CAGGGGACAGGCTGCAGCCGGTGCAGTTACACGTTTTCCTCCAAGGAGCCTCGGACGTTG
TCACGGGTTTGGGGTCGGGGACAGAGCAGTGACCATGGCCAGGCTGGCGTTGTCTCCTGT
GCCCAGCCACTGGATGGTGGCGTTGCTGCTGCTGCTCTCAGCTGAGCCAGTACCAGCAGC
CAGATCGGAGGACCGGTACCGGAATCCCAAAGGTAGTGCTTGTTCGCGGATCTGGCAGAG
CCCACGTTTCATAGCCAGGAAACGGGGCTTCACGGTGAAAATGCACTGCTACATGAACAG
CGCCTCCGGCAATGTGAGCTGGCTCTGGAAGCAGGAGATGGACGAGAATCCCCAGCAGCT
GAAGCTGGAAAAGGGCCGCATGGAAGAGTCCCAGAACGAATCTCTCGCCACCCTCACCAT
CCAAGGCATCCGGTTTGAGGACAATGGCATCTACTTCTGTCAGCAGAAGTGCAACAACAC
CTCGGAGGTCTACCAGGGCTGCGGCACAGAGCTGCGAGTCATGGGATTCAGCACCTTGGC
ACAGCTGAAGCAGAGGAACACGCTGAAGGATGGTATCATCATGATCCAGACGCTGCTGAT
CATCCTCTTCATCATCGTGCCTATCTTCCTGCTGCTGGACAAGGATGACAGCAAGGCTGG
CATGGAGGAAGATCACACCTACGAGGGCCTGGACATTGACCAGACAGCCACCTATGAGGA
CATAGTGACGCTGCGGACAGGGGAAGTGAAGTGGTCTGTAGGTGAGCACCCAGGCCAGGA
GTGAGAGCCAGGTCGCCCCATGACCTGGGTGCAGGCTCCCTGGCCTCAGTGACTGCTTCG
GAGCTGCCTGGCTCATGGCCCAACCCCTTTCCTGGACCCCCCAGCTGGCCTCTGAAGCTG
GCCCACCAGAGCTGCCATTTGTCTCCAGCCCCTGGTCCCCAGCTCTTGCCAAAGGGCCTG
GAGTAGAAGGACAACAGGGCAGCAACTTGGAGGGAGTTCTCTGGGGATGGACGGGACCCA
GCCTTCTGGGGGTGCTATGAGGTGATCCGTCCCCACACATGGGATGGGGGAGGCAGAGAC
TGGTCCAGAGCCCGCAAATGGACTCGGAGCCGAGGGCCTCCCAGCAGAGCTTGGGAAGGG
CCATGGACCCAACTGGGCCCCAGAAGAGCCACAGGAACATCATTCCTCTCCCGCAACCAC
TCCCACCCCAGGGAGGCCCTGGCCTCCAGTGCCTTCCCCCGTGGAATAAACGGTGTGTCC
TGAGAAACCA

FIG. 1

DNA225786

MARLALSPVPSHWMVALLLLLSAEPVPAARSEDRYRNPKGSACSRIWQSPRFIARKRGFT
VKMHCYMNSASGNVSWLWKQEMDENPQQLKLEKGRMEESQNESLATLTIQGIRFEDNGIY
FCQQKCNNTSEVYQGCGTELRVMGFSTLAQLKQRNTLKDGIIMIQTLLIILFIIVPIFLL
LDKDDSKAGMEEDHTYEGLDIDQTATYEDIVTLRTGEVKWSVGEHPGQE

Signal sequence.
amino acids 1-28.

Transmembrane domain.
amino acids 5-25, 159-179.

Immunoglobulin domain.
amino acids 58-124.

Immunoreceptor tyrosine-based activation motif.
amino acids 193-213.

N-glycosylation site.
amino acids 73-76, 101-104, 127-130, 128-131.

Protein kinase C phosphorylation site.
amino acids 49-51, 60-62, 156-158, 212-214.

Casein kinase II phosphorylation site.
amino acids 99-102, 156-159, 206-209, 221-224.

Tyrosine kinase phosphorylation site.
amino acids 113-120.

N-myristoylation site.
amino acids 40-45, 118-123.

FIG. 2

CHIMERIC ANTI-HUMAN CD79b (chMA79b) LIGHT CHAIN

CACTCCCAGCTCCAACTGCACCTCGGTTCTATCGATTGAATTCCACC**ATG**GGATGGTCATGT
ATCATCCTTTTTCTAGTAGCAACTGCAACTGGAGTACATTCAGATATCGTGCTGACCCAATC
TCCAGCTTCTTTGGCTGTGTCTCTGGGGCAGAGGGCCACCATCTCCTGCAAGGCCAGCCAAA
GTGTTGATTATGATGGTGATAGTTTTTTGAACTGGTACCAACAGAAACCAGGACAGCCACCC
AAACTCTTCATCTATGCTGCATCCAATCTAGAATCTGGGATCCCAGCCAGGTTTAGTGGCAG
TGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGGAGGAGGATGCTGCAACCT
ATTACTGTCAGCAAAGTAATGAGGATCCGCTCACGTTCGGGGCAGGCACCGAGCTGGAACTC
AAACGGACCGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC
TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT
GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGC
AAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACA
CAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA
ACAGGGGAGAGTGT**TAA**GCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGT
TACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAG
TTGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTCGGC

FIG. 3

CHIMERIC ANTI-HUMAN CD79b (chMA79b) LIGHT CHAIN

DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSFLNWYQQKPGQPPKLFIYAASNLES
GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPLTFGAGTELELKRTVAAPSVF
IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIG. 4

CHIMERIC ANTI-HUMAN CD79b (chMA79b) HEAVY CHAIN

TCGGTTCTATCGATTGAATTCCACC**ATG**GGATGGTCATGTATCATCCTTTTTCTAGTAGCAA
CTGCAACTGGAGTACATTCAGAAGTTCAGCTGCAGCAGTCTGGGGCTGAACTGATGAAGCCT
GGGGCCTCAGTGAAGATATCCTGCAAGGCTACTGGCTACACATTCAGTAGTTACTGGATAGA
GTGGGTAAAGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGAGATTTTACCTGGAGGTG
GTGATACTAACTACAATGAGATTTTCAAGGGCAAGGCCACATTCACTGCAGATACATCCTCC
AACACAGCCTACATGCAACTCAGCAGCCTGACATCTGAGGACTCTGCCGTCTATTACTGTAC
AAGACGAGTACCGGTTTACTTTGACTACTGGGGCCAAGGAACCTCAGTCACCGTCTCCTCAG
CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGC
ACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAA
CTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCT
ACTCCCTCAGCAGCGTGGTGACTGTGCCCTCTAGCAGCTTGGGCACCCAGACCTACATCTGC
AACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
CAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCC
TCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG
GTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
GGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCA
GCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCC
AACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGA
ACCACAGGTGTACACCCTGCCCCCATCCCGGGAAGAGATGACCAAGAACCAGGTCAGCCTGA
CCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG
CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTA
CAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGA
TGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA**TGA**
GTGCGACGGCCCTAGAGTCGACCTGCAGAAGCTTGGCCGCCAT

FIG. 5

CHIMERIC ANTI-HUMAN CD79b (chMA79b) HEAVY CHAIN

EVQLQQSGAELMKPGASVKISCKATGYTFSSYWIEWVKQRPGHGLEWIGEILPGGGDTNY
NEIFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCTRRVPVYFDYWGQGTSVTVSSAST
KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY
SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV
FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK
NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPG

FIG. 6

VL Sequences

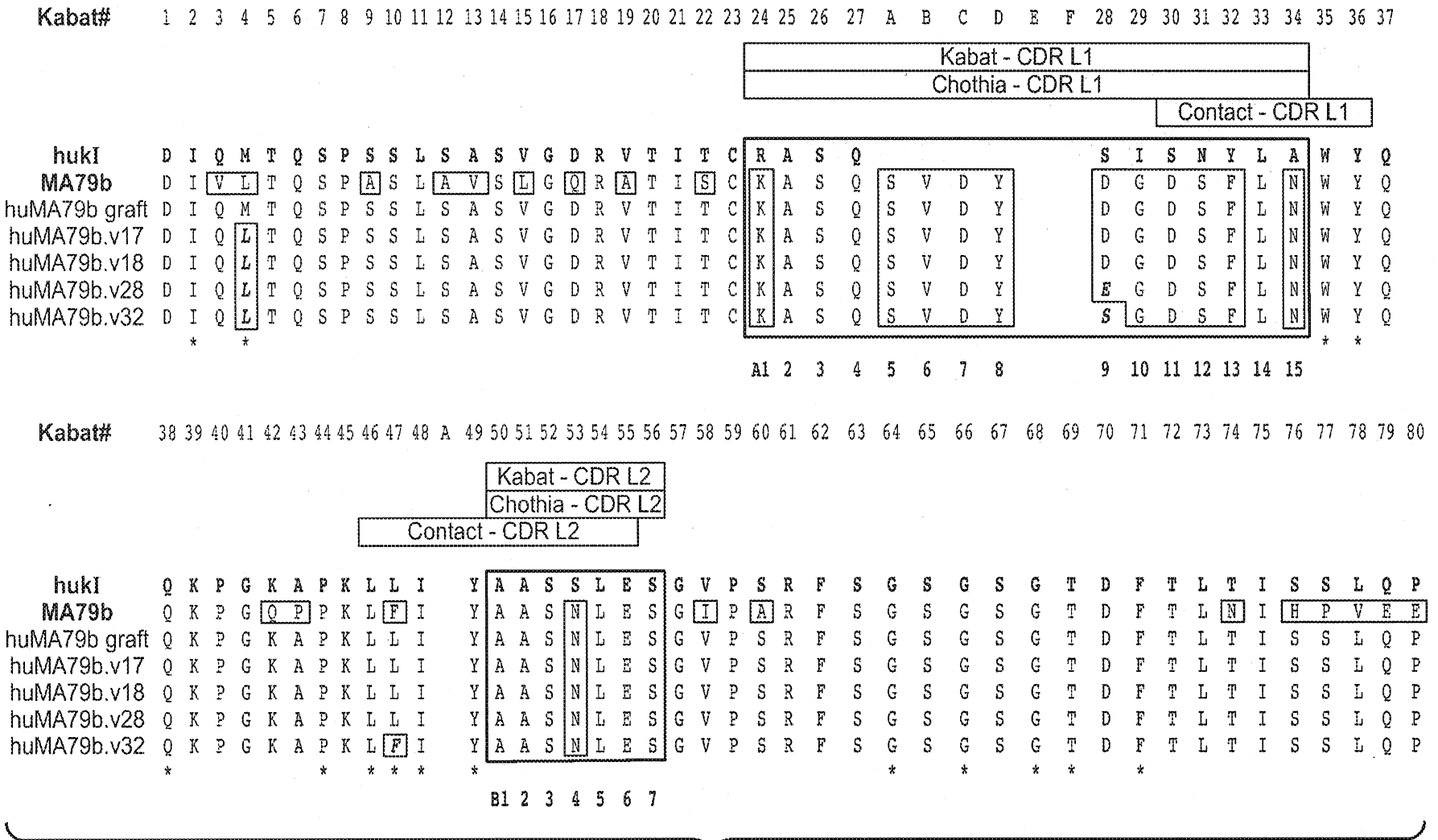


FIG. 7A

VL Sequences

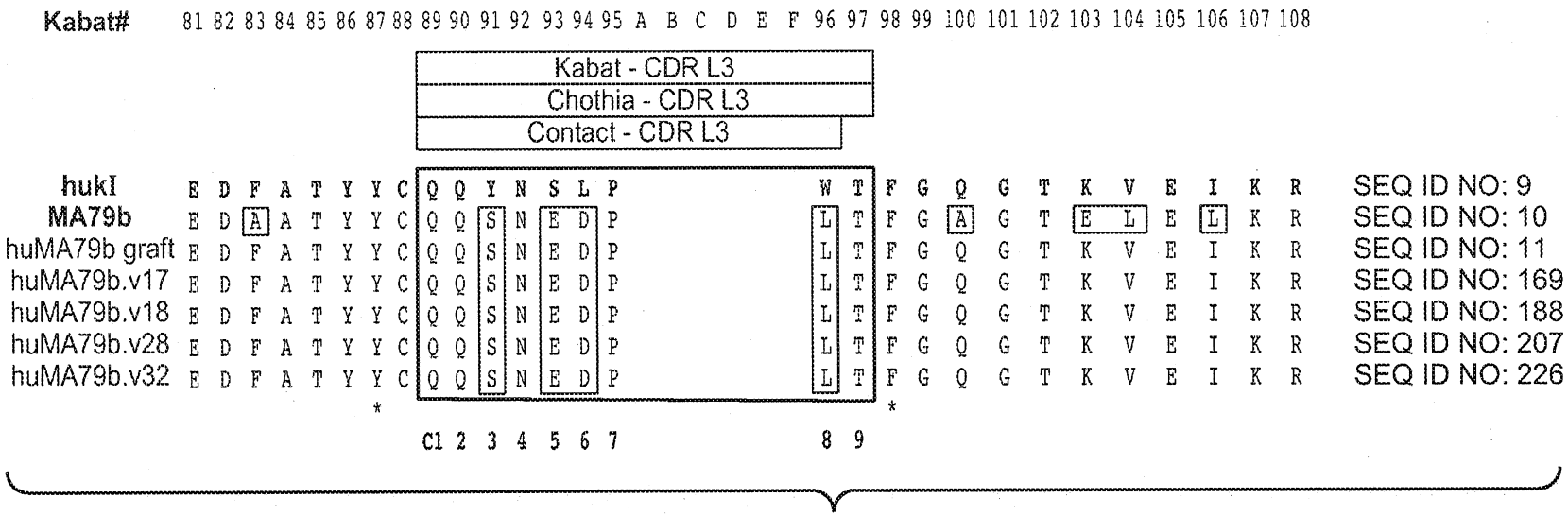


FIG. 7B

VH Sequences

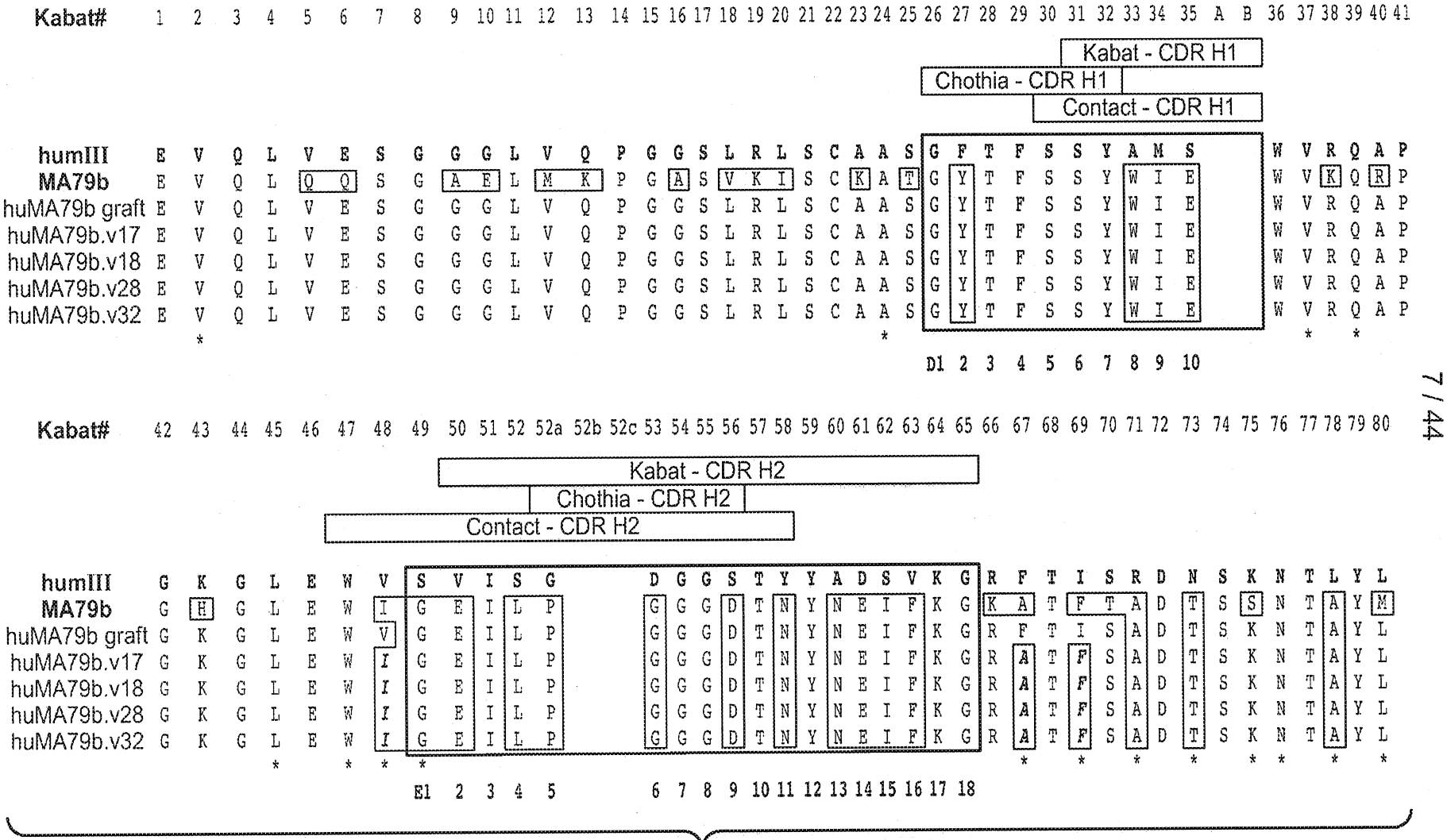


FIG. 8A

VH Sequences

Kabat#	81	82	A	B	C	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	A	B	C	D	E	F	G	H	I	J	K	101	102	103	104
																Kabat - CDR H3																								
																Chothia - CDR H3																								
																Contact - CDR H3																								
humIII	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	A	R	G																F	D	Y	W	G
MA79b	Q	L	S	S	L	T	S	E	D	S	A	V	Y	Y	C	T	R	R	V	P	V	Y												F	D	Y	W	G
huMA79b graft	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	T	R	R	V	P	V	Y												F	D	Y	W	G
huMA79b.v17	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	T	R	R	V	P	V	Y												F	D	Y	W	G
huMA79b.v18	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	T	R	R	V	P	*I*	*R*												*L*	D	Y	W	G
huMA79b.v28	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	T	R	R	V	P	*I*	*R*												*L*	D	Y	W	G
huMA79b.v32	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	T	R	R	V	P	*I*	*R*												*L*	D	Y	W	G
														*		*	*																				*	
																F1	2	3	4	5	6	7												8	9	10		

Kabat#	105	106	107	108	109	110	111	112	113	
humIII	Q	G	T	L	V	T	V	S	S	SEQ ID NO: 13
MA79b	Q	G	T	S	V	T	V	S	S	SEQ ID NO: 14
huMA79b graft	Q	G	T	L	V	T	V	S	S	SEQ ID NO: 15
huMA79b.v17	Q	G	T	L	V	T	V	S	S	SEQ ID NO: 170
huMA79b.v18	Q	G	T	L	V	T	V	S	S	SEQ ID NO: 189
huMA79b.v28	Q	G	T	L	V	T	V	S	S	SEQ ID NO: 208
huMA79b.v32	Q	G	T	L	V	T	V	S	S	SEQ ID NO: 227

FIG. 8B

	A	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	
L1	**K**	**A**	**S**	**Q**	**S**	**V**	**D**	**Y**	**D**	**G**	**D**	**S**	**F**	**L**	**N**		SEQ ID NO: 131
	K	A	S	K	S	V	D	Y	D	G	D	S	F	L	N		SEQ ID NO: 17; SPL-2

	B	1	2	3	4	5	6	7	
L2	**A**	**A**	**S**	**N**	**L**	**E**	**S**		SEQ ID NO: 132
	A	A	S	N	R	E	S		SEQ ID NO: 18
	A	A	S	N	L	K	S		SEQ ID NO: 19

	C	1	2	3	4	5	6	7	8	9	
L3	**Q**	**Q**	**S**	**N**	**E**	**D**	**P**	**L**	**T**		SEQ ID NO: 133
	Q	Q	S	N	S	D	P	L	T		SEQ ID NO: 20; SPL-5
	Q	Q	S	N	K	D	P	L	T		SEQ ID NO: 21

FIG. 9

	Biacore KD (nM)		
MA79b Variant IgG	Fab	IgG	Immobilized Antigen
MA79b	200	2	hu CD79b.ecd-Fc
		4.7	hu CD79b.ecd
hu MA79b graft		261	hu CD79b.ecd
hu MA79b L2-2	44		hu CD79b.ecd-Fc
	39	43	hu CD79b.ecd
hu MA79b H3-10		29	hu CD79b.ecd
hu MA79b H1-6		42	hu CD79b.ecd
hu MA79b L2/H3		2	hu CD79b.ecd-Fc
		3	hu CD79b.ecd
		1	16mer peptide

