

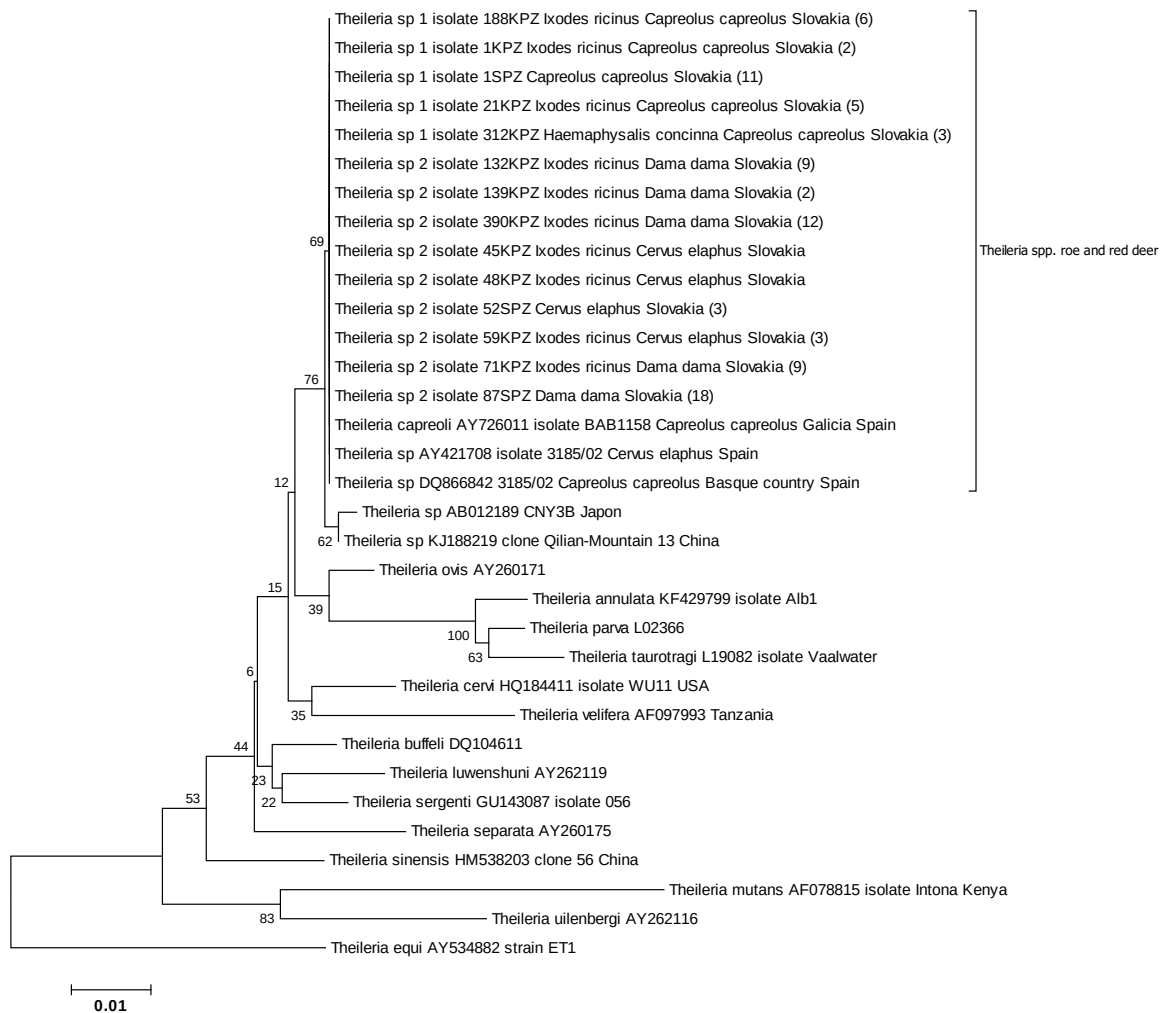


Figure S3 Neighbour-joining tree of hypervariable 18S rRNA gene sequences of *Theileria* parasites using neighbour-joining.

The sequences of isolates from Slovakia are labelled with isolate designation, tick and/or vertebrate host, geographic origin, and number of identical sequences (in brackets). The bootstrap values based of 1,000 replicates are displayed next to the branches. The tree is rooted using *Theileria equi* as the outgroup. Clades displaying a bootstrap value of ≥ 75 are considered relevant. The evolutionary distance is shown in the units of the number of base substitutions per site.