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Supplementary Materials for

A V_H1-69 antibody lineage from an infected Chinese donor potently neutralizes HIV-1 by targeting the V3 glycan supersite

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Table S1A. Neutralizing breadth and potency of sera from an HIV-1-infected Chinese donor (CBJC438) on the global panel of HIV-Env strains. [a]

Global Panel			CBJC438						
Clade	**Tier**	**Pseudovirus**	**2005-07-12**	**2006-04-06**	**2007-04-10**	**2008-03-20**	**2009-06-13**	**2009-12-15**	**2012-07-31**
A	**2**	**398-F1**	1277	893	102	829	1575	2038	254
B	**2**	**TRO.11**	260	348	54	358	334	492	122
	2	**X2278**	737	601	111	670	703	879	161
C	**2**	**25710**	498	294	72	323	308	241	129
	2	**Ce0217**	408	427	51	331	236	378	102
	2	**Ce1176**	341	303	25	496	318	385	126
G	**2**	**X1632**	101	91	23	214	116	138	91
CRF01_AE	**2**	**CNE55**	114	93	31	138	63	77	82
	2	**CNE8**	143	94	75	191	75	151	125
CRF07_BC	**2**	**BJOX2000**	414	400	22	248	298	621	150
	2	**CH119**	208	207	46	217	304	533	135
AC	**2**	**246**	162	150	81	253	205	224	138
Potency (GMTs)			292	253	50	311	258	352	129
Breadth% (>20)			100	100	100	100	100	100	100

[a]Global panel was developed by the Montefiori group at Duke University Medical Center.
The serum dilution values >1000 are highlighted in red, 200~1000 in orange, and 20~200 in green.

Table S1B. Neutralizing breadth and potency of monoclonal antibodies (mAbs) from an HIV-1-infected Chinese donor (CBJC438) on the global panel of HIV-Env strains. [a]

Global Panel			mAbs				
Clade	**Tier**	**Pseudovirus**	**438-B11**	**438-D5**	**438-D6**	**438-F11**	**VRC01**
A	**2**	**398-F1**	0.02	0.03	>50	>50	0.41
B	**2**	**TRO.11**	0.07	0.14	>50	>50	0.77
	2	**X2278**	0.09	0.08	>50	>50	0.35
C	**2**	**25710**	0.64	0.55	>50	>50	0.87
	2	**Ce0217**	4.53	1.67	>50	>50	0.42
	2	**Ce1176**	0.34	0.33	>50	>50	4.88
G	**2**	**X1632**	>50	>50	>50	>50	0.31
CRF01_AE	**2**	**CNE55**	>50	>50	>50	>50	0.64
	2	**CNE8**	>50	>50	>50	>50	0.56
CRF07_BC	**2**	**BJOX2000**	0.06	0.07	>50	>50	>50
	2	**CH119**	0.14	0.22	>50	>50	1.56
AC	**2**	**246**	>50	>50	>50	>50	0.51
Potency (GMTs)			0.18	0.19	n/a	n/a	0.69
Breadth% (<50µg/ml)			67	67	0	0	92

[a]Global panel was developed by the Montefiori group at Duke University Medical Center.
The neutralizing potency of the mAbs was measured as IC_{50} in µg/ml. Values < 0.2 µg/ml are highlighted in red, 0.2~2 µg/ml in yellow, and 2~50 µg/ml in green.

Table S1C. Neutralization activity of 438-B11, PGT121, PGT128 against a cross-clade 129-isolate HIV-1 Env pseudovirus panel (IC_{50}/IC_{80} in µg/ml).

Subtype	HIV.1 Isolate	IC_{50} (µg/ml)			IC_{80} (µg/ml)		
		B11	PGT121	PGT128	B11	PGT121	PGT128
A	0260.v5.c1	0.082	0.042	0.030	0.330	0.169	0.119
A	0330.v4.c3	0.081	0.039	0.165	0.324	0.158	0.659
A	191084 B7.19	0.039	0.049	0.345	0.156	0.194	1.380
A	191955 A11	>10.0	>10.0	1.559	>10.0	>10.0	6.235
A	92RW020	0.003	0.003	0.002	0.013	0.012	0.006
A	94UG103	3.031	5.184	0.030	>10.0	>10.0	0.119
A	BG505	>10.0	0.029	0.013	>10.0	0.115	0.053
A	KNH1144	0.833	0.107	0.009	3.334	0.429	0.036
A	MS208.A1	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
A1	Q168ENVa2	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
A1	Q23ENV17	0.009	0.004	0.004	0.036	0.016	0.017
A1	Q259ENVd2.17	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
A1	Q461ENVe2	>10.0	>10.0	6.441	>10.0	>10.0	>10.0
A1	Q769ENVd22	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
A1U	T278.5	>10.0	>10.0	0.029	>10.0	>10.0	0.117
AC	3301.v1.c24	1.412	0.007	0.207	5.647	0.029	0.827
AC	6041.v3.c23	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
AC	6540.v4.c1	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
AC	6545.v4.c1	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
ACD	0815.v3.c3	0.037	0.027	0.017	0.148	0.107	0.067
ACD	3103.v3.c10	0.022	0.012	0.005	0.088	0.048	0.018
AE	620345.c01	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
AE	92TH021	>10.0	>10.0	0.004	>10.0	>10.0	0.015
AE	BJOX009000.02.4	>10.0	>10.0	0.004	>10.0	>10.0	0.016
AE	BJOX010000.06.2	>10.0	>10.0	4.981	>10.0	>10.0	>10.0
AE	BJOX015000.11.5	>10.0	>10.0	0.012	>10.0	>10.0	0.048
AE	BJOX025000.01.1	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
AE	BJOX028000.10.3	>10.0	>10.0	0.029	>10.0	>10.0	0.115
AE	C1080.c03	>10.0	>10.0	0.081	>10.0	>10.0	0.325
AE	C3347.c11	>10.0	>10.0	0.003	>10.0	>10.0	0.012
AE	C4118.c09	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
AE	CNE5	>10.0	>10.0	0.047	>10.0	>10.0	0.187
AE	CNE8	>10.0	>10.0	0.007	>10.0	>10.0	0.030
AE	R1166.c01	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
AE	R2184.c04	>10.0	>10.0	0.958	>10.0	>10.0	3.833
AE	R3265.c06	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0

AG	928.28	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
AG	T211.9	>10.0	2.920	0.029	>10.0	>10.0	0.114
AG	T235.47	0.014	0.062	>10.0	0.056	0.248	>10.0
AG	T250.4	>10.0	0.001	0.001	>10.0	0.005	0.005
AG	T251.18	>10.0	>10.0	5.689	>10.0	>10.0	>10.0
AG	T255.34	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
AG	T257.31	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
AG	T263.8	>10.0	3.310	0.133	>10.0	>10.0	0.533
B	89.6	0.024	0.009	0.002	0.098	0.036	0.009
B	6535.3	0.011	0.003	0.003	0.043	0.011	0.013
B	1006.11.C3.1601	0.018	0.002	0.005	0.074	0.007	0.021
B	1012.11.TC21.3257	0.314	0.012	0.006	1.255	0.049	0.022
B	1054.07.TC4.1499	0.488	0.081	0.018	1.952	0.324	0.073
B	1056.10.TA11.1826	>10.0	0.035	0.003	>10.0	0.140	0.010
B	62357.14.D3.4589	>10.0	9.600	0.326	>10.0	>10.0	1.305
B	6240.08.TA5.4622	0.028	0.028	0.012	0.111	0.112	0.048
B	6244.13.B5.4567	0.043	0.072	0.014	0.174	0.290	0.058
B	92BR020	0.010	0.011	0.004	0.040	0.045	0.018
B	AC10.0.29	0.014	0.042	0.003	0.058	0.168	0.013
B	ADA	0.019	0.014	0.013	0.078	0.055	0.052
B	BaL.26	0.026	0.017	0.026	0.104	0.069	0.104
B	CAAN5342.A2	0.025	0.010	0.031	0.099	0.039	0.122
B	DH12	0.036	0.002	0.006	0.142	0.006	0.025
B	HxB2	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
B	JRCSF	0.034	0.063	0.006	0.137	0.253	0.022
B	JRFL	0.056	0.088	0.011	0.223	0.352	0.044
B	MN	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
B	PVO.4	4.419	0.126	0.004	>10.0	0.504	0.014
B	QHO692.42	>10.0	6.984	0.021	>10.0	>10.0	0.083
B	REJO.67	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
B	RHPA4.7	0.051	0.020	0.016	0.203	0.080	0.064
B	SC05.8C11.2344	0.014	0.022	0.007	0.058	0.087	0.027
B	SC422661.8	0.016	0.059	0.121	0.065	0.237	0.485
B	SF162	0.008	0.003	0.002	0.030	0.013	0.010
B	SS1196.1	0.009	0.004	0.004	0.038	0.016	0.015
B	TRJO.58	>10.0	9.008	0.011	>10.0	>10.0	0.043
B	TRO.11	0.023	0.008	0.006	0.092	0.032	0.023
B	WEAU.d15.410.787	0.026	0.026	0.005	0.104	0.102	0.022
B	WITO.33	>10.0	0.653	>10.0	>10.0	2.611	>10.0
B	YU2	0.047	0.089	0.035	0.190	0.356	0.139

BC	CNE17	>10.0	4.341	0.051	>10.0	>10.0	0.206
BC	CNE19	>10.0	0.012	>10.0	>10.0	0.050	>10.0
BC	CNE20	>10.0	4.89E-04	3.98E-04	>10.0	0.002	0.002
BC	CNE21	6.052	0.007	0.005	>10.0	0.027	0.018
BC	CNE30	1.196	0.049	0.245	4.782	0.197	0.981
BC	CNE52	>10.0	4.939	>10.0	>10.0	>10.0	>10.0
BC	CNE53	0.020	0.010	0.009	0.082	0.040	0.035
BC	CNE58	>10.0	>10.0	0.977	>10.0	>10.0	3.909
C	1394C9G1(Rev.)	>10.0	0.457	0.007	>10.0	1.828	0.026
C	7030102001E5(Rev.)	0.012	0.007	0.004	0.047	0.028	0.015
C	93IN905	0.009	0.003	0.004	0.036	0.010	0.016
C	BF1266.431a	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
C	CAP210.2.00.E8	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
C	CAP45.2.00.G3	>10.0	8.529	>10.0	>10.0	>10.0	>10.0
C	Ce0393 C3	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
C	Ce1172 H1	2.686	0.004	0.015	>10.0	0.015	0.059
C	Ce1176 A3	0.038	0.015	0.009	0.154	0.061	0.035
C	Ce2010 F5	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
C	Ce2060 G9	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
C	Ce703010054 2A2	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
C	Ce704809221 1B3	>10.0	0.031	0.013	>10.0	0.123	0.052
C	Du156.12	0.016	0.006	0.010	0.065	0.024	0.039
C	Du172.17	0.898	0.021	0.014	3.593	0.082	0.055
C	Du422.1	0.061	0.038	0.032	0.245	0.151	0.130
C	HIV-0013095.2.11	5.028	0.057	>10.0	>10.0	0.227	>10.0
C	HIV-001428.2.42	6.188	0.018	0.024	>10.0	0.074	0.097
C	HIV-16055.2.3	>10.0	0.626	>10.0	>10.0	2.502	>10.0
C	IAVIC22	0.008	0.001	0.003	0.033	0.006	0.010
C	ZM109F.PB4	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
C	ZM135M.PL10a	>10.0	1.260	7.496	>10.0	5.041	>10.0
C	ZM197M.PB7	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
C	ZM214M.PL15	>10.0	0.475	0.768	>10.0	1.898	3.071
C	ZM233M.PB6	>10.0	4.532	>10.0	>10.0	>10.0	>10.0
C	ZM246F.D5	>10.0	0.067	0.004	>10.0	0.268	0.014
C	ZM247F.F7	>10.0	0.028	0.016	>10.0	0.112	0.065
C	ZM249M.B10	>10.0	>10.0	1.238	>10.0	>10.0	4.950
C	ZM249M.PL1	>10.0	>10.0	1.235	>10.0	>10.0	4.941
C	ZM53M.PB12	>10.0	0.003	>10.0	>10.0	0.011	>10.0
CD	3817.v2.c59	>10.0	>10.0	0.007	>10.0	>10.0	0.030
CD	6480.v4.c25	0.006	0.005	>10.0	0.025	0.021	>10.0

CD	6811.v7.c18	0.012	0.002	0.013	0.048	0.008	0.054
CD	6952.v1.c20	>10.0	0.040	>10.0	>10.0	0.161	>10.0
CD	89.F1 2 25	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
D	231965.c01	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
D	3016.v5.c45	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
D	A07412M1.vrc12	>10.0	0.032	6.744	>10.0	0.127	>10.0
G	P0402 c2 11	0.316	0.004	0.006	1.263	0.015	0.026
G	P1981 C5 3	0.006	0.001	0.011	0.024	0.005	0.043
G	X1193 c1	>10.0	0.033	0.010	>10.0	0.132	0.041
G	X1254 c3	0.090	0.039	0.015	0.360	0.156	0.062
G	X1632 S2 B10	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
G	X2088 c9	0.015	0.005	7.559	0.059	0.020	>10.0
G	X2131 C1 B5	>10.0	0.010	0.009	>10.0	0.040	0.037
-	aMLV	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0
-	VSV	>10.0	>10.0	>10.0	>10.0	>10.0	>10.0

The neutralizing potency of the mAbs was measured as IC50/ IC80 in µg/ml. Values < 0.1 µg/ml are highlighted in red, 0.1-1 µg/ml in orange, 1-5 µg/ml in yellow, and 5-10 µg/m in green.

