



Additional file 2: Figure S2. Majority-rule consensus tree based on a PhyloBayes analysis of 18s rRNA sequences from Piroplasmida. The alignment is based on the 18s dataset from Papparini et al. (2015). A single contig from the platypus genome assembly, which contains a parasite-derived 18s rRNA fragment, was added to the alignment. Bayesian posterior probabilities are given at the nodes. The tree was rooted with *Cardiosporidium cionae*. All EMBL/Genbank acc. nos. are given in parentheses.