Supplementary Table 1. Serum neutralizing activity of selected donors.

			Clade A	Clade B		Clade C		CRF01_AE
Donor	presumed clade	Score	94UG103	92BR020	JRCSF	MGRM-C26	93IN905	92TH021
#36	CRF02_AG	3.67	900	900	≥2700	≥2700	≥2700	≥2700
#84	A or D	3.00	300	300	≥2700	300	≥2700	≥2700
#17	A	2.83	300	≥2700	900	≥2700	≥2700	<100
#39	C	2.83	300	900	900	≥2700	≥2700	100

Supplementary Table 2: Antibody sequence characteristics

Heavy Chain Sequences

Name	Donor	Putative V-gene[a]	Putative J-gene[a]	CDR3 length (amino acids)[b]	CDR3 sequence (amino acids)	Somatic mutations (nucleotides)[c]	Somatic mutations (amino acids)[c]	Mutation frequency (nucleotides)[c]	Mutation frequency (amino acids)[c]	Insertion/Deletions (number of amino acids/position)
PGT121	17	IGHV4-59*01	IGHJ6*03	24	TLHGRRIYGIVAFNEWFTYFYMDV	65	27	17 %	21 %	
PGT122					TKHGRRIYGVVAFKEWFTYFYMDV	68	31	18 %	24 %	
PGT123					ALHGKRIYGIVALGELFTYFYMDV	79	35	21 %	27 %	
PGT125	36	IGHV4-39*07	IGHJ5*02	19	FDGEVLVYNHWPKPAWVDL	78	36	20 %	27 %	+6 in CDR2
PGT126					FDGEVLVYHDWPKPAWVDL	67	30	17 %	23 %	+6 in CDR2
PGT127					FGGEVLVYRDWPKPAWVDL	58	30	15 %	23 %	+6 in CDR2
PGT128					FGGEVLRYTDWPKPAWVDL	75	36	19 %	28 %	+6 in CDR2
PGT130					SGGDILYYYEWQKPHWFSP	83	42	22 %	34 %	
PGT131					SGGDILYYIEWQKPHWFYP	84	41	23 %	33 %	
PGT135	39	IGHV4-39*07	IGHJ5*02	18	HRHHDVFMLVPIAGWFDV	67	37	17 %	29 %	+5 in CDR1
PGT136					HKYHDIFRVVPVAGWFDP	60	33	15 %	25 %	+5 in CDR1/+1 in CDR2
PGT137					HKYHDIVMVVPIAGWFDP	77	38	20 %	29 %	+5 in CDR1
PGT141	84	IGHV1-8*01	IGHJ6*02	31/32	GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV	51	29	12 %	21 %	0 or +1 in CDR3[d]
PGT142					GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV	51	31	12 %	23 %	0 or +1 in CDR3[d]
PGT143					GSKHRLRDYVLYDDYGLINYQEWNDYLEFLDV	51	29	12 %	21 %	0 or +1 in CDR3[d]
PGT144					GSKHRLRDYVLYDDYGLINQQEWNDYLEFLDV	59	33	14 %	24 %	0 or +1 in CDR3[d]
PGT145					GSKHRLRDYFLYNEYGPNYEEWGDYLATLDV	72	39	18 %	29 %	-1 or 0 in CDR3[d]

Light Chain Sequences

Name	Donor	Putative V-gene[a]	Putative J-gene[a]	CDR3 length (amino acids)[b]	CDR3 sequence (amino acids)	Somatic mutations (nucleotides)[c]	Somatic mutations (amino acids)[c]	Mutation frequency (nucleotides)[c]	Mutation frequency (amino acids)[c]	Insertion/Deletions (number of amino acids/position)
PGT121	17	IGLV3-21*02	IGLJ3*02	12	HIWDSRVPTKWV	56	31	18 %	30 %	-7 in FR1/+3 in FR3
PGT122					HIWDSRRPTNWV	58	27	19 %	26 %	-7 in FR1/+3 in FR3
PGT123					HIYDARGGTNWV	73	39	24 %	38 %	-7 in FR1/+3 in FR3
PGT125	36	IGLV2-8*01	IGLJ2*01 or IGLJ3*01	10	GSLVGNWDVI	46	23	15 %	22 %	-5 in CDR1
PGT126					SSLVGNWDVI	28	14	9 %	13 %	-5 in CDR1
PGT127					SSLVGNWDVI	27	13	9 %	12 %	-5 in CDR1
PGT128					GSLVGNWDVI	27	14	9 %	14 %	-5 in CDR1
PGT130					SSLFGRWDVV	39	21	12 %	19 %	
PGT131					SSLSGRWDIV	44	25	13 %	23 %	
PGT135	39	IGKV3-15*01	IGKJ1*01	9	QQYEEWPRT	51	29	16 %	28 %	
PGT136					QQYEEWPRT	39	22	12 %	21 %	
PGT137					QQYEEWPRT	35	19	11 %	18 %	
PGT141	84	IGKV2-28*01 or IGKV2D-28*01	IGKJ1*01	9	MQGLNRPWT	46	23	14 %	21 %	
PGT142					MQGLNRPWT	46	23	14 %	21 %	
PGT143					MQGLNRPWT	46	24	14 %	22 %	
PGT144					MQGLNRPWT	44	25	13 %	23 %	
PGT145					MQGLHSPWT	52	26	16 %	24 %	

a) Putative V- or J-gene of the common germline ancestor of each clonally related antibody cluster.

b) CDR3 lenghts according to the Kabat definiton.

c) Somatic mutations were counted over the whole variable region as nucleotides or amino acids differing from a putative germline sequence. For each cluster of clonally related antibodies, a germline sequence was composed of the putative V-gene, a consensus junction, the putative J-gene, and a consensus insertion where present. Sequences derived from 3' cloning primers were excluded from the frequency calculations.

d) Either an insertion in PGT141 to 144 or a deletion in PGT145.

e) Insertion of two amino acids in J-region due to mispriming in cloning PCR.

Supplementary Table 3: Median ICs and percent viruses neutralized

A) Median IC_{50} (μg/ml) against viruses neutralized with an $IC_{50} < 50$ μg/ml

Clade	n	PGT121	PGT122	PGT123	PGT125	PGT126	PGT127	PGT128	PGT130	PGT131	PGT135	PGT136	PGT137	PGT141	PGT142	PGT143	PGT144	PGT145	PG9	VRC01	PGV04	b12	2G12	4E10
A	26	0.02	0.07	0.02	0.01	0.01	0.02	0.01	0.09	0.09	0.64	2.34	0.72	0.22	0.25	0.27	2.81	0.40	0.12	0.26	0.14	6.98	17.20	5.95
B	31	0.02	0.02	0.02	0.02	0.02	0.06	0.01	0.09	0.07	0.15	13.19	8.55	0.48	0.40	0.39	3.37	0.09	0.43	0.24	0.17	0.80	0.82	5.19
C	27	0.02	0.03	0.01	1.83	0.18	0.55	0.04	0.15	0.78	0.05	7.52	0.23	0.33	0.09	0.17	0.85	0.14	0.23	0.48	0.79	5.46	2.93	3.98
D	25	0.01	0.02	0.02	0.09	0.04	0.49	0.02	0.65	0.85	1.69	0.05	6.30	0.37	0.19	0.28	2.13	1.07	0.10	0.44	0.44	1.47	4.57	4.54
F	15	0.13	0.43	0.09	0.04	0.08	0.65	0.52	0.07	0.56	0.21	4.75	6.23	0.24	0.22	0.36	0.51	0.82	0.09	0.39	0.18	na	9.23	2.26
G	15	0.02	0.05	0.04	0.02	0.18	0.22	0.04	4.14	3.54	0.14	18.95	0.23	0.30	0.21	0.21	3.84	0.11	0.27	0.10	0.08	2.99	31.03	1.44
AE	10	na	na	na	0.03	1.77	na	0.06	0.17	0.08	na	na	na	0.01	0.01	0.02	0.10	0.97	0.10	0.56	1.24	21.07	na	0.63
AG	10	0.49	2.75	0.61	0.01	0.03	0.04	0.67	0.04	0.18	27.37	29.11	28.30	0.50	2.16	1.11	18.62	0.16	0.56	0.12	0.10	10.40	0.95	1.42
All	**162**	**0.03**	**0.05**	**0.03**	**0.04**	**0.04**	**0.08**	**0.02**	**0.16**	**0.52**	**0.17**	**7.81**	**3.46**	**0.35**	**0.21**	**0.31**	**2.06**	**0.29**	**0.23**	**0.32**	**0.20**	**2.82**	**2.38**	**3.41**

B) Percent viruses neutralized with an $IC_{50} < 50$ μg/ml

Clade	n	PGT121	PGT122	PGT123	PGT125	PGT126	PGT127	PGT128	PGT130	PGT131	PGT135	PGT136	PGT137	PGT141	PGT142	PGT143	PGT144	PGT145	PG9	VRC01	PGV04	b12	2G12	4E10
A	26	62	58	58	65	54	50	58	50	38	19	4	23	65	69	65	46	81	85	92	100	31	35	96
B	31	84	84	81	74	81	81	81	65	45	39	19	19	52	52	52	39	77	74	100	94	58	71	97
C	27	85	81	85	56	74	52	78	48	41	37	33	33	70	70	70	52	70	67	89	70	26	11	89
D	25	48	40	48	40	52	48	60	44	36	24	4	12	28	28	28	16	72	76	84	76	48	24	96
F	15	93	80	80	20	33	27	80	33	13	60	13	20	67	67	67	53	100	67	100	93	0	20	93
G	15	80	80	80	27	53	40	67	47	40	40	27	33	67	67	67	33	80	80	93	87	13	20	100
AE	10	0	0	0	60	40	0	60	80	60	0	0	0	40	40	40	30	90	100	100	90	40	0	100
AG	10	70	60	60	30	50	40	90	50	40	20	10	10	50	60	50	20	70	80	90	100	30	50	100
All	**162**	**70**	**65**	**67**	**52**	**60**	**50**	**72**	**52**	**40**	**33**	**16**	**22**	**56**	**57**	**56**	**38**	**78**	**77**	**93**	**88**	**34**	**32**	**96**

C) Median IC_{50} (μg/ml) against all viruses

Clade	n	PGT121	PGT122	PGT123	PGT125	PGT126	PGT127	PGT128	PGT130	PGT131	PGT135	PGT136	PGT137	PGT141	PGT142	PGT143	PGT144	PGT145	PG9	VRC01	PGV04	b12	2G12	4E10
A	26	0.87	3.09	0.69	0.16	2.02	21.71	0.35	41.39	50.00	50.00	50.00	50.00	1.92	2.21	6.34	50.00	1.16	0.21	0.28	0.14	50.00	50.00	6.19
B	31	0.03	0.05	0.04	0.06	0.04	0.12	0.02	5.17	50.00	50.00	50.00	50.00	33.21	15.15	25.89	50.00	0.34	2.08	0.24	0.25	4.17	1.90	5.76
C	27	0.02	0.04	0.02	37.48	0.79	19.19	0.08	50.00	50.00	50.00	50.00	50.00	3.28	0.79	0.80	48.89	0.49	0.57	0.71	2.76	50.00	50.00	3.98
D	25	50.00	50.00	50.00	50.00	43.14	50.00	0.14	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	10.00	1.91	0.58	1.01	50.00	50.00	5.30
F	15	0.17	1.29	0.31	50.00	50.00	50.00	1.21	50.00	50.00	7.79	50.00	50.00	1.15	0.82	0.98	20.56	0.82	0.58	0.39	0.18	50.00	50.00	2.26
G	15	0.06	0.51	0.18	50.00	48.85	50.00	0.32	50.00	50.00	50.00	50.00	50.00	4.69	5.95	4.77	50.00	0.21	0.51	0.12	0.13	50.00	50.00	1.44
AE	10	50.00	50.00	50.00	1.61	50.00	50.00	0.31	0.58	2.60	50.00	50.00	50.00	50.00	50.00	50.00	50.00	1.17	0.10	0.56	1.26	50.00	50.00	0.63
AG	10	0.60	38.45	8.04	50.00	11.07	50.00	1.62	21.75	50.00	50.00	50.00	50.00	31.02	16.43	41.24	50.00	1.27	3.47	0.16	0.10	50.00	14.00	1.42
All	**162**	**0.31**	**2.02**	**0.35**	**34.97**	**1.08**	**42.83**	**0.10**	**22.98**	**50.00**	**50.00**	**50.00**	**50.00**	**16.01**	**9.46**	**13.76**	**50.00**	**0.86**	**0.62**	**0.34**	**0.30**	**50.00**	**50.00**	**3.50**

