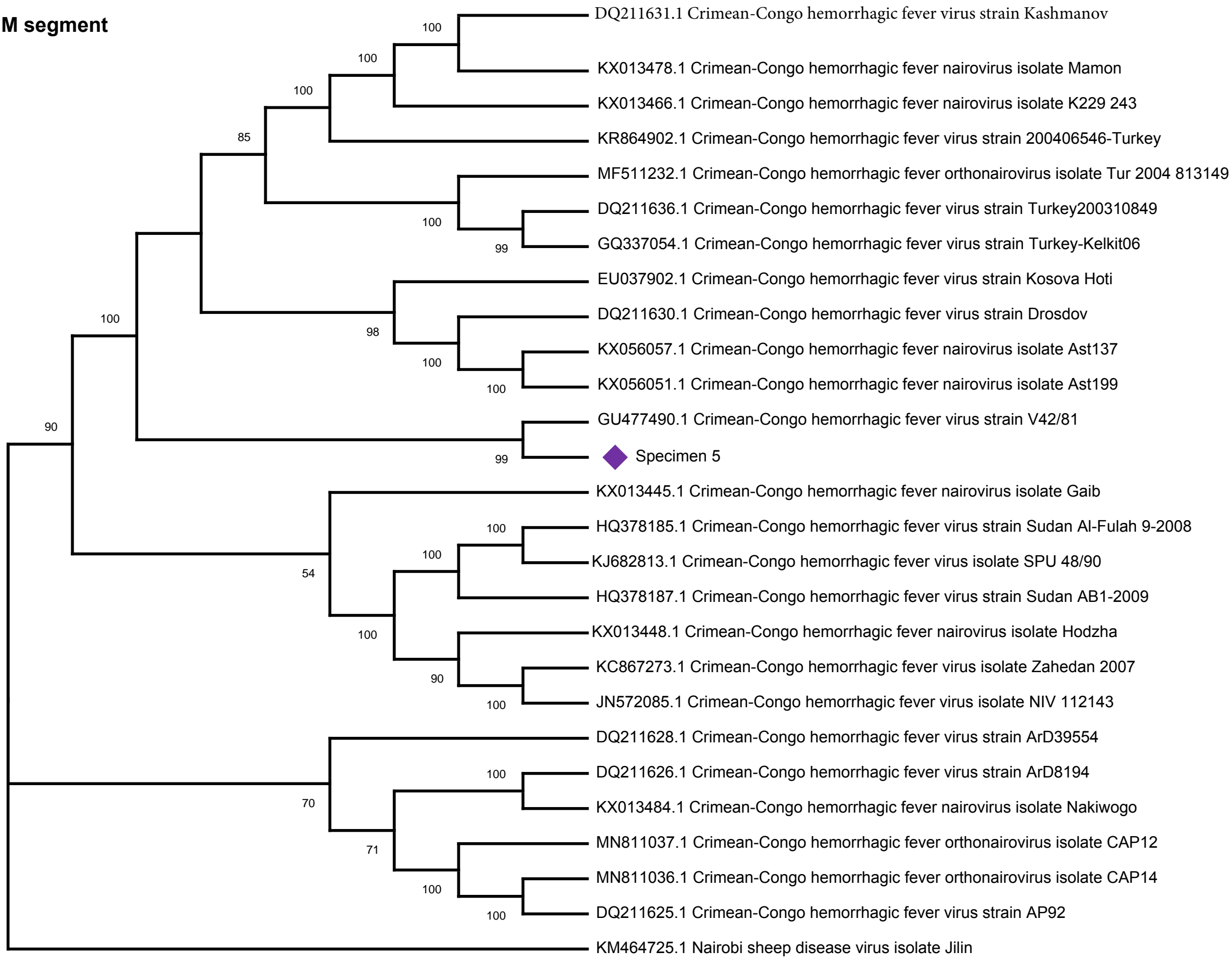


**FIGURE S2:** The maximum likelihood analysis of the CCHFV genome in individual segments. The bootstrap consensus trees are constructed using the Tamura-Nei model, gamma distributed with invariant sites (G+I) for 500 replications. The sequences generated in this study are indicated with a symbol and specimen code. Viruses included in the analyses are indicated by GenBank accession number and strain/isolate name. Nairobi sheep disease virus is analysed as an outgroup. Bootstrap values higher than 50 are shown in the trees. Major CCHFV clades are indicated in the L segment tree.

M segment



S segment

