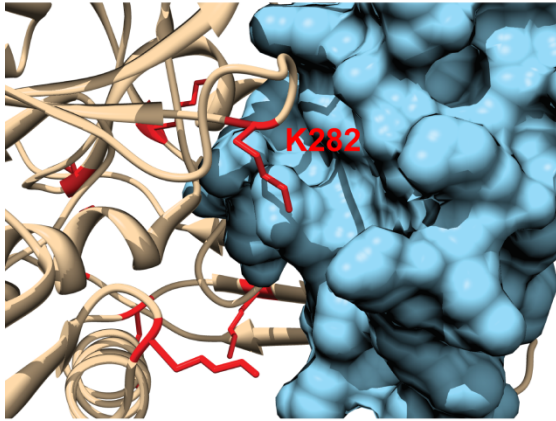
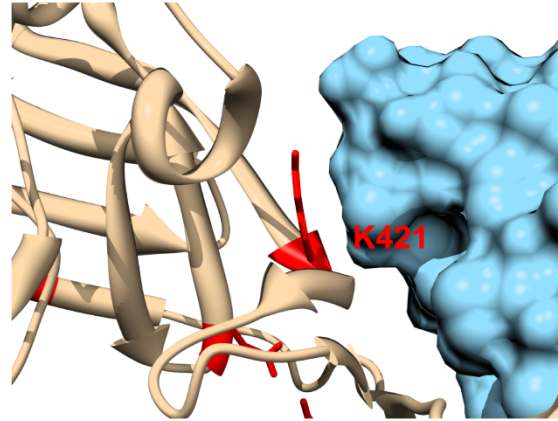


Supplementary Fig. 1: SPR analysis of the antigenicity of GLA cross-linked gp140. A+B: Titration series of unmodified (WT) or cross-linked (GLA) gp140 were passed over mAbs as indicated. Black curves show experimental data, red lines indicate results of a 1:1 langmuir analysis and vertical black lines show the end of the gp140 injection. B: sCD4 was added to gp140 either before (top right) or after (bottom right) cross-linking and samples were analysed as in A. C: Table shows the results from the 1:1 Langmuir analysis.

