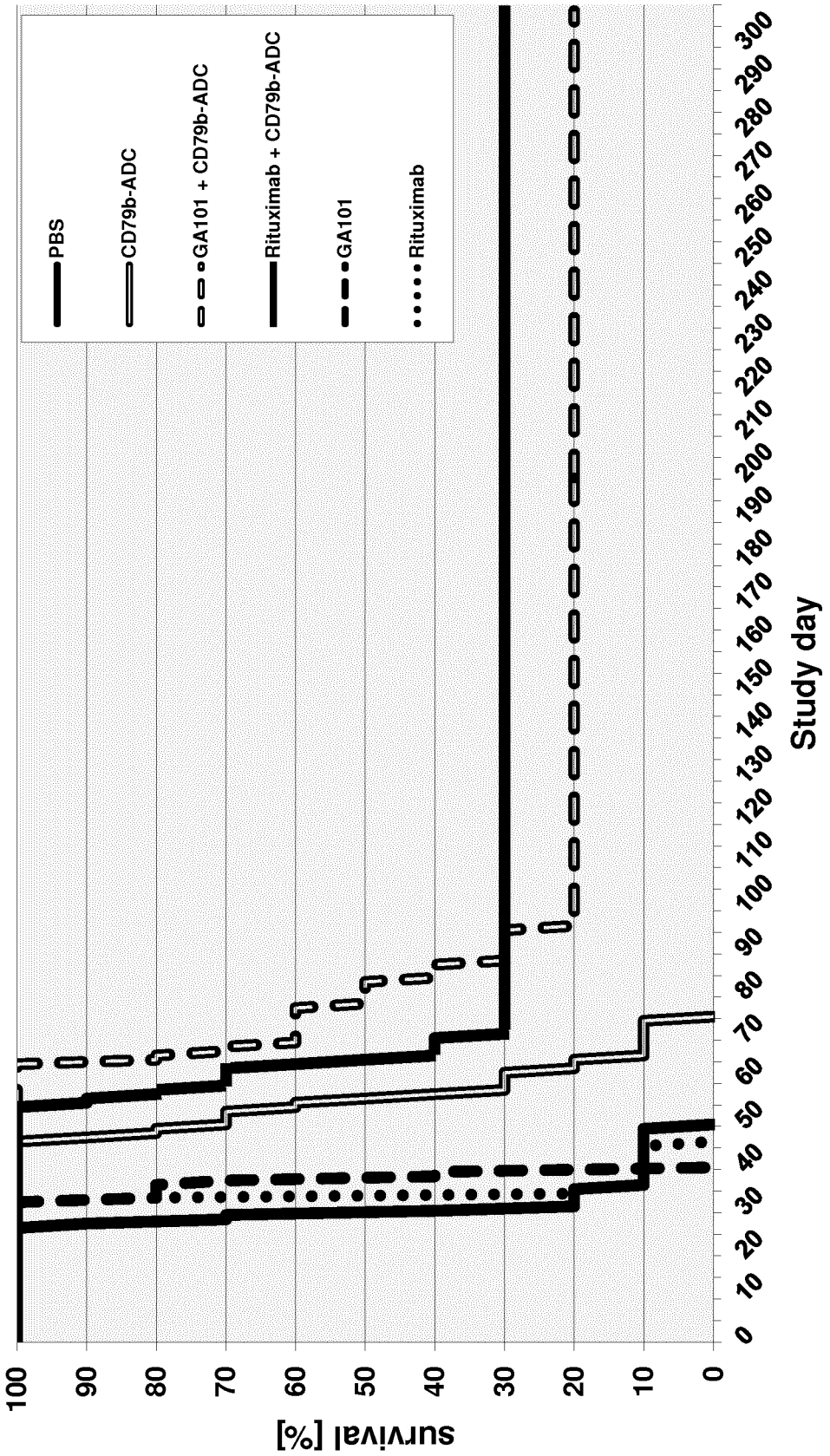

PBS
CD79b-ADC
GA101 + CD79b-ADC
Rituximab + CD79b-ADC
GA101
Rituximab
survival [%]
100
90
80
70
60
50
40
30
20
10
0
Study day
0
10
20
30
40
50
60
70
80
90
100
110
120
130
140
150
160
170
180
190
200
210
220
230
240
250
260
270
280
290
300

