

Supplemental Experimental Procedures

Recombinant Protein Expression and Purification

BiNAbs were generated using previously described approaches (Merchant et al., 1998; Ridgway et al., 1996; Schaefer et al., 2011). For correct heavy-light chain pairing, one of the parental mAbs was expressed in the CrossMab format (CH1-CL swapping), while for the other mAb, the wild-type domain architecture was maintained (Schaefer et al., 2011). For heavy chain heterodimerization, point mutations were introduced in the CH3 domain: Y349C/T366S/L368A/Y407V for the 1st mAb; S354C/T366W for the 2nd mAb (Merchant et al., 1998; Ridgway et al., 1996). Purification tags were added to the C terminus of each heavy chain (His or Strep-TagII) for determining heterodimer formation efficiency. Antibodies, gp140^{YU-2}, gp120^{YU-2}, and 2CC-core were generated by transient transfection of HEK293T or 293E cells, as previously described (Bournazos et al., 2014). Antibodies were purified using Protein G Sepharose 4 Fast Flow or MabSelect SuRe LX affinity purification media (GE Healthcare); Strep-tagged and His-tagged proteins were purified using the Strep-Tactin Superflow Plus Resin (Qiagen) and His-Tag isolation and pull-down dynabeads (ThermoFisher), respectively. Purified proteins were dialyzed in PBS and sterile filtered (0.22 µm). Purity was assessed by SDS-PAGE and Coomassie staining and was estimated to be >90%. Size exclusion chromatography (SEC) was performed using a Superose 6 Increase 10/300GL column (GE Healthcare) on an Äkta Pure 25 HPLC system. Protein Tm was determined using the Protein Thermal Shift Dye Kit (ThermoFisher) following manufacturer's instructions on a QuantStudio 12K Flex real-time thermal cycler.

In Vitro Neutralization Assay

In vitro neutralization activity of antibodies was assessed against a multiclade panel of HIV-1 envelope pseudoviruses, using previously described protocols (Montefiori, 2005). Neutralization assays were performed by the Collaboration for AIDS Vaccine Discovery (CAVD) core neutralization facility (Harvard University, Boston). IC₅₀ and IC₈₀ values reflect the amount of antibody sufficient to reduce luciferase activity (as measured by relative luminescence units (RLU)) by 50% and 80%, respectively. For comparison of the activity of biNAbs with the corresponding parental mAbs, fold change values were calculated by dividing the IC₅₀ or IC₈₀ titer of the most potent (lowest IC_{50/80}) of the two parental mAbs by the IC_{50/80} titer of the biNAb. Predicted neutralization activity of a mix of two mAbs was determined by selecting the lowest IC_{50/80} titer of the two mAbs for a given virus. For combinations involving 2 mAbs with non-overlapping epitope specificities, this predicted activity (theoretical IC_{50/80}) has been shown to be comparable to the neutralization activity of a 1:1 mAb mix determined experimentally (experimental IC_{50/80}) (Kong et al., 2015). Neutralization activity data of human IgG1 mAbs that were used for comparison in this study were obtained from the CATNAP database (<http://www.hiv.lanl.gov/>). For experiments involving the assessment of the *in vitro* neutralization activity of a mix of two bNAbs, antibodies were mixed at a ratio of 1:1 and the final concentration for determining IC_{50/80} titers was based on the total IgG concentration of the sample.

Anti-gp140 IgG ELISA

For epitope-specific ELISA, gp140^{YU-2}- or 2CC-Core-coated (1 µg/ml) microtiter plates (Nunc) were used, as previously described (Bournazos et al., 2014). Briefly, recombinant gp140^{YU-2}- or 2CC-Core (1 µg/ml) was immobilized into high-binding 96-well microtiter plates (Nunc) and following overnight incubation at 4°C, plates were blocked with PBS + 2% (w/v) BSA + 0.05% (v/v) Tween20 for 2 h. After blocking, plates were incubated for 1 h with IgG antibodies and plate-bound IgG was detected by HRP-conjugated goat anti-human IgG (Fcγ-specific, Jackson Immunoresearch), or goat anti-human kappa or lambda (Bethyl Laboratories). Plates were developed using the TMB (3,3',5,5'-Tetramethylbenzidine) two-component peroxidase substrate

kit (KPL) and reactions stopped with the addition of 1 M phosphoric acid. Absorbance at 450nm was immediately recorded using a SpectraMax Plus spectrophotometer (Molecular Devices) and background absorbance from negative control samples was subtracted. For competition ELISA, binding of biotinylated biNAb (1 µg/ml) to gp140-coated plates was competed with increasing amounts of mAbs, mAb mix (1:1) or biNAb (0.001-100 µg/ml), and detected using HRP-conjugated neutravidin (ThermoFisher). For the quantification of serum concentration of anti-HIV-1 mAbs, goat anti-human IgG (mouse IgG absorbed, Jackson Immunoresearch)-coated or gp140-coated plates were used (Bournazos et al., 2014). IgG binding was detected using HRP-conjugated goat anti-human IgG (mouse IgG absorbed; Jackson Immunoresearch), as previously described (Bournazos et al., 2014).

Surface Plasmon Resonance (SPR)

All experiments were performed with a Biacore T200 SPR system (Biacore, GE Healthcare) at 25°C in HBS-EP+ buffer (10 mM HEPES, pH 7.4; 150 mM NaCl; 3.4 mM EDTA; 0.005% (v/v) surfactant P20). For the measurement of the affinity of IgG hinge domain variants for mouse and human FcγRs, IgG antibodies (diluted at 25 µg/ml in 10 mM sodium acetate, pH 4.5) were immobilized on Series S CM5 chips by amine coupling at a density of 1000 RU. Recombinant human or mouse soluble FcγR ectodomains (Sinobiological) were injected through flow cells at a flow rate of 20 µl/min, with the concentration ranging from 15.625 – 2000 nM (1:2 successive dilutions). Association time was 120 s followed by a 300-s dissociation step. At the end of each cycle, sensor surface was regenerated with 50 mM NaOH (50 µl/min, 30 s). Background binding to blank immobilized flow cells was subtracted and affinity constants were calculated using BIACore T200 evaluation software (GE Healthcare) using the 1:1 Langmuir binding model.

Virus Production

HIV-1^{T251-18} was generated by cloning the T251-18 env gene (CRF02_AG; NIH AIDS Reagent program) to the NL4-3 HIV-1 vector backbone and produced by transfection in 293T cells, as previously described (Klein et al., 2012). HIV-1 virus preparations were quantified by p24 ELISA (Lenti-X p24 Rapid Titer Kit, Clontech), following manufacturer's recommendations.

In Vivo Experiments

All *in vivo* experiments were performed in compliance with federal laws and institutional guidelines and have been approved by the Rockefeller University Institutional Animal Care and Use Committee. Humanized NRG (NOD.Cg-Rag1^{tm1Mom}/I2rg^{tm1Wjl}/SzJ) mice were generated by intrahepatic human CD34⁺ HSCs injection of sublethally irradiated neonatal NRG mice, as previously described (Klein et al., 2012). Mice were screened at 6-8 wk of age for human leukocyte reconstitution by flow cytometry (as described in (Bournazos et al., 2014; Klein et al., 2012)) and mice with a measurable human CD45⁺ graft (10-15 weeks, males and females) were infected following i.p. injection of HIV-1^{T251-18} (180 ng p24). Viral load was quantified 3 weeks post-infection and mice with viral loads >10³ copies/ml were included in treatment experiments. Mice were randomly assigned to experimental groups and both groups had comparable baseline average viremia levels. Antibodies (either 1 mg of 3BNC117/PGT135 biNAb or 1 mg 1:1 mix of 3BNC117 (0.5 mg) and PGT135 (0.5mg)) were administered biweekly s.c. for 4 weeks. Each experimental group consisted of 9 mice; a group size previously determined to sufficiently detect response to antibody therapy (Bournazos et al., 2014; Klein et al., 2012). Plasma HIV-1 viral load was determined by quantitative reverse-transcriptase PCR as previously described (Bournazos et al., 2014; Klein et al., 2012). The lower limit of detection for this assay was previously determined to be 800 copies/ml (Klein et al., 2012).

HIV gp120 Sequence Analysis

Plasma-extracted viral RNA was reverse transcribed using the Superscript III first strand cDNA synthesis kit (Life Technologies) and the gp120 sequence-specific primer 5'-TAGCAATAGTTGTGGTCC-3'. Resulting cDNA was used as the template for PCR amplification using the following primer pairs: 5'-TAGCAATAGTTGTGGTCC-3' and 5'-ATTGCTCTGCTGTTGCACTATAC-3'. Products from this PCR reaction were subjected to a second PCR round using the following nested primer pairs: 5'-AGAAAGAGCAGAAGACAGTGGC-3' and 5'-TACCGTCAGCGTCATTGACGC-3'. All PCR reactions were performed using the Platinum *Taq* High Fidelity DNA polymerase (ThermoFisher) and PCR amplicons were ligated into pCR4-TOPO vectors. Inserts from individual colonies were sequenced (Genewiz) using M13F (5'-TGTAAAACGACGCCAGT-3'), M13R (5'-CAGGAAACAGCTATGAC-3'), and gp120-specific primers (5'-GTCTGGGCTACACATGCCTGC-3'; 5'-CCATGCAAAATGTCAGCACA-3'; 5'-GATGATATAACTCTCCAATGCAG-3'). Sequence reads were aligned to gp120^{T251-18} and mutations were numbered using HXBc2 numbering. To determine the presence of mutations within the gp120 ORF following bNAb therapy, virus gp120 was cloned from each mouse from plasma-extracted viral RNA obtained at the last experimental time point. Non-synonymous mutations present in the majority (>50%) of the analyzed clones (6-8 clones/mouse) were defined as recurrent mutations. Mice with evidence for recurrent mutations were further analyzed to determine viral gp120 sequence at baseline (i.e. prior to treatment initiation) to assess whether the observed mutations emerged following antibody treatment.