FIG. 11

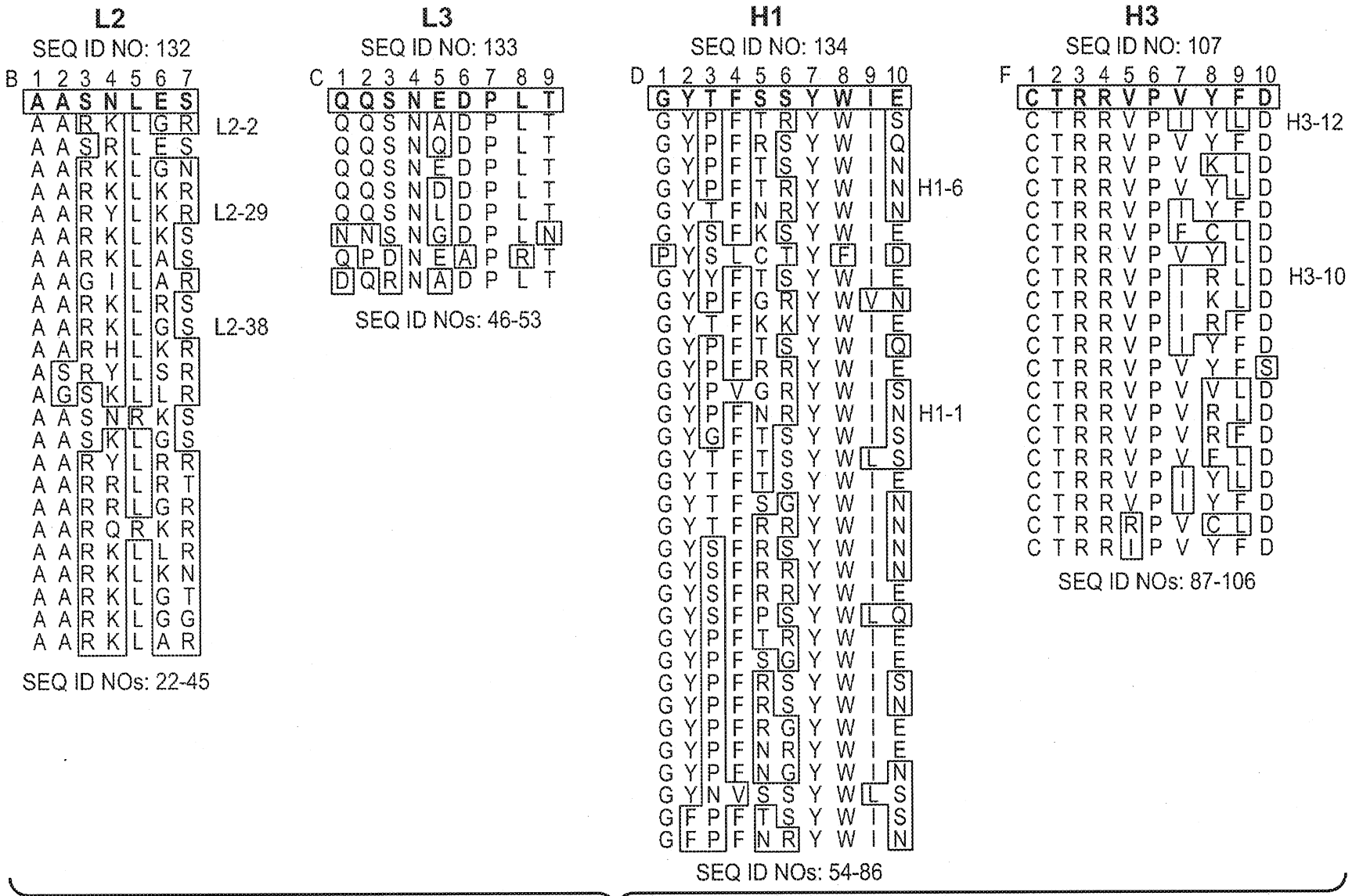

L2
SEQ ID NO: 132
B 1 2 3 4 5 6 7
A A S N L E S
A A R K L G R L2-2
A A S R L E S
A A R K L G N
A A R K L K R
A A R Y L K R L2-29
A A R K L K S
A A R K L A S
A A G I L A R
A A R K L R S
A A R K L G S L2-38
A A R H L K R
A S R Y L S R
A G S K L L R
A A S N R K S
A A S K L G S
A A R Y L R R
A A R R L R T
A A R R L G R
A A R Q R K R
A A R K L L R
A A R K L K N
A A R K L G T
A A R K L G G
A A R K L A R
SEQ ID NOs: 22-45
L3
SEQ ID NO: 133
C 1 2 3 4 5 6 7 8 9
Q Q S N E D P L T
Q Q S N A D P L T
Q Q S N Q D P L T
Q Q S N E D P L T
Q Q S N D D P L T
Q Q S N L D P L T
N N S N G D P L N
Q P D N E A P R T
D Q R N A D P L T
SEQ ID NOs: 46-53
H1
SEQ ID NO: 134
D 1 2 3 4 5 6 7 8 9 10
G Y T F S S Y W I E
G Y P F T R Y W I S
G Y P F R S Y W I Q
G Y P F T S Y W I N
G Y P F T R Y W I N H1-6
G Y T F N R Y W I N
G Y S F K S Y W I E
P Y S L C T Y F I D
G Y Y F T S Y W I E
G Y P F G R Y W V N
G Y T F K K Y W I E
G Y P F T S Y W I Q
G Y P F R R Y W I E
G Y P V G R Y W I S
G Y P F N R Y W I N H1-1
G Y G F T S Y W I S
G Y T F T S Y W L S
G Y T F T S Y W I E
G Y T F S G Y W I N
G Y T F R R Y W I N
G Y S F R S Y W I N
G Y S F R R Y W I N
G Y S F R R Y W I E
G Y S F P S Y W L Q
G Y P F T R Y W I E
G Y P F S G Y W I E
G Y P F R S Y W I S
G Y P F R S Y W I N
G Y P F R G Y W I E
G Y P F N R Y W I E
G Y P F N G Y W I N
G Y N V S S Y W L S
G F P F T S Y W I S
G F P F N R Y W I N
SEQ ID NOs: 54-86
H3
SEQ ID NO: 107
F 1 2 3 4 5 6 7 8 9 10
C T R R V P V Y F D
C T R R V P L Y L D H3-12
C T R R V P V Y F D
C T R R V P V K L D
C T R R V P V Y L D
C T R R V P I Y F D
C T R R V P F C L D
C T R R V P V Y L D
C T R R V P I R L D H3-10
C T R R V P I K L D
C T R R V P I R F D
C T R R V P I Y F D
C T R R V P V Y F S D
C T R R V P V V L D
C T R R V P V R L D
C T R R V P V R F D
C T R R V P V F L D
C T R R V P I Y L D
C T R R V P I Y F D
C T R R R P V C L D
C T R R I P V Y F D
SEQ ID NOs: 87-106

FIG. 10

huMA79 FW Variant IgG	Murine Framework Residues Present: VL	VH	Changes for Stability in VL	CDR-H3 seq	Bivalent Binding Fold $Kd_{variant}$ / $Kd_{chimera}$
	4 47	48 67 69 71 73 75 78 80	28 29 94 95		
huMA79 graft		71 73 78		wt	56
All Framework	4 47	48 67 69 71 73 75 78 80		wt	1
1		48 71 73 78		wt	9.4
2	47	71 73 78		wt	18
3		67 69 71 73 75 78 80		wt	5.5
4		69 71 73 75 78 80		wt	12
5		48 67 69 71 73 75 78 80		wt	3.5
6		48 67 71 73 78		wt	7.6
7		48 69 71 73 78		wt	3.5
8		48 67 69 71 73 78		wt	1.7
9		48 67 69 71 73 78 80		wt	1.8
10		48 67 69 71 73 75 78		wt	NA
11		48 67 69 71 73 75 78 80		H3-10	0.6
12		48 67 69 71 73 78		H3-10	0.5
13	47	48 69 71 73 78		wt	1.8
14	4	48 69 71 73 78		wt	1.1
15	4 47	48 69 71 73 78		wt	0.8
16	4	48 67 71 73 78		wt	1.6
17	4	48 67 69 71 73 78		wt	1.0
18	4	48 67 69 71 73 78		H3-10	0.4
19	4	48 67 69 71 73 78	S E	H3-10	NDB
20	4	48 67 69 71 73 78	S N	H3-10	NDB
21	4	48 67 69 71 73 78	E E	H3-10	NDB
22	4	48 67 69 71 73 78	E N	H3-10	NDB
23	4 47	48 67 69 71 73 78	S E	H3-10	25
24	4 47	48 67 69 71 73 78	S N	H3-10	NDB
25	4 47	48 67 69 71 73 78	E E	H3-10	NDB
26	4 47	48 67 69 71 73 78	E N	H3-10	NDB
27	4 47	48 67 69 71 73 78		H3-10	
28	4	48 67 69 71 73 78	E	H3-10	0.8
29		48 67 69 71 73 78	N	H3-10	very weak
30	4 47	48 67 69 71 73 78	A	H3-10	1.3
31	4 47	48 67 69 71 73 78	S	H3-10	1.0
32	4 47	48 67 69 71 73 78	S	H3-10	1.6
33	4 47	48 67 69 71 73 78	A	H3-10	very weak
34	4 47	48 67 69 71 73 78	E	H3-10	NDB

FIG. 12

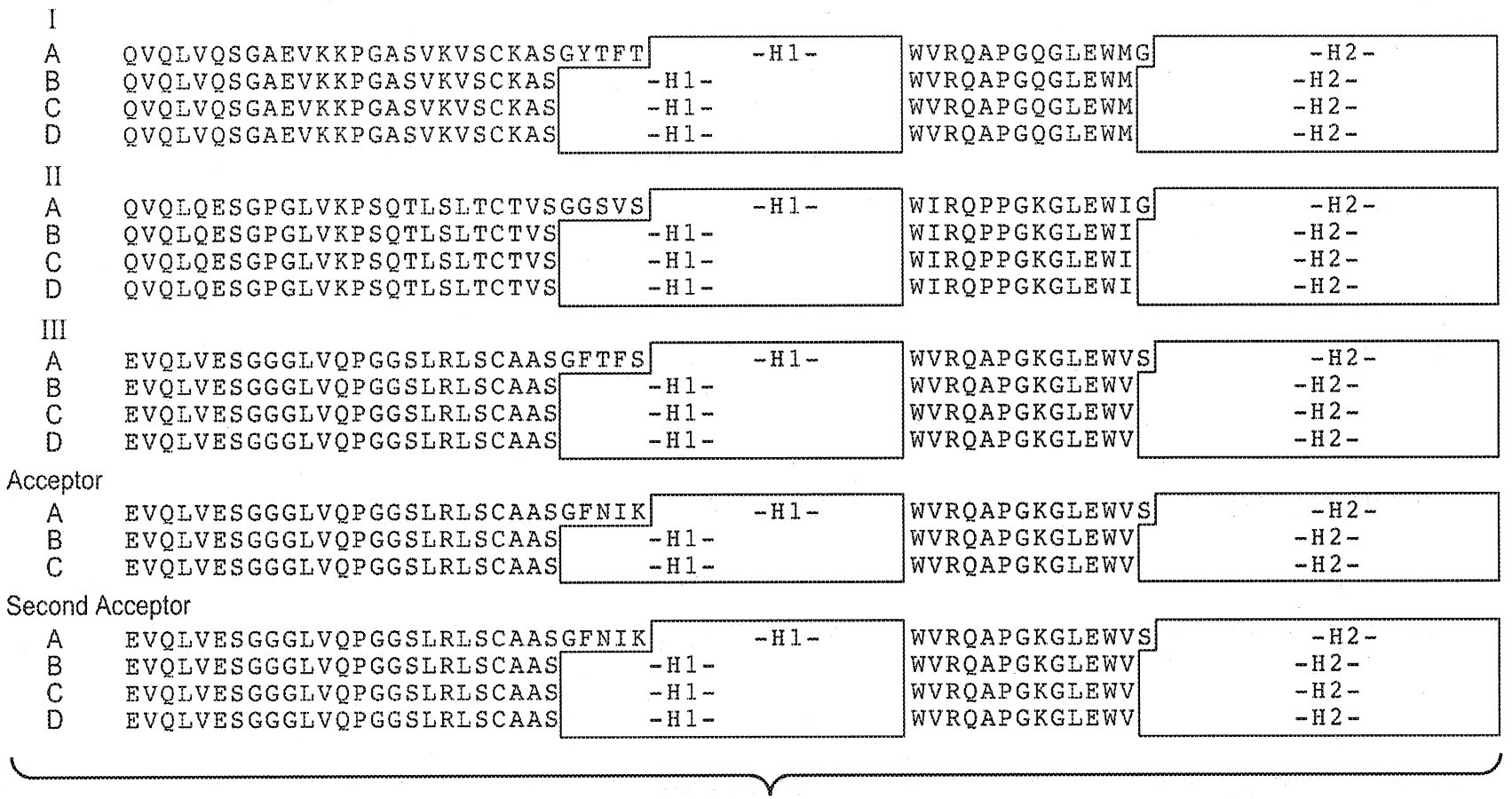

I
A QVQLVQSGAEVKKPGASVKVSCKASGYTFT -H1- WVRQAPGQGLEWMG -H2-
B QVQLVQSGAEVKKPGASVKVSCKAS -H1- WVRQAPGQGLEWM -H2-
C QVQLVQSGAEVKKPGASVKVSCKAS -H1- WVRQAPGQGLEWM -H2-
D QVQLVQSGAEVKKPGASVKVSCKAS -H1- WVRQAPGQGLEWM -H2-
II
A QVQLQESGPGLVKPSQTLSLTCTVSGGSVS -H1- WIRQPPGKGLEWIG -H2-
B QVQLQESGPGLVKPSQTLSLTCTVS -H1- WIRQPPGKGLEWI -H2-
C QVQLQESGPGLVKPSQTLSLTCTVS -H1- WIRQPPGKGLEWI -H2-
D QVQLQESGPGLVKPSQTLSLTCTVS -H1- WIRQPPGKGLEWI -H2-
III
A EVQLVESGGGLVQPGGSLRLSCAASGFTFS -H1- WVRQAPGKGLEWVS -H2-
B EVQLVESGGGLVQPGGSLRLSCAAS -H1- WVRQAPGKGLEWV -H2-
C EVQLVESGGGLVQPGGSLRLSCAAS -H1- WVRQAPGKGLEWV -H2-
D EVQLVESGGGLVQPGGSLRLSCAAS -H1- WVRQAPGKGLEWV -H2-
Acceptor
A EVQLVESGGGLVQPGGSLRLSCAASGFNIK -H1- WVRQAPGKGLEWVS -H2-
B EVQLVESGGGLVQPGGSLRLSCAAS -H1- WVRQAPGKGLEWV -H2-
C EVQLVESGGGLVQPGGSLRLSCAAS -H1- WVRQAPGKGLEWV -H2-
Second Acceptor
A EVQLVESGGGLVQPGGSLRLSCAASGFNIK -H1- WVRQAPGKGLEWVS -H2-
B EVQLVESGGGLVQPGGSLRLSCAAS -H1- WVRQAPGKGLEWV -H2-
C EVQLVESGGGLVQPGGSLRLSCAAS -H1- WVRQAPGKGLEWV -H2-
D EVQLVESGGGLVQPGGSLRLSCAAS -H1- WVRQAPGKGLEWV -H2-

FIG. 13A

I				
A	RVTITADTSTSTAYMELSSLRSEDTAVYYCAR	-H3-	WGQGTLVTVSS	SEQ ID NO.: 108
B	RVTITADTSTSTAYMELSSLRSEDTAVYYCAR	-H3-	WGQGTLVTVSS	SEQ ID NO.: 109
C	RVTITADTSTSTAYMELSSLRSEDTAVYYCA	-H3-	WGQGTLVTVSS	SEQ ID NO.: 110
D	RVTITADTSTSTAYMELSSLRSEDTAVYYC	-H3-	WGQGTLVTVSS	SEQ ID NO.: 111
II				
A	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	-H3-	WGQGTLVTVSS	SEQ ID NO.: 112
B	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	-H3-	WGQGTLVTVSS	SEQ ID NO.: 113
C	RVTISVDTSKNQFSLKLSSVTAADTAVYYCA	-H3-	WGQGTLVTVSS	SEQ ID NO.: 114
D	RVTISVDTSKNQFSLKLSSVTAADTAVYYC	-H3-	WGQGTLVTVSS	SEQ ID NO.: 115
III				
A	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	-H3-	WGQGTLVTVSS	SEQ ID NO.: 116
B	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	-H3-	WGQGTLVTVSS	SEQ ID NO.: 117
C	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA	-H3-	WGQGTLVTVSS	SEQ ID NO.: 118
D	RFTISRDNSKNTLYLQMNSLRAEDTAVYYC	-H3-	WGQGTLVTVSS	SEQ ID NO.: 119
Acceptor				
A	RFTISADTSKNTAYLQMNSLRAEDTAVYYCSR	-H3-	WGQGTLVTVSS	SEQ ID NO.: 120
B	RFTISADTSKNTAYLQMNSLRAEDTAVYYCSR	-H3-	WGQGTLVTVSS	SEQ ID NO.: 121
C	RFTISADTSKNTAYLQMNSLRAEDTAVYYCS	-H3-	WGQGTLVTVSS	SEQ ID NO.: 122
Second Acceptor				
A	RFTISADTSKNTAYLQMNSLRAEDTAVYYCAR	-H3-	WGQGTLVTVSS	SEQ ID NO.: 123
B	RFTISADTSKNTAYLQMNSLRAEDTAVYYCAR	-H3-	WGQGTLVTVSS	SEQ ID NO.: 124
C	RFTISADTSKNTAYLQMNSLRAEDTAVYYCA	-H3-	WGQGTLVTVSS	SEQ ID NO.: 125
D	RFTISADTSKNTAYLQMNSLRAEDTAVYYC	-H3-	WGQGTLVTVSS	SEQ ID NO.: 126

FIG. 13B

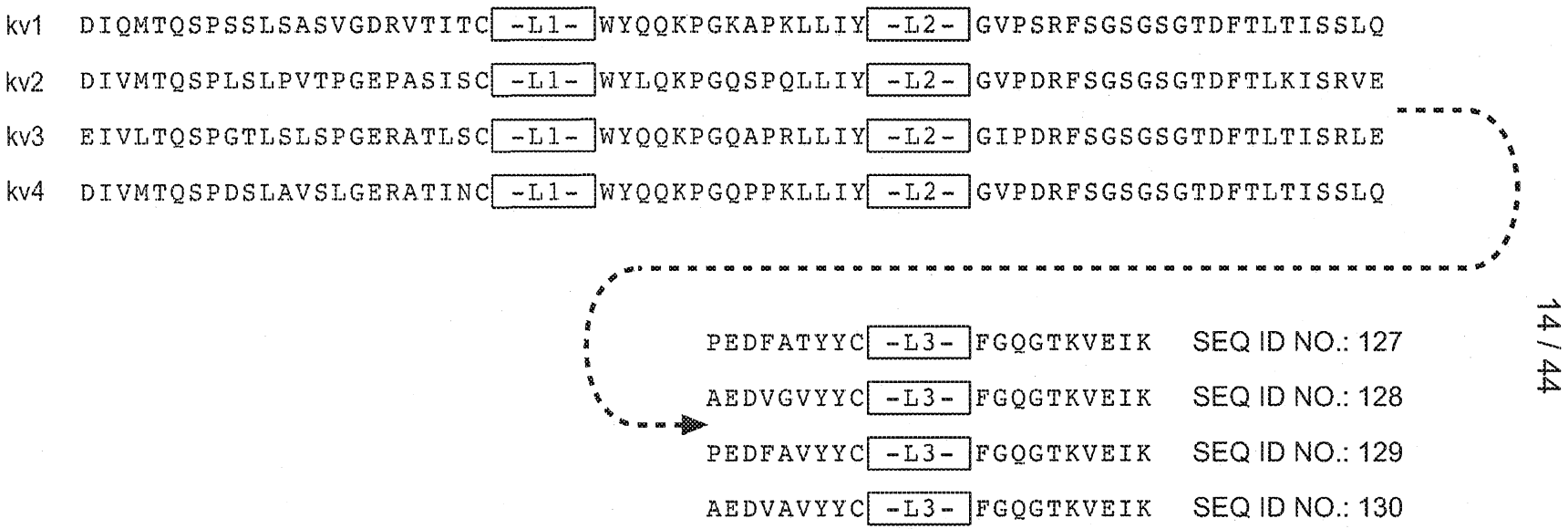

kv1 DIQMTQSPSSLSASVGDRVTITC -L1- WYQQKPGKAPKLLIY -L2- GVPSRFSGSGSGTDFTLTISSLQ
kv2 DIVMTQSPLSLPVTPGEPASISC -L1- WYLQKPGQSPQLLIY -L2- GVPDRFSGSGSGTDFTLKISRVE
kv3 EIVLTQSPGTLSLSPGERATLSC -L1- WYQQKPGQAPRLLIY -L2- GIPDRFSGSGSGTDFTLTISRLE
kv4 DIVMTQSPDSLAVSLGERATINC -L1- WYQQKPGQPPKLLIY -L2- GVPDRFSGSGSGTDFTLTISSLQ
PEDFATYYC -L3- FGQGTKVEIK SEQ ID NO.: 127
AEDVGVYYC -L3- FGQGTKVEIK SEQ ID NO.: 128
PEDFAVYYC -L3- FGQGTKVEIK SEQ ID NO.: 129
AEDVAVYYC -L3- FGQGTKVEIK SEQ ID NO.: 130

