

Figure 1: Comparison of the ability of 17415, 17552 and 4133 monoclonal antibodies to kill PBMC cells expressing CD45

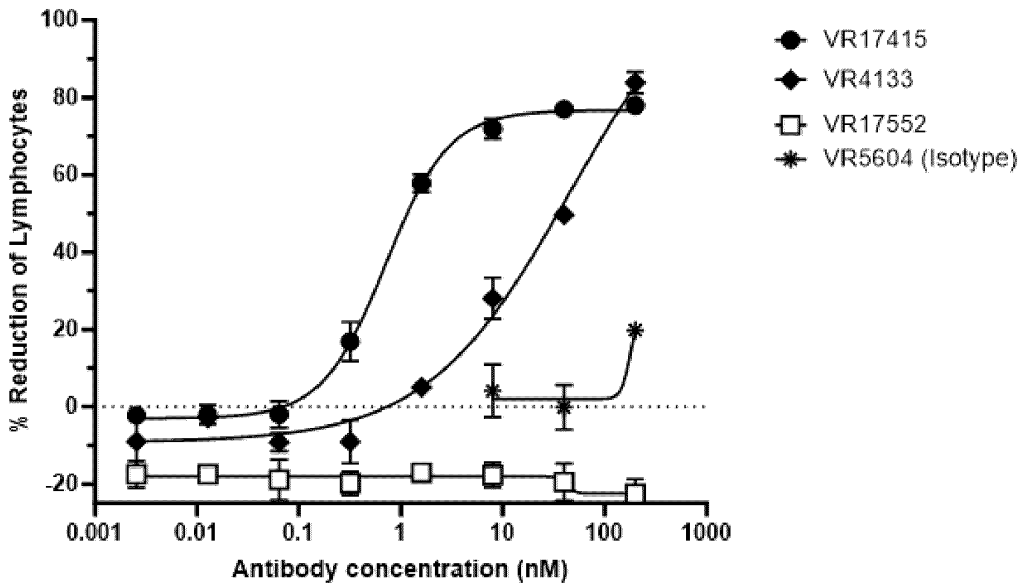


Figure 5A: Lymphocyte cell depletion - comparison of the 17415 IgG1 LALA heavy chain graft variant H1 paired with different light chain graft variants (L1-5).

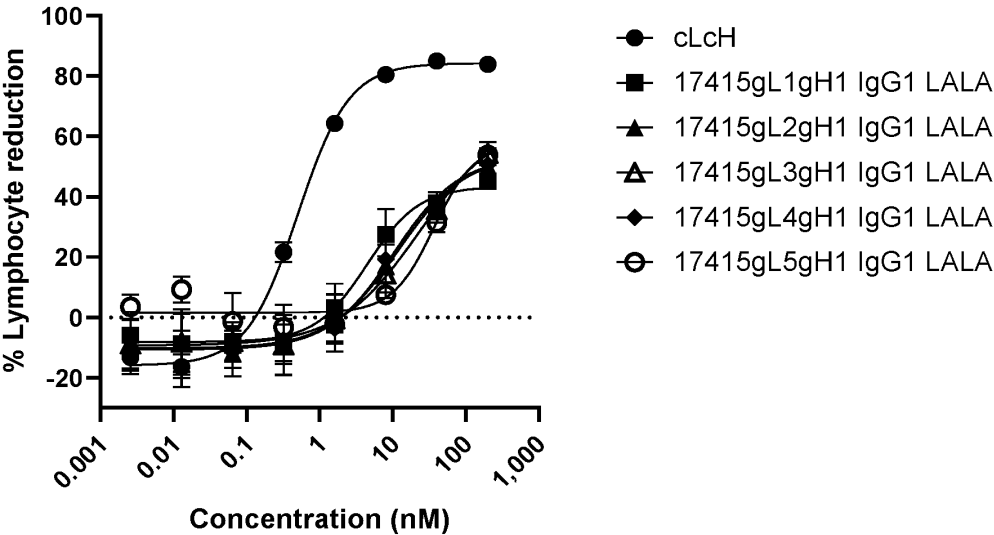


Figure 5B: Lymphocyte cell depletion - comparison of 17415 light chain L1 graft variant paired with different heavy chain grafts variants (H1-4).

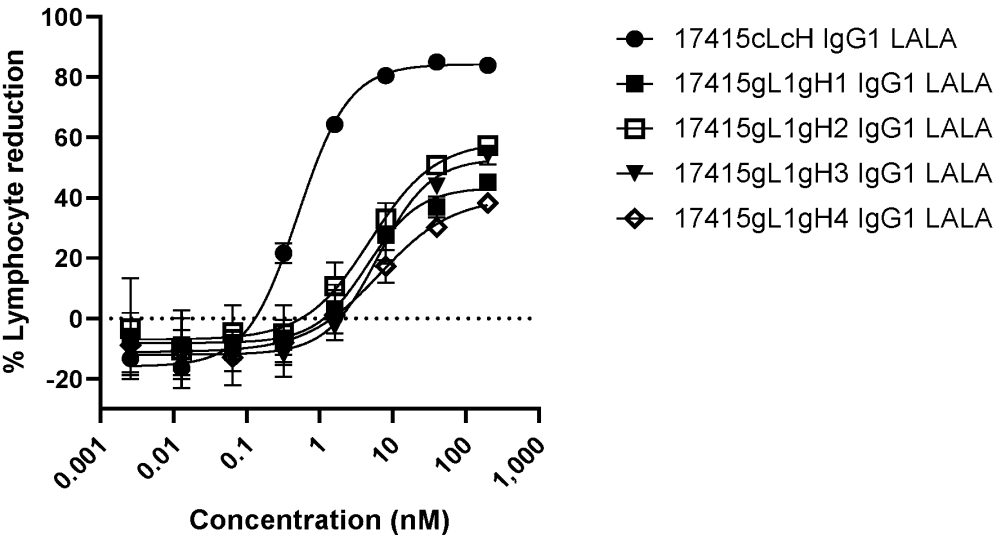


Figure 6A: Lymphocyte cell depletion - comparison of 17415 light chain graft variants L1-5 paired with chimeric 17415 heavy chain versus chimeric 1715 light and heavy chains paired together.

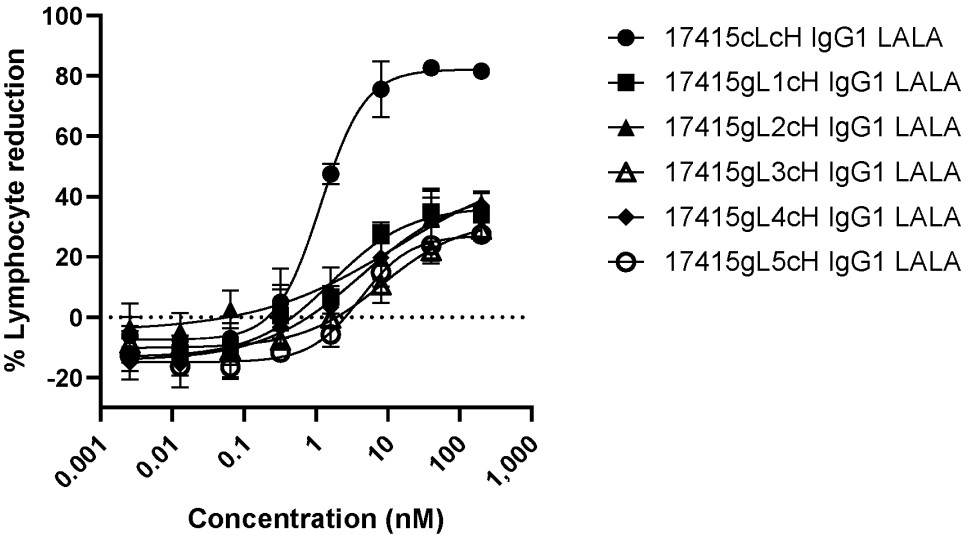


Figure 6B: Lymphocyte cell depletion - comparison of 17415 heavy chain graft variants H1-4 paired with chimeric 17415 light chain versus chimeric 17415 light and heavy chains paired together.

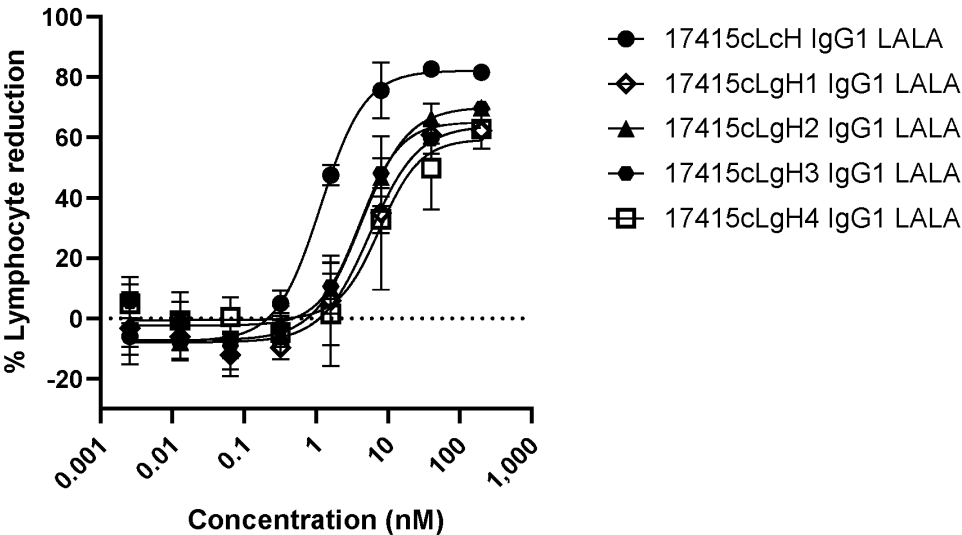


Figure 7A: T cell depletion - 17415 heavy chain graft variant H5 paired with further 17415 light chain graft variants L6, 7, 13, 14, 15 and 16.

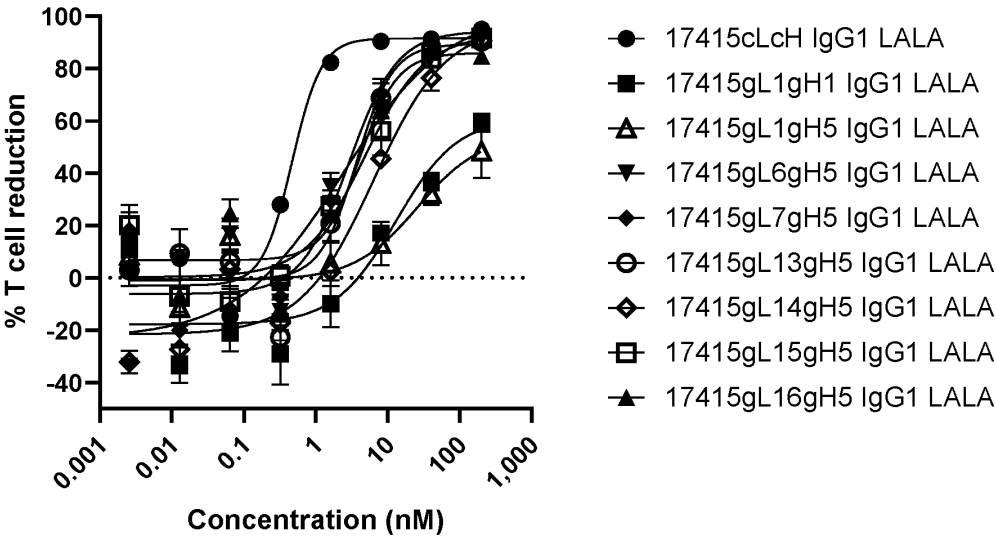


Figure 7B: T cell depletion - 17415 heavy chain graft variant H6 paired with further 17415 light chain graft variants L6, 7, 13, 14, 15 and 16.

