

1 **Figure S1.** Fully sampled sequence capture tree, estimated by weighted hybrid ASTRAL using
2 IQTREE genetree inputs. Branch support values are indicated at nodes and colored according to
3 value (white = 1; red <= 0.9).

4
5 **Figure S2.** Time calibrated species tree of microhylid frogs highlights with confidence intervals
6 indicated at nodes. Orange colored bars annotated with a circle indicate nodes calibrated by
7 fossil evidence. These correspond to (A) *Beelzebufo ampinga* as a 66 million year minimum on
8 the crown divergence of Neobatrachia; (B) *Calyptocephalella pichileufensis* as a 47.5 million year
9 minimum on the split between Calyptocephalellidae and Myobatrachoidae; (C) *Thamatosaurus*
10 *gezei* as a 33.9 million year minimum on the crown of Ranoidea; and (D) Ptychadenidae fossil as
11 a 25 million year minimum on the split of Ptychadenidae and Phrynobatrachidae.

12
13 **Figure S3.** IQTREE gene tree of concatenated mitochondrial loci (CYTB, ND4). Newly
14 assembled and placed samples are indicated by orange text. Incorporating new samples into the
15 alignments of Hill et al. (2023) allows for a shared understanding of Asterophryinae taxonomy
16 between mitochondrial and nuclear datasets.

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18 **Figure S4.** Visualizations of morphological dimensionality reduction and classification error
19 under three discrimination techniques (RF, LDA, FDA) are largely consistent.