FIG. 14

A. huMA79b.v17 Light Chain

FR1-LC: DIQLTQSPSSLSASVGDRVTITC (SEQ ID NO: 152)
FR2-LC: WYQQKPGKAPKLLIY (SEQ ID NO: 153)
FR3-LC: GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO: 154)
FR4-LC: FGQGTKVEIKR (SEQ ID NO: 155)
HVR1-LC: KASQSVDYDGDSFLN (SEQ ID NO: 156)
HVR2-LC: AASNLES (SEQ ID NO: 157)
HVR3-LC: QQSNEDPLT (SEQ ID NO: 158)
CL1: TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK
DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 159)

Light Chain:

DIQLTQSPSSLSASVGDRVTITCKASQSVDYDGDSFLNWYQQKPGKAPKLLIYAASNLESGVPSRFSGS
GSGTDFTLTISSLQPEDFATYYCQQSNEDPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC
LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS
PVTKSFNRGEC (SEQ ID NO: 303)

LC-Variable Domain:

DIQLTQSPSSLSASVGDRVTITCKASQSVDYDGDSFLNWYQQKPGKAPKLLIYAASNLESGVPSRFSGS
GSGTDFTLTISSLQPEDFATYYCQQSNEDPLTFGQGTKVEIKR (SEQ ID NO: 169)

B. huMA79b.v17 Heavy Chain

FR1-HC: EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO: 160)
FR2-HC: WVRQAPGKGLEWI (SEQ ID NO: 161)
FR3-HC: RATFSADTSKNTAYLQMNSLRAEDTAVYYC (SEQ ID NO: 162)
FR4-HC: WGQGTLVTVSS (SEQ ID NO: 163)
HVR1-HC: GYTFSSYWIE (SEQ ID NO: 164)
HVR2-HC: GEILPGGGDTNYNEIFKG (SEQ ID NO: 165)
HVR3-HC: TRRVPVYFDY (SEQ ID NO: 166)
CH1: ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT
(SEQ ID NO:167)
Fc: CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 168)

Heavy Chain:

EVQLVESGGGLVQPGGSLRLSCAASGYTFSSYWIEWVRQAPGKGLEWIGEILPGGGDTNYNEIFKGRAT
FSADTSKNTAYLQMNSLRAEDTAVYYCTRRVPVYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGG
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 304)

HC-Variable Domain:

EVQLVESGGGLVQPGGSLRLSCAASGYTFSSYWIEWVRQAPGKGLEWIGEILPGGGDTNYNEIFKGRAT
FSADTSKNTAYLQMNSLRAEDTAVYYCTRRVPVYFDYWGQGTLVTVSS (SEQ ID NO: 170)

FIG. 15

A. huMA79b.v18 Light Chain

FR1-LC: DIQLTQSPSSLSASVGDRVTITC (SEQ ID NO: 171)
FR2-LC: WYQQKPGKAPKLLIY (SEQ ID NO: 172)
FR3-LC: GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO: 173)
FR4-LC: FGQGTKVEIKR (SEQ ID NO: 174)
HVR1-LC: KASQSVDYDGDSFLN (SEQ ID NO: 175)
HVR2-LC: AASNLES (SEQ ID NO: 176)
HVR3-LC: QQSNEDPLT (SEQ ID NO: 177)
CL1: TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 178)

Light Chain:

DIQLTQSPSSLSASVGDRVTITCKASQSVDYDGDSFLNWYQQKPGKAPKLLIYAASNLESGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQSNEDPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC (SEQ ID NO: 305)

LC-Variable Domain:

DIQLTQSPSSLSASVGDRVTITCKASQSVDYDGDSFLNWYQQKPGKAPKLLIYAASNLESGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQSNEDPLTFGQGTKVEIKR (SEQ ID NO: 188)

B. huMA79b.v18 Heavy Chain

FR1-HC: EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO: 179)
FR2-HC: WVRQAPGKGLEWI (SEQ ID NO: 180)
FR3-HC: RATFSADTSKNTAYLQMNSLRAEDTAVYYC (SEQ ID NO: 181)
FR4-HC: WGQGTLVTVSS (SEQ ID NO: 182)
HVR1-HC: GYTFSSYWIE (SEQ ID NO: 183)
HVR2-HC: GEILPGGGDTNYNEIFKG (SEQ ID NO: 184)
HVR3-HC: TRRVPIRLDY (SEQ ID NO: 185)
CH1: ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO: 186)
Fc: CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 187)

Heavy Chain:

EVQLVESGGGLVQPGGSLRLSCAASGYTFSSYWIEWVRQAPGKGLEWIGEILPGGGDTNYNEIFKGRAT FSADTSKNTAYLQMNSLRAEDTAVYYCTRRVPIRLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 306)

HC-Variable Domain:

EVQLVESGGGLVQPGGSLRLSCAASGYTFSSYWIEWVRQAPGKGLEWIGEILPGGGDTNYNEIFKGRAT FSADTSKNTAYLQMNSLRAEDTAVYYCTRRVPIRLDYWGQGTLVTVSS (SEQ ID NO: 189)

FIG. 16

A. huMA79b.v28 Light Chain

FR1-LC: DIQLTQSPSSLSASVGDRVTITC (SEQ ID NO: 190)
FR2-LC: WYQQKPGKAPKLLIY (SEQ ID NO: 191)
FR3-LC: GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO: 192)
FR4-LC: FGQGTKVEIKR (SEQ ID NO: 193)
HVR1-LC: KASQSVDYEGDSFLN (SEQ ID NO: 194)
HVR2-LC: AASNLES (SEQ ID NO: 195)
HVR3-LC: QQSNEDPLT (SEQ ID NO: 196)
CL1: TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK
DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
(SEQ ID NO: 197)

Light Chain:

DIQLTQSPSSLSASVGDRVTITCKASQSVDYEGDSFLNWYQQKPGKAPKLLIYAASNLESGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQSNEDPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV
VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG
LSSPVTKSFNRGEC (SEQ ID NO: 307)

B. huMA79b.v28 Heavy Chain

FR1-HC: EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO: 198)
FR2-HC: WVRQAPGKGLEWI (SEQ ID NO: 199)
FR3-HC: RATFSADTSKNTAYLQMNSLRAEDTAVYYC (SEQ ID NO: 200)
FR4-HC: WGQGTLVTVSS (SEQ ID NO: 201)
HVR1-HC: GYTFSSYWIE (SEQ ID NO: 202)
HVR2-HC: GEILPGGGDTNYNEIFKG (SEQ ID NO: 203)
HVR3-HC: TRRVPIRLDY (SEQ ID NO: 204)
CH1: ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT
(SEQ ID NO: 205)
Fc: CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 206)

Heavy Chain:

EVQLVESGGGLVQPGGSLRLSCAASGYTFSSYWIEWVRQAPGKGLEWIGEILPGGGDTNYNEIFKGRA
TFSADTSKNTAYLQMNSLRAEDTAVYYCTRRVPIRLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 308)

FIG. 17

A. huMA79b.v32 Light Chain

FR1-LC: DIQLTQSPSSLSASVGDRVTITC (SEQ ID NO: 209)
FR2-LC: WYQQKPGKAPKLFIY (SEQ ID NO: 210)
FR3-LC: GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO: 211)
FR4-LC: FGQGTKVEIKR (SEQ ID NO: 212)
HVR1-LC: KASQSVDYSGDSFLN (SEQ ID NO: 213)
HVR2-LC: AASNLES (SEQ ID NO: 214)
HVR3-LC: QQSNEDPLT (SEQ ID NO: 215)
CL1: TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK
DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 216)

Light Chain:

DIQLTQSPSSLSASVGDRVTITCKASQSVDYSGDSFLNWYQQKPGKAPKLFIYAASNLESGVPSRFSGS
GSGTDFTLTISSLQPEDFATYYCQQSNEDPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC
LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS
PVTKSFNRGEC (SEQ ID NO: 309)

LC-Variable Domain:

DIQLTQSPSSLSASVGDRVTITCKASQSVDYSGDSFLNWYQQKPGKAPKLFIYAASNLESGVPSRFSGS
GSGTDFTLTISSLQPEDFATYYCQQSNEDPLTFGQGTKVEIKR (SEQ ID NO: 226)

B. huMA79b.v32 Heavy Chain

FR1-HC: EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO: 217)
FR2-HC: WVRQAPGKGLEWI (SEQ ID NO: 218)
FR3-HC: RATFSADTSKNTAYLQMNSLRAEDTAVYYC (SEQ ID NO: 219)
FR4-HC: WGQGTLVTVSS (SEQ ID NO: 220)
HVR1-HC: GYTFSSYWIE (SEQ ID NO: 221)
HVR2-HC: GEILPGGGDTNYNEIFKG (SEQ ID NO: 222)
HVR3-HC: TRRVPIRLDY (SEQ ID NO: 223)
CH1: ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT
(SEQ ID NO: 224)
Fc: CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 225)

Heavy Chain:

EVQLVESGGGLVQPGGSLRLSCAASGYTFSSYWIEWVRQAPGKGLEWIGEILPGGGDTNYNEIFKGRAT
FSADTSKNTAYLQMNSLRAEDTAVYYCTRRVPIRLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGG
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 310)

HC-Variable Domain:

EVQLVESGGGLVQPGGSLRLSCAASGYTFSSYWIEWVRQAPGKGLEWIGEILPGGGDTNYNEIFKGRAT
FSADTSKNTAYLQMNSLRAEDTAVYYCTRRVPIRLDYWGQGTLVTVSS (SEQ ID NO: 227)

FIG. 18


Signal Sequence
Test Peptide
hCD79b 1 MARLALSPVPSHWMVALLLLLSAEP-VPAARSEDRYRNPKGSACSRIWQS 49
CynCD79b 1 MARLALSPVSSHWLVALLLLLSAAEPVPAAKSEDLYPNPKGSACSRIWQS 50
mCD79b 1 MATLVLSSMPCHWLLFLLLLFSGEP-VPAMTSSDLPLNFQGSPCSQIWQH 49
hCD79b 50 PRFIARKRGFTVKMHCYMN-SASGNVSWLWKQEMDENPQQLKLEKGRMEE 98
CynCD79b 51 PRFIARKRGFTVKMHCYVTNSTFSIVSWLRKRETDKEPQQVNLEQGHMHQ 100
mCD79b 50 PRFAAKKRSSMVKFHCYTN---HSGALTWFRKRGSQQPQELVSEEGRIVQ 96
hCD79b 99 SQNESLATLTIQGIRFEDNGIYFCQQKCN-NTSEVYQGCGTELRVMGFST 147
CynCD79b 101 TQNSSVTTLIIQDIRFEDNGIYFCQQECS-KTSEVYRGCGTELRVMGFST 149
mCD79b 97 TQNGSVYTLTIQNIQYEDNGIYFCKQKCDSANHNVTDSCGTELLVLGFST 146
TM Domain
hCD79b 148 LAQLKQRNTLKDGIIMIQTLLIILFIIVPIFLLLDKDDSKAGMEEDHTYE 197
CynCD79b 150 LAQLKQRNTLKDGIIMIQTLLIILFIIVPIFLLLDKDDSKAGMEADHTYE 199
mCD79b 147 LDQLKRRNTLKDGIILIQTLLIILFIIVPIFLLLDKDDGKAGMEEDHTYE 196
ITAM Domain
hCD79b 198 GLDIDQTATYEDIVTLRTGEVKWSVGEHPGQE 229 SEQ ID NO: 2
CynCD79b 200 GLDIDQTATYEDIVTLRTGEVKWSVGEHPGQE 231 SEQ ID NO: 7
mCD79b 197 GLNIDQTATYEDIVTLRTGEVKWSVGEHPGQE 228 SEQ ID NO: 8

FIG. 19

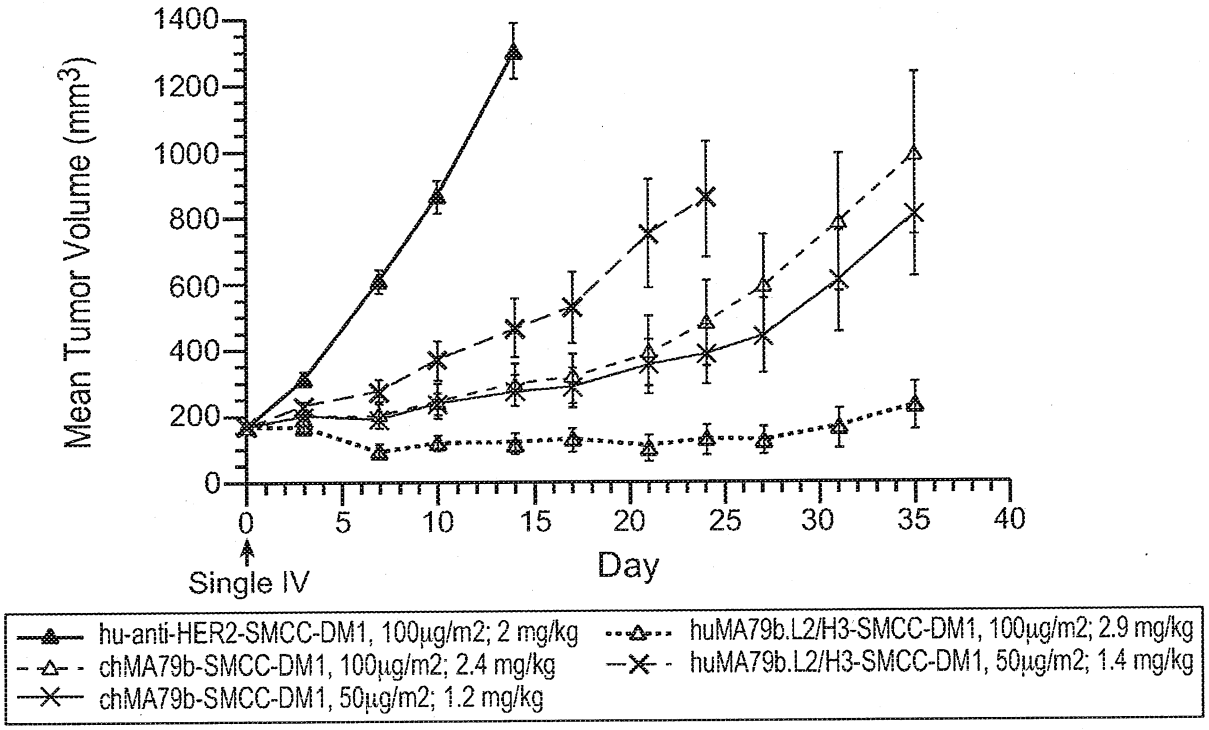

Mean Tumor Volume (mm3)
1400
1200
1000
800
600
400
200
0
0
5
10
15
20
25
30
35
40
Day
Single IV
hu-anti-HER2-SMCC-DM1, 100µg/m2; 2 mg/kg
chMA79b-SMCC-DM1, 100µg/m2; 2.4 mg/kg
chMA79b-SMCC-DM1, 50µg/m2; 1.2 mg/kg
huMA79b.L2/H3-SMCC-DM1, 100µg/m2; 2.9 mg/kg
huMA79b.L2/H3-SMCC-DM1, 50µg/m2; 1.4 mg/kg

