

Supplementary Figure 1. Phylogenetic trees to describe the HIV-1 subtype distribution in the treatment naïve cohort and in those patients experiencing ARV treatment failure. A curated set of HIV-1 RT coding sequences from the treatment naïve (a) and treatment failure cohorts (b) were aligned with a set of HIV-1 reference sequences using ClustalX and then a neighbor joining phylogenetic tree was drawn using Figtree v1.3.1.