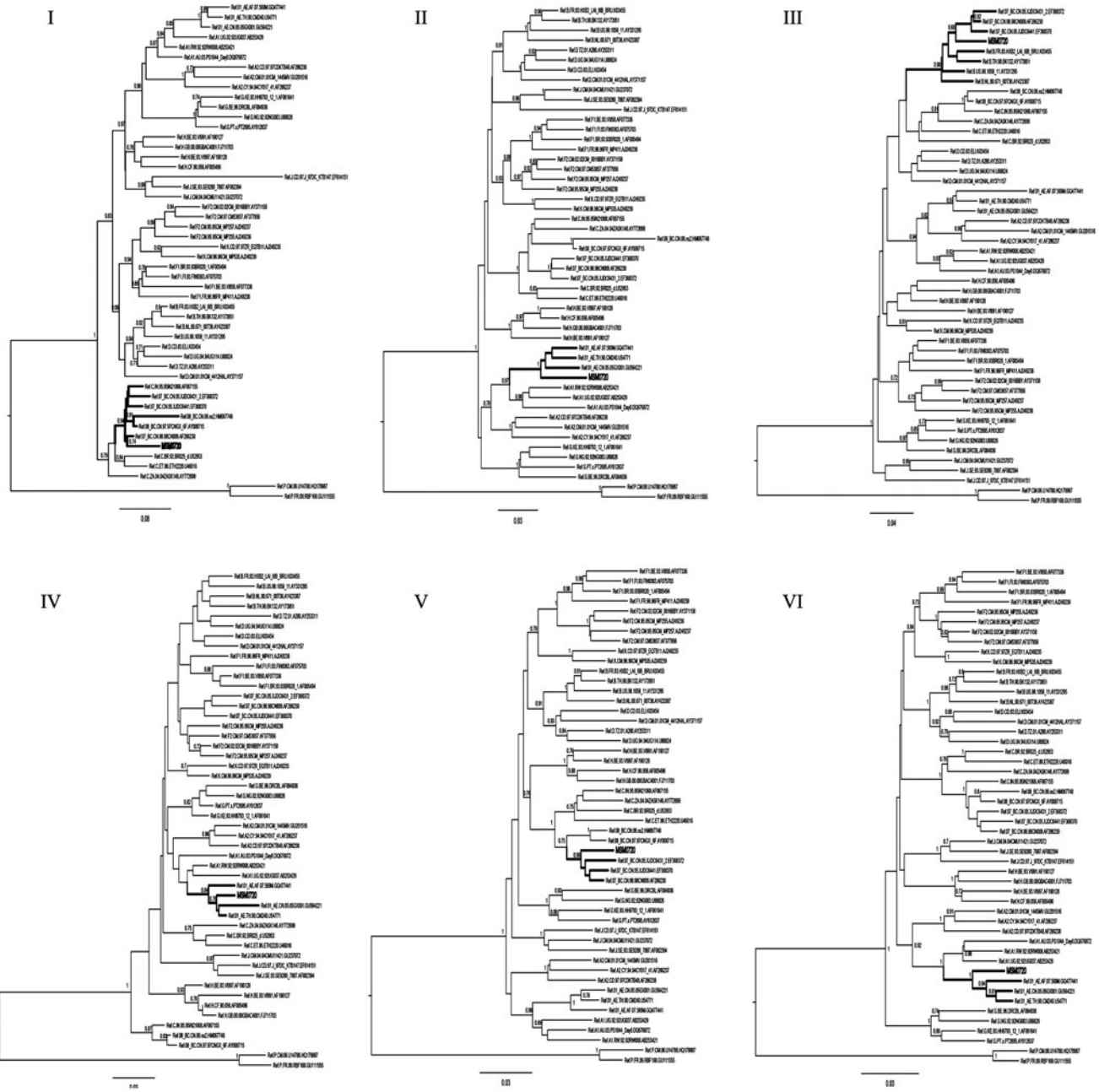# Supplementary Data

SUPPLEMENTARY FIG. S1. Phylogenetic analyses of 11 mosaic segments defined by bootscanning. The phylogenetic trees of the 11 mosaic segments were constructed with MEGA 5.0 using the neighbor-joining method. The subtype references are derived from the Los Alamos HIV Sequence Database. The stability of the nodes was assessed by bootstrap analysis with 1,000 replications, and only bootstrap values of >70 were shown at the corresponding nodes. The clades including MSM0720 are marked in red.

SUPPLEMENTARY FIG. S1. (Continued).