a

$$Antigenicity^{Score} = \sum_{i=1}^{N} w_i \times Fn_i \times \left(\frac{Fn_i}{Fn_i + Fp_i}\right)$$

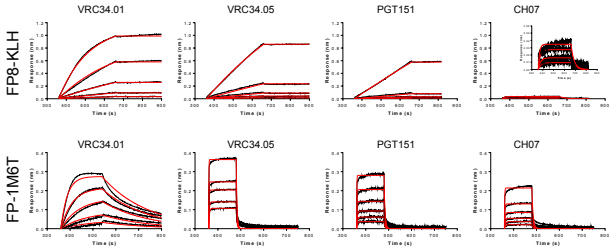
where $\sum_{i=1}^{N} w_i = 1$

w_i: weight for site i
Fn_i: Average binding of neutralizing antibodies targeting site i
Fp_i: Average binding of poorly/non-neutralizing antibodies targeting site i
N: Number of sites
Binding is defined as: $\frac{-\log(K_d) - \log(K_d^U)}{-\log(K_d^L) - (-\log(K_d^U))}$

K_d^U: upper bound of K_d assay limit (2000 nM)

K_d^L: lower bound of K_d assay limit (0.001 nM)

b

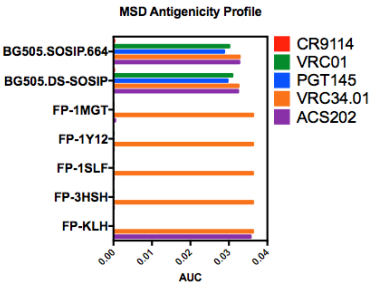


c

Construct	Scaffold configuration (EM)	Apparent K_D value (nM, with IgG avidity)						
		VRC34.01	VRC34.05	PGT151	CH07	ACS202	VRC01	447-52D
FP8-KLH	KLH particle	<0.001	<0.001	<0.001	N.B.	<0.001	N.B.	N.B.
FP-1M6T	Monomer	5.6	N.B.	N.B.	N.B.	N.B.	N.B.	N.B.
FP-1Y12	Dimer/Oligomer	3.7	N.B.	<0.001	N.B.	N.B.	N.B.	N.B.
FP-3HSH	Trimer	<0.001	25.4	47.2	N.B.	N.B.	N.B.	N.B.
FP-1SLF	Tetramer	<0.001	70.9	87.1	N.B.	N.B.	N.B.	N.B.
SOSIP.664	Env Trimer	<0.001	0.8	<0.001	N.B.	<0.001	<0.001	N.B.
DS SOSIP	Env Trimer	<0.001	0.6	<0.001	N.B.	<0.001	<0.001	N.B.
KLH	KLH particle	N.B.	N.B.	N.B.	N.B.	N.B.	N.B.	N.B.

N.B., apparent K_D>2000nM

d

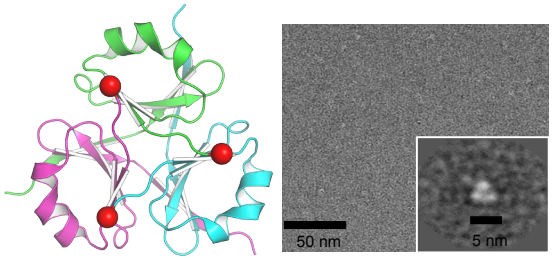


e

>FP-3HSH
AVGIGAVFLGGGGSSGVRLWATRQAMLGQVHEVPEGWLIFVAEQEELYVRVQNGFRKVQLEARTPLPRGGGSLEVLFQGP
>FP-1SLF
AVGIGAVFLGITGTWYNQLGSTFIVTAGADGALTGTYESAVGNAESRYVLTGRYDSAPATDGSGTALGWTVAWKNNYRNAHSATTWSGQYVGGAEARINTQWLLTSGTTEANAWKSTLVGHDTFTKVKPSAASGGLVPRGS

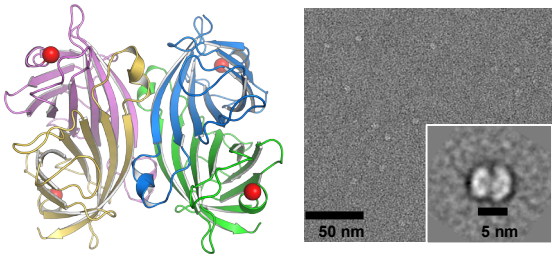
f

FP-3HSH



g

FP-1SLF

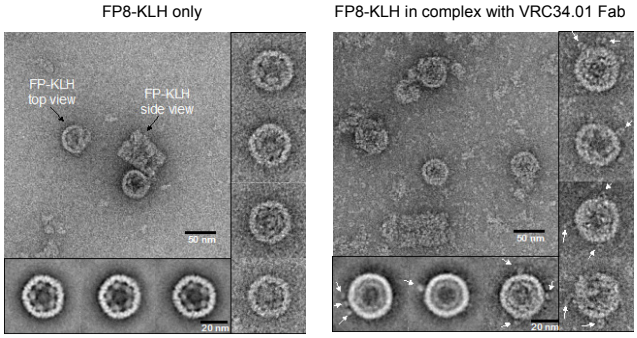


h

Physical stability of FP8-KLH

Retained fractional VRC34.01 reactivity						
Temp (ºC)		pH		Freeze Thaw	Osmolality (mM)	
50	70	3.5	10		10	3000
1.0	1.0	0.0	0.9	1.1	1.0	0.9

i



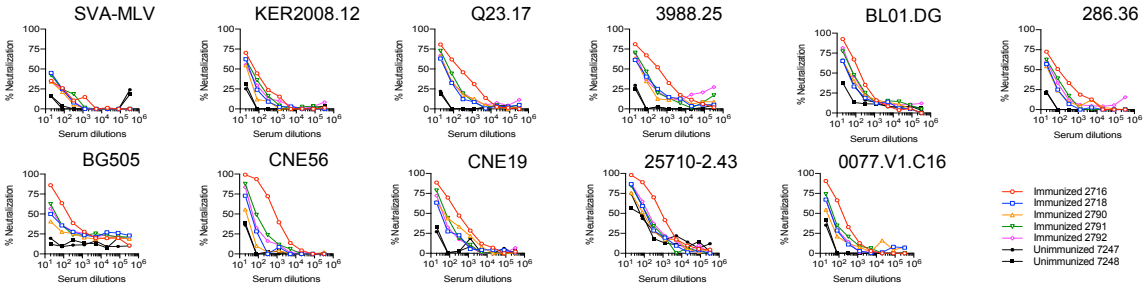
Supplementary Figure 1. Characteristics of FP immunogens. a, Metric of antigenicity. Here we focus on the FP site of vulnerability (N=1). VRC34.01, VRC34.05, PGT151, and ACS202 were used as the representative neutralizing antibodies targeting FP, and CH07 was used as the representative poorly/non-neutralizing antibody targeting FP. See (**c**) for K_D data. **b,** Antigenicity assessment of FP immunogens by BLI method with Octet. Examples of Octet-binding curves for FP8-KLH and FP-1M6T epitope scaffold are shown. **c,** FP-immunogen antigenicity. FP-directed antibodies VRC34.01, VRC34.02, PGT151 and ACS202 were considered neutralizing, whereas CH07 was considered weakly or non-neutralizing. **d,** Immunogen quality control by MSD**. e,** Amino acid sequences for FP scaffolds: FP-3HSH and FP-1SLF. Additional epitope scaffolds are described in Kong et al. 2016. **f,** Structural models of FP-3HSH and FP-1SLF. **g,** Negative-stain EM images (inset shows 2D-class averages). **h,** Physical stability of FP8-KLH. Fractional values refer to VRC34.01 reactivity retained after exposure to various physical extremes as compared to initial reactivity with VRC34.01. Affinity measured by biolayer interferometry. **i,** Binding of VRC34.01 Fab to FP8-KLH illustrated by negative-stain electron microscopy. Examples of micrographs for FP8-KLH (left) and FP8-KLH mixed with VRC34.01 Fab at a molar ratio of 1:10 (right). Right insets, examples of raw particles for FP8-KLH and FP8-KLH in complex with VRC34.01 Fab. White arrows indicate bound Fab fragments. Bottom insets, examples of 2D-class averages. White arrows indicate bound Fab fragments. For (**b, f, g and i**), n=3 experiments were performed independent with similar results.

a Neutralization assessment of 1st-generation murine immune sera

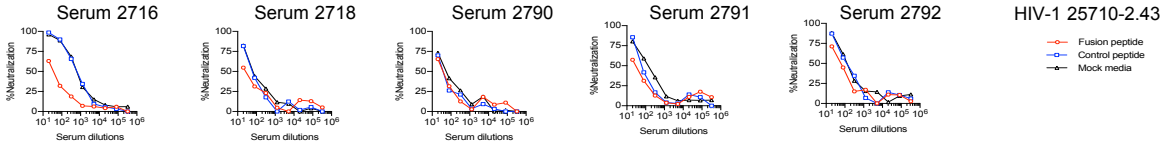
Viruses		Mice sera					
		1868	1882	1883	1884	2586	2602
SVA-MLV	ID50	50	23	25	<20	23	<20
	ID80	<20	<20	<20	<20	<20	<20
BG505 WT	ID50	<20	<20	<20	<20	<20	60
	ID80	<20	<20	<20	<20	<20	<20
BG505 Δ611 glycan	ID50	108	95	62	89	78	275
	ID80	20	<20	<20	<20	<20	22
BG505 Δ88+Δ611 glycans	ID50	493	320	239	205	239	575
	ID80	65	26	29	26	<20	55

ID50	ID80
<40	<20
40-100	20-100
100-1000	

b Sera neutralization curves on 10-isolate panel with MLV as control



c FP-competed sera neutralization



Summary of the effect of FP-competition to sera neutralization ID_{50} on HIV-1 strain 25710-2.43

Serum	Media	Fusion peptide			Control peptide		
	ID50	ID50	Fold change	% inhibition	ID50	Fold change	% inhibition
2716	610	33	18.5	95%	633	1.0	-4%
2718	68	27	2.5	60%	61	1.1	10%
2790	55	38	1.4	31%	36	1.5	35%
2791	141	31	4.5	78%	61	2.3	57%
2792	118	48	2.5	59%	128	0.9	-8%

d Summary of the effect of FP-competition to NHP sera and control antibody neutralization

Plasma	Virus	Clade	Media	Fusion peptide			Control peptide		
			ID50	ID50	Fold change	% inhibition	ID50	Fold change	% inhibition
NHP DFIW week 46	Q23.17	A	144	<20	>7.2	>86.1%	145	1.0	-0.7%
	45_01dG5	B	78	<20	>3.9	>74.3%	74	1.1	5.1%
	286.36	C	117	<20	>5.9	>82.9%	122	1.0	-4.3%
	0815.V3.C3	ACD	152	<20	>7.6	>86.8%	161	0.9	-5.9%

Antibody	Virus	Clade	Media	Fusion peptide			Control peptide		
			IC50	IC50	Fold change	% inhibition	IC50	Fold change	% inhibition
VRC34.01	Q23.17	A	0.10	14.10	139.6	99.3%	0.10	1.0	1.9%
	45_01dG5	B	0.31	18.00	58.6	98.3%	0.37	1.2	16.6%
	286.36	C	>50	>50	N/A	N/A	>50	N/A	N/A
	0815.V3.C3	ACD	0.04	1.72	44.1	97.7%	0.03	0.9	-14.7%
VRC01	Q23.17	A	0.12	0.14	1.1	11.9%	0.13	1.1	6.3%
	45_01dG5	B	0.03	0.01	0.6	-78.6%	0.03	1.1	7.4%
	286.36	C	0.46	0.38	0.8	-21.3%	0.48	1.0	4.6%
	0815.V3.C3	ACD	0.04	0.04	1.0	2.5%	0.04	1.1	9.3%

Supplementary Figure 2. Neutralization of immunized sera on 293T-derived HIV-1 Env-pseudotyped viruses in TZM-bl assay. a, Neutralization assessment of 1st-generation immune sera from immunized mice in Fig. 1. **b,** Neutralization assessment of 2nd-generation immune sera from immunized mice in Fig. 3c. Serum neutralization curves are shown for 5 immunized and 2 unimmunized control C57/BL6 mice, tested on 10 wildtype HIV-1 Env-pseudotyped viruses (5 with complete glycans around the FP site and 5 naturally missing glycans as shown in Fig. 3c along with ID_{50} titer). SVA-MLV was assessed as a control. **c,** FP-competed neutralization curves of indicated immunized mice sera on HIV-1 strain 25710-2.43. Sera were pre-incubated with the nine-amino acid FP (sequence AVGIGAVFL) (red), an non-cognate FLAG peptide (blue) or control media (black) before mixing with virus stock. ID_{50} titers are shown the summary table. ID_{50} fold change was calculated as ID50[media]/ID50[peptide]. % inhibition of FP or control peptide was calculated as (1-ID50[peptide]/ID50[media])*100. **d,** Neutralization summary for FP competition shown in Fig. 6b. For antibody neutralization, IC50 fold change was calculated as IC50[peptide]/IC50[media]. % inhibition of FP or control peptide was calculated as (1-IC50[media]/IC50[peptide])*100.

a

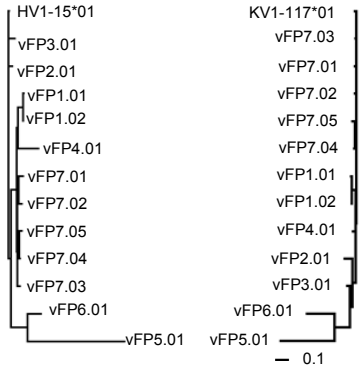
Mouse 1868

Class	Antibody	Heavy				Light			
		HV	HJ	HV identity (%)	CDR H3	KV	KJ	KV identity (%)	CDR L3
vFP1	vFP1.01	HV1-15*01	HJ1*03	94.5	LRNYWYFDV	KV1-117*01	KJ2*01	95.6	FQGSHVPYT
	vFP1.02	HV1-15*01	HJ1*03	94.5	LRNYWYFDV	KV1-117*01	KJ2*01	95.9	FQGSHVPYT
	vFP2.01	HV1-15*01	HJ2*01	96.5	LKRFYYFDY	KV1-117*01	KJ4*01	93.2	FQGSHVPYT
	vFP3.01	HV1-15*01	HJ2*01	95.2	LKRFYYFDY	KV1-117*01	KJ4*01	95.6	FQGSHFPFT
	vFP4.01	HV1-12*01	HJ1*03	94.6	LLPKWYFDV	KV1-117*01	KJ2*01	96.9	FQGSHVPYT
vFP5	vFP5.01	HV3-6*01	HJ3*01	94.9	EGNYRAY	KV6-23*01	KJ5*01	93.2	QQYSSYPLT
vFP6	vFP6.01	HV1-7*01	HJ2*01	93.1	GYVAFHY	KV2-112*01	KJ4*01	97.6	QQLVQHPFT

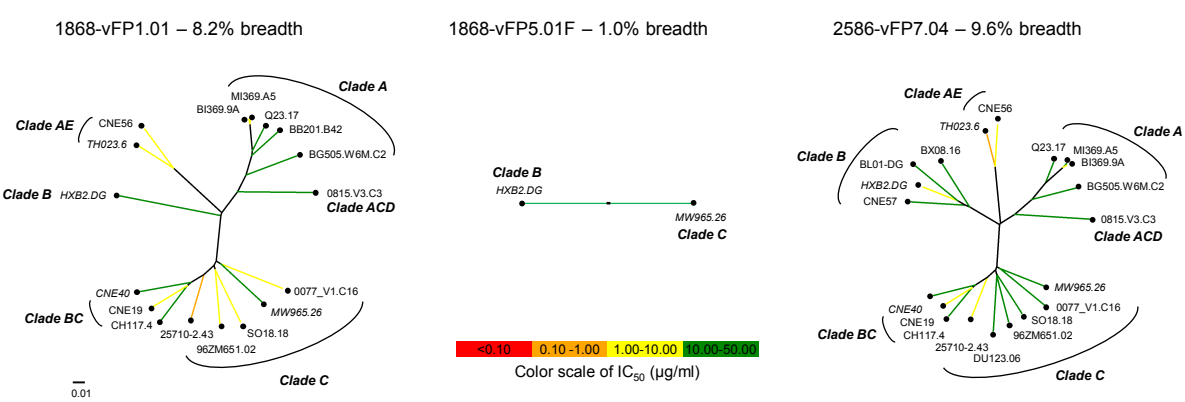
Mouse 2586

vFP1	vFP7.01	HV1-15*01	HJ1*03	96.5	LRLYGYFDV	KV1-117*01	KJ2*01	99.0	FQGSHIPYT
	vFP7.02	HV1-15*01	HJ1*03	96.9	LRLYGYFDV	KV1-117*01	KJ2*01	98.6	FQGSHVPYT
	vFP7.03	HV1-15*01	HJ1*03	96.5	LRLYWYFDV	KV1-117*01	KJ2.01	99.3	FQGSHVPYT
	vFP7.04	HV1-15*01	HJ1*03	97.9	LRLYWYFDV	KV1-117*01	KJ2*01	98.0	FQGSHVPYT
	vFP7.05	HV1-15*01	HJ1*03	96.2	LRLYWYFDV	KV1-117*01	KJ2*01	96.6	FQGSHVPYT