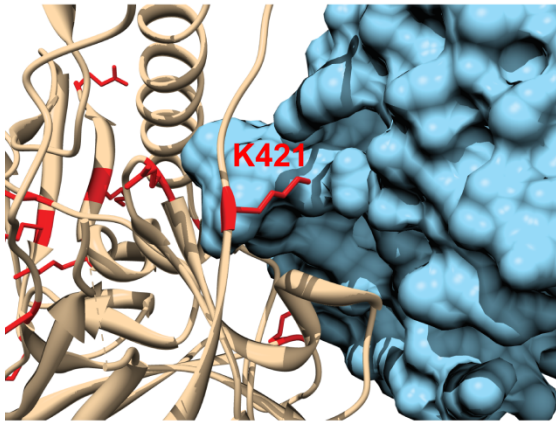
CD4



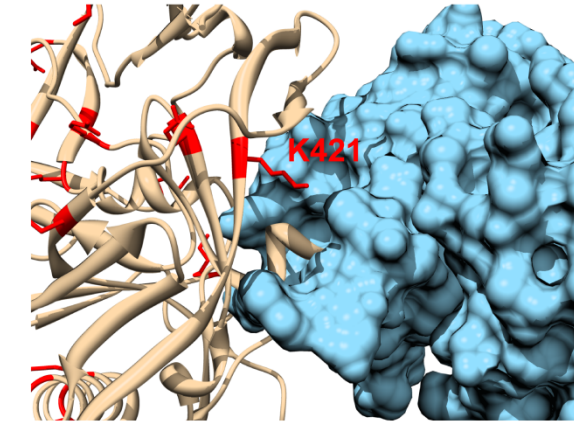
17b



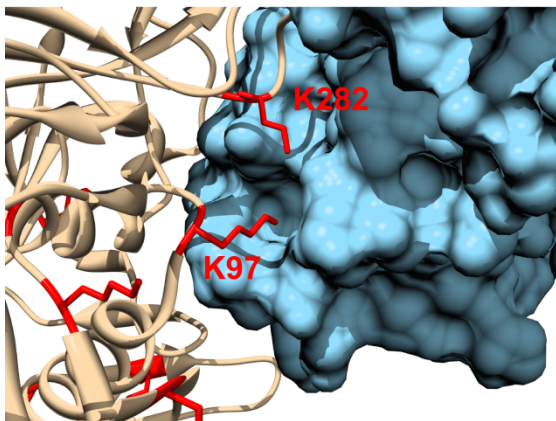
F105



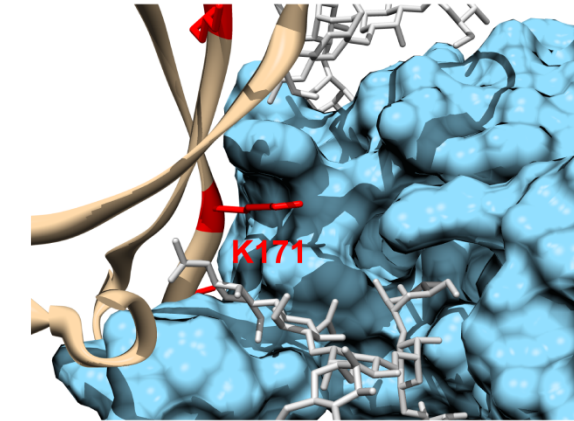