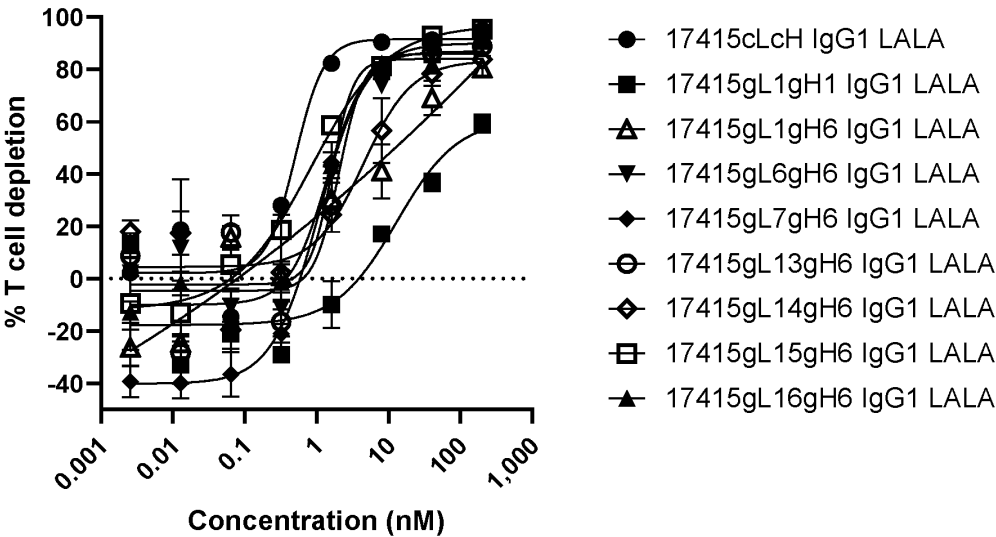


Figure 8A: Jurkat cell depletion - 17415 heavy chain graft variant H1 paired with different light chain graft variants (L1-5).

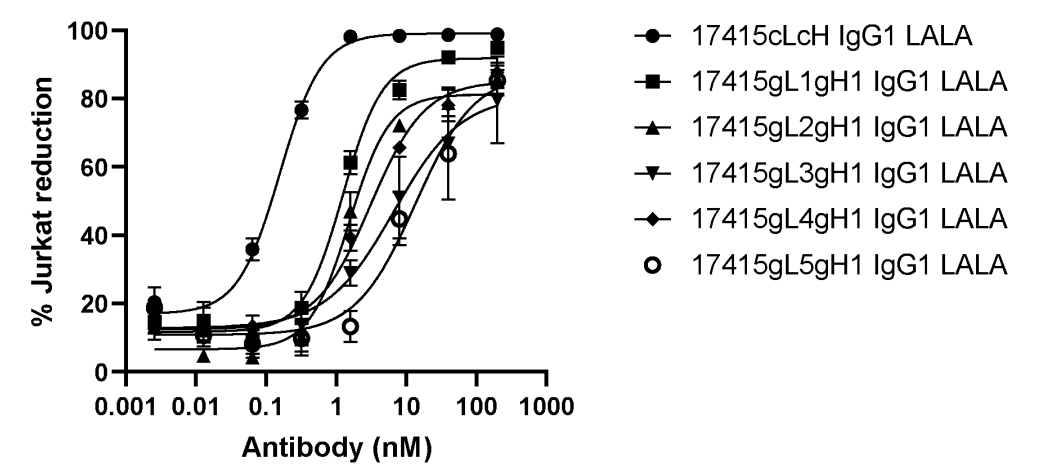


Figure 8B: Jurkat cell depletion - 17415 heavy chain graft variants H1-4 paired with light chain graft variant L1.

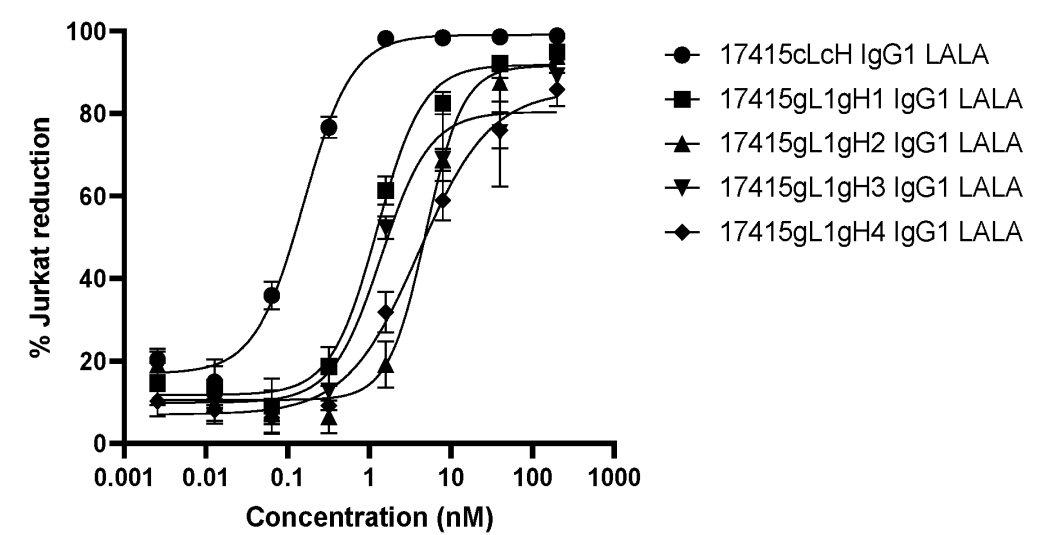


Figure 8C: Jurkat cell depletion - 17415 heavy chain graft variant H1-4 paired with chimeric 17415 light chain.

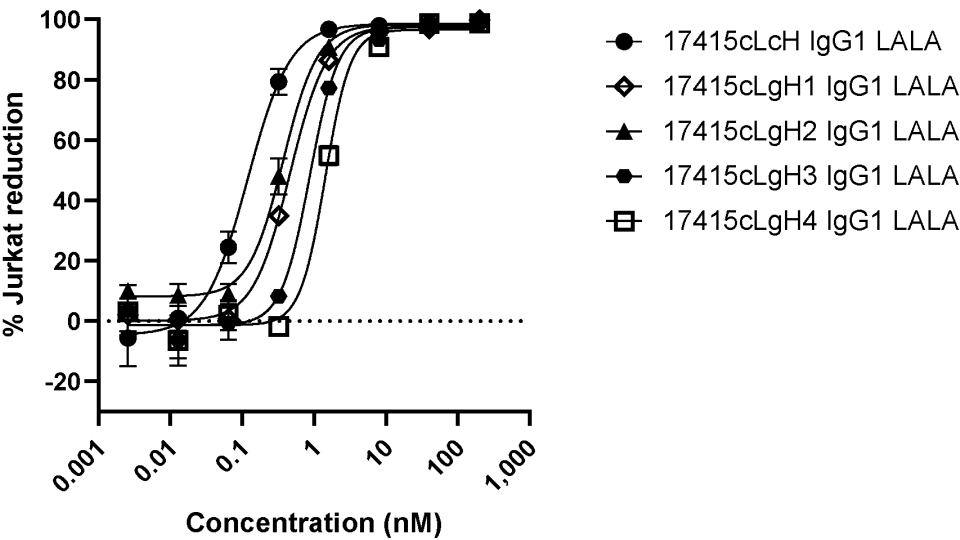


Figure 8D: Jurkat cell depletion - 17415 heavy chain graft variants H1-4 paired with chimeric light chain graft variant.

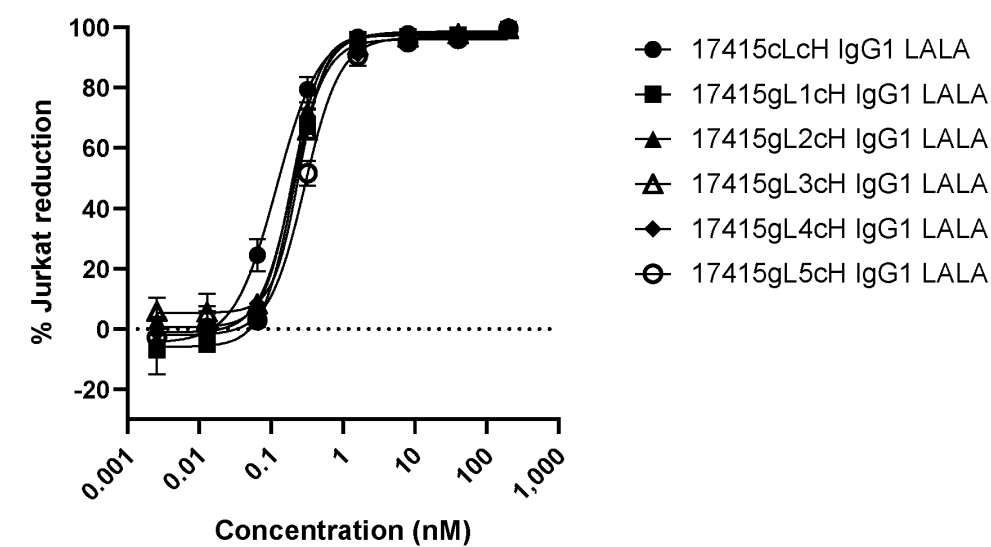


Figure 9: T cell depletion - comparison of 17415 light chain variants 7, 15 and 16 paired with heavy chain variant H6 and 17552 light chain variant L1 paired with heavy chain variants H1 and H4 for purified antibodies.

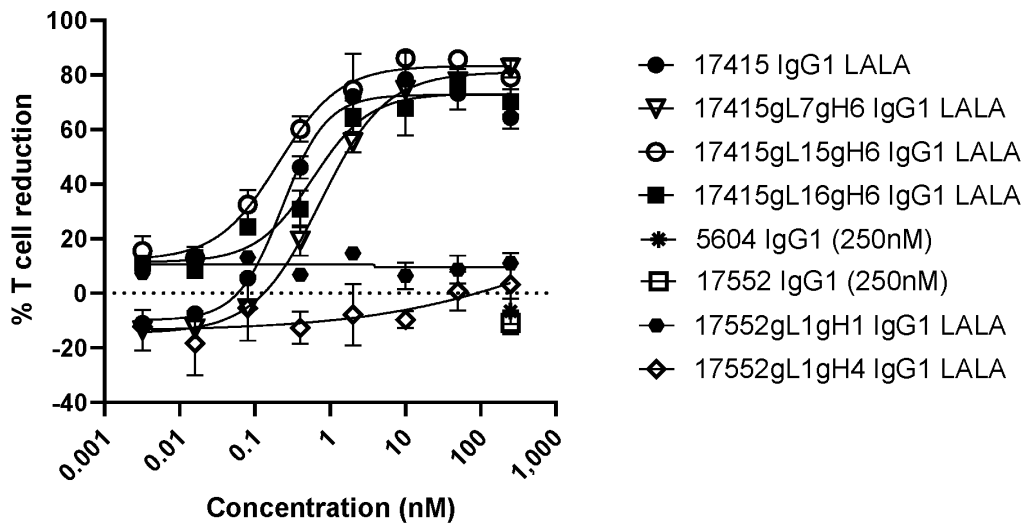


Figure 10: Jurkat cell depletion - comparison of 17415 light chain variants 7, 15 and 16 paired with heavy chain variant H6 for purified antibodies.

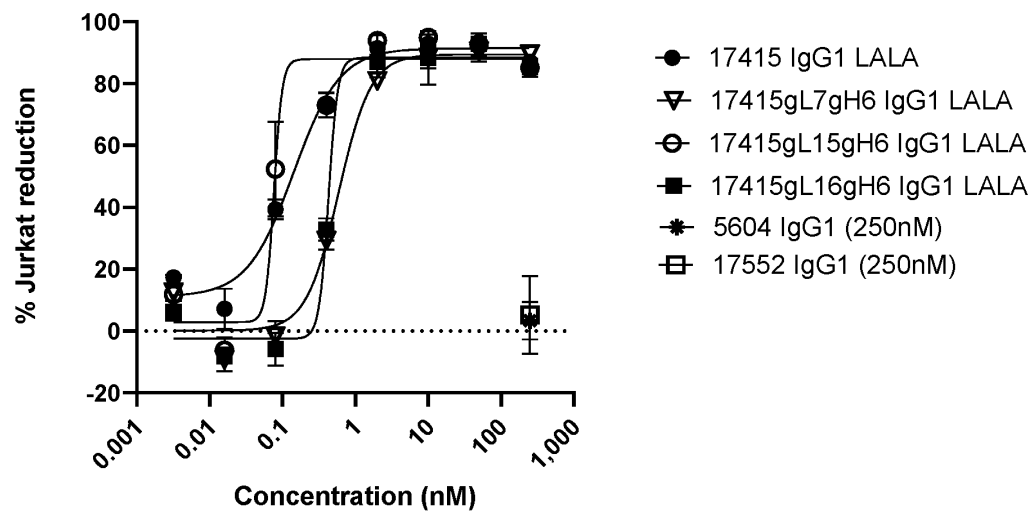


Figure 11: Binding of humanised 17415 IgG1 LALA grafts containing 17415 light chain variants 7, 15 and 16 paired with heavy chain variant H6 to human CD45.