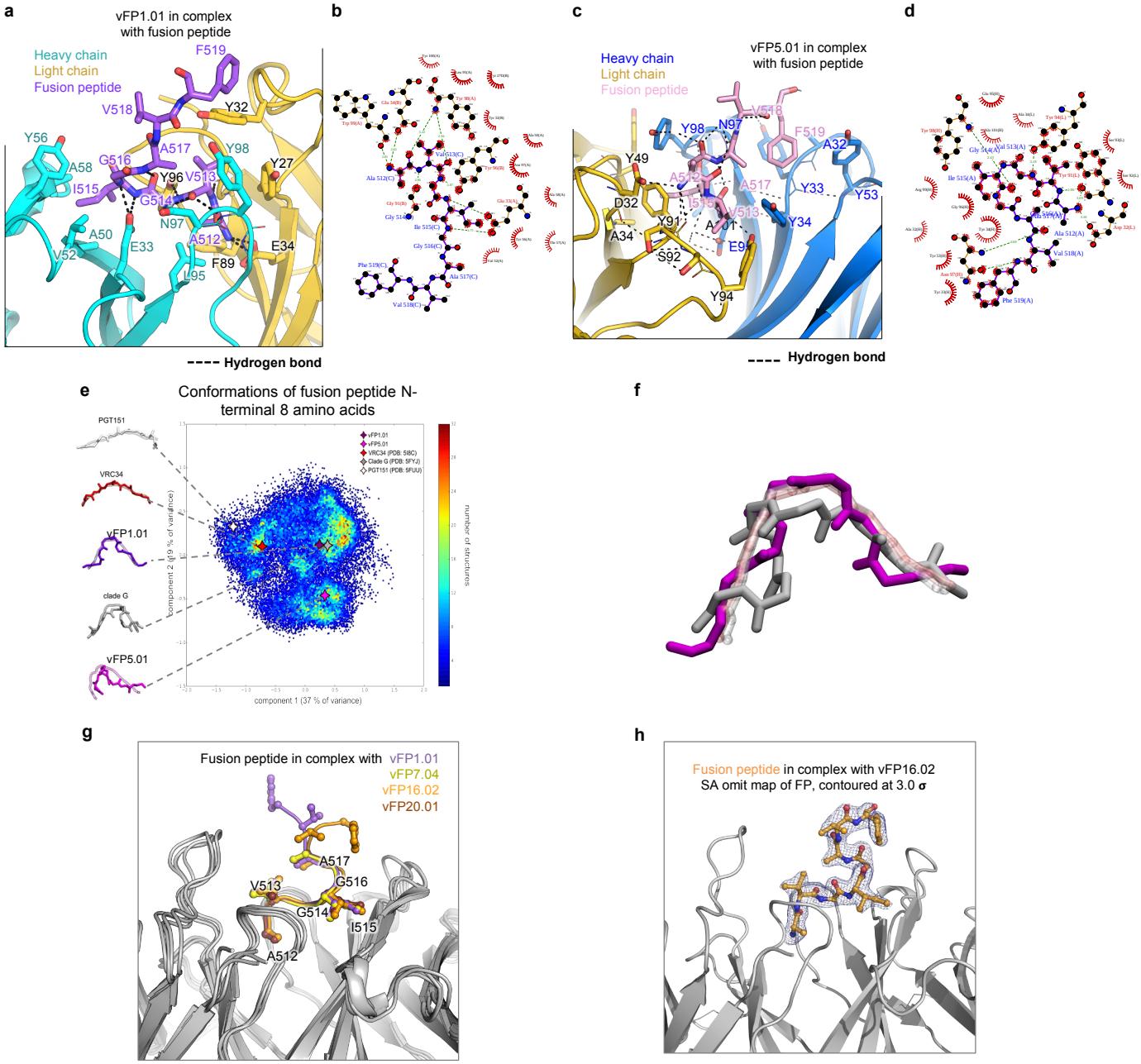
b



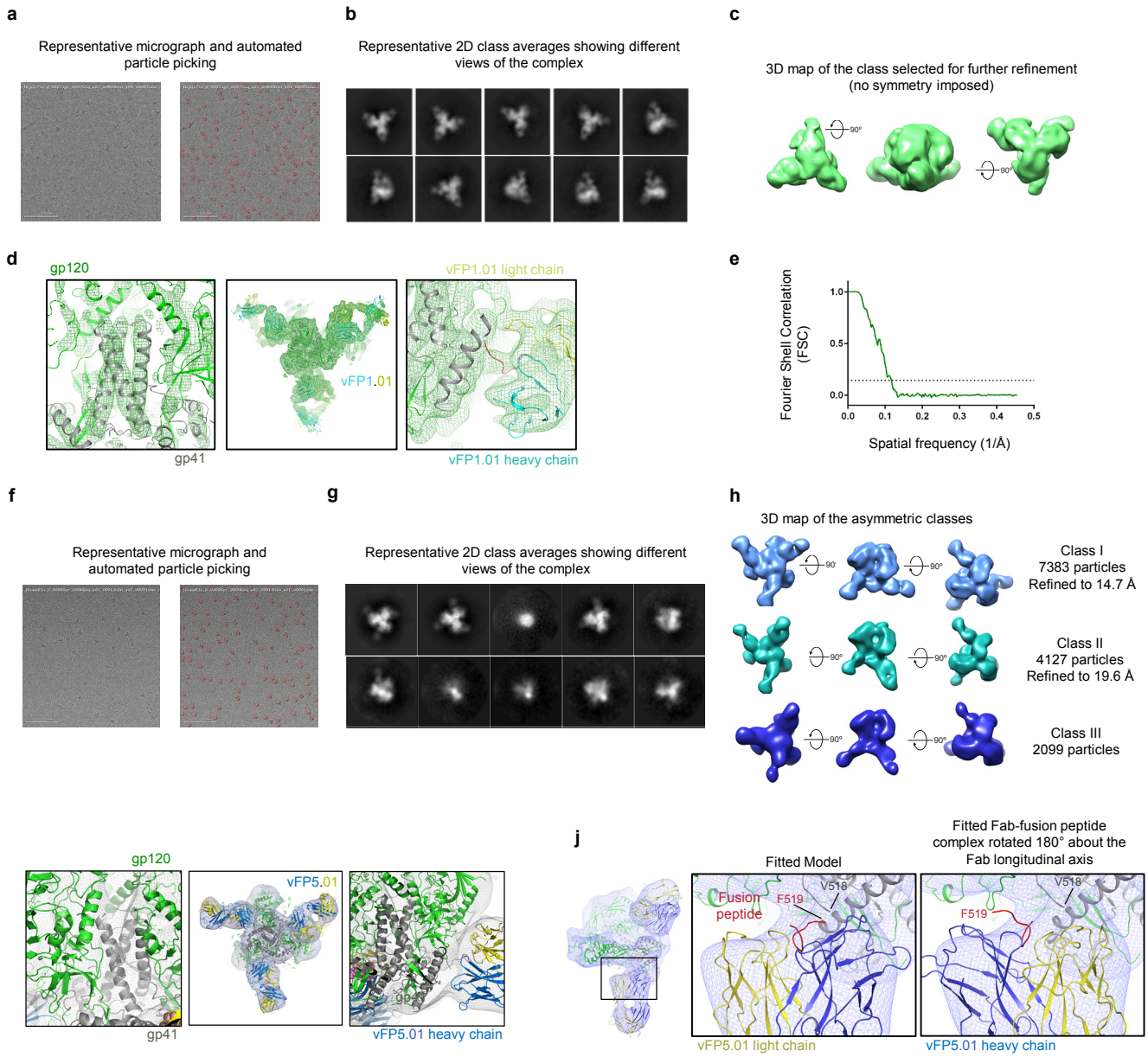
c



Supplementary Figure 3. First generation vaccine-elicited antibodies targeting FP neutralize up to ~10% of HIV-1 strains. a, Genetic characteristics of vaccine-elicited antibodies recognizing both HIV-1 Env and FP. Identity values are based on nucleotide sequence of the indicated heavy or light chain gene. **b,** Heavy and light chain phylogenetic tree. **c,** Neutralization dendrograms tested on 208-isolate panel for vaccine-elicited antibodies vFP1.01, vFP5.01 and vFP7.04, with branches only shown for neutralized strains and colored according to neutralization potency. Strains sensitive to V3-directed or CD4-induced antibodies shown in italics. See Supplementary Table 3a for titers.

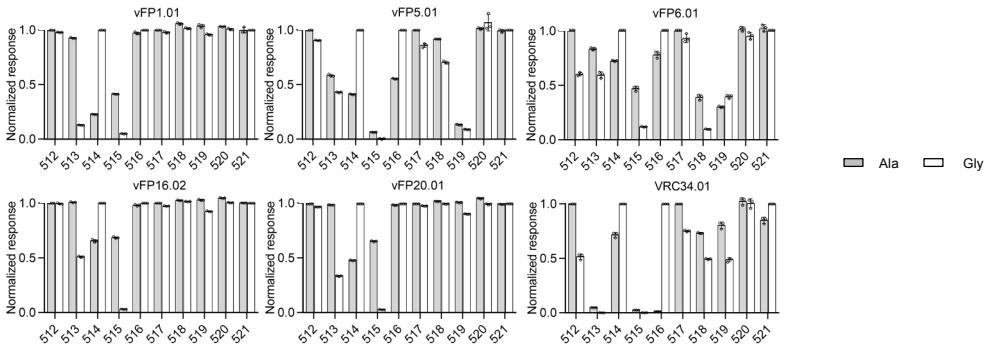


Supplementary Figure 4. Structural details of FP-conformational diversity and recognition by antibody. (**a-b**) vFP1.01 crystal structure with FP. **a,** Interaction between vFP1.01 and FP (contacting residues are shown as sticks). **b,** Ligplot showing the contact between vFP1.01 and FP. (**c-d**) vFP5.01 crystal structure with FP. **c,** Interaction between vFP5.01 and FP (contacting residues are shown as sticks). **d,** Ligplot showing the contact between vFP5.01 and FP. **e,** Principal component analysis of FP conformation based on molecular dynamics simulations of fully glycosylated HIV-1-Env trimer. Principal component projections (in transparency) are shown for HIV-1-fusion peptides bound by antibody (or for clade G Env trimer-5FYJ). Four prevalent clusters of fusion-peptide conformations were observed. Most prevalent was a symmetrical U-shaped conformation, which was recognized by FP1.01 and also observed in the fully glycosylated Env trimer from a Clade G isolate. A J-shaped conformation, recognized by FP5.01, was also highly prevalent, as was the extended linear conformation, recognized by VRC34.01. A related extended conformation was also recognized by antibody PGT151, though the conformational space sampled by the PGT151-bound antibody was substantially less dense than the other antibody-recognized conformations. **f,** Conformational superposition of the peptides analyzed in (**e**), along with the principal component projection (in transparency). Despite substantial difference in secondary structure, the two conformations share similar global shape. Thus, even though the FP-conformation in 5FYJ is slightly helical (one turn), both peptides adopt a symmetrical "U"-shape conformation. **g,** Superimposition of vFP1-class antibodies in complex with FP (residues 512-519). Antibody variable regions of vFP1-class antibodies, including vFP1.01, vFP7.04, vFP16.02 and vFP20.01, were aligned structurally. **h,** SA omit map of FP, in the crystal structure of vFP16.02 bound complex.

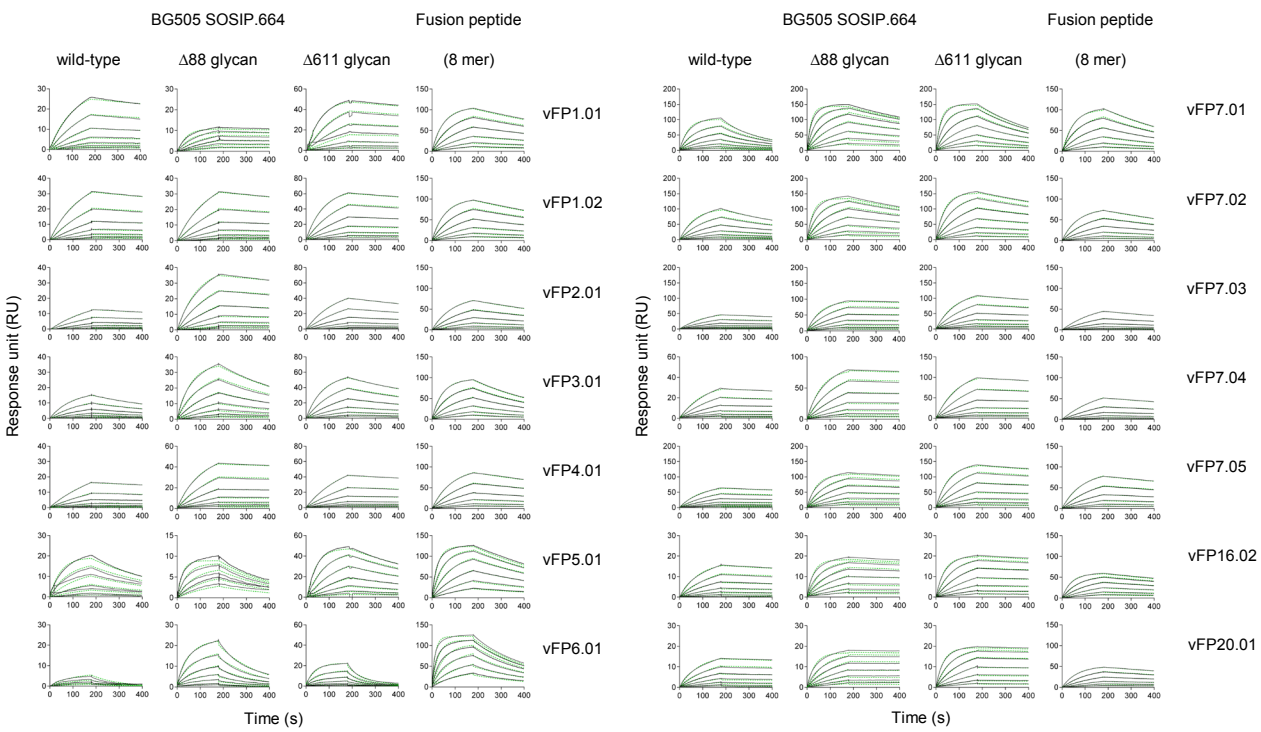


Supplementary Figure 5. Cryo-EM details for reconstructions of up to 8.6 Å resolution. (**a-e**) Details of cryo-EM structure of vFP1.01 complex with BG505 SOSIP trimer. **a,** Representative micrograph (left) with particles picked with DogPicker shown in red circles (right). **b,** Representative 2D class averages **c,** Views of the 3D class selected for refinement. **d,** Snapshot of density and fit of model at different regions of the complex. The panel on the left is shown at a higher map contour than the other two panels to highlight the fit around the gp41 region of the trimer, which is one of the most well-defined regions of the complex. **e,** Fourier shell correlation plot for the 3D refinement ($FSC_{0.143}$= 8.6 Å, indicated by the dotted line). (**f-i**) Details of cryo-EM structure of vFP5.01 complex with BG505 SOSIP trimer. **f,** Representative micrograph (left) with particles picked with DogPicker shown in red circles. **g,** Representative 2D class averages. **h,** Views of asymmetric 3D classes. **i,** Snapshot of refined Class I density and fit of model at different regions of the complex. **j,** Comparison of the orientation of the vFP5.01 Fab-fusion peptide crystal structure fitted into the cryo-EM map, with its orientation rotated 180° about the longitudinal axis of the Fab. In the fitted model, residue Phe519 of the fusion peptide bound to the Fab in the crystal structure is favorably placed near residue Val518 of the fitted trimer, whereas in the 180° rotated model, Phe519 diverges away from the electron density and gp41 in the fitted trimer. Cryo-EM data collection was performed once for each structure. The represented images in (**a**, **b**, **f** and **g**) was derived from the analysis of many particles in many images. Additional details on cryo-EM data collection, such as total number of particles, number of images, can be found in Supplementary Table 4.

a



b



c

Ligand	BG505.DS.SOSIP			BG505.DS.SOSIP.Δ88			BG505.DS.SOSIP.Δ611			Fusion peptide		
mAb	ka (1/Ms)	kd (1/s)	K_D (M)	ka (1/Ms)	kd (1/s)	K_D (M)	ka (1/Ms)	kd (1/s)	K_D (M)	ka (1/Ms)	kd (1/s)	K_D (M)
vFP1.01	4.73E+04	6.07E-04	1.28E-08	1.45E+05	3.04E-04	2.10E-09	9.02E+04	4.47E-04	4.96E-09	1.89E+05	1.35E-03	7.15E-09
vFP1.02	3.80E+04	4.77E-04	1.25E-08	1.01E+05	1.14E-04	1.13E-09	6.62E+04	3.89E-04	5.87E-09	1.66E+05	1.36E-03	8.19E-09
vFP2.01	2.43E+04	6.61E-04	2.72E-08	5.38E+04	4.24E-04	7.87E-09	3.69E+04	9.15E-04	2.48E-08	9.53E+04	1.48E-03	1.56E-08
vFP3.01	4.34E+04	2.20E-03	5.07E-08	7.64E+04	2.23E-03	2.95E-08	6.49E+04	1.47E-03	2.26E-08	1.91E+05	2.76E-03	1.44E-08
vFP4.01	1.93E+04	4.36E-04	2.26E-08	4.99E+04	1.92E-04	3.85E-09	2.92E+04	3.90E-04	1.33E-08	1.04E+05	1.02E-03	9.82E-09
vFP5.01	6.75E+04	3.10E-03	4.62E-08	2.23E+05	3.66E-03	1.64E-08	1.24E+05	1.88E-03	1.51E-08	3.88E+05	2.06E-03	5.29E-09
vFP6.01	1.12E+04	1.04E-02	9.28E-07	6.55E+04	5.72E-03	8.74E-08	1.55E+05	2.61E-02	1.69E-07	6.65E+05	3.48E-03	5.23E-09
vFP7.01	1.90E+05	5.14E-03	2.71E-08	3.00E+05	1.34E-03	4.46E-09	2.25E+05	3.12E-03	1.39E-08	4.79E+06	2.54E-03	5.30E-10
vFP7.02	7.22E+04	1.97E-03	2.72E-08	1.90E+05	1.19E-03	6.26E-09	1.34E+05	1.02E-03	7.61E-09	3.29E+06	1.48E-03	4.50E-10
vFP7.03	4.22E+04	6.10E-04	1.44E-08	8.83E+04	1.59E-04	1.80E-09	6.25E+04	5.59E-04	8.94E-09	1.26E+06	1.25E-03	9.94E-10
vFP7.04	5.07E+04	3.48E-04	6.86E-09	8.20E+04	1.32E-04	1.61E-09	5.55E+04	3.10E-04	5.59E-09	1.11E+06	8.94E-04	8.05E-10
vFP7.05	5.71E+04	4.38E-04	7.68E-09	1.59E+05	3.29E-04	2.07E-09	9.59E+04	4.11E-04	4.28E-09	2.52E+06	7.68E-04	3.05E-10
vFP16.02	5.82E+04	4.18E-04	7.19E-09	1.79E+05	3.11E-04	1.74E-09	1.41E+05	2.96E-04	2.10E-09	9.87E+05	1.05E-03	1.06E-09
vFP20.01	5.99E+04	2.22E-04	3.71E-09	1.49E+05	6.33E-05	4.26E-10	1.57E+05	1.47E-04	9.34E-10	5.88E+05	9.61E-04	1.64E-09
VRC34	5.25E+05	3.40E-04	6.48E-10	1.63E+06	3.27E-03	2.00E-09	1.59E+06	7.09E-04	4.46E-10	1.50E+06	9.24E-03	6.17E-09

Supplementary Figure 6. Binding of vaccine-elicited antibodies to HIV-1 Env trimers and His-tagged FP. a, Bar plots of Ala/Gly scan. Binding of indicated antibodies to alanine (grey bars) and glycine (white bars) mutants are shown, normalized by binding to the wild-type sequence. FP amino acids are shown on x-axis. Experiments were performed in triplicate (n=3 independent experiments), error bars indicating mean with SD are plotted for each residue position in the overlaid scatter dot plot. See Supplementary Table 5 for numerical details and additional vFP1-class antibodies**. b,** SPR sensorgrams of vFP1.01, vFP1.02, vFP2,01, vFP3.01, vFP4.01, VFP5.01, VFP6.01, vFP7.01, vFP7.02, vFP7.03, vFP7.04, vFP7.05, vFP16.02 and vFP20.01 binding to wild type, glycan-deleted BG505.DS-SOSIP trimers and His-tagged FP. Blank-corrected sensorgrams were shown in black and fitted data using a 1:1 Langmuir model of binding were shown in green dashed lines. **c,** SPR constants of all first and second generation vFPs Fabs binding to wild type, glycan-deleted BG505.DS-SOSIP, and FPs.