b12



VRC01

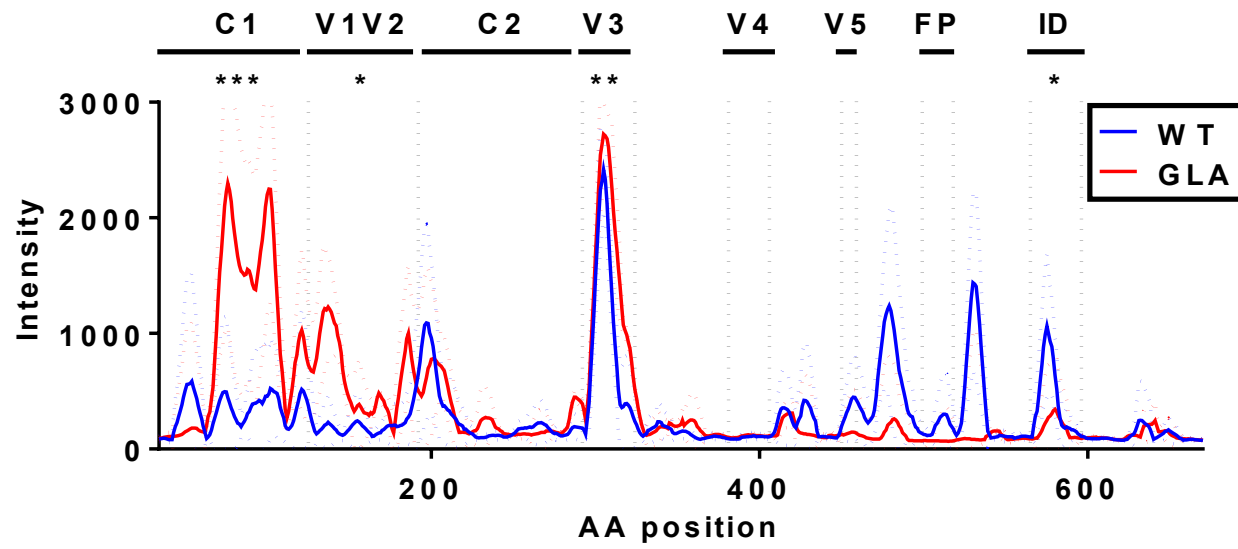


PG9



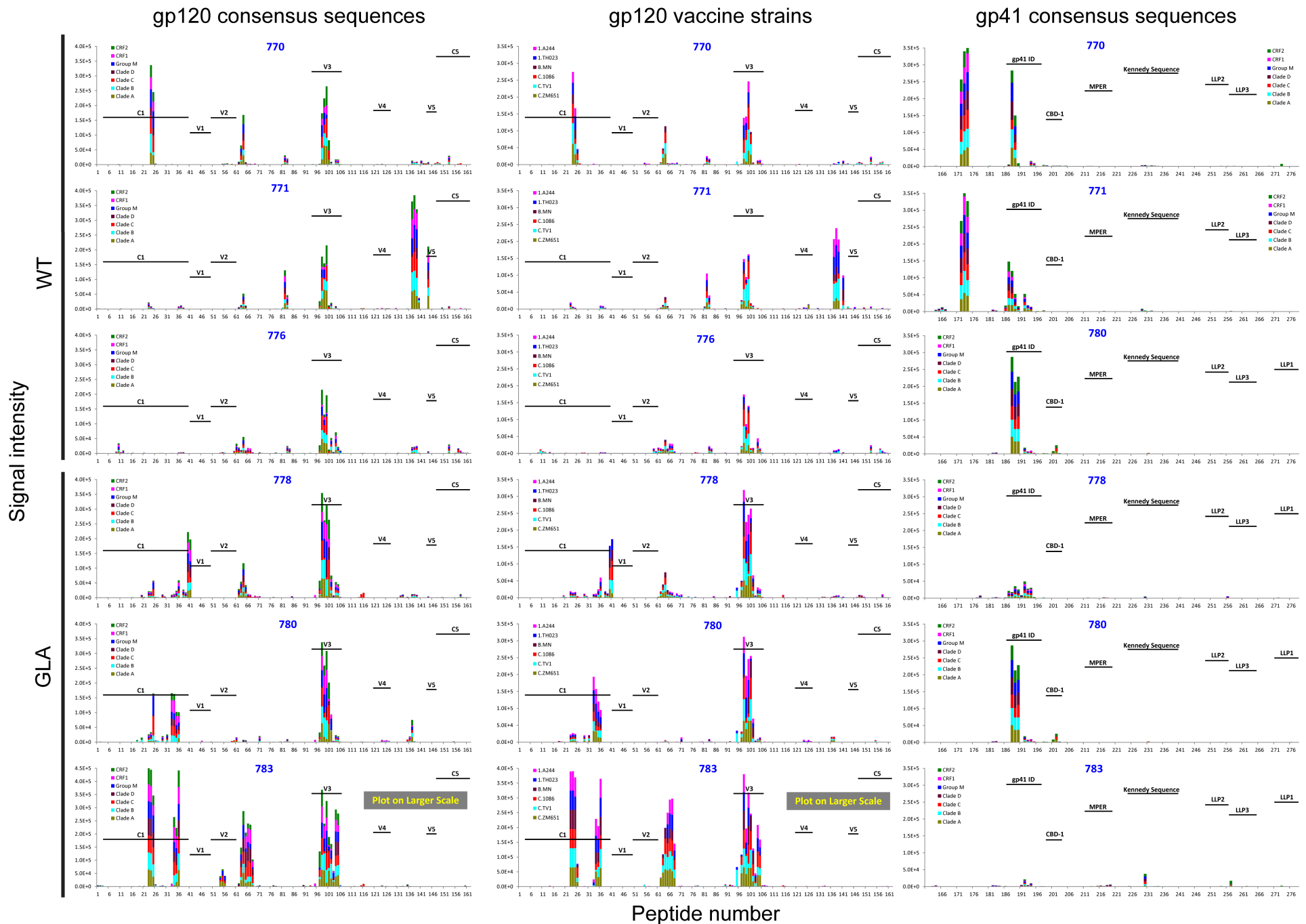
Supplementary Fig. 2: Modification sites within mAb epitopes.