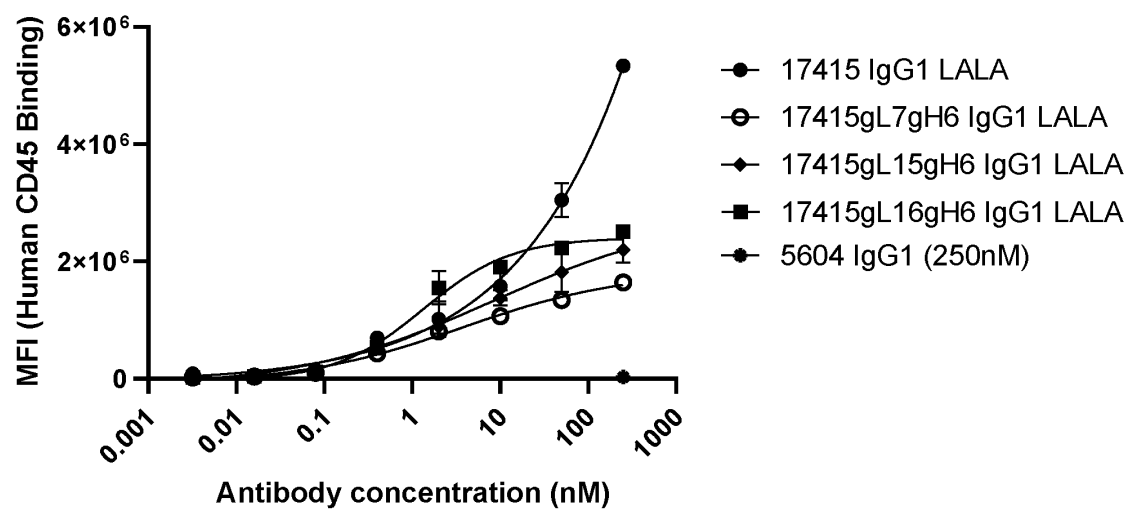


Figure 12A: Human CD45 binding of various biparatopic 17415/17552, 17415/5604 and 5604/17552 variants and monospecific 5604 antibody

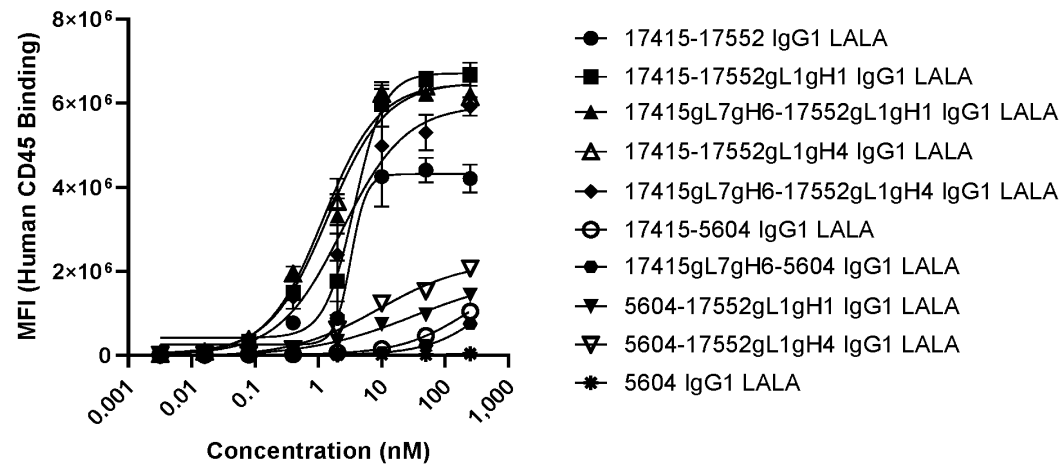


Figure 12B: Human CD45 binding of various biparatopic 17415/17552, 17415/5604 and 5604/17552 variants and monospecific 5604 antibody.

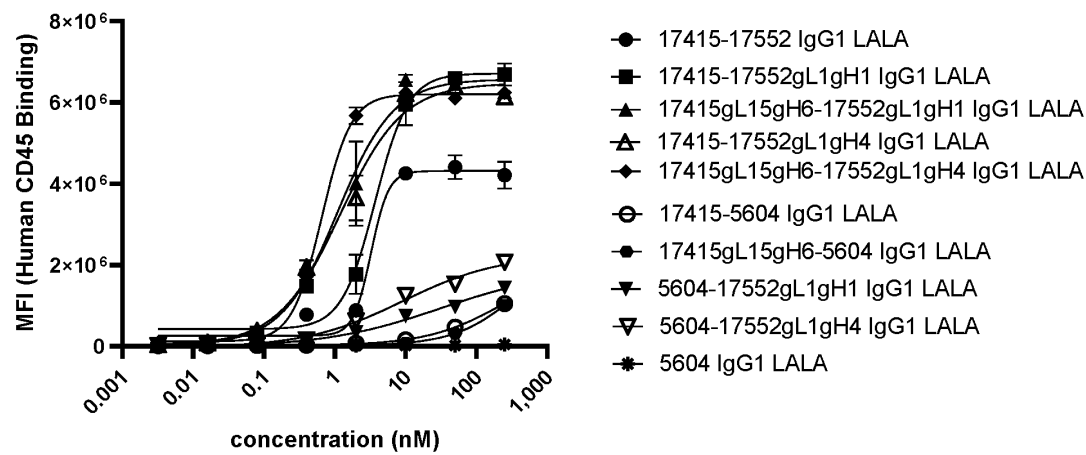


Figure 12C: Human CD45 binding of various biparatopic 17415/17552, 17415/5604 and 5604/17552 variants and monospecific 5604 antibody.

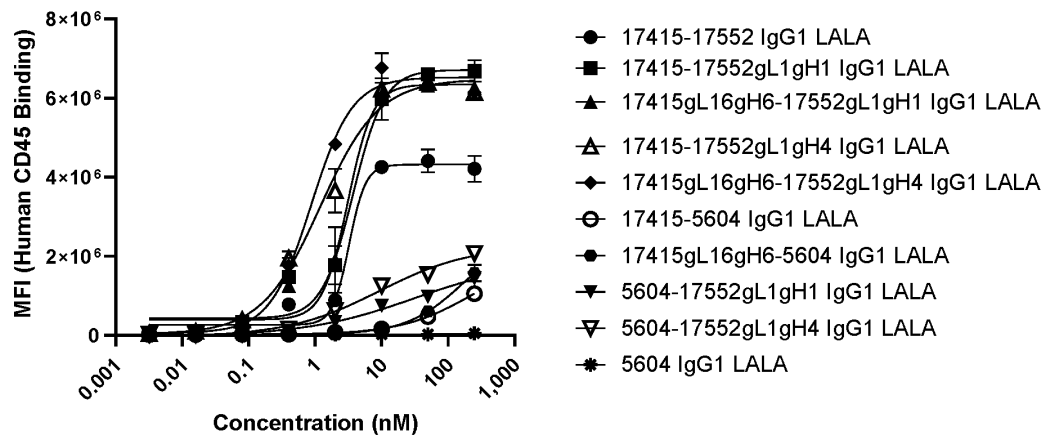


Figure 13A: Cyno CD45 binding of various biparatopic 17415/17552, 17415/5604 and 5604/17552 variants and monospecific 5604 antibody

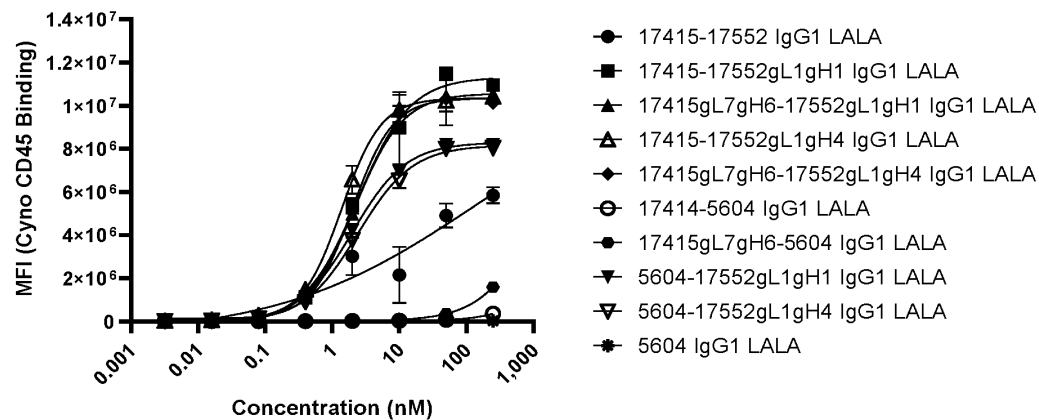


Figure 13B: Cyno CD45 binding of various biparatopic 17415/17552, 17415/5604 and 5604/17552 variants and monospecific 5604 antibody.

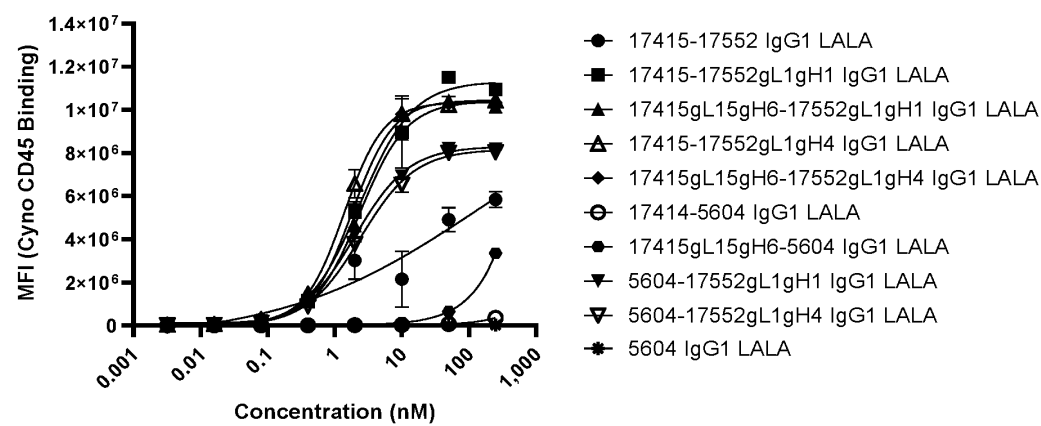


Figure 13C: Cyno CD45 binding of various biparatopic 17415/17552, 17415/5604 and 5604/17552 variants and monospecific 5604 antibody.

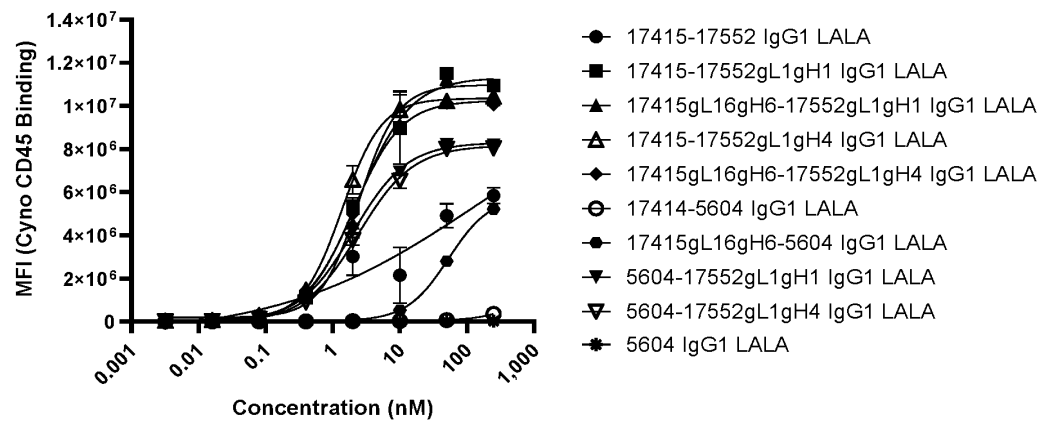


Figure 14A: T cell depletion of various biparatopic 17415/17552, 17415/5604 and 5604/17552 variants.

