

**Table S1. SPR analysis of antibody binding to BG505 GT1 and GT1.1.**

NAb (IgG)		Env trimer	$K_{on1}$ [1/Ms]	$K_{off1}$ [1/s]	$K_{D1}$ [nM]	$K_{on2}$ [1/Ms]	$K_{off2}$ [1/s]	$K_{D2}$ [nM]	$S_m$
VRC01	mature	BG505 SOSIP.v4.1- GT1 (n=2)	$2.2 \cdot 10^5$ $\pm 2.5 \cdot 10^4$	$< 10^{-5}$	$< 0.1$	$1.6 \cdot 10^3$ $\pm 4.6 \cdot 10^2$	$1.8 \cdot 10^{-3}$ $\pm 9.2 \cdot 10^{-4}$	$1.3 \cdot 10^3$ $\pm 9.4 \cdot 10^2$	2.3 $\pm 5.5 \cdot 10^{-2}$
		BG505 SOSIP.v4.1- GT1.1 (n=2)	$2.2 \cdot 10^5$ $\pm 5.0 \cdot 10^3$	$< 10^{-5}$	$< 0.1$	$1.4 \cdot 10^3$ $\pm 53$	$2.5 \cdot 10^{-3}$ $\pm 1.5 \cdot 10^{-4}$	$1.8 \cdot 10^3$ $\pm 1.8 \cdot 10^2$	2 $\pm 4.6 \cdot 10^{-3}$
	germline	BG505 SOSIP.v4.1- GT1 (n=2)	$9.4 \cdot 10^3$ $\pm 1.7 \cdot 10^2$	$1.7 \cdot 10^{-2}$ $\pm 7.5 \cdot 10^{-4}$	$1.8 \cdot 10^3$ $\pm 1.1 \cdot 10^2$	$8.6 \cdot 10^2$ $\pm 2.1 \cdot 10^2$	$8.5 \cdot 10^{-4}$ $\pm 8.2 \cdot 10^{-5}$	$1.0 \cdot 10^3$ $\pm 1.6 \cdot 10^2$	2.3 $\pm 5.1 \cdot 10^{-2}$
		BG505 SOSIP.v4.1- GT1.1 (n=2)	$1.2 \cdot 10^4$ $\pm 4.0 \cdot 10^2$	$4.2 \cdot 10^{-3}$ $\pm 6.0 \cdot 10^{-5}$	$3.6 \cdot 10^2$ $\pm 18$	$4.1 \cdot 10^3$ $\pm 1.5 \cdot 10^2$	$1.9 \cdot 10^{-3}$ $\pm 5.0 \cdot 10^{-5}$	$4.6 \cdot 10^2$ $\pm 4.6$	2.1 $\pm 1.4 \cdot 10^{-2}$
3BNC60	mature	BG505 SOSIP.v4.1- GT1 (n=3)	$2.5 \cdot 10^5$ $\pm 4.8 \cdot 10^4$	$< 10^{-5}$	$< 0.1$	$2.8 \cdot 10^3$ $\pm 2.0 \cdot 10^2$	$1.4 \cdot 10^{-3}$ $\pm 6.7 \cdot 10^{-4}$	$5.3 \cdot 10^2$ $\pm 3.0 \cdot 10^2$	2.4 $\pm 6.9 \cdot 10^{-3}$
		BG505 SOSIP.v4.1- GT1.1 (n=3)	$2.1 \cdot 10^5$ $\pm 1.9 \cdot 10^4$	$< 10^{-5}$	$< 0.1$	$3.2 \cdot 10^3$ $\pm 3.1 \cdot 10^2$	$9.3 \cdot 10^{-4}$ $\pm 1.8 \cdot 10^{-4}$	$3.1 \cdot 10^2$ $\pm 72$	2.2 $\pm 4.2 \cdot 10^{-2}$
	germline	BG505 SOSIP.v4.1- GT1 (n=2)	Minimal binding: <10 RU						

		BG505 SOSIP.v4.1- GT1.1  (n=2)	$3.9 \cdot 10^4$ $\pm 2.5 \cdot 10^3$	$3.0 \cdot 10^{-2}$ $\pm 6.5 \cdot 10^{-4}$	$7.8 \cdot 10^2$ $\pm 67$	$6.4 \cdot 10^2$ $\pm 26$	$2.1 \cdot 10^{-3}$ $\pm 8.0 \cdot 10^{-5}$	$3.3 \cdot 10^3$ $\pm 2.6 \cdot 10^2$	1.1 $\pm 3.7 \cdot 10^{-2}$
<b>12A12</b>	<i>germline</i>	BG505 SOSIP.v4.1- GT1  (n=2)	Minimal binding: <10 RU						
		BG505 SOSIP.v4.1- GT1.1  (n=2)	$4.2 \cdot 10^4$ $\pm 1.0 \cdot 10^3$	$8.5 \cdot 10^{-3}$ $\pm 2.0 \cdot 10^{-4}$	$2.0 \cdot 10^2$ $\pm 9.6$	$5.7 \cdot 10^8$ $\pm 1.4 \cdot 10^8$	$1.1 \cdot 10^2$ $\pm 30$	$1.9 \cdot 10^2$ $\pm 7.4$	1.6 $\pm 0.15$
<b>PGV19</b>	<i>germline</i>	BG505 SOSIP.v4.1- GT1  (n=2)	$4.1 \cdot 10^4$ $\pm 3.5 \cdot 10^2$	$3.7 \cdot 10^{-4}$ $\pm 1.0 \cdot 10^{-6}$	9.1 $\pm 0.10$	$2.1 \cdot 10^3$ $\pm 15$	$1.7 \cdot 10^{-3}$ $\pm 1.5 \cdot 10^{-5}$	$8.1 \cdot 10^2$ $\pm 13$	2.3 $\pm 5.4 \cdot 10^{-3}$
		BG505 SOSIP.v4.1- GT1.1  (n=2)	$5.3 \cdot 10^4$ $\pm 1.5 \cdot 10^2$	$1.3 \cdot 10^{-3}$ $\pm 6.7 \cdot 10^{-4}$	24 $\pm 12$	$1.6 \cdot 10^4$ $\pm 1.4 \cdot 10^4$	$2.2 \cdot 10^{-3}$ $\pm 3.3 \cdot 10^{-4}$	$4.6 \cdot 10^2$ $\pm 3.8 \cdot 10^2$	2.6 $\pm 0.32$

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<sup>a</sup> A bivalent model was fitted to the binding data for the specific response in response units [RU] over time [s]:  $k_{on1}$  [1/Ms] = on-rate constant for the first-point interaction;  $k_{off1}$  [1/s] = off-rate constant for the first-point interaction,  $10^{-5}$  [1/s] being the limit of detection;  $K_{D1}$  [nM] = equilibrium-dissociation constant for the first-point interaction;  $k_{on2}$  [1/Ms] = on-rate constant for the second-point interaction converted from [1/RUs];  $k_{off2}$  [1/s] = off-rate constant for the second-point interaction;  $K_{D2}$  [nM] = equilibrium-dissociation constant for the second-point interaction converted from [RU];  $S_m$  = the stoichiometric value of paratopes per trimer; n signifies the number of replicates.

