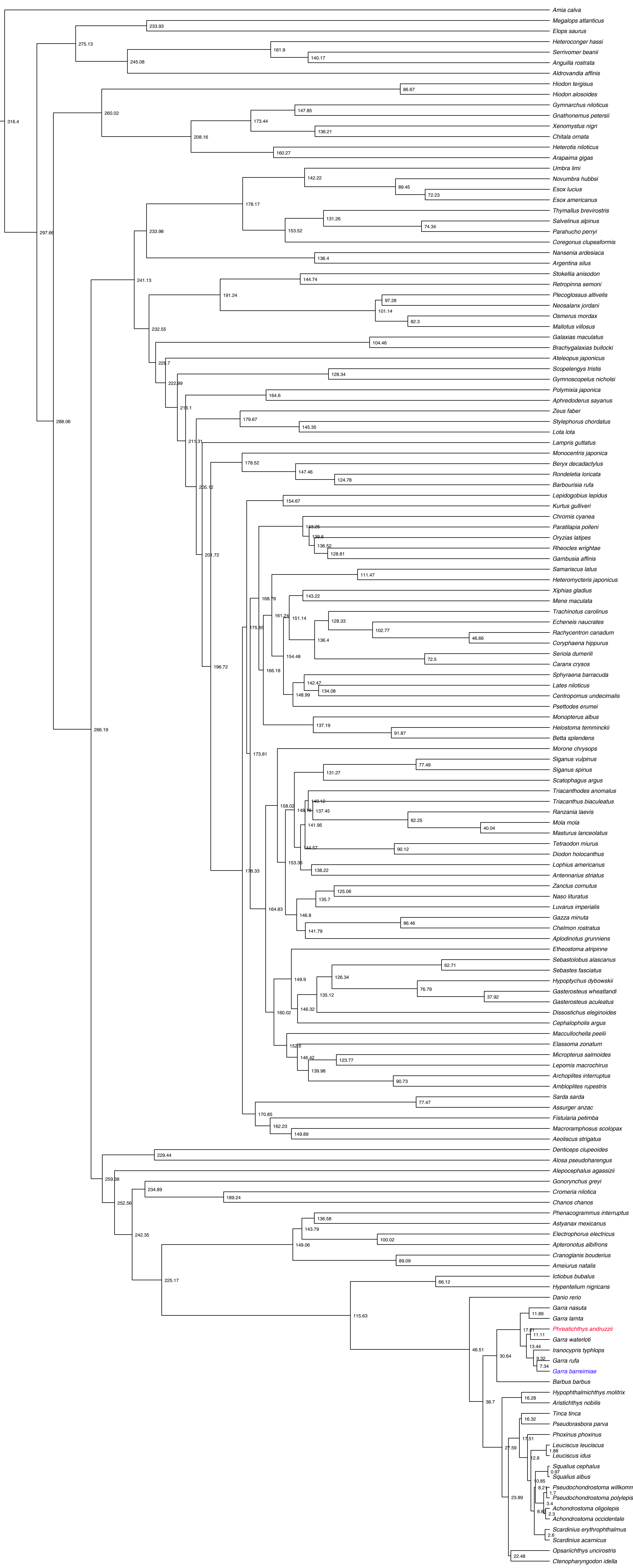


Supplementary figure 1. Full tree from the Bayesian analysis using Phylobayes and employing the CAT replacement model, the Birth-Death process as tree prior and multiple calibrations (Supplementary table 5, analysis 1). Numbers at each node represent mean divergence times.



350 300 250 200 150 100 50 0