Supplemental Tables

Table S1: Comparison of the *in vitro* neutralization activity of human IgG1 3BNC117 and 10-1074 mAbs and 3BNC117/10-1074 biNAb. *Related to Figure 1.*

Virus ID	Clade	3BNC117	10-1074	3BNC117 /10-1074	log Fold Change	Virus ID	Clade	3BNC117	10-1074	3BNC117 /10-1074	log Fold Change
6535.3	B	0.303	0.013	0.083	-0.805	Q769.d22	A	0.008	>20	0.028	-0.524
QH0692.42	B	0.238	0.073	0.282	-0.587	Q259.d2.17	A	0.016	11.912	0.359	-1.357
SC422661.8	B	0.045	0.072	0.108	-0.381	Q842.d12	A	0.002	12.812	0.019	-0.899
PVO.4	B	0.076	0.074	0.067	-0.043	0260.v5.c36	A	0.200	0.201	0.312	-0.193
TRO.11	B	0.062	0.014	0.060	-0.632	3415.v1.c1	A	0.115	>20	0.224	-0.291
AC10.0.29	B	7.028	0.037	0.248	-0.826	3365.v2.c2	A	0.015	0.160	0.066	-0.633
RHPA4259.7	B	0.026	0.049	0.030	-0.059	191955.A11	A (T/F)	>20	>20	>20	ND
THRO4156.18	B	2.552	>20	7.226	-0.452	191084.B7-19	A (T/F)	0.070	0.057	0.121	-0.327
REJO4541.67	B	0.030	>20	0.129	-0.635	9004SS.A3.4	A (T/F)	0.070	0.015	0.068	-0.656
TRJO4551.58	B	0.059	0.459	0.270	-0.661	T257-31	CRF02 AG	0.125	>20	0.369	-0.469
WITO4160.33	B	0.024	0.139	0.066	-0.438	928-28	CRF02 AG	0.153	1.911	0.424	-0.442
CAAN5342.A2	B	0.612	0.014	0.115	-0.915	263-8	CRF02 AG	0.028	0.793	0.053	-0.276
YU2.DG	B	0.034	0.110	0.037	-0.038	T250-4	CRF02 AG	>20	0.002	0.040	-1.301
WEAU_d15_410_787	B (T/F)	0.050	0.035	0.107	-0.485	T251-18	CRF02 AG	0.220	1.011	0.455	-0.315
1006_11_C3_1601	B (T/F)	0.030	0.001	0.018	-1.255	T278-50	CRF02 AG	>20	7.477	>20	-0.427
1054_07_TC4_1499	B (T/F)	0.070	0.113	0.177	-0.403	T255-34	CRF02 AG	0.037	>20	0.186	-0.697
1056_10_TA11_1826	B (T/F)	0.300	0.072	0.240	-0.523	211-9	CRF02 AG	0.350	0.203	0.680	-0.525
1012_11_TC21_3257	B (T/F)	0.020	0.023	0.029	-0.161	235-47	CRF02 AG	0.024	0.092	0.114	-0.670
6240_08_TA5_4622	B (T/F)	0.330	0.087	0.225	-0.413	620345.c01	CRF01 AE	>20	>20	>20	ND
6244_13_BS_4576	B (T/F)	0.040	0.197	0.107	-0.427	CNE8	CRF01 AE	0.026	>20	0.406	-1.194
62357_14_D3_4589	B (T/F)	0.060	>20	0.120	-0.301	C1080.c03	CRF01 AE	0.123	>20	0.400	-0.511
SC05_8C11_2344	B (T/F)	0.150	0.037	0.178	-0.682	R2184.c04	CRF01 AE	0.033	>20	0.062	-0.271
Du156.12	C	0.032	0.014	0.059	-0.625	R1166.c01	CRF01 AE	0.208	>20	0.354	-0.231
Du172.17	C	0.263	0.087	0.344	-0.597	R3265.c06	CRF01 AE	0.058	>20	3.613	-1.797
Du422.1	C	>20	0.082	0.964	-1.070	C2101.c01	CRF01 AE	0.059	>20	0.131	-0.347
ZM197M.PB7	C	0.354	>20	1.185	-0.525	C3347.c11	CRF01 AE	0.029	>20	0.077	-0.419
ZM214M.PL15	C	0.082	0.590	0.299	-0.562	C4118.c09	CRF01 AE	0.032	>20	0.462	-1.161
ZM233M.PB6	C	0.181	0.095	0.314	-0.519	CNE5	CRF01 AE	0.347	>20	1.950	-0.750
ZM249M.PL1	C	0.037	>20	0.224	-0.780	BJOX009000.02.4	CRF01 AE	0.400	>20	2.557	-0.806
ZM53M.PB12	C	0.212	>20	0.811	-0.584	BJOX015000.11.5	CRF01 AE (T/F)	0.050	>20	0.589	-1.071
ZM109P.PB4	C	0.052	>20	2.252	-1.635	BJOX010000.06.2	CRF01 AE (T/F)	1.580	>20	12.713	-0.906
ZM135M.PL10a	C	0.058	0.146	0.183	-0.502	BJOX025000.01.1	CRF01 AE (T/F)	0.050	>20	0.286	-0.757
CAP45.2.00.G3	C	1.399	>20	>20	-1.155	BJOX028000.10.3	CRF01 AE (T/F)	0.010	>20	0.044	-0.643
CAP210.2.00.E8	C	9.713	>20	>20	-0.314	X1193_c1	G	0.060	0.091	0.181	-0.480
HIV-001428-2.42	C	0.017	0.055	0.029	-0.229	P0402_c2.11	G	0.060	0.011	0.036	-0.515
HIV-0013095-2.11	C	0.243	>20	4.045	-1.222	X1254_c3	G	0.080	0.162	0.320	-0.602
HIV-16055-2.3	C	3.888	>20	>20	-0.711	X2088_c9	G	>20	0.004	0.126	-1.498
HIV-16845-2.22	C	>20	1.930	4.447	-0.363	X2131_C1_B5	G	0.430	0.023	0.171	-0.871
Ce1086_B2	C (T/F)	0.090	>50	1.722	-1.282	P1981_C5_3	G	0.740	0.005	0.077	-1.188
Ce0393_C3	C (T/F)	0.200	>50	0.916	-0.661	X1632_S2_B10	G	15.690	>20	>20	-0.105
Ce1176_A3	C (T/F)	0.220	0.022	0.211	-0.982	3016.v5.c45	D	0.834	>20	17.306	-1.317
Ce2010_F5	C (T/F)	0.050	>20	0.288	-0.760	A07412M1.vrc12	D	0.020	0.014	0.104	-0.871
Ce0682_E4	C (T/F)	0.030	>20	0.077	-0.409	231965.c01	D	0.039	>20	0.275	-0.844
Ce1177_H1	C (T/F)	>20	0.022	0.454	-1.315	231966.c02	D	0.290	>20	4.740	-1.213
Ce2060_G9	C (T/F)	0.240	>20	0.359	-0.175	191821_E6_1	D (T/F)	0.090	>20	0.902	-1.001
Ce703010054_A22	C (T/F)	0.370	>20	1.710	-0.665	3817.v2.c59	CD	0.191	1.151	0.916	-0.680
BF1266.431a	C (T/F)	0.030	>20	0.358	-1.077	6480.v4.c25	CD	0.010	0.005	0.034	-0.833
246F_C1G	C (T/F)	19.320	0.055	0.640	-1.066	6952.v1.c20	CD	0.150	0.030	0.251	-0.923
249M_B10	C (T/F)	0.100	>20	0.355	-0.550	6811.v7.c18	CD	0.030	0.002	0.029	-1.161
ZM247v1(Rev-)	C (T/F)	>20	0.060	1.538	-1.409	89-F1_2_25	CD	>20	>20	>20	ND
7030102001E5(Rev-)	C (T/F)	0.290	0.010	0.127	-1.104	3301.v1.c24	AC	0.028	0.020	0.066	-0.519
1394C9G1(Rev-)	C (T/F)	>20	0.038	0.592	-1.193	6041.v3.c23	AC	0.010	>20	0.197	-1.294
Ce704809221_1B3	C (T/F)	0.080	0.102	0.357	-0.650	6540.v4.c1	AC	>20	>20	>20	ND
CNE19	BC	0.020	0.344	0.124	-0.792	6545.v4.c1	AC	>20	>20	>20	ND
CNE20	BC	>20	0.001	0.054	-1.732	0815.v3.c3	ACD	0.015	0.088	0.029	-0.292
CNE21	BC	>20	0.049	0.548	-1.049	3103.v3.c10	ACD	0.220	0.041	0.265	-0.810
CNE17	BC	5.760	1.993	3.337	-0.224	Total Viruses		120	120	120	
CNE30	BC	0.280	0.353	0.772	-0.440	%Breadth		87.5	58.3	91.7	
CNE52	BC	0.020	1.711	0.174	-0.940	Geometric mean		0.103	0.071	0.242	
CNE53	BC	0.059	0.023	0.128	-0.745						
CNE58	BC	0.336	0.137	0.364	-0.424						
MS208.A1	A	0.016	>20	0.200	-1.092						
Q23.17	A	0.016	0.006	0.020	-0.523						
Q461.e2	A	0.059	>20	0.167	-0.455						

In vitro neutralization activity was determined by standardized TZM-bl assay.

IC₅₀ values are expressed as µg/ml.

Fold change values were calculated by dividing the IC₅₀ titer of the most potent (lowest IC₅₀) of the two parental mAbs (3BNC117 or 10-1074) by the IC₅₀ titer of the biNAb (3BNC117/10-1074).

