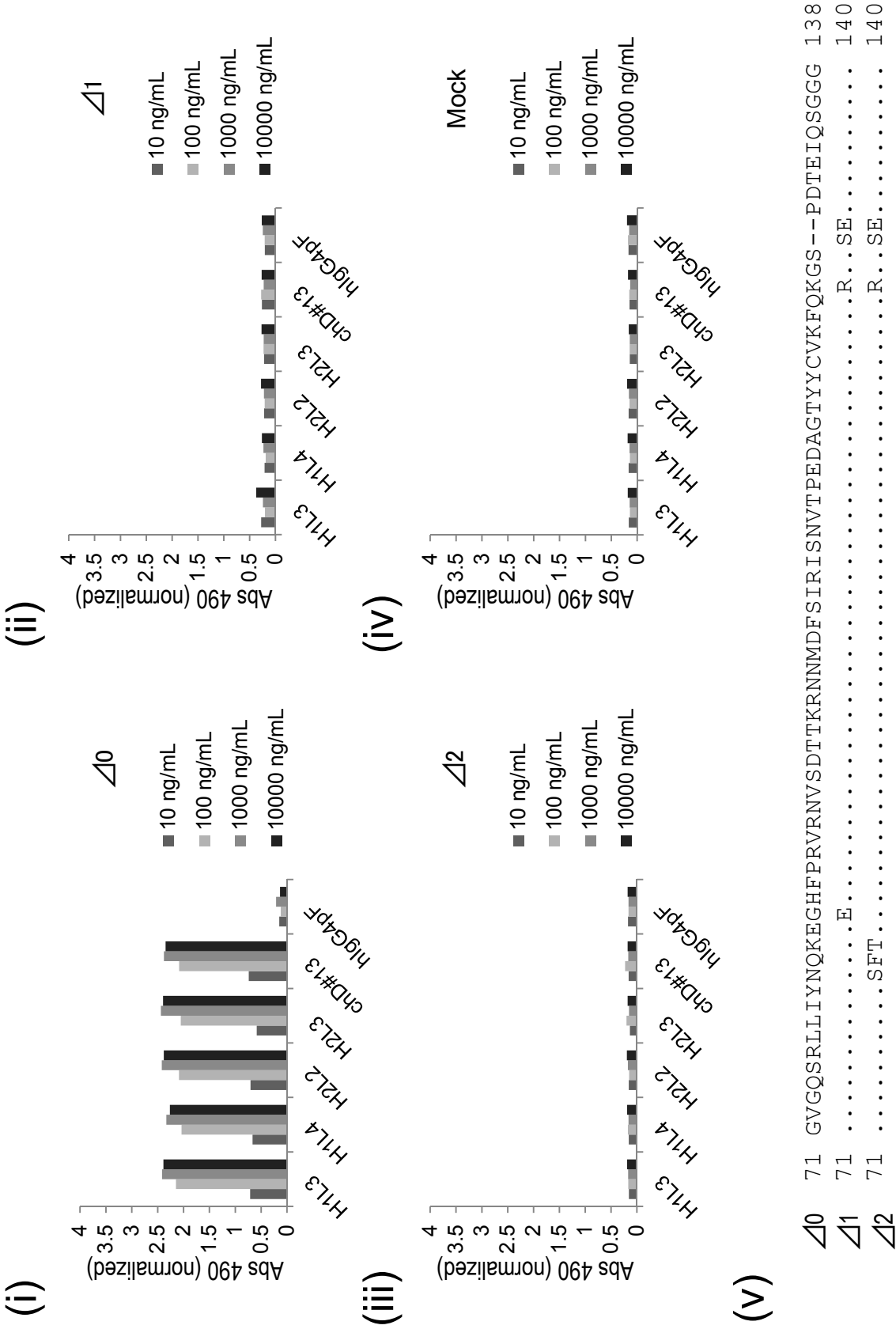


Fig. 2

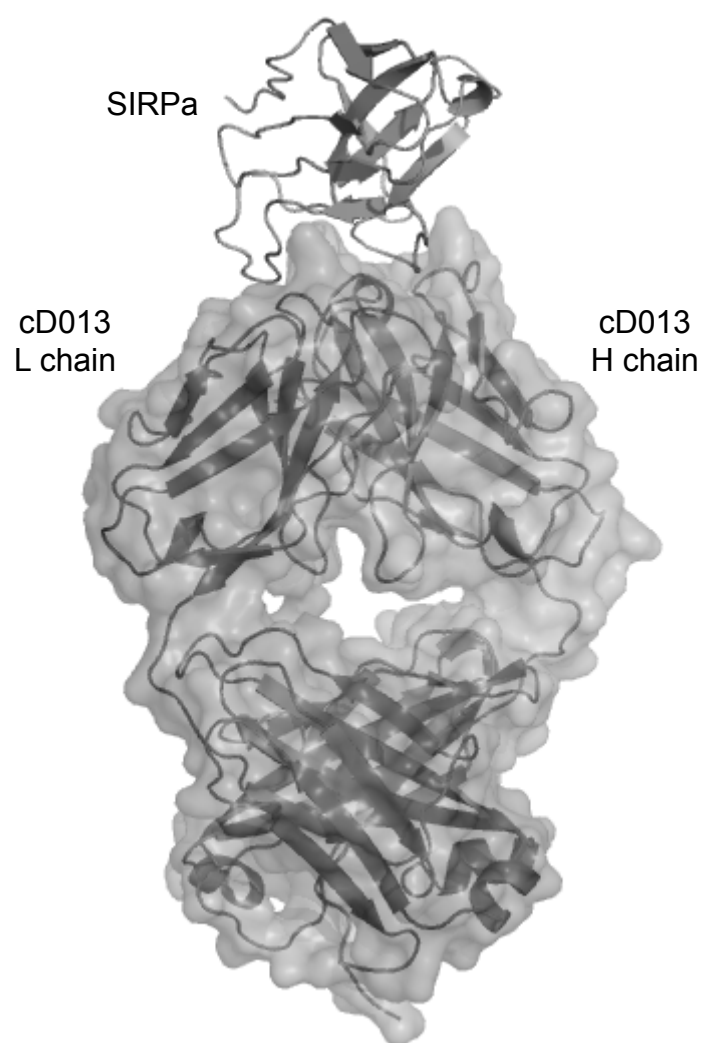
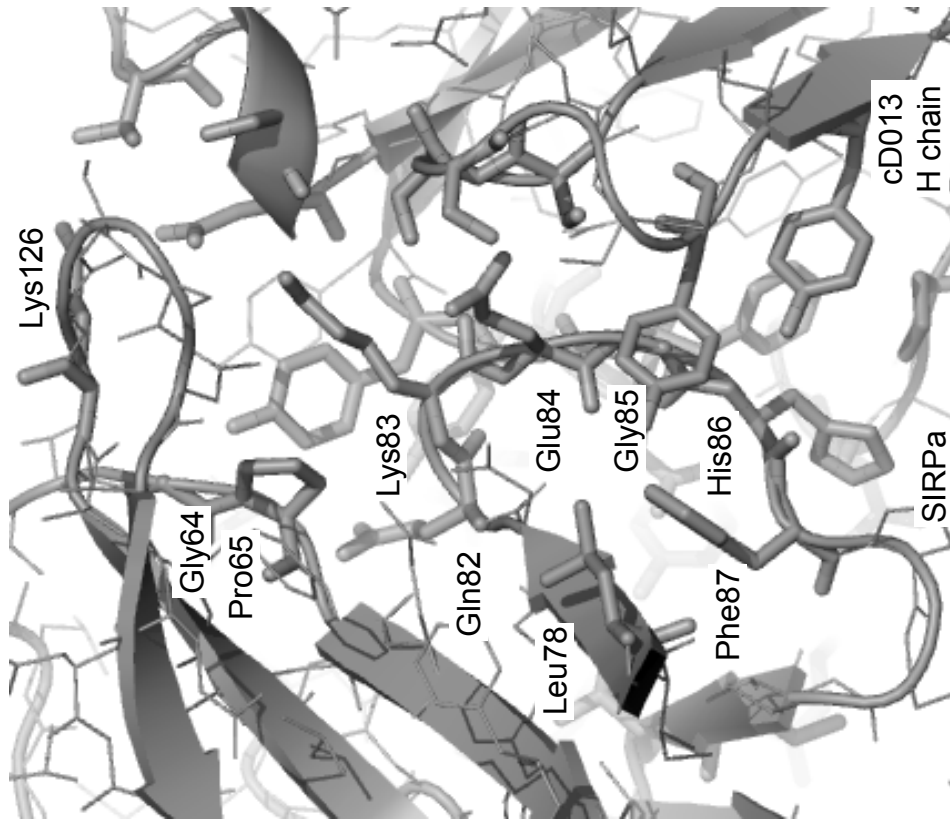


Fig. 3

A



B

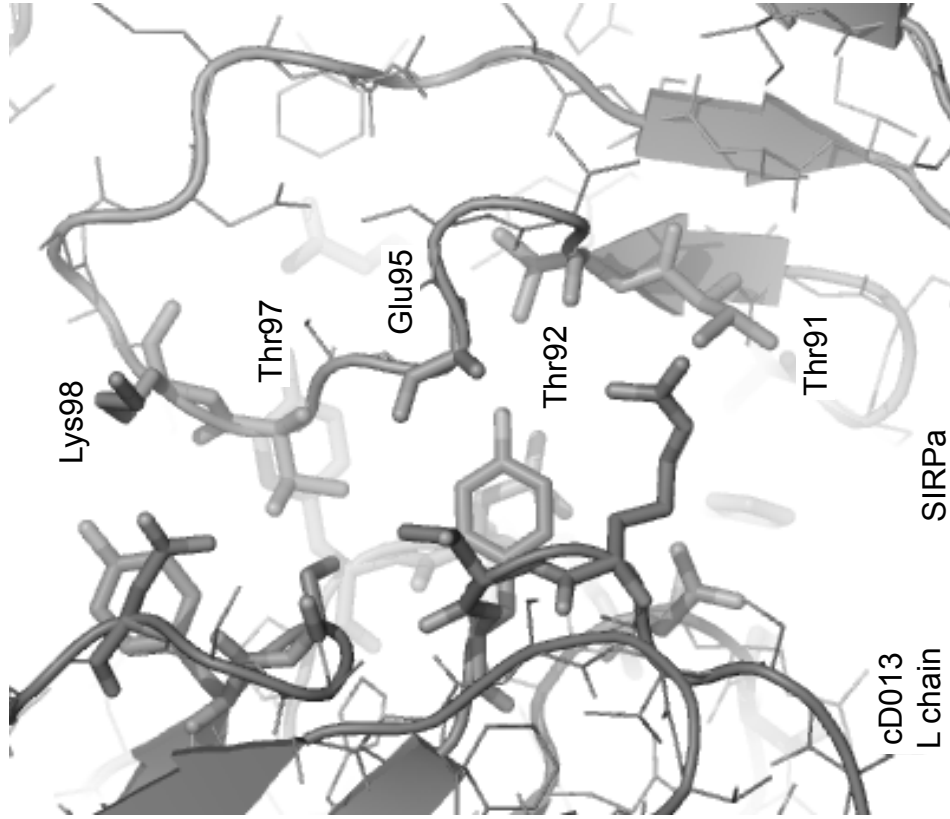


Fig. 4

V1	1	MEPAGAPGRGLGPLLCLLLAASCWAGVAGEEELQVIQPDKSVLVAAGETATLRCTATSL	60
V2	1	S.....S.I.H..V...	60
V3	1	S.....S.I.L..V...	60
V4	1	G.....S.....S.I.H.....	60
V5	1	F.....	60
V6	1		60
V7	1	S.....S.I.H..V...	60
V8	1		60
V9	1		60
V10	1	R.....S.....S.I.H..V...	60
V1	61	IPVGPIQWFRGAGPGRELIYNQKEGHFPRVTTVSDLTKRNNMDFSIRIGNITPADAGTYY	120
V2	61	A.....ES..E.....S.S.....	120
V3	61	A.....ES..E.....S.S.....	120
V4	61		120
V5	61		120
V6	61	P.....	120
V7	61	A.....ES..E.....S.S.....	120
V8	61	A.....ES..E.....S.S.....	120
V9	61		120
V10	61	A.....ES..E.....S.S.....	120
V1	121	CVKFRKGSPPDVEFKSGAGTELSVRA	146
V2	121	T-.....	145
V3	121	T-.....	145
V4	121		146
V5	121		146
V6	121		146
V7	121	T-.....G	145
V8	121	T-.....	145
V9	121		146
V10	121	T-.....	145