Ribbon representations of gp120 or gp120 fragments (fawn) are shown in complex with blue surface representations of CD4 or mAbs as indicated. Potential modification sites (lysine residues) are shown in red and residue numbers of lysines interacting with mAbs are labelled in red according to HXB2 numbering. Lysine residues were identified based on the sequence of strain CN54 except for PG9, in which case the sequence of strain UG37 was used consistent with the experiments performed in this study. PG9 interacts with a second lysine of UG37 (K168), which is shielded from view by PG9 in this orientation.



Supplementary Fig. 3: Homologous peptide scanning of week 24 serum responses.

Dotted curves indicated SD of 4 animals tested, dotted vertical lines indicated borders of epitopes.



Supplementary Fig. 4: Heterologous peptide scanning of week 24 serum responses.

Supplementary Table 2: A3R5 assay neutralization data

Group	Animal	Week	Ce0393_C3.Luc	CAP45.2.00.G3.	Ce1086_B2.Luc	DU151.2.LucR.T	Ce2010_F5.Luc	Du422.1.LucR.T	Ce0393_C3.Luc
			R.T2A.ecto	LucR.T2A.ecto	R.T2A.ecto	2A.ecto	R.T2A.ecto	2A.ecto	R.T2A.ecto
		Tier (Clade)	Tier 1A Clade C	Tier 1B Clade C	Tier 2 Clade C	Tier 2 Clade C	Tier 2 Clade C	Tier 2 Clade C	Tier 1A Clade C
WT	770	-1	14	<10	16	28	21	22	14
		14	493	119	80	83	63	100	493
		24	742	153	137	96	79	121	742
	771	-1	<10	<10	<10	20	<10	15	<10
		14	240	67	82	10	39	10	240
		24	427	220	139	71	47	67	427
	772	-1	14	<10	22	25	22	23	14
		14	451	131	113	10	10	76	451
		24	827	182	164	77	67	132	827
	773	-1	17	<10	25	21	22	20	17
		14	170	190	96	10	10	10	170
		24	374	376	263	76	43	37	374
	774	-1	20	<10	26	29	21	15	20
		14	73	32	169	10	10	10	73
		24	256	120	71	45	43	50	256
	775	-1	16	<10	27	21	15	17	16
		14	504	408	262	142	76	163	504
		24	1042	186	143	56	46	111	1042
	776	-1	30	25	42	41	48	42	30
		14	143	10	91	10	10	10	143
		24	522	384	97	36	28	49	522
	777	-1	18	13	36	36	32	40	18
		14	208	118	117	10	10	10	208
		24	614	281	191	43	89	90	614

GLA	778	-1	<10	<10	18	12	13	18	<10
		14	131	35	64	10	10	10	131
		24	463	134	108	35	47	59	463
	779	-1	17	<10	23	33	29	25	17
		14	719	40	106	10	10	10	719
		24	1763	159	113	93	53	79	1763
	780	-1	30	35	40	29	39	30	30
		14	580	514	113	10	10	116	580
		24	1870	142	129	118	51	139	1870
	781	-1	15	10	20	20	20	20	15
		14	123	95	91	10	10	10	123
		24	572	262	111	67	37	45	572
	782	-1	42	38	62	51	58	41	42
		14	551	10	10	10	10	10	551
		24	1063	107	187	84	89	202	1063
	783	-1	14	12	28	23	14	13	14
		14	182	181	10	10	10	10	182
		24	1789	291	49	35	40	43	1789
	784	-1	11	<10	16	21	<10	17	11
		14	346	73	117	10	34	76	346
		24	1096	170	103	64	47	83	1096
	785	-1	34	27	39	36	41	37	34
		14	514	151	10	10	10	10	514
		24	2049	308	112	78	58	152	2049