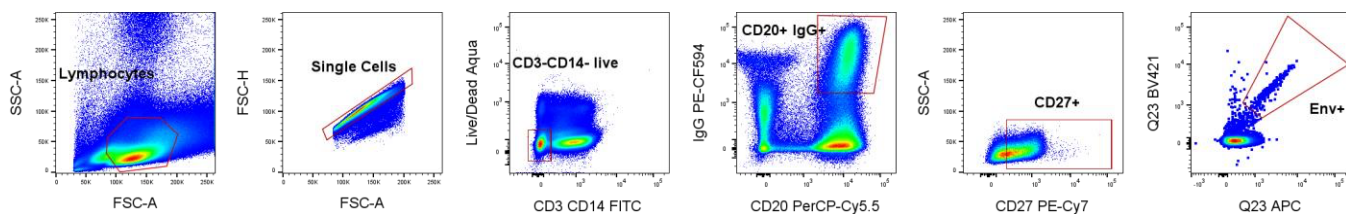

Supplementary information

Vaccination generates broadly cross-neutralizing antibodies to the HIV Env apex

In the format provided by the
authors and unedited



Supplementary Figure 1. FACS gating strategy

FACS gating strategy to isolate Env-specific macaque memory B cells from PBMCs. In brief, macaque PBMCs were first gated on lymphocytes based on FSC-A/SSC-A, followed by FSC-A/FSC-H to exclude doublets/select singlets. Dead cells, T cells, and monocytes were excluded using Aqua Live/Dead staining and CD3 CD14 markers, respectively. IgG⁺ B cells were defined as CD20⁺IgG⁺. Env-specific memory B cells were identified as CD27⁺Env⁺ (Q23, BG505, 16055) within the IgG⁺ B cell population.

Supplementary Table 1a. Sort statistics

Q7	sampling time point	probe	stained PBMCs (million)	sorted cell number	productive HC+LC pairs	mAb ID
	P6	Q23	8.75	376	208	Q7M-450 ⁸⁵ , Q7M-526, Q7M-562, Q7M-653, Q7M-675, Q7M-773 ⁸⁵
Q9	sampling time point	probe	stained PBMCs (million)	sorted cell number	productive HC+LC pairs	mAb ID
	P4	Q23	5	44	16	Q9M-001, Q9M-009 ^{***}
	P5	Q23	9.1	125	64	Q9M-023 ^{***} , Q9M-213 ^{***} , Q9M-218 ^{***}
	P6	Q23	7.4	188	137	Q9M-092, Q9M-225 ^{***} , Q9M-229 ^{***} , Q9M-231 ^{***} , Q9M-246 ^{***} , Q9M-247 ^{***}
Q10	sampling time point	probe	stained PBMCs (million)	sorted cell number	productive HC+LC pairs	mAb ID
	P4	Q23	5.85	234	112	Q10M-054 [*] , Q10M-055 [*] , Q10M-061 [*] , Q10M-092 [*] , Q10M-113 [*] , Q10M-100 ^{**} , Q10M-123 [*] , Q10M-048 [*] , Q10M-103 [*] , Q10M-083, Q10M-112, Q10M-122, Q10M-137
	P5	Q23	2.13	94	47	Q10M-209
Q12	sampling time point	probe	stained PBMCs (million)	sorted cell number	productive HC+LC pairs	mAb ID
	P4	Q23	2.7	36	10	Q12M-031 ^{***} , Q12M-032 ^{***} , Q12M-035
	P5	16055	1.8	41	33	Q1216M-031 ⁸⁵
	P5	16055+BG505	0.5	12	9	Q12B16M-007 ⁸⁵
	P5	BG505	11.4	119	80	Q12BBM-069 ⁸⁵ , Q12BBM-023 ^{***} , Q12BBM-068 ^{***} , Q12BBM-045 [*] , Q12BBM-056 [*] , Q12BBM-065 [*] , Q12BBM-085 [*] , Q12BBM-042 ²⁸⁸ , Q12BBM-076 ⁸⁵ , Q12BBM-022 ⁵ , Q12BBM-026 ⁵ , Q12BBM-044 ⁵ , Q12BBM-043
	P5	Q23+BG505	9	94	40	Q12QBM-007 ^{***} , Q12QBM-034 ⁵
	P6	Q23	8.8	376	221	Q12M-061 ⁸⁵ , Q12M-165 ⁸⁵ , Q12M-131 ⁵ , Q12M-158 ⁵ , Q12M-197 ⁵ , Q12M-190 ⁵ , Q12M-283 ⁵

