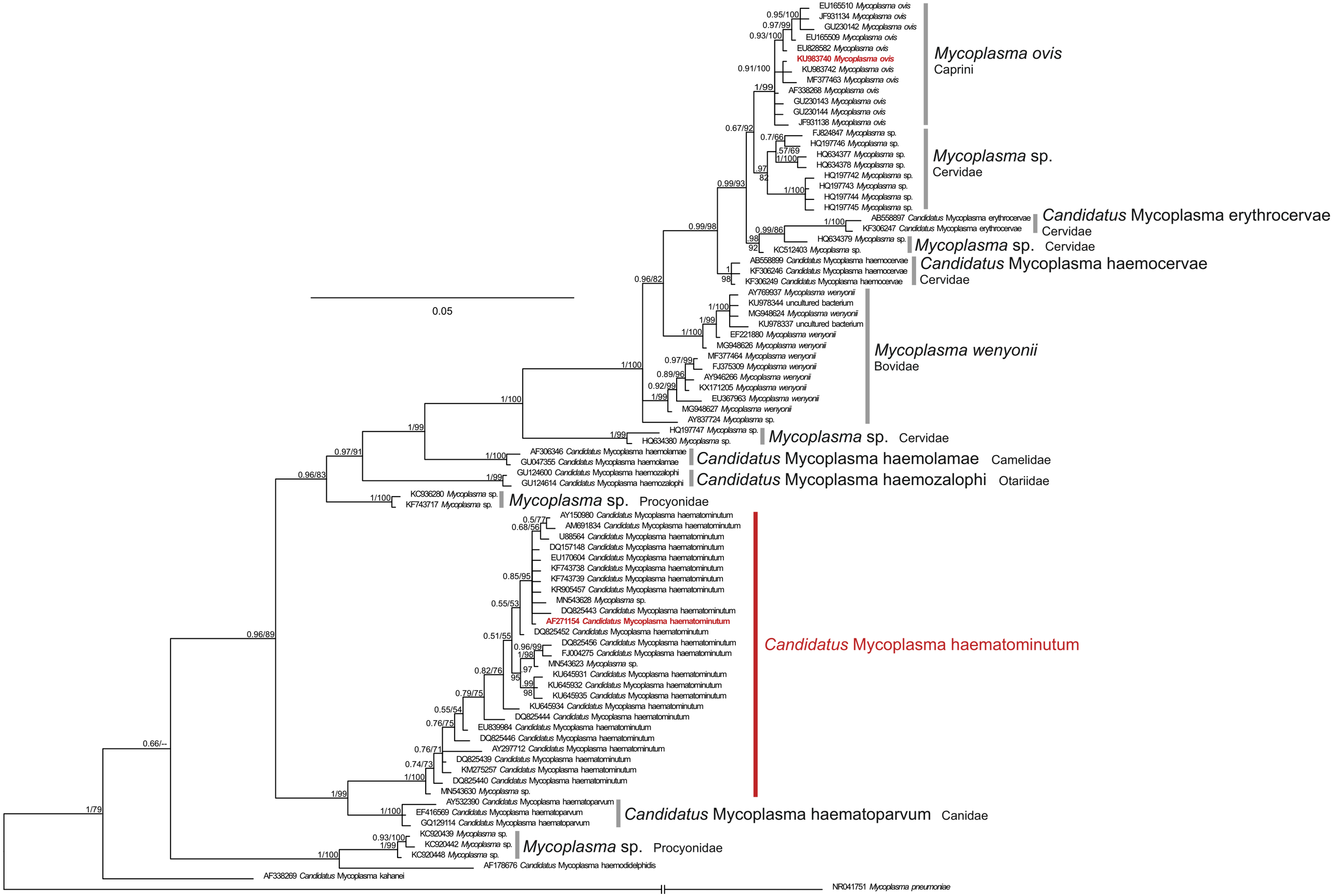

Supplement 1. Bayesian interference (BI) tree featuring *16S* rRNA sequences (969 nucleotide positions) of selected *Mycoplasma* spp. Nodes are marked with BI posterior probabilities and ML bootstrap values. Clades which are marked in red were used for calculation of the median-joining haplotype networks containing the sequences obtained in this study. Scale bar indicates the expected mean number of substitutions per site according to the model of sequence evolution applied.