D) Median IC_{90} (μg/ml) against viruses neutralized with an $IC_{90} < 50$ μg/ml

Clade	n	PGT121	PGT122	PGT123	PGT125	PGT126	PGT127	PGT128	PGT130	PGT131	PGT135	PGT136	PGT137	PGT141	PGT142	PGT143	PGT144	PGT145	PG9	VRC01	PGV04	b12	2G12	4E10
A	26	0.20	0.33	0.18	0.07	0.08	0.16	0.04	4.99	0.73	1.01	na	2.54	2.88	2.37	1.57	4.51	4.30	2.24	2.20	1.45	48.45	17.77	40.61
B	31	0.11	0.15	0.14	0.13	0.17	0.36	0.07	0.77	0.50	2.87	2.09	na	4.62	9.52	2.84	7.08	0.54	2.60	2.05	1.66	5.96	4.92	30.31
C	27	0.12	0.17	0.08	0.18	0.98	7.99	0.17	2.67	15.80	0.28	0.28	1.32	3.83	1.69	2.02	12.43	1.76	7.68	6.18	3.83	27.42	28.67	21.21
D	25	0.12	0.11	0.13	0.87	0.33	0.18	0.12	3.18	2.67	1.13	2.10	16.10	25.10	9.75	8.36	19.06	5.27	0.80	5.72	3.23	12.68	8.77	23.46
F	15	1.17	5.53	0.74	0.37	1.00	0.86	1.17	4.84	1.92	1.26	na	21.09	4.55	3.45	6.08	7.79	9.74	0.52	2.72	2.34	na	21.50	7.63
G	15	0.22	0.65	0.19	0.05	0.17	0.67	0.12	28.06	na	1.01	7.54	1.45	1.58	1.99	1.85	7.57	2.18	6.35	1.44	1.74	22.81	na	16.57
AE	10	na	na	na	0.22	19.58	na	1.47	0.08	0.21	na	na	na	0.03	0.03	0.05	3.41	11.09	1.02	4.08	8.18	12.68	na	12.96
AG	10	0.56	0.97	2.27	0.05	0.08	0.24	0.13	0.07	0.16	na	na	na	3.66	5.15	4.97	na	0.87	0.36	1.17	1.97	16.98	7.04	15.36
All	**162**	**0.13**	**0.26**	**0.16**	**0.16**	**0.17**	**0.46**	**0.12**	**1.68**	**0.54**	**1.13**	**2.09**	**2.10**	**3.89**	**3.75**	**2.60**	**8.37**	**2.10**	**1.22**	**2.79**	**2.00**	**16.01**	**6.96**	**22.37**

E) Percent viruses neutralized with an $IC_{90} < 50$ μg/ml

Clade	n	PGT121	PGT122	PGT123	PGT125	PGT126	PGT127	PGT128	PGT130	PGT131	PGT135	PGT136	PGT137	PGT141	PGT142	PGT143	PGT144	PGT145	PG9	VRC01	PGV04	b12	2G12	4E10
A	26	50	50	50	54	50	46	50	31	23	4	0	12	38	46	35	4	46	69	88	88	4	4	23
B	31	81	77	77	58	74	65	77	42	29	23	3	0	32	39	29	13	61	29	100	84	45	52	16
C	27	67	59	63	26	48	38	67	26	21	33	13	21	48	58	50	29	58	48	81	48	17	4	42
D	25	36	32	32	28	36	28	48	16	8	8	4	4	20	20	16	8	36	40	72	56	28	12	20
F	15	60	73	53	20	27	13	53	20	7	33	0	7	47	53	47	27	67	40	100	93	0	7	40
G	15	60	60	47	7	20	20	47	7	0	20	7	13	33	47	40	7	67	40	93	87	13	0	53
AE	10	0	0	0	40	20	0	50	50	40	0	0	0	30	30	30	20	60	70	100	80	10	0	70
AG	10	30	30	40	30	30	30	50	30	20	0	0	0	20	30	20	0	50	40	90	100	10	30	60
All	**162**	**55**	**54**	**52**	**37**	**45**	**36**	**57**	**28**	**19**	**17**	**5**	**7**	**35**	**40**	**33**	**14**	**53**	**46**	**89**	**77**	**19**	**15**	**34**

F) Median IC_{90} (μg/ml) against all viruses

Clade	n	PGT121	PGT122	PGT123	PGT125	PGT126	PGT127	PGT128	PGT130	PGT131	PGT135	PGT136	PGT137	PGT141	PGT142	PGT143	PGT144	PGT145	PG9	VRC01	PGV04	b12	2G12	4E10
A	26	47.89	48.07	23.26	26.63	6.27	50.00	9.38	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	2.71	2.38	1.62	50.00	50.00	50.00
B	31	0.23	0.41	0.42	0.49	0.29	1.17	0.12	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	6.51	50.00	2.05	2.05	50.00	44.23	50.00
C	27	0.47	7.99	7.29	50.00	50.00	50.00	2.54	50.00	50.00	50.00	50.00	50.00	50.00	43.11	50.00	50.00	30.57	22.11	6.71	50.00	50.00	50.00	50.00
D	25	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	8.77	7.58	50.00	50.00	50.00
F	15	1.88	23.47	5.05	50.00	50.00	50.00	38.14	50.00	50.00	50.00	50.00	50.00	50.00	34.51	50.00	50.00	16.34	50.00	2.72	2.52	50.00	50.00	50.00
G	15	2.10	26.35	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	9.93	50.00	1.69	2.07	50.00	50.00	29.65
AE	10	50.00	50.00	50.00	50.00	50.00	50.00	29.21	35.65	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	39.37	0.78	4.08	11.00	50.00	50.00	19.49
AG	10	50.00	50.00	50.00	50.00	50.00	50.00	42.87	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	50.00	35.44	50.00	1.40	1.97	50.00	50.00	26.15
All	**162**	**10.49**	**38.11**	**16.25**	**50.00**	**50.00**	**50.00**	**2.73**	**50.00**	**50.00**	**50.00**	**50.00**	**50.00**	**50.00**	**50.00**	**50.00**	**50.00**	**31.20**	**45.50**	**3.31**	**4.11**	**50.00**	**50.00**	**50.00**

Supplementary Table 4. Neutralizing activity of PGT mAbs against a cross-clade 162-pseudovirus panel.

		IC$_{50}$ (µg/mL)																				IC$_{50}$ (1/dil'n)			
Isolate	Subtype	PGT-121	PGT-122	PGT-123	PGT-125	PGT-126	PGT-127	PGT-128	PGT-130	PGT-131	PGT-135	PGT-136	PGT-137	PGT-141	PGT-142	PGT-143	PGT-144	PGT-145	VRC01	PGV04	PG9	#17	#84	#36	#39
92RW008	A	0.003	0.003	0.003	0.004	0.008	0.012	0.003	0.089	1.011	1.417	>50	0.148	0.579	0.447	0.385	>50	0.400	0.037	0.014	0.006	6500.7	9301.5	2084.1	644.0
92RW009		1.739	42.406	15.680	0.144	>50	>50	0.812	1.274	3.115	>50	>50	>50	0.022	0.006	0.010	0.893	0.026	0.187	0.108	0.050	463.6	1247.6	241.0	<100
92RW020		0.004	0.009	0.002	0.004	0.006	0.010	0.005	0.039	0.168	0.067	2.335	0.005	>50	31.523	>50	>50	0.997	0.130	0.055	0.141	5671.1	428.3	2617.1	2730.0
92RW021		0.009	0.021	0.005	0.005	0.006	0.011	0.005	0.004	0.012	>50	>50	3.516	>50	>50	>50	>50	1.620	0.066	0.038	0.027	2343.6	1092.2	4204.8	428.0
92RW024		>50	>50	>50	35.530	41.995	>50	>50	>50	>50	>50	>50	>50	0.175	0.069	0.122	16.346	0.069	0.327	0.310	0.258	<100	507.7	149.7	178.0
92RW026		0.014	0.036	0.012	0.007	0.008	0.024	0.010	0.037	0.041	0.068	>50	0.092	1.781	1.780	5.364	32.691	1.453	N/A	0.140	0.164	1561.0	717.3	2183.4	1046.0
92UG031		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.093	0.050	0.095	2.175	3.220	0.469	4.463	3.605	<100	282.5	422.2	459.0
92UG037		0.031	0.068	0.023	0.005	0.011	0.014	0.006	0.061	0.048	3.672	>50	>50	1.276	0.557	0.854	8.241	3.148	0.245	0.145	0.014	1120.4	501.8	1431.8	410.0
93RW029		>50	>50	>50	>50	>50	>50	>50	34.264	>50	>50	>50	>50	0.019	0.014	0.053	4.391	>50	1.570	0.540	0.690	<100	589.2	<100	270.0
93UG077		0.019	0.084	0.028	0.012	0.020	0.055	0.014	21.392	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.097	0.083	>50	1082.8	326.4	707.2	436.0
94UG103		2.518	2.041	0.678	0.008	0.008	0.017	0.011	1.402	1.097	>50	>50	>50	>50	>50	>50	>50	0.331	0.285	0.202	0.340	193.4	208.3	1138.4	568.0
MGRM-A-001		>50	>50	>50	12.392	>50	>50	>50	>50	>50	>50	>50	>50	0.209	0.169	0.274	1.111	0.062	>50	6.781	>50	<100	231.7	<100	149.0
MGRM-A-002		0.013	0.017	0.011	0.013	0.015	9.422	0.149	0.010	>50	>50	>50	>50	0.217	0.007	0.016	0.085	0.019	N/A	0.093	0.020	839.3	533.0	2782.2	264.0
MGRM-A-003		0.435	3.794	0.495	>50	>50	>50	>50	>50	>50	>50	>50	>50	7.961	9.239	11.154	>50	3.315	0.422	0.128	1.942	<100	612.2	<100	375.0
MGRM-A-004		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.007	0.002	0.007	0.855	0.068	1.064	0.175	0.020	<100	4567.2	<100	319.0
MGRM-A-005		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	11.112	9.695	7.483	18.590	0.128	0.095	0.134	0.750	<100	151.2	<100	282.0
MGRM-A-006		0.396	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.521	0.244	>50	260.6	646.5	120.0	564.0
MGRM-A-007		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	12.584	7.213	1.061	<100	<100	<100	556.0
MGRM-A-008		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.303	0.555	>50	<100	<100	<100	196.0
MGRM-A-009		0.006	0.012	0.004	0.009	0.004	0.013	0.005	0.308	0.035	>50	>50	>50	0.029	0.058	0.050	2.834	0.235	0.118	0.033	0.023	4535.8	2228.7	1611.4	286.0
MGRM-A-010		2.444	2.509	0.705	0.004	0.002	0.017	0.005	0.005	0.010	>50	>50	>50	0.022	0.015	0.019	2.791	0.028	0.325	0.205	0.022	271.3	1704.2	2779.2	279.0
MGRM-A-011		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.484	0.273	0.090	0.033	<100	242.3	<100	169.0
MGRM-A-012		0.092	0.257	0.192	0.177	0.097	0.105	0.025	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.230	>50	0.225	19.294	229.9	<100	270.6	215.0
MGRM-A-013		0.387	2.474	0.565	0.014	0.006	0.029	0.008	>50	>50	>50	>50	49.188	9.856	3.725	9.241	>50	1.761	0.152	0.086	0.122	892.0	162.8	835.9	776.0
MGRM-A-014		0.003	0.007	0.003	13.913	0.010	0.240	0.007	0.161	15.444	0.636	>50	18.576	0.628	0.367	1.071	>50	1.357	0.135	0.172	1.248	7222.6	412.6	705.2	681.0
VLGCA1		>50	>50	>50	0.078	>50	>50	0.838	>50	>50	>50	>50	>50	2.067	2.754	17.389	>50	8.009	0.163	0.024	0.069	<100	311.2	203.2	<100
94KE105	AC	0.029	0.056	0.024	0.004	0.006	0.023	0.007	0.004	0.013	0.063	>50	18.548	0.204	0.190	0.368	0.290	1.317	0.499	2.981	37.875	955.0	1035.2	4540.1	1633.0
92TH021	AE	>50	>50	>50	0.006	0.197	>50	0.010	0.009	0.014	>50	>50	>50	0.001	0.002	0.003	0.052	0.013	0.616	1.289	0.059	<100	5298.1	3301.2	212.0
CMU02		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	1.425	0.515	1.238	>50	<100	101.3	<100	312.0
MGRM-AE-001		>50	>50	>50	2.948	9.684	>50	0.069	1.005	4.805	>50	>50	>50	>50	>50	>50	>50	20.916	0.167	0.063	20.586	<100	<100	222.6	223.0
MGRM-AE-002		>50	>50	>50	>50	>50	>50	0.522	1.534	>50	>50	>50	>50	>50	>50	>50	>50	1.868	0.217	0.569	0.040	<100	169.1	254.0	249.0
MGRM-AE-003		>50	>50	>50	0.092	>50	>50	0.180	0.337	1.407	>50	>50	>50	>50	>50	>50	>50	0.552	0.685	6.401	0.044	<100	150.0	<100	181.0
MGRM-AE-004		>50	>50	>50	>50	>50	>50	>50	2.429	>50	>50	>50	>50	0.001	0.001	0.002	0.104	0.006	0.187	0.183	0.009	<100	6926.5	131.7	123.0
MGRM-AE-005		>50	>50	>50	0.010	0.324	>50	0.032	0.006	0.017	>50	>50	>50	>50	>50	>50	>50	0.967	0.029	0.051	0.282	<100	208.2	2772.2	265.0
MGRM-AE-006		>50	>50	>50	0.009	17.268	>50	0.044	0.009	0.026	>50	>50	>50	>50	>50	>50	>50	>50	4.648	>50	0.063	<100	117.5	1352.7	194.0
MGRM-AE-007		>50	>50	>50	0.876	>50	>50	>50	0.083	0.226	>50	>50	>50	33.133	6.697	13.558	>50	0.181	0.835	5.753	0.180	<100	270.9	444.5	184.0
MGRM-AE-008		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.101	0.080	0.135	3.553	1.464	1.715	1.513	31.482	<100	611.7	<100	341.0
MGRM-AG-001	AG	2.096	14.472	2.509	>50	>50	>50	4.730	>50	>50	>50	>50	>50	18.030	12.423	18.933	>50	0.164	0.228	0.218	17.125	174.8	292.1	302.2	499.0
MGRM-AG-002		>50	>50	>50	>50	>50	>50	4.987	>50	>50	>50	>50	>50	0.049	0.044	0.076	7.780	0.056	0.950	0.879	0.076	125.5	748.0	139.4	206.0
MGRM-AG-003		0.465	43.663	>50	>50	>50	>50	34.787	0.041	2.917	>50	>50	>50	>50	>50	>50	>50	>50	0.043	0.058	>50	<100	505.3	<100	121.0
MGRM-AG-005		0.649	33.861	0.149	>50	1.207	11.591	0.037	0.540	1.041	>50	>50	>50	0.497	0.383	1.114	>50	0.045	0.091	0.027	>50	517.3	775.6	865.9	708.0
MGRM-AG-006		0.014	0.028	0.014	0.008	0.010	0.021	0.009	0.009	0.019	17.890	29.108	28.298	>50	>50	>50	>50	6.603	0.344	1.230	>50	1105.3	321.1	4106.0	536.0
MGRM-AG-008		0.494	>50	19.162	>50	>50	>50	0.668	>50	>50	>50	>50	>50	19.242	12.125	34.009	>50	0.244	0.124	2.484	0.013	125.1	827.8	<100	692.0
MGRM-AG-009		0.080	0.128	0.073	0.026	0.030	0.059	0.021	9.461	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.148	>50	525.2	101.4	220.2	128.0
MGRM-AG-011		>50	>50	>50	>50	2.451	>50	3.931	>50	>50	>50	>50	>50	0.118	0.081	0.156	44.563	0.003	0.084	0.071	0.007	<100	2785.8	228.1	274.0
MGRM-AG-012		>50	>50	>50	>50	>50	>50	>50	>50	>50	41.885	>50	>50	>50	>50	>50	>50	>50	0.031	0.040	22.845	104.9	<100	136.6	235.0
MGRM-AG-013		0.557	0.521	3.371	0.004	0.008	0.018	0.004	0.010	0.030	>50	>50	>50	>50	21.719	>50	>50	14.387	0.197	0.030	0.259	321.2	319.1	2055.6	303.0

