Fig. 1


Extracellular Loop 1
CLDN6 (SEQ ID NO: 2) MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTG 60
CLDN9 (SEQ ID NO: 9) MASTGLELLGMTLAVLGWLGTLVSCALPLWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTG 60
CLDN4 (SEQ ID NO: 10) MASMGLQVMGIALAVLGWLAVMLCCALPMWRVTAFIGSNIVTSQTIWEGLWMNCVVQSTG 60
CLDN3 (SEQ ID NO: 11) -MSMGLEITGTALAVLGWLGTIVCCALPMWRVSAFIGSNIITSQNIWEGLWMNCVVQSTG 59
CLDN6 (SEQ ID NO: 2) QMQCKVYDSLLALPQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARLVLT 120
CLDN9 (SEQ ID NO: 9) QMQCKVYDSLLALPQDLQAARALCVIALLLALLGLLVAITGAQCTTCVEDEGAKARIVLT 120
CLDN4 (SEQ ID NO: 10) QMQCKVYDSLLALPQDLQAARALVIISIIVAALGVLLSVVGGKCTNCLEDESAKAKTMIV 120
CLDN3 (SEQ ID NO: 11) QMQCKVYDSLLALPQDLQAARALIVVAILLAAFGLLVALVGAQCTNCVQDDTAKAKITIV 119
Extracellular Loop 2
CLDN6 (SEQ ID NO: 2) SGIVFVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLLGGGL 180
CLDN9 (SEQ ID NO: 9) AGVILLLAGILVLIPVCWTAHAIIQDFYNPLVAEALKRELGASLYLGWAAAALLMLGGGL 180
CLDN4 (SEQ ID NO: 10) AGVVFLLAGLMVIVPVSWTAHNIIQDFYNPLVASGQKREMGASLYVGWAASGLLLLGGGL 180
CLDN3 (SEQ ID NO: 11) AGVLFLLAALLTLVPVSWSANTIIRDFYNPVVPEAQKREMGAGLYVGWAAAALQLLGGAL 179
CLDN6 (SEQ ID NO: 2) LCCTCPSGGSQGPSHYMARYSTSAPAISRGPSEYP-----TKNYV 220
CLDN9 (SEQ ID NO: 9) LCCTCPPPQVERPRG--PRLGYSIPSRS-GASGLD-----KRDYV 217
CLDN4 (SEQ ID NO: 10) LCCNCPPRT---DKPYSAK---YSAARSAAASN----------YV 209
CLDN3 (SEQ ID NO: 11) LCCSCPPR----EKKYTATKVVYSAPRSTGPGASLGTGYDRKDYV 220

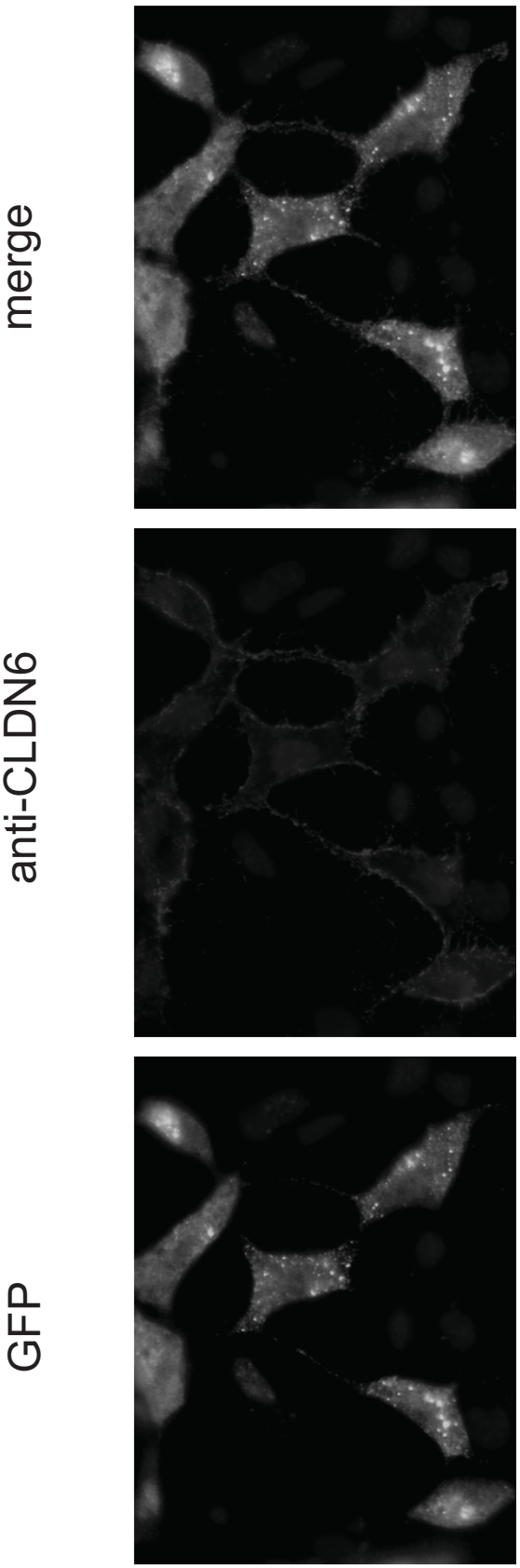


Fig. 2A

Fig. 2B

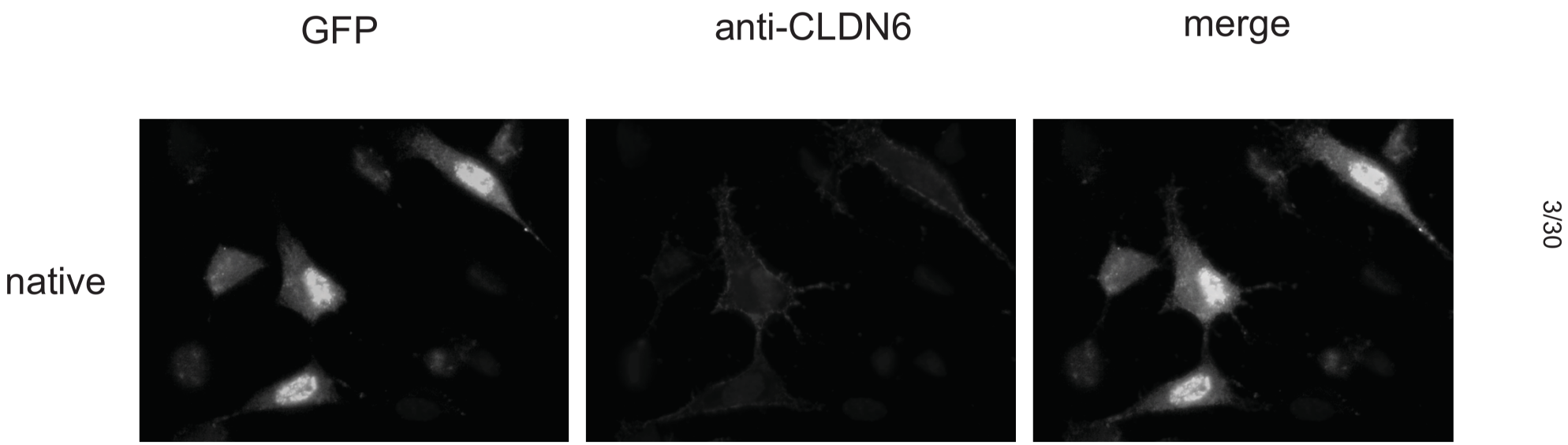


Fig. 3

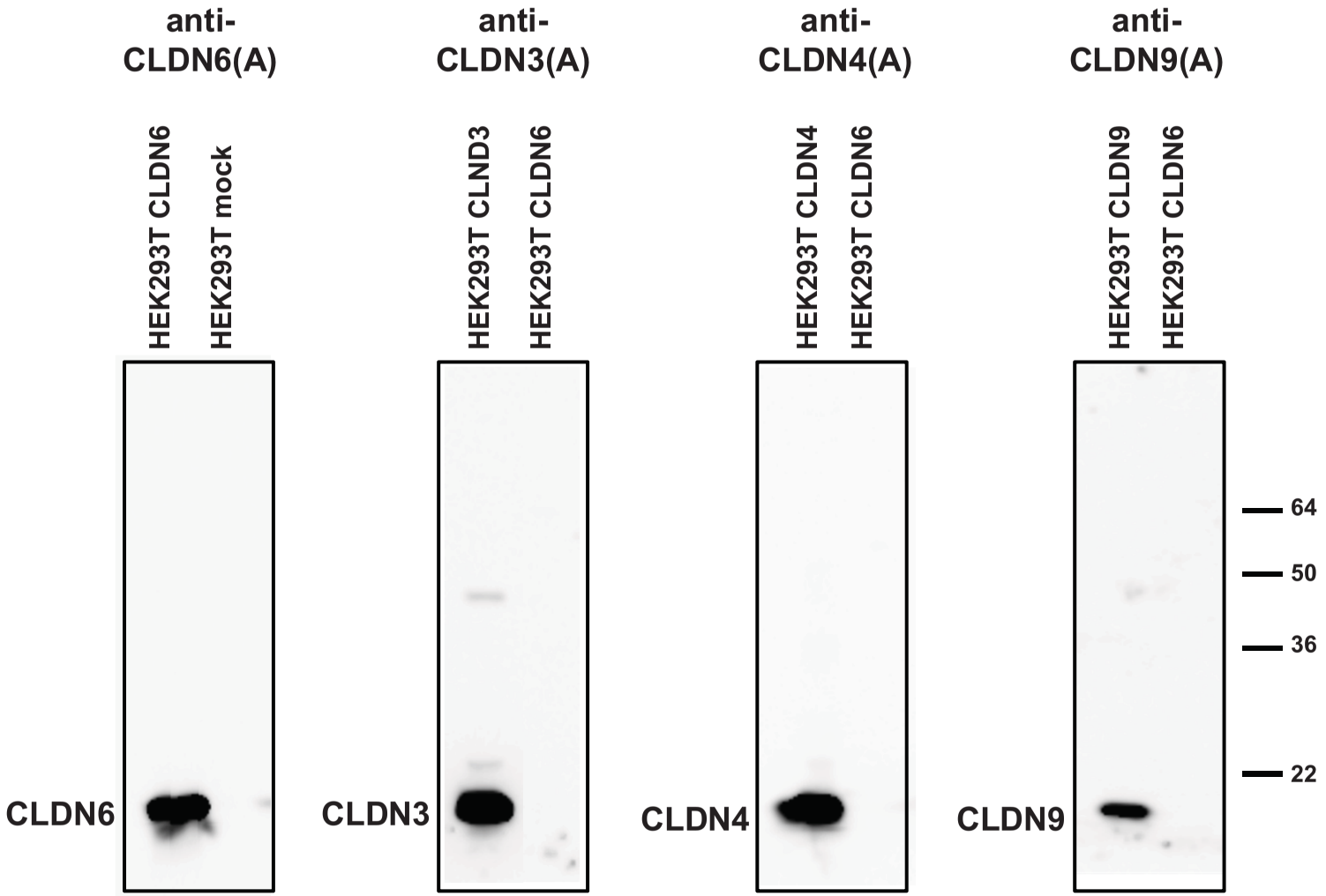

anti-
CLDN6(A)
HEK293T CLDN6
HEK293T mock
CLDN6
anti-
CLDN3(A)
HEK293T CLND3
HEK293T CLDN6
CLDN3
anti-
CLDN4(A)
HEK293T CLDN4
HEK293T CLDN6
CLDN4
anti-
CLDN9(A)
HEK293T CLDN9
HEK293T CLDN6
CLDN9
64
50
36
22

Fig. 4

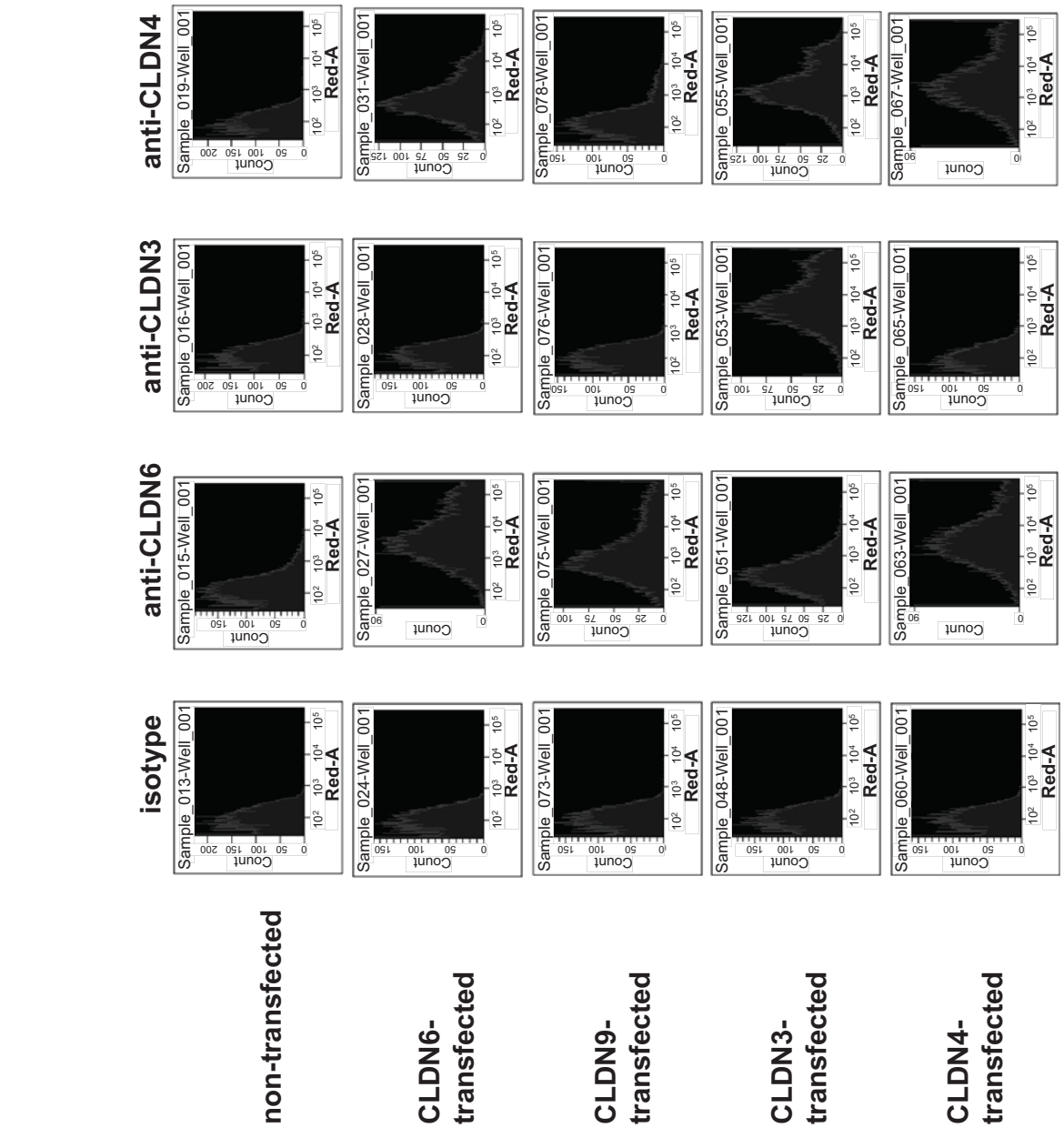

isotype
anti-CLDN6
anti-CLDN3
anti-CLDN4
non-transfected
CLDN6-transfected
CLDN9-transfected
CLDN3-transfected
CLDN4-transfected
Count
Red-A

