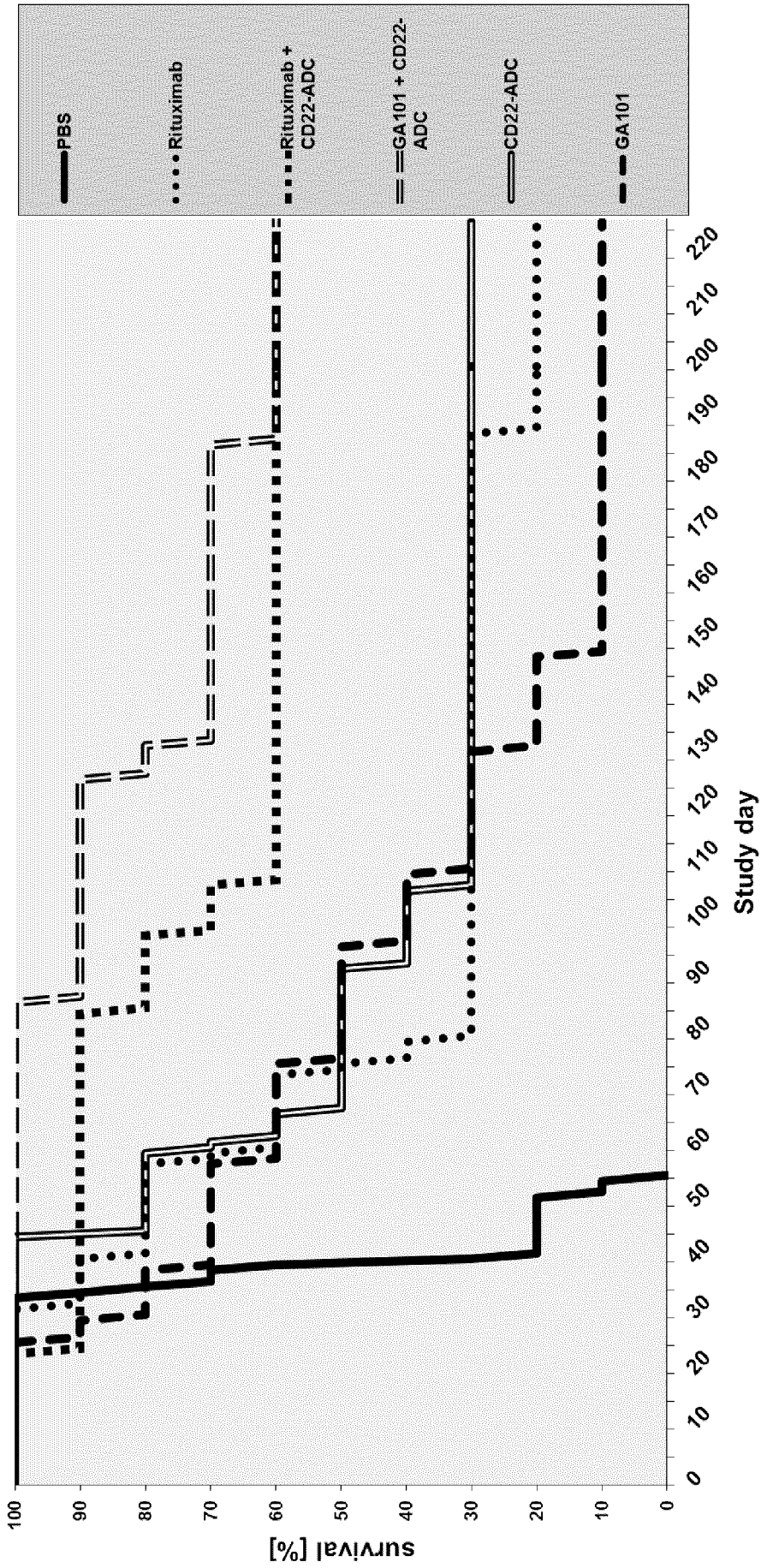

PBS
Rituximab
Rituximab + CD22-ADC
GA101 + CD22-ADC
CD22-ADC
GA101
survival [%]
Study day
0
10
20
30
40
50
60
70
80
90
100
110
120
130
140
150
160
170
180
190
200
210
220

Fig. 1

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

Group	PBS	CD22-ADC	GA101	GA101 + CD22-ADC	Rituximab	Rituximab + CD22-ADC
PBS	1.0000	<.0001*	0.0084*	<.0001*	0.0004*	0.0001*
CD22-ADC	<.0001*	1.0000	0.5022	0.0601	0.6193	0.1355
GA101	0.0084*	0.5022	1.0000	0.0041*	0.6962	0.0322*
GA101 + CD22-ADC	<.0001*	0.0601	0.0041*	1.0000	0.0198*	0.7848
Rituximab	0.0004*	0.6193	0.6962	0.0198*	1.0000	0.0435*
Rituximab + CD22-ADC	0.0001*	0.1355	0.0322*	0.7848	0.0435*	1.0000