Fig. 1

Pairwise Log-Rank Test (multiple test level = 0.00333)

Group	PBS	CD79b-ADC	GA101	GA101 + CD79b-ADC	Rituximab	Rituximab + CD79b-ADC
PBS	1.0000	<.0001*	0.0157*	<.0001*	0.1171	<.0001*
CD79b-ADC	<.0001*	1.0000	<.0001*	0.0002*	<.0001*	0.0234*
GA101	0.0157*	<.0001*	1.0000	<.0001*	0.1115	<.0001*
GA101 + CD79b-ADC	<.0001*	0.0002*	<.0001*	1.0000	<.0001*	0.6194
Rituximab	0.1171	<.0001*	0.1115	<.0001*	1.0000	<.0001*
Rituximab + CD79b-ADC	<.0001*	0.0234*	<.0001*	0.6194	<.0001*	1.0000

Pairwise Wilcoxon Test (multiple test level = 0.00333)

Group	PBS	CD79b-ADC	GA101	GA101 + CD79b-ADC	Rituximab	Rituximab + CD79b-ADC
PBS	1.0000	<.0001*	0.0020*	<.0001*	0.0109*	<.0001*
CD79b-ADC	<.0001*	1.0000	<.0001*	0.0003*	<.0001*	0.0199*
GA101	0.0020*	<.0001*	1.0000	<.0001*	0.0570	<.0001*
GA101 + CD79b-ADC	<.0001*	0.0003*	<.0001*	1.0000	<.0001*	0.2177
Rituximab	0.0109*	<.0001*	0.0570	<.0001*	1.0000	<.0001*
Rituximab + CD79b-ADC	<.0001*	0.0199*	<.0001*	0.2177	<.0001*	1.0000

Fig. 2

huMA79b.v17 Light Chain

FR1-LC: DIQLTQSPSSLSASVGDRVTITC (SEQ ID NO: 131)
FR2-LC: WYQQKPGKAPKLLIY (SEQ ID NO: 132)
FR3-LC: GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO: 133)
FR4-LC: FGQGTKVEIKR (SEQ ID NO: 134)
HVR1-LC: KASQSVDYDGDSFLN (SEQ ID NO: 47)
HVR2-LC: AASNLES (SEQ ID NO: 48)
HVR3-LC: QQSNEDPLT (SEQ ID NO: 49)
CL1: TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 135)

Light Chain:

DIQLTQSPSSLSASVGDRVTITCKASQSVDYDGDSFLNWYQQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQSNEDPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 176)

LC-Variable Domain:

DIQLTQSPSSLSASVGDRVTITCKASQSVDYDGDSFLNWYQQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQSNEDPLTFGQGTKVEIKR (SEQ ID NO: 53)

Fig. 3A

huMA79b.v17 Heavy Chain

FR1-HC: EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO: 136)
FR2-HC: WVRQAPGKGLEWI (SEQ ID NO: 137)
FR3-HC: RATFSADTSKNTAYLQMNSLRAEDTAVYYC (SEQ ID NO: 138)
FR4-HC: WGQGTLVTVSS (SEQ ID NO: 139)
HVR1-HC: GYTFSSYWIE (SEQ ID NO: 50)
HVR2-HC: GEILPGGGDTNYNEIFKG (SEQ ID NO: 51)
HVR3-HC: TRRVPVYFDY (SEQ ID NO: 52)
CH1: ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO: 140)
Fc: CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 141)

Heavy Chain:

EVQLVESGGGLVQPGGSLRLSCAASGYTFSSYWIEWVRQAPGKGLEWIGEILPGGGDTNYNEIFKGRATFSADTSKNTAYLQMNSLRAEDTAVYYCTRR
VPVYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 177)

