



Figure S2. Phylogenetic analysis of the CRF01_AE HIV-1 pol sequences.

The *pol* sequences of 2034 CRF01_AE-infected patients at baseline were analyzed by the maximum-likelihood method in FastTree v2.1.9. The nucleotide substitution model was GTR+G+I. Local support values were computed by the Shimodaira-Hasegawa test (SH test) with 1000 replicates. Node SH-like support value ≥ 0.9 was identified as a lineage and was indicated at relevant nodes. Three African CRF01_AE reference sequences were at the root of the ML tree. The various lineages were color-coded.