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 (ch2F2) LIGHT CHAIN

GATATCGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCCAT
CTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTGAATTGGTTAT
TACAGAGGCCAGGCCAGTCTCCAGAGCGCCTAATTTATCTGGTGTCTAAACTGGATTCTGGA
GTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTCACACTGAAAATCAGCAGAGT
GGAGGCTGAGGATTTGGGAGTTTATTGTTGCTGGCAAGGTACACATTTTCCGTACACGTTCG
GAGGGGGTACCAAGGTGGAGATCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCG
CCATCTGATGAGCAGTTGAAATCTGGAACTGCTTCTGTTGTGTGCCTGCTGAATAACTTCTA
TCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGG
AGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTG
AGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAG
CTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

FIG. 3

CHIMERIC ANTI-HUMAN CD79b (ch2F2) LIGHT CHAIN

DIVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPERLIYLVSKLDSG
VPDRFTGSGSGTDFTLKISRVEAEDLGVYCCWQGTHFPYTFGGGTKVEIKRTVAAPSVFIFP
PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL
SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIG. 4

CHIMERIC ANTI-HUMAN CD79b (ch2F2) HEAVY CHAIN

CAGGTTCAACTCCAGCAACCTGGGGCTGAGCTGGTGAGGCCTGGGGCTTCAGTGAAGCTGTC
CTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTG
GACAAGGCCTTGAATGGATTGGTATGATTGATCCTTCAGACAGTGAAACTCACTACAATCAT
ATCTTCAAGGACAAGGCCACTTTGACTGTAGACAAATCCTCCAGCACAGCCTACTTGCAGCT
CAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAAATCTCTACTTGTGGG
GTCAAGGAACCTCAGTCACCGTCTCCTTAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG
GCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCT
TCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACTGTGCCCTCT
AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGT
GGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCAC
CTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATG
ATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG
AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC
CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG
AAGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGAC
ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGT
GCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGC
AGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
AAGAGCCTCTCCCTGTCTCCGGGTAAA

FIG. 5

CHIMERIC ANTI-HUMAN CD79b (ch2F2) HEAVY CHAIN

QVQLQQPGAELVRPGASVKLSCKASGYTFTSYWMNWVKQRPGQGLEWIGMIDPSDSETHYNH
IFKDKATLTVDKSSSTAYLQLSSLTSEDSAVYYCARNLYLWGQGTSVTVSLASTKGPSVFPL
APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS
SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM
ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD
IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
KSLSLSPG