FIG. 20

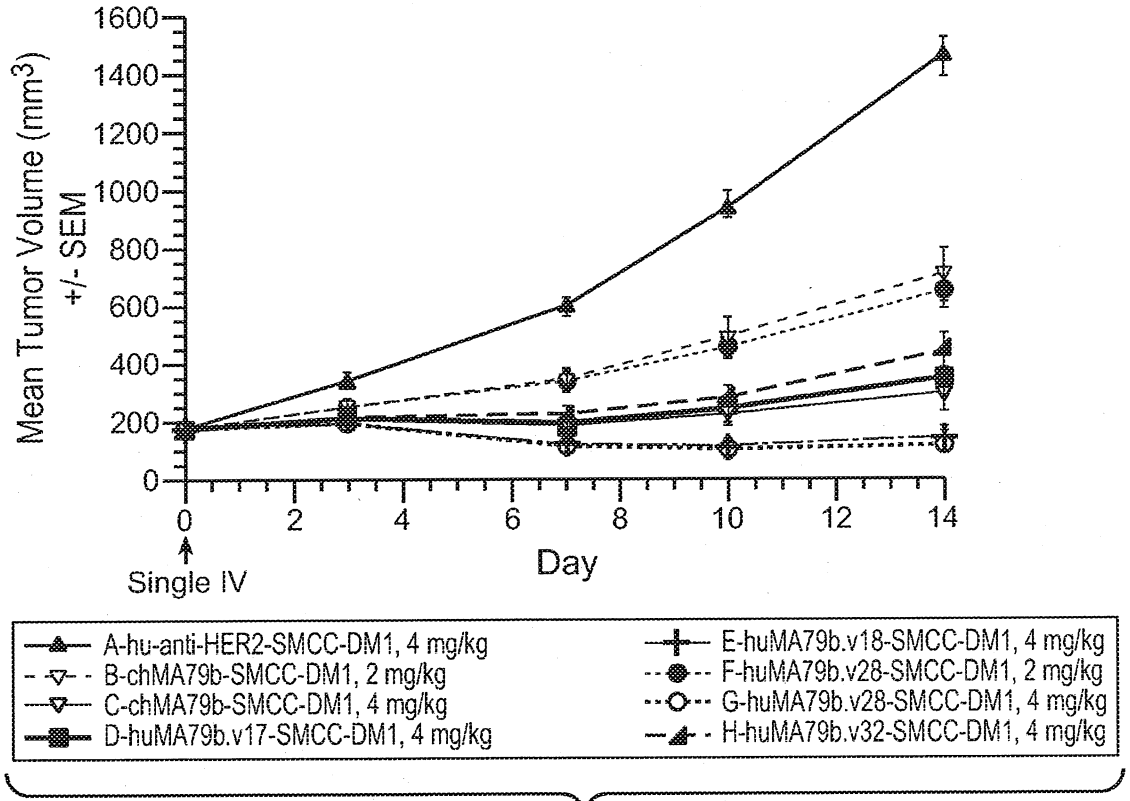


FIG. 21A

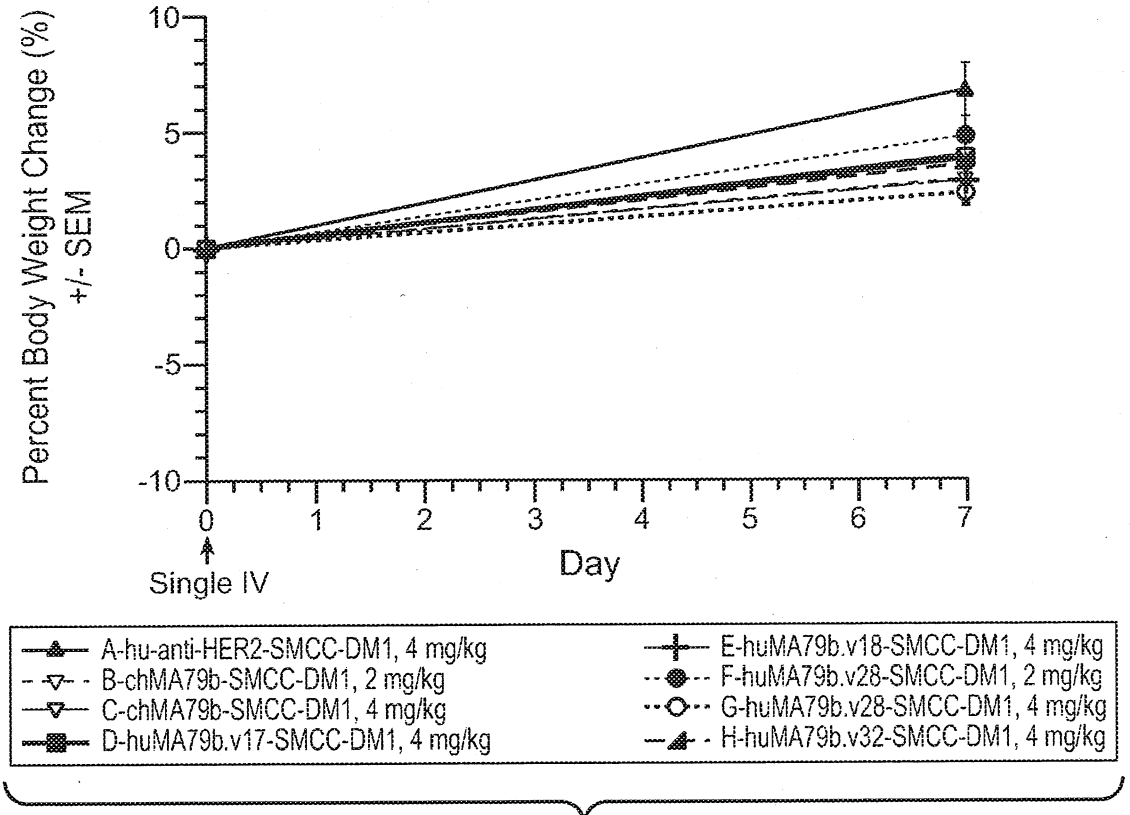


FIG. 21B

FIG. 22

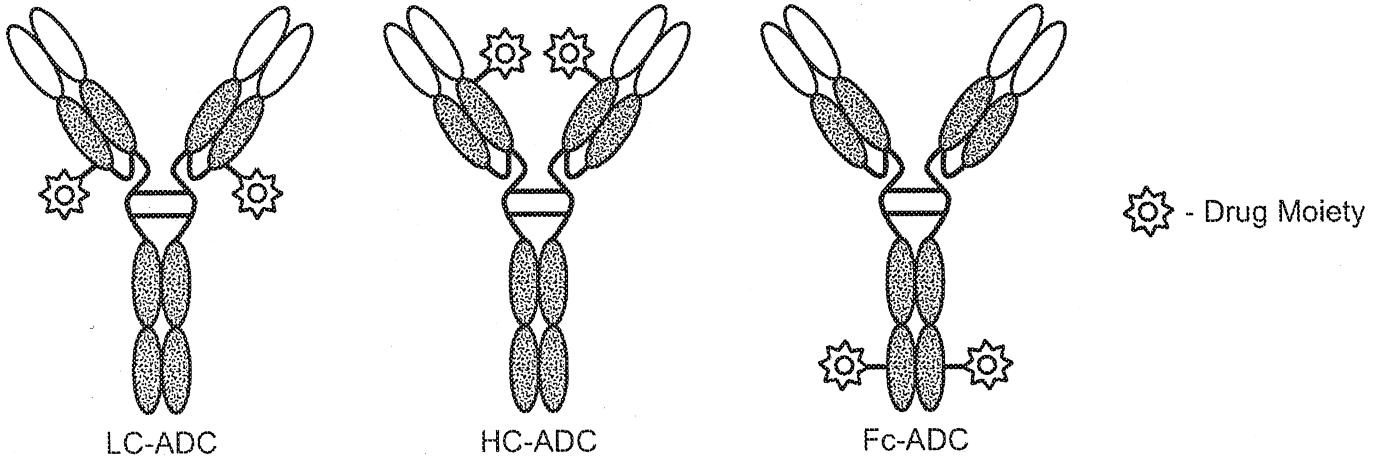
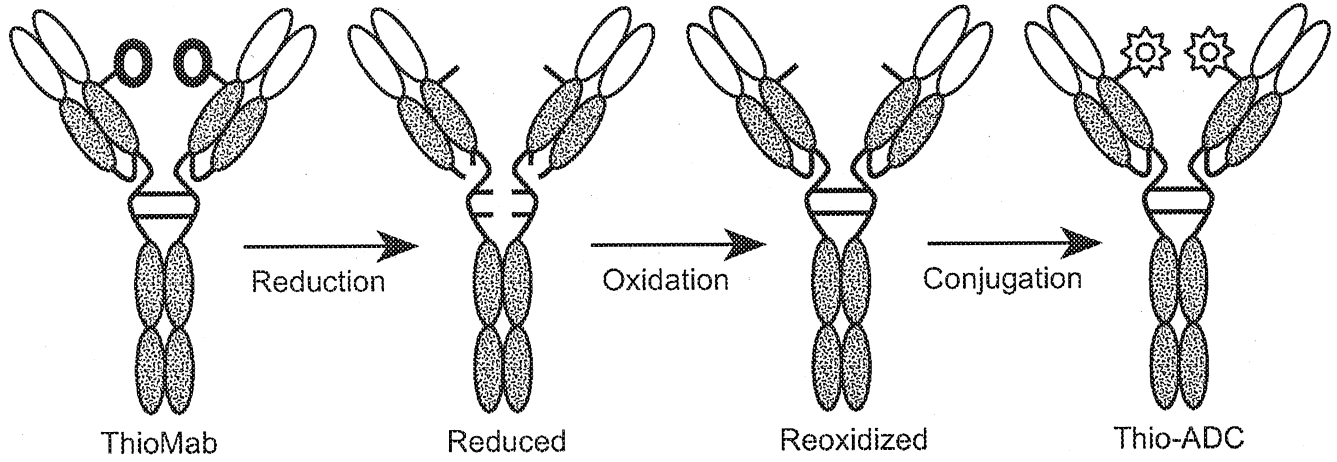

LC-ADC
HC-ADC
Fc-ADC
- Drug Moiety

FIG. 23


ThioMab
Reduction
Reduced
Oxidation
Reoxidized
Conjugation
Thio-ADC

Anti-CD79b A118C huMA79b.v17 Cysteine Engineered Heavy Chain ThioMAb

A. Light Chain Sequence
Thio-huMA79b.v17-HC-A118C (LC)

DIQLTQSPSSLSASVGDRVTITCKASQSVDYDGDSFLNWYQQKPGKAPKLLIYAASNLESGVPSRFSGS
GSGTDFTLTISSLQPEDFATYYCQQSNEDPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC
LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS
PVTKSFNRGEC (SEQ ID NO: 229)

B. Heavy Chain Sequence
Thio-huMA79b.v17-HC-A118C (HC)

EVQLVESGGGLVQPGGSLRLSCAASGYTFSSYWIEWVRQAPGKGLEWIGEILPGGGDTNYNEIFKGRATFSAD
TSKNTAYLQMNSLRAEDTAVYYCTRRVPVYFDYWGQGTLVTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS
CDKTHT*CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR*
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL
TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
(SEQ ID NO: 228)

FIG. 24

Anti-CD79b A118C huMA79b.v18 Cysteine Engineered Heavy Chain ThioMAb

A. Light Chain Sequence
Thio-huMA79b.v18-HC-A118C (LC)

DIQLTQSPSSLSASVGDRVTITCKASQSVDYDGDSFLNWYQQKPGKAPKLLIYAASNLESGVPSRFSGS
GSGTDFTLTISSLQPEDFATYYCQQSNEDPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC
LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS
PVTKSFNRGEC (SEQ ID NO: 231)

B. Heavy Chain Sequence
Thio-huMA79b.v18-HC-A118C (HC)

EVQLVESGGGLVQPGGSLRLSCAASGYTFSSYWIEWVRQAPGKGLEWIGEILPGGGDTNYNEIFKGRAT
FSADTSKNTAYLQMNSLRAEDTAVYYCTRRVPIRLDYWGQGTLVTVSSCSTKGPSVFPLAPSSKSTSGG
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS
NTKVDKKVEPKSCDKTHT*CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN*
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 230)

FIG. 25

Anti-CD79b A118C huMA79b.v28 Cysteine Engineered Heavy Chain ThioMAb

A. Light Chain Sequence
Thio-huMA79b.v28-HC-A118C (LC)

DIQLTQSPSSLSASVGDRVTITCKASQSVDYEGDSFLNWYQQKPGKAPKLLIYAASNLESGVPSRFSGS
GSGTDFTLTISSLQPEDFATYYCQQSNEDPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC
LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS
PVTKSFNRGEC (SEQ ID NO: 233)

B. Heavy Chain Sequence
Thio-huMA79b.v28-HC-A118C (HC)

EVQLVESGGGLVQPGGSLRLSCAASGYTFSSYWIEWVRQAPGKGLEWIGEILPGGGDTNYNEIFKGRAT
FSADTSKNTAYLQMNSLRAEDTAVYYCTRRVPIRLDYWGQGTLVTVSSCSTKGPSVFPLAPSSKSTSGG
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS
NTKVDKKVEPKSCDKTHT*CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN*
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 232)

FIG. 26

Anti-CD79b V205C chMA79b Cysteine Engineered Light Chain ThioMAb

A. Light Chain Sequence
Thio chMA79b-LC-V205C (LC)

DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSFLNWYQQKPGQPPKLFIYAASNLESGIPARFSGS
GSGTDFTLNIHPVEEEDAATYYCQQSNEDPLTFGAGTELELKRTVAAPSVFIFPPSDEQLKSGTASVVC
LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS
PCTKSFNRGEC (SEQ ID NO: 235)

B. Heavy Chain Sequence
Thio chMA79b-LC-V205C (HC)

EVQLQQSGAELMKPGASVKISCKATGYTFSSYWIEWVKQRPGHGLEWIGEILPGGGDTNYNEIFKGKAT
FTADTSSNTAYMQLSSLTSEDSAVYYCTRRVPVYFDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGG
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS
NTKVDKKVEPKSCDKTHT*CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN*
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 234)

FIG. 27

Anti-CD79b A118C chMA79b Cysteine Engineered Heavy Chain ThioMAb

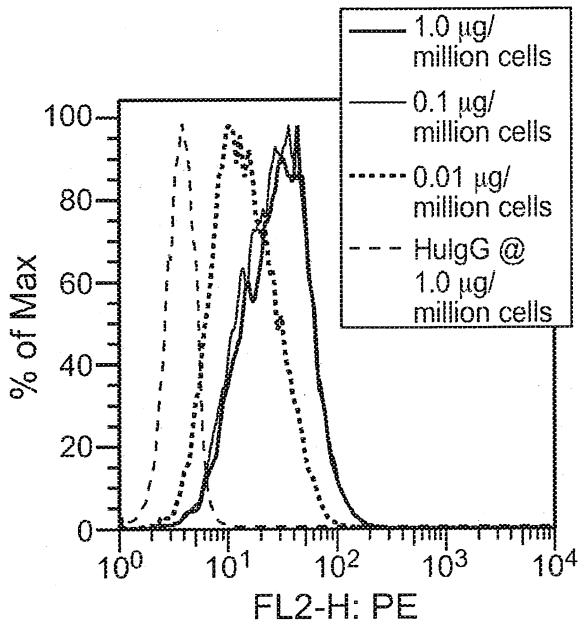
A. Light Chain Sequence
Thio chMA79b-HC-A118C (LC)

DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSFLNWYQQKPGQPPKLFIYAASNLESGIPARFSGS
GSGTDFTLNIHPVEEEDAATYYCQQSNEDPLTFGAGTELELKRTVAAPSVFIFPPSDEQLKSGTASVVC
LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS
PVTKSFNRGEC (SEQ ID NO: 237)

B. Heavy Chain Sequence
Thio chMA79b-HC-A118C (HC)

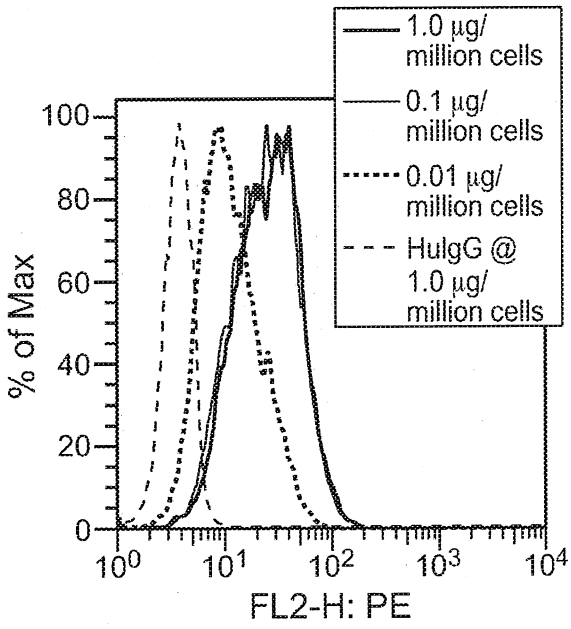
EVQLQQSGAELMKPGASVKISCKATGYTFSSYWIEWVKQRPGHGLEWIGEILPGGGDTNYNEIFKGKAT
FTADTSSNTAYMQLSSLTSEDSAVYYCTRRVPVYFDYWGQGTSVTVSSCSTKGPSVFPLAPSSKSTSGG
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS
NTKVDKKVEPKSCDKTHT*CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN*
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 236)

FIG. 28



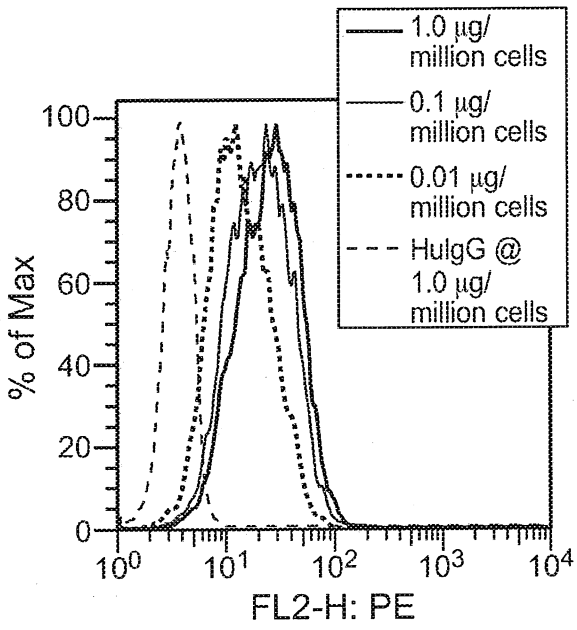
Binding of Thio chMA79b-LC(V205C)-MC-MMAF to BJAB-lucs

FIG. 29A



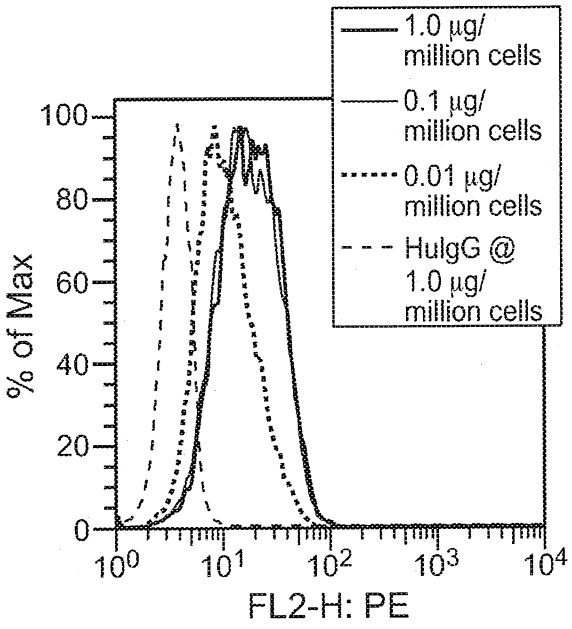
Binding of Thio chMA79b-HC(A118C)-MC-MMAF to BJAB-lucs

FIG. 29B



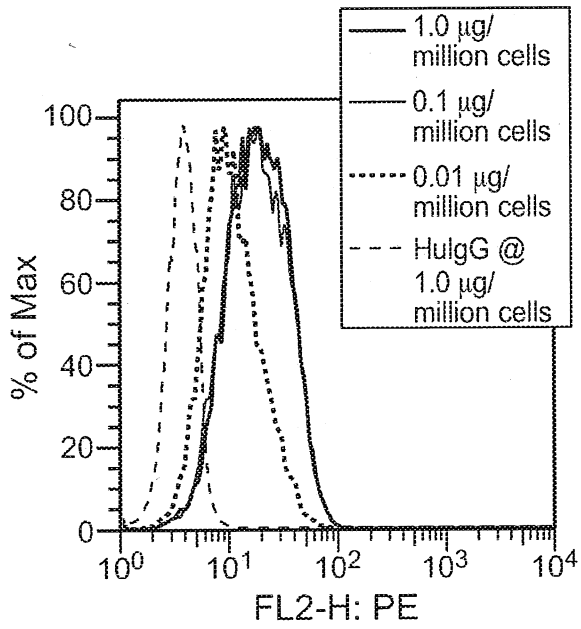
Binding of Naked Thio MA79b.v18-HC (A118C) to BJAB-lucs

FIG. 30A



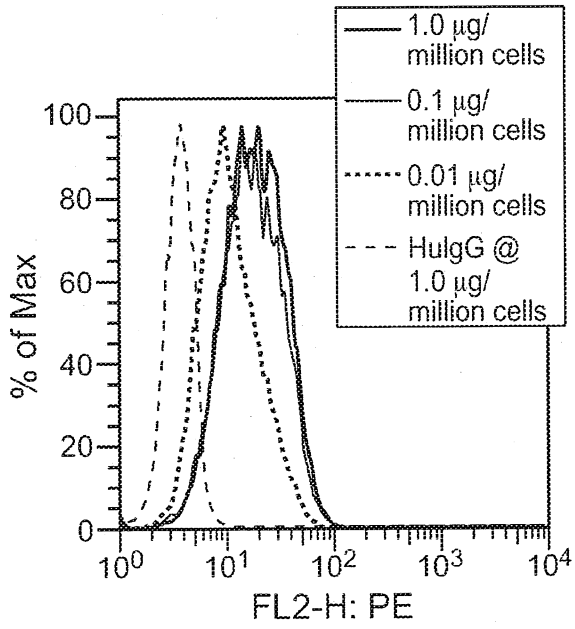
Binding of Thio MA79b.v18-HC (A118C)-MC-MMAF to BJAB-lucs

FIG. 30B



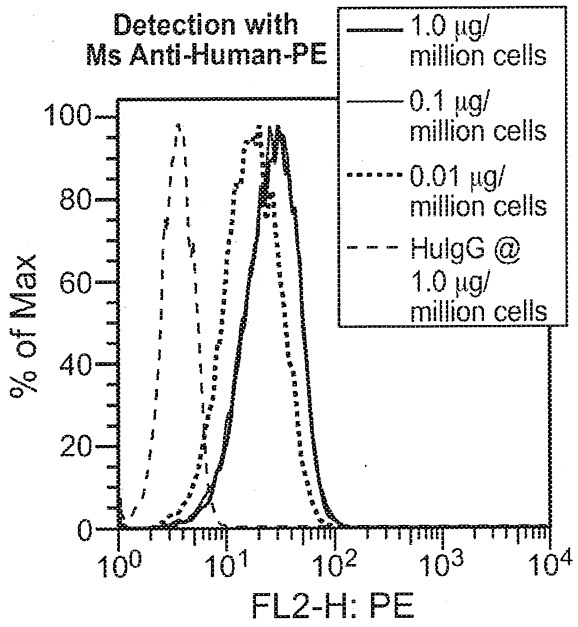
Binding of Thio MA79b.v18-HC (A118C)-MCvcPAB-MMAE to BJAB-lucs

FIG. 30C



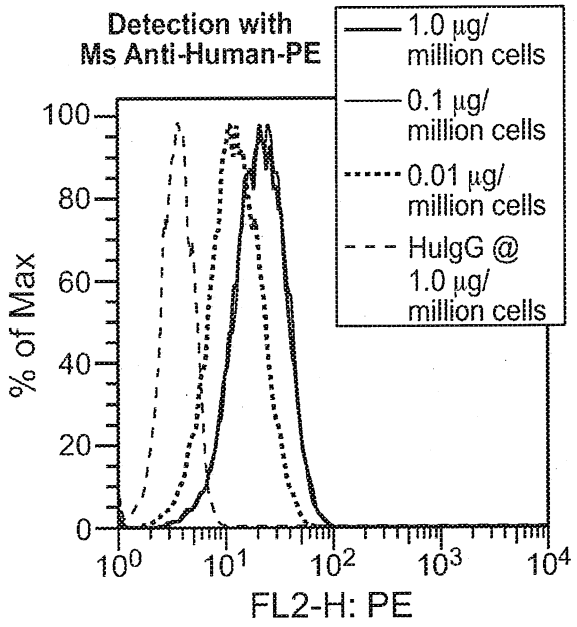
Binding of Thio MA79b.v18-HC (A118C)-BMPEO-DM1 to BJAB-lucs

