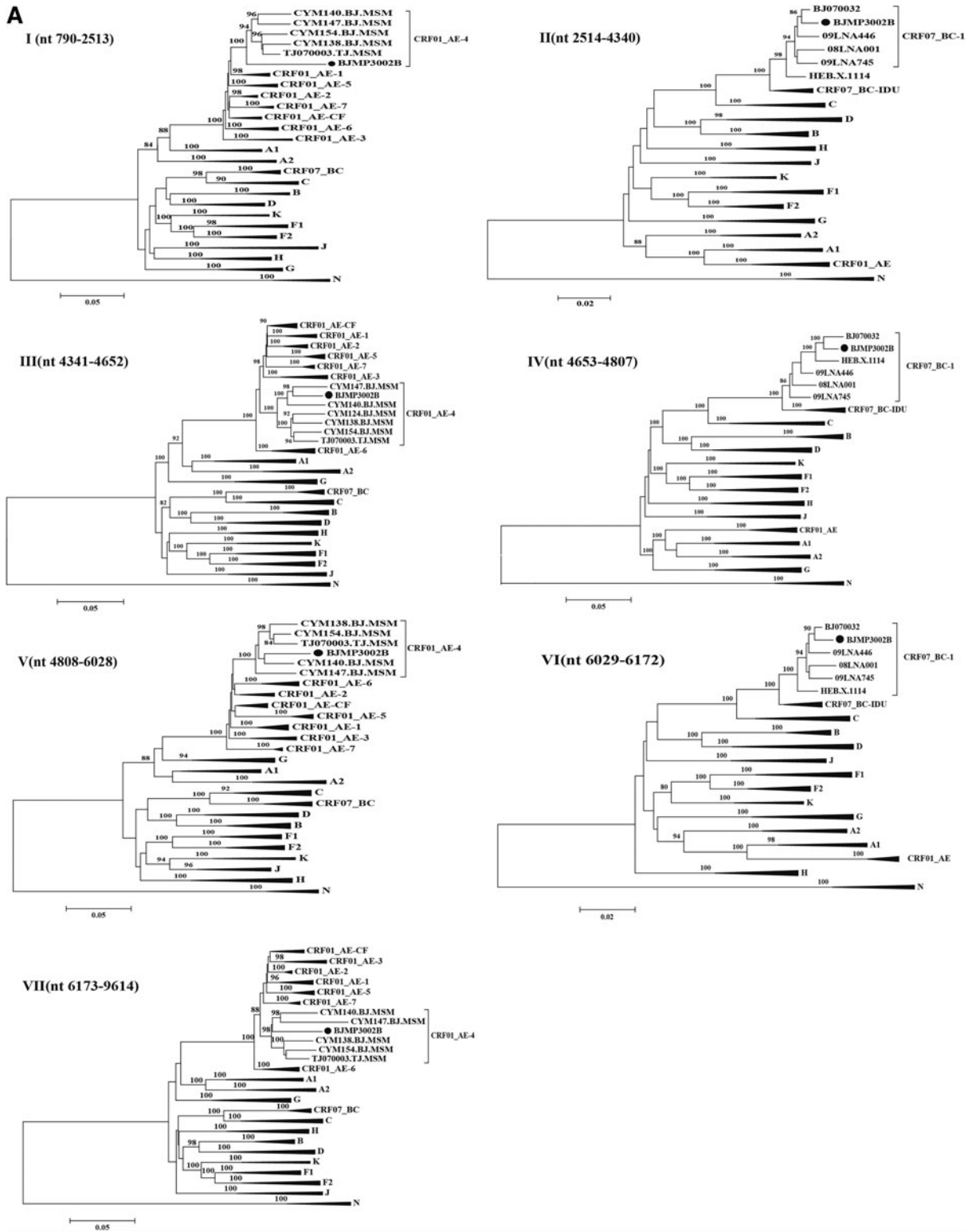


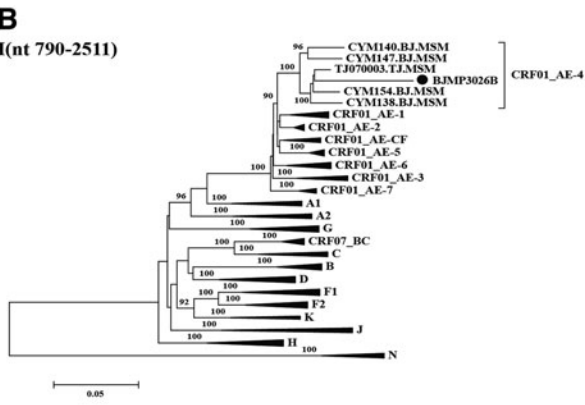
Supplementary Data



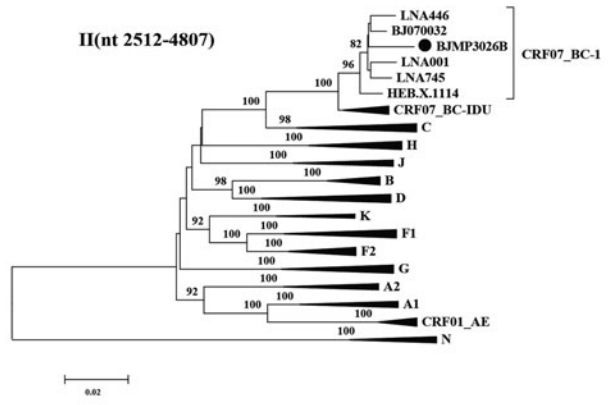
SUPPLEMENTARY FIG. S1. Phylogenetic analyses of mosaic segments defined by bootscanning. The phylogenetic trees of the mosaic segments were constructed with MEGA 6.0 using the neighbor-joining method. The subtype references