ND: not determined

Table S2: Comparison of the *in vitro* neutralization activity of human IgG1 PG16 and PGT121 mAbs and PG16/PGT121 biNAb. *Related to Figure 2.*

Virus ID	Clade	PG16	PGT121	PG16/ PGT121	log Fold Change	Virus ID	Clade	PG16	PGT121	PG16/ PGT121	log Fold Change
6535.3	B	0.653	0.008	1.333	-2.222	MS208 A1	A	0.002	>50	0.052	-1.415
QH0692.42	B	>50	1.041	>40	-1.585	Q23.17	A	0.008	0.01	0.001	0.903
SC422661.8	B	0.858	0.101	14.791	-2.166	Q461.e2	A	1.755	>50	5.863	-0.524
PVO.4	B	15.272	0.131	6.705	-1.709	Q769.d22	A	0.005	>50	0.176	-1.547
TRO.11	B	1.922	0.005	0.699	-2.146	Q259.d2.17	A	0.065	8.99	0.224	-0.537
AC10.0.29	B	0.023	0.037	0.055	-0.379	Q842.d12	A	0.032	0.023	0.023	0.000
RHPA4259.7	B	0.375	0.014	1.303	-1.969	Q260.v5.c36	A	1.538	0.054	0.817	-1.180
THRO4156.18	B	6.825	>50	10.836	-0.201	191955_A11	A (T/F)	0.009	>50	0.022	-0.388
REJO4541.67	B	0.039	3.607	0.091	-0.368	191084_BT-19	A (T/F)	0.024	0.042	0.034	-0.151
TRJO4551.58	B	1.008	3.728	4.837	-0.681	9004SS_A3_4	A (T/F)	0.020	0.008	0.026	-0.512
WITO4160.33	B	0.002	0.459	0.007	-0.544	T257-31	CRF02 AG	0.007	>50	0.017	-0.385
CAAN5342.A2	B	1.831	0.011	2.507	-2.358	928-28	CRF02 AG	0.034	>50	0.090	-0.423
YU2.DG	B	0.055	0.047	0.414	-0.946	263-8	CRF02 AG	0.347	3.347	0.531	-0.185
Bal_26	B	0.163	0.014	3.266	-2.353	T250-2	CRF02 AG	0.002	0.001	0.004	-0.602
WEAU_d15_410_787	B (T/F)	0.435	0.083	1.032	-1.095	T251-18	CRF02 AG	1.721	17.702	11.345	-0.819
1006_11_C3_1601	B (T/F)	>50	0.008	1.196	-2.175	T278-50	CRF02 AG	0.227	>50	6.072	-1.427
1054_07_TC4_1499	B (T/F)	>50	0.115	>40	0.782	T255-34	CRF02 AG	0.024	6.725	0.037	-0.188
1056_10_TA11_1826	B (T/F)	0.315	0.066	1.219	-1.266	211-9	CRF02 AG	0.029	1.455	0.027	0.031
1012_11_TC21_3257	B (T/F)	0.030	0.008	0.094	-1.070	235-47	CRF02 AG	0.092	0.332	1.039	-1.053
6240_08_TA5_4622	B (T/F)	>50	0.128	18.289	-2.155	620345.c01	CRF01 AE	>50	>50	>50	ND
6244_13_B5_4576	B (T/F)	>50	0.249	>40	2.206	C1080.c03	CRF01 AE	0.001	>50	0.002	-0.301
62357_14_D3_4589	B (T/F)	>50	1.036	>40	-1.587	R2184.c04	CRF01 AE	0.670	>50	5.155	-0.886
SC05_8C11_2344	B (T/F)	0.070	0.093	0.624	-0.950	R1166.c01	CRF01 AE	0.280	>50	4.583	-1.214
Du156.12	C	0.006	0.007	0.029	-0.684	R3265.c06	CRF01 AE	0.016	>50	0.052	-0.512
Du172.17	C	0.033	0.115	0.082	-0.395	C2101.c01	CRF01 AE	0.012	>50	0.012	0.000
Du422.1	C	0.261	0.029	0.096	-0.520	C3347.c11	CRF01 AE	0.008	>50	0.019	-0.376
ZM197M.PB7	C	1.496	>50	0.592	0.403	C4118.c09	CRF01 AE	0.022	>50	0.040	-0.260
ZM214M.PL15	C	>50	0.236	>40	2.229	CNE5	CRF01 AE	0.008	>50	0.004	0.301
ZM233M.PB6	C	0.002	1.451	0.002	0.000	BJOX009000.02.4	CRF01 AE	1.188	3.626	2.032	-0.233
ZM249M.PL1	C	0.127	>50	0.049	0.414	CNE55	CRF01 AE	1.006	>50	15.160	-1.178
ZM53M.PB12	C	0.007	0.001	0.011	-1.041	BJOX150000.11.5	CRF01 AE (T/F)	3.129	>50	10.879	-0.541
ZM109F.PB4	C	7.033	7.894	>40	-0.755	BJOX010000.06.2	CRF01 AE (T/F)	1.202	>50	10.276	-0.932
ZM135M.PL10a	C	>50	0.576	17.298	-1.478	BJOX025000.01.1	CRF01 AE (T/F)	0.071	>50	0.271	-0.582
CAP45.2.00.G3	C	0.001	0.083	0.001	0.000	X1193_c1	G	0.018	0.045	0.028	-0.192
CAP210.2.00.E8	C	0.010	5.082	0.242	-1.384	P0402_c2_11	G	0.025	0.02	0.914	-1.660
HIV-001428-2.42	C	0.039	0.026	0.001	1.415	X2088_c9	G	>50	0.011	7.752	-2.848
HIV-0013095-2.11	C	0.002	>50	0.019	-0.978	X2131_C1_B5	G	0.024	0.015	0.042	-0.447
HIV-16055-2.3	C	0.17	0.444	0.008	1.327	P1981_C5_3	G	0.376	0.004	0.348	-1.940
HIV-16845-2.22	C	3.126	12.685	9.374	-0.477	X1632_S2_B10	G	0.012	>50	0.063	-0.720
Ce1086_B2	C (T/F)	>50	0.001	1.274	-3.105	3016.v5.c45	D	>50	>50	>50	ND
Ce0393_C3	C (T/F)	0.002	>50	0.006	-0.477	A07412M1.vrc12	D	0.343	0.001	1.958	-3.292
Ce1176_A3	C (T/F)	0.003	0.017	0.009	-0.477	231965.c01	D	1.438	>50	0.540	0.425
Ce0682_E4	C (T/F)	0.026	>50	0.051	-0.293	231966.c02	D	0.007	>50	0.024	-0.535
Ce1172_H1	C (T/F)	0.007	0.023	0.021	-0.477	191821_E6_1	D (T/F)	9.600	>50	>40	-0.620
Ce2060_G9	C (T/F)	0.075	>50	0.398	-0.725	3817.v2.c59	CD	0.008	>50	0.011	-0.138
Ce703010054_2A2	C (T/F)	0.008	>50	0.036	-0.653	6480.v4.c25	CD	>50	0.017	1.846	-2.036
BF1266_431a	C (T/F)	0.003	>50	0.004	-0.125	6952.v1.c20	CD	21.865	0.085	1.797	-1.325
246F_C1G	C (T/F)	>50	0.083	37.288	-2.652	6811.v7.c18	CD	>50	0.004	1.227	-2.487
249M_B10	C (T/F)	0.026	>50	0.052	-0.301	89-F1_2_25	CD	47.612	>50	>40	0.076
ZM247V1(Rev-)	C (T/F)	0.016	0.027	0.038	-0.376	3301.v1.c24	AC	0.020	0.014	0.030	-0.331
703012001E5(Rev-)	C (T/F)	>50	0.01	4.466	-2.650	6041.v3.c23	AC	0.048	>50	0.050	-0.018
1394C9G1(Rev-)	C (T/F)	0.008	0.486	0.040	-0.699	6540.v4.c1	AC	0.035	>50	0.030	0.067
Ce704809221_B3	C (T/F)	0.021	0.098	0.033	-0.196	6545.v4.c1	AC	0.044	>50	0.205	-0.668
CNE19	BC	0.024	0.018	0.057	-0.501	0815.v3.c3	ACD	>50	0.022	15.225	-2.840
CNE20	BC	3.633	0.002	0.429	-2.331	3103.v3.c10	ACD	25.391	0.042	7.101	-2.228
CNE21	BC	0.007	0.02	0.051	-0.862						
CNE17	BC	0.029	45.289	0.060	-0.316						
CNE30	BC	>50	0.101	31.101	-2.488						
CNE52	BC	>50	0.055	3.604	-1.816						
CNE53	BC	>50	0.044	>50	0.033						
CNE58	BC				0.125						
Total Viruses											
%Breadth											
Geometric mean IC50											

In vitro neutralization activity was determined by standardized TZM-bl assay.

IC₅₀ values are expressed as µg/ml.

Fold change values were calculated by dividing the IC₅₀ titer of the most potent (lowest IC₅₀) of the two parental mAbs (PG16 or PGT121) by the IC₅₀ titer of the biNAb (PG16/PGT121).