HC-Variable Domain:

EVQLVESGGGLVQPGGSLRLSCAASGYTFSSYWIEWVRQAPGKGLEWIGEILPGGGDTNYNEIFKGRATFSADTSKNTAYLQMNSLRAEDTAVYYCTRR
VPVYFDYWGQGTLVTVSS (SEQ ID NO: 54)

Fig. 3B

huMA79b.v18 Light Chain

FR1-LC: DIQLTQSPSSLSASVGDRVTITC (SEQ ID NO: 142)
FR2-LC: WYQQKPGKAPKLLIY (SEQ ID NO: 143)
FR3-LC: GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO: 144)
FR4-LC: FGQGTKVEIKR (SEQ ID NO: 145)
HVR1-LC: KASQSVDYDGDSFLN (SEQ ID NO: 55)
HVR2-LC: AASNLES (SEQ ID NO: 56)
HVR3-LC: QQSNEDPLT (SEQ ID NO: 57)
CL1: TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 147)

Light Chain:

DIQLTQSPSSLSASVGDRVTITCKASQSVDYDGDSFLNWYQQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQSNEDPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 178)

LC-Variable Domain:

DIQLTQSPSSLSASVGDRVTITCKASQSVDYDGDSFLNWYQQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQSNEDPLTFGQGTKVEIKR (SEQ ID NO: 61)

Fig. 4A

huMA79b.v18 Heavy Chain

FR1-HC: EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO: 148)
FR2-HC: WVRQAPGKGLEWI (SEQ ID NO: 149)
FR3-HC: RATFSADTSKNTAYLQMNSLRAEDTAVYYC (SEQ ID NO: 150)
FR4-HC: WGQGTLVTVSS (SEQ ID NO: 151)
HVR1-HC: GYTFSSYWIE (SEQ ID NO: 58)
HVR2-HC: GEILPGGGDTNYNEIFKG (SEQ ID NO: 59)
HVR3-HC: TRRVPIRLDY (SEQ ID NO: 60)
CH1: ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO: 152)
Fc: CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 153)

Heavy Chain:

EVQLVESGGGLVQPGGSLRLSCAASGYTFSSYWIEWVRQAPGKGLEWIGEILPGGGDTNYNEIFKGRATFSADTSKNTAYLQMNSLRAEDTAVYYCTRR
VPIRLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 179)

HC-Variable Domain:

EVQLVESGGGLVQPGGSLRLSCAASGYTFSSYWIEWVRQAPGKGLEWIGEILPGGGDTNYNEIFKGRATFSADTSKNTAYLQMNSLRAEDTAVYYCTRR
VPIRLDYWGQGTLVTVSS (SEQ ID NO: 62)

Fig. 4B

huMA79b.v28 Light Chain

FR1-LC: DIQLTQSPSSLSASVGDRVTITC (SEQ ID NO: 154)
FR2-LC: WYQQKPGKAPKLLIY (SEQ ID NO: 155)
FR3-LC: GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO: 156)
FR4-LC: FGQGTKVEIKR (SEQ ID NO: 157)
HVR1-LC: KASQSVDYEGDSFLN (SEQ ID NO: 63)
HVR2-LC: AASNLES (SEQ ID NO: 64)
HVR3-LC: QQSNEDPLT (SEQ ID NO: 65)
CL1: TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 158)

Light Chain:

DIQLTQSPSSLSASVGDRVTITCKASQSVDYEGDSFLNWYQQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQSNEDPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 180)

Fig. 5A

huMA79b.v28 Heavy Chain

FR1-HC: EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO: 159)
FR2-HC: WVRQAPGKGLEWI (SEQ ID NO: 160)
FR3-HC: RATFSADTSKNTAYLQMNSLRAEDTAVYYC (SEQ ID NO: 161)
FR4-HC: WGQGTLVTVSS (SEQ ID NO: 162)
HVR1-HC: GYTFSSYWIE (SEQ ID NO: 66)
HVR2-HC: GEILPGGGDTNYNEIFKG (SEQ ID NO: 67)
HVR3-HC: TRRVPIRLDY (SEQ ID NO: 68)
CH1: ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO: 163)
Fc: CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 164)