Fig. 5A

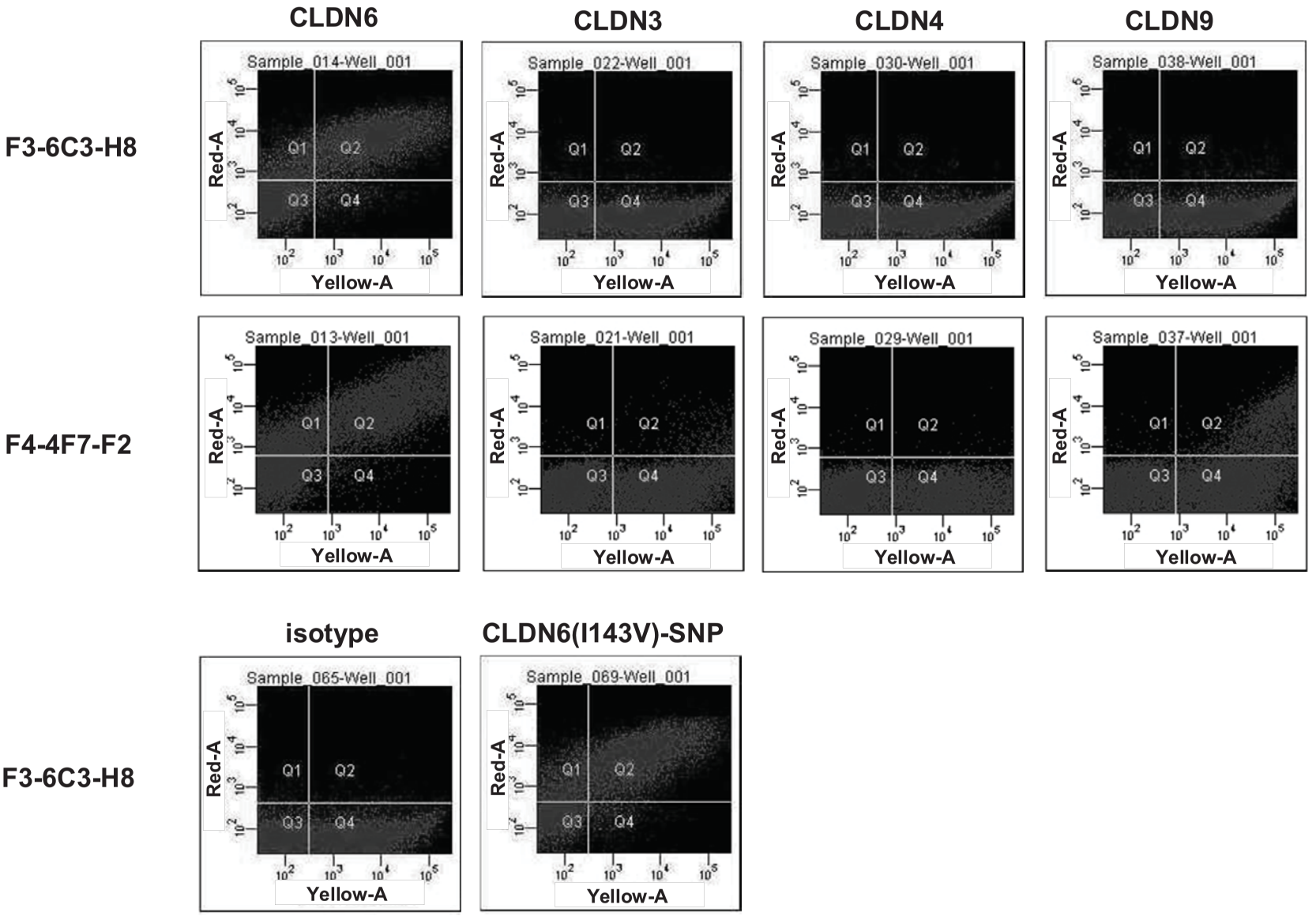
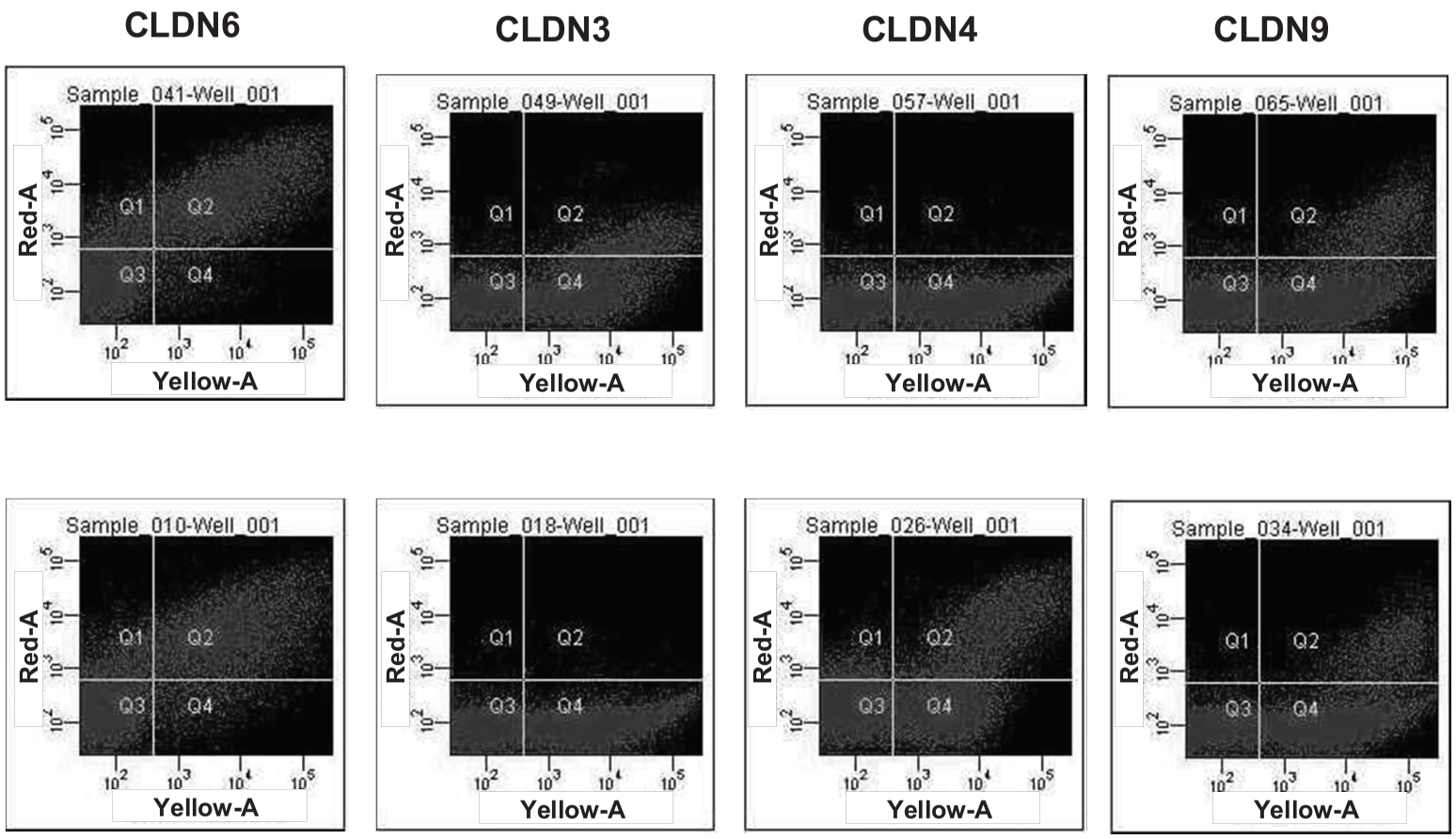

CLDN6
CLDN3
CLDN4
CLDN9
F3-6C3-H8
F4-4F7-F2
isotype
CLDN6(I143V)-SNP
F3-6C3-H8
Sample_014-Well_001
Sample_022-Well_001
Sample_030-Well_001
Sample_038-Well_001
Sample_013-Well_001
Sample_021-Well_001
Sample_029-Well_001
Sample_037-Well_001
Sample_065-Well_001
Sample_069-Well_001
Red-A
Yellow-A
Q1
Q2
Q3
Q4

Fig. 5B


CLDN6
CLDN3
CLDN4
CLDN9
F3-7B3-B4
F3-3F7-A5
Sample_041-Well_001
Sample_049-Well_001
Sample_057-Well_001
Sample_065-Well_001
Sample_010-Well_001
Sample_018-Well_001
Sample_026-Well_001
Sample_034-Well_001
Red-A
Yellow-A
Q1
Q2
Q3
Q4

CLDN	Q1	Q2
	Q3	Q4

reporter

Fig. 6

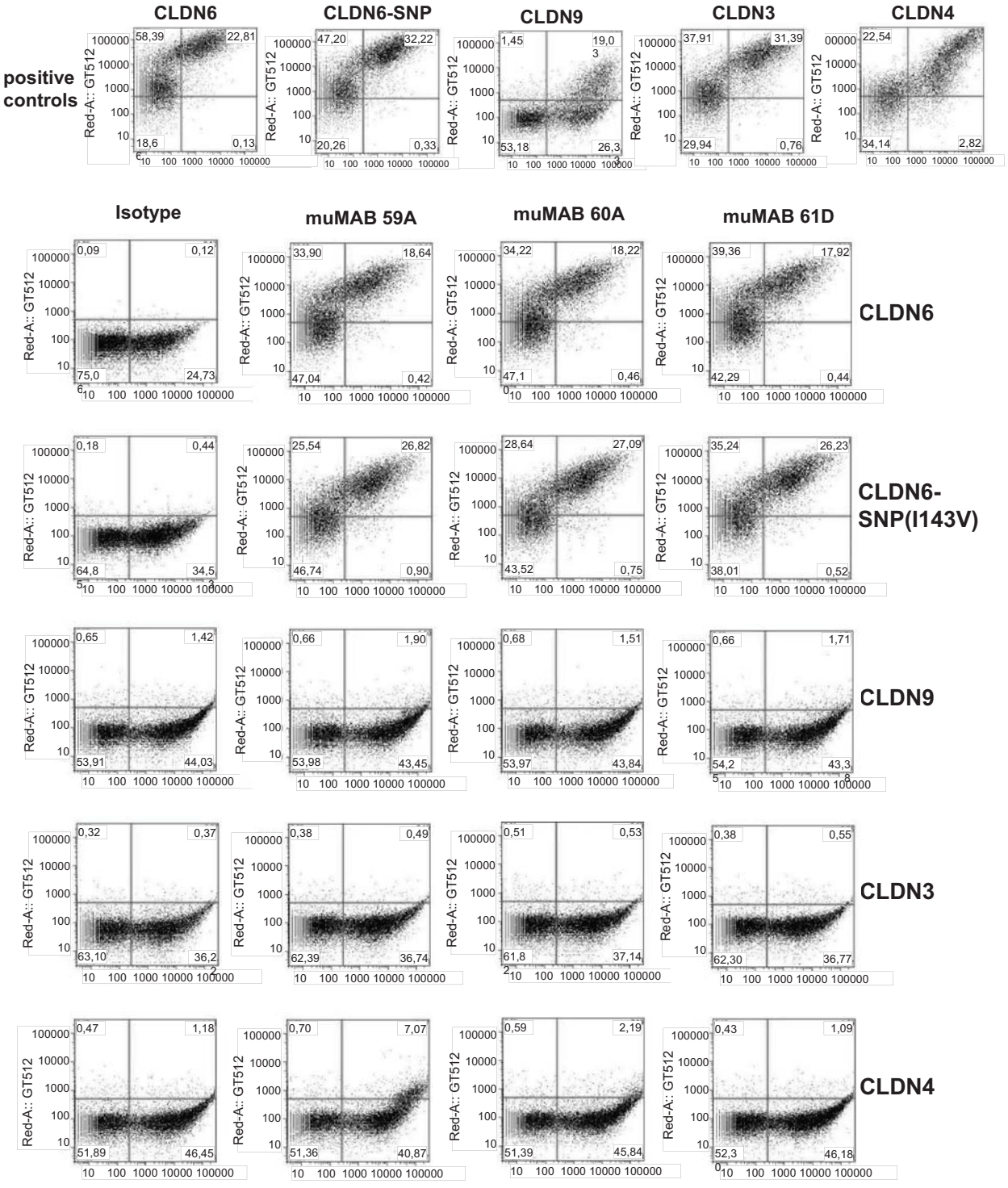


Fig. 6 (cont.)

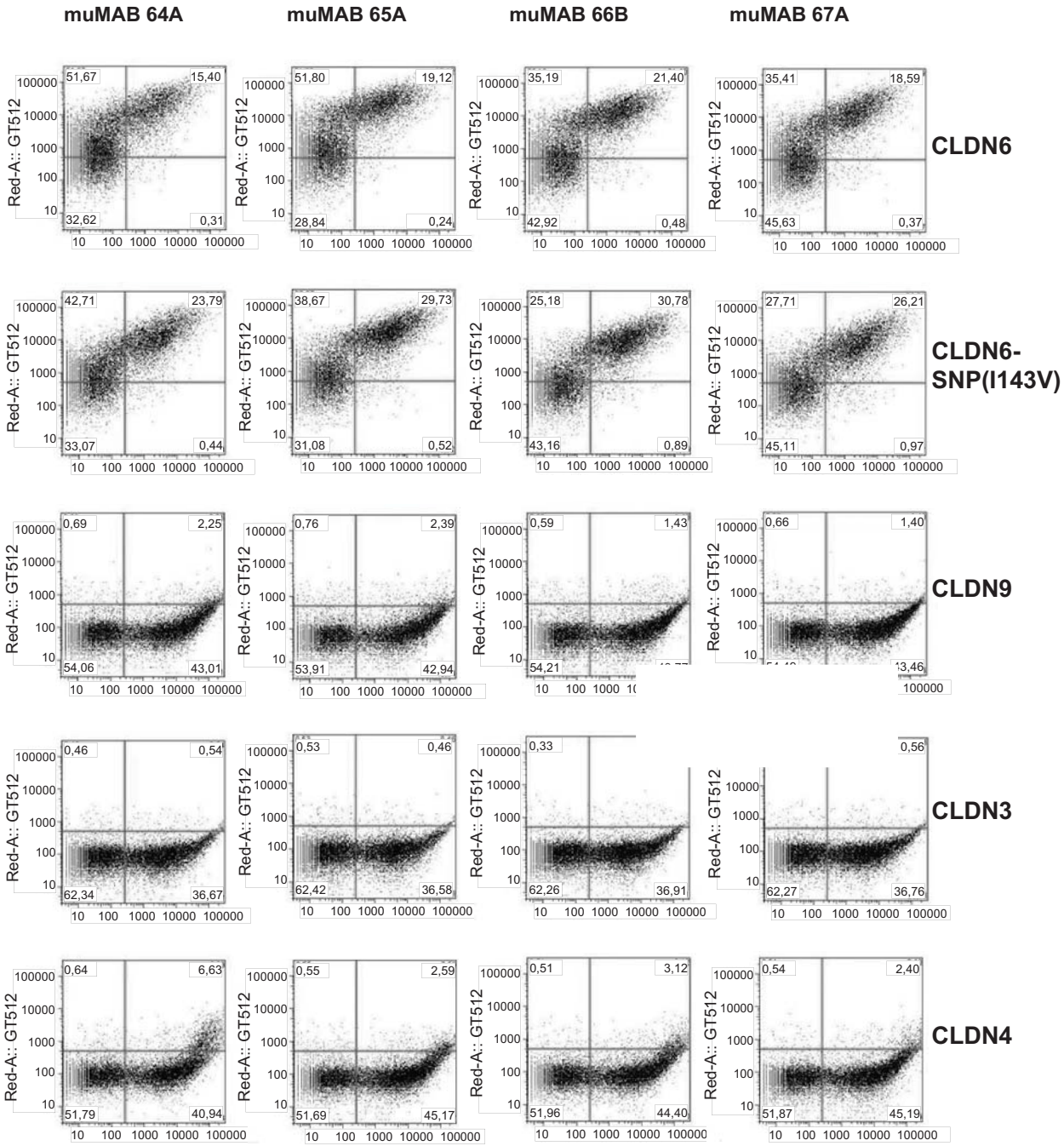

muMAB 64A
muMAB 65A
muMAB 66B
muMAB 67A
CLDN6
CLDN6-SNP(I143V)
CLDN9
CLDN3
CLDN4
Red-A:: GT512
51,67
15,40
32,62
0,31
51,80
19,12
28,84
0,24
35,19
21,40
42,92
0,48
35,41
18,59
45,63
0,37
42,71
23,79
33,07
0,44
38,67
29,73
31,08
0,52
25,18
30,78
43,16
0,89
27,71
26,21
45,11
0,97
0,69
2,25
54,06
43,01
0,76
2,39
53,91
42,94
0,59
1,43
54,21
0,66
1,40
0,46
0,54
62,34
36,67
0,53
0,46
62,42
36,58
0,33
62,26
36,91
0,56
62,27
36,76
0,64
6,63
51,79
40,94
0,55
2,59
51,69
45,17
0,51
3,12
51,96
44,40
0,54
2,40
51,87
45,19
10 100 1000 10000 100000