Table S2. GT1.1 pseudovirus characterization

GT1.1/GT1.2 neutralization phenotype by bNAbs/gl-bNAbs

bNAb	Epitope	IC50 (µg/mL) in TZM-bl cells	
		BG505 GT1.1 ΔCT	BG505 GT1.2 ΔCT
		293T	293T
sCD4	CD4bs	0.7	8.6
N6	CD4bs	<0.0023	<0.0023
VRC01	CD4bs	<0.00032	0.001
3BNC117	CD4bs	<0.00032	<0.00032
CH31	CD4bs	<0.01	<0.01
CH103	CD4bs	0.001	0.001
DH235.12	CD4bs	0.001	3.543
PG9	V2-apex	0.006	0.007
PG16	V2-apex	<0.00013	0.0004
CH01	V2-apex	0.045	0.035
PGDM1400	V2 apex	<0.0023	<0.0023
PGT128	V3-glycan	0.003	0.005
PGT121	V3-glycan	0.004	0.01
10-1074	V3 glycan	0.06	0.06
PGT151	gp120/gp41 interface	<0.0023	<0.0023
PGT145	gp120/gp41 interface	>5	>5
VRC34.01	gp120/gp41 interface	0.016	<0.01
2G12	OD-glycan	0.51	0.41
DH511.2_K3	MPER	0.017	0.034
2F5	MPER	0.05	<0.01
4E10	MPER	0.62	0.36
3074	Linear V3	11.7	10.5
3869	Linear V3	3.956	16.56
447-52D	Linear V3	>25	>25
838-12D	Linear V3	0.473	17.315
654-30D	CD4bs	>25	>25
1008-30D	CD4bs	>25	>25
1570	CD4bs	>25	>25
729-30D	CD4bs	>25	>25
F105	CD4bs	>25	>25

Neutralization curves plateau around 50% neutralization

gl-bNAb	Epitope	IC50 (µg/mL) in TZM-bl cells	
		BG505 GT1.1 ΔCT	BG505 GT1.2 ΔCT
		293T	293T
gl-VRC26	V2-apex	>50	>50
gl-PG9	V2-apex	>50	>50
gl-PG16	V2-apex	>50	>50
gl-PGT145	Apex	>50	>50
gl-PGT121	V3-glycan	>50	>50
gl-DH270	V3-glycan	>50	>50
gl-PGT128	V3-glycan	>50	>50
gl-VRC03	CD4bs	>50	>50
gl-VRC04	CD4bs	>50	>50
gl-VRC07	CD4bs	>50	>50
gl-VRC18	CD4bs	>50	>50
gl-VRC20	CD4bs	>50	>50
gl-VRC23	CD4bs	>50	>50
gl-CH30-34 (gl-CH31)	CD4bs	>50	>50
gl-CH103	CD4bs	>50	>50
gl-12A12	CD4bs	>50	>50
gl-PGV04	CD4bs	>50	>50
gl-1NC9	CD4bs	>50	>50
gl-3BNC60	CD4bs	>50	>50
gl-NIH45-46	CD4bs	>50	>50
gl-HOMA	CD4bs	>50	>50
gl-VRC01	V1/V2	>50	<b>49</b>
gl-DH235	CD4bs	>50	>50
gl-CH01	V1/V2	>50	>50
gl-PGV19	CD4bs	<b>29.22</b>	<b>30.181</b>

GT1.1/GT1.2 tier phenotype

Sample ID		IC50 (µg/mL) in TZM-bl cells	
		BG505 GT1.1 ΔCT	BG505 GT1.2 ΔCT
		293T	293T
SA-C10	Polyclonal IgG	436	513
SA-C48	Polyclonal IgG	197	262
SA-C72	Polyclonal IgG	168	182
SA-C74	Polyclonal IgG	34	21
SA-C90	Polyclonal IgG	2	1
<b>GMT</b>		<b>63</b>	<b>55</b>
<b>Tier</b>		<b>1A</b>	<b>1A</b>

Reference range:

Tier	IC50 Range
Tier 1A	<64
Tier 1B	64- 310
Tier 2	296-1603
Tier 3	>1603



**Table S3. MAb sequences.**

A b l D	A n i m a l	HC sequence (nt)	LC sequence (nt)
1 1 F 7	A 1 2 N 1 2 5	CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCAG TTGCGTTGTCTCTGATTACTCCATCAGCAGTGCTTTTGGCTGGAGCTGGATCCGCCAGCCCCA GGGAAGGGGCTGGAGTGGATTGCTCATATCGGTGGTAGTAGTGATGACACGAGCTACAATCCC TCCCTCAAGAGTCGAGTCGCCATTTCAAAGACACGTCCAAAGAATCAGTTCTCCCTGAAGCTGA GCTCTGTGACCGCCGCGGACACGGCCGTATTAATTCTGTGCGAGAGGGGTGGAGTTATTCTATTG GACGTTATAACTACGGTCTAGAGTACTTTGACTCCTGGGGCCAGGGAGTCTGGTCACCGTCT CTTCA	CAGTCTGTGCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGACAGAGGGTCACCATCTC CTGCACTGGGACTAGTTCCAACATTGGACGTCATTATGTATACTGGTACCAGCACCTCCCAGGA GTGGCCCCAAAGTCTCATCTATGACACTAATAAGCGACCATCAGGGGTTTCTGACCGATTCT CTGGCTCCAAGTCTGGTTCTCAGCCTCCCTGACCATCACTGGGCTCCAGACTGAGGATGAGG CTGATTACTGCTGCCAGTCCCATGACATCAACCTGAGTGGCCCCATCTTCGGTGTGGGACCC GGCTCACCGTCTCA
1 2 F 2 2	A 1 2 N 2 1 4 6	CAGGTCCAGCTGGTGCAGTCCGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAATGCAGCTCTC CTGCAAGGCTTCTGGATAACAATTCGGCCTCTATGCCATCAATTGGGTGCGACAGGCCCTGG ACAAGGCCCTTGAGTGGATGGGAGGGATCATCCCTCTTATTGGTTAACTACTATGCACAGAAG TTCCAGGGCAGAGTCACAATTAGCGCGGACACGTCCACAAACACAGCCACATGGAGCTGAGC AGCCTGGGATCTGAAGACACCGCCGTCTATTTCTGTGCGAGAGAGGGCTACGGTGTCCAGTCC GAGTCGGGCTGGTATTTGATTTCTGGGGCCCTGGCACCCAGTCACCATCTCCTCA	TCCTATGAGGTGACTCAGTCTCCCTCAGTGTTCGGTGTCCCCCGGACAGACAGCCAGCATCACC TGCTCTGGAGATGGGTTTGGGACTGCATATGGTACTGGTACCAGCAGAAGCCAGGCCAGGTC CCTGTTGCGGTCATCTATAAAAATACTAACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCT CCACCTCGGGGAACAGGCCACCTGACCATCAGCGGGTTCGAGGCTGGGGATGAGGCCGA CTATTATTGTGCACAAATTTGGCTCCGGGAGCAGCAGGTCATCTTCGGTCTGGGACC CGGCTCACCGTCTCA
1 2 C N 1 1	A 1 2 N 1 4 6	CAGGTCCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTTCAGAGACCCTGTCCCTCAC CTGCGCTGTCTCTGGCAACCCTGTACCGCTGGTTTTGACTGGACCTGGATCCGCCAGTCCCC GGGAAGGGGCTGGAGTGGATTGGCCATATCTATGGTGTAGTGGGAGCACCATAACAATCC GTCCCTCGAGAGTCGAGTACCATTTCAAGGGACGCGTCCAGGAACCAGTTCTCCCTGAAACT GACCACTGTGACCGCCGCGGACACGGCCGTCTATTACTGCGGAGACAGGGGGGATCATC GGTATTCGAGGATGCTTACATTTACTTTTACAAACTTCGACTTTTGGGGCCAGGGAGTCTGGT CACCGTCTCCTCA	CAGTCTGTGCTGACTCAGCCTCCCTCAGTGTCTGAGGCCGCCAGGAAGAGTGTCTCCATCTCC TGTTCTGGTAGCGACTCCAACATCGGCAGTAATAGTGTCTCCTGGTTCCAGCAGTTCCCAGGAA CAGCTCCCAAACCTCCTCATTTCATTTTAAATAAACAACGAGCCTCAGGTGTTTCTGACCGATTCTCT GGCTCCAAGTCTGGCAGTCTGCCTCCCTGGCCATCAGTGGACTCCAGACCGACGATGAGGCT GATTATTACTGCGCAGCTTGGGATGATAGCCTGACCGCTGCCGTCTTCGGTACTGGGACCCGG CTCACCGTCTCA
1 2 F 8	A 1 2 N 1 4 6	CAGGTCCAGCTGGTGCAGTCCGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAATGCAGCTCTC CTGCAAGGCTTCTGGATAACAATTCGGCCTCTATGCCATCAATTGGGTGCGACAGGCCCTGG ACAAGGCCCTTGAGTGGATGGGAGGGATCATCCCTCTCAATGGATTAACATATTATGTACAGAAG TTCCAGGGCAGACTACCATGACCGCGGACACGTCCACAAATACAGCCACATGGAGCTGAGC AGCCTGAGATCTGAGGACACCGCCGTTTATTCTGTGCGAGAGAGGGCTACGGTAGTAGACAC TCCGAGTCGGGCTGGTTTTTCGATCACTGGGGCCCTGGCACCCAGTCACCATCTCCTCA	TCCTATGAGGTGACTCAGTCTCCCTCAGTGTTCGGTGTCCCCCGGACAGACAGCCACCATCACC TGCTCTGGAGATGGGTTTGGGACTACATATGGTACTGGTACCAACAGAAGCCAGGCCAGGTC CCTGTTGCGGTCATCTATAAAAATACTCACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCT CCACCTCGGGGAACAGGCCACCTGACCATCAGCGGGTTCGAGGCTGGGGATGAGGCCGA CTATTATTGTGCACAAATTTGGCTCCGGGAGCAGCAGGTCATCTTCGGTCTGGGACC CGGCTCACCGTCTCA
2 1 N 7	A 1 1 N 1 6 0	CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCAC CTGCGCTGTCTCCGGTGGCCCATCAGCAGTGGTCACTACTACTGGACCTGGATCCGCCAACC CCAGGGAAGGGACTGGAGTGGATAGGGTTCATCACTTATGGTGGGACCACCGACTACAACCC GTCCCTCAAGAGTCGAGTACCTTTTCAACAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTG TCAAAAGTCGAGCCACATTTTCAAGCGGACATGTCCAAGAACCCTTCTCCCTGATACTGAGTTC AATTCTGTGACCGCCGCGGACACGGCCGTGATATTATTGTGTGAGAGATGCCCTCCCCACCTAT GGTGGTATAGAACTCGTGGGGCCGGGAGTCTGGTACCCTCTCCTCA	CAAGTTATATTGACTCAGTCTCCGGCCACCTGTCTTTGTACCGGGGGAAAGAGCCACCCTCT CCTGCAGGGCCAGTCAGAGTATTGGCAGCAGCTTAGCCTGGTACCAGCAGAAACCTGGGCAG GCCCCAGGCTCCTCATCTATGGTTTATCCAGCAGGGCCACTGGCATCCAGACAGGTTTCACT GGCAGTGGTCTGGGACAGAGTTCCTCTCACCATCAGCAGCCTGGAGCCTGAAGATTTTGT GTGTATTACTGTGAGAAGTATCATTCTCCCCGTGGAGTTCGGCCAAGGGACCAAGGTGGAAA TCAA
2 1 D 7	A 1 2 N 1 1 5	CAGGTGCAGGTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCAC CTGCGTTGTCTCTGGTGGCTCCATCGGCACTAACTACTGGAGCTGGTCCGCCAGTCCCCAGT GAAGGGACTGGAATGGATTGGACAAATCTATCTTAATTTTGGGACTACCAGTTATAATCCCTCCC TCAAAAGTCGAGCCACATTTTCAAGCGGACATGTCCAAGAACCCTTCTCCCTGATACTGAGTTC TGTGACCGCCGCGGACACGGCCGTCTATTAATTGTGCGAGAGGGGGCGGTAACCTACGTTGCTCT TGATATCTGGGGCCAGGGCTCAGGGTACAGTCTCTTCA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGGCTCCGGGCAGAGTGTACCATCTCT TGTTCTGGAGGCAGATCCAACATTGGAATAAATTATGTCTACTGGTACCAACACCTCCCAGGGA CGGCCCCAAAGTCGTATCTATTATACTAATCAGCGACCCTCAGGGGTCCTGACCGATTCTC TGGCTTAAGTCCGGCACCTCAGCCTCCCTGGCCATCAGTGGTGTCCGATCTGAGGATGAGGC TGATTATTACTGTACAGCCTGGGATGACAGTCTGACCCTGTTTTATTTCGGAGAGGGACCCGG TTGACCGTCTG
2 1 M 2 0	A 1 2 N 1 1 5	GAGGTGCAGTTGGTGGAGTCTGGGGCGGCTTGGCAAAGCCTGGGGGATCCCTGAGACTCTC CTGTGCAGCCTCAGGATTCACCTTCAAGTGGAGTATTATGCACTGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAATGGGTTTCAACTATTAATTATGCTGGTAGTACATACTACGCCGACTCCGTG AGGGGCCGATTCGTATCTCCAGGGACAACCTCAAAGAACACGCTCTCCCTACAAATGAACAGC GTGCGACCTGAGGACAGGGCCGTGTACTGTGCGAAGGATAAAGAGGGTACTATAGTGGT GGTTATCCCTTATGGTACTTCGATCTCTGGGGCCCTGGCACCCCTGTACCATCTCCTCA	GACGTCCAGATGACCCAGTCTCCTTCTCCCTGTCTGCCTCTGTTGGTGCACAAAGTCAGCATCA CTTCCGGGGCCAGTCAGGGCATTGCCGATGCTTTAGCCTGGTATCAGCAGAAACCAGGGAAAG CCCTAACTCCTGATCTATGGTGCATCCAACCTGAAAGTGGGGTCCCATCAAGATTCAGCG GCAGTGGTCTGGGACAGATTTCACTCTCACCATCAGTAGCCTGCAGGCTGAAGATTTTGCAG TCTATTACTGTCAACAGCGCAACAGTACCCTCCGACGTTCCGGCAAGGGACCGGGTGGAG TCAA