		IC_{50} (µg/ml)			**IC_{80} (µg/ml)**		
		438-B11	**PGT121**	**PGT128**	**438-B11**	**PGT121**	**PGT128**
Total Number of Viruses Tested		129	129	129	129	129	129
Total Number of Viruses Neutralized	IC_{50}/ IC_{80} >10.0 (µg/ml)	54	81	88	48	71	82
	IC_{50}/ IC_{80} >1.0 (µg/ml)	46	70	79	41	66	74
	IC_{50}/ IC_{80} >0.1 (µg/ml)	41	64	69	25	38	57
Percent of Viruses Neutralized	IC_{50}/ IC_{80} >10.0 (µg/ml)	41.9	62.8	68.2	37.2	55.0	63.6
	IC_{50}/ IC_{80} >1.0 (µg/ml)	35.7	54.3	61.2	31.8	51.2	57.4
	IC_{50}/ IC_{80} >0.1 (µg/ml)	31.8	49.6	53.5	19.4	29.5	44.2
Median IC_{50}/ IC_{80} (µg/ml)		0.027	0.028	0.013	0.098	0.080	0.046
Geometric IC_{50}/ IC_{80} Mean (µg/ml)		0.058	0.037	0.024	0.136	0.072	0.065

Antibody ID	**Geometric IC_{50} Mean**			
	Subtype A	Subtype B	Subtype C	Subtypes A, B, and C
438-B11	0.079	0.035	0.138	0.056
PGT121	0.045	0.039	0.049	0.043
PGT128	0.054	0.010	0.031	0.019

Table S1D. Characterization of four monoclonal antibodies isolated from an HIV-1-infected Chinese donor (CBJC438).

mAbs	Heavy chain					Light chain			
	IGHV	IGHD	IGHJ	CDR3 (aa)	SHM (%)	IGκ/λV	IGκ/λJ	CDR3 (aa)	SHM (%)
438-B11	1-69*01	3-3*01	3*01	21	25.4 (73/288)	3-20*01[a]	3*01[a]	9	12.7 (34/267)
438-D5	1-69*01	3-3*01	3*01	21	24.7 (71/288)	3-20*01[a]	3*01[a]	9	13.5 (36/267)
438-D6	3-48*02	1-20*01	4*02	8	8.7 (25/288)	2-11*01[b]	3*02[b]	10	2.6 (7/270)
438-F11	7-4-1*02	2-21*02	6*04	20	10.1 (29/288)	1-40*01[b]	2*01[b]	11	7.8 (21/270)

[a]438-B11 and 438-D5 use Kappa chains.

[b]438-D6 and 438-F11 use Lambda chains.

Table S1E. Next-generation sequencing and antibodyomics pipeline processing of CBJC438 B -cell repertoires. [a]

Time point	N_{Raw}	N_{Assign}	Chain	N_{Chain}	<Length> (nt)	N_{Usable}	$Perc_{Usable}$ (%)
2005	4,755,711	3,727,420	H	1,509,712	597.5	1,022,678	67.7%
			κ	1,106,927	600.5	617,666	55.8%
			λ	1,110,781	605.8	704,904	63.5%
2008	5,138,283	4,148,887	H	1,864,778	583.9	1,261,262	67.6%
			κ	1,135,577	567.7	672,894	59.3%
			λ	1,148,532	591.6	714,059	62.2%
2012	4,802,280	3,991,951	H	1,954,169	579.0	1,404,745	71.9%
			κ	1,016,963	591.0	647,514	63.7%
			λ	1,020,819	595.6	675,578	66.2%

[a] Listed items include the time point, total number of raw reads (N_{Raw}), number of reads with assigned germline V genes using a cutoff E-value of 10^{-3} (N_{Assign}), antibody chain type (Chain: H, κ, and λ), number of antibody chains (N_{Chain}), average read length (<length>), number of antibody chains after pipeline processing and removing sequences with a V-gene alignment of 250 bp or shorter (N_{Usable}), and percentage of the usable reads ($Perc_{Usable}=N_{Usable}/N_{Chain}\times100$). 5´-RACE PCR was used in library preparation. After template preparation on Ion Chef, the pooled antibody chain libraries were sequenced on Ion GeneStudio S5.

Table S2A. Expression of antibodies with selected 2005 heavy chain variants paired with the 438-D5 light chain.

No.	Chain type	Sequence index	Yield (mg/L culture sup)	Neutralization (%)	Sequence identity (%)	Amino acid sequence of variable domain
1[a]	H	656611	2.4	36	81.3	QVGLLQSGAEVKEPGSSVTVSCKPSGGTFTNYAISWVRQAPGQGRSSEGGRVPISGISKYAEQFQGRVRLYGDDSTKTVYLDPRSLTSDDTGVYYCARWRGCLDCHYDTGAYYNDASDIWGQGTMVTVSA
2[a]	H	3252240	0.8	14	81.5	QVRLVQSGGEVKKPGSSVTVSCKPSGGTFRNYAITGVRQAPGQGLQWMGGVPIIGGISKYAEQFQGRVRLYEDDSTKTVYLDLRSLTSDDTGVYYCARWRGCLDCHYDTGAYYNDASDIWGQGTMVTVSA
3[a]	H	4088606	1.0	42	77.9	QVRLLQSGAEVKEPGSSVTVSCKPSGGTFTKYAMHWVRQAPGQGLQWMGGRVPIIGVYKYAEQFQGRVRLYEDDSTKTVYLDLRSLTSDDTGVYYCARWRGCLDCHYDTGAYYNDASDIWGQGTMVTVSA
4[a]	H	2771371	1.0	17	81.8	RWRLLQSGAEVKEPGSSVTVSCKPFWRHLHQLWHYLHWVPPGPWTRRSGDGGRVPIIGVYKYAEQFQGRVRLYEDDSTKTVYLDLRSLTSDDTGVYYCARWRGCLDCHYDTGAYYNDASDIWGQGTMVTVSA
5[a]	H	4071948_dN	0.7	33	80.3	VAGLLQVWAEVRKPGSSVKVSCKPSGGTFTNYAMHWVPPGPGQGLQWMGGRVPIIGVYKYAEQFQGRVRLYEDDSTKTVYLDLRSLTSDDTGVYYCARWRGCLDCHYDTGAYYNDASDIWGQGTMVTVSA
6[b]	H	1018124	1.5	0	66.9	QVQLVQSGAEVKKPGSSVKVSCRASGGSFSQFSVNWVRQAPGLGLQWMGGIIPLLGITDYAQKFQGRVTITADDSTSTAYMDLSSLTSEDTAVYYCARAAPFDLRGIVGAYNYYYMDVWGKGTTVTVSS
7[b]	H	2859064	2.0	0	66.9	EVHLVQSGAEVKKPGSSVKVSCRASGGSFSQFAVNWVRQAPGLGLQWMGGIIPLLGITDYAQKFQGRVTITADDSTSTAYMDLSSLTSEDTAVYYCARAAPFDLRGIVGAYNYYYMDVWGKGTTVTVSS
8[b]	H	3069562	—	n/a	66.4	RVQLVQSGAEVKKPGSSVKVSCRASGGSFSQFSVNWVRQAPGPGLQWMGGIIPLLGITDYAQKFQGRVTITADDSTSTAYMDLSSLTSEDTAVYYCARAAPFDLRGIVGAYNYYYMDVWGKGTTVTVSS
9[b]	H	2438418	—	n/a	66.4	RWQLVQSGAEVKKPGSSVKVSCRASGGSFSNFDVNWVRQAPGLGRQWMGGIIPSLAITDYAQRFQGRVTITADDSTSTAYMDLSSLTSEDTAVYYCARAAPFDLRGIVGAYNYYYMDVWGKGTTVTVSS
10[b]	H	3749771	—	n/a	65.1	QVSQSRGCELVQVWAEVKKPGSCVKVSWRASGGGSFSQFSVKSWVRQAPGLGRKWMGGIIPLLGITDYAQKFQGRVTITADDSTSTAYMDLSSLTSEDTAVYYCARAAPFDLRGIVGAYNYYYMDVWGKGTTVTVSS

Listed items include sequence number, antibody chain type, sequence index in the PGM data set, protein yield, neutralization, sequence identity to 438-B11 heavy chain determined during the pipeline processing, and amino acid sequence. No expression (—) denotes protein yield less than 0.5 mg/L. Neutralizing activity was tested against viruses on Global Panel. n/a, not available.

[a] Heavy chains are related to 438-D5/B11 but cover a wide range of sequence identity and HCDR3 motifs.

[b] All sequences have a similar HCDR3 loop length of 20-23 aa.

Table S2B. Expression of antibodies with selected 2005 light chain variants paired with the 438-D5 heavy chain.

No.	Chain type	Sequence index	Yield (mg/L culture sup)	Neutralization (%)	Sequence identity (%)	Amino acid sequence of variable domain
1[a]	K	1020383	8.3	67	89.2	EIVLTQSPGTLSLSSGERGTLSCRASQNISSAYLAWYQQKRGQTPRLLIYAAFSRATATPDRFSGSGSGTDFTLTINRLEPEDFAVYYCQHYGGSFFSFGPGTQVDVK
2[a]	K	1031879	—	n/a	88.3	EIVLTQSPGTLSLSSGERGTLSCRASQNISSAYLAWYQQKRGQTPRLLIYAASSRATATPDRFSGSGSGTDFTLTINRLEPEGFAVYYCQHYGGSFFSFGPGTQVDVF
3[a]	K	158500	6.5	67	88.9	KIVLTQSPGTLSLSSGERGTLSCRASQNISSAYLAWYQQKRGQTPRLLIYAASSRATATPDRFSGSGSGTDFTLTINRLEPEDFAVYYCQHYGGSFFSFGPGTQVDVK
4[a]	K	1965944	7.2	67	88.6	KLVLTQSPGTLSLSSGERGTLSCRASHNISSAYLAWYQQKRGQTPRLLIYAASSRATATPDRFSGSGSGTDFTLTINRLEPEDFAVYYCQHYGGSFFSFGPGTQVDVK
5[a]	K	1043810	—	n/a	89.5	EIVLTQSPGTLSLSSGERGTLSCRASQNISSAYLAWYQQKRGQTPRLLIYAASSRATATPDRFSGSGSGTDFTLTINRLEPEGFAVYYCQHYGGSFFSFGPGTQVDVF

Listed items include sequence number, antibody chain type, sequence index in the PGM data set, protein yield, neutralization, sequence identity to 438-B11 light chain determined during the pipeline processing, and amino acid sequence. No expression (—) denotes protein yield less than 0.5 mg/L. Neutralizing activity was tested against viruses on Global Panel. n/a, not available.

[a] Kappa chains are related to 438-D5/B11 but cover a wide range of sequence identity and KCDR3 motifs.

Table S2C. Expression of antibodies with selected 2008 heavy chain variants paired with the 438-D5 light chain.