Fig. 7

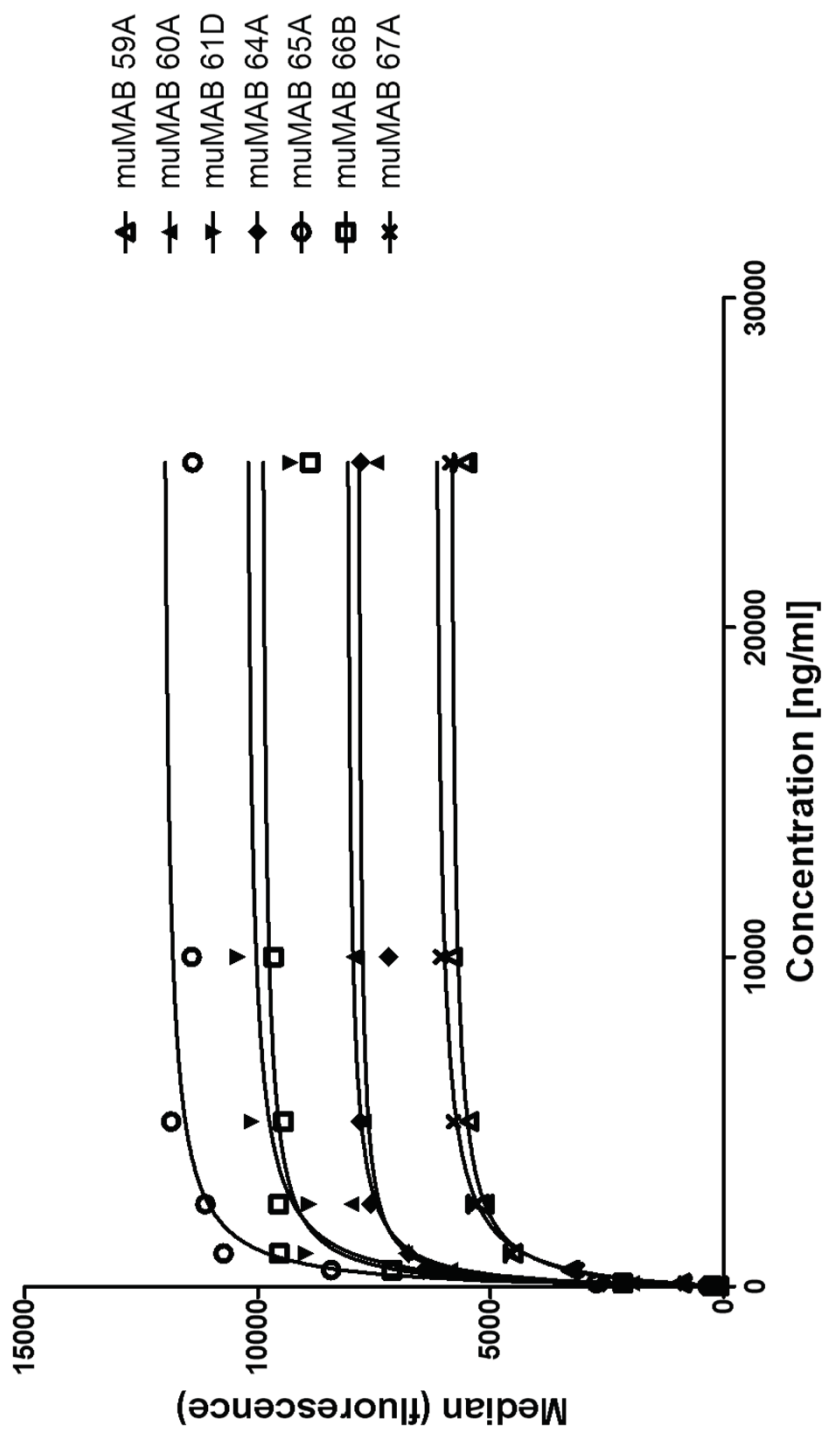
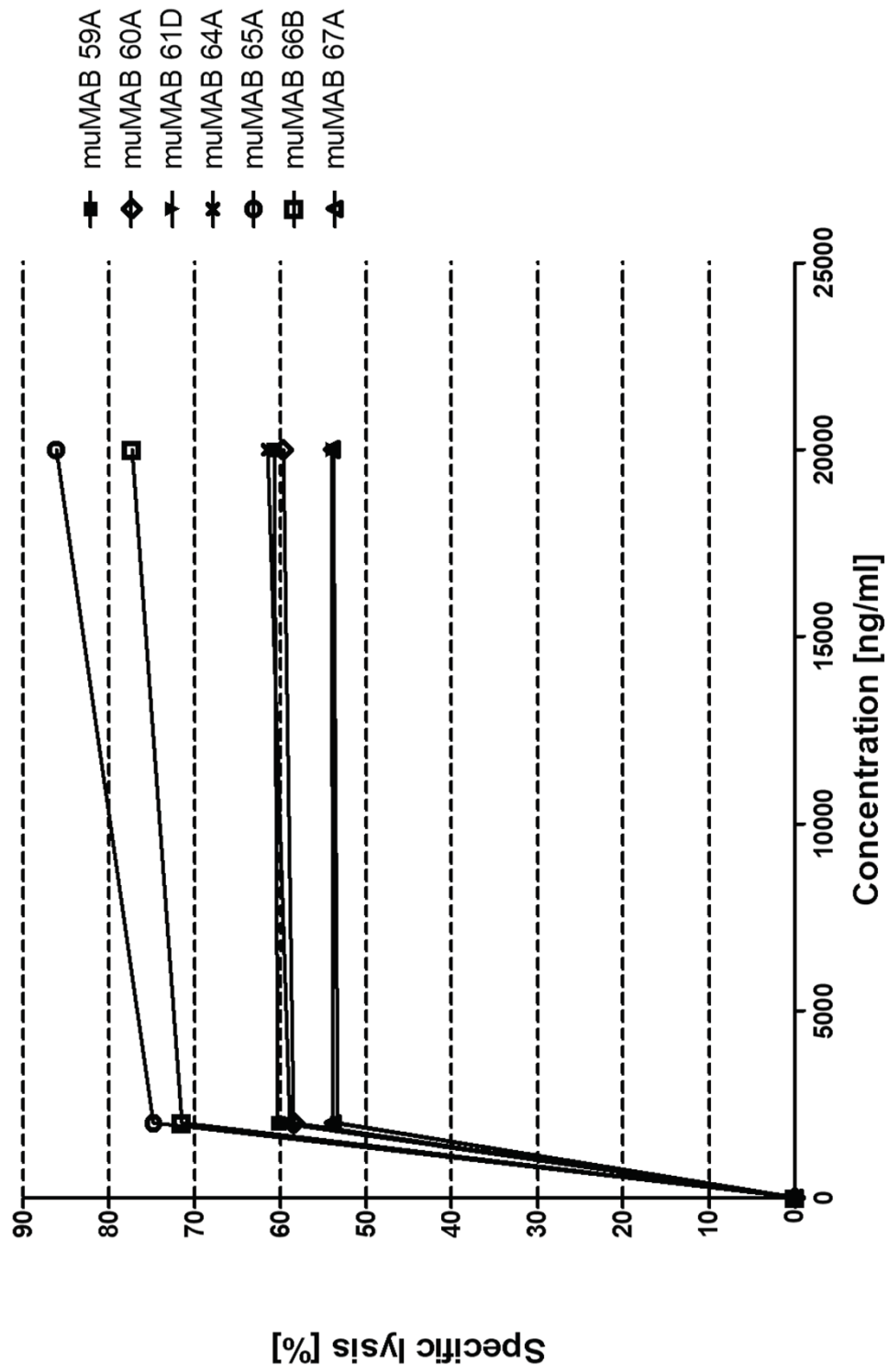

muMAB 59A
muMAB 60A
muMAB 61D
muMAB 64A
muMAB 65A
muMAB 66B
muMAB 67A
Median (fluorescence)
15000
10000
5000
0
0
10000
20000
30000
Concentration [ng/ml]

Fig. 8


muMAB 59A
muMAB 60A
muMAB 61D
muMAB 64A
muMAB 65A
muMAB 66B
muMAB 67A
Specific lysis [%]
0
10
20
30
40
50
60
70
80
90
0
5000
10000
15000
20000
25000
Concentration [ng/ml]

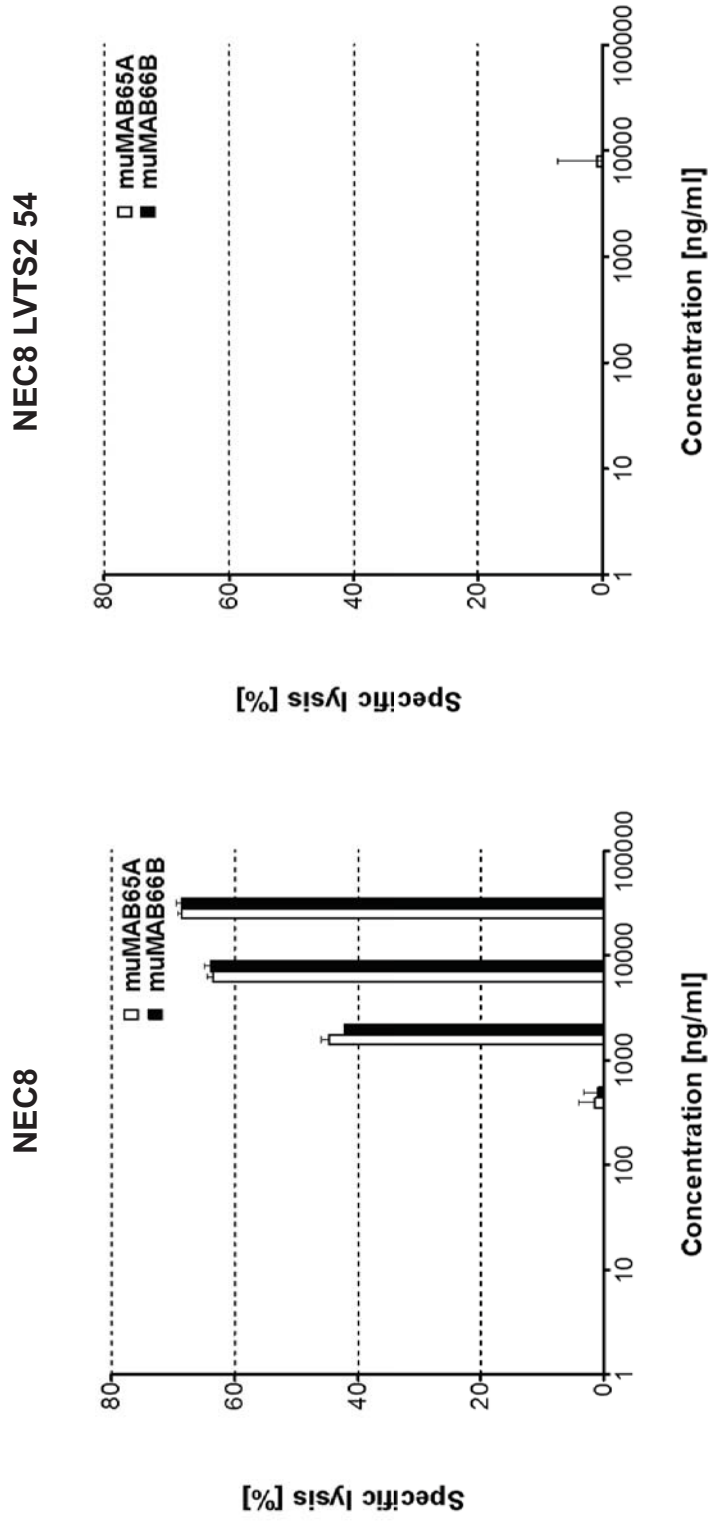

NEC8
muMAB65A
muMAB66B
Specific lysis [%]
0
20
40
60
80
1
10
100
1000
10000
100000
Concentration [ng/ml]
NEC8 LVTS2 54
muMAB65A
muMAB66B
Specific lysis [%]
0
20
40
60
80
1
10
100
1000
10000
100000
Concentration [ng/ml]

Fig. 9

Fig. 10

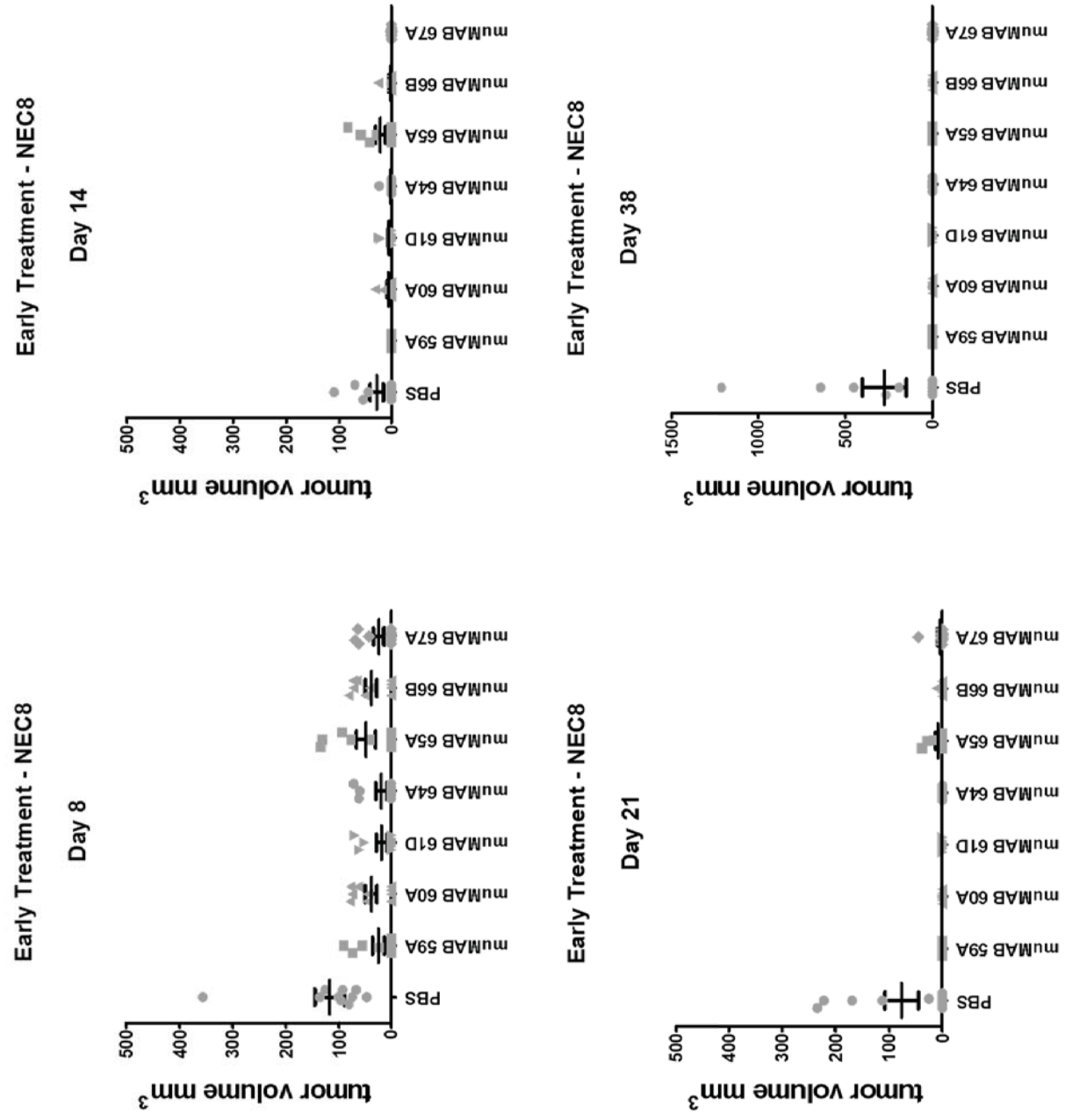
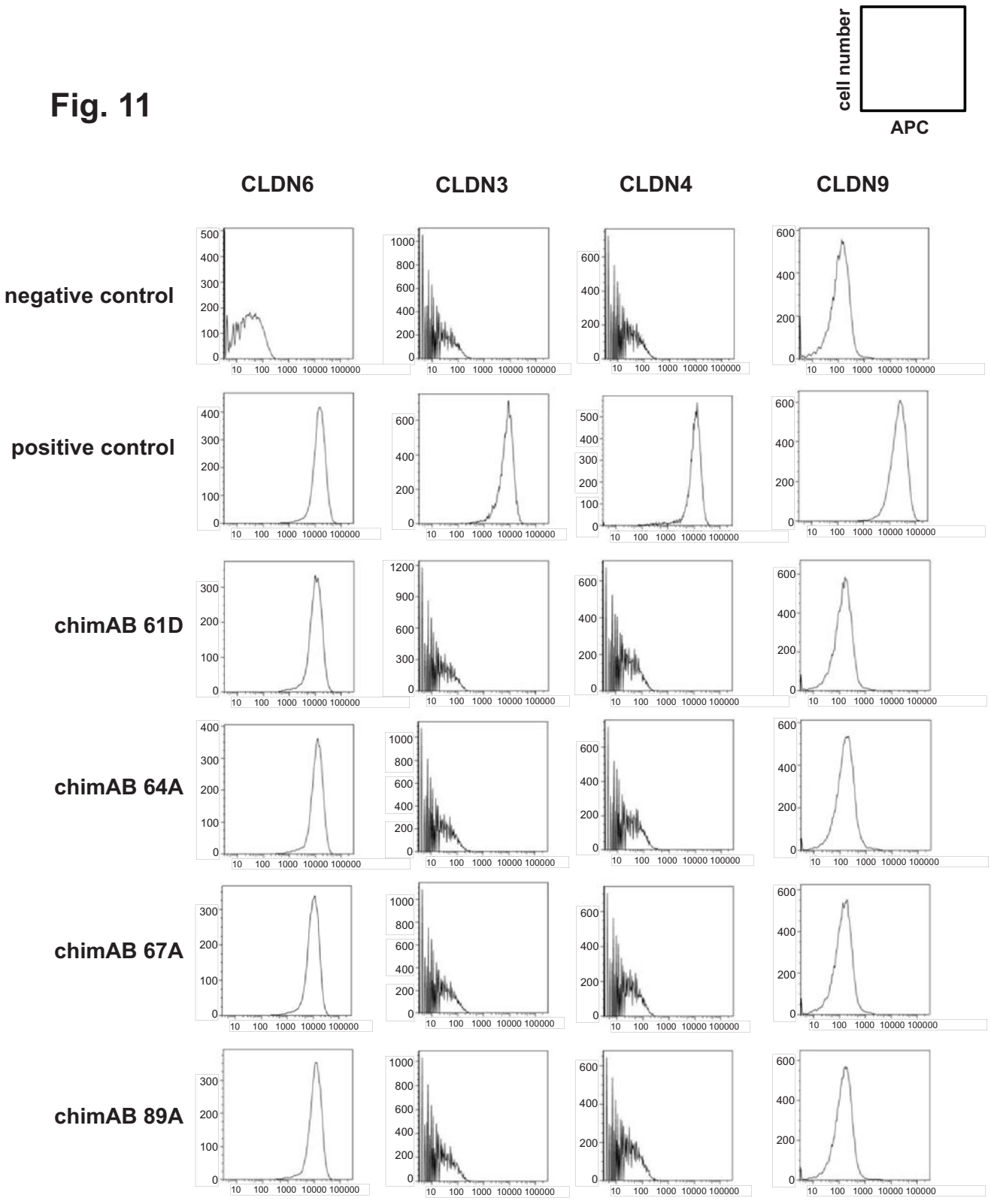