2 1 N 1 3	A 1 2 N 1 1 5	CAGGTGCAGCTTCAGGAGTCGGGCCAGGGCGGGTGAAGCCTTCGGAGACCCTGTCCCTCAC CTGCGCTGTCTCTGATGACTCTTTTGGTAGTAGTTATTTCTACTGGAGTTGGATCCGCCAGGCC CCAGGGAAGGGACTGGAGTGGATTGGTACATCGCTTACAGTGGGGCGCTCAGATAACAACC GTCCCTGTTCGAGTCGAGTCACCATTTCAAGAAACATACACGAGAGACAGTTCTACTGCGTCTG ACCTCTATGACCGCCGCGGACACGGCCGTCTACTACTGTGCGAGACATTGCGAAGATGATTAC GGTTACTATTCCGCCGCCAGTCATATGTTTTGGATTCTGGGGCCAAGGGATCGCCGTACC GTCTCCCA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTACCATCA CTTGCCGGACAAGTGAGAACGTTAACAACGTTTAAATTGGTATCAACAAAACCAGGGAAAGC CCCTAAGCTCCTGATCTATAGGACATCCACTTTGCAGAGAGGGGTCCCATCAAGGTTTCAGCGG CACTGGATCTGGGACAGATTACACTCTCACCATCAGCAGCCTGCAGTCTGAGGACTTTGGCACT TACTACTGTCAACATTATTATGGTACCCCGCTCACTTTCCGGCGGAGGGACCATGGTGACATCA AA
2 1 K 1 4	A 1 2 N 1 1 5	CAGTGTGCTGACTCAGCCACCCTCAGTGTCTGGGGCTCCCGGTGAGAGTGTACCATCTCT TGCTCTGGAAGCAGCTCCAACATTGGAAGTTATAATGTGTACTGGTATCAGCAGTTCCAGGAG CGCCCCCAGAGTCTCATCTGGGAGAATATTCATCGACCCTCAGGGGTCCCTGACCGATTCT CTGGCTTAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGTCTCCGATCTGAGGATGAGG CTGATTATTATTGTGCAGCATGGGACAACAGTCTGAGGAGTCCGGTTTTCCGGCGGAGGGACCC GGCTGACCGTCTCA	CAGTATGTGCTGACTCAGCCACCCTCAGTGTCTGGGGCTCCCGGTGAGAGTGTACCATCTCT TGCTCTGGAAGCAGCTCCAACATTGGAAGTTATAATGTGTACTGGTATCAGCAGTTCCAGGAG CGCCCCCAGAGTCTCATCTGGGAGAATATTCATCGACCCTCAGGGGTCCCTGACCGATTCT CTGGCTTAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGTCTCCGATCTGAGGATGAGG CTGATTATTATTGTGCAGCATGGGACAACAGTCTGAGGAGTCCGGTTTTCCGGCGGAGGGACCC GGCTGACCGTCTCA
2 3 F 1 9	A 1 2 N 1 1 8	CAGGTGCAGTTACAGGAGTCGGGCCAGGGCTGGTGAAGCCCTCGGAGACCCTGTCCCTCAC CTGCGCTGTCTCTGGTGGTCCATCAGCAGTGGTTTTACTACTGGACCTGGATCCGCCAGCC CCCCGGGAAGGGACTGGAATGGATTGGATACATCACTCATACTGGGAATGCCGACTACAGCCC GTCCCTCGAGAGTCGAGTACCATTTCCAGAGACACGTGGAAGAACCAGTTCTCCCTGACGCT GACGCTGTGACCGCCGCGGACACGGCCGTATATTACTGTGCGAGAAGGATGACTACAGCGACCAGA TATGAATACTCCGAAATGTGGGGCCAGGGGCGCCCTGGTACCCTCTCCTCA	CAAGTTATATTGACTCAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCT CTTGCCAGGGCCAGTCAAGTGTGGCAGTGCCTTAGCCTGGTATCAGCAGAAAACCTGGGCAGG CCCCCAGGCTCCTCGTCTATGGTGCTTCCAGCAGGGCCACTGACATCCCAGACAGGTTTCAGTG GCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGTCTAGAGCCTGAGGATTTTGCAG TGTATTATTGTGAGAGATAAATACCTCCCCTCGGAGCTTCCGGCAAGGGACCAAGGTGAAAT CAA
2 3 K 1 9	A 1 2 N 1 1 8	CAGGTGCAGCTGCAGGAATCGGGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGTTCTCAC CTGCGCTGTCTCTGGTGGCTCCATGAGTGTGATTACTACTGGACCTGGATCCGCCAGTCCCC AGGGAAGGGTCTGGAATGGATTGGTACATCTATGACGGAAGTGGGGCCACCAGTTACAACCC CTCATTCAAGAGTCGCGTCCGCATCTCAATTGACACGCTCCAAGAACCAGTTCTCCCTGACCCCTG AAGTCGGTCCAGCCGCGGACACGGCCATATTTCTGTGCGAGAGAGATTGTAGTCGTCCTC GAGAGAAGGGCGGTGGCGGACTCAGTGGATGCCTGGGGCCGGGAATTGCGGTACCCTCT CCTCA	GACATTGTGCTGACCCAGTCTCCAGCCTCTTTGGCCGTGTCTCCAGGGCAGAGGGCCACCATC ACCTGCAGAGCCAGCAGAGTGTGAGTTCGTTTTGGAGTATACTCATTCACTGGTATCAGCAGA AACCAGGACAATCTCCTAGACTCCTCATTACCAGGCAACCAATAAAGACTGTTGGGTCCCAGT CAGGTTACGCGCAGTGGGTCTGGGACCGATTTACCCTCACAAATTGATCCTGTGGAGCCTGA CGATGCTGCAGATTATTATTGTCTGCAGACTAAGAATTCTCCTCGGACGTTCCGGCCAAGGGACC AAGGTGGACATCAAA