FIG. 30D



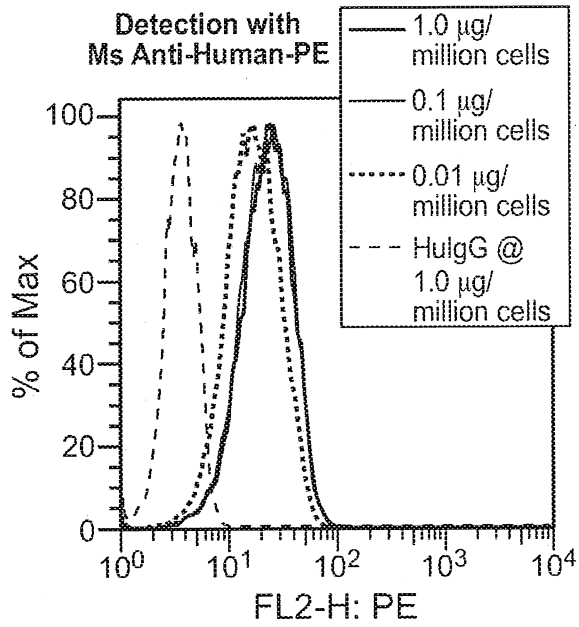
Binding of Naked Thio MA79b.v28-HC (A118C) to BJAB-lucs

FIG. 31A



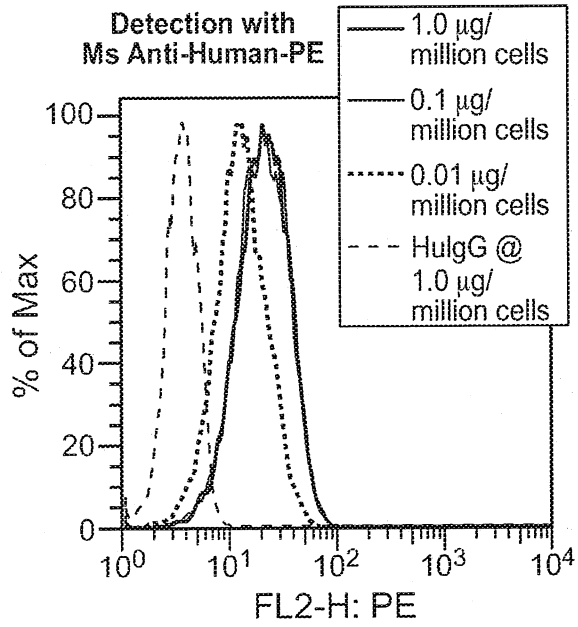
Binding of Thio MA79b.v28-HC (A118C)-MCvcPAB-MMAE to BJAB-lucs

FIG. 31B



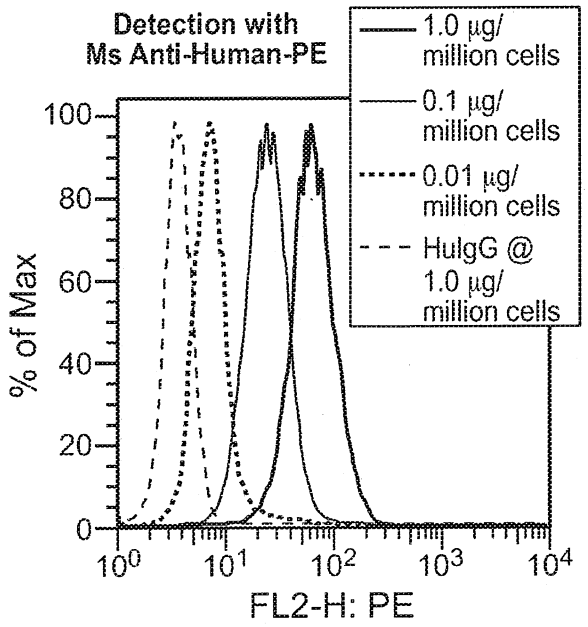
Binding of Thio MA79b.v28-HC (A118C)-BMPEO-DM1 to BJAB-lucs

FIG. 31C



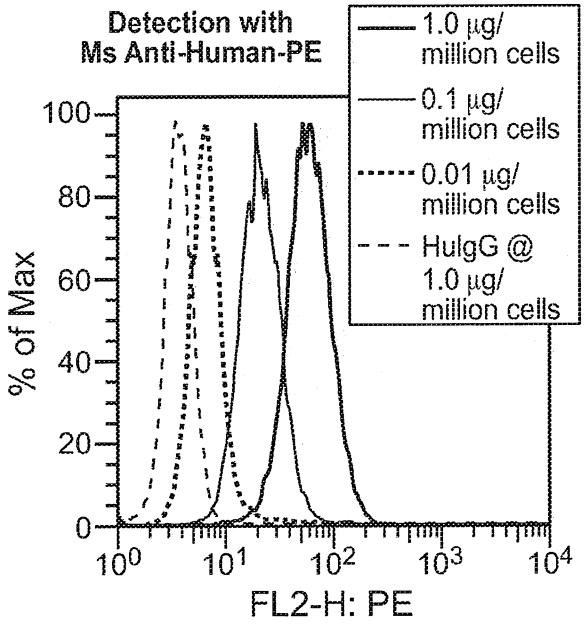
Binding of Thio MA79b.v28-HC (A118C)-MC-MMAF to BJAB-lucs

FIG. 31D



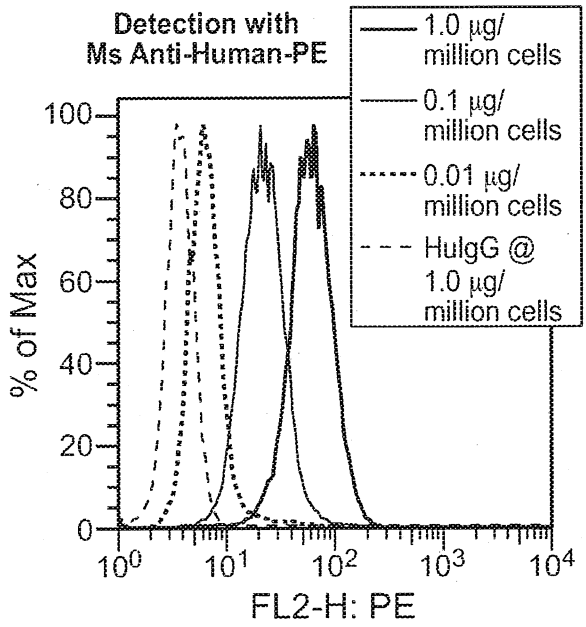
Binding of Naked Thio Anti-cynoCD79b (ch10D10)-HC(A118C) to BJAB-cynoCD79b Cells

FIG. 32A



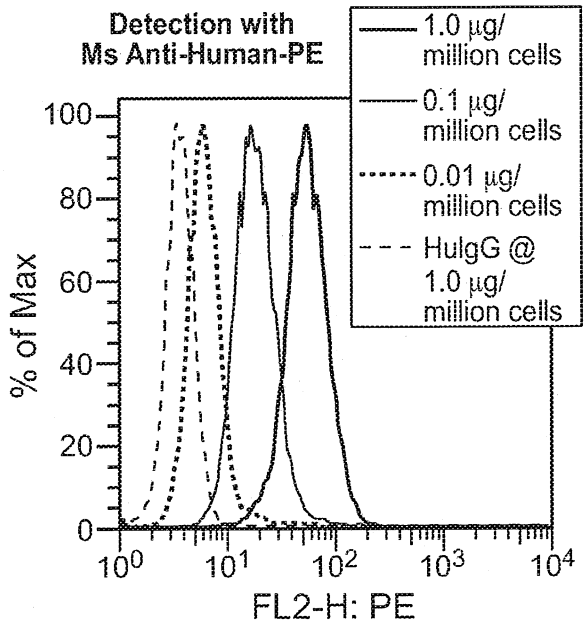
Binding of Thio Anti-cynoCD79b (ch10D10)-HC(A118C)-MCvcPAB-MMAE to BJAB-cynoCD79b Cells

FIG. 32B



Binding of Thio Anti-cynoCD79b (ch10D10)-HC(A118C)-BMPEO-DM1 to BJAB-cynoCD79b Cells

FIG. 32C



Binding of Thio Anti-cynoCD79b (ch10D10)-HC(A118C)-MC-MMAF to BJAB-cynoCD79b Cells