FIG. 6

VL Sequences

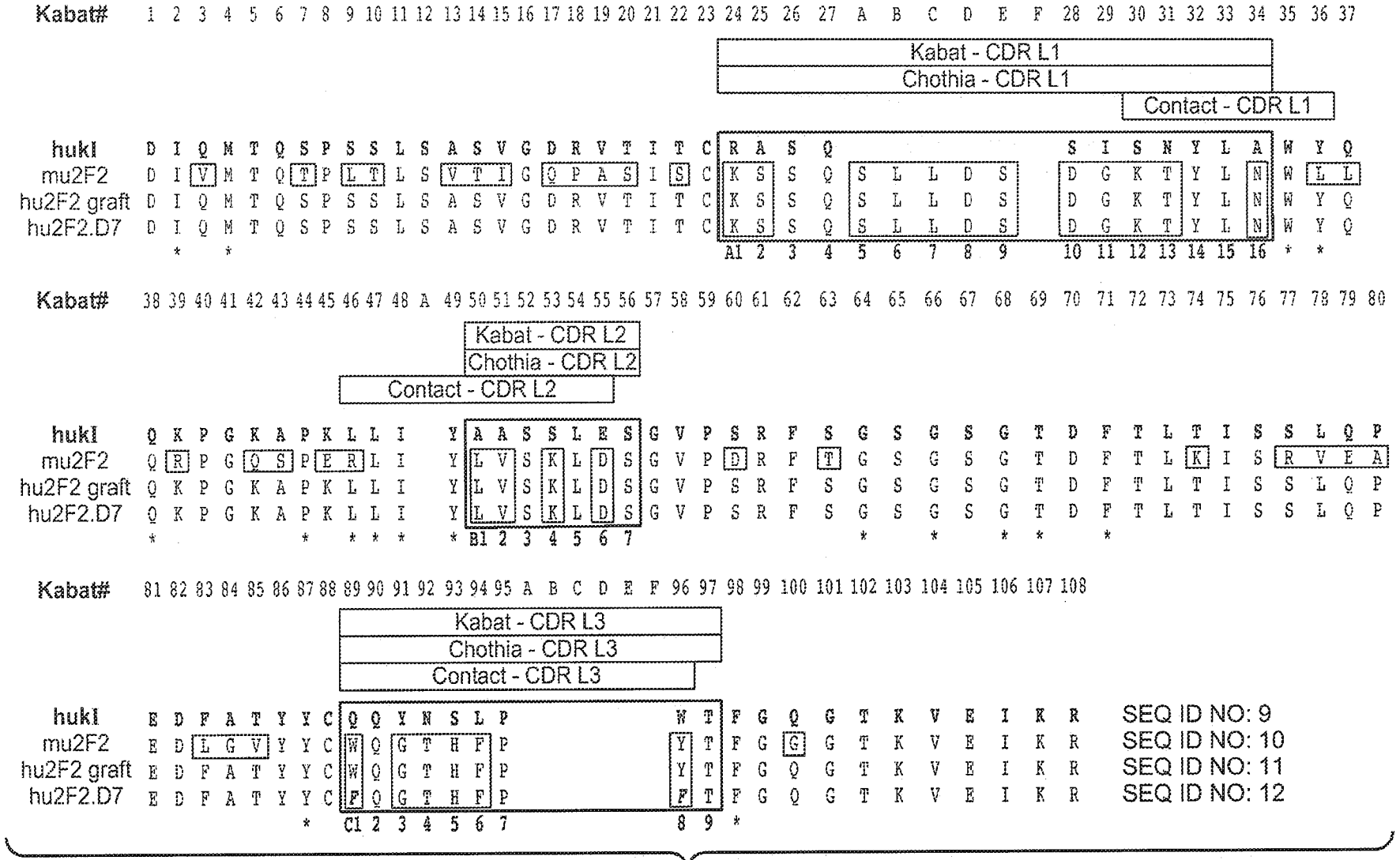


FIG. 7

VH Sequences

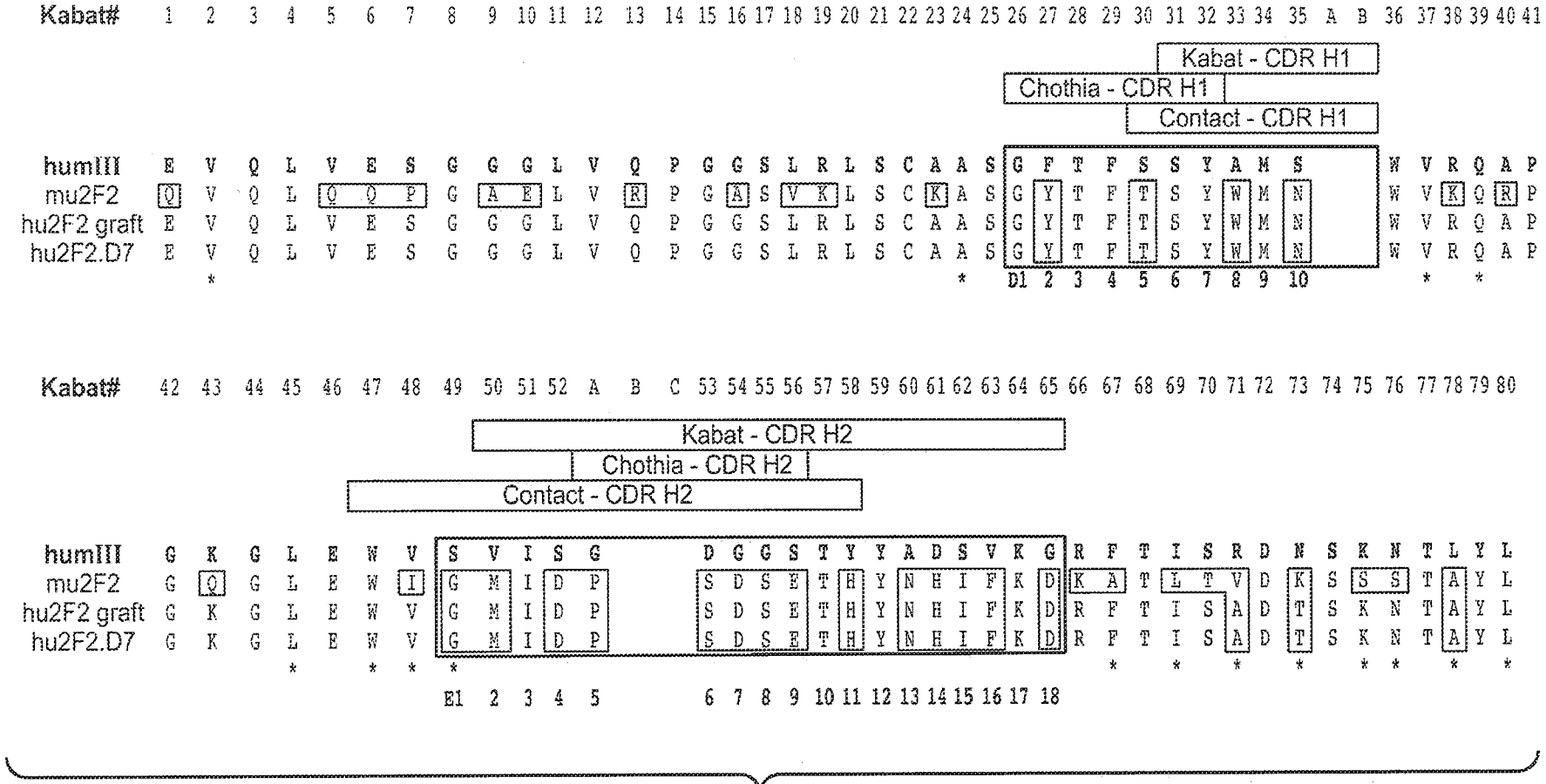


FIG. 8A

VH Sequences

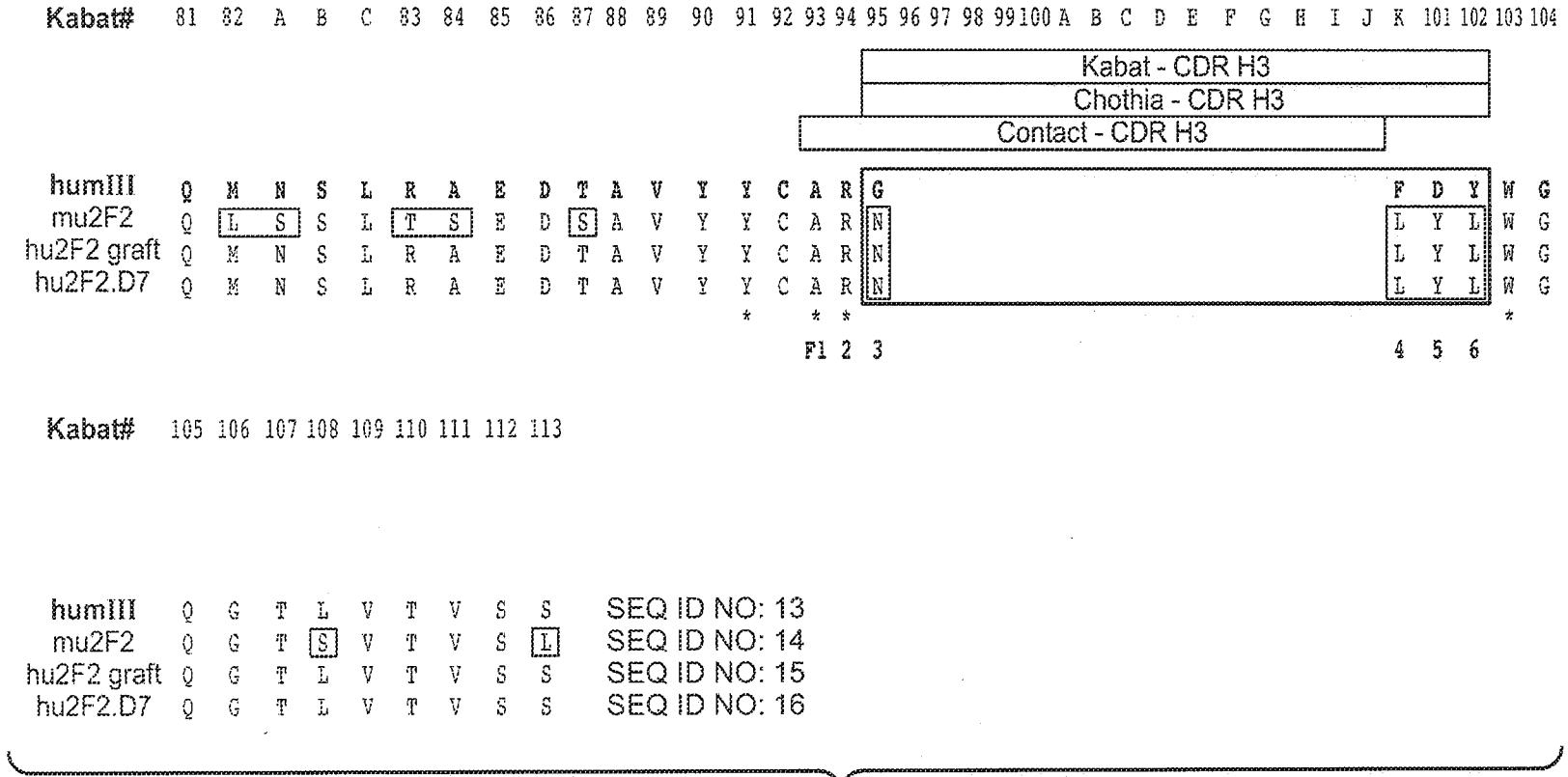


FIG. 8B

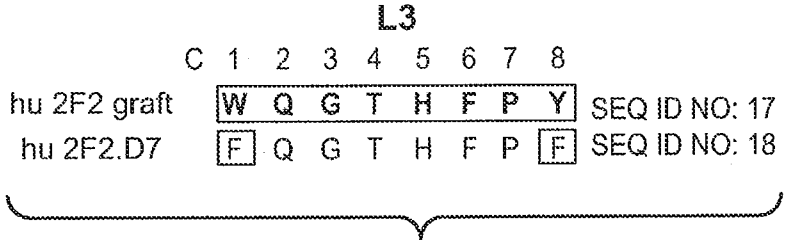


FIG. 9

	Biacore KD (nM)		
2F2 Variant	Fab	IgG	Immobilized Antigen
ch 2F2	108	2.7	hu CD79b.ecd-Fc
	111	1.4	hu CD79b.ecd
		2	15mer peptide
hu 2F2 graft	NB	NB	hu CD79b.ecd-Fc
		NB	hu CD79b.ecd
hu 2F2.D7	68	3.9	hu CD79b.ecd
		2.7	16mer peptide