		IC_{50} (µg/mL)																				IC_{50} (1/dil'n)			
Isolate	**Subtype**	**PGT-121**	**PGT-122**	**PGT-123**	**PGT-125**	**PGT-126**	**PGT-127**	**PGT-128**	**PGT-130**	**PGT-131**	**PGT-135**	**PGT-136**	**PGT-137**	**PGT-141**	**PGT-142**	**PGT-143**	**PGT-144**	**PGT-145**	**VRC01**	**PGV04**	**PG9**	**#17**	**#84**	**#36**	**#39**
6535.3	B	0.005	0.006	0.004	0.010	0.022	0.020	0.011	0.031	0.056	>50	>50	>50	>50	>50	>50	>50	>50	1.755	0.757	1.053	3712.0	477.8	848.0	387.0
92BR020		0.014	0.021	0.008	0.016	0.015	0.059	0.009	1.395	6.157	0.073	8.608	7.811	20.299	15.146	25.892	44.036	1.051	0.290	0.250	>50	1623.7	262.2	741.3	421.0
93TH305		0.007	0.013	0.008	0.008	0.013	0.017	0.006	0.021	0.016	>50	20.214	>50	>50	5.856	17.270	>50	0.032	0.243	0.255	8.124	3675.2	828.0	1520.7	306.0
APV_13		0.251	0.778	0.138	0.007	0.012	0.026	0.008	0.052	0.189	0.716	>50	>50	>50	>50	>50	>50	0.337	0.657	1.227	>50	177.8	211.6	1460.1	173.0
APV_17		0.066	0.250	0.114	8.063	0.353	10.378	0.016	10.661	>50	>50	>50	>50	0.590	0.628	1.108	10.298	0.488	0.477	0.309	34.778	470.0	161.5	279.4	482.0
APV_6		0.018	0.019	0.023	0.021	0.007	0.040	0.007	>50	>50	>50	>50	>50	14.216	4.725	13.968	>50	0.104	1.812	24.187	0.181	914.6	253.2	512.9	706.0
CAAN.A2		0.011	0.011	0.015	5.467	0.273	0.371	1.482	>50	>50	5.154	>50	>50	>50	>50	>50	>50	7.085	0.722	2.262	19.267	1743.1	173.1	148.8	222.0
JRFL		0.021	0.026	0.014	0.009	0.014	0.029	0.007	0.046	0.454	>50	>50	>50	>50	>50	>50	>50	30.401	0.034	0.032	>50	1291.5	348.5	858.2	471.0
MGRM-Chronic-B-001		0.102	0.138	0.150	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	3.223	0.066	0.048	>50	330.1	160.6	246.0	390.0
MGRM-Chronic-B-002		0.386	1.801	0.234	0.064	0.078	0.279	0.036	>50	>50	>50	>50	>50	>50	>50	>50	>50	3.672	0.117	0.142	3.439	200.1	<100	344.4	320.0
MGRM-Chronic-B-003		0.011	0.008	0.008	0.157	0.041	0.120	0.007	>50	>50	>50	>50	>50	0.400	0.484	0.854	7.408	0.045	0.100	0.258	>50	3664.9	307.2	370.4	103.0
MGRM-Chronic-B-004		0.009	0.008	0.008	0.007	0.010	0.018	0.009	0.010	0.040	>50	>50	>50	0.586	0.172	0.395	9.415	0.023	0.055	0.047	0.533	1874.9	796.5	1463.1	304.0
MGRM-Chronic-B-008		0.007	0.017	0.010	>50	5.890	21.515	0.143	5.183	>50	>50	>50	>50	>50	>50	>50	>50	1.903	0.155	0.166	8.784	2805.1	251.8	260.2	685.0
MGRM-Chronic-B-010		0.014	0.018	0.009	0.006	0.005	0.019	0.004	0.006	0.016	>50	>50	>50	>50	>50	>50	>50	>50	0.156	0.744	0.004	1145.5	443.0	3234.8	383.0
MGRM-Chronic-B-011		>50	>50	>50	3.228	0.108	0.297	0.020	0.153	6.468	>50	>50	>50	2.241	0.994	1.557	5.637	0.206	0.587	0.497	>50	130.8	458.4	1030.2	759.0
MGRM-Chronic-B-012		0.036	0.066	0.227	0.036	0.027	0.075	0.026	0.373	15.708	0.166	43.142	>50	>50	>50	>50	>50	9.062	1.033	>50	0.200	903.5	480.6	634.2	664.0
MGRM-Chronic-B-017		>50	5.664	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.147	0.076	0.145	0.712	0.054	0.141	0.129	0.688	132.7	317.6	<100	383.0
MGRM-Chronic-B-018		>50	>50	>50	>50	0.052	1.896	0.020	31.873	>50	>50	>50	>50	0.572	0.323	0.377	2.397	0.013	0.328	0.164	0.216	<100	612.7	289.3	375.0
MGRM-Chronic-B-020		0.004	0.005	0.005	0.087	0.021	0.050	0.007	0.014	0.053	0.057	>50	32.851	>50	>50	>50	>50	>50	0.424	1.262	>50	4132.2	390.1	858.8	305.0
MGRM-Chronic-B-023		0.005	0.010	0.055	>50	>50	>50	>50	>50	>50	0.329	>50	>50	0.318	0.486	0.236	>50	0.009	0.275	0.139	0.027	2216.5	950.0	196.7	523.0
MGRM-Chronic-B-024		0.195	2.308	>50	>50	>50	>50	>50	5.776	>50	>50	>50	>50	0.011	0.005	0.010	0.040	0.018	0.377	2.517	0.222	157.1	1060.2	104.1	110.0
PVO.4		0.137	0.689	0.105	0.042	0.017	0.164	0.005	5.171	>50	>50	>50	>50	0.113	0.066	0.162	0.535	0.299	0.218	0.454	24.752	212.9	239.4	420.8	123.0
QH0692.42		0.823	0.493	0.158	0.048	0.048	0.129	0.029	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	1.194	1.904	>50	175.1	<100	227.6	359.0
SC422661.8		0.098	0.103	0.039	30.138	0.119	36.688	1.578	>50	>50	21.751	>50	>50	1.656	3.153	2.017	>50	0.079	0.179	0.110	1.477	367.3	228.7	<100	220.0
SF162		0.005	0.009	0.005	0.004	0.003	0.019	0.007	0.007	0.025	0.023	0.482	3.407	>50	>50	>50	>50	>50	0.421	0.028	>50	5329.3	2049.0	5103.0	3043.0
THR0.18		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.007	0.012	0.016	0.029	0.013	2.461	>50	26.379	<100	1036.0	107.7	126.0
TRJ04551.58		7.095	>50	16.913	0.019	0.025	0.063	0.019	0.023	0.088	>50	>50	>50	>50	>50	>50	>50	>50	0.060	0.028	0.858	152.5	400.2	1416.1	617.0
TRO.11		0.008	0.011	0.008	0.111	0.041	0.079	0.018	0.257	1.913	0.030	0.073	9.349	0.383	0.270	0.219	4.728	0.044	0.186	0.121	16.865	2706.9	861.3	454.5	2740.0
VLGCB3		0.005	0.008	0.004	0.015	0.007	0.022	0.012	4.596	>50	0.142	>50	3.361	>50	>50	>50	>50	>50	0.108	0.045	0.022	2961.7	238.5	1333.0	754.0
NL43		>50	>50	>50	>50	>50	>50	>50	>50	>50	8.034	27.695	17.444	>50	>50	>50	>50	0.006	0.100	0.028	>50	418.2	3308.8	3033.8	1184.0
JRCSF		0.027	0.057	0.046	0.004	0.008	0.018	0.003	0.010	0.029	0.131	>50	>50	0.009	0.010	0.007	0.149	0.002	0.164	0.078	0.003	863.0	6255.4	2371.1	433.0
93IN905	C	0.005	0.013	0.004	0.009	0.015	0.024	0.009	0.020	0.177	0.011	0.011	0.042	0.001	0.001	0.002	0.132	0.002	0.138	0.332	0.035	4396.9	14817.0	1313.8	3667.0
93MW959		0.013	0.016	0.011	37.481	9.441	6.951	0.045	8.548	>50	>50	>50	>50	0.003	0.001	0.002	0.332	1.203	0.053	>50	0.054	1602.2	6171.8	176.1	506.0
97ZA012		0.002	0.004	0.002	2.465	0.042	>50	0.019	1.318	1.814	>50	>50	>50	>50	>50	>50	>50	0.915	0.088	0.041	3.400	8150.0	1083.1	433.0	594.0
98IN022		0.007	0.032	0.011	22.057	0.279	19.189	0.014	>50	>50	0.014	13.622	0.408	0.001	0.001	0.001	0.171	0.005	0.342	5.693	0.003	3711.8	15197.1	729.6	1918.0
MGRM-C-001		17.482	19.103	42.406	>50	>50	>50	>50	>50	>50	10.121	7.518	21.503	>50	>50	>50	>50	>50	1.369	>50	>50	<100	117.0	<100	174.0
MGRM-C-002		0.019	0.022	0.010	0.008	0.011	0.057	0.019	>50	>50	>50	>50	8.034	7.834	10.535	6.766	>50	0.008	0.577	>50	>50	1799.2	733.6	704.1	556.0
MGRM-C-004		0.011	0.020	0.009	1.825	0.033	0.532	0.025	2.756	3.714	0.046	0.034	0.026	>50	>50	>50	>50	>50	1.007	0.899	2.011	2177.9	234.5	327.9	2064.0
MGRM-C-005		0.015	0.027	0.012	2.087	0.298	0.570	0.030	0.935	1.356	>50	>50	>50	8.832	1.854	9.192	>50	>50	5.417	23.898	8.742	1323.5	405.1	383.0	600.0
MGRM-C-006		0.017	0.018	0.021	0.015	0.014	0.319	0.014	0.095	0.611	>50	>50	>50	0.330	0.478	0.369	48.894	0.010	2.202	>50	0.427	1681.6	1231.3	532.3	564.0
MGRM-C-007		0.196	3.348	0.547	>50	25.298	>50	0.111	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.064	330.7	244.2	<100	442.0
MGRM-C-008		0.012	0.028	0.011	>50	2.118	>50	0.373	7.277	>50	>50	>50	>50	>50	>50	>50	>50	>50	1.445	0.791	>50	1742.3	223.3	<100	903.0
MGRM-C-009		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.143	0.061	0.121	0.561	0.193	0.261	1.042	>50	<100	460.9	<100	224.0
MGRM-C-010		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.411	0.070	0.171	7.616	0.141	0.085	0.299	>50	<100	836.6	<100	316.0
MGRM-C-012		0.123	2.002	0.606	>50	0.111	1.073	0.058	>50	>50	0.017	>50	0.102	>50	>50	>50	>50	6.984	0.073	0.025	0.610	716.3	521.6	169.8	2150.0
MGRM-C-013		7.228	32.575	14.879	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	<100	<100	<100	453.0
MGRM-C-014		26.941	>50	1.003	>50	>50	>50	>50	>50	>50	>50	>50	>50	11.807	6.024	8.811	>50	5.816	>50	21.190	1.099	<100	702.6	<100	<100
MGRM-C-015		25.071	>50	13.141	>50	3.140	>50	0.196	0.344	1.015	0.104	11.066	1.983	0.033	0.038	0.085	0.236	0.120	1.569	0.983	0.427	141.6	544.2	253.4	1095.0
MGRM-C-017		0.009	0.015	0.010	2.358	0.170	3.397	1.065	>50	>50	>50	>50	>50	4.018	1.111	5.170	23.035	>50	0.366	0.383	2.688	3154.6	225.7	266.4	1587.0
MGRM-C-019		>50	>50	>50	0.130	0.006	0.017	0.010	0.010	0.021	0.264	20.100	>50	0.008	0.003	0.004	0.513	0.005	1.126	9.632	0.005	<100	4576.4	1383.6	424.0
MGRM-C-020		>50	13.955	>50	>50	>50	>50	5.846	>50	>50	>50	>50	>50	1.336	0.446	0.797	1.288	0.712	0.396	0.112	>50	110.9	245.6	115.3	<100
MGRM-C-022		0.015	0.012	0.010	1.233	0.960	0.410	0.042	0.127	0.780	>50	>50	>50	0.381	0.086	0.103	2.578	0.492	12.989	18.283	0.346	1972.8	921.3	725.8	658.0
MGRM-C-023		0.017	0.027	0.011	1.314	0.065	1.082	0.026	0.151	0.143	0.061	3.198	0.230	0.153	0.087	0.148	0.380	0.201	0.077	0.128	0.614	1046.6	354.6	285.3	1358.0
MGRM-C-024		0.052	0.102	0.195	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.101	0.030	0.050	2.064	0.174	3.395	>50	0.227	718.0	607.2	<100	170.0
MGRM-C-025		46.753	8.691	13.304	42.541	0.786	>50	10.489	>50	>50	>50	>50	>50	0.247	0.183	0.336	17.550	0.044	2.364	>50	0.148	228.2	886.0	129.6	651.0
MGRM-C-026		0.002	0.006	0.001	0.005	0.007	0.014	0.007	0.036	1.674	0.004	0.006	0.011	>50	>50	>50	>50	>50	0.707	0.303	0.060	12635.8	2201.2	2438.1	9554.0
MGRM-C-027		0.011	0.039	0.020	>50	15.557	>50	0.081	0.008	0.065	>50	>50	>50	3.275	0.792	0.598	>50	0.095	0.125	2.762	5.358	2368.0	859.3	1636.4	869.0
MGRM-C-028		0.472	2.216	0.402	14.023	0.196	7.567	14.423	>50	>50	1.474	33.676	>50	13.771	2.117	12.367	>50	0.099	0.319	0.149	0.067	115.0	363.0	<100	502.0

