

1 **Prolonged morphological expansion of spiny-rayed fishes 2 following the end-Cretaceous**

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4 Ava Ghezelayagh^{*1}, Richard C. Harrington^{*1}, Edward D. Burress¹, Matthew A. Campbell^{2,3},
5 Janet C. Buckner^{4,6}, Prosanta Chakrabarty⁴, Jessica R. Glass⁵, W. Tyler McCraney⁶, Peter J.
6 Unmack⁷, Christine E. Thacker^{8,9}, Michael E. Alfaro⁶, Sarah T. Friedman¹, William B. Ludt⁹,
7 Peter F. Cowman¹⁰, Matt Friedman^{11,12}, Samantha A. Price¹³, Alex Dornburg¹⁴, Brant C.
8 Faircloth⁴, Peter C. Wainwright¹⁵, Thomas J. Near^{1,16}

9
10 1. Department of Ecology and Evolutionary Biology, Yale University, New Haven, Connecticut
11 06520-8106, USA

12 2. Department of Animal Science, University of California, Davis, California 95616-5270, USA

13 3. University of Alaska Museum of the North, Fairbanks, Alaska 99775, USA

14 4. Museum of Natural Science and Department of Biological Sciences, Louisiana State
15 University, Baton Rouge, Louisiana 70803, USA

16 5. College of Fisheries and Ocean Sciences, University of Alaska Fairbanks, Fairbanks, Alaska
17 99775, USA

18 6. Department of Ecology and Evolutionary Biology, University of California, Los Angeles,
19 California 90095-1606, USA

20 7. Institute for Applied Ecology, University of Canberra, ACT 2601, Australia

21 8. Santa Barbara Museum of Natural History, Santa Barbara, California 93105, USA

22 9. Natural History Museum of Los Angeles County, Los Angeles, California 90007, USA

23 10. Queensland Museum, Townsville, QLD 4810, Australia

24 11. Department of Earth and Environmental Sciences, University of Michigan, Ann Arbor,
25 Michigan 48109-1079, USA

26 12. Museum of Paleontology, University of Michigan, Ann Arbor, Michigan 48109-1079, USA

27 13. Department of Biological Sciences, Clemson University, Clemson, South Carolina 29634,
28 USA

29 14. Department of Bioinformatics and Genomics, University of North Carolina, Charlotte, North
30 Carolina 28223, USA

31 15. Department of Evolution and Ecology, University of California, Davis, California 95616-
32 5270, USA

33 16. Peabody Museum of Natural History, Yale University, New Haven, Connecticut 06520-
34 8106, USA

35
36 * These authors contributed equally to this work

37 **Abstract**

38 **Spiny-rayed fishes (Acanthomorpha) dominate modern marine habitats and comprise**
39
40 **more than a quarter of all living vertebrate species¹⁻³. It is believed that this dominance**
41 **resulted from explosive lineage and phenotypic diversification coincident with the**
42 **Cretaceous-Paleogene (K-Pg) mass-extinction event⁴. It remains unclear, however, if living**
43 **acanthomorph diversity is the result of a punctuated burst or gradual accumulation of**
44 **diversity following the K-Pg. We assess these hypotheses with a time-calibrated phylogeny**
45 **inferred using ultraconserved elements from a sampling of species that represent over 91%**
46 **of all acanthomorph families, as well as an extensive body shape dataset of extant species.**
47 **Our results indicate that several million years after the end-Cretaceous, acanthomorphs**
48 **underwent a prolonged and significant expansion of morphological disparity primarily**
49 **driven by changes in body elongation, and that acanthomorph lineages containing the bulk**
50 **of the living species diversity originated throughout the Cenozoic. These acanthomorph**
51 **lineages radiated into distinct regions of morphospace and retained their iconic**
52 **phenotypes, including a large group of laterally compressed reef fishes, fast-swimming**
53 **open-ocean predators, bottom-dwelling flatfishes, seahorses, and pufferfishes. The**
54 **evolutionary success of spiny-rayed fishes is the culmination of a post K-Pg adaptive**
55 **radiation in which rates of lineage diversification were decoupled from periods of high**
56 **phenotypic disparity.**

57
58 **Main**

59 **The Cretaceous-Paleogene (K-Pg) mass extinction fundamentally affected the**
60
61 **evolutionary trajectory of terrestrial vertebrates, laying the foundation for spectacular radiations**

62 of eutherian mammals, neoavian birds, amphibians, and squamates⁵⁻¹². In contrast, the impact of
63 the K-Pg on marine vertebrate lineages is less clear. Most marine vertebrates are spiny-rayed
64 fishes (Acanthomorpha), which collectively represent over a quarter of all living vertebrates³. It
65 is hypothesized that the mass extinction of dominant Mesozoic plankton feeders following the K-
66 Pg relieved acanthomorph fishes from previous predation and competitive pressures, enabling
67 their occupation of vacated niches¹³. Paleogene fossils suggest a corresponding increase in
68 acanthomorph taxonomic diversity and morphological disparity¹⁴, and phylogenomic analyses
69 have prompted the complementary proposal that the origins of many major acanthomorph
70 lineages coincide with the K-Pg^{4,15}. However, the acanthomorph fossil record is sparse in the 20
71 million years around the end-Cretaceous¹⁶, and phylogenomic efforts to date have been limited
72 by sampling designs that inadequately represents the group's staggering taxonomic richness^{4,15}.
73 These factors have hindered the resolution of the timing and patterns of acanthomorph
74 diversification near the K-Pg; it remains uncertain if acanthomorph diversification in the
75 Cenozoic was gradual or punctuated, and whether there is a coupling of phenotypic and lineage
76 diversification that is considered a hallmark of adaptive radiation¹⁷. A well-resolved, time-
77 calibrated, phylogeny that includes all major lineages is critical to understanding the
78 evolutionary dynamics of spiny-rayed fishes in the wake of the K-Pg.

79
80 The largest challenge to acanthomorph evolutionary studies is inferring a phylogeny of its
81 more than 19,450 species³. The resolution of relationships within the subclade Percomorpha,
82 which contains more than 95% of all acanthomorph species, has been particularly difficult.
83 During most of the twentieth century, inferences of acanthomorph and percomorph relationships
84 relied on anatomical characters that resulted in largely unresolved phylogenetic hypotheses¹⁸.
85 Although these early morphological investigations defined major groups of acanthomorphs, their

conclusions were dramatically upended by the introduction of phylogenies inferred from a relatively small number of Sanger-sequenced mitochondrial and nuclear genes^{1,19-22}. For instance, molecular phylogenies placed the anglerfishes—long classified with the group of non-percomorph acanthomorphs that includes the economically-important cods (Gadiformes)—well within Percomorpha as the sister lineage of the pufferfishes¹⁹. In addition, molecular phylogenies have identified several major lineages of percomorphs that each encompass a large number of species and taxonomic families^{1,21}. As an example, one of these lineages discovered in molecular phylogenetic studies contains such disparate lineages as cichlids, blennies, guppies, flyingfishes, surfperches, and mullets²². Despite this progress, the interrelationships among and within the major lineages of percomorphs and acanthomorphs remain unresolved due to limited informativeness in Sanger DNA sequence datasets and limited taxonomic sampling of previous phylogenomic analyses^{1,4,15,19-23}.

Here, we present the results of comprehensive phylogenomic analyses and estimates of divergence times of 1,084 species representing 308 of the 337 (91.4%) acanthomorph taxonomic families. We additionally sampled nine species from Aulopiformes (lizardfishes), Myctophidae (lanternfishes), and Neoscopelidae (blackchins) to serve as outgroups. Our phylogenomic inferences are based on a DNA sequence alignment of 989 ultraconserved element (UCE) loci and our divergence time estimates were calibrated with 43 fossil constraints. We combine this new acanthomorph time tree with phenotypic data for 680 living acanthomorph species²⁴ to explore the patterns of body shape diversification in spiny-rayed fishes across the K-Pg boundary.

108

109 The maximum likelihood analysis of the concatenated UCE dataset departs from previous
110 efforts by providing confident phylogenetic resolution of nearly all sampled families of
111 acanthomorphs and percomorphs (Fig. 1, 2, Supplementary Figs. 1-25). The UCE phylogeny
112 differs from a phylogenomic analysis of exon capture data in the identification of
113 Paracanthopterygii as monophyletic, the resolution of a clade containing beardfishes (*Polymixia*)
114 and percopsiforms (troutperches, Pirate Perch, and amblyopsid cavefishes), and the placement of
115 Beryciformes (containing Berycoidei and Holocentridae) as the sister lineage of the species-rich
116 Percomorpha (Fig. 1, Extended Data Fig. 1)¹⁵. Our results are consistent with earlier molecular
117 analyses in regard to the resolution of major percomorph clades that each include a large number
118 of taxonomic families^{1,4,15,19-23}. For example, there is strong node support [Bootstrap support
119 (BSS) = 100%] for the percomorph subclade Acanthuriformes²⁵, a monophyletic group
120 comprising more than 2,325 species, including anglerfishes, pufferfishes, butterflyfishes, and
121 scores of other percomorph lineages that long evaded resolution in morphological and molecular
122 analyses (Fig. 2). The relationships among the most inclusive lineages of acanthomorphs inferred
123 from the concatenated datasets are largely corroborated in species tree estimates using coalescent
124 methods from individual gene trees (Supplementary Fig. 26). Exceptions include the placement
125 of codlets (*Bregmaceros*), Beryciformes, and several lineages of Eupercaria whose phylogenetic
126 relationships have historically been difficult to resolve^{1,21}.

127
128 In addition to yielding confident phylogenetic resolution among major lineages and
129 taxonomic families, the maximum likelihood UCE phylogeny reveals novel relationships among
130 some of the most scientifically interesting lineages of percomorph fishes (Figs. 1, 2,
131 Supplementary Figs. 1-25). For example, Sanger sequencing studies led to the discovery that the
132 enigmatic coral reef-dwelling engineer gobies (*Pholidichthys*) are the sister lineage of freshwater

133 cichlids (Fig. 1, Supplementary Fig. 11)^{1,21,22}. Whereas these Sanger analyses provided weak
134 resolution beyond the monophyly of these two lineages, our UCE phylogeny resolves the
135 freshwater tropical African and South American leaffishes (Polycentridae) as the sister lineage of
136 the *Pholidichthys*-cichlid clade (BSS = 100%), providing an opportunity for insight into the
137 evolution of the remarkable species richness and key morphological novelties found in cichlid
138 fishes. We also confidently resolve the near-shore rocky reef dwelling False Scorpionfish
139 (*Centrogenys vaigiensis*) as the sister lineage to a clade of more than 630 species of wrasses and
140 parrotfishes (Labridae; BSS = 100%) (Fig. 2, Supplementary Fig. 21). This newly discovered
141 relationship is not corroborated by the species tree analysis, but consistent with this discovery is
142 that wrasses and *Centrogenys vaigiensis* share ancestral, highly modified components of the
143 “labroid” pharyngeal jaw apparatus²². This result thereby reduces the number of independent
144 evolutions of pharyngognathia, an advanced feeding mechanism that promotes trophic
145 diversification by freeing the oral jaws from prey-processing functions²². The maximum
146 likelihood phylogeny inferred from our UCE dataset provides an important framework for
147 further exploration of the relationships among the most closely related lineages of acanthomorph
148 and percomorph fishes.

149
150 Divergence time estimates for Acanthomorpha, inferred from relaxed molecular clock
151 analyses calibrated with 43 well-justified fossil calibrations, allow for unprecedented resolution
152 of the timing and tempo of family-level lineage diversification. The mean Bayesian posterior age
153 estimates for stem lineages for 80% of living acanthomorph families post-date the K-Pg and are
154 primarily distributed across the Paleocene through the early Miocene (~65 – 15 Mya) (Extended
155 Data Fig. 2). This pattern contrasts with earlier hypotheses of an explosive origin of
156 acanthomorph familial diversity following the K-Pg mass extinction^{4,16}. Plotting the

157 accumulation of acanthomorph family origination times reveals an extended period of lineage
158 origination that persists for approximately 40 million years after the K-Pg (Fig. 2). Although
159 most of the taxonomic families assigned to living acanthomorphs originated in the Paleogene, we
160 detect no statistically supported mass extinctions or tree-wide shifts in lineage diversification
161 rates, indicating an indiscernible effect of the K-Pg on acanthomorph lineage diversification
162 (Extended Data Fig. 3). Moreover, stepping-stone simulations, used to evaluate the relative and
163 absolute fit of competing diversification models to the observed time-calibrated phylogeny,
164 strongly support a constant-rate birth-death model (Extended Data Table 1). Bayesian estimates
165 of the evolutionary rates of individual acanthomorph lineages are similarly homogenous across
166 the K-Pg and through the Cenozoic (Extended Data Fig. 4). We observe increases in speciation
167 rates in only a few percomorph clades, such as branches in the phylogeny leading to Apogonidae
168 (cardinalfishes), Pseudocrenilabrinae (most Middle Eastern and African cichlids),
169 Chaetodontidae (butterflyfishes), the species-rich *Sebastes* (rockfishes), and Lycodinae (a
170 lineage of eelpouts).

171
172 Although lineage diversification rate remained constant through the K-Pg boundary,
173 acanthomorph body shapes began diversifying sharply at the start of the Paleogene into distinct
174 regions of morphospace that correspond to iconic present-day ecomorphological types (Fig. 2,
175 Extended Data Fig. 5, Supplementary Fig. 27). Our analyses of body shape disparity through
176 time, repeated on a sample of 100 trees from the posterior distribution of BEAST time-trees,
177 show that the sudden diversification of acanthomorph body shapes began an average of
178 approximately five million years after the K-Pg (Supplementary Fig. 28). This period of high
179 between-clade phenotypic variation persisted until the early to mid-Eocene (~45 – 40 Mya) (Fig.
180 2). This pattern was not driven by a single clade, but rather occurred across all of

181 Acanthomorpha coincident with the origin of several major lineages (Figs. 1,2, Extended Data
182 Fig. 6a). In contrast, subsequent radiations of acanthomorphs primarily occurred within specific
183 percomorph lineages (Extended Data Fig. 5b, Supplementary Fig. 27). These clades expanded
184 into well recognized ecomorphological types, such as pufferfishes and allies (Tetraodontoiidei),
185 the charismatic seahorses and relatives (Syngnathiformes), a group of open ocean predators
186 (Scombriformes), bottom-dwelling flatfishes, a large clade of deep-bodied laterally compressed
187 reef fishes including surgeonfishes, butterflyfishes and rabbitfishes, and Perciformes, which
188 includes many large-mouthed predators that repeatedly invaded benthic habitats (Extended Data
189 Fig. 5, Supplementary Fig. 27).

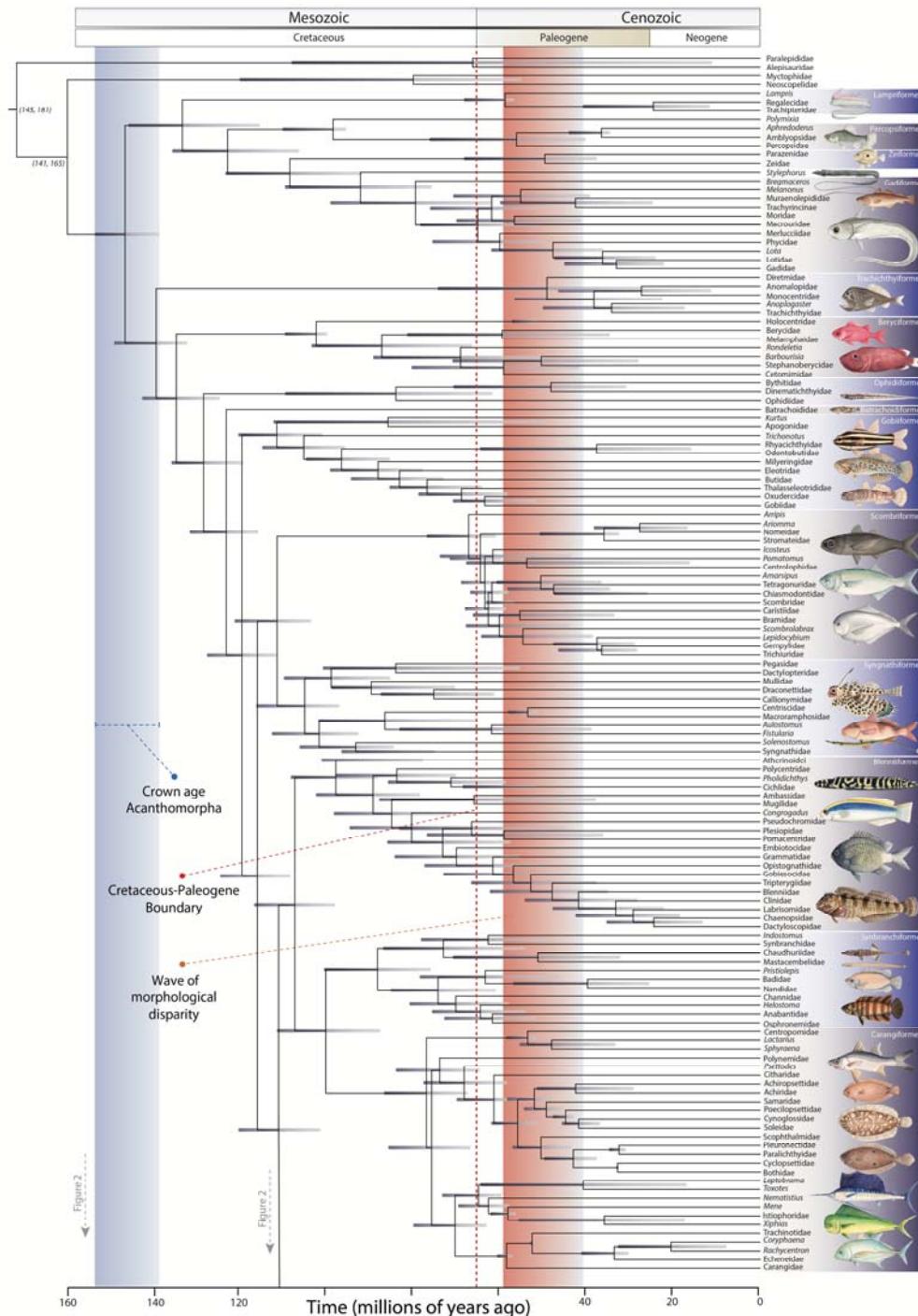
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191 Our estimate of the timing of acanthomorph body shape diversification at the onset of the
192 Paleogene refines inferences from the fossil record. Acanthomorph taxonomic diversity and
193 morphological disparity was low in the Late Cretaceous prior to the K-Pg event, after which
194 body shape disparity and taxonomic diversity became greatly elevated^{14,16}. The timing of this
195 diversification remained unclear due to a scarcity of deposits yielding abundant and well-
196 preserved teleost skeletons between the Campanian-Maastrichtian (~72 Mya) in the Late
197 Cretaceous to the Paleocene-Eocene boundary (~56 Mya)^{14,16}. Though isolated acanthomorph
198 otoliths are known throughout this interval, they remain little studied relative to those from
199 Eocene and younger deposits²⁶. Our analyses provide the precision lacking in the fossil record,
200 revealing that the disparity observed in early Cenozoic fossil acanthomorphs was likely the
201 product of an extended period of phenotypic diversification that began approximately 60 Mya
202 and lasted approximately 15-20 Myr. The initiation of a steady accumulation of living
203 acanthomorph families and morphological disparity following the K-Pg extends through much of

204 the acanthomorph fossil gap (Fig. 2), demonstrating that the rise of acanthomorph diversity in the
205 early Eocene was not punctuated¹⁶.

206
207 The prolonged expansion of morphological variation following the K-Pg was dominated
208 by divergences in body elongation between clades (Extended Data Fig. 5a, Extended Data Fig.
209 6b,c), a phenotypic trait that has adaptive consequences. Body elongation is a primary axis of
210 body shape variation in freshwater and marine fishes^{24,27} that is often coupled with habitat
211 transitions between pelagic, demersal and fully benthic habitats²⁸, including in the aftermath of
212 the K-Pg extinction²³. Our observations of diversification in body elongation shortly after the K-
213 Pg is therefore likely correlated with niche divergence along the benthic-pelagic axis. This
214 pattern of morphological diversification is consistent with the classic trend in phenotypic
215 evolution during adaptive radiation¹⁷, although it was not accompanied by changes in lineage
216 diversification rate. Nonetheless, our results imply that conditions in the aftermath of the global
217 K-Pg event promoted exceptional morphological diversification perhaps in response to the novel
218 landscape of ecological opportunity that took shape during the Paleogene¹³.

219
220 Our results provide a new perspective to the role of the K-Pg as a catalyst of vertebrate
221 diversification by demonstrating that its effects on acanthomorph lineage diversification rates
222 and disparity were decoupled. Although there is no indication that acanthomorph lineage
223 diversification rates increased near the K-Pg, much less explosively (Extended Data Fig. 3), the
224 time following the K-Pg undoubtedly played a critical role in increasing taxonomic diversity and
225 shaping the ecomorphological disparity of the vast majority of living spiny-rayed fishes (Fig. 2
226 and Extended Data Fig. 2). The approximately 15-20 Myr period following the K-Pg brought
227 about the origin of ecomorphological types that acted as a reservoir of diversity, setting the stage

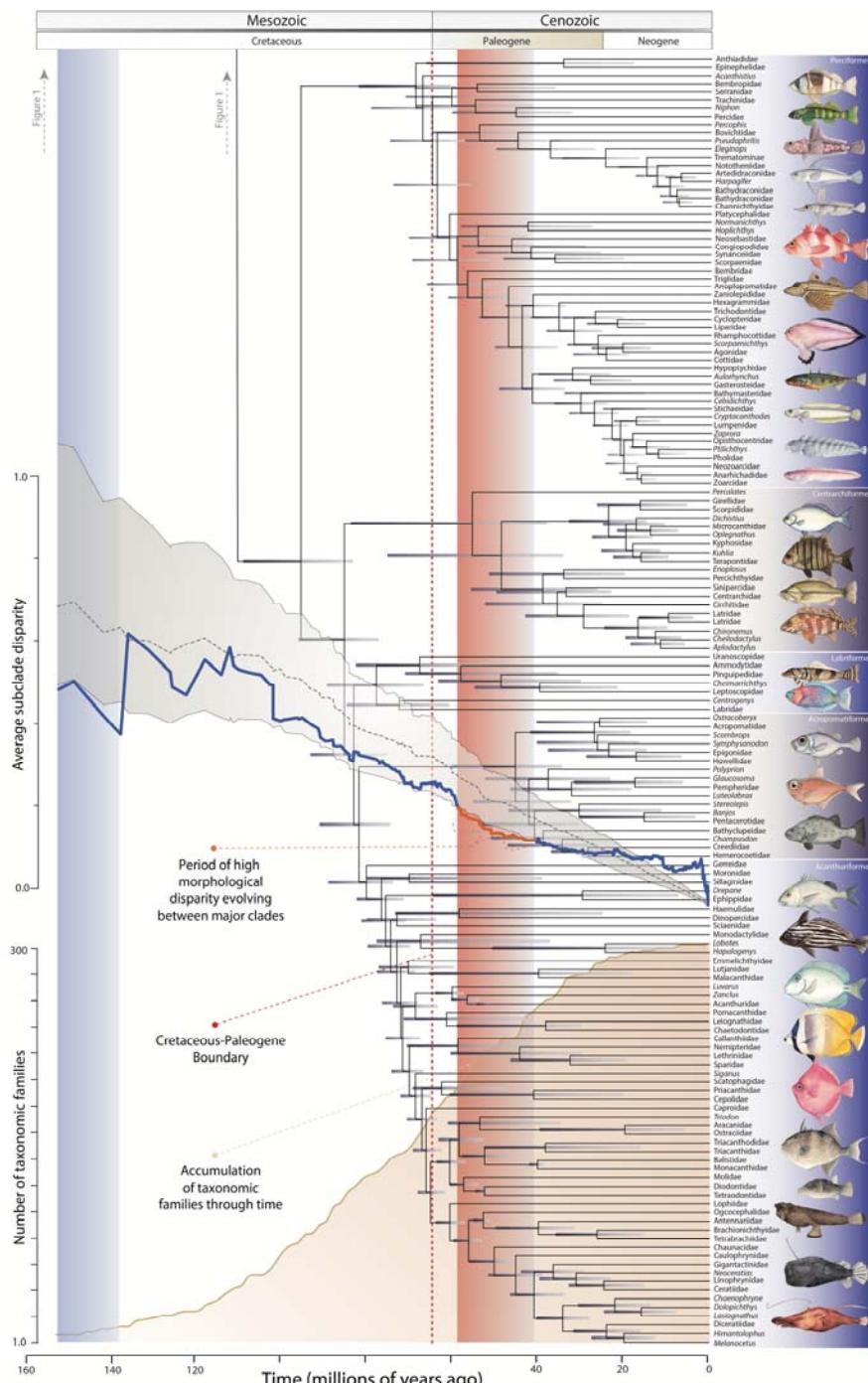
228 for more recent, phylogenetically or geographically localized radiations, including endothermic
229 open-ocean tunas, Antarctic notothenioids, parrotfishes on modern coral reefs, and African Rift
230 Lake cichlids²⁹⁻³². Though the decoupling of lineage and phenotypic diversification in
231 Acanthomorpha contradicts commonly invoked expectations of adaptive radiation¹⁷, this pattern
232 is evident in the evolutionary dynamics of other vertebrate adaptive radiations following the K-
233 Pg, including birds and placental mammals^{5,8,33,34}. Our findings illuminate the origin of
234 phenotypic diversity that characterizes the dominance of acanthomorph fishes in modern marine
235 habitats and broadens our understanding of adaptive radiation in species-rich vertebrate lineages
236 following the K-Pg mass extinction event.



237

238 **Fig. 1: Time-calibrated phylogeny of Acanthomorpha.**

239 The phylogeny is condensed to represent taxonomic families at the tips. For families containing a
240 single species or genus, the genus name is given at the tip. Shaded tabs to the right of taxon
241 labels identify inclusive taxonomic orders. Horizontal gray bars at each node portray the 95%
242 highest posterior density (HPD) of node age estimates. The blue shaded region reflects the 95%
243 HPD of the crown age of Acanthomorpha. Maximum likelihood bootstrap support values for
244 relationships are in Supplementary Figs. 1-25. The time-calibrated phylogeny continues in Fig. 2.



245

246 **Fig. 2: Time-calibrated phylogeny and disparity and lineage accumulation through time for**
247 **Acanthomorpha.**

248 Time-calibrated phylogeny condensed to represent taxonomic families at the tips (continued
249 from Fig. 1). The solid blue line (middle plot) shows observed morphological disparity through
250 time (DTT) and the red portion of the line represents the significant increase in among-clade
251 disparity in the early Eocene. The dashed black line and surrounding gray envelope represent the
252 median DTT and 95% confidence interval under Brownian evolution, respectively. The lower
253 plot estimates the cumulative number of taxonomic families through time. A vertical red dashed
254 line marks the K-Pg boundary.

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347

348 **Methods**

349
350 Detailed descriptions of all procedures are available in the Supplementary Information.
351

352 **Taxon sampling and procurement of sequence data**

353 This study incorporates ultraconserved element (UCE) sequence data from 1,109 specimens,
354 including nine outgroup taxa and 1,075 acanthomorph species spanning 308 recognized,
355 taxonomic families in Acanthomorpha (Supplementary Table 1). We generated new sequence
356 data from 647 specimens representing 628 species of acanthomorphs and six outgroups. We
357 extracted DNA from muscle or fin tissue following the standard protocol for Qiagen's DNeasy
358 Blood and Tissue kits. We prepared dual-indexed DNA libraries and targeted the 1,314 UCE loci
359 enriched by the myBaits UCE Acanthomorph kit from Arbor Biosciences⁴. Enriched libraries
360 were sequenced on Illumina HiSeq platforms in 2 × 150 bp paired-end runs. UCE data for 360
361 specimens came from five previous phylogenomic studies (Supplementary Table 1), and UCE
362 sequences for 96 species were extracted from whole genome shotgun sequence data published in
363 the NCBI GenBank^{35,36}

364

365 **Data processing and phylogenetic analyses**

366 We used the PHYLUCE^{35,36} computer package to process raw read data, conduct de novo
367 assembly and construct alignments of UCE loci. We generated two separate alignments of UCE
368 loci present in at least 75% of the samples: one consisting of all 1,109 specimens (1,084 species)

369 and another including only a subset of the 702 species that overlapped with the taxon sampling
370 of a previously published morphological dataset. The 1,084- and 702-taxon alignments consisted
371 of 987 loci (383,250 bp) and 989 loci (499,957 bp), respectively.

372

373 Using these two 75% complete data matrices, we conducted multiple phylogenetic analyses
374 using maximum likelihood methods in IQ-TREE v. 1.7³⁷ and RAxML-ng v. 0.9.0³⁸. We
375 topologically constrained the divergence time analyses represented in Figure 1 with phylogenies
376 inferred in IQ-TREE using single-partition alignments of the 702 taxa and 1,084 taxa datasets.
377 Both of these tree searches assumed the GTR+Gamma model of molecular evolution and used
378 ultrafast bootstrap approximation to generate 1,000 bootstrap replicates and 1,000 replicates of
379 the Shimodaira-Hasegawa approximate likelihood ratio test (SH-aLRT). We used the program
380 TOPD_v4.6³⁹ to ensure the phylogenies inferred using different partitioning schemes and
381 maximum likelihood programs presented similar tree topologies.

382

383 We also used IQ-TREE's ModelFinder Plus and ultrafast bootstrap approximation options to
384 infer maximum likelihood gene trees for each UCE locus. In TreeShrink⁴⁰, we used a false
385 positive tolerance rate parameter (alpha) of 0.05 to identify and remove potentially aberrant
386 sequences from the single-gene alignments. We re-aligned filtered alignments using
387 MAFFTv7.130b⁴¹ and used them to repeat inference of gene trees in IQ-TREE. We employed
388 the resulting gene trees to generate a summary species tree in ASTRAL-III v5.6.3⁴².

389

390 We applied Bayesian methods to understand the degree of topological discordance along the
391 backbone of the Acanthomorph tree. We inferred gene trees for UCE loci with Bayesian methods

392 for an 82-taxon alignment that represented the major acanthomorph subclades and was generated
393 using MAFFT. We ran these tree searches in MrBayes v. 3.2.7⁴³ for 2 million generations,
394 assuming a GTR+Gamma model of molecular evolution. Using an alpha value of 1.0, we
395 estimated genome-wide concordance factors in BUCKy⁴⁴ as a measure of the amount of
396 topological discordance between these Bayesian gene trees.

397

398 **Divergence time estimation**

399 We estimate divergence times for the 702- and 1,084-taxon phylogenies in BEAST v.2.5⁴⁵⁻⁴⁷ using
400 reduced datasets of randomly subsampled UCE loci^{29,48}. For both phylogenies, we repeated
401 dating analyses on three different alignments of 30 loci. For each of these alignments, we
402 accounted for site-specific variation in evolutionary patterns by selecting the best-fit partitioning
403 schemes using PartitionFinder2 v. 2.1.1⁴⁹. We performed at least three replicate analyses for each
404 30-locus dataset. We ran all BEAST analyses under a relaxed lognormal clock model and a birth-
405 death tree model, using the IQ-TREE phylogenies inferred from the single-partition, 702-taxon
406 and 1,084-taxon alignments as topological constraints. We used forty-three fossil constraints
407 (detailed in the Supplementary Information) to assign minimum age priors and ran BEAST
408 analyses for a minimum of 200 million generations after discarding a burnin of 200 million
409 iterations. We used Tracer v.1.7.1⁵⁰ to assess convergence of parameters across replicate MCMC
410 chains and ensure there were no directional trends in parameter estimates. For each set of random
411 loci, we combined replicate analyses in LogCombiner and constructed maximum clade
412 credibility (MCC) trees using TreeAnnotator in BEAST v1.8.4⁵¹, with summarized node heights
413 rescaled to reflect the posterior median heights. MCC trees for the 702-taxon datasets were

414 summarized from 10,000 post-burnin, randomly sampled trees, while MCC trees for the 1,084-
415 taxon datasets were summarized from 1,200 such trees.

416

417 **Diversification rate analyses**

418 We removed all outgroup and duplicate taxa from the 1,084 taxa maximum clade credibility tree
419 displaying the highest effective sample size (ESS) and used this pruned tree for all diversification
420 rate analyses. We used TESS⁵² to conduct stepping-stone simulations that estimated the marginal
421 likelihoods of eight birth-death models, allowing us to calculate Bayes Factors and assess the
422 competing models' relative and absolute fits to the time-calibrated phylogeny of
423 Acanthomorpha. We examined tree-wide speciation, extinction, and net-diversification rates
424 using TESS's CoMET model. For this analysis, we accounted for our incomplete sampling,
425 specified a uniform sampling strategy, and ran three replicate reversible-jump MCMC chains
426 until ESS values were ≥ 200 . CoMET runs were checked for within- and between-analysis
427 convergence of the diversification rate parameters as described in the Supplementary
428 Information. Using the same time-calibrated phylogeny, we also inferred rate heterogeneity
429 across lineages using BAMM v.2.5.0⁵³. BAMM analyses accounted for the incomplete taxon
430 sampling of taxonomic families and other major representative clades and used empirically
431 determined rate priors identified by the R package BAMMtools v.2.1.6⁵⁴. We ran 23 MCMC
432 chains with different combinations of parameters in BAMM, each for 100 million generations,
433 and we identified the rate shifts along specific branches that were predicted by at least sixteen of
434 these analyses.

435

436

437 **Phylogenetic comparative methods**

438 We pruned a body trait dataset of teleost fishes²⁴ to include maximum body depth, maximum fish
439 width, head depth, lower-jaw length, mouth width, minimum caudal-peduncle depth, and
440 minimum caudal-peduncle width for the 680 species that matched the species represented in the
441 702-taxon UCE phylogeny. To correct for body size, we regressed log-transformed trait values
442 against log-transformed standard fish lengths and calculated phylogenetic residuals in
443 PHYTOOLS⁵⁵. We assessed disparity through time using GEIGER⁵⁶ and the time-calibrated IQ-
444 TREE phylogeny. We repeated disparity through time analyses on 100 randomly sampled time
445 trees from the posterior distribution generated in BEAST, and summarized the mean and 95%
446 confidence interval for the 1.0 My time interval after the K-Pg during which average subclade
447 disparity first dropped below the value simulated under Brownian evolution, as well as the
448 proportion of trees through time that strayed from the Brownian prediction. We tested the
449 sensitivity of disparity through time analyses to the exclusion of body shape traits and of major
450 clades that arose immediately around the K-Pg boundary. Finally, we used PHYTOOLS to
451 visualize body shape morphospace using principal component analysis (PCA) and to generate
452 phenograms that visualize the evolutionary histories of the following seven major lineages:
453 Carangiformes, Lophioidei, Perciformes, Scombriformes, “Squamipinnes” (the clade in
454 Supplemental Fig. 23 defined by *Chaetodon kleinii* and *Luvarus imperialis*), Syngnathiformes
455 and Tetraodontoidei.

456

457 **Code availability**

458 Computer code for analyses can be obtained from the authors upon request.

459

460 **Data availability**

461 Alignments used to perform the analyses in this manuscript are available upon request. NCBI
462 BioSample Accession numbers corresponding to sequence data are listed in Supplementary
463 Table 1.

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529

530

531 **Acknowledgements**

532
533 We thank Julie Johnson for the fish illustrations in Figs. 1,2 and Supplementary Fig. 29, and the
534 numerous undergraduate and graduate researchers from the University of California, Davis and
535 Clemson University that helped collect morphological data. Portions of this research were
536 conducted with high performance computational resources provided by Louisiana State
537 University (<http://www.hpc.lsu.edu>). We are grateful to the ichthyology curators and staff of the
538 following collections for granting access to the tissues and specimens that made this study
539 possible: Smithsonian National Museum of Natural History (Washington, D.C.), University of
540 Florida Museum of Natural History (Gainesville), Scripps Institution of Oceanography (La
541 Jolla), South African Institute for Aquatic Biodiversity (Grahamstown), Southeastern Louisiana
542 University Museum of Biology (Hammond), American Museum of Natural History (New York),
543 Australian Museum (Sydney), Academy of Natural Sciences (Philadelphia), Field Museum of
544 Natural History (Chicago), California Academy of Sciences (San Francisco), Cornell University
545 Museum of Vertebrates (Ithaca), University of Tennessee David A. Etnier Ichthyological
546 Collection (Knoxville), Burke Museum of Natural History and Culture (Seattle), Academia
547 Sinica, Biodiversity Research Museum (Taipei), Natural History Museum and Institute (Chiba),
548 Australian National Fish Collection (Hobart), Kyoto University Museum, Mie University Fish
549 Collection of the Fisheries Research Laboratory (Shima), Hokkaido University Museum
550 (Sapporo), Illinois Natural History Survey (Champaign), Kagoshima University Museum

551 (Korimoto), University of Kansas Biodiversity Institute (Lawrence), Natural History Museum of
552 Los Angeles County, Universidade Estadual Paulista (São Paulo), Louisiana Museum of Natural
553 History (Baton Rouge), Harvard Museum of Comparative Zoology (Cambridge), Museo
554 Nacional de Ciencias Naturales (Madrid), Museo Nacional de Historia Natural (Santiago), North
555 Carolina Museum of Natural Sciences (Raleigh), National Museum of Natural History (New
556 Delhi), Museum of New Zealand Te Papa Tongarewa (Wellington), Museum Victoria
557 (Melbourne), National Museum of Nature and Science (Tokyo), Museums and Art Galleries of
558 the Northern Territory (Darwin), University of Tokyo Ocean Research Institute, Queensland
559 Museum (Brisbane), Royal Ontario Museum (Toronto), Seikai National Fisheries Research
560 Institute (Nagasaki), Universitetsmuseet i Bergen (Hordaland), University of Copenhagen
561 Zoological Museum, and Peabody Museum of Natural History (New Haven).

562

563 **Funding**

564 Authors were independently funded by the National Institute of Health Predoctoral Training
565 Program in Genetics T32 GM 007499 (to AG), the Bingham Oceanographic Fund maintained by
566 the Peabody Museum of Natural History, Yale University (to TJN), the Australian Research
567 Council DECRA Fellowship DE170100516 (to PFC), startup funds from Louisiana State
568 University (to BCF), and the following National Science Foundation grants: NSF DEB-1556953
569 (to SAP and PCW), NSF DEB-1655624 (to BCF), NSF DEB-1701323 (to PC and WBL), NSF
570 DEB-1830127 (to SAP), NSF DEB-1839915, and NSF IOS-1755242 (to AD).

571

572

573

574 **Author contributions**

575
576 The project was conceived and designed by TJN, AG, RCH, JRG, BCF, and PCW. AG, RCH,
577 JRG, MAC, JCB, WTM, WBL, BCF, PFC and TJN organized and executed the collection of
578 UCE sequence data. SAP, SFT, and PCW coordinated and collected morphological data. AG,
579 RCH, BCF, and AD carried out phylogenetic analyses. AG and RCH performed phylogenetic
580 divergence dating analyses, and AG performed analyses of lineage diversification rates. EDB
581 and PCW performed morphological comparative analyses. AG, RCH, AD, and TJN wrote the
582 first draft of the manuscript. All authors contributed to the writing of the final draft of the
583 manuscript.

584

585 **Ethics declarations**

586
587 **Competing interests**

588 The authors declare no competing interests.

589

590 **Additional information**

591
592 **Supplementary Information** is available for this paper.

593 Correspondence and requests for materials should be addressed to ava.ghezelayagh@yale.edu.

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595

596 **Extended data table and figure legends**

597
598 The Extended Data table and figures (with legends) are available in the document labelled
599 ExtendedDataTableAndFigs.pdf, but legends are also provided below.

600

601

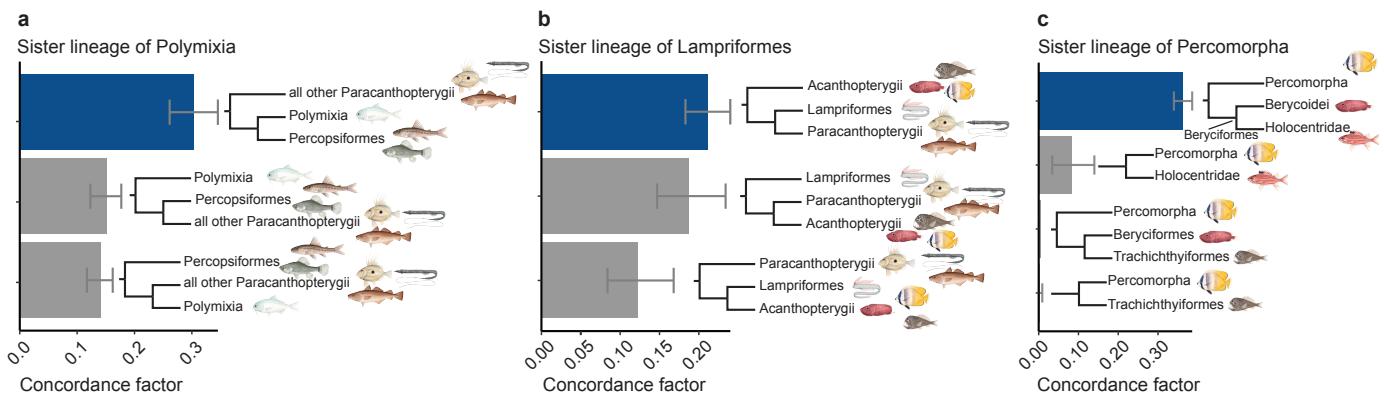
Extended Data Table 1: Pairwise comparisons of 8 birth-death (BD) branching process models.

Model 1 (Null)	Model 2 (Alternative)	2ln(BF)
Constant BD Uniform Sampling	Mass Extinction BD Diversified Sampling	55,487.1
Episodic BD (shift at 50 mya) Uniform Sampling	Mass Extinction BD Diversified Sampling	55,480.7
Decreasing Speciation Rate BD Uniform Sampling	Mass Extinction BD Diversified Sampling	55,477.2
Episodic BD (shift at 50 mya) Diversified Sampling	Mass Extinction BD Diversified Sampling	54,609.6
Decreasing Speciation Rate BD Diversified Sampling	Mass Extinction BD Diversified Sampling	50,634.5
Constant BD Diversified Sampling	Mass Extinction BD Diversified Sampling	49,838.1
Constant BD Uniform Sampling	Mass Extinction BD Uniform Sampling	29,863.0
Episodic BD (shift at 50 mya) Uniform Sampling	Mass Extinction BD Uniform Sampling	29,856.6
Decreasing Speciation Rate BD Uniform Sampling	Mass Extinction BD Uniform Sampling	29,853.1
Episodic BD (shift at 50 mya) Diversified Sampling	Mass Extinction BD Uniform Sampling	28,985.5
Mass Extinction BD Uniform Sampling	Mass Extinction BD Diversified Sampling	25,624.1
Decreasing Speciation Rate BD Diversified Sampling	Mass Extinction BD Uniform Sampling	25,010.4
Constant BD Diversified Sampling	Mass Extinction BD Uniform Sampling	24,214.0
Constant BD Uniform Sampling	Constant BD Diversified Sampling	5,649.0
Episodic BD (shift at 50 mya) Uniform Sampling	Constant BD Diversified Sampling	5,642.6
Decreasing Speciation Rate BD Uniform	Constant BD Diversified Sampling	5,639.1
Constant BD Uniform Sampling	Decreasing Speciation Rate BD Diversified Sampling	4,852.6
Episodic BD (shift at 50 mya) Uniform Sampling	Decreasing Speciation Rate BD Diversified Sampling	4,846.2
Decreasing Speciation Rate BD Uniform Sampling	Decreasing Speciation Rate BD Diversified Sampling	4,842.7
Episodic BD (shift at 50 mya) Diversified Sampling	Constant BD Diversified Sampling	4,771.5
Episodic BD (shift at 50 mya) Diversified Sampling	Decreasing Speciation Rate BD Diversified Sampling	3,975.1
Constant BD Uniform Sampling	Episodic BD (shift at 50 mya) Diversified Sampling	877.5
Episodic BD (shift at 50 mya) Uniform Sampling	Episodic BD (shift at 50 mya) Diversified Sampling	871.1
Decreasing Speciation Rate BD Uniform Sampling	Episodic BD (shift at 50 mya) Diversified Sampling	867.6
Decreasing Speciation Rate BD Diversified Sampling	Constant BD Diversified Sampling	796.4
Constant BD Uniform Sampling	Decreasing Speciation Rate BD Uniform Sampling	9.9
Constant BD Uniform Sampling	Episodic BD (shift at 50 mya) Uniform Sampling	6.4
Episodic BD (shift at 50 mya) Uniform Sampling	Decreasing Speciation Rate BD Uniform Sampling	3.5

TESS calculated Bayes Factors (2ln(BF)) from the pairwise comparisons of marginal likelihoods for 8 birth-death (BD) branching-process models with the following priors: 1.) constant diversification rate with uniform (random) sampling, 2.) constant diversification rate with diversified sampling (i.e. sampling results in even coverage of all clades), 3.) decreasing speciation rate with uniform sampling, 4.)

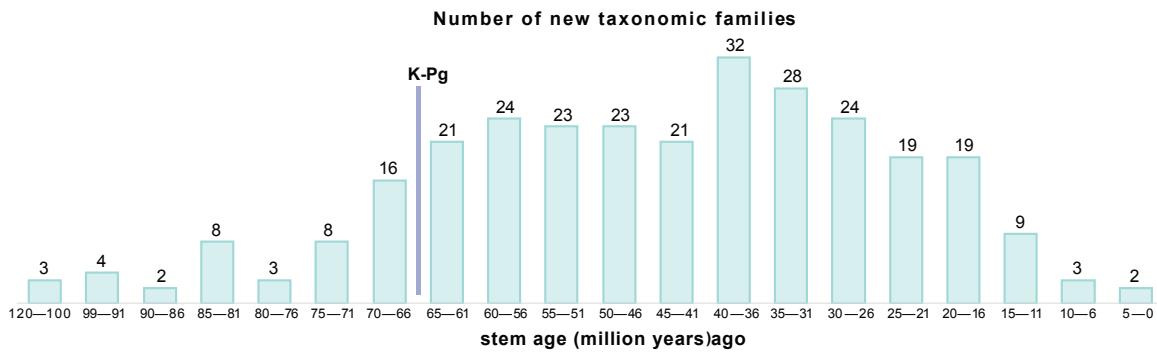
decreasing speciation rate with diversified sampling, 5.) constant diversification rate with a rate shift 50 Mya (“Episodic BD”) with uniform sampling, 6.) constant diversification rate with a rate shift 50 Mya (“Episodic BD”) with diversified sampling, 7.) constant speciation rate with a single mass extinction event occurring at any point in time (“Mass Extinction BD”) with uniform sampling, and 8.) constant speciation rate with a single mass extinction event occurring at any point in time (“Mass Extinction BD”) with diversified sampling. Observations of the pairwise comparisons note strong preference for a model that assumes uniform (random) sampling and strong support for either a constant rate BD model, or an episodic BD model that assumes a shift 50 mya. There is moderate Bayesian support ($2\ln(BF) = 6.4$) that among the models assuming uniform sampling, the constant rate model is preferred over the model with a shift 50 Mya.

Extended Data Fig. 1: Bayesian concordance analyses used to compare alternative phylogenetic hypotheses concerning the sister taxa of 3 major acanthomorph lineages.



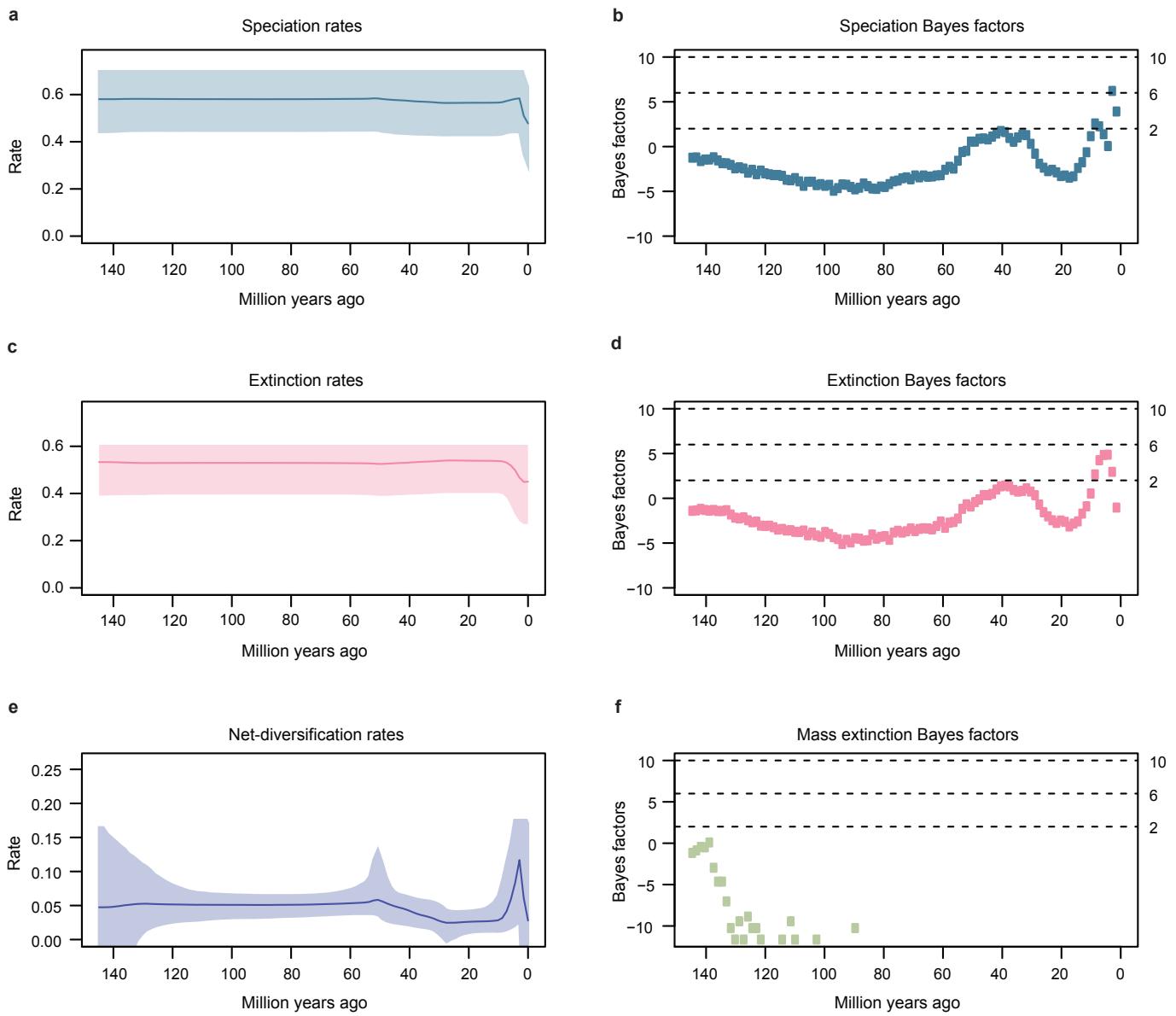
BUCKy-inferred genome-wide concordance factor estimates, with 95% confidence intervals, representing the proportion of gene trees exhibiting alternative topologies among major acanthomorph lineages. Blue bars reflect the concordance factor for the topology inferred in our concatenated analyses (see Figs. 1,2) and gray bars represent concordance factors of alternative topologies not observed in the concatenated phylogeny. **a**, Gene tree concordance for Percopsiformes, Polymixia, and all other Paracanthopterygii; **b**, Lampriformes, Paracanthopterygii, and Acanthopterygii; **c**, Alternative sister lineages of Percomorpha.

Extended Data Fig. 2: Acanthomorphs underwent a long, steady period of increased taxonomic family origination beginning at the K-Pg boundary.



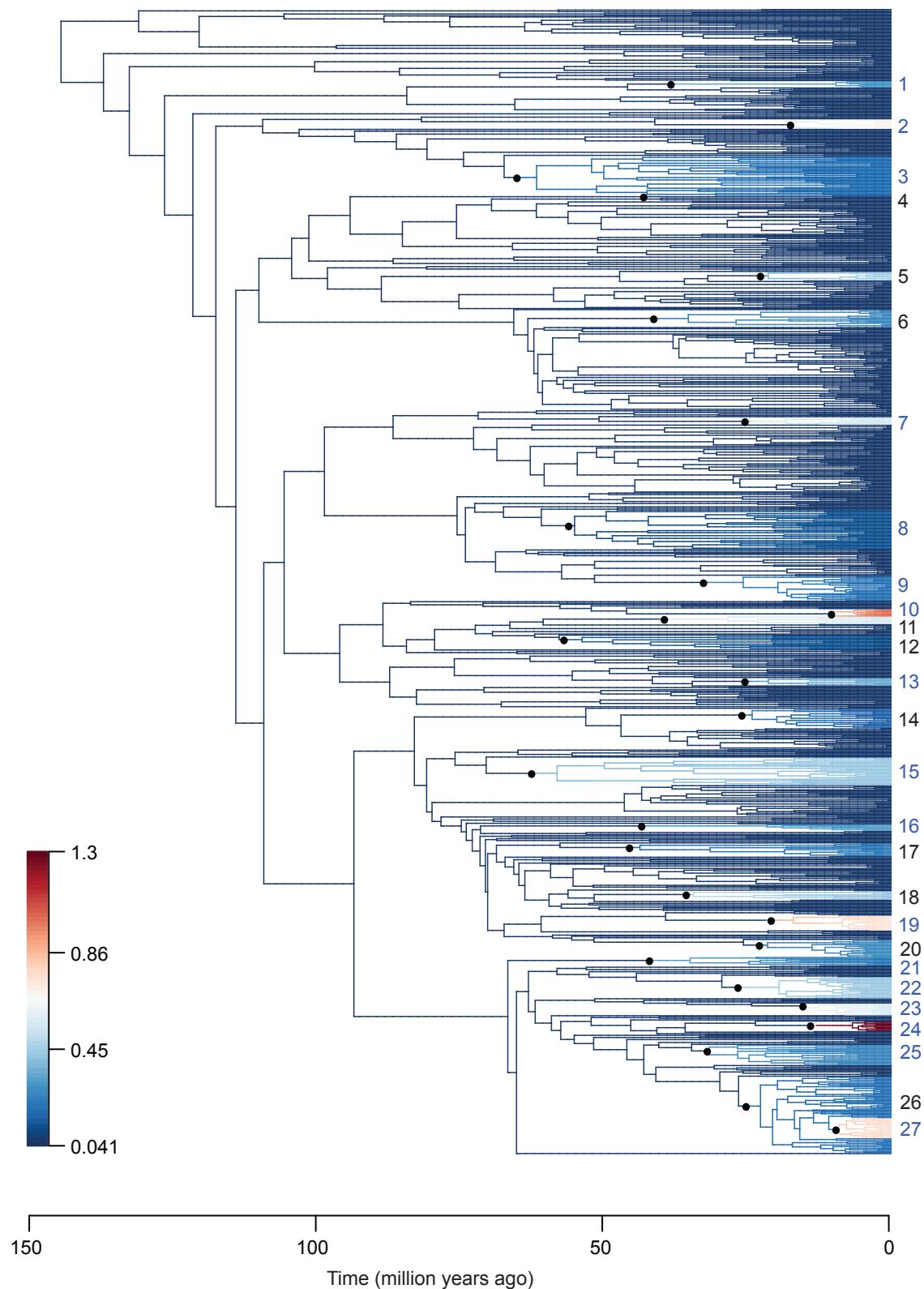
The bar plot of the estimated number of new taxonomic families originating during 5 million year bins. Note that the amounts of time represented by the first two bars are greater than the 5 million years represented by all other bars.

Extended Data Fig. 3: TESS-CoMET analyses indicate constant tree-wide diversification rates through most of the history of Acanthomorpha.



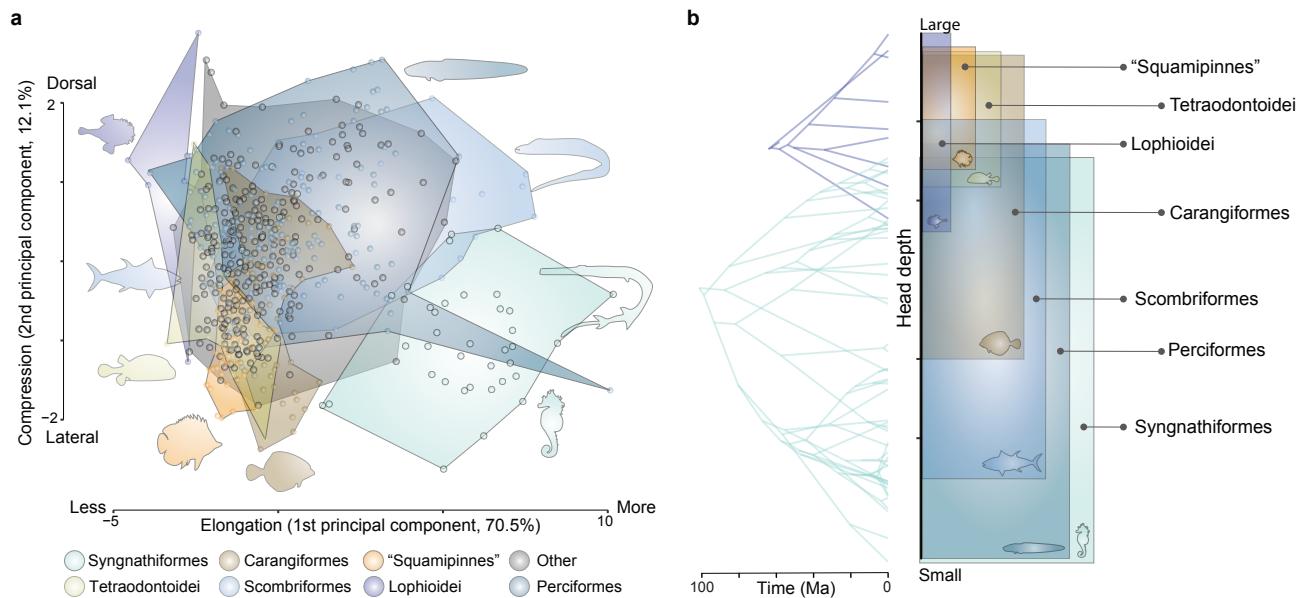
In **b**, **d**, and **e**, horizontal dashed lines and the right-hand y-axis mark statistical support cutoffs for rate shifts, with $2 \leq BF < 6$ considered to be low support, $6 \leq BF < 10$ considered to be moderate support and ≥ 10 considered to be high support. The rate shifts observed in **a**, **c**, and **e** over the last 10 million years are likely an artifact of the CoMET model (see **Supplementary Information** for further discussion). **a**, Speciation rate estimates through time for Acanthomorpha. **b**, Bayes factors (BF) support for a shift in speciation rate at every 1 Myr time period. **c**, Extinction rates through time for Acanthomorpha. **d**, Bayesian support (in Bayes factors) for a shift in extinction rate at every 1 Myr time period. **e**, Net-diversification (speciation minus extinction) rates through time for Acanthomorpha. Though this plot suggests that there is a small shift in net-diversification rate ~ 50 Mya, there is no statistical support for such a shift (see **b** and **d**). **f**, There is no statistical support (in Bayes factors) for a mass extinction event in Acanthomorpha at any 1 Myr time period.

Extended Data Fig. 4: Visual summary of shifts in speciation rates inferred using BAMM.