Early Treatment - NEC8
Day 8
tumor volume mm3
0
100
200
300
400
500
PBS
muMAB 59A
muMAB 60A
muMAB 61D
muMAB 64A
muMAB 65A
muMAB 66B
muMAB 67A
Early Treatment - NEC8
Day 14
tumor volume mm3
0
100
200
300
400
500
PBS
muMAB 59A
muMAB 60A
muMAB 61D
muMAB 64A
muMAB 65A
muMAB 66B
muMAB 67A
Early Treatment - NEC8
Day 21
tumor volume mm3
0
100
200
300
400
500
PBS
muMAB 59A
muMAB 60A
muMAB 61D
muMAB 64A
muMAB 65A
muMAB 66B
muMAB 67A
Early Treatment - NEC8
Day 38
tumor volume mm3
0
500
1000
1500
PBS
muMAB 59A
muMAB 60A
muMAB 61D
muMAB 64A
muMAB 65A
muMAB 66B
muMAB 67A

Fig. 11


cell number
APC
CLDN6
CLDN3
CLDN4
CLDN9
negative control
positive control
chimAB 61D
chimAB 64A
chimAB 67A
chimAB 89A
10 100 1000 10000 100000

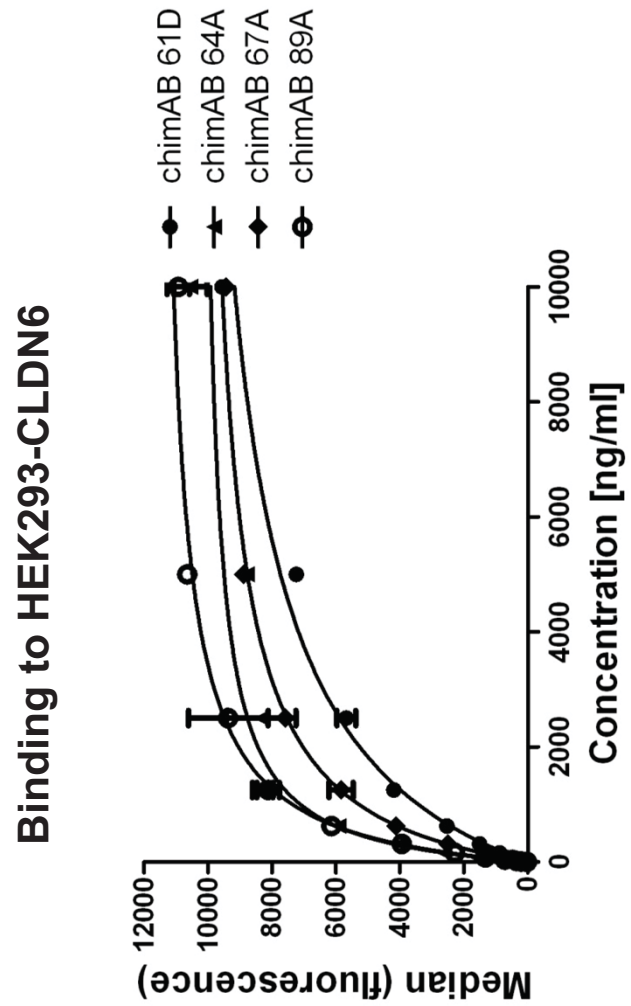

Binding to HEK293-CLDN6
chimAB 61D
chimAB 64A
chimAB 67A
chimAB 89A
Median (fluorescence)
0
2000
4000
6000
8000
10000
12000
0
2000
4000
6000
8000
10000
Concentration [ng/ml]

Fig. 12

Fig. 13

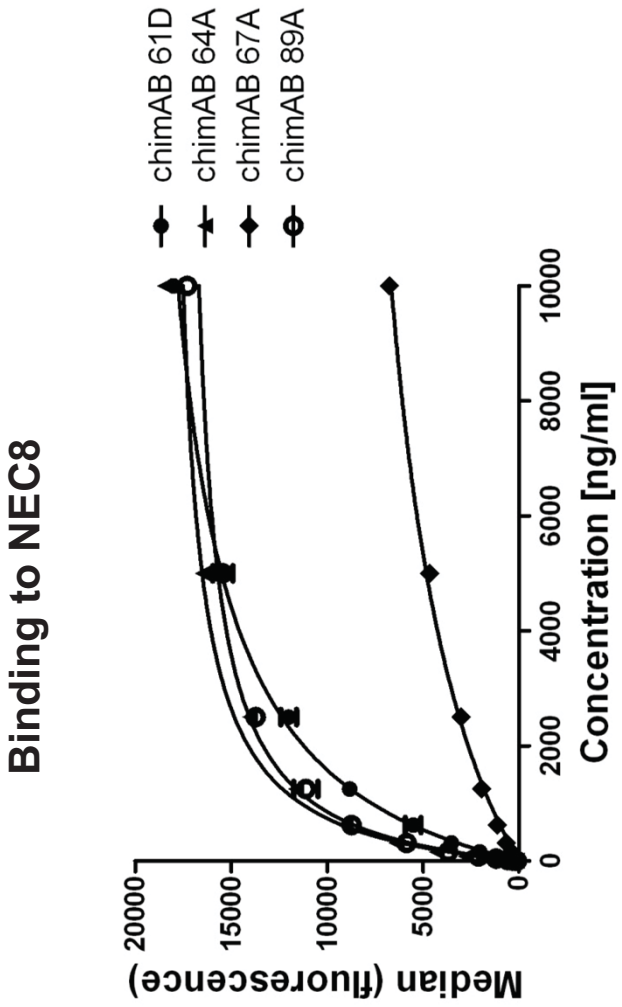

Binding to NEC8
chimAB 61D
chimAB 64A
chimAB 67A
chimAB 89A
Median (fluorescence)
20000
15000
10000
5000
0
0
2000
4000
6000
8000
10000
Concentration [ng/ml]

Fig. 14

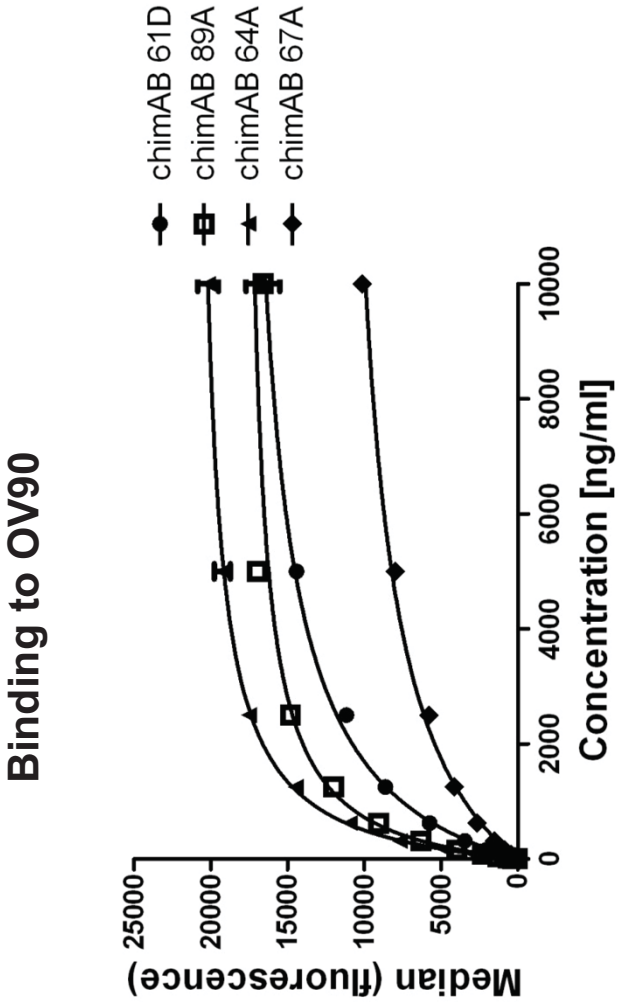

Binding to OV90
chimAB 61D
chimAB 89A
chimAB 64A
chimAB 67A
Median (fluorescence)
25000
20000
15000
10000
5000
0
0
2000
4000
6000
8000
10000
Concentration [ng/ml]

Fig. 15

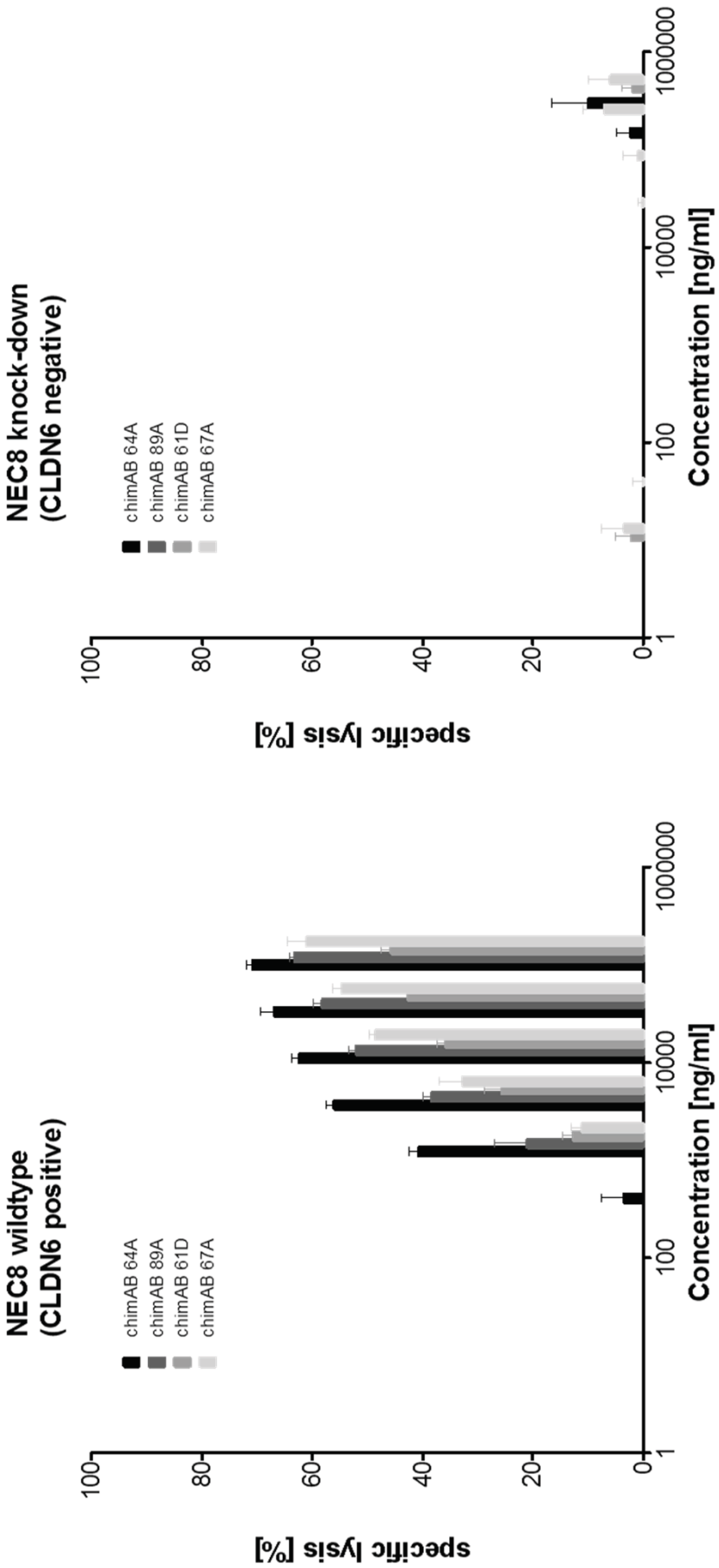

NEC8 knock-down
(CLDN6 negative)
chimAB 64A
chimAB 89A
chimAB 61D
chimAB 67A
specific lysis [%]
0
20
40
60
80
100
1
100
10000
1000000
Concentration [ng/ml]
NEC8 wildtype
(CLDN6 positive)
chimAB 64A
chimAB 89A
chimAB 61D
chimAB 67A
specific lysis [%]
0
20
40
60
80
100
1
100
10000
1000000
Concentration [ng/ml]

Fig. 16

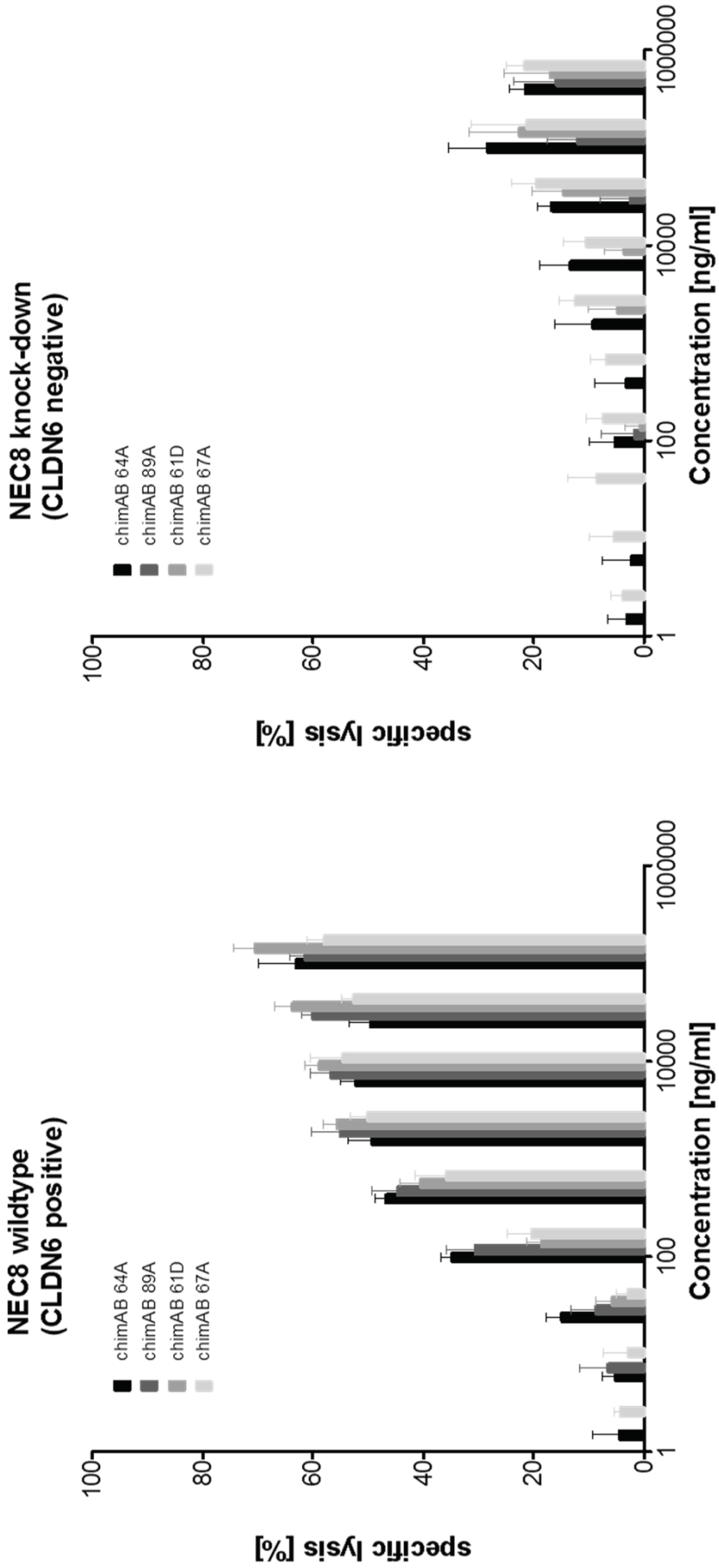
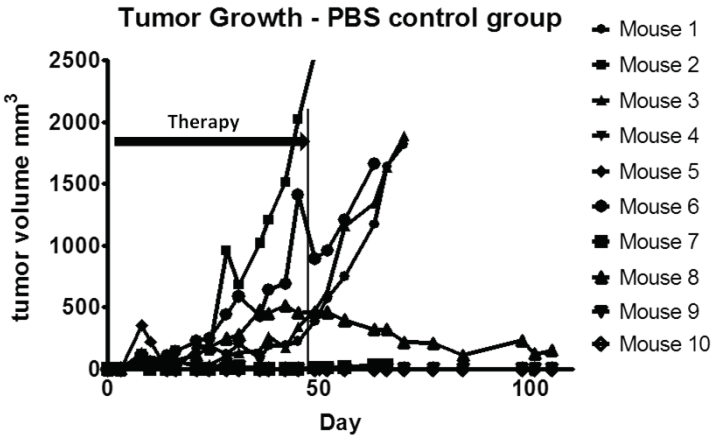
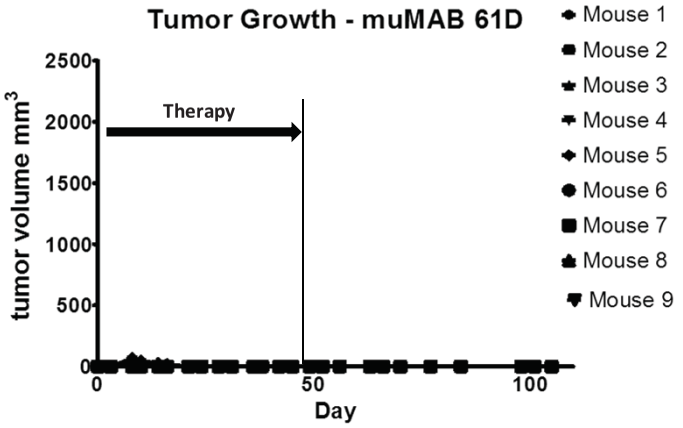
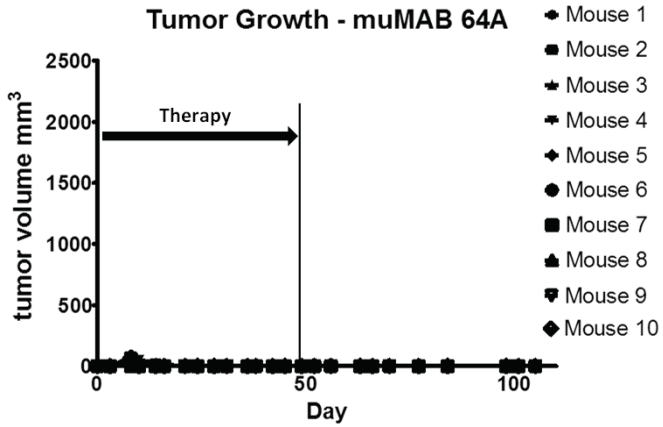