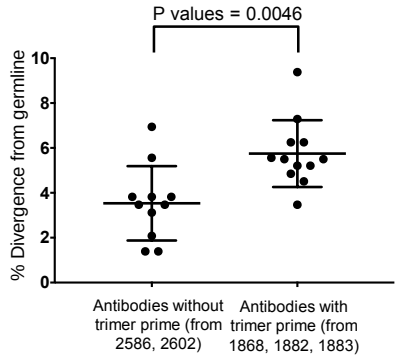
a

Mouse ID	Immunization 1	2	3	SVA-MLV ID50	SVA-MLV ID80	BG505 WT ID50	BG505 WT ID80	BG505 Δ611 glycan ID50	BG505 Δ611 glycan ID80	BG505 Δ88+Δ611 glycans ID50	BG505 Δ88+Δ611 glycans ID80	Hybridoma-identified antibodies (All vFP1 class)
2586	FP8	FP8		23	<20	<20	<20	78	<20	239	<20	*vFP7.01-vFP7.03, vFP7.04-vFP7.07, vFP7.08*
2602	FP8	FP8		<20	<20	60	<20	275	22	575	55	*vFP8.01, vFP8.02, vFP8.03*
1868	T1	FP8	FP8	50	<20	<20	<20	108	20	493	65	*vFP1.01-vFP1.02, vFP2.01, vFP3.01, vFP4.01*
1882	T1	FP8	FP8	23	<20	<20	<20	95	<20	320	26	*vFP9.01*
1883	T1	FP8	FP8	25	<20	<20	<20	62	<20	239	29	*vFP10.01-vFP10.05, vFP11.01*

Key:
FP8 = AVGIGAVF-KLH
T1 = BG505 SOSIP

ID50	ID80
<40	<20
40-100	20-100
100-1000	

b



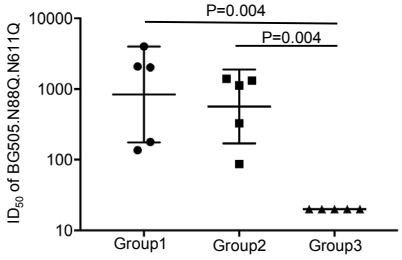
c

Group #	Immunizations 1	2	3	4	5	6	Animal ID	BG505.N88Q.N611Q ID50	BG505.N88Q.N611Q ID80
1	T1	FP8	FP7	FP6	T2	T2	4441	2029	280
							4442	136	<20
							4443	2087	348
							4444	4011	488
							4445	178	<20
2	T1	FP8	FP8	FP8	T2	T2	4446	1398	222
							4447	87	<20
							4448	1127	325
							4449	329	62
							4450	1312	302
3	T1	KLH only	KLH only	KLH only	T2	T2	4451	<20	<20
							4452	<20	<20
							4453	<20	<20
							4454	<20	<20
							4455	<20	<20

Key:
FP8 = AVGIGAVF-KLH
FP7 = AVGIGAV-KLH
FP6 = AVGIGA-KLH
T1 = BG505 SOSIP
T2 = BG505 DS SOSIP

ID50	ID80
<40	<20
40-100	20-100
100-1000	
1000-10000	

d



e

Week 18 sera neutralization of the guinea pig group, immunized with only 3x BG505.DS.SOSIP Env trimer

Clade	A	A	B	B	C	AE	BC	C	C	A	A	A	A	Wild type viruses neutralization #/10 in ID50
Glycan missing	Complete	Complete	Complete	Complete	Complete	241+611	448	241	241	241	88+241	241+611	88+241+611	
Viruses	KER2008.12	Q23.17	3988.25	BL01.DG	286.36	CNE56	CNE19	25710-2.43	0077.V1.C16	BG505	BG505 Δ88	BG505 Δ611	BG505 Δ88+Δ611	
Guinea pig ID	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	
CGP606-1	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	6,910 765	7,461 745	8,931 2,474	8,494 1,249	1
CGP606-2	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	2,434 330	1,149 205	5,499 1,608	2,736 502	1
CGP606-3	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	20,000 3,972	20,000 4,045	20,000 4,914	20,000 5,018	1
CGP606-4	<20 <20	-* -*	-* -*	-* -*	-* -*	-* -*	<20 <20	<20 <20	<20 <20	1,324 260	684 88	5,998 887	3,874 172	1
CGP606-5	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	1,315 288	611 119	5,394 2,026	2,583 309	1

* No enough sera to test

<20
20-100
100-1000
1000-10000
>10000

f

Week 18 sera neutralization of the NHP group, immunized with only 3x BG505.DS.SOSIP Env trimer

Clade	A	A	B	B	C	AE	BC	C	C	A	A	A	A	Wild type viruses neutralization #/10 in ID50
Glycan missing	Complete	Complete	Complete	Complete	Complete	241+611	448	241	241	241	88+241	241+611	88+241+611	
Viruses	KER2008.12	Q23.17	3988.25	BL01.DG	286.36	CNE56	CNE19	25710-2.43	0077.V1.C16	BG505	BG505 D88	BG505 D611	BG505 D88+611	
NHP ID	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	ID50 ID80	
A12V163	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	322 57	449 123	0
A12V193	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	66 <20	42 <20	139 27	363 74	1
A12V168	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	290 118	45 27	<20 <20	455 155	307 104	572 159	742 226	3
A12V049	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	1,034 272	787 251	909 278	1,280 447	1
A12V145	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	<20 <20	34 <20	70 <20	0

<20
20-100
100-1000
1000-10000
>10000

Supplementary Figure 7. Comparator mouse, guinea pig and NHP immunization experiments. a, FP8-KLH mouse immunizations with or without Env-trimer prime. Sera neutralization and antibody isolation is shown. **b,** Two tailed Mann-Whitney comparing of vFP1-class antibody SHM with and without Env-trimer prime (n=11 for Antibodies without trimer prime, n= 12 for Antibodies with trimer prime, means ± s.d were displayed). (**c-d**) Repeat immunization experiment of mouse ID 2716 with control. **c,** Experimental mouse immunization schema and neutralization on Δ88+611 BG505 virus. **d,** Statistical comparison, by single-tailed Mann-Whitney; Geometric mean and geometric SD were displayed, n= 5 animals. **e,** Week 18 sera neutralization of a guinea pig comparator group, immunized with 3x BG505 DS-SOSIP Env trimer at week 0, 4 and 16. **f,** Week 18 sera neutralization of a NHP comparator group, immunized with 3x BG505 DS-SOSIP Env trimer at week 0, 4 and 16.

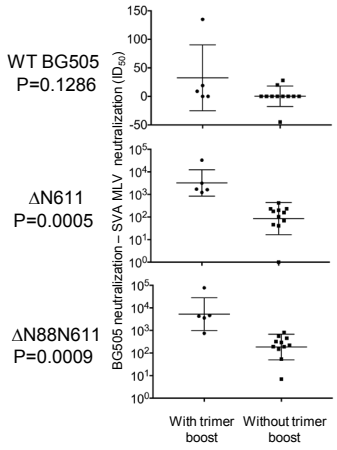
a

Immunization regimens								SVA MLV			BG505 WT			BG505 Δ611 glycan			BG505 Δ88+Δ611 glycans			Hybridoma-identified antibodies	
Mouse ID	Trimer prime	FP-KLH immunization				Trimer Boost	Days post-prime	ID50	ID80	Max % Neut	ID50	ID80	Max % Neut	ID50	ID80	Max % Neut	ID50	ID80	Max % Neut	Cross-clade ΔGlycan-only	Non-neutralizing
2703	T1	FP6	FP6	FP6			71	<20	<20	36	<20	<20	41	221	<20	79	471	48	85	*vFP12.01-06*	
2706	T1	FP7	FP7	FP7			71	<20	<20	50	<20	<20	36	66	<20	75	210	27	83	*vFP13.01-03*, vFP14.01-02	
2711	T1	FP9	FP9	FP9			74	<20	<20	49	<20	<20	36	441	74	90	834	139	94	*vFP15.01-07*	
2712	T1	FP10	FP10	FP10			80	195	<20	81	150	<20	70	155	49	81	202	54	86	*vFP16.01-02*	
2713	T1	FP10	FP10	FP10			80	128	<20	74	156	<20	68	169	21	81	182	53	86	*vFP17.01*	
2714	T1	FP10	FP10	FP10			78	90	<20	63	110	<20	73	269	41	91	282	78	92	vFP18.01-02, vFP19.01-02	
2716	T1	FP8	FP7	FP6		T2	91	<20	<20	35	155	38	86	33,118	8,844	100	77,279	17,983	99	*vFP20.01*	
2717	T1	FP8	FP7	FP6			74	<20	<20	38	<20	<20	40	251	48	89	574	68	89	*vFP21.01*	
2718	T1	FP8	FP9	FP10		T2	92	<20	<20	45	20	<20	50	1,732	187	95	4,292	382	95	vFP22.01	
2719	T1	FP8	FP9	FP10			78	<20	<20	35	<20	<20	47	123	22	82	241	67	94	*vFP23.01-03*, vFP24.01, vFP25.01-18	
2787	T1	FP8	FP8	FP8			68	<20	<20	34	<20	<20	44	178	<20	81	314	25	82	*vFP26.01-04*	
2788	T1	FP8	FP8	FP8	FP8		90	<20	<20	33	<20	<20	25	89	<20	78	167	<20	80	*vFP27.01*	
2789	T1	FP8	FP8	FP8	FP8		91	<20	<20	39	<20	<20	36	250	28	84	342	67	91	*vFP28.01, vFP29.01*	
2790	T1	FP8	FP8			T2	68	<20	<20	34	<20	<20	41	1,649	54	87	772	148	95	*vFP30.01-02*	
2791	T1	FP8	FP8			T2	69	<20	<20	42	39	<20	62	3,174	416	96	4,635	855	97	*vFP31.01*	
2792	T1	FP8	FP8			T2	69	<20	<20	35	29	<20	57	1,243	297	98	3,608	789	98	*vFP32.01-07*	

Key:
FP6 = AVGIGA
FP7 = AVGIGAV
FP8 = AVGIGAVF
FP9 = AVGIGAVFL
FP10 = AVGIGAVFLG
T1 = BG505 SOSIP
T2 = BG505 DS-SOSIP

ID50	ID80
<40	<20
40-100	20-100
100-1000	
1000-10000	
>10000	

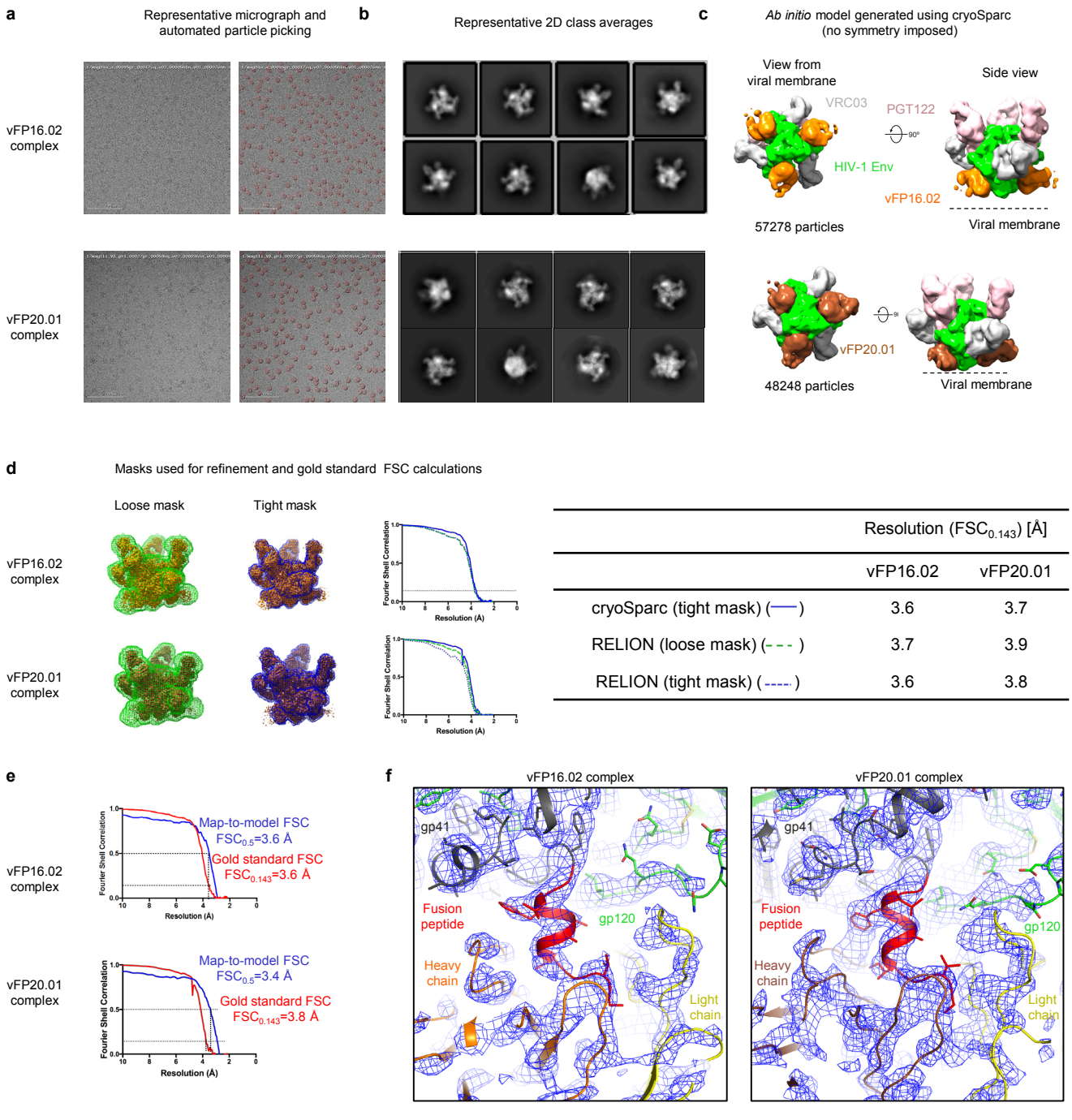
b



c Serum neutralization

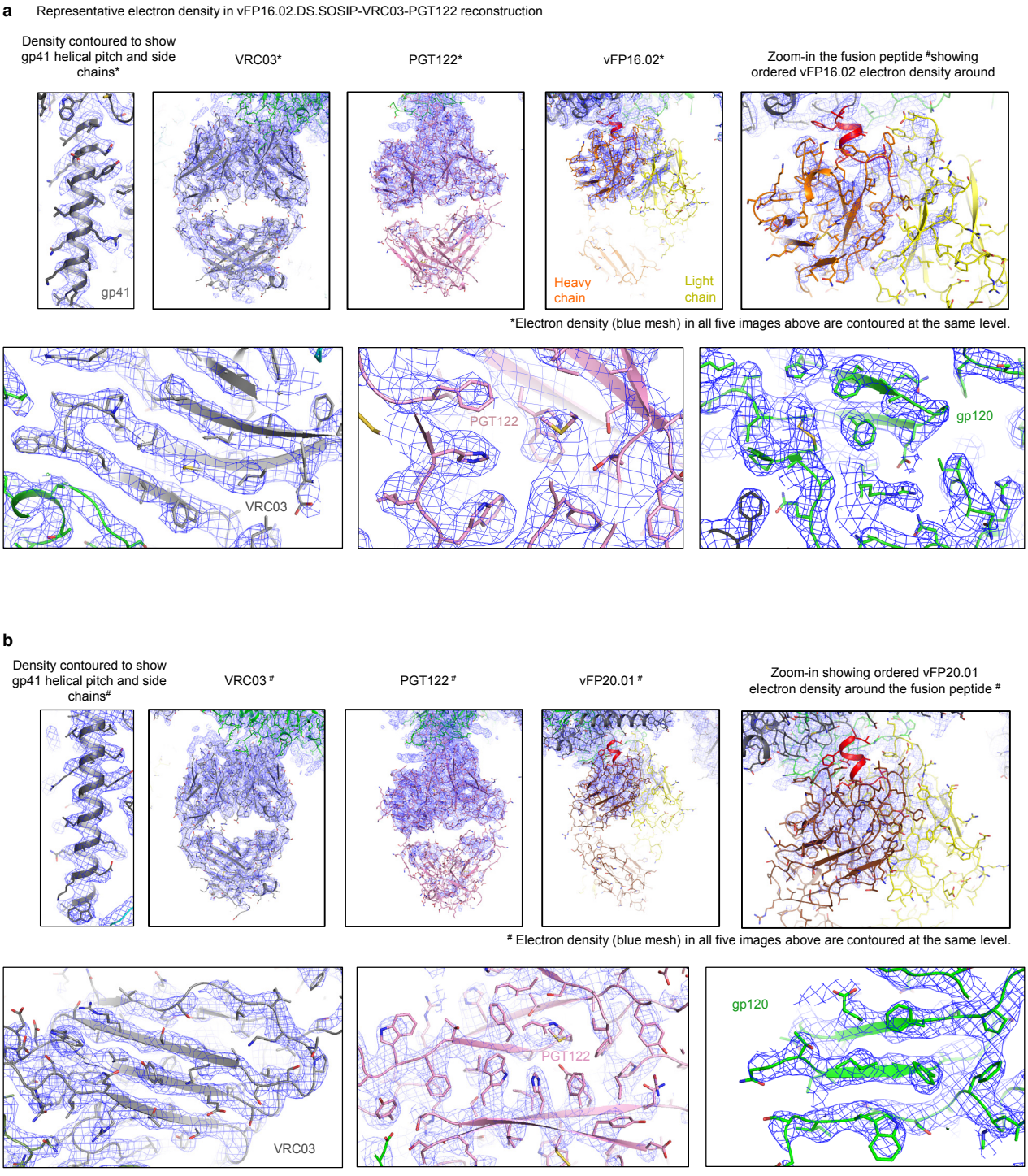
Clade			A		A		B		B		C		A		AE		BC		C		C	
Glycan missing			Complete		Complete		Complete		Complete		Complete		241		241/611		448		241		241	
Viruses	SVA-MLV		KER2008.12		Q23.17		3988.25		BL01.DG		286.36		BG505 WT		CNE56		CNE19		25710-2.43		0077.V1.C16	
Mouse ID	ID50	ID80	ID50	ID80	ID50	ID80	ID50	ID80	ID50	ID80	ID50	ID80	ID50	ID80	ID50	ID80	ID50	ID80	ID50	ID80	ID50	ID80
2716	<20	<20	60	<20	242	<20	339	22	158	46	90	<20	155	38	822	222	277	39	843	174	157	41
2718	<20	<20	28	<20	41	<20	40	<20	36	<20	26	<20	20	<20	59	<20	32	<20	119	32	35	<20
2790	<20	<20	22	<20	37	<20	42	<20	43	<20	23	<20	<20	<20	22	<20	65	<20	76	<20	23	<20
2791	<20	<20	39	<20	61	<20	69	<20	73	<20	45	<20	39	<20	75	25	61	<20	134	26	45	<20
2792	<20	<20	26	<20	37	<20	43	<20	69	21	36	<20	29	<20	46	21	50	<20	157	40	34	<20