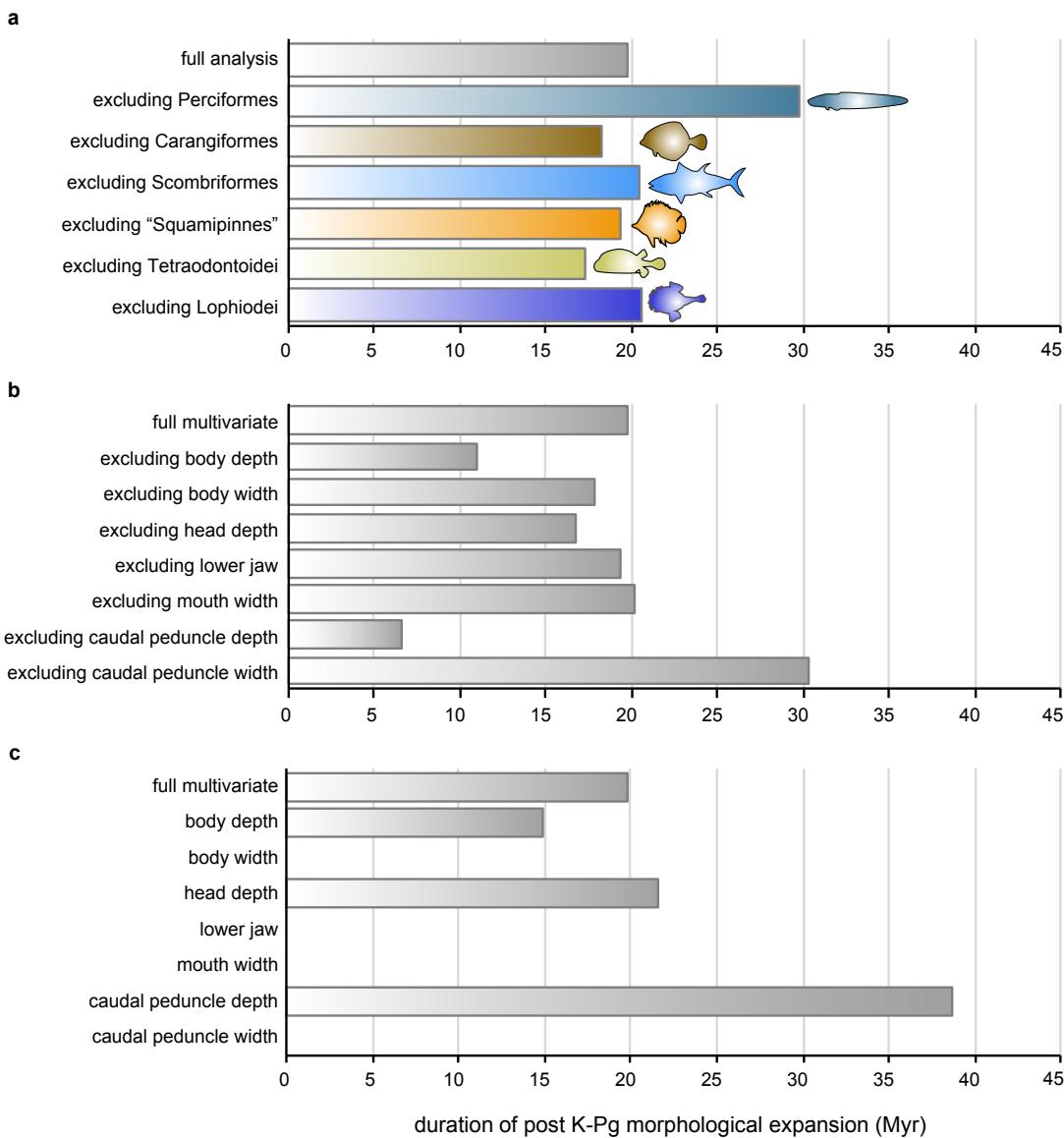
The configuration presented here is the maximum shift credibility (MSC) configuration for an analysis that expected 15 rate shifts under the prior. Darker pink colors depict relatively fast rates, while darker green colors depict relatively slow rates. Rate shifts along branches are denoted with filled, black circles and assigned identifying numbers. Shifts in speciation rate are estimated to have occurred on the branches leading to the following 27 clades: 1.) Dinematichthyidae, 2.) Apogonidae (to the exclusion of Pseudamia), 3.) Gobiidae and Oxudercidae, 4.) Solenostomus, 5.) Parupeneus and Pseudopeneus (in Mullidae), 6.) Ariomma, Nomeidae and Stromateidae, 7.) Mastacembelidae, 8.) the clade defined by Scophthalmidae and Soleidae, 9.) Carangidae (to the exclusion of Seriola), 10.) Pseudocrenilabrinae (in Cichlidae), 11.) Pomacentridae, 12.) the clade defined by Gobiesocidae and Dactyloscopidae, 13.) Poeciliidae, 14.) the clade defined by Scorpididae and Terapontidae, 15.) Labridae, 16.) Sciaenidae, 17.) the clade defined by Nemipteridae and Sparidae, 18.) Tetraodontidae, 19.) Chaetodontidae, 20.) Acanthuridae (to the exclusion of Prionurus and Naso), 21.) Anthiadinae and Epinephelidae, 22.) darters (Etheostomatinae), 23.) the clade defined by “Nototheniidae” and Channichthyidae, 24.) Sebastes, 25.) the clade defined by Trichodontidae and Psychrolutidae, 26.) the clade defined by Stichaeidae and Zoarcidae and 27.) the clade defined by Bothrocara and Lycodes concolor (in Zoarcidae). Shifts labelled with blue rather than black numbers are estimated to have occurred by 16 of the 23 BAMM analyses conducted in this study. Although shift number 20 and shift number 26 are labelled in black, the vast majority of BAMM analyses predicted a rate shift in branches leading to slightly more inclusive clades (specifically Acanthuridae minus Naso, and all of Lycodinae, respectively).

Extended Data Fig. 5: Changes in body elongation and compression.



Patterns of acanthomorph morphological disparification. **a**, The first two principal components of morphospace (elongation and compression), with seven major acanthomorph lineages color-coded by taxon. The proportion of variance explained by PC1 is 70.5% and by PC2 is 12.1%. **b**, Phenogram depicting the evolutionary history of head depth—which often reflects body elongation—across seven major lineages that arose around the K-Pg. Note that all major lineages except Syngnathiformes originate near the K-Pg boundary, but “Squamipinnes”, Lophioidei and Tetraodontoidei have markedly different ancestral trait values from Carangiformes, Scombriformes and Perciformes.

Extended Data Fig. 6: Robustness of DTT analyses.



Effect of individual lineages or body shape traits on the length of the estimated period of between-clade morphological expansion after the K-Pg (i.e., the period in which the observed disparity falls below that expected from a Brownian motion process). There is no single major lineage driving the extended duration of this period of phenotypic diversification, but the body shape traits related to elongation (body depth, head depth, and caudal peduncle depth) have more pronounced contributions to this pattern than the other body shape traits. **a**, Duration of the period of morphological expansion when a single major lineage is excluded from the analysis. **b**, Duration of the period of morphological expansion when data for one of the seven body shape traits in the original analysis is excluded. **c**, Duration of the period of morphological expansion when the DTT analysis is based on a single body shape trait.

1 **1. Supplementary Methods**

2

3 **a. Taxon sampling**

4 The phylogenetic analyses included UCE sequence data sampled from 1,109 specimens that
5 include 1,084 species. For this study, we collected new UCE sequence data from 653 specimens.
6 We retrieved UCE loci from the remaining 456 specimens at NCBI from previous studies of
7 acanthomorph phylogeny^{4,29,48,57,58} or from whole genomic data (Supplementary Table 1). This
8 study included representatives of all currently recognized acanthomorph taxonomic orders, 307
9 of the 331 (92.7%) described taxonomic families of Acanthomorpha and 276 of the 290 (95.2%)
10 families of Percomorpha³. Based on previous phylogenetic analyses^{15,20}, we sampled two species
11 of Aulopiformes and seven species of Myctophiformes as outgroups for the phylogenetic
12 analyses: *Notolepis coatsi*, *Alepisaura ferox*, *Scopelengys tristis*, *Neoscopelus macrolepidotus*,
13 *Neoscopelus microchir*, *Dasyscopelus selenops*, *Benthosema glaciale*, *Notoscopelus*
14 *caudispinosus*, and *Ceratoscopelus warmingii*. We sampled phenotypic data from 680 of the
15 1,075-acanthomorph species sampled in the UCE inferred phylogeny. We inferred phylogenies
16 from the UCE dataset for an inclusive taxon sampling of 1,084 species and for a set of 702
17 species that included the 680 for which corresponding morphological data was obtained. We
18 refer to these UCE datasets and resulting phylogenies as the 1,084 and 702 species datasets and
19 trees, respectively.

20

21 **b. Library preparation, target enrichment, and sequencing**

22 We isolated DNA from tissue biopsies using Qiagen DNeasy Blood and Tissue kits following the
23 manufacturer's protocol. We used a Qubit fluorometer (Life Technologies) to quantify 1-2 uL of
24 all DNA extractions. We sheared approximately 500 ng of genomic DNA from each sampled
25 specimen using a QSonica Q800R3 sonicator to obtain fragment sizes between 300-600 bp. For
26 library preparation and target enrichment of UCE loci, we followed protocols described in a
27 previous study⁴ using Kapa HyperPrep kits (Kapa Biosystems) and Illumina TruSeq iTru5 and
28 iTru7 adapters for dual indexing of genomic libraries⁵⁹. We used a bait set from Arbor
29 Biosciences designed to target 1,314 UCE loci in acanthomorph fishes for target-enrichment of
30 UCE loci⁴. Enriched libraries were sequenced using 150 bp paired-end sequencing on Illumina
31 HiSeq platforms.

32 **c. Assembly and alignment construction**

33 To process raw read data, construct assemblies, identify UCE sequences, and construct
34 alignments for each UCE locus, we used the PHYLUCE computer package^{35,36}, which uses
35 parallel wrapper functions around external programs to perform tasks required to process high-
36 throughput DNA sequence data. We used the illumiprocessor parallel wrapper program
37 (<https://github.com/faircloth-lab/illumiprocessor>) to implement Trimmomatic⁶⁰, which removes
38 adapter index sequences and low-quality bases from demultiplexed raw reads. We constructed
39 assemblies for each sample using *trinity* v.r2013-02-25⁶¹ and used the PHYLUCE program
40 *phyluce_assembly_match_contigs_to_loci.py* to identify which assembled contigs represented
41 UCE sequences by matching them to a FASTA file containing the UCE bait sequences.

42 To supplement these sequence data, we extracted UCE loci from existing genomes of 96
43 species (Supplementary Table 1). We downloaded genomes from NCBI and converted to 2bit
44 format using faToTwoBit from the UCSC Genome Browser Downloads
45 (<https://hgdownload.cse.ucsc.edu/admin/exe/>). Then, we located UCE loci in each genome
46 assembly by running the PHYLUCE program *run_multiple_lastzs_sqlite.py* with default
47 parameters and the FASTA file containing the UCE bait sequences. We extracted from each
48 assembly identified UCE loci along with ± 500 bp of sequence from each flank using
49 *phyluce_probe_slice_sequence_from_genomes.py* with default parameters. We used PHYLUCE
50 to run *match_contigs_to_loci.py* against the extracted loci, before the UCE data harvested from
51 genome assemblies were integrated with the UCE loci enriched from libraries.

52 We integrated these two data sets and used PHYLUCE programs to infer a separate set of
53 alignments and phylogenies for the 702 species including the sampling of morphological data
54 and the full 1,109 specimen sampling using the same protocols. We generated alignments for
55 each UCE locus using MAFFT v7.130b⁴¹ and trimmed with trimAL v1.4.rev⁶². For further
56 downstream phylogenetic analyses, we retained UCE loci that included at least 75% of the total
57 specimens in both the 1,084 and 702 species datasets.
58

59 **d. Phylogenetic analyses**

60 We inferred phylogenies for both the 1,084 and 702 species datasets using maximum likelihood
61 methods as implemented in IQ-TREE v. 1.7³⁷ and RAxML-ng 0.9.0³⁸. In IQ-TREE, we ran tree
62 searches using ultrafast bootstrap approximation until 1,000 bootstrap replicates and 1,000

63 replicates of the Shimodaira-Hasegawa approximate likelihood ratio test (SH-aLRT) were
64 generated⁶³. Phylogenies inferred in IQ-TREE using the unpartitioned alignments described
65 above served as the topological constraints for subsequent divergence time analyses. Maximum
66 likelihood tree searches conducted in IQ-TREE used the ModelFinderPlus⁶⁴ option, which
67 applies a relaxed hierarchical clustering search algorithm to determine partitioning schemes and
68 models of molecular evolution.

69 Before conducting analyses in RAxML-ng v0.9.0³⁸, we determined partitioning schemes
70 using PartitionFinder2 v2.1.1⁴⁹, with units of partitioning based on individual UCE loci. We
71 identified these partitioning schemes using a relaxed hierarchical clustering search algorithm
72 with a maximum cluster size set to 1000 data blocks, the Bayesian Information Criterion method
73 for partition model comparison, and GTR+Gamma as the model of molecular evolution. We
74 removed all fully undetermined columns from our partitioned, concatenated alignment using
75 RAxML-ng, compressed the alignment, and converted to binary. We performed maximum
76 likelihood tree searches on these alignments using the extended majority rule criterion method
77 implemented with the autoMRE command to continue bootstrapping until convergence.

78 We compared the tree topologies inferred in the concatenated analyses described above
79 using the program TOPD_v4.6³⁹. Phylogenies based on the 1,084 species dataset (IQ-TREE
80 single-partition, IQ-TREE multiple partitions, and RAxML-ng multiple partitions) were
81 compared to one another, and separate analyses compared the three phylogenies inferred from
82 the 702 species dataset. We utilized TOPD to calculate partition metrics, i.e., TOPD's "Split"
83 method⁶⁵, and path length metrics, i.e., TOPD's "Nodal" method⁶⁶. We produced lists of taxa
84 with different phylogenetic positions among the compared trees using TOPD's "Disagree"
85 method, which removes a single taxon at each iteration and calculates the reduction in trees' split
86 distance.

87 We inferred a summary species tree in ASTRAL-III v5.6.3⁴², using maximum likelihood
88 gene trees for each UCE locus generated with IQ-TREE v 1.6.12. For individual gene tree
89 inference, we applied the ModelFinder Plus⁶⁴ option to determine the optimal model of
90 molecular evolution as well as the ultrafast bootstrap approximation with a maximum of 10,000
91 bootstrap iterations. We used TreeShrink⁴⁰ to identify abnormally long branch lengths in the
92 individual UCE gene trees and to minimize the impact of misspecified sequences. We used a
93 false positive tolerance rate parameter (alpha) of 0.05 in our TreeShrink filtering to automate the

94 removal of potentially aberrant sequences from the UCE alignment. We re-aligned the
95 TreeShrink-pruned alignments using MAFFT v7.130b⁴¹ and re-inferred gene trees using IQ-
96 TREE, as above. We used these gene trees to infer a species tree in ASTRAL-III.
97

98 **e. Concordance factor analyses**

99 We used BUCKy⁴⁴ to estimate genome-wide concordance factors, which allows the evaluation
100 of phylogenetic discordance among individual UCE gene trees. We compared alternative
101 phylogenetic hypotheses among the major lineages of Acanthomorpha using these concordance
102 factors. BUCKy estimates the frequency of topological partitions that occur in a sample of
103 Bayesian gene tree posterior distributions and provides an estimate for their genome-wide
104 frequency and 95% confidence intervals. Because the number of possible topological
105 relationships among taxa increases non-linearly as the number of species included in the analysis
106 increases, large taxonomic datasets are intractable for thorough concordance factor analyses with
107 BUCKy. We therefore used a reduced taxonomic dataset of 82 species that represent each of the
108 major subclades of Acanthomorpha to reduce computational burden. For this reduced dataset, we
109 generated alignments of the 82 species using MAFFT (**Supplementary Table 1**). We used
110 MrBayes v. 3.2.7⁴³ to infer a Bayesian gene tree distributions for each UCE locus. We ran
111 MrBayes analyses with a GTR+Gamma molecular evolutionary model for 2 million generations,
112 with trees sampled every 2,000 generations. Using the BUCKy program mbsum, we discarded
113 the first 75% of sampled trees from the posterior sample of each UCE locus as burnin,
114 summarized branching patterns in the remaining post-burnin posterior distribution, and used an
115 alpha value of 1.0 for concordance factor estimation. These gene tree posterior distributions were
116 then used for subsequent BUCKy estimation of concordance factors.
117

118 **f. Divergence-time estimation**

119 We estimated divergence times for both the 702 and 1,084 species phylogenies using BEAST
120 v.2.5⁴⁵ following a protocol used in other UCE studies where BEAST analyses were run using
121 reduced datasets of 30 UCE loci^{29,48,67}. We constrained the phylogeny used in the BEAST runs
122 using the IQ-TREE analyses of the 1,084 and 702 species datasets. For both the 1,084 and 702
123 species datasets, we performed BEAST analyses on three different sets of 30 loci, each randomly
124 drawn without replacement from the entire set of ~1,000 UCE loci. Exploratory BEAST analyses

125 using sets of 25 and 50 loci yielded similar divergence time estimates, justifying the moderately
126 computationally expensive analyses using the 30 locus datasets. For each subset of 30 loci, we
127 determined the optimum partitioning scheme using the relaxed hierarchical clustering algorithm
128 in PartitionFinder2 v. 2.1.1⁴⁹. For divergence dating analyses performed in BEAST, we
129 employed a relaxed lognormal clock model and a birth-death tree model. We assigned minima
130 for age priors using forty-three fossil occurrences, described below. For each 30-locus dataset,
131 we ran at least three replicate analyses for a minimum of 200 million generations beyond a total
132 burnin of 200 million generations. As MCMC chains progressed, we accepted suggestions
133 provided by BEAST for improving operators' tuning parameter values. We used Tracer v.1.7.1
134 to observe effective sample size (ESS) values for posterior parameter estimates, to assess
135 convergence among replicate MCMC chains, and to check for directional trends in parameter
136 estimates⁵⁰. Though the large size of the phylogenies created computational limits that resulted in
137 moderate ESS values for some parameters, most parameter estimates reached ESS values well
138 above 200. Some analyses were run up to 900 million generations in length to obtain adequate
139 ESS values and ensure no directional trends in and unimodal distributions of parameter
140 estimates. We used LogCombiner in BEAST v.1.8.4^{51,68} to remove a burnin, and trees from each
141 replicate run were randomly thinned. We thinned the sets of 1,084-species trees such that a total
142 of 1,200 trees would remain across all runs, with an equal number of trees from each replicate
143 contributing to the final summary trees. We randomly thinned the sets of 702-species trees such
144 that 10,000 total trees remained across replicate runs. For each set of loci, we used LogCombiner
145 to combine trees from replicate runs and TreeAnnotator in BEAST v.1.8.4 (Drummond et al.
146 2012) to estimate maximum clade credibility trees.
147

148 ***g. Diversification rate analyses***

149 We performed diversification rate analyses on the time-calibrated 1,084-taxon phylogeny that was
150 run for the most generations and therefore had the highest ESS values for posterior parameter
151 estimates. Species diversity of acanthomorph lineages used to determine sampling fractions for
152 all diversification rate analyses were based on numbers of species presented in Eschmeyer's
153 Catalog of Fishes³, which at the time of the analyses included 19,219 species of Acanthomorpha.
154 We removed all outgroups and duplicate samples of the same species before performing
155 diversification rate analyses, leaving a phylogeny consisting of 1,075 acanthomorph species and

156 a sampling fraction of 0.056. We performed stepping-stone simulations within TESS⁵² to
157 estimate the marginal likelihoods of eight birth-death models and evaluate their fit to the
158 acanthomorph time-calibrated phylogeny. Competing models included those with constant
159 diversification rates, with episodically changing rates, or with decreasing speciation rates.
160 Variants of the constant rate model with and without a mass extinction event were also tested to
161 assess the potential impact of the K-Pg mass extinction on acanthomorph diversification. We
162 tested variants of the competing models that accommodated the effects of incomplete taxon
163 sampling by correcting for uniform (random) or diversified sampling methods.

164 Using the simulated marginal likelihoods of candidate models, we calculated Bayes
165 factors and compared the relative fits of models to the acanthomorph phylogeny (Extended Data
166 Table 1). With the exception of the models assuming a decreasing speciation rate, we ran
167 stepping-stone simulations for 10,000 iterations with 1,000 power posteriors (stepping stones)
168 and a burn-in period of 3,000 generations. Due to limited computational resources, we ran the
169 simulations of marginal likelihoods for the decreasing speciation rate (i.e., continuous) models
170 for 2,000 iterations (a burn-in of 500 generations was removed) with 100 power posteriors. This
171 test of relative model fit greatly favored models assuming uniform (random) sampling methods
172 over diversified methods (Extended Data Table 1), informing our model selection in downstream
173 TESS analyses.

174 We extracted the three branching process-models that were most favored in the tests of
175 relative model fit and assessed their absolute fit to the acanthomorph phylogeny using posterior-
176 predictive simulations. We compared the predictive distributions of the gamma statistic, number
177 of taxa, and lineage-through-time (LTT) plots to the empirical estimates.

178 We inferred the global speciation, extinction and net-diversification rates through time
179 using the CoMET model as employed by TESS. For CoMET analyses represented in Extended
180 Data Fig. 2, we specified a uniform (random) sampling strategy ($\rho = 0.056$), conditioned the
181 model on taxa survival, discarded a burn-in of 30,000 iterations, and ran three replicate
182 reversible-jump MCMC chains until the effective sample size (ESS) reached 200 or greater. We
183 assessed convergence within each CoMET run by calculating the effective sample sizes and
184 Geweke diagnostics for the diversification rate, and we assessed convergence of multiple runs
185 using the Rubin-Gelman test.

186 We inferred global diversification rates and examined rate heterogeneity across clades
187 using BAMM v.2.5.0⁵³. Our analyses corrected for incomplete sampling by accounting for the
188 sampling fractions of 304 major representative clades, most of which are taxonomic families, in
189 accordance with the number of species described by Eschmeyer's Catalog of Fishes³. We also
190 used the information on species diversity to appropriately adjust these clade-specific sampling
191 fractions for non-monophyletic taxonomic groups. As in the TESS analyses, we set the global
192 sampling fraction for all BAMM analyses to 0.056. We identified appropriate rate priors using
193 the function setBAMMpriors in the R package BAMMtools v.2.1.6⁶⁹, accounting for incomplete
194 taxon sampling.

195 We ran Markov chain Monte Carlo simulations for 100 million generations under the
196 default settings. We also used default settings for MCMC scaling operators and move
197 frequencies. We ran BAMM 23 times, each time under different conditions that might be
198 appropriate for a medium-sized tree consisting of ~1,000 taxa. Runs tested different
199 combinations of numbers of MCMC chains (2 or 4), temperature increment parameters (deltaT =
200 0.05 or 0.1) and expected number of diversification rate shifts (1, 5, 10, 15, 20, 25, 30, 35, 40
201 and 45). We tested the effect of changing the number of expected shifts—despite the
202 setBAMMpriors function in BAMMtools recommending an input of just one expected shift—
203 because preliminary runs suggested that the number of diversification rate shifts is greater than
204 20. For each analysis, we compared Bayes factors for competing prior models with different
205 numbers of expected rate shifts.

206

207 ***h. Body shape trait data***

208 We pruned a body trait dataset to the 680 species that matched those in the 702-species UCE
209 phylogeny²⁴. The body shape dataset included maximum body depth, maximum fish width, head
210 depth, lower-jaw length, mouth width, minimum caudal-peduncle depth, and minimum caudal-
211 peduncle width. We measured maximum body depth as the maximum linear distance from the
212 dorsal to ventral margin of the body, anywhere in the region between the posterior edge of the
213 operculum to the anterior portion of the caudal peduncle. We measured maximum fish width as
214 the maximum width anywhere along the body. We measured head depth as the vertical distance
215 from the dorsal to ventral margins of the head passing through the center of the eye. We
216 measured lower jaw length as the linear distance from the anterior end of the lower jaw to the

217 articular-quadrat joint. We measured mouth width as the linear distance between the left and
218 right articular-quadrat joints. We measured minimum caudal peduncle depth as the minimum
219 vertical distance from the dorsal to ventral margin of the caudal peduncle. We measured
220 minimum caudal peduncle width as the narrowest point along the caudal peduncle. Lastly, we
221 measured fish standard length as the linear distance from the anterior tip of the upper jaw to the
222 posterior edge of the hypural plate or to the posterior end of the vertebral column (i.e., in species
223 that lack a hypural plate). We accounted for size by regressing log-transformed lengths against
224 log-transformed standard fish length and calculating phylogenetic residuals using the phyl.resid
225 function implemented in PHYTOOLS⁵⁵. We used this matrix of residuals for seven traits for
226 phylogenetic comparative analyses using a multivariate framework.
227

228 *i. Disparity through time analyses*

229 We assessed disparity through time (DTT) using the dtt function implemented in GEIGER⁵⁶. We
230 incorporated uncertainty in divergence times by repeating analyses across 100 trees randomly
231 sampled from the posterior distribution. Since we were specifically interested in patterns around
232 and following the K-Pg boundary, we summarized disparity through time in 1 My intervals as
233 the proportion of trees in which the observed subclade disparity fell below that expected from a
234 Brownian motion process (i.e., the expected pattern if the clade is undergoing adaptive radiation)
235 (results in Supplementary Fig. 28). Focusing on the time following the K-Pg boundary, we
236 statistically summarized the 1 My time interval during which the observed subclade disparity
237 first dropped below that expected from a Brownian motion process (results in Supplementary Fig.
238 28). We tested the sensitivity of disparity through time analyses to body shape traits and to the
239 inclusion of major clades by repeating all analyses to the exclusion of clades that arose
240 immediately around the K-Pg boundary and to the exclusion of each trait, as well as repeating
241 the analyses for each trait separately in a univariate framework (results in Extended Data Fig. 6).
242 We also visualized the evolutionary histories of the following focal lineages using the
243 phenogram function implemented in PHYTOOLS⁵⁵: Carangiformes, Lophioidei, Perciformes,
244 Scombriformes, “Squamipinnes” (here defined as the clade containing *Chaetodon kleinii* and
245 *Luvarus imperialis*), Syngnathiformes, and Tetraodontidae. We visualized body shape
246 morphospace using principal component analysis (PCA) with the prcomp function. Since the
247 traits had different variances, we scaled all traits prior to performing PCA.

248 **2. Fossil calibrations for relaxed clock BEAST analyses**

249

250 **i. Node: Stem lineage Lampriformes**, dating the most recent common ancestor (MRCA) of
251 *Lampris guttatus* and *Stylephorus chordatus*, which is the MRCA of Lampriformes and all other
252 paracanthopterygians. *First occurrence*: †*Aipichthys minor*. Sannine Limestone, Hadjula,
253 Lebanon. *Resolution in phylogenetic analyses*: †*Aipichthys minor* is resolved as a lampriform
254 stem lineage in parsimony analyses of morphological characters^{70,71}. *Stratigraphy*: The Hadjula
255 fish beds are located below reported occurrence of *Mantelliceras mantelli*, which defines the first
256 complete ammonite zone of the Late Cretaceous. The top of the *Mantelliceras mantelli* Zone is
257 dated at 98.0 Ma⁷², from which we derive a minimum age for *Aipichthys*. *Minimum age*: 98.0
258 Ma. *Prior setting*: lognormal prior, minimum age 98.0 Ma, mean=1.0, S.D.=1.25, upper 95% CI:
259 119.0 Ma⁴⁸.

260

261 **ii. Node: Stem lineage Polymixiiformes**, dating the MRCA of *Polymixia lowei* and
262 *Aphredoderus sayanus*, which subtends the MRCA of Polymixia and Percopsiformes. *First*
263 *occurrence*: †*Homonotichthys dorsalis*. Lower Chalk of Sussex and Kent, UK⁷³. *Resolution in*
264 *phylogenetic analyses*: none. *Character states*: four full-sized branchiostegals; anterior
265 branchiostegals reduced and forming support for chin barbel^{16,73}. *Stratigraphy*: middle-upper
266 Cenomanian, zone of *Holoaster subglobosus*, corresponding to the late Cenomanian⁷³⁻⁷⁵. The
267 minimal age for †*Homonotichthys dorsalis* is provided by the age of Cenomanian-Turonian
268 boundary, which is dated as 93.9 Ma⁷². *Absolute age estimate*: 93.6 Ma (28). *Prior setting*:
269 lognormal prior, minimum age 93.6 Ma, mean = 1.06, S.D.=1.25, upper 95% CI: 116.35 Ma⁴.

270

271 **iii. Node: Stem lineage Aphredoderidae**, dating the MRCA of *Aphredoderus sayanus* and
272 *Typhlichthys subterraneus*, which subtends the MRCA of Aphredoderidae and Amblyopsidae.
273 *First occurrence*: †*Trichophanes foliarum*. Florissant Formation, Colorado, USA⁷⁶. *Resolution in*
274 *phylogenetic analyses*: †*Trichophanes* and *Aphredoderus* form a clade in a maximum parsimony
275 analysis of 47 morphological characters⁷⁷. *Character states*: ventral margins of lachrymal and
276 infraorbitals spiny; alveolar process of premaxilla divided into separate segments⁷⁶⁻⁷⁸.
277 *Stratigraphy*: The upper Priabonian Florissant Roadcut is dated radiometrically using ⁴⁰Ar/³⁹Ar

278 isotope ratios as 34.07 Ma⁷⁹. *Absolute age estimate*: 34.1 Ma. *Prior setting*: lognormal prior,
279 minimum age 34.1 Ma, mean=1.0, S.D.= 1.347, upper 95% CI: 59.0 Ma²⁰.

280

281 **iv. Node: Stem lineage *Zenopsis***, dating the MRCA of *Zenopsis* and *Zeus*. *First occurrence*:
282 †*Zenopsis clarus*, †*Z. tyleri*, and †*Z. hoernesi*. Lower Maikopian series, Psheka Horizon of the
283 Belaya River, Caucasus⁸⁰, and Lower Dysodylic shales, Strujinoasa-Drăgușina and Piatra Neamț,
284 Romania⁸¹; Lower Dysodylic shales, Piatra Neamț, Romania⁸¹; Laško (Tüffer), Slovenia⁸¹.

285 *Resolution in phylogenetic analyses*: maximum parsimony analysis of 45 morphological
286 characters resulted in a phylogeny where †*Zenopsis clarus*, †*Z. tyleri*, and †*Z. hoernesi*, and *Z.*
287 *oblongus* are resolved in a clade⁸². *Character states*: slender lachrymal; pelvic-fin spines absent;
288 buckler-like plates present along ventral midline of abdomen, and along dorsal ridge from middle
289 of spinous to end of soft dorsal fin⁸². *Stratigraphy*: lower Rupelian [P18], lower Khadumian
290 regional stage⁸³. *Absolute age estimate*: 32.0 Ma⁸⁴. *Prior setting*: lognormal prior, minimum age
291 32.0 Ma, mean=1.0, S.D.= 0.33, upper 95% CI: 36.7 Ma²⁰.

292

293 **v. Node: Stem lineage Lampridae**, dating the MRCA of *Lampris guttatus* and *Zu elongatus*,
294 which is the MRCA of Lampriformes. *First occurrence*: †*Turkmene finitimus*. Danatinsk Suite,
295 Ulyya-Kushlyuk locality, Turkmenistan^{85,86}. *Resolution in phylogenetic analysis*: none.
296 *Character states*: first dorsal fin pterygiophore strongly reclined posteriorly; enlarged pectoral
297 fins inserting high on flank; shoulder girdle broad ventrally, with expanded coracoid; long
298 parapophyses absent from abdominal vertebrate⁸⁶. *Stratigraphy*: uppermost Thanetian-lowermost
299 Ypresian⁸⁷. *Absolute age estimate*: 55.8 Ma⁸⁴. *Prior setting*: lognormal prior, minimum age 55.8
300 Ma, mean=1.0, S.D.= 1.411, upper 95% CI: 83.5 Ma²⁰.

301

302 **vi. Node: Stem lineage Holocentridae**, dating the MRCA of *Myripristis violacea* and
303 *Rondeletia loricata*, which subtends the MRCA of Holocentridae and Berycoidei. *First*
304 *occurrence*: †*Stichocentrus liratus* from the Sannine Limestone, Hadjula, Lebanon⁸⁸. *Resolution*
305 *in phylogenetic analyses*: none. *Character states*: The penultimate anal-fin spine of
306 †*Stichocentrus* is enlarged and represents a synapomorphy of holocentroids^{16,89}. *Stratigraphy*:
307 See discussion for Calibration i, †*Aipichthys minor*. *Absolute age estimate*: 98.0 Ma. *Prior*

308 *setting*: lognormal prior, minimum age 98.0 Ma, mean=1.0, S.D.= 0.8, upper 95% CI: 108.0
309 Ma⁴⁸.

310

311 **vii. Node: Stem lineage Myripristinae**, dating the MRCA of *Myripristis violacea* and
312 *Sargocentron coruscum*, which subtends the MRCA of Holocentridae. *First occurrence*:
313 †*Eoholocentrum macrocephalum*, †*Berybolcensis leptacanthus*, and †*Tenuicentrum pattersoni*.
314 Pesciara beds of ‘Calcari nummulitici’, Bolca, Italy⁹⁰⁻⁹². *Resolution in phylogenetic analyses*:
315 analysis of 72 morphological characters resolve †*Eoholocentrum*, †*Berybolcensis*, and
316 †*Tenuicentrum* as stem-lineage Myripristinae⁹³. *Character states*: tooth-bearing platform
317 expanded and overhangs lateral side of dentary near symphysis; premaxillary tooth field curves
318 dorsally toward ascending process at symphysis; edentulous ectopterygoid (†*Berybolcensis* and
319 †*Tenuicentrum*); spinous procurent caudal-fin rays reduced to four in the upper and three in the
320 lower lobe (†*Berybolcensis* and †*Tenuicentrum*)⁹³. *Stratigraphy*: upper Ypresian [NP14]^{94,95}.
321 *Absolute age estimate*: 50 Ma⁸⁴. *Prior setting*: lognormal prior, minimum age 50.0 Ma,
322 mean=1.0, S.D.= 0.6, upper 95% CI: 57.3 Ma²⁰.

323

324 **viii. Node: Crown lineage Syngnathiformes**, dating the MRCA of *Pegasus volitans* and
325 *Syngnathus scovelli*, which subtends the MRCA of Syngnathiformes. *First occurrence*:
326 †*Gasterorhamphos zuppichinii*. “Calcari di Melissano”, Porto Selvaggio, Lecce province,
327 Italy⁹⁶. *Resolution in phylogenetic analyses*: none, but Orr⁹⁷ argues that †*Gasterorhamphos* is a
328 stem lineage of a clade containing Macrorhamphosidae and Centriscidae. *Character states*: anal-
329 fin spine absent; enlarged dorsal-fin spine with serrated posterior margin; elongated tubular
330 snout; pleural ribs absent; cleithrum bears enlarged posterodorsal process; rod-like anteroventral
331 process of coracoid; pectoral rays simple^{97,98}. *Stratigraphy*: uppermost Campanian-lowermost
332 Maastrichtia⁹⁹. *Absolute age estimate*: 69.71 Ma⁴⁸. *Prior setting*: lognormal prior, minimum age
333 69.71 Ma, mean=1.0, S.D.= 0.785, upper 95% CI: 79.6 Ma⁴⁸.

334

335 **ix. Node: Stem lineage Centriscidae**, dating the MRCA of *Aeoliscus strigatus* and
336 *Macrorhamphosus gracilis*, which subtends the MRCA of Centriscidae. *First occurrence*:
337 †*Paramphisile weileri* and †*Paraeoliscus robinetae*. Pesciara beds of ‘Calcari nummulitici’,
338 Bolca, Italy¹⁰⁰. *Resolution in phylogenetic analyses*: none. *Character states*: caudal fin directed

339 posteroventrally (\dagger *Paraeoliscus*); dorsal spine jointed distally⁹⁷. *Stratigraphy*: See discussion for
340 Calibration viii \dagger *Eoholocentrum macrocephalum*. *Absolute age estimate*: 50 Ma⁸⁴. *Prior setting*:
341 lognormal prior, minimum age 50.0 Ma, mean=1.0, S.D.= 0.6, upper 95% CI: 57.3 Ma²⁰.

342

343 **x. Node: Crown lineage Ariomma**, dating the MRCA of *Ariomma indica* and *A. melana*. *First*
344 *occurrence*: \dagger *Ariomma geslini* from the diatomites of St Eugène, Chelif Basin, Algeria²⁹.
345 *Resolution in phylogenetic analyses*: none. *Character states*: extension of pleural ribs onto
346 caudal vertebrae^{101,102}, and a distinctive pattern of anal-fin skeleton shared with *A. bondi* and *A.*
347 *melana*, consisting of anterior pterygiophores that bend posteriorly, overlapping the similarly
348 curved shafts of successive pterygiophores^{102,103}. *Stratigraphy*: Details presented in Friedman et
349 al.²⁹. *Absolute age estimate*: 5.94 Ma. *Prior setting*: lognormal prior, minimum age 5.94 Ma,
350 mean=1.0, S.D.= 1.299, upper 95% CI: 28.96 Ma²⁹.

351

352 **xi. Node: stem lineage Stromateidae**, dating the MRCA of *Pampus argenteus* and *Ariomma*
353 *indica*, which subtends the MRCA Stromateidae and the clade that comprises *Ariomma* and
354 *Nameidae*. *First occurrence*: \dagger *Pinichthys pulcher* from the Pshekha Horizon \dagger *Planorbella* Beds,
355 Lower Maikop Caucasus¹⁰⁴. *Resolution in phylogenetic analyses*: none. *Character states*:
356 \dagger *Pinichthys* has a stellate, bony base of papillae in the region expected to bear pharyngeal
357 sacs¹⁰⁵. Synapomorphies of stromateiod displayed by \dagger *Pinichthys* include: a continuous dorsal
358 fin; a ventral articulation between the coracoid and ventral tip of the cleithrum; and an elongated
359 first anal fin pterygiophore that is strongly reclined¹⁰⁶. \dagger *Pinichthys* differs from extant lineages of
360 Stromateidae by having well-developed pelvic fins in adults and lacking extension of the first
361 anal fin pterygiophore posterior to the first haemal spine²⁹. \dagger *Pinichthys* is interpreted as a stem-
362 lineages stromateiod, which is consistent with previous interpretations¹⁰⁴. *Stratigraphy*: Details
363 presented in Friedman et al.²⁹. *Absolute age estimate*: 32.02 Ma. *Prior setting*: lognormal prior,
364 minimum age 32.02 Ma, mean=1.0, S.D.= 1.2, upper 95% CI: 51.6 Ma²⁹.

365

366 **xii. Node: stem lineage Chiasmodontidae**, dating the MRCA of *Kali kerberti* and *Tetragonurus*
367 *atlanticus*, which subtends the MRCA of Chiasmodontidae and *Tetragonurus*. *First occurrence*:
368 \dagger *Bannikovichthys paelynus* from the fish-bearing laminates of Toricella Paligna, Italy¹⁰⁷.
369 *Resolution in phylogenetic analyses*: none. *Character states*: The hypothesis that

370 †*Bannikovichthys* is related to living Chiasmodontidae is based on an absence of scales,
371 elongated opercles, delicate ossification of the interopercle and subopercle, and enlarged
372 hourglass-shaped radials¹⁰⁷. The relationships of †*Bannikovichthys* among living chiasmodontids
373 is uncertain, so it is conservatively treated as a stem-lineage taxon²⁹. *Stratigraphy*: Details
374 presented in Friedman et al.²⁹. *Absolute age estimate*: 11.9 Ma. *Prior setting*: lognormal prior,
375 minimum age 11.9 Ma, mean=1.0, S.D.= 1.454, upper 95% CI: 41.56 Ma²⁹.

376

377 **xiii. Node: within crown of *Scomber***, dating the MRCA of *Scomber australasicus* and *Scomber*
378 *japonicus*. *First occurrence*: *Scomber colias* from the Raz-el-Aïn, Oran, Algeria. *Resolution in*
379 *phylogenetic analyses*: This fossil is attributed to the living species *Scomber colias*, which is
380 resolved as the sister lineage of *S. japonicus* in a molecular phylogenetic analysis¹⁰⁸.
381 *Stratigraphy*: Details presented in Friedman et al.²⁹. *Absolute age estimate*: 5.94 Ma. *Prior*
382 *setting*: lognormal prior, minimum age 5.94 Ma, mean=1.0, S.D.= 1.255, upper 95% CI: 27.4
383 Ma²⁹.

384

385 **xiv. Node: stem lineage *Scomber***, dating the MRCA of *Scomber australasicus* and *Rastrelliger*
386 *kanagurta*. *First occurrence*: †*Scomber saadii* from the Padbeh Formation of Istehbanât, Iran¹⁰⁹.
387 *Resolution in phylogenetic analyses*: None. *Character states*: †*Scomber saadii* exhibits serrations
388 on the teeth that is a synapomorphy of *Scomber*^{108,110}. *Stratigraphy*: Details presented in
389 Friedman et al.²⁹. *Absolute age estimate*: 33.9 Ma. *Prior setting*: lognormal prior, minimum age
390 33.9 Ma, mean=1.0, S.D.= 1.02, upper 95% CI: 48.45 Ma²⁹.

391

392 **xv. Node: stem lineage *Acanthocybium***, dating the MRCA of *Acanthocybium solandri* and
393 *Scomberomorus maculatus*. *First occurrence*: †*Palaeocybium proosti* from the London Clay
394 Formation, Isle of Sheppey, UK¹¹¹. *Resolution in phylogenetic analysis*: none. *Character states*:
395 †*Palaeocybium* and *Acanthocybium* share closely spaced teeth with blunt tips and the holotype
396 specimen shows an elongate lower jaw that is similar to *Acanthocybium* and *Scomberomorus*¹¹²⁻
397 ¹¹⁴. *Stratigraphy*: Details presented in Friedman et al.²⁹. *Absolute age estimate*: 50.5 Ma. *Prior*
398 *setting*: lognormal prior, minimum age 50.5 Ma, mean=1.0, S.D.= 0.5, upper 95% CI: 56.72
399 Ma²⁹.

400

401 **xvi. Node: stem lineage Sardini + Thunnini**, dating the MRCA of *Scomberomorus maculatus*
402 and *Euthynnus affinis*. *First occurrence*: †*Eocoelopoma portentosum* from the Danatinsk
403 Formation, Turkmenistan¹¹⁵. *Resolution in phylogenetic analyses*: None. *Character states*:
404 Details presented in Friedman et al.²⁹. *Stratigraphy*: Details presented in Friedman et al.²⁹.
405 *Absolute age estimate*: 54.17 Ma. *Prior setting*: lognormal prior, minimum age 54.17 Ma,
406 mean=1.0, S.D.= 0.698, upper 95% CI: 62.71 Ma²⁹.

407

408 **xvii. Node: stem lineage Thunnus**, dating the MRCA of *Thunnus orientalis* and *Auxis rochei*,
409 which is the MRCA of Thunnini. *First occurrence*: †*Thunnus abchasicus* from the Kuma
410 Horizon, Pshekha River, Caucasus¹¹⁶. *Resolution in phylogenetic analyses*: None. *Character
411 states*: †*Thunnus abchasicus* exhibits several synapomorphies of *Thunnus* that include the
412 presence of small oral teeth and the shortened preural vertebrae¹¹⁶. The presence of a spine in the
413 second dorsal fin suggests that †*T. abchasicus* is a stem lineage *Thunnus*¹¹⁵. *Stratigraphy*: Details
414 presented in Friedman et al.²⁹. *Absolute age estimate*: 38.62 Ma. *Prior setting*: lognormal prior,
415 minimum age 38.62 Ma, mean=1.0, S.D.= 0.91, upper 95% CI: 50.78 Ma²⁹.

416

417 **xviii. Node: stem lineage Promethichthys**, dating the MRCA of *Promethichthys prometheus* and
418 *Diplospinus multistriatus*. *First occurrence*: †*Hemithyrsites maicopicus* from the Upper Maikop
419 of the Kurdzhips River, Adygea, Caucasus¹¹⁵. *Resolution in phylogenetic analyses*: None.
420 *Character states*: Derived traits shared by *Promethichthys* and †*Hemithyrsites maicopicus*
421 include reduction of the pelvic fin to a single spine and the presence of two pairs of dorsal and
422 anal finlets¹¹⁵. *Stratigraphy*: Details presented in Friedman et al.²⁹. *Absolute age estimate*: 15.97
423 Ma. *Prior setting*: lognormal prior, minimum age 15.97 Ma, mean=1.0, S.D.= 0.986, upper 95%
424 CI: 29.67 Ma²⁹.

425

426 **xix. Node: Stem lineage Channidae**, dating the MRCA of *Channa micropeltes* and *Helostoma
427 temminckii*, which subtends the MRCA of Channidae and a clade containing Helostoma,
428 Anabantidae, and Osphronemidae. *First occurrence*: †*Anchichanna kuldanensis* from the Ganda
429 Kas Area, Kuldana Formation, Kala Chitta Hills, Pakistan¹¹⁷. *Resolution in phylogenetic
430 analyses*: None. *Character states*: †*Anchichanna kuldanensis* exhibits the Channidae
431 synapomorphy of the outer wall of the auditory bulla formed mainly by the prootic, but is likely

432 a stem-lineage taxon because it does not share synapomorphies with either *Channa* or
433 *Parachanna*¹¹⁷. *Stratigraphy*: The Kuldana Formation and other vertebrate fossil localities of the
434 Kala Chitta Hills straddle the Ypresian-Lutetian boundary¹¹⁸. *Absolute age estimate*: 41.3 Ma.
435 *Prior setting*: lognormal prior, minimum age 41.3 Ma, mean=1.0, S.D.= 1.31, upper 95% CI:
436 64.7 Ma¹¹⁹.

437

438 **xx. Node: Stem lineage Sphyraenidae**, dating the MRCA of *Sphyraena jello* and *Lactarius*
439 *lactarius*. *First occurrence*: †*Sphyraena bolcensis*, Pesciara beds of ‘Calcare nummulitici’,
440 Bolca, Italy^{120,121}. *Resolution in phylogenetic analyses*: None. *Character states*: three ‘T’-shaped,
441 sutured predorsals or spineless pterygiophores¹²²; elongate gape; upper jaw non-protrusible;
442 enlarged fangs on dentary, premaxilla, and palatine. *Stratigraphy*: upper Ypresian [NP14]^{94,95}.
443 *Absolute age estimate*: 50.0 Ma⁹⁵. *Prior setting*: lognormal prior, minimum age 50.0 Ma,
444 mean=1.0, S.D.= 0.5999, upper 95% CI: 57.3 Ma¹.

445

446 **xxi. Node: Stem lineage Mene**, dating the MRCA of *Mene maculata* and *Xiphias gladius*. *First*
447 *occurrence*: †*Mene purdyi*, ‘Mancora Formation’, Perú¹²³; †*M. triangulum*, Danatinsk Suite,
448 Ulyya-Kushlyuk locality, Turkmenistan^{85,87}; and †*Mene* sp., ‘Stolle Klint clay’, Ølst Formation,
449 Denmark¹²⁴. *Resolution in phylogenetic analyses*: None. *Character states*: frontal vault; many
450 small infraorbitals; all anal fin rays short, with anteriormost rays plate like; anal fin spines
451 absent; postcleithrum broad and contacts first anal fin pterygiophore; disc-like body with deep
452 ventral keel; greatly elongated second anal fin ray¹²³. *Stratigraphy*: uppermost Thanetian-
453 lowermost Ypresian [NP14]^{87,124}. *Absolute age estimate*: 55.2 Ma¹²⁵. *Prior setting*: lognormal
454 prior, minimum age 55.2 Ma, mean=1.0, S.D.= 0.92, upper 95% CI: 67.5 Ma^{1,48}.

455

456 **xxii. Node: Stem lineage Carangidae**, dating the MRCA of *Caranx caninus* and *Trachinotus*
457 *goodei*, which subtends the MRCA of the clade comprising Carangidae, *Coryphaena*,
458 *Rachycentron*, Scomberoidinae, and Trachinotinae. *First occurrence*: †*Archaeus oblongus*.
459 Danatinsk Suite, Ulyya-Kushlyuk locality, Turkmenistan⁸⁵. *Resolution in phylogenetic analyses*:
460 None. *Character states*: broad gap between second and third anal-fin spines¹²⁶. *Stratigraphy*:
461 uppermost Thanetian-lowermost Ypresian⁸⁷. *Absolute age estimate*: 55.8 Ma⁸⁴. *Prior setting*:
462 lognormal prior, minimum age 55.8 Ma, mean=1.0, S.D.= 0.661, upper 95% CI: 63.9 Ma¹.

463 **xxiii. Node: Stem lineage Caranginae**, dating the MRCA of *Caranx caninus* and *Seriola*
464 *dumerili*, which subtends the MRCA of Carangidae. *First occurrence*: †*Eastmanalepes*
465 *primaevus*, Pesciara beds of ‘Calcare nummulitici’, Bolca, Italy¹²⁷. *Resolution in phylogenetic*
466 *analyses*: None. *Character states*: lateral line scales modified as thick scutes^{126,128}. *Stratigraphy*:
467 upper Ypresian [NP14]⁹⁴. *Absolute age estimate*: 49.0 Ma⁴⁸. *Prior setting*: lognormal prior,
468 minimum age 49.0 Ma, mean=1.0, S.D.= 0.1, upper 95% CI: 52.2 Ma^{1,48}.

469

470 **xxiv. Node: Stem lineage Echeneioidei**, dating the MRCA of *Echeneis naucrates* and
471 *Scomberoides lysan*, which subtends the MRCA of the clade comprising Echeneidae,
472 *Coryphaena*, *Rachycentron*, Scomberoidinae, and Trachinotinae. *First occurrence*: †*Ductor*
473 *vestenae* from the Pesciara locality of Bolca, Italy^{120,121}. *Resolution in phylogenetic analyses*:
474 parsimony and Bayesian analyses of morphology and combined molecular and morphological
475 datasets resolve †*Ductor vestenae* as either a stem echeneioid or as the sister the clade containing
476 *Rachycentron* and *Coryphaena*¹²⁹. We follow the conservative consideration of †*Ductor vestenae*
477 as a stem-lineage taxon, as used in Harrington et al.⁴⁸. *Character states*: Discussed in Friedman
478 et al.¹²⁹. *Stratigraphy*: upper Ypresian [between NP14 and SPZ11]⁹⁴. *Absolute age estimate*: 49.0
479 Ma⁴⁸. *Prior setting*: lognormal prior, minimum age 49.0 Ma, mean=1.0, S.D.= 0.1, upper 95%
480 CI: 52.2 Ma⁴⁸.

481

482 **xxv. Node: Stem lineage Echeneidae**, dating the MRCA of *Echeneis naucrates* and *Coryphaena*
483 *hippurus*, which subtends the MRCA of clade containing Echeneidae, *Coryphaena*, and
484 *Rachycentron*. *First occurrence*: unnamed Echeneidae undet. from the Frauenweiler clay pit,
485 Germany¹³⁰. *Resolution in phylogenetic analyses*: None. *Character states*: no supraneurals;
486 multiple anal fin pterygiophores insert anterior to first haemal spine; spinous dorsal fin modified
487 as adhesion disc^{129,131}. *Stratigraphy*: See discussion in Harrington et al.⁴⁸. *Absolute age estimate*:
488 29.62 Ma⁴⁸. *Prior setting*: lognormal prior, minimum age 29.62 Ma, mean=1.0, S.D.= 0.87,
489 upper 95% CI: 41.0 Ma⁴⁸.

490

491 **xxvi. Node: Stem lineage Scomberoides**, dating the MRCA of *Scomberoides lysan* and
492 *Trachinotus goodei*, which subtends the MRCA of Scomberoidinae and Trachinotinae. *First*
493 *occurrence*: *Scomberoides spinosus* from the Upper Maikop at Chernaya Rechka, Caucasus⁸⁷.

494 *Resolution in phylogenetic analyses:* None. *Character states:* *Scomberoides spinosus* exhibits
495 two synapomorphies of Scomberoidinae: 26 versus 24 vertebrae and posterior rays of the dorsal
496 and anal fin developed as finlets^{126,128,132}. *Stratigraphy:* See discussion in Harrington et al.⁴⁸.
497 *Absolute age estimate:* 19.3 Ma⁴⁸. *Prior setting:* lognormal prior, minimum age 19.3 Ma,
498 mean=1.0, S.D.= 1.095, upper 95% CI: 35.8 Ma⁴⁸.

499

500 **xxvii. Node: Stem lineage Citharidae**, dating the MRCA of *Gymnachirus melas* and
501 *Scophthalmus rhombus*, which subtends the MRCA of Citharidae and all other pleuronectoids
502 except *Psettidess*. *First occurrence:* †*Eobothus minimus* from the Pesciara beds of ‘Calcaro
503 nummulitico’, Bolca, Italy^{133,134}. *Resolution in phylogenetic analyses:* †*Eobothus* is the sister
504 lineage of *Citharus*¹³³. *Character states:* complete orbital asymmetry; dorsal fin extends above
505 orbit; hook-shaped urohyal; parahypural not in articulation with pectoral centrum 1; long neural
506 spine on preural centrum 2¹³³. *Stratigraphy:* See discussion in Harrington et al.⁴⁸. *Absolute age
507 estimate:* 49.0 Ma⁴⁸. *Prior setting:* lognormal prior, minimum age 49.0 Ma, mean=1.0, S.D.=
508 0.68, upper 95% CI: 57.3 Ma⁴⁸.

509

510 **xxviii. Node: Stem lineage of the clade containing Soleidae and Cynoglossidae**, dating the
511 MRCA of *Aseraggodes xenicus* and *Poecilopsetta plinthus*. *First occurrence:* †*Eobuglossus
512 eocenicus* from the Mokkatam Formation, Djebel Turah, Egypt¹³⁵. *Resolution in phylogenetic
513 analyses:* none. *Character states:* †*Eobuglossus* shows derived cranial features limited to
514 Soleidae, including blind side preopercular canal terminating on ventral margin of preopercular
515 and convex portion of blind side dentary anterior to angulo-articular^{135,136}. *Stratigraphy:* See
516 discussion in Harrington et al.⁴⁸. *Absolute age estimate:* 41.2 Ma⁴⁸. *Prior setting:* lognormal
517 prior, minimum age 41.9 Ma, mean=1.0, S.D.= 0.4, upper 95% CI: 46.4 Ma⁴⁸.

518

519 **xxix. Node: Stem lineage Bothidae**, dating the MRCA of *Bothus pantherinus* and *Cyclopsetta
520 frimbriata*, which subtends the MRCA of the clade containing Bothidae and Cyclopsettidae.
521 *First occurrence:* †*Oligobothus pristinus* from the Lower Dysodilic shales, Piatra Neamă,
522 Romania¹³⁷. *Resolution in phylogenetic analyses:* None. *Character states:* myorhabdoi
523 present¹³⁷. *Stratigraphy:* See discussion in Harrington et al.⁴⁸. *Absolute age estimate:* 29.62 Ma⁴⁸.

524 *Prior setting*: lognormal prior, minimum age 29.62 Ma, mean=1.0, S.D.= 0.06, upper 95% CI:
525 32.6 Ma⁴⁸.

526

527 **xxx. Node: Stem lineage Pleuronectidae**, dating the MRCA of *Pleuronichthys cornutus* and
528 *Paralichthys albigutta*, which subtends the MRCA of the clade containing Pleuronectidae and
529 Paralichthyidae. *First occurrence*: †*Oligopleuronectes germanicus* from the Frauenweiler fossil
530 site, Germany¹³⁸. *Resolution in phylogenetic analyses*: None. *Character states*: Suggested as a
531 member of Pleuronectidae based on †*Oligopleuronectes* being right-eyed and having a lateral
532 process on the eye-side frontal^{138,139}. *Stratigraphy*: See discussion in Harrington et al.⁴⁸. *Absolute
533 age estimate*: 29.62 Ma⁴⁸. *Prior setting*: lognormal prior, minimum age 29.62 Ma, mean=1.0,
534 S.D.= 0.45, upper 95% CI: 35.3 Ma⁴⁸.

535

536 **xxxi. Node: Stem lineage Bothus**, dating the MRCA of *Bothus pantherinus* and *Crossorhombus
537 azureus*. *First occurrence*: *Bothus* sp. from the Middle Tsurevsky Member of the Tsurevsky
538 Formation along the bank of the Psheka River, Caucasus¹⁴⁰. *Resolution in phylogenetic analyses*:
539 None. *Character states*: A specific affinity to *Bothus* is supported by the presence of robust
540 rectangular haemal spines^{140,141}. *Stratigraphy*: See discussion in Harrington et al.⁴⁸. *Absolute age
541 estimate*: 11.056 Ma⁴⁸. *Prior setting*: lognormal prior, minimum age 29.62 Ma, mean=1.0, S.D.=
542 0.84, upper 95% CI: 39.9 Ma⁴⁸.

543

544 **xxxii. Node: Stem lineage Pseudocrenilabrinae**, dating the MRCA of *Bathybates minor* and
545 *Amphilophus citrinellus*, which subtends the MRCA of the clade that contains
546 Pseudocrenilabrinae and Cichlinae. *First occurrence*: †*Mahengechromis plethos* from Mahenge,
547 Tanzania¹⁴². *Resolution in phylogenetic analyses*: Several phylogenetic resolutions of
548 †*Mahengechromis* place the taxon as either a crown lineage Cichlidae or crown lineage
549 Pseudocrenilabrinae^{142,143}. We follow Rabosky et al.¹¹⁹ in conservatively treating
550 †*Mahengechromis* as a stem-lineage Pseudocrenilabrinae. *Character states*: The identification
551 of †*Mahengechromis* as a cichlid is supported by the morphology of the lower pharyngeal jaw,
552 squamation, and meristics of vertebrae and median fins¹⁴²⁻¹⁴⁴. *Stratigraphy*: The Mahenge fossil
553 deposits accumulated in a crater formed by intrusion of kimberlite and U-Pb of a zircon crystal
554 dates the formation of the kimberlite at 45.83 +/-0.17 Ma¹⁴⁵. Because the lacustrine sediments

555 predate the kimberlite emplacement it was suggested the age of the fossil deposits are 0.2 to 0.1
556 Ma younger^{145,146}. We use the conservative date of 45 Ma used in Rabosky et al.¹¹⁹. Absolute age
557 estimate: 45.0 Ma. *Prior setting*: lognormal prior, minimum age 45.0 Ma, mean=1.0, S.D.= 1.29,
558 upper 95% CI: 67.3 Ma.

559

560 **xxxiii. Node: Crown lineage Exocetoidei**, dating the MRCA of *Xenentodon cancila* and
561 *Hemiramphus far*, which subtends the MRCA of Belonidae and Hemiramphidae. *First*
562 *occurrence*: †*Rhamphexocoetus volans* from Pesciara beds of ‘Calcarum nummulitici’, Bolca,
563 Italy¹⁴⁷. *Resolution in phylogenetic analyses*: None. *Character states*: lower jaw symphysis
564 extended; ventral lobe of caudal fin enlarged relative to dorsal lobe; pectoral fins greatly
565 expanded¹⁴⁸⁻¹⁵⁰. *Stratigraphy*: upper Ypresian [NP14]^{94,95}. *Absolute age estimate*: 49.0 Ma⁴.
566 *Prior setting*: lognormal prior, minimum age 49.0 Ma, mean=1.0, S.D.= 1.49, upper 95% CI:
567 80.52 Ma⁴.

568

569 **xxxiv. Node: Stem lineage Calotomus (Labridae)**, dating the MRCA of *Calotomus spinidens*
570 and *Sparisoma radians*. *First occurrence*: †*Calotomus preisli* from the Leitha Limestone, St.
571 Margarethen, Austria¹⁵¹. *Resolution in phylogenetic analyses*: None. *Character states*: Presence
572 of upper pharyngeal bones bearing 1 to 3 rows of teeth and presence of a lateral canine on the
573 premaxilla are synapomorphies for Scarinae. A conical tooth on the medial face of the
574 premaxilla is a synapomorphy of *Calotomus*¹⁵¹. *Stratigraphy*: The Leitha Limestone is
575 constrained by calcareous nannofossils to the standard biozone NN6¹⁵¹, which is entirely in the
576 Serravallian stage of the Miocene. The top of NN6 is dated at 11.9 Ma⁴. *Absolute age estimate*:
577 11.9 Ma⁴. *Prior setting*: lognormal prior, minimum age 11.9 Ma, mean=1.0, S.D.= 1.501, upper
578 95% CI: 43.95 Ma⁴.

579

580 **xxxv. Node: Stem lineage Luvaridae**, dating the MRCA of *Luvarus imperialis* and *Acanthurus*
581 *bahianus*, which subtends the MRCA of *Luvarus* and the clade containing *Zanclus cornutus* and
582 Acanthuridae. *First occurrence*: †*Avitoluvarus dianae*, †*A. mariannae*, †*Kushlukia permira*, and
583 †*Luvarus necopinatus*. Danatinsk Suite, Uyly-a-Kushlyuk locality, Turkmenistan¹⁵². *Resolution in*
584 *phylogenetic analyses*: a parsimony analysis of morphological characters resolves a clade that
585 contains †*Avitoluvarus*, †*Kushlukia*, †*Luvarus necopinatus*, and *L. imperialis*, which is sister to a

586 clade comprising *Zanclus* and Acanthuridae¹⁵². *Character states*: median pterygial truss
587 surrounding most of body; two or fewer dorsal-fin spines; no anal-fin spines; distal end of first
588 anal-fin pterygiophore greatly elongated anteriorly; hypurals 1-4 fused; caudal fins broadly
589 overlap hypural(s); pelvic fin rudimentary in adults; teeth absent or greatly reduced¹⁵².
590 *Stratigraphy*: uppermost Thanetian-lowermost Ypresian⁸⁷. *Absolute age estimate*: 55.8 Ma⁸⁴.
591 *Prior setting*: lognormal prior, minimum age 55.8 Ma, mean=1.0, S.D.= 0.661, upper 95% CI:
592 63.9 Ma²⁰.
593

594 **xxxvi. Node: Stem lineage Acanthurinae**, dating the MRCA of *Acanthurus bahianus* and *Naso*
595 *unicornis*, which subtends the MRCA of Acanthuridae. *First occurrence*: †*Proacanthurus tenius*
596 from the ‘Pesciara beds of ‘Calcare nummulitici’, Bolca, Italy¹⁵³. *Resolution in phylogenetic*
597 *analyses*: None. *Character states*: caudal peduncle bears folding spine¹⁵³. *Stratigraphy*: upper
598 Ypresian [NP14]⁹⁴. *Absolute age estimate*: 50 Ma⁹⁴. *Prior setting*: lognormal prior, minimum age
599 50.0 Ma, mean=1.0, S.D.= 0.6, upper 95% CI: 57.3 Ma¹.