Supplementary Table 1b. Antibody genetics

NHP ID	mAb ID	lineage name	IGHV allele	IGHD allele	IGHJ allele	HCDR3	% VH SHM nt aa	HCDR3 length	IGKV/IGLV allele	IGKJ/IGL J allele
Q7	Q7M-675	Q7M-450	IGHV4-NL_22*01_S8977	IGHD3-15*01	IGHJ5-4*01	VRDT EYNYPPDDYDYTY YTYGYNR FDV	13.2 25	25	IGKV1-NL_16*01_S1046_kim	IGKJ4*01
	Q7M-562		IGHV4-NL_17*01_S2469	IGHD3-15*01	IGHJ5-4*01	ARGA SYDDDDGYYYS EDRFDV	7.3 12.0	22	IGKV1-25*02_kim	IGKJ4*01
	Q7M-773		IGHV2-7*02_S1732	IGHD3-15*01	IGHJ3-2*01	ARSG GLFYED DYGYYP AMEDDA FDF	5.7 11.1	25	IGLV2-38*01_S7244_kim	IGLJ1*01
	Q7M-450		IGHV2-7*02_S1732	IGHD3-15*01	IGHJ3-2*01	ARSG GLFYED DYGYYP AKEDDA FDF	4.7 10.1	25	IGLV2-38*01_S7244_kim	IGLJ1*01
	Q7M-653		IGHV4-NL_17*01_S0147	IGHD3-15*01	IGHJ1-1*01	ARGARYEDDDSGYYYS RYFDL	5.3 11.0	21	IGKV1-94*01_S1549_kim	IGKJ4*01
	Q7M-526		IGHV4-150*01_S3825	IGHD3-15*01	IGHJ4-3*01	ARGA SFYEDARGASFY EDEGYFY FTYSP L FDF	3.4 4.1	31	IGKV1-94*01_S0326_kim	IGKJ4*01
	Q9M-246		IGHV4-117*01	IGHD3-15*01	IGHJ3-2*01	ASPI RVYYEE DDDYYT YEDAFHV	9.2 13.4	24	IGKV1-21*01_kim	IGKJ2*01
	Q9M-247		IGHV4-117*01	IGHD3-15*01	IGHJ3-2*01	ARPV RADHEE DDDGYT SYDDAFDL	11.2 18.4	24	IGKV1-21*01_kim	IGKJ2*01
	Q9M-225		IGHV4-117*01	IGHD3-15*01	IGHJ3-2*01	ARPM RVDYEE DDEYTY MYEDAFDI	7.5 11.2	24	IGKV1-21*01_kim	IGKJ2*01
	Q9M-229		IGHV4-117*01	IGHD3-15*01	IGHJ3-2*01	ARPV RADHEE DDDGYT SYDDAFDL	11.6 18.4	24	IGKV1-21*01_kim	IGKJ2*01
Q9	Q9M-023	Q9M-023	IGHV4-117*01	IGHD3-15*01	IGHJ3-2*01	ARPV RADHEE DDDGYT SYDDAFDL	8.8 13.3	24	IGKV1-21*01_kim	IGKJ2*01
	Q9M-009		IGHV4-117*01	IGHD3-15*01	IGHJ3-2*01	ARPI RVHYED DDEYTY MYEDAFDL	8.2 16.3	24	IGKV1-21*01_kim	IGKJ2*01
	Q9M-231		IGHV4-117*01	IGHD3-15*01	IGHJ3-2*01	GRPI RVYDYE DDEYTY MYEDAFEI	9.5 15.3	24	IGKV1-21*01_kim	IGKJ2*01
	Q9M-218		IGHV4-117*01	IGHD3-15*01	IGHJ3-2*01	ARPM RVDYEE DDEYTY MYEDAFDL	7.1 10.2	24	IGKV1-21*01_kim	IGKJ2*01
	Q9M-213		IGHV4-117*01	IGHD3-15*01	IGHJ3-2*01	ARPI RVYDYE DDDYTY MYEDAFEF	10.5 17.3	24	IGKV1-21*01_kim	IGKJ2*01
	Q9M-092		IGHV4-117*01	IGHD3-15*01	IGHJ6-6*01	AREG PRVEDD DGFYHY TSALDA	7.4 14.3	22	IGKV3-NL_6*01_S4875_kim	IGKJ2*01
	Q9M-001		IGHV4-144*01_S3113	IGHD3-15*01	IGHJ5-4*03	ATTS FYEEED SGYYT DDFRFDV	10.2 18.4	22	IGKV1-NL_10*01_S1234_kim	IGKJ3*01
	Q10M-055		IGHV4-117*01_S8404	IGHD3-15*01	IGHJ3-2*01	ASDL YEDDY GSYSEG LDVDF	8.8 16.3	22	IGKV3-42*02_kim	IGKJ1*01