Supplementary Figure 8. Second-generation murine immunization schema and elicited serum neutralization. a, 16 mice and 11 immunization schema (left), with neutralization (middle) and hybridoma-identified antibodies (right). Names for vFP1-class antibodies are italicized and colored according to neutralization properties as indicated. **b,** Trimer boost induced significantly higher serum neutralization titers by two-tailed Mann-Whitney. n=5 for "with trimer boost" group and n=11 for "without trimer group boost"; mean and SD were displayed for WT BG505 panel, and geometric mean and geometric SD were displayed for the other two panels. **c,** Neutralization by trimer-boosted sera on 10 wildtype isolates, 5 with complete glycans around FP and 5 naturally missing select glycans as specified, with ID50/ID80 colored as in (**a**). **d,** Neutralization dendrograms. Top row: 208-isolate panel for vaccine-elicited antibodies vFP16.02 and vFP20.01,

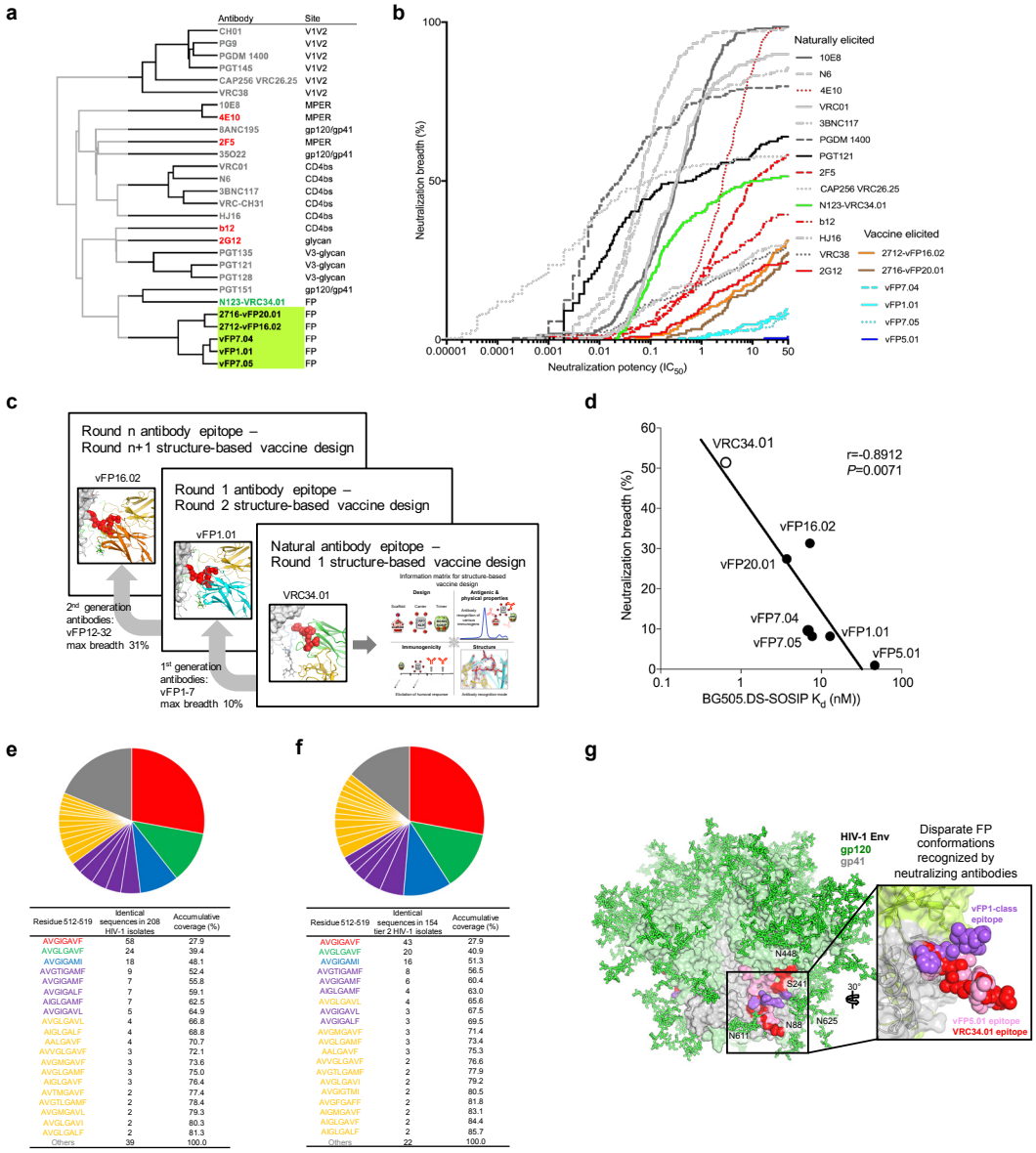


	Resolution ($FSC_{0.143}$) [Å]	
	vFP16.02	vFP20.01
cryoSparc (tight mask) (——)	3.6	3.7
RELION (loose mask) (- - -)	3.7	3.9
RELION (tight mask) (-----)	3.6	3.8

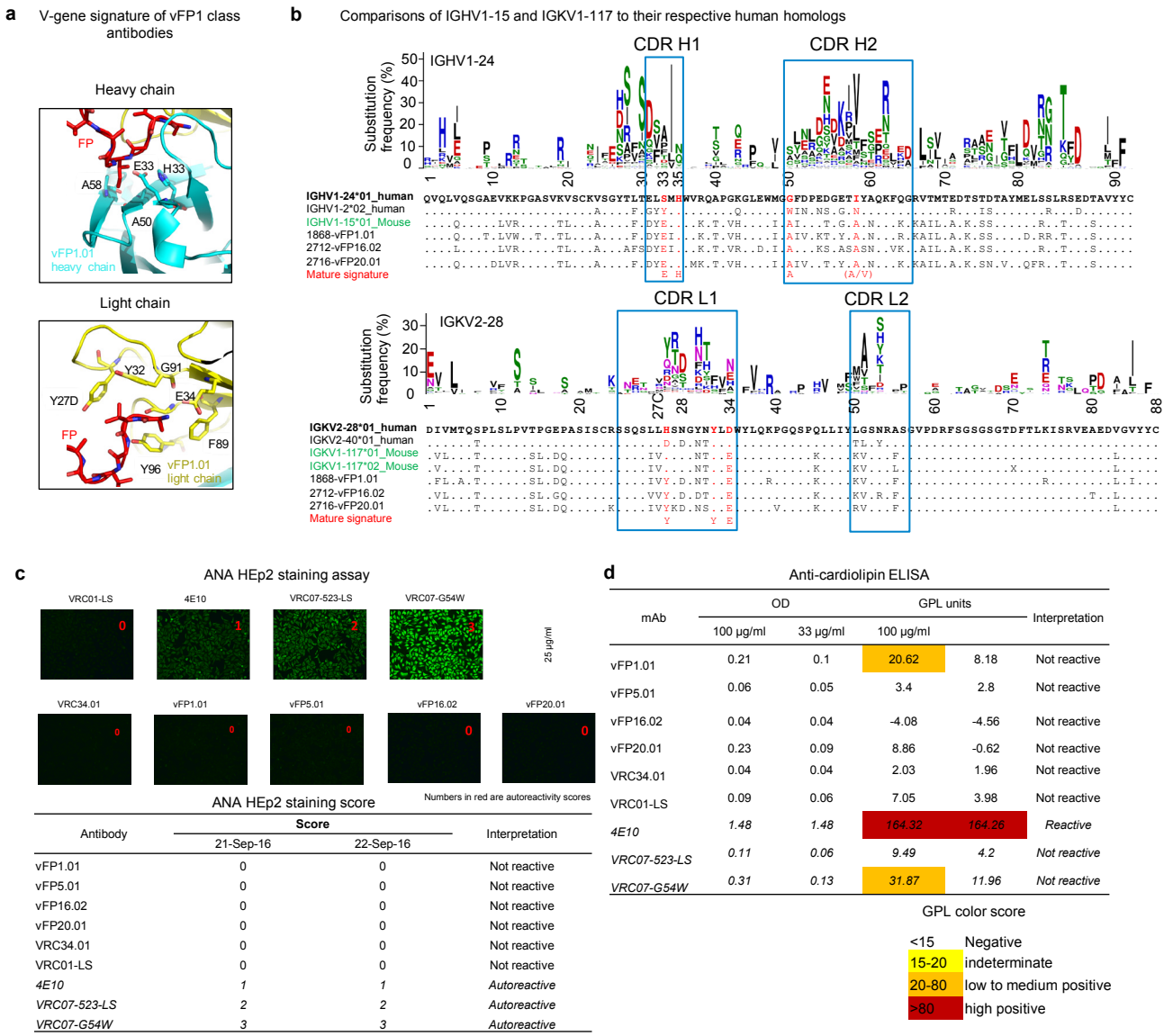
Supplementary Figure 9. Cryo-EM structural details for reconstructions of better than 4 Å resolution. (**a-f**) Details of cryo-EM structures of vFP16.02-BG505 DS-SOSIP-VRC03-PGT122 and vFP20.01-BG505 DS-SOSIP-VRC03-PGT122 complexes. **a,**. Representative micrograph (left) with particles picked with DogPicker shown in red circles (right). **b,** Representative 2D class averages. **c,** Ab initio models generated using cryoSparc. **d,** Refined map in orange with the mask used for the final iteration of cryoSparc refinement (green) and for FSC calculation (blue) shown as mesh. FSC plots and resolution values reported by cryoSparc and RELION according to the gold standard $FSC_{0.143}$ criterion ($FSC_{0.143}$ shown as dotted line. **e,** Gold standard (red) and map-to-model (blue) FSC correlation curves. The map-to-model FSC curve was calculated for protein residues within the complex excluding the antibody constant domains. **f,** Zoomed-in view of the region around the fusion peptide with electron density shown in blue mesh. Cryo-EM data collection was performed once for each structure. The represented images in (**a** and **b**) was derived from the analysis of many particles in many images. Additional details on cryo-EM data collection, such as total number of particles, number of images, can be found in Supplementary Table 4.



Supplementary Figure 10. Cryo-EM reconstructions reveal focused recognition of the HIV-1 fusion peptide by antibodies vFP16.02 and vFP20.01. a, Top panel. Focused recognition of fusion peptide by vFP16.01. Bottom panel. Representative electron density plots from different regions of the vFP16.02-DS.SOSIP-VRC03-PGT122 structure. **b,** Same as **a,** but for the vFP20.01-DS-SOSIP-VRC03-PGT122 complex.



Supplementary Figure 11. Iterative epitope-based vaccine development to achieve neutralization of heterologous viral strains. a, Dendrogram representing neutralization fingerprints shows vaccine-elicited antibodies to cluster with FP antibodies isolated from HIV-1 infected donors, though as a separate group. **b,** Comparison of HIV-1-neutralization breadth and potency by antibodies isolated from HIV-1 infected donors to vaccine-elicited antibodies. **c,** Schematic showing process of iterative structure-based vaccine design, which involves analysis of elicited antibodies to provide insight into the design and improvement of immunogens and immunization regimens for subsequent cycles of improvement. **d,** Neutralization breadth of FP-directed antibodies versus affinity for stabilized Env trimer. Pearson correlation was displayed, n=7 antibodies. **e,** Sequence diversity of the N-terminal eight residues of FP (residue 512 to 519) in the 208-isolate panel, in pie chart format (top) and table format ranked by their prevalence (bottom). The accumulative coverage of the sequence diversity of these five residues is also shown. **f,** Same as (**e**), but with 154 isolates resistant to neutralization by CD4-induced antibodies, V3-directed antibodies, and F105 antibody. **g,** vFP-defined site of vulnerability allows for target-site conformational diversity.



ANA HEp2 staining score

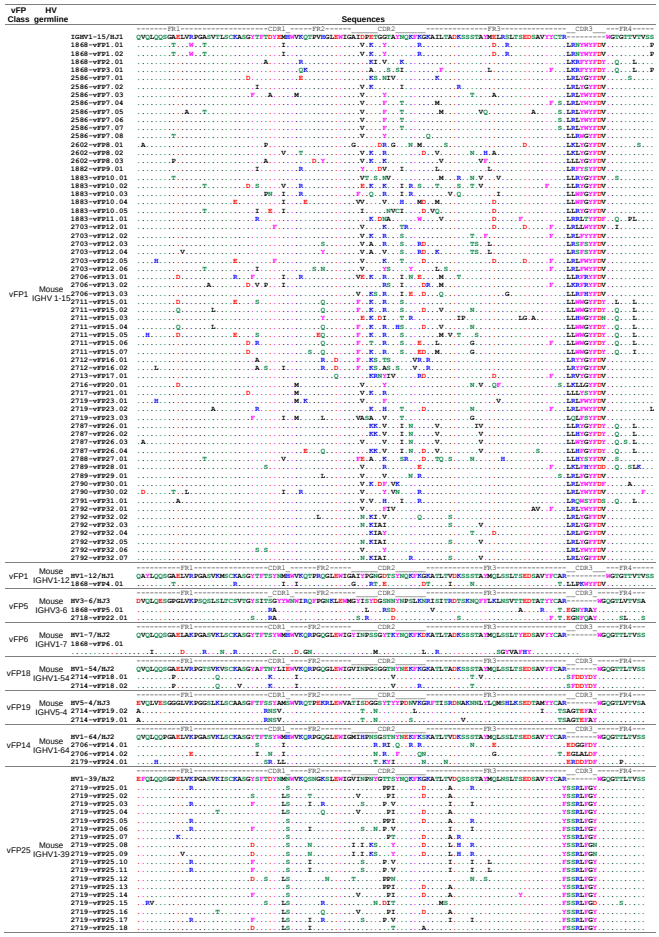
Antibody	Score 21-Sep-16	Score 22-Sep-16	Interpretation
vFP1.01	0	0	Not reactive
vFP5.01	0	0	Not reactive
vFP16.02	0	0	Not reactive
vFP20.01	0	0	Not reactive
VRC34.01	0	0	Not reactive
VRC01-LS	0	0	Not reactive
4E10	*1*	*1*	*Autoreactive*
VRC07-523-LS	*2*	*2*	*Autoreactive*
VRC07-G54W	*3*	*3*	*Autoreactive*

mAb	OD 100 µg/ml	OD 33 µg/ml	GPL units 100 µg/ml	GPL units	Interpretation
vFP1.01	0.21	0.1	20.62	8.18	Not reactive
vFP5.01	0.06	0.05	3.4	2.8	Not reactive
vFP16.02	0.04	0.04	-4.08	-4.56	Not reactive
vFP20.01	0.23	0.09	8.86	-0.62	Not reactive
VRC34.01	0.04	0.04	2.03	1.96	Not reactive
VRC01-LS	0.09	0.06	7.05	3.98	Not reactive
4E10	*1.48*	*1.48*	*164.32*	*164.26*	*Reactive*
VRC07-523-LS	*0.11*	*0.06*	*9.49*	*4.2*	*Not reactive*
VRC07-G54W	*0.31*	*0.13*	*31.87*	*11.96*	*Not reactive*

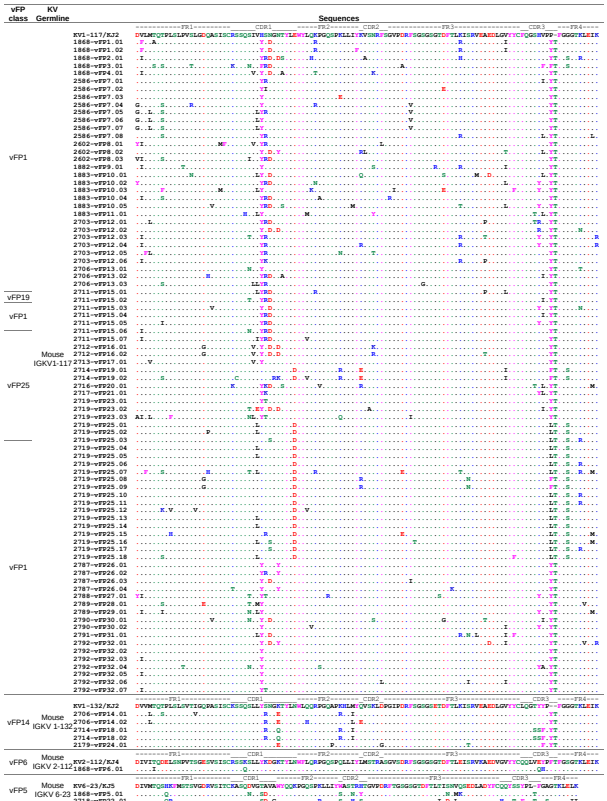
Supplementary Figure 12. vFP1-class antibodies: V-gene similarity to human homologues and autoreactivity. a, V-gene signature of vFP1 class antibodies. Signature residues for heavy chain (top) and light chain (bottom) are showed in sticks and labeled. **b,** Comparisons of IGHV1-15 and IGKV1-117 to their respective human homologs identified by IMGT/V-QUEST and mutation profile of human gene IGHV1-24 and IGKV2-28. Compared to mouse IGHV1-15, human IGHV1-24 contains the H35 signature, and the A50 and A/V58 signatures can be reproduced by somatic hypermutation with high frequencies (See gene-specific substitution profile of IGHV1-24 built from 190 mature human antibody lineages, with one sequence per lineage). This suggested similar key signatures may be reproduced by human antibodies. However, the alignment also showed multiple germline gene positions are diversified between the homolog genes, further investigations are required to understand whether they will affect FP recognition. The mouse IGKV1-117 was aligned to two human kappa chain genes, IGKV2-28 and IGKV2-40. Similar to mouse IGKV1-117, the IGKV2-28 also has a His-Ser-Asn motif in CDR L1. We built a substitution profile for IGKV2-28 using 104 antibody lineages derived from repertoires of three healthy human donors. The substitution profile showed that the key signatures of vFP1 antibodies, Y27d, Y32, and E34 are either germline residue or mutations with high frequency in human IGKV2-28 antibodies, suggesting the signatures observed in the vFP1 antibodies can be obtained with high frequency. V gene positions numbered using Kabat system.(**c-d**) Autoreactivity analysis of FP-directed antibodies. **c,** ANA Hep-2 staining analysis showed none of the five FP-directed antibodies are autoreactive. Control antibodies with known autoreactivity are italicized. The experiment was performed twice (n=2) independently. **d,** Anti-cardiolipin ELISA showed none of the three FP-directed antibodies to be reactive. Control values italicized as in (**c**). The experiment was performed only once.

Supplementary Table 1. Amino acid sequences and alignment of vFP antibodies.

a. Amino acid sequence alignment of heavy chain variable region.



b. Amino acid sequence alignment of light chain variable region.



