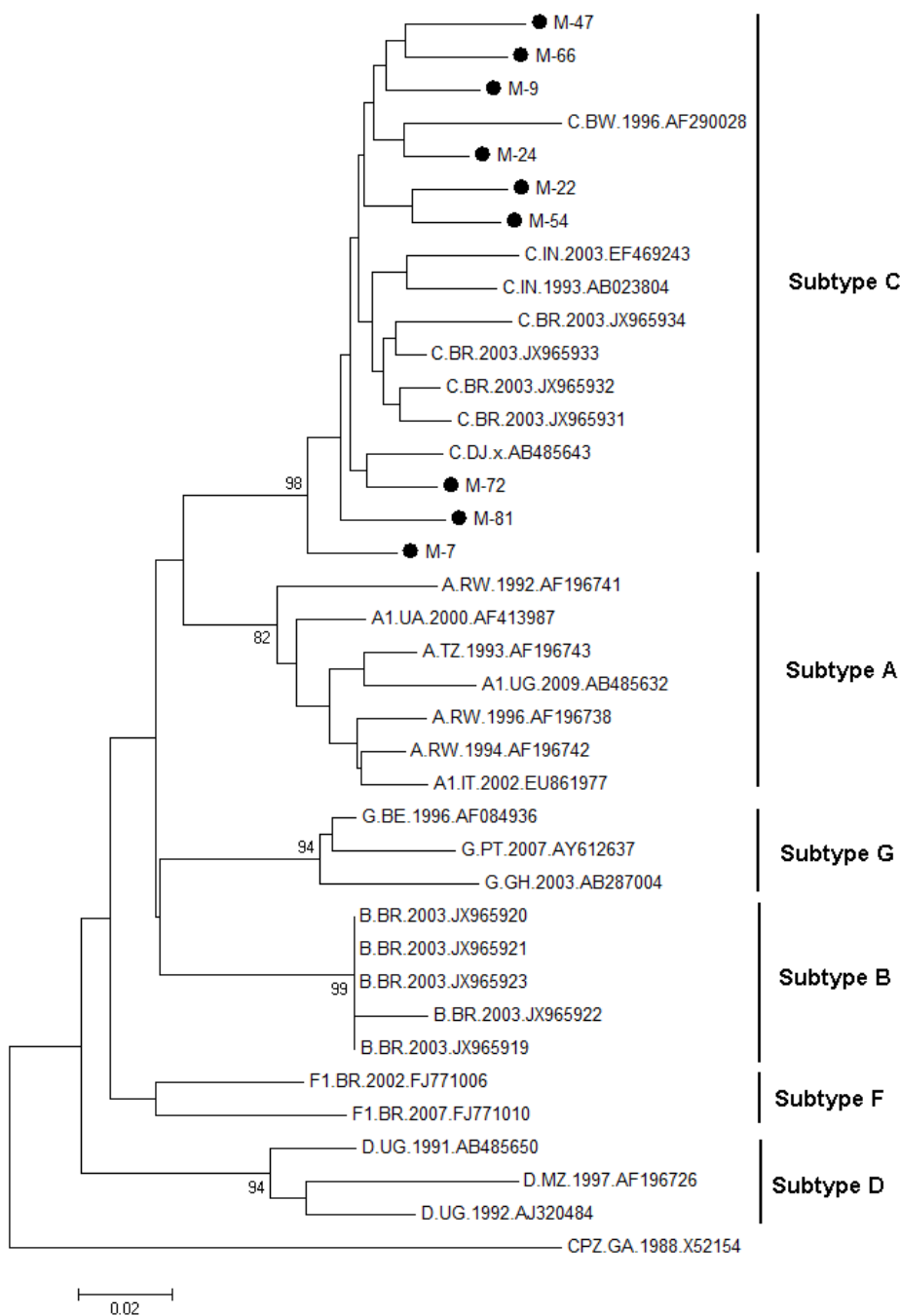


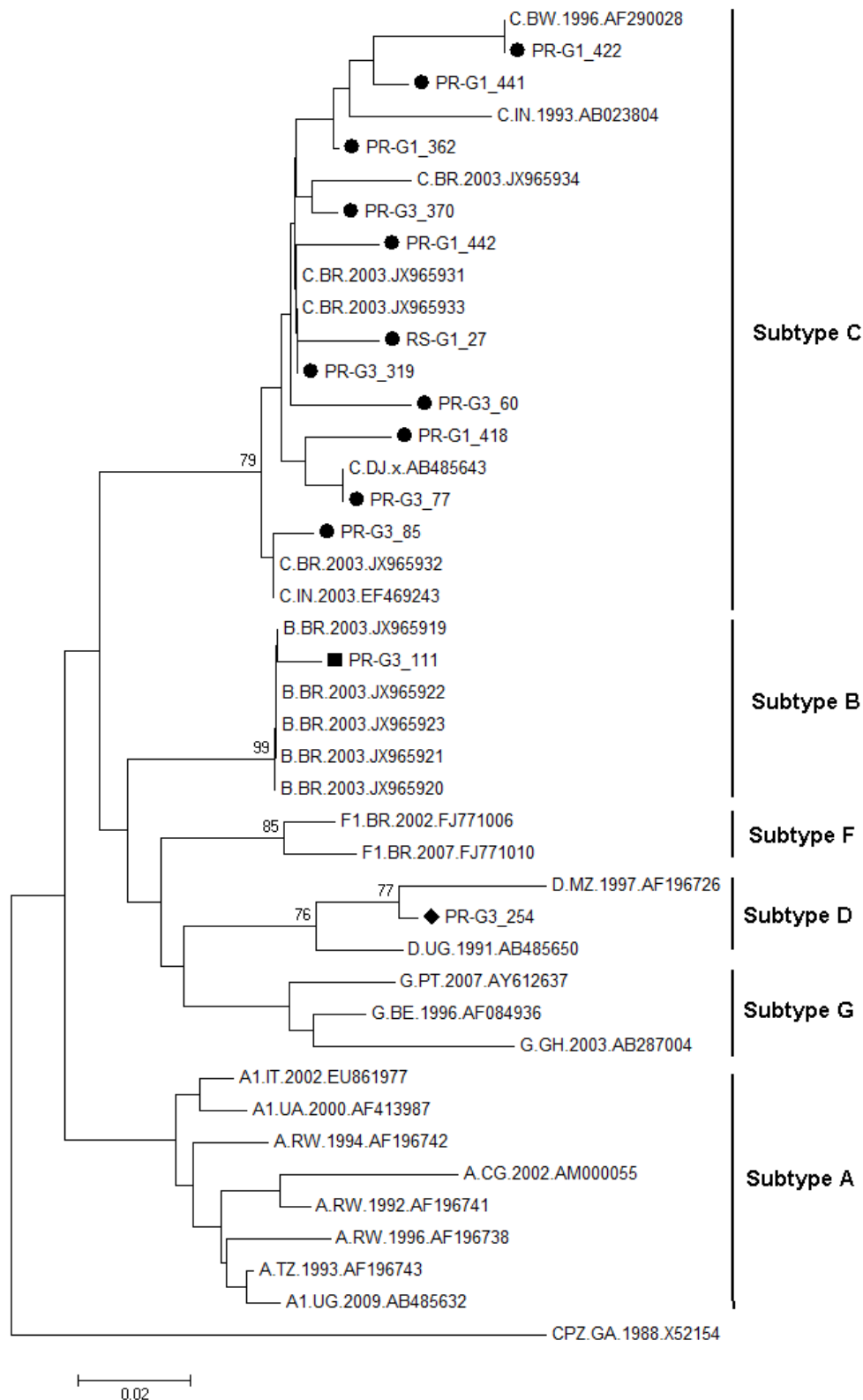
# Genetic Diversity in HIV-1 Subtype C LTR from Brazil and Mozambique Generates New Transcription Factor-Binding Sites

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**Supplementary Figure S1.** Rooted neighbor-joining tree based on long terminal repeat (LTR) sequences of Mozambican HIV-1 isolates (marked with ●). HIV-1 subtype reference sequences were obtained from the GenBank databases and the accession numbers are shown in figure. The tree was rooted using an SIV sequence. Only bootstrap values >70% are shown.



**Supplementary Figure 2.** Rooted neighbor-joining tree based on long terminal repeat (LTR) sequences of Brazilian HIV-1 isolates. The subtype C isolates is marked with ●, the subtype B isolate is marked with ■ and the subtype D isolate is marked with ◆. HIV-1 subtype reference sequences were obtained from the GenBank databases and the accession numbers are shown in figure. The tree was rooted using an SIV sequence. Only bootstrap values >70% are shown.



**Supplementary Figure 3.** Rooted neighbor-joining tree based on long terminal repeat (LTR) sequences of Brazilian HIV-1 isolates (marked with ●). HIV-1 subtype reference sequences were obtained from the GenBank databases and the accession numbers are shown in figure. The tree was rooted using an SIV sequence. Only bootstrap values >70% are shown.