FIG. 32D

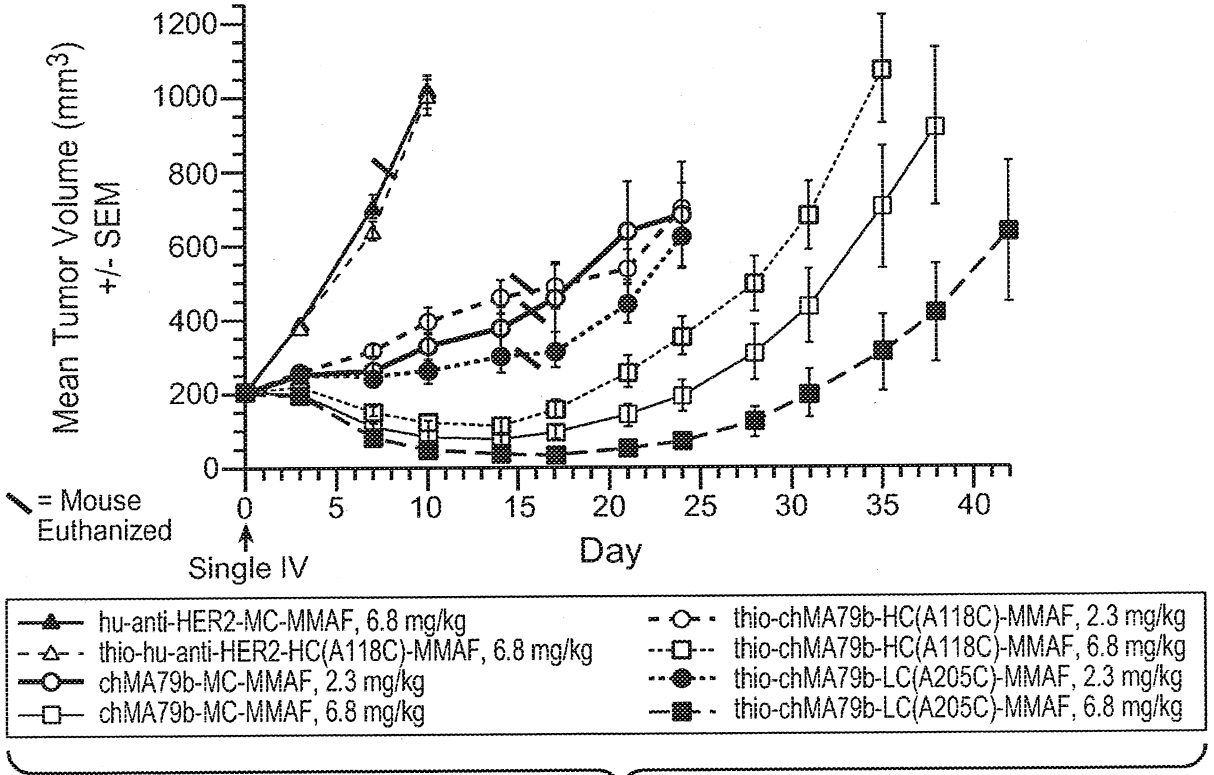


FIG. 33A

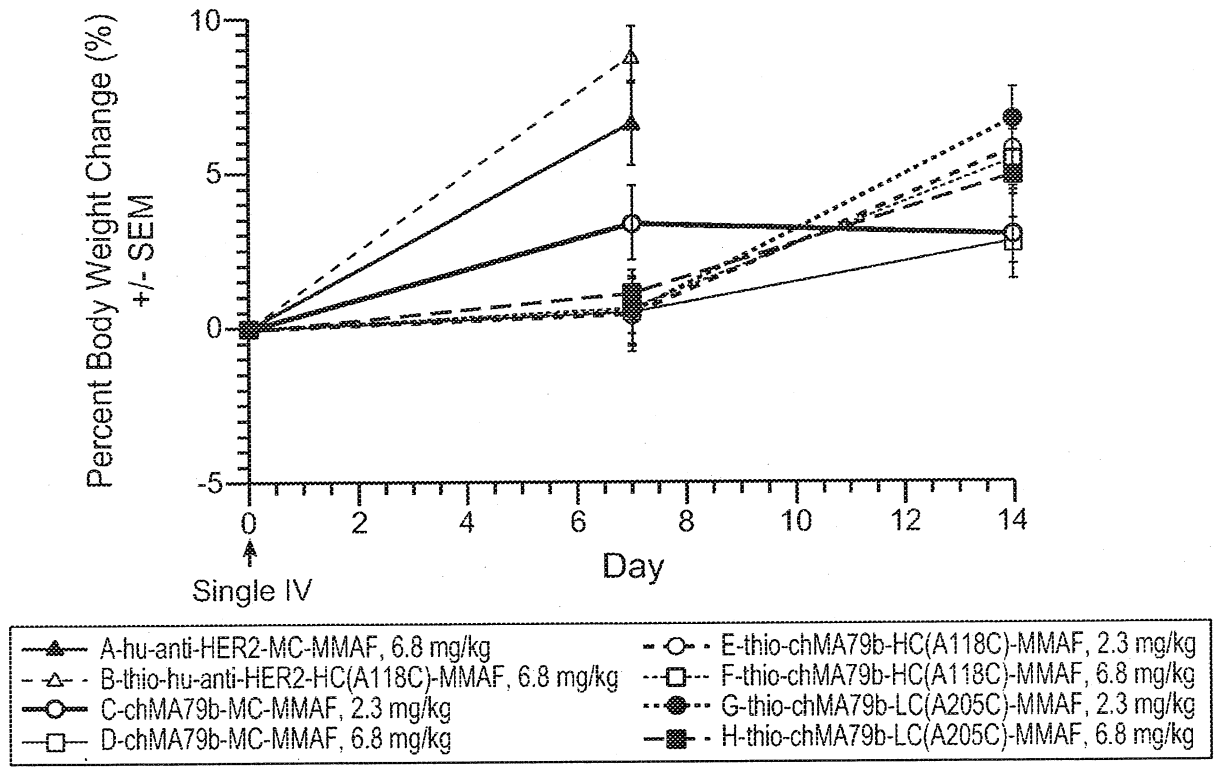


FIG. 33B

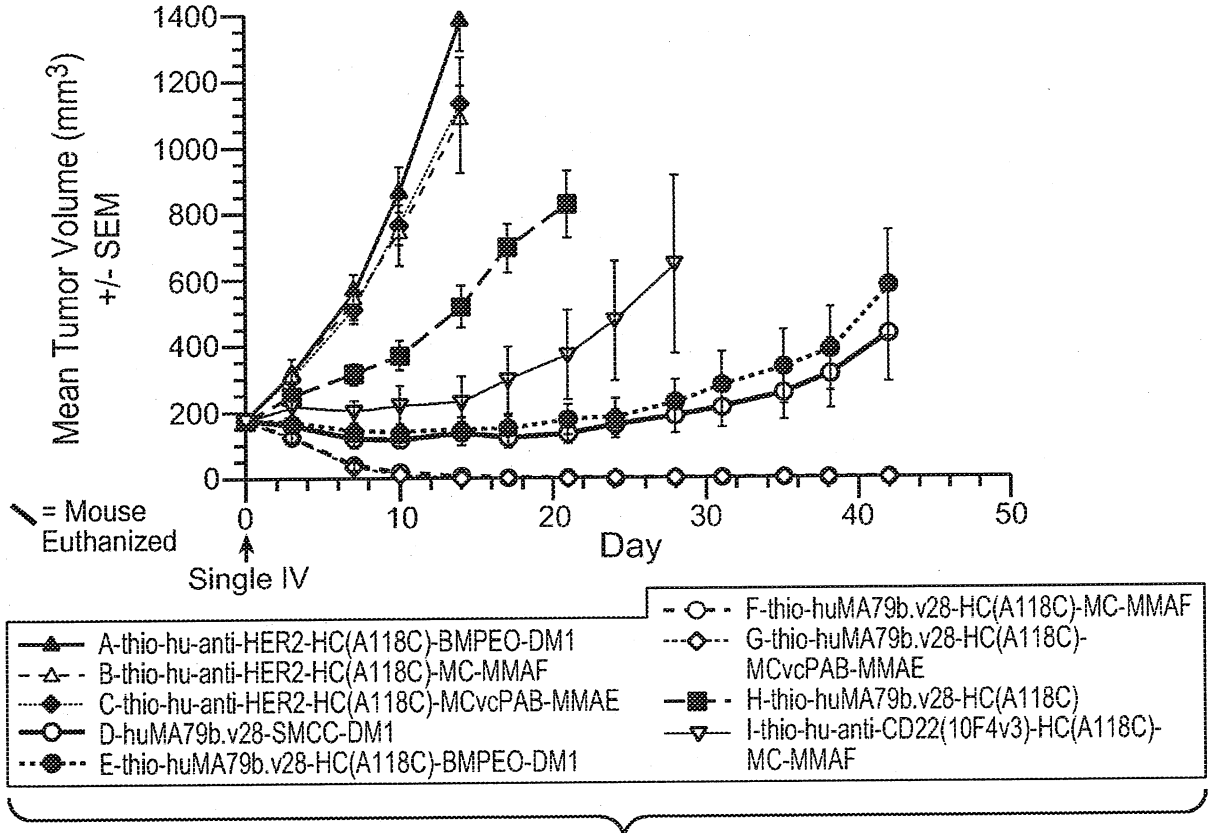


FIG. 34A

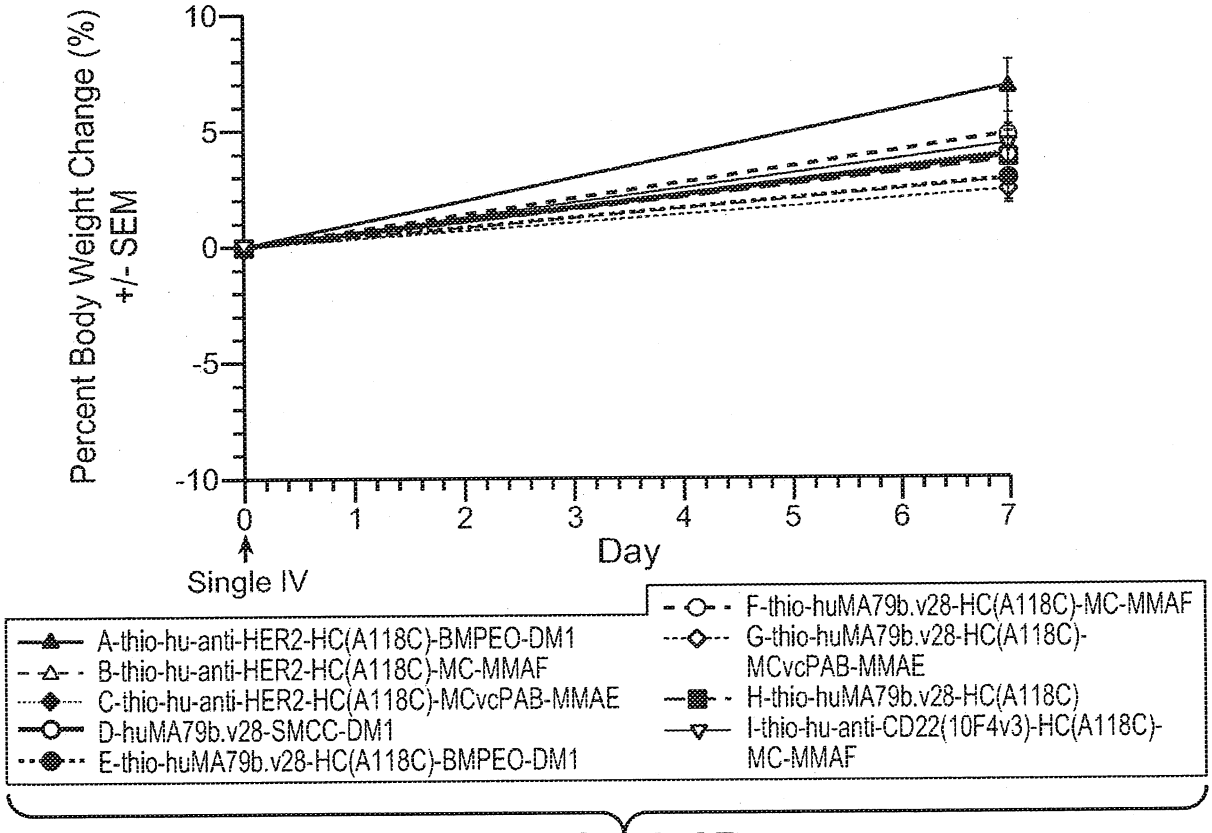


FIG. 34B

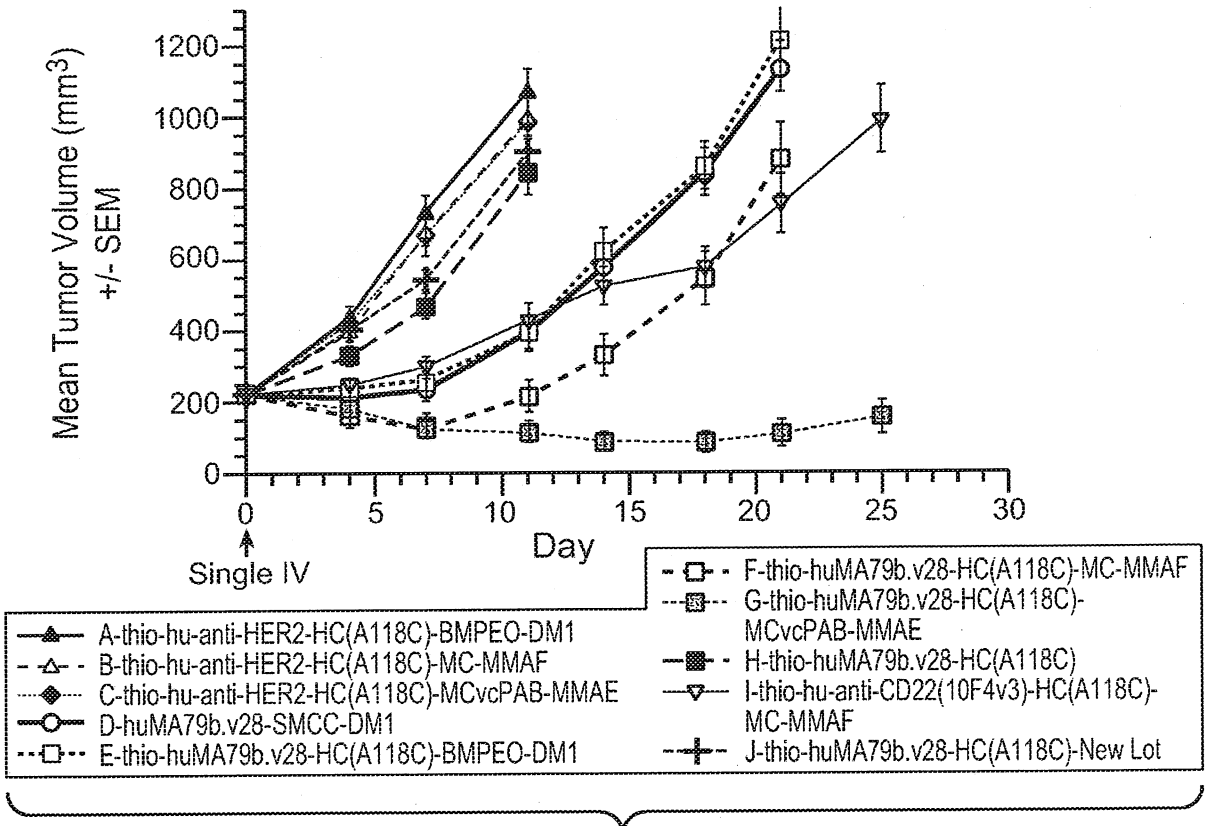


FIG. 35A

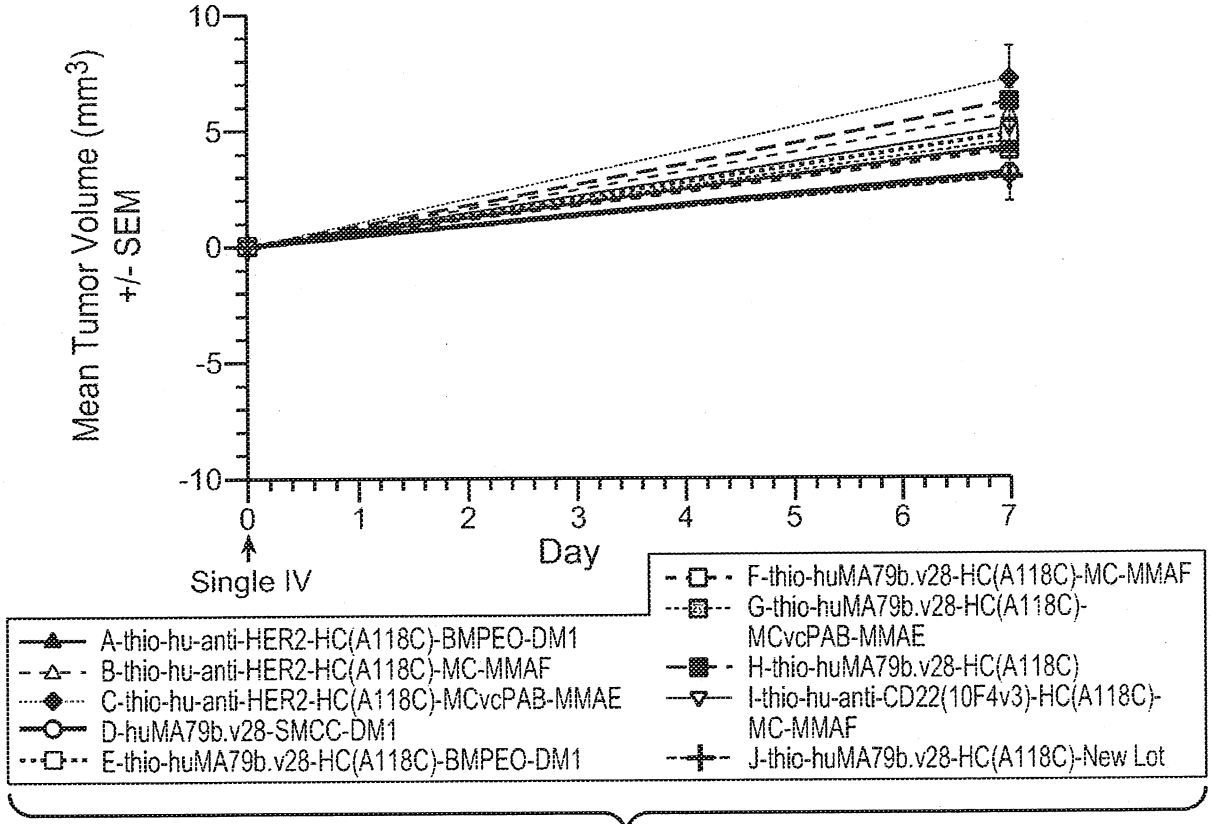


FIG. 35B

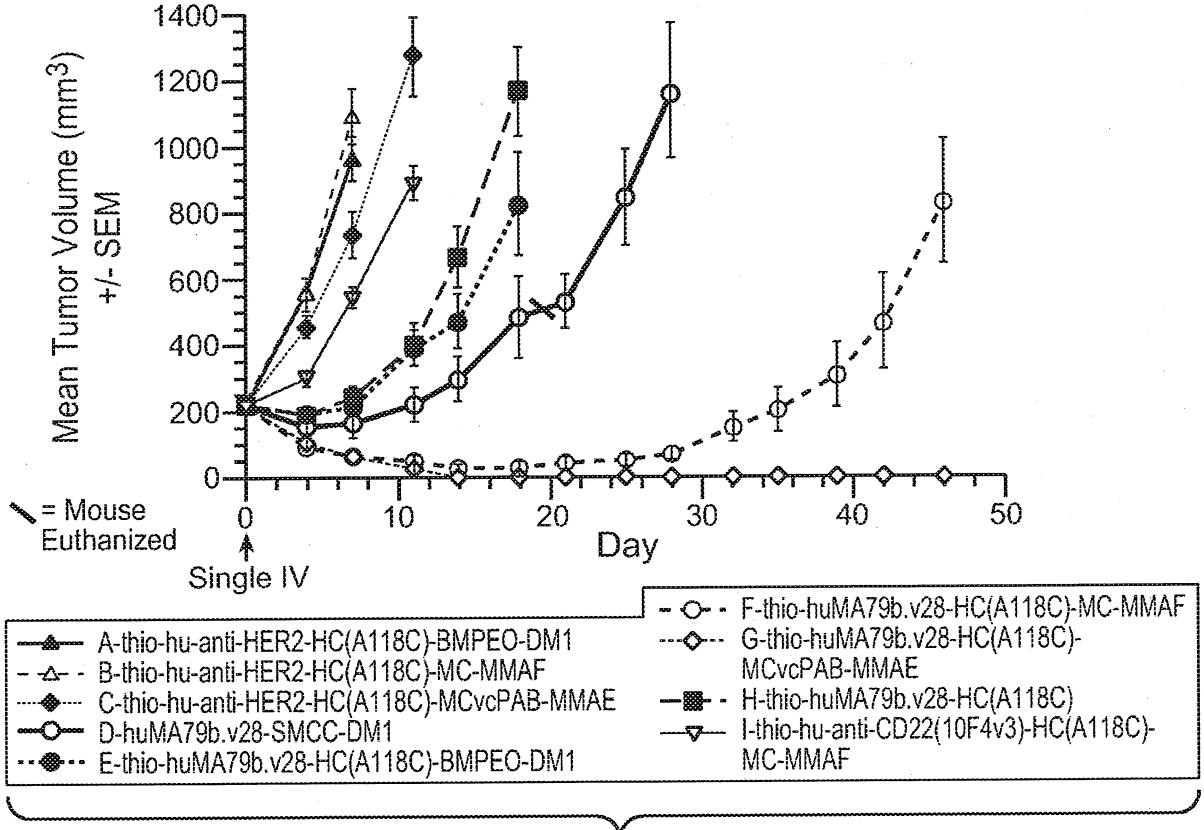

Mean Tumor Volume (mm3)
+/- SEM
1400
1200
1000
800
600
400
200
0
0
10
20
30
40
50
Day
= Mouse Euthanized
Single IV
A-thio-hu-anti-HER2-HC(A118C)-BMPEO-DM1
B-thio-hu-anti-HER2-HC(A118C)-MC-MMAF
C-thio-hu-anti-HER2-HC(A118C)-MCvcPAB-MMAE
D-huMA79b.v28-SMCC-DM1
E-thio-huMA79b.v28-HC(A118C)-BMPEO-DM1
F-thio-huMA79b.v28-HC(A118C)-MC-MMAF
G-thio-huMA79b.v28-HC(A118C)-MCvcPAB-MMAE
H-thio-huMA79b.v28-HC(A118C)
I-thio-hu-anti-CD22(10F4v3)-HC(A118C)-MC-MMAF

FIG. 36

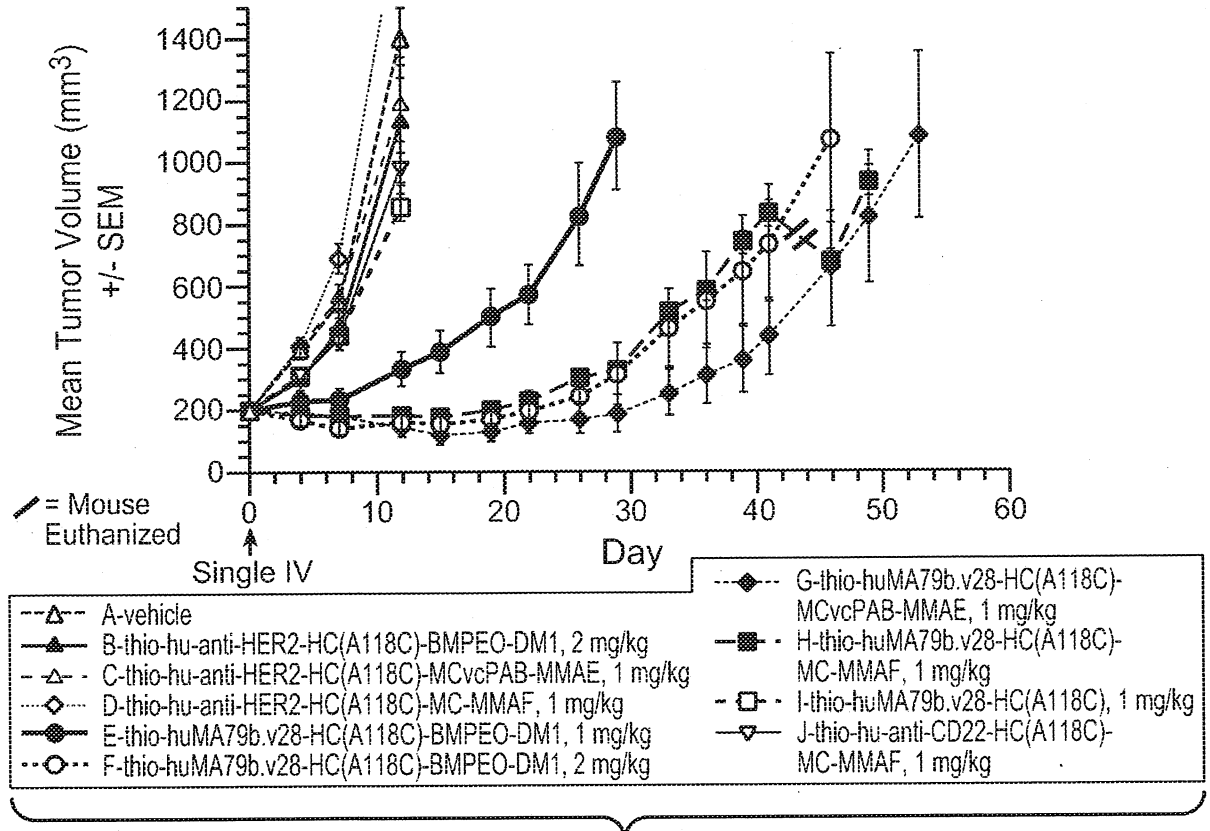

Mean Tumor Volume (mm3)
+/- SEM
1400
1200
1000
800
600
400
200
0
0
10
20
30
40
50
60
Day
= Mouse Euthanized
Single IV
A-vehicle
B-thio-hu-anti-HER2-HC(A118C)-BMPEO-DM1, 2 mg/kg
C-thio-hu-anti-HER2-HC(A118C)-MCvcPAB-MMAE, 1 mg/kg
D-thio-hu-anti-HER2-HC(A118C)-MC-MMAF, 1 mg/kg
E-thio-huMA79b.v28-HC(A118C)-BMPEO-DM1, 1 mg/kg
F-thio-huMA79b.v28-HC(A118C)-BMPEO-DM1, 2 mg/kg
G-thio-huMA79b.v28-HC(A118C)-MCvcPAB-MMAE, 1 mg/kg
H-thio-huMA79b.v28-HC(A118C)-MC-MMAF, 1 mg/kg
I-thio-huMA79b.v28-HC(A118C), 1 mg/kg
J-thio-hu-anti-CD22-HC(A118C)-MC-MMAF, 1 mg/kg