NEC8 knock-down
(CLDN6 negative)
chimAB 64A
chimAB 89A
chimAB 61D
chimAB 67A
specific lysis [%]
0
20
40
60
80
100
1
100
10000
1000000
Concentration [ng/ml]
NEC8 wildtype
(CLDN6 positive)
chimAB 64A
chimAB 89A
chimAB 61D
chimAB 67A
specific lysis [%]
0
20
40
60
80
100
1
100
10000
1000000
Concentration [ng/ml]

Fig. 17


Tumor Growth - PBS control group
tumor volume mm3
2500
2000
1500
1000
500
0
Therapy
0
50
100
Day
Mouse 1
Mouse 2
Mouse 3
Mouse 4
Mouse 5
Mouse 6
Mouse 7
Mouse 8
Mouse 9
Mouse 10


Tumor Growth - muMAB 61D
tumor volume mm3
2500
2000
1500
1000
500
0
Therapy
0
50
100
Day
Mouse 1
Mouse 2
Mouse 3
Mouse 4
Mouse 5
Mouse 6
Mouse 7
Mouse 8
Mouse 9


Tumor Growth - muMAB 64A
tumor volume mm3
2500
2000
1500
1000
500
0
Therapy
0
50
100
Day
Mouse 1
Mouse 2
Mouse 3
Mouse 4
Mouse 5
Mouse 6
Mouse 7
Mouse 8
Mouse 9
Mouse 10

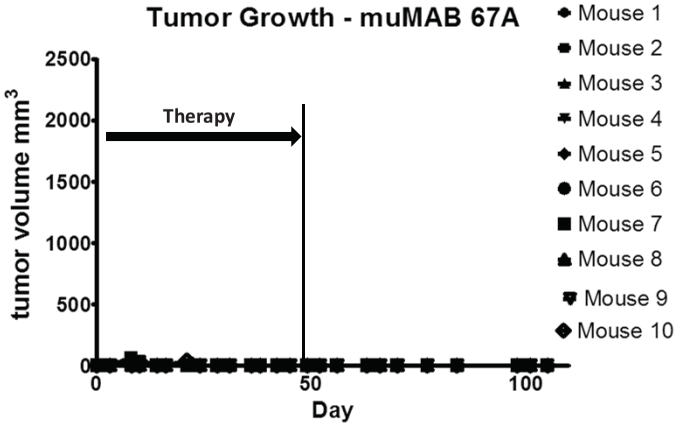
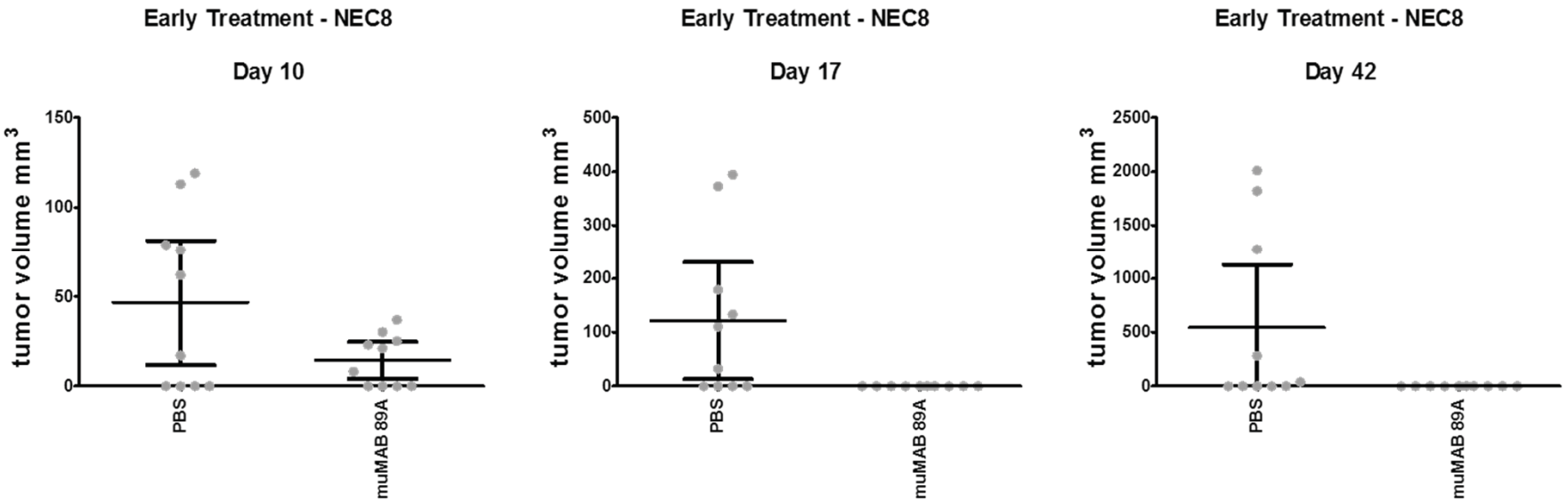

Tumor Growth - muMAB 67A
tumor volume mm3
2500
2000
1500
1000
500
0
Therapy
0
50
100
Day
Mouse 1
Mouse 2
Mouse 3
Mouse 4
Mouse 5
Mouse 6
Mouse 7
Mouse 8
Mouse 9
Mouse 10

Fig. 18

(A)


Early Treatment - NEC8
Day 10
tumor volume mm3
150
100
50
0
PBS
muMAB 89A
Early Treatment - NEC8
Day 17
tumor volume mm3
500
400
300
200
100
0
PBS
muMAB 89A
Early Treatment - NEC8
Day 42
tumor volume mm3
2500
2000
1500
1000
500
0
PBS
muMAB 89A

(B)

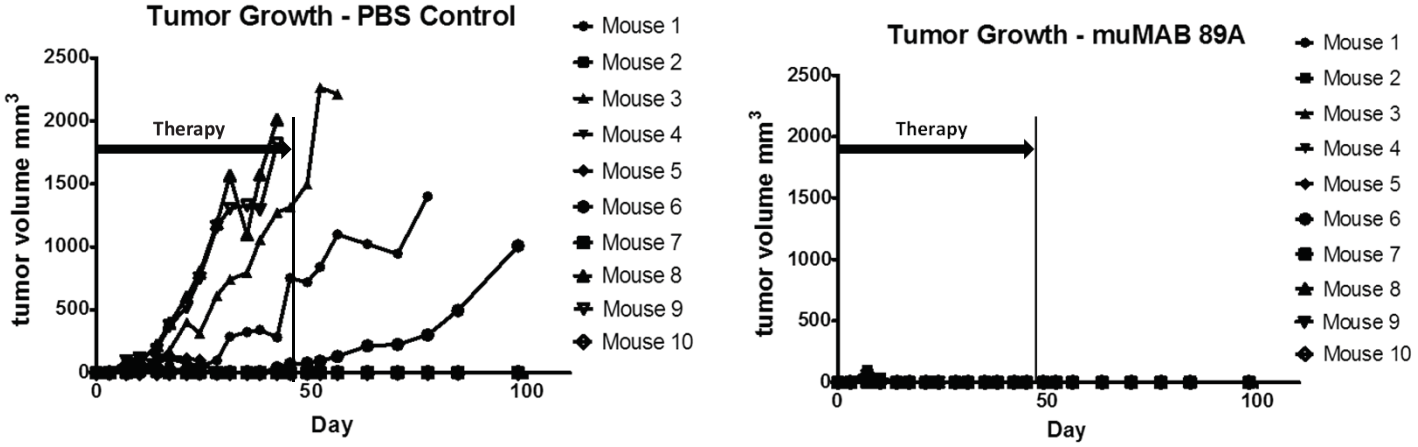

Tumor Growth - PBS Control
tumor volume mm3
2500
2000
1500
1000
500
0
Therapy
0
50
100
Day
Mouse 1
Mouse 2
Mouse 3
Mouse 4
Mouse 5
Mouse 6
Mouse 7
Mouse 8
Mouse 9
Mouse 10
Tumor Growth - muMAB 89A
tumor volume mm3
2500
2000
1500
1000
500
0
Therapy
0
50
100
Day
Mouse 1
Mouse 2
Mouse 3
Mouse 4
Mouse 5
Mouse 6
Mouse 7
Mouse 8
Mouse 9
Mouse 10

Fig. 19

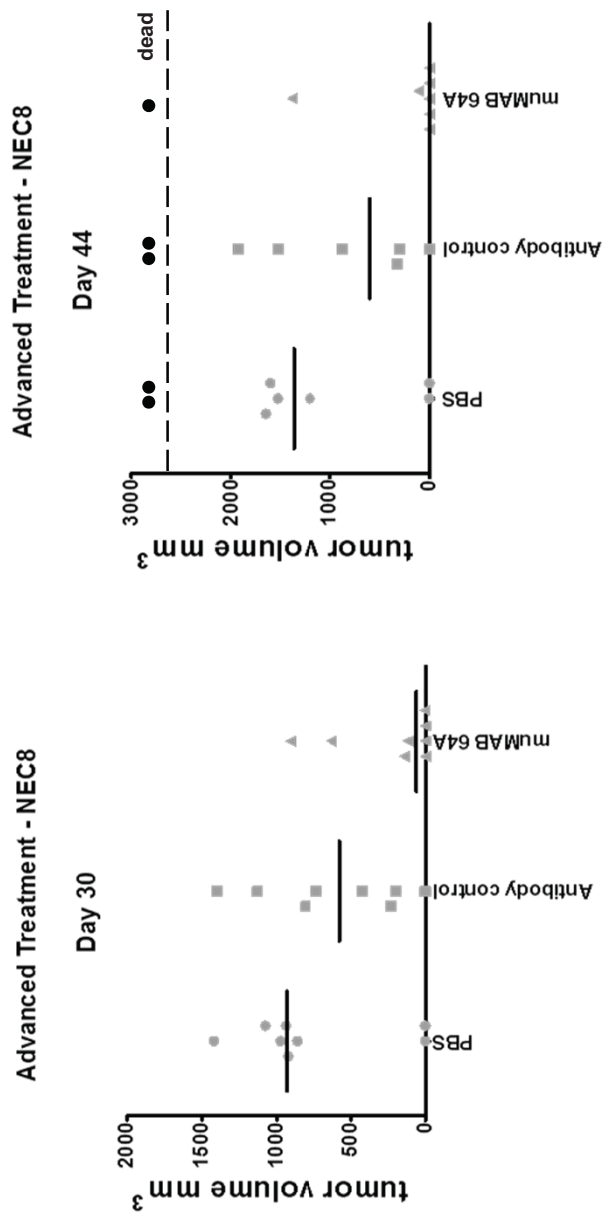
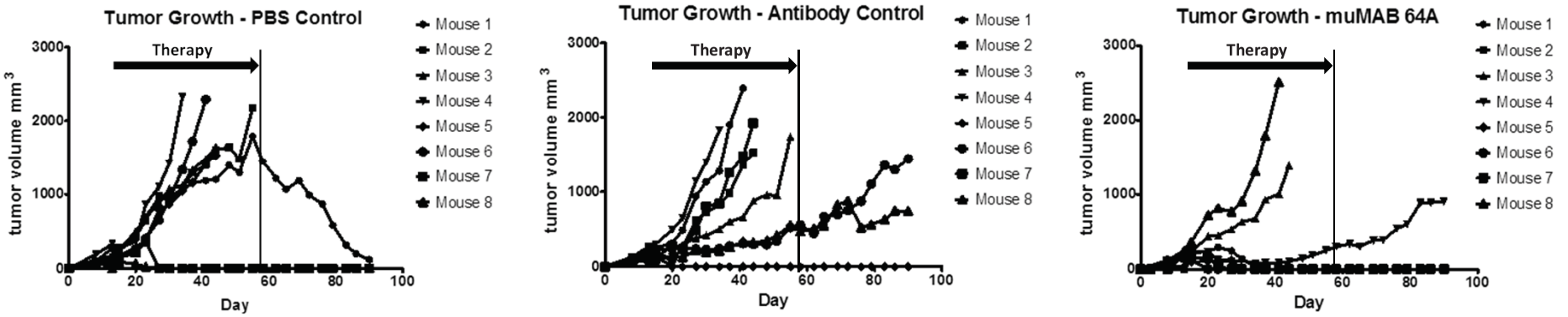

Advanced Treatment - NEC8
Day 15 - Initiation of Immunotherapy
tumor volume mm3
1000
800
600
400
200
0
PBS
Antibody control
muMAB 64A
Advanced Treatment - NEC8
Day 30
tumor volume mm3
2000
1500
1000
500
0
PBS
Antibody control
muMAB 64A
Advanced Treatment - NEC8
Day 44
tumor volume mm3
3000
2000
1000
0
dead
PBS
Antibody control
muMAB 64A

Fig. 20

(A)


Tumor Growth - PBS Control
Therapy
tumor volume mm3
Day
Mouse 1
Mouse 2
Mouse 3
Mouse 4
Mouse 5
Mouse 6
Mouse 7
Mouse 8
Tumor Growth - Antibody Control
Therapy
tumor volume mm3
Day
Tumor Growth - muMAB 64A
Therapy
tumor volume mm3
Day

(B)

