

**Supplementary Table 1** Analysis of Population Structure Between Replication Competent Virus and either Free Plasma Virus or Provirus Derived From Resting CD4<sup>+</sup>T Cells

Patient 154 <sup>a</sup>	Number of Independent Sequences				Slatkin-Maddison Analysis				AMOVA Analysis			Molecular Diversity ( $\pi$ )	
	Replication Competent Virus vs	Gene Amplified	Free Plasma Virus	Integrated Provirus	Replication Competent Virus	p-value	Adjusted p-value <sup>d</sup>	Migration Events (ML/BI)	% Variation Among / Within Populations	Adjusted p-value	Adjusted p-value <sup>d</sup>	Replication Competent Virus	Plasma Virus or Integrated Provirus
Free Plasma Virus	RT	238	0	19	0.024	0.029	17/17	42.89	0.000	0.000	0.023	0.011	
Integrated Provirus	RT	0	223	19	0.063	0.069	17/17	1.75	0.051	0.069	0.023	0.020	

<sup>a</sup> Patient sequences derived from Bailey *et al.* (1).

<sup>b</sup> ML indicates phylogenetic trees were generated via a classical maximum likelihood approach.

<sup>c</sup> BI indicates phylogenetic trees were generated via a Bayesian inference approach.

<sup>d</sup> p-values obtained for both the Slatkin-Maddison tests as well as the AMOVA tests were subjected to Benjamini-Hochberg false discovery rate corrections, treating p-values obtained using the ML approach separately from those obtained using BI, and both separately from the AMOVA tests (2).