FIG. 10


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. 11A

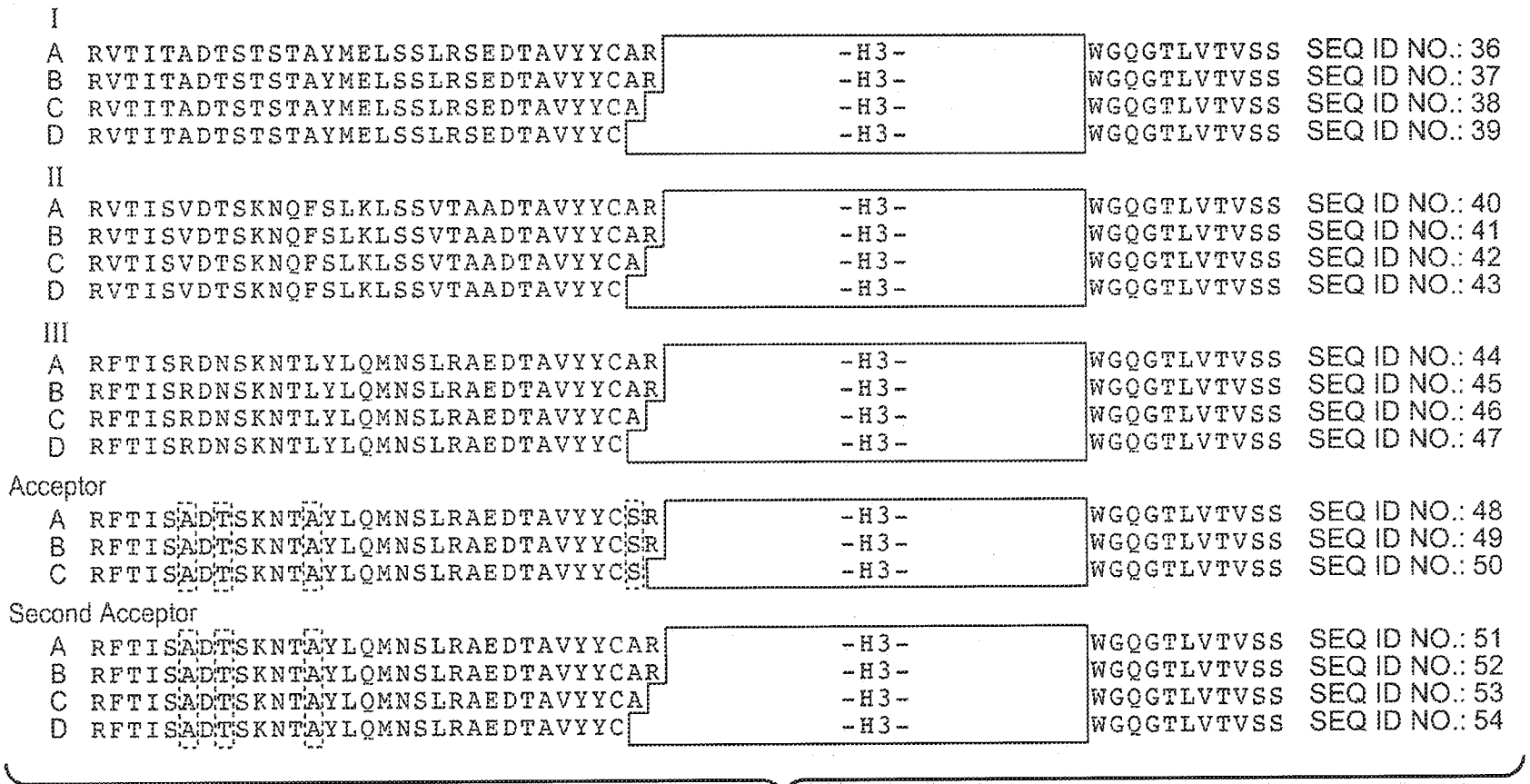

I
A RVTITADTSTSTAYMELSSLRSEDTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.: 36
B RVTITADTSTSTAYMELSSLRSEDTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.: 37
C RVTITADTSTSTAYMELSSLRSEDTAVYYCA -H3- WGQGTLVTVSS SEQ ID NO.: 38
D RVTITADTSTSTAYMELSSLRSEDTAVYYC -H3- WGQGTLVTVSS SEQ ID NO.: 39
II
A RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.: 40
B RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.: 41
C RVTISVDTSKNQFSLKLSSVTAADTAVYYCA -H3- WGQGTLVTVSS SEQ ID NO.: 42
D RVTISVDTSKNQFSLKLSSVTAADTAVYYC -H3- WGQGTLVTVSS SEQ ID NO.: 43
III
A RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.: 44
B RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.: 45
C RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA -H3- WGQGTLVTVSS SEQ ID NO.: 46
D RFTISRDNSKNTLYLQMNSLRAEDTAVYYC -H3- WGQGTLVTVSS SEQ ID NO.: 47
Acceptor
A RFTISADTSKNTAYLQMNSLRAEDTAVYYCSR -H3- WGQGTLVTVSS SEQ ID NO.: 48
B RFTISADTSKNTAYLQMNSLRAEDTAVYYCSR -H3- WGQGTLVTVSS SEQ ID NO.: 49
C RFTISADTSKNTAYLQMNSLRAEDTAVYYCS -H3- WGQGTLVTVSS SEQ ID NO.: 50
Second Acceptor
A RFTISADTSKNTAYLQMNSLRAEDTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.: 51
B RFTISADTSKNTAYLQMNSLRAEDTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.: 52
C RFTISADTSKNTAYLQMNSLRAEDTAVYYCA -H3- WGQGTLVTVSS SEQ ID NO.: 53
D RFTISADTSKNTAYLQMNSLRAEDTAVYYC -H3- WGQGTLVTVSS SEQ ID NO.: 54

