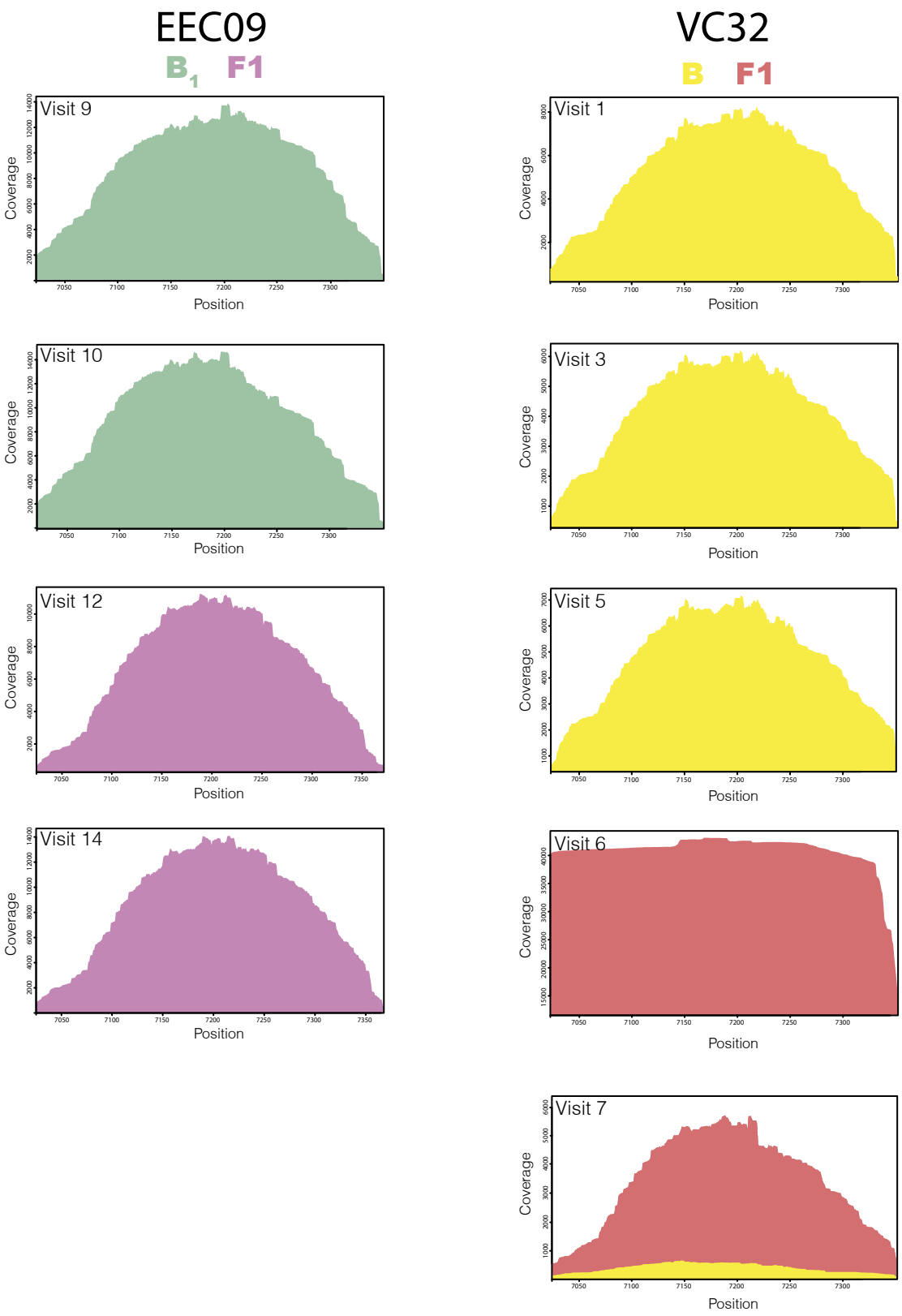
