Supplementary Fig. 1 – (**a** – **v**) Phylogenetic analyses of all patients utilized in the study. Sequences were derived from free plasma and cerebral spinal fluid (CSF) virus, and provirus derived from resting and activated CD4$^+$ T cells, monocytes, and unfractionated peripheral blood mononuclear cells (PBMC). The trees were generated using a classical maximum likelihood (ML) approach and were rooted with an M group ancestral sequence. In all instances, circles refer to proviral sequences and triangles refer to free virus. Clusters of five or more identical sequences are boxed.