

Supplementary Materials:

Figure S1

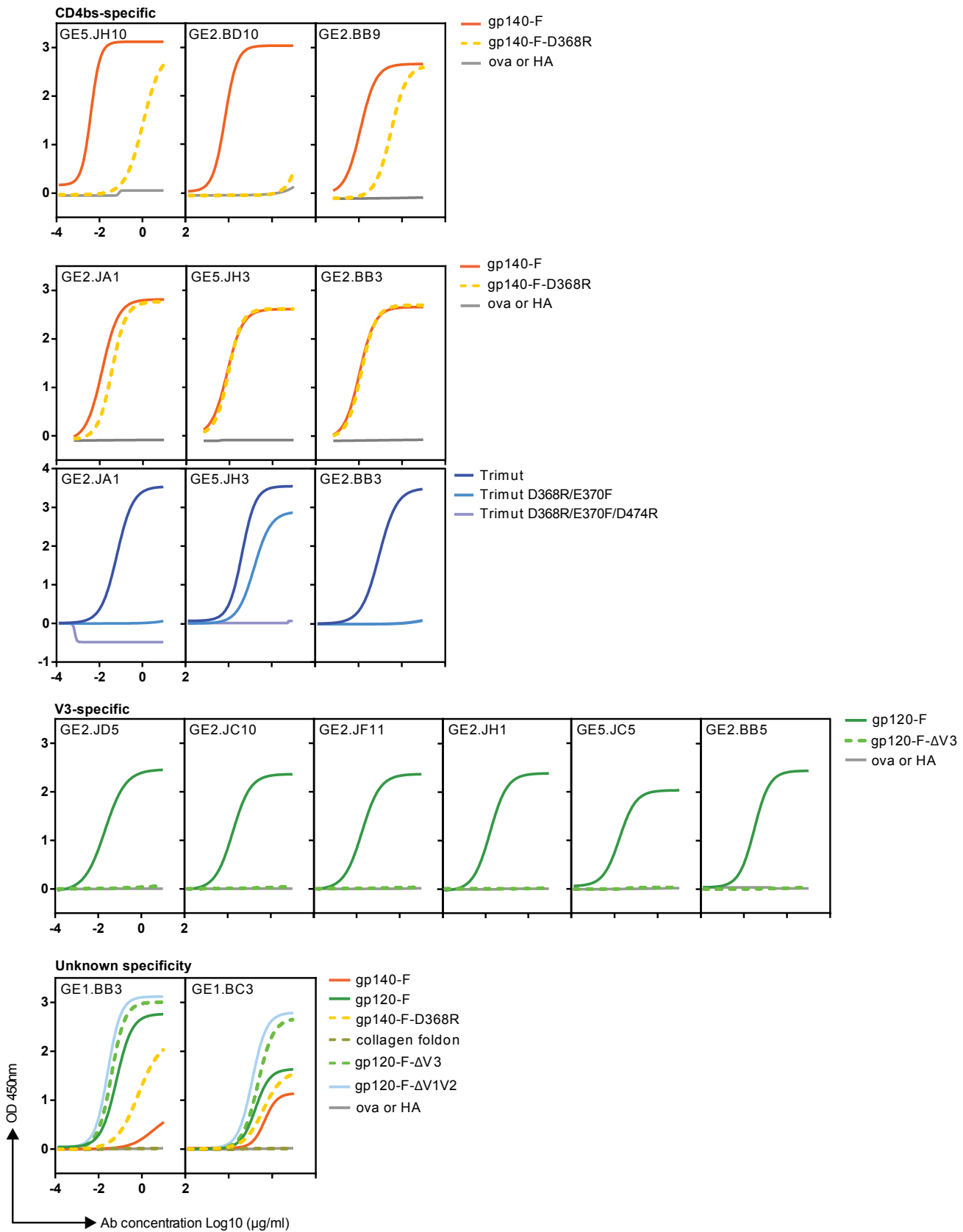


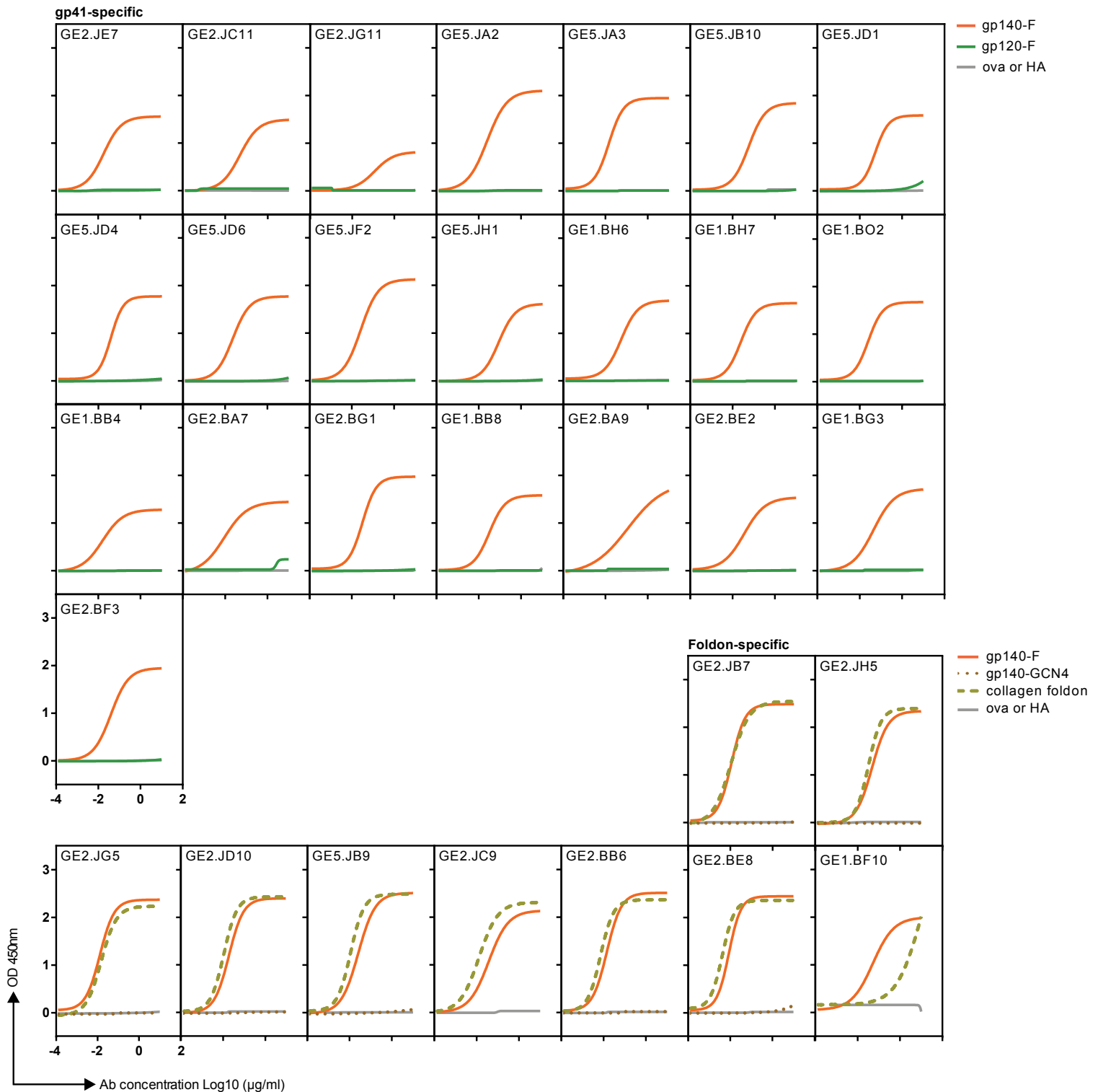
Figure S1

Figure S1. Epitope mapping of Env-specific MAbs. ELISA binding analyses of Env-specific MAbs were defined as follows: gp140-F and gp140-F-D368R (CD4bs-specific), gp120-F and gp120-F-ΔV3 (V3-specific), gp120-F and gp120-F-ΔV1V2 (V1V2-specific), gp140-F and gp120-F (gp41-specific), gp140-F, gp140-GCN4 and collagen foldon (foldon-specific). In addition to these probes, the CD4bs-directed MAbs that were insensitive to gp140-F-D368R were tested against TriMut, TriMut-D368R/E370F, and TriMut-D368R/E370F/D474R to confirm their CD4bs-epitope specificity. The MAbs that could not be mapped with this set of probes were designated as unknown specificity. Ova or influenza hemagglutinin-1 (HA1) were used as a controls. Titration curves are shown as Log10 dilutions (µg/ml). Representative binding curves are shown in Figure 1 and for the sub-specificities where more than one MAb was isolated the curves for the remaining MAbs are shown here.