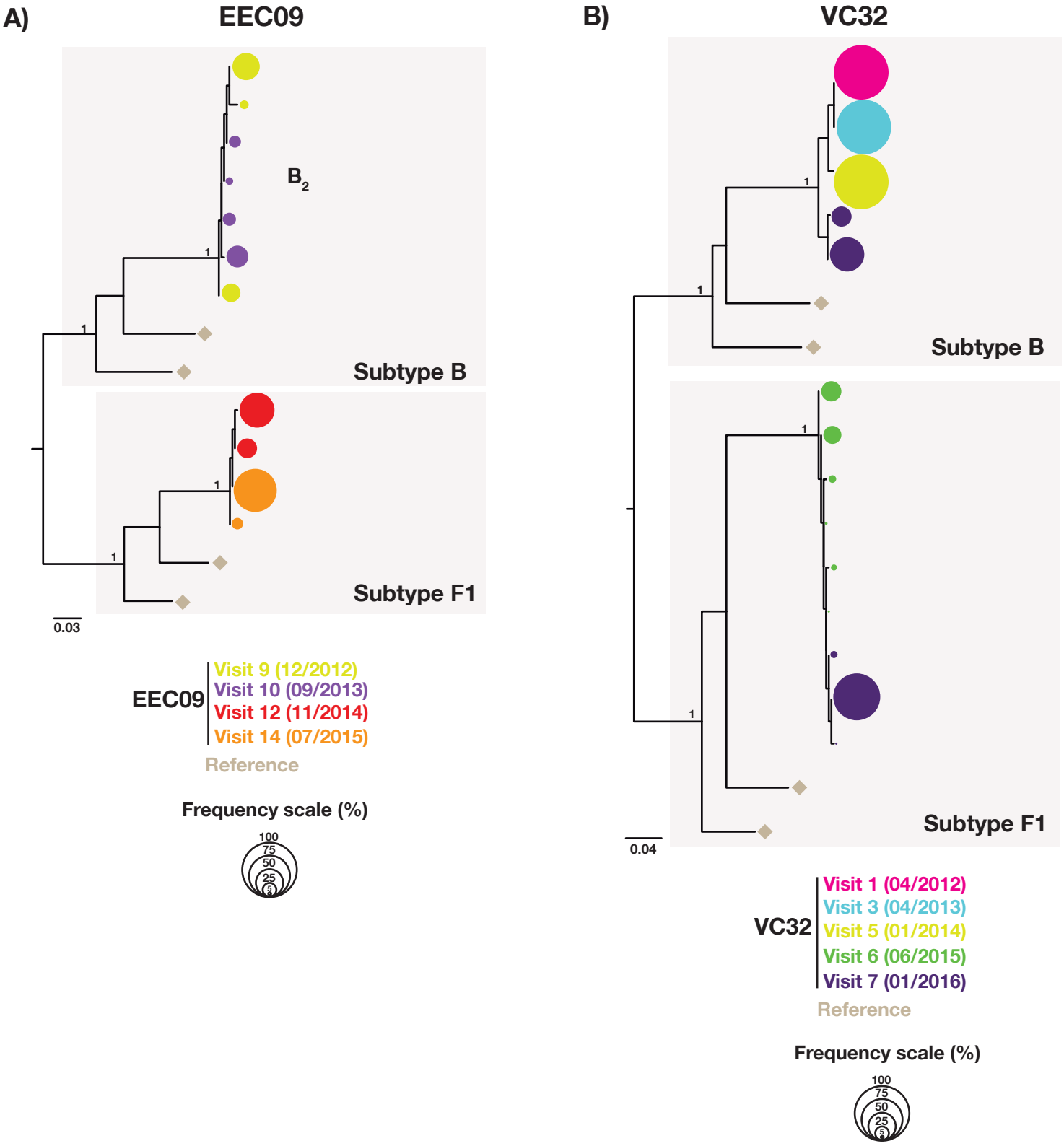


