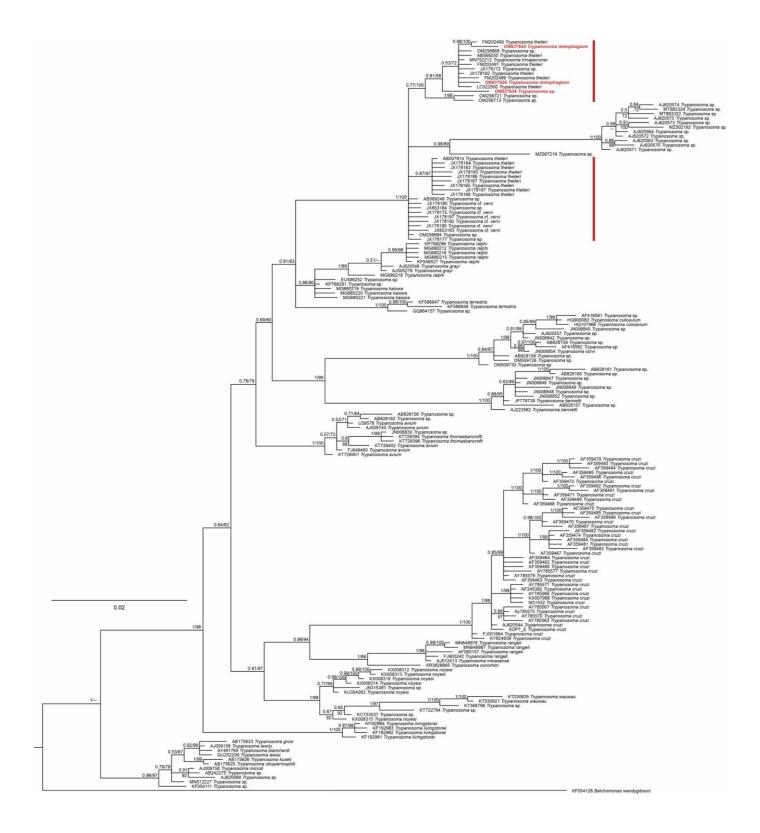**Supplementary Fig. 1.** Bayesian inference tree featuring gltA sequences (338 bp) of selected *Bartonella* spp. Nodes are marked with Bayesian inference posterior probabilities and Maximum likelihood bootstrap values. Clades which are marked with a red bar were used for calculation of the median-joining haplotype networks containing the sequences obtained in this study (font colour in red). Scale bar indicates the expected mean number of substitutions per site according to the model of sequence evolution applied

Supplementary Fig. 2. Bayesian inference tree featuring 18S rRNA sequences (701 bp) of selected *Trypanosoma* spp. Nodes are marked with Bayesian inference posterior probabilities and Maximum likelihood bootstrap values. Clades which are marked with a red bar were used for calculation of the median-joining haplotype networks containing the sequences obtained in this study (font colour in red). Scale bar indicates the expected mean number of substitutions per site according to the model of sequence evolution applied.