Pairwise Wilcoxon Test (multiple test level = 0.00333)

Group	PBS	CD22-ADC	GA101	GA101 + CD22-ADC	Rituximab	Rituximab + CD22-ADC
PBS	1.0000	0.0001*	0.0667	<.0001*	0.0026*	0.0011*
CD22-ADC	0.0001*	1.0000	0.5711	0.0278*	0.6226	0.1285
GA101	0.0667	0.5711	1.0000	0.0038*	0.7634	0.0615
GA101 + CD22-ADC	<.0001*	0.0278*	0.0038*	1.0000	0.0096*	0.6085
Rituximab	0.0026*	0.6226	0.7634	0.0096*	1.0000	0.0465*
Rituximab + CD22-ADC	0.0011*	0.1285	0.0615	0.6085	0.0465*	1.0000

Fig. 2

Heavy Chain Variable Domain
Sequence Alignment of Anti-CD22 10F4 variants

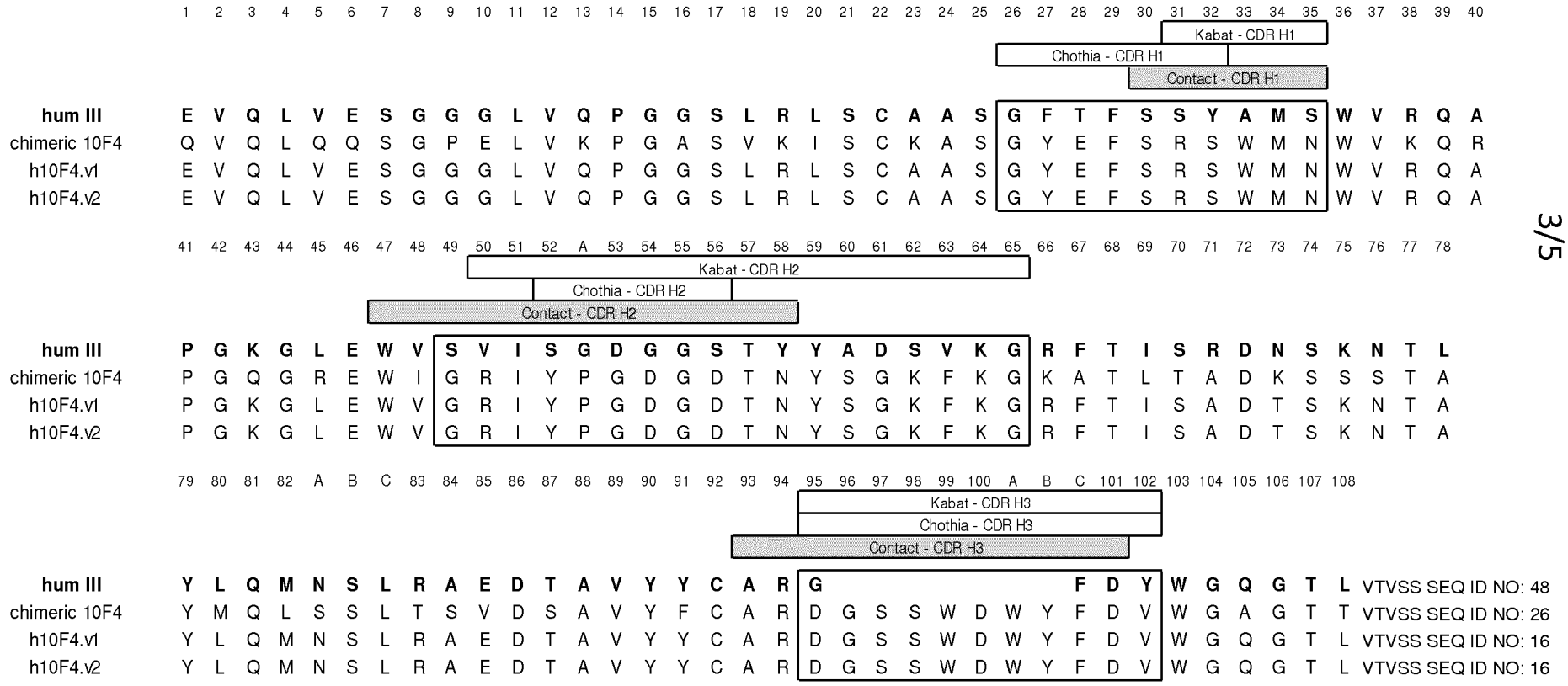


Figure 3A

Light Chain Variable Domain