Fig. 5

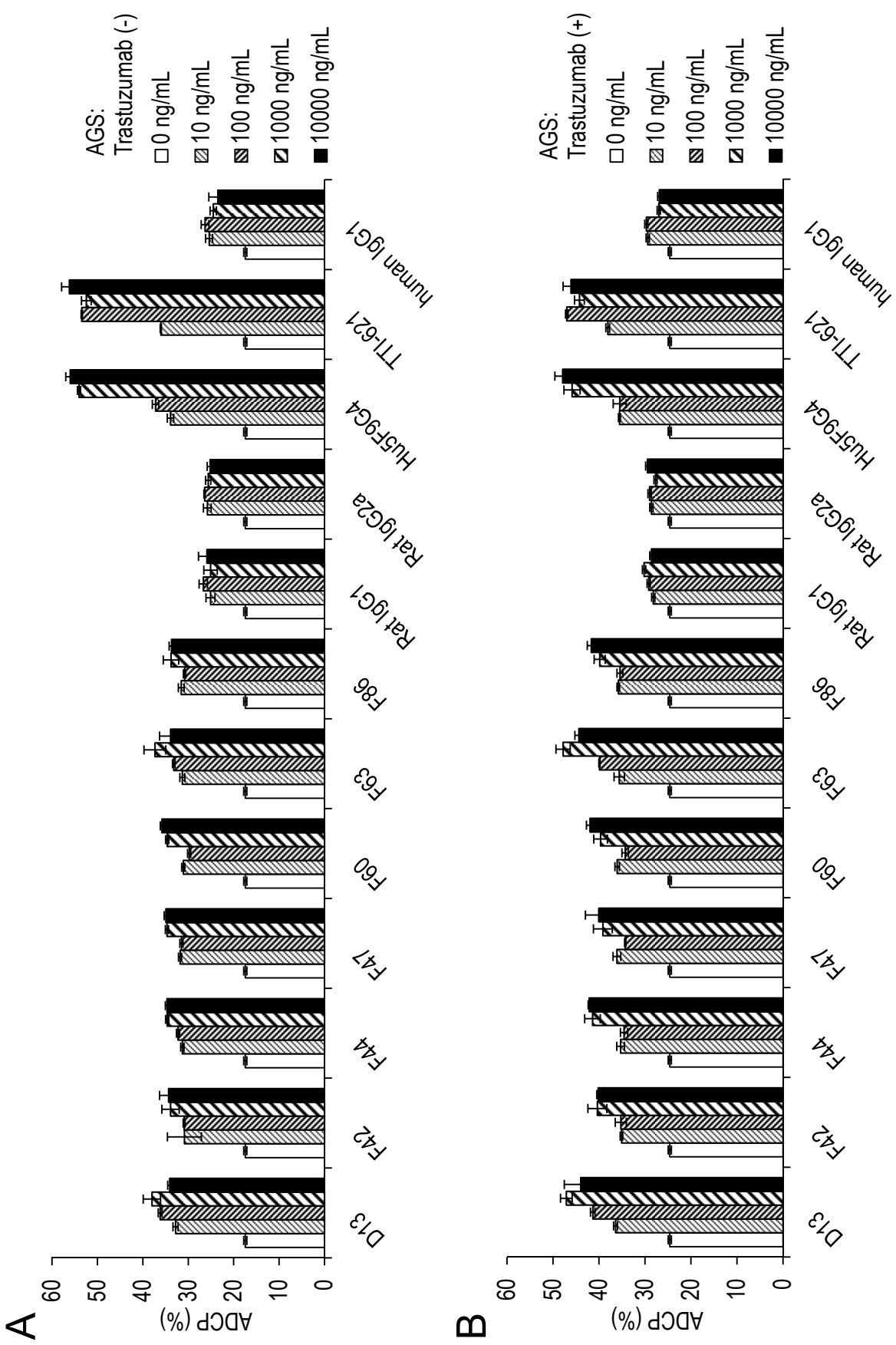


Fig. 6

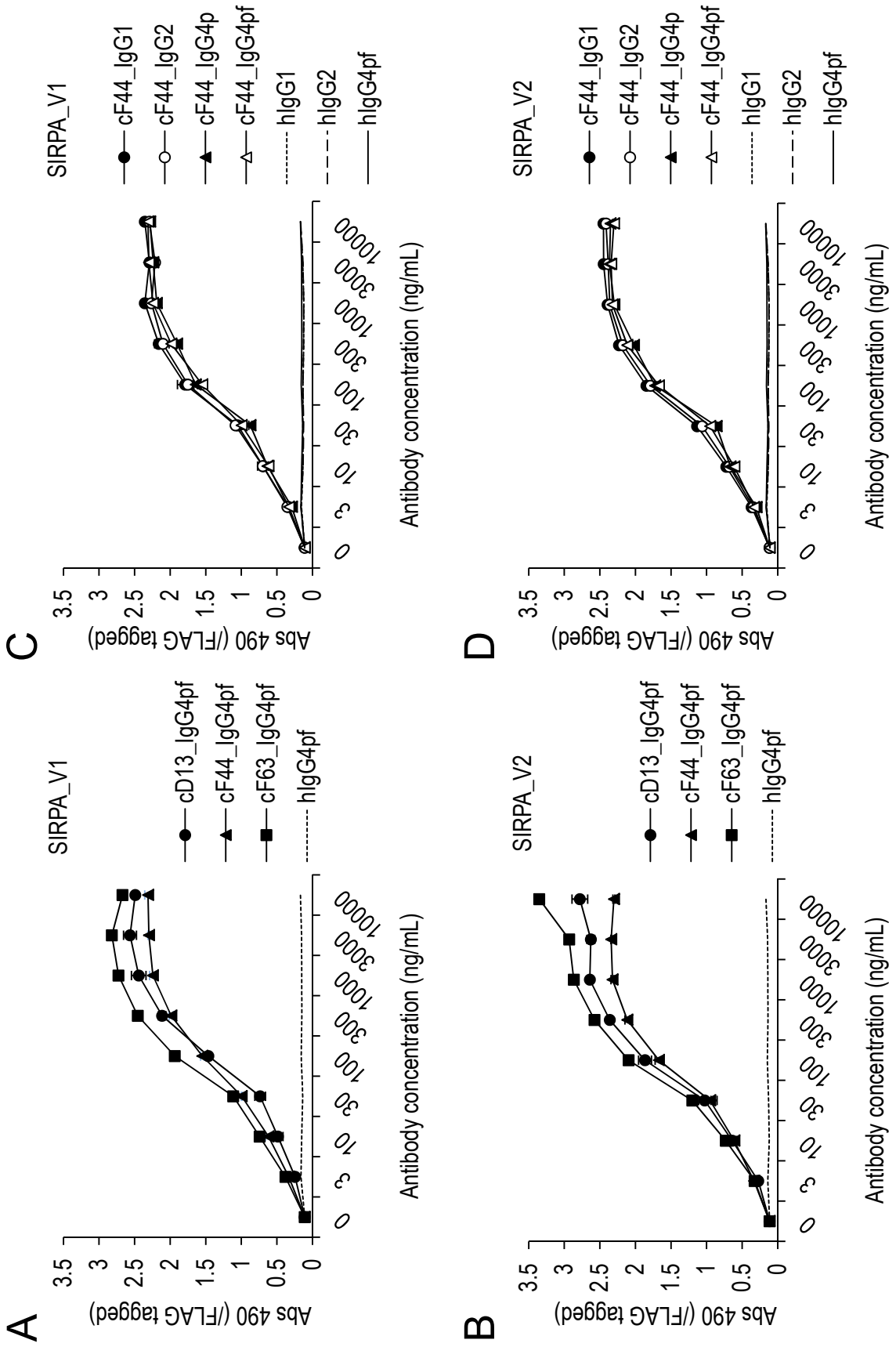


Fig. 7

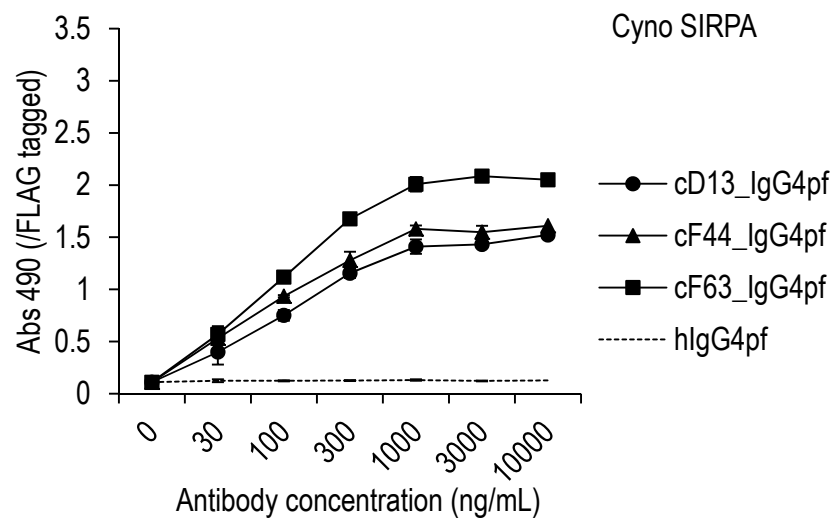


Fig. 8A

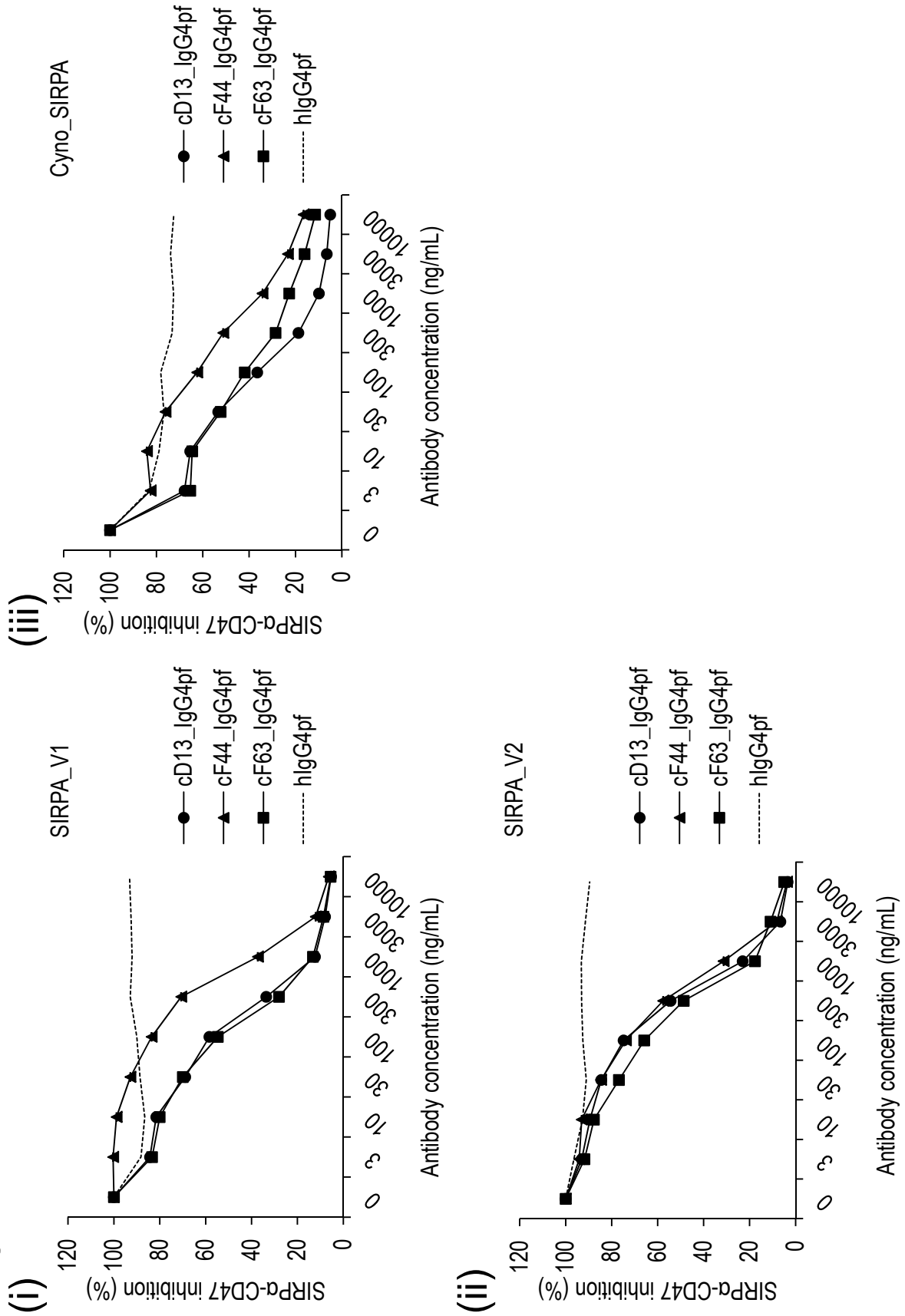


Fig. 8B

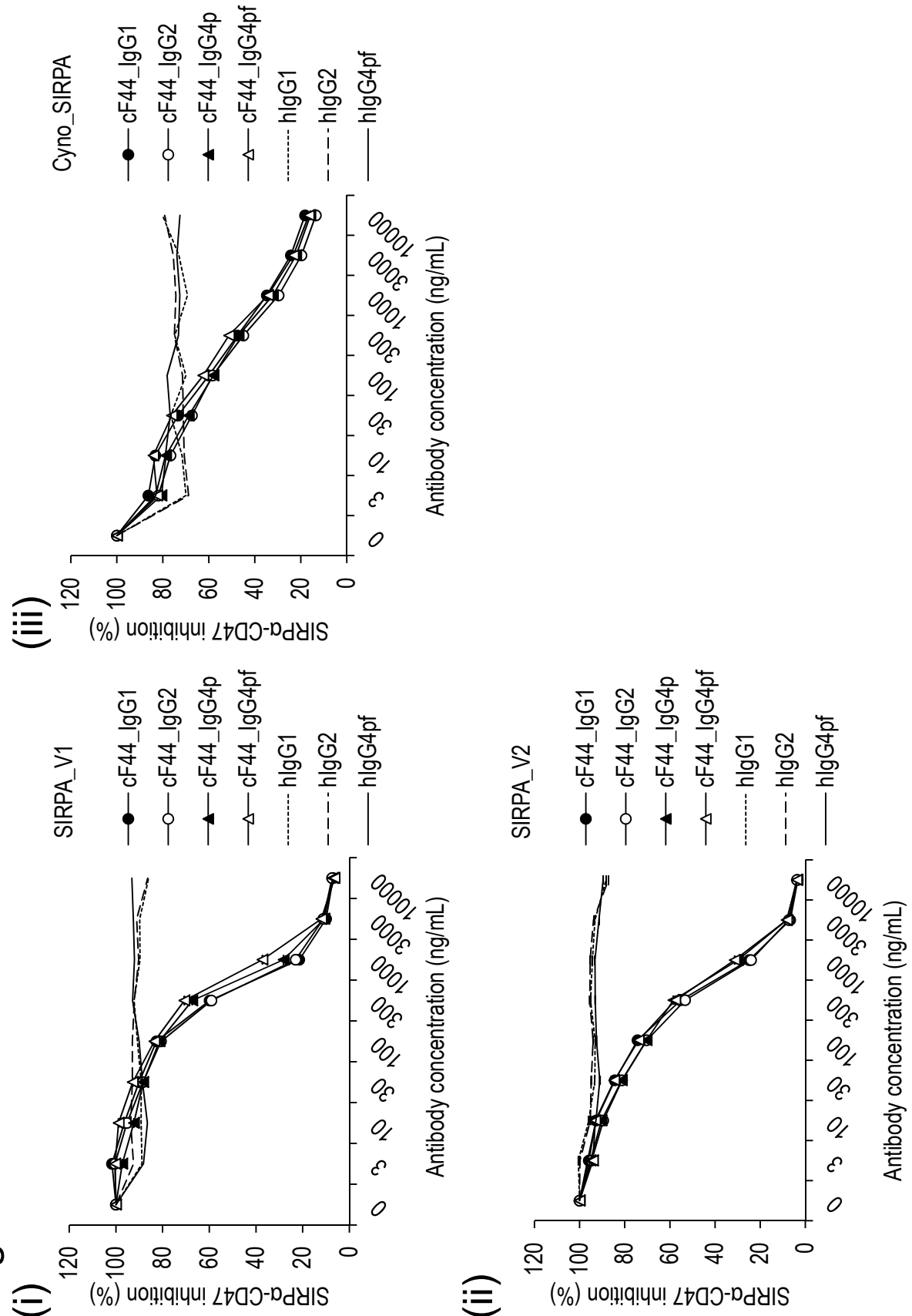


Fig. 9

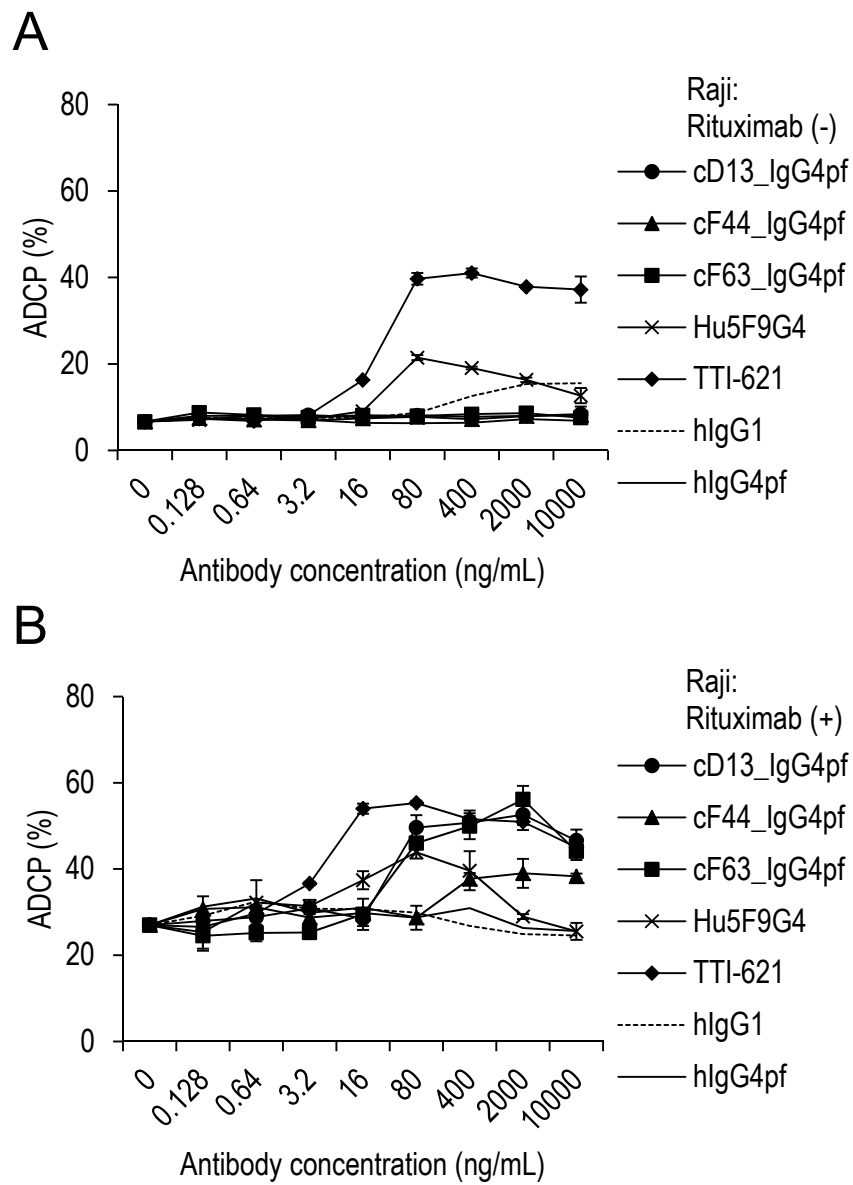


Fig. 10

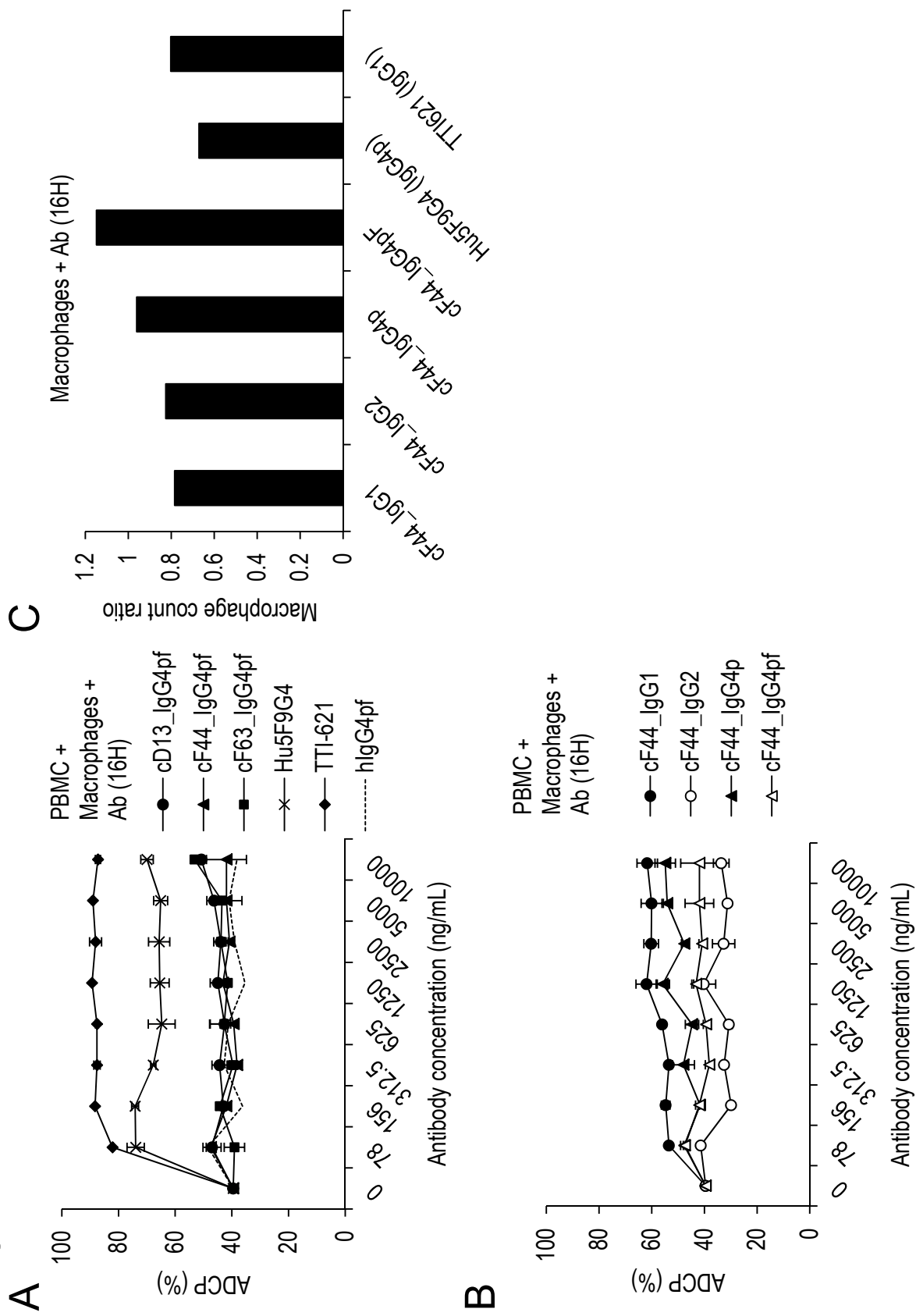


Fig. 11

cD13_H	1	MKHLWFFLLVAA	PRWVLSEVQLVESGGGLVQ	PGRSLKSLCLASGFTFSDY	GMIWVRQAP	60
hH1	1	Q.....	V.....R...A.....			60
hH2	1	V.....	R...A.....			60
cD13_H	61	GKGLEWVASIS	SSSYIYYADTVKGRFTISRENAKNTLFLHMTSLRSEDTALYYCARRY			120
hH1	61	S.....	D.S..R.Y.Q.N...A...V.....			120
hH2	61	S.....	D.S...Y.Q.N...A...V.....			120
cD13_H	121	GFNYPFDYWGQGV	MTVSS			139
hH1	121	T.....				139
hH2	121	T.....				139

Fig. 12

cD13_L	1	MVLQTQVFISLLLLWISGAYGDTVLTQSP-ALAVSLGQRVTTISCGASKSVRTYMHWYQQKS	59
hL2	1	AIQ.....SS.SA.V.....T.....P	60
hL3	1	Q.....SS.SA.V.....T.....P	60
hL4	1	DS.....A..N.....P	60
cD13_L	60	GQQPKLLIYSASNLEAGVPSRFSGSGGTFTLTIDPVEADDIANYYCQQSNEPPYTFGA	119
hL2	61	.KA.....SSLQPE.F.T.....Q	120
hL3	61	.K.....SSLQPE.F.T.....Q	120
hL4	61	SSLQ.E.V.....Q	120
cD13_L	120	GTKLELK	126
hL2	121	I.	127
hL3	121	I.	127
hL4	121	...V.I.	127

