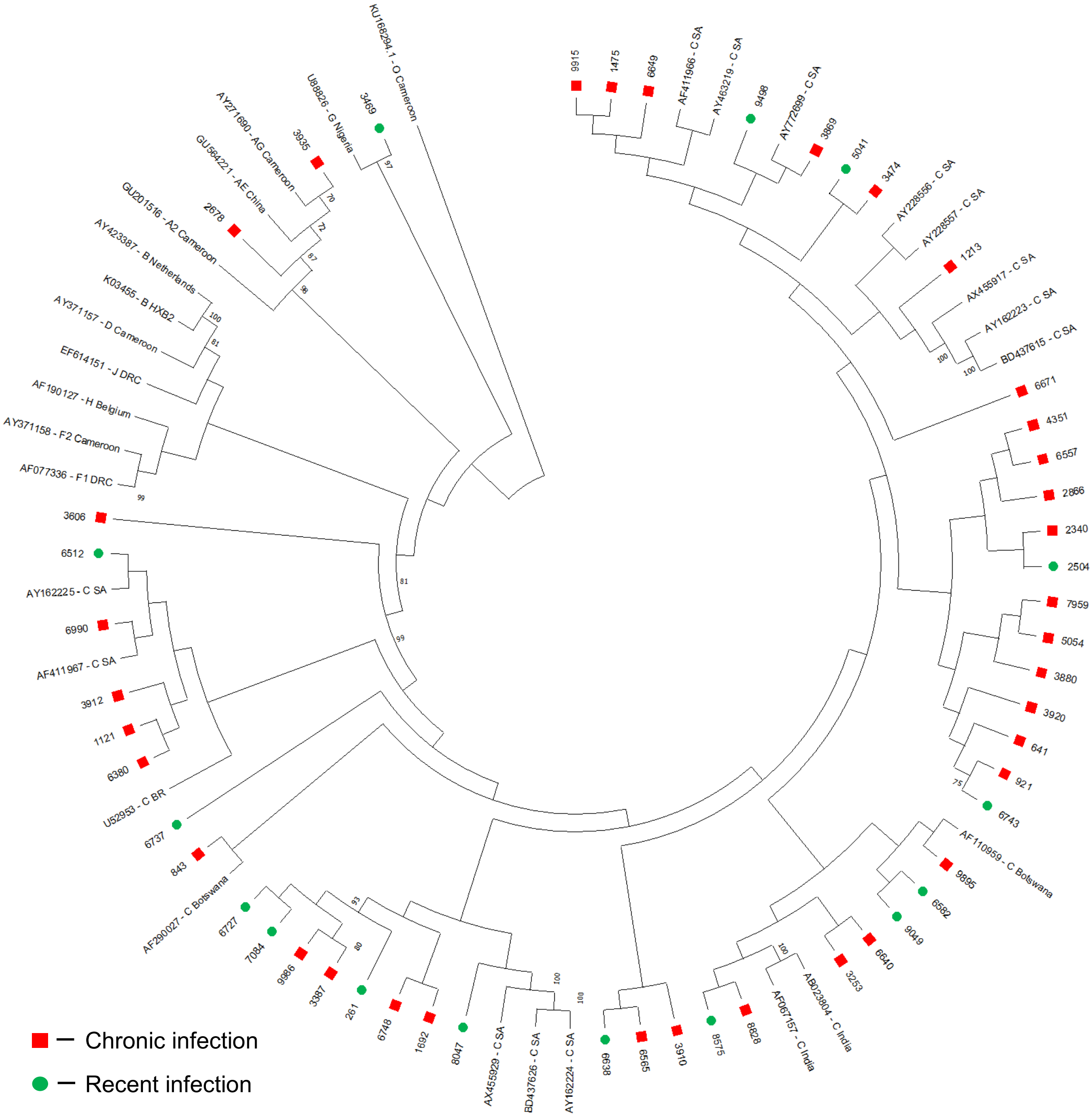

Supplementary Figure 1: Neighbor-joining phylogenetic tree drawn using both recent (green circles) and chronic (red squares) HIV-1 sequences. The majority (47/50, 94%) of the study sequences clustered with HIV-1 subtype C and a minority (3/50, 6%) clustered with non-subtype C sequences. HIV-1 – Human Immunodeficiency virus type 1; BR – Brazil; DRC – Democratic Republic of the Congo; SA – South Africa.