**Fig. S1.** Phylogenetic hypotheses obtained using Bayesian inference and maximum likelihood performed with 18S rRNA fragments of (A) up to 1000 bp, and (B) 585 bp sequences. The lineages obtained in this study are highlighted in bold font. Branches color indicates the parasite genus as follows: green for *Hepatozoon* sp., blue for *Hemolivia* sp., purple for *Karyolysus* sp., red for *Haemogregarina* and grey for the outgroup (*Dactylosoma* sp.). The silhouettes located near the clade nodes indicate the host from which the parasites were isolated: a frog for amphibians, a lizard for reptiles, a turtle for turtles and tortoises, and a bear for mammals. Bootstrap values and posterior probabilities are shown above the nodes. Nodal supports below 80/0.8 are not shown. The branch lengths are proportional to the amount of change. Scale bars indicating substitutions per site are provided.