No.	Chain type	Sequence index	Yield (mg/L culture sup)	Neutralization (%)	Sequence identity (%)	Amino acid sequence of variable domain
1[a]	H	1066709	30.2	67	97.7	QVRLLQSGAEVKKPGSSVTISCKPVGGTFTNFAIHWVRQAPGQGLEWVGGRVPVVGIYKYGKKFQDRLRLYEDDPMKTVFLELRSLTSDDTGVYYCTRWRGCGMCPYDTNSYYNDASDVWGPGTKVIVSA
2[a]	H	2437629	—	n/a	97.2	QVRLLQSGAEWTKPGSSVDNAPCKPVGGTFTNFAIHWVRQAPGQGLEWVGGRVPVVGIYKYGKKFHDRLRLYEDDPMKTVFLELRSLTSDDTGVYYCTRWRGCGMCPYDTSSYYNDASDVWGPGTKVIVSA
3[a]	H	3954697	—	n/a	93.8	QVRLLRSGAEVKKPGSSVSISCKPVGGTFTNFAITWVPQAPGQGLEWVGGRVPVVGILKYGKKFQVRLRLYEDDPMKTVFLELRSLTSDGTGVYYCTRWRGCGMCPYDTNSYYNDASDVWGPGTKVIVSA
4[a]	H	1067269	6.5	67	81.5	QVRLVQSGAVVKKPGSSVTVSCKPSGGTFTNFAIHWVRQAPGRGLQWMGGRVPIIGVYKYAEKFQDRMRLWEDDPAKTVFLDLRSLTPDDTGVYYCARWRGCGDCLYDTAAYYNDASDIWGQGTMVIVSA
5[a]	H	3795269	—	n/a	80.8	QVRLLQSGAVVKKPGSSVTVSCKPFGGTFTNFAIHWVRQAPGQGLQWMGGRVPIIGVYKYAEKFQGRLRLWEDDPAKTVYLDLRSLTPDDTGVYYCARWRGCGDCLYDTTAYYNDASGIWGQGTMVIVSA
6[a]	H	4500127	—	n/a	81.3	QVRLLQSGPGVARKPGSSVTVSCKPFGGTFTNFAQFSWVRQAPGRGLQWMGGRVPIIGVYKYAEKFQDRMRLWEDDPAKTVFLDLRSLTPDDTGVYYCARWRGCGDCLYDTTAYYNDASDIWGQGTMVIVSA
7[a]	H	881629	—	n/a	80.3	QVRLVQSGAVVKKPGSSVTVSCKPSGGTFTNFAISWVRQAPGQALQWMGGRVPISASTSYAEKFQGRLRLWEDDPAKTVYLDLRSLTPDDTGVYYCARWRGCGDCLYDTTAHYNDASDIWGQGTMVIVSA
8[a]	H	1021217	4.7	75	82.1	QVRLLQSGAEVKKPGSSVRVSCKPLGGFFTNHAIHWVRQAPGQGLEWMGGRVPVQGVYKYAKKFQDRLRLFEDDPMKIVYLELSGLTSDDTGIYYCTRWQGCLDCHADTTPYYNDASEIWGPGTMITVSA
9[a]	H	1071291	—	n/a	81.5	QVRLLQSGAEVKKPGSSVRVSCKPLGGLSFTNHAIHWVRQAPGQGLEWMGGARPVQGVYKYAKKFQDRLTTFEDDPMKIVYLELSGLTSDDTGVYYCTRWQGCLDCHADTSPYYNDASEIWGPGTMITVSA
10[a]	H	2032465	—	n/a	81.8	QVRLLQSGAEVKKPGSSVRVSCKPLGGFFSNHAIHWVRQAPGQGLEWMGGRVPVQGVYKYAKKFQDRLTTFEDDPMKIVYLELSGLTSDDTGVYYCTRWQGCLDCHADTSPYYNDASEIWGPGTMITVSA
11[a]	H	1141564	—	n/a	79.7	RVRLLQSGAVVKKPGSSVTVSCKPFGGTFTNFAISWVRQAPGQGLQWDGGRVPIIGVYKYAEKFQGRLRLWEDDPAKTVYLDLRSLTPDDTGVYYCARWRGCGDCLYDTTAYYNDASDIWGQGTMVIVSA
12[a]	H	4521170	—	n/a	79.0	RVRLLQVRAVVKKPGSSVTVSCKPFGGTFTNFAGFTWVRQALGRGLQWDGGRVPIIGGLKYAEKFQDRMRLWEDDPAKTVFLDLRSLTPDDTGVYYCARWRGCGDCLYDTTAYYDDASDIWGQGTMVIVSA
13[a]	H	1577295_dN	—	n/a	94.9	VAGLLQSGPMVTKPGSSLDISCKPVGGTFTNFAIHWVRQAPGQGLEWVGGRVPVVGIYKYGKKFHDRLRLYEDDPMKTVFLELRSLTSDDTGVYYCTRWRGCGMCPYDTSSYYNDASDVWGPGTKVIVSA
14[a]	H	3385754_dN	—	n/a	95.6	GRVLQSGAEWTKPGSTVDNAPCKTVGGTFTKFAIHWVRQAPGQGLEWVGGRVPVVGIYKYGKKFHDRLRLYEDDPMKTVFLELRSLTSDDTGVYYCTRWRGCGMCPYDTSSYYNDASDVWGPGTKVIVSA
15[a]	H	552047	—	n/a	96.7	RCPVPRCRLLQSGADGWNEPGSSVTISCKPVGGTFTNFAIHWVRQAPGQGLEWVGGRVPVVGIYKYGKKFHDRLRLYEDDPMKTVFLELRSLTSDDTGVYYCTRWRGCGMCPYDTSSYYNDASDVWGPGTKVIVSA
16[a]	H	1759061	—	n/a	94.6	HVRLLQSGAEVEKPGSSVTVSCKPVGGTFTNYAIHWVRQAPGQGLEWVGGRAPRVRNFIKYGKEKFHVRLRLYEDDPMKTVFLELRSLTSDDTGVYYCTRWRGCGMCPYDTSSYYNDASDVWGPGTKVIVSA
17[a]	H	1278991	—	n/a	95.9	HVRLLQSGADGWKKPGSSVTISCKPVGGTFSQFAIHWVRQAHGQGLEWVGGRVPVVGIYKYGKKFHDRLRLYEDDPMKTVFLELRSLTSDDTGVYYCTRWRGCGMCPYDTSSYYNDASDVWGPGTKVIVSA
18[a]	H	2288360	2.7	67	97.4	HVRLLQSGAEAKKPGSSVTISCKPVGGTFTNFAIHWVRQAPGQGLEWVGGRVPVVGIYKYGKKFHDRLRLYEDDPMKTVFLELRSLTSDDTGVYYCTRWRGCGMCPYDTSSYYNDASDVWGPGTKVIVSA
19[a]	H	1797956	6.4	33	82.8	TVRLLQSGAEVKKPGSSVRVSCKPLGGFFANHAIHWVRQAPGQGLEWMGGRVPVQGVYKYAKKFQDRLRLFEDDPMKIVYLELSGLTSDDTGVYYCTRWQGCLDCHADTSPYYNDASEIWGPGTMITVSA
20[a]	H	1719278_dN	—	n/a	97.9	VAGLLQSGAEVKKPGSSVTISCKPVGGTFTNFAIHWVRQAPGQGLEWVGGRVPVVGIYKYGKKFHDRLRLYEDDPMKTVFLELRSLTSDDTGVYYCTRWRGCGMCPYDTSSYYNDASDVWGPGTKVIVSA
21[a]	H	3140010	—	n/a	96.4	PVRLVQSGAEVEKPGSSVTISCKPVGGTFTNYAIHWVRQAPGQGLEWAGGRVPVVGIYKYGKKFHDRLRLYEDDPMKTVFLELRSLTSDDTGVYYCTRWRGCGMCPYDTSSYYNDASDVWGPGTKVIVSA
22[a]	H	364904	—	n/a	95.9	PVWLLQSGAEVKKPGSSVTISCKPVGGTFTNFAIHWVRQAPGQGLEWVGGRVPIVGIYKYGKKFQVRLRLYEDDPMKTVFLELRSLTSDDTGVYYCTRWRGCGMCPYDTNSYYNDASDVWGPGTKVTVSA
23[a]	H	3656520	2.8	0	97.9	TVRLVQSGAEVKKPGSSVTISCKPVGGTFNNFAIHWVRQAPGQGLEWVGGRVPVVGIYKYGKKFHDRLRLYEDDPMKAVFLELRSLTSDDTGVYYCTRWRGCGMCPYDTSSYYNDASNVWGPGTKVIVSA
24[a]	H	3639936	6.1	8	97.9	QVRLLQSGAEVKKPGSSVTISCKPVGGTFTNFAIHWVRQAPGQGLEWVGGRVPVVGIYKYGKKFHDRLRLYEDDPMKTVFLELRSLTSDDTGVYYCTRWRGCGMCPYDTSSHHNDASDVWGPGTKVIVSA
25[a]	H	2534625_dN	—	n/a	96.7	VAGLLQSGAEWKKPGSSVTISCKPVGGTFTNFAIHWVRQAPGQGLEWVGGRVPVVGIYKYGKKFHDRLRLYEDDPMKTVFLELRSLTSDDTGVYYCTRWRGCGMCPYDTSSYYNDASDVWGPGTKVIVSA
26[b]	H	3162349	1.0	0	69.0	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQALGQGLEWMGGIIPIVGIAKPYAQKFQGRVTITGDKSTSTAYMELSSLRSEDTAIYYCAREYYENDFWSGHYGINKAGYFDYWGQGTLVTVSS
27[b]	H	1064503	1.7	0	65.9	QVHLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQVLEWMGRIMPLLDIRNYAQEFQGRVTITADKSTSTAYMELSSLRSEDTAIYYCARDLIVLVPGDPEYSRREGSYCLDVWGKGTTVTVSS
28[b]	H	1201231	—	n/a	70.3	QVQLVQSGAEVKKPGSSVKVFCKASGDTFSRIAISWVRQAPGQGLEWLGGIIPSLGTATHAQNFQGRVTITADISTTTVYMELSSLRSEDTAVYYCAKDQSLDIVIQPAVILPNDAFGIWGQGTMVTVSS
29[b]	H	1047823	—	n/a	67.7	QVQLVQSGAEVKKPGSSVKASCKASGGTFSNYAISWLRQAPGQGLEWMGRIIPIFNVANYAQKFQGRVTISADKSAATAYMELSSLTSEDTAMYYCARVVPELEDIVAGPDVQDYYYMDVWGKGTTVIVSS
30[b]	H	1041439	—	n/a	63.6	QVQLVESGAEVKKPGSSVAVSCKASGGSLSRYSFNWVRQAPGQGLEWMGRVIPTHDKTVYAQKFQGRVTITADKSANTVYMELTSLRSEDTAVYYCARDGPPSYYDFFSGEMGNWFDPWGQGTLVTVSS
31[b]	H	129610	—	n/a	67.7	QVQLVQSGAEVKKPGSSVKVSCRASGGTFTSHTMNWVRQAPGQGLEWMGRFIPIVAISNYAQRFQGRVTITADKSTNTAYLELTGLRSEDTAVYYCARGQGFRPDSGSYSPYYYYYLDVWGKGTAVTVSS
32[b]	H	103511	—	n/a	66.4	QAQLHLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQGLEWLGGIIPIFGVTNYAQEFQGRVSVTADKSTSTAYMELSSLKSEDTAIYYCARDFIVVVPGAPEYSGREGSYYMDVWGKGTAVTAS
33[b]	H	1006836	4.7	33	70.0	RVQLVQSGPEVKKPGSSVKVSCKAAGDTFSRIAISWVRQAPGQGLEWLGGIIPSLGTATHAQNFQGRVTITADISTTTVYMELSSLRSEDTAVYYCAKDQSLDIVIQPAVILPNDAFGIWGQGTMVTVSS
34[b]	H	1730326	—	n/a	67.2	QVRLEQSGAEVQKPGSSVKVSRKTSGGTFDSQTISWVRQAPGQGPEWMARISPLVGVTIYAQKFKGRATITADKSTSTVNMELRSLRSDDTAVYYCARDRAEMDTNPPSYSSFYYYMDVWGEGTTVIVSS
35[b]	H	1168805	—	n/a	69.0	QVQLVQSGAEVKKPGSSVKVSCKASGGSFSSSAISWVRQAPGQGLEWMGGIIPMFGMANYGQNFQGGVTITADESTSTAYVELSNLRSDDTAVYYCVRGEDVYGGGVFEGDNFYYYLDVWGRGTTVTVSS

Listed items include sequence number, antibody chain type, sequence index in the PGM data set, protein yield, neutralization, sequence identity to 438-B11 heavy chain determined during the pipeline processing, and amino acid sequence. No expression (—) denotes protein yield less than 0.5 mg/L. Neutralizing activity was tested against viruses on Global Panel. n/a, not available.

[a] Heavy chains are related to 438-D5/B11 but cover a wide range of sequence identity and HCDR3 motifs.

[b] All sequences have a similar HCDR loop length of 20-23 aa

Table S2D. Expression of antibodies with selected 2008 light chain variants paired with the 438-D5 heavy chain.

No.	Chain type	Sequence index	Yield (mg/L culture sup)	Neutralization (%)	Sequence identity (%)	Amino acid sequence of variable domain
1[a]	K	1181460	2.1	67	97.2	DIVLTQSPVTLSLSSGEAGTLSCRASQNISSSWIAWYQQRRGQVPRLLISAASARAAGIPDRFTGRGSGTDFTLTISRLEPEDFGVYSCQYYGGSFFSFGPGTQVDVK
2[a]	K	1611025	8.6	67	87.3	DIVLTQSPGTLSLSSGETGTLSCRASQNISAAYLAWYHQRRGQVPRLLIYAASSRAGGIPDRFSGSGSGTDFTLTISRLEHGDFGLYYCQYYGGSFFTFGPGTPVDVK
3[a]	K	3391100	—	n/a	96.0	HIVLTQSPVTLSLSSGKTGTLSCRASQNISSSWIAWYQQRRGQSPRLLISAASARAAGIPDRFTGRGSGTDFTLTITRLEPEDFGVYSCQYYGGSFFTFGPGTQVDVK
4[a]	K	1540803	22.4	67	86.1	TIVLTQSPGTLSLSSGETGTLSCRASQNISAAYLAWYHQRRGQVPRLLIYATSSRAGGIPDRFSGSGSGTDFTLTISRLEHGDFGVYYCQYYGGSFFTFGPGTPVDVK
5[a]	K	1093646	3.2	67	96.9	TIVLTQSPVTLSLSSGETGTLSCRASQNISSSWIAWYQQRRGQVPRLLISAASARAAGIPDRFTGRGSGTDFTLTISRLEPEDFGVYSCQYYGGSFFSFGPGTQVDVK

Listed items include sequence number, antibody chain type, sequence index in the PGM data set, protein yield, neutralization, sequence identity to 438-B11 light chain determined during the pipeline processing, and amino acid sequence. No expression (—) denotes protein yield less than 0.5 mg/L. Neutralizing activity was tested against viruses on Global Panel. n/a, not available.