Fig. 13A

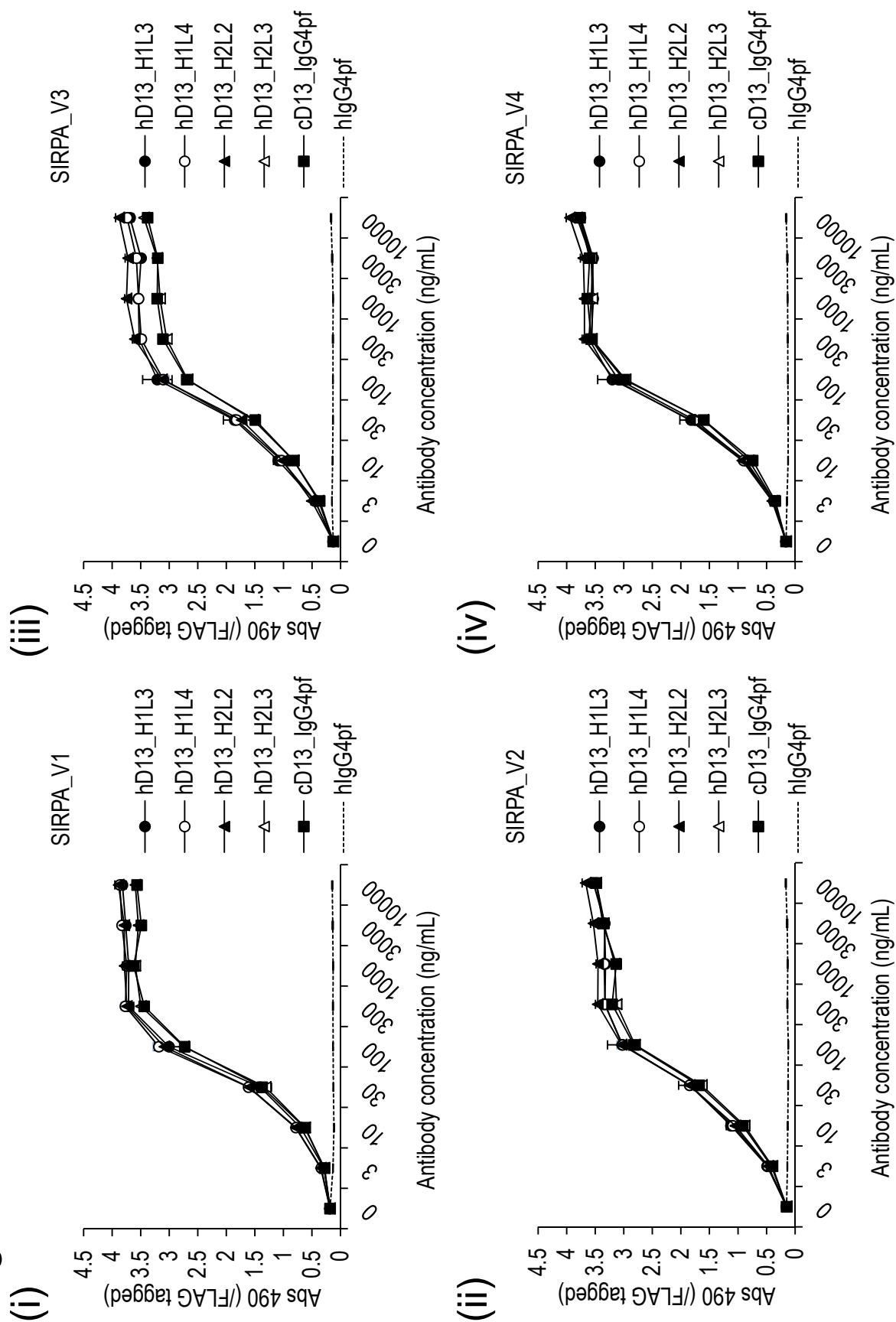


Fig. 13B

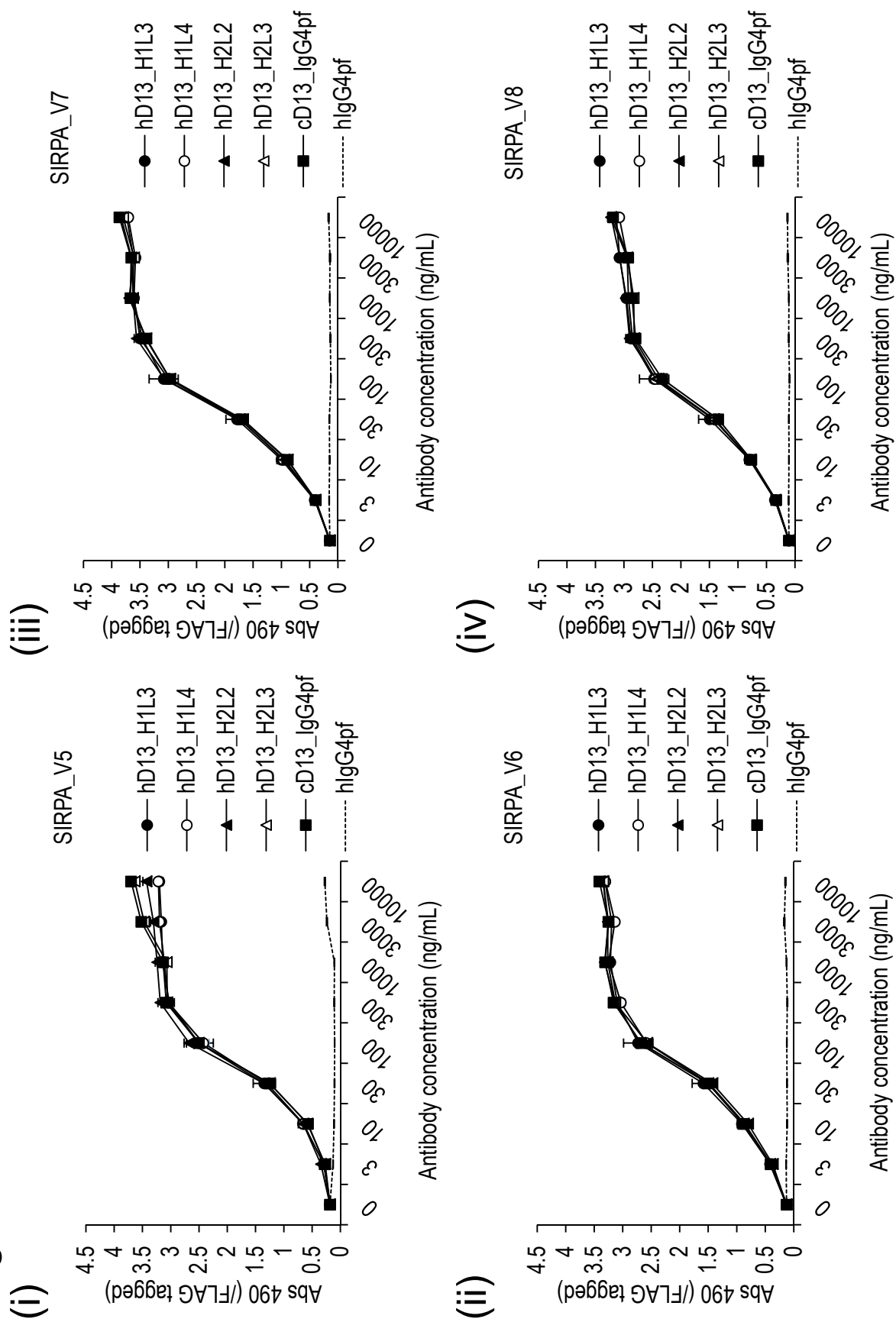


Fig. 13C

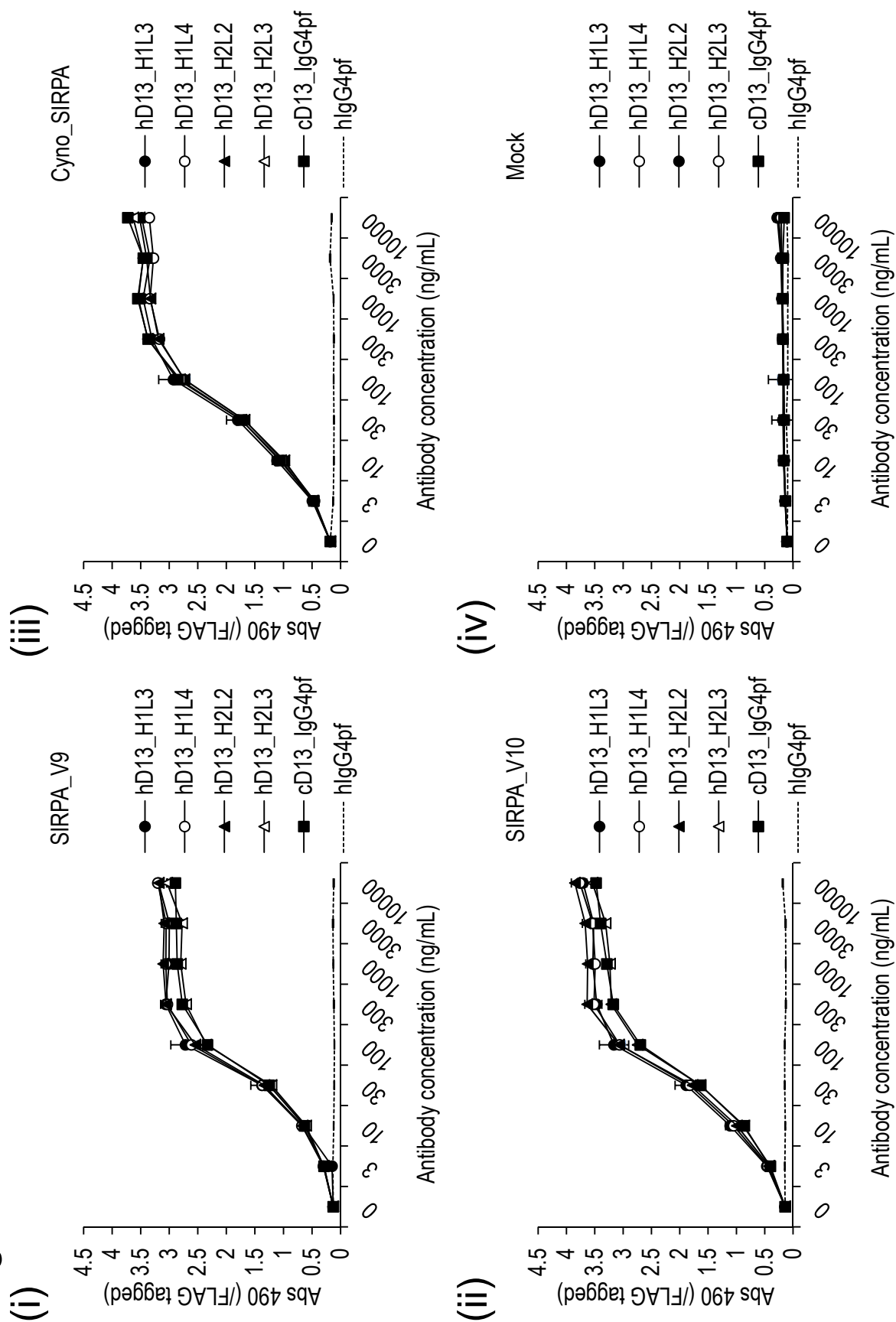


Fig. 14A

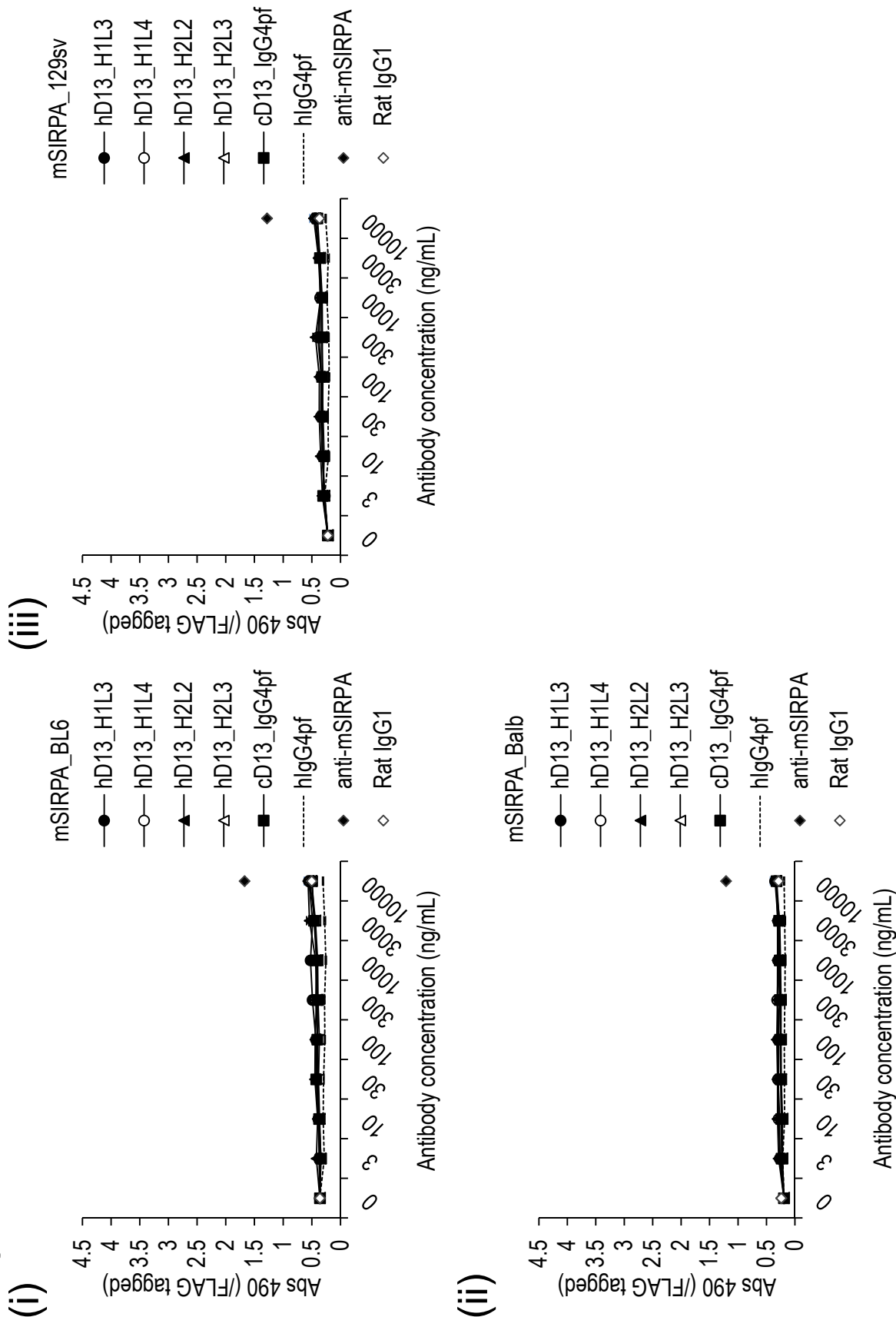
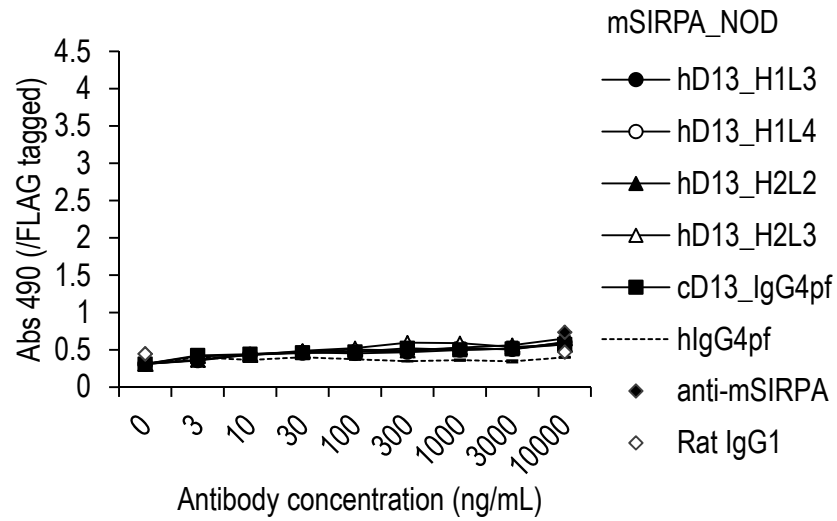