		IC$_{50}$ (µg/mL)																				IC$_{50}$ (1/dil'n)			
Isolate	**Subtype**	**PGT-121**	**PGT-122**	**PGT-123**	**PGT-125**	**PGT-126**	**PGT-127**	**PGT-128**	**PGT-130**	**PGT-131**	**PGT-135**	**PGT-136**	**PGT-137**	**PGT-141**	**PGT-142**	**PGT-143**	**PGT-144**	**PGT-145**	**VRC01**	**PGV04**	**PG9**	**#17**	**#84**	**#36**	**#39**
98CN009	CRF07_BC	0.009	0.013	0.007	0.030	0.019	0.090	0.025	0.136	4.051	0.071	0.428	5.059	1.277	3.999	10.206	>50	0.136	0.346	0.125	0.371	2551.0	1469.5	756.3	1430.0
98CN006	CRF08_BC	0.010	0.021	0.008	0.201	0.046	0.067	0.015	0.258	35.286	0.429	0.406	1.217	>50	>50	>50	>50	>50	0.655	1.320	>50	1908.7	365.2	367.0	980.0
92UG001	D	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	1.159	0.553	>50	<100	<100	<100	260.0
92UG005		18.292	>50	9.794	>50	0.037	1.107	0.018	0.959	0.854	>50	>50	>50	>50	>50	>50	>50	>50	0.576	0.440	>50	265.5	<100	590.3	480.0
92UG024		>50	>50	>50	>50	>50	>50	>50	>50	>50	0.010	0.052	0.106	>50	>50	>50	>50	1.600	0.576	0.201	1.861	<100	202.0	138.1	1930.0
92UG046		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	12.687	22.362	1.861	<100	200.5	<100	137.0
94UG114		0.004	0.011	0.005	0.349	0.038	7.091	0.083	>50	>50	1.289	>50	>50	>50	>50	>50	>50	20.113	0.330	0.461	40.608	5390.2	<100	292.1	548.0
MGRM-D-001		0.615	1.130	0.147	2.837	0.084	2.234	0.138	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.560	>50	>50	>50	<100	<100	112.8	<100
MGRM-D-002		0.006	0.005	0.012	0.118	0.039	0.600	0.011	0.869	11.150	>50	>50	>50	>50	>50	>50	>50	>50	0.252	0.322	0.021	5960.5	<100	726.4	442.0
MGRM-D-003		10.685	>50	3.736	0.065	0.021	0.029	0.019	0.651	19.624	>50	>50	>50	>50	>50	>50	>50	0.006	2.064	>50	0.033	183.1	695.8	414.7	176.0
MGRM-D-004		>50	>50	>50	0.371	>50	>50	24.887	1.208	2.007	>50	>50	>50	>50	>50	>50	>50	10.881	1.250	43.200	0.060	<100	125.9	108.5	397.0
MGRM-D-005		>50	>50	>50	>50	0.792	6.044	0.051	>50	>50	>50	>50	>50	5.154	1.153	1.414	14.807	10.398	>50	>50	1.802	<100	235.9	109.3	249.0
MGRM-D-008		>50	>50	>50	>50	43.139	>50	0.033	>50	>50	>50	>50	>50	0.371	0.174	0.153	9.849	0.025	0.854	3.564	11.454	<100	348.8	<100	356.0
MGRM-D-011		0.018	0.019	0.012	0.008	0.009	0.015	0.007	0.019	0.756	23.478	>50	6.297	>50	>50	>50	>50	14.655	0.075	0.025	0.071	1037.5	123.2	769.0	498.0
MGRM-D-012		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.216	0.125	16.182	<100	109.0	109.1	261.0
MGRM-D-013		>50	>50	>50	>50	>50	>50	8.847	0.429	4.141	>50	>50	>50	0.179	0.221	0.386	>50	3.480	0.087	0.088	0.210	<100	745.4	422.8	377.0
MGRM-D-014		0.009	0.012	0.009	0.120	0.030	0.393	0.013	0.061	0.516	2.209	>50	>50	0.010	0.005	0.009	0.113	2.511	0.332	0.194	0.023	2249.9	1526.5	428.0	322.0
MGRM-D-016		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.452	0.201	0.098	<100	282.7	203.4	253.0
MGRM-D-018		0.005	0.007	0.007	0.049	0.009	0.021	0.008	0.049	0.148	0.039	>50	15.100	>50	>50	>50	>50	0.065	>50	17.528	0.025	6632.6	259.2	1730.4	642.0
MGRM-D-019		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	1.655	0.155	0.277	>50	0.111	0.119	0.350	0.038	<100	296.7	260.0	467.0
MGRM-D-020		0.010	0.007	0.018	0.015	0.023	0.015	0.011	24.677	>50	>50	>50	>50	>50	>50	>50	>50	10.003	0.192	0.097	1.665	2488.0	<100	393.5	190.0
MGRM-D-021		5.334	11.735	11.120	0.040	0.047	0.056	0.014	0.156	0.106	>50	>50	>50	>50	>50	>50	>50	>50	33.445	>50	>50	<100	<100	457.5	148.0
MGRM-D-022		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	34.305	>50	>50	>50	<100	<100	<100	<100
MGRM-D-024		0.038	0.185	0.023	>50	0.376	1.945	0.067	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.224	0.366	>50	0.038	355.3	144.4	124.7	399.0
MGRM-D-026		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	32.480	12.512	44.566	>50	0.410	0.435	1.761	23.664	<100	401.4	103.2	<100
MGRM-D-028		0.009	3.338	0.132	>50	>50	>50	>50	0.825	>50	>50	>50	>50	>50	>50	>50	>50	0.721	0.377	1.008	20.234	2028.2	259.0	<100	563.0
MGRM-D-029		>50	>50	>50	>50	>50	>50	>50	>50	>50	30.849	>50	>50	0.057	0.192	0.200	0.459	0.030	3.224	1.557	>50	<100	291.4	<100	387.0
MGRM-F1-004	F	1.665	1.291	1.783	0.035	0.063	0.068	0.027	0.023	0.114	0.211	>50	40.343	0.021	0.013	0.036	0.105	0.361	0.305	0.580	0.175	260.7	874.0	687.6	366.0
MGRM-F1-006		5.328	3.266	6.894	0.361	0.078	7.172	0.763	>50	>50	>50	>50	>50	8.993	12.874	12.341	20.563	13.642	2.856	>50	7.249	<100	147.3	110.8	487.0
MGRM-F1-008		>50	>50	>50	>50	>50	>50	>50	0.065	2.742	>50	>50	>50	0.193	0.124	0.189	0.507	0.228	1.114	1.031	>50	<100	242.1	<100	308.0
MGRM-F1-010		0.016	0.024	0.016	>50	>50	>50	16.663	>50	>50	>50	>50	>50	>50	>50	>50	>50	3.321	0.097	0.184	0.012	825.3	420.4	<100	564.0
MGRM-F1-012		1.907	>50	22.222	>50	0.300	>50	0.007	>50	>50	0.010	>50	>50	>50	>50	>50	>50	0.113	0.488	0.250	0.023	573.3	332.3	299.8	1366.0
MGRM-F1-013		0.083	0.152	0.080	>50	>50	>50	12.723	>50	>50	21.080	>50	>50	0.043	0.023	0.013	0.509	0.402	0.170	0.084	1.253	283.9	2403.4	377.4	625.0
MGRM-F1-014		0.082	0.195	0.111	>50	>50	>50	0.277	11.795	>50	>50	>50	>50	0.001	0.001	0.001	0.014	0.009	0.056	0.020	0.020	314.2	6934.5	<100	538.0
MGRM-F1-015		28.359	31.437	>50	>50	>50	>50	>50	>50	>50	1.114	>50	>50	>50	>50	>50	>50	1.764	0.387	0.179	>50	<100	145.7	<100	234.0
MGRM-F1-016		0.931	4.808	4.948	>50	>50	>50	1.209	>50	>50	>50	>50	>50	>50	>50	>50	>50	17.531	0.517	0.268	0.518	110.3	103.0	<100	407.0
MGRM-F1-017		16.891	>50	>50	>50	>50	>50	11.659	>50	>50	7.788	>50	>50	30.829	23.465	26.279	>50	0.286	1.077	2.383	>50	<100	279.4	<100	832.0
MGRM-F1-018		0.040	0.563	0.054	>50	14.941	3.586	0.023	>50	>50	>50	>50	>50	0.785	0.404	0.701	>50	1.020	0.032	0.027	0.019	770.0	518.6	151.2	391.0
MGRM-F1-020		0.167	0.321	0.051	>50	>50	>50	0.355	9.728	>50	0.168	9.311	1.931	1.152	0.824	0.980	8.929	0.816	1.890	5.987	6.396	305.4	220.8	<100	306.0
MGRM-F1-021		0.099	2.301	0.307	>50	>50	>50	>50	>50	>50	0.065	>50	>50	>50	>50	>50	>50	8.038	0.039	0.031	>50	227.6	505.7	218.7	919.0
MGRM-F1-022		0.104	0.277	0.075	>50	>50	>50	4.545	>50	>50	0.964	2.418	6.231	0.114	0.040	0.082	0.382	0.009	0.055	0.072	0.028	350.0	1296.4	221.3	638.0
MGRM-F1-023		0.097	0.154	0.053	0.012	0.009	0.119	0.007	0.050	>50	0.088	>50	>50	0.307	0.602	0.972	1.163	5.879	0.392	0.171	>50	362.3	337.3	674.5	2177.0