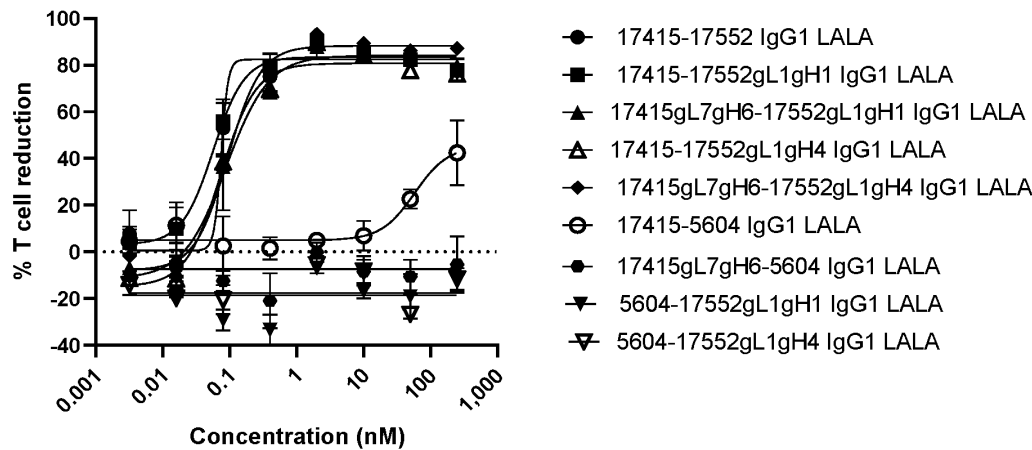


Figure 14B: T cell depletion of various biparatopic 17415/17552, 17415/5604 and 5604/17552 variants.

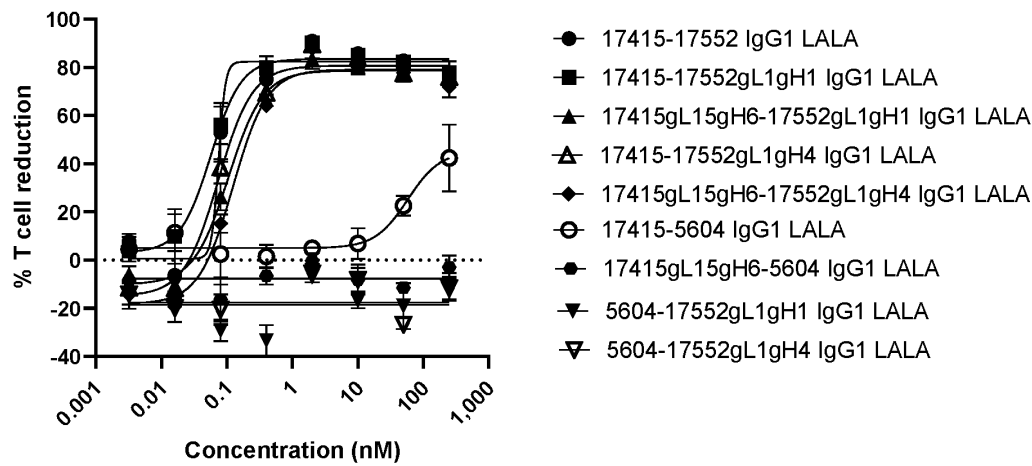


Figure 14C: T cell depletion of various biparatopic 17415/17552, 17415/5604 and 5604/17552 variants.

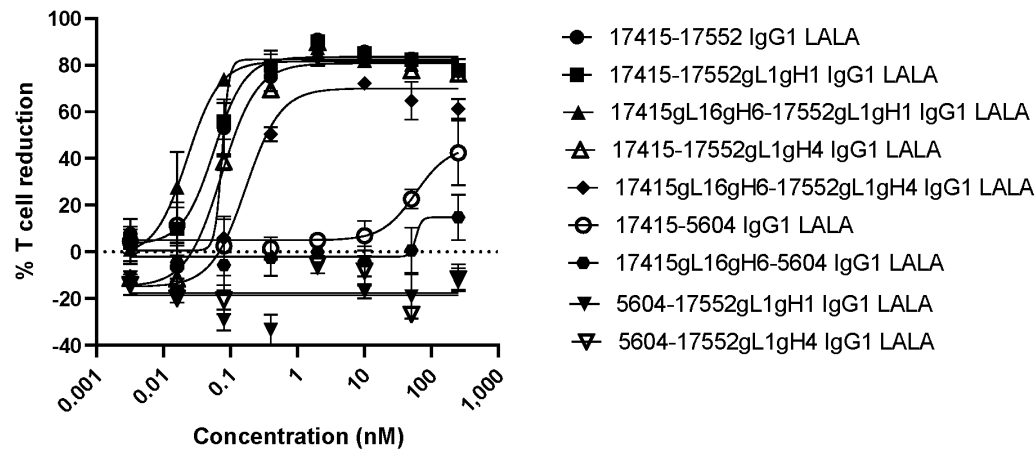


Figure 15A: Jurkat cell depletion of various biparatopic 17415/17552, 17415/5604 and 5604/17552 variants.

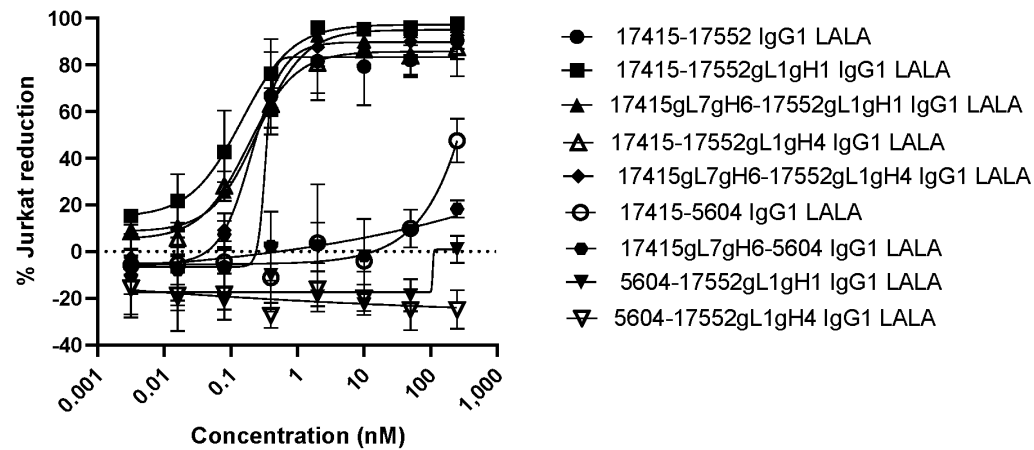


Figure 15B: Jurkat cell depletion of various biparatopic 17415/17552, 17415/5604 and 5604/17552 variants.

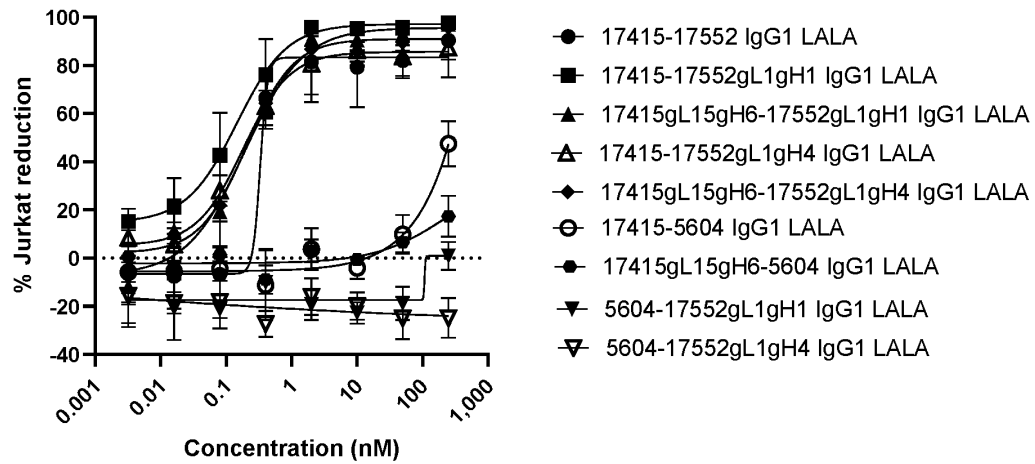


Figure 15C: Jurkat cell depletion of various biparatopic 17415/17552, 17415/5604 and 5604/17552 variants.

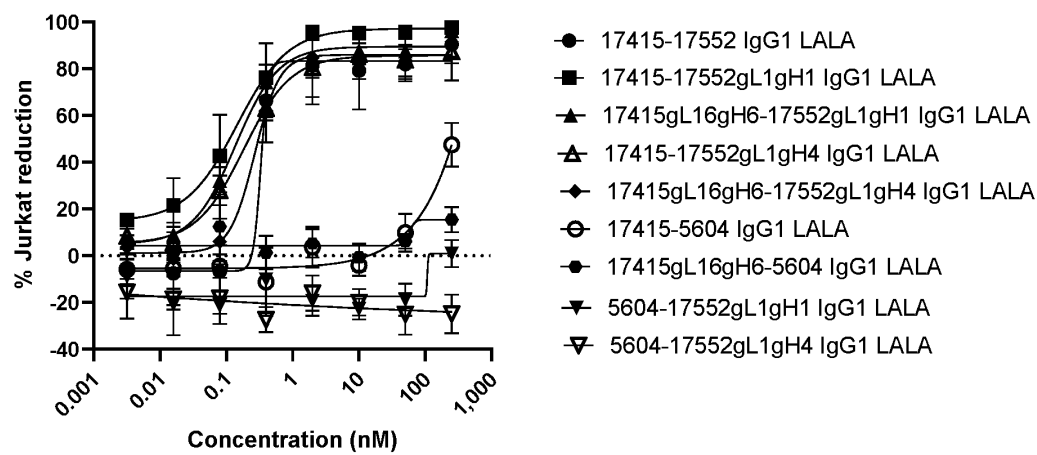


Figure 16: Cynomolgus T cell depletion in a PBMC population by 17415 IgG1, 17415-17552 IgG1 and 4133-6294 IgG1

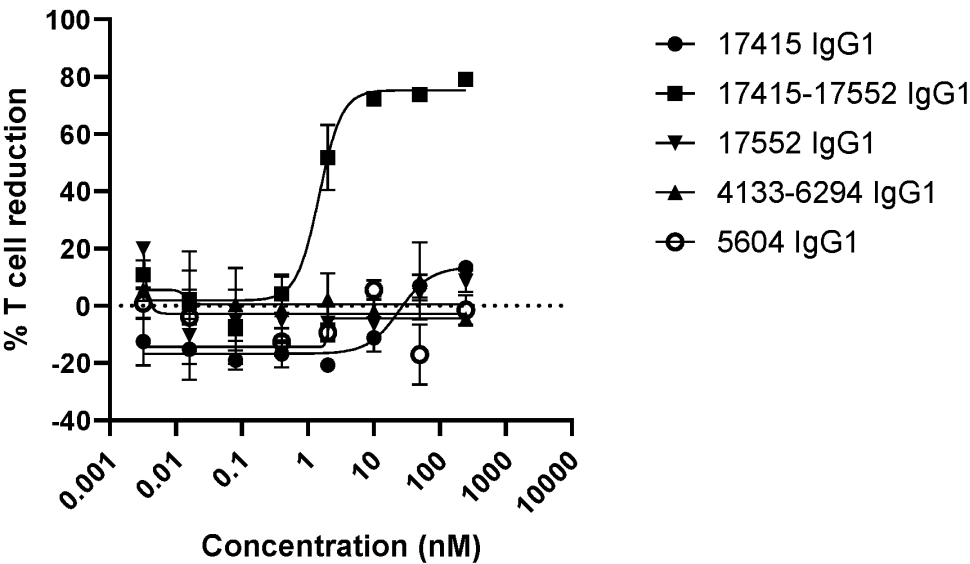


Figure 17: Comparison of the ability of 17415-17552 IgG1 and 4133-6294 IgG1 biparatopic antibodies to kill PBMC cells expressing CD45

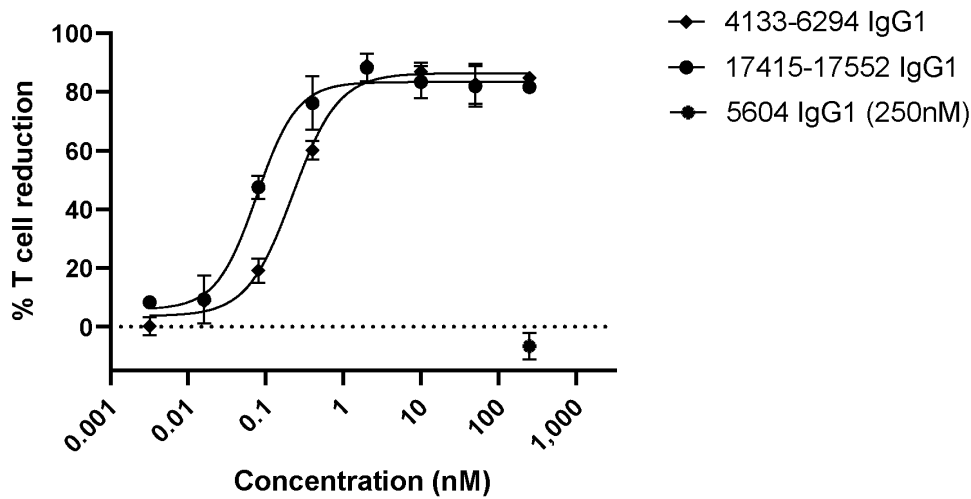


Figure 18: Comparison of the ability of 17415-17552 IgG1 and YTH24.5-YTH54.12 IgG1 antibodies to kill PBMC cells expressing CD45