Fig. 14B

(i)



(ii)

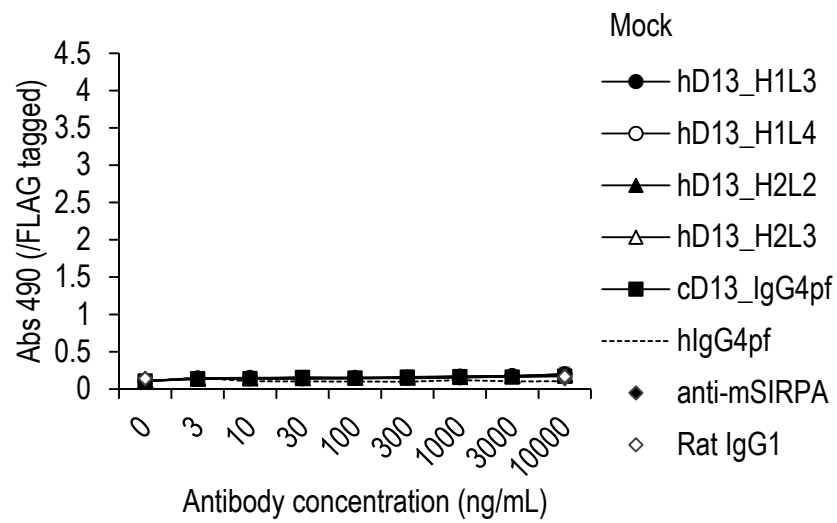


Fig. 15

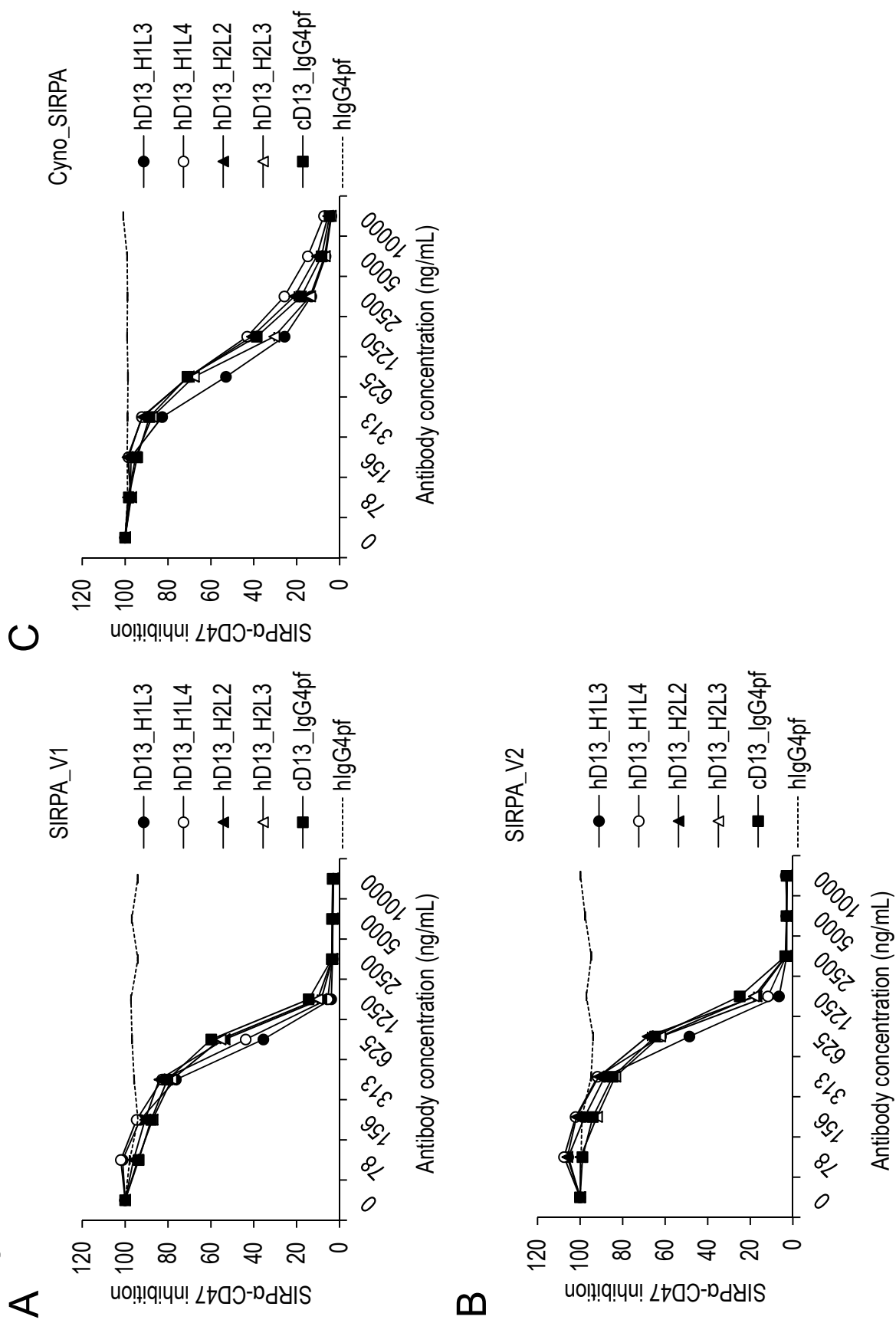


Fig. 16

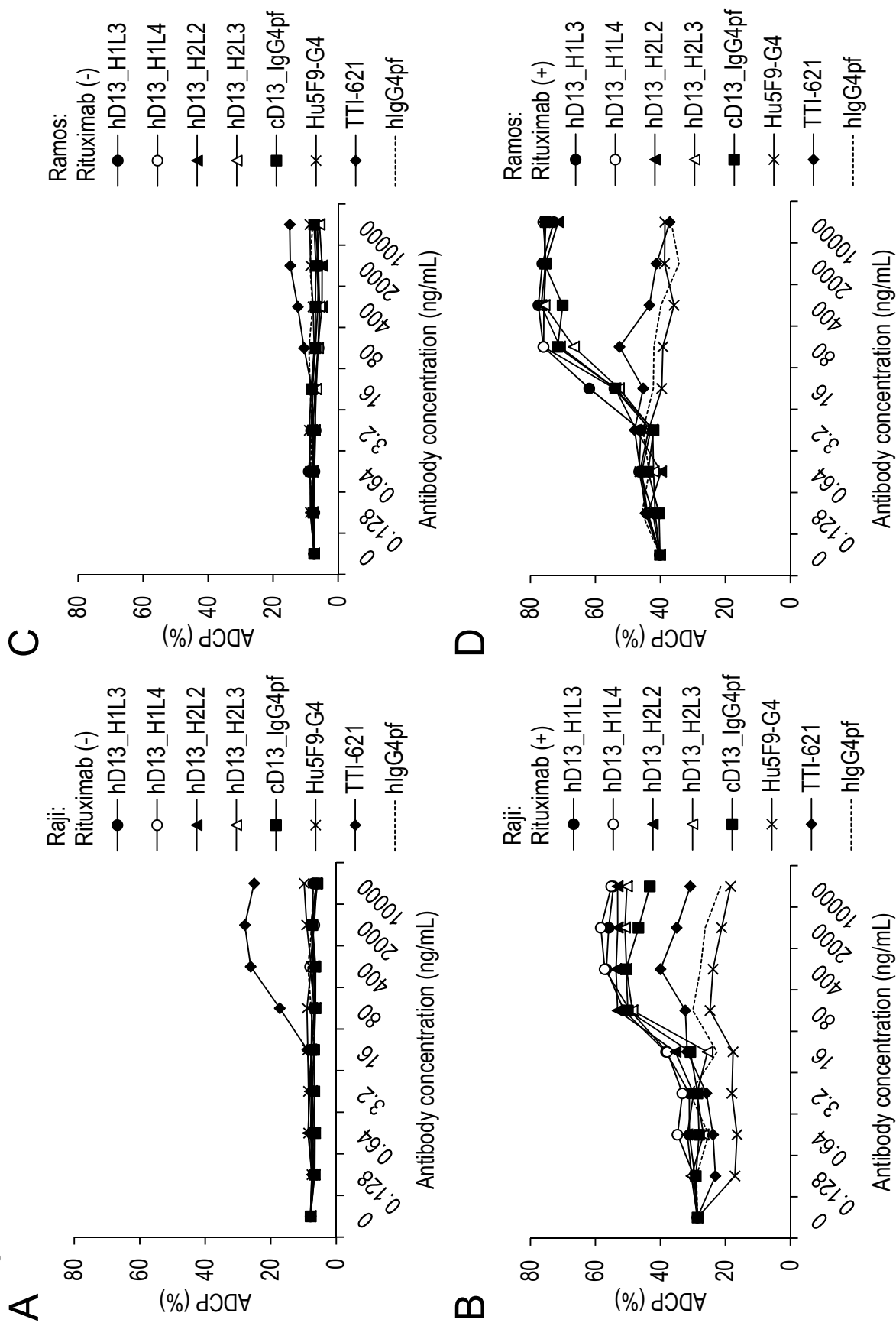


Fig. 17

SEQ ID NO: 22: Nucleotide sequence encoding cD13 light chain

```
ATGGTGCTGCAGACCCAGGTGTTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTA
CGGCGACACTGTGCTGACCCAGTCTCCTGCTTTGGCTGTGTCTCTAGGGCAGAGGG
TCACCATCTCTTGTGGGGCCAGCAAAAGTGTCCGTACATATATGCACTGGTACCAA
CAAAAATCGGGACAGCAACCCAAACTCCTGATCTATAGTGCATCCAACCTAGAGGC
TGGAGTCCCTTCCAGGTTTCAGTGGGAGTGGGTCTGGGACAGACTTTACCCTCACCA
TAGATCCTGTGGAGGCTGATGACATTGCAAACTATTACTGTCAGCAGAGTAATGAA
CCTCCGTACACGTTTGGAGCTGGGACCAAGCTGGAAGTGAACGGACGGTGGCCGC
CCCCTCCGTGTTTCATCTTCCCCCCTCCGACGAGCAGCTGAAGTCCGGCACCGCCT
CCGTGGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCAGTGGAAG
GTGGACAACGCCCTGCAGTCCGGGAAGTCCCAGGAGAGCGTGACCGAGCAGGACAG
CAAGGACAGCACCTACAGCCTGAGCAGCACCTGACCCTGAGCAAAGCCGACTACG
AGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGAGCTCCCCCGTC
ACCAAGAGCTTCAACAGGGGGGAGTGT
```

Signal sequence (1-60), variable region (61-378),
constant region (379-699)

SEQ ID NO: 23: Amino acid sequence of cD13 light chain
MVLQTQVFISLLWISGAYGDTVLTQSPALAVSLGQRVTISCGASKSVRTYMHWYQ
QKSGQQPKLLIYSASNLEAGVPSRFSGSGSGTDFTLTIDPVEADDIANYCYQQSNE
PPYTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPV
TKSFNRGEC

Signal sequence (1-20), variable region (21-126),
constant region (127-233)