	Q10M-054		IGHV4-117*01_S8404	IGHD3-15*01	IGHJ3-2*01	ASDL YEDDD GSYSEG LDVDF	12.8 19.4	22	IGKV3-42*02_kim	IGKJ1*01
	Q10M-061		IGHV4-117*01_S8404	IGHD3-15*01	IGHJ3-2*01	ARDI YEDDD GSYTG LDVDF	7.4 13.3	22	IGKV3-42*02_kim	IGKJ1*01
Q10	Q10M-092	Q10M-055	IGHV4-117*01_S8404	IGHD3-15*01	IGHJ3-2*01	ASDL YEDDY GSYSEG LDVDF	8.4 14.3	22	IGKV3-42*02_kim	IGKJ1*01
	Q10M-113		IGHV4-117*01_S8404	IGHD3-15*01	IGHJ3-2*01	ASDL YEDDY GSYSEG LDVDF	7.1 14.3	22	IGKV3-42*02_kim	IGKJ1*01
	Q10M-100		IGHV4-117*01	IGHD3-15*01	IGHJ5-4*02	ARDG FYDDDD DGYT DQWNV	8.8 16.3	22	IGKV3-42*02_kim	IGKJ1*01
	Q10M-123		IGHV4-117*01	IGHD3-15*01	IGHJ5-4*02	ARDG FYDDDD DGYT DQWNV	10.1 15.3	22	IGKV3-42*02_kim	IGKJ1*01
	Q10M-048		IGHV4-93*01	IGHD3-15*01	IGHJ4-3*01	VRDV SGRDYE DDDGYT FGRFFD F	7 12.1	23	IGKV1-NL_16*01_S1046_kim	IGKJ1*01
	Q10M-103		IGHV4-93*01	IGHD3-15*01	IGHJ4-3*01	VREI SGPVYE DDDGYT FGRVYD H	5 8.1	23	IGKV1-NL_16*01_S1046_kim	IGKJ1*01
	Q10M-083		IGHV4-117*01	IGHD3-15*01	IGHJ5-4*02	ARDG EYFDD DGSFPT QWDFD	8.4 16.3	22	IGKV3-12*02_kim	IGKJ4*01_S4126
	Q10M-112		IGHV5-15*02_S3096	IGHD3-15*01	IGHJ1-1*01	AKSP VYEDDY GSYTGAYDFD	5.8 7.1	21	IGLV1-NL_9*01_S1120_kim	IGLJ1*01
	Q10M-122		IGHV4-NL_1*01_S8621	IGHD3-15*01	IGHJ1-1*01	ATTR YDEDDY GYNYLE YFDV	6.5 10.3	20	IGLV6-112*01_kim	IGLJ3*01
	Q10M-137		IGHV5-15*02_S3096	IGHD3-15*01	IGHJ5-4*02	AKHD VYEDDY GSSSAS WFDV	8.5 15.3	20	IGLV1-NL_9*01_S1120_kim	IGLJ3*01
Q12	Q12M-209	Q12BBM-069	IGHV5-15*02_S3096	IGHD3-15*01	IGHJ4-3*01_S6302	ARAGEYEDD GSFYTA SHDFD	9.5 18.4	21	IGLV1-NL_9*01_S1120_kim	IGLJ2A*01
	Q12BBM-069		IGHV4-174*01	IGHD3-15*01	IGHJ2*01	TKDA IRGYED EFDGYT TLNDFY FDF	10.8 21.4	25	IGKV1-25*01_kim	IGKJ4*01
	Q12M-165		IGHV4-174*01	IGHD3-15*01	IGHJ2*01	AKEA IRGYED EFDGYT TLNDFY FDQ	14.5 21.4	25	IGKV1-25*01_kim	IGKJ4*01
	Q12M-061		IGHV4-174*01	IGHD3-15*01	IGHJ2*01	AKEA RVRYED EFDGYT TLNDFY FDF	13.9 22.4	25	IGKV1-25*01_kim	IGKJ4*01
	Q12BBM-007		IGHV4-117*01	IGHD3-15*01	IGHJ2*01	AKEA IRGYED EFDGYT TLNDFY YDV	7.2 15.5	25	IGKV1-25*01_kim	IGKJ4*01
	Q12BBM-023		IGHV4-117*01	IGHD3-15*01	IGHJ2*01	AKEA IRGYED EFDGYT TLNDFY FDF	9.1 17.3	25	IGKV1-25*01_kim	IGKJ4*01
	Q12BBM-068		IGHV4-117*01	IGHD3-15*01	IGHJ2*01	AKEA IRGYED EFDGYT TLNDFY FDF	9.8 17.3	25	IGKV1-25*01_kim	IGKJ4*01
	Q12M-031		IGHV4-117*01	IGHD3-15*01	IGHJ2*01	AKEA IRGYED DFDGYT TLNDFY FDL	11.1 19.4	25	IGKV1-25*01_kim	IGKJ4*01