FIG. 11B

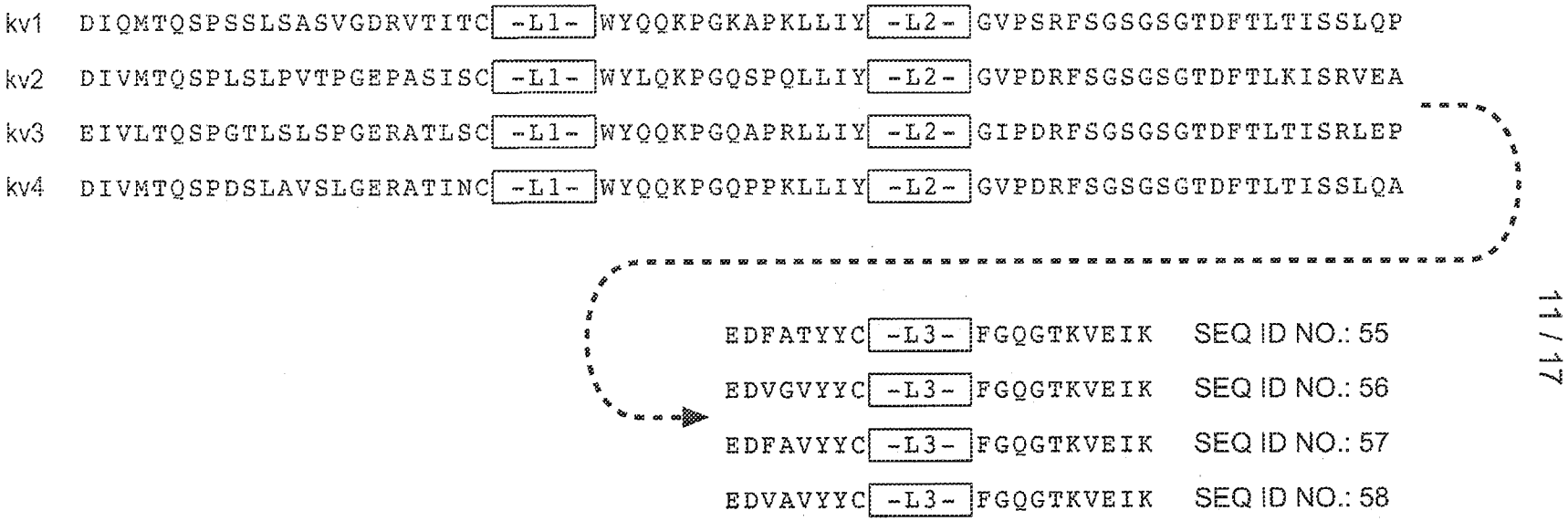

kv1 DIQMTQSPSSLSASVGDRVTITC -L1- WYQQKPGKAPKLLIY -L2- GVPSRFSGSGSGTDFTLTISSLQP
kv2 DIVMTQSPLSLPVTPGEPASISC -L1- WYLQKPGQSPQLLIY -L2- GVPDRFSGSGSGTDFTLKISRVEA
kv3 EIVLTQSPGTLSLSPGERATLSC -L1- WYQQKPGQAPRLLIY -L2- GIPDRFSGSGSGTDFTLTISRLEP
kv4 DIVMTQSPDSLAVSLGERATINC -L1- WYQQKPGQPPKLLIY -L2- GVPDRFSGSGSGTDFTLTISSLQA
EDFATYYC -L3- FGQGTKVEIK SEQ ID NO.: 55
EDVGVYYC -L3- FGQGTKVEIK SEQ ID NO.: 56
EDFAVYYC -L3- FGQGTKVEIK SEQ ID NO.: 57
EDVAVYYC -L3- FGQGTKVEIK SEQ ID NO.: 58

FIG. 12

A. hu2F2.D7 Light Chain

FR1-LC: DIQMTQSPSSLSASVGDRVTITC (SEQ ID NO: 19)
FR2-LC: WYQQKPGKAPKLLIY (SEQ ID NO: 20)
FR3-LC: GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO: 21)
FR4-LC: FGQGTKVEIKR (SEQ ID NO: 22)
HVR1-LC: KSSQSLLDSDGKTYLN (SEQ ID NO: 23)
HVR2-LC: LVSKLDS (SEQ ID NO: 24)
HVR3-LC: FQGTHFPFT (SEQ ID NO: 25)
CL1: TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
(SEQ ID NO: 26)

Light Chain:
DIQMTQSPSSLSASVGDRVTITCKSSQSLLDSDGKTYLNWYQQKPGKAPKLLIYLVSKLDSGVPS
RFSGSGSGTDFTLTISSLQPEDFATYYCFQGTHFPFTFGQGTKVEIKRTVAAPSVFIFPPSDEQL
KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHK
VYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 89)

LC-Variable Domain:
DIQMTQSPSSLSASVGDRVTITCKSSQSLLDSDGKTYLNWYQQKPGKAPKLLIYLVSKLDSGVPS
RFSGSGSGTDFTLTISSLQPEDFATYYCFQGTHFPFTFGQGTKVEIKR (SEQ ID NO: 12)

B. hu2F2.D7 Heavy Chain

FR1-HC: EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO: 27)
FR2-HC: WVRQAPGKGLEWV (SEQ ID NO: 28)
FR3-HC: RFTISADTSKNTAYLQMNSLRAEDTAVYYC (SEQ ID NO: 29)
FR4-HC: WGQGTLVTVSS (SEQ ID NO: 30)
HVR1-HC: GYTFTSYWMN (SEQ ID NO: 31)
HVR2-HC: GMIDPSDSETHYNHIFKD (SEQ ID NO: 32)
HVR3-HC: ARNLYL (SEQ ID NO: 33)
CH1: ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT
(SEQ ID NO: 34)
Fc: CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG
VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
(SEQ ID NO: 35)

Heavy Chain:
EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQAPGKGLEWVGMIDPSDSETHYNHIFK
DRFTISADTSKNTAYLQMNSLRAEDTAVYYCARNLYLWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI
CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV
DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
(SEQ ID NO: 90)

HC-Variable Domain:
EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQAPGKGLEWVGMIDPSDSETHYNHIFK
DRFTISADTSKNTAYLQMNSLRAEDTAVYYCARNLYLWGQGTLVTVSS (SEQ ID NO: 16)