ND: not determined

Table S3: Comparison of the *in vitro* neutralization activity of human IgG1 PG16 and PGT128 mAbs and PG16/PGT128 biNAb. **Related to Figure 2.**

Virus ID	Clade	PG16	PGT128	PG16/ PGT128	log Fold Change	Virus ID	Clade	PG16	PGT128	PG16/ PGT128	log Fold Change
6535.3	B	0.653	0.004	1.288	-2.508	Q23.17	A	0.008	0.009	0.001	0.903
QH0692.42	B	>50	0.029	>40	-3.140	Q461.e2	A	1.755	>50	7.703	-0.642
SC422661.8	B	0.858	1.078	>40	-1.669	Q769.d22	A	0.005	>50	0.135	-1.431
PVO_4	B	15.272	0.011	1.820	-2.219	Q259.d2.17	A	0.065	>50	0.213	-0.515
TRO.11	B	1.922	0.019	0.646	-1.531	Q842.d12	A	0.032	0.008	0.023	-0.459
AC10.0.29	B	0.023	0.008	0.040	-0.699	Q260.v5.c36	A	1.538	0.058	0.635	-1.039
RHPA4259.7	B	0.375	0.026	0.922	-1.550	Q330.v4.c3	A	0.005	1.604	0.014	-0.447
THRO4156.18	B	6.825	>50	15.441	-0.355	191955_A11	A (T/F)	0.009	14.195	0.029	-0.508
REJO4541.67	B	0.039	>50	0.027	0.160	191084_B7-19	A (T/F)	0.024	0.022	0.032	-0.163
TRJ04160.58	B	1.008	0.018	0.356	-1.296	9004SS_A3_4	A (T/F)	0.020	0.002	0.035	-1.243
WITO4160.33	B	0.002	>50	0.006	-0.477	T257-31	CRF02_AG	0.007	>50	0.019	-0.434
CAAN5342_A2	B	1.831	0.514	5.701	-1.045	928-28	CRF02_AG	0.034	>50	0.111	-0.514
YU2.DG	B	0.055	0.030	0.350	-1.074	263-8	CRF02_AG	0.347	0.342	0.323	0.025
Bal_26	B	0.163	0.021	4.691	-2.349	T250-4	CRF02_AG	0.002	0.001	0.002	-0.301
WEAU_d15_410_787	B (T/F)	0.435	0.032	2.310	-1.858	T251-18	CRF02_AG	1.721	>50	12.683	-0.867
1006_11_C3_1601	B (T/F)	>50	0.011	6.400	-2.765	T278-50	CRF02_AG	0.227	0.031	3.104	-2.001
1054_07_TC4_1499	B (T/F)	>50	0.035	>40	-3.058	T255-34	CRF02_AG	0.024	>50	0.051	-0.327
1056_10_TA11_1826	B (T/F)	0.315	0.001	0.42	-2.623	211-9	CRF02_AG	0.029	0.062	0.033	-0.056
1012_11_TC21_3257	B (T/F)	0.030	0.011	0.094	-0.932	235-47	CRF02_AG	0.092	>50	1.006	-1.039
6240_08_TA5_4622	B (T/F)	>50	0.019	12.085	-2.803	620345.c01	CRF01_AE	>50	>50	>50	ND
S244_13_B5_4576	B (T/F)	>50	0.020	12.702	-2.803	C1080.c03	CRF01_AE	0.001	0.283	0.003	-0.477
62357_14_D3_4589	B (T/F)	>50	1.144	>40	-1.544	R2184.c04	CRF01_AE	0.670	20.056	1.738	-0.414
SC05_8C11_2344	B (T/F)	0.070	0.017	0.502	-1.470	R1166.c01	CRF01_AE	0.280	>50	5.646	-1.305
Du156.12	C	0.006	0.017	0.035	-0.766	R3265.c06	CRF01_AE	0.016	>50	0.079	-0.694
Du172.17	C	0.033	0.028	0.096	-0.535	C2101.c01	CRF01_AE	0.012	>50	0.020	-0.222
Du422.1	C	0.261	0.039	0.081	-0.317	C3347.c11	CRF01_AE	0.008	0.001	0.015	-1.176
ZM197M_PB7	C	1.496	>50	0.574	0.416	C4118.c09	CRF01_AE	0.022	>50	0.030	-0.135
ZM214M_PL15	C	>50	1.498	>40	-1.427	CNE5	CRF01_AE	0.008	0.018	0.004	0.301
ZM233M_PB6	C	0.002	>50	0.006	-0.477	BJOX0090000.02.4	CRF01_AE	1.188	0.001	0.721	-2.858
ZM249M_PL1	C	0.127	39.657	0.040	0.502	CNE55	CRF01_AE	1.006	>50	24.829	-1.392
ZM53M_PB12	C	0.007	>50	0.018	-0.410	BJOX15000.11.5	CRF01_AE (T/F)	3.129	0.001	0.591	-2.772
ZM109F_PB4	C	7.033	>50	>40	-0.755	BJOX10000.06.2	CRF01_AE (T/F)	1.202	4.817	2.695	-0.351
ZM135M_PL10a	C	>50	>50	>50	ND	BJOX25000.01.1	CRF01_AE (T/F)	0.071	>50	0.086	-0.083
CAP45.2.00.G3	C	0.001	>50	0.002	-0.301	BJOX28000.10.3	CRF01_AE (T/F)	>50	0.024	1.159	-1.684
CAP210.2.00.E8	C	0.010	>50	0.186	-1.270	X1193_c1	G	0.018	>50	0.041	-0.358
HIV-001428-2.42	C	0.039	0.026	0.002	1.114	P0402_c2_11	G	0.025	0.007	1.352	-2.286
HIV-0013095-2.11	C	0.002	>50	0.024	-1.079	X1254_c3	G	0.023	>50	0.183	-0.901
HIV-16055-2.3	C	0.17	>50	0.013	1.117	X2131_C1_B5	G	0.024	>50	0.039	-0.211
HIV-16845-2.22	C	3.126	0.181	5.096	-1.450	P1981_C5_3	G	0.376	0.019	0.544	-1.457
Ce0393_C3	C (T/F)	0.002	>50	0.009	-0.653	X1632_S2_B10	G	0.012	>50	0.074	-0.790
Ce1176_A3	C (T/F)	0.003	0.009	0.011	-0.564	3016_V5_c45	D	>50	>50	>50	ND
Ce0682_E4	C (T/F)	0.026	>50	0.080	-0.488	A07412M1.vrc2	D	0.343	>50	2.317	-0.830
Ce1172_H1	C (T/F)	0.007	0.013	0.033	-0.673	231965.c01	D	1.438	>50	0.356	0.606
Ce2060_G9	C (T/F)	0.075	>50	0.404	-0.731	231966.c02	D	0.007	3.197	0.030	-0.632
Ce703010054_2A2	C (T/F)	0.008	>50	0.029	-0.559	191821_E6_1	D (T/F)	9.6	0.010	12.870	-3.110
BF1266_431a	C (T/F)	0.003	>50	0.006	-0.301	3817_V2_c59	CD	0.008	0.003	0.013	-0.637
246F_C1G	C (T/F)	>50	0.005	>40	-3.903	6480_V4_c25	CD	>50	0.003	7.987	-3.425
249M_B10	C (T/F)	0.026	7.868	0.041	-0.198	6952_V1_c20	CD	21.865	>50	36.091	-0.218
ZM247V1(Rev-)	C (T/F)	0.016	0.021	0.035	-0.340	6811_V7_c18	CD	>50	0.003	>40	-4.125
7030102001E5(Rev-)	C (T/F)	>50	0.007	>40	-3.757	69_F1_2_25	CD	47.612	>50	>40	ND
1394C9G1(Rev-)	C (T/F)	0.008	0.011	0.042	-0.720	3301_V1_c24	AC	0.020	0.067	0.030	-0.176
Ce704809221_1B3	C (T/F)	0.021	0.026	0.027	-0.109	6041_V3_c23	AC	0.048	>50	0.100	-0.319
CNE19	BC	0.024	>50	0.052	-0.336	6540_V4_c1	AC	0.035	11.798	0.029	0.082
CNE20	BC	3.633	0.001	0.256	-2.408	6545_V4_c1	AC	0.044	>50	0.135	-0.487
CNE21	BC	0.007	0.010	0.052	-0.871	0815_V3_c3	ACD	>50	0.030	24.937	-2.920
CNE17	BC	0.029	0.432	0.061	-0.323	3103_V3_c10	ACD	25.391	0.014	5.523	-2.596
CNE30	BC	>50	2.055	>40	-1.289	Total Viruses		117	117	117	
CNE52	BC	0.009	>50	0.038	-0.626	%Breadth		83.8	60.7	88.0	
CNE53	BC	>50	0.010	6.578	-2.818	Geometric mean IC50		0.071	0.043	0.167	
CNE58	BC	0.044	13.768	0.044	0.000						
MS208.A1	A	0.002	>50	0.050	-1.398						

In vitro neutralization activity was determined by standardized TZM-bl assay.

IC₅₀ values are expressed as µg/ml.

Fold change values were calculated by dividing the IC₅₀ titer of the most potent

(lowest IC₅₀) of the two parental mAbs (PG16 or PGT128) by the IC₅₀ titer of the

biNAb (PG16/PGT128).

ND: not determined

Table S4: Comparison of the *in vitro* neutralization activity of human IgG1 PG16 and 10-1074 mAbs and PG16/10-1074 biNAb.

Related to Figure 2.

Virus ID	Clade	PG16	10-1074	PG16/ 10-1074	log Fold Change
SC422661.8	B	0.858	0.072	0.224	-0.493
TRO.11	B	1.922	0.014	0.028	-0.301
THRO4156.18	B	6.825	>50	21.692	-0.502
TRJO4551.58	B	1.008	0.459	0.120	0.583
YU2.DG	B	0.055	0.110	0.113	-0.310
Du422.1	C	0.261	0.082	0.018	0.659
ZM249M.PL1	C	0.127	>50	0.240	-0.276
ZM109F.PB4	C	7.033	>50	>40	-0.755
ZM135M.PL10a	C	>50	0.146	0.428	-0.467
CAP210.2.00.E8	C	0.010	>50	0.575	-1.760
HIV-16845-2.22	C	3.126	1.930	0.402	0.681
249M.B10	C (T/F)	0.026	>50	0.146	-0.749
CNE30	BC	>50	0.363	1.264	-0.542
MS208.A1	A	0.002	45.556	0.156	-1.892
Q23.17	A	0.008	0.006	0.001	0.778
Q461.e2	A	1.755	>50	26.032	-1.171
0260.v5.c36	A	1.538	0.201	0.091	0.344
T257-31	CRF02 AG	0.007	>50	0.053	-0.879
263-8	CRF02 AG	0.347	0.763	0.222	0.194
T250-4	CRF02 AG	0.002	0.002	0.001	0.301
T251-18	CRF02 AG	1.721	1.011	2.028	-0.302
211-9	CRF02 AG	0.029	0.203	0.027	0.031
620345.c01	CRF01 AE	>50	>50	>50	ND
R1166.c01	CRF01 AE	0.280	>50	41.588	-2.172
R3265.c06	CRF01 AE	0.016	>50	0.424	-1.423
C2101.c01	CRF01 AE	0.012	>50	0.164	-1.136
X1193_c1	G	0.018	0.091	0.039	-0.336
X2131_C1_B5	G	0.024	0.023	0.012	0.283
3016.v5.c45	D	>50	>50	>50	ND
6952.v1.c20	CD	21.865	0.030	0.067	-0.349
6041.v3.c23	AC	0.048	21.720	2.038	-1.628
6540.v4.c1	AC	0.035	>50	0.258	-0.868
Total Viruses		32	32	32	
%Breadth		87.5	56.3	87.5	
Geometric mean IC₅₀		0.139	0.183	0.192	

In vitro neutralization activity was determined by standardized TZM-bl assay.
IC₅₀ values are expressed as µg/ml.