[a] Cover a wide range of sequence identity and KCDR3 motifs.

Table S2E. Expression of antibodies with selected 2012 heavy chain variants paired with the 438-D5 light chain.

No.	Chain type	Sequence index	Yield (mg/L culture sup)	Neutralization (%)	Sequence identity (%)	Amino acid sequence of variable domain
1[a]	H	1273901	5.0	67	97.4	QVRLLQSGAEVKKPGSSVTISCKPVGDTFTNFAIHWVRQAPGQGLEWVGGRVPVVGIYKYGKKFQDRLRLYEDDPMKAVFLELRSLTSDDTGVYYCTRWRGCGMCPYDTNSYYNDASDVWGPGTKVIVSA
2[a]	H	2070251	—	n/a	80.3	QVRLLQSGAEVKKPGSSVRVSCKPLGGFIHNHAIHWVRQAPGQGLEWMGGRVPVQGVYKYAKKFQDRLTTFEDDPMKIVYLELSGLTSDDTGVYYCTRWQGCLDCHADTTPYYNDASEIWGPGTMITVSA
3[b,c]	H	1128948	—	n/a	68.7	QVQLVQSGAEVKKPGSSLKVSCKASGGTFNSYAISWVRQAPGQGLEWLGGIIPVFGTVNYAQKFQGRVTITADEFTSTAYMELSSLTSEDTAVYYCARAYCTQSSCYPEWGYYYYYMDVWGKGTTVTASS
4[b,c]	H	1802268	2.4	8	69.2	QVQLVQSGAEVKKPGSFVKVSCKASGGTFNSYAISWVRQAPGQGLEWLGGIIPVFGTVNYAQKFQGRVTITADEFTSTAYMELSSLTSEDTAVYYCARAYCTQSSCYPEWGYYYYYMDVWGKGTTVTVSS
5[b]	H	130290	32.2	0	69.0	QVLLVQSGAEVKKPGSSVKVSCTTSGGTFGNFAIHWVRQAPGQGLEWMGGIIPVYGSADYADKFKGRVTMTADDSTSTAYLEVSSLRSDDSAVYYCARGSQSTKVSMRPAAVTYSYSYMDVWGKGTTVIVSS
6[b]	H	1044069	1.3	0	69.5	QVQLVQSGAEVKKPGSSVKVSCKASGGTLSNFVISWVRQAPGQGLEWLGGFIPIGDISNSAQNFQGRLTITADESNNTAYMDLSSLKFEDTAIYYCAIKTLTEAYYDDDGLYYYYYMDVWGKGTTVTVSS
7[b]	H	1023928	19.5	8	69.5	QVQLVQSGAEVKKPGSSVKVSCKASGGTFNNYSMNWVRQAPGQGLEWMGRIIPIFGVPNYAQKFQGRVTITADKSTRTAYMELSTLKSEDTAVYYCARDSSEYYNFWSGTYMTTRGAFDLWGQGTMVTVSS
8[b,c]	H	2390299	—	n/a	61.5	QVQLVQSGPEVNEPGSSVKVSCKASGGTFSKFLLSWVRSGPGQGIDWMGKIIPSFGTGHYAPKFQGRVSITADTSTNTVYMAMSVSGSEDTAVYYCATLGDCSRSSCLFPVRDGYMDVWGKGTTVIVSS
9[b,c]	H	3171013	—	n/a	64.4	QVQLVQSGPEVKKPGSSVKVSCKASGGTFSKISISWVRQAPGQGIEWMGKIIPLFGTGHYAPKFQGRVSITADTSTNTVYMAMSGLGSEDTAVYYCATLGDCSRSSCLFPVRTAYMDVWGKGTTCHVSS

Listed items include sequence number, antibody chain type, sequence index in the PGM data set, protein yield, neutralization, sequence identity to 438-B11 heavy chain determined during the pipeline processing, and amino acid sequence. No expression (—) denotes protein yield less than 0.50 mg/L. Neutralizing activity was tested against viruses on Global Panel. n/a, not available.

[a] Heavy chains are related to 438-D5/B11 but cover a wide range of sequence identity and HCDR3 motifs.

[b] All sequences have a similar HCDR3 loop length of 20-23 aa.

[c] The HCDR3 loop has the same characteristic disulfide bond as 438-B11.

Table S2F. Expression of antibodies with selected 2012 light chain variants paired with the 438-D5 heavy chain.

No.	Chain type	Sequence index	Yield (mg/L culture sup)	Neutralization (%)	Sequence identity (%)	Amino acid sequence of variable domain
1[a]	K	1720240	0.6	17	82.7	EIVLTQSPGTLSLSPGERATLSCRASQTVNNDYLAWYQQKPGQAPRLLIYGASSRPTGIPDRFSGSGSGTDFTLTISRLEPEDFAVFYCQQYASSLPFTFGQGTRLVIK
2[a]	K	3926609	—	n/a	86.7	EIVLTQSPGTLSLSPGERATLSCRASQSVSASYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSASGTDFTLTISRLEPEDFAVYHCQQYGGSPLFTFGPGTKVDIK

Listed items include sequence number, antibody chain type, sequence index in the PGM data set, protein yield, neutralization, sequence identity to 438-B11 light chain determined during the pipeline processing, and amino acid sequence. No expression (—) denotes protein yield less than 0.5 mg/L. Neutralizing activity was tested against viruses on Global Panel. n/a, not available.

[a] Germline-like kappa chains.

Table S3A. Neutralizing and binding activity of selected NGS-derived 438-B11/D5 somatic heavy variants paired with 438-D5 light chain.

Tier-1 virus and global panel			2005					2008							2012			control		
Clade	Tier	Pseudovirus	05HC-01	05HC-02	05HC-03	05HC-04	05HC-05	08HC-01	08HC-04	08HC-08	08HC-18	08HC-19	08HC-24	08HC-33	12HC-01	12HC-04	12HC-07	438-B11	438-D5	VRC01
B	1A	SF162	>50	>50	4.05	>50	9.52	0.01	0.01	0.04	0.01	1.74	>50	5.61	0.04	16.12	35.23	0.02	0.02	0.48
C	1A	MW965	50.00	>50	>50	>50	37.04	0.11	1.14	21.50	0.25	>50	>50	>50	11.69	>50	>50	1.19	1.75	0.07
A	2	398-F1[a]	23.81	41.67	20.83	37.04	--	0.02	0.03	0.13	0.01	25.78	41.08	11.57	0.18	19.05	47.38	0.02	0.03	0.41
B	2	TRO.11[a]	>50	>50	27.78	--	--	0.09	0.08	0.92	0.03	>50	>50	>50	0.93	>50	>50	0.07	0.14	0.77
	2	X2278[a]	45.45	--	33.33	--	--	0.03	0.03	0.08	0.04	14.22	>50	18.13	1.33	>50	>50	0.09	0.08	0.35
C	2	25710[a]	>50	>50	>50	>50	>50	0.23	0.53	10.16	0.18	>50	>50	>50	6.06	>50	>50	0.64	0.55	0.87
	2	Ce0217[a]	>50	>50	>50	>50	20.41	0.39	0.34	3.99	0.17	>50	>50	>50	24.39	>50	>50	4.53	1.67	0.42
	2	Ce1176[a]	>50	>50	>50	>50	>50	0.13	0.18	0.48	0.08	>50	>50	20.15	0.92	>50	>50	0.34	0.33	4.88
G	2	X1632[a]	>50	--	>50	--	--	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.31
CRF01_AE	2	CNE55[a]	>50	--	>50	--	--	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.64
	2	CNE8[a]	>50	--	>50	--	--	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.56
CRF07_BC	2	BJOX2000[a]	41.67	>50	47.62	>50	--	0.03	0.04	0.13	0.02	2.53	>50	>50	0.21	>50	>50	0.06	0.07	>50
	2	CH119[a]	37.04	>50	23.81	>50	--	0.10	0.21	0.57	0.05	17.93	>50	20.92	0.62	>50	>50	0.14	0.22	1.56
AC	2	246[a]	--	--	>50	--	--	>50	>50	20.66	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.51
Binding to BG505 probe[b]			+	+/-	++++	+	+++	++++	++++	++++	++++	++++	+++	++++	++++	++	++	++++	++++	++++
Potency on global panel			35.95	41.67	29.37	37.04	20.41	0.08	0.11	0.87	0.05	11.36	41.08	17.24	1.19	19.05	47.38	0.18	0.19	0.69
Breadth% on global panel			36	14	42	17	33	67	67	75	67	33	8	33	67	8	8	67	67	92

The neutralizing potency of the mAbs was measured as IC_{50} in μg/ml. Values < 0.2 μg/ml are highlighted in red, 0.2~2 μg/ml in yellow, 2~50 μg/ml in green.
The neutralizing breadth was calculated as the percentage of viruses neutralized with IC_{50} < 50 μg/ml.
"--": not tested.
[a]Global panel of 12 HIV-1 Env strains.
[b]Binding capacity was tested to the sorting probe BG505 by ELISA and categorized based on the OD450 value at the 10 μg/ml of antibody tested.
"++++": OD450 ⩾ 3.0; "+++": 2.0 ⩽ OD450 <3.0; "++": 1.0 ⩽ OD450 <2.0; "+": 0.2 ⩽ OD450 <1.0; "+/-": 0.1 ⩽ OD450 <0.2; "-": OD450 <0.1.

Table S3B. Neutralizing and binding activity of selected NGS-derived 438-B11/D5 somatic light variants paired with 438-D5 heavy chain.

Tier-1 virus and global panel			2005			2008				2012	control		
Clade	Tier	Pseudovirus	05KC-01	05KC-03	05KC-04	08KC-01	08KC-02	08KC-04	08KC-05	12KC-01	438-B11	438-D5	VRC01
B	1A	SF162	0.02	0.02	0.02	0.01	0.01	0.03	0.02	7.40	0.02	0.02	0.48
C	1A	MW965	0.40	0.24	0.08	2.04	6.19	8.07	1.80	>50	1.19	1.75	0.07
A	2	398-F1[a]	0.03	0.02	0.03	0.01	0.03	0.04	0.02	41.67	0.02	0.03	0.41
B	2	TRO.11[a]	0.20	0.22	0.22	0.08	0.15	0.19	0.11	>50	0.07	0.14	0.77
	2	X2278[a]	0.15	0.09	0.06	0.07	0.17	0.18	0.04	>50	0.09	0.08	0.35
C	2	25710[a]	1.26	0.90	1.23	0.36	2.38	4.13	0.73	>50	0.64	0.55	0.87
	2	Ce0217[a]	9.96	8.43	6.14	3.65	4.43	12.53	1.88	>50	4.53	1.67	0.42
	2	Ce1176[a]	0.20	0.21	0.27	0.13	0.19	0.24	0.11	>50	0.34	0.33	4.88
G	2	X1632[a]	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.31
CRF01_AE	2	CNE55[a]	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.64
	2	CNE8[a]	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.56
CRF07_BC	2	BJOX2000[a]	0.06	0.06	0.06	0.02	0.04	0.03	0.02	45.00	0.06	0.07	>50
	2	CH119[a]	0.23	0.20	0.23	0.10	0.19	0.22	0.13	>50	0.14	0.22	1.56
AC	2	246[a]	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.51
Binding to BG505 probe[b]			++++	++++	++++	++++	++++	++++	++++	++++	++++	++++	++++
Potency on global panel			0.27	0.23	0.24	0.11	0.24	0.32	0.12	43.30	0.18	0.19	0.69
Breadth% on global panel			67	67	67	67	67	67	67	17	67	67	92

The neutralizing potency of the mAbs was measured as IC_{50} in μg/ml. Values < 0.2 μg/ml are highlighted in red, 0.2~2 μg/ml in yellow, 2~50 μg/ml in green.
The neutralizing breadth was calculated as the percentage of viruses neutralized with IC_{50} < 50 μg/ml.
"--": not tested.
[a]Global panel of 12 HIV-1 Env strains.
[b] Binding capacity was tested to the sorting probe (HR1-redesigned BG505 trimer) by ELISA and categorized based on OD_{450} value at 10 μg/ml of antibody tested.
"++++": OD450 ⩾ 3.0; "+++": 2.0 ⩽ OD450 <3.0; "++": 1.0 ⩽ OD450 <2.0; "+": 0.2 ⩽ OD450 <1.0; "+/-": 0.1 ⩽ OD450 <0.2; "-": OD450 <0.1.

