Supplementary Figure 3. Hierarchical clustering analysis of single nucleotide polymorphisms (SNPs) in all HIV-1 coding regions plus the long-terminal regions (LTRs). Dendograms were calculated using the Euclidian distance and Complete cluster methods with 1000 bootstrap iterations as described in Los Alamos HIV Sequence Database (http://www.hiv.lanl.gov.content/sequence/HEATMAP/heatmap.html). Bootstrap values >60% are indicated by an asterisk. Green and grey blocks indicate the presence and absence of SNPs, respectively.