	Q12M-032		IGHV4-117*01	IGHD3-15*01	IGHJ2*01	AKEA LRGYED EFDGYT TLNDFY FDF	7.8 14.3	25	IGKV1-25*01_kim	IGKJ4*01
	Q12M-035		IGHV4-117*01	IGHD3-15*01	IGHJ4-3*01	AGDT EYFEDD GSYTG LDYFHS	7.8 17.3	22	IGKV1-NL_15*03_S6916_kim	IGKJ4*01
Q12	Q12M-131	Q12M-131	IGHV4-117*01	IGHD3-15*01	IGHJ2*01	AKDALGGYED DYGYT VNDFFY DV	7.5 12.4	24	IGKV1-25*01_kim	IGKJ4*01
	Q12M-158		IGHV4-117*01	IGHD3-15*01	IGHJ2*01	AKDALGGYED DYGYT VNDFFY DV	7.9 12.4	24	IGKV1-25*01_kim	IGKJ4*01
	Q12M-197		IGHV4-117*01	IGHD3-15*01	IGHJ2*01	AKDALGGYED DYGYT VNDFFY DV	9.2 14.4	24	IGKV1-25*01_kim	IGKJ4*01
	Q12M-190		IGHV4-117*01	IGHD3-15*01	IGHJ2*01_S5087	ARDG GAYTEE DDDFYT LDDWFFDI	5.7 9.2	24	IGKV1-25*01_kim	IGKJ4*01
	Q12M-283		IGHV4-117*01	IGHD3-15*01	IGHJ2*01_S5087	ARDG GAYHEE DYGYT TDGWFFDI	4.1 10.2	24	IGKV1-25*01_kim	IGKJ4*01
	Q12BBM-045		IGHV3-50*01	IGHD3-15*01	IGHJ3-2*01	ASLD YEDDY GYYYTG GVDFDL	5.8 11.3	21	IGKV1-NL_11*02_S1805_kim	IGKJ1*01
	Q12BBM-034		IGHV3-50*01	IGHD3-15*01	IGHJ3-2*01	ASLD YEDDY GYYYTG GVDFDL	8.2 16.5	21	IGKV1-NL_11*02_S1805_kim	IGKJ1*01
	Q12BBM-056		IGHV3-50*01	IGHD3-15*01	IGHJ3-2*01	ASLD YEDDY GYYYTG GVDFDL	12.1 17.6	21	IGKV1-NL_11*02_S1805_kim	IGKJ1*01
	Q12BBM-065		IGHV3-50*01	IGHD3-15*01	IGHJ3-2*01	ASLD YEDDY GYYYTG GVDFDL	6.5 13.4	21	IGKV1-NL_11*02_S1805_kim	IGKJ1*01
	Q12BBM-085		IGHV3-50*01	IGHD3-15*01	IGHJ3-2*01	ASLD YEDDY GYYYTG GVDFDL	6.5 8.2	21	IGKV1-NL_11*02_S1805_kim	IGKJ1*01
Q12	Q1216M-031	Q1216M-031	IGHV3-122*01	IGHD3-15*01	IGHJ5-5*01	ATTP TYSIEDG YGNSQVDSLVD	3.8 6.2	21	IGLV1-85*01_S8291_kim	IGLJ2A*01
	Q12B16M-007		IGHV3-122*01	IGHD3-15*01	IGHJ5-5*01	ATTP TYSIEDG YGNSQVDSLVD	3.8 7.2	21	IGLV1-85*01_S8291_kim	IGLJ2A*01
	Q12BBM-042		IGHV3-NL_17*01_S4250	IGHD3-15*01	IGHJ4-3*01	TFPD YVDYDG YFHTHL GGDY	4.7 6	20	IGKV2-72*01_kim	IGKJ3*01
	Q12BBM-076		IGHV3-NL_17*01_S4250	IGHD3-15*01	IGHJ4-3*01	TAAD FEDDYDG DFYTHL GGDY	4 7	20	IGKV2-72*01_kim	IGKJ3*01
	Q12BBM-022		IGHV4-NL_16*01_S3062	IGHD3-15*01	IGHJ5-5*01	ASED YEDDFG FYYNGV SLVD	7.7 15.2	20	IGKV1-43*02_kim	IGKJ1*01
	Q12BBM-026		IGHV4-NL_16*01_S3062	IGHD3-15*01	IGHJ5-5*01	ASED YEDDFG FYYNGV SVVD	11.7 18.2	20	IGKV1-43*02_kim	IGKJ1*01
	Q12BBM-044		IGHV4-NL_16*01_S3062	IGHD3-15*01	IGHJ5-5*01	ASED YEDDFG FYYNGV SVVD	9.7 19.2	20	IGKV1-43*02_kim	IGKJ1*01
	Q12BBM-043		IGHV3-128*01_S1128	IGHD3-15*01	IGHJ4-3*01	TTDD FEDDYDG SFYNGV GTDY	5 7	20	IGKV2-72*01_kim	IGKJ1*01