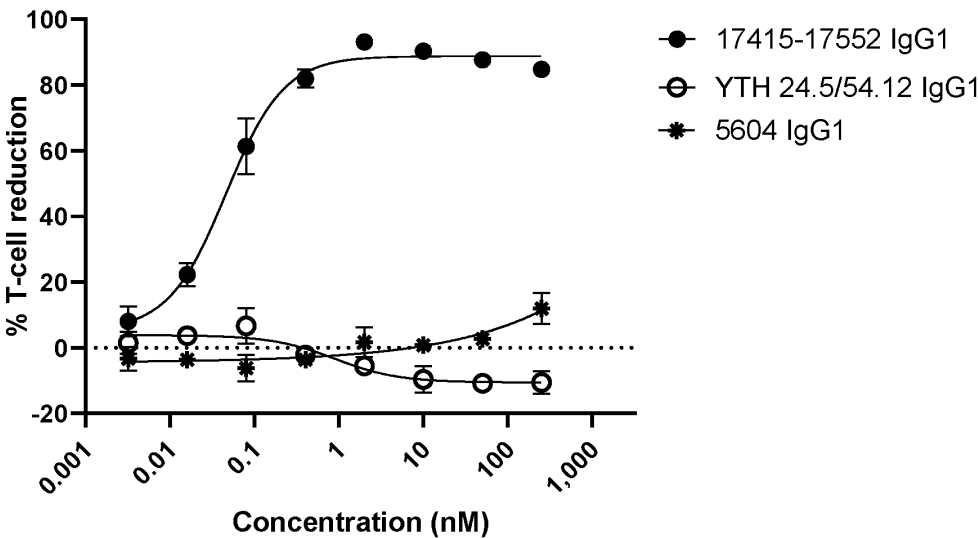


Figure 19: Comparison of the ability of 17415-17552 IgG1 and 4133-6294 IgG1 biparatopic antibodies to kill Jurkat cells expressing CD45

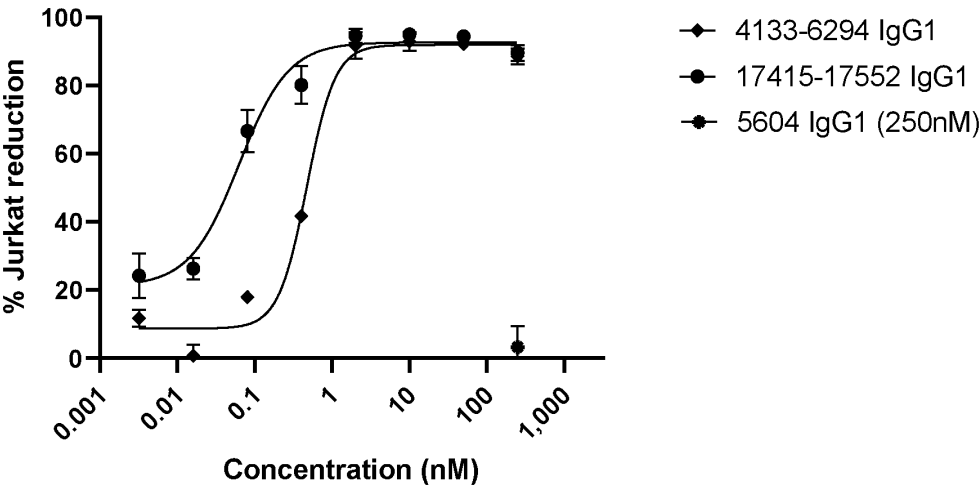


Figure 20A: Levels of IFN γ release in whole blood following 24-hour treatment with purified 17415gL15gH6-17552gL1gH4 biparatopic IgG1 LALA antibody, 17415gL15gH6 monoclonal IgG1 LALA antibody

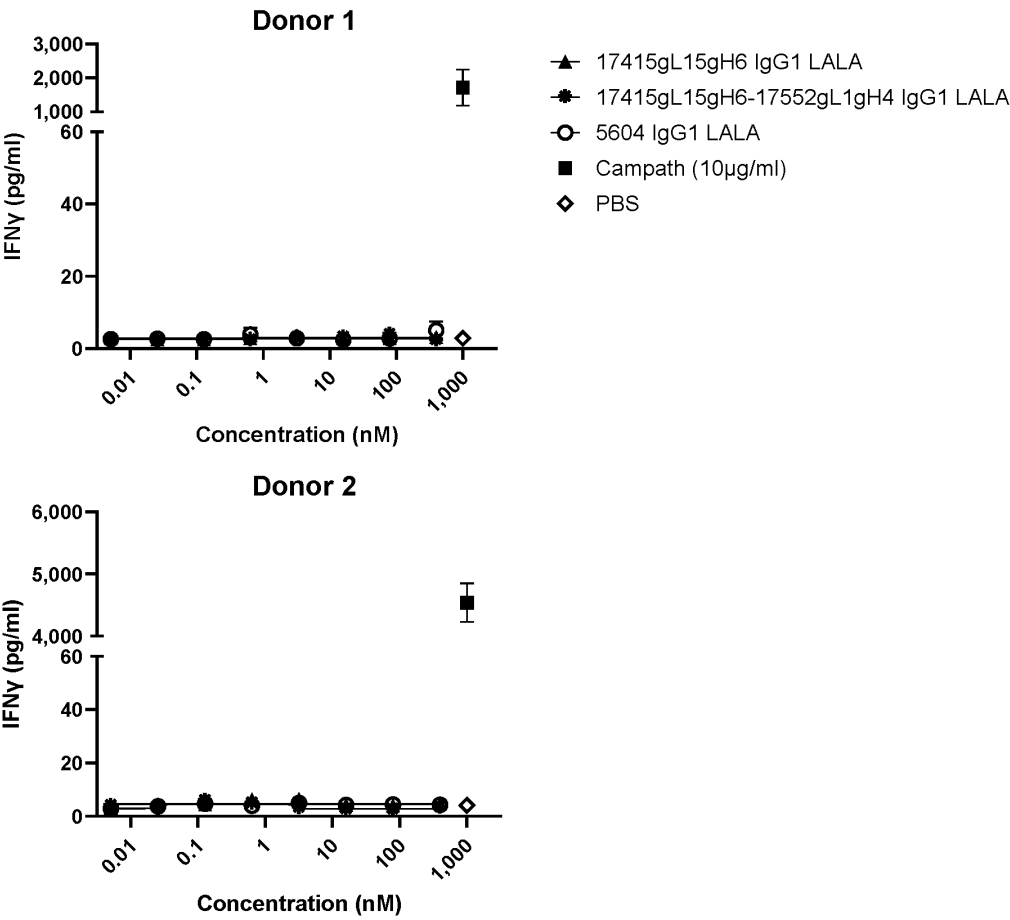


Figure 20B: Levels of IL-6 release in whole blood following 24-hour treatment with purified 17415gL15gH6-17552gL1gH4 biparatopic IgG1 LALA antibody, and 17415gL15gH6 monoclonal IgG1 LALA antibody

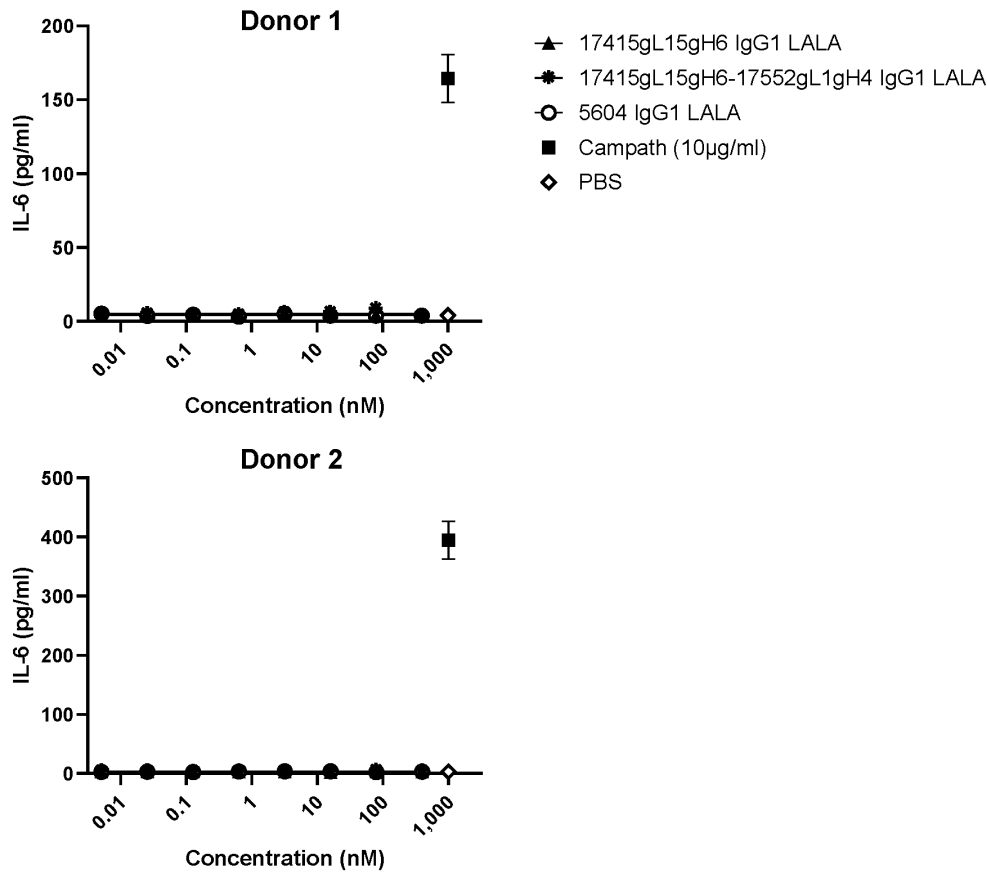


Figure 20C: Levels of TNF α release in whole blood following 24-hour treatment with purified 17415gL15gH6-17552gL1gH4 biparatopic and 17415gL15gH6 monoclonal IgG1 LALA antibodies

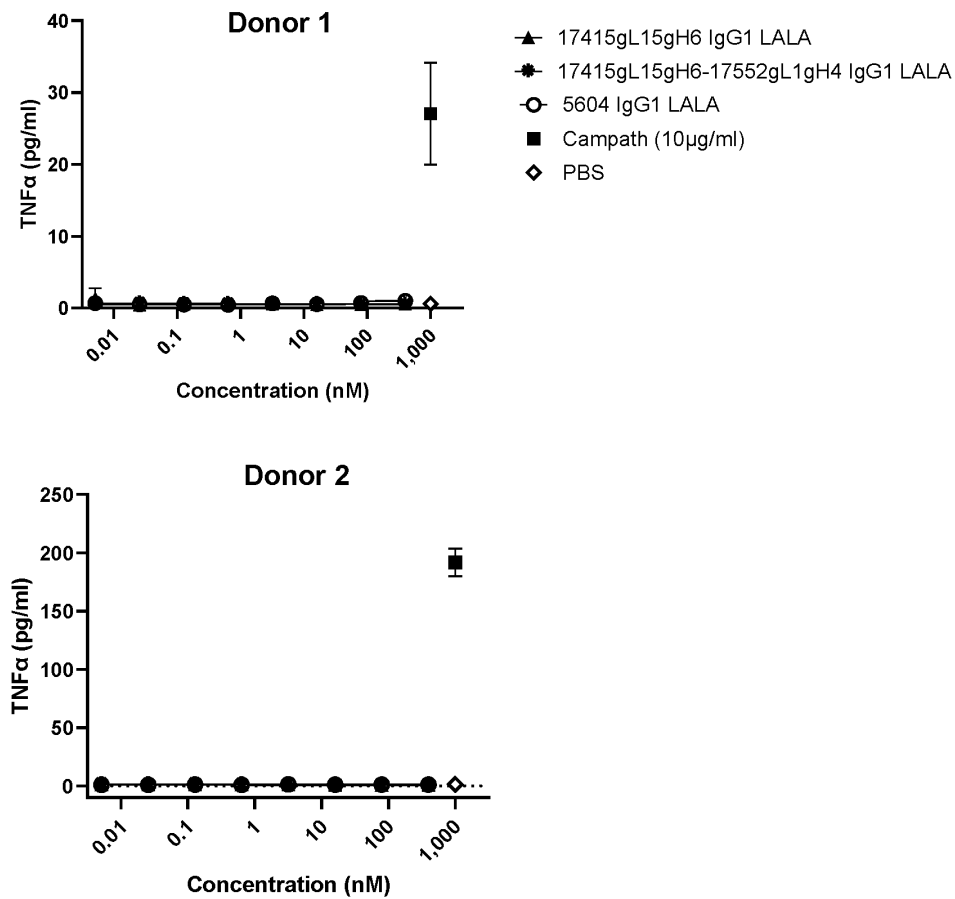


Figure 21: Comparison of the ability of 17415-17552 IgG1 and YTH24.5-YTH54.12 IgG1 antibodies to kill Jurkat cells expressing CD45

