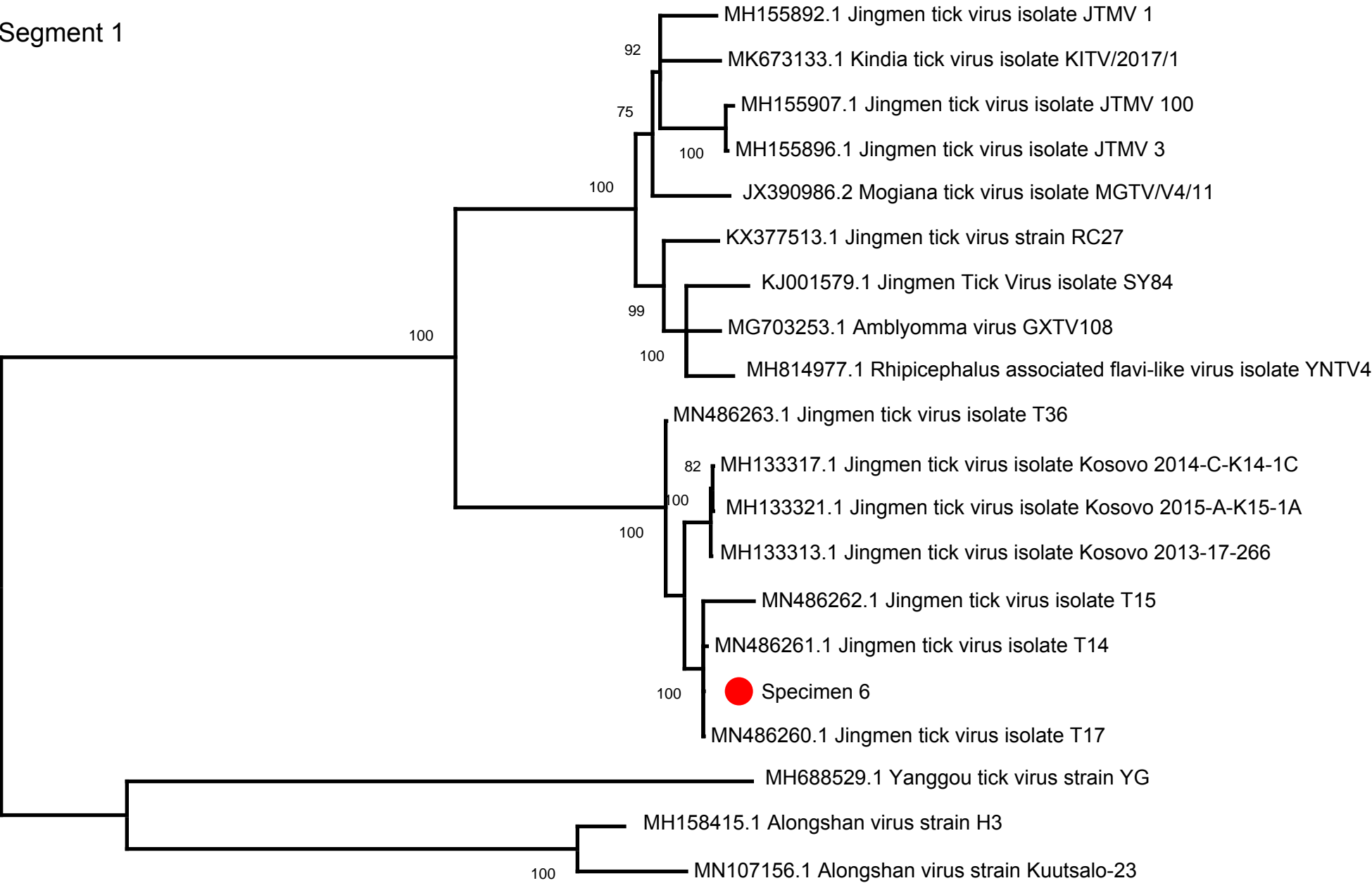


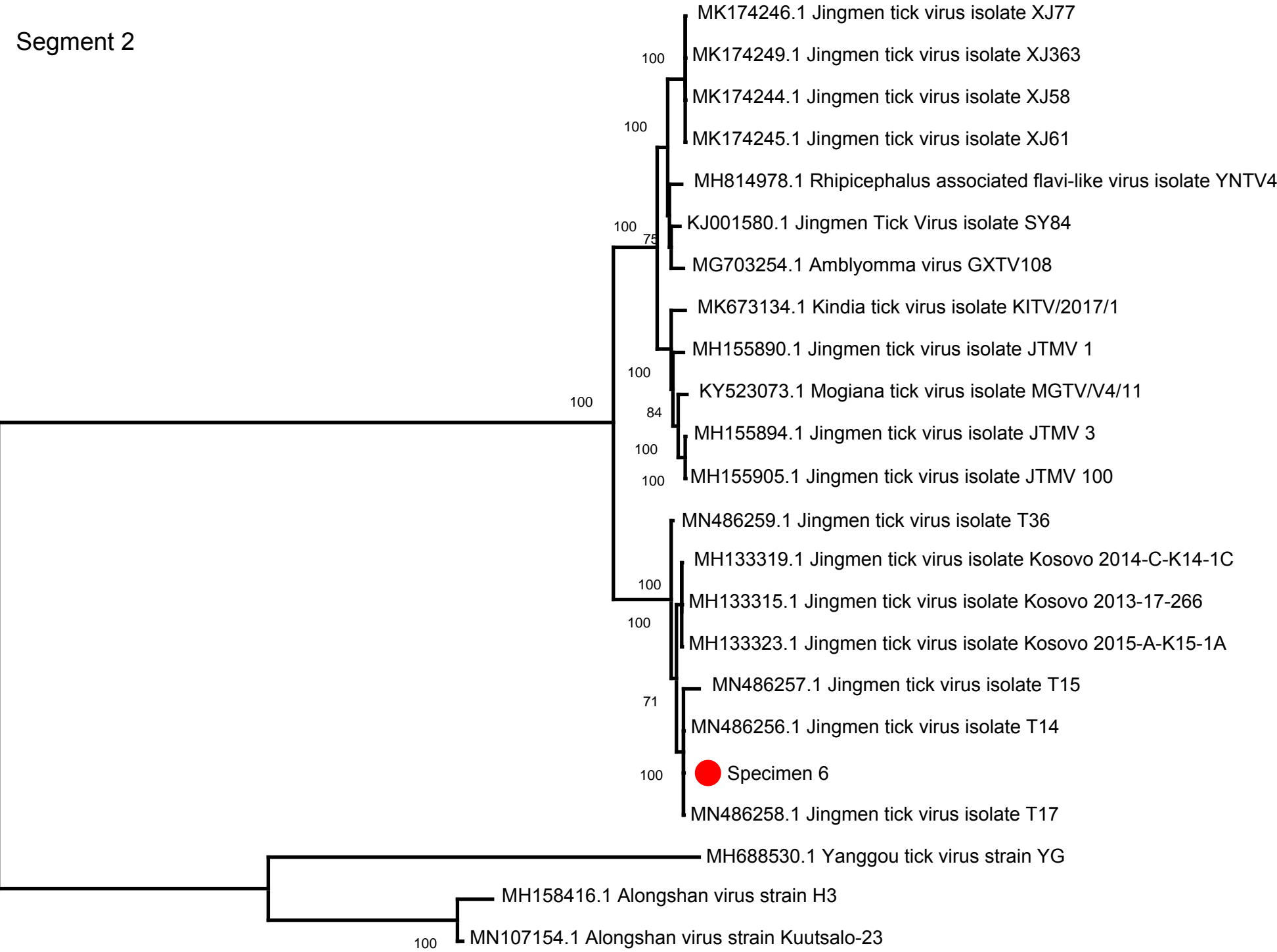
Segment 1



0.10

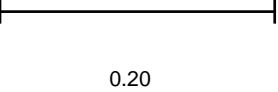
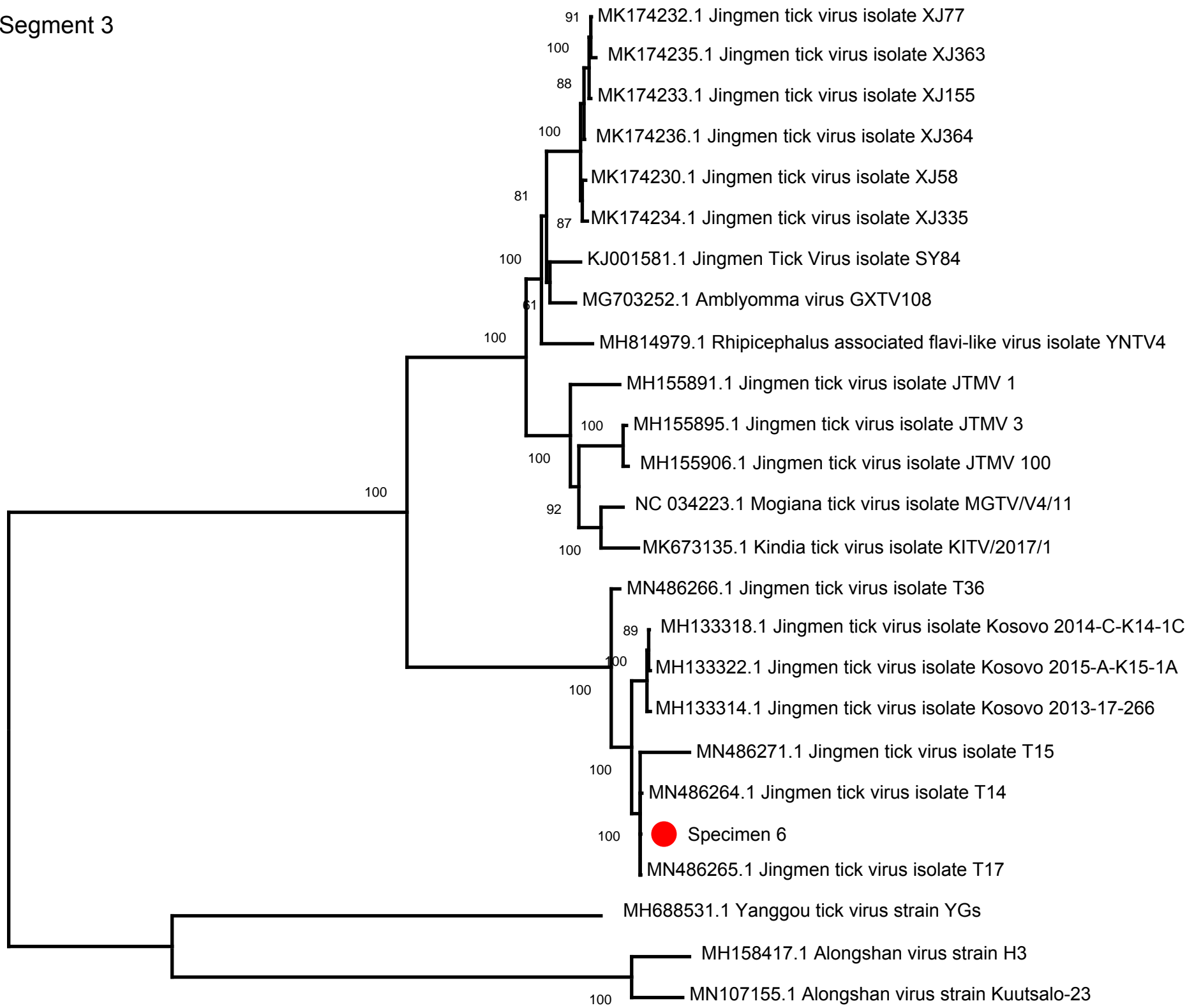
FIGURE S: The maximum likelihood analysis of the JMTV sequences in individual genomic segments. The trees are constructed using the general time reversible (GTR) model, gamma distributed with invariant sites (G+I) for 500 replications. The sequences generated in this study are indicated with a symbol and specimen code. Viruses included in the analyses are indicated by GenBank accession number and strain/isolate name. Bootstrap values higher than 50 are shown in the trees.