Heavy Chain:

EVQLVESGGGLVQPGGSLRLSCAASGYTFSSYWIEWVRQAPGKGLEWIGEILPGGGDTNYNEIFKGRATFSADTSKNTAYLQMNS LRAEDTAVYYCTRRVPIRLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG (SEQ ID NO: 181)

Fig. 5B

huMA79b.v32 Light Chain

FR1-LC: DIQLTQSPSSLSASVGDRVTITC (SEQ ID NO: 165)
FR2-LC: WYQQKPGKAPKLFIY (SEQ ID NO: 166)
FR3-LC: GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO: 167)
FR4-LC: FGQGTKVEIKR (SEQ ID NO: 168)
HVR1-LC: KASQSVDYSGDSFLN (SEQ ID NO: 71)
HVR2-LC: AASNLES (SEQ ID NO: 72)
HVR3-LC: QQSNEDPLT (SEQ ID NO: 73)
CL1: TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 169)

Light Chain:

DIQLTQSPSSLSASVGDRVTITCKASQSVDYSGDSFLNWYQQKPGKAPKLFIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQSNEDPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 182)

LC-Variable Domain:

DIQLTQSPSSLSASVGDRVTITCKASQSVDYSGDSFLNWYQQKPGKAPKLFIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFA TYYCQQSNEDPLTFGQGTKVEIKR (SEQ ID NO: 77)

Fig. 6A

huMA79b.v32 Heavy Chain

FR1-HC: EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO: 170)
FR2-HC: WVRQAPGKGLEWI (SEQ ID NO: 171)
FR3-HC: RATFSADTSKNTAYLQMNSLRAEDTAVYYC (SEQ ID NO: 172)
FR4-HC: WGQGTLVTVSS (SEQ ID NO: 173)
HVR1-HC: GYTFSSYWIE (SEQ ID NO: 74)
HVR2-HC: GEILPGGGDTNYNEIFKG (SEQ ID NO: 75)
HVR3-HC: TRRVPIRLDY (SEQ ID NO: 76)
CH1: ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO: 174)
Fc: CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 175)

Heavy Chain:

EVQLVESGGGLVQPGGSLRLSCAASGYTFSSYWIEWVRQAPGKGLEWIGEILPGGGDTNYNEIFKGRATFSADTSKNTAYLQMNSLR
AEDTAVYYCTRRVPIRLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
TQKSLSLSPG (SEQ ID NO: 146)

HC-Variable Domain:

EVQLVESGGGLVQPGGSLRLSCAASGYTFSSYWIEWVRQAPGKGLEWIGEILPGGGDTNYNEIFKGRATFSADTSKNTAYLQMNSLR
AEDTAVYYCTRRVPIRLDYWGQGTLVTVSS (SEQ ID NO: 78)

