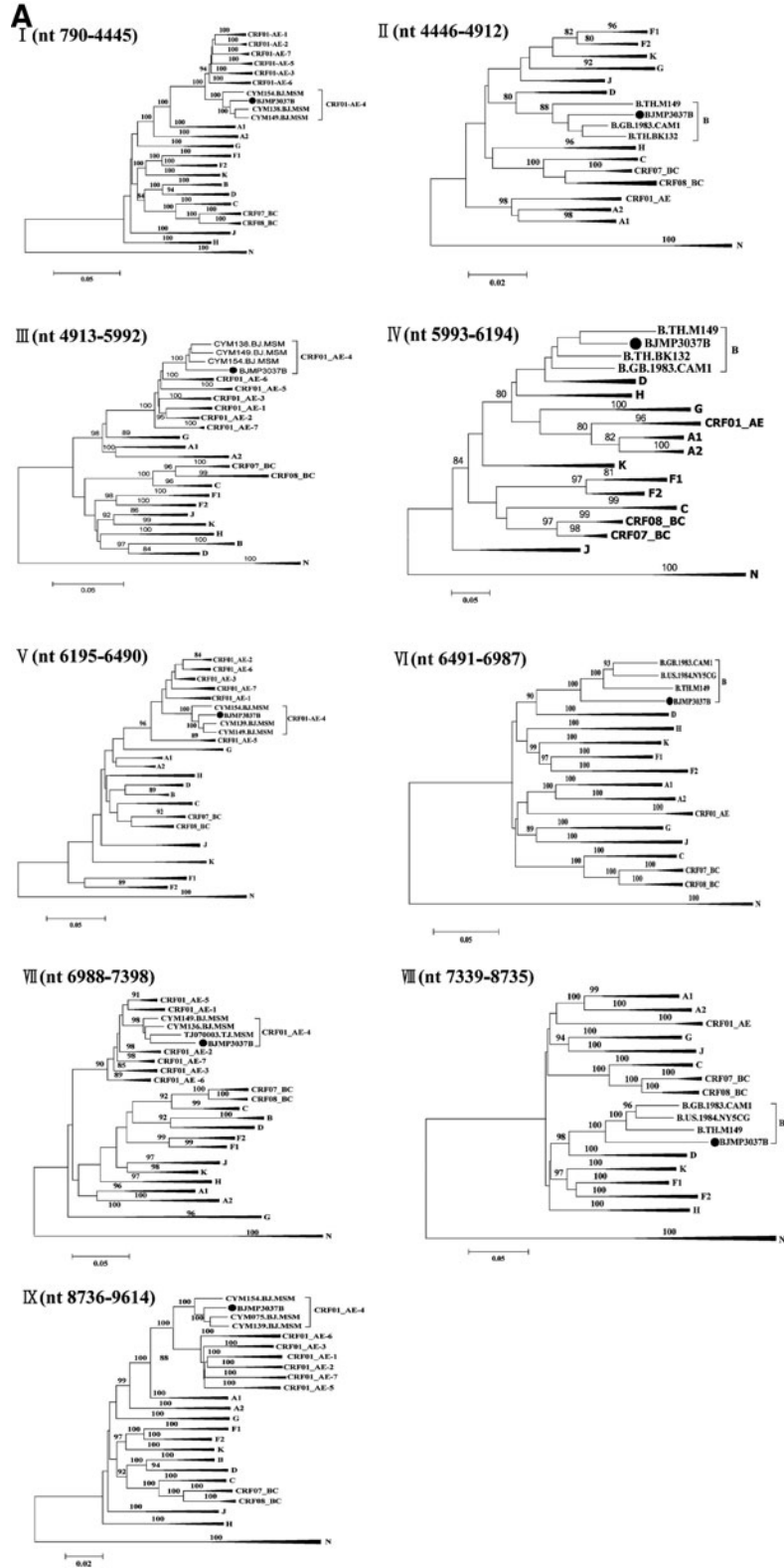


Supplementary Data



SUPPLEMENTARY FIG. S1. Phylogenetic analyses of mosaic segments defined by bootscanning. The phylogenetic trees of the mosaic segments were constructed with MEGA 6.0.6 using the neighbor-joining method. The subtype references are derived from the Los Alamos HIV Sequence Database. The trees also contain reference sequences from different HIV-positive populations. The stability of the nodes was assessed by bootstrap analysis with 1,000 replications, and only bootstrap values of >70 are shown at the corresponding nodes. The clades including our two samples are marked by a *solid circle* (●). (A) BJMP3037B; (B) BJMP3194B.