600
601 **xxxvii. Node: Stem lineage Siganidae**, dating the MRCA of *Siganus spinus* and *Scatophagus*
602 *argus*. *First occurrence*: †*Siganopygaeus rarus*. Danatinsk Suite, Uyly-a-Kushlyuk locality,
603 Turkmenistan¹⁵⁴. *Resolution in phylogenetic analyses*: parsimony analysis of morphological
604 characters resolves four Eocene and Oligocene taxa, including †*Siganopygaeus*, as stem-lineage
605 Siganidae¹⁵⁴. *Character states*: two pelvic-fin spines; seven or more anal-fin spines; ten or fewer
606 anal-fin rays¹⁵⁴. *Stratigraphy*: uppermost Thanetian-lowermost Ypresian⁸⁷. *Absolute age*
607 *estimate*: 55.8 Ma⁸⁴. *Prior setting*: lognormal prior, minimum age 55.8 Ma, mean=1.0, S.D.=
608 0.661, upper 95% CI: 63.9 Ma²⁰.
609

610 **xxxviii. Node: Stem lineage of Chaetodontidae**, dating the MRCA of *Chaetodon kleinii* and
611 *Leiognathus equula*, which subtends the MRCA of the clade that contains Chaetodontidae and
612 Leiognathidae. *First occurrence*: Chaetodontidae cf. *Chaetodon* (tholichthys-stage larvae) from
613 the ‘Fish shales’, Frauenweiler clay pit, Germany^{130,155}. *Resolution in phylogenetic analyses*:
614 None. *Character states*: overlapping, sequential articulation between first dorsal fin
615 pterygiophores, supraneurals, and supraoccipital crest; second infraorbital excluded from orbital
616 margin; two sets of lateral processes on each side of first dorsal fin pterygiophore define a clear

617 groove; distal head of second supraneural longer than that of first supraneural¹⁵⁵⁻¹⁵⁷.
618 *Stratigraphy*: The ‘Fish shales’ lie within NP23¹³⁸. *Absolute age estimate*: 29.62 Ma⁴. *Prior*
619 *setting*: lognormal prior, minimum age 29.62 Ma, mean=1.0, S.D.= 1.498, upper 95% CI: 61.6
620 Ma⁴.

621
622 **xxxix. Node: Stem lineage *Chaetodon***, dating the MRCA of *Chaetodon kleinii* and
623 *Prognathodes marcellae*. *First occurrence*: †*Chaetodon ficheuri* from the Saint-Denis du Sig,
624 Raz-el-Aïn, Les Planteurs, and Eugène, Algeria¹⁵⁶. *Resolution in phylogenetic analyses*: None.
625 *Character states*: overlapping, sequential articulation between first dorsal fin pterygiophores,
626 supraneurals, and supraoccipital crest; second infraorbital excluded from orbital margin; two sets
627 of lateral processes on each side of first dorsal fin pterygiophore define a clear groove; distal
628 head of second supraneural longer than that of first supraneural^{156,157}. *Stratigraphy*: Messinian¹⁵⁸⁻
629¹⁶⁰. *Absolute age estimate*: 7.1 Ma. *Prior setting*: lognormal prior, minimum age 7.1 Ma,
630 mean=0.26, S.D.= 0.2, upper 95% CI: 8.9 Ma²⁰.

631
632 **xl. Node: Stem lineage *Gazza***, dating the MRCA of *Gazza minuta* and *Leiognathus equula*.
633 *First occurrence*: †*Euleiognathus tottori* from the Iwami Formation, Tottori Group, Japan^{161,162}.
634 *Resolution in phylogenetic analyses*: none. *Character states*: long ascending processes of
635 premaxillae; paddle-like expansions of neural and haemal spine of preural centrum 4; single
636 supraneural; serrated anterior margins of fin spines; caniniform teeth¹⁶³. The final character is
637 unique to *Gazza* within leiognathids^{161,164}. The nesting of *Gazza* within the phylogeny of
638 Leiognathidae indicates caniniform teeth are derived within the clade^{163,165,166}. See Gill and
639 Michalski¹⁶⁷ who are sceptical that †*Euleiognathus* is a leiognathid. *Stratigraphy*: middle
640 Miocene^{161,162}. *Absolute age estimate*: 11.6 Ma¹⁶⁸. *Prior setting*: lognormal prior, minimum age
641 11.6 Ma, mean=0.8, S.D.= 1.0, upper 95% CI: 23.1 Ma²⁰.

642
643 **xli. Node: Stem lineage Diodontidae**, dating the MRCA of *Diodon liturosus* and *Canthigaster*
644 *rostrata*, which subtends the MRCA of Diodontidae and Tetraodontidae. *First occurrence*:
645 †*Prodiodon tenuispinus*, †*P. erinaceus*, †*Heptadiodon echinus*, and †*Zignodon fornasieroae*
646 from the Pesciara beds of ‘Calcare nummulitici’, Bolca, Italy¹⁶⁹. *Resolution in phylogenetic*
647 *analyses*: parsimony analysis of morphological characters resolves a clade containing

648 †*Prodiodon tenuispinus*, †*P. erinaceus*, †*Heptadiodon echinus*, †*Zignodon fornasieroae*, *Diodon*
649 *holocanthus*, and *Chilomycterus schoepfi*¹⁶⁹. *Character states*: premaxillae fused along midline;
650 dentaries fused along midline; jaws massive¹⁶⁹. *Stratigraphy*: upper Ypresian [NP14]⁹⁴. *Absolute*
651 *age estimate*: 50 Ma⁸⁴. *Prior setting*: lognormal prior, minimum age 50.0 Ma, mean=1.0, S.D.=
652 0.6, upper 95% CI: 57.3 Ma²⁰.

653

654 **xlii. Node: Stem lineage of Balistidae**, dating the MRCA of *Balistes capriscus* and *Aluterus*
655 *monoceros*, which subtends the MRCA of Balistidae and Monacanthidae. *First occurrence*:
656 †*Gornylistes prodigiosus* from the Kuma Horizon, Krasnodar Region, Caucasus¹⁷⁰. *Resolution in*
657 *phylogenetic analyses*: None. *Character states*: ventral shaft of second spine-bearing dorsal
658 pterygiophore absent; supraneural strut present between abdominal neural spine and final spine-
659 bearing dorsal pterygiophore; four anal-fin pterygiophores anterior to the haemal spine of the
660 third caudal vertebra¹⁶⁹. *Stratigraphy*: Bartonian [NP17] Kumian regional stage⁸³. *Absolute age*
661 *estimate*: 37.2 Ma⁸⁴. *Prior setting*: lognormal prior, minimum age 37.2 Ma, mean=1.0, S.D.=
662 0.42, upper 95% CI: 42.6Ma²⁰.

663

664 **xlii. Node: Stem lineage Antennarioidei**, dating the MRCA of *Antennarius striatus* and
665 *Ogcocephalus radiatus*. *First occurrence*: †*Eophryne bartutii* from the Pesciara beds of ‘Calcari
666 nummulitici’, Bolca, Italy¹⁷¹. *Resolution in phylogenetic analyses*: None. †*Eophryne* was
667 hypothesized to share common ancestry with Antennariidae based on overall morphological
668 similarity¹⁷¹. The phylogenetic placement used for this calibration is conservatively applied to
669 the more inclusive Antennarioidei. *Character states*: triradiate ectopterygoid; spatulate
670 postmaxillary process of premaxilla¹⁷¹⁻¹⁷³. *Stratigraphy*: upper Ypresian [NP14]⁹⁴. *Absolute age*
671 *estimate*: 50 Ma⁸⁴. *Prior setting*: lognormal prior, minimum age 50.0 Ma, mean=1.0, S.D.= 0.6,
672 upper 95% CI: 57.3 Ma¹.

673

674

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678

679 **3. Supplementary results and discussion**

680

681 **a. Phylogeny and classification of Acanthomorpha, and a new delimitation of taxonomic**
682 **orders in Percomorpha**

683 The maximum likelihood analyses of the 702-taxon and 1,084-taxon UCE datasets confidently
684 resolve the phylogenetic relationships of all sampled acanthomorph families. The phylogeny
685 inferred from the IQ-TREE analysis of the multiple-partition, concatenated 1084-taxon dataset is
686 represented in Supplementary Figs. 1-25. The results of the five other phylogenetic analyses are
687 available on Dryad. Bootstrap support values across the entire IQ-TREE phylogeny are high,
688 with most nodes being supported by 100% bootstrap support and only 27 of 1,107 nodes (2.4%)
689 having values $\leq 95\%$. Tree topologies inferred using the different methods described in *Section*
690 *1d* are largely consistent according to comparisons conducted in TOPD-FMTS v.4.6³⁹ (see
691 Supplementary Table 2). Robinson-Foulds metrics across all comparisons were low (≤ 0.033), as
692 were nodal distances (≤ 1.046). Supplementary Table 2 lists the 19 species that differ in their
693 phylogenetic relationships across the different analyses. Most of these species are found in areas
694 of the tree that have been historically difficult to resolve, such as Anthiadidae, Carangidae and
695 Apogonidae. Tree topologies inferred in IQ-TREE and RAxML using multiple-partition, 700-
696 taxon alignments were identical.

697 The non-percomorph acanthomorphs are classified into eight taxonomic orders:
698 Lampriformes, Percopsiformes, Polymixiiformes (a single genus, *Polymixia*) Zeiformes,
699 Gadiformes, Stylephoriformes (a single species, *Stylephorus chordatus*), Trachichthyiformes,
700 and Beryciformes (Fig. 1).

701 The new UCE-inferred phylogeny provides an opportunity to reevaluate the classification
702 of Percomorpha to identify inclusive taxonomic groupings that reflect phylogenetic relationships.
703 An initial effort at building classifications based on molecular phylogenies attempted to preserve
704 the ordinal ranks of the clades such as the Pleuronectiformes, Tetraodontiformes,
705 Atheriniformes, and Synbranchiformes¹⁷⁴. This classification proposed a delimitation of 33
706 taxonomic orders in Percomorpha that each contain an average of only 7.4 families and 492.9
707 species, and resulted in 10% of all percomorph families unassigned to a taxonomic order¹⁷⁴. In
708 Figs. 1 and 2, Supplementary Figs. 1-25, and Supplementary Table 3 we offer an alternative
709 delimitation of 13 clades that we treat as taxonomic orders to accommodate the classification of

710 all 290 percomorph families. In the proposed classification, each taxonomic order comprises an
711 average 2,226.8 species and 18.2 families.

712 The names of the orders in the proposed percomorph classification are consistent with
713 conventions in ichthyological systematics by establishing a link with one of the constituent
714 taxonomic families and using the “-iformes” suffix^{175,176}. For example, this delimitation of
715 Blenniiformes includes the Blenniidae and 48 other families (e.g., cichlids, livebearers, and
716 mullets) that were previously identified as a monophyletic group in molecular phylogenetic
717 studies^{1,4,15,21,22,177}. Previously named Ovalentaria²², this diverse clade of percomorphs had been
718 divided among seven orders¹⁷⁴, one of which, Mugiliformes, included a single family, Mugilidae
719 (mullets).

720

721 **b. Phylogeny of non-percomorph acanthomorphs**

722 *i. Monophyly and relationships of Paracanthopterygii*

723 Similar to other phylogenomic studies, this UCE inferred phylogeny resolves a monophyletic
724 and strongly supported Paracanthopterygii that includes *Polymixia* (beardfishes),
725 Percopsiformes, Zeiformes, *Stylephorus chordatus* (Tube-eye), and Gadiformes (Fig. 1,
726 Supplementary Fig. 1)^{4,15,178}. While relationships within Paracanthopterygii differ among
727 phylogenomic studies, the resolution of a clade containing *Polymixia* and Percopsiformes is the
728 best-supported topology in the concordance factor analysis, with the 95% credible interval of the
729 two alternative resolutions of *Polymixia* not overlapping with the optimal tree topology
730 (Extended Date Fig. 1a, Supplementary Fig. 1).

731

732 *ii. Phylogenetic relationships of Lampriformes*

733 The new UCE phylogeny of Acanthomorpha resolves Lampriformes as the sister lineage of
734 Paracanthopterygii (Fig. 1), which agrees with a previous phylogenetic analysis of UCE loci⁴.
735 Other studies offer conflicting phylogenetic positions for Lampriformes; a phylogenomic
736 analysis of ~1,000 exons resolve lampriforms as the sister lineage of the Acanthopterygii¹⁵,
737 while morphological phylogenies place the lampriforms as the sister lineage of all other
738 Acanthomorpha¹⁸. The Bayesian concordance factor analyses result in overlapping 95% credible
739 intervals for the phylogeny that places lampriforms as sister to Paracanthopterygii and the
740 phylogeny that resolves lampriforms as the sister lineage of all other acanthomorphs (Extended

741 Data Fig. 1b). The phylogeny that resolves lampriforms and Acanthopterygii as sister lineages
742 scored the lowest concordance factors and the 95% credible interval of its concordance factors
743 do not overlap with the credible interval of the phylogeny that resolves Lampriformes as the
744 sister lineage of Paracanthopterygii (Extended Data Fig. 1b).

745

746 *iii. Phylogenetic relationships of Gadiformes*

747 The new UCE phylogeny of Gadiformes is similar to a recent study that utilized DNA sequences
748 from more than 14,000 portions of protein coding genes¹⁷⁹. Results from the two analyses are
749 congruent in resolving *Bregmaceros* (codlets) as the sister lineage of all other Gadiformes, but
750 differ in three specific relationships. The UCE phylogeny resolves Muraenolepididae (eel cods)
751 and Trachyrincidae (armored grenadiers) as sister lineages, but the exon phylogeny resolves
752 *Melanonus* (pelagic cods) as the sister lineage of Muraenolepididae. The UCE phylogeny places
753 Merlucciidae (merluccid hakes) as the sister lineage of an inclusive clade containing Phycidae
754 (phycid hakes), Lotidae (hakes and burbots), and Gadidae (cods and haddocks), but the exon
755 phylogeny resolves Merlucciidae as the sister lineage of a clade containing *Eulichthys polynemus*
756 (Eucla cod), Muraenolepididae, *Melanonus*, Trachyrincidae, Moridae, *Macruronus* (blue
757 grenadiers), *Lyconus* (Atlantic hakes), Bathygadidae (rattails), *Steindachneria argenta*, and
758 Macrouridae. Lotidae is resolved as monophyletic in the exon phylogeny¹⁷⁹, but this lineage is
759 paraphyletic in the UCE phylogeny with *Lota lota* (Burbot) resolved as the sister lineage of a
760 clade containing *Brosme brosme* (Cusk), *Molva* (lings), and Gadidae (true cods) (Fig. 1,
761 Supplementary Fig. 1).

762

763 *iv. Phylogenetic relationships of Acanthopterygii and resolution of the sister lineage of the* 764 *hyper-diverse Percomorpha*

765 Acanthopterygii includes Trachichthyiformes, Beryciformes, and Percomorpha (Fig. 1). The
766 earliest molecular studies identified the sister lineage of percomorphs as either a monophyletic
767 group consisting of Trachichthyiformes and Beryciformes^{1,20} or the beryciform subclade
768 Holocentridae (squirrelfishes)²¹. The UCE inferred phylogeny presented in this study and
769 previous phylogenomic analyses resolve Trachichthyiformes as the sister lineage to all other
770 acanthopterygians and Beryciformes, which includes Holocentridae, as the percomorph sister
771 lineage^{4,15,178,180} (Fig. 1, Supplementary Fig. 2). This topology is also the most supported

772 hypothesis in the concordance factor analyses (Extended Data Fig. 1c). The alternative
773 hypotheses, including the phylogeny that places Holocentridae as sister to Percomorpha,
774 produced substantially lower Bayesian concordance factor scores with 95% credible intervals
775 that do not overlap with the scores of the optimal phylogeny (Extended Data Fig. 1c). The UCE
776 data presented here reject the hypothesis that Holocentridae is the sister lineage of Percomorpha.
777

778 **c. Phylogenetic relationships of Percomorpha**

779 Percomorphs are classified in an astounding 290 taxonomic families¹⁸¹, which is more than
780 living birds (252 families) and many more than mammals (167 families), squamates (58
781 families), amphibians (67 families), and turtles (11 families)¹⁸²⁻¹⁸⁴. By the middle of the 20th
782 century the vast majority of percomorph families were delimited and considered monophyletic
783 groups^{175,185}, but relationships among these delimited taxonomic families were woefully
784 unresolved at the start of the 21st century^{186,187}. This lack of phylogenetic resolution among the
785 nearly 300 taxonomic families led to the now famous analogy that Percomorpha was the “bush at
786 the top” of the teleost phylogeny¹⁸⁸. Since the start of the 21st century, however, molecular
787 studies have offered dramatic resolution of percomorph relationships^{1,4,15,21}. The UCE phylogeny
788 inferred in this study resolves the species sampled from 276 taxonomic families into one of
789 twelve taxonomic orders that contain more than one family. All 12 of these inclusive lineages are
790 monophyletic and strongly supported in the UCE phylogeny (Figs. 1,2, Supplementary Figs. 3-
791 25). Relationships are consistent with previous efforts using Sanger sequenced loci and
792 phylogenomic analyses, but no prior analysis included a high fraction (276 of 290) of the
793 percomorph families.

794 The UCE phylogeny has strong node support along the backbone of Percomorpha
795 including Eupercaria, which is an inclusive clade containing Perciformes, Centrarchiformes,
796 Labriformes, Acropomatiformes, and Acanthuriformes (Fig. 2, Supplementary Figs. 16-25).
797 Previous phylogenetic analyses strongly support monophyly of Eupercaria but provide little
798 resolution and node support for the interrelationships of its constituent lineages^{1,15,21}. The only
799 node in the UCE percomorph phylogeny shared among the delimited 13 taxonomic orders that is
800 not supported with a bootstrap score of 100% is the resolution of Acropomatiformes and
801 Acanthuriformes as a clade, which is supported with a bootstrap score of 99% (Supplementary
802 Fig. 22).

803

804 *i. The deepest node in the phylogeny of percomorphs: the phylogenetic relationships of*
805 *Ophidiiformes*

806 Ophidiiformes (cusk eels) is resolved as the sister lineage to all other percomorphs (Fig. 1).
807 Relationships within this species-rich lineage of mostly marine fishes are not well known and the
808 delimitation of taxonomic families is in flux¹⁸⁹. The UCE phylogeny resolves two clades in
809 Ophidiiformes that correspond to the suborders Bythitoidei and Ophidioidei (Fig. 1,
810 Supplementary Fig. 3). Within Bythitoidei, the families Dinematichthyidae (pygmy brotulas) and
811 Bythitidae (livebearing brotulas) are both monophyletic (Supplementary Fig. 3). As discovered
812 in previous studies¹⁸⁹⁻¹⁹¹, the formerly recognized taxonomic families Parabrotulidae and
813 Aphyonidae are phylogenetically nested in Bythitidae (Supplementary Fig. 3). Historically,
814 Ophidioidei contained Ophidiidae and Carapidae, but the UCE phylogeny (Fig. 1,
815 Supplementary Fig. 3) as well as previous studies using whole mtDNA genome sequences and
816 Sanger sequenced nuclear genes resolve Carapidae as phylogenetically nested within
817 Ophidiidae^{1,21,119,192}, prompting the synonymization of the family Carapidae with Ophidiidae¹⁷⁴.
818

819 *ii. Phylogenetic relationships of Batrachoididae*

820 There is limited taxon sampling of Batrachoididae in the UCE phylogeny, but the subfamily
821 Batrachoidinae (sampled with *Batrachoides pacifici* and *Opsanus tau*) is paraphyletic
822 (Supplementary Fig. 3). Porichthynae is paraphyletic in a phylogeny inferred from Sanger
823 sequenced mitochondrial and nuclear genes¹¹⁹.
824

825 *iii. Phylogeny of Gobiiformes*

826 One of the most surprising results from molecular analyses of percomorph phylogeny was the
827 discovery that gobies, cardinalfishes (Apogonidae), and nurseryfishes (Kurtidae) resolve in a
828 strongly supported monophyletic group^{20,193,194}. Subsequent molecular studies resolved two
829 competing hypotheses of relationships among the major lineages of Gobiiformes: 1) *Kurtus* and
830 Apogonidae resolved as a clade, or 2) Apogonidae as the sister lineage of a clade containing
831 *Trichonotus* (sand divers) and Gobioidei^{1,4,21,194-198}. The UCE phylogeny in this study resolves
832 two major lineages in Gobiiformes: the Apogonoidei that contains *Kurtus* and Apogonidae, and a
833 clade containing *Trichonotus* and Gobioidei (Fig. 1, Supplementary Figs. 3,4). The relationships

834 of the eight taxonomic families classified in Gobioidei are identical to phylogenies inferred using
835 Sanger sequenced mtDNA and nuclear genes^{197,198} (Fig. 1, Supplementary Fig. 4).

836

837 ***iv. Phylogenetic relationships of Scombriformes and Syngnathiformes***

838 Scombriformes (e.g., tunas, cutlassfishes and butterfishes) and Syngnathiformes (e.g., seahorses,
839 flying gurnards and dragonets) are resolved as sister lineages in the UCE phylogeny (Fig. 1), a
840 result that is consistent with other molecular phylogenetic analyses^{1,4,15}. This particular result has
841 the surprising implication that relative to all other percomorph teleosts, tunas and seahorses are
842 closely related.

843 Tunas, barracudas, cutlassfishes and swordfishes were historically classified in
844 Scombroidei. Early phylogenetic analyses of Sanger sequenced mtDNA and nuclear genes
845 resolved species classified in the traditional delimitation of Scombroidei into two distantly
846 related percomorph lineages¹⁹⁹. Xiphiidae (swordfishes), Istiophoridae (billfishes) and
847 Sphyraenidae (barracudas) were resolved in the clade Carangiformes along with flatfishes, jacks
848 and archerfishes (Fig. 1)⁴⁸. The remaining lineages of the historical Scombroidei—Scombridae
849 (tunas), Gempylinae (snake mackerels), Trichiurinae (cultassfishes) and *Pomatomus saltatrix*
850 (Bluefish)—are resolved in the clade Scombriformes that also includes the stromatioids, e.g.,
851 Stromateidae (butterfishes) and Chiasmodontidae (swallowers)²⁹. Other lineages in
852 Scombriformes include the enigmatic *Icosteus aenigmaticus* (Ragfish) and *Amarsipus carlsbergi*
853 (Bagless Glassfish), both of which are deep-branching, monotypic lineages that long evaded
854 phylogenetic resolution among percomorphs (Fig. 1, Supplementary Fig. 5). The UCE
855 phylogeny resolves *Lepidocybium flavobrunneum* (Escolar) as the sister lineage of a clade
856 containing Gempylidae and Trichiuridae (Fig. 1, Supplementary Fig. 6). *Lepidocybium*
857 *flavobrunneum* is traditionally classified in Gempylidae, which is paraphyletic in the UCE
858 phylogeny as the remaining gempylids are more closely related to species of Trichiuridae (Fig. 1,
859 Supplementary Fig. 6). This relationship has previously been resolved in a phylogenetic analysis
860 using morphological data¹²².

861 Syngnathiformes as consisting of seahorses and pipefishes, flying gurnards, goatfishes,
862 and dragonets was first resolved as a clade in phylogenetic analyses of Sanger sequenced
863 mtDNA and nuclear genes^{21,200}. Prior to the application of molecular phylogenetics,
864 Callionymidae (dragonets) and Draconettidae (draconetids) were classified as closely related to

865 Gobiesocidae (clingfishes)²⁰¹⁻²⁰⁴. As reflected in molecular phylogenies, Pietsch⁹⁸ proposed that
866 Dactylopteridae (helmet gurnards) were closely related to other syngnathiform lineages, but they
867 were classified by others with the sculpins, rockfishes and scorpionfishes in Scorpaeniformes.
868 Mullidae (goatfishes) were long classified in the wastebasket taxon Perciformes^{175,202,205} but
869 thought to be closely related to Haemulidae (grunts) and Sparidae (porgies)²⁰⁶. The UCE
870 phylogeny resolves two major lineages of Syngnathiformes: 1) a clade we delimit as Mulloidei
871 that contains Pegasidae (seamoths), Dactylopteridae, Mullidae, Callionymidae, and
872 Draconettidae and 2) a lineage we delimit as Syngnathoidei, consisting of Syngnathidae
873 (pipefishes and seahorses), Solenostomidae (ghost pipefishes), Aulostomidae (trumpetfishes),
874 Fistularidae (cornetfishes), Centriscidae (shrimpfishes) and Macroramphosidae (snipefishes)
875 (Fig. 1, Supplementary Figs. 7-9).

876

877 **v. Relationships among Blenniiformes, Synbranchiformes and Carangiformes**

878 The UCE phylogeny resolves a strongly supported monophyletic group where Blenniiformes
879 (e.g., blennies, cichlids, livebearers, and mullets) is the sister lineage of a clade containing
880 Synbranchiformes (e.g., swamp eels, gouramies, snakeheads, and leaffishes) and Carangiformes
881 (e.g., flatfishes, jacks and pompanos, billfishes, and barracudas). The discovery of this clade is
882 one of the many dramatic results from molecular phylogenetics of percomorphs¹, as this large
883 and inclusive group contains more than 7,300 species that are classified into 92 taxonomic
884 families.

885

886 **vi. Blenniiformes: Phylogenetic relationships of Atherinoidei (Cyprinodontoidea, Belonoidea 887 and Atherinoidea)**

888 The monophly of Blenniiformes—originally named Ovalentaria—resulted from a phylogenetic
889 analysis of Sanger sequenced nuclear genes²². In the UCE phylogeny, Blenniiformes is
890 monophyletic and contains two major clades: Atherinoidei (formerly Atherinomorpha) and all
891 other lineages of Blenniiformes. Atherinoidei contains three major lineages: 1) Belonoidea
892 (formerly Beloniformes, which includes needlefishes, medakas, halfbeaks, and flying fishes), 2)
893 Cyprinodontoidea (formerly Cyprinodontiformes, which includes killifishes, rivulines, pupfishes,
894 and livebearers), and 3) Atherinoidea (formerly Atheriniformes, which includes silversides and
895 rainbowfishes). Phylogenomic analysis of our UCE dataset results in a well-resolved phylogeny

896 of Atherinoidei, where every node along the backbone of the atherinoid tree is supported with a
897 100% bootstrap score (Fig. 1, Supplementary Fig. 10). Morphological phylogenies resolve
898 Atherinoidea as the sister lineage of a clade containing Belonoidea and Cyprinodontoidea^{149,207},
899 but the UCE phylogeny resolves Atherinoidea and Belonoidea as sister lineages (Fig. 1,
900 Supplementary Fig. 10).

901 Over the past 15 years, the number of taxonomic families recognized in
902 Cyprinodontoidea (killifishes, rivulines, pupfishes, and livebearers) increased from 10 to
903 16^{181,186}. The recognition of these six additional families resulted from phylogenetic analyses of
904 Sanger sequenced mtDNA and nuclear genes that overturned the results of morphological
905 studies²⁰⁸⁻²¹⁰ and demonstrated the non-monophyly of Cyprinodontidae (pupfishes) and
906 Poeciliidae (livebearers). The UCE phylogeny (Fig. 1, Supplementary Fig. 10) is consistent with
907 morphological phylogenetic analyses in the resolution of Rivulidae (New World rivulines),
908 Aplocheilidae (Asian rivulines), and Nothobranchiidae (African rivulines) as a monophyletic
909 group, as well as a clade containing Poeciliidae, Anablepidae (four-eyed fishes), *Valencia*
910 (toothcarps), Procatopodidae (African lampeyes), Fundulidae (topminnows), Cyprinodontidae,
911 *Profundulus* (Middle American killifishes), Goodeidae (goodeids), and *Cubanichthys* (Caribbean
912 killifishes)^{211,212}. Morphological and molecular phylogenetic studies show congruence on
913 specific relationships within Cyprinodontoidea. For example, the morphological analysis by
914 Costa²¹² identified *Profundulus* and Goodeidae as a clade. This result is supported in the UCE
915 phylogeny as well as studies from Sanger sequenced mtDNA and nuclear genes²⁰⁸⁻²¹⁰. Among
916 the notable differences between molecular and morphological phylogenies of cyprinodontoids is
917 the resolution of Cyprinodontidae and Fundulidae as sister lineages (Fig. 1, Supplementary Fig.
918 10).

919 Belonoidea is monophyletic in the UCE phylogeny, but despite limited taxon sampling
920 the families Zenarchopteridae and Hemiramphidae are found to be paraphyletic (Fig. 1,
921 Supplementary Fig. 10). Five families of Belonoidea are recognized in Eschmeyer's Catalog of
922 Fishes¹⁸¹. Phylogenies resulting from analyses of morphological characters and Sanger
923 sequenced mtDNA nest Scomberesocidae (sauries) well within Belonidae (needlefishes) and
924 resolve Hemiramphidae (halfbeaks) as paraphyletic relative to Exocoetidae (flyingfishes)^{213,214}.
925 In the UCE phylogeny, the hemiramphid *Oxyporhamphus micropterus* is more closely related to
926 the sampled species of Exocoetidae than the other two sampled hemiramphids (Fig. 1,

927 Supplementary Fig. 10), as previously inferred using morphological data²¹⁵. The new phylogeny
928 also resolves *Zenarchopterus dispar* as more closely related to the sampled belonid species
929 *Xenentodon cancila* than to the other two sampled zenarchopterid species (Fig. 1, Supplementary
930 Fig. 10).

931 There are 11 taxonomic families of Atherinoidea recognized in Eschmeyer's Catalog of
932 Fishes¹⁸¹, but Notocheiridae is well nested in Atherinopsidae in phylogenetic analyses of Sanger
933 sequenced mtDNA and nuclear genes^{216,217}. Of the ten other families, eight are sampled in the
934 UCE phylogeny. Missing from the analysis is the monotypic Dentatherinidae (Mercer's tusked
935 silverside) and Telmatherinidae (Celebes rainbowfishes). The UCE phylogeny is consistent with
936 current classifications and previous molecular and morphological phylogenetic analyses in
937 resolving Atherinopsidae (New World silversides) as the sister lineage of all other
938 atherinoids^{1,21,216,218} (Fig. 1, Supplementary Fig. 10). Another area of agreement in the UCE
939 phylogeny and previous molecular analyses is the resolution of a clade containing the
940 monogeneric Atherionidae (pricklenose silversides) and Phallostethidae (priapiumfishes)²¹⁷ (Fig.
941 1, Supplementary Fig. 10).

942 There are differences in the recognition of taxonomic families of Atherinoidea in
943 Eschmeyer's Catalog of Fishes¹⁸¹ and Nelson et al.¹⁷⁶ that involve lineages associated with
944 Melanotaeniidae (rainbowfishes). Following Dyer and Chernoff²¹⁸, Nelson et al.¹⁷⁶ treat
945 Bedotiidae (Madagascar rainbowfishes), Pseudomugilidae (blue eyes), and Telmatherinidae as
946 subfamilies of Melanotaeniidae. This delimitation of Melanotaeniidae is not supported in the
947 UCE phylogeny as Bedotiidae is resolved as the sister lineage of Atherinidae (Old World
948 silversides) (Fig. 1, Supplementary Fig. 10). In previous analyses of Sanger sequenced mtDNA
949 and nuclear genes, Melanotaeniidae is paraphyletic because the species *Cairinsichthys*
950 *rhombosomoides* is resolved as the sister lineage of a clade containing all sampled species of
951 Telmatherinidae and Pseudomugilidae^{216,217}; however, in the UCE phylogeny Melanotaeniidae—
952 sampled with *Cairinsichthys* and *Iriatherina werneri*—is monophyletic with strong node support
953 (Fig. 1, Supplementary Fig. 10). The non-monophyly of Melanotaeniidae in previous
954 phylogenetic analyses is likely driven by limited phylogenetic informativeness of Sanger
955 sequenced genes to resolve relationships among Atherinoidea, as evidenced by the low bootstrap
956 and Bayesian posterior node support values associated with these phylogenies^{216,217}.

957

958 **vii. Blenniiformes: Phylogenetic relationships of Cichlidae, Pholidichthys and Polycentridae**
959 Within Blenniiformes, the UCE phylogeny resolves a clade containing Cichlidae, *Pholidichthys*
960 (engineer gobies) and Polycentridae (leaffishes) (Fig. 1, Supplementary Fig. 11). Before the
961 advent of molecular phylogenetics, the morphology of the pharyngeal jaw apparatus was cited as
962 evidence to group Cichlidae with Labridae (wrasses and parrotfishes), Embiotocidae
963 (surfperches), and Pomacentridae (damselfishes) in a group named Labroidei²¹⁹⁻²²². Phylogenetic
964 analyses of ten Sanger sequenced nuclear genes strongly resolved *Pholidichthys* (engineer
965 gobies) and Cichlidae as sister lineages, but these analyses did not confidently identify a sister
966 lineage of this clade within the Blenniiformes^{1,22}. As recently delimited²²³, Polycentridae
967 contains five species classified among four genera distributed in freshwater habitats in Africa
968 and South America: *Afronandus sheljuzhkoi* (Africa), *Polycentropsis abbreviata* (Africa),
969 *Polycentrus* (two species in South America), and *Monocirrhus polyacanthus* (South America).
970 The resolution of the freshwater Polycentridae as the sister lineage of the clade containing
971 *Pholidichthys*-Cichlidae provides insight into the origin of freshwater blenniiform lineages and
972 the biogeographic relationships of freshwater fishes in South America and Africa^{224,225}.

973
974 **viii. Blenniiformes: Relationships of Mugilidae, Ambassidae, Pseudochromidae,
975 Congrogadidae and Pomacentridae**
976 The phylogenetic relationships of Mugilidae (mullets) have long vexed phylogenetic studies of
977 acanthomorphs, leading Stiassny²²⁶ to declare in a morphological phylogenetic study that
978 “without mullets our lives would be a lot simpler.” Morphological analysis of branchial
979 musculature supported a hypothesis that Mugilidae and Atherinoidei (formerly Atherinomorpha)
980 are sister lineages²²⁷, but analysis of pelvic girdle morphology supported an affinity with other
981 percomorph lineages²²⁶. The heterogeneity of relationships inferred from these two different
982 anatomical systems appears explained in the results of molecular phylogenetic analyses with
983 Mugilidae, Atherinoidei, or other “higher” percomorph lineages sensu Johnson and Patterson¹⁸
984 resolved in Blenniiformes. In Sanger sequencing efforts, the sister lineage of Mugilidae within
985 Blenniiformes varies between Plesiopidae (longfins) and Embiotocidae (surfperches), always
986 with weak node support^{1,22,177}. However, analysis of the UCE dataset and phylogenomic
987 inferences based on exon data¹⁵ both resolve Mugilidae and Ambassidae as sister lineages with
988 strong node support (Fig. 1, Supplementary Fig. 11).

989 In phylogenetic studies of Sanger sequenced mtDNA and nuclear genes,
990 Pseudochromidae (dottybacks) is resolved as paraphyletic relative to Plesiopidae (roundheads)
991 and Pomacentridae (damselfishes)^{1,21}. In the UCE phylogeny, Pseudochromidae is paraphyletic
992 because Congrogadidae (eelblennies) is resolved as the sister lineage of a clade containing the
993 remaining species of Pseudochromidae, Plesiopidae, Pomacentridae, Grammatidae (basslets),
994 Opistognathidae (jawfishes), Gobiesocidae (clingfishes), and Blennioidei (blennies) (Fig. 1,
995 Supplementary Fig. 11).

996

997 ***ix. Blenniiformes: Phylogenetic relationships of Grammatidae, Opistognathidae, Gobiesocidae
998 and Blennioidei***

999 The UCE phylogeny is congruent with trees inferred using exon data and Sanger sequenced
1000 mtDNA and nuclear genes in resolving a clade containing Grammatidae, Opistognathidae,
1001 Gobiesocidae, and Blennioidei^{1,15,21}, but differs in resolving Embiotocidae (surfperches) as the
1002 sister lineage of this clade (Fig. 1, Supplementary Fig. 11). Grammatidae and Opistognathidae
1003 are successive outgroups to a clade containing Gobiesocidae and Blennioidei (Fig. 1,
1004 Supplementary Fig. 11). In the UCE phylogeny, the relationships among the families of
1005 Blennioidei—Tripterygiidae (triplefin blennies), Dactyloscopidae (sand stargazers), Blenniidae
1006 (combtooth blennies), Clinidae (kelp blennies), Labrisomidae (labrisomid blennies), and
1007 Chaenopsidae (tube blennies)—are nearly identical to those inferred from Sanger sequenced
1008 mtDNA and nuclear genes^{1,21} (Fig. 1, Supplementary Fig. 11). However, a study with the largest
1009 sampling of blennioid species indicates that Labrisomidae and Chaenopsidae are both
1010 paraphyletic²²⁸.

1011

1012 ***x. Phylogenetic relationships of Synbranchiformes***

1013 Previous analyses of Sanger sequenced genes and phylogenomic datasets consistently resolve
1014 Synbranchoidei (swamp eels, earthworm eels, armored sticklebacks, and freshwater spiny eels)
1015 and Anabantoidei (gouramies, snakeheads, and Asian leaffishes) as a clade^{1,15,21,22,177}.

1016 One of the many surprises to emerge from the molecular phylogenies of percomorphs
1017 was the resolution of *Indostomus* (armored sticklebacks) as nested within
1018 Synbranchoidei^{1,177,192,229,230}. Traditionally, *Indostomus* was classified with seahorses,
1019 shrimpfish, and sticklebacks in the polyphyletic Gasterosteiformes based on the presence of

1020 dermal bony plates along the side of the body, a reduced cranial skeleton, and a small mouth
1021 size¹⁸⁶. Analysis of developmental ontogeny of several morphological traits led to the conclusion
1022 that *Indostomus* is closely related to sticklebacks (Gasterosteidae)²³¹. However, *Indostomus* and
1023 sticklebacks are distantly related in all molecular phylogenies and Gasterosteidae is classified
1024 here in Perciformes. Aside from the resolution of *Indostomus* as a synbranchoid, specifically as
1025 the sister lineage of Synbranchidae (swamp eels), the UCE phylogeny of Synbranchoidei is
1026 identical to relationships inferred from morphology where Synbranchidae is resolved as the sister
1027 lineage of a clade containing Chaudhuriidae (earthworm eels) and Mastacembelidae (freshwater
1028 spiny eels)²³² (Fig. 1, Supplementary Fig. 12).

1029 Anabantoidei—delimited here as including Nandidae (Asian leaffishes), Badidae
1030 (chameleonfishes), Pristolepididae (Malayan leaffishes), Channidae (snakeheads),
1031 Helostomatidae (Kissing Gourami), Anabantidae (climbing gouramies), and Osphronemidae
1032 (gouramies and fighting fishes)—is monophyletic in the UCE phylogeny and characterized by
1033 the unique possession of teeth on the parasphenoid^{223,233:9-12}. The UCE phylogeny resolves a
1034 clade containing Pristolepididae, Nandidae, and Badidae (Fig. 1, Supplementary Figs. 12, 13),
1035 which is supported with a unique morphology of the ventral gill arch musculature where the
1036 *rectus ventralis* IV has an additional insertion on the ceratobranchial 5^{223,234}. The clade
1037 containing Badidae and Nandidae is supported with two morphological traits: 1) a distally
1038 divided haemal spine on the second preural centrum and 2) the restriction of the attachments
1039 cells in eggs to the ventral side of the yolk sac^{223: Figs. 2d-f, 4}. Previous classifications grouped
1040 Pristolepididae and Badidae in Nandidae¹⁸⁶. Given that the current delimitation of Nandidae and
1041 Pristolepididae each contain a single genus and Badidae includes two genera, future
1042 classifications can reduce monogeneric families and limit redundant taxonomic group names by
1043 classifying all these lineages in Nandidae.

1044 The UCE phylogeny resolves Channidae, Helostomatidae, Anabantidae, and
1045 Osphronemidae as a strongly supported monophyletic group (Fig. 1, Supplementary Figs. 12,13).
1046 This phylogeny differs from those inferred using Sanger sequenced nuclear genes in resolving
1047 Helostomatidae as the sister lineage of a clade containing Anabantidae and Osphronemidae
1048 versus Helostomatidae as the sister lineage of Anabantidae or Osphronemidae^{1,223}.

1049
1050

1051 **xi. Phylogenetic relationships of Carangiformes**

1052 The UCE phylogeny is broadly congruent with other studies using UCEs⁴⁸, but differs in the
1053 relationships of *Lates*, *Centropomus* (snooks), and *Sphyraena* (barracudas) (Fig. 1,
1054 Supplementary Fig. 14). Analyses of Sanger sequenced nuclear genes consistently supported the
1055 monophyly of Carangiformes^{1,21,235,236}, but did not strongly support the relationships among the
1056 major carangiform clades. The UCE phylogeny includes a clade containing Centropomidae
1057 (sampled with *Lates* and *Centropomus*), *Lactarius lactarius* (False Trevally), and *Sphyraena*.
1058 Previous analyses using UCEs also resolved Centropomidae as monophyletic⁴⁸, but placed
1059 *Sphyraena* as the sister lineage of all other Carangiformes. A phylogenetic analysis of
1060 Carangiformes based on a dataset that combines a smaller number of UCE loci with discretely
1061 coded morphological characters resolves Centropomidae as paraphyletic with *Lates* and
1062 *Psammoperca*, forming a clade that is sister to a lineage containing *Centropomus*, *Lactarius* and
1063 *Sphyraena*²³⁷.

1064 The UCE phylogeny resolves three major lineages of Carangiformes: 1) an unnamed
1065 clade (discussed above) containing Centropomidae, *Lactarius*, and *Sphyraena*, 2) an unnamed
1066 clade containing Polynemidae (threadfins) and Pleuronectoidei (flatfishes), and 3) a clade
1067 delimited here as Carangoidei that contains *Leptobrama* (beachsalmons), *Toxotes* (archerfishes),
1068 *Nematistius pectoralis* (roosterfish), *Mene maculata* (moonfish), *Xiphias gladius* (swordfish),
1069 Istiophoridae (billfishes), and Carangoidea (Fig. 1, Supplementary Figs. 14,15).

1070 As resolved in several analyses using Sanger sequenced loci and UCE-based
1071 phylogenomic analyses^{1,21,25,48,119}, the traditional delimitation of Carangidae (jacks and
1072 pompanos) is paraphyletic. Carangidae, limited to the subfamilies Naucratinae and Caranginae,
1073 is the sister lineage of a clade containing the former carangid subfamilies Scomberoidinae and
1074 Trachinotinae, Echeneidae (remoras), *Rachycentron canadum* (cobia), and *Coryphaena*
1075 (dolphinfishes) (Fig. 1, Supplementary Fig. 15).

1076

1077 **xii. Eupercaria: relationships among Perciformes, Centrarchiformes, Labrifomes,
1078 Acropomatiformes and Acanthuriformes**

1079 Phylogenetic analyses of Sanger sequenced loci led to the resolution of Eupercaria, an inclusive
1080 clade that contains more than 37% of species and 53% of all taxonomic families in
1081 Percomorpha¹⁷⁴. While earlier studies resolved a clade containing Perciformes,

1082 Centrarchiformes, Labrifomes, Acropomatiformes, and Acanthuriformes, phylogenies inferred
1083 from Sanger sequenced genes provided little resolution for the relationships among the major
1084 lineages of Eupercaria^{1,21}. Analysis of the UCE dataset results in a phylogeny where Eupercaria
1085 is resolved as a clade with strong support for the relationships among the major lineages;
1086 Perciformes, Centrarchiformes, and Labrifomes are found to be successive outgroups to a clade
1087 containing Acropomatiformes and Acanthuriformes. All of the nodes along the backbone of the
1088 eupercarian phylogeny are supported with bootstrap values of 100% except the clade containing
1089 Acropomatiformes and Acanthuriformes (BSS = 99%) (Fig. 2, Supplementary Fig. 22). The
1090 phylogenomic analyses of the UCE loci resolve this substantial issue of the teleost phylogeny,
1091 which was once identified as the new bush on the top of the percomorph phylogeny²¹.

1092

1093 *xiii. Phylogenetic relationships of Perciformes*

1094 Prior to the application of molecular data to investigate the phylogenetic relationships of teleosts,
1095 the vast majority of percomorphs were classified in the catchall taxon Perciformes. In addition to
1096 perciforms, percomorphs included morphologically unique and disparate lineages such as
1097 Pleuronectiformes (flatfishes), Tetraodontiformes (pufferfishes), and Gasterosteiformes
1098 (sticklebacks and seahorses). Any lineage of percomorph that was not as morphologically
1099 distinctive as a flatfish or seahorse was classified in Perciformes. At the end of the 20th century
1100 Perciformes contained more than 10,000 species and 160 taxonomic families¹⁸⁶. Phylogenetic
1101 analyses of molecular datasets revealed that the perciform wastebasket contained lineages that
1102 spanned much of the backbone of the Percomorpha phylogeny. The UCE phylogeny offers a
1103 confirmation for the disassembly of Perciformes that involves the migration of more than 100
1104 taxonomic families into nearly all other major lineages of Percomorpha.

1105 An entirely different concept and delimitation of Perciformes emerged from molecular
1106 phylogenetic studies^{1,19,21,177,187,193,238-241}. No longer a taxonomic wastebasket, Perciformes (as
1107 delimited here) contains more than 3,200 species that are classified among at least 53 taxonomic
1108 families and comprises a diverse array of lineages that not only were previously classified as
1109 perciforms, but also as scorpaeniforms and gasterosteiforms^{3,176}. In addition to the namesake
1110 Percidae (perches, walleyes, and darters), the newer concept of Perciformes resulting from
1111 molecular phylogenetic analyses includes seabasses, scorpionfishes, rockfishes, sculpins,

1112 searobins, weaverfishes, notothenioids, eelpouts, sticklebacks, flatheads, and many others
1113 (Supplementary Table 3).

1114 Molecular analyses consistently resolve the traditional delimitation of Serranidae (sea
1115 basses), which contains more than 60 genera and 450 species, as non-monophyletic in
1116 Perciformes^{1,187,241}. In the UCE phylogeny, taxa comprising the traditional Serranidae resolve in
1117 four or five different lineages (Supplementary Fig. 16). Epinephelidae (groupers) and
1118 Anthiadidae (basslets and anthians) are resolved as successive sister lineages or as a
1119 monophyletic group that is the sister lineage of all other Perciformes. The less inclusive
1120 delimitation of Serranidae is strongly resolved as the sister lineage of Bembropidae (duckbills).
1121 *Acanthistius* is resolved as either the sister lineage of Anthiadidae, where it is traditionally
1122 classified, or as the sister lineage of all other perciforms except Epinephelidae and Anthiadidae.
1123 The enigmatic *Niphon spinosus*, which has long avoided a confident phylogenetic or taxonomic
1124 placement^{242,243}, strongly resolves as the sister lineage of Percidae (Fig. 2, Supplementary Fig.
1125 16).

1126 In addition to the non-monophyly of the traditional Serranidae, the molecular phylogeny
1127 of Perciformes provides several strongly supported relationships that were not anticipated from
1128 inferences using morphological characters^{18,205,244}. The UCE phylogeny is congruent with earlier
1129 analyses using Sanger sequenced loci but provides greater resolution and node support than
1130 obtained in earlier efforts. The commercially and scientifically important freshwater lineage
1131 Percidae is resolved in a clade that contains the marine *Niphon spinosus* and Trachinidae
1132 (weaverfishes), a lineage we refer to as Percoidei (Fig. 2, Supplementary Fig. 16, Supplementary
1133 Table 3). Notothenioidei includes the well-known Antarctic adaptive radiation as well as
1134 *Percophis brasiliensis* (Brazilian Flathead), which is distributed in the Atlantic Ocean from the
1135 coast of southern Brazil to central Argentina²⁴⁵. Notothenioidei is strongly resolved as the sister
1136 lineage of a new delimitation of Scorpaenoidei that includes almost all the lineages traditionally
1137 classified in Scorpaeniformes such as Platycephalidae (flatheads), Scorpaenidae (scorpionfishes
1138 and rockfishes), Triglidae (searobins), Bembridae (deepwater flatheads), Platycephalidae
1139 (flatheads), Hoplichthyidae (ghost flatheads), Hexagrammidae (greenlings), Trichodontidae
1140 (sandfishes), Cyclopteridae (lumpfishes), Liparidae (snailfishes), and Cottidae (sculpins). In
1141 addition to these classic scorpaeniform lineages the new delimitation of Scorpaenoidei includes

1142 Zoarcoidea (eelpouts, ronquils, and wolffishes) and Gasterosteoidae (sand eel, tubesnouts, and
1143 sticklebacks) (Fig. 2, Supplementary Figs. 17, 18).

1144 The UCE phylogeny of Scorpaenoidei is quite different from trees inferred using a
1145 dataset of morphological characters and Sanger sequenced mtDNA and nuclear genes²⁴⁶. For
1146 example, Smith et al.²⁴⁶ resolved Platyccephalidae as the sister lineage of Triglidae, but the UCE
1147 phylogeny places Platyccephalidae as the sister lineage of all other scorpaenoids (Fig. 2,
1148 Supplementary Fig. 17). In the UCE tree there are three major clades of Scorpaenoidei that
1149 contain multiple taxonomic families, but several families resolve along the backbone of the
1150 scorpaenoid phylogeny. Scorpaenoidea is here delimited as a strongly supported clade that
1151 includes *Normanichthys crockeri* (Mote Sculpin), Neosebastidae (gurnard scorpionfishes),
1152 Congiopodidae (horsefishes), Synanceiidae (stonefishes), and Scorpaenidae (Fig. 2,
1153 Supplementary Fig. 17). Bembridae, Triglidae, and Anoplopomatidae (sablefishes) resolve as
1154 successive sister lineages to a large clade containing all the lineages classified in Cottoidea
1155 (sculpins), Gasterosteoidae, and Zoarcoidea (Fig. 2, Supplementary Figs. 18, 19, Supplementary
1156 Table 3).

1157 Gasterosteoidae and Zoarcoidea resolve as sister lineages with strong node support,
1158 which is a result supported in earlier phylogenetic analyses of Sanger sequenced mtDNA and
1159 nuclear genes^{1,21}. Within Zoarcoidea the Bathymasteridae (ronquils) are resolved as the sister
1160 lineage of all other zoarcoids. In an earlier study using Sanger sequenced loci, Bathymasteridae
1161 was resolved as paraphyletic¹, but the UCE phylogenetic analyses sample all three bathymasterid
1162 genera and strongly support the lineage as a monophyletic group (Supplementary Fig. 18).
1163 *Scybalina cerdale* (Graveldiver) is nested well within Stichaeidae (Supplementary Fig. 18) while
1164 *Gymnoclinus cristulatus* (Trident Prickleback) is distantly related to other stichaeids
1165 (Supplementary Fig. 19), resolving as the sister lineage of Neozoarcidae. Previous phylogenetic
1166 analyses of morphology and Sanger sequenced mtDNA and nuclear genes resolve Stichaeidae as
1167 paraphyletic²⁴⁷⁻²⁴⁹. The zoarcoid lineages *Cryptacanthodes* (wrymouths), Lumpenidae
1168 (pricklebacks), *Zaprora silenus* (Prowfish), Opisthocentridae (ocellated blennies), *Ptilichthys*
1169 (*goodei*) (Quillfish), Pholidae (gunnels), *Gymnoclinus*, Neozoarcidae, Anarhichadidae
1170 (wolffishes), and Zoarcidae (eelpouts) resolve as a strongly supported clade that is the sister
1171 lineage of the paraphyletic Stichaeidae (Fig. 2, Supplementary Figs. 18,19).
1172

1173 **xiii. Phylogenetic relationships of Centrarchiformes**

1174 Phylogenetic analyses of Sanger sequenced mtDNA and nuclear genes led to the discovery of
1175 Centrarchiformes, a clade of approximately 300 species classified in at least 16 taxonomic
1176 families^{1,21,236,250,251}. Consistent with these earlier phylogenetic studies^{1,21,250,251}, the UCE
1177 phylogeny resolves *Percalates* as the sister lineage of all other Centrarchiformes (Fig. 2,
1178 Supplementary Fig. 20). Terapontoidei includes Girellidae (nibblers), Scorpidae (halfmoons),
1179 *Dichistius*, Microcanthidae, *Oplegnathus* (knifejaws), Kyphosidae (sea chubs), *Kuhlia* (flagtails),
1180 and Terapontidae (grunters) (Supplementary Fig. 20). Centrarchoidei is delimited here as a clade
1181 that includes *Enoplosus armatus* (Oldwife) and Percichthyidae (temperate perches),
1182 Centrarchoidea which includes Centrarchidae (sunfishes, blackbasses, and pygmy sunfishes) and
1183 Siniperidae (Chinese perches), and Cirrhitoidae which includes Cirrhitidae (hawkfishes),
1184 Latridae (trumpeters), *Chironemus* (kelpfishes), *Cheilodactylus*, and *Aplodactylus* (marblefishes)
1185 (Fig. 2, Supplementary Fig. 20, Supplementary Table 3).

1186 The classification of Centrarchiformes is dynamic and unsettled, reflected in part by a
1187 high proportion of families that contain a single genus. Molecular phylogenies consistently
1188 resolve two sets of traditionally delimited centrarchiform families as non-monophyletic. First,
1189 the two species of *Percalates* were traditionally classified as Percichthyidae²⁴⁴, but resolve as the
1190 sister lineage of all other centrarchiforms^{1,21,174,236,250}. There is no described taxonomic family to
1191 accommodate the classification of *Percalates*. Second, the classification of families within
1192 Cirrhitoidae was dramatically realigned as a result of molecular phylogenetic analyses.

1193 Traditionally, Cheilodactylidae (morwongs) contained three to five genera and approximately 20
1194 species^{202,252}. Previous phylogenetic analyses of mtDNA genes, morphological characters, and
1195 UCE data resolved Cheilodactylidae as polyphyletic, with all but two of the species traditionally
1196 classified as cheilodactylids nested within a paraphyletic Latridae²⁵³⁻²⁵⁵. The findings of these
1197 phylogenetic analyses resulted in a transfer of these species to Latridae from Cheilodactylidae.
1198 The new UCE phylogeny is consistent with these previous results, but differs from the
1199 phylogeny presented in Lüdt et al.²⁵⁵ in resolving *Aplodactylus* rather than *Chironemus* as the
1200 sister lineage of *Cheilodactylus* (Fig. 2, Supplementary Fig. 20).

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1203

1204 **xiv. Phylogenetic relationships of Labriformes**

1205 The UCE phylogeny strongly resolves a clade we delimit as Labriformes which contains two
1206 major lineages: Uranoscopoidei and Labroidei (Supplementary Fig. 21). As resolved in previous
1207 phylogenies inferred from Sanger sequenced nuclear genes¹⁹⁸, Uranoscopoidei contains
1208 Uranoscopidae (stargazers), Ammodytidae (sandlances), and Pinguipedidae (sandperches) as
1209 successive sister lineages to a clade containing the enigmatic *Cheimarrichthys fosteri*
1210 (Torrentfish) and Leptoscopidae (southern sandfishes) (Fig. 2, Supplementary Fig. 21).
1211 Morphological studies place *Cheimarrichthys* as closely related to Pinguipedidae or as the sister
1212 lineage of all “trachinoids,” which include all the lineages delimited here as Uranoscopoidei²⁵⁶⁻
1213 ²⁵⁸. The hypothesis that *Cheimarrichthys* and Pinguipedidae share common ancestry was rejected
1214 through the discovery that *Cheimarrichthys* shares more derived morphological character states
1215 with Leptoscopidae than any other “trachinoid” or uranoscopoid lineage²⁵⁹. Reflective of their
1216 shared common ancestry, *Cheimarrichthys* and Leptoscopidae have a similar geographic
1217 distribution; *Cheimarrichthys* is an anadromous species widely distributed among the rivers of
1218 New Zealand and leptoscopids are distributed along the Pacific and Indian coasts of Australia
1219 and New Zealand^{260,261}.

1220 Labroidei includes the sister lineages *Centrogenys vaigiensis* (False Scorpionfish) and
1221 Labridae (wrasses and parrotfishes) (Fig. 2, Supplementary Fig. 21). As discussed above
1222 regarding Blenniiformes, the species rich marine Labridae and the freshwater Cichlidae were
1223 hypothesized as closely related based on the morphology of the modified “labroid” pharyngeal
1224 jaw apparatus²¹⁹⁻²²¹, which is now known to have originated multiple times in Percomorpha²².
1225 Previous molecular phylogenetic analyses using Sanger sequenced nuclear genes demonstrated
1226 that labrids and cichlids are not closely related despite both having modified “labroid”
1227 pharyngeal jaws, but these early molecular studies resulted in an ambiguous and poorly
1228 supported resolution of the species rich Labridae^{1,22}. The resolution of Labridae and *Centrogenys*
1229 *vaigiensis* as sister lineages in the UCE phylogeny is interesting as both lineages have all three
1230 components of the modified labroid pharyngeal jaw apparatus²².

1231

1232 **xv. Phylogenetic relationships of Acropomatiformes**

1233 The discovery of Acropomatiformes resulted entirely from phylogenetic analyses of Sanger
1234 sequenced mtDNA and nuclear and genes^{1,198,236,245} and was never intimated through the study of

1235 morphology^{205,244}. The lineage is an odd assortment of deep sea and near shore percomorph
1236 lineages that were previously classified in the wastebasket version of Perciformes and the
1237 demonstrably polyphyletic Trachinoidei^{1,198,245}. While molecular studies consistently resolve
1238 Acropomatiformes as a clade, its monophyly is not strongly supported with Bayesian posteriors
1239 or bootstrap values and relationships within the clade differ dramatically across
1240 studies^{1,198,236,245,262}.

1241 The UCE phylogeny resolves Acropomatiformes as monophyletic with 100% bootstrap
1242 support (Fig. 2, Supplementary Fig. 22). All but two nodes within Acropomatiformes are present
1243 in 100% of the bootstrap replicates. First, the clade containing *Bathyclupea* (deepsea herrings),
1244 *Champsodon* (gapers), Creediidae (sandburrowers), and Hemerocoetidae (signalfishes) is
1245 supported with a bootstrap score of 97%. Second, the clade containing *Scombrops*
1246 (gnomefishes), Symphysanodontidae (slopefishes), Epigonidae (deepwater cardinalfishes), and
1247 Howellidae (oceanic basslets) is supported with a 99% bootstrap score (Fig. 2, Supplementary
1248 Fig. 22). The relationships among acropomatiforms in the UCE tree are quite different from any
1249 previous study and include the non-monophyly of Polyprionidae (wreckfishes) as *Polyprion* is
1250 resolved as the sister lineage of a clade containing *Glaucosoma* (pearl perches), Pempheridae
1251 (sweepers), and *Lateolabrax* (Asian seaperches) while *Stereolepis* is the sister lineage of a clade
1252 containing *Banjos* (banjofishes) and Pentacerotidae (armorheads). The resolution of Howellidae
1253 and Epigonidae as sister lineages in the UCE phylogeny is interesting in the context of four
1254 osteological traits shared between these two lineages and the possibility of additional shared
1255 traits in Howellidae and other acropomatiform lineages²⁶³. Future phylogenetic studies will
1256 round out the sampling of Acropomatiformes by including *Dinolestes lewini* (Long-finned Pike),
1257 Malakichthyidae (temperate ocean-basses), and Synagropidae (splitfin ocean-basses) to take
1258 advantage of the strong phylogenetic resolution provided by the UCE loci for this clade.
1259

1260 **xvi. Phylogenetic relationships of Acanthuriformes**

1261 The first wave of molecular phylogenetic analyses of percomorphs was based on whole
1262 mitochondrial genomes and small sets of Sanger sequenced mitochondrial and nuclear genes.
1263 The major lineages of percomorphs and their composition began to emerge because of these
1264 molecular phylogenetic analyses. The monophyly of the major percomorph lineages and their
1265 relationships to one another are well resolved in the UCE phylogeny and we delimit these

1266 inclusive clades as taxonomic orders (e.g., Gobiiformes, Scombriformes, and Perciformes).
1267 Hampering these earliest molecular phylogenetic studies of percomorphs was a lack of
1268 phylogenetic resolution for relationships within and between major lineages of Eupercaria which
1269 include Perciformes, Centrarchiformes, Acropomatiformes, and what Smith et al.²⁵ delimit as
1270 Acanthuriformes. The lack of phylogenetic resolution was particularly acute in Acanthuriformes,
1271 a lineage that includes more than 2,320 species classified in 56 taxonomic families. The
1272 phylogenies resulting from earlier molecular studies resolved taxonomic families within
1273 Acanthuriformes as monophyletic with high bootstrap support [e.g., Chaetodontidae
1274 (butterflyfishes), Acanthuridae (surgeonfishes), and Sparidae (porgies)], but had very poor
1275 support for relationships among these lineages^{1,21,25}.

1276 Acanthuriformes is monophyletic in the UCE phylogeny with strong bootstrap node
1277 support; however, six nodes along the backbone of the acanthuriform phylogeny have bootstrap
1278 scores ranging from 70% to 94% (Fig. 2, Supplementary Figs. 22-24). Despite this lower support
1279 for a small portion of the acanthuriform phylogeny, the UCE tree provides insight into several
1280 issues not resolved in earlier molecular studies of percomorph phylogenetics. First, Gerreidae
1281 (morjarras), which long evaded phylogenetic resolution, is the sister lineage of all other
1282 Acanthuriformes (Fig. 2, Supplementary Fig. 22). Second, Moronidae (temperate basses) and
1283 Sillaginidae (whitings) are resolved here as sister lineages (Fig. 2, Supplementary Fig. 22).
1284 Though they were resolved as a closely related in earlier molecular studies¹, Lutjanidae and
1285 Haemulidae are distantly related in the UCE phylogeny (Fig. 2, Supplementary Fig. 22,23).
1286 Finally, ten lineages identified as *incertae sedis* within Eupercaria by Betancur-R et al.¹⁷⁴ are
1287 phylogenetically resolved with moderate to high bootstrap support in Acanthuriformes (Fig. 2,
1288 Supplementary Figs. 22-24).

1289 One of the most surprising findings from molecular studies of the teleost phylogeny was
1290 the resolution of Lophioidei (anglerfishes, formerly Lophiiformes) and Tetraodontoidei (puffers
1291 and molas, formerly Tetraodontiformes) as sister lineages^{1,4,15,19-21,192}. An analogous
1292 rearrangement within Mammalia in terms of divergence times might be recognition of a clade of
1293 marsupials as the sister lineage of primates. In morphology-based classifications, the lophioids
1294 were placed in Paracanthopterygii^{186,264}, phylogenetically distant from other percomorph
1295 lineages. This migration of lophioids as paracanthopterygians into a derived clade of
1296 percomorphs is among the most significant changes in 21st century vertebrate phylogenetics.

