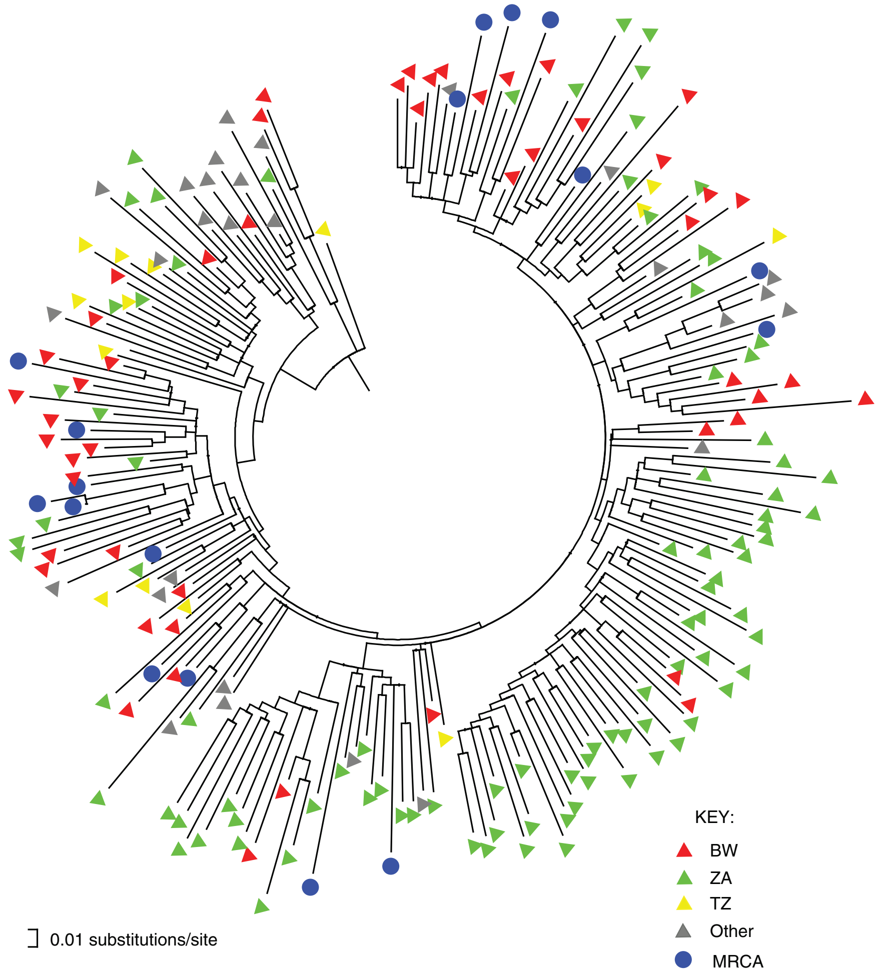
Supplementary Data



SUPPLEMENTARY FIG. S1. Maximum likelihood phylogeny inferred from our combined early and chronic HIV-1 *vif* sequences shows that the acute/early sequences are generally interspersed among the chronic ones. The phylogenetic tree was constructed using PhyML and the HKY85 nucleotide substitution model. The tree was visualized in FigTree v1.1.2 and Mega 5, labels and key for better visualization in Adobe Illustrator.