Fig. 6B

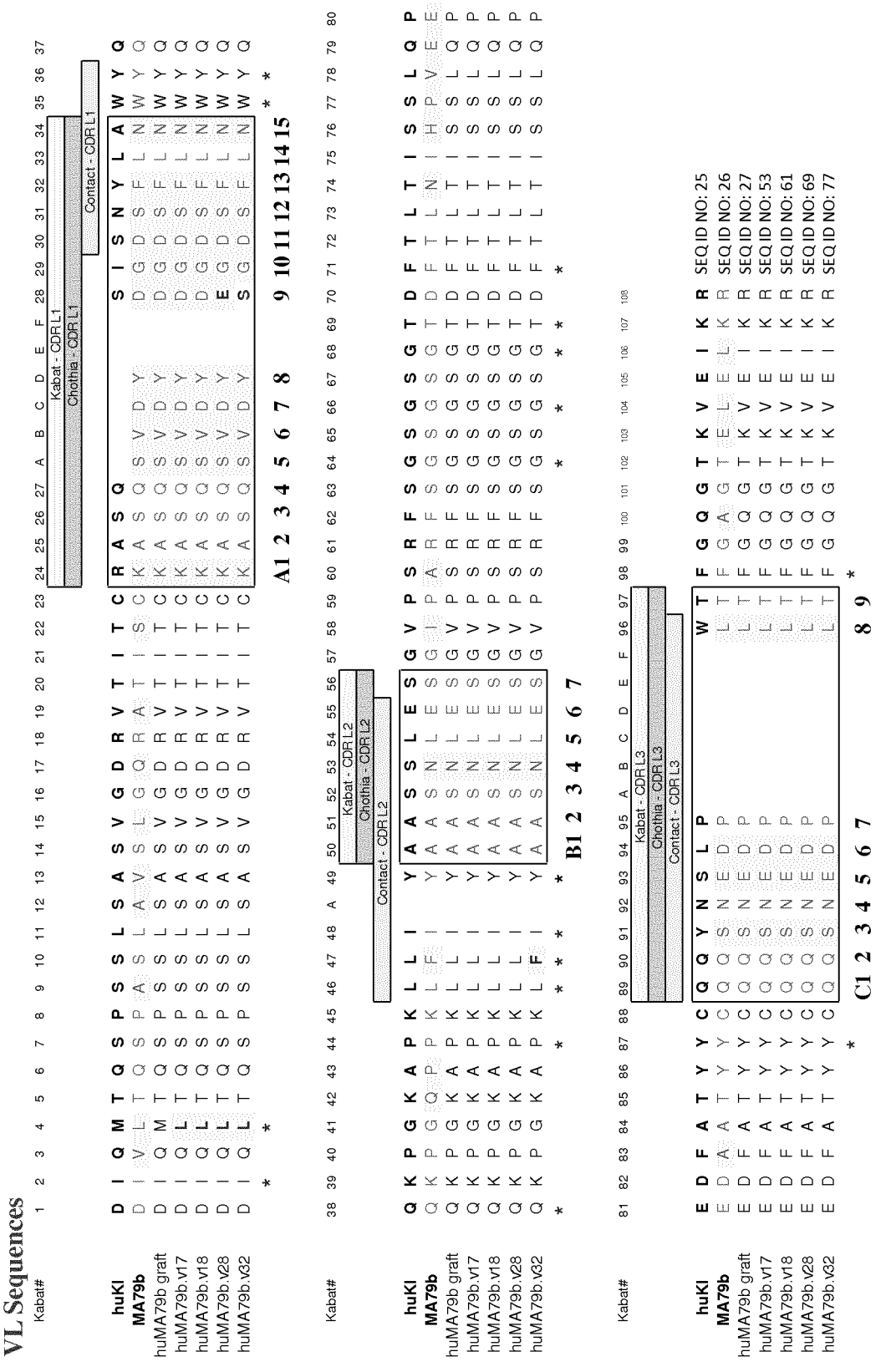

VL Sequences
Kabat - CDR L1
Chothia - CDR L1
Contact - CDR L1
Kabat - CDR L2
Chothia - CDR L2
Contact - CDR L2
Kabat - CDR L3
Chothia - CDR L3
Contact - CDR L3
huKI
MA79b
huMA79b graft
huMA79b.v17
huMA79b.v18
huMA79b.v28
huMA79b.v32
SEQ ID NO: 25
SEQ ID NO: 26
SEQ ID NO: 27
SEQ ID NO: 53
SEQ ID NO: 61
SEQ ID NO: 69
SEQ ID NO: 77