Fig. 18

SEQ ID NO: 24: Nucleotide sequence encoding cD13 heavy chain

```
ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGAGGTACAGCTGGTGGAGTCTGGAGGAGGCTTAGTGCAGCCTGGAAGGTCCCTGA
AACTCTCCTGTTTAGCCTCTGGATTCACTTTCAGTGACTATGGAATGATCTGGGTT
CGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGCATCTATTAGTAGTAGTAGCAG
TTACATCTACTATGCAGACACAGTGAAGGGCCGATTACCATCTCCAGAGAAAATG
CCAAGAACACCCTGTTTCCTGCACATGACCAGTCTGAGGTCTGAAGACACTGCCTTG
TATTACTGTGCAAGAAGATACTATGGGTTTAACTACCCTTTTGATTACTGGGGCCA
AGGAGTCATGGTCACAGTCAGCTCAGCCTCCACCAAGGGCCCTAGCGTGTTCCCTC
TGGCCCCCTTG TAGCAGAAGCACCAGCGAGTCTACAGCCGCCCTGGGCTGCCTCGTG
AAGGACTACTTTCCCGAGCCCGTGACCGTGTCTGGAAGTCTGGCGCTCTGACAAG
CGGCGTGACACCTTTCCAGCCGTGCTGCAGAGCAGCGGCCTGTACTCTCTGTCCA
GCGTCGTGACTGTGCCCAGCAGCTCTCTGGGCACCAAGACCTACACCTGTAACGTG
GACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCC
TCCCTGCCCTCCTTGCCCAGCCCCCTGAAGCCGCGGGCGGACCCTCCGTGTTCCCTGT
TCCCCCCAAAGCCCCAAGGACACCCTGATGATCAGCCGGACCCCCGAAGTGACCTGC
GTGGTGGTGGATGTGTCCCAGGAAGATCCCAGAGGTGCAGTTCAATTGGTACGTGGA
CGGCGTGGAAGTGCACAACGCCAAGACCAAGCCTAGAGAGGAACAGTTCAACAGCA
CCTACCGGGTGGTGTCCGTGCTGACAGTGCTGCACCAGGACTGGCTGAACGGCAAA
GAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCAGCTCCATCGAGAAAACCAT
CAGCAAGGCCAAGGGCCAGCCCCGCGAACCCCAGGTGTACACACTGCCTCCAAGCC
AGGAAGAGATGACCAAGAATCAGGTGTCCCTGACCTGTCTCGTGAAAGGCTTCTAC
CCCTCCGATATCGCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAA
GACCACCCCCCTGTGCTGGACTCCGATGGCTCATTCTTCCTGTACAGCAGACTGA
CCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTTCACTGCTCCGTGATGCAC
GAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGAGCCTGGGCAAA
```

Signal sequence (1-57), variable region (58-417),
constant region (418-1398)

SEQ ID NO: 25: Amino acid sequence of cD13 heavy chain

```
MKHLWFFLLLVAAPRWVLSEVQLVESGGGLVQPGRSLKLSCLASGFTFSDYGMIWV
RQAPGKGLEWVASISSSSSYIYYADTVKGRFTISRENAKNTLFLHMTSLRSED TAL
YYCARRYYGFNYPFDYWGGQVMVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV
DHKPSNTKVKDRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTC
VVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFY
PSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH
EALHNHYTQKSLSLSLGLK
```

Signal sequence (1-19), variable region (20-139),
constant region (140-466)

Fig. 19

SEQ ID NO: 26: Nucleotide sequence encoding cF44 light chain

```
ATGGTGCTGCAGACCCAGGTGTTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTA
CGGCGATGTCCAGATGACCCAGTCTCCATCTAATCTTGCTGCCTCTCCTGGAGAAA
GTGTTTCCATCAATTGCAAGGCAAGTAAGAGCATTAGCAAGTATTTAGCCTGGTAT
CAACAGAAACCTGGGAAAGCAAATAAGCTTCTTATCTACTCTGGGTCAACTTTGCA
ATCTGGAACCTCCATCGAGGTTTCAGTGGCAGTGGATCTGGTACAGATTTCACTCTCA
CCATCAGAAACCTGGAGCCTGAAGATTTTGGACTCTATTACTGTCAACAGCATAAT
GAATACCCACCCACGTTTGGAGCTGGGACCAAGTTGGAACCTGAAACGGACGGTGGC
CGCCCCCTCCGTGTTTCATCTTCCCCCCCCTCCGACGAGCAGCTGAAGTCCGGCACCG
CCTCCGTGGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCAGTGG
AAGGTGGACAACGCCCTGCAGTCCGGGAACTCCCAGGAGAGCGTGACCGAGCAGGA
CAGCAAGGACAGCACCTACAGCCTGAGCAGCACCCCTGACCCTGAGCAAAGCCGACT
ACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGAGCTCCCCC
GTCACCAAGAGCTTCAACAGGGGGGAGTGT
```

Signal sequence (1-60), variable region (61-381),
constant region (382-702)

SEQ ID NO: 27: Amino acid sequence of cF44 light chain
MVLQTQVFISLLWISGAYGDVQMTQSPSNLAASPGESVSINCKASKSISKYLAWY
QQKPGKANKLLIYSGSTLQSGTPSRFSGSGSGTDFTLTIRNLEPEDFGLYYCQQHN
EYPPTFGAGTKLELKRRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSP
VTKSFNRGEC

Signal sequence (1-20), variable region (21-127),
constant region (128-234)

Fig. 20

SEQ ID NO: 28: Nucleotide sequence encoding cF44 heavy chain

```
ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGAGGTGCAGCTGGTGAATCTGGGGGAGGCTTAGTGCAGCCTGGAAGGTCCCTGA
AACTCTCCTGTGCAGCCTCAGGATTCACTTTCAGTAACTATTACATGGCCTGGGTC
CGCCAGGCTCCAACGAAGGGTCTGGAGTGGGTCACATACATTACTACTGGTGGTGG
TAGCACTTACTTTTCGAGACTCCGTGAAGGGCCGATTCACTATCTCCAGAGATAATG
CAGAAAGCACCCCTATACCTGCAAAATGGACAGTCTGAGGTCTGAGGACACGGCCACT
TATTACTGTACAGCAGCTAACTACGGAGGGTCTTACTTTGATTACTGGGGCCAAGG
AGTCATGGTGCAGTCAGCTCAGCCTCCACCAAGGGCCCTAGCGTGTTCCTCTGG
CCCCTTGTAGCAGAAGCACCAAGCGAGTCTACAGCCGCCCTGGGCTGCCTCGTGAAG
GACTACTTTCCCGAGCCCGTGACCGTGTCTGGAATCTGGCGCTCTGACAAGCGG
CGTGACACACCTTTCCAGCCGTGCTGCAGAGCAGCGGCCTGTACTCTCTGTCCAGCG
TCGTGACTGTGCCCAGCAGCTCTCTGGGCACCAAGACCTACACCTGTAACGTGGAC
CACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGAATCTAAGTACGGCCCTCC
CTGCCCTCCTTGCCCAGCCCCCTGAAGCCGCGGGCGGACCCTCCGTGTTCTCTGTTCC
CCCCAAAGCCCAAGGACACCCCTGATGATCAGCCGGACCCCCGAAGTGACCTGCGTG
GTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGTGGACGG
CGTGGAAGTGCACAACGCCAAGACCAAGCCTAGAGAGGAACAGTTCAACAGCACCT
ACCGGGTGGTGTCCGTGCTGACAGTGCTGCACCAGGACTGGCTGAACGGCAAAGAG
TACAAGTGCAAGGTGTCCAACAAGGGCCTGCCAGCTCCATCGAGAAAACCATCAG
CAAGGCCAAGGGCCAGCCCCGCGAACCCAGGTGTACACACTGCCTCCAAGCCAGG
AAGAGATGACCAAGAATCAGGTGTCCCTGACCTGTCTCGTGAAAGGCTTCTACCCC
TCCGATATCGCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGAC
CACCCCCCTGTGCTGGACTCCGATGGCTCATTCTTCTGTACAGCAGACTGACCG
TGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTTCAGCTGCTCCGTGATGCACGAG
GCCCTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGAGCCTGGGCAA
```

Signal sequence (1-57), variable region (58-414),
constant region (415-1395)

SEQ ID NO: 29: Amino acid sequence of cF44 heavy chain

```
MKHLWFFLLLVAAAPRWVLSEVQLVESGGGLVQPGRSLKLSCAASGFTFSNYMAWV
RQAPTKGLEWVTYIITGGGSTYFRDSVKGRFTISRDNASTLYLQMDSLRSEDAT
YYCTAANYGGSYFDYWGQGMVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGKTYTCNVD
HKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDNLNGKE
YKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVME
ALHNHYTQKSLSLSLGK
```

Signal sequence (1-19), variable region (20-138),
constant region (139-465)

Fig. 21

SEQ ID NO: 30: Nucleotide sequence encoding cF63 light chain

```
ATGGTGCTGCAGACCCAGGTGTTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTA
CGGCCAGTTCACGCTGACTCAACCAAAGTCCGTGTCAGGAGCTTTAAGAAGCACTA
TCACCATTCCCTGTGAGCGCAGCAGTGGTGACATTGGAGATAGCTATGTGAGCTGG
TACCAGCGACACTTGGGAAGACCCCCCATCAATGTGATCTATGCTGATGATCAAAG
ACCATCTGAAGTGTCTGATCGGTTCTCGGGCTCCATCGACAGCTCCTCTAACTCAG
CCTCACTGACCATCACTAATCTGCAGATGGATGATGAGGCCGACTACTTCTGTCAG
TCTTACGATAGTAAGATTGACATTTTTCGGCGGTGGAACCAAGCTCACTGTCCTAGG
CCAGCCTAAGGCTGCCCCTAGCGTGACCCTGTTCCCTCCTTCCAGCGAGGAGCTTC
AAGCTAACAAGGCCACCCTGGTGTGTCTTATCTCTGACTTCTACCCTGGCGCTGTG
ACCGTGGCCTGGAAGGCTGACAGCTCCCCTGTGAAGGCCGGAGTGGAGACCACCAC
ACCTAGCAAGCAGTCTAACAACAAGTACGCTGCCAGCTCCTACCTGAGCCTTACCC
CTGAGCAGTGGAAGTCTCACAGAAGCTACTCCTGTCAAGTGACCCACGAGGGCAGC
ACCGTGGAGAAGACCGTGGCTCCTACCGAGTGTTCC
```

Signal sequence (1-60), variable region (61-390),
constant region (391-708)

SEQ ID NO: 31: Amino acid sequence of cF63 light chain

```
MVLQTQVFISLLWISGAYGQFTLTQPKSVSGALRSTITIPCERSSSGDIGDSYVSW
YQRHLGRPPINVIYADDQRPSEVSDRFSGSIDSSSNSASLTITNLQMDDEADYFCQ
SYDSKIDIFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAV
TVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGS
TVEKTVAPTECS
```

Signal sequence (1-20), variable region (21-130),
constant region (131-236)

Fig. 22

SEQ ID NO: 32: Nucleotide sequence encoding cF63 heavy chain

```
ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CCAGGTGCAGCTGAAGGAGTCAGGACCTGGTCTGGTGCAGCCCTCAGAGACCCTGT
CCCTCACCTGCACTGTCTCTGGGTTCTCACTAGCCAGCTATAGTTTAAAGTTGGGT
CGCCAGCCTTCAGGAAAAGGTCCTGAGTGGATGGGAAGAATGTACTATGATGGAGA
CACAGCATATAATTCACTCTCAAATCCCGACTGAGCATCAGCAGGGACACCTCCA
AGAACCAAGTTTTCTTAAAAATGAACAGTCTGCAAACCTGATGACACAGGCACCTAC
TACTGTACCAGAGATAGGAGTATGTTTGGTACGGATTATCCCCACTGGTACTTTGA
CTTCTGGGGCCCAGGAACCATGGTCACCGTGAGCTCAGCCTCCACCAAGGGCCCTA
GCGTGTTCCCTCTGGCCCCCTGTAGCAGAAGCACCAGCGAGTCTACAGCCGCCCTG
GGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTGACCGTGTCTGGAACCTCTGG
CGCTCTGACAAGCGGCGTGACACCTTTCCAGCCGTGCTGCAGAGCAGCGGCCTGT
ACTCTCTGTCCAGCGTCTGTGACTGTGCCCAGCAGCTCTCTGGGCACCAAGACCTAC
ACCTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGAATC
TAAGTACGGCCCTCCCTGCCCTCCTTGCCCAGCCCCCTGAAGCCGCGGGCGGACCCT
CCGTGTTCTGTTCCTCCCCCAAGCCCAAGGACACCCTGATGATCAGCCGGACCCCC
GAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAA
TTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCTAGAGAGGAAC
AGTTCAACAGCACCTACCGGGTGGTGTCCGTGCTGACAGTGCTGCACCAGGACTGG
CTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCAGCTCCAT
CGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAACCCCAGGTGTACACAC
TGCTCTCAAGCCAGGAAGAGATGACCAAGAATCAGGTGTCCCTGACCTGTCTCGTG
AAAGGCTTCTACCCCTCCGATATCGCCGTGGAATGGGAGAGCAACGGCCAGCCGA
GAACAACCTACAAGACCACCCCCCTGTGCTGGACTCCGATGGCTCATTCTTCCTGT
ACAGCAGACTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTTCAGCTGC
TCCGTGATGCACGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGAG
CCTGGGCAAA
```

Signal sequence (1-57), variable region (58-429),
constant region (430-1410)

SEQ ID NO: 33: Amino acid sequence of cF63 heavy chain

```
MKHLWFFLLLVAAPRWVLSQVQLKESGPGLVQPSETLSLTCTVSGFSLASYSLSWV
RQPSGKGPEWMGRMYDGDYNSALKSRLSISRDTSKNQVFLKMNSLQTDGTGY
YCTRDRSMFGTDYPHWYFDWGPVTMVTVSSASTKGPSVFPLAPCSRSTSESTAAL
GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKEY
TCNVDPKPSNTKVDKRVESKYGPPCPPAPEAAGGPSVFLFPPKPKDTLMISRTPE
VTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDW
LNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLV
KGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSC
SVMHEALHNHYTQKSLSLGLK
```

Signal sequence (1-19), variable region (20-143),
constant region (144-470)