Segment 2

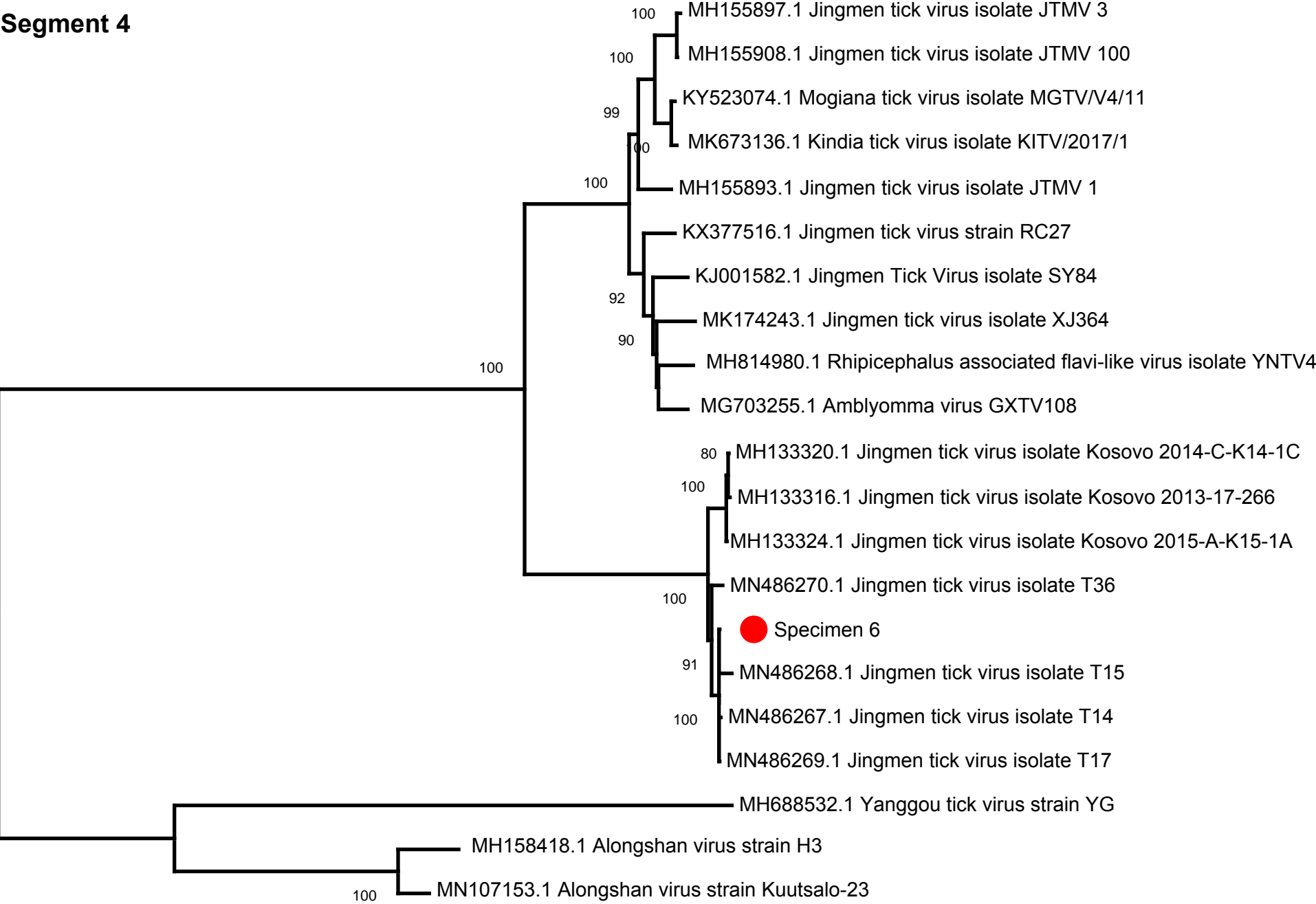


0.50

Segment 3



Segment 4



0.20