Supplementary Table 1. Sort statistics and antibody genetics

(a) Sort statistics from NHPs Q7, Q9, Q10, and Q12. Sampling time points, probes used for sorting, numbers of stained PBMCs, sorted cells, productive paired chains, and cloned mAbs are shown. Clonally related mAbs are indicated with identical symbols. (b) Genetic features of the expressed mAbs from NHPs Q7, Q9, Q10, and Q12. The mAbs highlighted in red are shown in Figure 3b.

Supplementary Table 2. X-ray Data collection and refinement statistics (molecular replacement)

	Q9M-023	Q10M-055	Q12BQM-007	Q12BBM-069
Data collection				
Space group	P 21 21 21	P 21 21 21	P 21 21 21	P 21 21 21
Cell dimensions				
<i>a</i> , <i>b</i> , <i>c</i> (Å)	61.7 73.0 132.5	50.7 74.5 135.6	72.9 89.1 89.8	56.4 72.5 175.2
α , β , γ (°)	90 90 90	90 90 90	90 90 90	90 90 90
Resolution (Å)	33.13 - 2.34	33.73 - 1.63	35.14 - 1.54	33.50 - 1.79
	(2.38 - 2.34)	(1.66 - 1.63)	(1.57 - 1.54)	(1.82 - 1.79)
<i>R</i> _{sym} or <i>R</i> _{merge}	0.22 (2.5)	0.08 (2.5)	0.10 (1.4)	0.12 (2.4)
<i>I</i> / σI	8.5 (1.2)	15.5 (1.0)	13.0 (1.0)	13.9 (1.3)
Completeness (%)	99.9 (99.5)	100.0 (100.0)	98.2 (83.3)	99.6 (99.2)
Redundancy	13.7 (14.1)	13.6 (13.9)	10.3 (5.2)	13.8 (13.7)
Refinement				
Resolution (Å)	33.13 - 2.34	33.73 - 1.63	35.14 - 1.54	33.50 - 1.79
No. reflections	26,094 (1289)	65,008 (3204)	84,729 (4039)	68,711 (3407)
<i>R</i> _{work} / <i>R</i> _{free}	0.23 / 0.27	0.22 / 0.25	0.19 / 0.21	0.21 / 0.24
No. atoms	3367	3472	3658	3576
Protein	3347	3238	3372	3355
Ligand/ion	-	-	-	-
Water	20	234	286	221
<i>B</i> -factors				
Protein	53	31	21	34
Ligand/ion	-	-	-	-
Water	45	35	29	38
R.m.s. deviations				
Bond lengths (Å)	0.002	0.012	0.013	0.013
Bond angles (°)	0.5	1.2	1.3	1.3

*Values in parentheses are for highest-resolution shell.