CDR regions are defined according to kabat numbering system. We define antibody lineages to be members of the same antibody class if lineage members have the same mode of recognition and utilize similar B cell pathways of development (Kwong and Mascola, 2012).

Chemical Characteristics	Amino Acids
Polar Positive charge	HKR
Polar Negative charge	DE
Polar Neutral	CNQST
Non-polar Neutral	AGILMPV
Nonpolar Aromatic Neutral	FWY

Supplementary Table 2. V(D)J recombination of vFP lineages. (continued on next page)

a

Germline nucleotide and amino acid residues are shown in black with the corresponding junctions colored in light blue. Somatic hypermutation events are colored red. Nucleotides deleted by exonuclease trimming are crossed out. The N, P additions occurring at the junctions and the gene assignment are from IMGT Vquest (http://www.imgt.org/IMGT_vquest/share/textes/).

Supplementary Table 2. V(D)J Recombination of vFP lineages. (continued from prior page)

b

1868

Light chain

H \ L	vFP1.01	vFP1.02	vFP2.01	vFP3.01	vFP4.01	vFP5.01	vFP6.01
vFP1.01		0	15	15	0	132	93
vFP1.02	0		15	15	0	132	93
vFP2.01	20	20		0	15	143	96
vFP3.01	17	17	3		15	143	96
vFP4.01	41	41	56	58		132	93
vFP5.01	177	177	174	174	179		140
vFP6.01	81	81	63	66	76	173	

Heavy chain

2706

Light chain

H \ L	vFP13.01	vFP13.02	vFP13.03	vFP14.01	vFP14.02
vFP13.01		0	0	65	65
vFP13.02	13		0	65	65
vFP13.03	13	0		65	65
vFP14.01	66	62	62		0
vFP14.02	65	60	60	2	

Heavy chain

1883

Light chain

H \ L	vFP10.01	vFP10.02	vFP10.03	vFP10.04	vFP10.05	vFP11.01
vFP10.01		0	0	0	0	0
vFP10.02	1		0	0	0	0
vFP10.03	3	2		0	0	0
vFP10.04	3	2	0		0	0
vFP10.05	1	0	2	2		0
vFP11.01	31	31	31	31	31	

Heavy chain

2714

Light chain

H \ L	vFP18.01	vFP18.02	vFP19.01	vFP19.02
vFP18.01		0	73	73
vFP18.02	0		73	73
vFP19.01	148	148		0
vFP19.02	148	148	0	

Heavy chain

2789

Light chain

H \ L	vFP28.01	vFP29.01
vFP28.01		0
vFP29.01	17	

Heavy chain

2719

Light chain

H \ L	vFP23.01	vFP23.02	vFP23.03	vFP24.01	vFP25.01	vFP25.02	vFP25.03	vFP25.04	vFP25.05	vFP25.06	vFP25.07	vFP25.08	vFP25.09	vFP25.10	vFP25.11	vFP25.12	vFP25.13	vFP25.14	vFP25.15	vFP25.16	vFP25.17	vFP25.18
vFP23.01		0	0	65	0	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
vFP23.02	0		0	65	0	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
vFP23.03	0	0		65	0	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
vFP24.01	80	80	80		65	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73
vFP25.01	85	85	85	62		8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
vFP25.02	85	85	85	62	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
vFP25.03	85	85	85	62	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
vFP25.04	85	85	85	62	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0
vFP25.05	85	85	85	62	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0
vFP25.06	85	85	85	62	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0
vFP25.07	85	85	85	62	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0
vFP25.08	85	85	85	62	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0
vFP25.09	85	85	85	62	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0
vFP25.10	85	85	85	62	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0
vFP25.11	85	85	85	62	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0
vFP25.12	85	85	85	62	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0
vFP25.13	85	85	85	62	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0
vFP25.14	83	83	83	60	21	21	21	21	21	21	21	21	21	21	21	21	21		0	0	0	0
vFP25.15	86	86	86	63	1	1	1	1	1	1	1	1	1	1	1	1	1	22		0	0	0
vFP25.16	81	81	81	66	10	10	10	10	10	10	10	10	10	10	10	10	10	22	11		0	0
vFP25.17	85	85	85	62	0	0	0	0	0	0	0	0	0	0	0	0	0	21	1	10		0
vFP25.18	85	85	85	62	0	0	0	0	0	0	0	0	0	0	0	0	0	21	1	10	0	

Heavy chain

For each mouse with more than one vFP lineage, we performed pairwise comparison of nucleotide differences separating germline versions of heavy (blue) and light (yellow) chain variable regions. Mouse ID is listed in upper left of each table.

Supplementary Table 3. vFP antibody and sera neutralization.

a. vFP antibody neutralization against a panel of 208 isolates.

High Throughput Antibody Screen - FP mAbs
Assay - Luc/TZM-bl
values represent in ug/ml

Color key: <0.001 | .001-.01 | .01-.100 | .100-1.00 | 1.00-10.0 | >10.0

IC50

	HT Panel:	V	V	W	W	24	24	26	V	B	J	A	V	J	R
Virus ID	**Clade**	**vFP1.01**	**vFP5.01**	**vFP7.04**	**vFP7.05**	**vFP20.01**	**vFP16.02**	**vFP16.02**	**VRC34.01**	**17b**	**48d**	**F105**	**3074**	**447-52D**	**PGT151**
0260.v5.c36	A	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.018
0330.v4.c3	A	>100	>100	>100	>100	>100	>100	>500	0.039	>50	>50	>50	>50	>50	0.005
0439.v5.c1	A	>100	>100	>100	>100	>100	36.6	101	0.275	>50	>50	>50	>50	>50	0.021
3365.v2.c20	A	>100	>100	>100	>100	58.1	56.0	35.0	0.036	>50	>50	>50	0.689	>50	0.004
3415.v1.c1	A	>100	>100	>100	>100	>100	>100	>500	0.068	>50	>50	>50	>50	>50	0.003
3718.v3.c11	A	>100	>100	>100	>100	>100	>100	>500	0.752	>50	>50	>50	>50	>50	0.026
398-F1_F6_20	A	62.6	>100	>100	38.0	2.62	4.19	5.07	0.112	>50	>50	>50	>50	>50	0.006
BB201.B42	A	40.3	>100	51.6	>100	1.69	0.531	0.650	0.053	>50	>50	>50	>50	>50	0.019
BB539.2B13	A	>100	>100	>100	>100	54.4	>100	178	1.33	>50	>50	>50	>50	>50	0.002
BG505.W6M.C2	A	21.9	>100	14.7	49.0	1.70	2.51	2.52	0.083	>50	>50	>50	>50	>50	0.001
BI369.9A	A	1.42	>100	2.68	4.40	0.631	0.400	0.920	0.058	>50	>50	>50	>50	>50	0.034
BS208.B1	A	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	0.765	>50	0.017
KER2008.12	A	>100	>100	56.0	>100	11.2	1.13	1.55	0.036	>50	>50	>50	>50	>50	0.006
KER2018.11	A	>100	>100	>100	>100	>100	>100	>500	0.182	>50	>50	>50	>50	>50	0.007
KNH1209.18	A	>100	>100	>100	>100	35.6	>100	119	0.401	>50	>50	>50	>50	>50	0.008
MB201.A1	A	>100	>100	51.0	>100	1.09	0.453	0.790	0.046	>50	>50	>50	>50	>50	0.011
MB539.2B7	A	>100	>100	>100	>100	>100	11.3	21.0	0.256	>50	>50	>50	>50	>50	0.013
MI369.A5	A	4.31	>100	15.4	>100	1.19	0.340	0.630	0.147	>50	>50	>50	>50	>50	0.030
MS208.A1	A	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	18.0	>50	0.003
Q23.17	A	18.8	>100	13.9	44.4	2.16	0.733	0.560	0.098	>50	>50	>50	>50	>50	0.007
Q259.17	A	>100	>100	>100	>100	>100	17.7	43.6	1.58	>50	>50	>50	>50	>50	>50
Q769.d22	A	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
Q769.h5	A	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
Q842.d12	A	>100	>100	>100	>100	25.2	15.5	31.6	0.091	>50	>50	>50	>50	>50	0.006
QH209.14M.A2	A	>100	>100	>100	>100	3.52	50.0	51.2	0.143	>50	>50	>50	>50	>50	0.005
RW020.2	A	>100	>100	>100	>100	26.8	21.4	34.5	2.71	>50	>50	>50	34.0	>50	0.006
UG037.8	A	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
246-F3.C10.2	AC	>100	>100	>100	>100	34.7	>100	71.2	0.316	>50	>50	>50	>50	>50	>50
3301.V1.C24	AC	>100	>100	>100	>100	18.5	11.2	11.5	0.105	>50	>50	>50	>50	>50	0.024
3589.V1.C4	AC	>100	>100	>100	>100	>100	>100	>500	0.075	>50	>50	>50	>50	>50	0.003
6540.v4.c1	AC	>100	>100	>100	>100	>100	>100	>500	0.185	>50	>50	>50	>50	>50	0.007
6545.V4.C1	AC	>100	>100	>100	>100	>100	>100	>500	0.149	>50	>50	>50	>50	>50	0.008
0815.V3.C3	ACD	12.8	>100	11.0	98.0	1.02	0.247	0.170	0.024	>50	>50	>50	>50	>50	>50
6095.V1.C10	ACD	>100	>100	>100	>100	>100	>100	>500	>100	8.88	16.4	4.69	>50	0.551	>50
3468.V1.C12	AD	>100	>100	>100	>100	>100	>100	>500	0.105	>50	>50	>50	>50	>50	0.066
Q168.a2	AD	>100	>100	>100	>100	59.3	59.9	81.1	0.230	>50	>50	>50	>50	>50	0.011
Q461.e2	AD	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
620345.c1	AE	>100	>100	>100	>100	>100	77.9	99.3	>100	>50	>50	>50	>50	>50	>50
BJOX009000.02	AE	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
BJOX010000.06	AE	>100	>100	>100	>100	97.9	14.7	14.5	>100	>50	>50	>50	>50	>50	>50
BJOX025000.01	AE	>100	>100	>100	>100	>100	>100	58.5	>100	>50	>50	>50	>50	>50	>50
BJOX028000.10	AE	>100	>100	>100	>100	>100	>100	>500	57	>50	>50	>50	>50	>50	>50
C1080.c3	AE	>100	>100	>100	>100	>100	19.0	15.0	4.46	>50	>50	>50	>50	>50	>50
C2101.c1	AE	>100	>100	>100	>100	71.4	11.7	13.1	0.218	>50	>50	>50	>50	>50	>50
C3347.c11	AE	>100	>100	>100	>100	>100	>100	344	>100	>50	>50	>50	>50	>50	>50
C4118.09	AE	>100	>100	>100	>100	>100	57.9	70.8	>100	>50	>50	>50	>50	>50	>50
CM244.ec1	AE	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
CNE3	AE	>100	>100	>100	>100	>100	>100	>500	6.93	>50	>50	>50	>50	>50	>50
CNE5	AE	>100	>100	>100	>100	>100	>100	156	>100	>50	>50	>50	>50	>50	>50
CNE55	AE	>100	>100	>100	>100	>100	45.3	53.9	>100	>50	>50	>50	>50	>50	>50
CNE56	AE	5.91	>100	2.18	1.44	0.508	0.405	0.380	>100	>50	>50	>50	>50	>50	>50
CNE59	AE	>100	>100	>100	>100	>100	47.8	48.3	>100	>50	>50	>50	>50	>50	>50
CNE8	AE	>100	>100	>100	>100	>100	>100	276	23.6	>50	>50	>50	0.890	>50	>50
M02138	AE	>100	>100	>100	>100	15.8	3.98	10.3	>100	>50	>50	>50	>50	>50	>50
R1166.c1	AE	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
R2184.c4	AE	>100	>100	>100	>100	>100	>100	321	>100	>50	>50	>50	>50	>50	>50
R3265.c6	AE	>100	>100	>100	>100	>100	58.0	52.3	>100	>50	>50	>50	>50	>50	>50
TH023.6	AE	2.14	>100	0.362	0.630	0.358	0.091	0.160	>100	>50	>50	>50	0.043	>50	>50
TH966.8	AE	>100	>100	>100	>100	>100	>100	172	>100	>50	>50	>50	>50	>50	>50
TH976.17	AE	>100	>100	>100	>100	>100	>100	269	>100	>50	>50	>50	>50	>50	>50
235-47	AG	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
242-14	AG	>100	>100	>100	>100	>100	>100	>500	0.107	>50	>50	>50	15.4	>50	0.006
263-8	AG	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
269-12	AG	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.002
271-11	AG	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	0.091	>50	>50
928-28	AG	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
DJ263.8	AG	>100	>100	>100	>100	>100	>100	187	0.167	>50	>50	>50	0.125	22.9	0.005
T250-4	AG	>100	>100	>100	>100	>100	>100	>500	0.150	>50	>50	>50	>50	>50	0.002
T251-18	AG	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.072
T253-11	AG	>100	>100	>100	>100	>100	>100	>500	0.385	>50	>50	>50	>50	>50	0.009
T255-34	AG	>100	>100	>100	>100	>100	>100	>500	0.021	>50	>50	>50	0.403	>50	0.004
T257-31	AG	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.004
T266-60	AG	>100	>100	>100	>100	>100	>100	>500	0.070	>50	>50	>50	>50	>50	0.013
T278-50	AG	>100	>100	>100	>100	>100	>100	>500	0.024	>50	>50	>50	>50	>50	0.030
T280-5	AG	>100	>100	>100	>100	>100	>100	>500	0.069	>50	>50	>50	>50	>50	0.014
T33-7	AG	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
3988.25	B	>100	>100	>100	>100	5.06	18.7	10.7	0.059	>50	>50	>50	>50	>50	0.008
5768.04	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.040
6101.10	B	>100	>100	>100	>100	39.2	23.7	30.0	0.366	>50	>50	>50	>50	>50	0.013
6535.3	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	3.08	3.04	0.412	0.006
7165.18	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
45_01dG5	B	>100	>100	>100	>100	47.0	>100	133	0.771	>50	>50	>50	>50	>50	0.013
89.6.DG	B	>100	>100	>100	>100	7.87	3.14	6.63	0.041	>50	>50	>50	>50	0.005	>50
AC10.29	B	>100	>100	>100	26.4	1.90	6.47	15.5	>100	>50	>50	>50	>50	>50	0.007
ADA.DG	B	>100	>100	>100	>100	>100	>100	>500	>100	0.269	3.57	2.02	0.162	0.016	>50
Bal.01	B	>100	>100	>100	>100	3.25	3.78	2.47	0.616	>50	>50	>50	0.645	0.084	0.018
BaL.26	B	>100	>100	>100	>100	73.6	23.0	26.7	>100	>50	>50	10.9	0.855	0.028	0.016
BG1168.01	B	>100	>100	>100	>100	>100	>100	>500	2.14	>50	>50	>50	>50	>50	0.021
BL01.DG	B	78.1	>100	22.8	27.6	2.87	1.15	1.85	0.051	>50	>50	>50	>50	>50	0.006
BR07.DG	B	>100	>100	>100	>100	2.94	6.02	9.95	>100	>50	41.3	>50	>50	0.390	>50
BX08.16	B	>100	>100	22.4	13.7	2.59	2.06	5.04	0.341	1.86	24.7	9.73	1.97	0.064	0.002
CAAN.A2	B	>100	>100	>100	>100	>100	>100	>500	1.93	>50	>50	>50	>50	>50	0.012
CNE10	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
CNE12	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.020
CNE14	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.007
CNE4	B	>100	>100	>100	>100	>100	>100	>500	0.234	14.7	4.20	13.6	>50	7.49	>50
CNE57	B	>100	>100	43.4	>100	3.39	0.825	0.610	0.029	49.3	>50	>50	>50	2.26	0.006
HO86.8	B	>100	>100	>100	>100	15.2	2.26	2.77	0.440	>50	>50	>50	>50	14.4	>50
HT593.1	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	15.1	>50	>50	2.56	0.007
HXB2.DG	B	1.21	49.0	1.01	0.840	0.217	0.177	0.220	0.132	2.28	0.594	0.167	>50	0.006	0.014
JRCSF.JB	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	3.03	0.157	0.013
JRFL.JB	B	>100	>100	>100	>100	23.0	25.8	50.7	0.087	>50	>50	>50	>50	3.68	0.008
MN.3	B	>100	81.7	>100	>100	>100	>100	>500	>100	0.419	0.065	>50	0.489	0.001	>50
PVO.04	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
QH0515.01	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.005
QH0692.42	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.224
REJO.67	B	>100	>100	>100	>100	37.6	14.5	19.1	>100	>50	>50	>50	15.8	>50	0.045
RHPA.7	B	>100	>100	>100	>100	77.8	>100	213	1.30	>50	>50	>50	>50	>50	0.013
SC422.8	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.010
SF162.LS	B	>100	>100	>100	>100	>100	>100	>500	0.165	0.402	11.3	2.92	0.017	0.028	0.014
SS1196.01	B	>100	>100	>100	>100	>100	>100	>500	>100	11.9	13.7	6.24	0.960	0.365	>50
THRO.18	B	>100	>100	>100	>100	>100	>100	>500	>100	34.2	>50	>50	>50	>50	>50
TRJO.58	B	>100	>100	>100	>100	>100	>100	>500	9.03	>50	>50	>50	>50	>50	0.373
TRO.11	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
WITO.33	B	>100	>100	>100	>100	>100	>100	>500	0.149	>50	>50	>50	>50	33.0	0.012
X2278.C2.B6	B	>100	>100	>100	>100	>100	>100	>500	2.22	>50	>50	>50	>50	>50	0.014
YU2.DG	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	12.1	>50
BJOX002000.03	BC	>100	>100	>100	>100	89.4	>100	132	0.177	>50	>50	>50	>50	>50	0.005
CH038.12	BC	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	31.4	>50	>50
CH070.1	BC	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
CH117.4	BC	34.8	>100	45.6	45.0	1.47	0.393	0.710	0.047	>50	>50	>50	>50	>50	>50
CH119.10	BC	>100	>100	>100	>100	7.32	2.98	3.75	0.053	>50	>50	>50	>50	>50	0.012
CH181.12	BC	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
CNE15	BC	>100	>100	>100	>100	7.85	4.25	11.7	>100	>50	>50	>50	>50	>50	0.020
CNE19	BC	2.69	>100	1.35	2.80	0.253	0.051	0.080	0.023	>50	>50	>50	>50	>50	0.007
CNE20	BC	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	8.71	>50	>50
CNE21	BC	>100	>100	>100	>100	12.0	7.63	14.3	0.039	>50	>50	>50	>50	>50	0.004
CNE40	BC	44.7	59.2	32.6	>100	1.32	0.346	0.620	0.129	0.062	>50	0.242	0.008	0.152	>50
CNE7	BC	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.017
286.36	C	80.4	>100	>100	>100	10.4	3.50	4.14	0.515	>50	>50	>50	>50	>50	0.010
288.38	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	8.30	>50	>50
0013095-2.11	C	>100	>100	>100	>100	66.6	63.6	89.8	>100	>50	>50	>50	3.18	>50	>50
001428-2.42	C	>100	>100	>100	>100	>100	>100	>500	0.051	>50	>50	>50	>50	>50	>50
0077_V1.C16	C	5.20	>100	17.0	25.2	3.66	0.643	0.380	0.607	>50	>50	>50	>50	>50	0.002
00836-2.5	C	>100	>100	>100	>100	>100	9.42	10.8	>100	>50	>50	>50	13.6	>50	0.056
0921.V2.C14	C	>100	>100	>100	>100	66.9	77.4	117	>100	>50	>50	>50	>50	>50	>50
16055-2.3	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
16845-2.22	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
16936-2.21	C	>100	>100	>100	>100	>100	>100	>500	0.072	>50	>50	>50	>50	>50	>50
25710-2.43	C	0.578	>100	1.08	5.02	0.211	0.104	0.070	3.09	>50	>50	>50	15.7	>50	>50
25711-2.4	C	>100	>100	>100	>100	>100	>100	120	>100	>50	>50	>50	>50	>50	0.004
25925-2.22	C	>100	>100	>100	>100	>100	>100	>500	0.086	>50	>50	>50	>50	>50	0.005
26191-2.48	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
3168.V4.C10	C	>100	>100	>100	>100	>100	>100	>500	2.55	>50	>50	>50	>50	>50	>50
3637.V5.C3	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
3873.V1.C24	C	>100	>100	>100	>100	13.7	36.7	40.7	0.214	>50	>50	>50	5.32	>50	0.002
426c	C	>100	>100	>100	>100	49.9	44.4	69.6	0.079	>50	>50	>50	>50	>50	0.005
6322.V4.C1	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
6471.V1.C16	C	>100	>100	>100	>100	>100	93.7	91.7	>100	>50	>50	>50	>50	>50	>50
6631.V3.C10	C	>100	>100	>100	>100	>100	24.9	42.7	>100	>50	>50	>50	>50	>50	0.006
6644.V2.C33	C	>100	>100	>100	>100	>100	>100	>500	0.026	>50	>50	2.30	0.022	>50	>50
6785.V5.C14	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
6838.V1.C35	C	>100	>100	>100	>100	>100	>100	>500	0.034	>50	>50	>50	>50	>50	>50
96ZM651.02	C	4.91	>100	21.8	21.8	0.504	0.240	0.490	0.038	>50	>50	>50	>50	>50	0.009
BR025.9	C	>100	>100	>100	>100	41.8	22.0	28.5	0.300	>50	>50	>50	0.619	>50	>50
CAP210.E8	C	>100	>100	>100	>100	>100	43.8	77.5	0.091	>50	>50	>50	>50	>50	0.018
CAP244.D3	C	>100	>100	>100	>100	>100	>100	178	>100	>50	>50	>50	>50	>50	>50
CAP256.206.C9	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
CAP45.G3	C	>100	>100	>100	>100	>100	6.65	12.8	0.045	>50	>50	>50	>50	>50	0.008
Ce1176.A3	C	>100	>100	>100	>100	33.4	29.4	70.1	0.154	>50	>50	>50	>50	>50	0.006
CE703010217.B	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
CNE30	C	>100	>100	>100	>100	>100	>100	>500	0.158	>50	>50	>50	>50	>50	>50
CNE31	C	>100	>100	>100	>100	>100	>100	142	0.061	>50	>50	>50	>50	>50	0.005
CNE53	C	>100	>100	>100	>100	>100	>100	>500	0.058	>50	>50	>50	>50	>50	>50
CNE58	C	>100	>100	>100	>100	37.5	>100	85.6	0.124	>50	>50	>50	>50	>50	0.002
DU123.06	C	>100	>100	36.2	>100	3.23	0.281	0.250	6.07	>50	>50	>50	15.5	>50	>50
DU151.02	C	>100	>100	>100	>100	>100	>100	>500	2.20	>50	>50	>50	>50	>50	0.040
DU156.12	C	>100	>100	>100	>100	>100	78.2	67.1	>100	>50	>50	>50	>50	>50	0.005
DU172.17	C	>100	>100	>100	>100	19.7	24.7	65.3	0.062	>50	>50	>50	>50	>50	0.003
DU422.01	C	>100	>100	>100	>100	>100	>100	>500	1.03	>50	>50	>50	>50	>50	>50
MW965.26	C	14.6	17.2	19.2	28.6	3.32	1.47	1.83	35.8	0.247	>50	>50	0.004	0.048	0.017
SO18.18	C	6.44	>100	27.0	7.98	1.01	0.963	1.38	0.091	>50	>50	>50	>50	>50	0.007
TV1.29	C	>100	>100	>100	>100	21.3	20.5	36.2	0.129	>50	>50	>50	3.38	>50	0.004
TZA125.17	C	>100	>100	>100	>100	>100	>100	180	>100	>50	>50	>50	>50	>50	0.096
TZBD.02	C	>100	>100	>100	>100	36.8	12.9	102	0.662	>50	>50	>50	>50	>50	0.006
ZA012.29	C	>100	>100	>100	>100	>100	>100	>500	1.23	>50	>50	>50	>50	>50	0.059
ZM106.9	C	>100	>100	>100	>100	3.82	1.40	1.75	>100	>50	>50	>50	>50	>50	>50
ZM109.4	C	>100	>100	>100	>100	>100	>100	100	1.29	>50	>50	>50	1.20	>50	>50
ZM135.10a	C	>100	>100	>100	>100	>100	29.5	44.0	>100	>50	>50	>50	>50	>50	>50
ZM176.66	C	>100	>100	>100	>100	35.8	10.6	8.87	0.318	>50	>50	>50	>50	>50	0.005
ZM197.7	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.005
ZM214.15	C	>100	>100	>100	>100	>100	>100	76.9	0.269	>50	>50	>50	>50	>50	0.017
ZM215.8	C	>100	>100	>100	>100	>100	>100	>500	3.56	>50	>50	>50	>50	>50	0.046
ZM233.6	C	>100	>100	>100	>100	15.5	20.2	33.8	0.033	>50	>50	>50	35.8	>50	0.010
ZM249.1	C	>100	>100	>100	>100	>100	>100	>500	0.033	>50	>50	>50	>50	>50	0.006
ZM53.12	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
ZM55.28a	C	>100	>100	>100	>100	26.6	50.2	101	0.155	>50	>50	>50	>50	>50	0.005
3326.V4.C3	CD	>100	>100	>100	>100	>100	>100	>500	16.2	>50	>50	>50	>50	>50	0.442
3337.V2.C6	CD	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	0.663	>50	0.300
3817.v2.c59	CD	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
191821.E6.1	D	>100	>100	>100	>100	>100	>100	>500	3.88	>50	>50	>50	>50	>50	0.112
231965.c1	D	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.015
247-23	D	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
3016.v5.c45	D	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	35.2	>50	0.500
57128.vrc15	D	>100	>100	>100	>100	>100	>100	>500	>100	13.9	3.99	0.940	2.26	45.0	>50
6405.v4.c34	D	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.026
A03349M1.vrc4	D	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
A07412M1.vrc1	D	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
NKU3006.ec1	D	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
UG021.16	D	>100	>100	>100	>100	>100	>100	>500	>100	0.144	>50	0.382	>50	>50	0.010
UG024.2	D	>100	>100	>100	>100	>100	>100	>500	>100	0.046	1.35	0.043	>50	>50	>50
P0402.c2.11	G	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.004
P1981.C5.3	G	>100	>100	>100	>100	>100	>100	>500	1.17	>50	>50	>50	>50	>50	>50
X1193.c1	G	>100	>100	>100	>100	>100	>100	>500	0.430	>50	>50	>50	>50	>50	0.019
X1254.c3	G	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.015
X1632.S2.B10	G	>100	>100	>100	>100	>100	>100	>500	6.45	>50	>50	>50	2.81	>50	>50
X2088.c9	G	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
X2131.C1.B5	G	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	0.551	>50	0.007
SIVmac251.30.	NA	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
SVA.MLV	NA	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50

