Codon position (HXB2 numbering)	Amino Acid Frequency			Env sites and domains		Fisher`s-exact *p*-value
	HXB2_K0345.1 (Reference strain)	**Plasma (n=16 SGS)**	**CSF (n=30 SGS)**	**gp120**	**gp41**	
62	D	E (6%), K (94%)	E (97%), K (3%)	CD4bs	-	4.85E-10
136 “NI” insertion	-	NI insertion (6%)	NI insertion (100%)	V1, N-linked glycosylation	-	3.10E-11
187	D	E (6%), N (12%), D (82%)	E (93%), D (7%)	V2	-	4.80E-07
252	R	K (19%), R (81%)	K (90%, R (10%)	C2	-	2.30E-06
319	T	A (100%)	A (7%), T (93%)	V3	-	1.50E-10
322	K	A (6%), E (94%)	A (100%)	V3	-	3.10E-11
343	L	I (56%), L (44%)	I (7%), L (93%)	C3	-	4.00E-04
345	Q	R (100%)	R (7%), Q (93%)	C3	-	1.50E-10
347	A	V (12%), A (88%)	V (93%), A (7%)	C3	-	5.30E-08
399	S	N (100%)	N (7%), T (93%)	V4, N-linked glycosylation	-	1.50E-10
420	R	K (6%), R (94%)	K (94%), R (6%)	V4	-	4.00E-09
449	N	Y (50%), N (50%)	N (100%)	C4	-	5.00E-05
462	S	G (69%), R (6%), deletion (25%)	G (7%), deletion (93%)	V5	-	1.90E-05
464 “QXXT” insertion	-	K (31.5%), N (37%), T (31.5%)	N (7%), K (93%)	C5	-	1.90E-05
782	I	I (25%), V (75%)	I (93%), V (7%)	-	cytoplasmic domain	3.40E-06

Supplemental Table 3. Frequencies of plasma/CSF compartmentalizing amino acids in HIV-1 *env* single genomes. We used two-sided Fisher`s-exact tests to compare amino acid frequency of dominant alleles in CSF, compared to those detected in plasma at week 54, during PML-IRIS; p-values shown.