Sequence	Residues				Nonsynonymous				Isofunctional			
	V1V2	V1	V2	V3	V1V2	Glycan V2	V3	V3 Crown	V1V2	Glycan V2	V3	V3 Crown
6501-1 con	68	30	39	35	--	--	--	--	--	--	--	--
6501-5 con	89	42	48	35	44	2	4	0	8	2	1	1
6501-6 con	92	45	48	35	43	2	5	0	10	1	1	1
Antigen	66	22	45	35	25	3	6	2	12	4	2	2
6564-1 con	76	30	47	35	--	--	--	--	--	--	--	--
6564-2 con1	70	31	40	35	22	2	9	3	10	2	1	1
6564-2 con2	70	31	40	35	21	3	10	4	11	3	1	1
6564-3 con1	70	31	40	35	21	4	10	4	13	4	1	1
6564-3 con2	70	31	40	35	22	3	8	3	11	3	1	1
6564-4 con	66	27	40	35	22	3	8	3	12	3	1	1
Antigen	66	22	45	35	28	4	8	3	8	4	2	1

Sequence	Charge				Tropism	Potential N glycosylation sites		
	V1V2	Glycan V2	V3	V3 Crown		Env	V1V2	V3
6501-1 con	5+	2+	2+	2+	R5	23	4	1
6501-5 con	0	0	3+	2+	R5	28	6	1
6501-6 con	4-	0	4+	2+	R5	27	6	1
Antigen	0	2+	4+	3+	R5	24*	5*	1*
6564-1 con	1+	2+	3+	2+	X4	27	6	1
6564-2 con1	2+	3+	1+	1+	R5	25	6	1
6564-2 con2	2+	3+	2+	2+	R5	26	6	1
6564-3 con1	2+	3+	2+	2+	R5	26	6	1
6564-3 con2	2+	3+	1+	1+	R5	26	6	1
6564-4 con	1+	3+	1+	1+	R5	25	6	1
Antigen	0	2+	4+	3+	R5	24*	5*	1*

S3 Table. Comparison of amino acid characteristics of the envelope clones' variable loops. Number of amino acid residues, nonsynonymous & isofunctional mutations (compared against first time point sequences), potential N-glycosylation sites, tropism, and charges of the V1V2, V1, V2, Glycan V2, V3, V3 crown regions of consensus *Env* sequences from NYU6501 and NYU6564.

Alignments and potential N-glycosylation sites were determined as described in methods. Genotypic prediction of coreceptor tropism was done using Geno2pheno with 5% false positive rate (see methods). V1V2 and V3 antigens as well as HXB2 (indicated with *) were used as Reference strains. Consensus sequences were generated as described in methods; the generation of two consensus sequences was done according to similarity in the highlighter plots in **S2 Fig**. Consensus sequences after SI are filled in with red