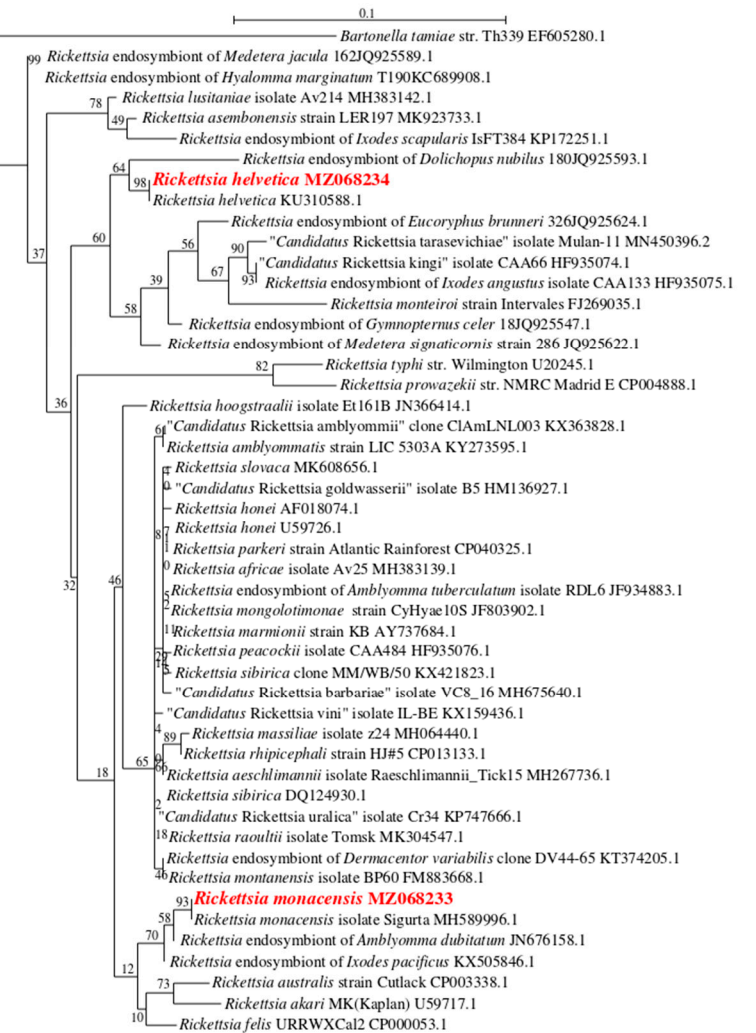


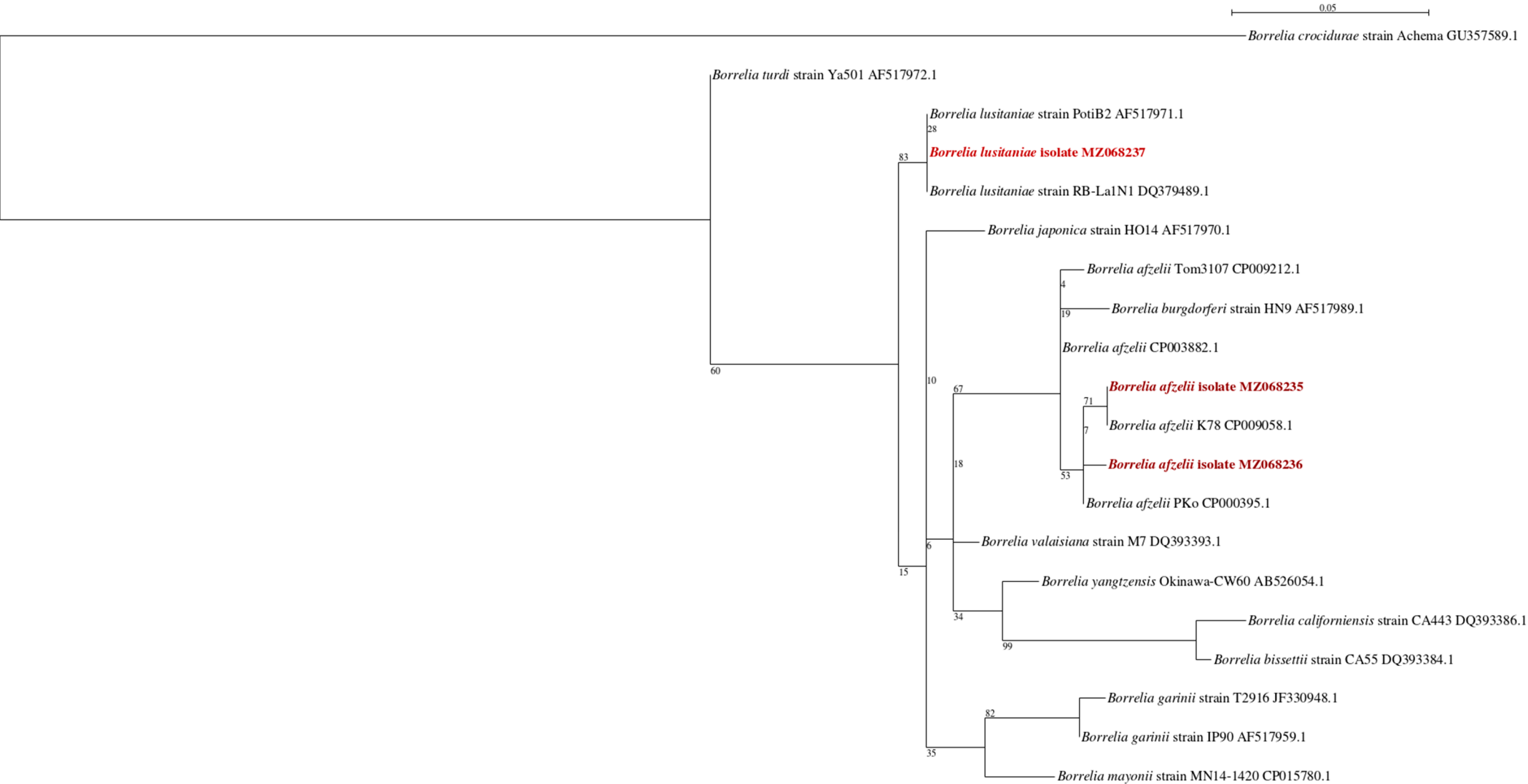
Figure S1

Phylogenetic inference of the obtained gene sequences. Phylogenetic inference performed on the obtained gene sequences for the following tick-borne pathogens: a) Spotted Fever Group *Rickettsia* spp., b) *Borrelia burgdorferi* s.l., c) *Anaplasma* spp./*Neoehrlichia* spp., d) *Babesia* spp. Phylogenetic inferences were performed