are derived from the Los Alamos HIV Sequence Database. The trees also contain 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) BJMP3002B and (B) BJMP3026B.

B

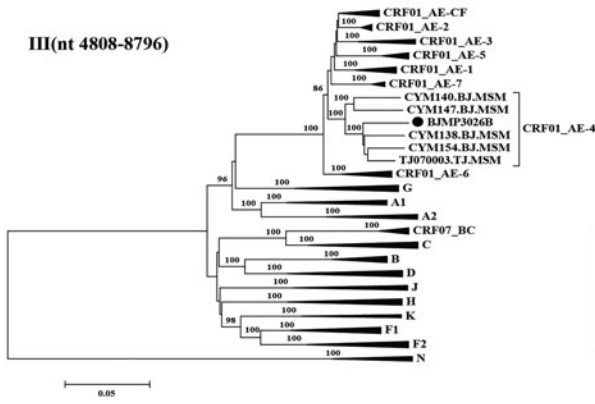
I(nt 790-2511)



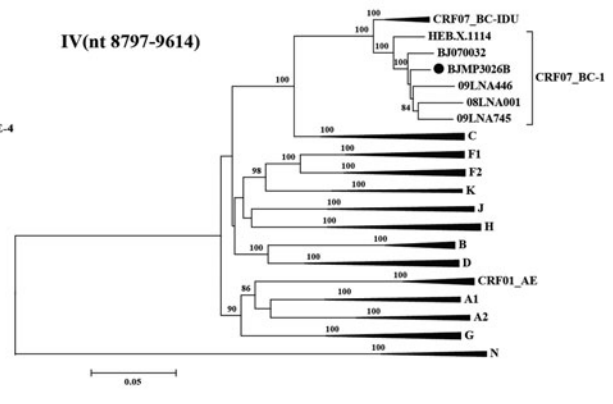
II(nt 2512-4807)



III(nt 4808-8796)



IV(nt 8797-9614)



SUPPLEMENTARY FIG. S1. (Continued)