FIG. 13

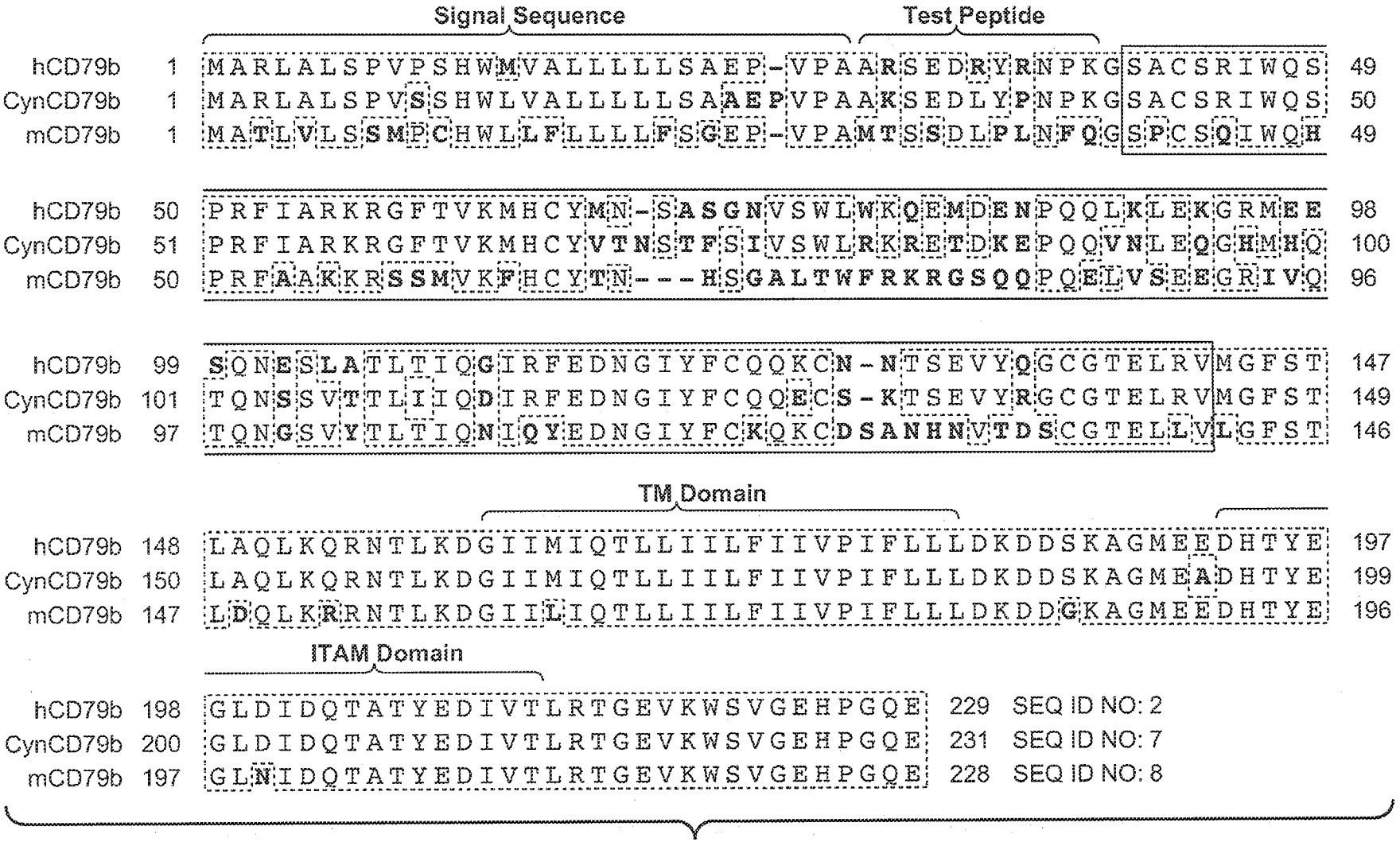

Signal Sequence
Test Peptide
hCD79b 1 MARLALSPVPSHWMVALLLLLSAEP-VPAARSEDRYRNPKGSACSRIWQS 49
CynCD79b 1 MARLALSPVSSHWLVALLLLLSAAEPVPAAKSEDLYPNPKGSACSRIWQS 50
mCD79b 1 MATLVLSSMPCHWLLFLLLLFSGEP-VPAMTSSDLPLNFQGSPCSQIWQH 49
hCD79b 50 PRFIARKRGFTVKMHCYMN-SASGNVSWLWKQEMDENPQQLKLEKGRMEE 98
CynCD79b 51 PRFIARKRGFTVKMHCYVTNSTFSIVSWLRKRETDKEPQQVNLEQGHMHQ 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. 14

FIG. 15

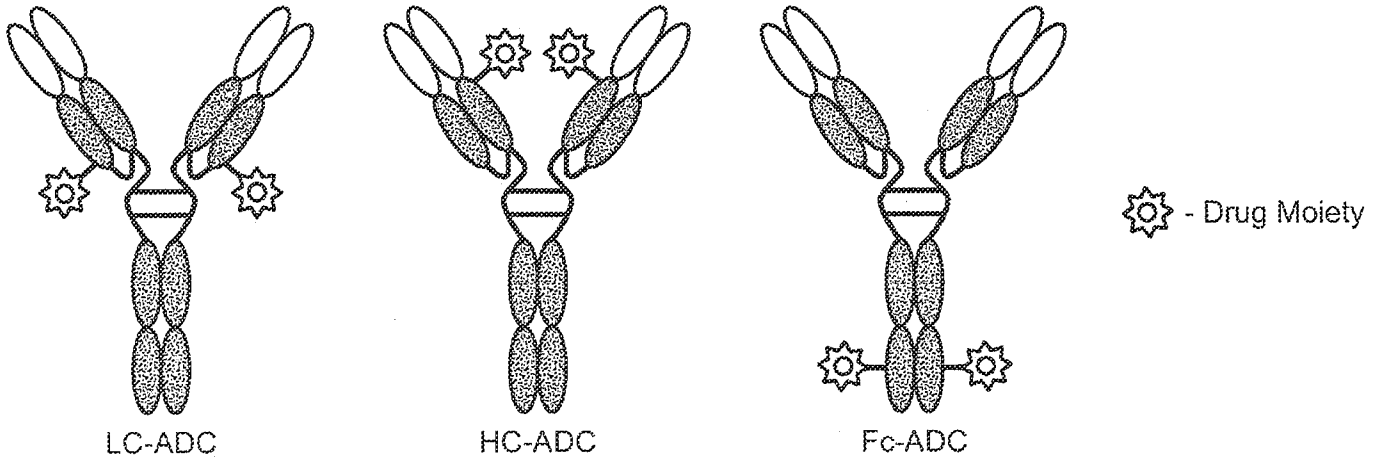
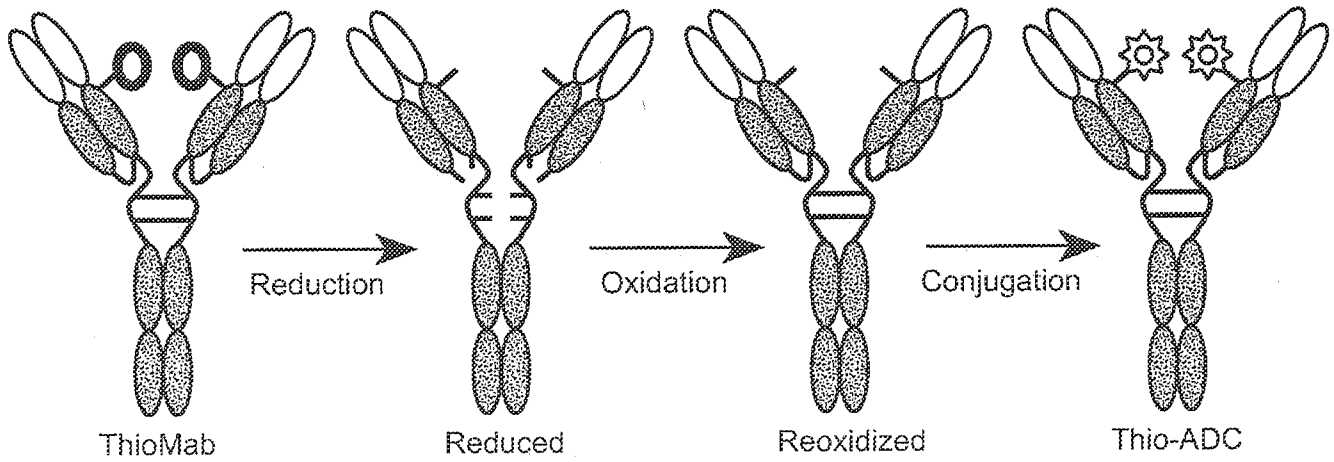