2 3 C 1 5	A 1 2 N 1 1 8	GAGGTGCAACTGGTGGAGTCTGGGGCGGGCTTGGCAAAGCCCGGGGATCCCTGAGACTCTC CTGTGAAGCCTCTGGATTCATCTTCAGTAGTTATGCTATGCACTGGGTCCGCCAGGCTCCGGG GAAGGGGCTGGTGTGGGTCTCAGGTGTCAATAGTAGTGGTGGCACATACTACGGAGACTCCGT GAAGGGCCGATTACCATTCCAGAGACAACCTCAAAGAACACGCTCTCCCTGAAATGAACAG CCTGAGAATTGAGGACACGGCCGTGTATTACTGTGCGAAAGATCTTGCTAGTTATTCTCGTTT GGCGGTTTGGATTCTGGGGCCAAGGGTCTGCTGTCACCGTCTCCTCA	CACTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACTCCCGGCCAGAGTGTCTCCATCTCT TGCTCTGGAAGCTACTCCAATATTGGAGTTATTTGTATATTGGTACCAGCAGTTGCCAGGGG CGGCCCCAAACTCCTCATCCATTATAATGATCAGCGACCCTCAGGGGTCCCTGACCGATTCTC TGGTCCCAAGTCTGGCAGGTGAGCCTCCCTGGCCATCACTGGTCCGGTCTGAAGATGAGGC TGATTATTACTGTGCAGTTTTGGGATGACAGACTGAGCAATGTGTTATTCCGGAGGAGGGACCCG GCTGACCGTCTCA
2 3 C 1 9	A 1 2 N 1 1 8	CGGATGCAGCTGCAGGAGTCGGGCCAGGAATGGTGAAGCCTTCGGAGACCCTGTCCCTCAC CTGCGTTGTCTCTACTGGCTCCATCAGCAGTGGTTTTCTACTACTGGACCTGGATCCGCCAGCCC CCGGGGAAGGGACTGGAGTGGATTGGTCTTATCCACAGTAATAATCAGAATACCAATTACAATC CCTCCCTCAAGAGTCGAGTACCATTTCAAAGACACGTCCAAAATCTGTTCTCCCTGGAAC GCGCTCTGTGACCGCCGCGGACACGGCCATGATTTCTGTGCGAGAGGTGCGCTACGATTGG GTTTGGGTTCTGGGGCCAGGGGTCGTGTCACCGTACCTCA	GATATTGTGTTGACCCAGACTCCACCCTCGTTGCCGTGACCCCTGGAGAGCCGGCCTCCATC TCCTGCAGGTCTAGTCAAACCCTTCTACATAGTAATGGAATCACCTATTTGCATTGGTACCTCCA GAAGCCAGGCCAGTCTCCACGGCTCCTGATCTATAAAGTTACCAGTCCGGGAATTTGGGGTCCC AGACAGGTTTCAGTGGCAGTGGGTGAGCCACAGAGTTCACACTGAAAATCAGCAGGGTGGAGC CTGAGGATGTTGGTGTATTACTGCATGCAGTGTACAGAGGATCCGTGGACGTTCCGGCCAAG GGACTAAGGTGGAATCAAA
2 3 C 2 1	A 1 2 N 1 1 8	GAAGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTACAGCCTGGGGGTCCCTGAGACTCTT GTGTACAGCCTCTGGATTCACCTTTGATGATCATGCCATGCACTGGGTCCGCCAAGCTCCAGG GAAGGGTCTGGAGTGGATCTGATATTACCTGGAATGGTGAAGAAACACTATGGAGACTCC GTGAAGGGCCGATTACCATTTCCAGAGACAACGGCAACGCTCCCTGATCTGGACATGAAC AGACTGAGGCCTGAAGACACAGCCTTCTATTACTGTGCGCGAGGGGGTCTAGCAGCTGGGATC GCTGAGTCTTCAATTGTGGGGCCAGGGGCGCCCTGGTACCCTCTCCTCA	GATATTGTGATGACCCAGACTCCACTCTCCCTGCCGTGACCCCTGGAGAGCCGGCCTCCATC TCCTGCAGGTCTAGTCAAGCCTTCTGGATTCTGAAGATGGAAGACCTATTTGGATTGGTACC TCCAGAAGCCGGGAGTCTCCACAGGCCTGATTATGAGGTTTCCAATCGGGCCTCTGGAG TCCCAGACAGGTTGAGTGGCAGTGGGTGAGACACTGATTTACACTGAAAATCAGCAGAGTGG AGGCTGAGGATGTTGGGGTTTATTACTGCATGCAATATACAGTTTTTCTCCATTTTCCGGCGG AGGGACCAAGGTGGAGATCAAG
2 4 N 1 4	A 1 2 N 1 0 7 4	CAGGTGCAGTTGCAGGAGTCGGGCCAGGACTGGTGAAGCCATCGGAGACCCTGTCCCTCAC CTGCGATATTTCTGGTACTCCTTCAAGTCGATGATGACTTCTGGAGTTGGATCCGCCAGGCC CCAGGGAAGGGACTGGAGTGGATTGGACACCTCACCTATGGAGGGACCAGTATACAATCCG TCCCTCGAGAGTCGAGTACCATTTCAAGAGACACGTCCAAGAACCAGGTTCTCCTGAAGTTAA AGTCTGTGAGCGCCGCGGACGCGGCCATATTTCTGTGTAAGAGATGCGAAGCTGACCTACG GTTCCGATACCTGGGGCCAGGGGTCGCGTCATCGTCTCCTCA	CAAGTTGTGTTGACTCAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCT CCTGCAGGGCCAGTCAAGTGTGGCAGCGCCTTAGCCTGGTACCAGCAGAAAACCTGGACAG GCCCCCAGGCTCGTATCTATGGTGCCTCTACTACGGCCCTGGCATCCCTGACAGGTTCCGT GGCAGTGGGTCTGGGACAGAGTTCCTCTCACCATCAACAGCCTGGAGCCTGAAGATTTTGG CTATATTACTGTGAGAGGTACAACACCCCCCGACAATTTTGGCCAGGGGACCAGAGTAGAC ATGAAA