1297 While the discovery that Lophioidei and Tetraodontoidei are closely related was based on
1298 phylogenetic analyses of molecular data, subsequent investigation of their morphology identified
1299 several soft tissue characters that are likely synapomorphies of a lophioid-tetraodontoid clade²⁶⁵.
1300 It has also been discovered that the larvae of these two lineages exhibit unique morphology and
1301 pigmentation²⁶⁶. Congruent with earlier studies, the UCE tree resolves an inclusive lineage
1302 containing *Siganus* (rabbitfishes), Scatophagidae (scats), Priacanthidae (bigeyes), Cepolidae
1303 (bandfishes), and Caproidae (boarfishes) as the sister lineage of the Lophioidei-Tetraodontoidei
1304 clade. These nodes in the UCE phylogeny are all characterized by high bootstrap support values
1305 (Fig. 2, Supplementary Figs. 24,25).

1306

1307 **xvii. Acanthuriformes: phylogenetic relationships of Tetraodontoidei**

1308 Some of the earliest phylogenetic analyses of ray-finned fishes focused on relationships within
1309 Tetraodontoidei, resulting in numerous phylogenetic analyses based on morphological and
1310 molecular datasets^{21,169,267-274}. While there are important differences among nearly all the
1311 phylogenies of tetraodontoids, most analyses consistently resolve three to four sets of sister
1312 lineages that include Triacanthodidae (spikefishes)-Triacanthidae (triplespines), Diodontidae
1313 (porcupinefishes)-Tetraodontidae (puffers), Balistidae (triggerfishes)-Monacanthidae (filefishes),
1314 and Aracanidae (deepwater boxfishes)-Ostraciidae (boxfishes)^{1,21,169,267,274}, but all these
1315 phylogenies differ in how these lineages relate to one another. They are also incongruent
1316 regarding the relationships of *Triodon macropterus* (Threetooth Puffer) and Molidae (molas and
1317 ocean sunfishes). The UCE phylogeny and most of the earlier molecular phylogenies do not
1318 resolve the subclade formerly named Tetraodontoidei, which contained Triodontidae, Molidae,
1319 Diodontidae, and Tetraodontidae^{1,21,269-272}. The monophyly of this group was inferred, in part,
1320 based on the beak-like teeth in the upper and lower jaws and on a non-protractile upper jaw¹⁶⁹.

1321 The relationships of Tetraodontoidei in the UCE phylogeny are strongly supported with
1322 high bootstrap values at every node (Fig. 2, Supplementary Fig. 24), but differ from all previous
1323 topologies inferred using morphology, molecules, or combined morphological and molecular
1324 datasets. The UCE phylogeny resolves the relationships of *Triodon* and Molidae and contains
1325 three major lineages: 1) a clade containing *Triodon*, Aracanidae, and Ostraciidae, 2) a clade
1326 containing Triacanthodidae, Triacanthidae, Balistidae, and Monacanthidae, and 3) a clade
1327 containing Molidae, Diodontidae, and Tetraodontidae (Fig. 2, Supplementary Fig. 24).

1328 **xviii. Acanthuriformes: phylogenetic relationships of Lophioidei**

1329 The UCE phylogeny includes 16 of 18 recognized taxonomic families of Lophioidei; the
1330 monotypic Centrophrynidae and Lophichthyidae are not sampled. Phylogenies of Lophioidei
1331 inferred from morphological characters, whole mtDNA genome sequences, and Sanger
1332 sequenced mtDNA and nuclear genes all differ from one another^{1,21,275,276}. Congruent with all
1333 other phylogenetic analyses, the UCE phylogeny resolves the Lophiidae (goosefishes) as the
1334 sister lineage of all other Lophioidei (Fig. 2, Supplementary Fig. 25). It is also congruent with a
1335 previous phylogenetic analysis of lophioids in resolving Ogcocephalidae (batfishes) as the sister
1336 lineage of a clade previously named Antennarioidei that contains Antennariidae (frogfishes),
1337 Tetrabrachiidae (tetrabranchid frogfishes), and Brachionichthyidae (handfishes)²⁷⁷. All nodes
1338 along the backbone of the UCE lophioid phylogeny have high bootstrap support (Fig. 2,
1339 Supplementary Fig. 25).

1340 The UCE phylogeny is congruent with previous molecular phylogenetic analyses in
1341 resolving Chaunacidae (coffinfishes) as the sister lineage of the eleven taxonomic families that
1342 comprise the deepsea anglerfishes^{1,21,275}, delimited here as Ceratioidea (Fig. 2, Supplementary
1343 Fig. 25, Supplementary Table 3). The UCE phylogeny and previous molecular analyses using
1344 whole mitochondrial genomes resolve Thaumatichthyidae (wolftrap anglers) as paraphyletic with
1345 *Lasiognathus* nested within Oneirodidae (dreamers)²⁷⁵. Within the ceratioids, the UCE
1346 phylogeny resolves *Neoceratias spinifer* (Toothed Seadevil), Linophrynidae (leftvents), and
1347 Ceratiidae (seadevils) as a monophyletic group (Fig. 2, Supplementary Fig. 25). These three
1348 lineages all exhibit male obligate sexual parasitism and dramatically altered their immune
1349 systems through losing the capacity for somatic diversification of antigen receptor genes²⁷⁸. All
1350 previous morphological and molecular phylogenetic analyses of ceratioids resulted in the non-
1351 monophyly of the lineages exhibiting obligate male sexual parasitism, implying multiple origins
1352 of this unique reproductive mode^{275,278,279}. In contrast, the UCE phylogeny implies a single
1353 evolutionary origin of this unique trait (Fig. 2, Supplementary Fig. 25).

1354

1355 **d. ASTRAL-III species tree analysis**

1356 The ASTRAL-III inferred summary species tree is similar to the phylogeny inferred from
1357 the concatenated data analyses (Figs. 1,2, Supplementary Figs. 1-25) in resolving Lampriformes
1358 as the sister lineage of a monophyletic Paracanthopterygii, monophyly of Acanthopterygii, and

1359 very similar relationships among the major lineages of Percomorpha (Supplementary Fig. 26).
1360 The non-collapsed species tree is available on Dryad. The ASTRAL-III species tree differs from
1361 the concatenated-dataset, maximum likelihood phylogeny in the inference of Trachichthyiformes
1362 and Beryciformes as a clade that is sister to Percomorpha, the gadiform *Bregmaceros* as the
1363 sister lineage of a clade containing *Stylephorus* and all other gadiforms, the placement of
1364 *Centrogenys*, and the non-monophyly of Acropomatiformes and Labriformes. The ASTRAL-III
1365 species tree also does not resolve Gerreidae as the sister lineage of all other Acanthuriformes. In
1366 general, the phylogenetic placement of major eupercarian clades in the tree estimated under the
1367 multi-species coalescent model differs from the topology of the concatenated-dataset, maximum
1368 likelihood trees, but nodal support values were significantly stronger for the backbone
1369 relationships inferred using maximum likelihood methods (Supplementary Figs. 1-26).

1370

1371 *e. Divergence-time estimates*

1372 For both the 702- and 1,084-taxon phylogenies, our relaxed-clock molecular dating analyses
1373 estimated similar stem lineage ages across the multiple subsamples of UCE loci, with
1374 overlapping 95% highest posterior densities for most nodes (Supplementary Table 4). There
1375 were also no observable differences in the median node heights reported in Maximum Clade
1376 Credibility trees built using post-burn-in trees that were randomly sampled (as in the tree
1377 represented in Figs. 1,2), or using post-burn-in trees that were systematically sampled after a
1378 certain number of MCMC iterations (Supplementary Table 4).

1379 Our age estimates are largely in agreement with those presented in previous
1380 phylogenomic analyses of ~1,000 UCE loci⁴ and ~1,100 exons¹⁵ (Supplementary Fig. 29). For
1381 most major clades, our analyses inferred slightly older stem ages, but with 95% highest posterior
1382 densities that overlap with the dates reported in previous studies (Supplementary Fig. 29).
1383 However, our analyses inferred comparably younger stem lineage ages for *Polymixia*,
1384 Percopsiformes, and clades within Eupercaria^{4,15}. Our stem lineage age estimates are
1385 significantly older for Gobiiformes and the Syngnathiformes-Scombriformes clade⁴. Perhaps as a
1386 result of incongruent phylogenetic topologies, our analyses inferred younger stem age estimates
1387 for Acanthuriformes than estimated in the phylogenomic analysis of exon data¹⁵.

1388 We similarly estimate crown lineage ages for major clades with 95% highest posterior
1389 densities that largely overlap with previous phylogenomic analyses^{4,15}. Exceptions include the

1390 crown age estimates of Acanthuriformes, Syngnathiformes and Scombriformes,
1391 Trachichthyiformes, Beryciformes, Gobiiformes, Syngnathiformes and Blenniiformes. Many of
1392 the discrepancies in crown ages likely result from differences among inferred phylogenetic trees
1393 (especially within Eupercaria), or from the relatively sparse taxon sampling in previous
1394 phylogenomic studies^{4,15}.

1395

1396 *f. Diversification rate analyses*

1397 Our results do not support a significant effect of the K-Pg on acanthomorph lineage
1398 diversification rates. TESS-CoMET results indicate constant tree-wide diversification rates
1399 through most of the history of Acanthomorpha, with no evidence of a mass extinction (Extended
1400 Data Fig. 3). Although Extended Data Fig. 3e suggest a brief increase in the global net-
1401 diversification (speciation minus extinction) rate at approximately 50 mya (followed by a
1402 decline), we observe very low Bayesian support for these rate shifts (Extended Data Fig. 3b,d).
1403 Parameter estimates for speciation and extinction rates converged in all TESS-CoMET runs (ESS
1404 values > 200 and Geweke statistics within the 95% confidence intervals for all time points).
1405 Convergence results for the CoMET run visualized in Extended Data Fig. 3 are available in
1406 Supplementary Fig. 30. All replicate analyses produced diversification plots that were virtually
1407 indistinguishable from one another. The results of the Gelman-Rubin test, which calculates the
1408 ratio of within-sample variance to between-sample variance, ensured that rate parameters and
1409 shift time parameters converged across the independent, replicate analyses (Rubin-Gelman
1410 statistic < 1.05) (Supplementary Fig. 31).

1411 The CoMET results do report moderately supported shifts ($2 \leq 2\ln \text{Bayes Factors} \leq 6$) in
1412 speciation and extinction rates in the last 10 million years (Extended Data Fig. 3a-e). We
1413 strongly suspect, however, that these shifts are an artefact of the CoMET model, perhaps due to
1414 how it accounts for incomplete taxon sampling. This suspicion is supported by diversification
1415 patterns reported in numerous other studies^{10,280-282}, which all demonstrate (often dramatic) rate
1416 shifts close to the present-day. It remains unclear how these recent patterns may affect the
1417 inference of older rate shifts. May et al.²⁸³ describe that more recent mass extinction events may
1418 cause a “shadow effect” that diminishes the signal of earlier mass extinctions. As it stands, we
1419 have no evidence that the rate shift we observe in the mid- to late-Neogene could be
1420 overshadowing or weakening a signal for an earlier shift in diversification rates.

Indeed, our tests of relative model fit in TESS corroborate CoMET's estimate of constant diversification rates (Extended Data Table 1). Pairwise comparisons of marginal likelihoods using Bayes Factors suggested that a constant branching-process model best represents the pattern of diversification in Acanthomorpha. In general, this test of relative model fit strongly favored models assuming uniform sampling methods over diversified methods. Therefore, after the model assuming a constant birth-death process and uniform sampling, the next most-favored branching process models were an episodic model that accounted for a rate shift 50 mya (in accordance with the blip in net-diversification rates from the CoMET analysis) and a model with speciation rates that decreased through time, both of which assumed uniform sampling. The predictive distributions of the gamma statistic, number of taxa, and lineage-through-time (LTT) plots for the three most-favored branching process models are reported in Supplementary Fig. 32. The models assuming a tree-wide rate shift at 50 my or a decreasing speciation rate produce posterior-predictive distributions that are in accordance with the empirical estimates from the time-calibrated acanthomorph phylogeny (Supplementary Fig. 32b,c,e,f,h,i). However, the distribution under a simpler, constant rate model is also in agreement and appears to produce the most similar LTT plots to the empirical data (Supplementary Fig. 32a,d,g).

There is controversy surrounding the popular macroevolutionary modeling program BAMM^{284,285}, so indications of lineage diversification rate heterogeneity in the time-calibrated acanthomorph phylogeny are viewed with a degree of skepticism. Since the size of the phylogeny is so large, in every analysis BAMM estimated multiple shift configurations that were relatively equiprobable. We therefore chose not to examine configurations with the maximum a posteriori probability. Rather, for each analysis we chose to interrogate the maximum shift credibility (MSC) configuration, which considers only configurations sampled in the reversible-jump MCMC simulations and maximizes the product of the marginal branch-specific shift probabilities. In the 23 BAMM analyses that were conducted using the time-calibrated 1,084-taxon phylogeny, MSC configurations inferred anywhere between 22 and 33 well-supported rate shifts (Supplementary Fig. 33). The regression line in Supplementary Fig. 33 suggests that the prior number of shifts specified in BAMM does not dramatically affect the estimated number of rate shifts in the posterior prediction (slope = 0.1049). The average number of rate shifts among the MSC configurations was approximately 28. Bayes factor comparisons for each analysis, however, supported models with a number of diversification rate shifts in the upper 30s or low

1452 40s, depending on the specified priors. This was true even for analyses with prior models that
1453 expected one rate shift in the phylogeny.

1454 In Extended Data Fig. 4, we present the MSC configuration resulting from an analysis
1455 with a prior model that expected 15 rate shifts and ran a 2-chain MCMC simulation with a deltaT
1456 value of 0.5. Log-likelihood values across all analyses were similar, but the analyses with prior
1457 models assuming 15 or 40 expected shifts displayed the highest effective sample sizes (ESS) for
1458 their log-likelihoods and for the number of shift events. Since the estimated number and
1459 positions of the rate shifts were similar across analyses with different priors, we take note of the
1460 19 clades with leading branches that were estimated to have undergone rate shifts by at least 16
1461 ($\geq 70\%$) of the 23 BAMM analyses. The 19 shared clades, several of which (e.g. zoarcoids,
1462 darters, notothenioids, labrids, cichlids and gobies) have previously been described as having
1463 undergone radiations, are labeled with blue numbers in Extended Data Fig. 4. They include: 1)
1464 Dinematichthyidae, 2) Apogoninae (Apogonidae to the exclusion of *Pseudamia*), 3) Gobiidae
1465 and Oxudercidae, 4) Mastacembelidae, 5) the clade defined by Scopthalmidae and Soleidae, 6)
1466 Carangidae (to the exclusion of *Seriola*), 7) Pseudocrenilabrinae (in Cichlidae), 8) Poeciliidae, 9)
1467 Labridae, 10) Sciaenidae, 11) Chaetodontidae, 12) Acanthuridae (to the exclusion of *Naso*), 13)
1468 Anthiadinae and Epinephelidae, 14.) darters (Etheostomatinae), 15) the clade defined by
1469 “Nototheniidae” and Channichthyidae (see Supplementary Fig. 17 for clarification), 16) *Sebastes*,
1470 17) the clade defined by Trichodontidae and Psychrolutidae, 18) Lycodinae (in Zoarcidae), and
1471 19) the clade defined by Stichaeidae and Zoarcidae. We chose to present the configuration in
1472 Extended Data Fig. 4 because the analysis assuming 40 rate shifts had more rate shifts beyond
1473 these 19 clades than the analysis assuming 15 expected rate shifts. Still, the MSC configuration
1474 presented in Extended Data Fig. 4 highlights eight additional rate shifts that are labelled with
1475 black numbers and are not present in this list of 19. Furthermore, while the MSC configuration in
1476 Extended Data Fig. 4 identifies rate shifts occurring within Acanthuridae and Zoarcidae, these
1477 shifts occur along a different-yet-nearby internal branch than in most of the other configurations.
1478 Specifically, the configuration in Extended Data Fig. 4 flags one rate shift in the branch leading
1479 to Acanthuridae to the exclusion of *Naso* and *Prionurus*, and another in the lineage defined by
1480 *Bothrocara* and *Lycodes concolor* (within Zoarcidae).

1481 The fact that many of the rate shifts identified by BAMM occur along tipwards branches
1482 may indicate that the species richness of Acanthomorpha is driven by relatively recent, more

1483 phylogenetically or geographically localized radiations instead of a burst of diversification after
1484 the K-Pg. This pattern does not seem to be unique to acanthomorphs; numerous radiations have
1485 shown to have a similar pattern of constant diversification across the K-Pg boundary despite
1486 bursts in the origin of disparity in morphological and ecological traits⁷. Nevertheless, there is a
1487 chance that this pattern is the by-product of analytical corrections for incomplete sampling. Such
1488 corrections may reduce the statistical power to infer shifts in diversification rates and increase
1489 the probability of Type II error when rate variation is present²⁸⁶. It is also known that Bayesian
1490 methods of diversification rate estimation, including BAMM and TESS, penalize parameter-rich
1491 diversification models and favor less-complex models even under liberal priors. Given the
1492 infinite number of possible diversification scenarios that could result in the observed
1493 phylogeny²⁸⁷, it is therefore possible that TESS estimated a constant-rate model to best fit our
1494 data because of its simplicity rather than its accuracy.
1495

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086 **Supplementary Table 1: Binomial names and higher taxonomic classification of species included in the**
087 **phylogeny, institutional voucher information for specimens (if applicable), and NCBI SRA BioSample**
088 **accession numbers.** The sixth column ('Morphology Analyses') denotes whether species were included in the
089 body shape analyses, and the seventh column ('Concordance Analyses') denotes if samples were included in the
090 BUCKy concordance factor analyses. NCBI BioSample numbers denoted with an asterisk (*) indicate samples
091 for which UCE data were extracted from whole genome sequence data.

Order	Higher Taxa (Family or Genus)	Species Name	Voucher ID	NCBI BioSample	Morphology Analyses	Concordance Analyses
Aulopiformes	Alepisauridae	<i>Alepisaurus ferox</i>	YPM ICH 25657	SAMN05915027	✓	
Aulopiformes	Paralepididae	<i>Notolepis coatsi</i>	YPM ICH 022576		✓	
Myctophiformes	Myctophidae	<i>Benthosema glaciale</i> <i>Ceratoscopelus warmingii</i>	See NCBI SRA	SAMEA4028768*	✓	
Myctophiformes	Myctophidae	<i>Dasy scopelus selenops</i> <i>Notoscopelus caudispinosus</i>	SIO 0510-09-28	SAMN05915048	✓	
Myctophiformes	Myctophidae	<i>Neoscopelus macrolepidotus</i>	YPM ICH 25697		✓	✓
Myctophiformes	Myctophidae	<i>Neoscopelus macrolepidotus</i>	YPM ICH 028430		✓	
Myctophiformes	Neoscopelidae	<i>Neoscopelus microchir</i>	ASIZP 0913636		✓	
Myctophiformes	Neoscopelidae	<i>Scopelengys tristis</i>	ASIZO 0910701		✓	✓
Myctophiformes	Neoscopelidae	<i>Lampris guttatus</i>	UW 115136		✓	
Lampriformes	<i>Lampris</i>	<i>Regalecus glesne</i>	SIO 04-195	SAMN05915079	✓	✓
Lampriformes	Regalecidae	<i>Zu elongatus</i>	YPM ICH 26237	SAMN05915116		
Lampriformes	Trachipteridae	<i>Polymixia lowei</i>	P.042029/TS3	NMNZ	✓	✓
Polymixiiformes	<i>Polymixia</i>	<i>Aphredoderus sayanus</i>	YPM ICH 25183	SAMN05915031	✓	✓
Percopsiformes	Amblyopsidae	<i>Typhlichthys subterraneus</i>	See NCBI SRA	SAMEA4028771*	✓	
Percopsiformes	Percopsidae	<i>Percopsis omiscomyces</i>	YPM ICH 017307	SAMN05915097		✓
Percopsiformes	Percopsidae	<i>Percopsis transmontana</i>	See NCBI SRA	SAMEA4028770*		
Zeiformes	Parazenidae	<i>Cyttopsis rosea</i>	See NCBI SRA	SAMEA4028773*	✓	✓
Zeiformes	Zeidae	<i>Zenopsis conchifera</i>	MCZ 155779	SAMN05915138	✓	
Zeiformes	Zeidae	<i>Zeus faber</i>	NSMT 62233	SAMN05915139	✓	✓
Stylephoriformes		<i>Stylephorus chordatus</i>	YPM ICH 25672	SAMN05915127	✓	✓
Gadiformes	<i>Bregmaceros</i>	<i>Bregmaceros cantori</i>	See NCBI SRA	SAMEA4028775*	✓	✓
Gadiformes	<i>Melanonus</i>	<i>Melanonus zugmayeri</i> <i>Muraenolepis marmoratus</i>	See NCBI SRA	SAMEA4028779*	✓	
Gadiformes	Muraenolepididae	<i>Trachyrincus murrayi</i>	See NCBI SRA	SAMEA4028780*		
Gadiformes	Trachyrincidae	<i>Trachyrincus scabrus</i>	See NCBI SRA	SAMEA4028782*		
Gadiformes	Trachyrincidae	<i>Laemonema laureysi</i>	See NCBI SRA	SAMEA4028784*	✓	
Gadiformes	Moridae	<i>Mora moro</i>	See NCBI SRA	SAMEA4028783*	✓	

		<i>Bathygadus</i>				
Gadiformes	Macrouridae	<i>melanobranchus</i>	See NCBI SRA	SAMEA4028785*	✓	
Gadiformes	Macrouridae	<i>Coryphaenoides</i>				
		<i>rupestris</i>	YPM ICH 025367	SAMN05915057	✓	
		<i>Coryphaenoides</i>				
Gadiformes	Macrouridae	<i>rupestris</i>	See NCBI SRA	SAMN08010939*		
Gadiformes	Macrouridae	<i>Macrourus berglax</i>	See NCBI SRA	SAMEA4028786*	✓	
		<i>Malacocephalus</i>				
Gadiformes	Macrouridae	<i>occidentalis</i>	See NCBI SRA	SAMEA4028787*	✓	
Gadiformes	Merlucciidae	<i>Merluccius capensis</i>	See NCBI SRA	SAMEA4028778*		
Gadiformes	Merlucciidae	<i>Merluccius merluccius</i>	See NCBI SRA	SAMEA4028777*	✓	
Gadiformes	Phycidae	<i>Lotella phycis</i>	See NCBI SRA	SAMEA4028789*		
Gadiformes	Phycidae	<i>Phycis blennoides</i>	See NCBI SRA	SAMEA4028788*	✓	
Gadiformes		<i>Lota lota</i>	See NCBI SRA	SAMEA4028790*	✓	
Gadiformes	Lotidae	<i>Brosme brosme</i>	See NCBI SRA	SAMEA4028792*	✓	
Gadiformes	Lotidae	<i>Molva molva</i>	See NCBI SRA	SAMEA4028791*	✓	
Gadiformes	Gadidae	<i>Arctogadus glacialis</i>	See NCBI SRA	SAMEA4028798*		
Gadiformes	Gadidae	<i>Boreogadus saida</i>	See NCBI SRA	SAMEA4028799*	✓	
Gadiformes	Gadidae	<i>Gadiculus argenteus</i>	See NCBI SRA	SAMEA4028794*	✓	
Gadiformes	Gadidae	<i>Gadus chalcogrammus</i>	See NCBI SRA	SAMEA4028800*		
Gadiformes	Gadidae	<i>Gadus morhua</i>	YPM ICH 020859	SAMN05915065	✓	✓
Gadiformes	Gadidae	<i>Gadus morhua</i>	See NCBI SRA	SAMEA4028801*		
		<i>Melanogrammus</i>		SAMEA104602249		
Gadiformes	Gadidae	<i>aeglefinus</i>	See NCBI SRA	*	✓	
Gadiformes	Gadidae	<i>Merlangius merlangus</i>	See NCBI SRA	SAMEA4028797*	✓	
Gadiformes	Gadidae	<i>Pollachius virens</i>	See NCBI SRA	SAMEA4028795*	✓	
Gadiformes	Gadidae	<i>Trisopterus minutus</i>	See NCBI SRA	SAMEA4028793*	✓	
		<i>Diretmoides</i>				
Trachichthyiformes	Diretmidae	<i>pauciradiatus</i>	YPM ICH 028266			✓
Trachichthyiformes	Diretmidae	<i>Diretmus argenteus</i>	Pers. Coll.: N. Merrett, "JMS"		✓	
Trachichthyiformes	Anomalopidae	<i>Anomalops katoptron</i>	YPM ICH 020676			
Trachichthyiformes	Monocentridae	<i>Monocentris japonica</i>	ORIUT 1183		✓	
Trachichthyiformes	Anoplogaster	<i>Anoplogaster cornuta</i>	YPM ICH 025640	SAMN05915028	✓	✓
		<i>Aulotrachichthys</i>				
Trachichthyiformes	Trachichthyidae	<i>prosthemius</i>	ASIZD 0910678			
Trachichthyiformes	Trachichthyidae	<i>Hoplostethus</i>				
		<i>occidentalis</i>	YFTC 14563, n.v.		✓	
Trachichthyiformes	Trachichthyidae	<i>Paratrachichthys</i>				
		<i>sajademalensis</i>	YFTC 14534, n.v.			
Beryciformes	Holocentridae	<i>Holocentrus rufus</i>	See NCBI SRA	SAMEA4028806*	✓	✓
Beryciformes	Holocentridae	<i>Myripristis jacobus</i>	See NCBI SRA	SAMEA4028805*	✓	
			Pers. Coll.: M.Alfaro, Alfaro			
Beryciformes	Holocentridae	<i>Myripristis leiognathus</i>	875	SAMN05915086	✓	
			Pers. Coll.: P.Wainwright,			
Beryciformes	Holocentridae	<i>Myripristis violacea</i>	PW2260B	SAMN05915087	✓	✓
Beryciformes	Holocentridae	<i>Neoniphon sammara</i>	See NCBI SRA	SAMEA4028807*	✓	

Beryciformes	Holocentridae	<i>Sargocentron coruscum</i>	YPM ICH 23957	SAMN05915119	✓
Beryciformes	Berycidae	<i>Beryx decadactylus</i>	YFTC 13731, n.v.		✓
Beryciformes	Berycidae	<i>Beryx splendens</i>	See NCBI SRA	SAMEA4028808*	✓
Beryciformes	Berycidae	<i>Centroberyx druzhinini</i>	ASIZD 0911026		✓
Beryciformes	Melamphaidae	<i>Melamphaes longivelis</i>	YPM ICH 028501		✓
Beryciformes	Melamphaidae	<i>Poromitra gibbsi</i>	YPM ICH 028486		✓
Beryciformes	Melamphaidae	<i>Scopelogadus beanii</i>	YPM ICH 028434		✓
Beryciformes	<i>Rondeletia</i>	<i>Rondeletia bicolor</i>	YPM ICH 027515		✓
Beryciformes	<i>Rondeletia</i>	<i>Rondeletia loricata</i>	YPM ICH 25674	SAMN05915117	✓
Beryciformes	Cetomimidae	<i>Ataxolepis apus</i>	YPM ICH 025531		
Beryciformes	Cetomimidae	<i>Cetostoma regani</i>	YPM ICH 028287		✓
Beryciformes	Cetomimidae	<i>Ditropichthys storeri</i>	YPM ICH 028280		✓
Beryciformes	Cetomimidae	<i>Mirapinna esau</i>	YFTC 26026, n.v.		
Beryciformes		<i>Barbourisia rufa</i>	YPM ICH 010068		✓
Beryciformes	Stephanoberycidae	<i>Acanthochaenus luetkenii</i>	YFTC 24122, n.v.		✓
Beryciformes	Stephanoberycidae	<i>Acanthochaenus luetkenii</i> <i>Malacosarcus</i>	YFTC 24124, n.v.		
Beryciformes	Stephanoberycidae	<i>macrostoma</i>	USNM 400019		
Ophidiiformes	Dinematichyidae	<i>Diancistrus jeffjohnsoni</i>	YFTC 32439, n.v.		✓
Ophidiiformes	Dinematichyidae	<i>Dinematicichthys</i> <i>iluocoeteoides</i>	USNM 334123		✓
Ophidiiformes	Dinematichyidae	<i>Diancistrus tongaensis</i>	USNM 374200		✓
Ophidiiformes	Dinematichyidae	<i>Ogilbia cayorum</i>	ZMUC P771463		
Ophidiiformes	Dinematichyidae	<i>Ogilbichthys</i> sp.	USNM 349073		
Ophidiiformes	Dinematichyidae	<i>Typhliasina pearsei</i>	ZMUC P771455		
Ophidiiformes	Bythitidae	<i>Aphyonus gelatinosus</i>	ZMUB/MAR 3880		
Ophidiiformes	Bythitidae	<i>Bidenichthys capensis</i>	KU 6466		
Ophidiiformes	Bythitidae	<i>Brosmophyciops pautzkei</i>	SAIAB 86260		
Ophidiiformes	Bythitidae	<i>Cataetyx messieri</i> <i>Diplacanthopoma</i> <i>brachysoma</i>	ZMUC P771617		✓
Ophidiiformes	Bythitidae	<i>Megacataetyx niki</i>	MCZ 155341		
Ophidiiformes	Bythitidae	<i>Parabrotula tanseimaru</i>	NMNZ P.41257		
Ophidiiformes	Ophidiidae	<i>Acanthonus armatus</i>	CBM 10557	SAMN18716611*	
Ophidiiformes	Ophidiidae	<i>Apagesoma australe</i>	MNHN 2004-1311		
Ophidiiformes	Ophidiidae	<i>Bassogigas walkeri</i>	ZMUC P771525		
Ophidiiformes	Ophidiidae	<i>Brotula barbata</i>	SIO 08-109		✓
Ophidiiformes	Ophidiidae	<i>Carapus acus</i>	See NCBI SRA	SAMEA4028811*	✓
Ophidiiformes	Ophidiidae	<i>Carapus bermudensis</i>	KU 18739	SAMN05915045	
Ophidiiformes	Ophidiidae	<i>Chilara taylori</i>	KU 28277		✓
Ophidiiformes	Ophidiidae	<i>Dannevigia tusca</i>	YFTC 32428, n.v.		
Ophidiiformes	Ophidiidae	<i>Dicrolene intronigra</i>	KU 3677		✓

Ophidiiformes	Ophidiidae	<i>Holcomycteronus brucei</i>	ZMUC P771528		
Ophidiiformes	Ophidiidae	<i>Lamprogrammus exutus</i>	See NCBI SRA	SAMEA4028812*	✓
Ophidiiformes	Ophidiidae	<i>Lepophidium profundorum</i>	KU 27197		✓
Ophidiiformes	Ophidiidae	<i>Monomitopus garmani</i>	ZMUC P771573		
Ophidiiformes	Ophidiidae	<i>Porogadus miles</i>	ZMUB/MAR 2661		
Ophidiiformes	Ophidiidae	<i>Ventichthys biospeedoi</i>	MNHN 2004-2038		
Batrachoidiformes	Batrachoididae	<i>Batrachoides pacifici</i>	See NCBI SRA	SAMN05915038	
Batrachoidiformes	Batrachoididae	<i>Chatrabus melanurus</i>	See NCBI SRA	SAMEA4028814*	✓
Batrachoidiformes	Batrachoididae	<i>Halobatrachus didactylus</i>	YFTC 17238, n.v.		✓ ✓
Batrachoidiformes	Batrachoididae	<i>Opsanus tau</i>	YPM ICH 24156		✓ ✓
Batrachoidiformes	Batrachoididae	<i>Porichthys notatus</i>	Pers. Coll.: P.Wainwright, PW267: B50		✓
Gobiiformes	<i>Kurtus</i>	<i>Kurtus gulliveri</i>	TMB 09-2	SAMN05915077	✓ ✓
Gobiiformes	<i>Kurtus</i>	<i>Kurtus indicus</i>	AMNH 251591		
Gobiiformes	Apogonidae	<i>Astrapogon stellatus</i>	YPM ICH 021834		✓
Gobiiformes	Apogonidae	<i>Cheilodipterus quinquelineatus</i>	Pers. Coll.: P.Wainwright, PW1704B Pers. Coll.: P.Wainwright,		✓
Gobiiformes	Apogonidae	<i>Fibramia lateralis</i>	PW2294B	SAMN05915032	
Gobiiformes	Apogonidae	<i>Ostorhinchus doederleini</i>	LACM 000974		✓
Gobiiformes	Apogonidae	<i>Ostorhinchus nigrofasciatus</i>	LACM-T 000970	SAMN05915092	✓
Gobiiformes	Apogonidae	<i>Paroncheilus affinis</i>	Pers. Coll.: M. Alfaro, MEA		
Gobiiformes	Apogonidae	<i>Phaeoptyx pigmentaria</i>	LACM-T 000493	SAMN05915099	✓
Gobiiformes	Apogonidae	<i>Pristiopogon kallopterus</i>	YPM ICH 026618		✓
Gobiiformes	Apogonidae	<i>Pseudamia gelatinosa</i>	n.v.		✓ ✓
Gobiiformes	Apogonidae	<i>Taeniamia biguttata</i>	LACM 000975		
Gobiiformes	<i>Trichonotus</i>	<i>Trichonotus filamentosus</i>	LSUMZ 14120		✓ ✓
Gobiiformes	Rhyacichthyidae	<i>Rhyacichthys aspro</i>	NSMT-P 97135		
Gobiiformes	Odontobutidae	<i>Odontobutis obscura</i>	See NCBI SRA	SAMN05915089	✓ ✓
Gobiiformes	Odontobutidae	<i>Sineleotris saccharae</i>	LACM-T, n.v.		
Gobiiformes	Milyeringidae	<i>Milyeringa veritas</i>	SAMA, n.v.		
Gobiiformes	Milyeringidae	<i>Typhleotris madagascariensis</i>	FMNH 116498		
Gobiiformes	Eleotridae	<i>Dormitator maculatus</i>	LACM 000017		✓
Gobiiformes	Eleotridae	<i>Eleotris pisonis</i>	LACM 000019		✓
Gobiiformes	Eleotridae	<i>Eretelis smaragdus</i>	LACM-T 000042	SAMN05915063	✓
Gobiiformes	Eleotridae	<i>Gobiomorphus hubbsi</i>	LACM-T, n.v.		✓
Gobiiformes	Eleotridae	<i>Gobiomorus dormitor</i>	NCSM 068278 Pers. Coll.:		✓
Gobiiformes	Eleotridae	<i>Guavina micropus</i>	VanTass/Rob		✓
Gobiiformes	Eleotridae	<i>Hemieleotris latifasciata</i>	LACM 000018		✓
Gobiiformes	Eleotridae	<i>Hypseleotris compressa</i>	LACM 000104		✓

Gobiiformes	Eleotridae	<i>Microphilypnus ternetzi</i>	ANSP 180643		
Gobiiformes	Eleotridae	<i>Mogurnda adspersa</i>	LACM-T 000069	SAMN05915085	✓
Gobiiformes	Eleotridae	<i>Ratsirakia legendrei</i>	LACM 000007		
Gobiiformes	Eleotridae	<i>Tateurndina ocellicauda</i>	LACM 000066		✓
Gobiiformes	Butidae	<i>Butis butis</i>	LACM 000045		
Gobiiformes	Butidae	<i>Kribia nana</i>	LACM 000077		✓
Gobiiformes	Butidae	<i>Ophiocara porocephala</i>	LACM-T 000001	SAMN05915091	
Gobiiformes	Butidae	<i>Oxyeleotris lineolata</i>	LACM-T 000021		✓
Gobiiformes	Butidae	<i>Oxyeleotris nullipora</i>	LACM-T 000596		
Gobiiformes	Butidae	<i>Oxyeleotris selheimi</i>	LACM-T 000006		✓
Gobiiformes	Thalasseleotrididae	<i>Grahamichthys radiata</i>	YPM ICH 26585		✓
Gobiiformes	Thalasseleotrididae	<i>Thalasseleotris iota</i>	YPM ICH 26584		
Gobiiformes	Oxudercidae	<i>Acanthogobius flavimanus</i>	LACM 000295		✓
Gobiiformes	Oxudercidae	<i>Acanthogobius flavimanus</i>	LACM-T 000295		
Gobiiformes	Oxudercidae	<i>Boleophthalmus pectinirostris</i>	See NCBI SRA	SAMN03201692*	✓
Gobiiformes	Oxudercidae	<i>Evorthodus minutus</i>	LACM-T 000265	SAMN05915064	✓
Gobiiformes	Oxudercidae	<i>Gillichthys seta</i>	LACM-T 000281	SAMN05915066	✓
Gobiiformes	Oxudercidae	<i>Gnatholepis cauerensis</i>	LACM 001122		✓
Gobiiformes	Oxudercidae	<i>Gobiopterus semivestitus</i>	LACM 000090		
Gobiiformes	Oxudercidae	<i>Mugilogobius rivulus</i>	LACM 000262		✓
Gobiiformes	Oxudercidae	<i>Pandaka lidwilli</i>	LACM 000254		
Gobiiformes	Oxudercidae	<i>Periophthalmodon schlosseri</i>	See NCBI SRA	SAMN03201695*	
Gobiiformes	Oxudercidae	<i>Periophthalmus barbarus</i>	LACM-T 000273	SAMN05915098	✓
Gobiiformes	Oxudercidae	<i>Periophthalmus magnuspinatus</i>	See NCBI SRA	SAMN03201694*	
Gobiiformes	Oxudercidae	<i>Scartelaos histophorus</i>	See NCBI SRA	SAMN03201693*	✓
Gobiiformes	Oxudercidae	<i>Typhlogobius californiensis</i>	LACM 000025		✓
Gobiiformes	Gobiidae	<i>Amblyeleotris guttata</i>	LACM 001025		✓
Gobiiformes	Gobiidae	<i>Amblygobius phalaena</i>	LACM 000195		✓
Gobiiformes	Gobiidae	<i>Asterropteryx ensifera</i>	LACM 001050		✓
Gobiiformes	Gobiidae	<i>Bathygobius soporator</i>	LACM-T 000511	SAMN05915037	✓
Gobiiformes	Gobiidae	<i>Bryaniinops yongei</i>	LACM 000164		✓
Gobiiformes	Gobiidae	<i>Callogobius sclateri</i>	LACM 000172		✓
Gobiiformes	Gobiidae	<i>Corygalops anomolus</i>	LACM 000243		
Gobiiformes	Gobiidae	<i>Coryphopterus glaucofraenum</i>	LACM 000578		✓
Gobiiformes	Gobiidae	<i>Cryptocentrus cinctus</i>	LACM 001086		✓
Gobiiformes	Gobiidae	<i>Elacatinus oceanops</i>	LACM 000230		✓
Gobiiformes	Gobiidae	<i>Exyrias belissimus</i>	LACM 000168		✓
Gobiiformes	Gobiidae	<i>Glossogobius flaviginnis</i>	LACM 000311		✓

Gobiiformes	Gobiidae	<i>Gobiodon histrio</i>	LACM 000239	✓	
Gobiiformes	Gobiidae	<i>Istigobius rigilius</i>	LACM 001078	✓	
Gobiiformes	Gobiidae	<i>Koumansetta rainfordi</i>	n.v.		
Gobiiformes	Gobiidae	<i>Lesueurigobius sanzi</i>	See NCBI SRA	SAMEA4028816*	✓
Gobiiformes	Gobiidae	<i>Lythrypnus dalli</i>	LACM 000190		✓
Gobiiformes	Gobiidae	<i>Microdesmus longipinnis</i>	LACM 000617		
Gobiiformes	Gobiidae	<i>Nes longus</i>	LACM 000222	✓	
Gobiiformes	Gobiidae	<i>Priolepis cincta</i>	LACM 000904 Pers. Coll.: P.Wainwright, PW2064B	✓	
Gobiiformes	Gobiidae	<i>Ptereleotris evides</i>	LACM 000594	SAMN05915113	✓
Gobiiformes	Gobiidae	<i>Ptereleotris zebra</i>	LACM 001049		✓
Gobiiformes	Gobiidae	<i>Stonogobiops xanthorhinica</i>	LACM-T 000898	SAMN05915136	✓
Gobiiformes	Gobiidae	<i>Valenciennea strigata</i>	FAKU 82391	SAMN13222433	✓
Scombriformes	<i>Arripis</i>	<i>Arripis trutta</i>	YPM ICH 025637	SAMN13222429	✓
Scombriformes	<i>Ariomma</i>	<i>Ariomma bondi</i>	NSMT 64808	SAMN13222430	✓
Scombriformes	<i>Ariomma</i>	<i>Ariomma indica</i>	MCZ 161902	SAMN13222431	✓
Scombriformes	<i>Ariomma</i>	<i>Ariomma melana</i>	YPM ICH 027642	SAMN13222432	
Scombriformes	Nomeidae	<i>Cubiceps whiteleggi</i>	SNFR 14797	SAMN13222449	✓
Scombriformes	Nomeidae	<i>Cubiceps baxteri</i>	SIO 98-26	SAMN13222448	✓
Scombriformes	Nomeidae	<i>Psenes cyanophrys</i>	YPM ICH 025740	SAMN13222496	✓
Scombriformes	Nomeidae	<i>Psenes arafurensis</i>	SNFR 14835	SAMN13222495	✓
Scombriformes	Stromateidae	<i>Pampus argenteus</i>	LSUMZ 5282	SAMN13222483	✓
Scombriformes	Stromateidae	<i>Pampus chinensis</i>	LSUMZ 5300	SAMN13222484	
Scombriformes	Stromateidae	<i>Pampus echinogaster</i>	KAUM 64926	SAMN13222485	
Scombriformes	Stromateidae	<i>Pampus punctatissimus</i>	CBM 12672		
Scombriformes	Stromateidae	<i>Peprilus burti</i>	KU 5086	SAMN13222490	✓
Scombriformes	Stromateidae	<i>Peprilus paru</i>	KU 5169	SAMN13222489	✓
Scombriformes	Stromateidae	<i>Peprilus simillimus</i>	KU 9394	SAMN13222491	✓
Scombriformes	Stromateidae	<i>Peprilus triacanthus</i>	YPM ICH 024677 Pers. Coll.: P.Wainwright, PW1568	SAMN13222492	
Scombriformes		<i>Pomatomus saltatrix</i>	SAMN05915106	✓	
Scombriformes	Centrolophidae	<i>Hyperoglyphe antarctica</i>	SNFR 16241	SAMN13222465	✓
Scombriformes	Centrolophidae	<i>Hyperoglyphe japonica</i>	CBM 13628	SAMN13222466	✓
Scombriformes	Centrolophidae	<i>Psenopsis anomala</i>	Miya-11-231	SAMN05915108	✓
Scombriformes	Centrolophidae	<i>Schedophilus velaini</i>	SNFR 16403	SAMN13222508	✓
Scombriformes	Icosteidae	<i>Icosteus aenigmaticus</i>	SIO 99-95	SAMN13222467	✓
Scombriformes		<i>Amarsipus carlsbergi</i>	CBM 17750	SAMN10081044 *	✓
Scombriformes	Tetragonuridae	<i>Tetragonurus atlanticus</i>	YPM ICH 027663	SAMN13222521	✓
Scombriformes	Tetragonuridae	<i>Tetragonurus cuvieri</i>	NSMT 65749	SAMN13222522	

Scombriformes	Tetragonuridae	<i>Tetragonurus pacificus</i>	SNFR 15336	SAMN13222523	
Scombriformes	Chiasmodontidae	<i>Chiasmodon niger</i>	YPM ICH 25663	SAMN05915052	✓
Scombriformes	Chiasmodontidae	<i>Dysalotus alcocki</i>	YPM ICH 025665	SAMN13222451	✓
Scombriformes	Chiasmodontidae	<i>Dysalotus oligoscolus</i>	YPM ICH 025654	SAMN13222452	
Scombriformes	Chiasmodontidae	<i>Kali kerberti</i>	UW 115135	SAMN05915076	✓
Scombriformes	Chiasmodontidae	<i>Kali macrodon</i>	YPM ICH 027772	SAMN13222468	✓
Scombriformes	Chiasmodontidae	<i>Kali macrura</i> <i>Pseudoscopelus altipinnis</i>	KU 8140	SAMN13222469	
Scombriformes	Chiasmodontidae	<i>Pseudoscopelus astronesthidens</i>	YPM ICH 027632	SAMN13222498	
Scombriformes	Chiasmodontidae	<i>Pseudoscopelus obtusifrons</i>	KU 6518	SAMN13222499	
Scombriformes	Chiasmodontidae	<i>Pseudoscopelus odontoglossum</i>	YPM ICH 027787	SAMN13222501	
Scombriformes	Chiasmodontidae	<i>Pseudoscopelus scutatus</i>	YPM ICH 025805	SAMN13222503	
Scombriformes	Scombridae	<i>Acanthocybium solandri</i>	KU 5425	SAMN13222425	✓
Scombriformes	Scombridae	<i>Auxis rochei</i>	CBM 14077	SAMN13222436	✓
Scombriformes	Scombridae	<i>Auxis thazard</i>	CBM 12877	SAMN13222437	
Scombriformes	Scombridae	<i>Euthynnus affinis</i> <i>Gasterochisma melampus</i>	CBM 12671	SAMN13222455	✓
Scombriformes	Scombridae	<i>Gymnosarda unicolor</i>	NSMT 93197	SAMN13222462	
Scombriformes	Scombridae	<i>Katsuwonus pelamis</i>	CBM 12672	SAMN13222471	✓
Scombriformes	Scombridae	<i>Rastrelliger kanagurta</i>	NSMT 76071	SAMN13222505	✓
Scombriformes	Scombridae	<i>Scomber australasicus</i>	CBM 12636		✓
Scombriformes	Scombridae	<i>Scomber japonicus</i>	CBM 12641	SAMN13222509	✓
Scombriformes	Scombridae	<i>Scomber scombrus</i>	YPM ICH 020681	SAMN05915123	✓
			Pers. Coll.: P.Wainwright, PW1207		
Scombriformes	Scombridae	<i>Scomberomorus maculatus</i> <i>Scomberomorus niphonius</i>	CBM 14469	SAMN13222512	
Scombriformes	Scombridae	<i>Scomberomorus regalis</i>	KU 30178		✓
Scombriformes	Scombridae	<i>Thunnus orientalis</i>	NSMT-P 93077		✓
Scombriformes	Scombridae	<i>Thunnus tonggol</i>	SNFR 16558		
Scombriformes	Caristiidae	<i>Caristius macropus</i>	UW 113533	SAMN13222445	
Scombriformes	Caristiidae	<i>Paracaristius maderensis</i>	YPM ICH 027617	SAMN13222486	
Scombriformes	Caristiidae	<i>Paracaristius nudarcus</i>	YPM ICH 25618		
Scombriformes	Bramidae	<i>Brama caribbea</i>	YPM ICH 025808	SAMN13222442	✓
Scombriformes	Bramidae	<i>Brama dussumieri</i>	CBM 15373	SAMN13222443	✓
Scombriformes	Bramidae	<i>Brama japonica</i>	SIO 01-183	SAMN05915040	✓
Scombriformes	Bramidae	<i>Eumegistus illustris</i>	n.v. tissue only	SAMN13222454	
Scombriformes	Bramidae	<i>Pterycombus brama</i>	KU 8137	SAMN13222504	✓
Scombriformes	Bramidae	<i>Pterycombus petersii</i>	OCF-P 20071225		✓

Scombriformes	Bramidae	<i>Taractes asper</i>	SIO 00-165	SAMN05915132	
Scombriformes	Bramidae	<i>Taractes rubescens</i>	CBM 14224	SAMN13222517	
Scombriformes	Bramidae	<i>Taractichthys longipinnis</i>	KU 5403	SAMN13222518	
Scombriformes	Bramidae	<i>Taractichthys steindachneri</i>	CBM 14163	SAMN13222519	✓
Scombriformes		<i>Scombrolabrax heterolepis</i>	NMNZ 40456	SAMN13222514	
Scombriformes		<i>Lepidocybium flavobrunneum</i>	CBM 12751	SAMN13222474	
Scombriformes	Gempylidae	<i>Diplospinus multistriatus</i>	YPM ICH 025671	SAMN13222450	✓
Scombriformes	Gempylidae	<i>Epinnula magistralis</i>	NSMT 62524	SAMN13222453	
Scombriformes	Gempylidae	<i>Gempylus serpens</i>	NSMT 62526	SAMN13222463	✓
Scombriformes	Gempylidae	<i>Neoepinnula americana</i>	KU 3543	SAMN13222480	✓
Scombriformes	Gempylidae	<i>Nesiarchus nasutus</i>	NSMT 75668	SAMN13222481	✓
Scombriformes	Gempylidae	<i>Paradiplospinus antarcticus</i>	KU 925	SAMN13222487	✓
Scombriformes	Gempylidae	<i>Paradiplospinus gracilis</i>	YPM ICH 022377	SAMN13222488	
Scombriformes	Gempylidae	<i>Promethichthys prometheus</i>	CBM 13627	SAMN13222494	✓
Scombriformes	Gempylidae	<i>Rexea prometheoides</i>	OCF-P 20140707-2	SAMN13222506	
Scombriformes	Gempylidae	<i>Ruvettus pretiosus</i>	SIO 06-116	SAMN05915118	✓
Scombriformes	Gempylidae	<i>Thyrsitoides marleyi</i>	NSMT 73382	SAMN13222526	
Scombriformes	Trichiuridae	<i>Aphanopus carbo</i>	HUMZ 220745	SAMN13222427	✓
Scombriformes	Trichiuridae	<i>Assurger anzac</i>	SIO 18126	SAMN05915034	
Scombriformes	Trichiuridae	<i>Benthodesmus elongatus</i>	YPM ICH 025649	SAMN13222438	✓
Scombriformes	Trichiuridae	<i>Benthodesmus simonyi</i>	MCZ 158586	SAMN13222439	✓
Scombriformes	Trichiuridae	<i>Benthodesmus tenuis</i>	HUMZ 220516	SAMN13222440	
Scombriformes	Trichiuridae	<i>Evoxymetopon macrophthalmus</i>	SNFR 14546	SAMN13222456	
Scombriformes	Trichiuridae	<i>Evoxymetopon poeyi</i>	NSMT 77666	SAMN13222457	
Scombriformes	Trichiuridae	<i>Evoxymetopon taeniatus</i>	KU 5249	SAMN13222458	✓
Scombriformes	Trichiuridae	<i>Lepidopus altifrons</i>	KU 3546	SAMN13222475	✓
Scombriformes	Trichiuridae	<i>Lepidopus caudatus</i>	KU 8084	SAMN13222476	✓
Scombriformes	Trichiuridae	<i>Lepturacanthus savala</i>	LSUMZ 78	SAMN13222477	✓
Scombriformes	Trichiuridae	<i>Tentoriceps cristatus</i>	SNFR 17729	SAMN13222520	✓
Scombriformes	Trichiuridae	<i>Trichiurus lepturus</i>	CBM 12994	SAMN13222527	✓
Scombriformes	Trichiuridae	<i>Trichiurus</i> sp. 1	SNFR 17528	SAMN13222528	
Scombriformes	Trichiuridae	<i>Trichiurus</i> sp. 2	SNFR 17533	SAMN13222529	
Sygnathiformes	Pegasidae	<i>Eurypegasus draconis</i>	See NCBI SRA	SAMN06563069	
Sygnathiformes	Pegasidae	<i>Pegasus volitans</i>	See NCBI SRA	SAMN06563109	✓
Sygnathiformes	Dactylopteridae	<i>Dactyloptena orientalis</i>	See NCBI SRA	SAMN06563054	✓
Sygnathiformes	Dactylopteridae	<i>Dactyloptena peterseni</i>	See NCBI SRA	SAMN06563055	✓
Sygnathiformes	Dactylopteridae	<i>Dactylopterus volitans</i>	See NCBI SRA	SAMN06563056	✓
Sygnathiformes	Mullidae	<i>Mulloidichthys dentatus</i>	See NCBI SRA	SAMN06563097	

		<i>Mulloidichthys</i>				
Sygnathiformes	Mullidae	<i>martinicus</i>	See NCBI SRA	SAMN06563098	✓	
Sygnathiformes	Mullidae	<i>Mulloidichthys vanicolensis</i>	See NCBI SRA	SAMN06563099	✓	
Sygnathiformes	Mullidae	<i>Mullus auratus</i>	See NCBI SRA		✓	
		<i>Parupeneus barberinoides</i>	See NCBI SRA	SAMN06563103	✓	
Sygnathiformes	Mullidae	<i>Parupeneus barberinus</i>	See NCBI SRA		✓	
Sygnathiformes	Mullidae	<i>Parupeneus barberinus</i>	See NCBI SRA	SAMN06563108		
Sygnathiformes	Mullidae	<i>Parupeneus cyclostomus</i>	See NCBI SRA	SAMN06563105	✓	
Sygnathiformes	Mullidae	<i>Parupeneus multifasciatus</i>	See NCBI SRA	SAMN06563106	✓	
Sygnathiformes	Mullidae	<i>Parupeneus rubescens</i>	See NCBI SRA	SAMN06563107		
Sygnathiformes	Mullidae	<i>Pseudupeneus grandisquamis</i>	See NCBI SRA	SAMN06563113	✓	✓
Sygnathiformes	Mullidae	<i>Pseudupeneus maculatus</i>	See NCBI SRA	SAMN06563112	✓	
Sygnathiformes	Mullidae	<i>Upeneichthys lineatus</i>	See NCBI SRA	SAMN06563144	✓	
Sygnathiformes	Mullidae	<i>Upeneus tragula</i>	See NCBI SRA	SAMN06563145	✓	
Sygnathiformes	Draconettidae	<i>Draconetta xenica</i>	YFTC 25957; Pers. Coll.: Eri Katayama			
Sygnathiformes	Callionymidae	<i>Anaora tentaculata</i>	See NCBI SRA	SAMN06563036		
Sygnathiformes	Callionymidae	<i>Callionymus belcheri</i>	See NCBI SRA	SAMN06563039	✓	✓
Sygnathiformes	Callionymidae	<i>Callionymus calcaratus</i>	See NCBI SRA	SAMN06563114		
Sygnathiformes	Callionymidae	<i>Callionymus curvicornis</i>	See NCBI SRA	SAMN06563040	✓	
Sygnathiformes	Callionymidae	<i>Callionymus delicatulus</i>	See NCBI SRA	SAMN06563041	✓	
Sygnathiformes	Callionymidae	<i>Callionymus limiceps</i>	See NCBI SRA	SAMN06563042	✓	
Sygnathiformes	Callionymidae	<i>Calliurichthys grossi</i>	See NCBI SRA	SAMN06563043		
Sygnathiformes	Callionymidae	<i>Calliurichthys scaber</i>	See NCBI SRA	SAMN06563044		
Sygnathiformes	Callionymidae	<i>Dactylopus dactylopus</i>	See NCBI SRA	SAMN06563057	✓	
Sygnathiformes	Callionymidae	<i>Diplogrammus goramensis</i>	See NCBI SRA	SAMN06563058	✓	
Sygnathiformes	Callionymidae	<i>Draculo mirabilis</i>	See NCBI SRA	SAMN06563066		
Sygnathiformes	Callionymidae	<i>Repomucenus calcaratus</i>	See NCBI SRA			
Sygnathiformes	Callionymidae	<i>Synchiropus agassizii</i>	See NCBI SRA	SAMN06563075		
Sygnathiformes	Callionymidae	<i>Synchiropus altivelis</i>	See NCBI SRA	SAMN06563120		
Sygnathiformes	Callionymidae	<i>Synchiropus atrilabiatus</i>	See NCBI SRA	SAMN06563121	✓	
Sygnathiformes	Callionymidae	<i>Synchiropus goodenbeani</i>	See NCBI SRA			
Sygnathiformes	Callionymidae	<i>Synchiropus masudai</i>	See NCBI SRA	SAMN06563077		
Sygnathiformes	Callionymidae	<i>Synchiropus moyeri</i>	See NCBI SRA	SAMN06563122		
Sygnathiformes	Callionymidae	<i>Synchiropus ocellatus</i>	See NCBI SRA	SAMN06563123		
Sygnathiformes	Callionymidae	<i>Synchiropus picturatus</i>	See NCBI SRA	SAMN06563124	✓	
Sygnathiformes	Callionymidae	<i>Synchiropus splendidus</i>	See NCBI SRA	SAMN06563125	✓	
Sygnathiformes	Callionymidae	<i>Synchiropus stellatus</i>	See NCBI SRA	SAMN06563101	✓	
Sygnathiformes	Centriscidae	<i>Aeoliscus strigatus</i>	See NCBI SRA	SAMN06563035	✓	
Sygnathiformes	Centriscidae	<i>Centriscus scutatus</i>	See NCBI SRA	SAMN06563045		✓

Sygnathiformes	Centriscidae	<i>Macroramphosus gracilis</i>	See NCBI SRA	SAMN06563091	✓
Sygnathiformes	Centriscidae	<i>Macroramphosus scolopax</i>	See NCBI SRA	SAMN06563092	✓
Sygnathiformes	<i>Aulostomus</i>	<i>Aulostomus chinensis</i>	SAIAB 77945		✓
Sygnathiformes	<i>Aulostomus</i>	<i>Aulostomus maculatus</i>	See NCBI SRA	SAMN06563038	✓
Sygnathiformes	<i>Fistularia</i>	<i>Fistularia commersonii</i>	See NCBI SRA	SAMN06563071	✓
Sygnathiformes	<i>Fistularia</i>	<i>Fistularia corneta</i>	See NCBI SRA	SAMN06563072	✓
Sygnathiformes	<i>Fistularia</i>	<i>Fistularia petimba</i>	See NCBI SRA	SAMN06563073	✓
Sygnathiformes	<i>Fistularia</i>	<i>Fistularia tabacaria</i>	See NCBI SRA	SAMN06563074	
Sygnathiformes	<i>Solenostomus</i>	<i>Solenostomus cyanopterus</i>	See NCBI SRA	SAMN06563117	
Sygnathiformes	<i>Solenostomus</i>	<i>Solenostomus paradoxus</i>	See NCBI SRA	SAMN06563118	
Sygnathiformes	Syngnathidae	<i>Choeroichthys sculptus</i>	See NCBI SRA	SAMN06563046	
Sygnathiformes	Syngnathidae	<i>Corythoichthys amplexus</i>	See NCBI SRA	SAMN06563047	✓
Sygnathiformes	Syngnathidae	<i>Corythoichthys haematopterus</i>	See NCBI SRA	SAMN06563049	✓
Sygnathiformes	Syngnathidae	<i>Corythoichthys intestinalis</i>	See NCBI SRA	SAMN06563050	✓
Sygnathiformes	Syngnathidae	<i>Corythoichthys schultzi</i>	See NCBI SRA	SAMN06563051	✓
Sygnathiformes	Syngnathidae	<i>Cosmocampus arctus</i>	See NCBI SRA	SAMN06563052	✓
Sygnathiformes	Syngnathidae	<i>Doryichthys boaja</i>	See NCBI SRA	SAMN06563059	
Sygnathiformes	Syngnathidae	<i>Doryichthys martensii</i>	See NCBI SRA	SAMN06563060	
Sygnathiformes	Syngnathidae	<i>Doryrhamphus excisus</i>	See NCBI SRA	SAMN06563061	✓
Sygnathiformes	Syngnathidae	<i>Doryrhamphus janssi</i>	See NCBI SRA	SAMN06563062	
Sygnathiformes	Syngnathidae	<i>Dunckerocampus boylei</i>	See NCBI SRA	SAMN06563064	
Sygnathiformes	Syngnathidae	<i>Dunckerocampus dactyliophorus</i>	See NCBI SRA		
Sygnathiformes	Syngnathidae	<i>Enneacampus ansorgii</i>	See NCBI SRA	SAMN06563067	
Sygnathiformes	Syngnathidae	<i>Entelurus aequoreus</i>	See NCBI SRA	SAMN06563068	✓
Sygnathiformes	Syngnathidae	<i>Festucalex wassi</i>	See NCBI SRA	SAMN06563070	
Sygnathiformes	Syngnathidae	<i>Halicampus crinitus</i>	See NCBI SRA	SAMN06563093	✓
Sygnathiformes	Syngnathidae	<i>Halicampus dunckeri</i>	See NCBI SRA	SAMN06563078	✓
Sygnathiformes	Syngnathidae	<i>Hippichthys penicilllus</i>	See NCBI SRA	SAMN06563079	✓
Sygnathiformes	Syngnathidae	<i>Hippocampus abdominalis</i>	See NCBI SRA	SAMN06563080	✓
Sygnathiformes	Syngnathidae	<i>Hippocampus barbouri</i>	See NCBI SRA		✓
Sygnathiformes	Syngnathidae	<i>Hippocampus comes</i>	See NCBI SRA	SAMN06563082	✓
Sygnathiformes	Syngnathidae	<i>Hippocampus ingens</i>	See NCBI SRA		✓
Sygnathiformes	Syngnathidae	<i>Hippocampus kuda</i>	See NCBI SRA		✓
Sygnathiformes	Syngnathidae	<i>Hippocampus reidi</i>	See NCBI SRA	SAMN06563087	✓
Sygnathiformes	Syngnathidae	<i>Hippocampus subelongatus</i>	See NCBI SRA	SAMN06563088	
Sygnathiformes	Syngnathidae	<i>Hypselognathus rostratus</i>	See NCBI SRA	SAMN06563089	
Sygnathiformes	Syngnathidae	<i>Idiotropiscis lumnitzeri</i>	See NCBI SRA	SAMN06563090	
Sygnathiformes	Syngnathidae	<i>Microphis brachyurus</i>	See NCBI SRA	SAMN06563094	✓

