

**Cell, Volume 180**

## **Supplemental Information**

### **Restriction of HIV-1 Escape**

#### **by a Highly Broad and Potent Neutralizing Antibody**

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**Table S1. HIV-1-Reactive Antibody Clones Isolated by Single Cell Cloning from Individual IDC561, Related to Figure 1**

Clone	Antibody	Heavy Chain					Light Chain					Activity			Single Cell Sort Summary by Clone					
		Genes			CDRH3	Length	Notes	Genes			CDRL3	Length	Notes	Binding (ELISA) BG505* YU2**	Neutralization Global panel***	Identifying Baits				
		V <sub>H</sub>	D <sub>H</sub>	J <sub>H</sub>				Sequence	κ/λ	V <sub>L</sub>						J <sub>L</sub>	Sequence	Length	Notes	Clone
1	561_01_35	1-2*02	6-19*01	4*02	ARDRPSVGGWYVPGSD	16 aa			λ	1-47*01	3*02	ASWDDRLSVGV	11 aa	-	-	-	1	2	+	-
2	561_09_03	1-69*01	6-19*01	2*01	AREGGSPVAIYVFFDV	17 aa			λ	1-40*01	1*01	QSYDGNFV	9 aa	-	-	-	2	18	+	-
3	561_01_05	4-4*07	2-8*01	2*01	VDRDRPILIGAVPRFDF	17 aa			κ	2-29*02	2*01	MQGILYPT	9 aa	-	-	-	3	106	+	-
4.1	561_01_18	1-46*01	3-10*01	6*03	ARDPFGDRAPHYNYHMDV	18 aa	6 aa ins. in CDRH1	κ	3-20*01	3*01	QRYGGTPIT	9 aa	+	+	+	4.1	37	+	+	
4.1	561_01_21	1-46*01	5-24*01	6*03	ARDPFGDMYPHYNYHMDV	18 aa	6 aa ins. in CDRH1	κ	3-20*01	3*01	QRYGGTPIT	9 aa	+	+	+					
4.1	561_01_33	1-46*01	3-10*01	6*03	ARDPFGDMYPHYNYHMDV	18 aa	6 aa ins. in CDRH1	κ	3-20*01	3*01	QRYGGTPIT	9 aa	+	+	+					
4.1	561_01_54	1-46*01	3-10*01	6*03	ARDPFGDMYPHYNSHMDV	18 aa	6 aa ins. in CDRH1	κ	3-20*01	3*01	QRYGGTPIT	9 aa	+	+	+					
4.1	561_01_55	1-46*01	3-10*01	6*03	ARDPFGDMYPHYNYHMDV	18 aa	6 aa ins. in CDRH1	κ	3-20*01	3*01	QRYGGTPIT	9 aa	+	+	+					
4.1	561_02_10	1-46*01	3-10*01	6*03	ARDPFGNMPHYNYHMDV	18 aa	6 aa ins. in CDRH1	κ	3-20*01	4*01	QRYGGTPIT	9 aa	+	+	+					
4.1	561_02_22	1-46*01	3-10*01	6*03	ARDPFGDMYPHYNYHMDV	18 aa	6 aa ins. in CDRH1	κ	3-20*01	3*01	QRYGGTPIT	9 aa	+	+	+					
4.1	561_02_27	1-46*01	3-10*01	6*03	ARDPFGDMYPHYNYHMDV	18 aa	6 aa ins. in CDRH1	κ	3-20*01	3*01	QRYGGTPIT	9 aa	+	+	+					
4.1	561_02_47	1-46*01	3-10*01	6*03	ARDPFGDMYPHYNYHMDV	18 aa	6 aa ins. in CDRH1	κ	3-20*01	3*01	QRYGGTPIT	9 aa	+	+	+					
4.1	561_03_59	1-46*01	3-10*01	6*03	ARDPFGDRAPHYNYHMDV	18 aa	6 aa ins. in CDRH1	κ	3-20*01	4*01	QRYGATPIT	9 aa	+	+	+					
4.1	561_05_18	1-46*01	5-24*01	6*03	ARDPFGDMYPHYNYHMDV	18 aa	6 aa ins. in CDRH1	κ	3-20*01	4*01	QRYGGTPIT	9 aa	+	+	+					
4.1	561_08_10	1-46*01	3-10*01	6*03	ARDPFGDRAPHYNYHMDV	18 aa	6 aa ins. in CDRH1	κ	3-20*01	4*01	QRYGGTPIT	9 aa	+	+	+					