2 4 E 1 6	A 1 2 N 0 7 4	GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCGCAGCCTGGGGGGTCCCTGGGACTCT CCTGTGCAGCCTCTGGATTGAGTTCACTAGATACTACATGATTGGGTCCGCCAGACTCCAGG GAAGGGGCTGGAGTGGATCTCATCTCTTGATGCTGGTGGGAAACCACATACTACTCAGACTC CGTGAAGGGCCGATTACCATTTCCAGAGACAACCAAGAATACGGTCTCCCTACTAATGGTC AGCCTGAGACCTGAGGACACGGCCGTATATTACTGTGCGAAAGGCGCAATGTTGGTAACTCA TTGGATGTCTGGGGCCGGGGGTTCTGGTACCCTCTCCCTCA	GATATTGTGATGACCCAGACTCCACTCTCCCTATCCGTCAACACTGGAGAGCCGGCTTCCATGT CCTGCAGGTCCAGTCAGAGACTCCTGCATAGTAATGGGAACACCTATTTGCATTGGTACTTGCA GAAGCCGGGCCAGTCTCCACAGCTCCTGATCTATGAGTTTCCAACCGGGCCTCTGGAGTCCC TGACAGGTTTCAGTGGCAGTGGGTGAGGACTGATTTACCCCTGAGAATCAGCCGGGTGGAGG CTGAGGATGTTGGGATTTATTACTGCGAACAAAGTCTACACATTCGCGCACTTTTCGGCGGAGG GACCAAGGTGGATATCAAA
2 4 J 9	A 1 2 N 0 7 4 A	CAGGTGCAGCTGCAGGAGTGGGGCCAGGACTAGTGAAGCCTTTGGAGACCCTGTCCCTCAC CTGCACTGTCTCTGGTGGCTCTATCAGCAGTAACACTGGAGTTGGATCCGCCAGCCCCCAGG AAAGGGACTGGAATGGATTGGATATATCTATGGCAGTGGTGGGAGCACCGACAGCAACCCCTC CCTCAAGAGTCGAGTACCCTGTGAGTGGACAGTCCAAGAACCAGTTCTCCCTGAGGTTGAG TTCTGTGACCGCCGCGGACACGGCCGTCTATTACTGTGCGAGAGATCGCCATTACAATGTCTG GACTGGGTACCCATATTACGCTCTGGATACCTGGGGCCAAGGGGTGCTCGTACCCTCTCATC	CAGGCTGCCCCGACTCAGCCTCCCTCTGTGTCCGGGCCCTCCTGGACAGTCGGTACCATCTCC TGACTGGAACCAACAGTGATATTGGGTATTTAATGCTGTGTCTTGGTACCAGCAGCGTCCAG GCGAAGCCCCAAACTCATGATTCATGAGGTCACTAAGCGGCCCTCAGGGGTCTCTGGTCGCT TCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGAATGAGGATG AGGTTGATTATTACTGCAGCTCATATGCAGGCGACAATACTCTCATATTCGGCGGAGGGACCCG GCTGACCGTCTCTG
2 4 C 6	A 1 2 N 0 7 4	CAGGTGCAGCTACAGGAGTGGGGCCAGCAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCAC CTGCGCTGTCTCTGGTGGCTCCATCAGCAGTAGTAGTTGGTGGAACTGGATCCGCCAGTCCCC AGGGCAGGGGCTGGAATGGATTGGGGGTATCCATGGTAGTGCTGGAAACACCAATAACAACC CCTCCCTCAAGAGTCGAGCCACCATTTCAAGAGACGCGTCCAAGAACCAGTTCTCCCTGAAGG TGAACATGTGACCGCCGCGGACACCGCCGTGATTACTGTGCGAGACGCCCCCCAGTTTTTA TAACTGGAAGTGCAGGCTTTGACTACTGGGGCCAGGGAGTCTGATACCCTCTCCTCA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGAGACAGAGTCACCATCA CTTGTCCGGCAAGTCAGGGCATTAGAAGTTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAG CCCCAACCCTCCTGATCTATAAGGCATCCACTTTGCAAAGTGGGGTCCCATCAAGTTTCAGCGG CAGTGGATCTGGGACAGATTTCACTCTCACCATCAGTAGCCTGCAGCCTGAAGATTTTGAAC TATTACTGTCAACAGCATATTAGTGACCCGTACAGTTTTGGCCAGGGGACCAAGTGGAGATCA AA
2 4 E 1 7	A 1 2 N 0 7 4	CAGGTACCTTGAAGGAGTCTGGTCTGCGCTCGTGAAGCCACACAGACCCTCACGCTGACC TGCACCTTCTCTGGGTTCTCACTACCACTTCTGCAACAGGTGTGGGCTGGATCCGTACGCC CCAGGGAAAGGCCCTGGAATGGCTTGCCAGCGTTTTTTGGAGTGATAATAAATACTACATCACAT CGATGAAGAGCAGGCTCACCATCTCCAAGGACACCTCCAAAACCAGGTGGTTCTAAGAATGA CAAACATGGACCCTATGGACACAGCCACATATTACTGTGACCGGATAATAGCGGGAGCTACGC GATGGTACGGTTTGGATTCTGGGGCCAAGGGGTGCTCGTCAATTGTCTCCTCA	GAAGTTGTAATGACGCAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAACAGCCACCCTCT CCTGCAGGGCCAGTGAGAGTATTGGCAGCGACTTAGCCTGGTCCAGCAGAAACCTGGGCAG GCTCCCAAGCTCCTTGTCCGTGGTACATACTTCAGGGCCACTGGCATCCAGACAGGTTTCAGT GGCAGCGGGTCTGGGACAGAGTTCACTCTCACCATTAACAGCCTGGAGCCTGAAGATGTTGGA GTTTATCACTGTGAGCAGTATAATGACTTGCTGTTCACTTTTCGGCGGAGGGACAGGGTGGAG CTCAAA
2 4 D 2 2	A 1 2 N 0 7 4	GAAGTGCAGCTGGTGCAGTCTGGATCAGAGGTGAAAAGGCCCGGGGAGTCTCTGACGATCTC CTGCCAGACTTCTGGATACACCTTACCGACAATTGGATCAATTGGGTGCGCCAGCTGCCCGG GAGAGGCCTAGAGTGGATGGGGAGCATCTATCCTGGTATTCTGATACGAGATAACAACCCGTC CTTCCAAGGCCACGTCACTATCTCAGCCGACAAGTCCATCGGCGCCACCTACCTGCAGTGGGA CCGCCCTGAGGGCCTCGGACACCGCCACATACTATTGTGCTGCCAGGCCTGTCGTGATGATGG CTGTTCTTACACTTTGACTGGTGGGGCCAGGGAGTCTGGTACCCTCTCCCA	CAGTCTGTGCTGACGCAGCCGCCCTCAACATCTGGGGCCCCCGGGCAGAGGGTACCATCTC CTGCACTGGGAGTAGTTCCAACATCGGGGCGAATCATTATGTTTCTGGTACCACAGTTCCCA GGAACAGCCCCCAAAGTCCCTCATCTTTGAAAATACTGAGCGACCCTCAGGGGTCTCTGGCCGA TTCTCTGGCTCCAAGTCTGGTACCTCAGCCTCCCTGACCATCACTGGACTCCAATCTGAGGATG AGGCTGATTATTACTGCTCAGCATGGGATAGCAGCCTCAATTTTTCAGATATTCGGCGGAGGGAC CCGGCTGACCGTCTCA



