

Supplementary Figures

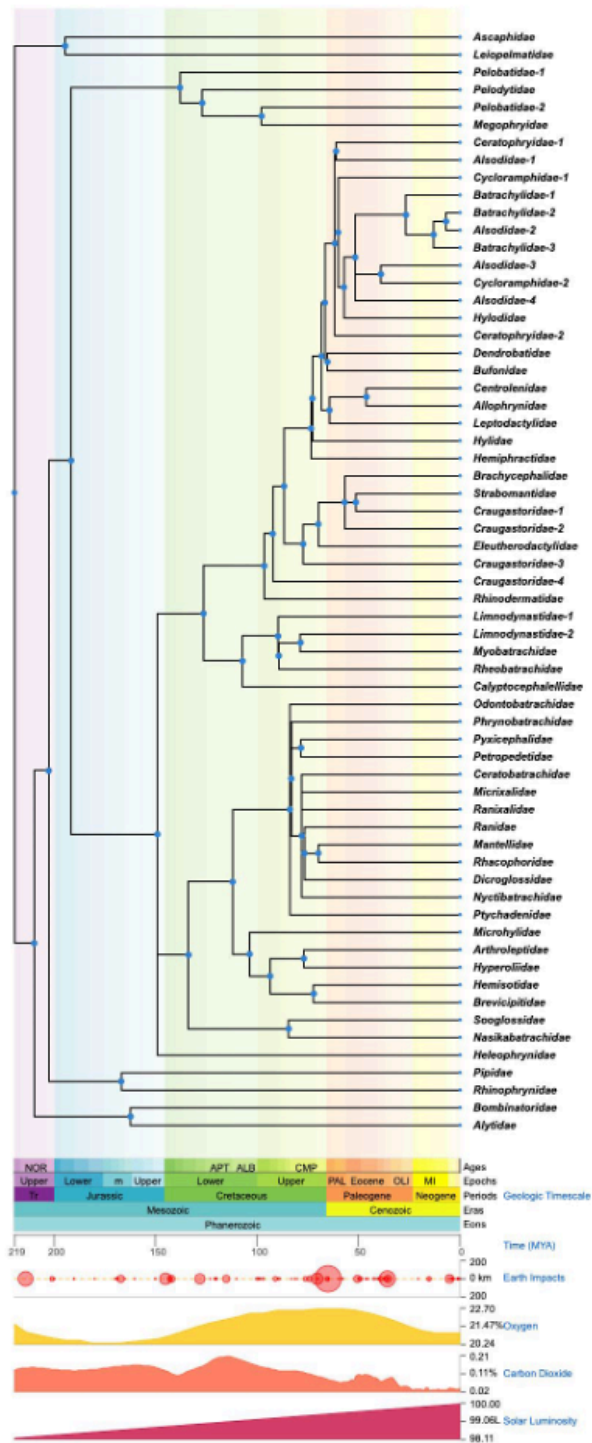


Figure S1: Time calibrated anuran family tree generated from [Timetree.org](https://timetree.org/).