Sygnathiformes	Syngnathidae	<i>Microphis cuncalus</i>	See NCBI SRA	SAMN06563095	
Sygnathiformes	Syngnathidae	<i>Microphis deocata</i>	See NCBI SRA	SAMN06563096	
Sygnathiformes	Syngnathidae	<i>Nerophis ophidion</i>	See NCBI SRA	SAMN06563102	✓
Sygnathiformes	Syngnathidae	<i>Phycodurus eques</i>	See NCBI SRA	SAMN06563110	
Sygnathiformes	Syngnathidae	<i>Phyllopteryx taeniolatus</i>	See NCBI SRA	SAMN06563111	
Sygnathiformes	Syngnathidae	<i>Siokunichthys nigrolineatus</i>	See NCBI SRA	SAMN06563116	
Sygnathiformes	Syngnathidae	<i>Stigmatopora nigra</i>	See NCBI SRA	SAMN06563119	
Sygnathiformes	Syngnathidae	<i>Stigmatopora nigra</i> <i>Syngnathoides biaculeatus</i>	See NCBI SRA	SAMN06563126	✓
Sygnathiformes	Syngnathidae	<i>Syngnathus abaster</i>	See NCBI SRA	SAMN06563127	✓
Sygnathiformes	Syngnathidae	<i>Syngnathus acus</i>	See NCBI SRA	SAMN06563128	
Sygnathiformes	Syngnathidae	<i>Syngnathus auliscus</i>	See NCBI SRA	SAMN06563129	
Sygnathiformes	Syngnathidae	<i>Syngnathus californiensis</i>	See NCBI SRA	SAMN06563130	✓
Sygnathiformes	Syngnathidae	<i>Syngnathus exilis</i>	See NCBI SRA	SAMN06563131	
Sygnathiformes	Syngnathidae	<i>Syngnathus floridae</i>	See NCBI SRA	SAMN06563132	✓
Sygnathiformes	Syngnathidae	<i>Syngnathus fuscus</i>	See NCBI SRA	SAMN06563133	✓
Sygnathiformes	Syngnathidae	<i>Syngnathus leptorhynchus</i>	see Longo <i>et al.</i> 2017		✓
Sygnathiformes	Syngnathidae	<i>Syngnathus louisianae</i>	See NCBI SRA see Longo <i>et al.</i> 2017	SAMN06563135	
Sygnathiformes	Syngnathidae	<i>Syngnathus pelagicus</i>			✓
Sygnathiformes	Syngnathidae	<i>Syngnathus rostellatus</i>	See NCBI SRA	SAMN06563137	✓
Sygnathiformes	Syngnathidae	<i>Syngnathus scovelli</i>	See NCBI SRA	SAMN06563138	✓
Sygnathiformes	Syngnathidae	<i>Syngnathus springeri</i>	See NCBI SRA	SAMN06563139	
Sygnathiformes	Syngnathidae	<i>Syngnathus taenionotus</i>	See NCBI SRA	SAMN06563140	
Sygnathiformes	Syngnathidae	<i>Syngnathus typhle</i> <i>Trachyrhamphus bicoarctatus</i>	See NCBI SRA	SAMN06563141	✓
Sygnathiformes	Syngnathidae	<i>Vanacampus phillipi</i>	See NCBI SRA	SAMN06563143	✓
Sygnathiformes	Syngnathidae	<i>Vanacampus poecilolaemus</i>	See NCBI SRA	SAMN06563146	✓
Sygnathiformes	Syngnathidae			SAMN06563147	
Blenniiformes	Adrianichthyidae	<i>Adrianichthys oophorus</i>	USNM 38982		✓
Blenniiformes	Adrianichthyidae	<i>Oryzias latipes</i> <i>Nomorhamphus celebensis</i>	YFTC 32445, n.v.		✓
Blenniiformes	Belonidae		YPM ICH 021568 Pers. Coll.: M.Alfaro, Alfaro 586		✓
Blenniiformes	Belonidae	<i>Xenentodon cancila</i>		SAMN05915137	✓
Blenniiformes	Belonidae	<i>Zenarchopterus dispar</i>	CAS 222403		
Blenniiformes	Exocoetidae	<i>Prognichthys occidentalis</i>	KU 30212		✓
Blenniiformes	Exocoetidae	<i>Oxyporhamphus micropterus</i>	LACM 46125.003		✓
Blenniiformes	Hemiramphidae	<i>Hyporhamphus dussumieri</i>	KU 37091		✓
Blenniiformes	Hemiramphidae	<i>Hemiramphus far</i>	KU 6756		✓

Blenniiformes	Atherinopsidae	<i>Atherinella panamensis</i>	YFTC 16681, n.v.	✓
Blenniiformes	Atherinopsidae	<i>Melanorhinus microps</i>	LACM T-000545	
Blenniiformes	<i>Atherion</i>	<i>Atherion elymus</i>	YFTC 16683, n.v.	
Blenniiformes	Phallostethidae	<i>Neostethus bicornis</i>	YFTC 16684, n.v.	✓
Blenniiformes	Phallostethidae	<i>Phenacostethus smithi</i>	USNM 329346	
Blenniiformes	<i>Iso</i>	<i>Iso rhothophilus</i>	YFTC 16682, n.v.	✓
Blenniiformes	Atherinidae	<i>Atherina presbyter</i> <i>Bedotia</i> <i>madagascariensis</i>	KU 8637	
Blenniiformes	Bedotiidae	<i>Pseudomugil gertrudae</i> <i>Cairnsichthys</i> <i>rhombosomoides</i>	YFTC 21585, n.v. tissued whole	✓
Blenniiformes	Pseudomugilidae	<i>Iriatherina werneri</i> <i>Austrofundulus</i> <i>leohoignei</i>	KU 1696	✓
Blenniiformes	Melanotaeniidae	<i>Austrolebias nigripinnis</i>	YFTC 16675, n.v.	
Blenniiformes	Melanotaeniidae	<i>Kryptolebias marmoratus</i>	YPM ICH 025213	✓
Blenniiformes	Rivulidae	<i>Aplocheilidae</i> <i>Aplocheilus panchax</i>	Pers. Coll.: Reznick Lab UCRiverside	✓
Blenniiformes	Rivulidae	<i>Nothobranchius furzeri</i> <i>Nothobranchius</i> <i>orthonotus</i>	See NCBI SRA	SAMN03490872*
Blenniiformes	Aplocheilidae	<i>Aplocheilus lineatus</i>	See NCBI SRA	SAMN04622665*
Blenniiformes	Aplocheilidae	<i>Aplocheilus panchax</i>	YPM ICH 025220	✓
Blenniiformes	Nothobranchiidae	<i>Aphyosemion thysi</i>	AMNH 258919	✓
Blenniiformes	Nothobranchiidae	<i>Epiplatys spilargyreia</i>	AMNH 257025	✓
Blenniiformes	Nothobranchiidae	<i>Nothobranchius furzeri</i> <i>Nothobranchius</i> <i>orthonotus</i>	See NCBI SRA	SAMEA2698544*
Blenniiformes	Cubanichthys	<i>Cubanichthys pengelleyi</i>	YFTC 16678, n.v.	
Blenniiformes	Goodeidae	<i>Goodea atripinnis</i>	SLU 6644	✓
Blenniiformes	Profundulidae	<i>Tlaloc labialis</i>	SLU 8114	
Blenniiformes	Cyprinodontidae	<i>Cyprinodon nevadensis</i>	See NCBI SRA	SAMN03072616*
Blenniiformes	Cyprinodontidae	<i>Cyprinodon variegatus</i>	See NCBI SRA	SAMN02736898*
Blenniiformes	Cyprinodontidae	<i>Floridichthys carpio</i>	KU 35360	✓
Blenniiformes	Fundulidae	<i>Fundulus heteroclitus</i>	See NCBI SRA	SAMN03277211*
Blenniiformes	Fundulidae	<i>Fundulus zebrinus</i>	YFTC 16686, n.v.	✓
Blenniiformes	Fundulidae	<i>Leptolucania ommata</i>	YFTC 23708, n.v.	
Blenniiformes	Procatopodidae	<i>Poropanchax normani</i>	YPM ICH 025212	
Blenniiformes	<i>Valencia</i>	<i>Valencia hispanica</i>	MNCN/ADN 63424	✓
Blenniiformes	<i>Valencia</i>	<i>Valencia letourneuxi</i>	YFTC 25747, n.v.	
Blenniiformes	Poeciliidae	<i>Anableps anableps</i>	YPM ICH 024513	✓
Blenniiformes	Poeciliidae	<i>Gambusia affinis</i>	See NCBI SRA	SAMN07157452*
Blenniiformes	Poeciliidae	<i>Gambusia holbrooki</i>	MNCN/ADN 59090	✓
Blenniiformes	Poeciliidae	<i>Poecilia latipinna</i>	See NCBI SRA	SAMN02048973*
Blenniiformes	Poeciliidae	<i>Poecilia mexicana</i>	See NCBI SRA	SAMN02048972*
Blenniiformes	Poeciliidae	<i>Poecilia reticulata</i>	See NCBI SRA	SAMN02404645*

Blenniiformes	Poeciliidae	<i>Xiphophorus couchianus</i>	See NCBI SRA	SAMN03922721*	✓	
Blenniiformes	Poeciliidae	<i>Xiphophorus hellerii</i>	See NCBI SRA	SAMN09545741*	✓	
Blenniiformes	Polycentridae	<i>Monocirrhus polyacanthus</i>	Pers. Coll.: P.Wainwright, PW1656		✓	✓
Blenniiformes	Polycentridae	<i>Polycentrus schomburgkii</i>	Pers. Coll.: P.Wainwright, PW1659 Pers. Coll.: P.Wainwright,			
Blenniiformes	<i>Pholidichthys</i>	<i>leucotaenia</i>	PW1329	SAMN05915100	✓	✓
Blenniiformes	Cichlidae	<i>Amphilophus citrinellus</i>	See NCBI SRA	SAMEA2698536*	✓	
Blenniiformes	Cichlidae	<i>Bathybates minor</i>	See NCBI SRA	SAMN04011497	✓	
Blenniiformes	Cichlidae	<i>Ectodus descampsii</i>	See NCBI SRA	SAMN04011500		
Blenniiformes	Cichlidae	<i>Eretmodus cyanostictus</i>	See NCBI SRA	SAMN04011501	✓	
Blenniiformes	Cichlidae	<i>Haplotaxodon microlepis</i>	See NCBI SRA	SAMN04011503		
Blenniiformes	Cichlidae	<i>Lamprologus callipterus</i>	See NCBI SRA	SAMN04011505	✓	
Blenniiformes	Cichlidae	<i>Paratilapia polleni</i>	YPM ICH 023179			
Blenniiformes	Cichlidae	<i>Paretroplus dambabe</i>	YPM ICH 023180		✓	✓
Blenniiformes	Cichlidae	<i>Pseudotropheus flavus</i>	See NCBI SRA	SAMN04011494		
Blenniiformes	Cichlidae	<i>Pterophyllum leopoldi</i>	YPM ICH 023150	SAMN05915114		✓
Blenniiformes	Cichlidae	<i>Ptychochromis oligacanthus</i>	YPM ICH 023177		✓	
Blenniiformes	Cichlidae	<i>Telmatochromis temporalis</i>	See NCBI SRA	SAMN04011535	✓	
Blenniiformes	Ambassidae	<i>Ambassis urotaenia</i>	YPM ICH 020542		✓	
Blenniiformes	Ambassidae	<i>Parambassis ranga</i>	YFTC 1064, n.v.		✓	✓
Blenniiformes	Mugilidae	<i>Crenimugil crenilabis</i>	YPM ICH 026701			
Blenniiformes	Mugilidae	<i>Osteomugil engeli</i>	YFTC 23617, n.v.			
Blenniiformes	Congrogadidae	<i>Congrogadus subducens</i>	YPM ICH 25208			
Blenniiformes	Plesiopidae	<i>Plesiops caeruleolineatus</i>	YPM ICH 026606 Pers. Coll.: M.Alfaro, Alfaro 13MS4			
Blenniiformes	Plesiopidae	<i>Plesiops</i> sp.		SAMN05915101		
Blenniiformes	Pseudochromidae	<i>Labracinus cyclophthalmus</i>	Pers. Coll.: P.Wainwright, PW1689			✓
Blenniiformes	Pseudochromidae	<i>Pseudochromis flavivertex</i>	CAS LR151	SAMN05915110	✓	
Blenniiformes	Pseudochromidae	<i>Pseudochromis fuscus</i>	See NCBI SRA	SAMEA4028829*	✓	
Blenniiformes	Pseudochromidae	<i>Pseudochromis sankeyi</i>	CAS LR117	SAMN05915111	✓	
Blenniiformes	Pomacentridae	<i>Acanthochromis polyacanthus</i>	See NCBI SRA	SAMN06347167*	✓	✓
Blenniiformes	Pomacentridae	<i>Amphiprion ocellaris</i>	See NCBI SRA	SAMN07982614*	✓	
Blenniiformes	Pomacentridae	<i>Amphiprion percula</i>	See NCBI SRA	SAMN08615572*	✓	
Blenniiformes	Pomacentridae	<i>Chromis chromis</i>	See NCBI SRA	SAMEA4028828*	✓	
Blenniiformes	Pomacentridae	<i>Chromis enchrysura</i>	CAS CEN01	SAMN05915054	✓	
Blenniiformes	Pomacentridae	<i>Pomacentrus philippinus</i>	YPM ICH 026633		✓	
Blenniiformes	Pomacentridae	<i>Stegastes partitus</i>	YPM ICH 24711		✓	
Blenniiformes	Embiotocidae	<i>Embiotoca jacksoni</i>	Pers. Coll.: P.Wainwright, PW227: B09		✓	✓

Blenniiformes	Embiotocidae	<i>Hyperprosopon ellipticus</i>	INHS 45420	✓	
Blenniiformes	Embiotocidae	<i>Phanerodon furcatus</i>	Pers. Coll.: P.Wainwright, PW269: B52	✓	
Blenniiformes	Grammatidae	<i>Gramma loreto</i>	CAS GLO01	SAMN05915067	✓
Blenniiformes	Opistognathidae	<i>Opistognathus aurifrons</i>	YPM ICH 025216	✓	
Blenniiformes	Gobiesocidae	<i>Gobiesox maeandricus</i>	Pers. Coll.: P.Wainwright, PW2497 SAMEA104026382	✓	✓
Blenniiformes	Gobiesocidae	<i>Gouania willdenowi</i>	See NCBI SRA *		✓
Blenniiformes	Gobiesocidae	<i>Lepadichthys lineatus</i>	CAS 224422		
Blenniiformes	Tripterygiidae	<i>Enneanectes boehlkei</i>	USNM 327602		
Blenniiformes	Tripterygiidae	<i>Lepidonectes corallicolus</i>	SIO 02-82		
Blenniiformes	Blenniidae	<i>Parablennius parvicornis</i>	See NCBI SRA	SAMEA4028827*	✓
Blenniiformes	Blenniidae	<i>Scartella cristata</i>	CAS SCR01	SAMN05915120	✓
Blenniiformes	Clinidae	<i>Gibbonsia metzi</i>	Pers. Coll.: P.Wainwright, PW221: B03	✓	
Blenniiformes	Clinidae	<i>Muraenoclinus dorsalis</i>	KU 6488		
Blenniiformes	Labrisomidae	<i>Labrisomus nuchipinnis</i>	CAS LNU08	SAMN05915078	
Blenniiformes	Chaenopsidae	<i>Emblemariopsis</i> sp.	CAS EMB01	SAMN05915061	
Blenniiformes	Dactyloscopidae	<i>Dactyloscopus lacteus</i>	SIO 02-88-1		
Blenniiformes	Dactyloscopidae	<i>Gillellus semicinctus</i>	SIO 01-167	✓	
Anabantiformes	<i>Indostomus</i>	<i>Indostomus crocodilus</i>	YPM ICH 23894		
Anabantiformes	<i>Indostomus</i>	<i>Indostomus paradoxus</i>	n.v. tissued whole Per. Coll.: W.L.Smith 22	✓	✓
Anabantiformes	Synbranchidae	<i>Monopterus albus</i> <i>Ophisternon</i> <i>aenigmaticum</i>	LSUMZ 16237		
Anabantiformes	Synbranchidae	<i>Ophisternon bengalense</i>	UF 235970		
Anabantiformes	Synbranchidae	<i>Synbranchus marmoratus</i>	KU 41318		
Anabantiformes	Chaudhuriidae	<i>Chaudhuria caudata</i>	UF 173154		
Anabantiformes	Mastacembelidae	<i>Macrognathus aculeatus</i> <i>Macrognathus</i> <i>circumcinctus</i>	UF 161615		
Anabantiformes	Mastacembelidae		UF 170247		
Anabantiformes	Mastacembelidae	<i>Macrognathus zebrinus</i>	Pers. Coll.: J.Day	✓	
Anabantiformes	Mastacembelidae	<i>Mastacembelus armatus</i>	Pers. Coll.: J.Day	✓	
Anabantiformes	Mastacembelidae	<i>Mastacembelus flavidus</i> <i>Mastacembelus</i> <i>mastacembelus</i>	SAIAB 79915 Pers. Coll.: J.Day JF1390		
Anabantiformes	Mastacembelidae	<i>Mastacembelus unicolor</i>	UF 166011		✓
Anabantiformes	<i>Pristolepis</i>	<i>Pristolepis fasciata</i>	UF 162364	✓	
Anabantiformes	Badidae	<i>Badis badis</i>	Pers. Coll.: J.Day	✓	
Anabantiformes	Badidae	<i>Badis pyema</i>	YFTC 18189, n.v. tissued whole	✓	
Anabantiformes	Badidae	<i>Dario dario</i>	YFTC 18190, n.v. tissued whole		
Anabantiformes	Badidae	<i>Dario hysginon</i>	YFTC 20196, n.v. tissued whole	✓	
Anabantiformes	Nandidae	<i>Nandus andrewi</i>	Pers. Coll.: P.Wainwright, PW1657		
Anabantiformes	Nandidae	<i>Nandus nandus</i>	Pers. Coll.: P.Wainwright, PW1663	✓	
Anabantiformes	Nandidae	<i>Nandus nebulosus</i>	Pers. Coll.: P.Wainwright, PW1660	✓	

			Pers. Coll.:	
Anabantiformes	Nandidae	<i>Nandus</i> cf. <i>oxyrhynchus</i>	W.L.Smith 488	✓
Anabantiformes	Channidae	<i>Channa andrao</i>	Pers. Coll.: J.Day	
Anabantiformes	Channidae	<i>Channa argus</i>	CBM 12593	
Anabantiformes	Channidae	<i>Channa aurantimaculata</i>	Pers. Coll.: J.Day	
Anabantiformes	Channidae	<i>Channa bleheri</i>	Pers. Coll.: J.Day	
Anabantiformes	Channidae	<i>Channa gachua</i>	Pers. Coll.: J.Day	✓
Anabantiformes	Channidae	<i>Channa lucius</i>	UF 236121	
Anabantiformes	Channidae	<i>Channa marulius</i>	UF 237264 Pers. Coll.: W.L.Smith 355	✓
Anabantiformes	Channidae	<i>Channa micropeltes</i>	UF 173357	✓
Anabantiformes	Channidae	<i>Parachanna insignis</i>	CUMV 96133	
Anabantiformes	Channidae	<i>Parachanna obscura</i>	CUMV 96491 Pers. Coll.: W.L.Smith 36	
Anabantiformes		<i>Helostoma temminckii</i>		✓
Anabantiformes	Anabantidae	<i>Anabas testudineus</i>	UF 237404	✓
Anabantiformes	Anabantidae	<i>Ctenopoma acutirostre</i>	CUMV 93049	✓
Anabantiformes	Anabantidae	<i>Ctenopoma gabonense</i>	CUMV 87803	
Anabantiformes	Anabantidae	<i>Ctenopoma kingsleyae</i>	CUMV 91505	✓
Anabantiformes	Anabantidae	<i>Ctenopoma maculatum</i>	CUMV 92275	
Anabantiformes	Anabantidae	<i>Ctenopoma multispine</i>	CUMV 91229	
Anabantiformes	Anabantidae	<i>Ctenopoma muriei</i>	CUMV 94531	✓
Anabantiformes	Anabantidae	<i>Ctenopoma nigropannosum</i>	CUMV 96662 Pers. Coll.: W.L.Smith 279	✓
Anabantiformes	Anabantidae	<i>Ctenopoma ocellatum</i> <i>Microctenopoma</i> <i>ansorgii</i>		
Anabantiformes	Anabantidae	<i>Microctenopoma fasciolatum</i>	YPM ICH 025197	✓
Anabantiformes	Anabantidae	<i>Microctenopoma nanum</i>	YPM ICH 32030	
Anabantiformes	Anabantidae	<i>Microctenopoma pekkolai</i>	CUMV 94529	
Anabantiformes	Anabantidae	<i>Microctenopoma uelense</i>	CUMV 91502	
Anabantiformes	Anabantidae	<i>Sandelia bainsii</i>	SAIAB 199798	
Anabantiformes	Anabantidae	<i>Sandelia capensis</i>	SAIAB 186085	✓
Anabantiformes	Anabantidae	<i>Sandelia capensis</i>	SAIAB 186114	
Anabantiformes	Anabantidae	<i>Sandelia capensis</i>	SAIAB 186029	
Anabantiformes	Osphronemidae	<i>Belontia hasselti</i>	UF 165962	✓
Anabantiformes	Osphronemidae	<i>Betta albimarginata</i>	Pers. Coll.: J.Day	
Anabantiformes	Osphronemidae	<i>Betta macrostoma</i>	Pers. Coll.: J.Day	✓
Anabantiformes	Osphronemidae	<i>Betta mandor</i>	YPM ICH 34720	
Anabantiformes	Osphronemidae	<i>Betta splendens</i>	Pers. Coll.: J.Day	✓
Anabantiformes	Osphronemidae	<i>Ctenops nobilis</i>	YPM ICH 33735	
Anabantiformes	Osphronemidae	<i>Luciocephalus aura</i>	UF 167012	✓

			Pers. Coll.:		
Anabantoformes	Osphronemidae	<i>Luciocephalus pulcher</i>	W.L.Smith 718		
Anabantoformes	Osphronemidae	<i>Macropodus ocellatus</i>	CBM 12607		
Anabantoformes	Osphronemidae	<i>Macropodus opercularis</i>	Pers. Coll.: J.Day Pers. Coll.:	✓	
Anabantoformes	Osphronemidae	<i>Osphronemus goramy</i>	W.L.Smith 536	✓	
Anabantoformes	Osphronemidae	<i>Osphronemus laticlavius</i>	YFTC 20201, n.v.		
Anabantoformes	Osphronemidae	<i>Paraspheerichthys ocellatus</i>	YPM ICH 32028	✓	
Anabantoformes	Osphronemidae	<i>Parosphromenus deissneri</i>	Pers. Coll.: J.Day	✓	
Anabantoformes	Osphronemidae	<i>Parosphromenus linkei</i>	YFTC 20193, n.v.		
Anabantoformes	Osphronemidae	<i>Pseudosphromenus cupanus</i>	YPM ICH 33699		
Anabantoformes	Osphronemidae	<i>Sphaerichthys ospromenoides</i>	Pers. Coll.: W.L.Smith 308	✓	
Anabantoformes	Osphronemidae	<i>Sphaerichthys vaillanti</i>	Pers. Coll.: J.Day		
Anabantoformes	Osphronemidae	<i>Trichogaster chuna</i>	Pers. Coll.: J.Day		
Anabantoformes	Osphronemidae	<i>Trichogaster labiosa</i>	YPM ICH 32029	✓	
Anabantoformes	Osphronemidae	<i>Trichogaster lalius</i>	Pers. Coll.: J.Day	✓	
Anabantoformes	Osphronemidae	<i>Trichopodus leerii</i>	Pers. Coll.: J.Day	✓	
Anabantoformes	Osphronemidae	<i>Trichopodus microlepis</i>	Pers. Coll.: J.Day		
Anabantoformes	Osphronemidae	<i>Trichopodus pectoralis</i>	YPM ICH 021566	✓	
Anabantoformes	Osphronemidae	<i>Trichopodus trichopterus</i>	LSUMZ 13914	✓	
Anabantoformes	Osphronemidae	<i>Trichopsis pumila</i>	n.v. tissued whole	✓	
Anabantoformes	Osphronemidae	<i>Trichopsis vittata</i>	UF 162202	✓	
Carangiformes	Centropomidae	<i>Lates calcarifer</i>	NTM 92	SAMN05785344	✓
Carangiformes	Centropomidae	<i>Centropomus ensiferus</i>	LSUMZ 16022		✓
Carangiformes	Centropomidae	<i>Centropomus mediuss</i>	KU 8498	SAMN05915046	✓
Carangiformes		<i>Lactarius lactarius</i>	NSMT-P 91244		
Carangiformes	<i>Sphyraena</i>	<i>Sphyraena barracuda</i>	LSUMZ 15881		✓
Carangiformes	<i>Sphyraena</i>	<i>Sphyraena jello</i>	LSUMZ 17037		✓
Carangiformes	<i>Sphyraena</i>	<i>Sphyraena pinguis</i>	LSUMZ 17074		✓
Carangiformes	<i>Sphyraena</i>	<i>Sphyraena putnamiae</i>	KU 6785	SAMN05915126	✓
Carangiformes	<i>Sphyraena</i>	<i>Sphyraena sphyraena</i>	Pers. Coll.: W.L.Smith 499	SAMN05785363	
Carangiformes	Polynemidae	<i>Eleutheronema tetradactylum</i>	Pers. Coll.: H.Larson	SAMN05785336	✓
Carangiformes	Polynemidae	<i>Polydactylus approximans</i>	LSUMZ 17875		✓
Carangiformes	Polynemidae	<i>Polydactylus sexfilis</i>	KU 6829	SAMN05915103	
Carangiformes	Polynemidae	<i>Polynemus melanochir</i>	LSUMZ 14165		
Carangiformes	<i>Psettodes</i>	<i>Psettodes eneumeri</i>	LSUMZ 5295	SAMN05785354	✓
Carangiformes	Citharidae	<i>Brachypleura novaezeelandiae</i>	LSUMZ 13790		
Carangiformes	Citharidae	<i>Citharus linguatula</i>	Pers. Coll.: W.L.Smith 596	SAMN05785330	
Carangiformes	Citharidae	<i>Citharoides macrolepis</i>	KU 2468	SAMN05915055	✓

Carangiformes	Achiridae	<i>Gymnachirus melas</i>	KU 5187	SAMN05785338	✓
Carangiformes	Achiridae	<i>Trinectes maculatus</i>	KU 1501 Pers. Coll.:	SAMN05785371	✓
Carangiformes	Achiropsettidae	<i>Mancopsetta maculata</i>	W.L.Smith 714 Pers. Coll.:	SAMN05785346	
Carangiformes	Achiropsettidae	<i>Neoachiropsetta milfordi</i>	W.L.Smith 715	SAMN05785350	
Carangiformes	Samaridae	<i>Samaris cristatus</i>	SAIAB 82287		✓
Carangiformes	Samaridae	<i>Samariscus filipectoralis</i>	LSUMZ 13484		
Carangiformes	Samaridae	<i>Samariscus xenicus</i>	KU 2484	SAMN05785357	✓
Carangiformes	Poecilopsettidae	<i>Poecilopsetta natalensis</i>	SAIAB 81888		
Carangiformes	Poecilopsettidae	<i>Poecilopsetta plinthus</i>	KU 2473	SAMN05915102	✓
Carangiformes	Poecilopsettidae	<i>Poecilopsetta zanzibarensis</i>	SAIAB 82402		
Carangiformes	Cynoglossidae	<i>Cynoglossus lingua</i>	LSUMZ 17034		✓
Carangiformes	Cynoglossidae	<i>Paraplagusia japonica</i>	LSUMZ 17060		
Carangiformes	Cynoglossidae	<i>Syphurus plagiusa</i>	AMNH 474	SAMN05785364	
Carangiformes	Soleidae	<i>Aseraggodes xenicus</i>	KU 5719	SAMN05915093	✓
Carangiformes	Soleidae	<i>Austroglossus pectoralis</i>	SAIAB 200601		
Carangiformes	Soleidae	<i>Dagetichthys marginatus</i>	SAIAB 200744		
Carangiformes	Soleidae	<i>Heteromycteris capensis</i>	SAIAB 191581		
Carangiformes	Soleidae	<i>Solea turbynei</i>	SAIAB 82350		✓
Carangiformes	Scophthalmidae	<i>Scophthalmus maximus</i>	See NCBI SRA	SAMN08049846*	✓
Carangiformes	Scophthalmidae	<i>Scophthalmus rhombus</i>	KU 5416	SAMN05785360	✓
Carangiformes	Pleuronectidae	<i>Pleuronichthys cornutus</i>	LSUMZ 17067		✓
Carangiformes	Pleuronectidae	<i>Pleuronichthys guttulatus</i>	SIO 01-179		
Carangiformes	Pleuronectidae	<i>Pseudopleuronectes yokohamae</i>	LSUMZ 17053		✓
Carangiformes	Paralichthyidae	<i>Ancylopsetta dilecta</i>	LSUMZ 15797		
Carangiformes	Paralichthyidae	<i>Paralichthys alboguttata</i>	AMNH Uncat E172		✓
Carangiformes	Paralichthyidae	<i>Paralichthys oblongus</i>	KU 1493	SAMN05915073	✓
Carangiformes	Paralichthyidae	<i>Pseudorhombus elevatus</i>	LSUMZ 16603		✓
Carangiformes	Cyclopsettidae	<i>Citharichthys spilopterus</i>	LSUMZ 15927		
Carangiformes	Cyclopsettidae	<i>Cyclopsetta fimbriata</i>	KU 3985	SAMN05785333	✓
Carangiformes	Cyclopsettidae	<i>Etropus cyclosquamus</i>	KU 5241	SAMN05785337	✓
Carangiformes	Cyclopsettidae	<i>Syacium gunteri</i>	LSUMZ 15543		✓
Carangiformes	Bothidae	<i>Bothus pantherinus</i>	KU 5642	SAMN05915039	✓
Carangiformes	Bothidae	<i>Crossorhombus azureus</i>	LSUMZ 14148		✓
Carangiformes	Bothidae	<i>Crossorhombus kobensis</i>	KU 2485		
Carangiformes	Bothidae	<i>Engyophrys senta</i>	LSUMZ 15538		
Carangiformes	Bothidae	<i>Trichopsetta ventralis</i>	LSUMZ 15806		
Carangiformes	Leptobrama	<i>Leptobrama muelleri</i>	FMNH 119722	SAMN05785345	✓
Carangiformes	Toxotes	<i>Toxotes blythii</i>	YPM ICH 32036		✓
Carangiformes	Toxotes	<i>Toxotes jaculatorix</i>	YPM ICH 020543	SAMN05915135	✓

Carangiformes		<i>Nematistius pectoralis</i>	LSUMZ 18084 Pers. Coll.:		
Carangiformes		<i>Mene maculatus</i>	W.L.Smith 370 Pers. Coll.:	SAMN05915082	✓
Carangiformes		<i>Xiphias gladius</i>	W.L.Smith 787	SAMN05785372	✓
Carangiformes	Istiophoridae	<i>Istiophorus platypterus</i>	KU 5428	SAMN05915075	
Carangiformes	Istiophoridae	<i>Kajikia audax</i> <i>Tetrapturus</i>	SIO 06-38		
Carangiformes	Istiophoridae	<i>angustirostris</i> <i>Scomberoides</i>	SIO 05-31	SAMN05785366	
Carangiformes	Trachinotidae	<i>commersonnianus</i>	KU 8988	SAMN05785359	✓
Carangiformes	Trachinotidae	<i>Scomberoides lyisan</i>	LSUMZ 14159 SAIAB AV-2010-		✓
Carangiformes	Trachinotidae	<i>Scomberoides tol</i>	091		✓
Carangiformes	Trachinotidae	<i>Trachinotus baillonii</i>	SAIAB RB-09-160		✓
Carangiformes	Trachinotidae	<i>Trachinotus blochii</i>	KU 6793	SAMN05785368	
Carangiformes	Trachinotidae	<i>Trachinotus goodei</i>	YFTC 1994, n.v.		✓
Carangiformes		<i>Rachycentron canadum</i>	KU 3521	SAMN05915115	
Carangiformes		<i>Coryphaena hippurus</i>	KU 7212	SAMN05915056	✓
Carangiformes	Echeneidae	<i>Echeneis naucrates</i>	SAIAB HM07-581		✓
Carangiformes	Echeneidae	<i>Echeneis neucratoides</i>	KU 27104 SAIAB ACEP-09-	SAMN05785335	
Carangiformes	Echeneidae	<i>Phtheirichthys lineatus</i>	224		✓
Carangiformes	Echeneidae	<i>Remora albescens</i>	SIO 05-37		✓
Carangiformes	Echeneidae	<i>Remora brachyptera</i>	SIO 07-91		✓
Carangiformes	Echeneidae	<i>Remora osteochir</i>	SIO 11-34 SAIAB ACEP-08-		✓
Carangiformes	Echeneidae	<i>Remora remora</i>	1660		✓
Carangiformes	Carangidae	<i>Alectis indicus</i>	KU 8966	SAMN05915025	✓
Carangiformes	Carangidae	<i>Alepes kleinii</i>	KU 8966	SAMN05915026	
Carangiformes	Carangidae	<i>Alepes vari</i>	QM A01251		
Carangiformes	Carangidae	<i>Alepes vari</i>	QM I39515		
Carangiformes	Carangidae	<i>Carangichthys dinema</i>	FRLM 48738		
Carangiformes	Carangidae	<i>Carangooides armatus</i>	LSUMZ 16745		
Carangiformes	Carangidae	<i>Carangooides armatus</i>	LSUMZ 16745		
Carangiformes	Carangidae	<i>Carangooides chrysophrrys</i>	SAIAB Event Number: AV/2010-04; n.v.		✓
Carangiformes	Carangidae	<i>Carangooides ferdau</i>	SAIAB Event Number: PCH 2005-27; n.v.		✓
Carangiformes	Carangidae	<i>Carangooides praeustus</i>	FRLM 51405		
Carangiformes	Carangidae	<i>Caranx caninus</i>	LSUMZ 17829 SAIAB Event Number JRG-PDO-15-215;		✓
Carangiformes	Carangidae	<i>Caranx heberii</i>	n.v.		
Carangiformes	Carangidae	<i>Caranx latus</i>	UF 180908		✓
Carangiformes	Carangidae	<i>Caranx latus</i>	UF 183512		
Carangiformes	Carangidae	<i>Caranx melampygus</i>	KU 5657	SAMN05915044	✓
Carangiformes	Carangidae	<i>Caranx vinctus</i>	LSUMZ 14570		
Carangiformes	Carangidae	<i>Caranx vinctus</i>	LSUMZ 14585		

Carangiformes	Carangidae	<i>Chloroscombrus orqueta</i>	KU 8495	SAMN05915053	✓
Carangiformes	Carangidae	<i>Decapterus maruadsi</i>	KU 8984	SAMN05785334	✓
Carangiformes	Carangidae	<i>Gnathanodon speciosus</i>	LSUMZ 17993		✓
Carangiformes	Carangidae	<i>Hemicarax bicolor</i>	MNHN 1913-0110		✓
Carangiformes	Carangidae	<i>Megalaspis cordyla</i>	KU 4705	SAMN05785347	✓
Carangiformes	Carangidae	<i>Parastromateus niger</i>	LSUMZ 17039		✓
Carangiformes	Carangidae	<i>Selaroides leptolepis</i>	LSUMZ 14065		✓
Carangiformes	Carangidae	<i>Selene peruviana</i>	SIO 07-88L		
Carangiformes	Carangidae	<i>Selene vomer</i>	LSUMZ 14271		✓
Carangiformes	Carangidae	<i>Seriola dumerili</i>	Pers. Coll.: P.Wainwright, PW2629 SAIAB ACEP-09-314		✓
Carangiformes	Carangidae	<i>Seriola dumerili</i>	314		
Carangiformes	Carangidae	<i>Seriola zonata</i>	KU 1188	SAMN05915125	✓
Carangiformes	Carangidae	<i>Trachurus trachurus</i>	KU 8077	SAMN05785370	✓
Perciformes	Epinephelidae	<i>Cephalopholis argus</i>	CAS CAG01	SAMN05915047	✓
Perciformes	Epinephelidae	<i>Cephalopholis cruentata</i>	YPM ICH 24718 Pers. Coll.: G.		✓
Perciformes	Epinephelidae	<i>Diploprion drachi</i>	Bernardi		✓
Perciformes	Epinephelidae	<i>Jeboehlkia gladifer</i>	AMNH CUR13192		✓
Perciformes	Epinephelidae	<i>Liopropoma rubre</i>	YPM ICH 24752		✓
Perciformes	Epinephelidae	<i>Rypticus subbifrenatus</i>	YPM ICH 24697		✓
Perciformes	Anthiadidae	<i>Acanthistius cinctus</i>	KER 427 Pers. Coll.: M.Alfaro, Alfaro-		✓
Perciformes	Anthiadidae	<i>Pseudanthias squamipinnis</i>	969	SAMN05915109	✓
Perciformes	Anthiadidae	<i>Trachypoma macracanthus</i>			✓
Perciformes	Bembropidae	<i>Bembrops anatirostris</i>	YFTC 14558, n.v.		✓
Perciformes	Bembropidae	<i>Chriomema furunoi</i>	NSMT-P 78494		
Perciformes	Serranidae	<i>Chelidoperca hirundinacea</i>	NSMT-P115036 Pers. Coll.: M.Alfaro, Alfaro-		
Perciformes	Serranidae	<i>Hypoplectrus puella</i>	1010.1	SAMN05915074	✓
Perciformes	Serranidae	<i>Serranus tigrinus</i>	Pers. Coll.: P.Wainwright, PW1343: mea207		✓
Perciformes	Trachinidae	<i>Echiichthys vipera</i>	YFTC 24258, n.v.		
Perciformes	Trachinidae	<i>Trachinus radiatus</i>	n.v.		✓
Perciformes		<i>Niphon spinosus</i>	SIO 00-174		✓
Perciformes	Percidae	<i>Allohistium cinereum</i>	UT 91.7531		✓
Perciformes	Percidae	<i>Ammocrypta beanii</i>	INHS 38611		✓
Perciformes	Percidae	<i>Ammocrypta pellucida</i>	YPM ICH 017573		✓
Perciformes	Percidae	<i>Crystallaria asprella</i>	YFTC 686, n.v.		✓
Perciformes	Percidae	<i>Etheostoma baileyi</i>	UT 91.7240		✓
Perciformes	Percidae	<i>Etheostoma basilare</i>	n.v. whole fish in tissue tube		✓
Perciformes	Percidae	<i>Etheostoma blennius</i>	YPM ICH 024144		

Perciformes	Percidae	<i>Etheostoma histrio</i>	YPM ICH 016102	✓
Perciformes	Percidae	<i>Etheostoma pholidotum</i>	YPM ICH 015608	
Perciformes	Percidae	<i>Etheostoma swaini</i>	YPM ICH 027128	
Perciformes	Percidae	<i>Etheostoma variatum</i>	YPM ICH 23724	✓
Perciformes	Percidae	<i>Etheostoma zonale</i>	UT 91.6631	✓
Perciformes	Percidae	<i>Nothonotus juliae</i>	INHS 38559	
Perciformes	Percidae	<i>Nothonotus rufilineatus</i>	UT 91.7011	
Perciformes	Percidae	<i>Perca flavescens</i>	YPM ICH 027384	✓
Perciformes	Percidae	<i>Perca fluviatilis</i>	See NCBI SRA	SAMN08954933*
Perciformes	Percidae	<i>Percina aurantiaca</i>	INHS 64349	✓
Perciformes	Percidae	<i>Percina caprodes</i>	YPM ICH 27964	✓
Perciformes	Percidae	<i>Percina cymatotaenia</i>	YPM ICH 018551	✓
Perciformes	Percidae	<i>Percina evides</i>	YPM ICH 023560	✓
Perciformes	Percidae	<i>Percina macrocephala</i>	YPM ICH 024352; ex UT 91.7318	✓
Perciformes	Percidae	<i>Percina tanasi</i>	YFTC 25474, n.v.	✓
Perciformes	Percidae	<i>Sander canadensis</i>	n.v.	✓
Perciformes		<i>Percophis brasiliensis</i>	LBP 8654 T35304	✓
Perciformes	Bovichtidae	<i>Bovichtus chilensis</i>	YPM ICH 027476	✓
Perciformes	Bovichtidae	<i>Cottoperca trigloides</i>	YFTC 3925, n.v.	✓
Perciformes		<i>Pseudaphritis urvillii</i>	YFTC 16619, n.v.	✓
Perciformes		<i>Eleginops maclovinus</i>	YPM ICH 016549	✓
Perciformes	"Nototheniidae"	<i>Notothenia coriiceps</i>	YPM ICH 016542	✓
Perciformes	"Nototheniidae"	<i>Patagonotothen ramsayi</i>	YFTC 24090, n.v.	✓
Perciformes	Harpagifer	<i>Harpagifer bispinis</i>	YFTC 21691, n.v.	✓
Perciformes	Harpagifer	<i>Harpagifer kerguelensis</i>	YFTC 4830, n.v.	
Perciformes	Artedidraconidae	<i>Arteididracos</i> <i>glareobarbatus</i>	YFTC 14511, n.v.	✓
Perciformes	Artedidraconidae	<i>Pogonophryne</i> <i>cerebropogon</i>	YFTC 24233, n.v.	✓
Perciformes	"Bathydraconidae"	<i>Akarotaxis nudiceps</i>	YPM ICH 024118	✓
Perciformes	"Bathydraconidae"	<i>Parachaenichthys</i> <i>charcoti</i>	YPM ICH 022368	
Perciformes	Channichthyidae	<i>Chaenocephalus</i> <i>aceratus</i>	See NCBI SRA	SAMEA4028820*
Perciformes	Channichthyidae	<i>Chionodraco</i> <i>rastrospinosus</i>	YPM ICH 016672	✓
Perciformes	Channichthyidae	<i>Pageotopsis macropterus</i>	NZNM 043556	
Perciformes	Platycephalidae	<i>Platycephalus indicus</i>	ASIZ 10910261	✓
Perciformes		<i>Normanichthys crockeri</i>	Pers. Coll.: Leonardo Castro	✓
Perciformes	<i>Hoplichthys</i>	<i>Hoplichthysgilberti</i>	ASIZP 9010790	✓
Perciformes	<i>Hoplichthys</i>	<i>Hoplichthys langsdorffii</i>	ASIZP 0913594	✓
Perciformes	Neosebastidae	<i>Neosebastesthetidis</i>	NMV A 22113	✓
Perciformes	Congiopodidae	<i>Congiopodus</i> <i>leucopaecilus</i>	NZNM 044580	✓

Perciformes	Synanceiidae	<i>Inimicus didactylus</i>	Pers. Coll.: P.Wainwright, PCW 3785	✓	
Perciformes	Synanceiidae	<i>Minous trachycephalus</i>	NMV A 29712-004	✓	
Perciformes	Scorpaenidae	<i>Sebastes aleutianus</i>	See NCBI SRA	SAMN03964772*	✓
Perciformes	Scorpaenidae	<i>Sebastes koreanus</i>	See NCBI SRA	SAMN10490951*	
Perciformes	Scorpaenidae	<i>Sebastes minor</i>	See NCBI SRA	SAMN03354192*	
Perciformes	Scorpaenidae	<i>Sebastes nigroinctus</i>	See NCBI SRA	SAMN02981553*	✓
Perciformes	Scorpaenidae	<i>Sebastes norvegicus</i>	See NCBI SRA	SAMEA4028819*	✓
Perciformes	Scorpaenidae	<i>Sebastes nudus</i>	See NCBI SRA	SAMN10490952*	
Perciformes	Scorpaenidae	<i>Sebastes rubrivinctus</i>	See NCBI SRA	SAMN02981552*	
Perciformes	Scorpaenidae	<i>Sebastes schlegelii</i>	See NCBI SRA	SAMN10490953*	✓
Perciformes	Scorpaenidae	<i>Sebastes steindachneri</i>	See NCBI SRA Pers. Coll.: M.Alfaro-	SAMN03579458*	✓
Perciformes	Scorpaenidae	<i>Taenianotus triacanthus</i>	889	SAMN05915130	✓
Perciformes	Bembridae	<i>Bembras japonicus</i>	ASIZPO 910626		
Perciformes	Bembridae	<i>Parabembras curtus</i>	ASIZPO 910628		
Perciformes	Triglidae	<i>Prionotus evolans</i>	YPM ICH 017358		✓
Perciformes	Triglidae	<i>Pterygotrigla hemisticta</i>	ASIZP 091046		
Perciformes	Anoplopomatidae	<i>Anoplopoma fimbria</i>	See NCBI SRA	SAMN02144194*	✓
Perciformes	Anoplopomatidae	<i>Erilepis zonifer</i>	YPM ICH 026411		
Perciformes	Zaniolepididae	<i>Oxylebius pictus</i>	UW 113229		✓
Perciformes	Zaniolepididae	<i>Zaniolepis frenata</i>	UW 119888		✓
Perciformes	Zaniolepididae	<i>Zaniolepis latipinnis</i>	FMNH 121496		
Perciformes	Hexagrammidae	<i>Hexagrammos decagrammus</i>	INHS 45417		✓
Perciformes	Trichodontidae	<i>Trichodon trichodon</i>	UW 117635		✓
Perciformes	Cyclopteridae	<i>Eumicrotremus orbis</i>	Pers. Coll.: P.Wainwright, PW2499		✓
Perciformes	Liparidae	<i>Liparis mucosus</i>	n.v.		✓
Perciformes	Liparidae	<i>Paraliparis meganchus</i>	YPM ICH 022466		✓
Perciformes	Liparidae	<i>Pseudoliparis</i> sp.	See NCBI SRA Pers. Coll.: M.Miya 01-054	SAMN10662039*	
Perciformes	Rhamphocottidae	<i>Ereunias grallator</i>			
Perciformes	Rhamphocottidae	<i>Rhamphocottus richardsoni</i>	Pers. Coll.: P.Wainwright, PW2440		✓
Perciformes		<i>Scorpaenichthys marmoratus</i>	Pers. Coll.: P.Wainwright, PW222: B04		✓
Perciformes		<i>Aspidophoroides monopterygius</i>	YPM ICH 020685		✓
Perciformes	Agonidae	<i>Blepsias cirrhosus</i>	Pers. Coll.: P.Wainwright, PW2441		✓
Perciformes	Agonidae	<i>Hemitripterus bolini</i>	UW 151146		✓
Perciformes	Agonidae	<i>Stellerina xyosterna</i>	n.v.		✓
Perciformes	Cottidae	<i>Cottus carolinae</i>	YPM ICH 021076		✓
Perciformes	Cottidae	<i>Cottus rhenanus</i>	See NCBI SRA	SAMN04145896*	
Perciformes	Psychrolutidae	<i>Cottunculus thomsonii</i>	MCZ 159183		✓
Perciformes	Psychrolutidae	<i>Malacobocetus zonorus</i>	KU 28057		✓

Perciformes	Psychrolutidae	<i>Myoxocephalus aenaeus</i>	YPM ICH 021194	✓
Perciformes	Psychrolutidae	<i>Myoxocephalus scorpius</i>	See NCBI SRA	SAMEA4028818*
Perciformes	Psychrolutidae	<i>Triglops murrayi</i>	YPM ICH 020694	✓
Perciformes		<i>Hypoptichus dybowskii</i>	NSMT-P72827	
Perciformes		<i>Aulichthys japonicus</i>	NSMT-P72829	✓
Perciformes	Gasterosteidae	<i>Gasterosteus islandicus</i>	YFTC 16641, n.v.	✓
Perciformes	Gasterosteidae	<i>Pungitius pungitius</i>	See NCBI SRA	SAMN05210078*
Perciformes	Gasterosteidae	<i>Spinachia spinachia</i> <i>Bathymaster</i>	YFTC 16669, n.v.	✓
Perciformes	Bathymasteridae	<i>caeruleofasciatus</i>	UW 150110	✓
Perciformes	Bathymasteridae	<i>Bathymaster leurolepis</i>	UW 48567	✓
Perciformes	Bathymasteridae	<i>Bathymaster signatus</i>	UW 119600	✓
Perciformes	Bathymasteridae	<i>Rathbunella hypoplecta</i>	n.v.	
Perciformes	Bathymasteridae	<i>Ronquilus jordani</i>	UW 116967	✓
Perciformes		<i>Cebidichthys violaceus</i>	INHS 45421	✓
Perciformes	Stichaeidae	<i>Alectrias alectrolophus</i>	UW 47876	✓
Perciformes	Stichaeidae	<i>Anoplarchus insignis</i> <i>Anoplarchus</i> <i>purpurescens</i>	UW 47871	✓
Perciformes	Stichaeidae		UW 151344	✓
Perciformes	Stichaeidae	<i>Bryozoichthys lysimus</i>	UW 150624	✓
Perciformes	Stichaeidae	<i>Bryozoichthys marjorius</i>	UW 150104	✓
Perciformes	Stichaeidae	<i>Chirolophis decoratus</i>	UW 119212	✓
Perciformes	Stichaeidae	<i>Chirolophis japonicus</i>	UW 47908	
Perciformes	Stichaeidae	<i>Chirolophis snyderi</i> <i>Ernogrammus</i>	UW 150723	
Perciformes	Stichaeidae	<i>hexagrammus</i> <i>Eumesogrammus</i>	UW 47891	✓
Perciformes	Stichaeidae	<i>praecisus</i>	UW 150174	✓
Perciformes	Stichaeidae	<i>Phytichthys chiru</i>	UW 151660	
Perciformes	Stichaeidae	<i>Scybalina cerdale</i>	YPM ICH 026410	
Perciformes	Stichaeidae	<i>Stichaeopsis nana</i>	UW 47889	
Perciformes	Stichaeidae	<i>Stichaeus grigorjewi</i>	UW 47895	✓
Perciformes	Stichaeidae	<i>Stichaeus nozawai</i>	UW 47894	✓
Perciformes	Stichaeidae	<i>Stichaeus punctatus</i>	UW 150124	✓
Perciformes	Stichaeidae	<i>Xiphister atropurpureus</i>	UW 151673	
Perciformes	Stichaeidae	<i>Xiphister mucosus</i> <i>Cryptacanthodes</i> <i>aleutensis</i>	UW 151678	✓
Perciformes	<i>Cryptacanthodes</i>	<i>Cryptacanthodes</i> <i>giganteus</i>	UW 48737	
Perciformes	<i>Cryptacanthodes</i>	<i>Cryptacanthodes</i> <i>maculatus</i>	UW 48792	
Perciformes	<i>Cryptacanthodes</i>	<i>Acantholumpenus</i>	YPM ICH 020687	✓
Perciformes	Lumpenidae	<i>mackayi</i>	UW 150276	✓
Perciformes	Lumpenidae	<i>Anisarchus medius</i>	UW 49373	✓
Perciformes	Lumpenidae	<i>Anisarchus medius</i>	UW 152055	

Perciformes	Lumpenidae	<i>Leptoclinus maculatus</i>	UW 49369	✓
Perciformes	Lumpenidae	<i>Leptoclinus maculatus</i>	UW 151205	✓
Perciformes	Lumpenidae	<i>Lumpenella longirostris</i>	UW 151000	✓
Perciformes	Lumpenidae	<i>Lumpenus sagitta</i>	UW 150616	✓
Perciformes	Lumpenidae	<i>Poroclinus rothrocki</i>	UW 150577	✓
Perciformes		<i>Zaprora silenus</i>	UW 152655	✓
Perciformes		<i>Zaprora silenus</i>	UW 150107	
Perciformes	Opisthocentridae	<i>Askoldia variegata</i>	UW 44508	
Perciformes	Opisthocentridae	<i>Opisthocentrus ocellatus</i>	UW 44935	✓
Perciformes	Opisthocentridae	<i>Opisthocentrus tenuis</i>	UW 47877	✓
Perciformes	Opisthocentridae	<i>Opisthocentrus zonope</i>	UW 47885	✓
Perciformes	Opisthocentridae	<i>Pholidapus dybowskii</i>	UW 47882	
Perciformes		<i>Ptilichthys goodei</i>	Pers. Coll.: P.Wainwright, PCW 2416	✓
Perciformes	Pholidae	<i>Apodichthys flavidus</i>	UW 151663	✓
Perciformes	Pholidae	<i>Pholis clemensi</i>	UW 47872	
Perciformes	Pholidae	<i>Pholis laeta</i>	UW 43793	
Perciformes	Pholidae	<i>Pholis ornata</i>	Pers. Coll.: P.Wainwright, PW244: B27	✓
Perciformes	Pholidae	<i>Pholis ornata</i> <i>Rhodymenichthys dolichogaster</i>	UW 151676	
Perciformes	Pholidae	<i>Gymnoclinus cristulatus</i>	UW 44509	
Perciformes	Neozoarcidae	<i>Neozoarces steindachneri</i>	UW 47875	
Perciformes	Anarhichadidae	<i>Anarhichas orientalis</i>	UW 150194	✓
Perciformes	Anarhichadidae	<i>Anarhichas orientalis</i>	UW 111905	
Perciformes	Anarhichadidae	<i>Anarrhichthys ocellatus</i>	UW 49014	
Perciformes	Zoarcidae	<i>Bothrocara brunneum</i>	UW 150525	✓
Perciformes	Zoarcidae	<i>Bothrocara molle</i>	UW 111363	✓
Perciformes	Zoarcidae	<i>Bothrocara pusillum</i>	UW 151315	✓
Perciformes	Zoarcidae	<i>Bothrocara zestum</i>	UW 150975	
Perciformes	Zoarcidae	<i>Gymnelus viridis</i>	UW 150119	✓
Perciformes	Zoarcidae	<i>Lycenchelys camchatica</i>	UW 119335	✓
Perciformes	Zoarcidae	<i>Lycenchelys crotalinus</i>	UW 118611	✓
Perciformes	Zoarcidae	<i>Lycodapus fierasfer</i>	UW 115137	✓
Perciformes	Zoarcidae	<i>Lycodapus mandibularis</i>	UW 152155	✓
Perciformes	Zoarcidae	<i>Lycodes akuugun</i>	UW 117198	
Perciformes	Zoarcidae	<i>Lycodes beringi</i>	UW 150976	✓
Perciformes	Zoarcidae	<i>Lycodes brevipes</i>	UW 151235	✓
Perciformes	Zoarcidae	<i>Lycodes concolor</i>	UW 150529	✓
Perciformes	Zoarcidae	<i>Lycodes cortezianus</i>	UW 115164	✓
Perciformes	Zoarcidae	<i>Lycodes diapterus</i>	YFTC 13952, n.v.	✓

Perciformes	Zoarcidae	<i>Lycodes diapterus</i>	UW 119963		
Perciformes	Zoarcidae	<i>Lycodes mucosus</i>	UW 152426		
Perciformes	Zoarcidae	<i>Lycodes pacificus</i>	UW 119472	✓	
Perciformes	Zoarcidae	<i>Lycodes pacificus</i>	UW 113585		
Perciformes	Zoarcidae	<i>Lycodes palearis</i>	UW 152045	✓	
Perciformes	Zoarcidae	<i>Lycodes polaris</i>	UW 152421	✓	
Perciformes	Zoarcidae	<i>Lycodes raridens</i>	UW 152485	✓	
Perciformes	Zoarcidae	<i>Lycodes turneri</i>	UW 150133	✓	
Perciformes	Zoarcidae	<i>Puzanovia rubra</i>	UW 150349		
Perciformes	Zoarcidae	<i>Zoarces elongatus</i>	UW 44917 Pers. Coll.: Peter Unmack	✓	
Centrarchiformes	<i>Perca</i>	<i>Perca californiensis</i>			✓
Centrarchiformes	Girellidae	<i>Girella nigricans</i>	Pers. Coll.: Giacomo Bernardi	✓	✓
Centrarchiformes	Scorpididae	<i>Medialuna californiensis</i>	YFTC 21006, n.v. Pers. Coll.: JP	✓	
Centrarchiformes	Scorpididae	<i>Scorpis georgiana</i>	Hobbs	✓	
Centrarchiformes	<i>Dichistius</i>	<i>Dichistius capensis</i>	SAIAB 87252		
Centrarchiformes	<i>Dichistius</i>	<i>Dichistius multifasciatus</i>	SAIAB 86789 Pers. Coll.: JP		
Centrarchiformes	Microcanthidae	<i>Microcanthus strigatus</i>	Hobbs Pers. Coll.: JP		
Centrarchiformes	Microcanthidae	<i>Tilodon sexfasciatus</i>	Hobbs		
Centrarchiformes	<i>Oplegnathus</i>	<i>Oplegnathus conwayi</i>	SIO 05-48		
Centrarchiformes	<i>Oplegnathus</i>	<i>Oplegnathus fasciatus</i>	See NCBI SRA	SAMN07331350*	✓
Centrarchiformes	<i>Oplegnathus</i>	<i>Oplegnathus peacocki</i>	SAIAB 86857		
Centrarchiformes	Kyphosidae	<i>Kyphosus sectatrix</i>	YPM ICH 024907	✓	
Centrarchiformes	Kyphosidae	<i>Kyphosus vaigiensis</i>	NMND 403373	✓	
Centrarchiformes	<i>Kuhlia</i>	<i>Kuhlia marginata</i>	UF 162616	✓	
Centrarchiformes	<i>Kuhlia</i>	<i>Kuhlia rupestris</i>	KU 5666 Pers. Coll.: Peter	✓	
Centrarchiformes	Terapontidae	<i>Bidyanus bidyanus</i>	Unmack Pers. Coll.: Peter	✓	
Centrarchiformes	Terapontidae	<i>Hephaestus fuliginosus</i>	Unmack Pers. Coll.: Peter	✓	
Centrarchiformes	Terapontidae	<i>Scortum barcoo</i>	Unmack Pers. Coll.: Peter		
Centrarchiformes	Terapontidae	<i>Terapon jarbua</i>	Unmack	✓	
Centrarchiformes		<i>Enoplosus armatus</i>	Pers. Coll.: P.Wainwright, PW 3119	✓	
Centrarchiformes	Percichthyidae	<i>Maccullochella peelii</i>	Pers. Coll.: P.Wainwright, PW 1633	✓	
Centrarchiformes	Percichthyidae	<i>Nannoperca australis</i>	Pers. Coll.: Peter Unmack Pers. Coll.: Peter		
Centrarchiformes	Percichthyidae	<i>Percilia gillissi</i>	Unmack Pers. Coll.: Peter		
Centrarchiformes	Percichthyidae	<i>Percilia irwini</i>	Unmack Pers. Coll.: Peter		
Centrarchiformes	Siniperidae	<i>Coreoperca herzi</i>	YPM ICH 026803	✓	
Centrarchiformes	Siniperidae	<i>Siniperca chuatz</i>	YPM ICH 023856	✓	
Centrarchiformes	Centrarchidae	<i>Elassoma okfenokee</i>	Pers. Coll.: P.Wainwright, PW667: FL18	✓	

Centrarchiformes	Centrarchidae	<i>Elassoma zonatum</i>	YPM ICH 021245	✓
Centrarchiformes	Centrarchidae	<i>Enneacanthus chaetodon</i>	UF 236219	✓
Centrarchiformes	Centrarchidae	<i>Micropterus salmoides</i>	YPM ICH 023651	SAMN05915084
Centrarchiformes	Cirrhitidae	<i>Amblycirrhitus pinos</i>	USNM 349043	✓
Centrarchiformes	Cirrhitidae	<i>Cirrhitichthys falco</i>	USNM 334280	✓
Centrarchiformes	Cirrhitidae	<i>Chirodactylus brachydactylus</i>	KU 6471	✓
Centrarchiformes	Latridae	<i>Latridopsis fosteri</i>	YFTC 24241, n.v. SAMA ABTC	
Centrarchiformes	Latridae	<i>Latris lineata</i>	102988	
Centrarchiformes	<i>Chironemus</i>	<i>Chironemus bicornis</i>	FMNH 107336 Pers. Coll.: Chris	✓
Centrarchiformes	<i>Cheilodactylus</i>	<i>Cheilodactylus fasciatus</i>	Burridge	SRX5100538
Centrarchiformes	<i>Aplodactylus</i>	<i>Aplodactylus arctidens</i>	NMV A 24857 Pers. Coll.: Chris	✓
Centrarchiformes	<i>Aplodactylus</i>	<i>Aplodactylus lophodon</i>	Burridge	SRR8285884
Labrifomes	Uranoscopidae	<i>Astroscopus y graecum</i>	KU 22957	✓
Labrifomes	Uranoscopidae	<i>Kathetostoma averruncus</i>	KU 28152	✓
Labrifomes	Ammodytidae	<i>Ammodytes hexapterus</i>	Pers. Coll.: P.Wainwright, PW2451	✓
Labrifomes	Pinguipedidae	<i>Parapercis hexophtalma</i>	SAIAB 77885	✓
Labrifomes		<i>Cheimarrichthys fosteri</i>	See NCBI SRA	SAMN05915051
Labrifomes	Leptoscopidae	<i>Crapatalus munroi</i>	CSIRO H 7106-01	
Labrifomes	Leptoscopidae	<i>Lesueurina platycephala</i>	CSIRO H 7106-03	
Labrifomes		<i>Centrogenys vaigiensis</i>	LSUMZ 16511	✓
Labrifomes		<i>Centrogenys vaigiensis</i>	LSUMZ 16559	✓
Labrifomes		<i>Centrogenys vaigiensis</i>	LSUMZ 16559	
Labrifomes	Labridae	<i>Achoerodus viridis</i>	Pers. Coll.: D.Bellwood M507, n.v.	
Labrifomes	Labridae	<i>Bodianus rufus</i>	Pers. Coll.: D.Bellwood M383, n.v.	✓
Labrifomes	Labridae	<i>Bolbometopon muricatum</i>	Pers. Coll.: D.Bellwood Choat_SIO1, n.v.	✓
Labrifomes	Labridae	<i>Calotomus spinidens</i>	Pers. Coll.: H.Choat G2118, n.v.	✓
Labrifomes	Labridae	<i>Cetoscarus bicolor</i>	Pers. Coll.: H.Choat G113, n.v.	✓
Labrifomes	Labridae	<i>Cheilinus fasciatus</i>	Pers. Coll.: D.Bellwood M215, n.v.	✓
Labrifomes	Labridae	<i>Cheilio inermis</i>	Pers. Coll.: D.Bellwood M1187, n.v.	✓
Labrifomes	Labridae	<i>Chlorurus japanensis</i>	Pers. Coll.: H.Choat PFC5870, n.v.	✓
Labrifomes	Labridae	<i>Choerodon anchorago</i>	Pers. Coll.: D.Bellwood M12, n.v.	✓
Labrifomes	Labridae	<i>Coris atlantica</i>	Pers. Coll.: D.Bellwood M1692, n.v.	
Labrifomes	Labridae	<i>Coris gaimard</i>	Pers. Coll.: D.Bellwood M1359, n.v. Pers. Coll.: P.Wainwright, PW1897B	✓
Labrifomes	Labridae	<i>Epibulus insidiator</i>	Pers. Coll.: SAMN05915062	✓
Labrifomes	Labridae	<i>Halichoeres poeyi</i>	P.Wainright, PW46	SAMN05915071
Labrifomes	Labridae	<i>Halichoeres radiatus</i>	CAS HRA01	SAMN05915072
Labrifomes	Labridae	<i>Heteroscarus acroptilus</i>	Pers. Coll.: D.Bellwood M492, n.v.	✓

