

Supplementary Material to “Evolutionary patterns in squamate mitogenomes: are selective regimes associated with fossoriality and limblessness?”

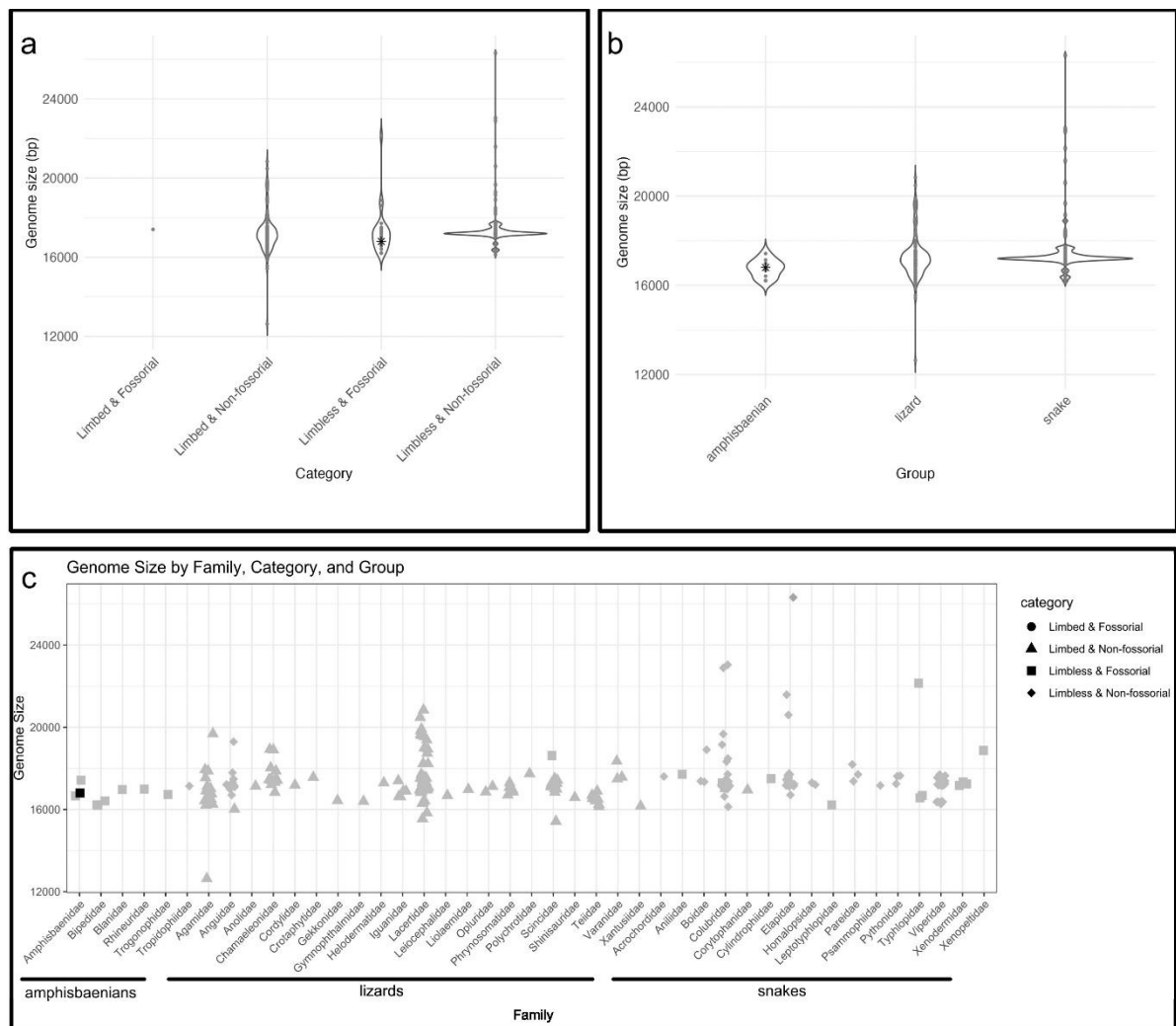


Figure S2 – Mitochondrial genome size across squamates. (a) Genome size by ecological category (limbed fossorial, limbed non-fossorial, limbless fossorial, limbless non-fossorial). The asterisk marks *Amphisbaena alba*, which falls within the range of limbless-fossorial species. (b) Genome size across major squamate groups (Amphisbaenia, lizards, and snakes). *Amphisbaena alba* is highlighted with an asterisk and lies within the amphisbaenian range. The five largest genomes correspond to snakes: *Hydrophis ornatus* (26,316 bp), *Leptodeira polysticta* (23,038 bp), *Sibon nebulatus* (22,887 bp), *Indotyphlops braminus* (22,144 bp), and *Sinomicrurus japonicus* (22,144 bp). (c) Genome size grouped by family, with *Amphisbaena alba* indicated in black.