



Supplement 2. Bayesian inference (BI) tree featuring 18S rRNA (539 nucleotide positions) sequences of *Hepatozoon* spp. and other members of the suborder Adeleorina. 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 or creation of the pie charts 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.