Table S3C. Anti-viral human antibodies with intra-HCDR3 disulfide bond(s).[a]

Antibody	HCDR3	Germline	PDB ID	Virus Target (epitope)
438-B11 (this study)	WRGCGMCPYDTSSYYNDASDV	IGHV1-69	6UUH *	HIV-1 Env (Glycan supersite)
438-D5 (this study)	WRGCGMCPYDTSSYYNDASDV	IGHV1-69	6UUL *	HIV-1 Env (Glycan supersite)
VRC03	VRRGSCDYCGDFPWQY	IGHV1-02	5JXA *	HIV-1 Env (RBS)
VRC03GL	ARRGSCDYCGDFPWQY	IGHV1-02	5JOF *	HIV-1 Env (RBS)
VRC06B	VRKGPSCPHCGDFHWQH	IGHV1-02	4XNZ *	HIV-1 Env (RBS)
45-VRC01.H03+06.D-001739	VRKGPSCPHCGDFHWQH	IGHV1-02	4S1Q *	HIV-1 Env (RBS)
VRC06	VRRGSSCPHCGDFHFEH	IGHV1-02	4JB9 *	HIV-1 Env (RBS)
45-VRC01.H5.F-185917	VRTADCERDPCKGWVFPH	IGHV1-02	4S1S *	HIV-1 Env (RBS)
VRC08	VRGRSCCGGRRHCNGADCFNWDFQH	IGHV1-02	4XMP **	HIV-1 Env (RBS)
VRC08c	VRGKSCCNGRRYCNGADCFNWDFEY	IGHV1-02	4XNY **	HIV-1 Env (RBS)
45.VRC01.H08.F-117225	VRGKSCCGGRRYCNGADCFNWDFEH	IGHV1-02	4S1R **	HIV-1 Env (RBS)
CAP256-VRC26.03	AKDLREDECEEWWSDYYDFGKQLPCRKSRGVAGIFDG	IGHV3-30	4OD1 *	HIV-1 Env (V1-V2)
CAP256-VRC26.04	AKDLREDECEEWWSDYYDFGKQLPCRKSRGVAGIFDK	IGHV3-30	4ORG *	HIV-1 Env (V1-V2)
CAP256-VRC26.07	AKDLREDECEEWWSDYYDFGKKLPCRKSRGVAGVFDK	IGHV3-30	4OD3 *	HIV-1 Env (V1-V2)
CAP256-VRC26.10	AKDMREYECEYWTSDYYDFGRPQPCIDRRGVVGIFDM	IGHV3-30	4OCS *	HIV-1 Env (V1-V2)
CAP256-VRC26.25	AKDLREDECEEWWSDYYDFGKQLPCAKSRGGLVGIADN	IGHV3-30	5DT1 *	HIV-1 Env (V1-V2)
CAP256-VRC26.06	ARDLRELECEEWTLYNYYDFGSRGPCVDPRGVAGSFDV	IGHV3-30	4OCW *	HIV-1 Env (V1-V2)
F045-092	AGPSITESHYCLDCAAKDYYYGLDV	IGHV1-69	4O58 *	Influenza HA (RBS)
FluA-20	ARGTEDLGYCSSGSCPNH	IGHV4-61	6OBZ *	Influenza HA (trimer interface)
F10	ARSPSYICSGGTCVFDH	IGHV1-69	3FKU *	Influenza HA (stem region)
FLD194	HASCSARSCYWGPVDY	IGHV5-51	5A3I *	Influenza HA (RBS)
HEPC3	ARDGVRYCGGGRCYNWFDP	IGHV1-69	6MED *	Hepatitis-C E2
HEPC74	ARDLLKYCGGGNCHSLLVDP	IGHV1-69	6MEE *	Hepatitis-C E2
AR3A	VRPETPRYCSGGFCYGEFDN	IGHV1-69	6BKB *	Hepatitis-C E2
AR3C	VRSVTPRYCGGGFCYGEFDY	IGHV1-69	4MWF *	Hepatitis-C E2
ADI-19425	ARLGYCSGGSCHFDY	IGHV3-21	6APC *	RSV F
CB0002.5	ARSGFCSDDACYRRGSWFDP	IGHV4-4/59	6BLI *	RSV G
CR9501	AACGAYVLISNCGWFDS	IGHV4-31	6OE4 *	RSV F
8f9	ARDGKCGGGRCYSGLLDY	IGHV3-30	3EYF *	humCMV Env (AD2S1)
m336	ARVGYCSSTSCNRGAFDI	IGHV1-69	4XAK *	MERS-CoV (RBS)
CDC2-C2	AREGGHQGYCSGGSCYDFDY	IGHV1-69	6C6Z *	MERS-CoV (RBS)
R13	ASLPYCSGRICRPRTDY	IGHV4-31	6IEA *	RVFV Env Gn
CR1-10	ARLTSDCSGGNCYQAFDY	IGHV4-31	5W1K *	JUNV Env GP1 (RBS)

[a] Human antibodies targeting non-viral antigens (e.g. PBD IDs: 4PTU, 4VID, 4N2U, 2HFG, 2IG2, 5IFJ, and 5BV7) are not listed in this table.

RBS = Receptor-binding site

RSV = Respiratory Syncytial Virus

HA = Hemagglutinin

humCMV = human cytomegalovirus

MERS-CoV = Middle East respiratory syndrome coronavirus

RVFV = Rift Valley fever virus

JUNV = Junin virus (causing human hemorrhagic fever)

* One intra-HCDR3 disulfide bond; ** Two intra-HCDR3 disulfide bonds

Table S3D. X-ray crystallographic data collection and refinement statistics

Data collection	BG505 UFO.664, Fabs 438-B11, 35O22	Fab 438-B11 & PG	Fab 438-B11ΔSS	Fab 438-D5
X-ray Source	APS 23ID-D	SSRL 12-2	APS 23ID-D	APS 23ID-D
Wavelength (Å)	1.033	0.979	1.033	1.033
Detector	Pilatus	Pilatus	Pilatus	Pilatus
Space group	H32	$P2_1$	$P2_1$	$P2_12_12_1$
Unit cell parameters	a = b = 247.3, c = 257.6 Å	a = 71.1, b = 72.7, c = 108.7 Å β = 101.1˚	a = 104.1, b = 66.1, c = 108.8 Å β = 117.9˚	a = 92.7, b = 97.8, c = 125.5 Å
Resolution (Å)	50.00 - 3.80 (3.87 – 3.80) [a]	50.00 – 2.70 (2.75 – 2.70)[a]	50.00 – 2.10 (2.14 – 2.10)	50.00 – 2.07 (2.14 -2.07)
Observations	293,758	86,956	449,748	833,571
Unique reflections	29,804 (1,403) [a]	29,107 (1,479) [a]	76,942 (3,836) [a]	71,245 (6,892) [a]
Redundancy	9.9 (6.4) [a]	3.0 (3.0) [a]	5.8 (5.9) [a]	11.7 (9.7) [a]
Completeness (%)	99.6 (95.2) [a]	96.6 (97.8) [a]	99.9 (99.6) [a]	99.8 (98.2) [a]
$<I/\sigma I>$ [b]	13.0 (1.0) [a]	12.9 (1.4) [a]	9.1 (1.2) [a]	22.8 (1.0) [a]
R_{sym} [c]	0.17 (1.19) [a]	0.10 (0.96) [a]	0.17 (1.28) [a]	0.19 (>1.0) [a]
R_{pim} [c]	0.05 (0.42) [a]	0.05 (0.53) [a]	0.07 (0.52) [a]	0.05 (0.79) [a]
$CC_{1/2}$	0.89 (0.47)[a]	0.89 (0.54)[a]	0.84 (0.46)[a]	0.88 (0.56)[a]
Refinement statistics				
Resolution (Å)	49.44 – 3.80	48.23 – 2.70	48.08 – 2.10	46.37 – 2.07
Reflections (work)	29,787	29,094	76,912	71,132
R_{cryst} (%) [d] / R_{free} (%) [e]	29.9 / 31.7	22.7 / 26.0	22.9 / 26.8	20.0 / 24.5
No. atoms				
Protein	11,441	7,644	6,724	6,653
Glycan	978	110	28	52
Water	-	-	534	407
Average *B*-value (Å^2)	163	57	37	55
Protein	163	56	36	54
Glycan	163	97	94	132
Water	-	-	40	54
Wilson *B*-value (Å^2)	132	57	28	41
RMSD from ideal geometry				
Bond length (Å)	0.004	0.003	0.003	0.003
Bond angles (°)	0.77	0.67	0.58	0.59
Ramachandran statistics (%) [f]				
Favored	90.31	97.16	97.13	97.33
Allowed	8.87	2.84	2.87	2.67
Outliers	0.82	0	0	0
PDB ID	6UTK	6UUH	6UUM	6UUL

[a] Numbers in parentheses refer to the highest resolution shell.
[b] Calculated as average(*I*)/average(σ*I*)

[c] $R_{sym} = \Sigma_{hkl}\Sigma_i \mid I_{hkl,i} - \langle I_{hkl} \rangle \mid / \Sigma_{hkl}\Sigma_i I_{hkl,I}$, where $I_{hkl,i}$ is the scaled intensity of the i^{th} measurement of reflection h, k, l, $\langle I_{hkl} \rangle$ is the average intensity for that reflection, and n is the redundancy. R_{pim} is a redundancy-independent measure of the quality of intensity measurements. $R_{pim} = \Sigma_{hkl} (1/(n-1))^{1/2} \Sigma_i \mid I_{hkl,i} - \langle I_{hkl} \rangle \mid / \Sigma_{hkl} \Sigma_i I_{hkl,I}$, where $I_{hkl,i}$ is the scaled intensity of the i^{th} measurement of reflection h, k, l, $\langle I_{hkl} \rangle$ is the average intensity for that reflection, and n is the redundancy.

[d] $R_{cryst} = \Sigma_{hkl} \mid F_o - F_c \mid / \Sigma_{hkl} \mid F_o \mid \times 100$

[e] R_{free} was calculated as for R_{cryst}, but on a test set comprising 5% of the data excluded from refinement.

[f] These values were calculated using MolProbity (http://molprobity.biochem.duke.edu/).

Table S3E. X-ray crystallographic data collection and refinement statistics

Data collection	BG505 UFO.664, Fabs 438-B11ΔSS, 35O22
X-ray Source	SSRL 12-2
Wavelength (Å)	0.979
Detector	Pilatus
Space group	H3
Unit cell parameters	a = b= 148.5, c = 843.5 Å
Resolution (Å)	50.00 – 6.51 (6.62 – 6.51) [a]
Observations	55,947
Unique reflections	13,313 (638) [a]
Redundancy	4.2 (3.2) [a]
Completeness (%)	97.5 (95.5) [a]
$<I/\sigma I>$ [b]	7.3 (1.0) [a]
R_{sym} [c]	0.19 (1.19) [a]
R_{pim} [c]	0.09 (0.64) [a]
$CC_{1/2}$	0.85 (0.62)[a]
Refinement statistics	
Resolution (Å)	46.71 – 6.51
Reflections (work)	13,258
R_{cryst} (%) [d] / R_{free} (%) [e]	30.7 / 35.5
No. atoms	
Protein	22820
Glycan	642
Water	-
Average *B*-value (Å^2)	282
Protein	283
Glycan	252
Water	-
Wilson *B*-value (Å^2)	234
RMSD from ideal geometry	
Bond length (Å)	0.003
Bond angles (°)	0.64
Ramachandran statistics (%) [f]	
Favored	90.44
Allowed	8.74
Outliers	0.82
PDB ID	6V6W

[a] Numbers in parentheses refer to the highest resolution shell.
[b] Calculated as average(*I*)/average(σ*I*)

[c] $R_{sym} = \Sigma_{hkl}\Sigma_i \mid I_{hkl,i} - \langle I_{hkl} \rangle \mid / \Sigma_{hkl}\Sigma_i I_{hkl,I}$, where $I_{hkl,i}$ is the scaled intensity of the i^{th} measurement of reflection h, k, l, $\langle I_{hkl} \rangle$ is the average intensity for that reflection, and n is the redundancy. R_{pim} is a redundancy-independent measure of the quality of intensity measurements. $R_{pim} = \Sigma_{hkl} (1/(n-1))^{1/2} \Sigma_i \mid I_{hkl,i} - \langle I_{hkl} \rangle \mid / \Sigma_{hkl} \Sigma_i I_{hkl,I}$, where $I_{hkl,i}$ is the scaled intensity of the i^{th} measurement of reflection h, k, l, $\langle I_{hkl} \rangle$ is the average intensity for that reflection, and n is the redundancy.

[d] $R_{cryst} = \Sigma_{hkl} \mid F_o - F_c \mid / \Sigma_{hkl} \mid F_o \mid \times 100$

[e] R_{free} was calculated as for R_{cryst}, but on a test set comprising 5% of the data excluded from refinement.

[f] These values were calculated using MolProbity (http://molprobity.biochem.duke.edu/).