Supplementary Table 3. CryoEM data collection, refinement and validation statistics

	Q10M-055 Fab + Q23 NFL TD CC3+ (EMD-72009) (PDB 9PY5)	Q12QBM-007 Fab + BG505 NFL TD CC3+ (EMD-72031) (PDB 9PYD)	Q12BBM-069 Fab + BG505 NFL TD CC3+ (EMD-72035) (PDB 9PYK)	Q9M-023 Fab + BG505 NFL TD CC3+ (EMD-72033) (PDB 9PYH)	Q7M-675 Fab + WITO NFL TD CC3+ (EMD-74449)
Data collection and processing					
Microscope	TFS Glacios 2	TFS Glacios 2	TFS Glacios 2	TFS Glacios 2	TFS Glacios 2
Voltage (keV)	200	200	200	200	200
Camera	TFS Falcon 4i	TFS Falcon 4i	TFS Falcon 4i	TFS Falcon 4i	TFS Falcon 4i
Collection mode	Counting	Counting	Counting	Counting	Counting
Magnification	190,000x	190,000x	190,000x	190,000x	190,000x
Pixel size at detector (Å)	0.718	0.718	0.718	0.718	0.718
Total electron exposure (e ⁻ /Å ²)	45.2	44.9	45.0	45.0	45.1
Exposure rate (e ⁻ /pixel/sec)	7.56	6.68	7.30	7.84	7.78
Number of EER frames	40	40	40	40	40
Defocus range (µm)	-0.8 to -1.7	-0.8 to -1.7	-0.8 to -1.8	-0.8 to -1.8	-0.8 to -1.8
Automation software	EPU	EPU	EPU	EPU	EPU
Micrographs collected (no.)	7,036	7,003	7,001	7,021	10,912
Micrographs used (no.)	4,663	5,551	6,207	6,766	10,169
Initial particle images (no.)	425,148	947,031	790,420	645,545	1,708,227
Final particle images (no.)	24,541	81,859	72,419	131,528	24,436
Map pixel size (Å)	1.034	1.005	1.034	0.718	0.718
Symmetry	C1	C1	C1	C1	C1
Map resolution (masked/unmasked Å)	3.5/7.1	3.3/4.2	3.3/4.1	3.3/3.8	4.3/7.3
FSC threshold	0.143	0.143	0.143	0.143	0.143
Map sharpening <i>B</i> factor (Å ²)	-45	-62	-66	-87	-92
Map resolution range (Å) [#]	3.0-5.0	2.5-4.5	2.5-4.5	2.5-4.0	<i>n/a</i>
Refinement					
Initial model source	AlphaFold3	AlphaFold3 & PDB 6V0R	AlphaFold3	AlphaFold3	<i>n/a</i>
Refinement package	Phenix RSR	Phenix RSR	Phenix RSR	Phenix RSR	<i>n/a</i>
Model resolution (Å)	3.8	3.5	3.5	3.4	<i>n/a</i>
FSC threshold	0.5	0.5	0.5	0.5	<i>n/a</i>
EMRinger score	2.05	2.16	2.40	3.13	<i>n/a</i>
CC (mask)	0.78	0.79	0.81	0.82	<i>n/a</i>
<i>Model composition</i>					
Non-hydrogen atoms	16,706	15,794	15,785	15,625	<i>n/a</i>
Protein residues	1,966	1,896	1,883	1,857	<i>n/a</i>
Ligands	84	65	71	73	<i>n/a</i>
<i>Mean B factors (Å²)</i>					
Protein	101	66	49	64	<i>n/a</i>
Ligand	108	79	71	81	<i>n/a</i>
<i>R.m.s. deviations</i>					
Bond lengths (Å)	0.005	0.007	0.006	0.005	<i>n/a</i>
Bond angles (°)	0.999	1.279	1.112	0.879	<i>n/a</i>
<i>Validation</i>					
MolProbity score	1.12	1.34	1.25	1.16	<i>n/a</i>
Clashscore	1.82	2.66	1.44	1.13	<i>n/a</i>
Poor rotamers (%)	0.81	0.42	0.54	0.00	<i>n/a</i>
<i>Ramachandran plot</i>					
Favored (%)	96.99	95.82	94.55	95.19	<i>n/a</i>
Allowed (%)	3.01	4.18	5.45	4.81	<i>n/a</i>
Disallowed (%)	0.00	0.00	0.00	0.00	<i>n/a</i>
Cβ outliers (%)	0.00	0.00	0.00	0.00	<i>n/a</i>
CaBLAM outliers (%)	1.48	2.80	2.18	3.24	<i>n/a</i>

[#]modeled regions

Supplementary Table 4. Antibody heavy and light chains Env contacts and SHM

Antibody residues contacting Env are highlighted in color with Env region denoted in grey. Antibody residues resulting from SHM are marked with an asterisk in bold font. SHM only annotated to residue 94.

y. Antibody residues resulting from SHM are marked with an