		IC_{50} (µg/mL)																				IC_{50} (1/dil'n)			
Isolate	**Subtype**	**PGT-121**	**PGT-122**	**PGT-123**	**PGT-125**	**PGT-126**	**PGT-127**	**PGT-128**	**PGT-130**	**PGT-131**	**PGT-135**	**PGT-136**	**PGT-137**	**PGT-141**	**PGT-142**	**PGT-143**	**PGT-144**	**PGT-145**	**VRC01**	**PGV04**	**PG9**	**#17**	**#84**	**#36**	**#39**
MGRM-G-001	G	0.004	0.005	0.009	0.033	0.038	0.113	0.019	0.198	0.404	0.393	8.113	41.703	0.392	0.362	0.423	>50	0.028	0.371	>50	0.166	5296.0	557.6	635.9	169.0
MGRM-G-004		0.115	2.146	0.181	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	600.5	157.8	107.3	574.0
MGRM-G-006		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.043	0.019	0.031	3.843	0.286	0.055	0.083	1.983	<100	548.1	<100	<100
MGRM-G-009		0.020	0.514	33.546	>50	>50	>50	>50	>50	>50	>50	>50	>50	1.890	2.811	2.968	>50	0.982	0.073	0.043	10.704	160.3	336.3	<100	345.0
MGRM-G-011		3.167	31.299	14.900	>50	7.318	>50	8.212	>50	>50	>50	>50	>50	0.086	0.046	0.074	1.577	0.028	0.065	0.780	0.335	<100	641.1	<100	891.0
MGRM-G-013		3.991	3.448	3.969	>50	48.845	7.699	0.995	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	0.553	0.168	>50	100.5	561.4	480.3	629.0
MGRM-G-014		0.009	0.008	0.005	0.007	0.009	0.009	0.004	2.226	4.313	>50	>50	>50	0.222	0.076	0.107	0.562	0.144	0.056	0.056	16.478	3593.5	389.5	1058.0	295.0
MGRM-G-015		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	10.465	0.548	0.333	6.599	<100	<100	<100	266.0
MGRM-G-016		>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	4.690	8.170	7.600	>50	0.081	0.063	0.019	1.363	<100	681.8	106.0	440.0
MGRM-G-017		0.004	0.032	0.026	>50	>50	>50	0.319	>50	>50	0.137	>50	34.905	0.164	0.125	0.107	9.972	0.205	0.124	0.065	0.104	1582.3	701.7	282.9	420.0
MGRM-G-019		0.011	0.016	0.008	>50	0.018	0.429	0.010	27.938	>50	0.145	44.285	0.126	20.310	5.949	4.773	>50	0.041	0.060	0.027	14.559	1416.7	253.3	354.8	524.0
MGRM-G-024		0.014	0.033	0.032	>50	>50	>50	0.095	5.838	10.730	0.062	0.152	0.051	0.051	0.054	0.048	7.923	0.060	0.025	0.033	0.163	1077.4	388.2	131.5	516.0
MGRM-G-025		0.063	0.079	0.046	>50	17.054	19.279	0.017	8.452	7.750	0.592	>50	>50	>50	>50	>50	>50	>50	0.292	1.608	>50	396.1	129.5	164.2	213.0
MGRM-G-027		0.124	0.606	0.182	34.414	0.875	>50	0.313	4.137	2.904	0.062	45.222	0.228	>50	>50	>50	>50	0.433	0.360	0.125	0.007	289.0	140.8	143.4	676.0
MGRM-G-028		0.014	0.010	0.008	0.012	0.012	0.032	0.008	0.074	0.466	>50	>50	>50	24.888	30.309	42.988	>50	0.046	0.164	0.352	0.891	2769.4	522.4	1201.4	621.0
aMLV	negative	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	<100	<100	<100	<100

Supplementary Table 5. Binding activity of PGT mAbs.

		EC$_{50}$ (µg/ml)[a]			
Donor	**mAb**	**WT JR-FL gp120**	**JR-FL gp120 ΔV1/ΔV2**	**JR-FL gp120 ΔV3**	**Endo H treated JR-FL gp120**
#17	**121**	**0.2**	**0.2**	**>10**	**>10**
	122	**0.3**	**0.3**	**>10**	**>10**
	123	**0.2**	**0.3**	**>10**	**>10**
#36	**125**	**0.2**	**0.6**	**>10**	**>10**
	126	**0.1**	**0.3**	**>10**	**>10**
	127	**0.1**	**0.7**	**>10**	**>10**
	128	**0.1**	**0.3**	**7.8**	**>10**
	130	**0.2**	**>10**	**>10**	**>10**
	131	**0.4**	**>10**	**>10**	**>10**
#39	**135**	**0.1**	**0.1**	**0.2**	**>10**
	136	**0.2**	**0.3**	**0.1**	**>10**
	137	**0.1**	**0.2**	**0.1**	**>10**

[a] Binding was evaluated by ELISA. EC$_{50}$ values were derived by nonlinear regression analysis.
Experiments were performed in duplicate, and data represent an average of at least two independent experiments.

Supplementary Table 6. Neutralizing activity of PGT mAbs against a panel of JR-CSF alanine mutants.

		Fold IC_{50} increase relative to wild-type[c]									
Mutation[a]	**gp120 domain[b]**	**PGT-121**	**PGT-122**	**PGT-123**	**PGT-125**	**PGT-126**	**PGT-127**	**PGT-128**	**PGT-130**	**PGT-131**	**PGT-135**
D113A	C1	1.2	1.0	1.1	1.1	1.2	0.3	0.5	0.8	ND	0.8
V120A		0.8	1.2	1.1	0.5	0.7	1.5	1.4	0.8	0.7	1.4
L125A		0.9	2.4	2.5	1.6	1.2	1.4	2.9	2.5	2.5	0.9
V127A		0.7	1.0	1.2	0.9	1.3	2.5	1.1	0.8	0.6	1.4
N134A	V1	0.2	0.3	0.4	0.5	0.6	1.0	1.2	0.6	0.5	0.2
N156A	V2	0.9	1.1	6.2	3.6	1.8	1.6	0.4	1.5	1.0	0.3
N160K		1.1	1.1	1.0	0.5	0.5	0.8	1.0	3.4	0.4	7.7
T162A		0.3	0.6	0.7	0.5	0.6	1.1	1.1	0.6	0.6	0.9
I165A		3.3	3.0	2.2	2.3	2.5	1.7	2.1	3.2	2.4	4.0
R166A		1.4	0.9	0.9	1.5	1.0	1.6	2.7	1.2	1.6	0.9
D167A		1.0	1.1	1.2	1.7	1.6	1.6	0.3	1.2	1.2	0.7
K168A		1.5	0.8	0.8	0.9	0.7	1.9	1.1	1.2	1.7	0.4
E172A		1.4	1.0	1.1	1.8	0.7	2.1	2.5	1.4	ND	1.3
Y177A		1.4	2.4	2.4	1.1	0.9	2.9	1.4	3.6	5.3	0.3
L179A		1.9	1.1	1.2	1.3	2.6	2.5	2.8	2.4	4.8	1.2
V182A		2.1	2.2	2.8	1.3	1.4	1.6	1.2	1.2	1.1	1.5
D185A		1.0	1.8	1.9	0.6	1.0	2.0	1.5	0.9	0.7	1.3
N188A		0.8	1.0	1.1	0.7	0.8	0.8	1.3	1.0	0.9	0.4
N197A	C2 (V1/V2 stem)	1.1	1.4	1.4	1.0	1.1	0.6	1.0	1.2	1.1	0.3
S199A		0.8	1.0	1.1	0.7	0.8	3.0	1.0	0.9	1.6	0.3
T202A		1.2	1.5	1.2	0.8	0.8	1.8	1.1	1.2	2.7	1.8
F210A	C2	1.5	2.6	2.8	1.4	1.5	0.8	0.8	1.7	1.0	1.3
N241A		0.5	1.4	0.8	0.5	0.6	0.6	0.7	0.6	0.7	0.1
N262A		1.1	1.1	0.5	0.9	1.0	1.4	1.6	0.7	0.4	2.1
N276A		0.8	1.4	1.1	0.9	0.9	1.6	0.6	1.0	0.8	2.5