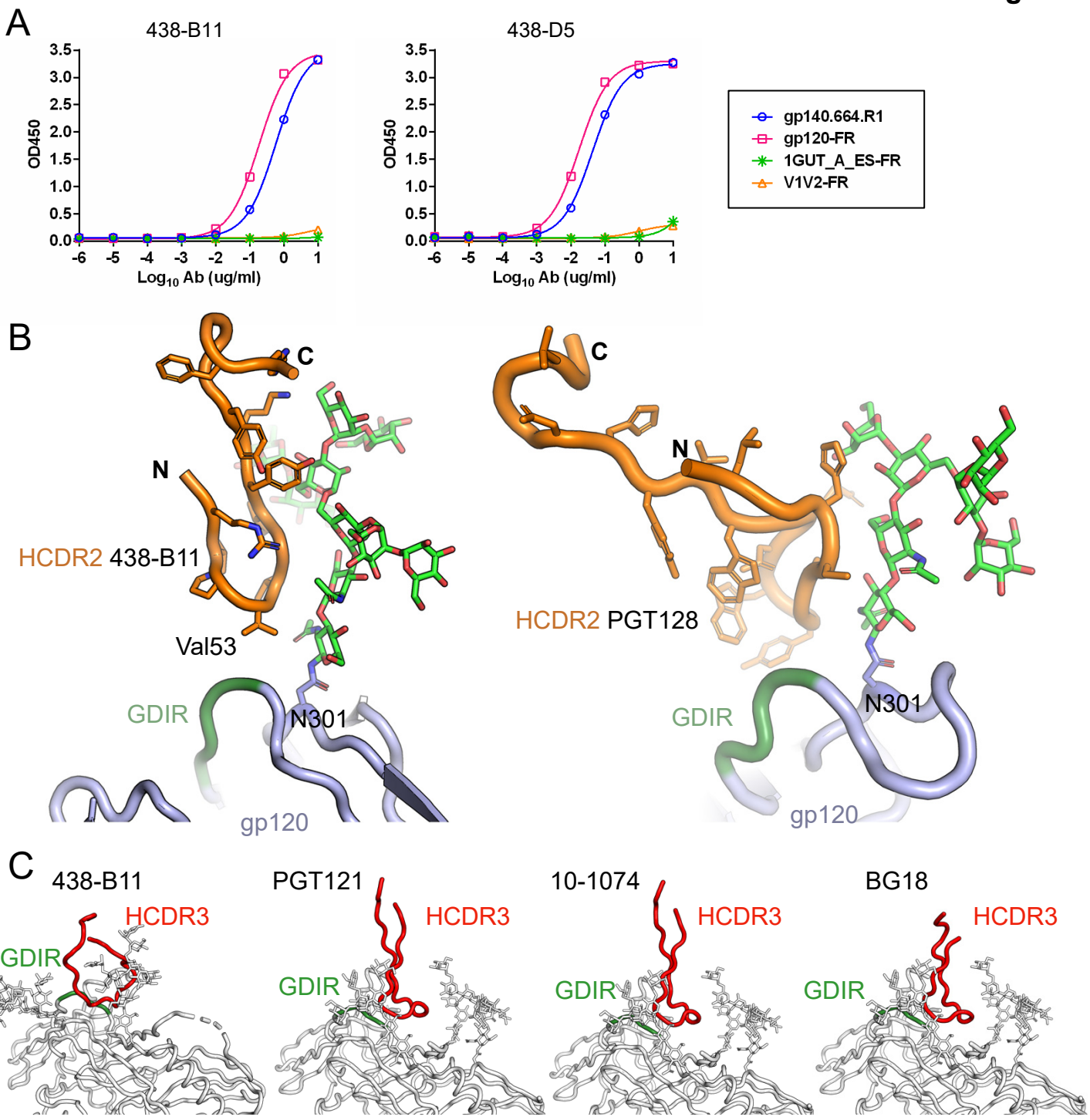
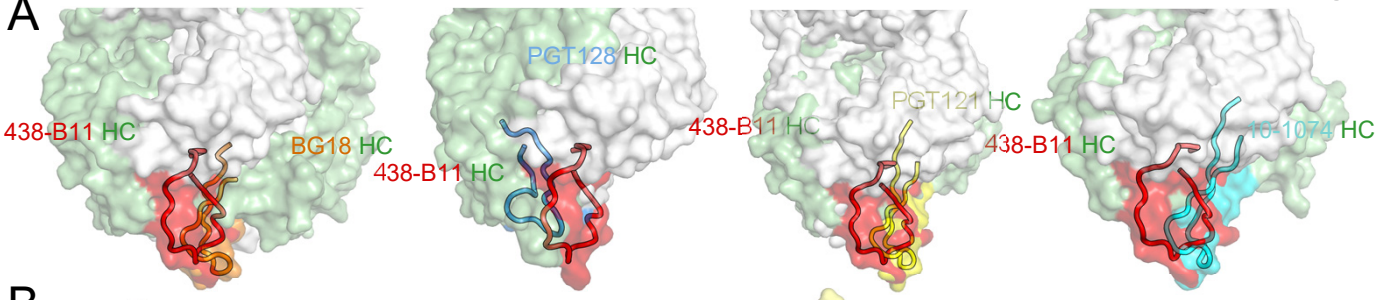
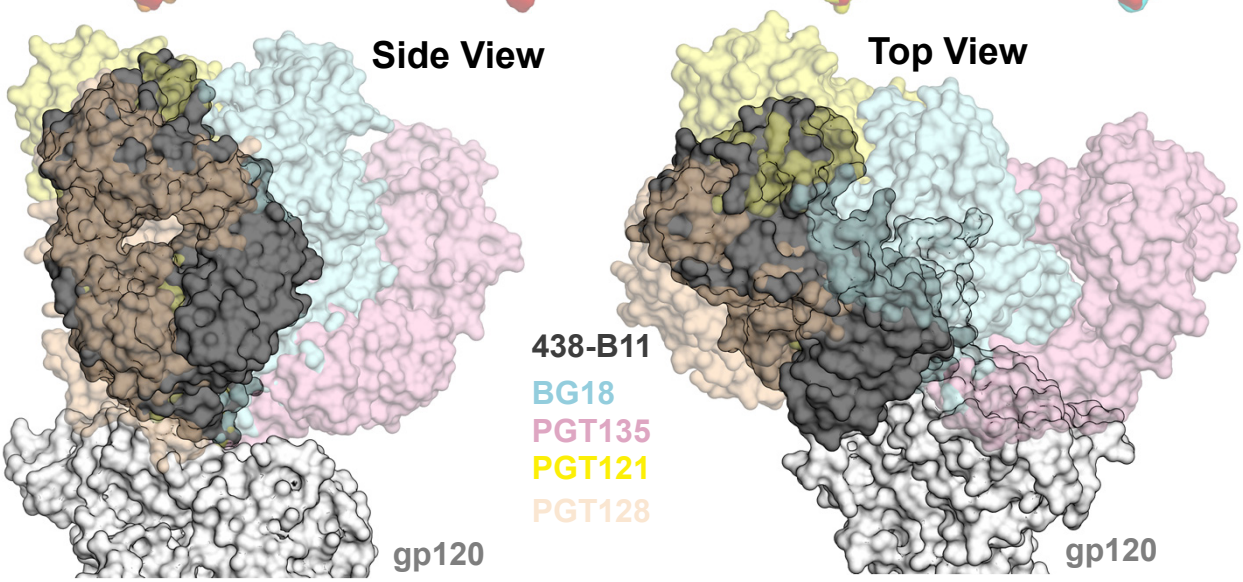


fig. S1. Binding of monoclonal antibodies (mAbs) to the HIV-1 Env. (A) 438-B11 and 438-D5 binding to the untagged HR1-redesigned trimer, BG505 gp140.664.R1, and four epitope antigens including a gp120-ferritin nanoparticle (gp120-FR), an N332 epitope-presenting ferritin nanoparticle (1GUT_A_ES-FR), and a ZM109 V1V2 ferritin nanoparticle (V1V2-FR). (**B**) Interaction of the apolar face of N-linked glycans at Asn301 of gp120 (blue) with HCDR2 (orange) of 438-B11 in complex with BG505 UFO.664 (left) and PGT128 with a modified gp120 (right, PDB ID: 3TYG). **(C)** HCDR3 (red) of different bNAbs buried in the N332 glycan pocket.

A



B



C

BnAbs (PDB ID)	Heavy chain	Light chain	Total BSA (Å^2)
438-B11 (this study)	412 (682)	- (221)	412 (903)
PGT121 precursor (5CEZ)	298 (308)	304 (267)	602 (575)
10-1074 (5T3X)	251 (287)	278 (313)	529 (600)
BG18 (6CH7)	251 (640)	262 (164)	513 (804)
PGT128 (3TYG)	356 (884)	- (227)	356 (1111)
PGT135 (4JM2)	441 (686)	- (592)	441 (1278)

D

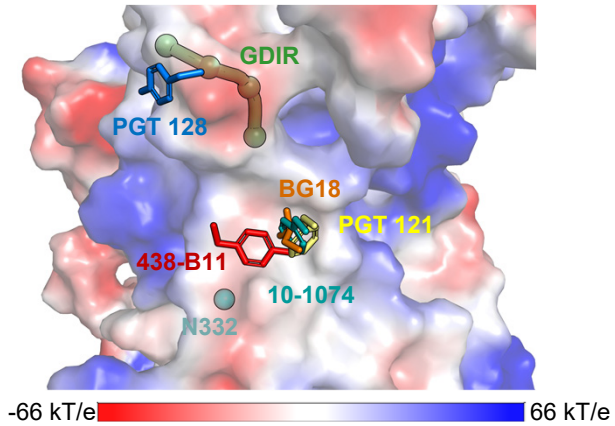


fig. S2. Analysis of bNAbs HCDR3 orientation, angle of approach, and interaction hotspots on gp120. (A) Superposition of the gp120 of Env-bound bNAbs (HC: green; and LC: grey) showing the relative HCDR3 orientation of 438-B11 (red), BG18 (orange), PGT128 (blue), PGT121 (yellow) and 10-1074 (cyan). **(B)** Side and top views of N332/V3 glycan-class bNAbs angle of approach to the gp120. **(C)** Buried surface area (BSA) in Å^2 contributed by bNAb heavy and light chain CDRs on the protein and glycan (shown in parentheses) components of the gp120 surface. **(D)** Residue at the tip of HCDR3 (PGT128: marine; 438-B11: red; PGT121 precursor: yellow; BG18: orange; and 10-174: cyan) are shown in sticks and interact with gp120 on the Env. The electrostatic surface of gp120 is shown with the bar below indicating negatively to positively charged molecular surfaces.

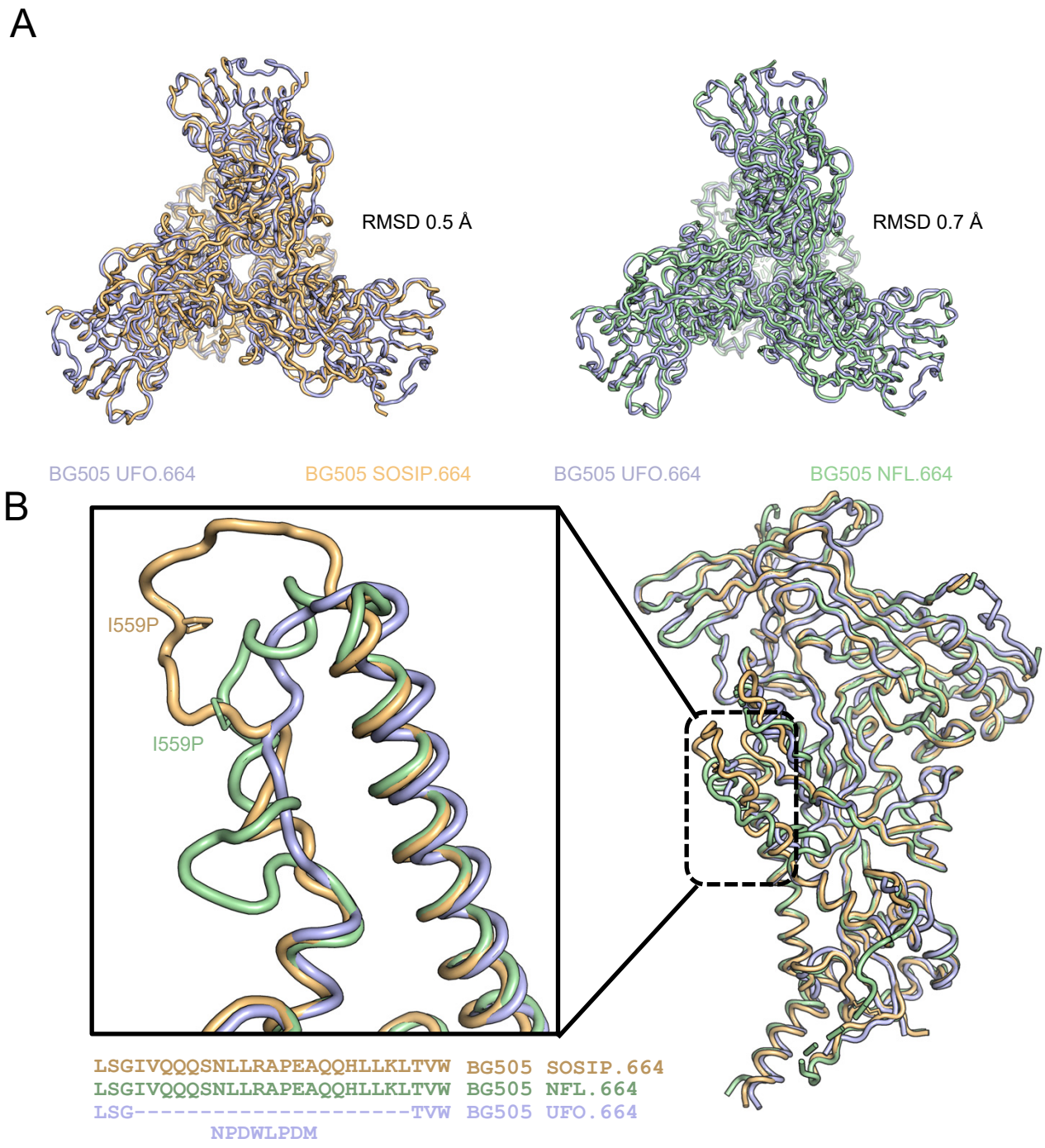


fig. S3. BG505 trimers of SOSIP, NFL, and UFO designs share a highly similar architecture. (A) Superimposition of cleaved BG505 SOSIP.664 (orange), uncleaved BG505 NFL.664 (green) and UFO.664 (blue). **(B)** Superimposition of SOSIP (orange), NFL (green) and UFO (blue) BG505 protomers. The inset on the left shows a close-up view of the superimposed heptad repeat 1 (HR1) N-terminal region ($HR1_N$) from the three trimer designs. The I559P mutation is labeled for SOSIP and NFL. Sequence alignment of $HR1_N$ in three trimer designs is shown below the insert.