4.1	561_09_23	1-46*01	3-10*01	6*03	ARDPFGERAPHYNYHMDV	18 aa	6 aa ins. in CDRH1	κ	3-20*01	4*01	QRFGATPIT	9 aa	+	+	+					
4.1	561_10_07	1-46*01	3-10*01	6*03	ARDPFGDRAPHYNYHMDV	18 aa	6 aa ins. in CDRH1	κ	3-20*01	4*01	QRYGGTPIT	9 aa	+	+	+					
4.2	561_08_52	1-46*01	6-13*01	6*03	ARDPLGEKSPAYSHHMDV	18 aa	2 aa del. in FWR1	κ	3-20*01	4*01	QTYGATPIT	10 aa	2 aa ins. in FWR3	+	+					+
4.2	561_09_89	1-46*01	1-26*01	6*03	ARDPLGEKSPAYSHHMDV	18 aa	2 aa del. in FWR1	κ	3-20*01	4*01	QTYGATPIT	10 aa	2 aa ins. in FWR3	+	+					+
4.3	561_09_71	1-46*01	3-16*01	6*04	ARDSFGETFRRHSGDQPYQMDV	21 aa	2 aa del. in FWR1	κ	3-20*01	4*01	QSYGSITPLI	10 aa	+	+	+					
4.4	561_01_23	1-46*01	3-16*01	6*04	ARDSFGETFRRHSGDQPYQMDV	20 aa	2 aa del. in FWR1	κ	3-20*01	4*01	QSYGSITPLV	10 aa	+	+	+					
4.4	561_01_29	1-46*01	3-16*01	6*04	ARDSFGETFRRHSGDQPYQMDL	20 aa	2 aa del. in FWR1	κ	3-20*01	4*01	QSYGSITPLV	10 aa	+	+	+					
4.4	561_02_12	1-46*01	3-16*01	6*04	ARDPFGETFRGHDPYRMDV	20 aa	2 aa del. in FWR1	κ	3-20*01	4*01	QSYGSITPLV	10 aa	+	+	+					
4.4	561_02_21	1-46*01	3-16*01	6*04	ARDPFGETFRGREQPYQMDV	20 aa	2 aa del. in FWR1	κ	3-20*01	4*01	QSYGPITPLV	10 aa	+	+	+					
4.4	561_03_07	1-46*01	3-16*01	6*04	ARDPFGETFRGHDPYRMDV	20 aa	2 aa del. in FWR1	κ	3-20*01	4*01	QSYGSITPLV	10 aa	+	+	+					
4.4	561_03_78	1-46*01	3-16*01	6*04	ARDPFGETFRGHDPYQMDV	20 aa	2 aa del. in FWR1	κ	3-20*01	4*01	QSYGSITPLV	10 aa	+	+	+					
6	561_01_30	3-30*18	4-17*01	6*03	VKDGEVDYGDYAYYYMDV	21 aa		λ	1-47*01	1*01	AAWDDSLSGRYV	12 aa	-	-	-	6	2	+	-	
7	561_01_50	3-13*01	3-3*01	6*03	TRGEAPYDFWGGHLDYHYFYMDI	23 aa		κ	2-30*02	2*01	MQASHWPHA	9 aa	+	+	+	7	17	+	+	
8	561_01_02	5-51*01	5-24*01	3*02	ARPLCGQDVTCINAFDI	17 aa		κ	4-1*01	2*01	EQFYDTPYT	9 aa	+	+	+	8	12	+	+	
8	561_02_17	5-51*01	5-24*01	3*02	ARPLCGQDVTCINAFDI	17 aa		κ	4-1*01	2*01	EQFYDTPYT	9 aa	+	+	+	8	12	+	+	
9	561_02_32	4-34*01	3-10*01	6*03	VRYYLPHMDV	10 aa		κ	2-24*01	2*01	MQASQFPHT	9 aa	2 aa del. in FWR1	-	-	-	9	7	+	-
10	561_08_24	1-69*01	1-26*01	6*02	AVGSNVNGFFHMDH	14 aa	6 aa del. in FWR3	λ	3-10*01	2*01	YLADRNNMGI	11 aa	+	+	+	10	8	+	-	
11	561_02_73	1-69*01	2-21*02	6*03	VRGDVGGSVLTETDYQQMDV	24 aa		κ	3-15*01	2*03	QYNNWPPYS	10 aa	+	+	+	11	9	+	+	
13	561_05_16	1-18*01	2-8*02	4*02	ARDLNYPFCTETTCYETLAY	20 aa		κ	1-39*01	2*01	QQSYTPYT	9 aa	+	+	+	13	5	-	+	
14	561_05_75	1-2*02	3-3*01	6*03	ARAKTATMFIIRNPKSGNNYMDA	24 aa		κ	3-20*01	4*01	QQYATSVT	8 aa	-	+	-	14	5	+	+	
