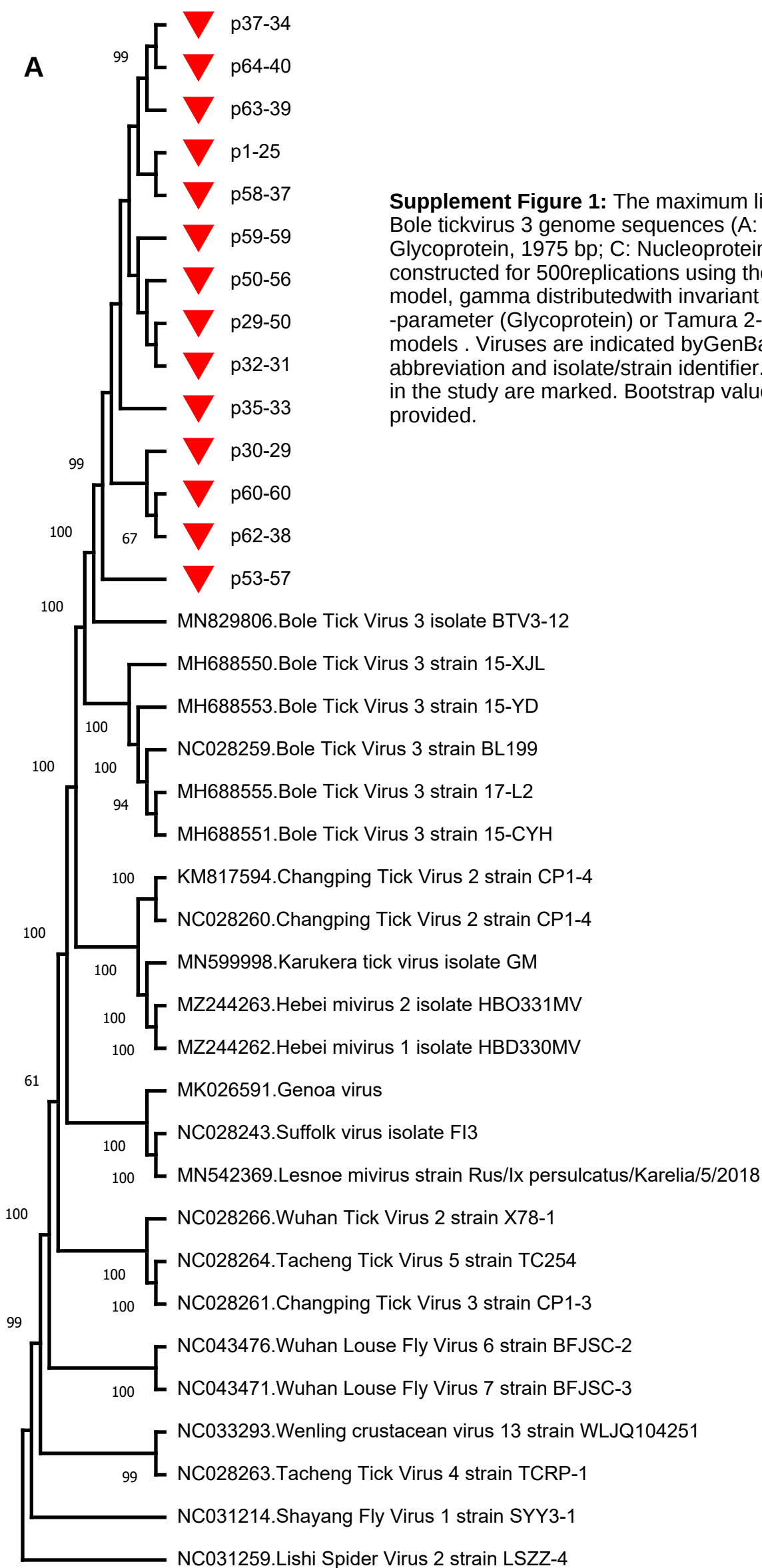




Supplement Figure 1: The maximum likelihood analysis of the Bole tickvirus 3 genome sequences (A: Replicase, 6994 bp; B: Glycoprotein, 1975 bp; C: Nucleoprotein, 1240 bp). The tree is constructed for 500 replications using the general time reversible model, gamma distributed with invariant sites (Replicase), Kimura 2-parameter (Glycoprotein) or Tamura 2-parameter (Nucleoprotein) models. Viruses are indicated by GenBank accession number, abbreviation and isolate/strain identifier. The sequences obtained in the study are marked. Bootstrap values higher than 60 are provided.

B