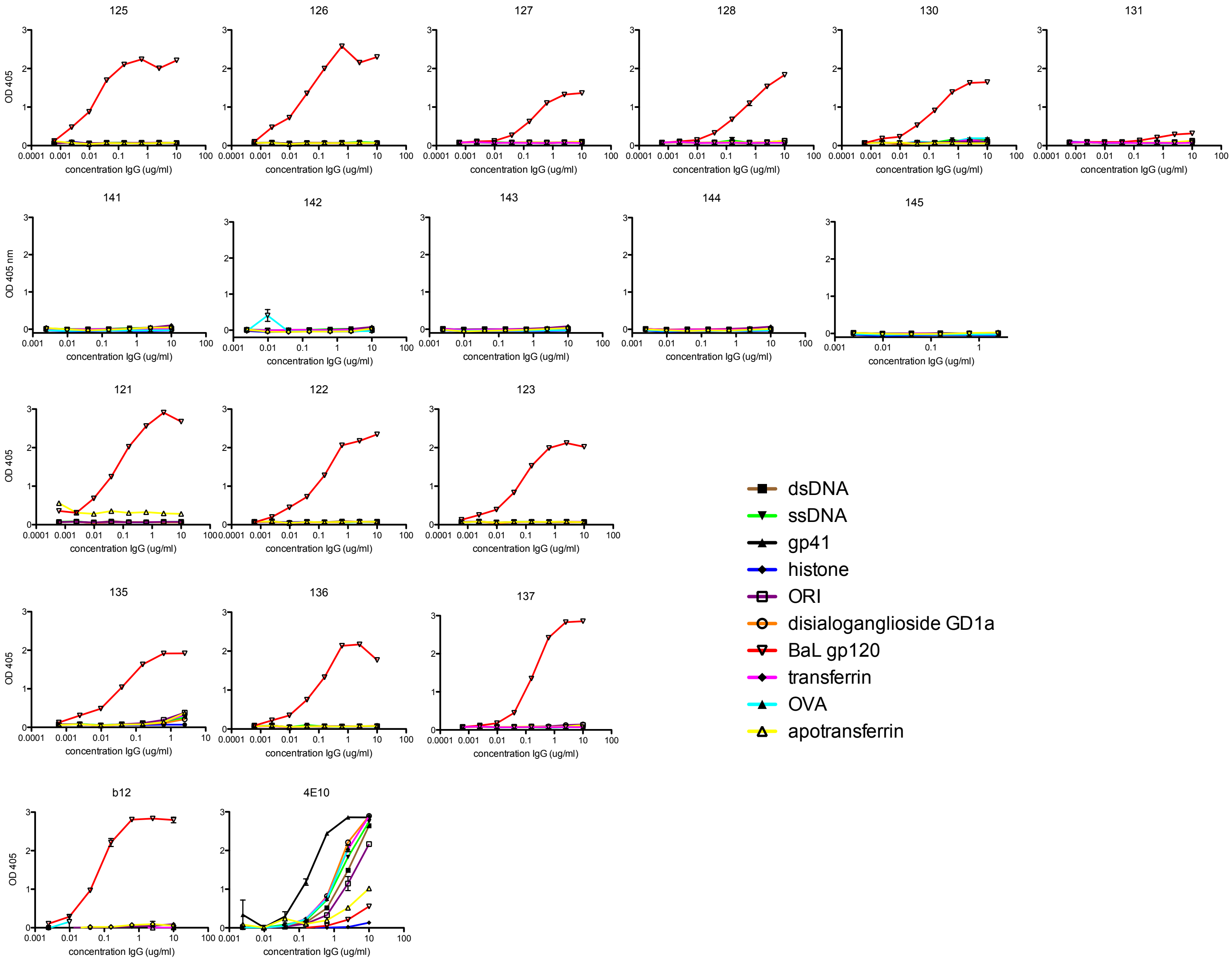
		Fold IC_{50} increase relative to wild-type[c]									
Mutation[a]	**gp120 domain[b]**	**PGT-121**	**PGT-122**	**PGT-123**	**PGT-125**	**PGT-126**	**PGT-127**	**PGT-128**	**PGT-130**	**PGT-131**	**PGT-135**
V292A	V3	2.7	1.3	1.7	3.3	5.0	0.9	2.1	0.9	1.4	2.0
N295A		0.6	0.7	1.2	0.8	0.9	2.3	1.0	0.7	2.1	>18
T297A		0.7	0.6	0.3	0.9	0.8	1.7	1.1	0.9	1.2	>30
P299A		0.2	0.5	0.7	0.2	0.2	0.2	1.2	0.8	2.0	0.36
N301A		0.4	0.4	1.0	213	314	>250	10.7	>1000	>170	0.5
N302A		0.7	1.1	1.3	0.7	0.9	3.0	1.5	1.1	1.0	0.8
T303A		0.7	2.5	1.1	>250	>250	>500	>500	>250	>170	0.3
R304A		1.7	0.7	0.7	1.9	1.8	0.4	0.7	2.5	1.5	0.7
K305A		1.9	3.0	1.9	1.9	1.0	2.6	1.8	6.9	ND	0.2
S306A		0.7	0.5	0.5	1.2	0.7	0.6	1.1	1.5	0.7	0.4
I307A		3.7	3.8	5.9	5.0	1.8	10.2	3.7	1000.0	>170	0.3
I309A		1.1	2.1	1.6	1.0	1.2	6.0	2.8	>77.9	8.8	0.3
P313A		0.5	0.4	0.2	0.3	0.4	1.3	1.0	0.3	0.52	0.5
R315A		0.9	0.5	0.7	0.9	1.0	0.3	0.4	0.6	0.7	1.8
F317A		1.7	3.4	3.1	1.8	1.0	0.2	0.8	17.0	96	0.5
T319A		1.3	0.5	0.4	1.1	0.8	1.0	0.5	1.6	0.9	0.4
T320A		1.2	0.7	0.7	0.8	0.6	1.8	1.0	0.9	4.5	0.5
E321aA		0.3	0.4	0.6	1.0	0.6	1.9	1.3	1.7	1.8	0.8
I323A		1.9	2.2	1.0	0.9	0.9	4.0	3.0	0.8	38.0	1.5
G324A		16.6	12.5	14.5	1.7	3.3	ND	ND	>50	ND	0.4
D325A		2.0	44.0	64.0	0.4	0.5	0.93	0.5	>1000	>170	0.5
I326A		0.7	0.6	0.4	0.9	0.8	3.5	1.6	1.3	1.7	1.2
R327A		2.5	1.7	1.7	2.1	2.2	1.8	2.5	2.4	19.0	0.67
H330A		0.8	0.5	0.3	0.7	0.5	0.5	0.3	0.9	0.5	>250
N332A		>200	>200	>200	2.0	181	>100	1.4	0.6	0.5	>250
S334A		>50	>50	>50	0.8	>30	>500	1.4	0.5	0.4	>30
Q337A	C3	1.0	0.5	0.5	0.8	0.4	0.5	0.7	1.0	1.3	2.1
N339A		0.5	0.4	0.8	0.9	0.6	1.1	0.8	0.2	1.0	1.2
T341A		0.5	0.3	0.3	1.1	0.5	1.7	1.3	0.8	1.3	0.6
K343A		0.6	0.3	0.3	0.7	1.2	1.0	1.0	1.1	1.1	1.1
R350A		0.8	0.6	0.5	0.6	0.7	1.1	1.0	0.5	1.3	0.9
N355A		1.4	0.8	0.5	1.2	0.2	1.4	0.7	1.3	2.3	0.8
N386A		1.3	1.2	1.4	0.8	0.9	0.6	1.1	0.1	1.1	0.3
S387A		0.5	0.9	0.9	0.6	0.6	1.0	1.2	0.7	1.1	0.6
T388A		0.9	0.3	0.2	0.6	0.6	0.5	1.0	1.0	0.6	0.1

		Fold IC_{50} increase relative to wild-type[c]									
Mutation[a]	**gp120 domain**[b]	**PGT-121**	**PGT-122**	**PGT-123**	**PGT-125**	**PGT-126**	**PGT-127**	**PGT-128**	**PGT-130**	**PGT-131**	**PGT-135**
N392Q	**V4**	**0.9**	**1.0**	**1.0**	**1.2**	**1.6**	**1.1**	**0.9**	**1.2**	**0.4**	**>250**
S393A		**0.6**	**0.5**	**0.6**	**0.5**	**0.5**	**1.2**	**1.4**	**0.7**	**1.1**	**0.9**
T394A		**0.2**	**0.6**	**0.4**	**0.6**	**0.6**	**1.6**	**3.0**	**1.2**	**0.9**	**>75**
W395A		**0.5**	**0.4**	**0.4**	**0.9**	**0.6**	**1.6**	**0.8**	**0.6**	**0.5**	**0.6**
N396A		**1.3**	**1.1**	**1.2**	**1.6**	**1.7**	**2.4**	**0.9**	**1.0**	**0.9**	**1**
N411A		**0.4**	**0.7**	**0.5**	**0.5**	**0.7**	**0.8**	**0.7**	**0.6**	**0.6**	**0.2**
T413A		**0.5**	**0.8**	**0.4**	**0.5**	**0.7**	**0.8**	**1.0**	**0.6**	**0.6**	**0.3**
I414A		**0.5**	**0.5**	**0.3**	**0.3**	**0.4**	**2.2**	**1.4**	**0.7**	**1.0**	**1.2**
I415A		**0.6**	**0.4**	**0.4**	**0.3**	**0.3**	**2.1**	**0.7**	**0.6**	**0.6**	**5**
L416A		**0.6**	**1.0**	**0.9**	**0.8**	**0.8**	**1.0**	**1.1**	**1.0**	**1.0**	**1.2**
D417A		**0.7**	**0.5**	**0.7**	**0.5**	**1.0**	**0.4**	**0.5**	**1.0**	**1.0**	**5.0**
R419A	**C4**	**1.8**	**0.8**	**0.7**	**1.0**	**1.2**	**2.5**	**0.5**	**2.6**	**1.7**	**3.9**
I420A		**3.3**	**3.5**	**3.2**	**1.1**	**0.6**	**1.8**	**0.8**	**9.8**	**153**	**1.4**
K421A		**1.3**	**1.2**	**0.9**	**1.2**	**0.7**	**1.5**	**2.0**	**2.9**	**11.0**	**0.3**
Q422A		**1.2**	**1.1**	**0.8**	**1.2**	**1.1**	**0.1**	**0.2**	**1.0**	**1.9**	**0.8**
I423A		**3.3**	**2.8**	**1.5**	**5.0**	**1.1**	**0.5**	**2.6**	**>1000**	**>80**	**0.1**
I424A		**0.9**	**0.8**	**0.5**	**0.7**	**0.4**	**2.0**	**1.3**	**3.9**	**4.8**	**0.1**
E466A	**V5**	**1.2**	**0.9**	**0.60**	**1.6**	**1.4**	**0.9**	**0.6**	**1.7**	**1.7**	**0.5**
F468A		**0.8**	**1.0**	**0.50**	**1.0**	**0.7**	**3.0**	**0.5**	**0.4**	**1.6**	**1.1**
P470A		**0.9**	**2.1**	**0.8**	**1.6**	**2.7**	**1.0**	**0.6**	**2.4**	**1.0**	**0.8**
G471A		**0.8**	**1.8**	**1.3**	**1.0**	**1.2**	**1.2**	**0.9**	**0.8**	**1.2**	**3**
D474A		**1.3**	**1.8**	**1.1**	**1.4**	**3.3**	**1.5**	**0.8**	**2.0**	**1.6**	**1.2**
R476A		**1.1**	**0.9**	**2.0**	**1.9**	**1.5**	**1.2**	**0.7**	**1.3**	**1.0**	**0.8**
D477A		**1.9**	**0.9**	**2.3**	**3.4**	**1.1**	**1.7**	**0.7**	**1.1**	**1.0**	**1.5**
N478A		**0.8**	**0.9**	**0.6**	**1.5**	**1.0**	**1.2**	**0.8**	**0.8**	**1.0**	**0.7**
R480A		**0.8**	**1.4**	**1.7**	**2.1**	**1.9**	**0.2**	**0.1**	**1.0**	**1.5**	**1.4**

[a] Amino acid numbering is based on the sequence of HIV-$1_{HxB2.}$

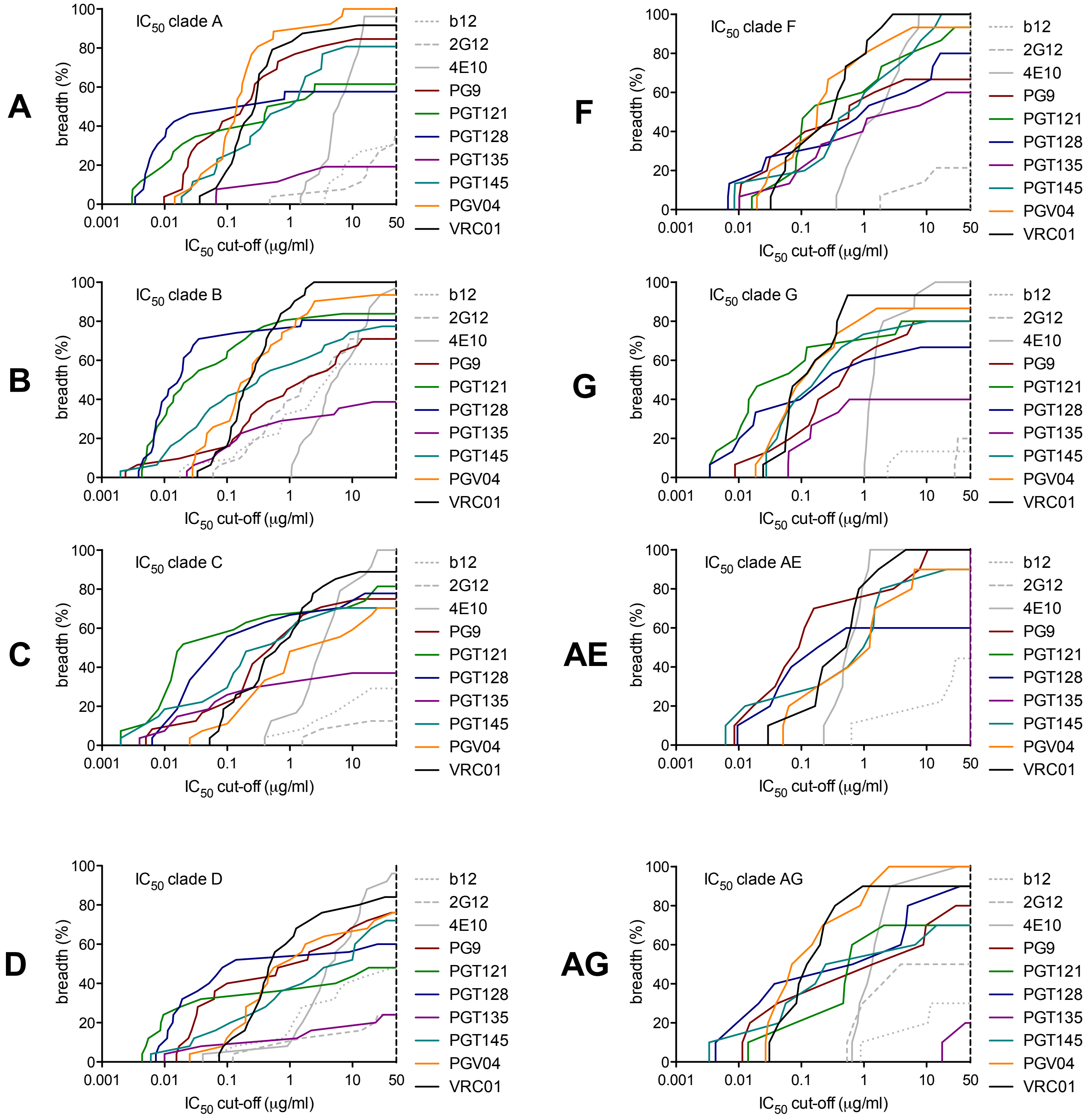
[b] C refers to constant domains and V refers to variable loops.