17	561_05_54	1-69*01	3-9*01	4*02	EGRYKYGSSSTSGPFD	17 aa		κ	1-33*01	3*01	QQYDNIIPRAT	11 aa	+	+	-	17	4	-	+	
18	561_05_11	1-69*01	3-9*01	4*02	VGRYKYRSASTSGPFD	17 aa		κ	1-33*01	3*01	QQCDNIIPRAT	11 aa	+	+	-	18	8	-	+	
20	561_02_33	1-69*01	3-9*01	4*02	VARYKQHGNSGPFD	16 aa		κ	1-33*01	3*01	QQYDNIIPRAT	11 aa	+	+	-	20	21	+	+	
21	561_05_02	1-69*01	3-3*01	3*02	ARNTISNGDDAFDI	15 aa		λ	2-8*01	2*01	GSLVGNWDVI	10 aa	6 aa del. in CDRL1	-	-	-	21	5	-	+
22	561_05_44	1-69*11	5-18*01	6*03	ARSSLVTVMDEAELEEESHYYMDV	26 aa		κ	4-1*01	4*01	HQYNTPLT	9 aa	+	+	+	22	13	-	+	
23	561_06_44	1-69*12	3-10*01	6*03	ARGSDVTVLEFETERLEENYYYYMDV	26 aa		κ	4-1*01	4*01	QQYFSIPLT	9 aa	+	+	+	23	3	-	+	
24	561_05_83	3-23*01	4-17*01	4*02	ARGPLLRFFDL	11 aa		λ	2-23*02	2*01	SSYARGTSFL	10 aa	+	+	+	24	6	-	+	
25	561_06_09	3-23*04	3-10*01	4*02	TKDQGLLRAHDY	12 aa		λ	2-14*01	2*01	SSYTSRSTSS	10 aa	+	+	-	25	6	-	+	
26	561_05_65	3-23*04	3-16*01	4*02	ASILTAQISTFTDVGFLH	19 aa		κ	1-9*01	2*01	HQLNSPRYT	9 aa	+	+	-	26	6	-	+	
27	561_05_09	3-30*18	6-13*01	4*02	AKDKAPRARKQGFDF	15 aa		κ	10-12*01	2*01	QQANSFPFT	9 aa	+	+	-	27	5	-	+	
28	561_06_69	3-30*3*02	5-18*01	4*02	ARGGFTYGLFDY	13 aa		κ	2-29*03	2*01	LQGVLDPPYT	10 aa	+	+	-	28	6	-	+	
30	561_05_23	4-34*01	6-6*01	5*02	AGTKRVANRPKGGWFD	17 aa		κ	1-39*01	2*01	QQSYTPYT	9 aa	+	+	-	30	8	-	+	
32	561_05_10	4-34*01	3-16*01	5*02	ARLRAKNGYVDWFD	15 aa		λ	1-47*01	1*01	AAWDDSFYV	10 aa	+	+	-	32	7	-	+	
34	561_07_60	4-34*01	1-7*01	4*02	AGRLAGTRNFNS	12 aa		κ	1-5*03	3*01	QQYNSIERLFT	11 aa	+	+	-	34	2	-	+	
36	561_07_83	4-34*01	6-6*01	4*02	ARGPKGPRPFGGPDQ	16 aa		κ	3-15*01	5*01	QQYYWPSIT	10 aa	+	+	-	36	3	-	+	
37	561_07_14	1-69*01	3-16*01	6*03	ARGSDVTVMFEGAGRWEEENFYADV	26 aa		κ	4-1*01	4*01	QQYFTIPLT	9 aa	+	+	-	37	4	-	+	
40	561_07_07	3-23*01	6-25*01	4*02	ASVLAQAISTFITDVGFLH	19 aa		κ	1-9*01	2*01	HQLNSPRYT	9 aa	+	+	-	40	6	-	+	
41	561_05_78	1-69*12	3-16*01	6*03	ATDGGAGASITAADNPFYDYSYLYMDV	32 aa		κ	3-20*01	3*01	QQYSSPVT	9 aa	+	+	-	41	6	+	+	
43	561_07_10	3-7*03	3-9*01	4*02	VRYFDSRASEARLDF	16 aa		λ	3-10*01	1*01	YSTDKKGLHV	11 aa	+	+	-	43	2	+	+	
45	561_05_25	3-11*01	2-21*01	3*02	ARDRRQVLKFTGAGDAFMS	19 aa		λ	3-21*02	3*02	QVVDYSRIHCV	11 aa	+	+	+	45	3	-	+	
54	561_09_01	1-69*06	6-6*01	4*02	ARSAAPRRFLDASGLNLP	20 aa	9 aa ins. in CDRH2	κ	3-11*01	4*01	QQSSAWPLT	9 aa	+	+	-	54	10	+	+	

aa, amino acids; ins., insertion; del., deletion; \*, BG505<sub>505P664</sub>; \*\*, YU2<sub>90140</sub> fold-on trimer; \*\*\* Neutralization defined as neutralizing activity detected against at least one viral strain.