IC80

	HT Panel:	V	V	W	W	24	24	26	V	B	J	A	V	J	R
Virus ID	**Clade**	**vFP1.01**	**vFP5.01**	**vFP7.04**	**vFP7.05**	**vFP20.01**	**vFP16.02**	**vFP16.02**	**VRC34.01**	**17b**	**48d**	**F105**	**3074**	**447-52D**	**PGT151**
0260.v5.c36	A	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
0330.v4.c3	A	>100	>100	>100	>100	>100	>100	>500	0.121	>50	>50	>50	>50	>50	0.018
0439.v5.c1	A	>100	>100	>100	>100	>100	>100	>500	2.19	>50	>50	>50	>50	>50	>50
3365.v2.c20	A	>100	>100	>100	>100	>100	>100	259	0.130	>50	>50	>50	16.1	>50	0.014
3415.v1.c1	A	>100	>100	>100	>100	>100	>100	>500	0.421	>50	>50	>50	>50	>50	0.010
3718.v3.c11	A	>100	>100	>100	>100	>100	>100	>500	10.3	>50	>50	>50	>50	>50	0.081
398-F1_F6_20	A	>100	>100	>100	>100	51.5	70.5	76.4	5.76	>50	>50	>50	>50	>50	0.025
BB201.B42	A	>100	>100	>100	>100	>100	>100	214	0.231	>50	>50	>50	>50	>50	0.461
BB539.2B13	A	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.008
BG505.W6M.C2	A	>100	>100	34.4	>100	5.10	9.56	10.0	0.418	>50	>50	>50	>50	>50	0.006
BI369.9A	A	>100	>100	>100	>100	12.0	5.11	14.7	0.517	>50	>50	>50	>50	>50	>50
BS208.B1	A	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
KER2008.12	A	>100	>100	>100	>100	>100	10.9	14.5	0.111	>50	>50	>50	>50	>50	0.065
KER2018.11	A	>100	>100	>100	>100	>100	>100	>500	0.575	>50	>50	>50	>50	>50	0.022
KNH1209.18	A	>100	>100	>100	>100	>100	>100	>500	1.80	>50	>50	>50	>50	>50	0.024
MB201.A1	A	>100	>100	>100	>100	58.8	>100	54.4	0.144	>50	>50	>50	>50	>50	0.102
MB539.2B7	A	>100	>100	>100	>100	>100	66.9	91.8	1.12	>50	>50	>50	>50	>50	0.035
MI369.A5	A	>100	>100	>100	>100	45.4	13.2	17.5	0.808	>50	>50	>50	>50	>50	>50
MS208.A1	A	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.007
Q23.17	A	>100	>100	>100	>100	37.5	8.25	9.15	0.582	>50	>50	>50	>50	>50	0.025
Q259.17	A	>100	>100	>100	>100	>100	>100	241	>100	>50	>50	>50	>50	>50	>50
Q769.d22	A	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
Q769.h5	A	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
Q842.d12	A	>100	>100	>100	>100	>100	>100	241	0.405	>50	>50	>50	>50	>50	0.018
QH209.14M.A2	A	>100	>100	>100	>100	23.1	>100	316	0.751	>50	>50	>50	>50	>50	0.013
RW020.2	A	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.019
UG037.8	A	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
246-F3.C10.2	AC	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
3301.V1.C24	AC	>100	>100	>100	>100	>100	>100	167	0.304	>50	>50	>50	>50	>50	0.179
3589.V1.C4	AC	>100	>100	>100	>100	>100	>100	>500	0.276	>50	>50	>50	>50	>50	0.016
6540.v4.c1	AC	>100	>100	>100	>100	>100	>100	>500	0.707	>50	>50	>50	>50	>50	0.032
6545.V4.C1	AC	>100	>100	>100	>100	>100	>100	>500	0.487	>50	>50	>50	>50	>50	0.036
0815.V3.C3	ACD	>100	>100	>100	>100	18.1	2.05	2.09	0.069	>50	>50	>50	>50	>50	>50
6095.V1.C10	ACD	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
3468.V1.C12	AD	>100	>100	>100	>100	>100	>100	>500	2.03	>50	>50	>50	>50	>50	>50
Q168.a2	AD	>100	>100	>100	>100	>100	>100	358	0.757	>50	>50	>50	>50	>50	0.030
Q461.e2	AD	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
620345.c1	AE	>100	>100	>100	>100	>100	>100	367	>100	>50	>50	>50	>50	>50	>50
BJOX009000.02	AE	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
BJOX010000.06	AE	>100	>100	>100	>100	>100	32.1	57.4	>100	>50	>50	>50	>50	>50	>50
BJOX025000.01	AE	>100	>100	>100	>100	>100	>100	289	>100	>50	>50	>50	>50	>50	>50
BJOX028000.10	AE	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
C1080.c3	AE	>100	>100	>100	>100	>100	>100	101	>100	>50	>50	>50	>50	>50	>50
C2101.c1	AE	>100	>100	>100	>100	>100	71.5	66.5	>100	>50	>50	>50	>50	>50	>50
C3347.c11	AE	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
C4118.09	AE	>100	>100	>100	>100	>100	>100	307	>100	>50	>50	>50	>50	>50	>50
CM244.ec1	AE	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
CNE3	AE	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
CNE5	AE	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
CNE55	AE	>100	>100	>100	>100	>100	>100	255	>100	>50	>50	>50	>50	>50	>50
CNE56	AE	28.6	>100	7.38	4.14	1.31	0.996	1.08	>100	>50	>50	>50	>50	>50	>50
CNE59	AE	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
CNE8	AE	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
M02138	AE	>100	>100	>100	>100	>100	25.6	59.6	>100	>50	>50	>50	>50	>50	>50
R1166.c1	AE	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
R2184.c4	AE	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
R3265.c6	AE	>100	>100	>100	>100	>100	>100	235	>100	>50	>50	>50	>50	>50	>50
TH023.6	AE	>100	>100	14.3	>100	5.02	0.903	1.93	>100	>50	>50	>50	>50	>50	>50
TH966.8	AE	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
TH976.17	AE	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
235-47	AG	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
242-14	AG	>100	>100	>100	>100	>100	>100	>500	0.348	>50	>50	>50	>50	>50	0.034
263-8	AG	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
269-12	AG	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.008
271-11	AG	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	0.720	>50	>50
928-28	AG	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
DJ263.8	AG	>100	>100	>100	>100	>100	>100	>500	0.441	>50	>50	>50	0.632	>50	0.014
T250-4	AG	>100	>100	>100	>100	>100	>100	>500	0.911	>50	>50	>50	>50	>50	0.007
T251-18	AG	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
T253-11	AG	>100	>100	>100	>100	>100	>100	>500	2.69	>50	>50	>50	>50	>50	0.034
T255-34	AG	>100	>100	>100	>100	>100	>100	>500	0.109	>50	>50	>50	27.4	>50	0.012
T257-31	AG	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.012
T266-60	AG	>100	>100	>100	>100	>100	>100	>500	5.53	>50	>50	>50	>50	>50	>50
T278-50	AG	>100	>100	>100	>100	>100	>100	>500	0.167	>50	>50	>50	>50	>50	0.200
T280-5	AG	>100	>100	>100	>100	>100	>100	>500	0.399	>50	>50	>50	>50	>50	0.036
T33-7	AG	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
3988.25	B	>100	>100	>100	>100	77.4	>100	476	0.267	>50	>50	>50	>50	>50	0.024
5768.04	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	2.00
6101.10	B	>100	>100	>100	>100	>100	>100	326	1.37	>50	>50	>50	>50	>50	0.044
6535.3	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	2.65	0.020
7165.18	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
45_01dG5	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.035
89.6.DG	B	>100	>100	>100	>100	92.4	36.4	72.0	0.228	>50	>50	>50	>50	0.178	>50
AC10.29	B	>100	>100	>100	>100	35.4	>100	325	>100	>50	>50	>50	>50	>50	0.043
ADA.DG	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	3.96	2.33	>50
Bal.01	B	>100	>100	>100	>100	>100	31.8	28.1	30.3	>50	>50	>50	4.07	0.382	0.126
BaL.26	B	>100	>100	>100	>100	>100	>100	128	>100	>50	>50	>50	3.05	0.257	0.062
BG1168.01	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.143
BL01.DG	B	>100	>100	>100	>100	15.8	7.32	9.43	0.513	>50	>50	>50	>50	>50	0.035
BR07.DG	B	>100	>100	>100	>100	>100	>100	272	>100	>50	>50	>50	>50	3.05	>50
BX08.16	B	>100	>100	>100	>100	38.6	26.7	49.8	4.24	>50	>50	28.1	39.5	0.939	0.012
CAAN.A2	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.102
CNE10	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
CNE12	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
CNE14	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.113
CNE4	B	>100	>100	>100	>100	>100	>100	>500	1.60	>50	43.8	>50	>50	>50	>50
CNE57	B	>100	>100	>100	>100	75.0	9.77	9.04	0.094	>50	>50	>50	>50	24.0	0.025
HO86.8	B	>100	>100	>100	>100	>100	19.9	19.2	6.86	>50	>50	>50	>50	>50	>50
HT593.1	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.033
HXB2.DG	B	5.46	>100	3.08	2.96	0.808	0.483	0.570	1.05	6.04	2.33	0.624	>50	0.114	0.064
JRCSF.JB	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	8.49	0.837	0.058
JRFL.JB	B	>100	>100	>100	>100	>100	>100	478	0.321	>50	>50	>50	>50	39.5	0.030
MN.3	B	>100	>100	>100	>100	>100	>100	>500	>100	1.77	0.173	>50	>50	0.004	>50
PVO.04	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
QH0515.01	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.020
QH0692.42	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
REJO.67	B	>100	>100	>100	>100	>100	96.8	151	>100	>50	>50	>50	>50	>50	0.296
RHPA.7	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.045
SC422.8	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.034
SF162.LS	B	>100	>100	>100	>100	>100	>100	>500	1.39	13.5	>50	20.4	0.067	0.181	0.056
SS1196.01	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	5.56	2.61	>50
THRO.18	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
TRJO.58	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	22.5
TRO.11	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
WITO.33	B	>100	>100	>100	>100	>100	>100	>500	0.634	>50	>50	>50	>50	>50	0.079
X2278.C2.B6	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.103
YU2.DG	B	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
BJOX002000.03	BC	>100	>100	>100	>100	>100	>100	>500	0.624	>50	>50	>50	>50	>50	0.017
CH038.12	BC	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
CH070.1	BC	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
CH117.4	BC	>100	>100	>100	>100	16.7	4.20	7.07	5.37	>50	>50	>50	>50	>50	>50
CH119.10	BC	>100	>100	>100	>100	58.9	12.7	22.8	0.245	>50	>50	>50	>50	>50	0.094
CH181.12	BC	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
CNE15	BC	>100	>100	>100	>100	>100	>100	202	>100	>50	>50	>50	>50	>50	9.00
CNE19	BC	20.4	>100	12.0	58.6	1.57	0.218	0.280	>100	>50	>50	>50	>50	>50	>50
CNE20	BC	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
CNE21	BC	>100	>100	>100	>100	95.4	50.7	64.5	0.110	>50	>50	>50	>50	>50	0.011
CNE40	BC	>100	>100	>100	>100	9.18	2.17	3.93	0.507	0.246	>50	1.78	0.033	4.75	>50
CNE7	BC	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
286.36	C	>100	>100	>100	>100	>100	29.2	52.2	>100	>50	>50	>50	>50	>50	0.326
288.38	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
0013095-2.11	C	>100	>100	>100	>100	>100	>100	131	>100	>50	>50	>50	40.7	>50	>50
001428-2.42	C	>100	>100	>100	>100	>100	>100	>500	0.214	>50	>50	>50	>50	>50	>50
0077_V1.C16	C	30.5	>100	71.2	>100	13.3	1.65	1.36	>100	>50	>50	>50	>50	>50	0.009
00836-2.5	C	>100	>100	>100	>100	>100	76.1	71.2	>100	>50	>50	>50	>50	>50	>50
0921.V2.C14	C	>100	>100	>100	>100	>100	>100	483	>100	>50	>50	>50	>50	>50	>50
16055-2.3	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
16845-2.22	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
16936-2.21	C	>100	>100	>100	>100	>100	>100	>500	0.216	>50	>50	>50	>50	>50	>50
25710-2.43	C	3.09	>100	5.32	34.6	0.722	0.316	0.250	>100	>50	>50	>50	>50	>50	>50
25711-2.4	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
25925-2.22	C	>100	>100	>100	>100	>100	>100	>500	0.299	>50	>50	>50	>50	>50	>50
26191-2.48	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
3168.V4.C10	C	>100	>100	>100	>100	>100	>100	>500	11.8	>50	>50	>50	>50	>50	>50
3637.V5.C3	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
3873.V1.C24	C	>100	>100	>100	>100	>100	>100	294	>100	>50	>50	>50	>50	>50	0.007
426c	C	>100	>100	>100	>100	>100	>100	465	0.305	>50	>50	>50	>50	>50	0.015
6322.V4.C1	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
6471.V1.C16	C	>100	>100	>100	>100	>100	>100	286	>100	>50	>50	>50	>50	>50	>50
6631.V3.C10	C	>100	>100	>100	>100	>100	>100	481	>100	>50	>50	>50	>50	>50	0.032
6644.V2.C33	C	>100	>100	>100	>100	>100	>100	>500	0.078	>50	>50	11.5	0.107	>50	>50
6785.V5.C14	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
6838.V1.C35	C	>100	>100	>100	>100	>100	>100	>500	0.114	>50	>50	>50	>50	>50	>50
96ZM651.02	C	65.6	>100	>100	>100	3.31	1.84	3.03	0.119	>50	>50	>50	>50	>50	0.157
BR025.9	C	>100	>100	>100	>100	>100	>100	176	4.04	>50	>50	>50	15.3	>50	>50
CAP210.E8	C	>100	>100	>100	>100	>100	>100	>500	0.548	>50	>50	>50	>50	>50	>50
CAP244.D3	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
CAP256.206.C9	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
CAP45.G3	C	>100	>100	>100	>100	>100	63.1	120	0.141	>50	>50	>50	>50	>50	>50
Ce1176.A3	C	>100	>100	>100	>100	>100	>100	315	0.706	>50	>50	>50	>50	>50	0.017
CE703010217.B	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
CNE30	C	>100	>100	>100	>100	>100	>100	>500	0.485	>50	>50	>50	>50	>50	>50
CNE31	C	>100	>100	>100	>100	>100	>100	>500	0.211	>50	>50	>50	>50	>50	0.020
CNE53	C	>100	>100	>100	>100	>100	>100	>500	0.294	>50	>50	>50	>50	>50	>50
CNE58	C	>100	>100	>100	>100	>100	>100	>500	0.476	>50	>50	>50	>50	>50	0.008
DU123.06	C	>100	>100	>100	>100	25.2	1.95	1.77	>100	>50	>50	>50	>50	>50	>50
DU151.02	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
DU156.12	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.029
DU172.17	C	>100	>100	>100	>100	98.5	>100	323	0.237	>50	>50	>50	>50	>50	0.013
DU422.01	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
MW965.26	C	61.1	>100	84.2	>100	9.46	5.05	5.27	>100	0.629	>50	>50	0.016	1.02	0.059
SO18.18	C	>100	>100	>100	93.0	12.0	15.6	14.6	>100	>50	>50	>50	>50	>50	0.040
TV1.29	C	>100	>100	>100	>100	>100	99.4	219	0.450	>50	>50	>50	14.5	>50	0.020
TZA125.17	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
TZBD.02	C	>100	>100	>100	>100	>100	39.3	499	>100	>50	>50	>50	>50	>50	0.023
ZA012.29	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
ZM106.9	C	>100	>100	>100	>100	94.2	38.7	38.4	>100	>50	>50	>50	>50	>50	>50
ZM109.4	C	>100	>100	>100	>100	>100	>100	307	8.40	>50	>50	>50	35.2	>50	>50
ZM135.10a	C	>100	>100	>100	>100	>100	>100	119	>100	>50	>50	>50	>50	>50	>50
ZM176.66	C	>100	>100	>100	>100	>100	42.2	64.6	>100	>50	>50	>50	>50	>50	0.015
ZM197.7	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.060
ZM214.15	C	>100	>100	>100	>100	>100	>100	>500	15.1	>50	>50	>50	>50	>50	0.714
ZM215.8	C	>100	>100	>100	>100	>100	>100	>500	14.2	>50	>50	>50	>50	>50	0.489
ZM233.6	C	>100	>100	>100	>100	72.6	>100	226	0.101	>50	>50	>50	>50	>50	>50
ZM249.1	C	>100	>100	>100	>100	>100	>100	>500	0.128	>50	>50	>50	>50	>50	0.016
ZM53.12	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
ZM55.28a	C	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.016
3326.V4.C3	CD	>100	>100	>100	>100	>100	>100	>500	41.2	>50	>50	>50	>50	>50	>50
3337.V2.C6	CD	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	4.12	>50	>50
3817.v2.c59	CD	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
191821.E6.1	D	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	4.40
231965.c1	D	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.048
247-23	D	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
3016.v5.c45	D	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
57128.vrc15	D	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	32.3	>50	>50
6405.v4.c34	D	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
A03349M1.vrc4	D	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
A07412M1.vrc1	D	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
NKU3006.ec1	D	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
UG021.16	D	>100	>100	>100	>100	>100	>100	>500	>100	1.81	>50	2.53	>50	>50	0.043
UG024.2	D	>100	>100	>100	>100	>100	>100	>500	>100	0.311	4.82	0.569	>50	>50	>50
P0402.c2.11	G	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	0.015
P1981.C5.3	G	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
X1193.c1	G	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
X1254.c3	G	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
X1632.S2.B10	G	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	15.9	>50	>50
X2088.c9	G	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
X2131.C1.B5	G	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	11.5	>50	0.070
SIVmac251.30.	NA	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50
SVA.MLV	NA	>100	>100	>100	>100	>100	>100	>500	>100	>50	>50	>50	>50	>50	>50