Fold change values were calculated by dividing the IC₅₀ titer of the most potent (lowest IC₅₀) of the two parental mAbs (PG16 or 10-1074) by the IC₅₀ titer of the biNAb (PG16/10-1074).

ND: not determined

Table S5: Comparison of the *in vitro* neutralization activity of human IgG1 PGT151 and 35O22 mAbs and PGT151/35O22 biNAb. *Related to Figure 2.*

Virus ID	Clade	PGT151	35O22	PGT151/35O22		<i>log Fold Change</i>	Virus ID	Clade	PGT151	35O22	PGT151/35O22		<i>log Fold Change</i>
					<i>log Fold Change</i>								
6535.3	B	0.005	>50	0.020	-0.602		Q769.d22	A	>50	>50	>50		ND
OH0692.42	B	0.078	9.621	0.150	-0.284		Q259.d2.17	A	50.000	>50	5.890	0.929	
SC422661.8	B	0.012	>50	0.032	-0.426		Q842.d12	A	0.024	11.580	0.045	-0.273	
PVO_4	B	0.129	>50	0.424	-0.517		0260.v5.c36	A	0.355	>50	0.680	-0.282	
TRO.11	B	>50	>50	>50	ND		3415.v1.c1	A	0.009	>50	0.024	-0.426	
AC10.0.29	B	0.007	8.782	0.028	-0.602		3365.v2.c2	A	0.011	>50	0.065	-0.772	
RHPA4259.7	B	0.035	>50	0.068	-0.288		191955_A11	A (T/F)	0.016	20.351	0.043	-0.429	
REJO4541.67	B	0.096	0.355	0.075	0.107		191084_B7-19	A (T/F)	0.014	>50	0.044	-0.497	
TRJO4551.58	B	1.053	5.474	0.752	0.146		9004SS_A3_4	A (T/F)	0.027	>50	0.051	-0.276	
WITO4160.33	B	0.005	>50	0.024	-0.681		T257-31	CRF02_AG	0.006	>50	0.024	-0.602	
CAAN5342.A2	B	0.013	1.591	0.058	-0.649		928-28	CRF02_AG	>50	>50	>50	ND	
YU2.DG	B	11.373	>50	41.362	-0.561		263-8	CRF02_AG	>50	>50	>50	ND	
WEAU_d15_410_787	B (T/F)	0.098	>50	0.112	-0.058		T250-4	CRF02_AG	0.011	>50	0.024	-0.339	
1006_11_C3_1601	B (T/F)	3.367	>50	6.427	-0.281		T251-18	CRF02_AG	0.782	>50	1.504	-0.284	
1054_07_TC4_1499	B (T/F)	0.015	>50	0.023	-0.186		T278-50	CRF02_AG	0.260	>50	0.460	-0.248	
1056_10_TA11_1826	B (T/F)	0.023	>50	0.188	-0.912		T255-34	CRF02_AG	0.014	>50	0.026	-0.269	
1012_11_TC21_3257	B (T/F)	>50	>50	>50	ND		211-9	CRF02_AG	0.006	12.641	0.022	-0.564	
6240_08_TA5_4622	B (T/F)	0.112	4.100	0.406	-0.559		235-47	CRF02_AG	>50	>50	>50	ND	
6244_13_B5_4576	B (T/F)	>50	>50	>50	ND		620345.c01	CRF01_AE	>50	>50	>50	ND	
62357_14_D3_4589	B (T/F)	0.024	0.243	0.034	-0.151		CNE8	CRF01_AE	>50	>50	>50	ND	
SC05_8C11_2344	B (T/F)	0.153	>50	1.320	-0.936		C1080.c03	CRF01_AE	50.000	>50	29.517	0.229	
Du156.12	C	0.011	>50	0.046	-0.621		R2184.c04	CRF01_AE	>50	16.954	45.045	-0.424	
Du172.17	C	0.008	>50	0.029	-0.559		R1166.c01	CRF01_AE	>50	>50	>50	ND	
Du422.1	C	1.149	13.085	0.454	-0.403		R3265.c06	CRF01_AE	>50	>50	>50	ND	
ZM197M.PB7	C	0.011	>50	0.095	-0.936		C2101.c01	CRF01_AE	50.000	>50	29.517	0.229	
ZM214M.PL15	C	0.034	>50	0.038	-0.048		C3347.c11	CRF01_AE	>50	>50	>50	ND	
ZM233M.PB6	C	0.038	1.406	0.060	-0.198		C4118.c09	CRF01_AE	>50	0.097	0.173	-0.251	
ZM249M.PL1	C	0.010	0.221	0.033	-0.519		CNE5	CRF01_AE	>50	>50	>50	ND	
ZM53M.PB12	C	>50	>50	>50	ND		BJOX009000.02.4	CRF01_AE	>50	>50	>50	ND	
ZM109F.PB4	C	0.501	>50	2.487	-0.696		BJOX015000.11.5	CRF01_AE (T/F)	>50	>50	>50	ND	
ZM135M.PL10a	C	>50	>50	>50	ND		BJOX010000.06.2	CRF01_AE (T/F)	>50	>50	>50	ND	
CAP45.2.00.G3	C	0.103	2.224	0.120	-0.066		BJOX025000.01.1	CRF01_AE (T/F)	>50	>50	>50	ND	
CAP210.2.00.E8	C	0.020	0.422	0.095	-0.677		BJOX028000.10.3	CRF01_AE (T/F)	50.000	>50	24.369	0.312	
HIV-001428-2.42	C	0.078	>50	0.329	-0.625		X1193_c1	G	0.027	5.092	0.058	-0.332	
HIV-0013095-2.11	C	2.075	>50	11.832	-0.756		P0402_c2_11	G	0.012	41.444	0.030	-0.398	
HIV-16055-2.3	C	0.174	>50	1.828	-1.021		X1254_c3	G	0.263	>50	1.977	-0.876	
HIV-16845-2.22	C	>50	>50	>50	ND		X2088_c9	G	>50	>50	>50	ND	
Ce1086_B2	C (T/F)	0.250	>50	0.419	-0.224		X2131_C1_B5	G	0.019	>50	0.076	-0.602	
Ce0393_C3	C (T/F)	>50	>50	>50	ND		P1981_C6_3	G	0.133	0.622	0.176	-0.122	
Ce1176_A3	C (T/F)	0.007	1.551	0.017	-0.385		X1632_S2_B10	G	1.207	>50	0.714	0.228	
Ce2010_F5	C (T/F)	>50	2.719	46.524	-1.252		3016.v5.c45	D	0.641	>50	1.785	-0.445	
Ce0682_E4	C (T/F)	>50	>50	>50	ND		A07412M1.vrc12	D	0.808	>50	6.110	-0.879	
Ce1172_H1	C (T/F)	>50	>50	>50	ND		231965.c01	D	0.019	>50	0.048	-0.402	
Ce2060_G9	C (T/F)	0.902	>50	2.570	-0.455		231966.c02	D	0.159	>50	0.913	-0.759	
Ce703010054_2A2	C (T/F)	0.047	17.054	0.137	-0.465		191821_E6_1	D (T/F)	0.276	>50	1.153	-0.621	
BF1266_431a	C (T/F)	>50	>50	>50	ND		3817.v2.c59	CD	>50	>50	>50	ND	
246F_C1G	C (T/F)	>50	25.031	2.924	-0.933		6480.v4.c25	CD	>50	>50	>50	ND	
249M_B10	C (T/F)	0.021	1.034	0.050	-0.377		64952.v1.c20	CD	>50	>50	>50	ND	
ZM247V1(Rev-)	C (T/F)	0.068	>50	0.248	-0.562		6811.v7.c18	CD	>50	>50	>50	ND	
7030102001E5(Rev-)	C (T/F)	0.009	>50	0.032	-0.551		89-F1_2_25	CD	>50	>50	>50	ND	
1394CG91(Rev-)	C (T/F)	0.051	>50	0.088	-0.237		CD	>50	>50	>50	ND		
Ce704809221_1B3	C (T/F)	>50	0.565	2.460	-0.639		3301.v1.c24	AC	0.036	24.840	0.077	-0.330	
CNE19	BC	0.049	0.651	0.063	-0.109		6041.v3.c23	AC	0.034	>50	0.076	-0.349	
CNE20	BC	>50	>50	>50	ND		6540.v4.c1	AC	0.024	>50	0.065	-0.433	
CNE21	BC	0.004	>50	0.019	-0.677		6545.v4.c1	AC	0.023	>50	0.062	-0.431	
CNE17	BC	0.231	>50	1.922	-0.920		0815.v3.c3	ACD	>50	10.664	0.102	2.019	
CNE30	BC	39.348	>50	6.218	0.801		3103.v3.c10	ACD	0.115	>50	0.311	-0.432	
CNE52	BC	0.022	>50	0.049	-0.348								
CNE53	BC	>50	>50	>50	ND		Total Viruses	120	120	120			
CNE58	BC	0.007	42.173	0.031	-0.646		%Breadth	64.2	27.5	72.5			
MS208-A1	A	0.006	>50	0.032	-0.727		Geometric mean IC50	0.077	2.840	0.220			
Q23.17	A	0.018	2.797	0.040	-0.347								
Q461.e2	A	2.569	0.231	0.306	-0.122								

In vitro neutralization activity was determined by standardized TZM-bl assay.