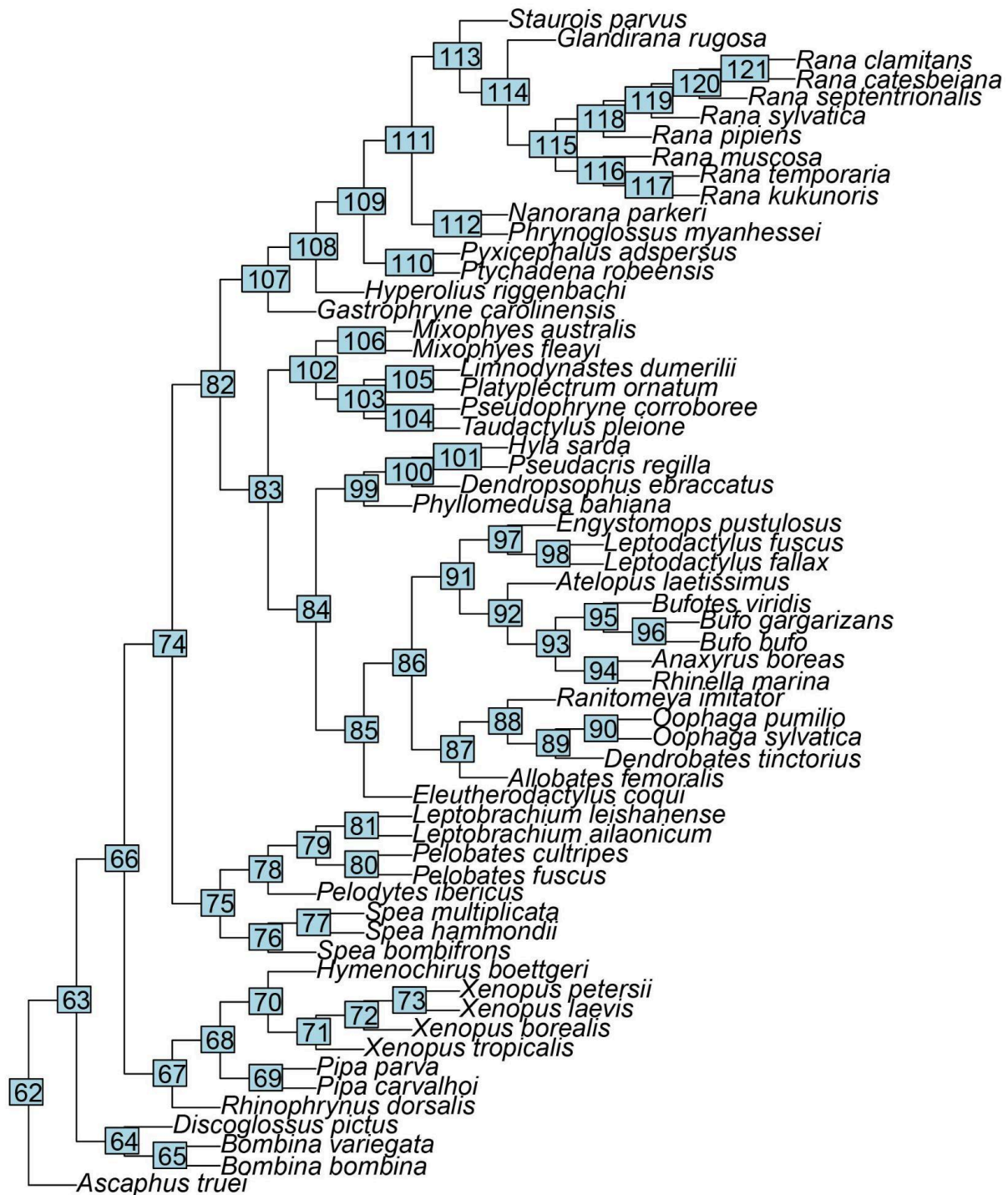


Figure S2. Anuran phylogeny with labeled nodes for reference in comparing overlapping confidence intervals for ancestral character state estimates (see Supplementary Table XX). All branch lengths set to 1 to highlight tree branching.

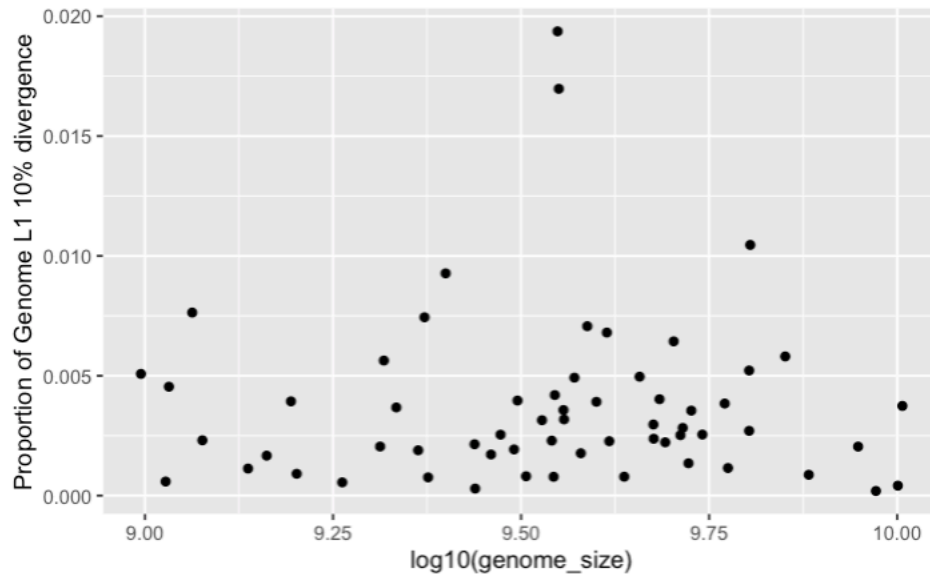


Figure S3: Relationship between proportion of amphibian genome composed of recently active L1 elements and genome size. Elements were considered recently active if the integrated genome sequence had less than 10% divergence from L1 RepeatModeler consensus sequences. Each point represents the per species genome proportion composed of recently active L1 elements (OLS regression p-value=0.95).