Labriformes	Labridae	<i>Hipposcarus harid</i>	Pers. Coll.: H.Choat PFC6379, n.v.	✓
Labriformes	Labridae	<i>Labrichthys unilineatus</i>	Pers. Coll.: D.Bellwood M254, n.v.	✓
Labriformes	Labridae	<i>Labrus bergylta</i>	See NCBI SRA SAMEA3939555*	✓
Labriformes	Labridae	<i>Lachnolaimus maximus</i>	Pers. Coll.: D.Bellwood M397, n.v.	✓
Labriformes	Labridae	<i>Pseudodax moluccanus</i>	Pers. Coll.: D.Bellwood M62, n.v.	✓
Labriformes	Labridae	<i>Scarus flavipectoralis</i>	Pers. Coll.: H.Choat G228, n.v.	✓
Labriformes	Labridae	<i>Scarus taeniopterus</i>	Pers. Coll.: H.Choat G754, n.v.	✓
Labriformes	Labridae	<i>Sparisoma radians</i>	Pers. Coll.: H.Choat A10, n.v.	✓
Labriformes	Labridae	<i>Syphodus melops</i>	See NCBI SRA SAMEA4028821*	✓
Labriformes	Labridae	<i>Thalassoma ballieui</i>	CAS TBA-04 SAMN05915134	✓
Labriformes	Labridae	<i>Wetmorella albofasciata</i>	Pers. Coll.: D.Bellwood M288, n.v.	✓
Acropomatiformes	<i>Ostracoberyx</i>	<i>Ostracoberyx dorygenys</i>	ASIZPO 911526	
Acropomatiformes	Acropomatidae	<i>Acropoma japonica</i>	YPM ICH 010066	✓
Acropomatiformes	Acropomatidae	<i>Doederleinia berycoides</i>	NMV Z 6813	
Acropomatiformes	<i>Scombrops</i>	<i>Scombrops boops</i>	YFTC 24186, n.v.	
Acropomatiformes	<i>Scombrops</i>	<i>Scombrops gilberti</i>	YFTC 24191, n.v.	
Acropomatiformes	<i>Scombrops</i>	<i>Scombrops gilberti</i>	YFTC 24192, n.v.	
Acropomatiformes	<i>Scombrops</i>	<i>Scombrops gilberti</i>	YFTC 24193, n.v.	
Acropomatiformes	<i>Sympysanodon</i>	<i>Sympysanodon berryi</i>	YPM ICH 028303	✓
Acropomatiformes	<i>Sympysanodon</i>	<i>Sympysanodon octoactinus</i>	USNM 406214	✓
Acropomatiformes	Epigonidae	<i>Brinkmannella carpenteri</i>	YPM ICH 028297	
Acropomatiformes	Howellidae	<i>Howella atlantica</i>	YPM ICH 028408	
Acropomatiformes	Howellidae	<i>Howella brodiei</i>	YPM ICH 027798	
Acropomatiformes	<i>Polyprion</i>	<i>Polyprion americanus</i>	AMS I.42844-002	✓
Acropomatiformes	<i>Glaucosoma</i>	<i>Glaucosoma hebraicum</i>	YFTC 18186, n.v.	
Acropomatiformes	Pempheridae	<i>Pempheris schomburgkii</i>	YPM ICH 24903 SAMN05915096	✓
Acropomatiformes	<i>Lateolabrax</i>	<i>Lateolabrax japonicus</i>	YFTC 25777, n.v.	✓
Acropomatiformes	<i>Lateolabrax</i>	<i>Lateolabrax japonicus</i>	See NCBI SRA SAMN07680090*	
Acropomatiformes	<i>Lateolabrax</i>	<i>Lateolabrax latus</i>	KAUM 51068	
Acropomatiformes	<i>Stereolepis</i>	<i>Stereolepis gigas</i>	SIO 03-74	✓
Acropomatiformes	<i>Banjos</i>	<i>Banjos banjos</i>	ASIZPO 801399	✓
Acropomatiformes	Pentacerotidae	<i>Pentaceros japonicus</i>	ASIZD 0800699	
Acropomatiformes	Pentacerotidae	<i>Pseudopentaceros wheeleri</i>	UW 116954	
Acropomatiformes	Bathyclupeidae	<i>Neobathyclupea argentea</i>	YPM ICH 028270	
Acropomatiformes	Bathyclupeidae	<i>Neobathyclupea gracilis</i>	NMV A 25118-003	
Acropomatiformes	<i>Champsodon</i>	<i>Champsodon sechellensis</i>	SAIAB 84026	
Acropomatiformes	<i>Champsodon</i>	<i>Champsodon snyderi</i>	ASIZPO 910951	
Acropomatiformes	Creediidae	<i>Limnichthys</i> sp.	KU 782 NMNZ P.044479/TS1	
Acropomatiformes	Creediidae	<i>Tewara cranwellae</i>		

Acropomatiformes	Hemerocoetidae	<i>Enigmapercis</i> sp.	NSMT-P 114722		✓
Acropomatiformes	Hemerocoetidae	<i>Osopsaron formosensis</i>	NSMT-P 77318		✓
Acropomatiformes	Hemerocoetidae	<i>Pteropsaron evolans</i>	NSMT-P 77317		
Euperciformes	Gerreidae	<i>Eucinostomus jonesii</i>	YPM ICH 24864		✓
Euperciformes	Gerreidae	<i>Gerres cinereus</i>	YPM ICH 24843 Pers. Coll.: F.J. Sanchez Vazques, U. of Murica		✓
Euperciformes	Moronidae	<i>Dicentrarchus labrax</i>	Murica		✓
Euperciformes	Moronidae	<i>Morone saxatilis</i>	YPM ICH 018448 Pers. Coll.: W.L.Smith		✓
Euperciformes	Sillaginidae	<i>Sillago chondrops</i>			
Euperciformes	Sillaginidae	<i>Sillago sihama</i>	SAIAB 77085		✓
Euperciformes	<i>Drepane</i>	<i>Drepane punctata</i>	ROM 69918		✓
Euperciformes	Ephippidae	<i>Platax orbicularis</i>	SAIAB 77666		✓
Euperciformes	Dinopercidae	<i>Dinoperca petersi</i>	SAIAB 81789		✓
Euperciformes	Haemulidae	<i>Haemulon album</i>	CAS HAL01	SAMN05915068	✓
Euperciformes	Haemulidae	<i>Haemulon flavolineatum</i>	CAS HFG04	SAMN05915069	✓
Euperciformes	Haemulidae	<i>Haemulon parra</i>	CAS HPA01	SAMN05915070	✓
Euperciformes	Sciaenidae	<i>Collichthys lucidus</i>	See NCBI SRA	SAMN10225518*	✓
Euperciformes	Sciaenidae	<i>Larimichthys crocea</i>	See NCBI SRA	SAMN10434301*	✓
Euperciformes	Sciaenidae	<i>Micropogonias undulatus</i>	YPM ICH 023546	SAMN05915083	✓
Euperciformes	Sciaenidae	<i>Miichthys miuy</i>	See NCBI SRA	SAMN02486174*	✓
Euperciformes	Sciaenidae	<i>Nibea albiflora</i>	See NCBI SRA	SAMEA1067819*	✓
Euperciformes	Sciaenidae	<i>Pareques acuminatus</i>	CAS PAC20	SAMN05915094	✓
Euperciformes	Monodactylidae	<i>Monodactylus sebae</i> <i>Hapalogrenys dampieriensis</i>	YPM ICH 020540		✓
Euperciformes	Lobotidae		NMV Z 6535		
Euperciformes	Lobotidae	<i>Lobotes surinamensis</i>	Pers. Coll.: P.Wainwright, PW2610		✓
Euperciformes	Emmelichthyidae	<i>Erythrocles schlegelii</i>	KU 7270		✓
Euperciformes	Lutjanidae	<i>Lutjanus goreensis</i>	CAS LG001	SAMN05915081	✓
Euperciformes	Malacanthidae	<i>Caulolatilus princeps</i>	SIO 08-66		✓
Euperciformes	Malacanthidae	<i>Malacanthus plumieri</i>	Pers. Coll.: P.Wainwright, PW1198		✓
Euperciformes	Pomacanthidae	<i>Centropyge flavissima</i> <i>Chaetodontoplus melanosoma</i>	YPM ICH 026532		✓
Euperciformes	Pomacanthidae		Pers. Coll.: P.Wainwright, PW643		✓
Euperciformes	Pomacanthidae	<i>Holocanthus passer</i>	Pers. Coll.: P.Wainwright, PW642		✓
Euperciformes	Pomacanthidae	<i>Pomacanthus paru</i>	CAS PPA01	SAMN05915105	✓
Euperciformes	Leiognathidae	<i>Gazza minuta</i>	YFTC 18187, n.v.		✓
Euperciformes	Leiognathidae	<i>Karalla daura</i>	LSUMZ 8791		✓
Euperciformes	Leiognathidae	<i>Leiognathus equula</i>	LSUMZ 8683		✓
Euperciformes	Leiognathidae	<i>Secutor nuconius</i>	LSUMZ 8682 Pers. Coll.: P.Wainwright, PW2291B		✓
Euperciformes	Chaetodontidae	<i>Chaetodon kleinii</i>		SAMN05915049	✓
Euperciformes	Chaetodontidae	<i>Chaetodon leucopleura</i>	See NCBI SRA	SAMN09765312	

Euperciformes	Chaetodontidae	<i>Chaetodon melapterus</i>	See NCBI SRA	SAMN09765325		
Euperciformes	Chaetodontidae	<i>Chaetodon ocellatus</i>	CAS CAC01	SAMN05915050	✓	
Euperciformes	Chaetodontidae	<i>Chaetodon trichrous</i>	See NCBI SRA	SAMN09765350	✓	✓
Euperciformes	Chaetodontidae	<i>Chaetodon trifascialis</i>	See NCBI SRA	SAMN09765353	✓	
Euperciformes	Chaetodontidae	<i>Chaetodon unimaculatus</i>	See NCBI SRA	SAMN09765358	✓	
Euperciformes	Chaetodontidae	<i>Chaetodon vagabundus</i>	See NCBI SRA	SAMN09765361	✓	
Euperciformes	Chaetodontidae	<i>Chaetodon xanthurus</i>	See NCBI SRA	SAMN09765364	✓	
Euperciformes	Chaetodontidae	<i>Forcipiger longirostris</i>	See NCBI SRA	SAMN09765373	✓	✓
Euperciformes	Chaetodontidae	<i>Heniochus acuminatus</i>	See NCBI SRA	SAMN09765375	✓	
Euperciformes	Chaetodontidae	<i>Heniochus diphyreutes</i>	See NCBI SRA	SAMN09765376	✓	
Euperciformes	Chaetodontidae	<i>Prognathodes aculeatus</i>	See NCBI SRA	SAMN09765385	✓	✓
Euperciformes	Chaetodontidae	<i>Prognathodes marcellae</i>	See NCBI SRA	SAMN09765386	✓	
Euperciformes		<i>Luvarus imperialis</i>	MCZ 159566		✓	
Euperciformes		<i>Zanclus cornutus</i>	Pers. Coll.: P.Wainwright, PW1782B		✓	
Euperciformes	Acanthuridae	<i>Acanthurus bahianus</i>	ANSP 191513 Pers. Coll.: M.Alfaro, Alfaro-	SAMN05915021	✓	
Euperciformes	Acanthuridae	<i>Acanthurus bariene</i>	909	SAMN05915022		
Euperciformes	Acanthuridae	<i>Acanthurus chirurgus</i>	Pers. Coll.: D.Bellwood M1523, n.v.		✓	
Euperciformes	Acanthuridae	<i>Acanthurus coeruleus</i>	Pers. Coll.: D.Bellwood M284, n.v.		✓	
Euperciformes	Acanthuridae	<i>Acanthurus lineatus</i>	Pers. Coll.: D.Bellwood M579, n.v.		✓	
Euperciformes	Acanthuridae	<i>Acanthurus nigricans</i>	Pers. Coll.: D.Bellwood M309, n.v.		✓	
Euperciformes	Acanthuridae	<i>Acanthurus nigrofasciatus</i>	Pers. Coll.: D.Bellwood M1452, n.v. Pers. Coll.: M.Alfaro, Alfaro-		✓	
Euperciformes	Acanthuridae	<i>Acanthurus olivaceus</i>	878 Pers. Coll.: M.Alfaro, Alfaro-	SAMN05915023	✓	
Euperciformes	Acanthuridae	<i>Acanthurus pyroferus</i>	907	SAMN05915024	✓	
Euperciformes	Acanthuridae	<i>Acanthurus triostegus</i>	Pers. Coll.: D.Bellwood M677, n.v.		✓	
Euperciformes	Acanthuridae	<i>Ctenochaetus striatus</i>	Pers. Coll.: D.Bellwood M747, n.v.		✓	
Euperciformes	Acanthuridae	<i>Ctenochaetus truncatus</i>	Pers. Coll.: D.Bellwood M310, n.v.			
Euperciformes	Acanthuridae	<i>Naso elegans</i>	Pers. Coll.: D.Bellwood M1206, n.v. Pers. Coll.: M.Alfaro, Alfaro-			
Euperciformes	Acanthuridae	<i>Naso unicornis</i>	mv010.12	SAMN05915088	✓	
Euperciformes	Acanthuridae	<i>Paracanthurus hepatus</i>	Pers. Coll.: D.Bellwood M1432, n.v.		✓	
Euperciformes	Acanthuridae	<i>Prionurus biafraensis</i>	Pers. Coll.: D.Bellwood M1695, n.v.		✓	
Euperciformes	Acanthuridae	<i>Zebrasoma desjardinii</i>	Pers. Coll.: D.Bellwood M1454, n.v.			
Euperciformes	Acanthuridae	<i>Zebrasoma flavescens</i>	Pers. Coll.: D.Bellwood M2031, n.v.		✓	
Euperciformes	Acanthuridae	<i>Zebrasoma rostratum</i>	Pers. Coll.: D.Bellwood M2030, n.v. NMNZ			
Euperciformes	Callanthiidae	<i>Callanthias australis</i>	P.052282/TS2			
Euperciformes	Nemipteridae	<i>Parascolopsis eriomma</i>	SAIAB 80609		✓	
Euperciformes	Nemipteridae	<i>Scolopsis ghanam</i>	SAIAB 80378			

Euperciformes	Nemipteridae	<i>Scolopsis vosmeri</i>	SAIAB 80713	✓	
Euperciformes	Lethrinidae	<i>Lethrinus erythropterus</i>	Pers. Coll.: P.Wainwright, PW2049B	✓	
Euperciformes	Lethrinidae	<i>Monotaxis grandoculis</i>	Pers. Coll.: P.Wainwright, PW2159B	✓	
Euperciformes	Sparidae	<i>Calamus calamus</i>	Pers. Coll.: P.Wainwright, PW102: 960	✓	
Euperciformes	Sparidae	<i>Pagrus major</i>	See NCBI SRA	SAMD00076252*	✓
Euperciformes	Sparidae	<i>Sparus aurata</i>	See NCBI SRA	SAMN09603368*	✓
Euperciformes	Sparidae	<i>Spicara australis</i>	SAIAB 81795		
Euperciformes	Sparidae	<i>Spicara smaris</i>	SAIAB 81064	✓	
Euperciformes	Sparidae	<i>Spondyliosoma cantharus</i>	See NCBI SRA	SAMEA4028822*	✓
Euperciformes	Sparidae	<i>Stenotomus chrysops</i>	YPM ICH 017360		
Euperciformes	<i>Siganus</i>	<i>Siganus spinus</i>	KU 4159	✓	
Euperciformes	<i>Siganus</i>	<i>Siganus vulpinus</i>	Pers. Coll.: P.Wainwright, PW1601	✓	
Euperciformes	Scatophagidae	<i>Scatophagus argus</i>	YPM ICH 020538	✓	
Euperciformes	Priacanthidae	<i>Priacanthus arenatus</i>	KU 27012	✓	
Euperciformes	Cepolidae	<i>Cepola schlegelii</i>	ASIZPO 800615	✓	
Euperciformes	Cepolidae	<i>Owstonia tosaensis</i>	ASIZPO 801455		
Euperciformes	Caproidae	<i>Antigonia capros</i>	YPM ICH 25915 Pers. Coll.: W.L. Smith	SAMN05915030	✓
Tetraodontiformes		<i>Triodon macropterus</i>			
Tetraodontiformes	Aracanidae	<i>Aracana aurita</i>	Pers. Coll.: P.Wainwright, PW1285	✓	
Tetraodontiformes	Ostraciidae	<i>Lactophrys bicaudalis</i>	YPM ICH 24800	✓	
Tetraodontiformes	Triacanthodidae	<i>Triacanthodes ethiops</i>	SAIAB 82125	✓	
Tetraodontiformes	Triacanthidae	<i>Triacanthus biaculeatus</i>	NSMT 59287 Pers. Coll.: P.Wainwright, PW2623		✓
Tetraodontiformes	Balistidae	<i>Balistes capriscus</i>	Pers. Coll.: P.Wainwright, PW1740B	SAMN05915036	✓
Tetraodontiformes	Monacanthidae	<i>Acreichthys tomentosus</i>			
Tetraodontiformes	Monacanthidae	<i>Aluterus monoceros</i>	YPM ICH 027566	✓	
Tetraodontiformes	Moridae	<i>Masturus lanceolatus</i>	KU 5252		
Tetraodontiformes	Moridae	<i>Mola mola</i>	ORIUT 910		
Tetraodontiformes	Diodontidae	<i>Chilomycterus schoepfi</i>	Pers. Coll.: P.Wainwright, PW1225	✓	
Tetraodontiformes	Diodontidae	<i>Cyclichthys orbicularis</i>	SAIAB 190092		
Tetraodontiformes	Diodontidae	<i>Diodon liturosus</i>	SAIAB 78248 Pers. Coll.: M.Alfaro, Alfaro-		✓
Tetraodontiformes	Tetraodontidae	<i>Canthigaster figureiredoi</i>	491	SAMN05915041	✓
Tetraodontiformes	Tetraodontidae	<i>Canthigaster margaritata</i>	CAS LR03	SAMN05915042	
Tetraodontiformes	Tetraodontidae	<i>Canthigaster rostrata</i>	CAS CRO42	SAMN05915043	✓
Tetraodontiformes	Tetraodontidae	<i>Dichotomyctere nigroviridis</i>	See NCBI SRA Pers. Coll.: M.Alfaro, Alfaro- 666	SAMEA3138311*	
Tetraodontiformes	Tetraodontidae	<i>Pao suvattii</i>	666	SAMN05915133	
Tetraodontiformes	Tetraodontidae	<i>Takifugu bimaculatus</i>	See NCBI SRA	SAMN10524747*	✓

Tetraodontiformes	Tetraodontidae	<i>Takifugu flavidus</i>	See NCBI SRA	SAMN10077091*	
Tetraodontiformes	Tetraodontidae	<i>Takifugu rubripes</i>	See NCBI SRA	SAMEA3138310*	✓
Lophiiformes	Lophiidae	<i>Lophius gastrophysus</i>	Pers. Coll.: J.Moore, JAM99-109 Pers. Coll.: M.Alfaro, Alfaro-1152		✓
Lophiiformes	Ogcocephalidae	<i>Ogcocephalus radiatus</i>	Pers. Coll.: M.Alfaro, Alfaro-961	SAMN05915090	✓
Lophiiformes	Antennariidae	<i>Antennarius striatus</i>	961	SAMN05915029	✓
Lophiiformes	Antennariidae	<i>Antennarius striatus</i>	Brachionichthyidae	See NCBI SRA	SAMEA4028823*
Lophiiformes	Tetrabrachiidae	<i>Brachionichthys australis</i>	e	CSIRO H 4465-01	
Lophiiformes	Tetrabrachiidae	<i>Tetrabrachium ocellatum</i>		UW A50	✓
Lophiiformes	Tetrabrachiidae	<i>Tetrabrachium ocellatum</i>		UW A67	
Lophiiformes	Chaunacidae	<i>Chaunax stigmaeus</i>		MCZ 166061	
Lophiiformes	Chaunacidae	<i>Chaunax suttkusi</i>		MCZ 166070	✓
Lophiiformes	Chaunacidae	<i>Chaunax</i> sp.		UW 25870 NMNZ	
Lophiiformes	Caulophrynidiae	<i>Caulophryne pelagica</i>		P.043296/TS3	
Lophiiformes	Gigantactinidae	<i>Gigantactis ios</i>		MCZ 163303	
Lophiiformes	Gigantactinidae	<i>Gigantactis vanhoeffeni</i>		YPM ICH 027791	
Lophiiformes		<i>Neoceratias spinifer</i>		UW D17 NMNZ	
Lophiiformes	Linophrynidiae	<i>Haplophryne mollis</i>		P.041209/TS3	
Lophiiformes	Ceratiidae	<i>Cryptopsaras couesi</i>		YPM ICH 25702	SAMN05915058
Lophiiformes	Oneirodidae	<i>Chaenophryne longiceps</i>		YPM ICH 25647	
Lophiiformes	Oneirodidae	<i>Dolopichthys karsteni</i>		MCZ 165969	
Lophiiformes	Oneirodidae	<i>Lasiognathus intermedius</i>		YPM ICH 25927	
Lophiiformes	Diceratiidae	<i>Bufoaceratias thele</i>		UW D6	
Lophiiformes	Diceratiidae	<i>Diceratias pileatus</i>		UW D7	
Lophiiformes	Diceratiidae	<i>Diceratias</i> sp.		UW D27	
Lophiiformes	Himantolophidae	<i>Himantolophus albinares</i>		MCZ 161521	
Lophiiformes	Himantolophidae	<i>Himantolophus sagamius</i>		SIO 02-2	
Lophiiformes	Melanocetidae	<i>Melanocetus johnsonii</i>		UW 115879	✓
Lophiiformes	Melanocetidae	<i>Melanocetus murrayi</i>		YPM ICH 027583	✓

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Institutional Abbreviations: AMNH, American Museum of Natural History, New York; AMS, Australian Museum, Sydney; ANSP, Academy of Natural Sciences, Philadelphia; ASIZ, Academia Sinica, Biodiversity Research Museum, Taipei; CAS, California Academy of Sciences, San Francisco; CBM, Natural History Museum and Institute, Chiba; CSIRO, Commonwealth Scientific and Industrial Research Organisation, Division of Marine and Atmospheric Research, Australian National Fish Collection, Hobart; CUMV, Cornell University Museum of Vertebrates, Ithaca; FAKU, Kyoto University Museum, Kyoto University, Yoshida, Sakyo; FMNH, Field Museum of Natural History, Chicago; FRLM, Fish Collection of the Fisheries Research

100 Laboratory, Mie University, Wagu, Shima; HUMZ, The Hokkaido University Museum, Sapporo; INHS, Illinois
101 Natural History Survey, Champaign; KAUM, Kagoshima University Museum, Korimoto; KU, University of
102 Kansas Biodiversity Institute, Lawrence; LACM, Natural History Museum of Los Angeles County, Los
103 Angeles; LBP, Laboratório de Biologia e Genética de Peixes, Departamento de Morfologia, Universidade
104 Estadual Paulista “Júlio de Mesquita Filho”, Campus de Rio Claro, São Paulo; LSUMZ, Louisiana Museum of
105 Natural History, Baton Rouge; MCZ, Museum of Comparative Zoology, Harvard University, Cambridge,
106 Massachusetts; MNCN, Museo Nacional de Ciencias Naturales (CSIC), Madrid; MNHN, Museo Nacional de
107 Historia Natural, Zoología, Santiago; NCSM, North Carolina Museum of Natural Sciences, Raleigh; NMND,
108 National Museum of Natural History, New Delhi; NMNZ, Museum of New Zealand Te Papa Tongarewa,
109 Wellington; NMV, Museum Victoria, Melbourne; NSMT, National Museum of Nature and Science, Ueno Park,
110 Tokyo; NTM, Museums and Art Galleries of the Northern Territory, Darwin; ORIUT, University of Tokyo,
111 Ocean Research Institute, Tokyo; QM, Queensland Museum, Centre for Biodiversity, Brisbane; ROM, Royal
112 Ontario Museum, Department of Natural History, Toronto; SAIAB, South African Institute for Aquatic
113 Biodiversity, Grahamstown; SAMA, South Australian Museum, Adelaide; SIO, Scripps Institution of
114 Oceanography, Marine Vertebrate Collection, University of California, San Diego, La Jolla; SLU, Southeastern
115 Louisiana University, Museum of Biology, Hammond; SNFR, Seikai National Fisheries Research Institute,
116 Nagasaki; UF, University of Florida, Florida Museum of Natural History, Gainesville; USNM, National
117 Museum of Natural History, Smithsonian Institution, Department of Vertebrate Zoology, Washington, D.C.; UT,
118 University of Tennessee, Department of Ecology and Evolutionary Biology, David A. Etnier Ichthyological
119 Collection, Knoxville; UW, University of Washington, Burke Museum of Natural History and Culture, Seattle;
120 YFTC, Yale Fish Tissue Collection, Department of Ecology and Evolutionary Biology, Yale University, New
121 Haven; YPM, Yale University, Peabody Museum of Natural History, New Haven; ZMUB, Universitetsmuseet i
122 Bergen, Bergen, Hordaland; ZMUC, Zoological Museum, University of Copenhagen, Copenhagen.

123 **Supplementary Table 2: Summary of TOPD pairwise comparisons of tree topologies inferred using**
124 **different methods.**

702-taxon trees		1,084-taxon trees		
Multiple-partition vs IQ-TREEsingle*		IQ-TREEsingle* vs IQ-TREEmulti†		IQ-TREEmulti† vs RAxML
<i>Acanthistius cinctus</i>		<i>Acanthistius cinctus</i>	<i>Acanthistius cinctus</i>	<i>Apogon affinis</i>
<i>Arripis trutta</i>		<i>Acanthurus triostegus</i>	<i>Acanthurus triostegus</i>	<i>Astrapogon stellatus</i>
<i>Chloroscombrus orqueta</i>		<i>Icosteus aenigmaticus</i>	<i>Apogon affinis</i>	<i>Cryptopsaras couesii</i>
<i>Icosteus aenigmaticus</i>			<i>Astrapogon stellatus</i>	<i>Ectodus descampsii</i>
<i>Lycodes concolor</i>			<i>Cryptopsaras couesii</i>	<i>Haplotaxodon microlepis</i>
<i>Pomatomus saltatrix</i>			<i>Ectodus descampsii</i>	<i>Nomorhamphus celebensis</i>
<i>Pseudanthias squamipinnis</i>			<i>Haplotaxodon microlepis</i>	<i>Phaeoptyx pigmentaria</i>
<i>Selaroides leptolepis</i>			<i>Icosteus aenigmaticus</i>	<i>Xenentodon cancila</i>
<i>Sillago sihama</i>			<i>Nomorhamphus celebensis</i>	<i>Zenarchopterus dispar</i>
			<i>Phaeoptyx pigmentaria</i>	
			<i>Xenentodon cancila</i>	
			<i>Zenarchopterus dispar</i>	
Robinson-Foulds split distances	0.033	0.006	0.012	0.007
# Disagreeing Splits / Total	46 / 1398	14 / 2212	26 / 2212	16 / 2212
Nodal distance	1.05	0.49	0.61	0.51

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126 *IQ-TREEsingle = tree resulting from an IQ-TREE analysis using an unpartitioned alignment

127 † “IQ-TREEmulti = tree resulting from an IQ-TREE analysis using the ModelFinder Plus option

128 Columns list taxa with different phylogenetic positions among the compared trees. Robinson-Foulds split
129 distances, the number of disagreeing splits, and nodal distances are provided at the bottom of each column. All
130 RAxML-ng analyses were performed on multiple-partition alignments that were partitioned with PartitionFinder2.
131 The topologies of the 702-taxon trees inferred using multiple-partition alignments in IQ-TREE and RAxML-ng
132 were identical.

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139 **Supplementary Table 3: Classification of Acanthomorpha.** The number of species in each taxonomic order
140 is offered in the second column. Though every family is classified in an order, not every family is classified in a
141 suborder or superfamily.

Order	Number of species	Suborder-Superfamily	Family
Polymixiiformes	10		Polymixiidae
Percopsiformes	12		Amblyopsidae
			Aphredoderidae
			Percopsidae
Zeiformes	33		Cyttidae
			Grammicolepididae
			Oreosomatidae
			Parazenidae
			Zeidae
			Zeniontidae
Stylephoriformes	1		Stylephoridae
Gadiformes	615		Bathygadidae
			Bregmacerotidae
			Eulichthyidae
			Gadidae
			Gaidropsaridae
			Lotidae
			Lyconidae
			Macrouridae
			Macruronidae
			Melanonidae
			Merlucciidae
			Moridae
			Muraenolepididae
			Phycidae
			Ranicipitidae
			Steindachneriidae
			Trachyrincidae
Lampriformes	29		

		Lampridae	
		Lophotidae	
		Radiicephalidae	
		Regalecidae	
		Trachipteridae	
		Veliferidae	
Trachichthyiformes	66	Anomalopidae	
		Anoplogasteridae	
		Diretmidae	
		Monocentridae	
		Trachichthyidae	
Beryciformes	211	Holocentridae	
		Rondeletiidae	
		Stephanoberycidae	
		Barbourisiidae	
		Cetomimidae	
		Berycidae	
		Melamphaidae	
		Gibberichthyidae	
		Hispidoberyidae	
Ophidiiformes	545	Bythitidae	
		Dinematichthyidae	
		Ophidiidae	
Batrachoidiformes	84	Batrachoididae	
Gobiiformes (=Gobiaria)	2,638	Gobioidei	Rhyacichthyidae
		Gobioidei	Odontobutidae
		Gobioidei	Butidae
		Gobioidei	Eleotridae
		Gobioidei	Milyeringidae
		Gobioidei	Thalasseleotrididae
		Gobioidei	Oxudercidae
		Gobioidei	Gobiidae

		Trichonotidae
		Kurtidae
		Apogonidae
Scombriformes (=Pelagiaria)	285	
		Amarsipidae
		Ariommataidae
		Arripidae
		Bramidae
		Caristiidae
		Centrolophidae
		Chiasmodontidae
		Gempylidae
		Icosteidae
		Lepidocybidae
		Nameidae
		Pomatomidae
		Scombridae
		Scombrolabracidae
		Stromateidae
		Tetragonuridae
		Trichiuridae
Syngnathiformes (=Syngnatharia)	674	
		Syngnathoidei
		Callionymoidei
		Callionymoidei
Blenniiformes (=Ovalentaria)	5,865	
		Blennioidei
		Blenniidae

Blennioidei	Chaenopsidae
Blennioidei	Clinidae
Blennioidei	Dactyloscopidae
Blennioidei	Gobiesocidae
Blennioidei	Labrisomidae
Blennioidei	Tripterygiidae
Atherinoidei-Belonoidea	Adrianichthyidae
Atherinoidei-Belonoidea	Belonidae
Atherinoidei-Belonoidea	Exocoetidae
Atherinoidei-Belonoidea	Hemiramphidae
Atherinoidei-Cyprinodontoidea	Anablepidae
Atherinoidei-Cyprinodontoidea	Aphaniidae
Atherinoidei-Cyprinodontoidea	Aplocheilidae
Atherinoidei-Cyprinodontoidea	Rivulidae
Atherinoidei-Cyprinodontoidea	Cyprinodontidae
Atherinoidei-Cyprinodontoidea	Fluviphylacidae
Atherinoidei-Cyprinodontoidea	Fundulidae
Atherinoidei-Cyprinodontoidea	Goodeidae
Atherinoidei-Cyprinodontoidea	Nothobranchiidae
Atherinoidei-Cyprinodontoidea	Pantanodontidae
Atherinoidei-Cyprinodontoidea	Poeciliidae
Atherinoidei-Cyprinodontoidea	Profundulidae
Atherinoidei-Cyprinodontoidea	Procatopodidae
Atherinoidei-Cyprinodontoidea	Valenciidae
Atherinoidei-Atherinoidea	Atherinidae
Atherinoidei-Atherinoidea	Atherinopsidae
Atherinoidei-Atherinoidea	Atherionidae
Atherinoidei-Atherinoidea	Bedotiidae
Atherinoidei-Atherinoidea	Dentatherinidae
Atherinoidei-Atherinoidea	Isonidae
Atherinoidei-Atherinoidea	Melanotaeniidae
Atherinoidei-Atherinoidea	Phallostethidae
Atherinoidei-Atherinoidea	Pseudomugilidae
Atherinoidei-Atherinoidea	Telmatherinidae
Cichloidei	Cichlidae
Cichloidei	Pholidichthyidae
	Ambassidae
	Embiotocidae

		Grammatidae
		Mugilidae
		Opistognathidae
		Plesiopidae
		Polycentridae
		Pomacentridae
		Pseudochromidae
		Congrogadidae
		Plesiopidae
Synbranchiformes	400	
(=Anabantaria)		
		Synbranchoidei
		Anabantoidei
		Carangiformes
(=Carangaria)	1,100	
		Carangoidei-Carangoidea
		Carangoidei-Xiphioidea
		Carangoidei-Xiphioidea
		Carangoidei
		Pleuronectoidei
		Pleuronectoidei-Pleuronectoidea
		Achiridae
		Istiophoridae
		Xiphiidae
		Leptobramidae
		Menidae
		Nemastiidiae
		Toxotidae
		Psettodidae

Perciformes	3,192	
		Percoidei
		Percoidei
		Percoidei
		Notothenioidei
		Scorpaenoidei
		Achiropsettidae
		Bothidae
		Citharidae
		Cyclopsetidae
		Cynoglossidae
		Oncopteridae
		Paralichthyidae
		Paralichthodidae
		Pleuronectidae
		Poecilopsettidae
		Rhombosoleidae
		Samaridae
		Scophthalmidae
		Soleidae
		Centropomidae
		Lactariidae
		Polynemidae
		Sphyraenidae
		Percidae
		Trachinidae
		Niphonidae
		Epinephelidae
		Grammistidae
		Liopropomatidae
		Serranidae
		Anthiadidae
		Bembropidae
		Percophidae
		Bovichtidae
		Pseudaphritidae
		Eleginopsidae
		Artedidraconidae
		Bathydraconidae
		Channichthyidae
		Harpagiferidae
		Nototheniidae
		Platycephalidae

Scorpaenoidei	Bembridae
Scorpaenoidei	Congiopodidae
Scorpaenoidei	Neosebastidae
Scorpaenoidei	Hoplichthyidae
Scorpaenoidei	Normanichthyidae
Scorpaenoidei	Synanceiidae
Scorpaenoidei	Triglidae
Scorpaenoidei	Scorpaenidae
Scorpaenoidei	Anoplopomatidae
Scorpaenoidei	Hexagrammidae
Scorpaenoidei	Zaniolepididae
Scorpaenoidei	Trichodontidae
Scorpaenoidei	Cyclopteridae
Scorpaenoidei	Liparidae
Scorpaenoidei	Scorpaenichthyidae
Scorpaenoidei	Agonidae
Scorpaenoidei	Cottidae
Scorpaenoidei	Psychrolutidae
Scorpaenoidei	Rhamphocottidae
Scorpaenoidei	Anarhichadidae
Scorpaenoidei	Bathymasteridae
Scorpaenoidei	Cryptacanthodidae
Scorpaenoidei	Pholidae
Scorpaenoidei	Ptilichthyidae
Scorpaenoidei	Scythalinidae
Scorpaenoidei	Stichaeidae
Scorpaenoidei	Zaproridae
Scorpaenoidei	Eulophiidae
Scorpaenoidei	Opisthocentridae
Scorpaenoidei	Lumpenidae
Scorpaenoidei	Neozoarcidae
Scorpaenoidei	Zoarcidae
Scorpaenoidei	Aulorhynchidae
Scorpaenoidei	Gasterosteidae
Scorpaenoidei	Hypoptychidae

		Cheilodactylidae
		Chironemidae
		Cirrhitidae
		Dichistiidiae
		Enoplosidae
		Girellidae
		Kuhliidae
		Kyphosidae
		Microcanthidae
		Scorpididae
		Latridae
		Oplegnathidae
		Percichthyidae
		Siniperidae
		Terapontidae
Labrifomes	757	
		Labroidei
		Labroidei
		Uranoscopoidei
Acropomatiformes	308	
		Acropomatidae
		Banjosidae
		Bathyclupeidae
		Champsodontidae
		Creediidae
		Dinolestidae
		Epigonidae
		Glaucosomatidae
		Hemerocoetidae
		Howellidae
		Lateolabracidae
		Leptoscopidae
		Malakichthyidae
		Ostracoberycidiae

		Pempheridae
		Pentacerotidae
		Polyprionidae
		Stereolepidae
		Scombropidae
		Synagropidae
		Sympysanodontidae
Acanthuriformes	2,350	
		Acanthuridae
	Acanthuroidei	Zanclidae
	Acanthuroidei	Luvaridae
	Acanthuroidei	Gerreidae
		Moronidae
		Sillaginidae
		Drepaneidae
		Ephippidae
		Dinopercidae
		Haemulidae
		Sciaenidae
		Monodactylidae
		Lobotidae
		Emmelichthyidae
		Lutjanidae
		Malacanthidae
		Pomacanthidae
		Leiognathidae
		Chaetodontidae
		Callanthiidae
		Lethrinidae
		Nemipteridae
		Sparidae
		Siganidae
		Scatophagidae
		Priacanthidae
		Cepolidae
		Caproidae
	Lophioidei	Antennariidae
	Lophioidei	Brachionichthyidae

Lophioidei	Caulophrynidae
Lophioidei	Centrophrynidae
Lophioidei	Ceratiidae
Lophioidei	Chaunacidae
Lophioidei	Diceratiidae
Lophioidei	Gigantactinidae
Lophioidei	Himantolophidae
Lophioidei	Linophrynidae
Lophioidei	Lophichthyidae
Lophioidei	Lophiidae
Lophioidei	Melanocetidae
Lophioidei	Neoceratiidae
Lophioidei	Ogcocephalidae
Lophioidei	Oneirodidae
Lophioidei	Tetrabrachiidae
Tetraodontoidei	Aracanidae
Tetraodontoidei	Balistidae
Tetraodontoidei	Diodontidae
Tetraodontoidei	Molidae
Tetraodontoidei	Monacanthidae
Tetraodontoidei	Ostraciidae
Tetraodontoidei	Tetraodontidae
Tetraodontoidei	Triacanthidae
Tetraodontoidei	Triacanthodidae
Tetraodontoidei	Triodontidae

144 **Supplementary Table 4: Divergence date estimates in millions of years (Mya) and 95% Highest Posterior
145 Densities (HPD) for major acanthomorph clades, generated using six alignments of 30 UCE loci in
146 BEAST.** Estimates from the 702-taxon and 1,084-taxon time trees are both represented. All stem and crown
147 ages are calculated from median node heights.

Clade	# of Taxa	Loci Set	Stem Age (Mya)	Stem 95% HPD (Mya)	Crown Age (Mya)	Crown 95% HPD (Mya)
Lampriformes	1,084	30 loci set A	131.28	[112.28, 145.67]	58.09	[55.84, 69.71]
		30 loci set B	134.87	[117.46, 147.27]	57.83	[55.82, 67.74]
		30 loci set C	133.75	[116.00, 146.56]	58.15	[55.82, 72.19]
	702	30 loci set D	133.07	[115.53, 145.96]	57.90	[55.83, 69.38]
		30 loci set E	137.30	[123.25, 147.73]	57.99	[55.81, 69.90]
		30 loci set F	137.28	[119.55, 152.47]	57.90	[55.81, 69.26]
Polymixia	1,084	30 loci set A	96.79	[93.96, 108.22]		
		30 loci set B	98.33	[93.99, 120.28]		
		30 loci set C	97.52	[93.96, 112.48]		
	702	30 loci set D	97.16	[93.94, 111.95]		
		30 loci set E	96.69	[93.92, 108.91]		
		30 loci set F	96.77	[93.93, 109.90]		
Percopsiformes	1,084	30 loci set A	96.79	[93.96, 108.22]	53.54	[40.12, 72.36]
		30 loci set B	98.33	[93.99, 120.28]	53.04	[38.36, 71.85]
		30 loci set C	97.52	[93.96, 112.48]	54.02	[39.34, 75.18]
	702	30 loci set D	97.16	[93.94, 111.95]	36.57	[34.12, 51.86]
		30 loci set E	96.69	[93.92, 108.91]	36.34	[34.12, 46.72]
		30 loci set F	96.77	[93.93, 109.90]	36.40	[34.12, 47.56]
Zeiformes	1,084	30 loci set A	105.92	[88.81, 122.96]	49.98	[37.33, 72.02]
		30 loci set B	109.87	[94.35, 129.43]	54.86	[38.88, 77.00]
		30 loci set C	109.41	[94.58, 125.37]	50.10	[37.46, 66.39]
	702	30 loci set D	108.97	[92.86, 124.77]	50.09	[36.68, 72.93]
		30 loci set E	112.40	[97.33, 127.83]	52.23	[36.27, 73.79]
		30 loci set F	110.89	[87.82, 127.33]	54.95	[40.48, 79.84]
Stylephorus	1,084	30 loci set A	88.48	[72.87, 105.39]		
		30 loci set B	92.97	[75.31, 112.39]		
		30 loci set C	94.55	[79.52, 110.80]		
	702	30 loci set D	94.04	[78.07, 110.29]		
		30 loci set E	97.74	[82.02, 113.36]		
		30 loci set F	93.74	[73.39, 112.47]		

Gadiformes	1,084	30 loci set A	88.48	[72.87, 105.39]	77.01	[61.50, 92.18]
		30 loci set B	92.97	[75.31, 112.39]	79.22	[63.54, 97.57]
		30 loci set C	94.55	[79.52, 110.80]	81.29	[65.42, 97.97]
	702	30 loci set D	94.04	[78.07, 110.29]	87.13	[71.95, 103.23]
		30 loci set E	97.74	[82.02, 113.36]	84.64	[68.98, 99.22]
		30 loci set F	93.74	[73.39, 112.47]	80.19	[60.80, 99.93]
Trachichthyiformes	1,084	30 loci set A	137.42	[129.12, 147.30]	46.58	[24.68, 75.50]
		30 loci set B	136.40	[127.79, 144.74]	42.47	[24.82, 72.22]
		30 loci set C	138.07	[129.74, 145.62]	44.99	[25.20, 78.24]
	702	30 loci set D	138.73	[129.73, 147.16]	46.53	[20.28, 78.59]
		30 loci set E	138.45	[129.72, 147.34]	46.02	[23.89, 77.49]
		30 loci set F	138.55	[125.63, 151.42]	51.89	[27.55, 90.99]
Beryciformes	1,084	30 loci set A	132.91	[123.97, 143.13]	100.57	[98.23, 107.44]
		30 loci set B	132.29	[122.95, 141.24]	100.35	[98.28, 107.45]
		30 loci set C	133.93	[126.23, 141.83]	100.57	[98.35, 107.08]
	702	30 loci set D	134.77	[126.10, 144.04]	100.69	[98.18, 108.19]
		30 loci set E	134.80	[125.53, 143.44]	100.70	[98.18, 108.29]
		30 loci set F	134.23	[116.61, 148.64]	100.69	[98.17, 108.06]
Ophidiiformes	1,084	30 loci set A	126.76	[116.96, 135.68]	84.50	[59.31, 111.29]
		30 loci set B	126.31	[117.66, 135.78]	88.86	[66.89, 115.30]
		30 loci set C	127.63	[120.65, 136.57]	92.32	[65.49, 115.42]
	702	30 loci set D	128.36	[119.08, 137.65]	85.49	[57.95, 115.91]
		30 loci set E	127.61	[117.49, 137.46]	83.87	[58.20, 110.70]
		30 loci set F	127.09	[105.34, 141.44]	80.24	[53.46, 114.16]
Batrachoididae	1,084	30 loci set A	121.85	[113.37, 130.94]	49.09	[25.28, 76.27]
		30 loci set B	121.66	[111.66, 130.20]	50.84	[29.93, 78.15]
		30 loci set C	123.25	[114.82, 130.23]	43.56	[23.91, 70.03]
	702	30 loci set D	123.43	[114.13, 133.12]	43.41	[19.20, 76.30]
		30 loci set E	123.23	[113.51, 133.45]	43.46	[18.07, 75.89]
		30 loci set F	121.76	[104.77, 139.03]	50.55	[27.08, 83.20]
Gobiiformes	1,084	30 loci set A	117.81	[108.89, 126.63]	109.64	[98.88, 119.95]
		30 loci set B	118.22	[107.12, 126.70]	111.01	[99.69, 121.14]
		30 loci set C	119.73	[111.67, 127.22]	112.57	[103.28, 121.44]
	702	30 loci set D	119.80	[110.41, 129.24]	111.76	[100.58, 122.53]
		30 loci set E	119.71	[108.92, 129.01]	111.91	[99.63, 122.86]
		30 loci set F	117.80	[97.66, 132.04]	110.32	[94.89, 124.32]
Syngnathiformes	1,084	30 loci set A	110.30	[101.51, 120.65]	104.59	[95.01, 114.75]

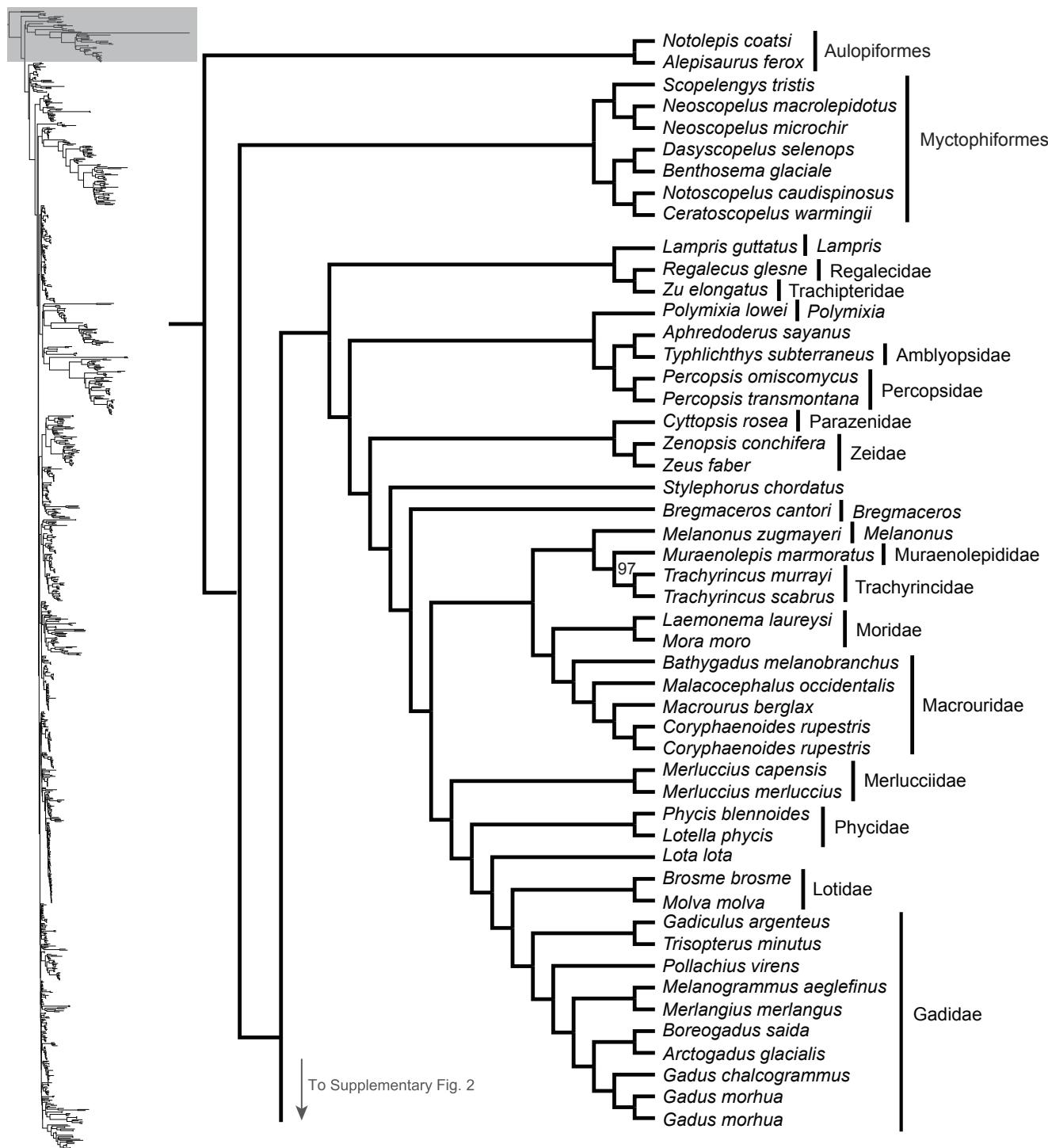
		30 loci set B	110.65	[97.59, 119.08]	104.49	[93.39, 114.84]
		30 loci set C	111.82	[101.46, 120.96]	105.30	[92.93, 115.32]
Scombriformes	1,084	30 loci set D	109.82	[99.69, 119.86]	102.66	[91.04, 112.38]
		30 loci set E	109.64	[98.89, 119.71]	101.48	[88.91, 111.90]
		30 loci set F	107.73	[87.68, 122.92]	98.93	[80.57, 113.81]
	702	30 loci set A	110.30	[101.51, 120.65]	65.83	[59.72, 74.36]
		30 loci set B	110.65	[97.59, 119.08]	68.10	[61.74, 79.89]
		30 loci set C	111.82	[101.46, 120.96]	66.96	[60.70, 76.91]
Blenniiformes	1,084	30 loci set D	109.82	[99.69, 119.86]	63.99	[58.44, 71.70]
		30 loci set E	109.64	[98.89, 119.71]	64.74	[59.56, 70.85]
		30 loci set F	107.73	[87.68, 122.92]	63.05	[58.28, 69.03]
	702	30 loci set A	105.90	[96.11, 115.30]	96.20	[86.23, 105.98]
		30 loci set B	107.22	[96.59, 118.94]	96.77	[84.99, 108.06]
		30 loci set C	106.45	[95.78, 117.40]	95.84	[83.69, 106.66]
Synbranchiformes	1,084	30 loci set D	107.79	[97.99, 120.19]	98.25	[88.06, 109.92]
		30 loci set E	104.16	[93.40, 114.87]	93.99	[83.25, 104.93]
		30 loci set F	102.17	[87.07, 117.66]	90.17	[78.27, 104.02]
	702	30 loci set A	98.87	[87.37, 110.69]	86.89	[73.15, 100.03]
		30 loci set B	99.34	[86.57, 113.26]	85.96	[72.16, 98.73]
		30 loci set C	98.46	[85.78, 111.44]	88.14	[75.77, 102.19]
Carangiformes	1,084	30 loci set D	99.93	[85.23, 111.97]	87.17	[72.00, 101.38]
		30 loci set E	95.32	[81.12, 108.53]	81.86	[66.73, 96.64]
		30 loci set F	97.98	[78.90, 112.10]	83.95	[66.38, 100.05]
	702	30 loci set A	98.87	[87.37, 110.69]	75.72	[66.44, 86.53]
		30 loci set B	99.34	[86.57, 113.26]	73.94	[65.91, 85.40]
		30 loci set C	98.46	[85.78, 111.44]	73.12	[65.15, 85.06]
Perciformes	1,084	30 loci set D	99.93	[85.23, 111.97]	75.66	[65.74, 88.17]
		30 loci set E	95.32	[81.12, 108.53]	73.30	[64.89, 83.24]
		30 loci set F	97.98	[78.90, 112.10]	71.38	[63.27, 81.47]
	702	30 loci set A	93.73	[81.70, 107.69]	66.86	[55.18, 78.00]
		30 loci set B	87.35	[77.09, 101.56]	58.70	[48.42, 71.23]
		30 loci set C	86.31	[76.71, 99.62]	61.77	[51.99, 71.14]
Centrarchiformes	1,084	30 loci set D	86.27	[76.37, 98.52]	63.53	[52.65, 77.01]
		30 loci set E	87.27	[76.89, 100.23]	59.84	[48.61, 71.50]
		30 loci set F	88.41	[77.47, 104.10]	59.33	[49.69, 72.02]
	702	30 loci set A	83.17	[75.26, 92.76]	53.26	[35.65, 78.06]
		30 loci set B	80.67	[73.27, 90.20]	50.84	[35.00, 77.08]

		30 loci set C	80.55	[73.40, 89.02]	78.34	[59.02, 88.96]
Labriformes	702	30 loci set D	81.63	[73.63, 91.51]	54.56	[36.97, 79.62]
		30 loci set E	80.75	[73.11, 89.16]	61.09	[38.33, 84.46]
		30 loci set F	82.97	[73.07, 93.94]	46.08	[31.65, 71.94]
	1,084	30 loci set A	81.03	[73.25, 89.30]	76.07	[66.21, 86.95]
		30 loci set B	78.81	[71.72, 87.07]	76.55	[67.89, 85.94]
		30 loci set C	79.34	[72.06, 87.16]	75.25	[65.80, 84.60]
Acropomatiformes	702	30 loci set D	79.91	[72.33, 88.93]	74.89	[64.69, 85.59]
		30 loci set E	79.06	[71.80, 86.93]	76.45	[73.11, 89.16]
		30 loci set F	81.47	[71.92, 91.68]	77.08	[66.51, 88.21]
	1,084	30 loci set A	80.09	[73.10, 88.58]	46.53	[32.55, 60.96]
		30 loci set B	77.12	[70.67, 84.95]	47.39	[33.95, 65.12]
		30 loci set C	78.32	[71.11, 85.72]	46.24	[33.17, 59.99]
Acanthuriformes	702	30 loci set D	78.83	[71.72, 87.89]	23.78	[14.06, 35.85]
		30 loci set E	77.45	[70.87, 85.19]	22.06	[13.60, 33.15]
		30 loci set F	80.07	[70.93, 89.84]	21.41	[12.44, 31.76]
	1,084	30 loci set A	80.09	[73.10, 88.58]	78.52	[72.01, 86.64]
		30 loci set B	77.12	[70.67, 84.95]	75.78	[69.13, 82.30]
		30 loci set C	78.32	[71.11, 85.72]	76.51	[70.12, 84.05]
Percomorpha	1,084	30 loci set A	132.91	[123.97, 143.13]	126.76	[116.96, 135.68]
		30 loci set B	132.29	[122.95, 141.24]	126.31	[117.66, 135.78]
		30 loci set C	133.93	[126.23, 141.83]	127.63	[120.65, 136.57]
	702	30 loci set D	134.77	[126.10, 144.04]	128.36	[119.08, 137.65]
		30 loci set E	134.80	[125.53, 143.44]	127.61	[117.49, 137.46]
		30 loci set F	134.23	[116.61, 148.64]	127.09	[105.34, 141.44]

148

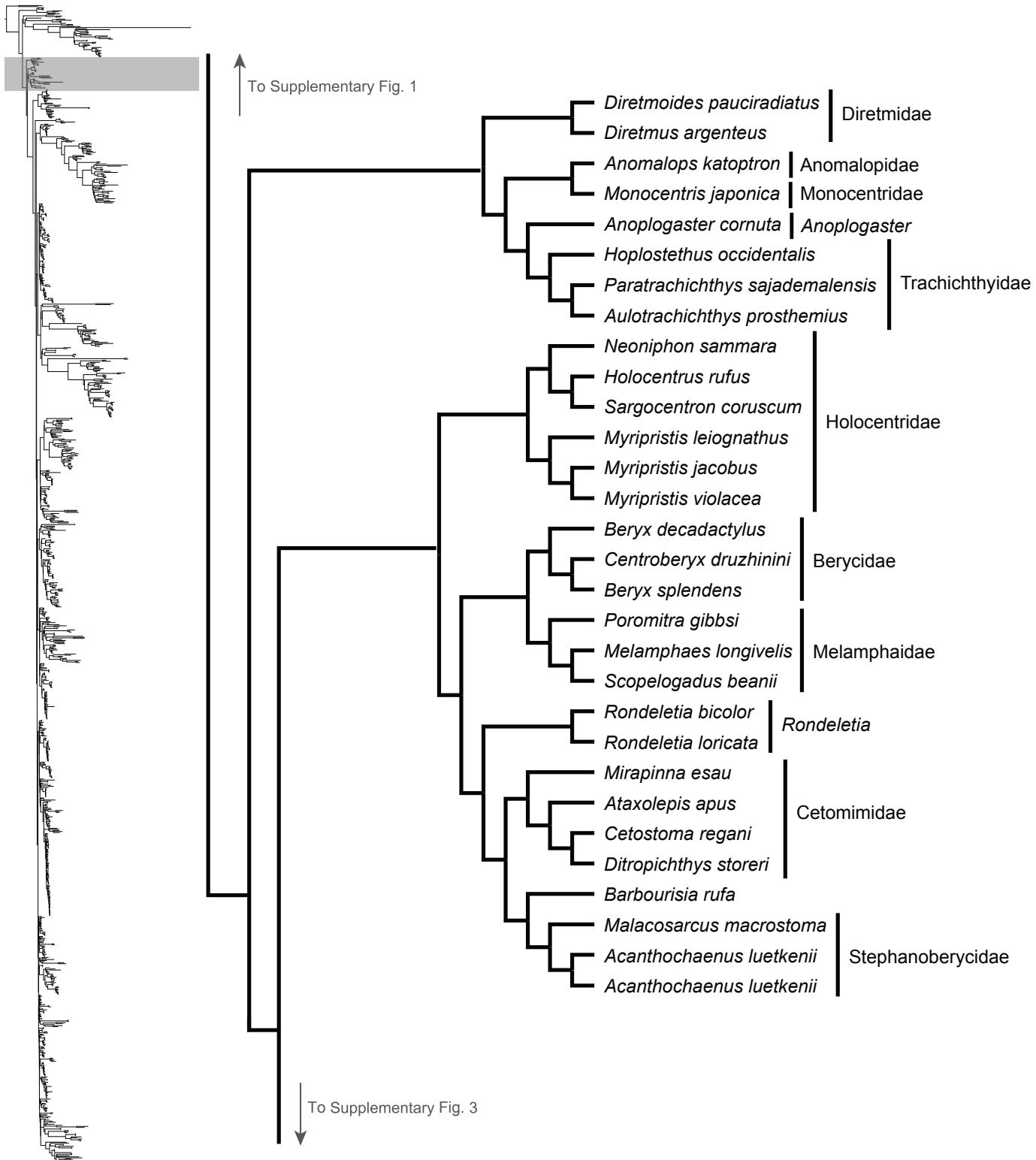
149

150



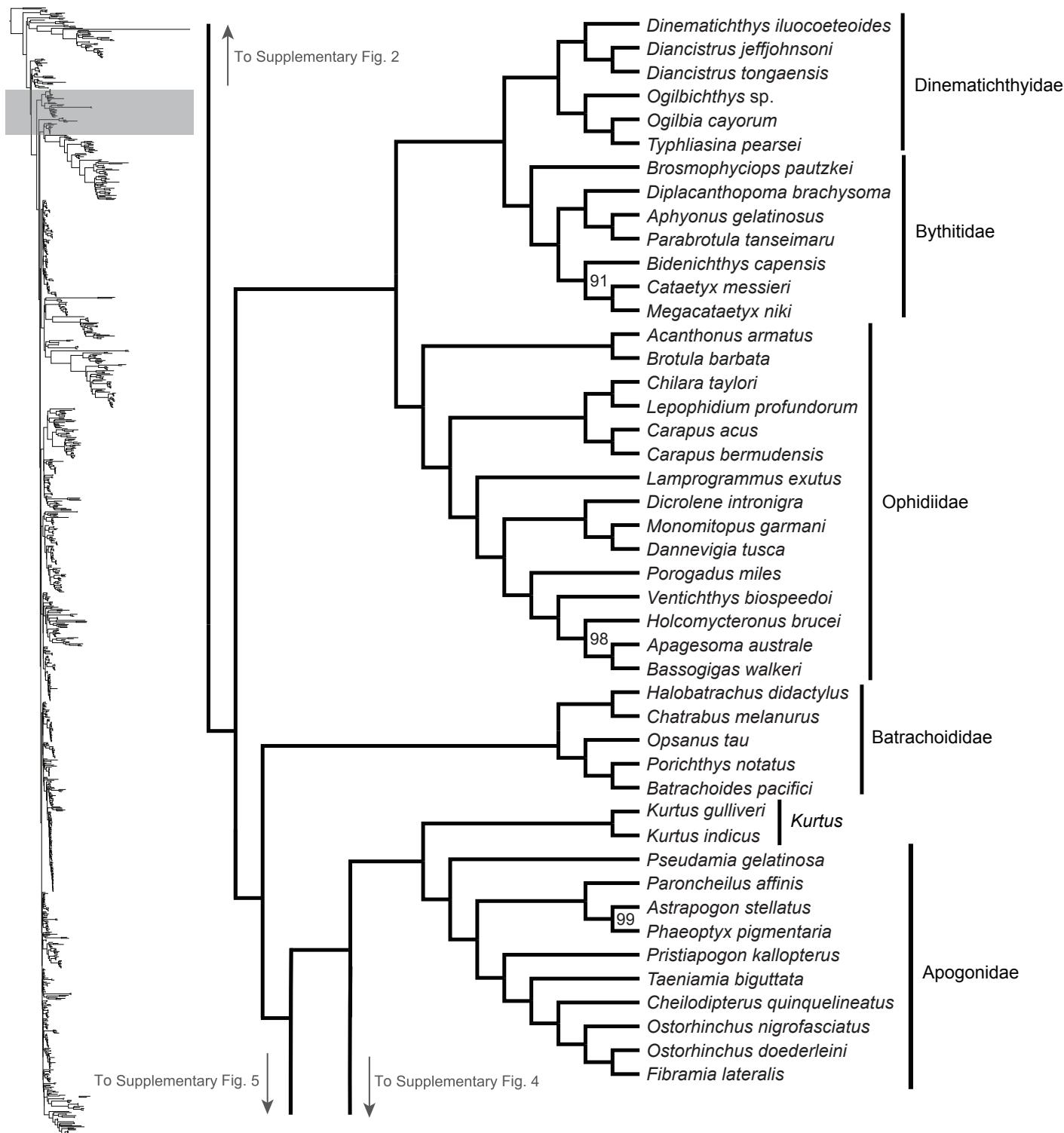
Supplementary Fig. 1: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars. Any tips left unassigned to a higher taxon are monotypic or monogeneric taxa.