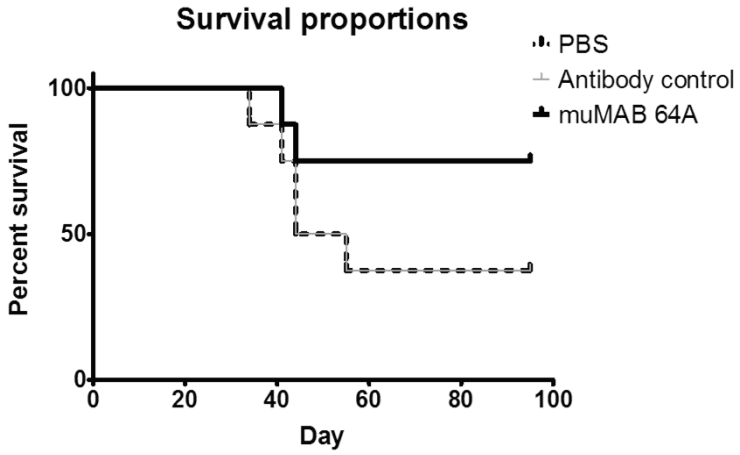
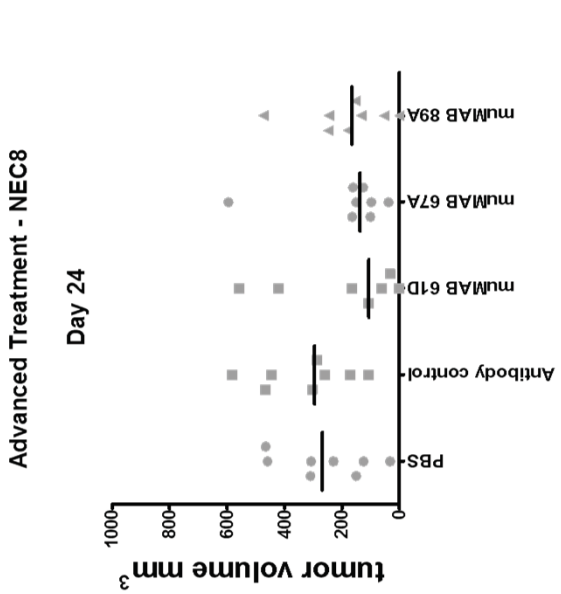
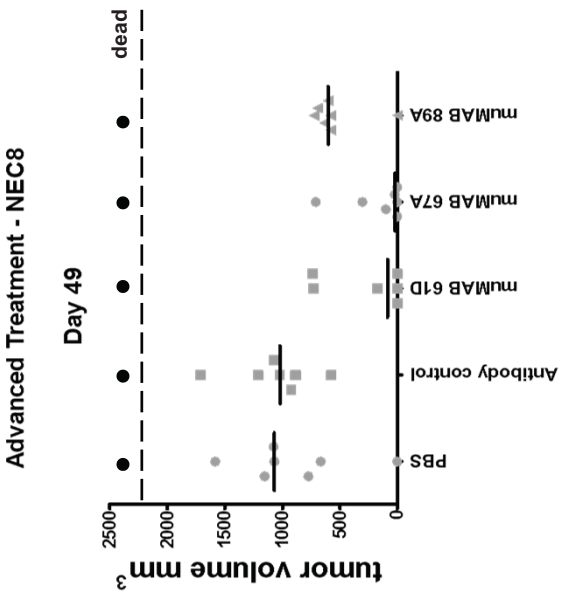
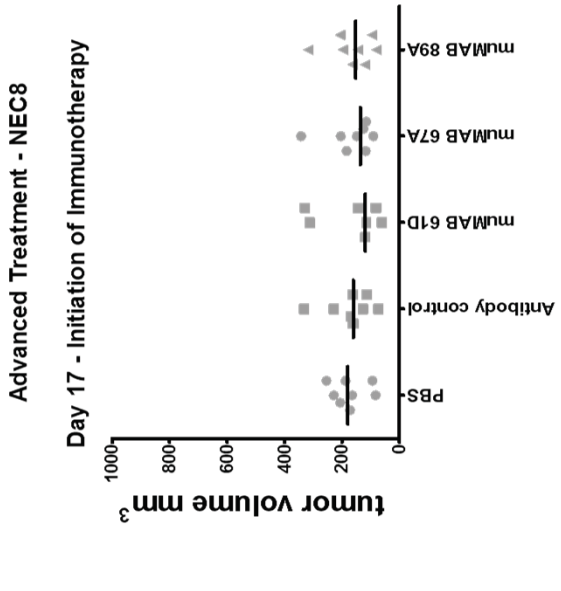

Survival proportions
PBS
Antibody control
muMAB 64A
Percent survival
Day

Fig. 21


Advanced Treatment - NEC8
Day 24
tumor volume mm3
0
200
400
600
800
1000
PBS
Antibody control
muMAB 61D
muMAB 67A
muMAB 89A


Advanced Treatment - NEC8
Day 49
dead
tumor volume mm3
0
500
1000
1500
2000
2500
PBS
Antibody control
muMAB 61D
muMAB 67A
muMAB 89A


Advanced Treatment - NEC8
Day 17 - Initiation of Immunotherapy
tumor volume mm3
0
200
400
600
800
1000
PBS
Antibody control
muMAB 61D
muMAB 67A
muMAB 89A

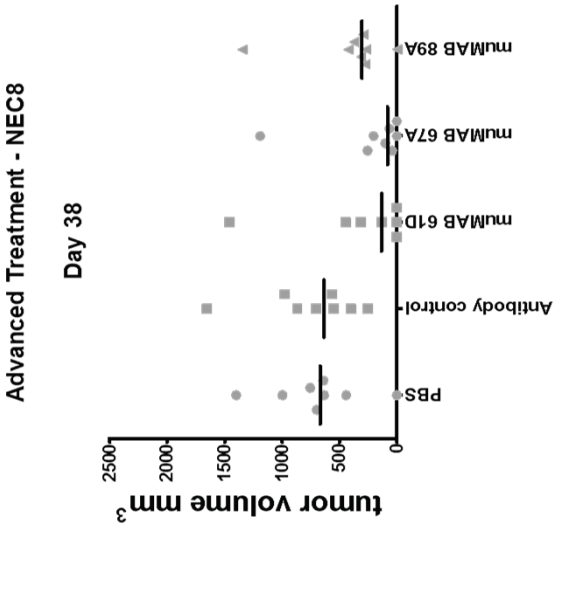
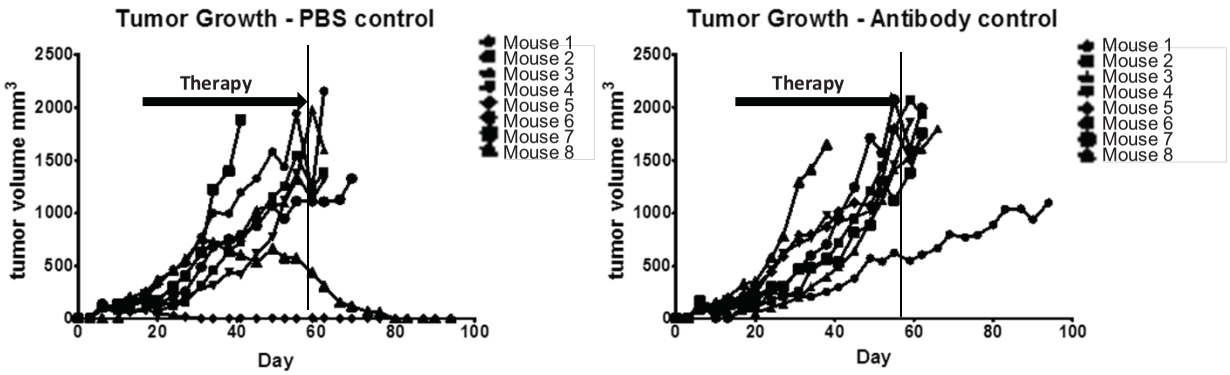
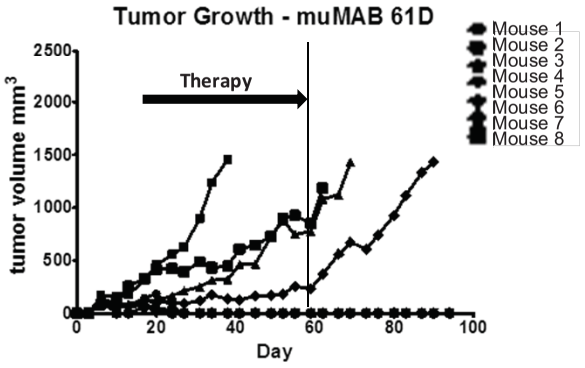

Advanced Treatment - NEC8
Day 38
tumor volume mm3
0
500
1000
1500
2000
2500
PBS
Antibody control
muMAB 61D
muMAB 67A
muMAB 89A

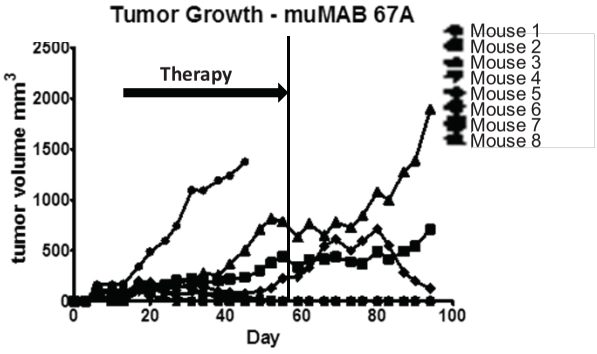
Fig. 22

(A)


Tumor Growth - PBS control
Therapy
tumor volume mm3
Day
Mouse 1
Mouse 2
Mouse 3
Mouse 4
Mouse 5
Mouse 6
Mouse 7
Mouse 8

Tumor Growth - Antibody control
Therapy
tumor volume mm3
Day
Mouse 1
Mouse 2
Mouse 3
Mouse 4
Mouse 5
Mouse 6
Mouse 7
Mouse 8


Tumor Growth - muMAB 61D
Therapy
tumor volume mm3
Day
Mouse 1
Mouse 2
Mouse 3
Mouse 4
Mouse 5
Mouse 6
Mouse 7
Mouse 8


Tumor Growth - muMAB 67A
Therapy
tumor volume mm3
Day
Mouse 1
Mouse 2
Mouse 3
Mouse 4
Mouse 5
Mouse 6
Mouse 7
Mouse 8

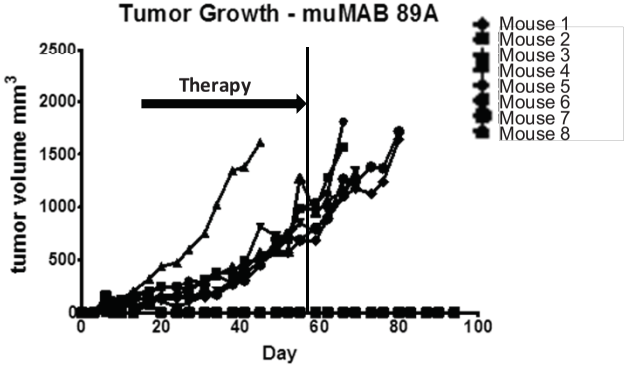

Tumor Growth - muMAB 89A
Therapy
tumor volume mm3
Day
Mouse 1
Mouse 2
Mouse 3
Mouse 4
Mouse 5
Mouse 6
Mouse 7
Mouse 8

Fig. 22

(B)

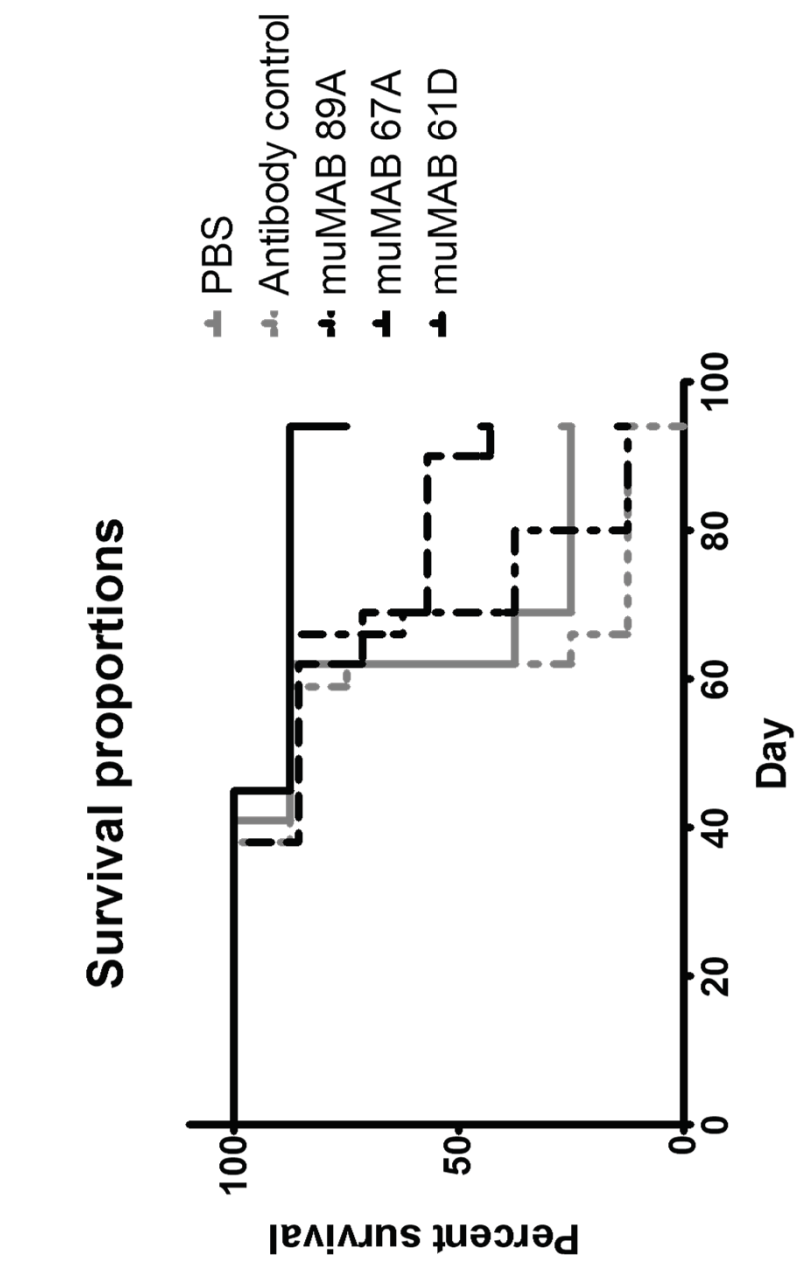

Survival proportions
PBS
Antibody control
muMAB 89A
muMAB 67A
muMAB 61D
Percent survival
100
50
0
0
20
40
60
80
100
Day

Fig. 23

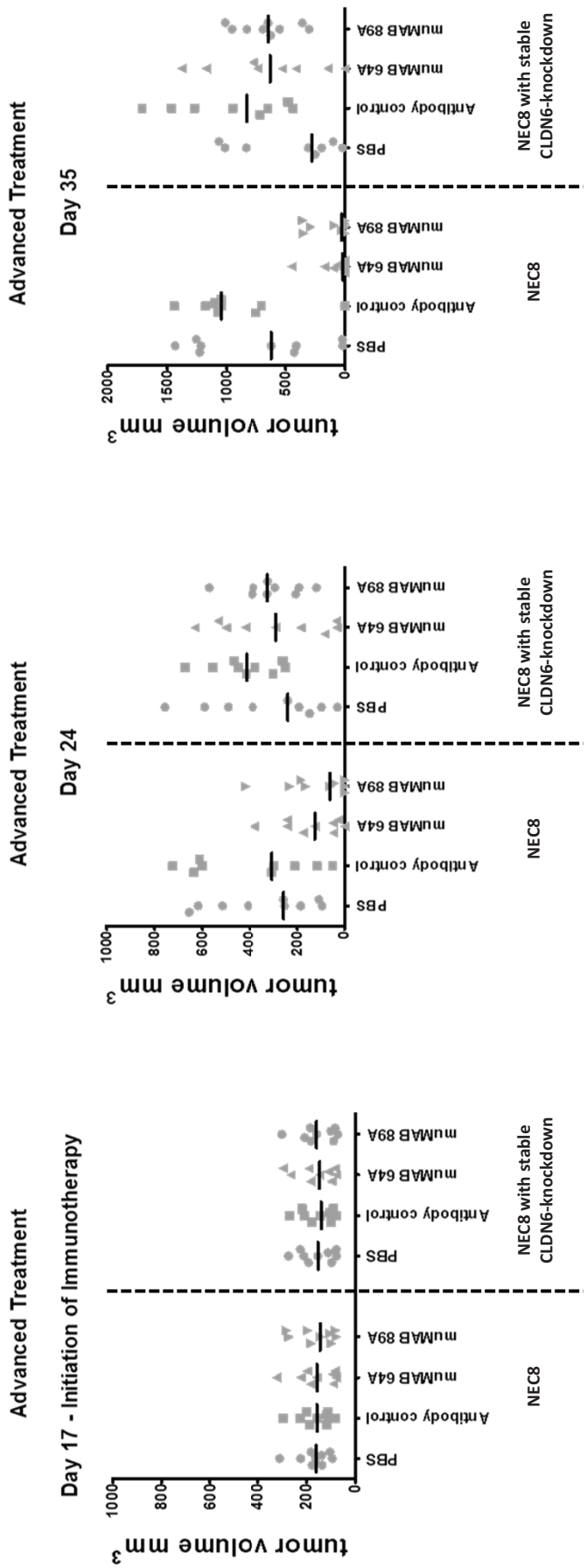

Advanced Treatment
Day 17 - Initiation of Immunotherapy
Day 24
Day 35
tumor volume mm3
0
200
400
600
800
1000
500
1000
1500
2000
PBS
Antibody control
muMAB 64A
muMAB 89A
NEC8
NEC8 with stable CLDN6-knockdown