**Table S4. Additional extended multiclade virus panel neutralization for NAb 12C11.**

Virus ID	Clade*	Titer in TZM.bl cells (ug/ml)	
		12C11	
		IC50	IC80
6535.3	B	>100	>100
QH0692.42	B	>100	>100
SC422661.8	B	>100	>100
PVO.4	B	>100	>100
TRO.11	B	>100	>100
AC10.0.29	B	>100	>100
RHPA4259.7	B	>100	>100
THRO4156.18	B	>100	>100
REJO4541.67	B	>100	>100
TRJO4551.58	B	>100	>100
WITO4160.33	B	>100	>100
CAAN5342.A2	B	>100	>100
WEAU_d15_410_787	B (T/F)	>100	>100
1006_11_C3_1601	B (T/F)	>100	>100
1054_07_TC4_1499	B (T/F)	>100	>100
1056_10_TA11_1826	B (T/F)	>100	>100
1012_11_TC21_3257	B (T/F)	>100	>100
6240_08_TA5_4622	B (T/F)	>100	>100
6244_13_B5_4576	B (T/F)	>100	>100
62357_14_D3_4589	B (T/F)	>100	>100
SC05_8C11_2344	B (T/F)	>100	>100
Du156.12	C	>100	>100
Du172.17	C	>100	>100
Du422.1	C	>100	>100
ZM197M.PB7	C	>100	>100
ZM214M.PL15	C	>100	>100
ZM233M.PB6	C	>100	>100
ZM249M.PL1	C	>100	>100
ZM53M.PB12	C	>100	>100
ZM109F.PB4	C	<b>42.850</b>	>100
ZM135M.PL10a	C	>100	>100
CAP45.2.00.G3	C	>100	>100
CAP210.2.00.E8	C	>100	>100
HIV-001428-2.42	C	>100	>100
HIV-0013095-2.11	C	>100	>100
HIV-16055-2.3	C	<b>56.950</b>	>100
HIV-16845-2.22	C	>100	>100
Ce1086_B2	C (T/F)	<b>65.038</b>	>100
Ce0393_C3	C (T/F)	<b>58.964</b>	>100
Ce1176_A3	C (T/F)	>100	>100
Ce2010_F5	C (T/F)	>100	>100
Ce0682_E4	C (T/F)	>100	>100
Ce1172_H1	C (T/F)	>100	>100
Ce2060_G9	C (T/F)	>100	>100
Ce703010054_2A2	C (T/F)	>100	>100
BF1266.431a	C (T/F)	>100	>100

246F C1G	C (T/F)	>100	>100
249M B10	C (T/F)	<b>90.726</b>	>100
ZM247v1(Rev-)	C (T/F)	>100	>100
7030102001E5(Rev-)	C (T/F)	>100	>100
1394C9G1(Rev-)	C (T/F)	<b>29.523</b>	>100
Ce704809221_1B3	C (T/F)	>100	>100
CNE19	BC	<b>22.815</b>	>100
CNE20	BC	>100	>100
CNE21	BC	>100	>100
CNE17	BC	>100	>100
CNE30	BC	>100	>100
CNE52	BC	>100	>100
CNE53	BC	>100	>100
CNE58	BC	<b>2.605</b>	<b>13.351</b>
MS208.A1	A	>100	>100
Q23.17	A	>100	>100
Q461.e2	A	>100	>100
Q769.d22	A	<b>1.786</b>	<b>6.399</b>
Q259.d2.17	A	>100	>100
Q842.d12	A	<b>52.758</b>	>100
0260.v5.c36	A	>100	>100
3415.v1.c1	A	>100	>100
3365.v2.c2	A	>100	>100
191955_A11	A (T/F)	>100	>100
191084 B7-19	A (T/F)	<b>20.210</b>	<b>80.854</b>
9004SS_A3_4	A (T/F)	>100	>100
T257-31	CRF02_AG	>100	>100
928-28	CRF02_AG	>100	>100
263-8	CRF02_AG	>100	>100
T250-4	CRF02_AG	>100	>100
T251-18	CRF02_AG	>100	>100
T278-50	CRF02_AG	>100	>100
T255-34	CRF02_AG	>100	>100
211-9	CRF02_AG	>100	>100
235-47	CRF02_AG	>100	>100
620345.c01	CRF01_AE	>100	>100
CNE8	CRF01_AE	>100	>100
C1080.c03	CRF01_AE	>100	>100
R2184.c04	CRF01_AE	>100	>100
R1166.c01	CRF01_AE	>100	>100
R3265.c06	CRF01_AE	>100	>100
C2101.c01	CRF01_AE	>100	>100
C3347.c11	CRF01_AE	>100	>100
C4118.c09	CRF01_AE	>100	>100
CNE5	CRF01_AE	>100	>100
BJOX009000.02.4	CRF01_AE	>100	>100
BJOX015000.11.5	CRF01_AE (T/F)	>100	>100