Fig. 23

SEQ ID NO: 34: Nucleotide sequence encoding hL2

ATGGTGCTGCAGACCCAGGTGTTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTA
CGGCGCCATTCAGCTGACACAGAGCCCTAGCAGCCTGAGCGCCTCTGTGGGCCAGA
GAGTGACCATTACCTGCGGCGCCAGCAAGAGCGTGCGGACCTACATGCACTGGTAT
CAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAGCGCCTCCAATCTGGA
AGCCGGCGTGCCAGCAGATTTTCCGGCTCTGGCAGCGGCACCGACTTCACCCTGA
CAATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCTACTACTGCCAGCAGAGCAAC
GAGCCCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGCGTACGGTGGC
CGCCCCCTCCGTGTTTCATCTTCCCCCCCCTCCGACGAGCAGCTGAAGTCCGGCACCG
CCTCCGTGGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCAGTGG
AAGGTGGACAACGCCCTGCAGTCCGGGAACCTCCAGGAGAGCGTGACCGAGCAGGA
CAGCAAGGACAGCACCTACAGCCTGAGCAGCACCTGACCCTGAGCAAAGCCGACT
ACGAGAAGCACAAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGAGCTCCCCC
GTCACCAAGAGCTTCAACAGGGGGGAGTGT

Signal sequence (1-60), variable region (61-381),
constant region (382-702)

SEQ ID NO: 35: Amino acid sequence of hL2

MVLQTQVFISLLLWISGAYGAIQLTQSPSSLSASVGQRVTITCGASKSVRTYMHY
QQKPGKAPKLLIYSASNLEAGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSN
EPPYTFGQGKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSP
VTKSFNRGEC

Signal sequence (1-20), variable region (21-127),
constant region (128-234)

Fig. 24

SEQ ID NO: 36: Nucleotide sequence encoding hL3

ATGGTGCTGCAGACCCAGGTGTTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTA
CGGCGATACCCAGCTGACACAGAGCCCTAGCAGCCTGTCTGCCAGCGTGGGCCAGA
GAGTGACCATTACCTGCGGCGCCAGCAAGAGCGTGCGGACCTACATGCACTGGTAT
CAGCAGAAGCCCGGCAAGCAGCCCAAGCTGCTGATCTACAGCGCCTCCAACCTGGA
AGCCGGCGTGCCAGCAGATTTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGA
CAATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCTACTACTGCCAGCAGAGCAAC
GAGCCCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGCGTACGGTGGC
CGCCCCCTCCGTGTTTCATCTTCCCCCCCCTCCGACGAGCAGCTGAAGTCCGGCACCG
CCTCCGTGGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCAGTGG
AAGGTGGACAACGCCCTGCAGTCCGGGAACCTCCAGGAGAGCGTGACCGAGCAGGA
CAGCAAGGACAGCACCTACAGCCTGAGCAGCACCTGACCCTGAGCAAAGCCGACT
ACGAGAAGCACAAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGAGCTCCCCC
GTCACCAAGAGCTTCAACAGGGGGGAGTGT

Signal sequence (1-60), variable region (61-381),
constant region (382-702)

SEQ ID NO: 37: Amino acid sequence of hL3

MVLQTQVFISLLLWISGAYGDTQLTQSPSSLSASVGQRVTITCGASKSVRTYMHWY
QQKPGKQPKLLIYSASNLEAGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSN
EPPYTFGQGKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDSSTLSKADYEKHKVYACEVTHQGLSSP
VTKSFNRGEC

Signal sequence (1-20), variable region (21-127),
constant region (128-234)

Fig. 25

SEQ ID NO: 38: Nucleotide sequence encoding hL4

```
ATGGTGCTGCAGACCCAGGTGTTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTA
CGGCGATACCGTGCTGACCCAGAGCCCTGATAGCCTGGCCGTGTCCCTGGGACAGA
GAGCCACCATCAATTGCGGCGCCAGCAAGAGCGTGCGGACCTACATGCACTGGTAT
CAGCAGAAGCCCGGCCAGCAGCCCAAGCTGCTGATCTACAGCGCCTCCAACCTGGA
AGCCGGCGTGCCAGCAGATTTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGA
CAATCAGCTCCCTGCAGGCCGAGGACGTGGCCGTGTACTACTGCCAGCAGAGCAAC
GAGCCCCCTACACCTTTGGCCAGGGCACCAAGGTGGAAATCAAGCGTACGGTGGC
CGCCCCCTCCGTGTTTCATCTTCCCCCCCCTCCGACGAGCAGCTGAAGTCCGGCACCG
CCTCCGTGGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCAGTGG
AAGGTGGACAACGCCCTGCAGTCCGGGAAGTCCCAGGAGAGCGTGACCGAGCAGGA
CAGCAAGGACAGCACCTACAGCCTGAGCAGCACCTGACCCTGAGCAAAGCCGACT
ACGAGAAGCACAAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGAGCTCCCCC
GTCACCAAGAGCTTCAACAGGGGGGAGTGT
```

Signal sequence (1-60), variable region (61-381),
constant region (382-702)

SEQ ID NO: 39: Amino acid sequence of hL4

```
MVLQTQVFISLLLWISGAYGDTVLTQSPDSLAVSLGQRATINCGASKSVRTYMHY
QQKPGQQPKLLIYSASNLEAGVPSRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSN
EPPYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSP
VTKSFNRGEC
```

Signal sequence (1-20), variable region (21-127),
constant region (128-234)

Fig. 26

SEQ ID NO: 40: Nucleotide sequence encoding hH1

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CCAGGTGCAGCTGGTGGAAATCTGGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGA
GACTGAGCTGTGCCGCCAGCGGCTTCACCTTCAGCGACTACGGCATGATCTGGGTG
CGCCAGGCCCTTGGCAAAGGCCTGGAATGGGTGGCCAGCATCAGCAGCAGCTCCAG
CTACATCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACAACA
GCAAGAACCGGCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTG
TACTATTGCGCCAGACGGTACTACGGCTTCAACTACCCCTTCGACTACTGGGGCCA
GGGCACAATGGTCAACGTCAGCTCAGCCTCCACCAAGGGCCCTAGCGTGTTCCCTC
TGGCCCCTTGTAGCAGAAGCACCAGCGAGTCTACAGCCGCCCTGGGCTGCCTCGTG
AAGGACTACTTTCCCGAGCCCGTGACCGTGTCTGGAATCTGGCGCTCTGACAAG
CGGCGTGCACACCTTTCCAGCCGTGCTGCAGAGCAGCGGCCTGTACTCTCTGTCCA
GCGTCGTGACTGTGCCCAGCAGCTCTCTGGGCACCAAGACCTACACCTGTAACGTG
GACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAACTCTAAGTACGGCCC
TCCCTGCCCTCCTTGCCAGCCCCCTGAAGCCGCGGGCGGACCCTCCGTGTTCCCTGT
TCCCCCAAAGCCCAAGGACACCCTGATGATCAGCCGGACCCCCGAAGTGACCTGC
GTGGTGGTGGATGTGTCCCAGGAAGATCCCAGAGTGCAGTTCAATTGGTACGTGGA
CGGCGTGGAAAGTGCACAACGCCAAGACCAAGCCTAGAGAGGAACAGTTCAACAGCA
CCTACCGGGTGGTGTCCGTGCTGACAGTGTGACACAGGACTGGCTGAACGGCAAA
GAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCAGCTCCATCGAGAAAACCAT
CAGCAAGGCCAAGGGCCAGCCCCGCGAACCCCAGGTGTACACACTGCCTCCAAGCC
AGGAAGAGATGACCAAGAATCAGGTGTCCCTGACCTGTCTCGTGAAAGGCTTCTAC
CCCTCCGATATCGCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAA
GACCACCCCCCTGTGCTGGACTCCGATGGCTCATTCTTCCCTGTACAGCAGACTGA
CCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTTACGCTGCTCCGTGATGCAC
GAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGAGCCTGGGCAAA

Signal sequence (1-57), variable region (58-417),
constant region (418-1398)

SEQ ID NO: 41: Amino acid sequence of hH1

MKHLWFFLLLVAAPRWVLSQVQLVESGGGVVQPGRSLRLSCAASGFTFSDYGMIVV
RQAPGKGLEWVASISSSSSYIYYADSVKGRFTISRDN SKNRLYLQMNSLR AEDTAV
YYCARRYYGFNYPFDYWQGQTMVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLG TKTYTCNV
DHKPSNTKVDKRVESKYGPCCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTC
VVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKGLPSSIEKTI SKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFY
PSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH
EALHNHYTQKSLSLSLGK

Signal sequence (1-19), variable region (20-139),
constant region (140-466)

Fig. 27

SEQ ID NO: 42: Nucleotide sequence encoding hH2

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGAAGTGCAGCTGGTGGAATCTGGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGA
GACTGAGCTGTGCCGCCAGCGGCTTCACCTTCAGCGACTACGGCATGATCTGGGTG
CGCCAGGCCCTGGCAAAGGCCTGGAATGGGTGGCCAGCATCAGCAGCAGCTCCAG
CTACATCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACAACA
GCAAGAACACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTG
TACTATTGCGCCAGACGGTACTACGGCTTCAACTACCCCTTCGACTACTGGGGCCA
GGGCACAATGGTCAACGTCAGCTCAGCCTCCACCAAGGGCCCTAGCGTGTTCCCTC
TGGCCCCTTGTAGCAGAAGCACCAGCGAGTCTACAGCCGCCCTGGGCTGCCTCGTG
AAGGACTACTTTCCCGAGCCCGTGACCGTGTCTGGAATCTGGCGCTCTGACAAG
CGGCGTGCACACCTTTCCAGCCGTGCTGCAGAGCAGCGGCCTGTACTCTCTGTCCA
GCGTCGTGACTGTGCCCAGCAGCTCTCTGGGCACCAAGACCTACACCTGTAACGTG
GACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAACTCTAAGTACGGCCC
TCCCTGCCCTCCTTGCCAGCCCCCTGAAGCCGCGGGCGGACCCTCCGTGTTCCCTGT
TCCCCCAAGGCCAAGGACACCTGATGATCAGCCGGACCCCGAAGTGACCTGC
GTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGTGGA
CGGCGTGGAAAGTGCACAACGCCAAGACCAAGCCTAGAGAGGAACAGTTCAACAGCA
CCTACCGGGTGGTGTCCGTGCTGACAGTGTGACACAGGACTGGCTGAACGGCAAA
GAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCAGCTCCATCGAGAAAACCAT
CAGCAAGGCCAAGGGCCAGCCCCGCGAACCCAGGTGTACACACTGCCTCCAAGCC
AGGAAGAGATGACCAAGAATCAGGTGTCCCTGACCTGTCTCGTGAAAGGCTTCTAC
CCCTCCGATATCGCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAA
GACCACCCCCCTGTGCTGGACTCCGATGGCTCATTCTTCCCTGTACAGCAGACTGA
CCGTGGACAAGAGCCGTGGCAGGAAGGCAACGTGTTTACGCTGCTCCGTGATGCAC
GAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGAGCCTGGGCAA

Signal sequence (1-57), variable region (58-417),
constant region (418-1398)

SEQ ID NO: 43: Amino acid sequence of hH2

MKHLWFFLLLVAAPRWVLSEVQLVESGGGVVQGRSLRLSCAASGFTFSDYGMIVV
RQAPGKGLEWVASISSSSSYIYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAV
YYCARRYYGFNYPFDYWQGTMTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKTYTCNV
DHKPSNTKVDKRVESKYGPCCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTC
VVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFY
PSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH
EALHNHYTQKSLSLSLGK

Signal sequence (1-19), variable region (20-139),
constant region (140-466)