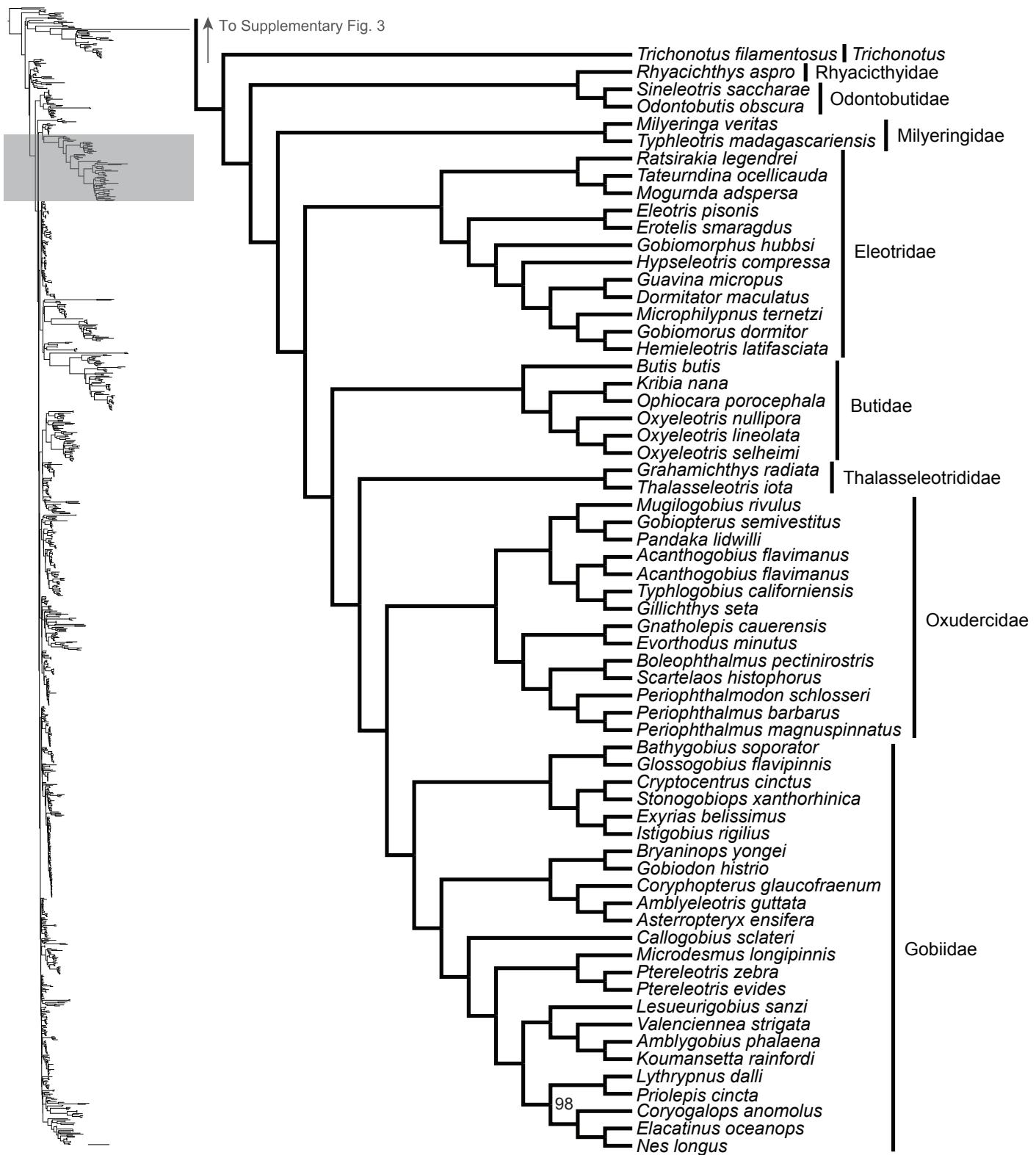
Supplementary Fig. 2: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. All nodes have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars. Any tips left unassigned to a higher taxon are monotypic or monogeneric taxa.



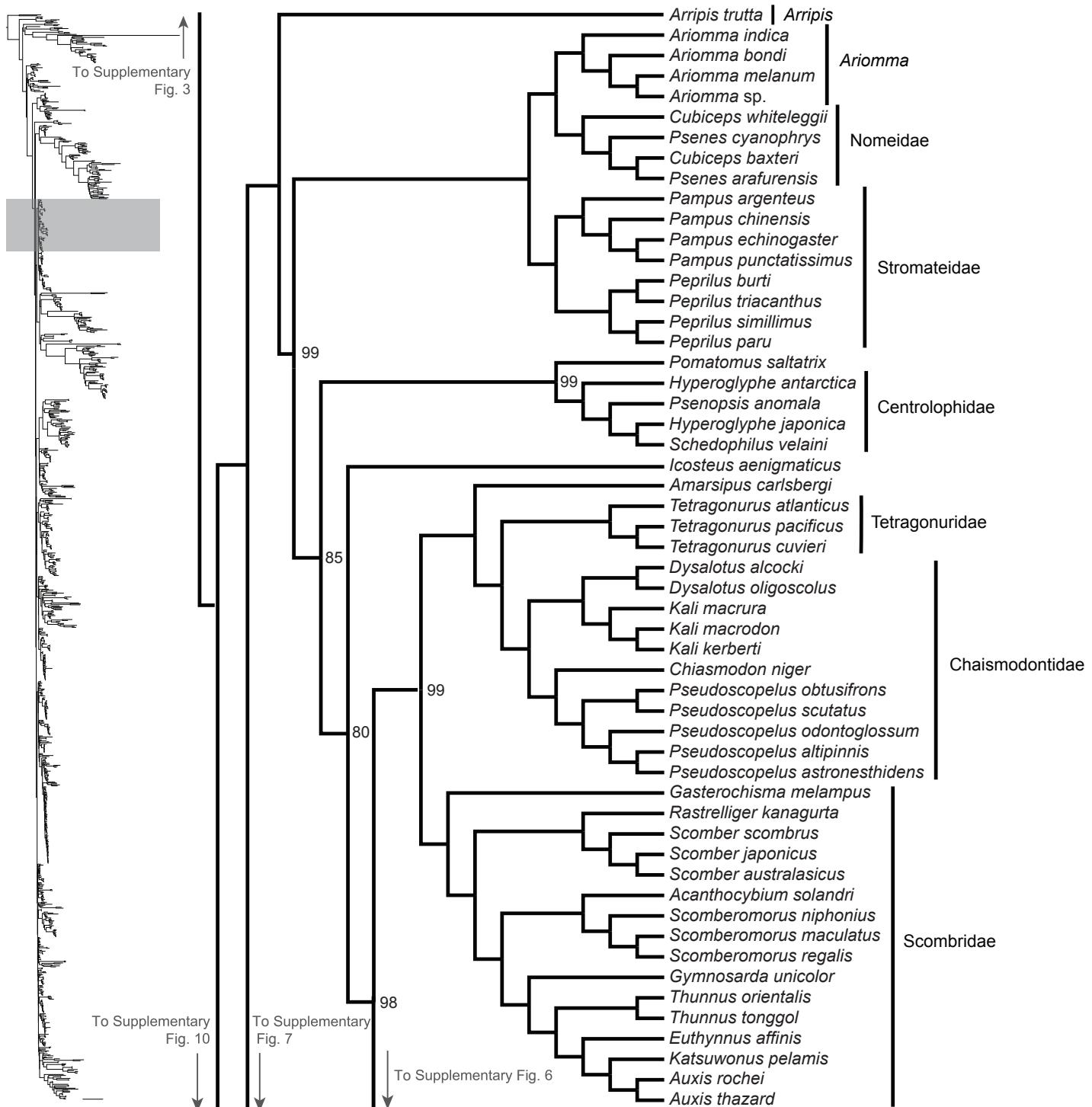
Supplementary Fig. 3: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars.



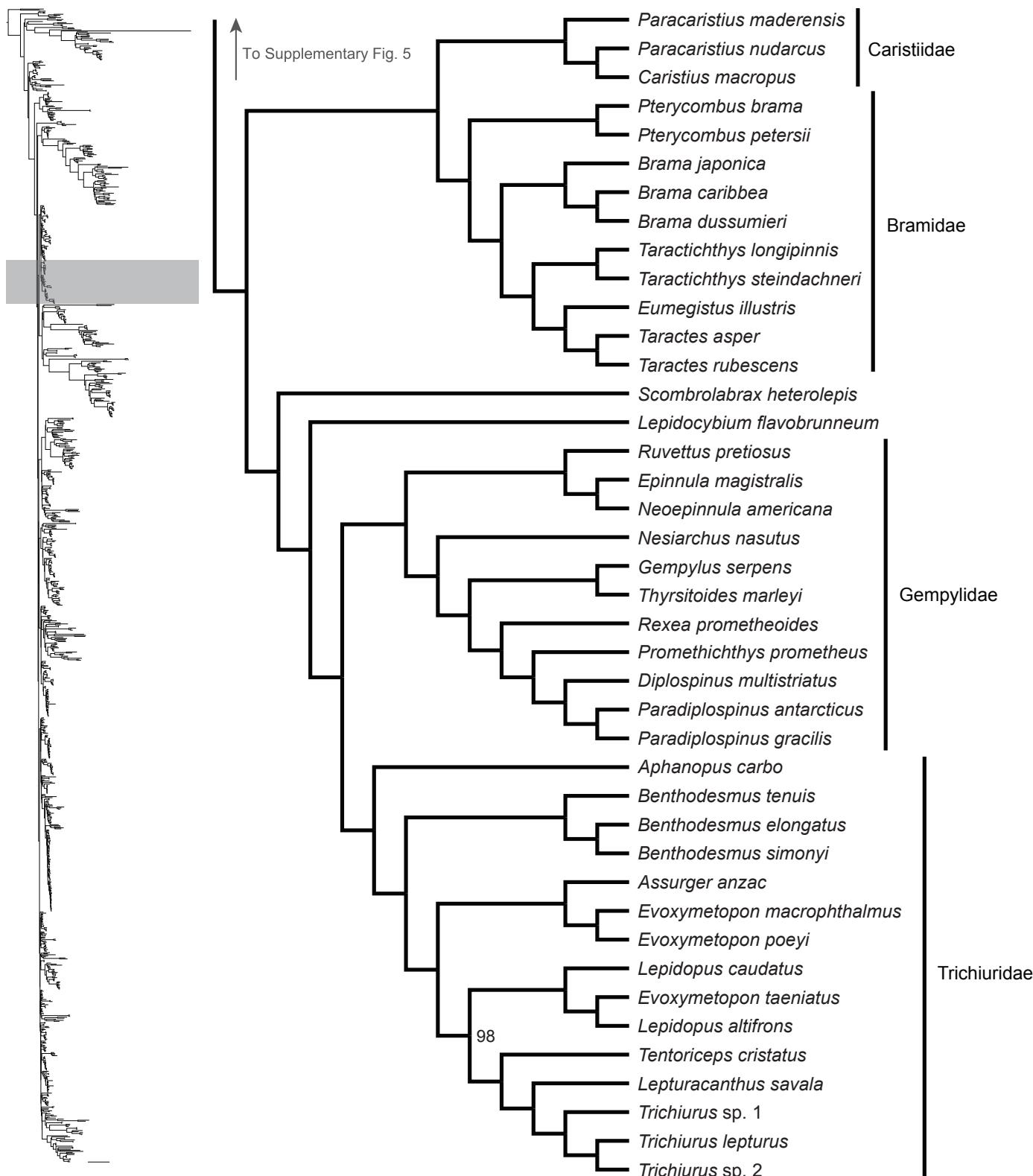
Supplementary Fig. 4: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars.



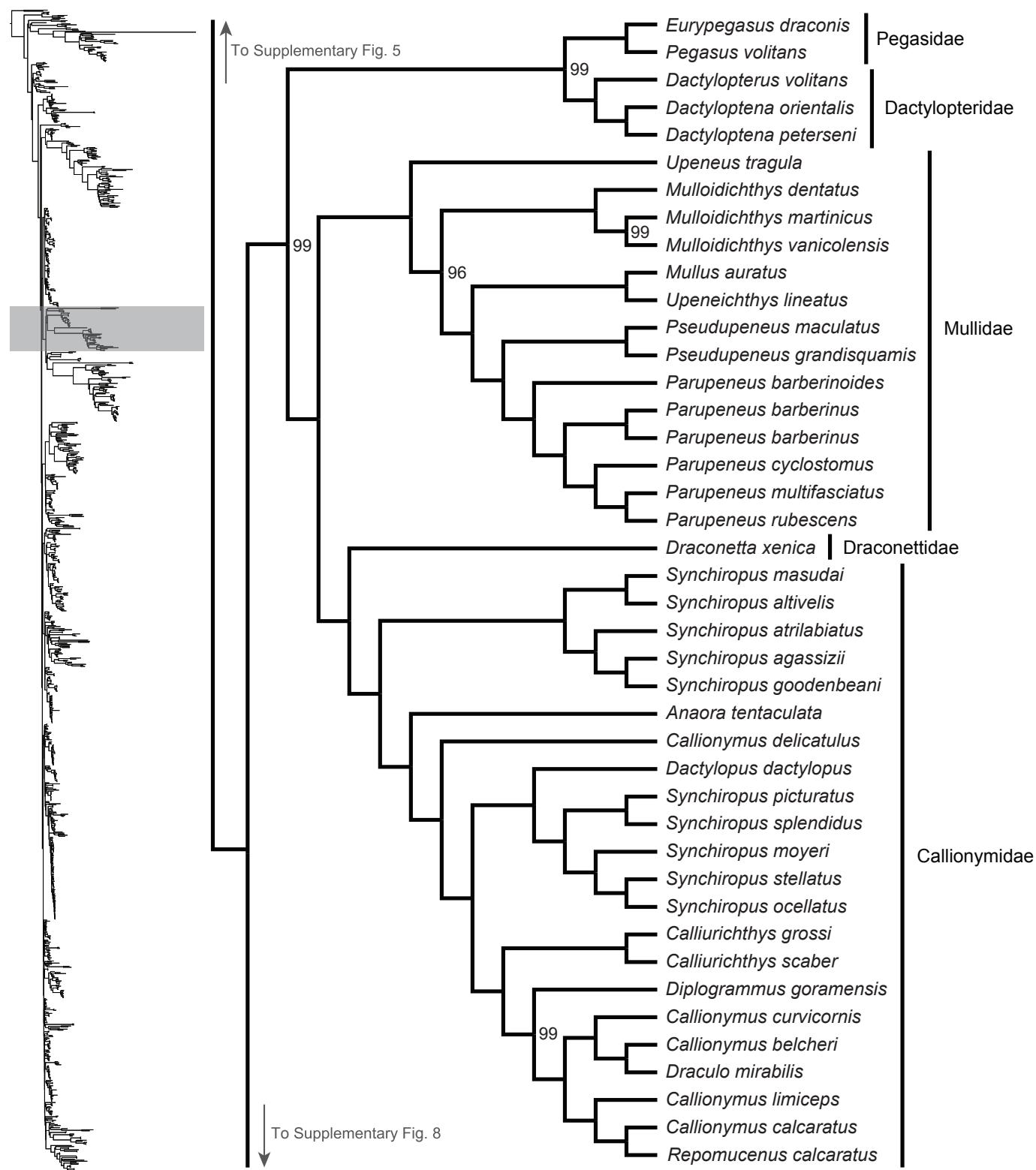
Supplementary Fig. 5: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars. Any tips left unassigned to a higher taxon are monotypic or monogenetic taxa.



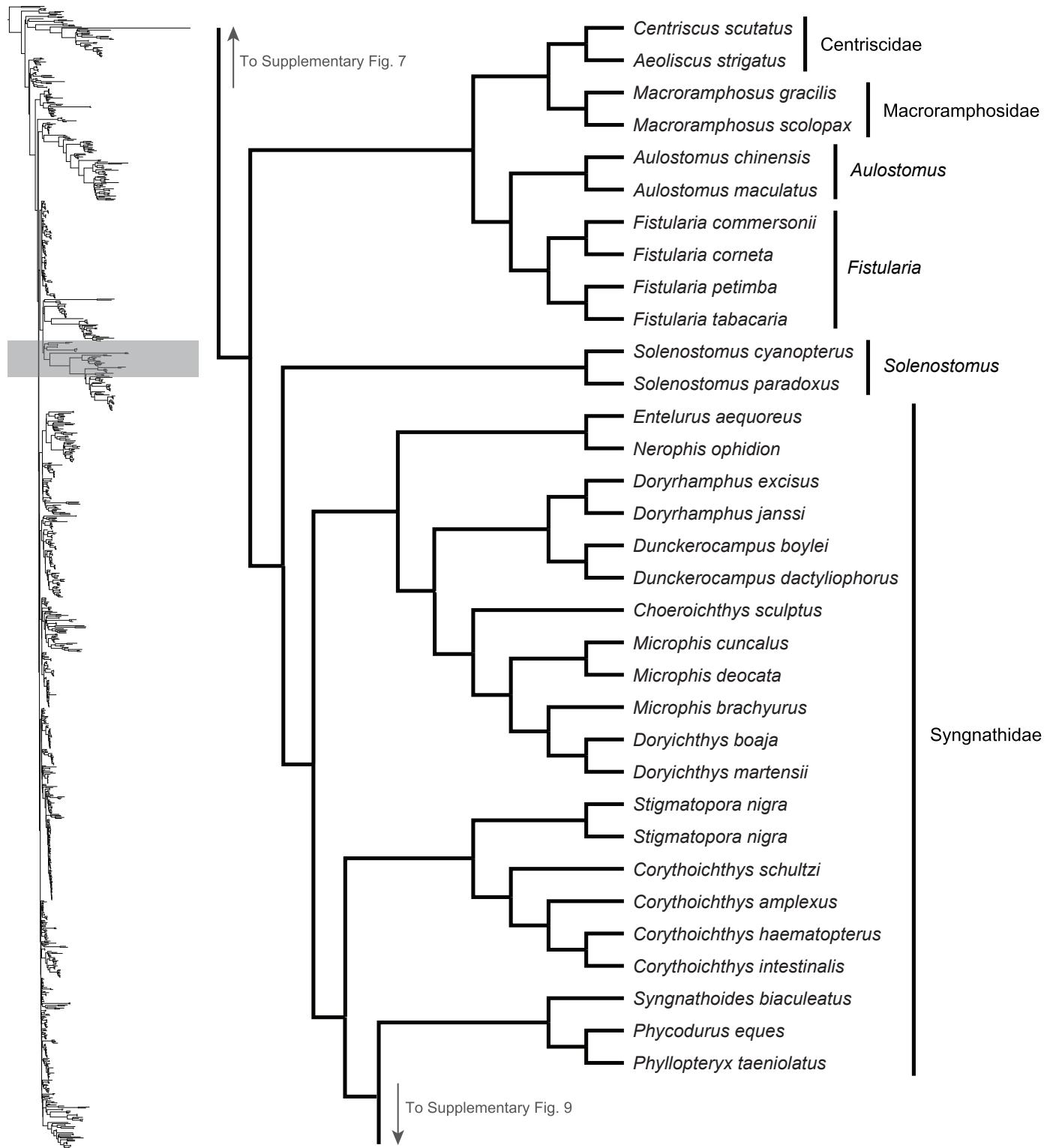
Supplementary Fig. 6: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars. Any tips left unassigned to a higher taxon are monotypic or monogeneric taxa.



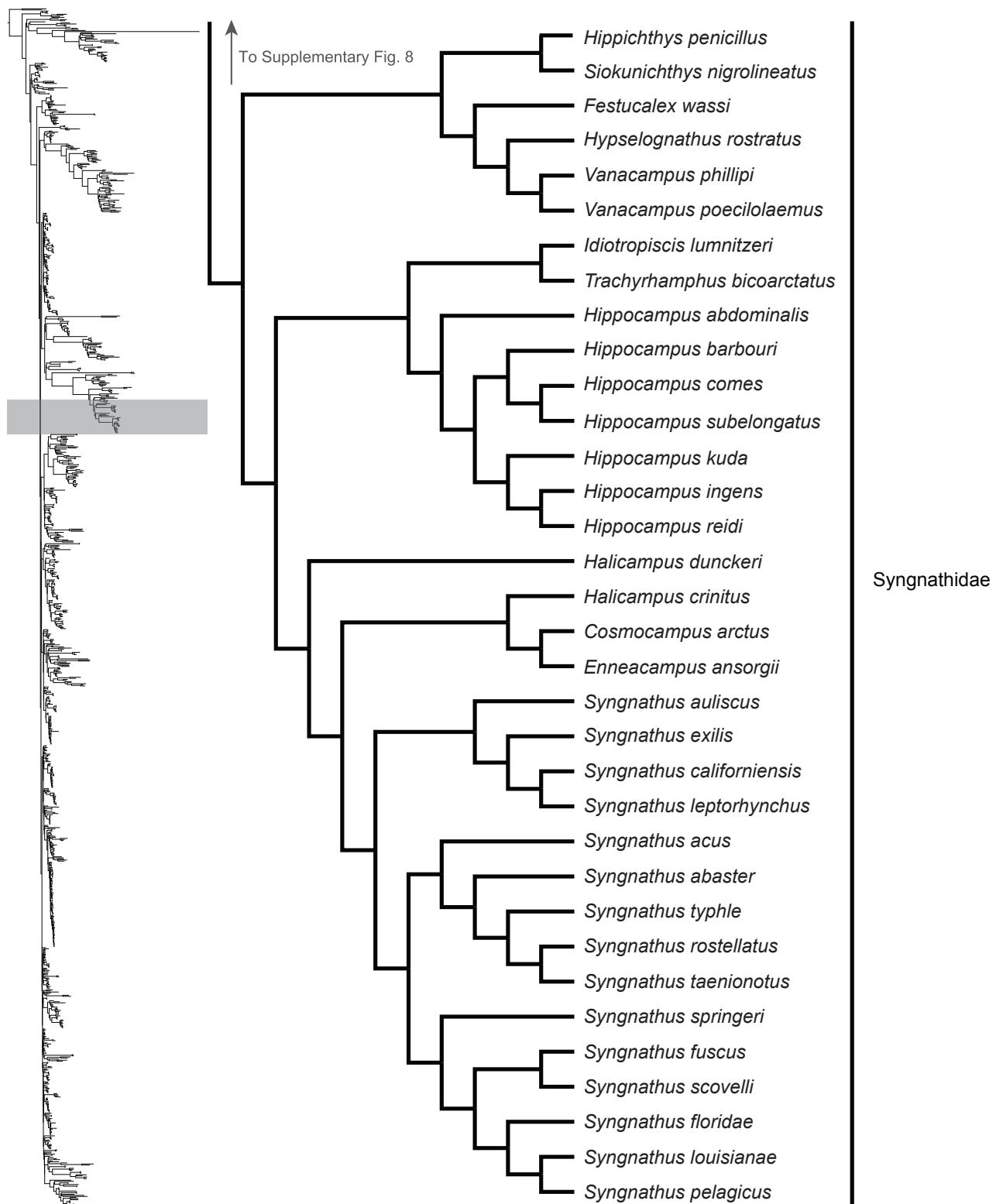
Supplementary Fig. 7: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars.



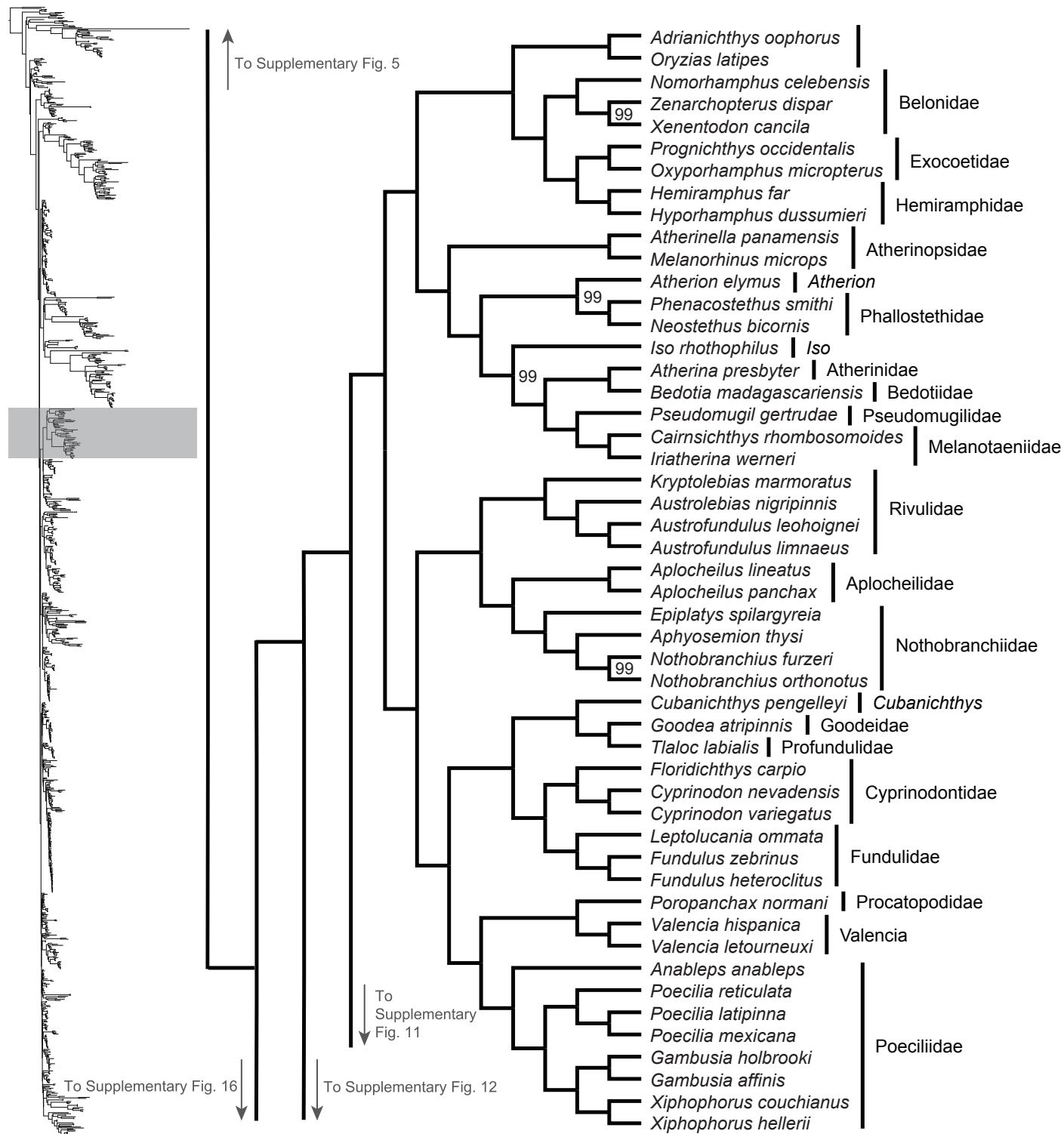
Supplementary Fig. 8: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. All nodes have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars.



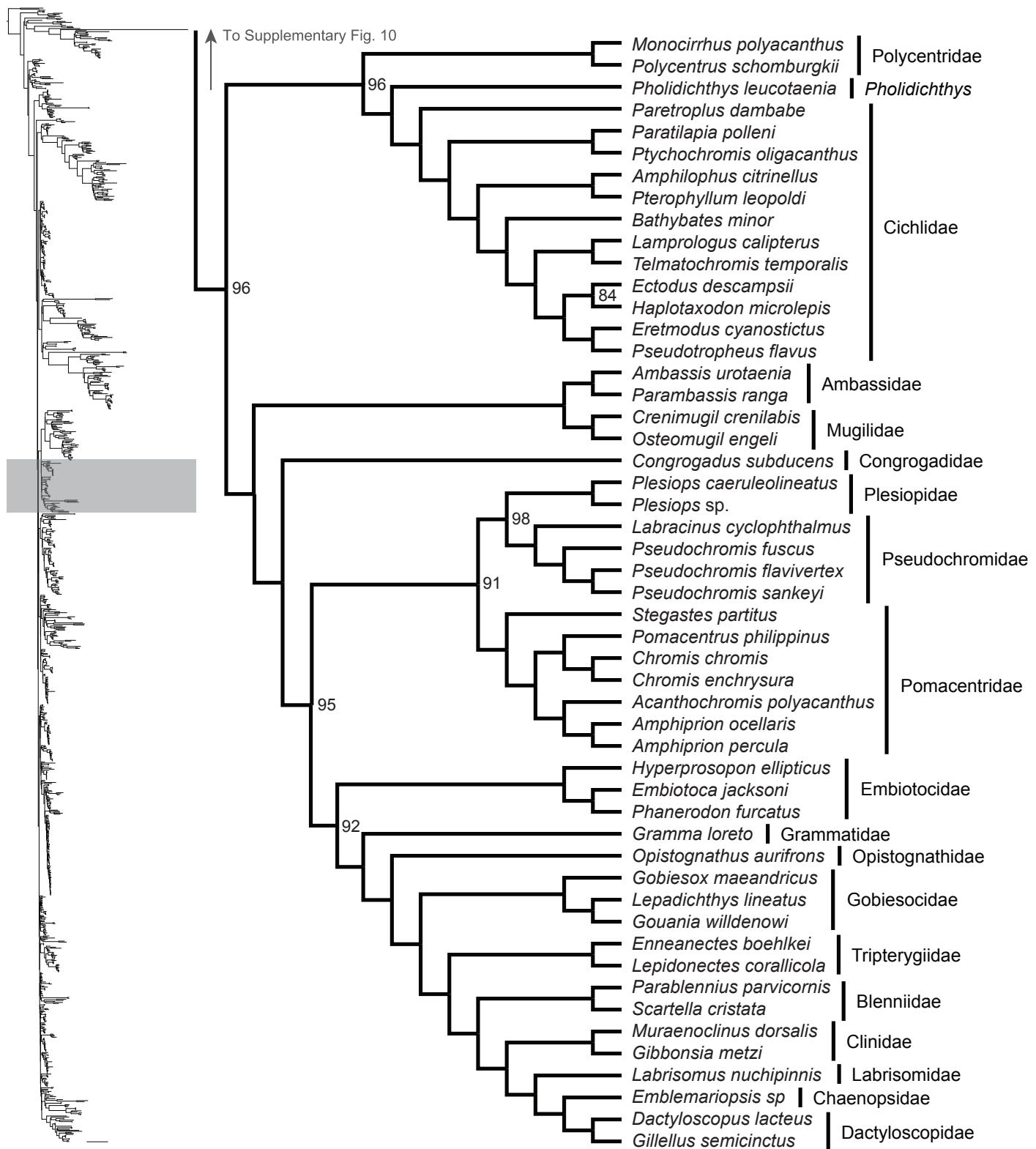
Supplementary Fig. 9: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. All nodes have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars.



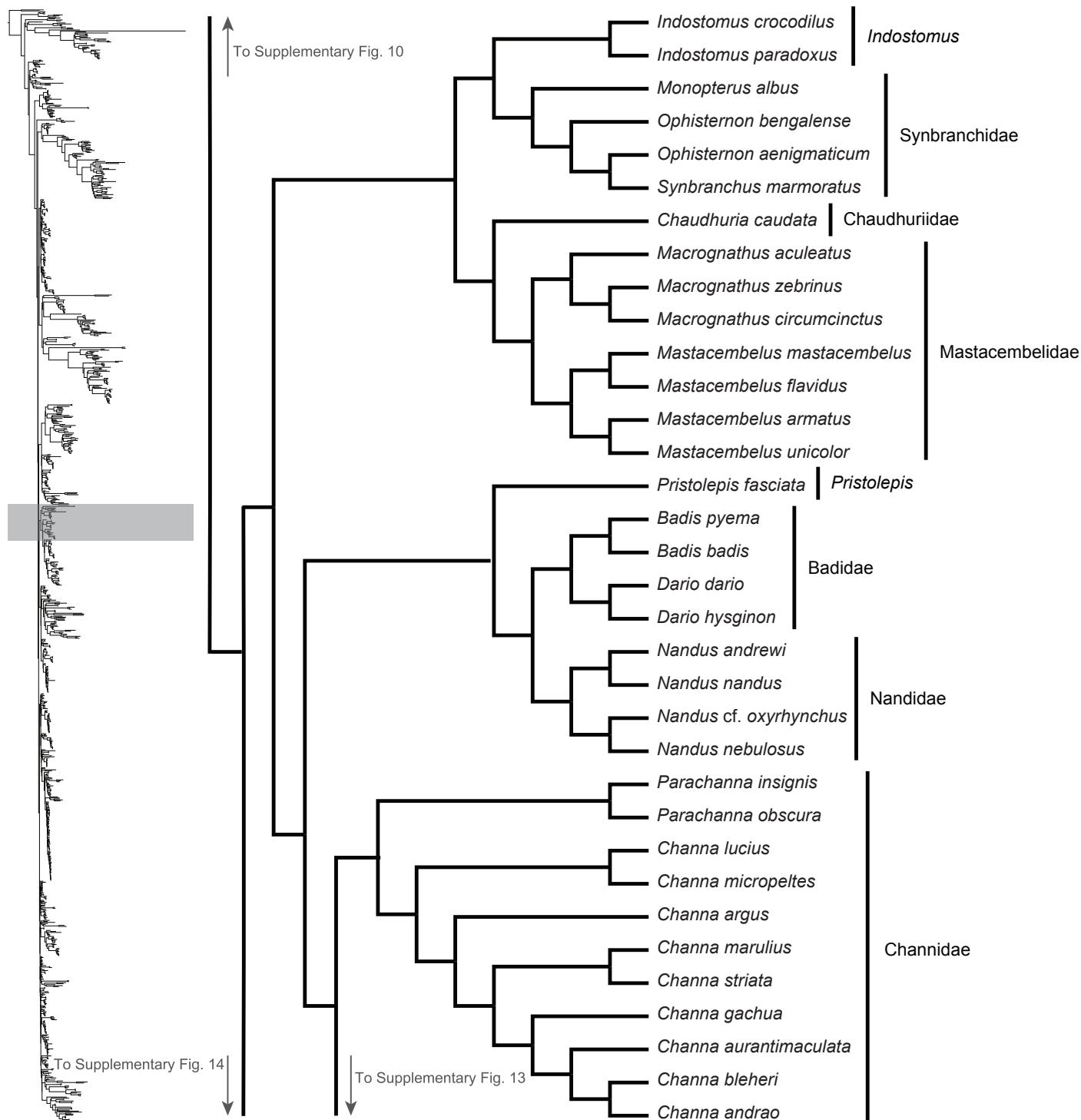
Supplementary Fig. 10: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars.



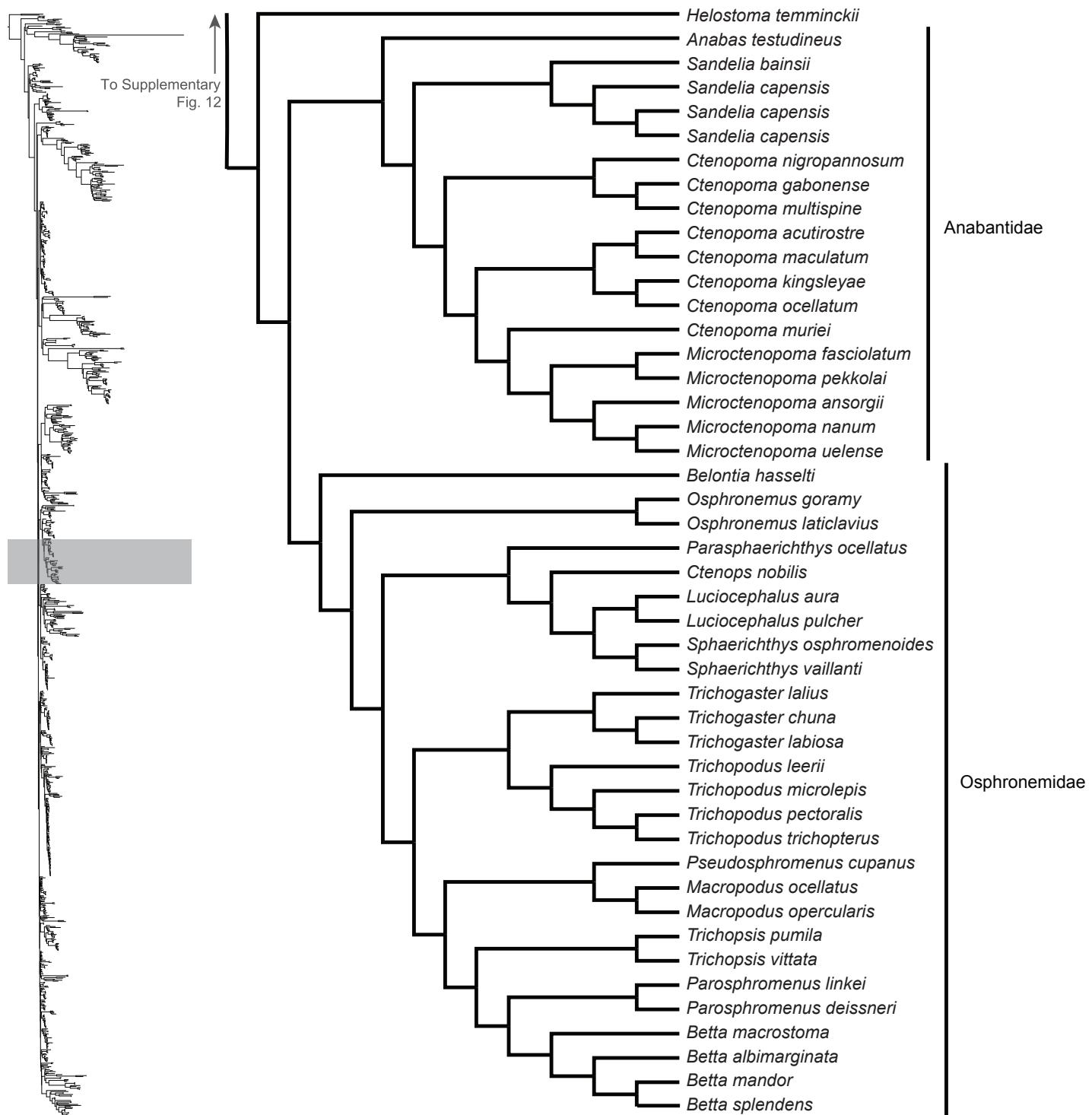
Supplementary Fig. 11: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars.



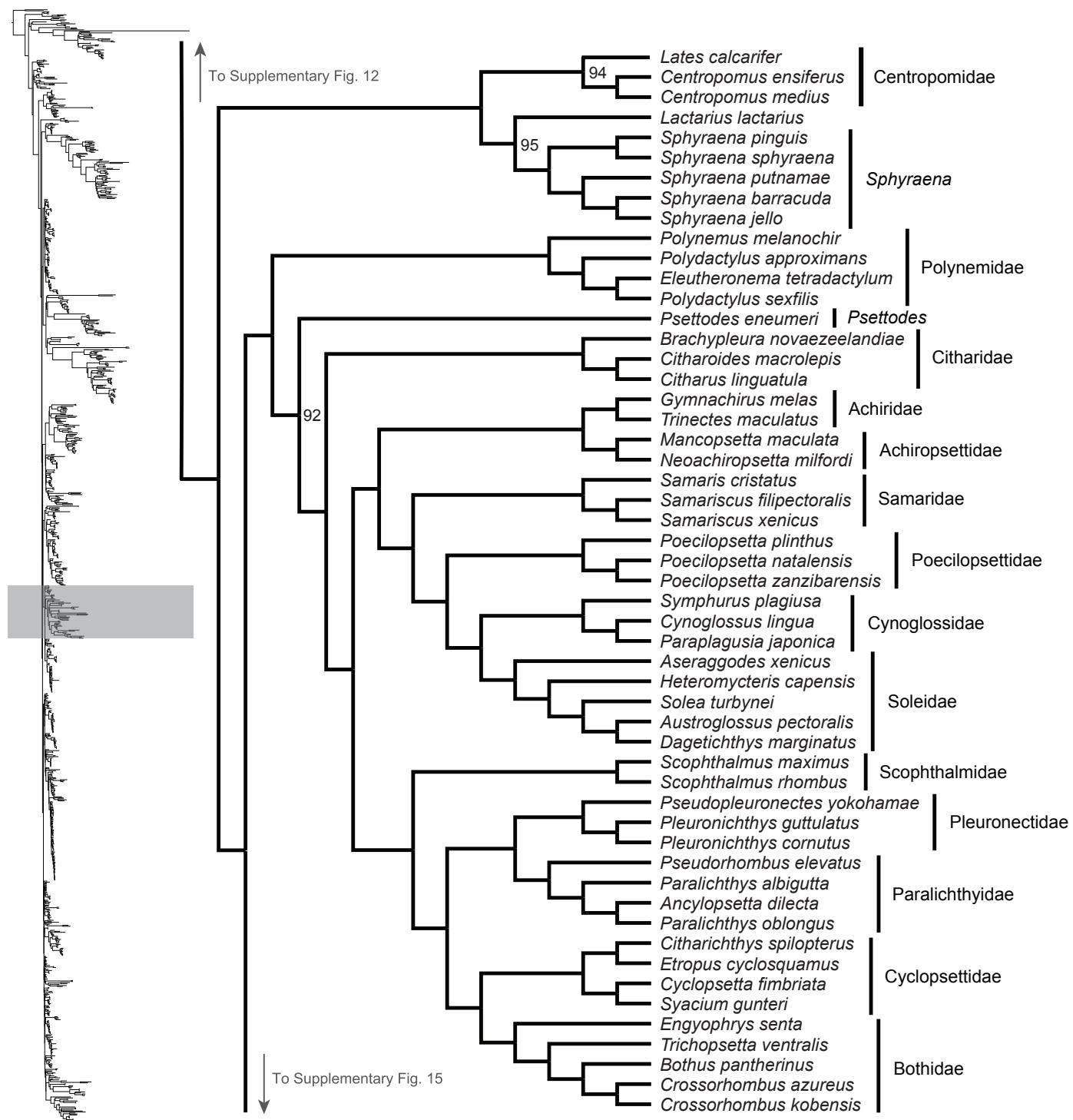
Supplementary Fig. 12: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. All nodes have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars.



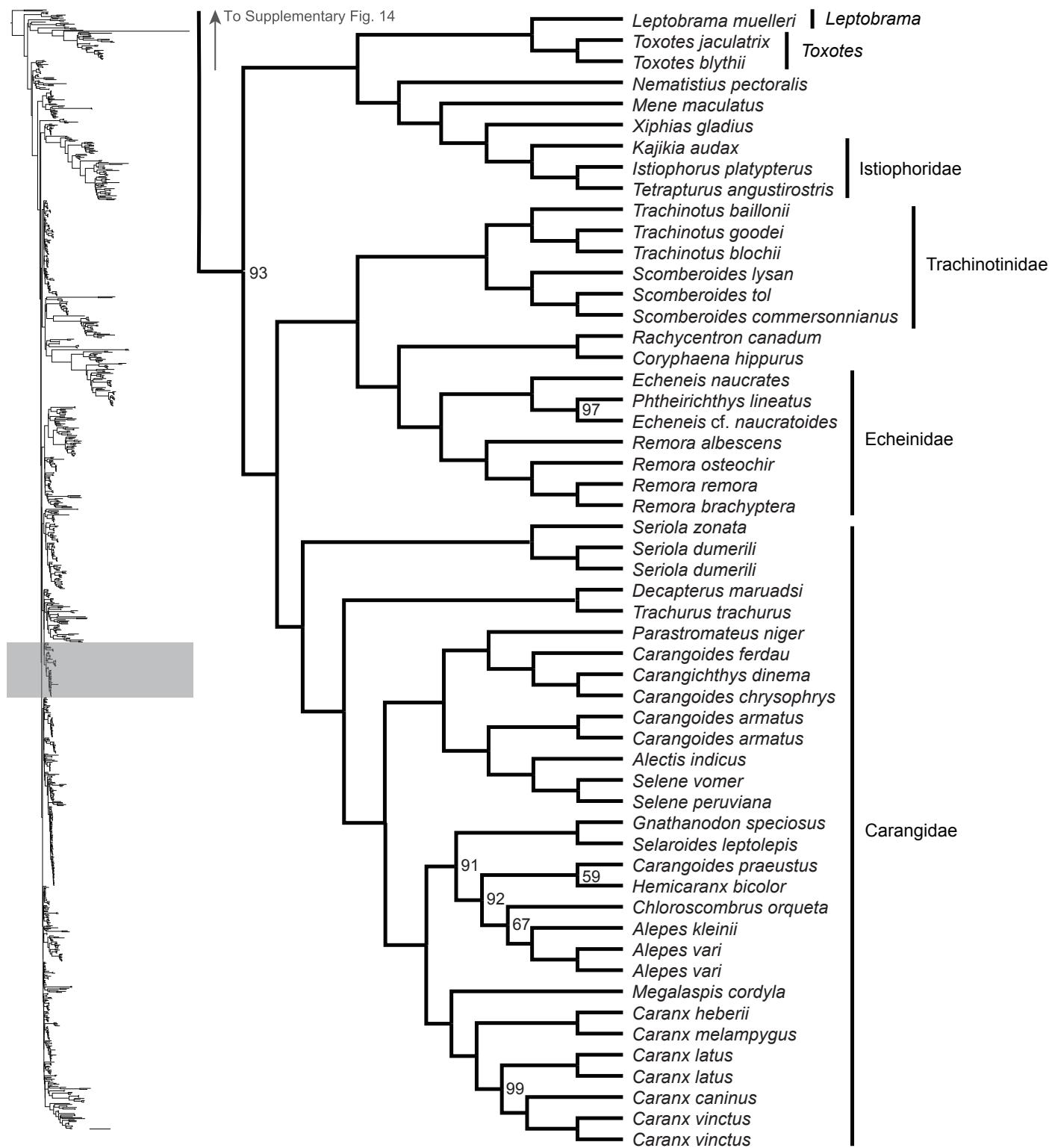
Supplementary Fig. 13: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. All nodes have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars. Any tips left unassigned to a higher taxon are monotypic or monogenetic taxa.



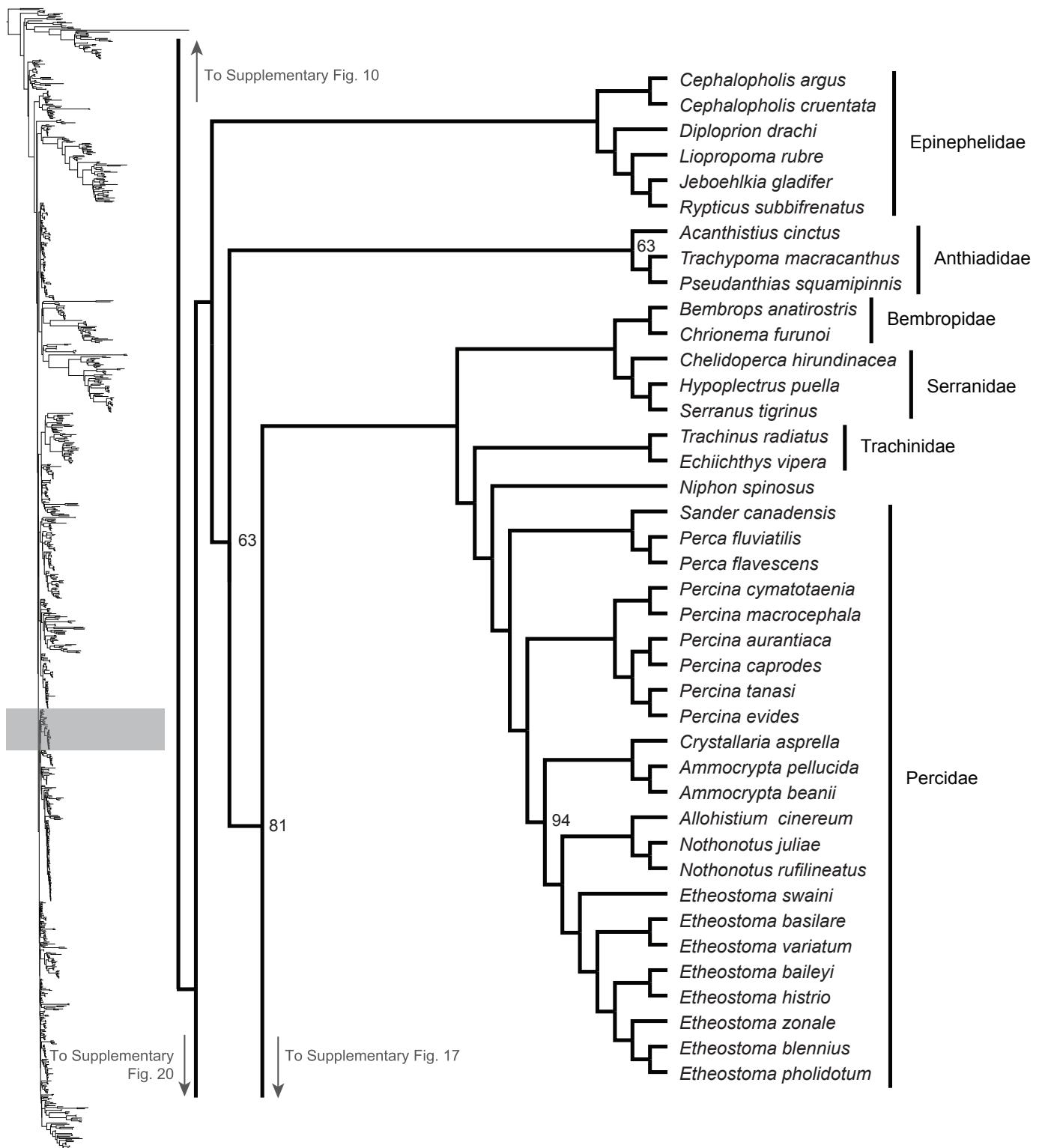
Supplementary Fig. 14: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars. Any tips left unassigned to a higher taxon are monotypic or monogeneric taxa.



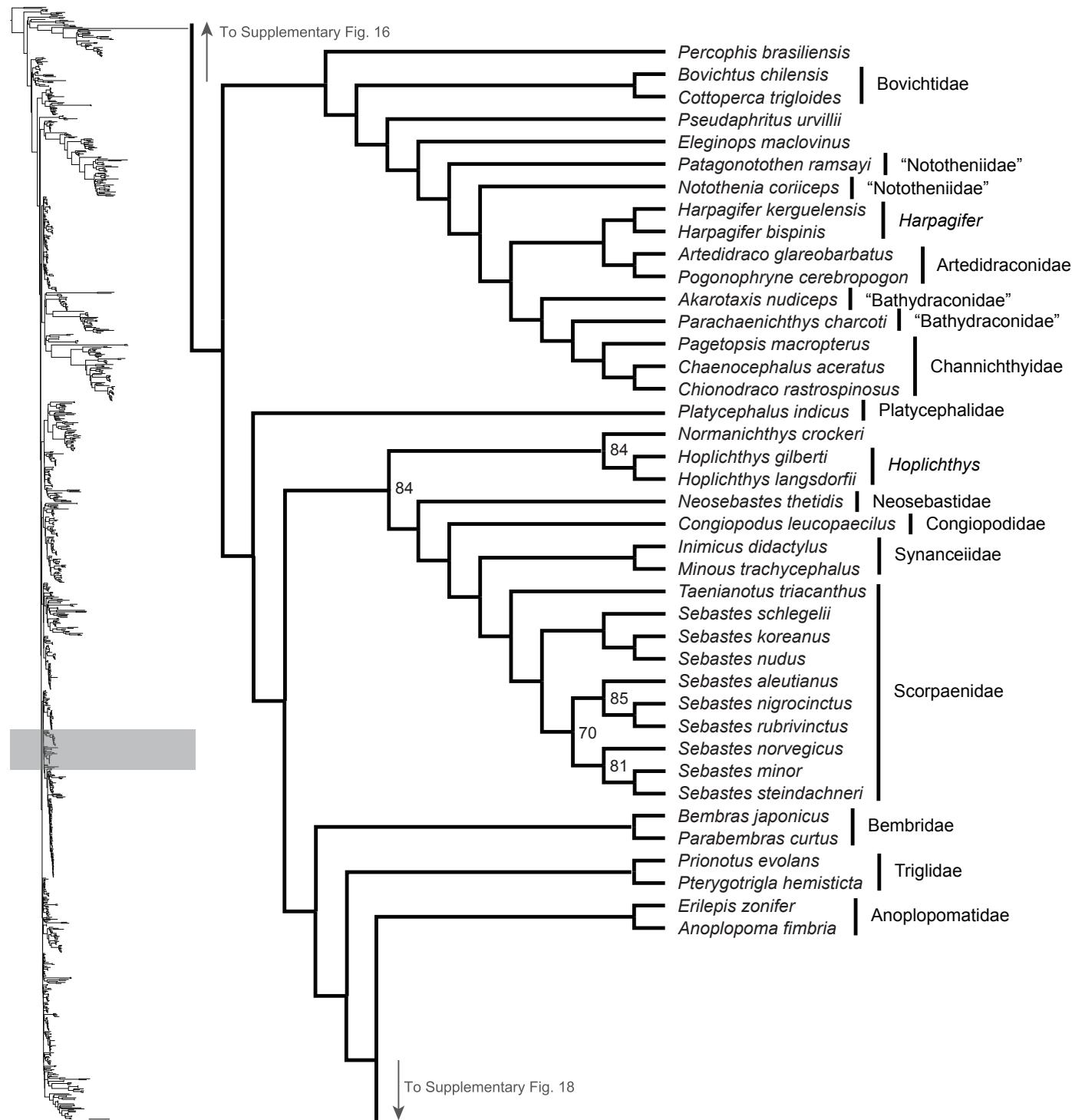
Supplementary Fig. 15: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars. Any tips left unassigned to a higher taxon are monotypic or monogeneric taxa.



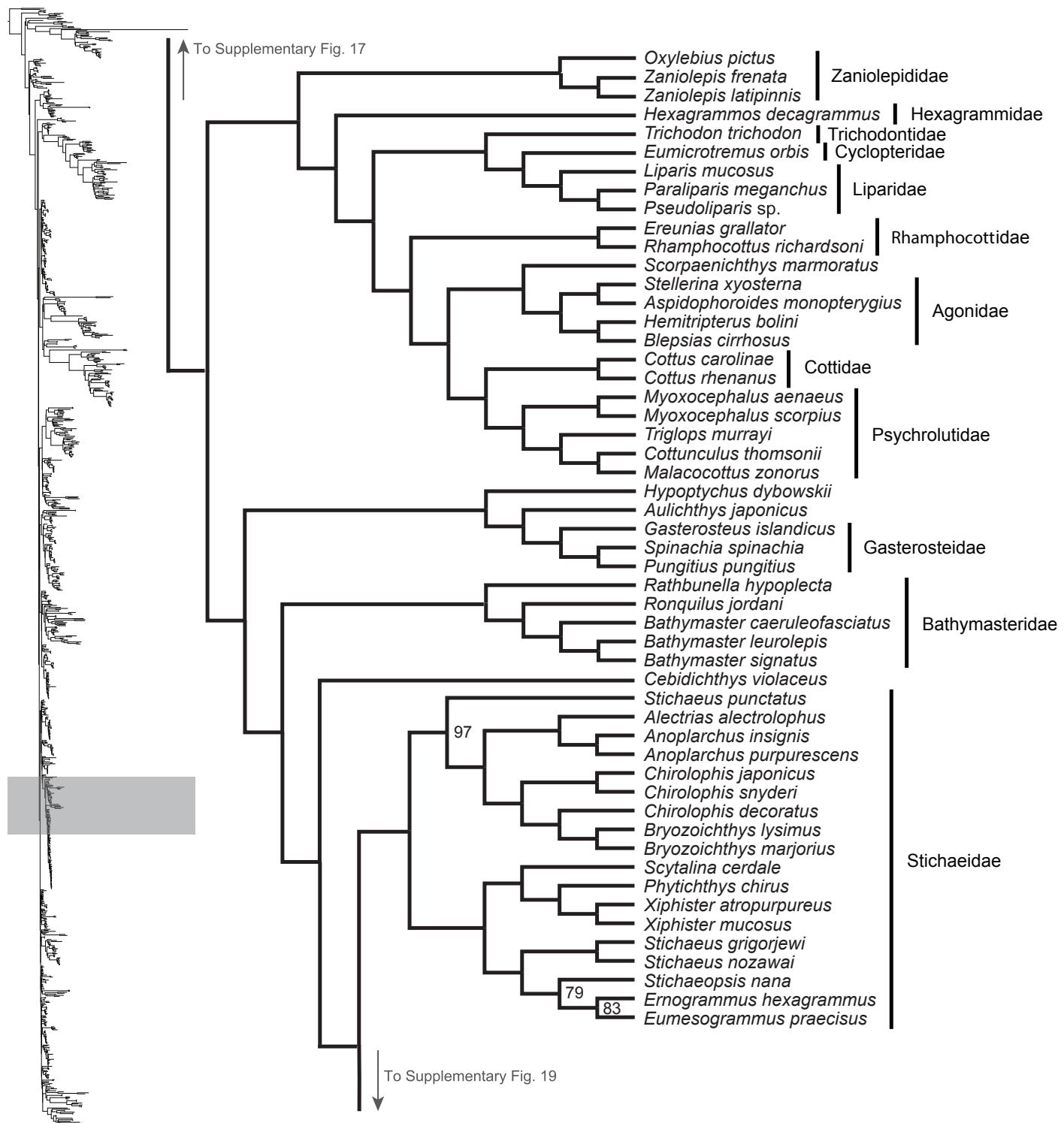
Supplementary Fig. 16: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars. Any tips left unassigned to a higher taxon are monotypic or monogeneric taxa.