Sequence Alignment of Anti-CD22 10F4 variants

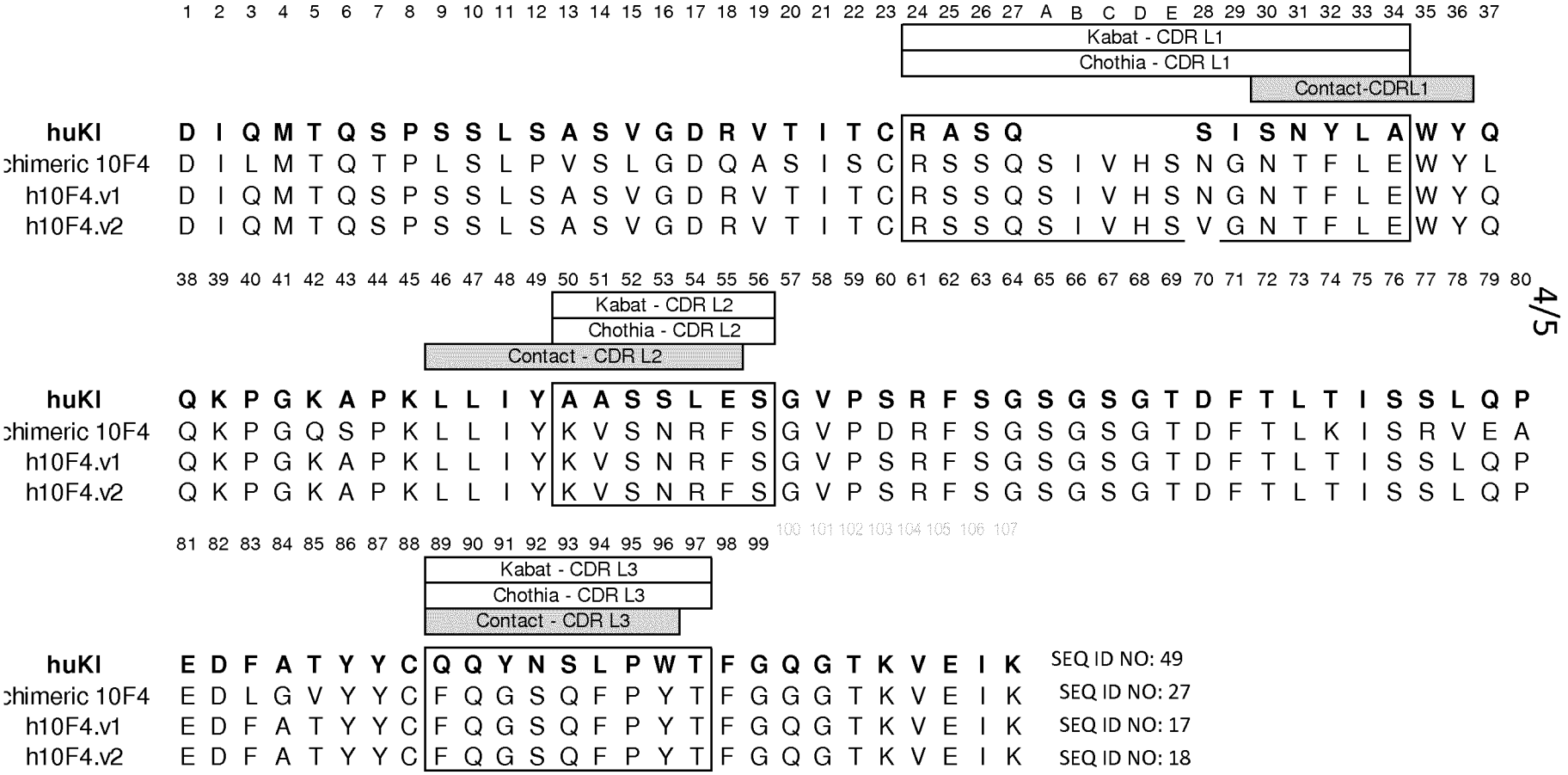


Figure 3B

Anti-CD22 h10F4v2 light chain

DIQMTQSPSSLSASVGDRVTITCRSSQSIVHSVGNTFLEWYQQKPGKAP
KLLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQGSQF
PYTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHK
VYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:50)

Anti-CD22 h10F4v2 heavy chain

EVQLVESGGGLVQPGGSLRLSCAASGYEFSRSWMNWVRQAPGKGLEWVGRIYPGDGDTNYSGKFKGRFTISADTSKNTAYL
QMNSLRAEDTAVYYCARDGSSWDWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN
SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:51)

Figure 4