A

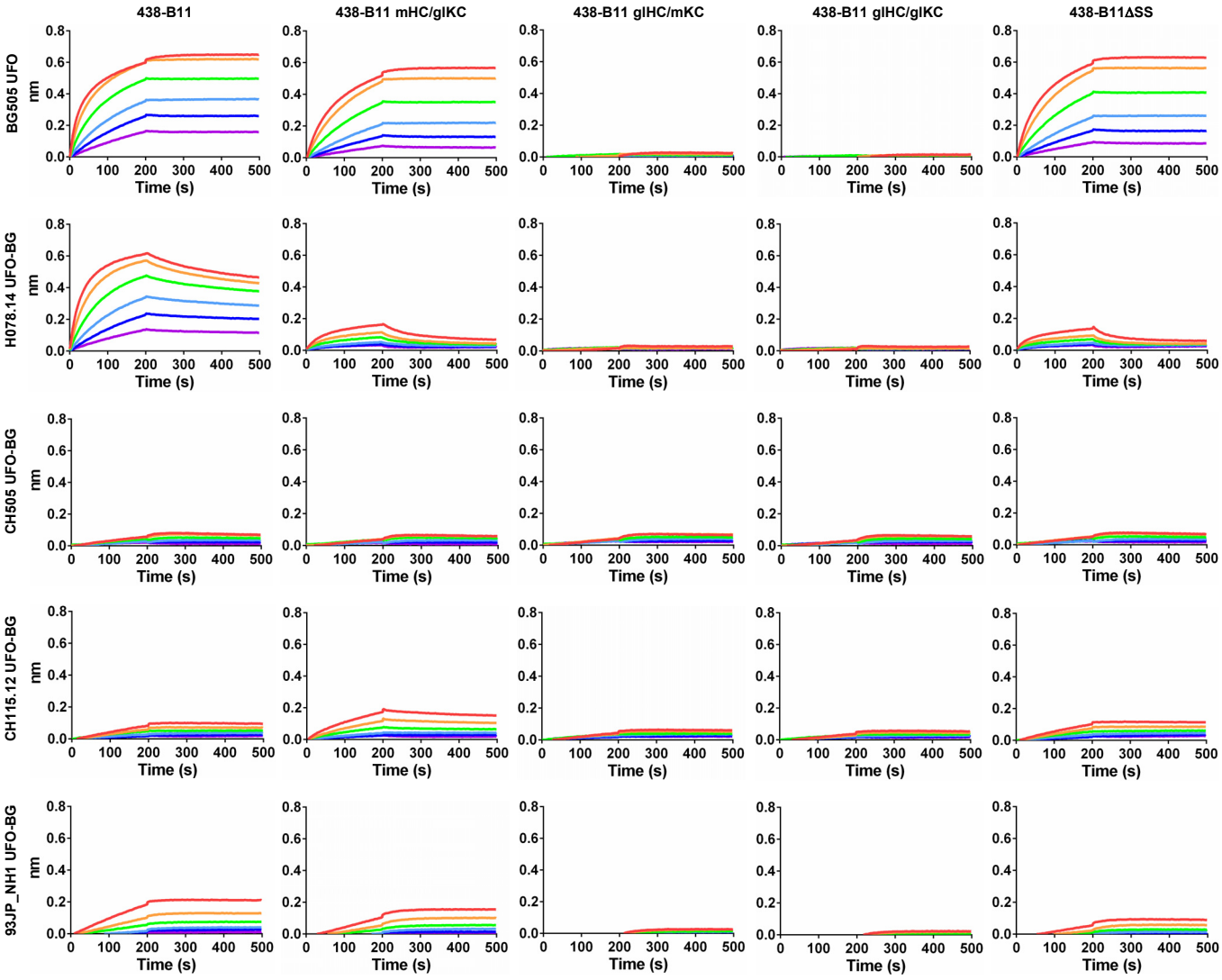
B11 HC reversion (IGHV1-69*01+IGHJ3*01)

```
438-B11 HC          QVQLVQSGAEVRKPGSSVTISCKPVGGTFTNFAIHWVRQAPGQGLEWVGGRVPVVGIYKYGKKFH
438-B11 glHC        QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQ
                    ***********:******.:***. ****:.:** ************:** :*:.*  :*.:**:
                                                                HCDR3
438-B11 HC          DRLRLYEDDPMKTVFLELRSLTSDDTGVYYCTRWRGCGMCPYDTSSYYNDASDVWGPGTKVIVSA
438-B11 glHC        GRVTITADESTSTAYMELSSLRSEDTAVYYCTRWRGCGMCPYDTSSYYNDASDVWGQGTMVTVSS
                    .*: :  *:. .*.::** ** *:**.***************************** ** * **:
```

B11 KC reversion (IGKV3-20*01+IGKJ3*01)

```
438-B11 KC          EIVLTQSPVTLSLSSGETGTLSCRASQNISSSWIAWYQQRRGQVPRLLISAASARAAGIPDRFTG
438-B11 glKC        EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSG
                    ******** *****.** .********.:****::*****: **.***** .**:**:******:*
                                              KCDR3
438-B11 KC          RGSGTDFTLTITRLEPEDFGVYSCQYYGGSFFTFGPGTQVDVK
438-B11 glKC        SGSGTDFTLTISRLEPEDFAVYYCQYYGGSFFTFGPGTKVDIK
                    **********:*******.** ***************:**:*
```

B



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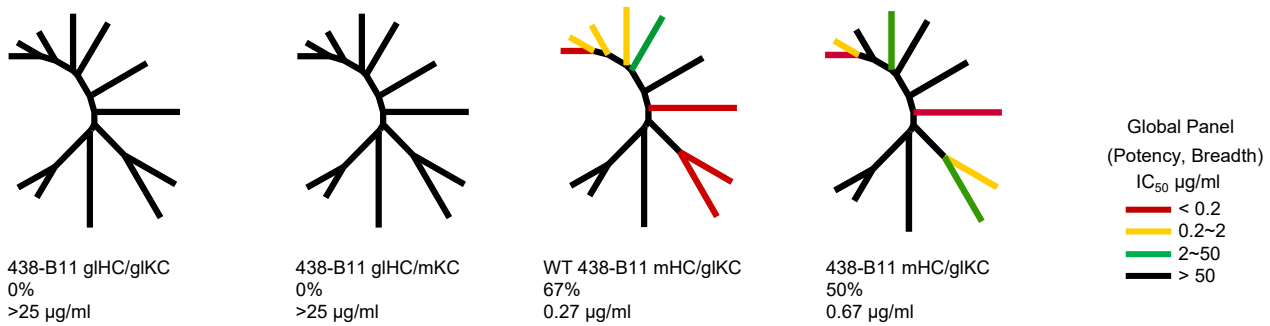

fig. S4. Characterization of 438-B11 germline revertants and 438-B11ΔSS mutant. **(A)** Sequence alignment 438-B11 HC and KC revertants with their respective wildtype sequences. Putative germline genes and CDR3 regions (Kabat number) are labeled. **(B)** Binding of 438-B11 revertants and 438-B11ΔSS mutant to UFO/UFO-BG trimers derived from five representative HIV-1 Envs, including clade-A BG505, clade-B H078.14, clade-C CH505, clade-BC CH115.12, and clade-AE 93JP_NH1. BLI sensorgrams were obtained from an Octet RED96 instrument using a titration series of six trimer concentrations (200-6.25 nM by 2-fold dilution). **(C)** Neutralization breadth (%) and potency (µg/ml) of germline revertants and mature 438-B11 against the global panel. The color-coding scheme is based on potency.

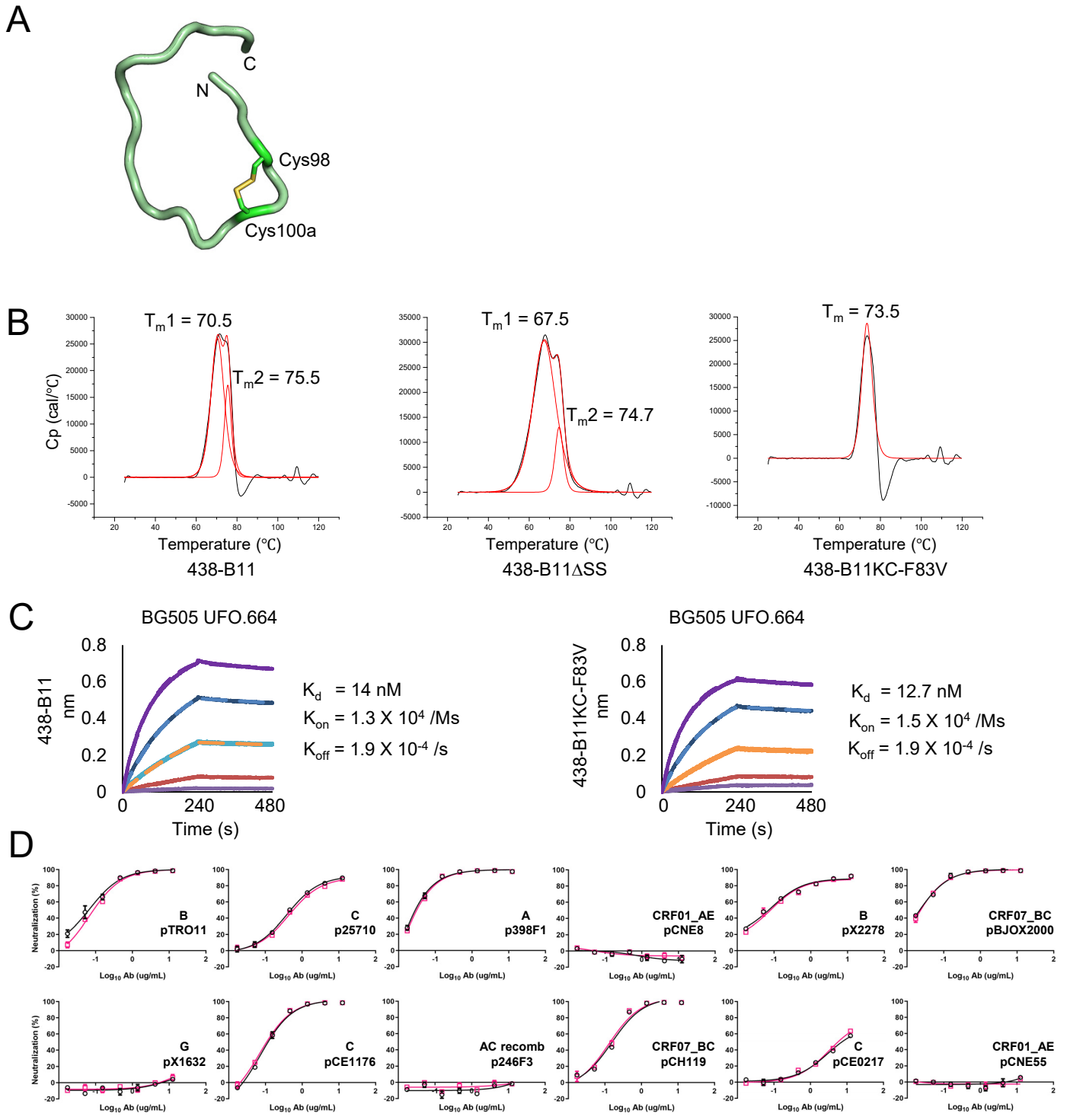

fig. S5. Structure, binding and neutralization of 438-B11, 438-B11ΔSS, and 438-B11KC-F83V. (A) Structure of the U-shaped 438-B11 HCDR3 loop with the intra-HCDR3 disulfide bond (Cys98-Cys100a). **(B)** Differential scanning calorimetry (DSC) analysis of 438-B11, 438-B11ΔSS, and 438-B11KC-F83V. Melting temperatures (T_M) are labeled after the fitting. (**C**) Binding of 438-B11 and 438-B11KC-F83V for BG505 UFO.664 trimer. BLI sensorgrams were obtained from an Octet RED96 instrument using a titration series of five trimer concentrations (800-50 nM by 2-fold dilution). (**D**) Neutralization of global panel by 438-B11 (black) and 438-B11KC-F83V (pink).