FIG. 37

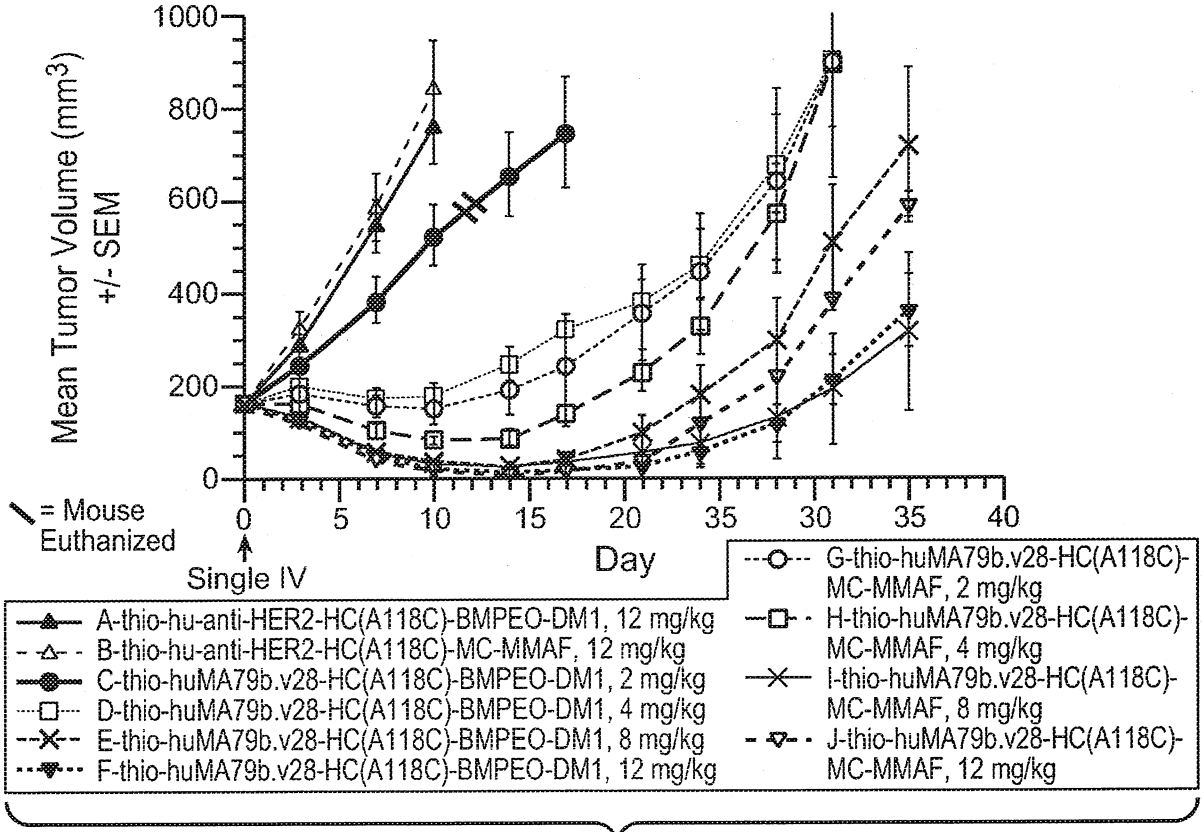


FIG. 38A

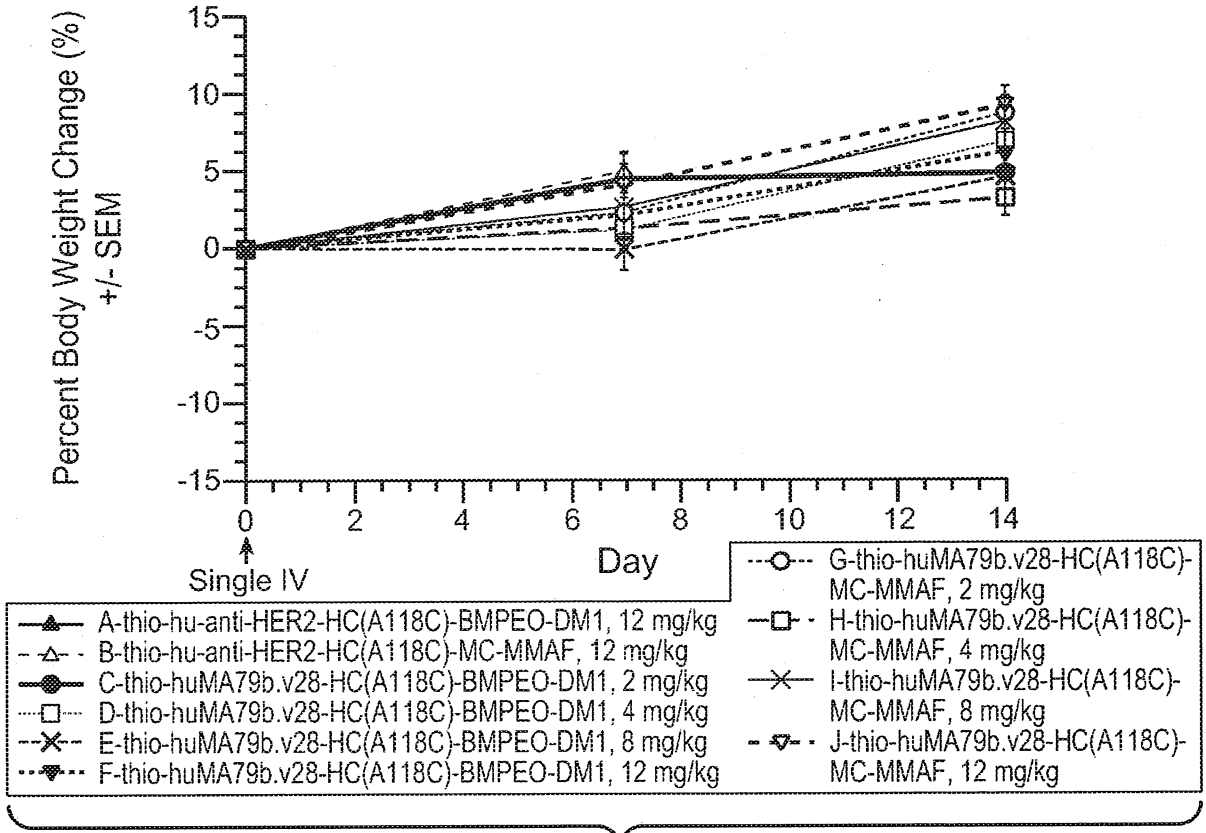


FIG. 38B

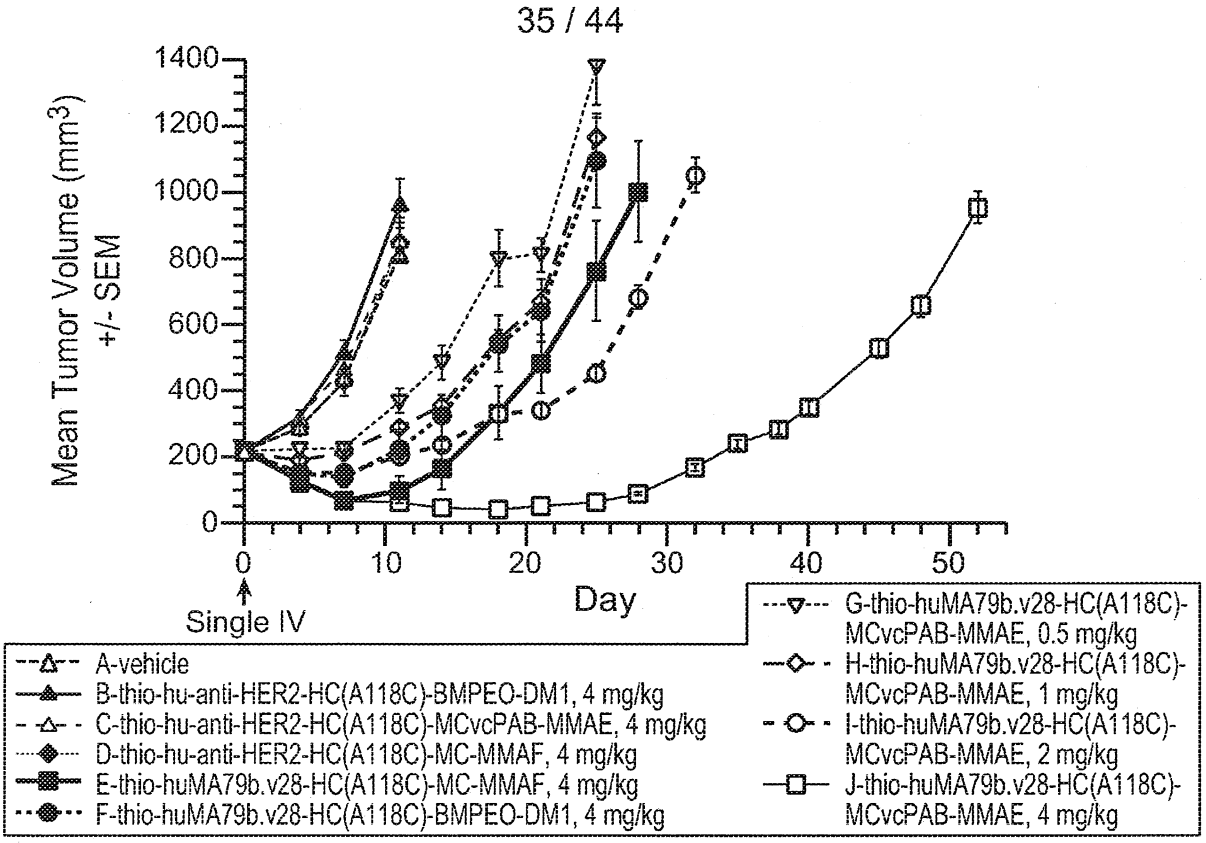

Mean Tumor Volume (mm3)
+/- SEM
1400
1200
1000
800
600
400
200
0
0
10
20
30
40
50
Day
Single IV
A-vehicle
B-thio-hu-anti-HER2-HC(A118C)-BMPEO-DM1, 4 mg/kg
C-thio-hu-anti-HER2-HC(A118C)-MCvcPAB-MMAE, 4 mg/kg
D-thio-hu-anti-HER2-HC(A118C)-MC-MMAF, 4 mg/kg
E-thio-huMA79b.v28-HC(A118C)-MC-MMAF, 4 mg/kg
F-thio-huMA79b.v28-HC(A118C)-BMPEO-DM1, 4 mg/kg
G-thio-huMA79b.v28-HC(A118C)-MCvcPAB-MMAE, 0.5 mg/kg
H-thio-huMA79b.v28-HC(A118C)-MCvcPAB-MMAE, 1 mg/kg
I-thio-huMA79b.v28-HC(A118C)-MCvcPAB-MMAE, 2 mg/kg
J-thio-huMA79b.v28-HC(A118C)-MCvcPAB-MMAE, 4 mg/kg

FIG. 39

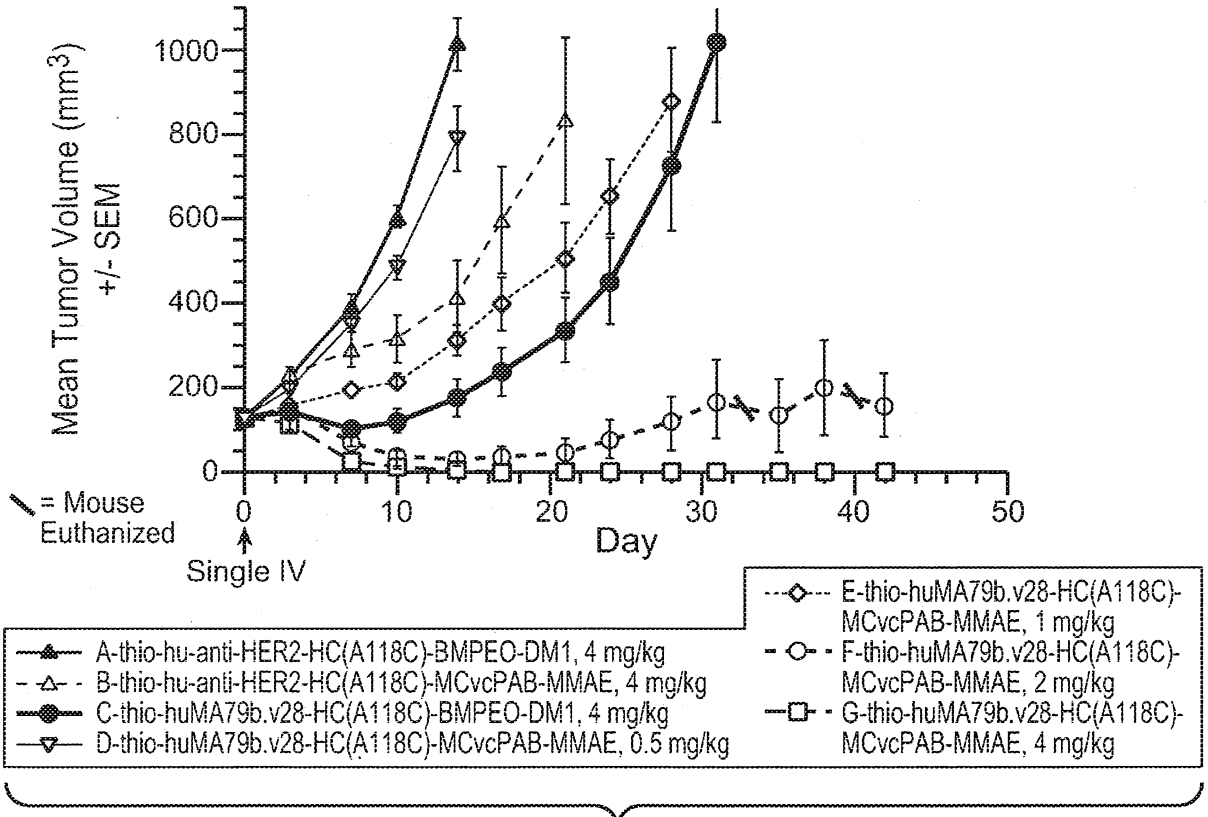

Mean Tumor Volume (mm3)
+/- SEM
1000
800
600
400
200
0
= Mouse Euthanized
0
10
20
30
40
50
Day
Single IV
A-thio-hu-anti-HER2-HC(A118C)-BMPEO-DM1, 4 mg/kg
B-thio-hu-anti-HER2-HC(A118C)-MCvcPAB-MMAE, 4 mg/kg
C-thio-huMA79b.v28-HC(A118C)-BMPEO-DM1, 4 mg/kg
D-thio-huMA79b.v28-HC(A118C)-MCvcPAB-MMAE, 0.5 mg/kg
E-thio-huMA79b.v28-HC(A118C)-MCvcPAB-MMAE, 1 mg/kg
F-thio-huMA79b.v28-HC(A118C)-MCvcPAB-MMAE, 2 mg/kg
G-thio-huMA79b.v28-HC(A118C)-MCvcPAB-MMAE, 4 mg/kg

FIG. 40

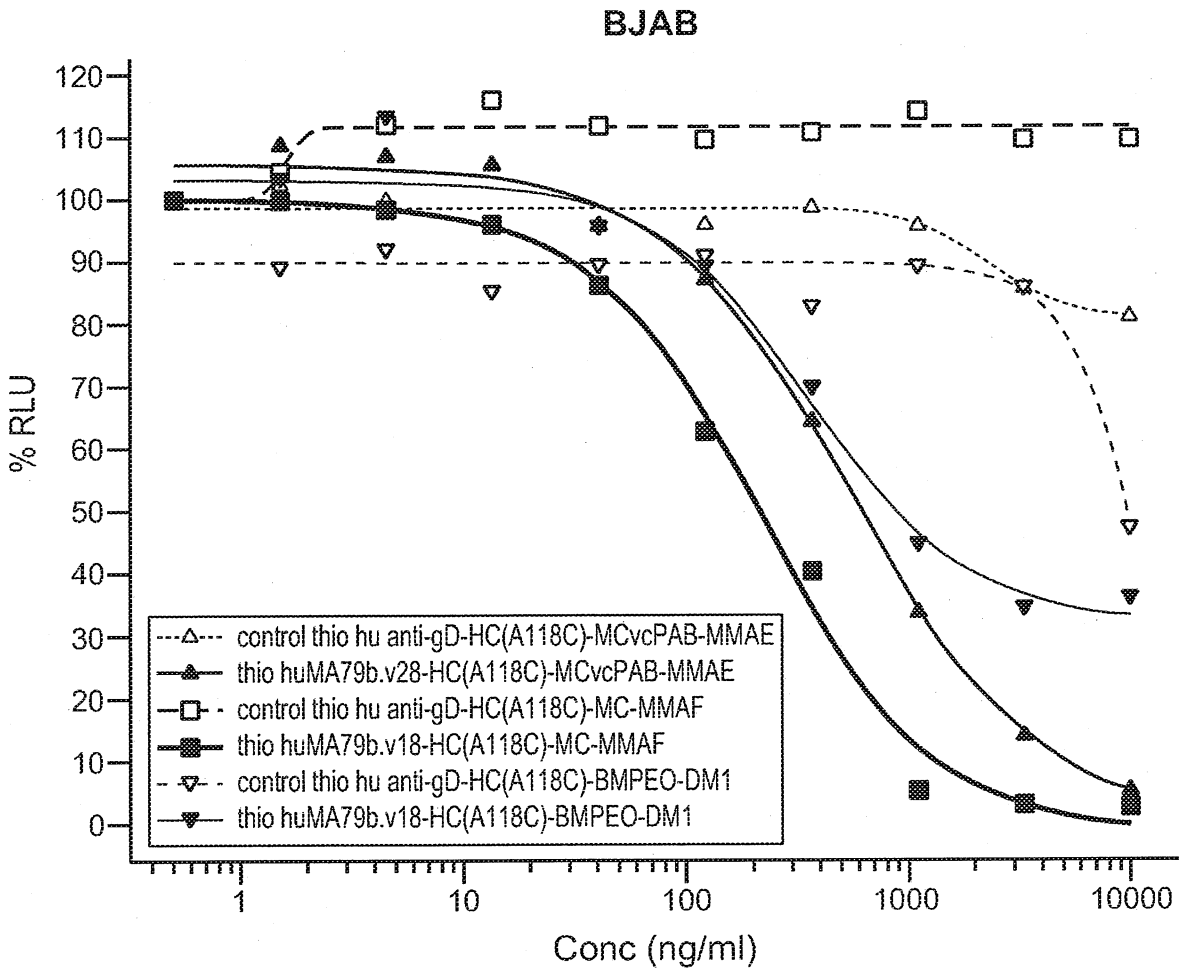

BJAB
% RLU
120
110
100
90
80
70
60
50
40
30
20
10
0
1
10
100
1000
10000
Conc (ng/ml)
control thio hu anti-gD-HC(A118C)-MCvcPAB-MMAE
thio huMA79b.v28-HC(A118C)-MCvcPAB-MMAE
control thio hu anti-gD-HC(A118C)-MC-MMAF
thio huMA79b.v18-HC(A118C)-MC-MMAF
control thio hu anti-gD-HC(A118C)-BMPEO-DM1
thio huMA79b.v18-HC(A118C)-BMPEO-DM1

FIG. 41A

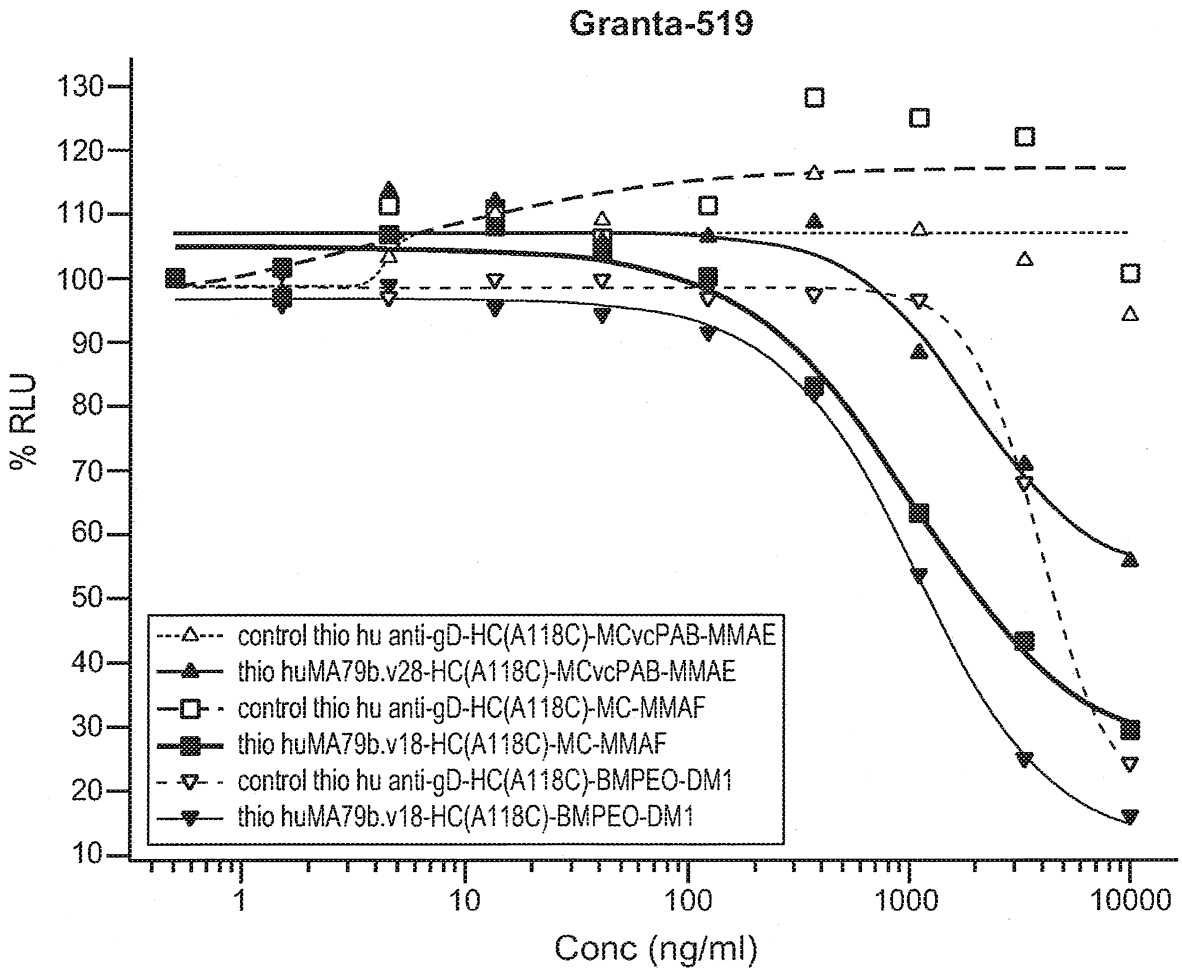

Granta-519
% RLU
130
120
110
100
90
80
70
60
50
40
30
20
10
1
10
100
1000
10000
Conc (ng/ml)
control thio hu anti-gD-HC(A118C)-MCvcPAB-MMAE
thio huMA79b.v28-HC(A118C)-MCvcPAB-MMAE
control thio hu anti-gD-HC(A118C)-MC-MMAF
thio huMA79b.v18-HC(A118C)-MC-MMAF
control thio hu anti-gD-HC(A118C)-BMPEO-DM1
thio huMA79b.v18-HC(A118C)-BMPEO-DM1

FIG. 41B

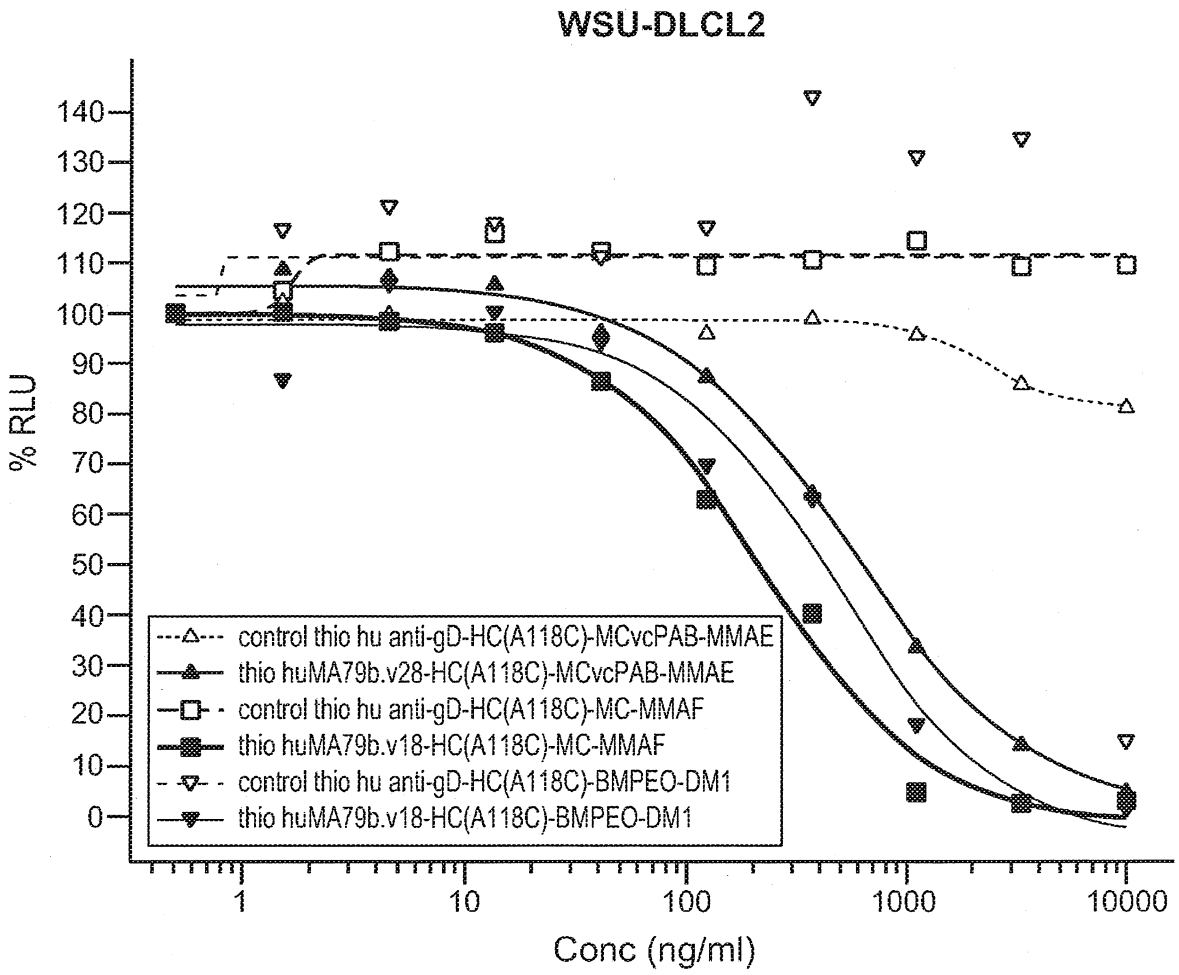

WSU-DLCL2
% RLU
140
130
120
110
100
90
80
70
60
50
40
30
20
10
0
1
10
100
1000
10000
Conc (ng/ml)
control thio hu anti-gD-HC(A118C)-MCvcPAB-MMAE
thio huMA79b.v28-HC(A118C)-MCvcPAB-MMAE
control thio hu anti-gD-HC(A118C)-MC-MMAF
thio huMA79b.v18-HC(A118C)-MC-MMAF
control thio hu anti-gD-HC(A118C)-BMPEO-DM1
thio huMA79b.v18-HC(A118C)-BMPEO-DM1