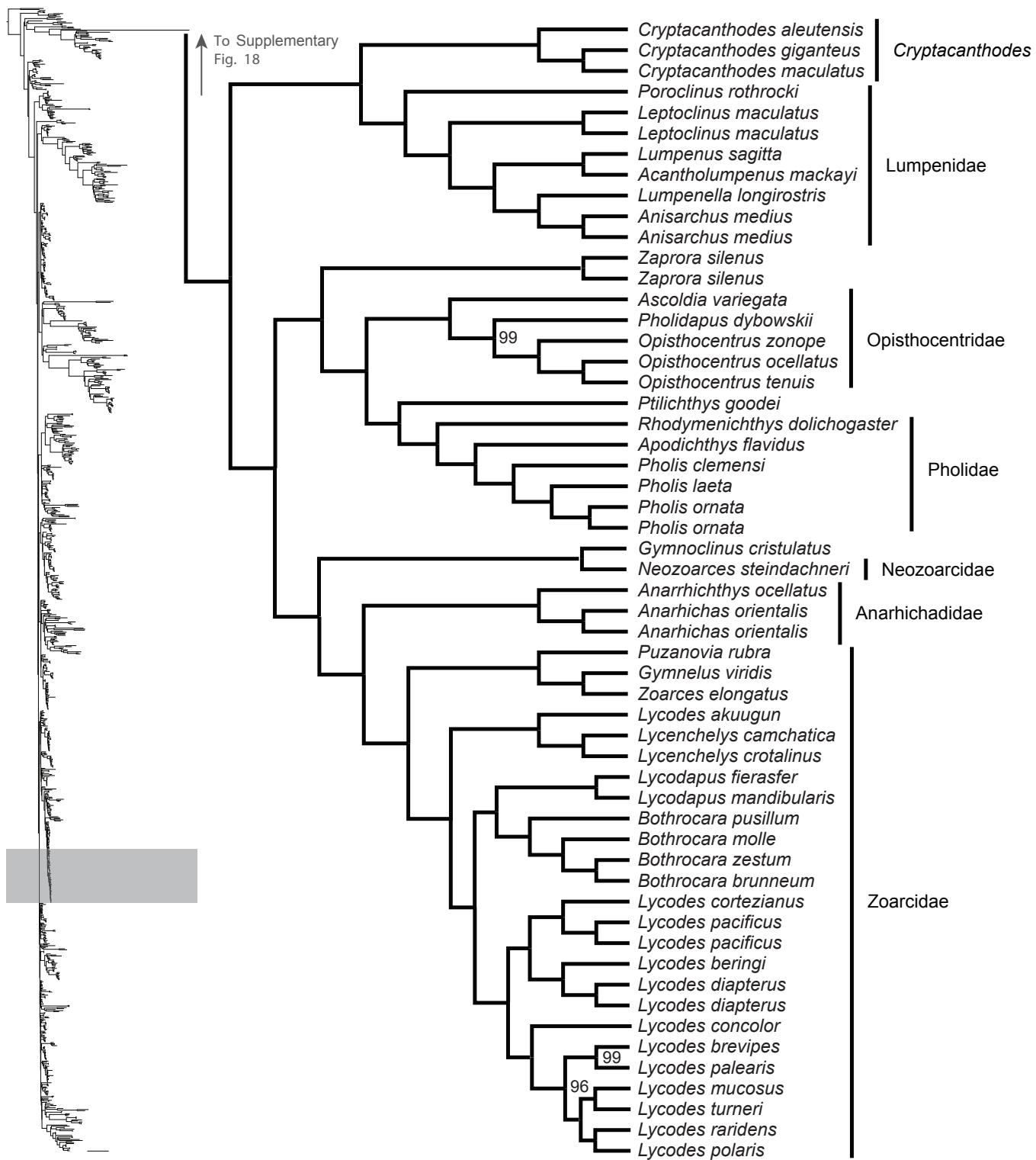
Supplementary Fig. 17: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars. Any tips left unassigned to a higher taxon are monotypic or monogenetic taxa.



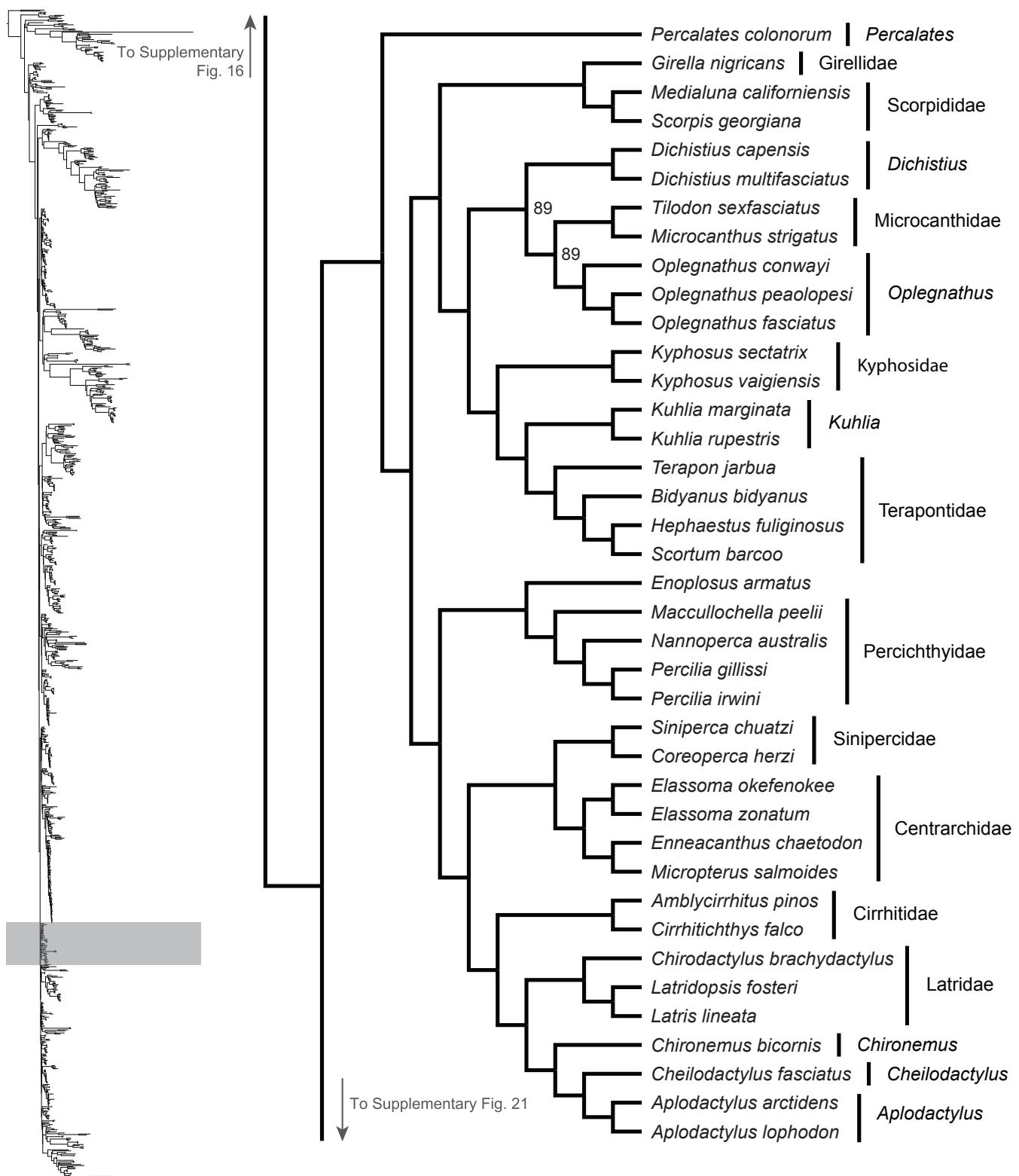
Supplementary Fig. 18: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars. Any tips left unassigned to a higher taxon are monotypic or monogeneric taxa.



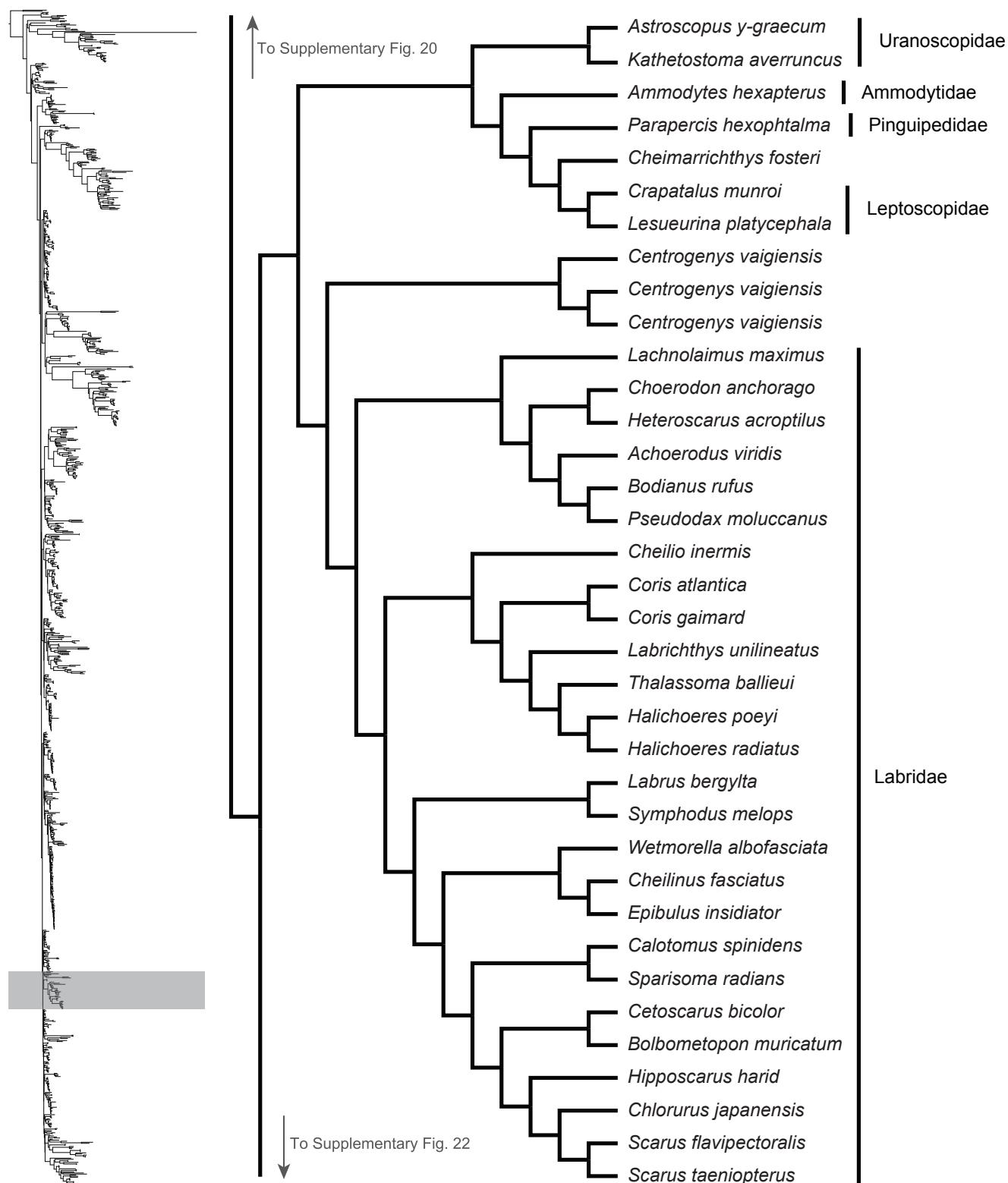
Supplementary Fig. 19: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars. Any tips left unassigned to a higher taxon are monotypic or monogeneric taxa.



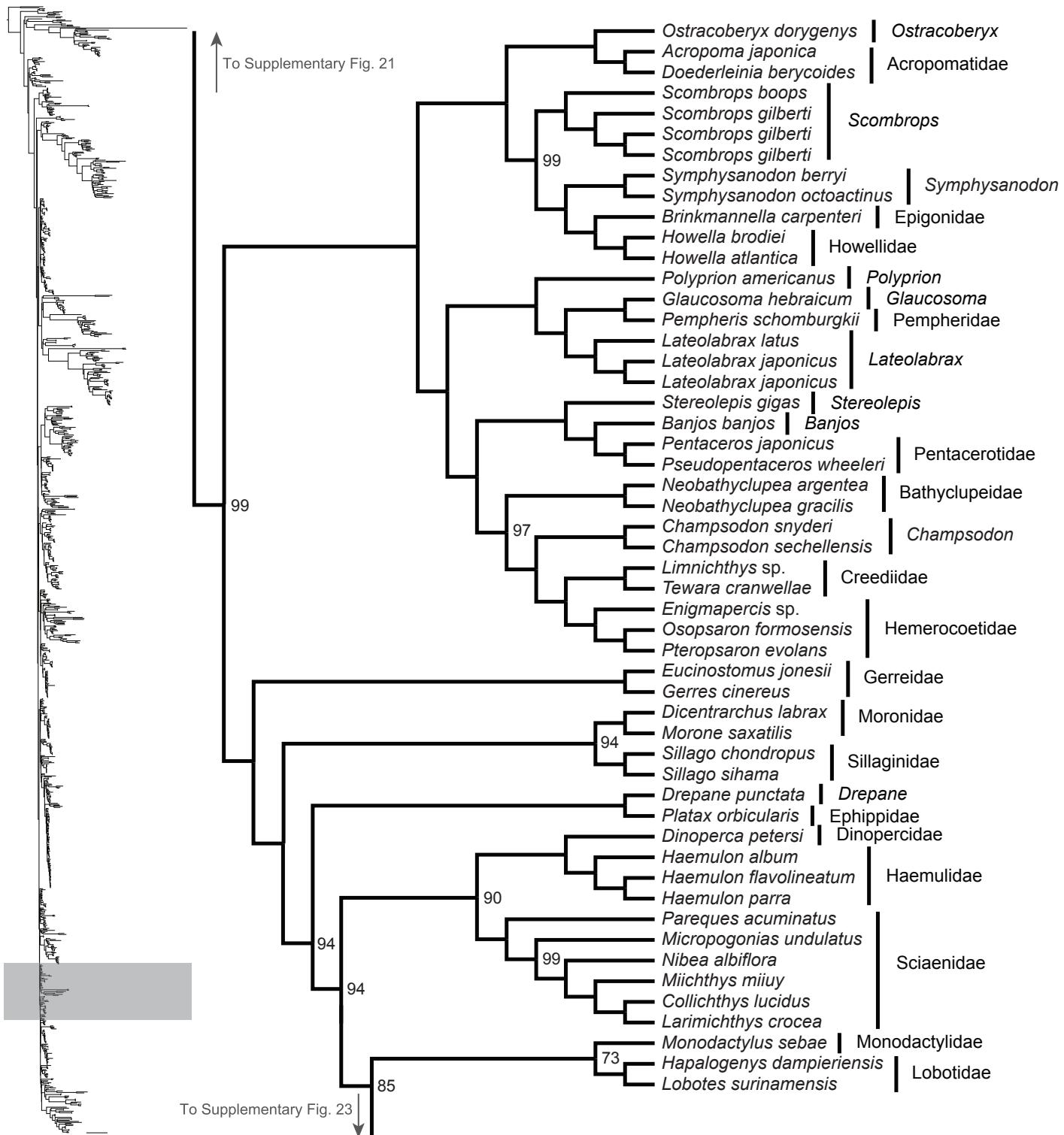
Supplementary Fig. 20: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars. Any tips left unassigned to a higher taxon are monotypic or monogeneric taxa.



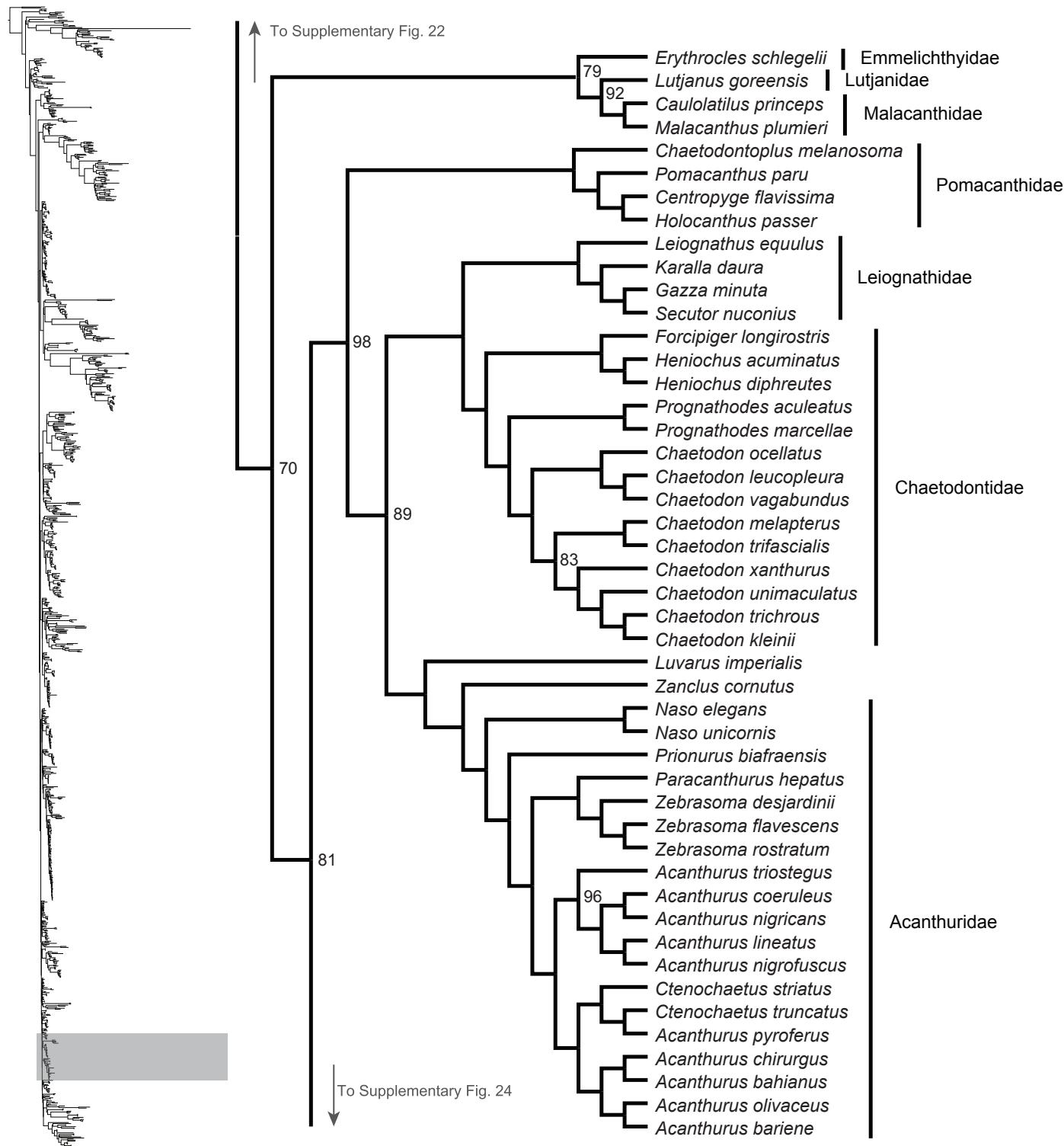
Supplementary Fig. 21: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. All nodes have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars. Any tips left unassigned to a higher taxon are monotypic or monogeneric taxa.



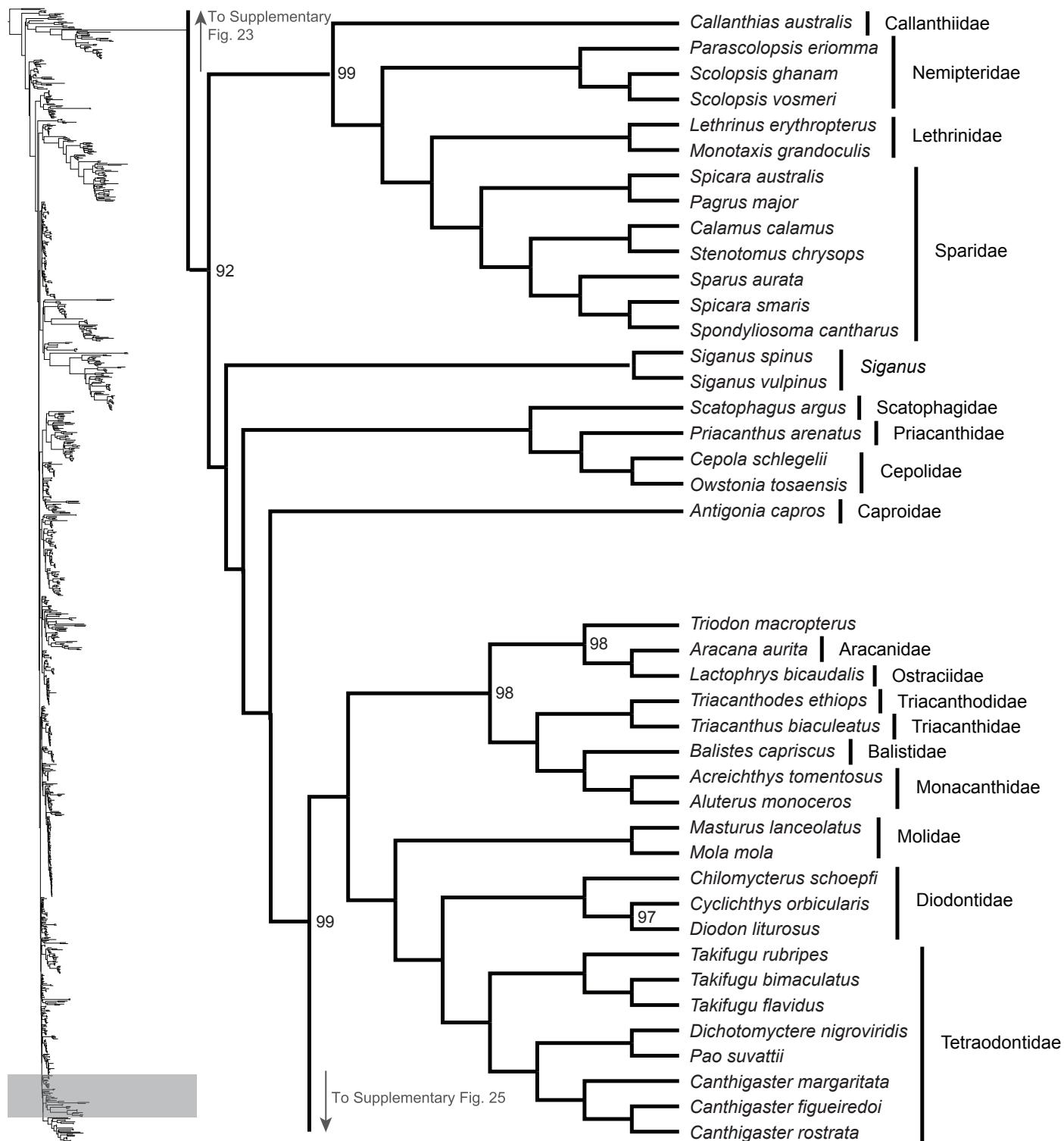
Supplementary Fig. 22: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars.



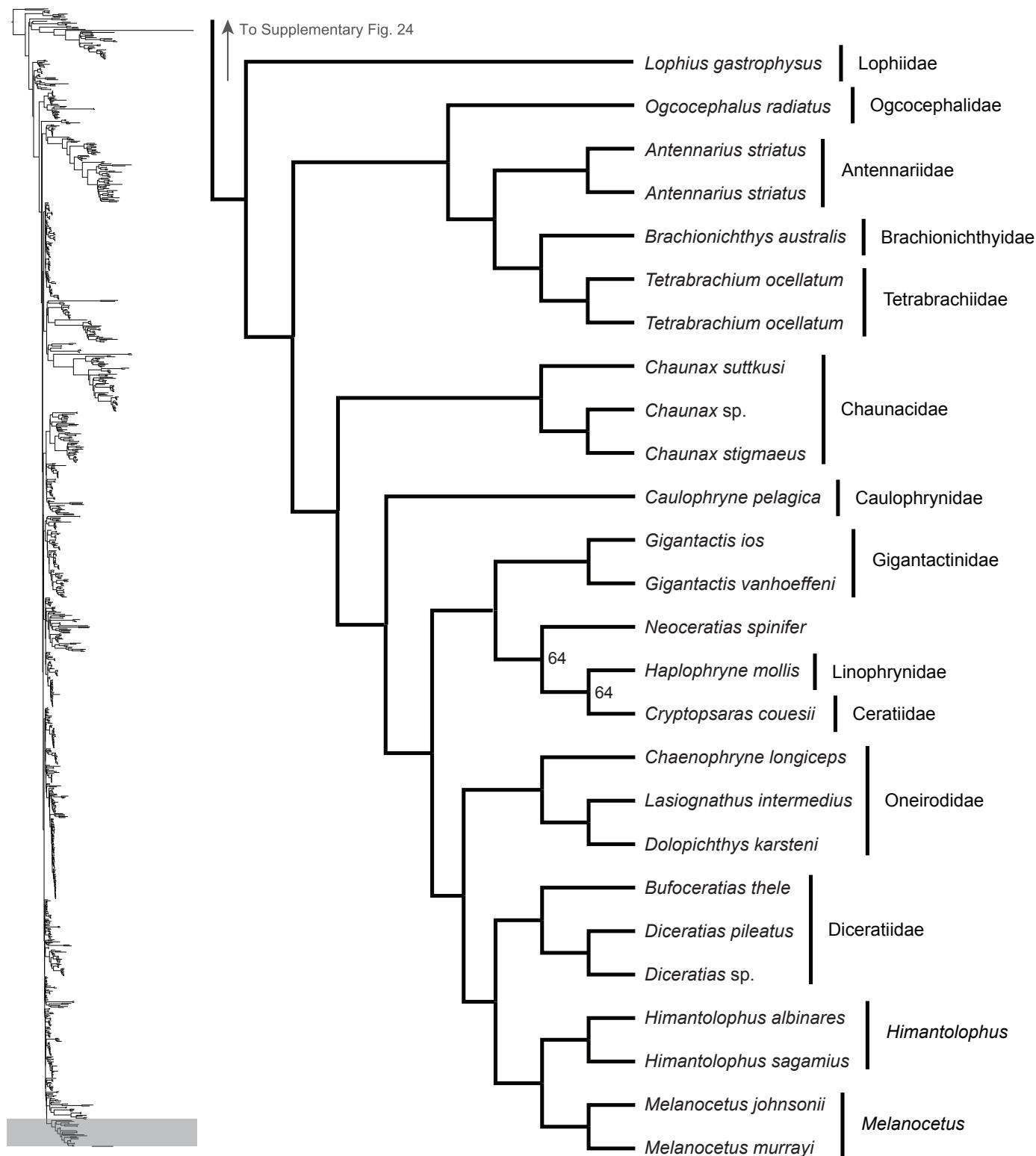
Supplementary Fig. 23: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars. Any tips left unassigned to a higher taxon are monotypic or monogeneric taxa.



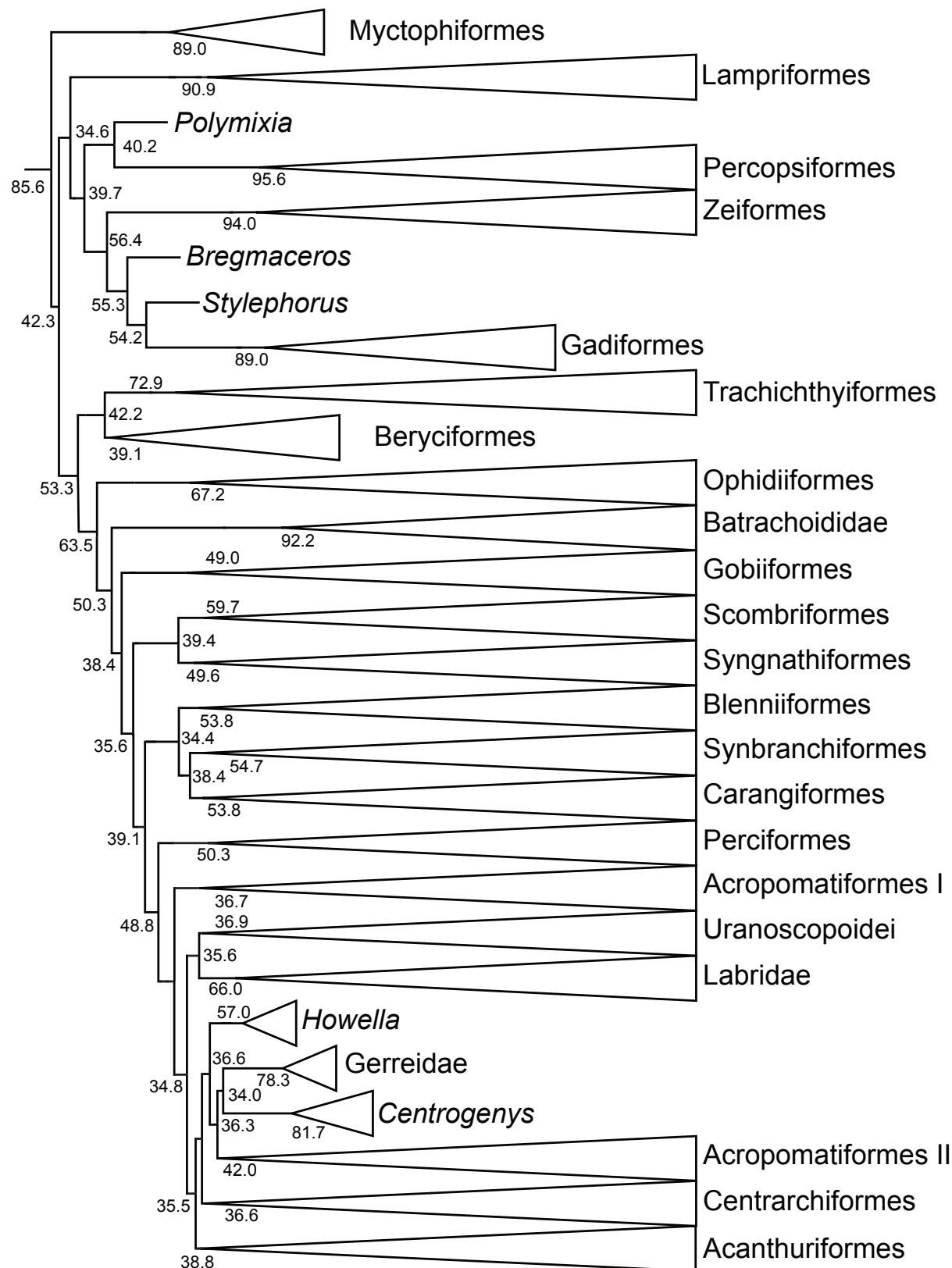
Supplementary Fig. 24: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars. Any tips left unassigned to a higher taxon are monospecific taxa.



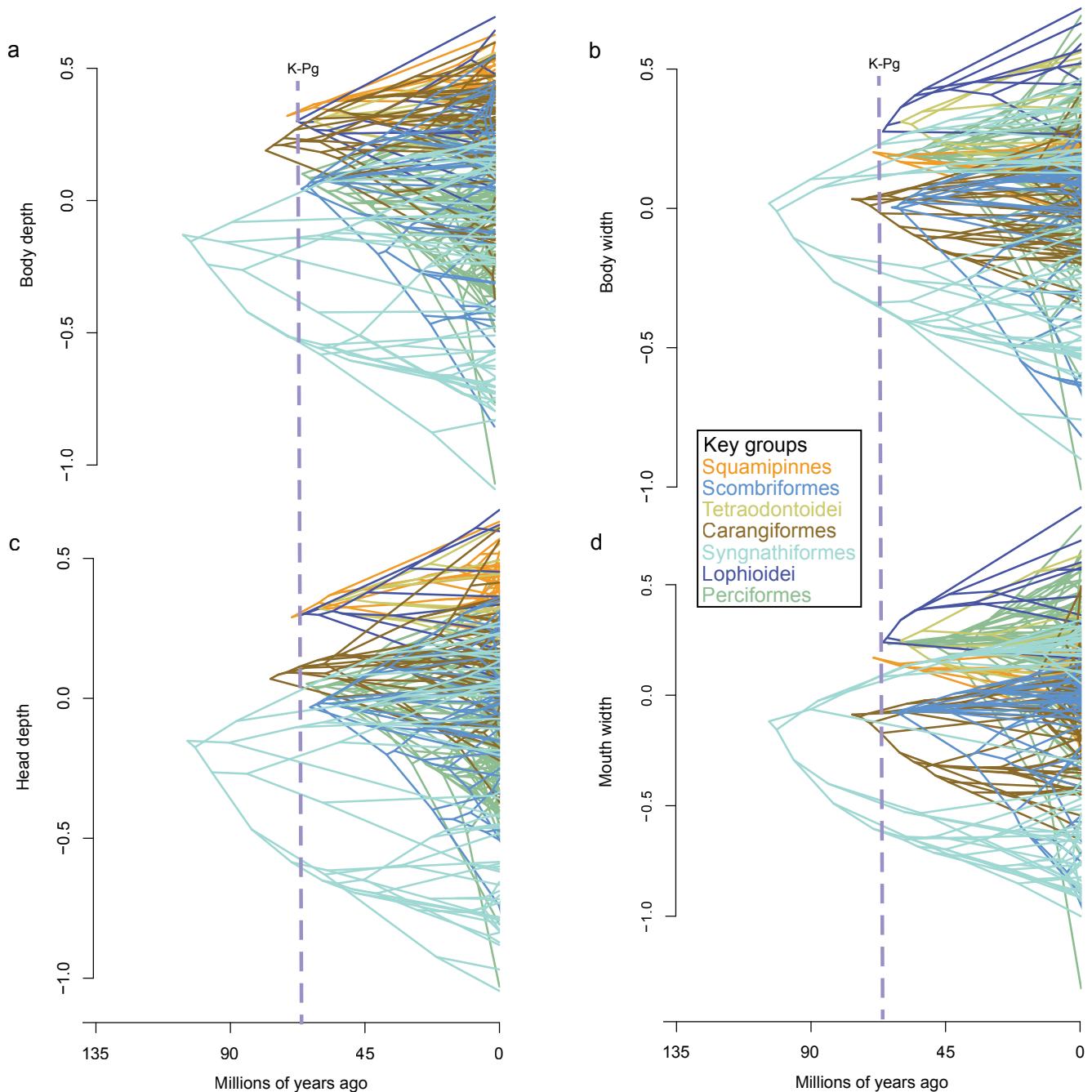
Supplementary Fig. 25: Maximum likelihood phylogeny inferred in IQ-TREE.

A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars. Any tips left unassigned to a higher taxon are monotypic or monogeneric taxa.



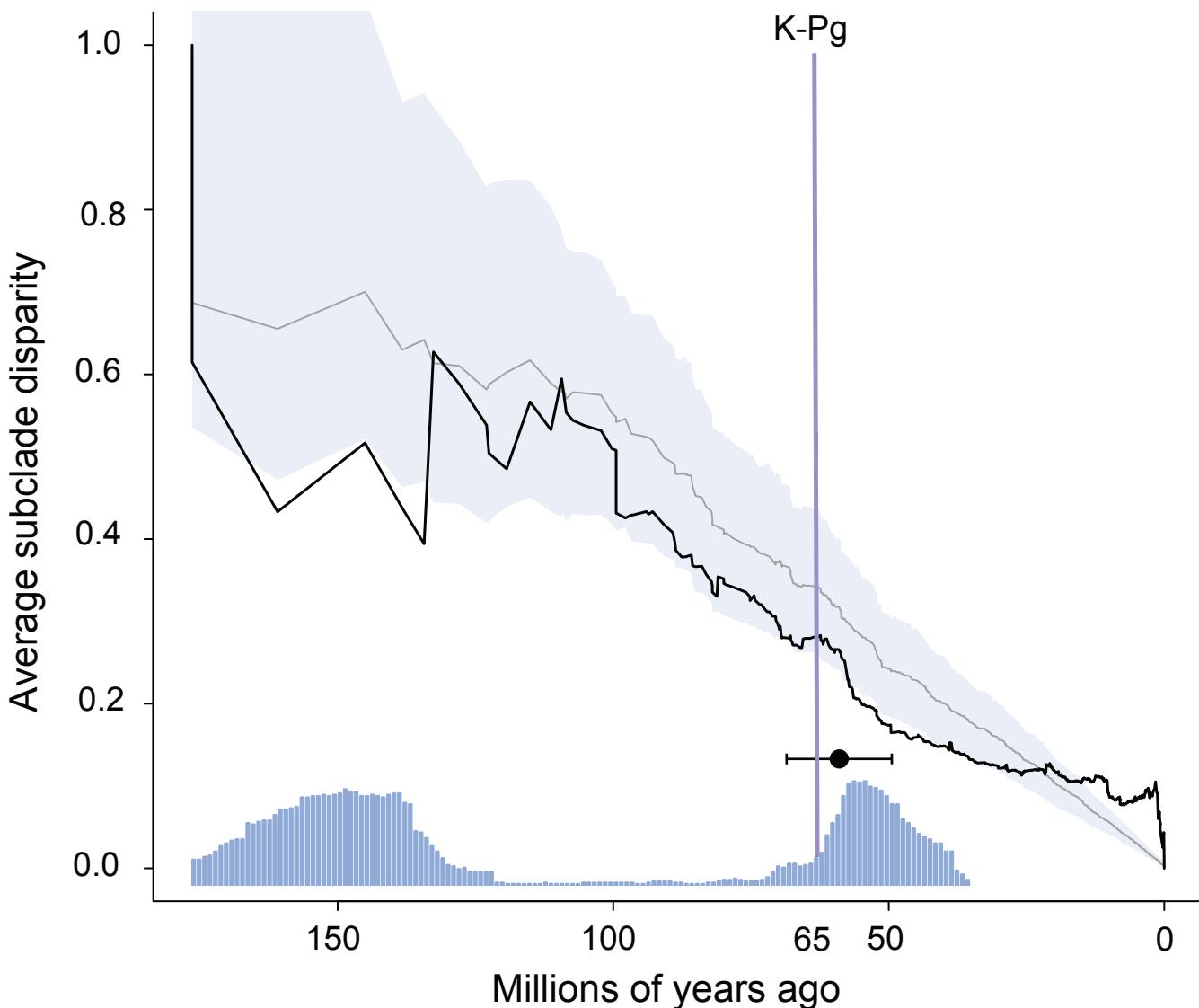
Supplementary Fig. 26: ASTRAL-III inferred species tree.

Collapsed species tree inferred under the multi-species coalescent model. Local posterior probability values at nodes do not measure support for bipartitions, but rather are a function of the frequencies of the shown quartet topologies among all gene trees.



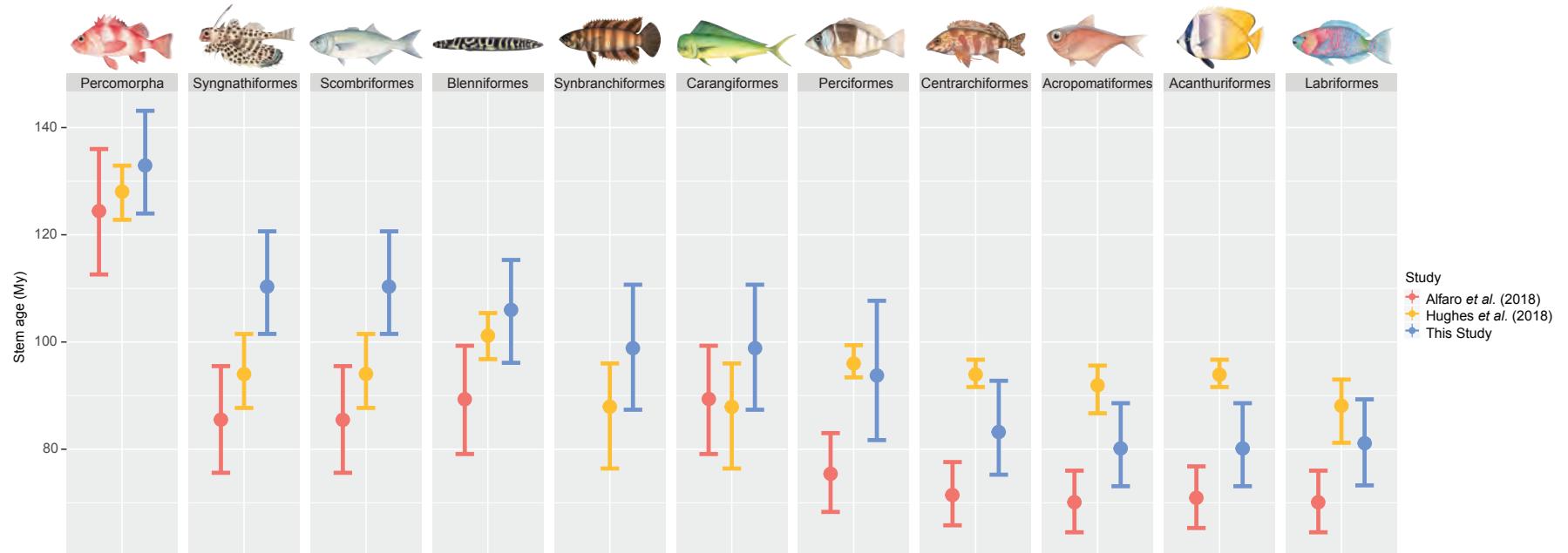
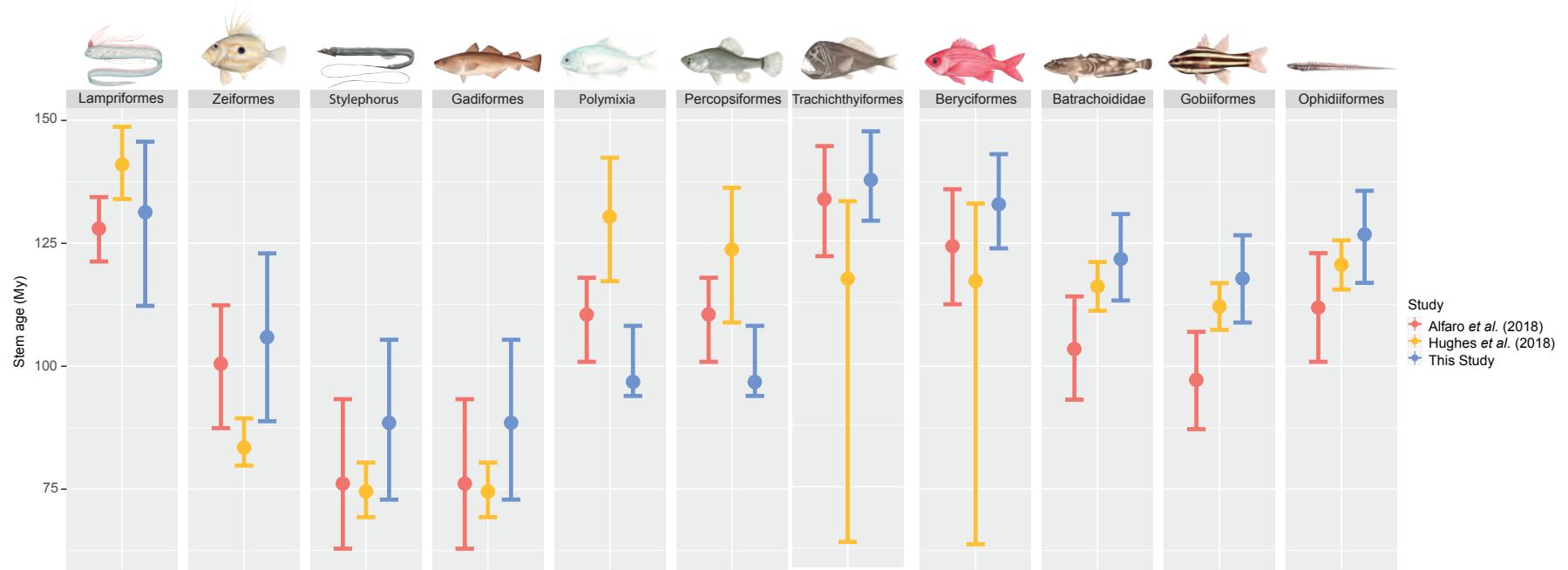
Supplementary Fig. 27: Phenograms depicting the evolutionary history of four phenotypic traits (body depth and width, and head depth and width) across seven major lineages that arose around the K-Pg.

The vertical dashed line marks the K-Pg boundary.



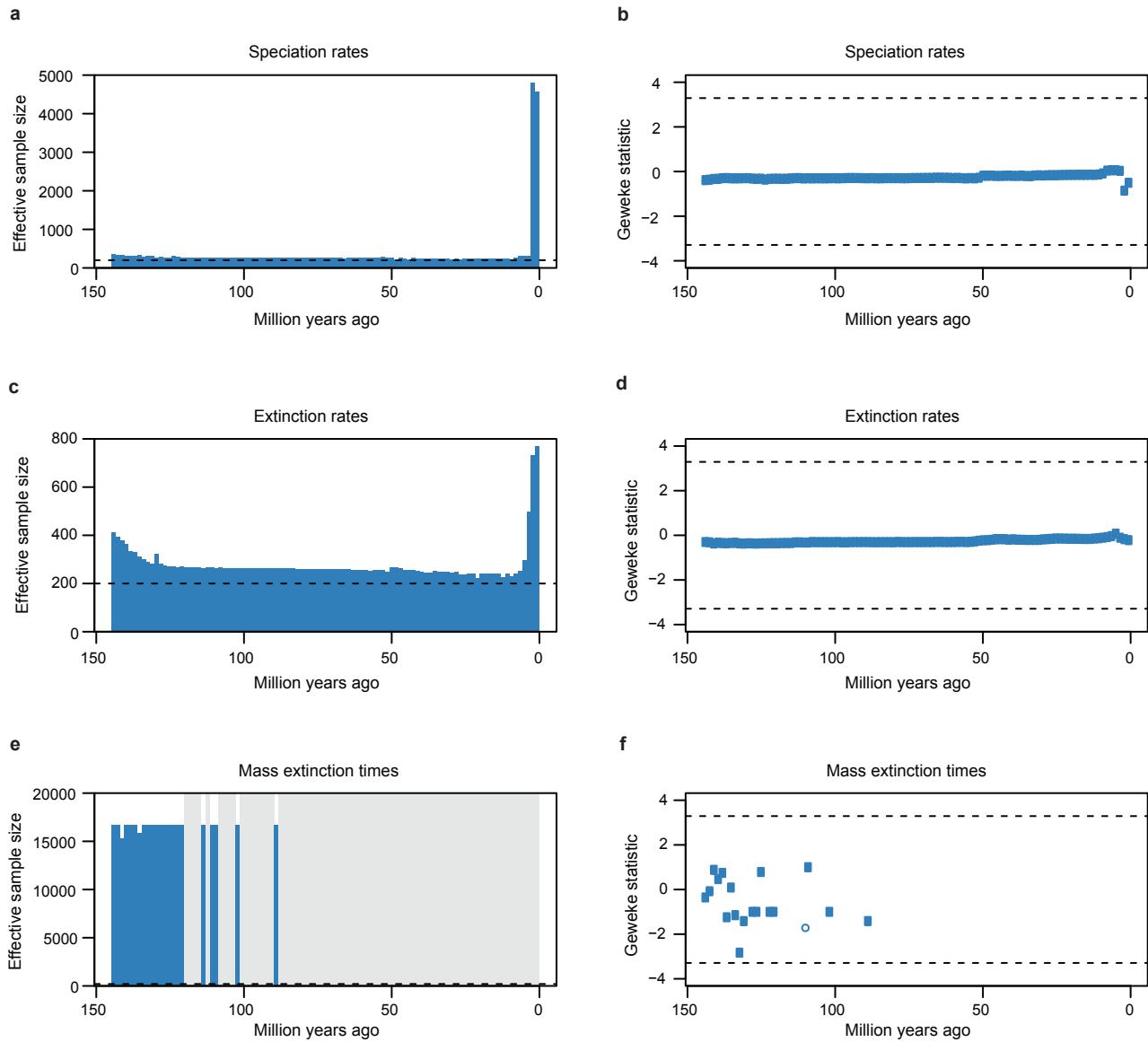
Supplementary Fig. 28: Disparity through time (DTT) for the combined morphological data, repeated on a sample of 100 trees from the posterior distribution of time-trees.

The gray line and blue shaded region indicate the median and 95% confidence interval (CI) expected under a Brownian motion model (BM) of evolution, respectively, and solid black line indicates observed pattern of disparity. This is the same plot visualized in Fig. 2, but note that the early portion of the DTT plot that includes the outgroup is not shown in Fig. 2. Acanthomorph body shapes radiated for approximately 20 million years in the aftermath of the K-Pg, followed by within-lineage phenotypic diversification. The blue histogram along the x-axis shows the proportion of time-calibrated trees for which observed disparity falls outside of the BM model's 95% CI in each one-million year interval. The inset, black box and whisker plot depicts the mean ($\pm 95\%$ CI) of the initial time point at which the observed disparity dropped below that expected from BM following the K-Pg.



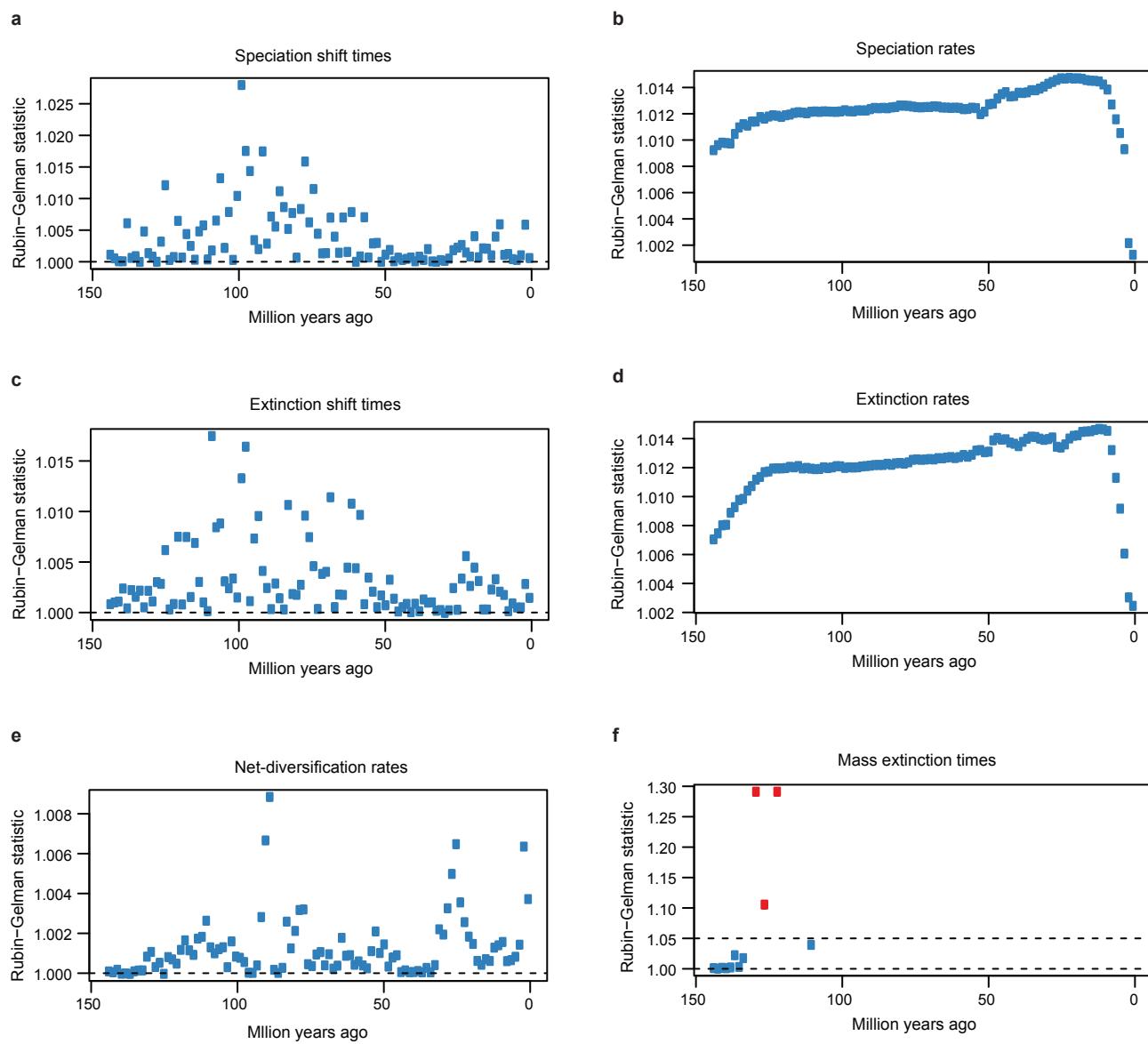
Supplementary Fig. 29: Median stem age estimates and 95% Highest Posterior Densities (HPD) for 22 major acanthomorph clades, as reported in the following 3 phylogenomic studies: Alfaro et al. (2018), Hughes et al. (2018) and this study.

Estimates for this study are the raw node heights reported in the 1,084-taxon time tree from Figs. 1 and 2. The 95% HPD of stem ages for most of the represented clades overlap with previous estimates, but we observe some major discrepancies, likely due to differences in tree topologies and taxon sampling.



Supplementary Fig. 30: Effective sample sizes (ESS) of parameters and Geweke diagnostics reflect within-chain convergence in the TESS-CoMET analysis depicted in Extended Data Fig.3.

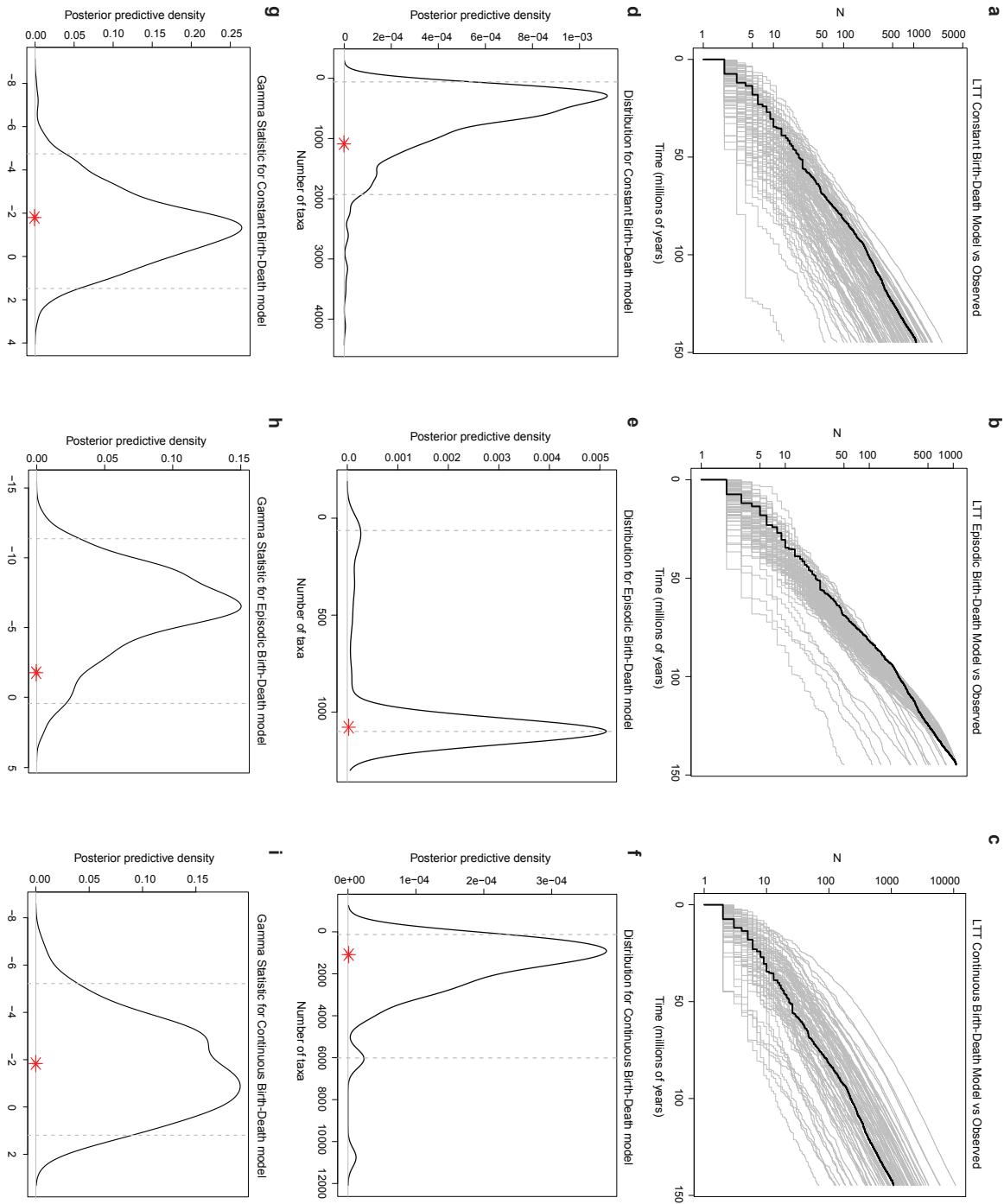
Blue bars and dots reflect that the run successfully converged for the parameter at a given time interval. Horizontal dashed lines reflect canonical, acceptable threshold values or 95% confidence intervals for the two diagnostics ($\text{ESS} \geq 200$ for a, c, and e; $P > 0.05$ for b, d, and f). a, Effective sample size for speciation rate estimates. b, Geweke statistic for post-burn-in speciation rate estimates. c, Effective sample size for extinction rate estimates. d, Geweke statistic for post-burn-in extinction rate estimates. e, Effective sample size for mass extinction times. f, Geweke statistic for post-burn-in mass extinction times.

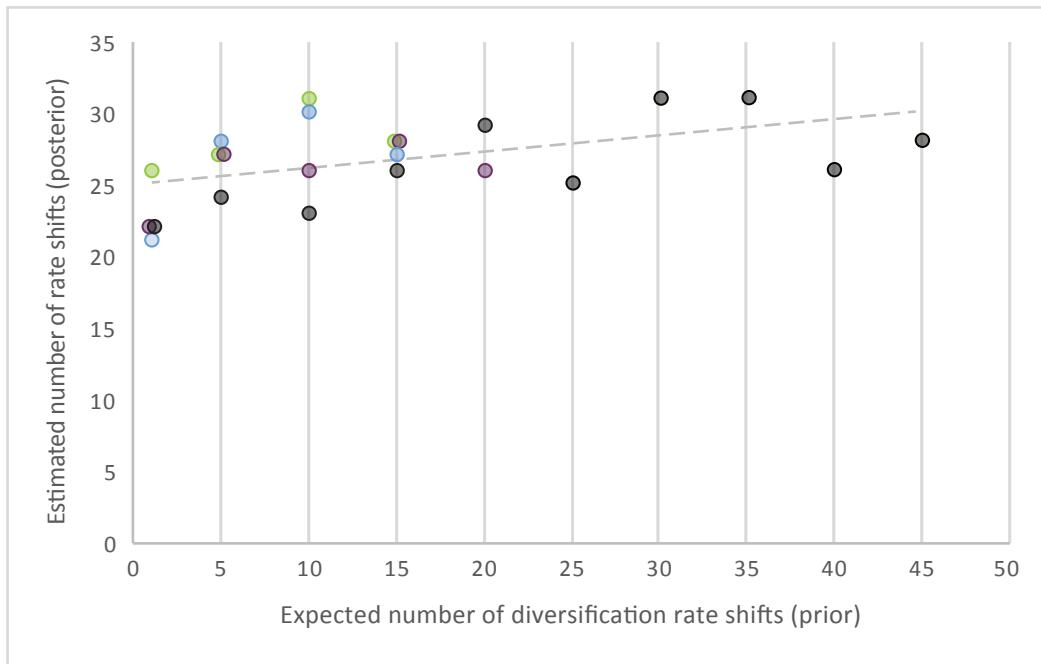


Supplementary Fig. 31: Results of the Gelman-Rubin test show convergence of three independent replicates of the TESS-CoMET analysis represented in Extended Data Fig.3. Blue dots indicate that the ratio of within-chain variance to between-chain variance is <1.05 , suggesting the independent MCMC simulations have converged on the same distribution of parameter values. Red dots indicate failed convergence of runs for those time interval-specific parameter estimates. Horizontal dashed lines represent the ideal value (1.00) for the diagnostic. a, Rubin-Gelman statistic for speciation shift times. b, Rubin-Gelman statistic for speciation rates. c, Rubin-Gelman statistic for extinction shift times. d, Rubin-Gelman statistic for extinction rates. e, Rubin-Gelman statistic for net-diversification rates. f, Rubin-Gelman statistic for mass extinction time estimates. A second horizontal dashed line marks the critical value (1.05) above which the test is considered to have failed for that estimate.

Supplementary Fig. 32: Assessment of the absolute fit of three candidate birth-death (BD) models to the time-calibrated phylogeny of Acanthomorpha.

Figures a-c compare lineage-through-time (LTT) curves for simulated trees under a given model (grey lines) to the LTT curve observed for the acanthomorph phylogeny (black line). Figures d-e plot the posterior-predictive distributions for the total number of species estimated to exist in the tree under each model. Dashed lines represent the 95% credible interval for the distribution and red asterisks indicate the total number of acanthomorph species (1,075) in the empirical data. Figures g-i plot the posterior-predictive distributions for the gamma statistic. Dashed lines represent the 95% credible interval for the distribution and red asterisks indicate the value of the gamma statistic empirically calculated for the acanthomorph phylogeny. Candidate models include: 1.) a constant rate birth-death model, 2.) an episodic birth-death model with a rate shift 50 Mya and 3.) a birth-death model with decreasing speciation rates through time. All three candidate models assume uniform (random) incomplete taxon sampling.





Supplementary Fig. 33: The posterior number of shifts in speciation rates inferred in BAMM is weakly predicted by the prior.

Our BAMM analyses used varying numbers of expected speciation rate shifts, and so the resulting maximum shift credibility (MSC) configurations displayed different numbers of estimated rate shifts, shown here as a scatterplot. The slope of the dashed, regression line (0.1049) suggests that changing the inputted prior parameter does not greatly affect the posterior prediction ($y = 0.1049x + 25.063$; $R^2 = 0.217$). The standard error of the prior coefficient is 0.0436 and of the intercept is 0.8393. Colors of data points correspond to the settings used when running Markov Chain Monte Carlo (MCMC) simulations in BAMM: black corresponds to 4 MCMC chains in the analysis with a ΔT of 0.05, purple corresponds to 4 MCMC chains in the analysis with a ΔT of 0.1, blue corresponds to 2 MCMC chains in the analysis with a ΔT of 0.05, and green corresponds to 2 MCMC chains in the analysis with a ΔT of 0.1.