[c] Neutralization activity is reported as fold increase in IC_{50} value relative to WT JR-CSF and was calculated using the equation (IC_{50} mutant / IC_{50} WT). Experiments were performed in duplicate and values represent an average of at least two independent experiments.

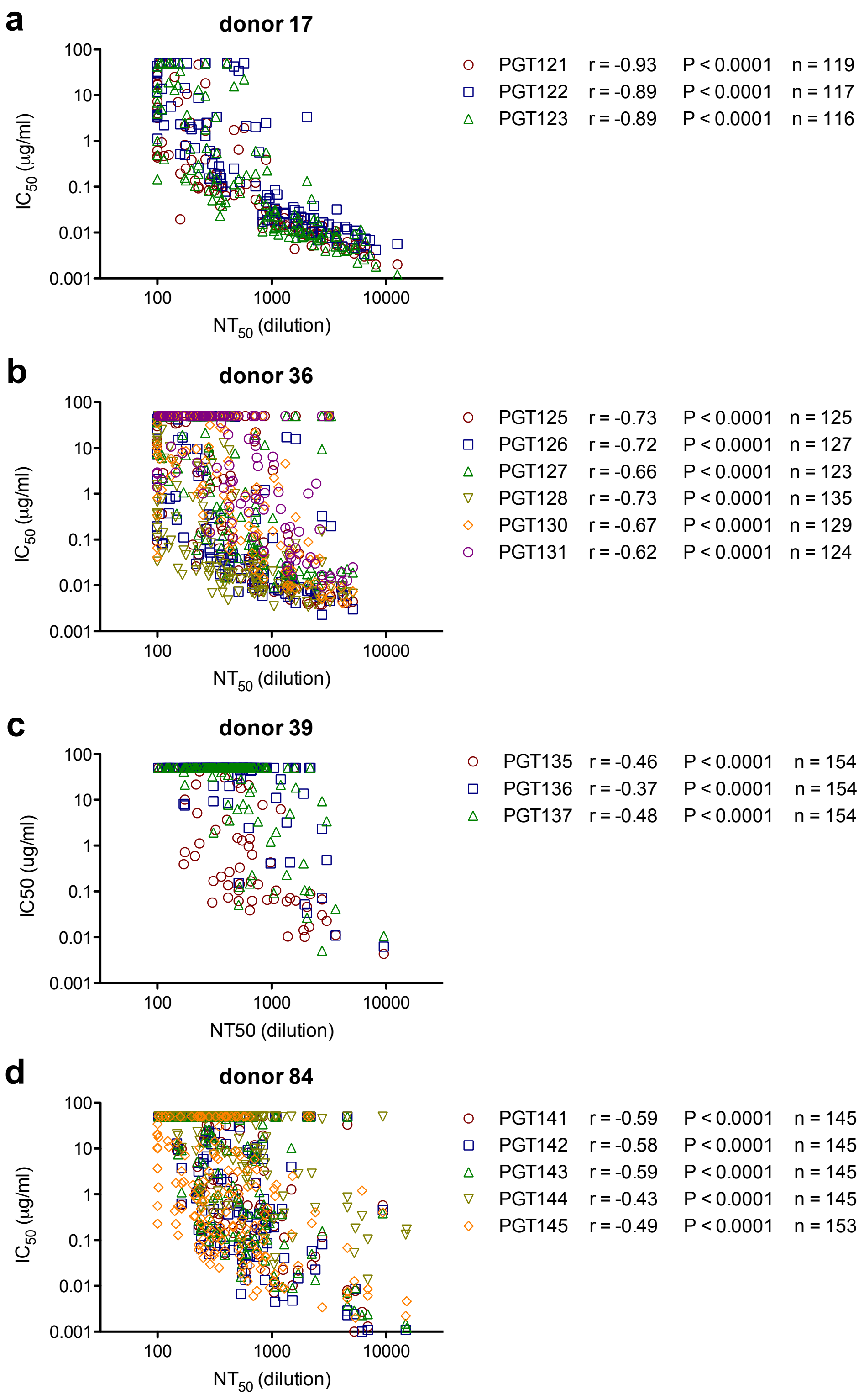


Supplementary Figure 1. Polyreactivity ELISA assay. PGT mAbs were tested for ELISA reactivity against a panel of antigens.

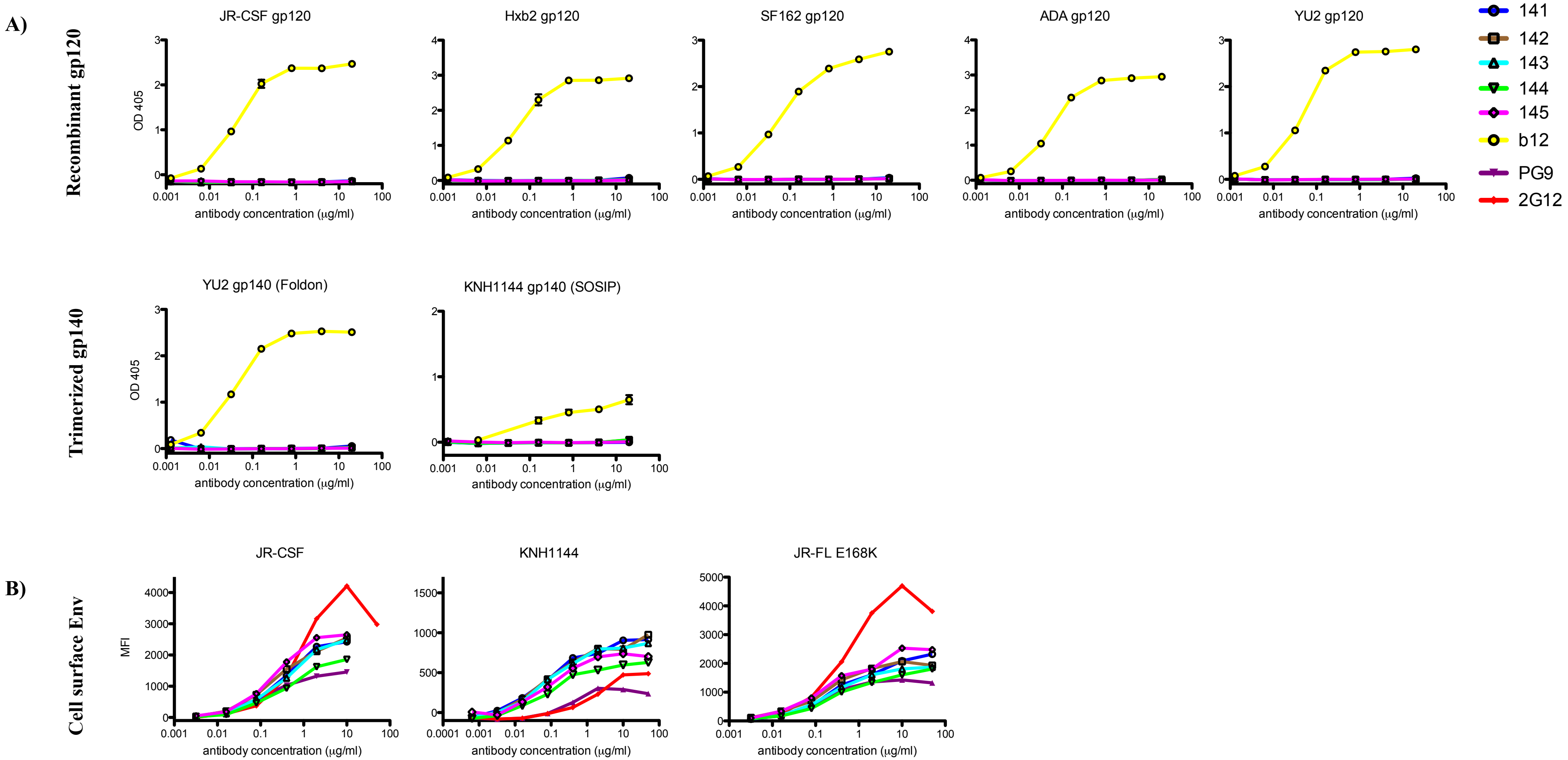
The bNAbs b12 and 4E10 were also included for comparison. d.s, double-stranded; s.s, single-stranded.



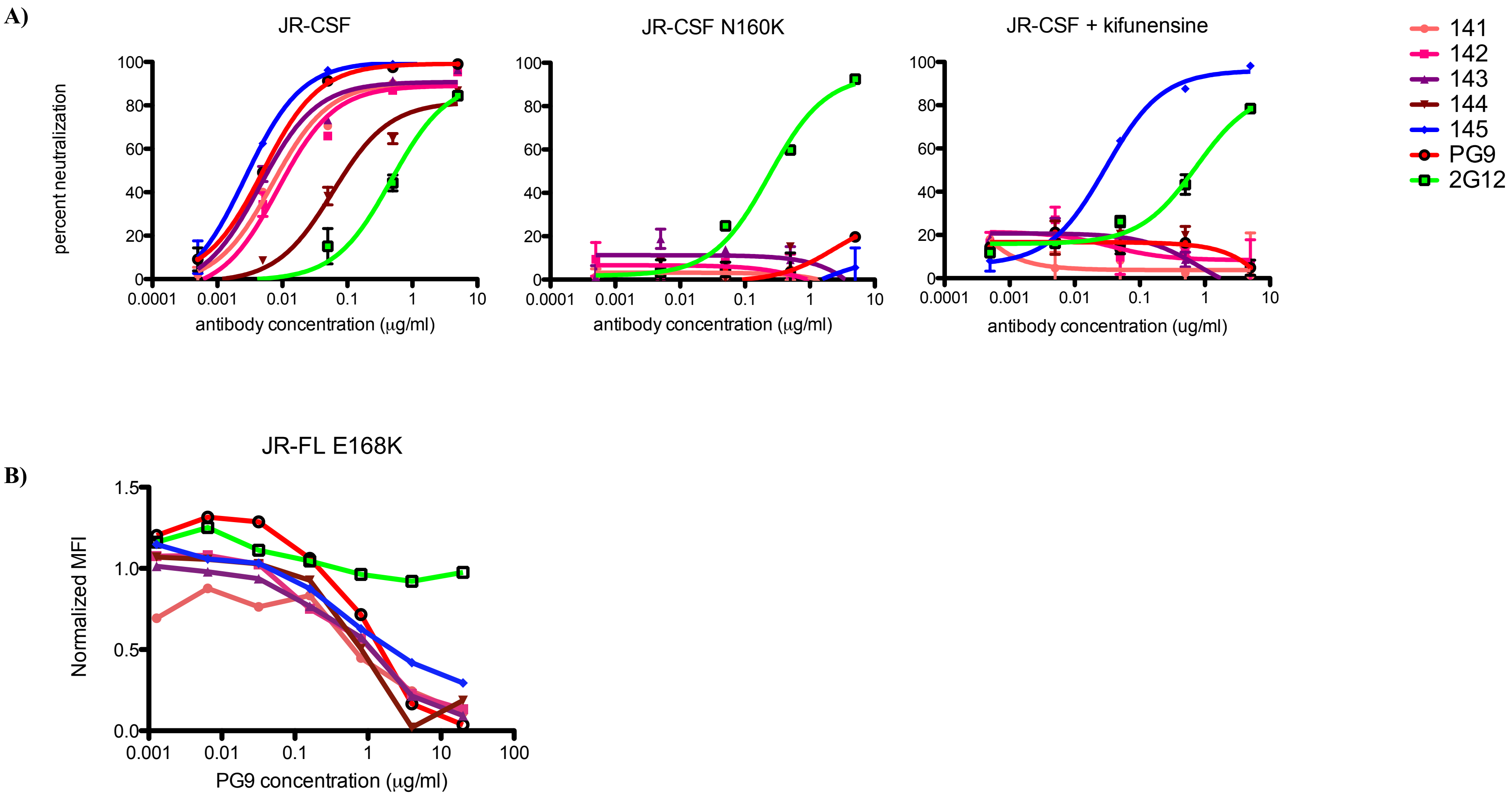
Supplementary Figure 2. Analysis of neutralization activity by virus clades. Cumulative frequency distribution of IC_{50} values of broadly neutralizing MAbs tested against a 162 virus panel separated by clades A, B, C, D, F, G, AE and AG.