LC-ADC
HC-ADC
Fc-ADC
- Drug Moiety

FIG. 16


ThioMab
Reduction
Reduced
Oxidation
Reoxidized
Conjugation
Thio-ADC

Anti-CD79b A118C hu2F2.D7 Cysteine Engineered Heavy Chain ThioMAb

A. Light Chain Sequence
Thio-hu2F2.D7-HC-A118C (LC)

DIQMTQSPSSLSASVGDRVTITCKSSQSLLDSDGKTYLNWYQQKPGKAPKLLIYLVSKLDSGVPS
RFSGSGSGTDFTLTISSLQPEDFATYYCFQGTHFPFTFGQGTKVEIKRTVAAPSVFIFPPSDEQL
KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHK
VYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 86)

B. Heavy Chain Sequence
Thio-hu2F2.D7-HC-A118C (HC)

EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQAPGKGLEWVGMIDPSDSETHYNHIFK
DRFTISADTSKNTAYLQMNSLRAEDTAVYYCARNLYLWGQGTLVTVSSCSTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI
CNVNHKPSNTKVDKKVEPKSCDKTHT*CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV*
DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
(SEQ ID NO: 85)

FIG. 17

Anti-CD79b V205C hu2F2.D7 Cysteine Engineered Light Chain ThioMAb

A. Light Chain Sequence
Thio-hu2F2.D7-LC-V205C (LC)

DIQMTQSPSSLSASVGDRVTITCKSSQSLLDSDGKTYLNWYQQKPGKAPKLLIYLVSKLDSGVPS
RFSGSGSGTDFTLTISSLQPEDFATYYCFQGTHFPFTFGQGTKVEIKRTVAAPSVFIFPPSDEQL
KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHK
VYACEVTHQGLSSPCTKSFNRGEC (SEQ ID NO: 88)

B. Heavy Chain Sequence
Thio-hu2F2.D7-LC-V205C (HC)

EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMNWVRQAPGKGLEWVGMIDPSDSETHYNHIFK
DRFTISADTSKNTAYLQMNSLRAEDTAVYYCARNLYLWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI
CNVNHKPSNTKVDKKVEPKSCDKTHT*CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV*
DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
(SEQ ID NO: 87)