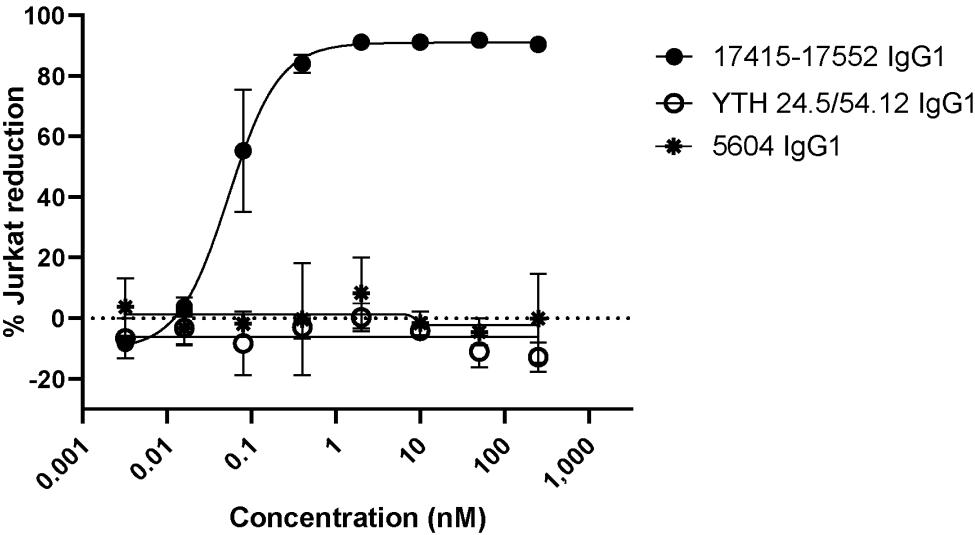
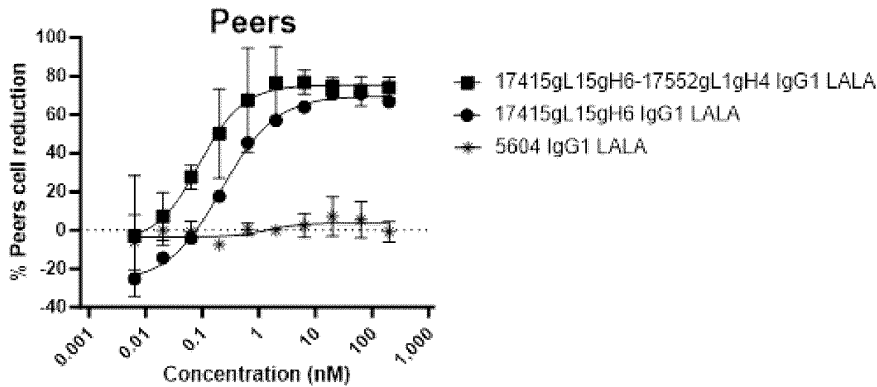
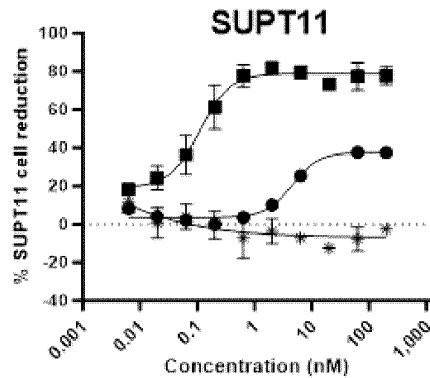


Figure 22: Leukaemic T cell line depletion - comparison between selected 17415gL15gH6-17552gL1gH4 biparatopic and 17415gL15gH6 monoclonal IgG1 LALA antibodies

A



B



C

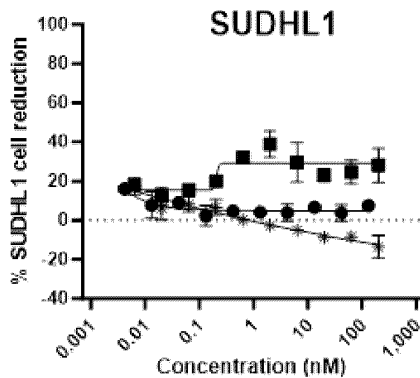


Figure 23: Leukaemic B cell line depletion - comparison between selected 17415gL15gH6-17552gL1gH4 biparatopic and 17415gL15gH6 monoclonal IgG1 LALA antibodies

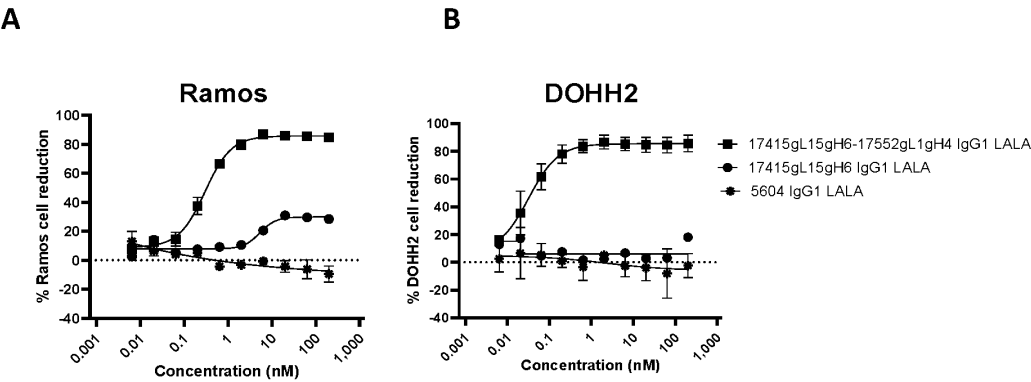
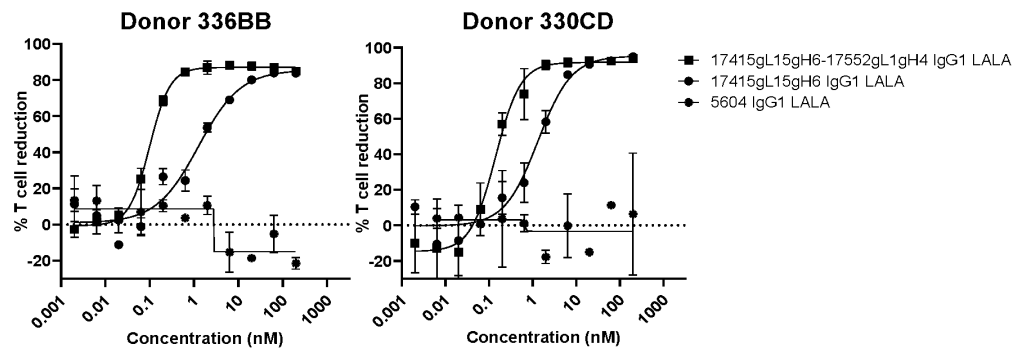


Figure 24: T-cell depletion in PBMC derived from healthy volunteers and a T-cell leukaemia patient – purified 17415gL15gH6-17552gL1gH4 biparatopic and 17415gL15gH6 monoclonal IgG1 LALA antibodies

A



B

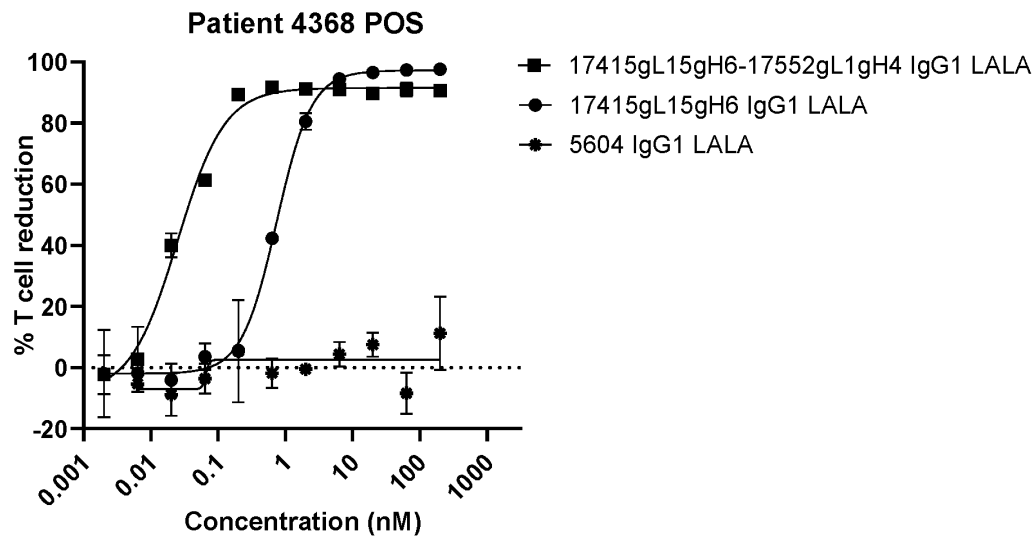
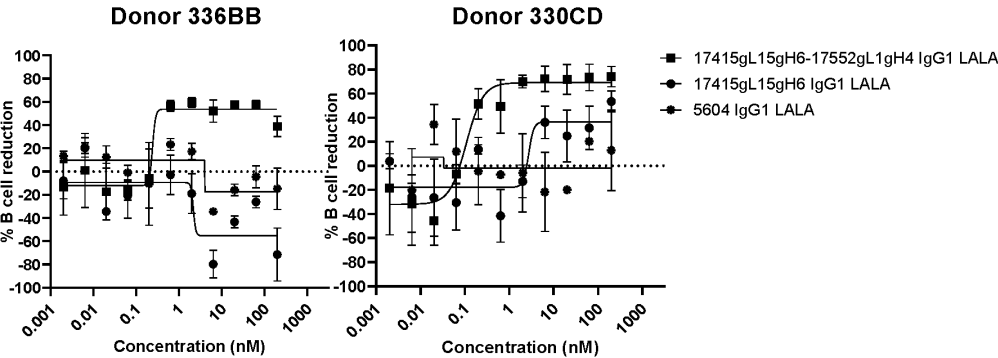


Figure 25: B-cell depletion in PBMC derived from healthy volunteers and a B-cell leukaemia patient – purified 17415gL15gH6-17552gL1gH4 biparatopic and 17415gL15gH6 monoclonal IgG1 LALA antibodies

A



B

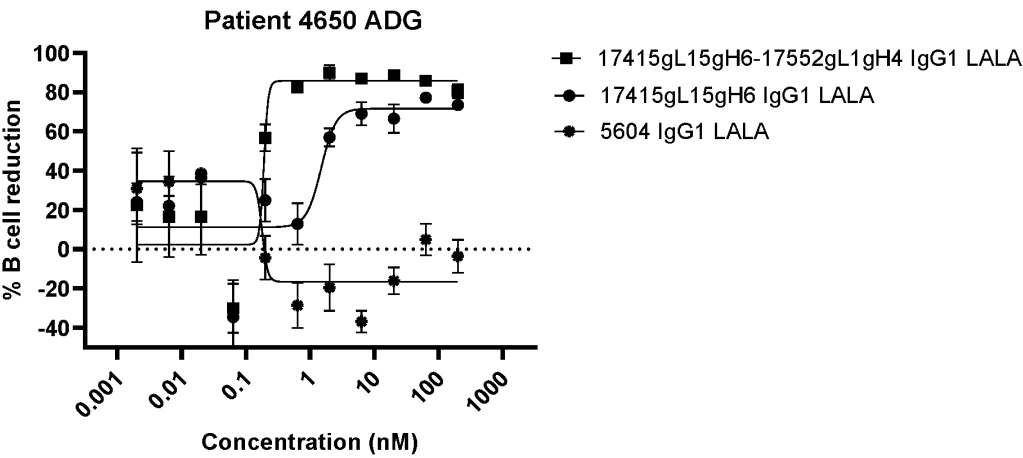


Figure 26
Summary of results for examples of preferred monospecifics

Antibody	T lymphocyte depletion assay		Jurkat depletion assay		Human CD45 SPR			Cyno CD45 SPR			Human CD45 Cell Binding	
	EC50 (nM)	Emax (%)	EC50 (nM) (n=1)	Emax (%)	k _a (M ⁻¹ s ⁻¹)	k _d (s ⁻¹)	Affinity (KD) nM	k _a (M ⁻¹ s ⁻¹)	k _d (s ⁻¹)	Affinity (KD) nM	EC50 (nM) (n=1)	Emax MFI
17415 IgG1 LALA	0.28 (n=3) Range (0.22 - 0.40)	70.4 (n=3) Range (65.1 - 73.5)	0.14	91.4	4.11E+04	3.92E-03	95.36	-	-	-	-	5.34E+06
17415gLT7gH6 IgG1 LALA	0.78 (n=3) Range(0.74 - 0.85)	75.5 (n=3) Range (66.9 - 81.0)	0.59	89.4	4.18E+04	9.13E-03	218.11	-	-	-	3.72	1.85E+06
17415gLT15gH6 IgG1 LALA	0.34 (n=3) Range (0.21 - 0.40)	74.7 (n=3) Range (63.4 - 83.3)	0.08	87.9	3.41E+04	5.94E-03	174.17	-	-	-	8.39	2.81E+06
17415gLT16gH6 IgG1 LALA	0.61 (n=3) Range (0.59 - 0.76)	65.4 (n=3) Range (57.7 - 73.1)	0.43	88.4	3.38E+04	4.79E-03	141.51	-	-	-	1.34	2.41E+06