using RAxML 8.2.4 (100 bootstraps, -p 123, -x 1234). The evolutionary models applied for phylogenetic inference were: GTR+I+G for *Babesia* spp. and *Anaplasma* spp./*Neoehrlichia* spp., HKY+I+G for *Borrelia* spp., and *Rickettsia* spp. The species detected in this work are indicated in red font, GenBank accession numbers are found next to the species names.

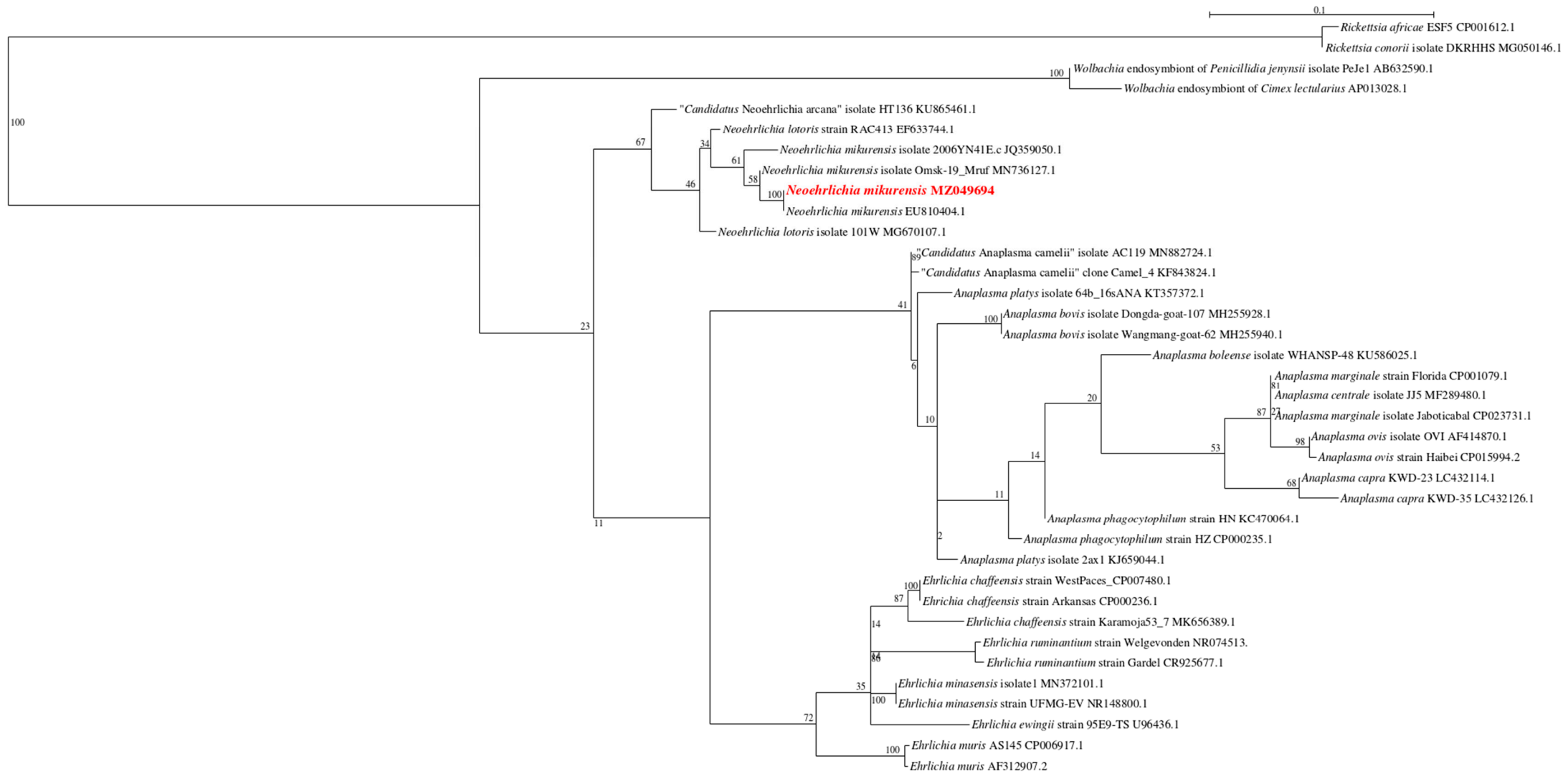
a)



b)



c)



d)