IC₅₀ values are expressed as µg/ml.

Fold change values were calculated by dividing the IC₅₀ titer of the most potent (lowest IC₅₀) of the two parental mAbs (PGT151 or 35O22) by the IC₅₀ titer of the biNAb (PGT151/35O22).

ND: not determined

Related to Figure 4.

Table S6: *In vitro* neutralization activity (IC_{50} and IC_{80} titers) of hinge variants of 3BNC117/10-1074 biNAb.

In vitro neutralization activity was determined by standardized TZM-bl assay.

IC_{50} and IC_{80} values are expressed as $\mu\text{g}/\text{ml}$.

Fold change values were calculated by dividing the IC₅₀ or IC₈₀ titer of the

IgG3C- with that of IgG1 hinge variant biNAb.

ND: not determined

Table S8: Comparison of the *in vitro* neutralization activity of IgG3C- hinge variants of 8ANC195 and PGT128 mAbs and 8ANC195/PGT128 biNAb. *Related to Figure 5.*

Virus ID	Clade	8ANC195/				<i>log Fold</i>		Virus ID	Clade	8ANC195/				<i>log Fold</i>	
		IC50	IC80	PGT128	PGT128	IC50	IC80			IC50	IC80	PGT128	PGT128	IC50	IC80
6535_3	B	0.093	0.664	0.007	0.032	0.008	0.036	-0.058	-0.051					ND	ND
GH0692_42	B	1.229	5.089	0.016	0.051	0.018	0.062	-0.051	-0.085					-0.213	-0.220
SC422661.8	B	0.173	1.199	1.772	13.645	0.025	0.115	0.840	1.018					-0.319	-0.325
PVO_4	B	0.095	0.606	0.010	0.037	0.011	0.054	-0.041	-0.164						
TRO_11	B	0.103	0.434	0.026	0.089	0.014	0.047	0.268	0.277						
AC10_0.29	B	0.544	2.180	0.006	0.028	0.009	0.044	-0.176	-0.246						
RHPA4259.7	B	0.231	1.167	0.019	0.108	0.011	0.056	0.237	0.285						
THRO4156.18	B	>30	>30	>30	>30	>30	>30	ND	ND						
REJO4541.67	B	0.127	0.581	>30	>30	0.076	0.366	0.223	0.201						
TRJO4551.58	B	0.319	1.091	0.034	0.098	0.049	0.113	-0.159	-0.062						
WITO4160.33	B	>30	>30	>30	>30	0.316	12.866	1.977	0.368						
CAAN5342_A2	B	>30	>30	0.145	>30	0.088	0.945	0.217	1.902						
WEAU_d15_410_787	B (T/F)	>30	>30	0.016	0.074	0.030	0.229	-0.273	-0.491						
1006_11_C3_1601	B (T/F)	0.157	1.812	0.009	0.035	0.006	0.299	0.176	0.082						
1054_07_TC4_1499	B (T/F)	0.205	5.572	0.043	0.267	0.013	0.081	0.520	0.518						
1056_10_TA11_1826	B (T/F)	>30	>30	0.004	0.019	0.008	0.035	-0.301	-0.265						
1012_11_TC21_3257	B (T/F)	>30	>30	0.011	0.040	0.017	0.118	-0.189	-0.470						
6240_08_TA5_4622	B (T/F)	>30	>30	0.020	0.060	0.024	0.099	-0.079	-0.217						
6244_13_BS_4576	B (T/F)	>30	>30	0.033	0.119	0.045	0.163	-0.135	-0.137						
62357_14_D3_4589	B (T/F)	>30	>30	0.731	7.088	0.053	0.441	1.144	1.206						
SC05_8C11_2344	B (T/F)	0.242	1.117	0.025	0.070	0.018	0.052	0.143	0.129						
Du172_17	C	5.923	24.128	0.032	0.148	0.035	0.125	-0.039	0.073						
D422_1	C	>30	>30	0.063	0.189	0.043	0.196	0.166	-0.016						
ZM197MPB7	C	7.711	>30	>30	>30	6.715	>30	0.060	ND						
ZM214MPL15	C	0.487	6.454	1.057	9.008	0.040	0.256	1.085	1.402						
ZM233MPB6	C	4.877	19.132	>30	>30	2.403	9.770	0.307	0.292						
ZM249MP1	C	>30	>30	1.786	16.798	0.097	0.937	1.265	1.253						
ZM53MPB12	C	12.846	>30	>30	>30	18.396	>30	-0.156	ND						
ZM109PB4	C	>30	>30	>30	>30	>30	>30	ND	ND						
ZM135MP10a	C	>30	>30	1.981	15.180	0.134	0.864	1.170	1.245						
CA452_0.20_G3	C	>30	>30	>30	>30	1.947	26.265	1.186	0.058						
CA210_2.00_E8	C	>30	>30	>30	>30	4.888	>30	0.788	ND						
HIV-001428_2.42	C	>30	>30	0.037	0.125	0.034	0.119	0.037	0.021						
HIV-0013095_2.11	C	0.168	0.612	>30	>30	0.192	0.694	-0.058	-0.056						
HIV-16055_2.3	C	10.158	>30	>30	>30	7.924	>30	0.108	ND						
HIV-16845_2.22	C	2.223	14.223	0.183	0.670	0.089	0.332	0.313	0.305						
Ce1086_B2	C (T/F)	4.899	>30	>30	>30	0.468	4.293	1.020	0.844						
Ce0393_C3	C (T/F)	4.574	>30	>30	>30	8.026	>30	-0.244	ND						
Ce1176_A3	C (T/F)	2.411	10.873	0.019	0.047	0.024	0.070	-0.101	-0.173						
Ce2010_F5	C (T/F)	>30	>30	>30	>30	>30	>30	ND	ND						
Ce0682_E4	C (T/F)	0.777	0.565	>30	>30	0.077	0.520	0.000	0.036						
Ce1172_H1	C (T/F)	25.431	>30	0.015	0.044	0.029	0.079	-0.286	-0.264						
Ce2060_G9	C (T/F)	1.695	11.108	>30	>30	0.483	2.275	0.545	0.689						
Ce703010054_A2	C (T/F)	8.789	>30	>30	>30	9.749	>30	-0.045	ND						
BF1266_431a	C (T/F)	>30	>30	>30	>30	>30	>30	ND	ND						
246F_C1G	C (T/F)	21.211	>30	0.007	0.020	0.011	0.070	-0.196	-0.217						
249M_B10	C (T/F)	>30	>30	3.302	29.230	0.173	1.369	1.281	1.329						
ZM247v1(Rev-)	C (T/F)	1.599	7.988	0.032	0.092	0.020	0.065	0.204	0.151						
Z030102001E5(Rev-)	C (T/F)	1.079	5.390	0.014	0.034	0.011	0.042	0.105	-0.092						
1394C9G1(Rev-)	C (T/F)	>30	>30	0.033	0.085	0.020	0.087	-0.217	-0.010						
Ce704809221_B3	C (T/F)	0.367	3.003	0.036	0.136	0.024	0.117	-0.177	0.065						
CNE19	BC	0.280	1.889	>30	>30	0.150	1.059	0.271	0.251						
CNE20	BC	0.833	3.879	0.005	0.011	0.007	0.017	-0.146	-0.189						
CNE21	BC	0.311	2.260	0.009	0.028	0.013	0.041	-0.160	-0.166						
CNE17	BC	2.555	9.747	0.456	1.618	0.227	0.742	0.303	0.339						
CNE30	BC	7.120	>30	0.927	8.819	0.161	0.736	0.761	1.079						
CNE52	BC	0.879	8.534	>30	>30	0.198	1.885	0.647	0.705						
CNE53	BC	>30	>30	0.027	0.082	0.030	0.114	-0.046	-0.143						
CNE58	BC	>30	>30	5.236	>30	0.320	1.621	1.214	1.267						
MS208_A1	A	>30	>30	>30	>30	>30	>30	ND	ND						
Q23_17	A	0.291	1.405	0.018	0.050	0.016	0.045	0.051	0.046						
Q461_e2	A	0.925	3.292	>30	>30	0.128	0.441	0.859	0.873						
Q769_d22	A	0.093	0.600	>30	>30	0.111	1.081	-0.077	-0.256						
		Total Viruses 116 116 116 116 116 116													
		%Breadth 65.5 56.9 65.5 58.6 90.5 81.9													
		Geometric mean 0.645 2.373 0.068 0.164 0.084 0.237													

In vitro neutralization activity was determined by standardized TZM-bl assay.

IC₅₀ and IC₈₀ values are expressed as µg/ml.

Fold change values were calculated by dividing the IC₅₀ or IC₈₀ titer of the most potent (lowest IC_{50/80}) of the two parental mAbs (8ANC195 or PGT128) by the IC_{50/80} titer of the biNAb (8ANC195/PGT128).