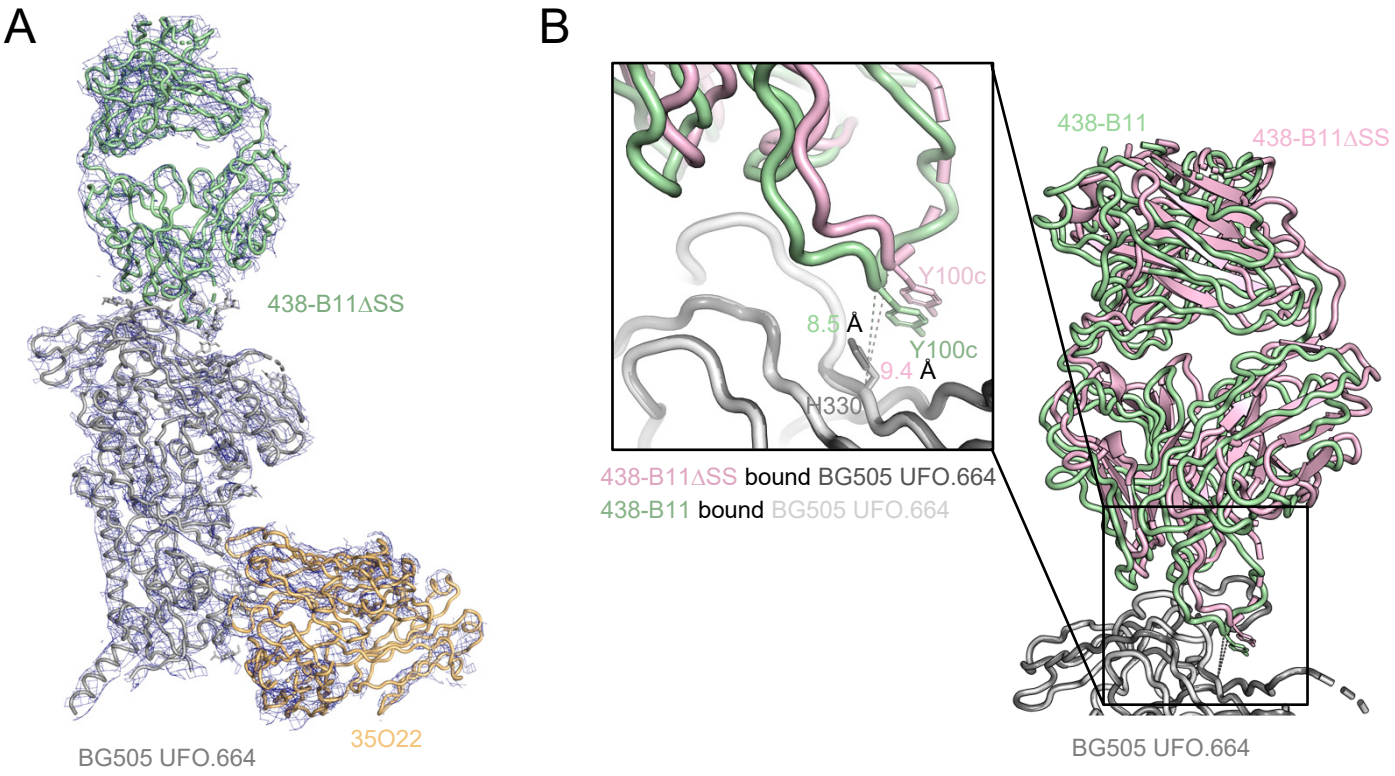

fig. S6. Crystallographic analysis of the 438-B11 disulfide bond mutant. **(A)** Crystal structure of the BG505 UFO.664 trimer (gp140:grey) trimer in complex with Fabs 438-B11ΔSS (green) and 35O22 (orange) at 6.5 Å resolution. The side view of the Env protomer is shown here. **(B)** Superposition of the complex crystal structures of WT 438-B11 (green) and 438-B11ΔSS (pink) bound to the BG505 UFO.664 trimer. The left inset shows an ~1Å upward movement of Fab 438-B11ΔSS compared to WT 438-B11 on the gp120 protein surface. The distances are measured in Å between the Cα atoms of gp120 His330 and 438-B11 HCDR3 Tyr100c.

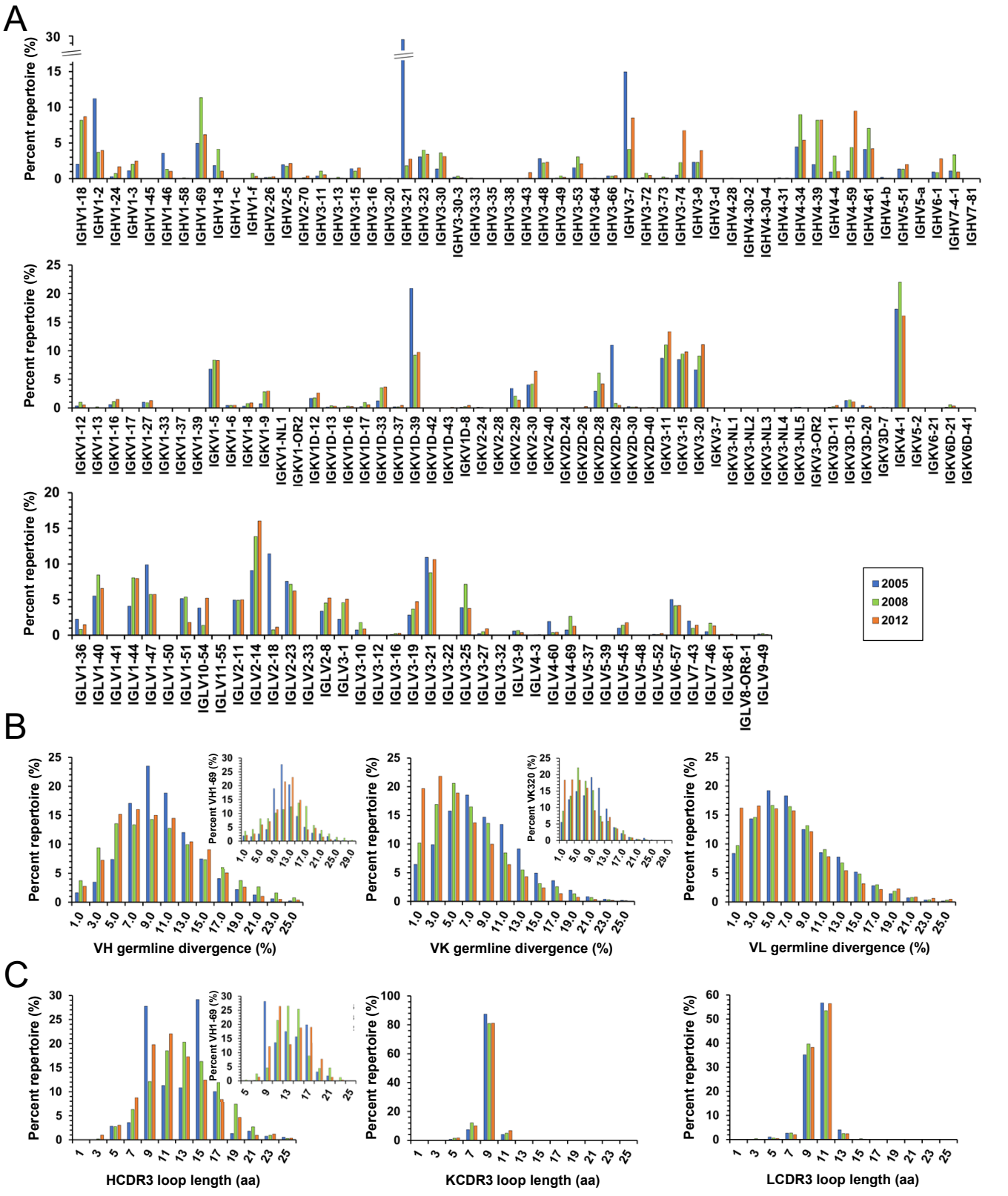

fig. S7. B cell repertoire profiles of an HIV-1-infected Chinese donor (CBJC438) at three time points. The distribution is plotted for **(A)** germline V gene usage for heavy and light (κ and λ) chains, **(B)** germline gene divergence, or degree of SHM, and **(C)** CDR3 loop length (H: heavy chain; K: κ chain; L: λ chain). Color coding denotes the time point analyzed with 2005 shown in blue, 2008 in green, and 2012 in orange.

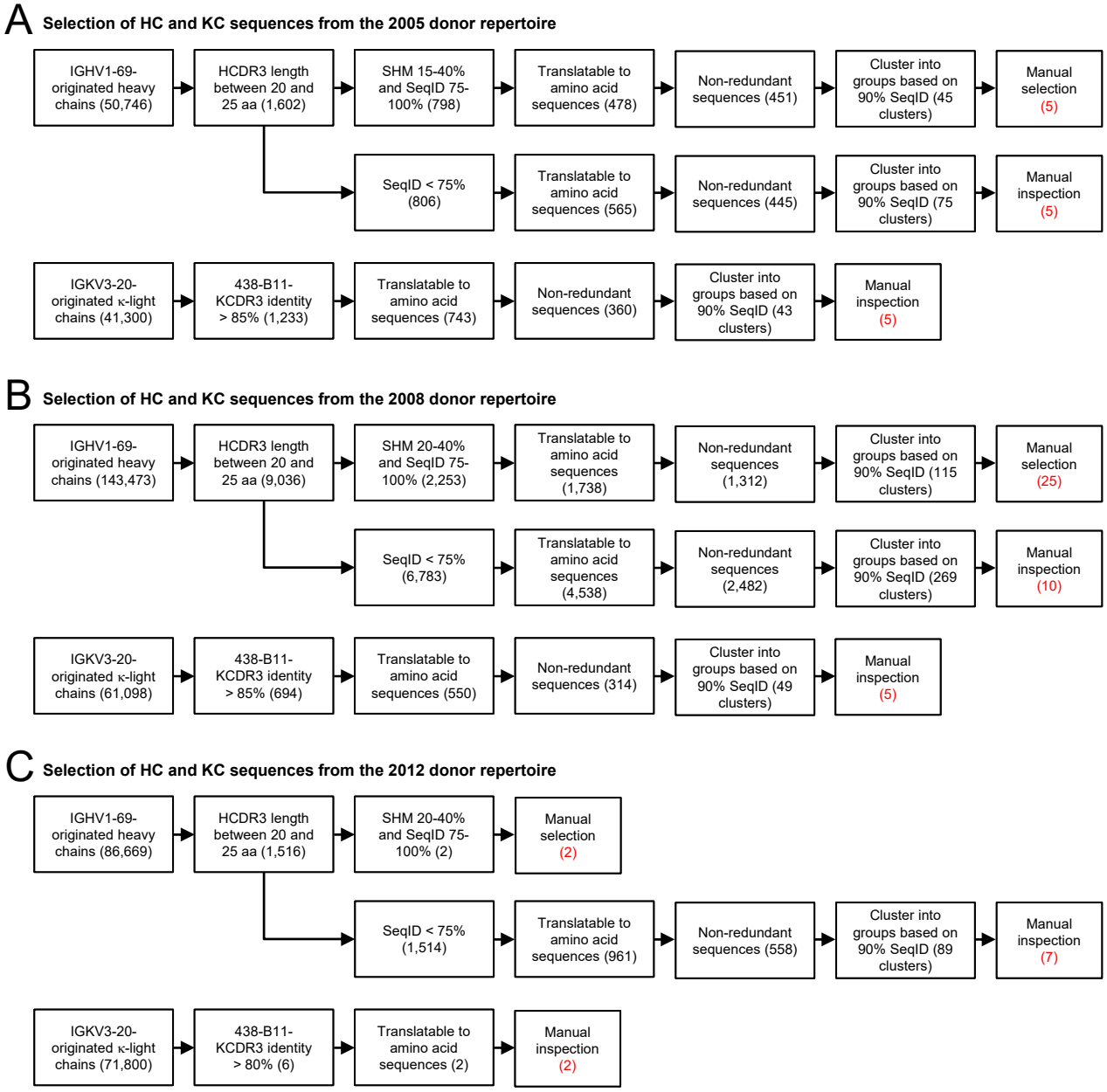

fig. S8. Bioinformatics procedure used for selecting sequences from repertoire NGS data of an HIV-1-infected Chinese donor (CBJC438) for antibody synthesis and characterization. (A) 2005 repertoire. **(B)** 2008 repertoire. **(C)** 2012 repertoire**.** The number of remaining sequences at each step of the process is labeled.