Figure S2

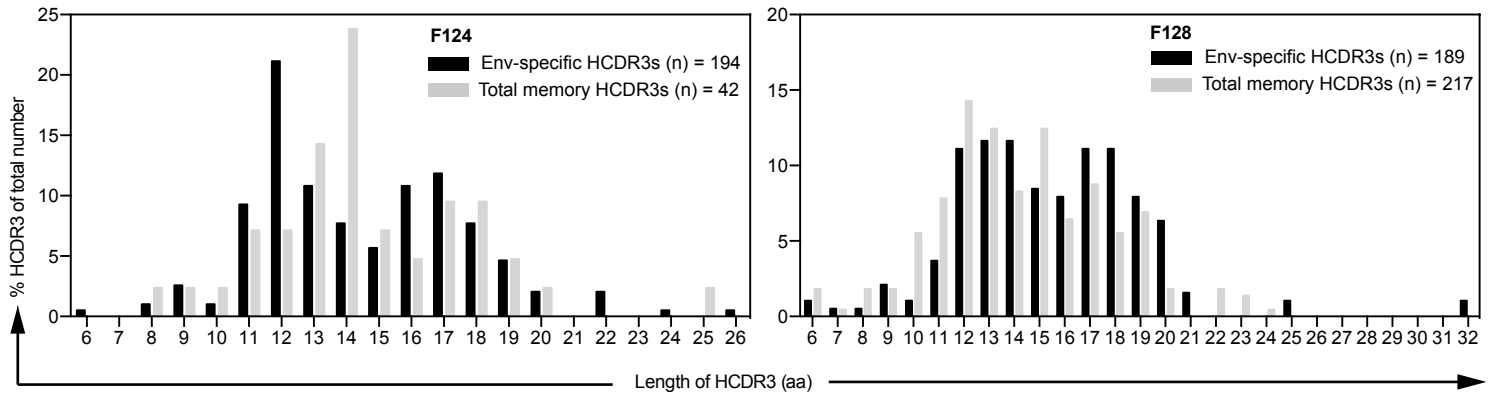
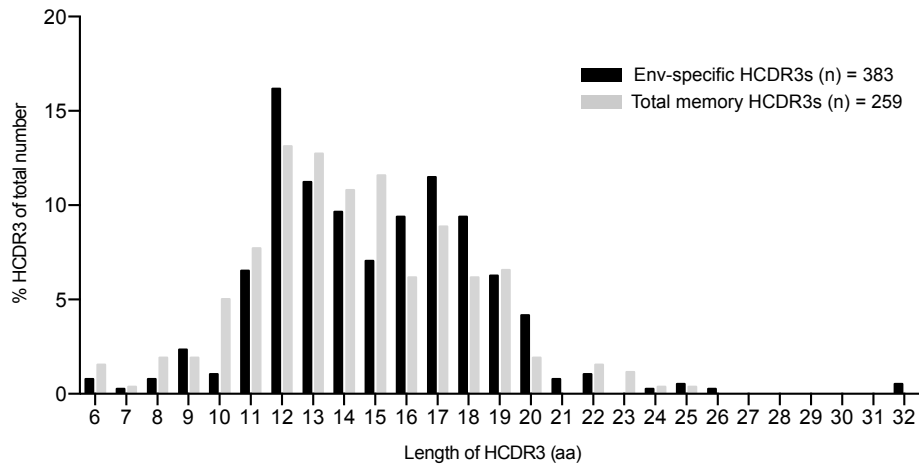


Figure S2A. HCDR3 analyses of Env-specific and total memory IgG sequences. The bars indicate the percentage HCDR3 sequences (Y-axis) of a given amino acid length (X-axis) of Env-specific (n=383) (black) and total memory (n=259) (gray) sequences from animals F124 and F128 (top panel) with the contribution from each donor shown separately (lower panels).