Fig. 24

	EC1 (aa 27-81)																																																					
	L	P	M	W	K	V	T	A	F	I	G	N	S	I	V	V	A	Q	V	V	W	E	G	L	W	M	S	C	V	V	Q	S	T	G	Q	M	Q	C	K	V	Y	D	S	L	L	A	L	P	Q	D	L	Q	A	A	R
Name	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81
GT512chimAB 61D		X		X																			X	X	X			X										X																	
GT512chimAB 64A		X		X																			X	X	X			X										X																	
GT512chimAB 67A		X		X																			X	X	X			X										X																	
GT512chimAB 89A		X		X																			X	X	X			X										X																	
R&D		X		X																			X	X	X			X										X																	

	EC2 (aa 137-161)																								
	C	W	T	A	H	A	I	I	R	D	F	Y	N	P	L	V	A	E	A	Q	K	R	E	L	G
Name	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161
GT512chimAB 61D																									
GT512chimAB 64A																									
GT512chimAB 67A																									
GT512chimAB 89A																									
R&D																									

X altered transport to the membrane

no influence on antibody binding

contributes to antibody binding

essential for antibody binding

Fig. 25

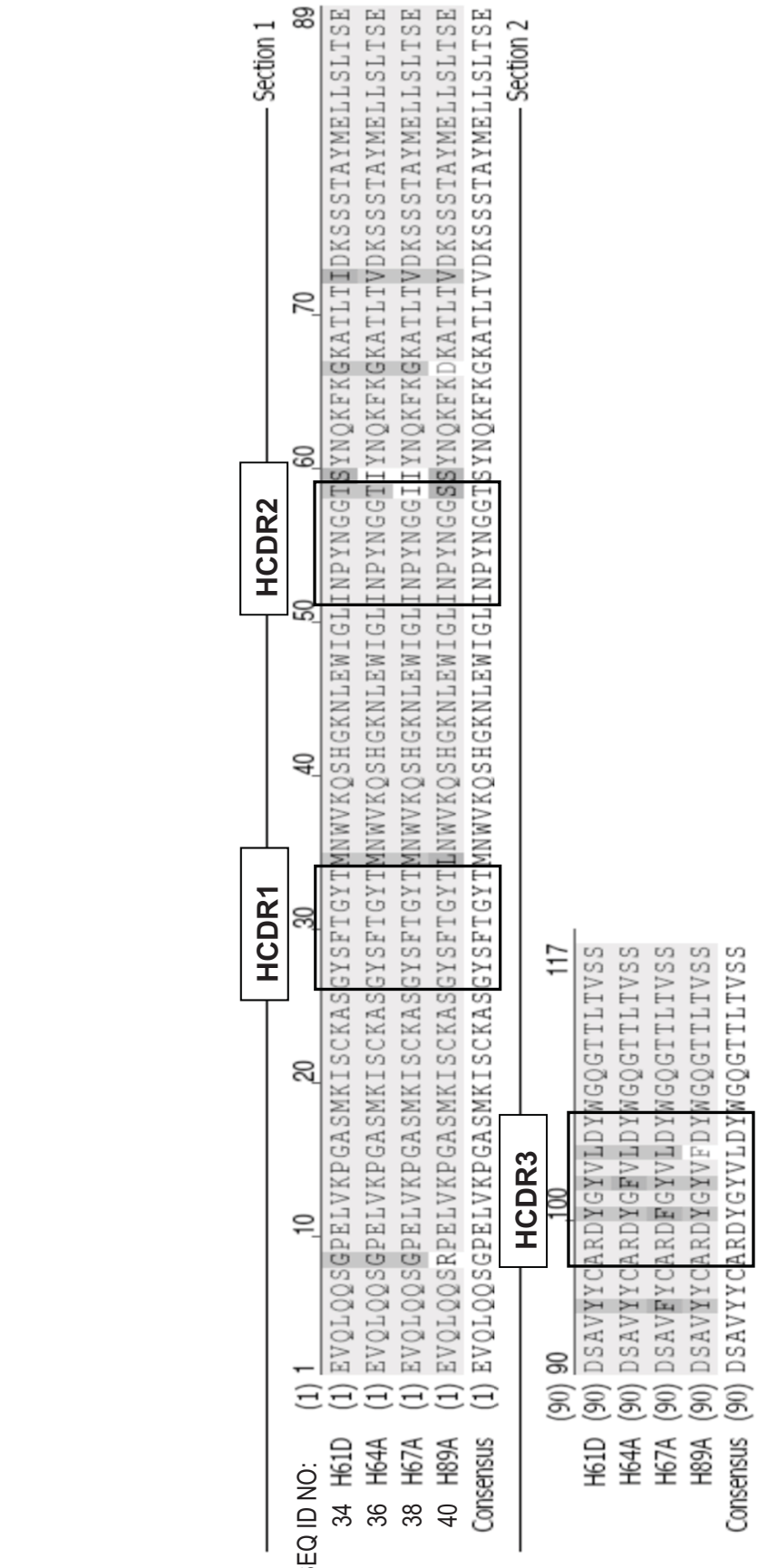
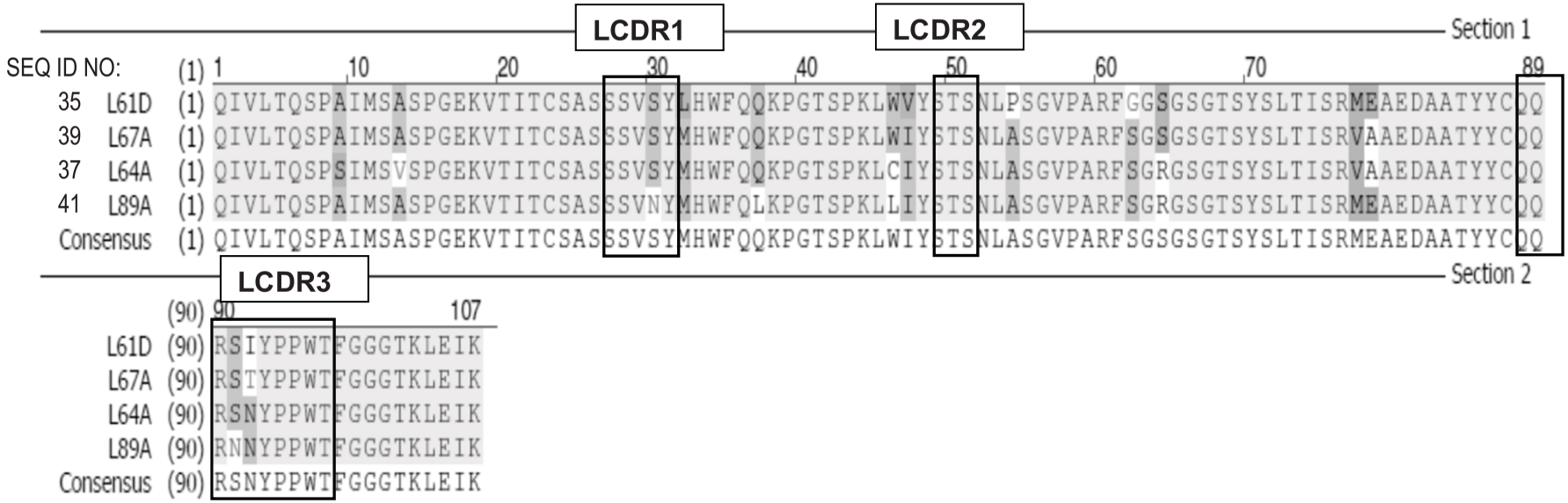

Section 1
Section 2
HCDR1
HCDR2
HCDR3
SEQ ID NO:
34 H61D
36 H64A
38 H67A
40 H89A
Consensus
(1) EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMNWVKQSHGKNLEWIGLINPYNGGTSYNQKFKGKATLTVDKSSSTAYMELLSLTSE
(90) DSAVYYCARDYGYVLDYWGQGTTLTVSS

Fig. 26


LCDR1
LCDR2
Section 1
SEQ ID NO:
(1) 1 10 20 30 40 50 60 70 89
35 L61D (1) QIVLTQSPAIMSASPGEKVTITCSASSSVSYLHWFQQKPGTSPKLWVYSTSNLPSGVPARFGGSGSGTSYSLTISRMEAEDAATYYCQQ
39 L67A (1) QIVLTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISRVAAEDAATYYCQQ
37 L64A (1) QIVLTQSPSIMSVSPGEKVTITCSASSSVSYMHWFQQKPGTSPKLCIYSTSNLASGVPARFSGRGSGTSYSLTISRVAAEDAATYYCQQ
41 L89A (1) QIVLTQSPAIMSASPGEKVTITCSASSSVNYMHWFQLKPGTSPKLLIYSTSNLASGVPARFSGRGSGTSYSLTISRMEAEDAATYYCQQ
Consensus (1) QIVLTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQ
LCDR3
Section 2
(90) 90 107
L61D (90) RSIYPPWTFGGGTKLEIK
L67A (90) RSTYPPWTFGGGTKLEIK
L64A (90) RSNYPPWTFGGGTKLEIK
L89A (90) RNNYPPWTFGGGTKLEIK
Consensus (90) RSNYPPWTFGGGTKLEIK

SEQUENCE LISTING

<110> Ganymed Pharmaceuticals AG; and
Johannes Gutenberg-Universität Mainz

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<151> 2009-11-11

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<151> 2010-07-06

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<151> 2010-07-06

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<151> 2009-11-11

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<211> 1369
<212> DNA
<213> Homo sapiens

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atggcctctg ccggaatgca gatcctggga gtcgtcctga cactgctggg ctgggtgaat 120

ggcctggtct cctgtgccct gcccatgtgg aaggtgaccg ctttcatcgg caacagcatc 180

gtggtggccc aggtggtgtg ggagggcctg tggatgtcct gcgtggtgca gagcaccggc 240

cagatgcagt gcaaggtgta cgactcactg ctggcgctgc cacaggacct gcaggctgca 300

cgtgccctct gtgtcatcgc cctccttgtg gccctgttcg gcttgctggt ctaccttgct 360

ggggccaagt gtaccacctg tgtggaggag aaggattcca aggcccgcct ggtgctcacc 420

tctgggattg tctttgtcat ctcaggggtc ctgacgctaa tccccgtgtg ctggacggcg 480

catgccatca tccgggactt ctataacccc ctggtggctg aggcccaaaa gcgggagctg 540

ggggcctccc tctacttggg ctgggcggcc tcaggccttt tgttgctggg tgggggggttg 600

ctgtgctgca cttgcccctc gggggggtcc cagggcccca gccattacat ggcccgctac 660

tcaacatctg cccctgccat ctctcggggg ccctctgagt accctaccaa gaattacgtc 720

tgacgtggag gggaatgggg gctccgctgg cgctagagcc atccagaagt ggcagtgccc 780

aacagctttg ggatgggttc gtacctttg tttctgcctc ctgctatttt tcttttgact 840

gaggatattt aaaattcatt tgaaaactga gccaaggtgt tgactcagac tctcacttag 900

gctctgctgt ttctcaccct tggatgatgg agccaaagag gggatgcttt gagattctgg 960

atcttgacat gcccatctta gaagccagtc aagctatgga actaatgcgg aggctgcttg 1020

ctgtgctggc tttgcaacaa gacagactgt ccccaagagt tcctgctgct gctgggggct 1080

gggcttccct agatgtcact ggacagctgc cccccatcct actcaggtct ctggagctcc 1140

tctcttcacc cctggaaaaa caaatgatct gttaacaaag gactgcccac ctccggaact 1200

tctgacctct gtttcctccg tcctgataag acgtccaccc cccagggcca ggtcccagct 1260

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<210> 2
<211> 220
<212> PRT
<213> Homo sapiens

<400> 2

Met Ala Ser Ala Gly Met Gln Ile Leu Gly Val Val Leu Thr Leu Leu
1 5 10 15

Gly Trp Val Asn Gly Leu Val Ser Cys Ala Leu Pro Met Trp Lys Val
20 25 30

Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val Val Trp Glu
35 40 45

Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys
50 55 60

Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala
65 70 75 80

Arg Ala Leu Cys Val Ile Ala Leu Leu Val Ala Leu Phe Gly Leu Leu
85 90 95

Val Tyr Leu Ala Gly Ala Lys Cys Thr Thr Cys Val Glu Glu Lys Asp
100 105 110

Ser Lys Ala Arg Leu Val Leu Thr Ser Gly Ile Val Phe Val Ile Ser
115 120 125

Gly Val Leu Thr Leu Ile Pro Val Cys Trp Thr Ala His Ala Ile Ile
130 135 140

Arg Asp Phe Tyr Asn Pro Leu Val Ala Glu Ala Gln Lys Arg Glu Leu
145 150 155 160

Gly Ala Ser Leu Tyr Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu
165 170 175

Gly Gly Gly Leu Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly
180 185 190

Pro Ser His Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser
195 200 205

Arg Gly Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
210 215 220

<210> 3
<211> 805
<212> DNA
<213> Artificial

<220>
<223> codon-optimized nucleic acid sequence encoding human claudin 6

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agcttgccac catggccagc gccggcatgc agatcctggg agtggtgctg accctgctgg 120

gctgggtgaa cggcctggtg tcctgcgccc tgcccatgtg gaaagtgacc gccttcatcg 180

gcaacagcat cgtggtggcc caggtcgtgt gggagggcct gtggatgagc tgtgtggtgc 240

agagcaccgg ccagatgcag tgcaaggtgt acgacagcct gctggccctg cctcaggatc 300

tgcaggccgc cagagccctg tgtgtgatcg ccctgctggt cgccctgttc ggcctgctgg 360

tgtacctcgc tggcgccaag tgcaccacct gtgtggagga aaaggacagc aaggcccggc 420

tggtcctgac aagcggcatc gtgttcgtga tcagcggcgt gctgacactg atccccgtgt 480

gctggaccgc ccacgccatc atccgggact tctacaaccc tctggtggcc gaggcccaga 540

agagagagct gggcgccagc ctgtatctgg gatgggccgc ctcaggactg ctgctgctgg 600

gcggaggcct gctgtgctgt acatgtccta gcggcggctc ccagggccct agccactaca 660

tggcccggta cagcaccagc gcccctgcca tcagcagagg ccccagcgag taccccacca 720

agaactacgt gtgataggaa ttcgagctct tatggcgcgc ccaattcgcc ctatagtgag 780

tcgtattacg tcgcgctcac tggcc 805

<210> 4
<211> 165
<212> DNA
<213> Artificial

<220>
<223> codon-optimized nucleic acid sequence encoding the predicted extracellular loop 2 (EC2) of human claudin 6

<400> 4
ggcgcgccaa ggtaccaagc ttgccaccat ggaaaccgac accctgctgc tgtgggtgct 60

gctcctgtgg gtcccaggct ctacaggcga cgccgcccag cccagagact tctacaaccc 120

cctggtggcc gaggcccaga agctcgagtc tagagggtta attaa 165

<210> 5
<211> 38
<212> PRT
<213> Artificial

<220>
<223> predicted 2nd extracellular loop of human claudin 6 containing an Ig kappa leader sequence

<220>
<221> SIGNAL
<222> (1)..(21)
<223> Ig kappa leader sequence

<220>
<221> DOMAIN
<222> (26)..(38)
<223> predicted 2nd extracellular loop (EC2) of human claudin 6

<400> 5

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Ala Ala Gln Pro Arg Asp Phe Tyr Asn Pro Leu
20 25 30

Val Ala Glu Ala Gln Lys
35

<210> 6
<211> 13
<212> PRT
<213> Homo sapiens

<400> 6

Arg Asp Phe Tyr Asn Pro Leu Val Ala Glu Ala Gln Lys
1 5 10

<210> 7
<211> 53
<212> PRT
<213> Homo sapiens

<400> 7

Pro Met Trp Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala
1 5 10 15

Gln Val Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr
20 25 30

Gly Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln

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        35                  40                  45

Asp Leu Gln Ala Ala
    50
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<210> 8
<211> 220
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (143)..(143)
<223> human claudin 6 I143V polymorphism

<400> 8

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Met Ala Ser Ala Gly Met Gln Ile Leu Gly Val Val Leu Thr Leu Leu
1               5                   10                  15

Gly Trp Val Asn Gly Leu Val Ser Cys Ala Leu Pro Met Trp Lys Val
            20                  25                  30

Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val Val Trp Glu
        35                  40                  45

Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys
    50                  55                  60

Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala
65                  70                  75                  80

Arg Ala Leu Cys Val Ile Ala Leu Leu Val Ala Leu Phe Gly Leu Leu
                85                  90                  95

Val Tyr Leu Ala Gly Ala Lys Cys Thr Thr Cys Val Glu Glu Lys Asp
            100                 105                 110

