Supplementary Figure 1: Neighbour-joining phylogenetic analysis of Illumina consensus and Sanger consensus sequences for baseline samples. Sanger and Illumina consensus of the same sample significantly clustered together. Majority of the sequences clustered with HIV-1 subtype C references. HIV group O was used for rooting the tree and a bootstrap value of 1000 was used for analysis. S = Sanger sequencing; D = Deep sequencing.