ND: not determined

Table S9: Comparison of the *in vitro* neutralization activity of IgG3C- hinge variants of PGT151 and 10-1074 mAbs and PGT151/10-1074 biNAb. **Related to Figure 5.**

Virus ID	Clade	PGT151/10-1074						Fold Change Log								
		PGT151			10-1074			PGT151			10-1074			Log		
		IC50	IC80	IC50	IC80	IC50	IC80	IC50	IC80	IC50	IC80	IC50	IC80	IC50	IC80	IC50
6535.3	B	0.007	0.017	0.010	0.030	0.003	0.017	0.368	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OH0692.42	B	0.028	0.572	0.090	0.340	0.019	0.079	0.184	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SC422661.8	B	0.013	0.044	0.053	0.268	0.014	0.058	-0.032	-0.120	0.000	0.000	0.000	0.000	0.000	0.000	0.000
PVO_4	B	0.028	6.403	0.050	0.234	0.020	0.094	0.161	0.400	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TRO_11	B	>30	>30	0.024	0.059	0.042	0.121	-0.243	-0.087	0.000	0.000	0.000	0.000	0.000	0.000	0.000
AC10.29	B	0.008	0.036	0.018	0.093	0.016	0.055	-0.301	-0.184	0.000	0.000	0.000	0.000	0.000	0.000	0.000
DHPA4259.7	B	0.012	0.058	0.031	0.115	0.014	0.061	-0.067	-0.022	0.000	0.000	0.000	0.000	0.000	0.000	0.000
THRO4156.18	B	>30	>30	>30	>30	>30	>30	>30	>30	ND	ND	ND	ND	ND	ND	ND
REJO4541.67	B	0.043	0.355	>30	>30	0.071	0.367	-0.218	-0.14	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TRJ04551.58	B	0.951	7.935	0.493	2.332	0.366	1.579	0.129	0.169	0.000	0.000	0.000	0.000	0.000	0.000	0.000
WIT04160.33	B	0.007	0.061	0.178	1.858	0.014	0.053	-0.301	0.061	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CAANS342.02	B	0.008	0.031	0.019	0.043	0.004	0.020	0.301	0.190	0.000	0.000	0.000	0.000	0.000	0.000	0.000
YU2_DG	B	>30	>30	0.121	0.568	0.100	0.464	0.083	0.088	0.000	0.000	0.000	0.000	0.000	0.000	0.000
WEAU_d15_410_787	B (T/F)	0.032	>30	0.054	0.239	0.010	0.037	0.505	0.810	0.000	0.000	0.000	0.000	0.000	0.000	0.000
1006_11_TC21_3257	B (T/F)	1.467	>30	0.001	0.005	0.007	0.028	-0.845	-0.748	0.000	0.000	0.000	0.000	0.000	0.000	0.000
1054_07_TC4_1499	B (T/F)	0.004	0.028	0.023	0.161	0.010	0.043	-0.398	-0.171	0.000	0.000	0.000	0.000	0.000	0.000	0.000
1056_10_TA11_1826	B (T/F)	0.012	0.058	0.034	0.244	0.019	0.070	-0.200	-0.082	0.000	0.000	0.000	0.000	0.000	0.000	0.000
1012_11_TC21_3257	B (T/F)	>30	>30	0.013	0.059	0.078	0.276	-0.778	-0.670	0.000	0.000	0.000	0.000	0.000	0.000	0.000
6249_08_TA5_4622	B (T/F)	0.101	1.195	0.102	0.353	0.077	0.210	0.118	0.226	0.000	0.000	0.000	0.000	0.000	0.000	0.000
6244_13_B5_4576	B (T/F)	>30	>30	0.240	0.783	0.095	0.418	0.402	0.272	0.000	0.000	0.000	0.000	0.000	0.000	0.000
62357_14_D3_4586	B (T/F)	0.005	0.031	1.290	26.815	0.011	0.044	-0.342	-0.152	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SC05_8C11_2344	B (T/F)	0.022	0.246	0.037	0.112	0.031	0.112	-0.149	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Du156_12	C	0.010	0.030	0.022	0.100	0.019	0.052	-0.279	-0.239	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Du172_17	C	0.003	0.020	0.086	0.303	0.013	0.038	-0.637	-0.279	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Du422_1	C	0.185	>30	0.078	0.203	0.051	0.178	0.185	0.057	0.000	0.000	0.000	0.000	0.000	0.000	0.000
ZM197M_PB7	C	0.001	0.021	>30	>30	0.026	0.115	-1.418	-0.738	0.000	0.000	0.000	0.000	0.000	0.000	0.000
ZM214M_PL15	C	0.009	0.118	0.077	1.066	0.011	0.074	-0.087	0.203	0.000	0.000	0.000	0.000	0.000	0.000	0.000
ZM233M_PB6	C	0.015	0.225	0.054	0.202	0.012	0.049	0.097	0.615	0.000	0.000	0.000	0.000	0.000	0.000	0.000
ZM249M_PL1	C	0.009	0.025	>30	>30	0.021	0.063	-0.419	-0.401	0.000	0.000	0.000	0.000	0.000	0.000	0.000
ZM53M_PB12	C	>30	>30	>30	>30	>30	>30	>30	>30	ND	ND	ND	ND	ND	ND	ND
ZM109F_PB4	C	0.744	>30	>30	0.30	0.358	>30	0.318	ND	ND	ND	ND	ND	ND	ND	ND
ZM135M_PL10a	C	0.004	0.017	>30	>30	0.024	0.078	-0.778	-0.662	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CAP45_2.00_G3	C	0.005	0.033	>30	>30	0.026	0.166	-0.716	-0.702	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CAP210_2.00_E8	C	0.022	0.488	20.730	>30	0.042	0.242	-0.281	0.305	0.000	0.000	0.000	0.000	0.000	0.000	0.000
HIV-001428-2.42	C	0.058	>30	0.056	0.189	0.024	0.079	0.368	0.379	0.000	0.000	0.000	0.000	0.000	0.000	0.000
HIV-0013095-2.11	C	0.025	>30	5.293	>30	0.033	0.287	-1.121	-2.019	0.000	0.000	0.000	0.000	0.000	0.000	0.000
HIV-16055-2.3	C	0.096	>30	>30	>30	0.104	0.846	-0.35	1.850	0.000	0.000	0.000	0.000	0.000	0.000	0.000
HIV-16845-2.22	C	>30	>30	0.862	3.053	0.105	0.792	0.914	0.586	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Ce1086_B2	C (T/F)	0.069	11.107	>30	>30	0.093	0.881	-1.130	1.101	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Ce0393_C3	C (T/F)	>30	>30	>30	>30	>30	>30	>30	>30	ND	ND	ND	ND	ND	ND	ND
Ce1776_A3	C (T/F)	0.003	0.016	0.026	0.094	0.007	0.022	-0.368	-0.138	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Ce2010_F5	C (T/F)	>30	>30	>30	>30	>30	>30	>30	>30	ND	ND	ND	ND	ND	ND	ND
Ce0682_E4	C (T/F)	>30	>30	>30	>30	>30	>30	6.882	>30	0.639	ND	ND	ND	ND	ND	ND
Ce1772_H1	C (T/F)	>30	>30	0.060	0.210	0.032	1.642	-1.023	-0.893	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Ce2060_G9	C (T/F)	0.120	>30	13.310	>30	0.079	0.772	0.182	1.690	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Ce7_03010054_2A2	C (T/F)	0.023	0.157	>30	>30	0.051	0.304	-0.348	-0.287	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BF1266_431a	C (T/F)	>30	>30	>30	>30	>30	>30	>30	>30	ND	ND	ND	ND	ND	ND	ND
246F_C1G	C (T/F)	13.267	>30	0.051	0.144	0.056	0.269	-0.401	-0.271	0.000	0.000	0.000	0.000	0.000	0.000	0.000
249M_C1G	C (T/F)	0.007	0.029	>30	>30	0.019	0.068	-0.434	-0.370	0.000	0.000	0.000	0.000	0.000	0.000	0.000
ZM247v1(Rev)	C (T/F)	0.013	>30	0.037	0.110	0.010	0.045	0.114	0.388	0.000	0.000	0.000	0.000	0.000	0.000	0.000
7030102001E5(Rev)	C (T/F)	0.005	0.016	0.009	0.028	0.008	0.016	-0.301	-0.426	0.000	0.000	0.000	0.000	0.000	0.000	0.000
1394C9G1(Rev)	C (T/F)	0.023	0.254	0.041	0.149	0.020	0.073	0.061	0.310	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Ce704809221_1B3	C (T/F)	>30	>30	0.079	0.687	0.192	0.670	-0.386	-0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CNE19	BC	0.098	0.167	0.078	>30	0.008	0.036	0.000	0.666	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CNE20	BC	>30	>30	0.003	0.010	0.010	0.032	-0.523	-0.505	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CNE21	BC	0.004	0.012	0.050	0.198	0.008	0.032	-0.301	-0.426	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CNE17	BC	0.019	13.704	1.279	6.471	0.030	0.150	-0.198	1.638	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CNE30	BC	>30	>30	0.356	1.243	0.086	0.430	0.617	0.461	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CNE52	BC	0.013	0.064	1.534	9.008	0.014	0.075	-0.032	-0.069	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CNE53	BC	>30	>30	0.029	0.109	0.044	0.116	-0.181	-0.027	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CNE58	BC	0.011	0.036	0.312	0.919	0.025	0.069	-0.357	-0.283	0.000	0.000	0.000	0			

Table S10: Comparison of the *in vitro* neutralization activity of IgG3C- hinge variants of 3BNC117 and PGT135 mAbs and 3BNC117/PGT135 biNAb. *Related to Figure 5.*