Ser Lys Ala Arg Leu Val Leu Thr Ser Gly Ile Val Phe Val Ile Ser
        115                 120                 125

Gly Val Leu Thr Leu Ile Pro Val Cys Trp Thr Ala His Ala Val Ile
    130                 135                 140

Arg Asp Phe Tyr Asn Pro Leu Val Ala Glu Ala Gln Lys Arg Glu Leu
145                 150                 155                 160

Gly Ala Ser Leu Tyr Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu
                165                 170                 175
```

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Gly Gly Gly Leu Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly
            180                 185                 190

Pro Ser His Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser
        195                 200                 205

Arg Gly Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
    210                 215                 220
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<210> 9
<211> 217
<212> PRT
<213> Homo sapiens

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1               5                   10                  15

Gly Trp Leu Gly Thr Leu Val Ser Cys Ala Leu Pro Leu Trp Lys Val
            20                  25                  30

Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val Val Trp Glu
        35                  40                  45

Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys
    50                  55                  60

Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala
65                  70                  75                  80

Arg Ala Leu Cys Val Ile Ala Leu Leu Leu Ala Leu Leu Gly Leu Leu
                85                  90                  95

Val Ala Ile Thr Gly Ala Gln Cys Thr Thr Cys Val Glu Asp Glu Gly
            100                 105                 110

Ala Lys Ala Arg Ile Val Leu Thr Ala Gly Val Ile Leu Leu Leu Ala
        115                 120                 125

Gly Ile Leu Val Leu Ile Pro Val Cys Trp Thr Ala His Ala Ile Ile
    130                 135                 140

Gln Asp Phe Tyr Asn Pro Leu Val Ala Glu Ala Leu Lys Arg Glu Leu
145                 150                 155                 160

Gly Ala Ser Leu Tyr Leu Gly Trp Ala Ala Ala Ala Leu Leu Met Leu
                165                 170                 175

Gly Gly Gly Leu Leu Cys Cys Thr Cys Pro Pro Pro Gln Val Glu Arg
```

180 185 190

Pro Arg Gly Pro Arg Leu Gly Tyr Ser Ile Pro Ser Arg Ser Gly Ala
195 200 205

Ser Gly Leu Asp Lys Arg Asp Tyr Val
210 215

<210> 10
<211> 209
<212> PRT
<213> Homo sapiens

<400> 10

Met Ala Ser Met Gly Leu Gln Val Met Gly Ile Ala Leu Ala Val Leu
1 5 10 15

Gly Trp Leu Ala Val Met Leu Cys Cys Ala Leu Pro Met Trp Arg Val
20 25 30

Thr Ala Phe Ile Gly Ser Asn Ile Val Thr Ser Gln Thr Ile Trp Glu
35 40 45

Gly Leu Trp Met Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys
50 55 60

Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala
65 70 75 80

Arg Ala Leu Val Ile Ile Ser Ile Ile Val Ala Ala Leu Gly Val Leu
85 90 95

Leu Ser Val Val Gly Gly Lys Cys Thr Asn Cys Leu Glu Asp Glu Ser
100 105 110

Ala Lys Ala Lys Thr Met Ile Val Ala Gly Val Val Phe Leu Leu Ala
115 120 125

Gly Leu Met Val Ile Val Pro Val Ser Trp Thr Ala His Asn Ile Ile
130 135 140

Gln Asp Phe Tyr Asn Pro Leu Val Ala Ser Gly Gln Lys Arg Glu Met
145 150 155 160

Gly Ala Ser Leu Tyr Val Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu
165 170 175

Gly Gly Gly Leu Leu Cys Cys Asn Cys Pro Pro Arg Thr Asp Lys Pro
180 185 190

Tyr Ser Ala Lys Tyr Ser Ala Ala Arg Ser Ala Ala Ala Ser Asn Tyr
195 200 205

Val

<210> 11
<211> 220
<212> PRT
<213> Homo sapiens

<400> 11

Met Ser Met Gly Leu Glu Ile Thr Gly Thr Ala Leu Ala Val Leu Gly
1 5 10 15

Trp Leu Gly Thr Ile Val Cys Cys Ala Leu Pro Met Trp Arg Val Ser
20 25 30

Ala Phe Ile Gly Ser Asn Ile Ile Thr Ser Gln Asn Ile Trp Glu Gly
35 40 45

Leu Trp Met Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys Lys
50 55 60

Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg
65 70 75 80

Ala Leu Ile Val Val Ala Ile Leu Leu Ala Ala Phe Gly Leu Leu Val
85 90 95

Ala Leu Val Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Asp Thr Ala
100 105 110

Lys Ala Lys Ile Thr Ile Val Ala Gly Val Leu Phe Leu Leu Ala Ala
115 120 125

Leu Leu Thr Leu Val Pro Val Ser Trp Ser Ala Asn Thr Ile Ile Arg
130 135 140

Asp Phe Tyr Asn Pro Val Val Pro Glu Ala Gln Lys Arg Glu Met Gly
145 150 155 160

Ala Gly Leu Tyr Val Gly Trp Ala Ala Ala Ala Leu Gln Leu Leu Gly
165 170 175

Gly Ala Leu Leu Cys Cys Ser Cys Pro Pro Arg Glu Lys Lys Tyr Thr
180 185 190

Ala Thr Lys Val Val Tyr Ser Ala Pro Arg Ser Thr Gly Pro Gly Ala
195 200 205

Ser Leu Gly Thr Gly Tyr Asp Arg Lys Asp Tyr Val
210 215 220

<210> 12
<211> 159
<212> DNA
<213> Artificial

<220>
<223> codon-optimized nucleic acid sequence encoding the predicted extracellular loop 1 (EC1) of human claudin 6

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gagggcctgt ggatgagctg cgtggtgcag agcaccggcc agatgcagtg caaggtgtac 120

gacagcctgc tggccctgcc tcaggatctg caggctgct 159

<210> 13
<211> 106
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<223> predicted 1st extracellular loop of human claudin 6 containing an Ig kappa leader sequence

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<221> Signal
<222> (1)..(21)
<223> Ig kappa leader sequence

<220>
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1 5 10 15

Gly Ser Thr Gly Asp Ala Ala Gln Pro Pro Met Trp Lys Val Thr Ala
20 25 30

Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val Val Trp Glu Gly Leu
35 40 45

Trp Met Ser Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys Lys Val
50 55 60

Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Leu Glu
65 70 75 80

Ser Arg Gly Pro Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
85 90 95

Met His Thr Gly His His His His His His
100 105

<210> 14
<211> 13
<212> PRT
<213> Homo sapiens

<400> 14

Pro Met Trp Lys Val Thr Ala Phe Ile Gly Asn Ser Ile
1 5 10

<210> 15
<211> 15
<212> PRT
<213> Homo sapiens

<400> 15

Met Trp Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala
1 5 10 15

<210> 16
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<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide

<400> 16
tccatgacgt tcctgacgtt 20

<210> 17
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 17
gagaaagctt gccgccacca tgggatggag ctggatcttt ctc 43

<210> 18
<211> 43
<212> DNA
<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 18
gagagggccc ttggtggagg ctgaagagac tgtgagagtg gtg 43

<210> 19
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 19
gagagggccc ttggtggagg ctgaggagac tgtgagagtg gtg 43

<210> 20
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 20
gagagggccc ttggtggagg ctgaggagac tgtgagagtg gtg 43

<210> 21
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 21
gagaaagctt gccgccacca tgcattttca agtgcagatt ttcagc 46

<210> 22
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 22
cacacgtacg tttgatttcc agcttggtgc ctc 33

<210> 23
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 23
cacacgtacg tttgatttcc agcttggtgc ctc 33

<210> 24
<211> 993
<212> DNA
<213> Homo sapiens

<400> 24
gcctccacca agggcccaag cgtgttcccc ctggccccca gcagcaagag caccagcggc 60

ggcacagccg ccctgggctg cctggtgaag gactacttcc ccgagcccgt gaccgtgagc 120

tggaacagcg gagccctgac ctccggcgtg cacaccttcc ccgccgtgct gcagagcagc 180

ggcctgtaca gcctgagcag cgtggtgacc gtgcccagca gcagcctggg cacccagacc 240

tacatctgca acgtgaacca caagcccagc aacaccaagg tggacaagag agtggagccc 300

aagagctgcg acaagaccca cacctgcccc ccctgcccag ccccagagct gctgggcgga 360

cccagcgtgt tcctgttccc ccccaagccc aaggacaccc tgatgatcag caggaccccc 420

gaggtgacct gcgtggtggt ggacgtgagc cacgaggacc cagaggtgaa gttcaactgg 480

tacgtggacg gcgtggaggt gcacaacgcc aagaccaagc ccagagagga gcagtacaac 540

agcacctaca gggtggtgtc cgtgctgacc gtgctgcacc aggactggct gaacggcaag 600

gaatacaagt gcaaggtctc caacaaggcc ctgccagccc ccatcgaaaa gaccatcagc 660

aaggccaagg gccagccacg ggagccccag gtgtacaccc tgcccccag ccgggaggag 720

atgaccaaga accaggtgtc cctgacctgt ctggtgaagg gcttctaccc agcgacatc 780

gccgtggagt gggagagcaa cggccagccc gagaacaact acaagaccac ccccccagtg 840

ctggacagcg acggcagctt cttcctgtac agcaagctga ccgtggacaa gtccaggtgg 900

cagcagggca acgtgttcag ctgcagcgtg atgcacgagg ccctgcacaa ccactacacc 960

cagaagtccc tgagcctgag ccccggcaag tag 993

<210> 25
<211> 330
<212> PRT
<213> Homo sapiens

<400> 25

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

```
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225                 230                 235                 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320
```

```
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
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<210> 26
<211> 324
<212> DNA
<213> Homo sapiens

<400> 26
cgtacggtgg ccgctcccag cgtgttcatc ttcccccca gcgacgagca gctgaagtcc 60

ggcaccgcca gcgtggtgtg cctgctgaac aacttctacc cccgggaggc caaggtgcag 120

tggaaggtgg acaacgccct gcagagcggc aacagccagg agagcgtcac cgagcaggac 180

agcaaggact ccacctacag cctgagcagc accctgaccc tgagcaaggc cgactacgag 240

aagcacaagg tgtacgcctg cgaggtgacc caccagggcc tgtccagccc cgtgaccaag 300

agcttcaaca ggggcgagtg ctag 324

<210> 27
<211> 107
<212> PRT
<213> Homo sapiens

<400> 27

```
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1               5                  10                  15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
            20                  25                  30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        35                  40                  45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
    50                  55                  60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65                  70                  75                  80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
                85                  90                  95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            100                 105
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<210> 28
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<220>
<221> misc_feature
<222> (31)..(32)
<223> any nucleotide

<400> 28
ttttttttt ttttttttt ttttttttt nn 32

<210> 29
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 29
aagcagtggt atcaacgcag agtacgcggg 30

<210> 30
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 30
ctgctcactg gatggtggga agatgg 26

<210> 31
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 31
acaggggcca gtggatagac cgatg 25

<210> 32
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 32
gtaatacgac tcactatagg gcaagcagtg gtatcaacgc agagt 45

<210> 33
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 33
gtaatacgac tcactatagg gc 22

<210> 34
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VH sequence

<400> 34

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30

Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
35 40 45

Gly Leu Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ile Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Gly Tyr Val Leu Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser
115

<210> 35
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VL sequence

<400> 35

Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15

```
Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Leu
            20                  25                  30

His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Val Tyr
        35                  40                  45

Ser Thr Ser Asn Leu Pro Ser Gly Val Pro Ala Arg Phe Gly Gly Ser
    50                  55                  60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
65                  70                  75                  80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ile Tyr Pro Pro Trp
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 36
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VH sequence

<400> 36

```
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15

Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
            20                  25                  30

Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
        35                  40                  45

Gly Leu Ile Asn Pro Tyr Asn Gly Gly Thr Ile Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Tyr Gly Phe Val Leu Asp Tyr Trp Gly Gln Gly Thr Thr
            100                 105                 110
```

Leu Thr Val Ser Ser
115

<210> 37
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VL sequence

<400> 37

Gln Ile Val Leu Thr Gln Ser Pro Ser Ile Met Ser Val Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Cys Ile Tyr
35 40 45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Arg
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Ala Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Asn Tyr Pro Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 38
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VH sequence

<400> 38

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30

Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
35 40 45

```
Gly Leu Ile Asn Pro Tyr Asn Gly Gly Ile Ile Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Phe Tyr Cys
                85                  90                  95

Ala Arg Asp Phe Gly Tyr Val Leu Asp Tyr Trp Gly Gln Gly Thr Thr
            100                 105                 110

Leu Thr Val Ser Ser
        115
```

<210> 39
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VL sequence

<400> 39

```
Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1               5                   10                  15

Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            20                  25                  30

His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr
        35                  40                  45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
    50                  55                  60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Ala Ala Glu
65                  70                  75                  80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Pro Trp
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 40
<211> 117
<212> PRT
<213> Artificial Sequence

<220>

<223> Antibody VH sequence

<400> 40

```
Glu Val Gln Leu Gln Gln Ser Arg Pro Glu Leu Val Lys Pro Gly Ala
1               5                  10                  15

Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
            20                  25                  30

Thr Leu Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
        35                  40                  45

Gly Leu Ile Asn Pro Tyr Asn Gly Gly Ser Ser Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Tyr Gly Tyr Val Phe Asp Tyr Trp Gly Gln Gly Thr Thr
            100                 105                 110

Leu Thr Val Ser Ser
        115
```

<210> 41
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VL sequence

<400> 41

```
Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1               5                  10                  15

Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Asn Tyr Met
            20                  25                  30

His Trp Phe Gln Leu Lys Pro Gly Thr Ser Pro Lys Leu Leu Ile Tyr
        35                  40                  45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Arg
    50                  55                  60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
65                  70                  75                  80
```

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Asn Asn Tyr Pro Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 42
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VH CDR3 sequence

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Any amino acid, preferably Leu or Phe, more preferably Leu

<400> 42

Xaa Gly Xaa Val Xaa
1 5

<210> 43
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VH CDR3 sequence

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>

<221> MISC_FEATURE
<222> (6)..(6)
<223> Any amino acid, preferably Leu or Phe, more preferably Leu

<400> 43

Asp Xaa Gly Xaa Val Xaa
1 5

<210> 44
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VH CDR3 sequence

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Any amino acid, preferably Leu or Phe, more preferably Leu

<400> 44

Xaa Gly Xaa Val Xaa Asp
1 5

<210> 45
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VH CDR3 sequence

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>

<221> MISC_FEATURE
<222> (6)..(6)
<223> Any amino acid, preferably Leu or Phe, more preferably Leu

<400> 45

Asp Xaa Gly Xaa Val Xaa Asp
1 5

<210> 46
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VH CDR3 sequence

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Any amino acid, preferably an aromatic amino acid, more preferably Phe or Tyr, most preferably Tyr

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Any amino acid, preferably Leu or Phe, more preferably Leu

<400> 46

Ala Arg Asp Xaa Gly Xaa Val Xaa Asp Tyr
1 5 10

<210> 47
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VH CDR1 sequence

<400> 47

Gly Tyr Ser Phe Thr Gly Tyr Thr
1 5

<210> 48
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VH CDR2 sequence

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Any amino acid, preferably Thr, Ser or Ile, most preferably Thr

<400> 48

Ile Asn Pro Tyr Asn Gly Gly Xaa
1 5

<210> 49
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VL CDR3 sequence

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Any amino acid, preferably Ser or Asn, most preferably Ser

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Any amino acid, preferably Tyr, Ser, Ile, Asn or Thr, more preferably Tyr, Ser, or Asn, most preferably Asn

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Any amino acid, preferably Ser or Tyr, more preferably Tyr

<400> 49

Arg Xaa Xaa Xaa Pro
1 5

<210> 50
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VL CDR3 sequence

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Any amino acid, preferably Ser or Asn, most preferably Ser

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Any amino acid, preferably Tyr, Ser, Ile, Asn or Thr, more preferably Tyr, Ser, or Asn, most preferably Asn

<220>

<221> MISC_FEATURE
<222> (5)..(5)
<223> Any amino acid, preferably Ser or Tyr, more preferably Tyr

<400> 50

Gln Arg Xaa Xaa Xaa Pro Pro
1 5

<210> 51
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VL CDR3 sequence

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Any amino acid, preferably Ser or Asn, most preferably Ser

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Any amino acid, preferably Tyr, Ser, Ile, Asn or Thr, more preferably Tyr, Ser, or Asn, most preferably Asn

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Any amino acid, preferably Ser or Tyr, more preferably Tyr

<400> 51

Gln Gln Arg Xaa Xaa Xaa Pro Pro Trp Thr
1 5 10

<210> 52
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody VL CDR1 sequence

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Any amino acid, preferably Ser or Asn, most preferably Ser

<400> 52

Ser Ser Val Xaa Tyr
1 5

<210> 53
<211> 3
<212> PRT

<213> Artificial Sequence

<220>
<223> Antibody VL CDR2 sequence

<400> 53

Ser Thr Ser
1