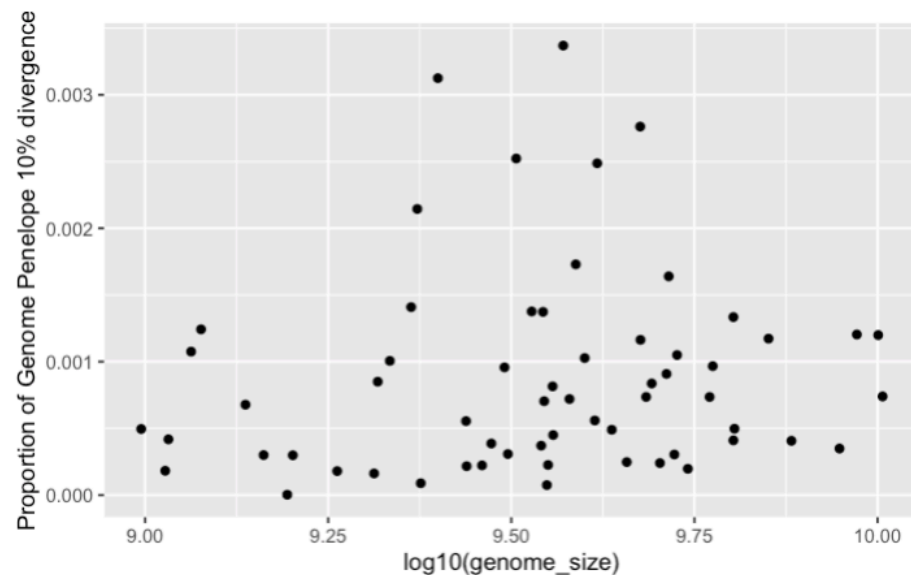


Figure S4: Relationship between proportion of amphibian genome composed of recently active Penelope elements and genome size. Elements were considered recently active if the integrated genome sequence had less than 10% divergence from Penelope RepeatModeler consensus sequences. Each point represents the per species genome proportion composed of recently active Penelope elements (OLS regression p-value = 0.37).

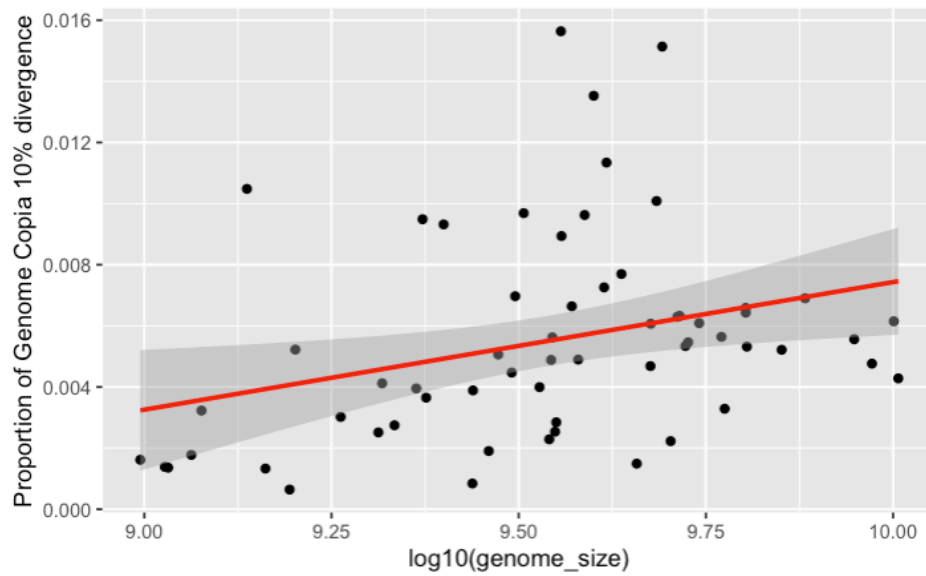


Figure S5: Relationship between proportion of amphibian genome composed of recently active Copia elements and genome size. Elements were considered recently active if the integrated genome sequence had less than 10% divergence from Copia RepeatModeler consensus sequences. Each point represents the per species genome proportion composed of recently active Copia elements (OLS regression p-value = 0.01, $R^2=0.09$, $\beta=0.004$).