

**Supplementary figure 2.** Phylogenetic affinities and divergence times based on *cytb*.

Detail of the consensus tree from a Bayesian analysis using Phylobayes and employing the CAT replacement model, the Birth-Death process as tree prior and multiple calibrations. The age of nodes correspond to the mean posterior divergence time; bars indicate 95% Highest Posterior Densities (HPD). Black mean estimate and black bar: statistics for the split of *G. barreimiae* from *P. andruzzii*. The full tree is shown in Supplementary Figure 1. Results obtained with other replacement models or tree priors are shown in blue (GTR model, Birth-Death) and red (CAT model, Uniform) (Supplementary Table 5). Po: Pliocene, P-H: Pleistocene-Holocene.