Supplemental Fig. 1. Sequencing coverage of the env amplicon from RNA from plasma samples. The depth of each base's coverage is indicated on the y-axis while the corresponding position in the HIV-1 genome is indicated on the x-axis (according to the HXB2 coordinates). Plots were colored according to the viral variant/s detect at each visit.



Supplemental Fig. 2. Frequency of viral haplotypes at different points in time found in the plasma compartment of the HIV controllers. ML phylogenetic tree of env sequences from subjects EEC09 (A) and VC32 (B) (circles) and HIV-1 subtype reference sequences (diamonds). The circles in the tips are colored according to the time point analyzed and their sizes are proportional to the haplotype frequency according to the scale at the right corner. Horizontal branch lengths are proportional to the bar at the bottom indicating nucleotide substitutions per site. The subtype of each cluster is indicated in the footer of the shaded boxes.

Supplemental Table 1. Coreceptor tropism prediction in quasispecies from PBMC and plasma compartments.

Patient ID	Variants	Visits	Source	V3 loop	Frequency of clones[a]	Predicted coreceptor use	Geno2pheno[b]
EEC09	B_1	V1-14	PBMC	CTRPSNNTRKGIHIGPGRAFYATGDIIGDIRQAHC	98	R5	51.8
		V6	PBMC	CTRPSNNTRKGIHIGPGRAFYATGDRIGDIRQAHC	1		21.4
		V10	PBMC	CTRPSNNTRKGIHIGPGRAFYATGDIIGDIR-A--	1		91.7
	B_2	V1-9	PBMC	CTRPNNNTRKGIHMGWGKALYATEKIIGDIRQAHC	100	X4	4
		V9,10	Plasma	CTRPNNNTRKGIHVGWGRALYATEKIIGDIRQAHC	100		2.6
	F1	V10,12,14	PBMC	CTRPNNNTRKSIPIGPGRAFYATGEIIGDIRKAHC	98	R5	59.2
		V12,14	Plasma		100		59.2
		V10	PBMC	CTRPNNNTRKSIPIGLGRAFYATGEIIGDIRKAHC	2		38
VC32	B	V1-8	PBMC	CTRPNNNTRKSINIGPGRAFYATGEIIGDIRQAHC	32	R5	64
		V1-8	PBMC	CTRPNNNTRKSIHIGPGRAFYATGEIIGDIRQAHC	22		42.6
		V1-8	PBMC	CTRPNNNTRKSINIGPGRAFYATEEIIGDIRQAHC	14		17
		V5	Plasma		100		
		V1-8	PBMC	CTRPNNNTRKSINIGPGRAFYATEGIIGDIRQAHC	13.5		13.5
		V1,3	Plasma		100		
		V1-8	PBMC	CTRPNNNTRKSINIGPGRAFYATGKIIGDIRQAHC	11.5		11.5
		V7	Plasma		100		
		V1,7,8	PBMC	CTRPNNNTRKSIHIGPGKAFYATGEIIGDIRQAHC	3		49.9
		V1,3	PBMC	CTRPNNNTRKSINIGPGRAFYATKGIIGDIRQAHC	2		30.1
		V1,5	PBMC	CTRPNNNTRKSINIGPGRAFYATGEVIGDIRQAHC	1		50.5
		V5	PBMC	CTRPNNNTRKSINIAPGRAFYATGEIIGDIRQAHC	0.5		88
		V8	PBMC	CTRPNNNTRKSIHIGPGRAFYATGEIIGDIRQAYC	0.5		38
	F1	V6-8	PBMC	CTRPNNNTRKGIHLGPGRTFYATGDIIGDIRQAQC	100		75.6
		V6,7	Plasma		100		

[a] Frequency represented in percentages (%); [b] Predicted using geno2pheno with a false positive rate (FPR) cutoff of 5%. Red shades represent changes related to the major haplotype of each variant. Grey shades highlight the crown of the V3 loop region.

Supplemental Table 2. Virological characteristics of HIV controllers EEC09 and VC32.

Patient ID	Visit (month/year)	RNA load (cp/mL)[a]	DNA load (cp/10^6cells)	Viral variant DNA-PBMCs			Viral variant RNA-Plasma	
EEC09	V1 (Feb 2009)	< 50	61	B_1= 9 (47%) π^c = 0.9%	B_2=10 (53%) π = 0.2%	-	-	-
	V2 (Dec 2009)	< 50	< 40	B_1= 13 (87%) π = 0.2%	B_2= 2 (13%) π = 1.2%	-	-	-
	V6 (Aug 2011)	< 50	43	B_1= 27 (96%) π = 0.7%	B_2 = 1 (4%) π = ND	-	-	-
	V9 (Dec 2012)	170	< 40	B_1= 13 (87%) π = 0.3%	B_2= 2 (13%) π = 0.2%	-	B_2 = 100% π = 0.5%	-
	V10 (Sep 2013)	159	< 40	B_1= 11 (58%) π = 1.4%	B_2= 8 (42%) π = 0.2%	F1 = 8 (42%) π = 0.2%	B_2 = 100% π = 0.3%	-
	V12 (Nov 2014)	388	87	B_1 = 12 (36%) π = 0.5%		F1= 21 (64%) π = 0.2%	-	F1 = 100% π = 0.1%
	V14 (Jul 2015)	581	45	B_1 = 1 (4%) π = ND		F1= 26 (96%) π = 0.3%	-	F1 = 100% π = 0.1%
VC32	V1 (Apr 2012)	82	ND[b]	B = 33 (100%) π = 3.2%		-	B = 100% π =ND	-
	V3 (Apr 2013)	136	136	B = 30 (100%) π = 3.6%		-	B = 100% π = ND	-
	V5 (Jan 2014)	403	106	B = 34 (100%) π = 3.0%		-	B = 100% π = ND	-
	V6 (Jun 2015)	722	74	B = 17 (89%) π = 3.5%		F1 = 2 (11%) π = 0.1%	-	F1 = 100% π = 0.3%
	V7 (Jan 2016)	472	< 40	B = 19 (90%) π = 2.7%		F1 = 2 (10%) π = 0%	B = 10% π = 0.1%	F1 = 90% π = 0.1%
	V8 (Apr 2016)	58	< 40	B = 27 (96%) π = 3.3%		F1 = 1 (4%) π = ND	-	-

[a]cp, copies/ml; [b]ND, not determined; [c]π, mean nucleotide diversity.