Fig. 7

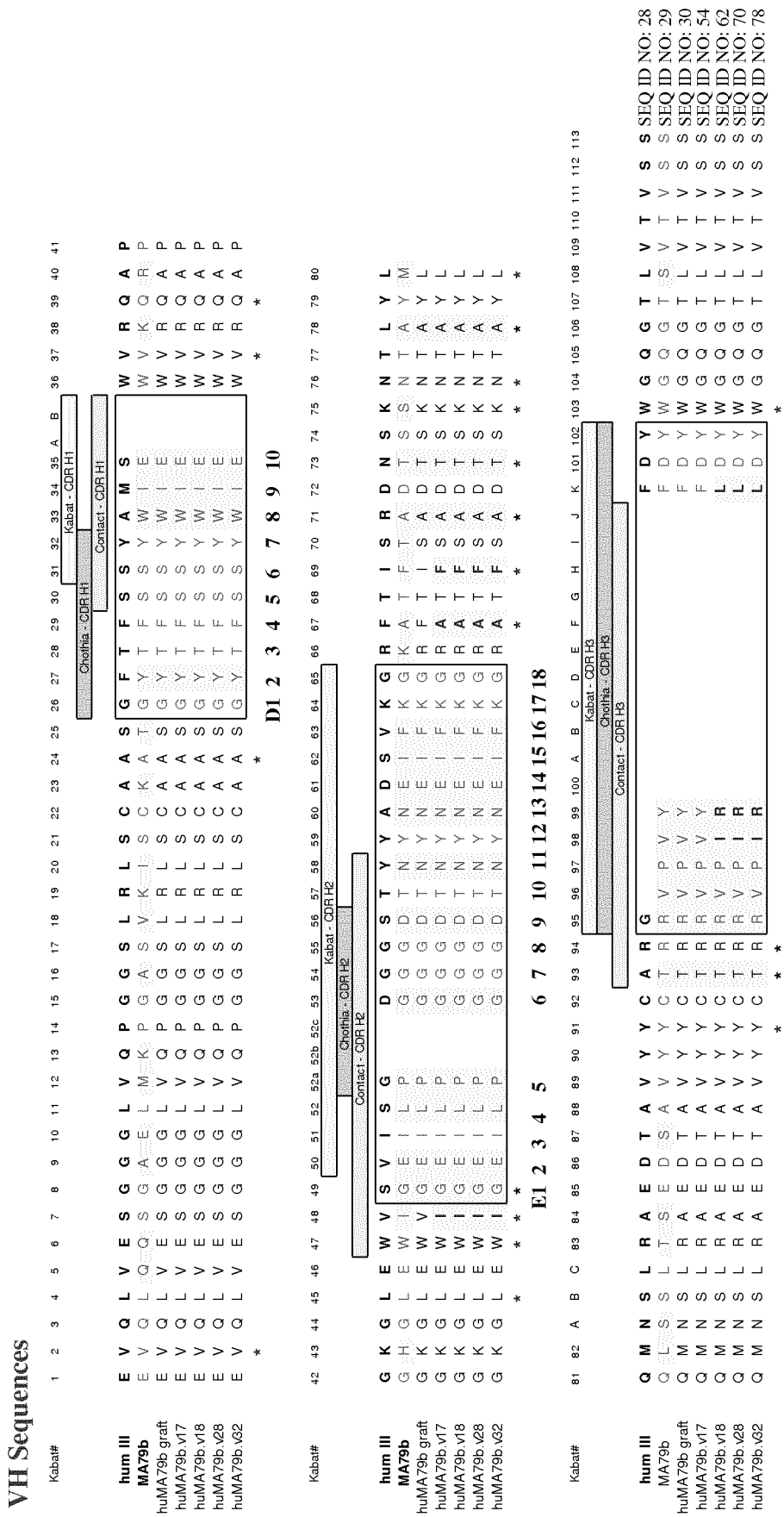

VH Sequences
Kabat - CDR H1
Chothia - CDR H1
Contact - CDR H1
Kabat - CDR H2
Chothia - CDR H2
Contact - CDR H2
Kabat - CDR H3
Chothia - CDR H3
Contact - CDR H3
hum III
MA79b
huMA79b graft
huMA79b.v17
huMA79b.v18
huMA79b.v28
huMA79b.v32
SEQ ID NO: 28
SEQ ID NO: 29
SEQ ID NO: 30
SEQ ID NO: 54
SEQ ID NO: 62
SEQ ID NO: 70
SEQ ID NO: 78

Fig. 8