Summary (IC50)

	vFP1.01	vFP5.01	vFP7.04	vFP7.05	vFP20.01	vFP16.02	vFP16.02	VRC34.01	17b	48d	F105	3074	447-52D	PGT151
# Viruses	208	208	208	208	208	208	208	208	208	208	208	208	208	208
Total VS Neutralized														
IC50 <500ug/ml							97							
IC50 <100ug/ml	20	4	23	18	67	76	76	108						
IC50 <50ug/ml	17	2	20	17	57	65	58	107	15	12	14	40	24	115
IC50 <10ug/ml	10	0	6	7	32	37	32	104	10	6	12	30	19	115
IC50 <1.0ug/ml	1	0	1	2	7	18	17	83	7	2	5	19	15	115
IC50 <0.1ug/ml	0	0	0	0	0	2	2	40	2	1	1	6	9	109
IC50 <0.01ug/ml	0	0	0	0	0	0	0	0	0	0	0	2	3	59
% VS Neutralized														
IC50 <500ug/ml							47							
IC50 <100ug/ml	10	2	11	9	32	37	37	52						
IC50 <50ug/ml	8	1	10	8	27	31	28	51	7	6	7	19	12	55
IC50 <10ug/ml	5	0	3	3	15	18	15	50	5	3	6	14	9	55
IC50 <1.0ug/ml	0	0	0	1	3	9	8	40	3	1	2	9	7	55
IC50 <0.1ug/ml	0	0	0	0	0	1	1	19	1	0	0	3	4	52
IC50 <0.01ug/ml	0	0	0	0	0	0	0	0	0	0	0	1	1	28
Median IC50	9.62	54	19.2	23.5	11.2	10.9	31.6	0.155	1.86	7.75	2.61	1.59	0.378	0.009
Geometric Mean	9.61	44.9	11.7	11.9	8.00	5.82	15.2	0.251	1.55	4.72	1.65	1.34	0.378	0.011

Summary (IC80)

	vFP1.01	vFP5.01	vFP7.04	vFP7.05	vFP20.01	vFP16.02	vFP16.02	VRC34.01	17b	48d	F105	3074	447-52D	PGT151
# Viruses	208	208	208	208	208	208	208	208	208	208	208	208	208	208
Total VS Neutralized														
<500ug/ml							72							
<100ug/ml	7	0	8	5	31	39	36	75						
<50ug/ml	5	0	6	3	21	31	25	75	7	4	7	22	16	88
<10ug/ml	2	0	3	2	9	17	15	69	6	3	4	12	14	87
<1.0ug/ml	0	0	0	0	2	5	3	53	3	1	2	6	8	84
<0.1ug/ml	0	0	0	0	0	0	0	3	0	0	0	3	1	70
<0.01ug/ml	0	0	0	0	0	0	0	0	0	0	0	0	1	8
% VS Neutralized														
<500ug/ml							35							
<100ug/ml	3	0	4	2	15	19	17	36						
<50ug/ml	2	0	3	1	10	15	12	36	3	2	3	11	8	42
<10ug/ml	1	0	1	1	4	8	7	33	3	1	2	6	7	42
<1.0ug/ml	0	0	0	0	1	2	1	25	1	0	1	3	4	40
<0.1ug/ml	0	0	0	0	0	0	0	1	0	0	0	1	0	34
<0.01ug/ml	0	0	0	0	0	0	0	0	0	0	0	0	0	4
Median	28.6	>100	13.1	34.6	23.1	13.2	96	0.485	1.77	3.58	2.53	7.03	0.980	0.033
Geometric Mean	19.8	>100	16.0	18.7	17.9	10.6	55	0.647	1.44	3.04	3.76	3.41	0.918	0.043

Note: Median and Geometric Mean titers are calculated only for viruses neutralized

Values "less than" the lowest concentration assayed were assigned that value for calculation purposes. Indicated in italics

*To assess for non-specific neutralization at 500 ug/ml, the non-HIV-1 murine antibody 5C4 (specific for RSV neutralization) was tested at 500 ug/ml; two strains, HXB2.DG and DU123.06 were neutralized at 264 and 483 ug/ml, respectively, over 1000-fold less sensitively than by vFP16.02.

Supplementary Table 3. vFP antibody and sera neutralization.

b. vFP antibody neutralization against a panel of 10 isolates.

	IC50										IC80									
HIV strains	KER2008.12	Q23.17	3988.25	BL01.DG	286.36	BG505.W6M.C2	CNE56	CNE19	25710-2.43	0077.V1.C16	KER2008.12	Q23.17	3988.25	BL01.DG	286.36	BG505.W6M.C2	CNE56	CNE19	25710-2.43	0077.V1.C16
1868-vFP1.01	19.1	3.01	>100	>50	>50	21.9	4.49	2.96	0.756	7.1	>50	>50	>100	>50	>50	>100	39.9	31.7	4.32	44.3
2586-vFP7.07	28.3	34.6	>50	>50	>50	43.6	9.2	9.18	4.63	>50	>50	>50	>50	>50	>50	>50	40.4	>50	30.3	>50
2602-vFP8.02	7.35	1.01	1.96	5.86	10.9	2.2	0.715	0.48	0.513	3.39	>50	>50	>50	43.2	>50	22.3	2.92	3.36	2.26	12.1
2602-vFP8.03	>50	21.3	17.9	>50	18.1	>50	12.5	36.8	18.4	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50
2682-vFP9.01	6.29	6.83	>50	>50	>50	26.9	16	1.32	1.69	18.3	>50	>50	>50	>50	>50	>50	>50	9.97	8.49	>50
2703-vFP12.01	>50	13.9	5.01	>50	>50	>50	25.9	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50
2703-vFP12.02	>50	11.3	36.1	>50	>50	>50	8.04	7.53	8.13	38.5	>50	>50	>50	>50	>50	>50	30.3	49.3	40.7	>50
2703-vFP12.04	11.4	4.31	3.58	8.16	35.6	6.96	0.831	3.9	0.796	8.47	>50	>50	>50	41.3	>50	>50	3.47	23.8	4.06	36.1
2703-vFP12.06	36.1	28.2	5.67	32.6	>50	15.3	8.6	5.96	6.45	>50	>50	>50	>50	>50	>50	49.1	30.5	39.2	23.1	>50
2711-vFP15.01	45.5	24.5	>50	>50	40.3	44.9	6.07	9.61	2.97	>50	>50	>50	>50	>50	>50	>50	31.1	>50	24.8	>50
2711-vFP15.02	4.15	1.55	6.68	32.3	20	9.24	2.85	2.38	1.51	13.2	>50	>50	>50	>50	>50	>50	10.4	24.3	5.05	>50
2711-vFP15.03	3.97	14.4	>50	>50	10.9	21.2	27.6	0.922	0.562	23.8	>50	>50	>50	>50	>50	>50	>50	7.42	2.05	>50
2711-vFP15.04	19.8	5.16	>50	>50	>50	36.1	3.79	4.66	1.73	23.3	>50	>50	>50	>50	>50	>50	16.3	>50	9.56	>50
2711-vFP15.05	23	6.39	4.75	>50	13.7	17.9	7.38	3.34	2.09	23.5	>50	>50	>50	>50	>50	>50	15.8	42.4	8.88	>50
2711-vFP15.07	2.01	5.91	45.2	>50	18.2	>50	6.52	3.82	0.751	6.84	>50	>50	>50	>50	>50	>50	25.4	>50	3.03	44.3
2712-vFP16.02	1.44	0.84	6.72	3.26	2.67	2.64	1.06	0.203	0.355	1.29	14	13.4	>50	14.3	35	9.31	3.6	0.688	1.21	3.83
2713-vFP17.01	>50	>50	7.2	12.3	>50	18.9	19.3	4.05	1.46	23.7	>50	>50	>50	>50	>50	>50	>50	>50	13	>50
2716-vFP20.01	2.84	1.67	1.16	3.91	6.56	2.47	1.82	0.644	0.608	4.39	>50	40.7	>50	23.2	>50	8.15	6.96	3.63	3.39	20.3
2787-vFP26.02	>50	15.1	8.51	>50	>50	28.5	17.1	23.1	3.95	18.5	>50	>50	>50	>50	>50	>50	>50	>50	22.6	>50
2787-vFP26.03	3.96	27.7	>50	22.7	>50	39.2	8.43	0.539	0.574	9.46	>50	>50	>50	>50	>50	>50	29.6	3.54	2.37	>50
2787-vFP26.04	4.25	2.91	8.42	19.8	28.8	6.04	10.6	1.3	1.23	15.2	>50	>50	>50	>50	>50	25.7	>50	8.24	4.49	>50
2788-vFP27.01	1.84	6.9	9.55	>50	24.8	16.4	11	1.45	1.03	28.2	>50	>50	>50	>50	>50	>50	46.3	11.1	5.41	>50
2790-vFP30.01	5.48	3.18	9.71	7.39	40.2	1.73	4.17	2.12	2.03	7.28	>50	>50	>50	42.3	>50	5.6	12.1	14.1	8.11	30.3
2791-vFP31.01	7.05	1.92	14.8	17.3	36.9	21.5	3.92	1.27	1.14	9.7	>50	>50	>50	>50	>50	>50	21.6	7.47	3.5	>50
2792-vFP32.01	35.9	30.4	>50	35.3	>50	9.38	10.7	2.86	3.13	11.2	>50	>50	>50	>50	>50	32	40.6	17.4	12.7	40.8
2792-vFP32.03	>50	33.1	>50	2.33	>50	0.751	1.11	7.93	1.27	2.53	>50	>50	>50	17.9	>50	2.03	2.62	>50	8.05	11.8
2792-vFP32.04	34.3	4.75	>50	8.55	>50	17.2	4.46	2.38	1.03	26.7	>50	>50	>50	47.9	>50	>50	23	22.3	3.73	>50
2792-vFP32.06	20.2	44.8	>50	>50	>50	24.6	10.9	2.4	2.42	44.2	>50	>50	>50	>50	>50	>50	49.8	24.9	19.2	>50
2792-vFP32.07	>50	8.49	>50	2.86	>50	1.67	1.17	10.7	1.14	2.93	>50	>50	>50	23.9	>50	6.09	3.66	>50	7	15.4
N123-VRC34.01	0.028	0.083	0.028	0.048	4.11	0.069	>50	0.033	0.128	0.721	0.138	0.36	0.111	0.193	>50	0.331	>50	1.54	6.22	24.2

Supplementary Table 3. vFP antibody and sera neutralization.

c. NHP sera neutralization against a panel of 58 isolates with matching FP sequence in the first 8 residues to the immunogens and naturally missing glycans highlighted in gray.