Virus ID	Clade	3BNC117/ PGT135						Fold Change Log		Virus ID	Clade	3BNC117/ PGT135						Fold Change Log	
		IC50	IC80	IC50	IC80	IC50	IC80	IC50	IC80			IC50	IC80	IC50	IC80	IC50	IC80	IC50	IC80
6535.3	B	0.599	5.030	>30	>30	0.051	0.405	1.070	1.094	Q461.e2	A	0.133	0.445	>30	>30	0.026	0.091	0.709	0.689
OH0692.42	B	0.146	0.514	>30	>30	0.017	0.218	0.934	0.373	Q769.d22	A	0.023	0.095	>30	>30	0.011	0.052	0.320	0.262
SC422661.8	B	0.095	0.251	7.753	>30	0.009	0.063	0.766	0.600	Q259.d21.17	A	0.064	0.208	>30	>30	0.022	0.105	0.464	0.297
PVO_4	B	0.027	0.125	>30	>30	0.015	0.099	0.755	0.128	Q842.d12	A	0.024	0.068	>30	>30	0.007	0.029	0.535	0.370
TRO_11	B	0.072	0.203	0.049	0.143	0.018	0.067	0.435	0.329	3415.v1.c1	A	0.092	0.568	0.315	2.032	0.017	0.064	0.733	0.948
AC10.0.29	B	>30	>30	>30	>30	3.149	>30	0.979	ND	3365.v2.c2	A	0.062	0.170	0.222	0.837	0.017	0.065	0.562	0.418
RHPA4259.7	B	0.023	0.069	>30	>30	0.009	0.045	0.407	0.186	191955_A11	A (T/F)	>30	>30	>30	2.349	>30	1.145	ND	ND
THRO4156.18	B	3.909	16.176	>30	>30	0.249	2.023	1.196	0.903	191084_B7-19	A (T/F)	0.111	0.539	0.157	1.288	0.008	0.060	1.142	0.953
REJO4541.67	B	0.040	0.228	>30	>30	0.015	0.093	0.426	0.389	W1084_SS_A3_4	A (T/F)	0.121	0.545	>30	>30	0.014	0.071	0.937	0.885
TRJO4551.58	B	0.193	0.676	>30	>30	0.019	0.154	1.007	0.642	T257-31	CRF02 AG	0.270	1.251	>30	>30	0.028	0.171	0.984	0.864
WITO4160.33	B	0.027	0.104	>30	>30	0.016	0.057	0.227	0.261	928-28	CRF02 AG	0.234	1.121	>30	>30	0.038	0.184	0.789	0.775
CAAN5342.A2	B	0.646	2.512	3.421	26.634	0.061	1.313	1.025	0.904	263-8	CRF02 AG	0.071	0.212	>30	>30	0.009	0.041	0.897	0.714
YU2.DG	B	0.031	0.086	16.810	>30	0.014	0.070	0.345	0.089	T250-4	CRF02 AG	>30	>30	>30	>30	8.963	29.034	0.525	0.014
WEAU_d15_410_787	B (T/F)	0.065	0.335	0.208	1.782	0.017	0.084	0.582	0.601	T251-18	CRF02 AG	0.279	0.948	>30	>30	0.028	0.113	0.998	0.924
1004_11_C3_1601	B (T/F)	0.048	0.173	>30	>30	0.016	0.061	0.477	0.406	T278-50	CRF02 AG	>30	>30	>30	>30	ND	ND	ND	ND
1054_07_TC4_1499	B (T/F)	0.127	0.534	>30	>30	0.019	0.094	0.825	0.736	T255-34	CRF02 AG	0.132	0.455	>30	>30	0.016	0.074	0.916	0.789
1056_10_TA11_1826	B (T/F)	0.196	3.113	>30	>30	0.050	0.349	0.593	0.950	211-9	CRF02 AG	0.826	4.135	>30	>30	0.115	0.520	0.856	0.900
1012_11_TC21_3257	B (T/F)	0.016	0.084	26.241	>30	0.009	0.048	0.250	0.243	235-47	CRF02 AG	0.153	1.276	6.511	>30	0.015	0.065	1.009	1.293
6240_08_TA5_4622	B (T/F)	0.688	1.814	>30	>30	0.053	0.237	1.113	0.884	620345.co1	CRF01 AE	>30	>30	>30	>30	ND	ND	ND	ND
6244_13_B5_4576	B (T/F)	0.109	0.342	0.530	2.397	0.020	0.073	0.736	0.671	C1080.co3	CRF01 AE	0.160	0.967	>30	>30	0.023	0.140	0.842	0.839
6235_14_D3_4589	B (T/F)	0.066	0.438	>30	>30	0.019	0.099	0.541	0.646	R2184.co4	CRF01 AE	0.030	0.120	>30	>30	0.009	0.047	0.590	0.407
SC05_8C11_2344	B (T/F)	0.225	0.752	5.363	>30	0.151	0.523	0.173	0.158	R2166.co1	CRF01 AE	0.151	2.787	>30	>30	0.044	0.272	0.536	0.111
Du156_12	C	0.114	0.459	>30	>30	0.067	0.299	0.231	0.199	R3265.co6	CRF01 AE	0.248	0.847	>30	>30	0.027	0.122	0.963	0.842
Du172_17	C	1.348	12.316	>30	>30	0.375	1.354	0.556	0.959	C2101.co1	CRF01 AE	0.033	0.235	>30	>30	0.007	0.058	0.673	0.608
Du422_1	C	>30	>30	>30	>30	ND	ND	ND	ND	C3347.co11	CRF01 AE	0.023	0.104	>30	>30	0.007	0.050	0.517	0.318
ZM197MPB7	C	0.527	1.810	>30	>30	0.039	0.194	1.131	0.965	C4118.co9	CRF01 AE	0.068	0.457	>30	>30	0.028	0.141	0.385	0.511
ZM214MP1.15	C	0.119	0.785	>30	>30	0.024	0.113	0.695	0.842	CNE5	CRF01 AE	0.482	1.728	>30	>30	0.077	0.377	0.797	0.661
ZM233MPB6	C	0.445	1.570	0.439	9.943	0.033	0.118	1.124	1.124	E191821_E009000.024	CRF01 AE	0.894	3.167	>30	>30	0.086	0.417	1.017	0.886
ZM240MP1.1	C	0.079	0.363	>30	>30	0.026	0.127	0.483	0.456	X2042.co2	CRF01 AE	0.110	0.392	>30	>30	0.029	0.151	0.579	0.414
ZM53MPB12	C	0.363	1.738	>30	>30	0.063	0.310	0.761	0.749	X2088.c9	CRF01 AE	0.204	0.560	4.107	>30	0.037	0.186	0.741	0.479
ZM109FPB4	C	0.250	1.459	>30	>30	0.031	0.231	0.907	0.800	X2131_C1_B5	CRF01 AE	0.399	2.263	0.023	0.097	0.025	0.161	-0.036	-0.220
ZM135MP10a	C	0.121	0.538	>30	>30	0.021	0.075	0.761	0.856	P1981_C3_5	CRF01 AE	1.080	6.349	>30	>30	0.060	0.294	1.255	1.328
CAP45.2.00.G3	C	16.603	>30	>30	>30	0.031	0.676	2.729	1.647	X1632_SS_B10	CRF01 AE	>30	>30	0.020	0.308	3.176	0.989		
CAP210.2.00.E8	C	>30	>30	>30	>30	0.368	3.720	1.911	0.906	X1193_c1	G	0.066	0.325	0.055	0.249	0.017	0.065	0.510	0.583
HIV-001428-2.42	C	0.009	0.026	0.051	0.228	0.003	0.015	0.477	0.239	X2130_E002	G	0.110	0.392	>30	>30	0.029	0.151	0.579	0.414
HIV-013095-2.11	C	0.830	7.653	>30	>30	0.024	0.131	1.539	1.767	X2088.c9	G	0.204	0.560	4.107	>30	0.037	0.186	0.741	0.479
HIV-16055-2.23	C	>30	>30	>30	>30	0.063	>30	2.678	ND	X2131_C1_B5	G	0.399	2.263	0.023	0.097	0.025	0.161	-0.036	-0.220
HIV-16845-2.22	C	>30	>30	0.998	>30	0.176	2.873	1.795	0.019	P1981_C3_5	G	0.1080	6.349	>30	>30	0.060	0.294	1.255	1.328
Ce1086_B2	C (T/F)	0.190	0.888	>30	>30	0.037	0.242	0.711	0.565	X1632_SS_B10	G	>30	>30	0.020	0.308	3.176	0.989		
Ce0393_C3	C (T/F)	0.267	1.260	>30	>30	0.032	0.155	0.921	0.910	A07412M1.vrc12	D	4.872	>30	>30	>30	0.146	1.983	1.523	ND
Ce1176_A3	C (T/F)	0.246	1.236	11.617	>30	0.022	0.109	1.049	0.055	X071965.co1	D	0.057	0.291	11.815	>30	0.017	0.088	0.525	0.519
Ce2010_F5	C (T/F)	0.076	0.272	>30	>30	0.014	0.067	0.735	0.608	X191821_E6_1	D (T/F)	0.334	2.256	>30	>30	0.033	0.154	1.005	1.171
Ce0682_E4	C (T/F)	0.050	0.145	>30	>30	0.014	0.061	0.553	0.376	X31966.co2	D	0.643	6.279	>30	>30	0.028	0.243	1.410	1.412
Ce1172_H1	C (T/F)	>30	>30	>30	>30	>30	>30	ND	ND	X31966.co2	D	0.122	0.558	>30	>30	0.032	0.218	0.581	0.407
Ce2060_G9	C (T/F)	0.235	0.815	>30	>30	0.029	0.108	0.909	0.878	X31966.co2	D	0.643	6.279	>30	>30	0.028	0.243	1.410	1.412
Ce70301_02001E5(Rev-)	C (T/F)	0.306	1.547	>30	>30	0.029	0.144	1.023	1.031	X31966.co2	D	0.334	2.256	>30	>30	0.033	0.154	1.005	1.171
1394C9G1(Rev-)	C (T/F)	>30	>30	0.300	4.429	0.519	3.264	-0.238	0.133	X31966.co2	D	0.643	6.279	>30	>30	0.028	0.243	1.410	1.412
Cer0704809221_1B3	C (T/F)	0.119	0.566	>30	>30	0.027	0.094	0.644	0.780	X31966.co2	D	0.643	6.279	>30	>30	0.028	0.243	1.410	1.412
CNE19	BC	0.042	0.175	0.010	0.047	0.009	0.024	0.046	0.310	AC	0.066	0.185	>30	>30	0.016	0.054	0.615	0.535	
CNE20	BC	>30	>30	0.007	0.020	0.051	0.145	-0.662	-0.860	AC	0.031	0.204	>30	>30	0.007	0.029	0.646	0.847	
CNE21	BC	>30	>30	0.054	0.253	0.093	0.443	-0.236	-0.243	AC	>30	>30	>30	>30	ND	ND	ND	ND	
CNE17	BC	12.003	>30	>30	>30	0.166	0.982	1.859	1.485	AC	0.023	0.097	>30	>30	0.008	0.037	0.459	0.419	
CNE30	BC	0.934	3.007	>30	>30	0.082	0.288	1.057	1.019	AC	1.502	3.823	7.981	28.871	0.067				

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