Fig. 28

SEQ ID NO: 1: D13 CDRL1
GASKSVRTYMH

SEQ ID NO: 2: D13 CDRL2
SASNLEA

SEQ ID NO: 3: D13 CDRL3
QQSNEPPYT

SEQ ID NO: 4: D13 CDRH1
GFTFSDYGMI

SEQ ID NO: 5: D13 CDRH2
SISSSSSYIY

SEQ ID NO: 6: D13 CDRH3
RYYGFNYPFDY

Fig. 29

SEQ ID NO: 7: F44 CDRL1
KASKSISKYLA

SEQ ID NO: 8: F44 CDRL2
SGSTLQS

SEQ ID NO: 9: F44 CDRL3
QQHNEYPPT

SEQ ID NO: 10: F44 CDRH1
GFTFSNYMA

SEQ ID NO: 11: F44 CDRH2
YITTGGGSTY

SEQ ID NO: 12: F44 CDRH3
ANYGGSYFDY

Fig. 30

SEQ ID NO: 13: F63 CDRL1
ERSSGDIGDSYVS

SEQ ID NO: 14: F63 CDRL2
ADDQRPS

SEQ ID NO: 15: F63 CDRL3
QSYDSKIDI

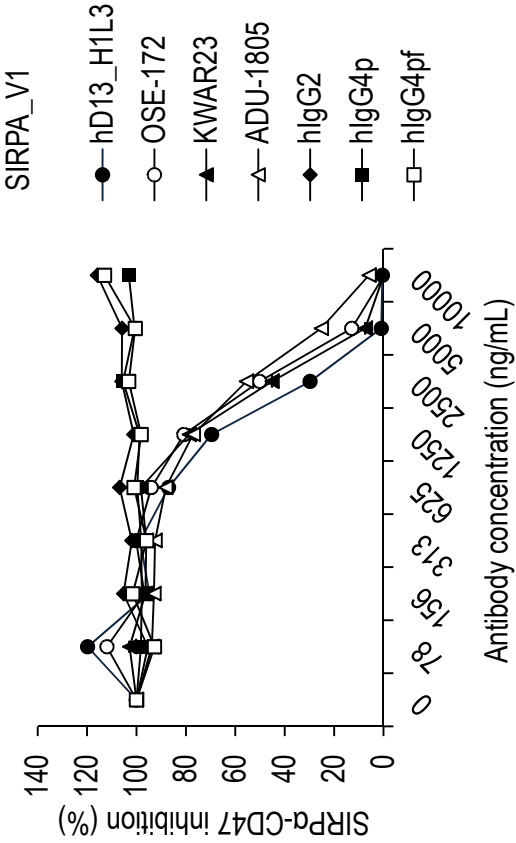
SEQ ID NO: 16: F63 CDRH1
GFSLASYSLS

SEQ ID NO: 17: F63 CDRH2
RMYDGDGA

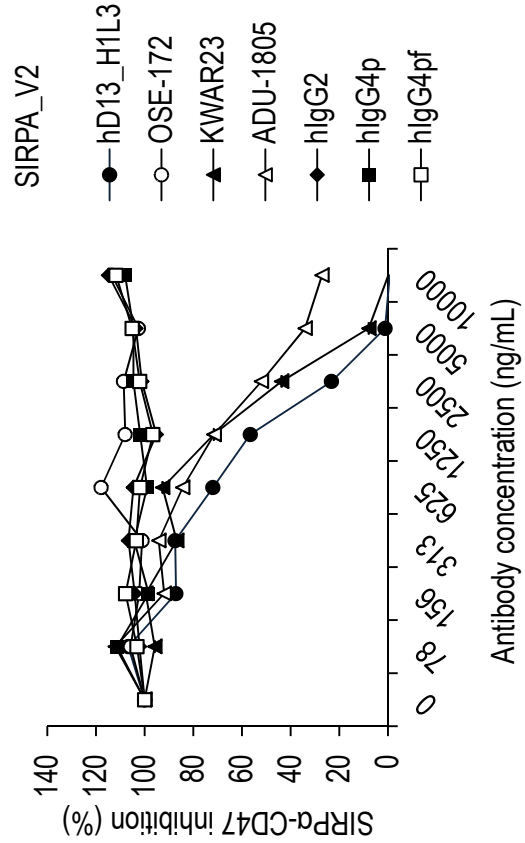
SEQ ID NO: 18: F63 CDRH3
DRSMFGTDYPHWYFDF

Fig. 31

A



B



C

	IC50 (ng/mL)	
	V1	V2
hD13_H1L3	1578	1303
OSE-172	2320	Above quantitation limit
KWAR	2244	2186
ADU-1805	2968	2119

Fig. 32

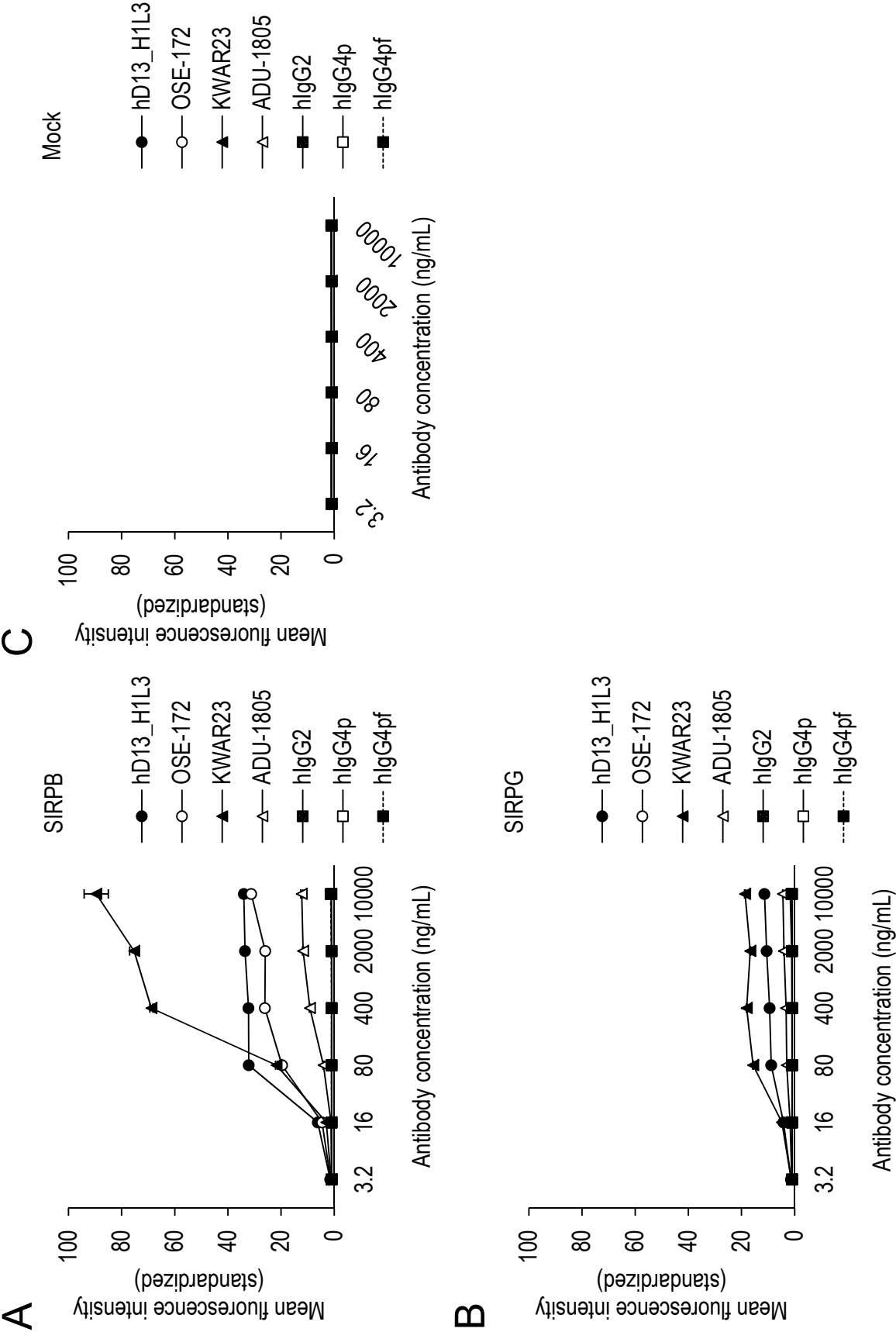


Fig. 33

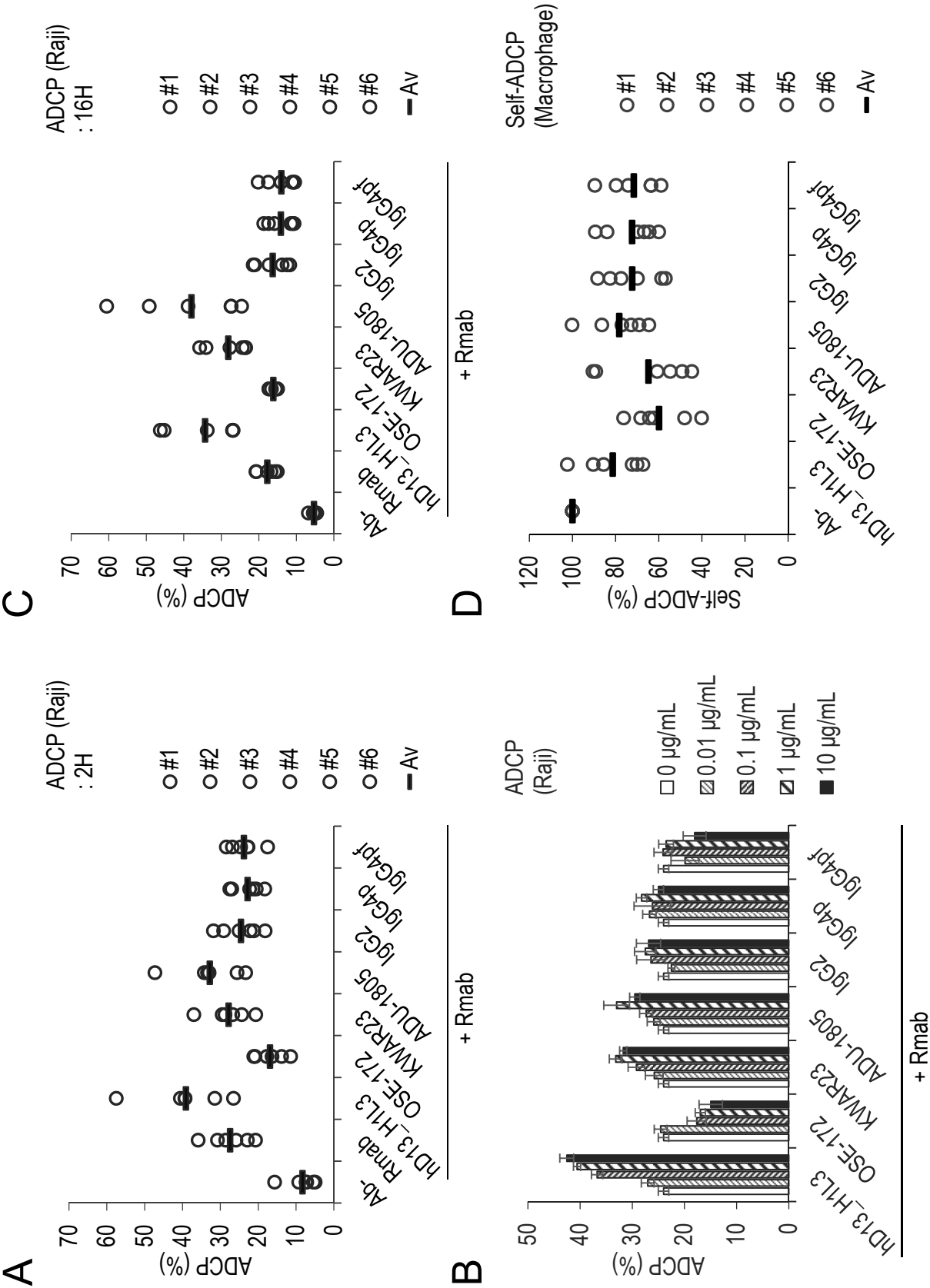


Fig. 34

SEQ ID NO: 81: Amino acid sequence of OSE-172 antibody heavy chain (OSE-172_hG4Pro)

MKHLWFFLLLVAAPRWVLSEVQLVQSGAEVKKPGESLRISCKASGYSFTSYWVHWV
RQMPGKGLEWMGNIDPSDS DTHYSPSFQGHVTL SVDKSISTAYLQLSSLKASDTAM
YYCVRGGTGTLAYFAYWGQGLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKYTCNV
DHKPSNTKVKDRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTC
VVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFY
PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH
EALHNHYTQKSLSLSPGK*

SEQ ID NO: 82: Amino acid sequence of OSE-172 antibody light chain (OSE-172_hK)

MVLQQTQVFISLLWISGAYGDVVMVTQSPSLPVTLGQPASISCRSSQSLVHSYGNT
YLYWFQQRPGQSPRLLIYRVSNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYY
CFQGTHVPYTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQ
GLSSPVTKSFNRGEC*

Fig. 35

SEQ ID NO: 83: Amino acid sequence of KWAR23 antibody heavy chain (KWAR23_hG4Pro)

MKHLWFFLLLVAAPRWVLSEVQLQQSGAELVKPGASVKLSCTASGFNIKDYIHWV
QQRTEQGLEWIGRIDPEDGETKYAPKFQDKATITADTSSNTAYLHLSSLTSED
TAVYYCARWGAYWGQGLTVTVSAASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP
VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGKTYTCNV
DHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSQ
EDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV
SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHY
TQKSLSLSLGK*

SEQ ID NO: 84 Amino acid sequence of KWAR23 antibody light chain (KWAR23_hK)

MVLQQTQVFISLLWISGAYGQIVLTQSPAISASPGEKVTLTCSASSSVSSSYLYW
YQQKPGSSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISSMEEAEDAASYFCHQW
SSYPRTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS
PVTKSFNRGEC*

Fig. 36

SEQ ID NO: 85: Amino acid sequence of ADU-1805 antibody heavy chain (ADU-1805_hG2)

MKHLWFFLLLVAAPRWVLSEVQLVQSGAEVVKPGASVKLSCKASGSTFTSYWMHWV
KQAPGQGLEWIGAIYPVNSDTTYNQKFKGKATLTVDKSASTAYMELSSLRSED
TAVYYCTRSFYYSLDAAWFVYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSNFGTQTYTC
NVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVSVLTVVHQDWLNG
KEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVM
HEALHNHYTQKSLSLSPGK*

SEQ ID NO: 86: Amino acid sequence of ADU-1805 antibody light chain (ADU-1805_hK)

MVLQQTQVFISLLWISGAYGDIQMTQSPSSLSASVGDRVTITCRASQDIGSRLNWL
QQKPGKAPKRLIYATSSLD SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQYA
SSPFTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSP
VTKSFNRGEC*