S3 Fig. Substitution saturation analysis. (a) HIV-1$_{CRF35\_AD}$ datasets, **(b)** HIV-1$_{CRF35\_AD+A1/D}$ datasets. Transitions (blue line) and Transversions (green line) are plotted against divergence. The genetic distance is computed with the GTR nucleotide substitution model. The results show that all the datasets contain enough evolutionary information for reliable phylogenetic and molecular clock inferences.