FIG. 41C

<p1.cynoCD79b

TCATGGTGATGGTGATGATGACCGGTACGCGTAGAATCGAGACCGAGGAGAGGGTTAGGGATAGG
CTTACCTTCGAACCGCGGGCCCTCTAGACTCGAGCGGCCGCCACTGTGCTGGATATCTGCAGAAT
TGCCCTTGGGGACAGAGCAGTGACC**ATG**GCCAGGCTGGCGTTGTCTCCTGTGTCCAGCCACTGGC
TGGTGGCGTTGCTGCTGCTGCTCTCAGCAGCTGAGCCAGTGCCAGCAGCCAAATCAGAGGACCTG
TACCCGAATCCCAAAGGTAGTGCTTGTTCTCGGATCTGGCAGAGCCCACGTTTCATAGCCAGGAA
ACGGGGCTTCACGGTGAAAATGCACTGCTACGTGACCAACAGCACCTTCAGCATCGTGAGCTGGC
TCCGGAAGCGGGAGACGGACAAGGAGCCCCAACAGGTGAACCTGGAGCAGGGCCACATGCATCAG
ACCCAAAACAGCTCTGTCACCACCCTCATCATCCAAGACATCCGGTTTGAGGACAACGGCATCTA
CTTCTGTCAGCAGGAGTGCAGCAAGACCTCGGAGGTCTACCGGGGCTGCGGCACGGAGCTGCGAG
TCATGGGGTTCAGCACCTTGGCACAGCTGAAGCAGAGGAACACGCTGAAGGATGGCATCATCATG
ATCCAGACGCTGCTGATCATCCTCTTCATCATCGTGCCCATCTTCCTGCTGCTGGACAAGGATGA
CAGCAAGGCCGGCATGGAGGAAGATCACACCTACGAGGGCCTGGACATTGACCAGACGGCCACCT
ACGAGGACATAGTGACGCTGCGGACAGGGGAAGTGAAGTGGTCTGTGGGTGAGCACCCAGGTCAG
GAG**TGA**GAGCCAGGACCTCCCCACGGCCTGGGTGCAGGCTCCCCAGCC

FIG. 42

<p1.cynoCD79b
DNA548455

MARLALSPVSSHWLVALLLLLSAAEPVPAAKSEDLYPNPKGSACSRIWQSPRFIARKRGFT
VKMHCYVTNSTFSIVSWLRKRETDKEPQQVNLEQGHMHQTQNSSVTTLIIQDIRFEDNGIY
FCQQECSKTSEVYRGCGTELRVMGFSTLAQLKQRNTLKDGIIMIQTLLIILFIIVPIFLLL
DKDDSKAGMEEDHTYEGLDIDQTATYEDIVTLRTGEVKWSVGEHPGQE

Signal sequence.
amino acids 1-26.

Transmembrane domain.
amino acids 161-181.

Immunoglobulin domain.
amino acids 59-126.

Immunoreceptor tyrosine-based activation motif.
amino acids 195-215.

Immunoglobulin V-set domain.
amino acids 44-145.

N-glycosylation site.
amino acids 70-73, 103-106.

cAMP- and cGMP-dependent protein kinase phosphorylation site.
amino acids 81-84.

Protein kinase C phosphorylation site.
amino acids 50-52, 61-63, 84-86, 158-160, 214-216.

Casein kinase II phosphorylation site.
amino acids 22-25, 84-87, 158-161, 208-211, 223-226.

Tyrosine kinase phosphorylation site.
amino acids 115-122.

N-myristoylation site.
amino acids 41-46, 120-125.

FIG. 43

CHIMERIC ANTI-CYNO CD79b (ch10D10) LIGHT CHAIN

ACCTCGGTTC TATCGATTGA ATTCCACCAT GGGATGGTCA TGTATCATCC TTTTTCTAGT
AGCAACTGCA ACTGGAGTAC ATTCAGATAT CGTGCTGACC CAATCTCCAC CCTCTTTGGC
TGTGTCTCTA GGGCAGAGGG CCACCATATC CTGCAGAGCC AGTGAAAGTG TTGATAGTTA
TGGCAAAACT TTTATGCACT GGCACCAGCA GAAACCAGGA CAGCCACCCA AACTCCTCAT
CTATCGTGTA TCCAACCTAG AATCTGGGAT CCCTGCCAGG TTCAGTGGCA GTGGGTCAAG
GACAGACTTC ACCCTCACCA TTAATCCTGT GGAGGCTGAT GATGTTGCAA CCTATTACTG
TCAGCAAAGT AATGAGGATC CGTTCACGTT CGGTGGAGGC ACCAAGCTGG AAATCAAACG
GACCGTGGCT GCACCATCTG TCTTCATCTT CCCGCCATCT GATGAGCAGT TGAAATCTGG
AACTGCCTCT GTTGTGTGCC TGCTGAATAA CTTCTATCCC AGAGAGGCCA AAGTACAGTG
GAAGGTGGAT AACGCCCTCC AATCGGGTAA CTCCCAGGAG AGTGTCACAG AGCAGGACAG
CAAGGACAGC ACCTACAGCC TCAGCAGCAC CCTGACGCTG AGCAAAGCAG ACTACGAGAA
ACACAAAGTC TACGCCTGCG AAGTCACCCA TCAGGGCCTG AGCTCGCCCG TCACAAAGAG
CTTCAACAGG GGAGAGTGTT AAGCTTGGCC GCCATGGCCC AACTTGTTTA TTGCAGCTTA
TAATGGTTAC AAATAAAGCA

FIG. 44

CHIMERIC ANTI-CYNO CD79b (ch10D10) LIGHT CHAIN

DIVLTQSPPSLAVSLGQRATISCRASESVDSYGKTFMHWHQQKPGQPPKLLIYRVSNLESGIPAR
FSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPFTFGGGTKLEIKRTVAAPSVFIFPPSDEQLK
SGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKV
YACEVTHQGLSSPVTKSFNRGEC

FIG. 45

CHIMERIC ANTI-CYNO CD79b (ch10D10) HEAVY CHAIN

CACCTCGGTT CTATCGATTG AATTCCACCA TGGGATGGTC ATGTATCATC CTTTTTCTAG
TAGCAACTGC AACTGGAGTA CATTCAGAAG TTCAGCTGCA GGAGTCGGGA CCTGGCCTGG
TGAAACCTTC TCAGTCTCTG TCCCTCACCT GCACTGTCAC TGGCTACTCA ATCACCAGTG
ATTATGCCTG GAACTGGATC CGGCAGTTTC CAGGAAACAA ACTGGAGTGG ATGGGCAACA
TATGGTACAG TGGTAGCACT ACCTACAACC CATCTCTCAA AAGTCGAATC TCTATCACTC
GAGACACATC CAAGAACCAG TTCTTCCTGC AGTTGAATTC TGTGACTTCT GAGGACACAG
CCACATATTA CTGTTCAAGA ATGGACTTCT GGGGTCAAGG CACCACTCTC ACAGTCTCCT
CAGCCTCCAC CAAGGGCCCA TCGGTCTTCC CCCTGGCACC CTCCTCCAAG AGCACCTCTG
GGGGCACAGC GGCCCTGGGC TGCCTGGTCA AGGACTACTT CCCCGAACCG GTGACGGTGT
CGTGGAACTC AGGCGCCCTG ACCAGCGGCG TGCACACCTT CCCGGCTGTC CTACAGTCCT
CAGGACTCTA CTCCCTCAGC AGCGTGGTGA CTGTGCCCTC TAGCAGCTTG GGCACCCAGA
CCTACATCTG CAACGTGAAT CACAAGCCCA GCAACACCAA GGTGGACAAG AAAGTTGAGC
CCAAATCTTG TGACAAAACT CACACATGCC CACCGTGCCC AGCACCTGAA CTCCTGGGGG
GACCGTCAGT CTTCCTCTTC CCCCCAAAAC CCAAGGACAC CCTCATGATC TCCCGGACCC
CTGAGGTCAC ATGCGTGGTG GTGGACGTGA GCCACGAAGA CCCTGAGGTC AAGTTCAACT
GGTACGTGGA CGGCGTGGAG GTGCATAATG CCAAGACAAA GCCGCGGGAG GAGCAGTACA
ACAGCACGTA CCGTGTGGTC AGCGTCCTCA CCGTCCTGCA CCAGGACTGG CTGAATGGCA
AGGAGTACAA GTGCAAGGTC TCCAACAAAG CCCTCCCAGC CCCCATCGAG AAAACCATCT
CCAAAGCCAA AGGGCAGCCC CGAGAACCAC AGGTGTACAC CCTGCCCCCA TCCCGGGAAG
AGATGACCAA GAACCAGGTC AGCCTGACCT GCCTGGTCAA AGGCTTCTAT CCCAGCGACA
TCGCCGTGGA GTGGGAGAGC AATGGGCAGC CGGAGAACAA CTACAAGACC ACGCCTCCCG
TGCTGGACTC CGACGGCTCC TTCTTCCTCT ACAGCAAGCT CACCGTGGAC AAGAGCAGGT
GGCAGCAGGG GAACGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC AACCACTACA
CGCAGAAGAG CCTCTCCCTG TCTCCGGGTA AATGAGTGCG ACGGCCCTAG AGTCGACCTG
CAGAAGCTTG GCCGCCATGG CCCAACTTGT TTATTGCAGC TTATAATGGT TACAAATAAA

FIG. 46

CHIMERIC ANTI-CYNO CD79b (ch10D10) HEAVY CHAIN

EVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGNIWYSGSTTYNPSLK
SRISITRDTSKNQFFLQLNSVTSEDTATYYCSRMDFWGQGTTLTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

FIG. 47

Anti-cyno CD79b ch10D10 A118C Cysteine Engineered Heavy Chain ThioMAb

A. Light Chain Sequence
Thio-anti-cyno CD79b (ch10D10)-HC-A118C (LC)

DIVLTQSPPSLAVSLGQRATISCRASESVDSYGKTFMHWHQQKPGQPPKLLIYRVSNLESGIPAR
FSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPFTFGGGTKLEIKRTVAAPSVFIFPPSDEQLK
SGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKV
YACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 245)

B. Heavy Chain Sequence
Thio-anti-cyno CD79b (ch10D10)-HC-A118C (HC)

DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGNIWYSGSTTYNPSLK
SRISITRDTSKNQFFLQLNSVTSEDTATYYCSRMDFWGQGTTLTVSSCSTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKVEPKSCDKTHT*CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD*
VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
(SEQ ID NO: 244)

FIG. 48

Anti-cyno CD79b ch10D10 V205C Cysteine Engineered Light Chain ThioMAb

A. Light Chain Sequence
Thio-anti-cyno CD79b (ch10D10)-HC-V205C (LC)

DIVLTQSPPSLAVSLGQRATISCRASESVDSYGKTFMHWHQQKPGQPPKLLIYRVSNLESGIPAR
FSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPFTFGGGTKLEIKRTVAAPSVFIFPPSDEQLK
SGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKV
YACEVTHQGLSSPCTKSFNRGEC (SEQ ID NO: 300)

B. Heavy Chain Sequence
Thio-anti-cyno CD79b (ch10D10)-HC-V205C (HC)

DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGNIWYSGSTTYNPSLK
SRISITRDTSKNQFFLQLNSVTSEDTATYYCSRMDFWGQGTTLTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKVEPKSCDKTHT*CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD*
VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 299)

FIG. 49

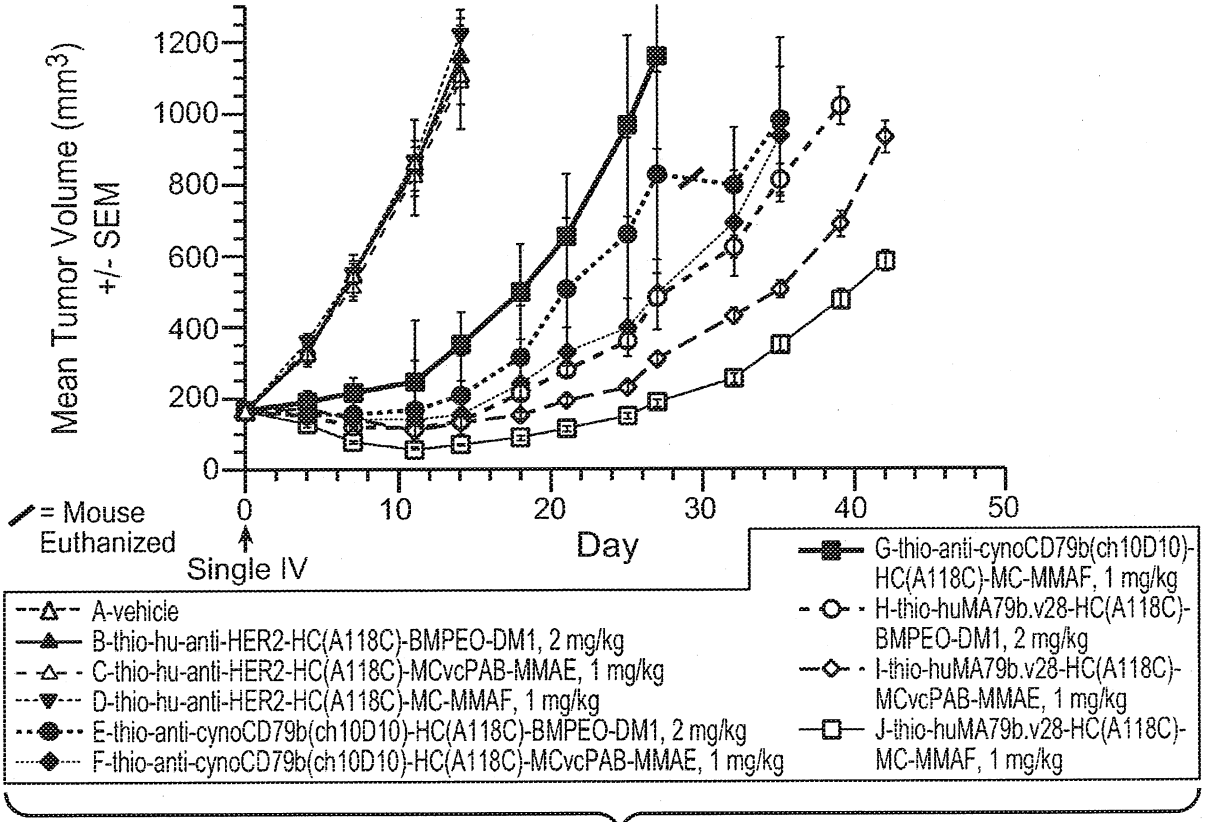

Mean Tumor Volume (mm3)
+/- SEM
1200
1000
800
600
400
200
0
0
10
20
30
40
50
Day
= Mouse Euthanized
Single IV
A-vehicle
B-thio-hu-anti-HER2-HC(A118C)-BMPEO-DM1, 2 mg/kg
C-thio-hu-anti-HER2-HC(A118C)-MCvcPAB-MMAE, 1 mg/kg
D-thio-hu-anti-HER2-HC(A118C)-MC-MMAF, 1 mg/kg
E-thio-anti-cynoCD79b(ch10D10)-HC(A118C)-BMPEO-DM1, 2 mg/kg
F-thio-anti-cynoCD79b(ch10D10)-HC(A118C)-MCvcPAB-MMAE, 1 mg/kg
G-thio-anti-cynoCD79b(ch10D10)-HC(A118C)-MC-MMAF, 1 mg/kg
H-thio-huMA79b.v28-HC(A118C)-BMPEO-DM1, 2 mg/kg
I-thio-huMA79b.v28-HC(A118C)-MCvcPAB-MMAE, 1 mg/kg
J-thio-huMA79b.v28-HC(A118C)-MC-MMAF, 1 mg/kg

FIG. 50

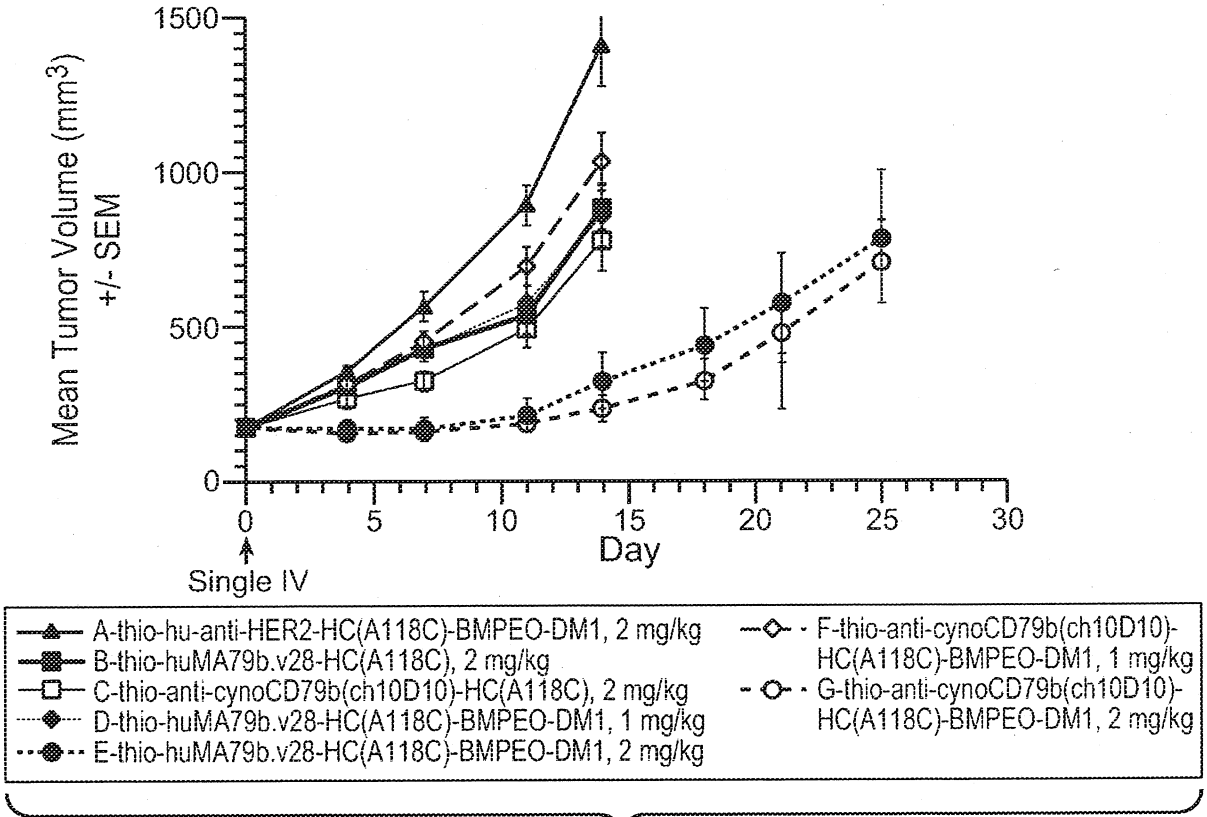

Mean Tumor Volume (mm3)
+/- SEM
1500
1000
500
0
0
5
10
15
20
25
30
Day
Single IV
A-thio-hu-anti-HER2-HC(A118C)-BMPEO-DM1, 2 mg/kg
B-thio-huMA79b.v28-HC(A118C), 2 mg/kg
C-thio-anti-cynoCD79b(ch10D10)-HC(A118C), 2 mg/kg
D-thio-huMA79b.v28-HC(A118C)-BMPEO-DM1, 1 mg/kg
E-thio-huMA79b.v28-HC(A118C)-BMPEO-DM1, 2 mg/kg
F-thio-anti-cynoCD79b(ch10D10)-HC(A118C)-BMPEO-DM1, 1 mg/kg
G-thio-anti-cynoCD79b(ch10D10)-HC(A118C)-BMPEO-DM1, 2 mg/kg

FIG. 51