Virus ID	Clade	Naturally missing glycan in FP region				Env trimer only (Wk18)		FP-KLH + Env trimer (Wk46)									
						NHP A12V049		NHP DF3R		NHP DFPE		NHP DF1W		NHP DF4B		NHP 0PV	
		88	241	448	611	ID50	ID80	ID50	ID80	ID50	ID80	ID50	ID80	ID50	ID80	ID50	ID80
0439.v5.c1	A					<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20
3365.v2.c20	A					<20	<20	<20	<20	<20	<20	34	<20	<20	<20	<20	<20
398-F1_F6_20	A					<20	<20	<20	<20	<20	<20	111	<20	<20	<20	32	<20
BB201.B42	A					<20	<20	<20	<20	<20	<20	55	<20	<20	<20	24	<20
BB539.2B13	A					<20	<20	<20	<20	<20	<20	62	<20	<20	<20	<20	<20
BG505.W6M.C2	A					526	149	129	<20	133	<20	240	31	33	<20	48	<20
BI369.9A	A					<20	<20	<20	<20	<20	<20	73	<20	<20	<20	<20	<20
KER2008.12	A					<20	<20	<20	<20	<20	<20	76	<20	<20	<20	<20	<20
KNH1209.18	A					<20	<20	<20	<20	<20	<20	40	<20	<20	<20	<20	<20
MB201.A1	A					<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20
MB539.2B7	A					<20	<20	<20	<20	<20	<20	24	<20	<20	<20	<20	<20
MI369.A5	A					<20	<20	<20	<20	<20	<20	144	<20	<20	<20	23	<20
Q23.17	A					<20	<20	<20	<20	35	<20	214	39	<20	<20	40	<20
Q259.17	A					<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20
Q842.d12	A					<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20
QH209.14M.A2	A					<20	<20	<20	<20	<20	<20	182	29	<20	<20	<20	<20
RW020.2	A					<20	<20	<20	<20	27	<20	100	27	<20	<20	24	<20
246-F3.C10.2	AC					<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20
3301.V1.C24	AC					<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20
3589.V1.C4	AC					<20	<20	<20	<20	<20	<20	21	<20	<20	<20	<20	<20
0815.V3.C3	ACD					<20	<20	<20	<20	30	<20	228	29	<20	<20	26	<20
Q168.a2	AD					<20	<20	<20	<20	<20	<20	32	<20	<20	<20	<20	<20
3988.25	B					<20	<20	<20	<20	<20	<20	45	<20	<20	<20	<20	<20
45_01dG5	B					<20	<20	<20	<20	<20	<20	64	<20	<20	<20	<20	<20
89.6.DG	B					<20	<20	<20	<20	20	<20	23	<20	<20	<20	<20	<20
Bal.01	B					<20	<20	<20	<20	<20	<20	78	<20	<20	<20	<20	<20
BL01.DG	B					<20	<20	<20	<20	<20	<20	123	34	<20	<20	<20	<20
CNE57	B					<20	<20	<20	<20	34	<20	20	<20	<20	<20	37	<20
HO86.8	B					<20	<20	<20	<20	26	<20	52	<20	<20	<20	<20	<20
JRFL.JB	B					<20	<20	<20	<20	<20	<20	61	<20	<20	<20	<20	<20
BJOX002000.03.2	BC					<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20
CH117.4	BC					<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20
CH119.10	BC					<20	<20	<20	<20	26	<20	36	<20	<20	<20	<20	<20
CNE15	BC					<20	<20	<20	<20	<20	<20	45	<20	<20	<20	<20	<20
CNE19	BC					54	<20	<20	<20	93	28	198	20	28	<20	64	<20
CNE21	BC					<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20
CNE40	BC					33	<20	22	<20	<20	<20	<20	<20	<20	<20	<20	<20
286.36	C					<20	<20	<20	<20	<20	<20	154	27	<20	<20	<20	<20
0921.V2.C14	C					<20	<20	<20	<20	<20	<20	27	<20	<20	<20	<20	<20
25710-2.43	C					23	<20	<20	<20	100	24	859	244	22	<20	123	40
3873.V1.C24	C					<20	<20	<20	<20	<20	<20	147	36	<20	<20	<20	<20
426c	C					<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20
96ZM651.02	C					<20	<20	<20	<20	44	<20	169	<20	<20	<20	32	<20
BR025.9	C					<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20
CAP210.E8	C					<20	<20	<20	<20	23	<20	21	<20	<20	<20	<20	<20
Ce1176.A3	C					<20	<20	<20	<20	<20	<20	97	<20	<20	<20	<20	<20
CNE31	C					<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20
CNE58	C					<20	<20	<20	<20	<20	<20	121	<20	<20	<20	<20	<20
DU172.17	C					<20	<20	<20	<20	<20	<20	42	<20	<20	<20	<20	<20
MW965.26	C					92	40	151	54	77	34	130	40	32	20	83	40
TV1.29	C					<20	<20	<20	<20	<20	<20	28	<20	<20	<20	<20	<20
ZA012.29	C					<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20
ZM109.4	C					<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20
ZM135.10a	C					<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20
ZM176.66	C					<20	<20	<20	<20	<20	<20	145	32	<20	<20	<20	<20
ZM214.15	C					<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20
ZM233.6	C					<20	<20	<20	<20	<20	<20	71	<20	<20	<20	<20	<20
ZM55.28a	C					<20	<20	<20	<20	<20	<20	102	21	<20	<20	<20	<20
SVA.MLV	NA					<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20	<20
					Total number of tested	58	58	58	58	58	58	58	58	58	58	58	58
					Number of neutralized (ID50/80>criteria)	5	2	3	1	12	3	41	13	4	0	12	2
					% neutralized of tested	9%	3%	5%	2%	21%	5%	71%	22%	7%	0%	21%	3%
					at least % neutralized of total 208	2%	1%	1%	0%	6%	1%	20%	6%	2%	0%	6%	1%
					Geometric mean ID50/80 of neutralized	72	77	75	54	42	28	75	35	28	20	40	40

100-1000
20-100
<20

Supplementary Table 4. Data collection and refinement statistics.

a. Crystal data collection and refinement statistics (molecular replacement)

	vFP1.01:FP	**vFP5.01:FP**	**vFP7.04:FP**	**vFP16.02:FP**	**vFP20.01:FP**
PDB accession code	5TKJ	5TKK	6CDM	6CDO	6CDP
Data collection					
Space group	P 2_1 2_1 2_1	P 2_1	P 2_1	P 4_1 2_1 2	C 2 2 2_1
Cell dimensions					
a, *b*, *c* (Å)	76.16, 120.18, 226.18	36.24, 82.23, 72.26	79.57, 61.03, 88.65	141.03, 141.03, 77.64	60.46, 192.31, 87.56
α, β, γ (°)	90.00, 90.00, 90.00	90.00, 90.23, 90.00	90.00, 91.89, 90.00	90.00, 90.00, 90.00	90.00, 90.00, 90.00
Resolution (Å)	50 - 2.12 (2.16 - 2.12)*	50 - 1.55 (1.58 - 1.55)	50 - 2.41 (2.49 - 2.41)	50 - 2.10 (2.17 - 2.10)	50 - 2.46 (2.54 - 2.46)
R_{sym} or R_{merge}	0.093 (0.517)	0.066 (0.468)	0.127 (0.412)	0.108 (0.931)	0.118 (0.423)
I / σI	20.7 (2.4)	16.1 (2.1)	10.0 (2.0)	30.9 (2.2)	19.8 (2.1)
Completeness (%)	99.6 (97.8)	97.2 (85.2)	99.3 (94.1)	99.8 (98.3)	97.4 (83.2)
Redundancy	7.1 (5.4)	3.5 (2.1)	3.5 (2.8)	13.9 (9.7)	6.4 (4.9)
Refinement					
Resolution (Å)	43.54 - 2.12 (2.16 - 2.12)	25.47 - 1.55 (1.58 - 1.55)	44.3 - 2.41 (2.49 - 2.41)	41.95 - 2.10 (2.17 - 2.10)	48.17 - 2.46 (2.54 - 2.46)
No. reflections	843,512	209,617	113,946	641,724	118,218
R_{work} / R_{free}	0.20 (0.24) / 0.24 (0.29)	0.21 (0.31) / 0.25 (0.39)	0.18 (0.22) / 0.22 (0.28)	0.19 (0.26) / 0.23 (0.31)	0.21 (0.32) / 0.26 (0.39)
No. atoms	14,526	3693	7075	3805	3478
Protein	13,412	3356	6724	3460	3406
Ligand/ion (SO_4)	35			50	10
Water	1079	337	351	295	62
B-factors (Å^2)	47	38	28	45	55
Protein	47	37	27	44	55
Ligand/ion	56			75	66
Water	43	42	32	49	49
R.m.s. deviations					
Bond lengths (Å)	0.008	0.01	0.005	0.008	0.003
Bond angles (°)	1.01	1.28	0.91	0.98	0.63

One crystal was used for each structure
*Values in parentheses are for highest-resolution shell.

b. Cryo-EM data collection and refinement statistics

	vFP16.02-DS-SOSIP-VRC03-PGT122 EMD-7460 6CDI	**vFP20.01-DS-SOSIP-VRC03-PGT122** EMD-7459 6CDE	**vFP1.01-DS-SOSIP** EMD-8420	**vFP5.01-DS-SOSIP** EMD-8421, EMD-8422
Data collection and processing				
Magnification	22500	130000	22500	22500
Voltage (kV)	300	300	300	300
Electron exposure (e–/Å^2)	67.18	70.70	67.39	68.58
Defocus range (μm)	~ -1.0 - -4.0	~ -2.0 - -3.0	~-1.8- -4.0	~-1.0- -3.5
Pixel size (Å)	1.07	1.06	1.07	1.07
Symmetry imposed	C3	C3	C3	C1
Initial particle images (no.)	206112	108962	53263	45231
Final particle images (no.)	57278	48248	14931	7383, 41278
Map resolution (Å)	3.6	3.8	8.6	14.7, 19.6
FSC threshold	0.143	0.143	0.143	0.143
Map resolution range (Å)	3.4-8.9	3.4-8.7		
Refinement				
Initial model used (PDB code)	5FYL, 3SE8, 6CDO	5FYL, 3SE8, 6CDP		
Model resolution (Å)	3.7	3.9		
FSC threshold	0.5	0.5		
Model resolution range (Å)	10-3.6	10-3.4		
Map sharpening *B* factor (Å^2)	-68.00	-69.47		
Model composition				
Non-hydrogen atoms	33165	33057		
Protein residues	3849	3852		
B factors (Å^2)				
Protein	103.84	97.66		
R.m.s. deviations				
Bond lengths (Å)	0.008	0.007		
Bond angles (°)	1.02	0.960		
Validation				
MolProbity score	1.69	1.65		
Clashscore	7.62	5.15		
Poor rotamers (%)	0.18	0		
Ramachandran plot				
Favored (%)	93.84	94.47		
Allowed (%)	6.16	5.53		
Disallowed (%)	0	0		

Supplementary Table 5. Impact of alanine and glycine mutations at different FP residue positions on binding of FP-directed antibodies.

a

	vFP1.01	vFP1.02	vFP2.01	vFP3.01	vFP4.01	vFP5.01	vFP6.01	vFP7.01	vFP7.02	vFP7.03	vFP7.04	vFP7.05	vFP16.02	vFP20.01	VRC34.01
512	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
513	0.93	0.97	0.69	0.70	0.44	0.59	0.83	0.90	0.97	1.02	1.04	1.02	1.01	0.99	0.05
514	0.24	0.21	0.06	0.04	0.01	0.41	0.72	0.08	0.10	0.04	0.09	0.09	0.66	0.48	0.72
515	0.44	0.44	0.10	0.04	0.05	0.07	0.47	0.25	0.32	0.27	0.29	0.23	0.69	0.66	0.03
516	1.03	1.07	1.01	1.05	0.75	0.56	0.78	0.99	0.99	0.99	1.02	1.00	0.98	0.99	0.01
517	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
518	0.96	1.06	1.03	1.00	1.02	0.92	0.39	1.01	1.03	1.06	1.02	1.06	1.03	1.02	0.73
519	0.93	1.03	0.98	1.02	1.03	0.14	0.30	0.98	1.02	1.04	1.02	1.03	1.03	1.01	0.80
520	0.99	1.06	1.01	1.07	1.05	1.01	1.01	1.03	1.03	1.05	1.01	1.04	1.05	1.05	1.02
521	0.98	1.08	1.02	1.09	1.01	0.99	1.02	1.03	1.02	1.02	1.02	1.00	1.00	1.00	0.85

< 0.25 | 0.25 - 0.50 | 0.50 - 0.75 | > 0.75

Binding of indicated antibodies to alanine mutants normalized to binding to the wild-type FP sequence. Experiments were performed in triplicate (n=3 independent experiments).

b

	vFP1.01	vFP1.02	vFP2.01	vFP3.01	vFP4.01	vFP5.01	vFP6.01	vFP7.01	vFP7.02	vFP7.03	vFP7.04	vFP7.05	vFP16.02	vFP20.01	VRC34.01
512	0.98	1.03	0.85	1.09	0.85	0.91	0.60	0.81	0.94	0.88	0.98	0.96	1.00	0.97	0.52
513	0.12	0.09	0.06	0.03	0.04	0.43	0.59	0.13	0.14	0.17	0.30	0.27	0.51	0.34	0.00
514	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
515	0.05	0.03	0.02	0.02	0.01	0.01	0.12	0.04	0.01	0.01	0.01	0.01	0.03	0.03	0.00
516	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
517	0.83	0.96	0.93	0.93	0.96	0.86	0.93	0.94	0.92	0.94	0.97	0.94	0.97	0.98	0.75
518	0.98	1.02	0.96	0.86	1.01	0.71	0.10	0.95	0.98	1.00	0.98	0.99	1.02	1.00	0.49
519	0.95	0.97	0.84	0.95	0.88	0.09	0.39	0.87	0.92	0.90	0.89	0.90	0.92	0.91	0.49
520	0.99	1.06	0.97	1.09	1.03	1.07	0.95	0.97	0.99	1.00	0.98	1.00	1.01	1.00	1.01
521	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

< 0.25 | 0.25 - 0.50 | 0.50 - 0.75 | > 0.75

Binding of indicated antibodies to glycine mutants normalized to binding to the wild-type sequence. Experiments were performed in triplicate (n=3 independent experiments).

Supplementary Table 6. Prevalence of FP residue 512-519 by clades.

Clades A/ACD/AD		Clade AC		Clade AE		Clade AG		Clade B		Clades C/BC		Clades D/CD		Clade G	
Residue 512-519	Count	Residue 512-519	Count	Residue 512-519	Count	Residue 512-519	Count	Residue 512-519	Count	Residue 512-519	Count	Residue 512-519	Count	Residue 512-519	Count
AVGIGAVF	19	AVGIGAVF	3	AVGIGAMI	18	AVGLGAVF	8	AVGIGAVF	8	AVGIGAVF	28	AIGLGAMF	6	AVGMGAVL	2
AVGLGAVF	3	AVGLGAVF	2	AVGIGTMI	2	AVVGLGAVF	2	AVGTIGAMF	8	AVGLGAVF	10	AIGLGALF	4	EVTLGALF	1
AVTMGAVF	2			AVTIGAMI	1	AVGMGALI	1	AVGIGALF	5	AVGLGAVL	4	AIGLGAVF	3	AVGLGAVI	1
AVGFGAFF	2			AVGIGIMI	1	AVGMGALF	1	AVGIGAMF	3	AVGIGAVL	4	AIGMGALF	1	AVGLGAFL	1
AVVELGAVF	1			AVGIGALL	1	AVGLGALF	1	AVGTLGAMF	2	AVGIGAMF	4			AIGMGAVL	1
AVGMGAVF	1					AVGLGAFF	1	AVGLGAMF	2	AALGAVF	3			AIGLGTVL	1
AVGMAAVF	1					AIGMGAVF	1	TVGIGALF	1	AVGMGAVF	2				
AVGMAALF	1					AALGAVF	1	DLGLGALF	1	AVGIGAVI	2				
AIGMGAVF	1							AVTLGAVF	1	AVGIGALF	2				
AIGLGAMF	1							AVTLGAMF	1	TVGIGAVF	1				
								AVGMLGAMF	1	AVVGLGAVF	1				
								AVGLGAVF	1	AVGVGAVM	1				
								AVGLGALF	1	AVGTIGAMF	1				
								AVGIVGAMF	1	AVGLGAVI	1				
								AVGIGAVL	1	AVGLGAMI	1				
								AMGIGAMF	1	AVGLGAMF	1				
								AIGIGAVF	1	AVGGIGAVF	1				
								AALGALF	1	AVGGFGAMI	1				
								AAIGALF	1	AALGALF	1				
										AAGIGAVI	1				

Supplementary Table 7. Association of FP-proximal *N*-glycan sequons (N88, N241, N448, and N611) and neutralization based on the 208-isolate panel.

	vFP1.01	vFP7.04	vFP7.05	vFP16.02	vFP20.01	VRC34.01
88	**1**	1	1	1	1	0.7037
241	**0.0122**	**0.0233**	**0.0122**	0.9382	0.7846	0.7424
448	1	1	1	0.5804	0.6812	**0.0327**
611	0.4714	0.5504	0.4714	0.3986	0.9479	0.7037

Values displayed are P-values from the two-tailed Fisher's exact test and were corrected for multiple testing using Hohm metric. Statistically significant adjusted P-values are highlighted in red and corresponding contingency tables shown below. n=208 HIV-1 strains.

vFP1.01 - 241

	Resistant	Sensitive
Glycan	190	16
Non-glycan	1	1

vFP7.04 - 241

	Resistant	Sensitive
Glycan	183	16
Non-glycan	5	4

vFP7.05 - 241

	Resistant	Sensitive
Glycan	186	13
Non-glycan	5	4

vFP34.01 - 448

	Resistant	Sensitive
Glycan	94	86
Non-glycan	7	21

Supplementary Table 8. vFP antibody neutralization statistics from the 208-virus isolate panel.

IC_{50}<50 µg/ml	1868-vFP1.01	1868-vFP5.01	2586-vFP7.04	2586-vFP7.05	2712-vFP16.02	2716-vFP20.01	N123-VRC34.01
Neutralization breadth on 208 virus panel	8.17%	0.96%	9.62%	8.17%	31.3%	27.4%	51.4%
Neutralization breadth on global virus panel	8.33%	0%	8.33%	16.7%	41.7%	41.7%	75.0%
Neutralization breadth against neutralization-resistant isolates	7.69%	0%	8.33%	8.33%	28.9%	25.0%	50.0%
Neutralization breadth on FP8-sequence viruses	20.7%	1.72%	22.4%	17.2%	72.4%	74.1%	94.8%

IC_{50}<100 µg/ml	1868-vFP1.01	1868-vFP5.01	2586-vFP7.04	2586-vFP7.05	2712-vFP16.02	2716-vFP20.01	N123-VRC34.01
Neutralization breadth on 208 virus panel	9.62%	1.92%	11.1%	8.65%	36.5%	32.2%	51.92%
Neutralization breadth on global virus panel	16.7%	0%	8.33%	16.7%	41.7%	50.0%	75.0%
Neutralization breadth neutralization-resistant isolates	7.69%	0%	10.3%	8.97%	34.0%	28.9%	50.6%
Neutralization breadth on FP8-sequence viruses	25.9%	3.45%	27.6%	19.0%	81.0%	82.8%	94.8%

IC_{50}<500 µg/ml	2712-vFP16.02
Neutralization breadth on 208 virus panel	46.6%
Neutralization breadth on global virus panel	66.7%
Neutralization breadth neutralization-resistant isolates	46.1%
Neutralization breadth on FP8-sequence viruses	96.6%

Neutralization breadth of FP targeting neutralizing antibodies evaluated based on different virus panels: a 208-isolate panel evaluated in this study; the global panel (deCamp et al. 2013 JVI); the neutralization-resistant strains in the 208-isolate panel (154 strains that were not neutralized by antibodies 17b, 48d, F105, 447-52D and 3074); the 58 strains in the 208-isolate panel that have the identical N-terminal 8-mer of the FP as BG505. Breadth statistics for IC_{50}<50 µg/ml are shown at top, statistics for IC_{50}<100 µg/ml are shown in the middle, and statistics for IC_{50}<500 µg/ml are shown at bottom.