Figure 27

Summary of results for examples of preferred biparatopics

Antibody	T lymphocyte depletion assay		Jurkat depletion assay		Human CD45 SPR			Cyno CD45 SPR			Human CD45 Cell Binding		Cyno CD45 Cell Binding	
	EC50 (nM)	Emax (%)	EC50 (nM) (n=1)	Emax (%)	k_a (M ⁻¹ s ⁻¹)	k_d (s ⁻¹)	Affinity (KD) nM	k_a (M ⁻¹ s ⁻¹)	k_d (s ⁻¹)	Affinity (KD) nM	EC50 (nM) (n=1)	Emax MFI	EC50 (nM) (n=1)	Emax MFI
17415-17552 IgG1 LALA	0.09 (n=3) Range (0.06 - 0.13)	84 (n=3) Range (79.9 - 89.6)	0.33	83.3	5.02E+04	6.33E-04	12.62	3.20E+04	7.21E-06	0.31	3.24	4.32E+06	-	11,523,460.00
17415g17gH6-17552g1gH1 IgG1 LALA	0.12 (n=3) Range (0.08 - 0.18)	82.2 (n=3) Range (80.7 - 84.1)	0.26	95.0	5.11E+04	4.43E-04	8.66	3.01E+04	4.26E-07	0.33	1.4	6.49E+06	2.2	10,570,888.00
17415g115gH6-17552g1gH1 IgG1 LALA	0.17 (n=3) Range (0.11 - 0.29)	75.5 (n=3) Range (73.2 - 78.7)	0.19	95.7	5.28E+04	5.98E-04	11.32	3.11E+04	1.55E-07	0.32	1.1	6.57E+06	2.38	10,401,719.00
17415g116gH6-17552g1gH1 IgG1 LALA	0.05 (n=3) Range (0.02 - 0.08)	78.0 (n=3) Range (71.8 - 81.7)		89.5	4.67E+04	5.33E-04	11.41	2.88E+04	1.08E-05	0.37	3.1	6.34E+06	2.46	10,969,848.00
17415g17gH6-17552g1gH4 IgG1 LALA	0.09 (n=3) Range (0.08 - 0.09)	83.7 (n=3) Range (78.9 - 88.2)	0.21	89.8	4.13E+04	4.28E-04	10.36	2.18E+04	1.17E-05	0.54	2.39	5.95E+06	2.01	10,341,609.00
17415g115gH6-17552g1gH4 IgG1 LALA	0.13 (n=3) Range (0.09 - 0.17)	77.6 (n=3) Range (76.1 - 79.2)	0.21	91.1	4.07E+04	4.69E-04	11.54	2.14E+04	9.95E-06	0.47	0.65	6.21E+06	1.83	10,443,785.00
17415g116gH6-17552g1gH4 IgG1 LALA	0.16 (n=3) Range (0.10 - 0.21)	65.9 (n=3) Range (60.2 - 70.0)	0.27	86.1	4.11E+04	4.84E-04	11.77	2.19E+04	9.30E-06	0.46	0.87	6.53E+06	2.03	10,243,631.00

Figure 28 – Sequence of human CD45 SEQ ID NO: 127 (SEQ ID NO: 41 of WO 2022/079199)

Met	Tyr	Leu	Trp	Leu	Lys	Leu	Leu	Ala	Phe	Gly	Phe	Ala	Phe	Leu	Asp
1				5					10					15	
Thr	Glu	Val	Phe	Val	Thr	Gly	Gln	Ser	Pro	Thr	Pro	Ser	Pro	Thr	Gly
			20					25					30		
Leu	Thr	Thr	Ala	Lys	Met	Pro	Ser	Val	Pro	Leu	Ser	Ser	Asp	Pro	Leu
		35				40					45				
Pro	Thr	His	Thr	Thr	Ala	Phe	Ser	Pro	Ala	Ser	Thr	Phe	Glu	Arg	Glu
	50					55					60				
Asn	Asp	Phe	Ser	Glu	Thr	Thr	Ser	Leu	Ser	Pro	Asp	Asn	Thr	Ser	
65				70					75				80		
Thr	Gln	Val	Ser	Pro	Asp	Ser	Leu	Asp	Asn	Ala	Ser	Ala	Phe	Asn	Thr
			85					90					95		
Thr	Gly	Val	Ser	Ser	Val	Gln	Thr	Pro	His	Leu	Pro	Thr	His	Ala	Asp
		100						105					110		
Ser	Gln	Thr	Pro	Ser	Ala	Gly	Thr	Asp	Thr	Gln	Thr	Phe	Ser	Gly	Ser
		115					120					125			
Ala	Ala	Asn	Ala	Lys	Leu	Asn	Pro	Thr	Pro	Gly	Ser	Asn	Ala	Ile	Ser
	130					135					140				
Asp	Val	Pro	Gly	Glu	Arg	Ser	Thr	Ala	Ser	Thr	Phe	Pro	Thr	Asp	Pro
145				150					155					160	
Val	Ser	Pro	Leu	Thr	Thr	Thr	Leu	Ser	Leu	Ala	His	His	Ser	Ser	Ala
			165					170					175		
Ala	Leu	Pro	Ala	Arg	Thr	Ser	Asn	Thr	Thr	Ile	Thr	Ala	Asn	Thr	Ser
		180					185					190			
Asp	Ala	Tyr	Leu	Asn	Ala	Ser	Glu	Thr	Thr	Thr	Leu	Ser	Pro	Ser	Gly
	195					200					205				
Ser	Ala	Val	Ile	Ser	Thr	Thr	Thr	Ile	Ala	Thr	Thr	Pro	Ser	Lys	Pro
	210					215					220				
Thr	Cys	Asp	Glu	Lys	Tyr	Ala	Asn	Ile	Thr	Val	Asp	Tyr	Leu	Tyr	Asn
225				230					235				240		
Lys	Glu	Thr	Lys	Leu	Phe	Thr	Ala	Lys	Leu	Asn	Val	Asn	Glu	Asn	Val
			245						250				255		
Glu	Cys	Gly	Asn	Asn	Thr	Cys	Thr	Asn	Asn	Glu	Val	His	Asn	Leu	Thr
		260						265				270			
Glu	Cys	Lys	Asn	Ala	Ser	Val	Ser	Ile	Ser	His	Asn	Ser	Cys	Thr	Ala
	275					280					285				
Pro	Asp	Lys	Thr	Leu	Ile	Leu	Asp	Val	Pro	Pro	Gly	Val	Glu	Lys	Phe
	290					295					300				
Gln	Leu	His	Asp	Cys	Thr	Gln	Val	Glu	Lys	Ala	Asp	Thr	Thr	Ile	Cys
305				310					315					320	
Leu	Lys	Trp	Lys	Asn	Ile	Glu	Thr	Phe	Thr	Cys	Asp	Thr	Gln	Asn	Ile
			325					330					335		
Thr	Tyr	Arg	Phe	Gln	Cys	Gly	Asn	Met	Ile	Phe	Asp	Asn	Lys	Glu	Ile
	340						345					350			
Lys	Leu	Glu	Asn	Leu	Glu	Pro	Glu	His	Glu	Tyr	Lys	Cys	Asp	Ser	Glu
	355					360					365				
Ile	Leu	Tyr	Asn	Asn	His	Lys	Phe	Thr	Asn	Ala	Ser	Lys	Ile	Ile	Lys
	370					375					380				
Thr	Asp	Phe	Gly	Ser	Pro	Gly	Glu	Pro	Gln	Ile	Ile	Phe	Cys	Arg	Ser
385				390					395					400	
Glu	Ala	Ala	His	Gln	Gly	Val	Ile	Thr	Trp	Asn	Pro	Pro	Gln	Arg	Ser
			405						410				415		
Phe	His	Asn	Phe	Thr	Leu	Cys	Tyr	Ile	Lys	Glu	Thr	Glu	Lys	Asp	Cys
	420						425					430			
Leu	Asn	Leu	Asp	Lys	Asn	Leu	Ile	Lys	Tyr	Asp	Leu	Gln	Asn	Leu	Lys
	435					440					445				
Pro	Tyr	Thr	Lys	Tyr	Val	Leu	Ser	Leu	His	Ala	Tyr	Ile	Ile	Ala	Lys
	450					455					460				
Val	Gln	Arg	Asn	Gly	Ser	Ala	Ala	Met	Cys	His	Phe	Thr	Thr	Lys	Ser
465				470					475					480	
Ala	Pro	Pro	Ser	Gln	Val	Trp	Asn	Met	Thr	Val	Ser	Met	Thr	Ser	Asp
			485						490				495		
Asn	Ser	Met	His	Val	Lys	Cys	Arg	Pro	Pro	Arg	Asp	Arg	Asn	Gly	Pro
	500						505					510			
His	Glu	Arg	Tyr	His	Leu	Glu	Val	Glu	Ala	Gly	Asn	Thr	Leu	Val	Arg
	515					520					525				
Asn	Glu	Ser	His	Lys	Asn	Cys	Asp	Phe	Arg	Val	Lys	Asp	Leu	Gln	Tyr
	530					535					540				
Ser	Thr	Asp	Tyr	Thr	Phe	Lys	Ala	Tyr	Phe	His	Asn	Gly	Asp	Tyr	Pro
545				550					555					560	

Figure 28 (continued) – Sequence of human CD45 SEQ ID NO: 127 (SEQ ID NO: 41 of WO 2022/079199)