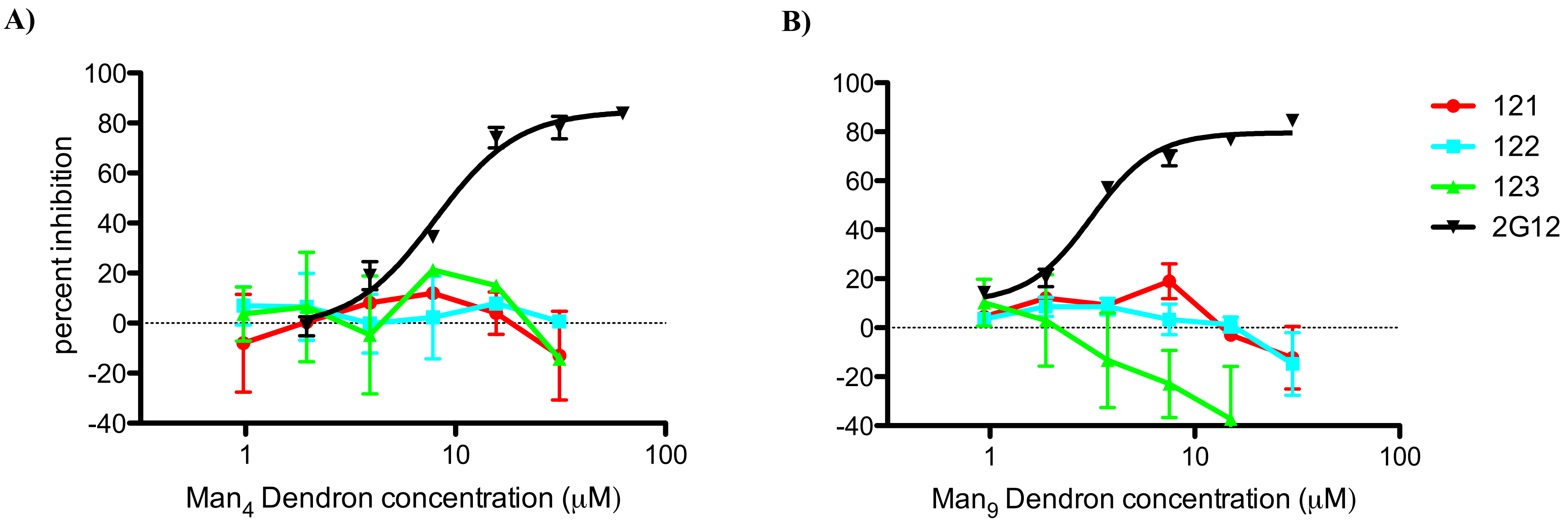
Supplementary Figure 3. MAb neutralization correlates strongly with serum neutralization. Correlation of IC$_{50}$s of the MAbs and serum NT$_{50}$s of the corresponding donors 17 (**a**), 36 (**b**), 39 (**c**) and 84 (**d**) is shown. Spearman correlation was used for statistical analyses. Only viruses neutralized by either the MAb (IC$_{50}$ < 50 µg/ml) or the serum (NT$_{50}$ > 100) were included.



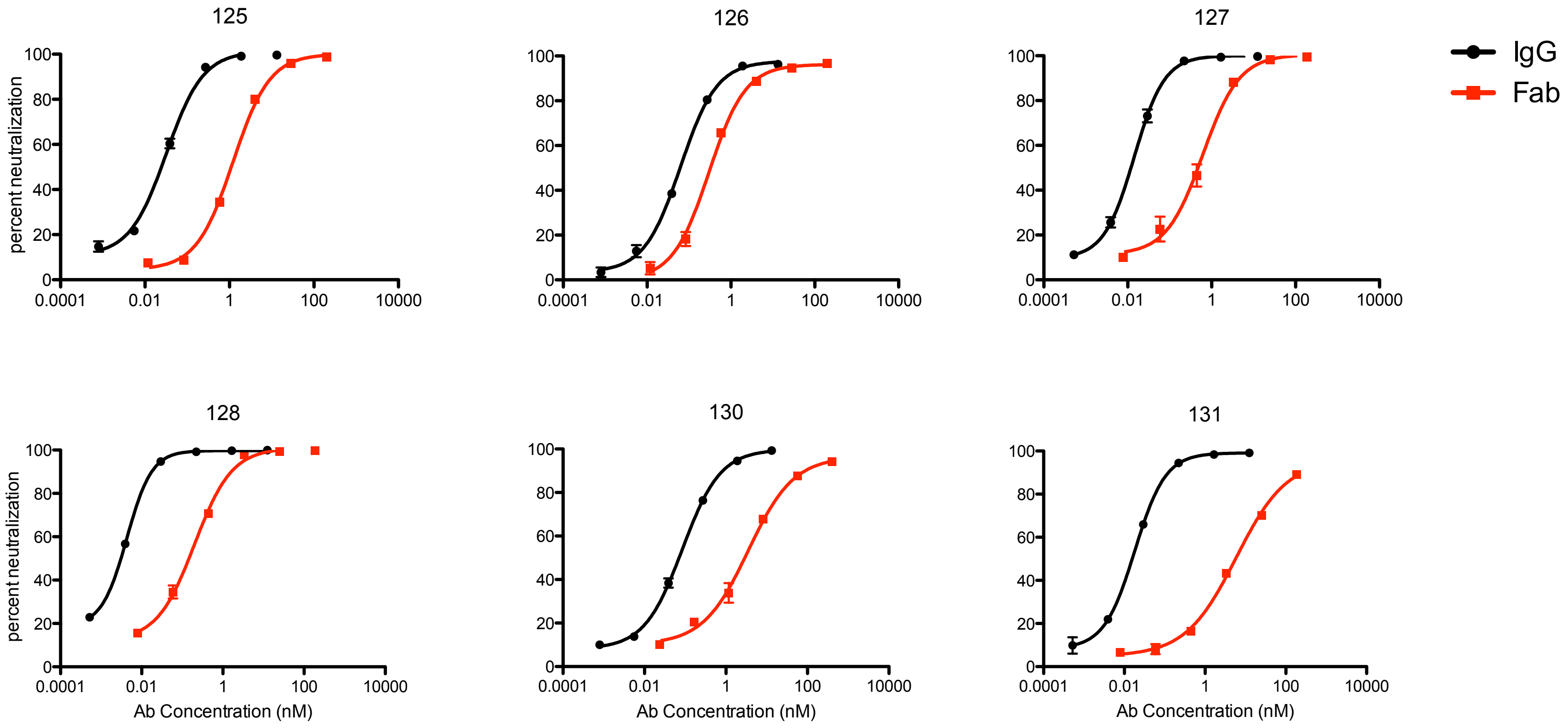
Supplementary Figure 4. PGT 141-145 bind preferentially to cell-surface expressed trimers. A) Binding of PGTs 141-145 to monomeric gp120 and artificially trimerized gp140 constructs as determined by ELISA. The bNAbs b12 and PG9 are included for comparison. OD, optical density (absorbance at 450 nm). B) Binding of PGTs 141-145 to Env expressed on the surface of 293T cells as determined by flow cytometry. The bNAbs 2G12 and PG9 are included for comparison.



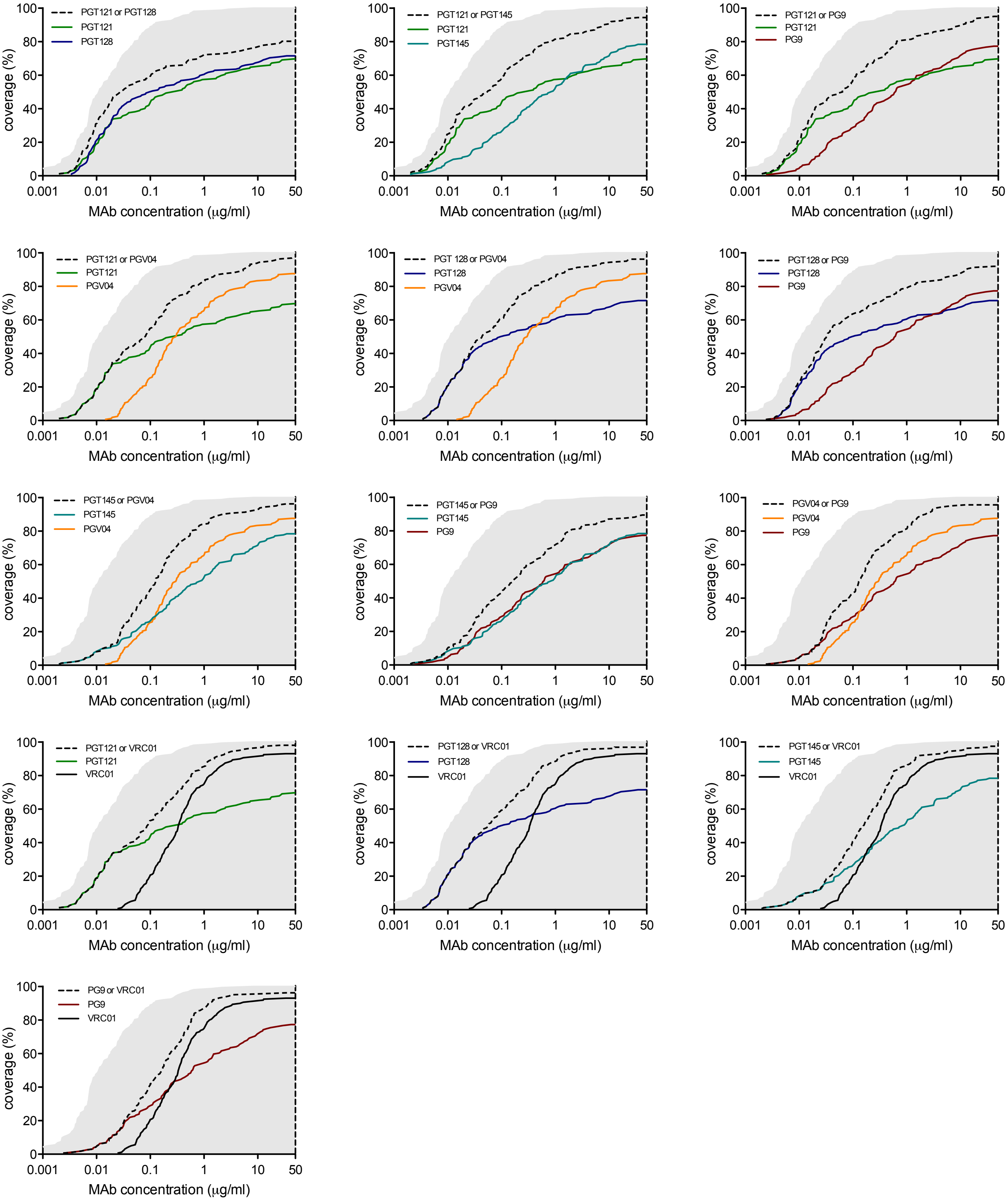
Supplementary Figure 5. PGT mAbs 141-145 bind to epitopes overlapping those of PG9 and PG16. A) PGTs 141-145 are sensitive to the N160K mutation and PGTs 141-144 fail to neutralize pseudoviruses produced in the presence of kifunensine. The bNAb 2G12 was also included for comparison. **B)** PG9 competes with PGTs 141-145 for binding to cell-surface trimers. The bNAb 2G12 was included as a negative control.



Supplementary Figure 6. PGTs 121, 122 and 123 competition with oligodendrons. Unlike PGTs 125, 126, 127, 128 and 130, the binding of PGTs 121, 122 and 123 to gp120 could not be competed by A) Man$_4$ or B) Man$_9$ dendrons.



Supplementary Figure 7. Neutralization activity of Fab fragments. Fab fragments of PGTs-125, 126, 127, 128, 130 and 131 were generated by Lys-C digestion and the neutralizing activity tested against HIV-1$_{\text{JR-CSF}}$ using a single round of replication pseudovirus assay.



Supplementary Figure 8. Percent viruses covered by single MAbs (solid lines) or by at least one of the MAbs in dual combinations (dashed black lines) dependent on individual concentrations. The grey area in all panels is the coverage of 26 MAbs tested on the 162-virus panel (PGT121-123, PGT125-128, PGT130-131, PGT135-137, PGT141-145, PG9, PG16, PGC14, VRC01, PGV04, b12, 2G12, 4E10, 2F5) and depicts the theoretical maximal achievable coverage known to date.

Supporting Notes

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