BJOX010000.06.2	CRF01_AE (T/F)	>100	>100
BJOX025000.01.1	CRF01_AE (T/F)	>100	>100
BJOX028000.10.3	CRF01_AE (T/F)	>100	>100
X1193_c1	G	>100	>100
P0402_c2_11	G	<b>29.342</b>	<b>87.411</b>
X1254_c3	G	>100	>100
X2088_c9	G	>100	>100
X2131_C1_B5	G	>100	>100
P1981_C5_3	G	>100	>100
X1632_S2_B10	G	<b>27.006</b>	>100
3016.v5.c45	D	>100	>100
A07412M1.vrc12	D	>100	>100
231965.c01	D	>100	>100
231966.c02	D	>100	>100
6405.v4.c34	D	>100	>100
3817.v2.c59	CD	>100	>100
6480.v4.c25	CD	<b>9.025</b>	<b>53.006</b>
6952.v1.c20	CD	>100	>100
6811.v7.c18	CD	<b>32.440</b>	>100
89-F1_2_25	CD	>100	>100
3301.v1.c24	AC	>100	>100
6041.v3.c23	AC	>100	>100
6540.v4.c1	AC	>100	>100
6545.v4.c1	AC	>100	>100
0815.v3.c3	ACD	>100	>100
3103.v3.c10	ACD	>100	>100
MuLV	Neg. Control	>100	>100

**Table S5. CryoEM data collection, processing and model building statistics.**

Map	GT1.1 + 12C11 + RM20A3	GT1.1 + 21N13 + 21M20 + RM20A3
EMDB	EMD-40796	EMD-40797
<b>Data collection</b>		
Microscope	TFS Glacios	TFS Glacios
Voltage (kV)	200	200
Detector	TFS Falcon 4	TFS Falcon 4
Recording mode	Counting	Counting
Nominal magnification	190,000x	190,000x
Movie micrograph pixelsize (Å)	0.725	0.725
Number of frames (Falcon 4 EER fractions)	40	40
Total dose (e <sup>-</sup> /Å <sup>2</sup> )	40	40
Defocus range (µm)	-0.5 to -1.8	-0.5 to -1.8
<b>EM data processing</b>		
Number of movie micrographs	9,459	9,547
Number of molecular projection images in map	456,166	242,098
Symmetry	C3	C1
Map pixel size	1.009	1.044
Map resolution (FSC 0.143; Å)	2.8	2.9
Map sharpening B-factor (Å <sup>2</sup> )	-104.1	-70.7
<b>Structure building and validation</b>		
<i>Composition</i>		
Atoms	24,819	26,323
Residues (protein)	3,099	3,303
Residues (ligands)	60	47
MolProbity score	0.99	1.08
Clashscore	1.76	2.93
Map correlation coefficient (mask)	0.75	0.82
EMRinger score	4.35	4.31
d FSC model (0.5; Å)	2.9	3.0
<i>RMSD from ideal</i>		
Bond length (Å)	0.006	0.007
Bond angles (°)	1.332	1.142
<i>Ramachandran plot</i>		
Favored (%)	97.73	98.08
Allowed (%)	2.27	1.92
Outliers (%)	0.00	0.00
Side chain rotamer outliers (%)	0.19	0.14
Cβ outliers (%)	0.00	0.00
PDB	8sw3	8sw4

**Table S6. X-ray data collection and refinement statistics**

	21N13 Fab	21N13 Fab +BG505 + 35O22 scFv
<b>Data Collection</b>		
Beamline	APS-23ID-D	SSRL12-1
<b>Resolution (Å)</b>	47.68-2.50 (2.54-2.50)	43.63-4.70 (4.78-4.70)
Wavelength, Å	1.0332	0.9795
Space group	C 1 2 1	P2 <sub>1</sub> 3
Unit cell a, b, c (Å)	260.5 45.2 84.6	265.4 265.4 265.4
$\alpha, \beta, \gamma$ (°)	90 98.5 90	90 90 90
Copies per ASU	2	1
Completeness	99.9 (99.9)	100.0 (100.0)
Redundancy	6.1 (5.8)	40.3 (35.3)
No. total reflections	213,542	1,319,858
No. unique reflections	34,904 (1698)	32,727(1623)
I/ $\sigma$	8.9 (3.2)	14.2 (1.0)
R <sub>sym</sub>	0.34 (1.7)	0.35 (4.2)
R <sub>pim</sub>	0.15 (0.75)	0.06 (0.71)
CC1/2	0.83 (0.35)	0.99 (0.30)
<b>Refinement Statistics</b>		
Resolution (Å)	47.68-2.46 (2.53-2.50)	43.63-4.69 (4.83-4.70)
No. reflections total/Rfree	33,176 / 1711	31,038 /1733
R <sub>cryst</sub>	18.2 (23.8)	28.4 (36.9)
R <sub>free</sub>	22.0 (29.6)	30.5 (37.1)
RMSD bond length (Å)	0.007	0.04
RMSD bond angles (°)	0.96	0.61
Number of atoms		
All proteins	6544	11435
21N13 Fab	6544	3358
35O22 scFv	/	1839
gp120	/	3587
gp41	/	1166
Water	383	/
Glycan	/	705
Average B-value (Å <sup>2</sup> )		
All proteins	27	302
21N13 Fab	27	287
35O22 scFv	/	322
gp120	/	303
gp41	/	306
Water	29	/
Glycan	/	373

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Wilson B-value (Å <sup>2</sup> )	25	249
Ramachandran Favored%	98.1	95.1
Ramachandran Outliers%	0	0
PDB	8D01	8D0Y

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