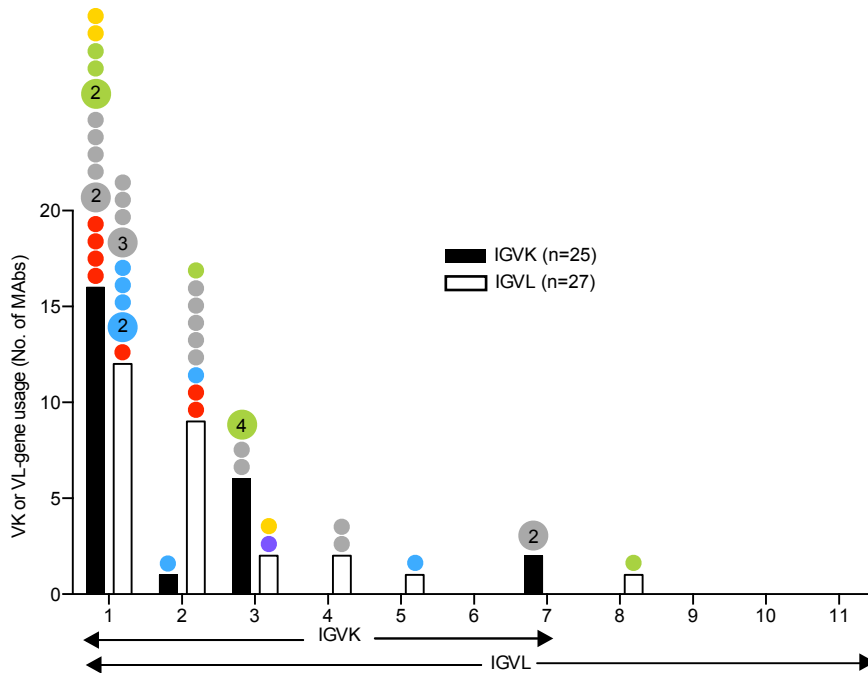


Figure S2B. Analysis of light chains of Env-specific MAbs. The number kappa and lambda light chain V gene usage by Env-specific MAbs indicated by black (VK) and white (VL) bars. The V gene families of kappa (1 to 7) and lambda (1 to 11) are shown on the X-axis. The colored dots above each bar indicate the epitope specificity of expressed MAbs using a given VK or VL family and larger dots indicate the number of clonally related MAbs identified.

Figure S3

		V3-region of HIV-1																																					
Viruses	YU2	1	C	T	R	P	N	N	N	T	R	K	S	I	N	-	I	G	P	G	R	A	L	Y	T	G	E	I	I	G	D	I	R	Q	A	H	C	35	
	HxBc2	1	C	T	R	P	N	N	N	T	R	K	R	I	R	I	Q	R	G	P	G	R	A	F	V	T	I	G	-	K	I	G	N	M	R	Q	A	H	C
	YU2	1	C	T	R	P	N	N	N	T	R	K	S	I	N	I	G	P	G	R	A	L	Y	T	G	E	I	I	G	D	I	R	Q	A	H	C	35		
	JRFL	1	C	T	R	P	N	N	N	T	R	K	S	I	H	I	G	P	G	R	A	F	Y	T	T	G	E	I	I	G	D	I	R	Q	A	H	C	35	
	89.6	1	C	T	R	P	N	N	N	T	R	R	L	S	I	G	P	G	R	A	F	Y	A	R	R	N	I	I	G	D	I	R	Q	A	H	C	35		
	DJ263.8	1	C	P	R	P	N	N	N	T	R	K	S	V	R	I	G	P	G	Q	T	F	Y	A	T	G	D	I	I	G	D	I	R	Q	A	H	C	35	
	MN	1	C	T	R	P	Y	N	N	R	R	T	R	I	H	I	G	P	G	R	A	F	Y	T	T	K	N	I	K	G	T	I	R	Q	A	H	C	35	
	SF162	1	C	T	R	P	N	N	N	T	R	K	S	I	T	I	G	P	G	R	A	F	Y	A	T	G	D	I	I	G	D	I	R	Q	A	H	C	35	
	ADA	1	C	T	R	P	N	N	N	T	R	K	S	I	H	I	G	P	G	R	A	F	Y	T	T	G	E	I	I	G	D	I	R	Q	A	H	C	35	
	BaL.26	1	C	T	R	P	N	N	N	T	R	K	S	I	H	I	G	P	G	R	A	F	Y	T	T	G	E	I	I	G	D	I	R	Q	A	H	C	35	
	SS1196.1	1	C	T	R	P	N	N	N	T	R	K	S	I	H	I	G	P	G	R	A	F	Y	A	T	G	G	V	I	G	D	I	R	Q	A	H	C	35	
	JRCSF	1	C	T	R	P	S	N	N	T	R	K	S	I	H	I	G	P	G	R	A	F	Y	T	T	G	E	I	I	G	D	I	R	Q	A	H	C	35	
	MW965.26	1	C	T	R	P	N	N	N	T	R	K	S	V	R	I	G	P	G	Q	T	F	Y	A	T	G	A	I	I	G	D	I	R	Q	A	H	C	35	

Figure S3. Sequence analysis of V3-regions of HIV-1. Amino acid alignment of the V3-region of tier 1 and tier 2 HIV-1 isolates from clade A, B, and C are grouped as ‘V3-sensitive’ and ‘V3-insensitive’ based on their neutralization sensitivity against V3-directed MAbs. The V3 epitope targeted by the vaccine-induced V3-directed MAbs is highlighted in red. The V3 region sequences were obtained from the GenBank with the accession number as follows: M89973 (YU2), K03455 (HxBc2), U63632 (JRFL), U39362 (89.6), AF063223 (DJ263.8), AF443202 (MN), U08455 (SF162), AY426119 (ADA), DQ318211 (BaL.26), AY835442 (SS1196.1), M38429 (JRCSF), U08455 (MW965.26).