FIG. 18

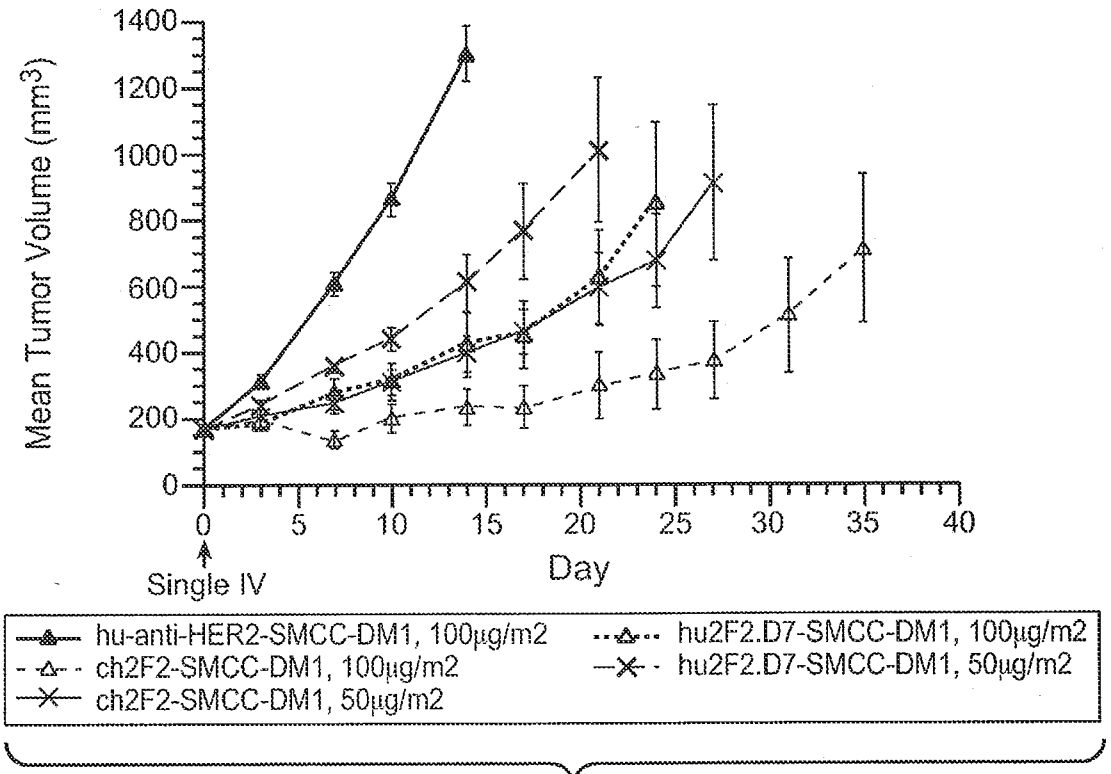

Mean Tumor Volume (mm3)
1400
1200
1000
800
600
400
200
0
0
5
10
15
20
25
30
35
40
Day
Single IV
hu-anti-HER2-SMCC-DM1, 100µg/m2
ch2F2-SMCC-DM1, 100µg/m2
ch2F2-SMCC-DM1, 50µg/m2
hu2F2.D7-SMCC-DM1, 100µg/m2
hu2F2.D7-SMCC-DM1, 50µg/m2

FIG. 19

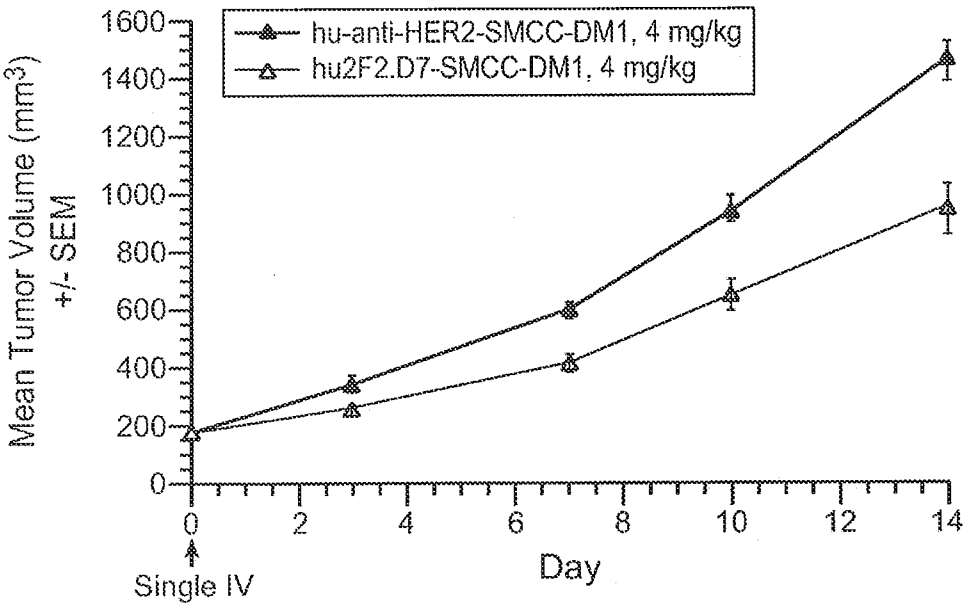


FIG. 20A

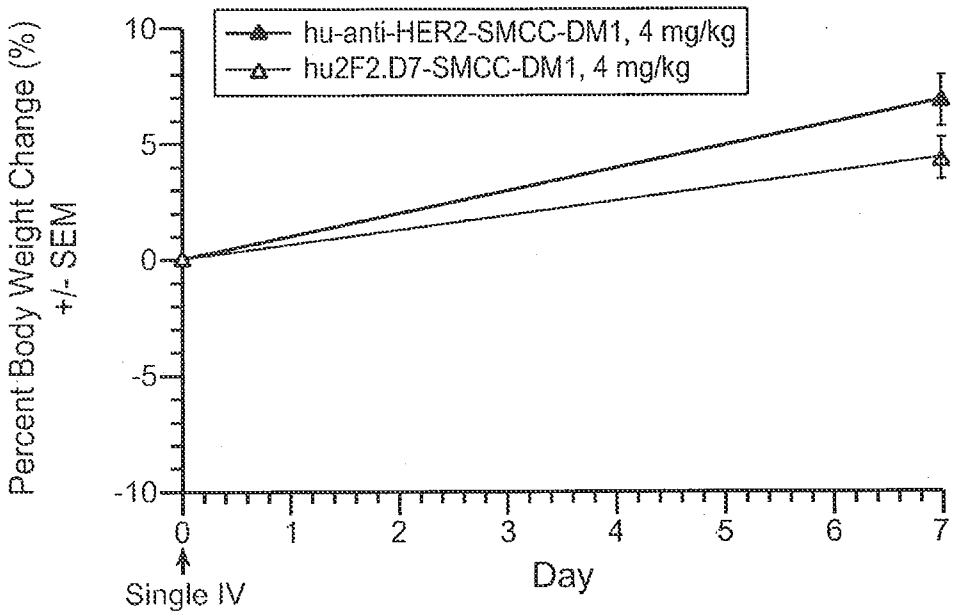


FIG. 20B