Gly Glu Pro Phe Ile Leu His His Ser Thr Ser Tyr Asn Ser Lys Ala
 565 570 575
 Leu Ile Ala Phe Leu Ala Phe Leu Ile Ile Val Thr Ser Ile Ala Leu
 580 585 590
 Leu Val Val Leu Tyr Lys Ile Tyr Asp Leu His Lys Lys Arg Ser Cys
 595 600 605
 Asn Leu Asp Glu Gln Gln Glu Leu Val Glu Arg Asp Asp Glu Lys Gln
 610 615 620
 Leu Met Asn Val Glu Pro Ile His Ala Asp Ile Leu Leu Glu Thr Tyr
 625 630 635 640
 Lys Arg Lys Ile Ala Asp Glu Gly Arg Leu Phe Leu Ala Glu Phe Gln
 645 650 655
 Ser Ile Pro Arg Val Phe Ser Lys Phe Pro Ile Lys Glu Ala Arg Lys
 660 665 670
 Pro Phe Asn Gln Asn Lys Asn Arg Tyr Val Asp Ile Leu Pro Tyr Asp
 675 680 685
 Tyr Asn Arg Val Glu Leu Ser Glu Ile Asn Gly Asp Ala Gly Ser Asn
 690 695 700
 Tyr Ile Asn Ala Ser Tyr Ile Asp Gly Phe Lys Glu Pro Arg Lys Tyr
 705 710 715 720
 Ile Ala Ala Gln Gly Pro Arg Asp Glu Thr Val Asp Asp Phe Trp Arg
 725 730 735
 Met Ile Trp Glu Gln Lys Ala Thr Val Ile Val Met Val Thr Arg Cys
 740 745 750
 Glu Glu Gly Asn Arg Asn Lys Cys Ala Glu Tyr Trp Pro Ser Met Glu
 755 760 765
 Glu Gly Thr Arg Ala Phe Gly Asp Val Val Val Lys Ile Asn Gln His
 770 775 780
 Lys Arg Cys Pro Asp Tyr Ile Ile Gln Lys Leu Asn Ile Val Asn Lys
 785 790 795 800
 Lys Glu Lys Ala Thr Gly Arg Glu Val Thr His Ile Gln Phe Thr Ser
 805 810 815
 Trp Pro Asp His Gly Val Pro Glu Asp Pro His Leu Leu Leu Lys Leu
 820 825 830
 Arg Arg Arg Val Asn Ala Phe Ser Asn Phe Phe Ser Gly Pro Ile Val
 835 840 845
 Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Tyr Ile Gly Ile
 850 855 860
 Asp Ala Met Leu Glu Gly Leu Glu Ala Glu Asn Lys Val Asp Val Tyr
 865 870 875 880
 Gly Tyr Val Val Lys Leu Arg Arg Gln Arg Cys Leu Met Val Gln Val
 885 890 895
 Glu Ala Gln Tyr Ile Leu Ile His Gln Ala Leu Val Glu Tyr Asn Gln
 900 905 910
 Phe Gly Glu Thr Glu Val Asn Leu Ser Glu Leu His Pro Tyr Leu His
 915 920 925
 Asn Met Lys Lys Arg Asp Pro Pro Ser Glu Pro Ser Pro Leu Glu Ala
 930 935 940
 Glu Phe Gln Arg Leu Pro Ser Tyr Arg Ser Trp Arg Thr Gln His Ile
 945 950 955 960
 Gly Asn Gln Glu Glu Asn Lys Ser Lys Asn Arg Asn Ser Asn Val Ile
 965 970 975
 Pro Tyr Asp Tyr Asn Arg Val Pro Leu Lys His Glu Leu Glu Met Ser
 980 985 990
 Lys Glu Ser Glu His Asp Ser Asp Glu Ser Ser Asp Asp Ser Asp
 995 1000 1005
 Ser Glu Glu Pro Ser Lys Tyr Ile Asn Ala Ser Phe Ile Met Ser
 1010 1015 1020
 Tyr Trp Lys Pro Glu Val Met Ile Ala Ala Gln Gly Pro Leu Lys
 1025 1030 1035
 Glu Thr Ile Gly Asp Phe Trp Gln Met Ile Phe Gln Arg Lys Val
 1040 1045 1050
 Lys Val Ile Val Met Leu Thr Glu Leu Lys His Gly Asp Gln Glu
 1055 1060 1065
 Ile Cys Ala Gln Tyr Trp Gly Glu Gly Lys Gln Thr Tyr Gly Asp
 1070 1075 1080
 Ile Glu Val Asp Leu Lys Asp Thr Asp Lys Ser Ser Thr Tyr Thr
 1085 1090 1095
 Leu Arg Val Phe Glu Leu Arg His Ser Lys Arg Lys Asp Ser Arg
 1100 1105 1110
 Thr Val Tyr Gln Tyr Gln Tyr Thr Asn Trp Ser Val Glu Gln Leu
 1115 1120 1125

Figure 28 (continued) – Sequence of human CD45 SEQ ID NO: 127 (SEQ ID NO: 41 of WO 2022/079199)

Pro	Ala	Glu	Pro	Lys	Glu	Leu	Ile	Ser	Met	Ile	Gln	Val	Val	Lys
1130						1135					1140			
Gln	Lys	Leu	Pro	Gln	Lys	Asn	Ser	Ser	Glu	Gly	Asn	Lys	His	His
1145						1150					1155			
Lys	Ser	Thr	Pro	Leu	Leu	Ile	His	Cys	Arg	Asp	Gly	Ser	Gln	Gln
1160						1165					1170			
Thr	Gly	Ile	Phe	Cys	Ala	Leu	Leu	Asn	Leu	Leu	Glu	Ser	Ala	Glu
1175						1180					1185			
Thr	Glu	Glu	Val	Val	Asp	Ile	Phe	Gln	Val	Val	Lys	Ala	Leu	Arg
1190						1195					1200			
Lys	Ala	Arg	Pro	Gly	Met	Val	Ser	Thr	Phe	Glu	Gln	Tyr	Gln	Phe
1205						1210					1215			
Leu	Tyr	Asp	Val	Ile	Ala	Ser	Thr	Tyr	Pro	Ala	Gln	Asn	Gly	Gln
1220						1225					1230			
Val	Lys	Lys	Asn	Asn	His	Gln	Glu	Asp	Lys	Ile	Glu	Phe	Asp	Asn
1235						1240					1245			
Glu	Val	Asp	Lys	Val	Lys	Gln	Asp	Ala	Asn	Cys	Val	Asn	Pro	Leu
1250						1255					1260			
Gly	Ala	Pro	Glu	Lys	Leu	Pro	Glu	Ala	Lys	Glu	Gln	Ala	Glu	Gly
1265						1270					1275			
Ser	Glu	Pro	Thr	Ser	Gly	Thr	Glu	Gly	Pro	Glu	His	Ser	Val	Asn
1280						1285					1290			
Gly	Pro	Ala	Ser	Pro	Ala	Leu	Asn	Gln	Gly	Ser				
1295						1300								

**Figure 29 – Sequence of human CD45 extracellular domains 1 to - SEQ ID NO: 128
(SEQ ID NO: 113 of WO 2022/079199)**

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Asp Ala Val Val Thr Gln Glu Ser Ala Leu Thr Ser Ser Pro Gly Glu
1      5      10      15
Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20      25      30
Asn Tyr Ala Ser Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly
35      40      45
Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg Phe
50      55      60
Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65      70      75      80
Gln Thr Glu Asp Glu Ala Ile Tyr Phe Cys Val Leu Trp Tyr Ser Asp
85      90      95
His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
100     105     110
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115     120     125
Gly Ser Asp Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Ala Pro
130     135     140
Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Leu Leu Thr
145     150     155     160
Asp Tyr Gly Val Asn Trp Val Arg Gln Ser Pro Gly Lys Cys Leu Glu
165     170     175
Trp Leu Gly Val Ile Trp Gly Asp Gly Ile Thr Asp Tyr Asn Ser Ala
180     185     190
Leu Lys Ser Arg Leu Ser Val Thr Lys Asp Asn Ser Lys Ser Gln Val
195     200     205
Phe Leu Lys Met Asn Ser Leu Gln Ser Gly Asp Ser Ala Arg Tyr Tyr
210     215     220
Cys Val Thr Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
225     230     235     240
Val Ser Ser Ala Ala Ala His His His His His His Glu Gln Lys Leu
245     250     255
Ile Ser Glu Glu Asp Leu
260

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Figure 30 - Sequence of cynomolgus monkey CD45 - SEQ ID NO: 129

MTMCLWLKLLAFVFAFLDTEVFVTGQGSTPSPSTGVSSALTPHLPTHADSQTPSTGTDQTTPSGSAANTTL
SPTPRSDISVSYLNASETTTPSPSGSTVISTPTIATTTSKPTCAEKYATIPVDYLYNNKTKLFTAKLNV
NENVECTNNNHTHNICTNNEVLNLPECKEMNVFVSHNSCTDRHKELKLDVPPEVEKFQLDDCTPDVEANT
TICLKWKIIETFACDKSKITYRFQCGNKTYNKEGIYLENLEPEYEEKDSEILYNNHKYINITKLIKTD
GIPGQPQNVVCRHEDAHQGVITWNPPQRSFHNFTLCYVSKTAKKCLSLDKHLTTYHLQNLKPYTNYSLSL
HAYIIAKVQRNGTAATCNFTTESAPPSQVQNMIVSTSDNSMRVKCEAPRDVNGPTELYLLEVEAGNTLVR
NLSQSECDFSVNNLQYSTYYNLKAYYHNGKYSGEPIVIRESTSYNSKALIAFLAFLIIVTSIALLVVLYK
IYDLHKKRSCNLDEQQELVERDDEKQLMNVEPIHADILLETYKRKIADEGRFLAEFQSI PRVFSKFPIK
EARKPFNQKNRYVDILPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAQGPRDETVDDFWRMI
WEQKATVIVM/TRCEEGRNRNKCAEYWPSMEEGTRAFGDVVVKINQHKRCPDYIIQKLNIVNKKEKATGRE
VTHIQFTSWPDHGVPEDPHLLKLRRRVNAFSNFFSGPIVVHCSAGVGRGTGYIGIDAMLEGLEAENKVD
VYGYVVKLRRQRCLMVQVEAQYILIHQALVEYNQFGETEVNLSELHPYLHNMKKRDPPEPSPLEAEFQR
LPSYRSWRTQHIGNQEENKNKNRNSNVI PYDYNRVPLKHELEMSKESDHDSDESSDDSDSEEPSKYINA
SFIMSYWKPEVMIAAQGPLKETIGDFWQMI FQRKVIVM/TELKHGDQEICAQYWGEKGQTYGDIEVDM
KDTNKSSTYTLRVFELRHSKRKDSRTVYQYQYTNWSVEQLPAEPKELVSLIQVLKEKLPQKNSSEGNKHH
KSTPLLIHCRDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARPGMVSTFEQYQFLYDIIASTYP
AQNGQVKNNHQEDKIEFDNEVDKVKQDANCVNPLGATEKLPEAKEQATGSEPTSGTEGPEHSVNGPASP
ALNQGS

Figure 31

	Amino acid sequences
VR174 15gI15 gH6 IgG1 LALA	Full VR17415 gH6 heavy chain sequence (SEQ ID NO: 140): EVQLVESGGGLVQPGGSLRLSCTASGLSFIGNYISWVRQAPGKGLEWIGSIYTGSSGSTYYASWAKGRFTISKDSSTSVYLQMNLSKTEDTAVVYCELDAYTYAFWQQGT LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPEAAAGGSPVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLS PGK Full VR17415 gL15 light chain sequence (SEQ ID NO: 141): DWVLTQSPDLSVSLGERVTINCOASQSIYSNLAWYQQKPKAPKLLIYAASNLAGSVPSRFKSGSGTEFTLTISLQAEDAATYYCQSTNYGSGYVNTFGGGTEVWIKRT VAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQQLSSPVTKSFNRGEC

Figure 32

	Amino acid sequences
VR174 15g115 gH6 x VR175 52g118 H4 IgG1 LALA	Full VR17415 gH6 heavy chain sequence (SEQ ID NO: 147) - heavy chain constant region has "knob" modification shaded: EVQLVESGGGLVQPGGSLRLSCTASGLSFIGNYYISWVRQAPGKGLEWIGSIYTGSSGTYASWAKGRFTISKDSSTSVLQMNSLKTEDTAVYYCELDAYTFAFWGQGT LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSL SPGK Full VR17415 gL15 light chain sequence (SEQ ID NO: 141): DVVLTSQPSLSVSLGERVTINCOASQSIYSNLAWYQQKPKAPKLLIYAASNLASGVPSRFKSGSGTEFTLTISLQAEDAATYYCQSTNYGSGVYVNTFGGGTEVVIKRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYLSSTLTLSKADYEKHKVYACEVTHQQLSSPVTKSFNRGEC Full VR17552 gH4 heavy chain sequence (SEQ ID NO: 142) - heavy chain constant region has "holes" modification shaded: EVQLQESGPGLVKPSGTLSTICTVSGFSLDYMIWVRQPPGKGLVIGAISYGGSAYYLSWAKGRFTISKDSKNQVSLKLSVTAADTAVYYCTRGIW DAGSGGPWG YF DIWGGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHN HYTQKSLSLSPGK Full VR17552 gL1 light chain sequence (SEQ ID NO: 143): ALVMTQSPSSFSASTGDRVTITCQASQSITTALAWYQQKPKAPKLLIYRASTLASGVPSRFEGSGSGTDFTLTISLSQSEDFATYWCQEYYSSSDVDNTFGGGTKVEIKRTV AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYLSSTLTLSKADYEKHKVYACEVTHQQLSSPVTKSFNRGEC

Figure 33

	Light chain constant region amino acid sequence
	<i>Light chain constant region sequence (SEQ ID NO: 145):</i> RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
	Heavy chain constant region amino acid sequence without knobs into holes modifications
	<i>Heavy chain constant region sequence (SEQ ID NO: 144):</i> ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTCPPAPEAA GGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYV LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
	Constant region amino acid sequences – Heavy chains with knobs-into-holes modifications
	<i>Heavy chain constant region sequence with knob mutation shaded - T336W - (SEQ ID NO: 148):</i> ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTCPPAPEAA GGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYV LPPSRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK <i>Heavy chain constant region sequence with hole mutations shaded – T366S, L368S & Y407V (SEQ ID NO: 146):</i> ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTCPPAPEAA GGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYV LPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK