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

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Abstract

Spiny-rayed fishes (Acanthomorpha) dominate modern marine habitats and comprise more than a quarter of all living vertebrate species[1-3]. It is believed that this dominance resulted from explosive lineage and phenotypic diversification coincident with the Cretaceous-Paleogene (K-Pg) mass-extinction event[4]. It remains unclear, however, if living acanthomorph diversity is the result of a punctuated burst or gradual accumulation of diversity following the K-Pg. We assess these hypotheses with a time-calibrated phylogeny inferred using ultraconserved elements from a sampling of species that represent over 91% of all acanthomorph families, as well as an extensive body shape dataset of extant species. Our results indicate that several million years after the end-Cretaceous, acanthomorphs underwent a prolonged and significant expansion of morphological disparity primarily driven by changes in body elongation, and that acanthomorph lineages containing the bulk of the living species diversity originated throughout the Cenozoic. These acanthomorph lineages radiated into distinct regions of morphospace and retained their iconic phenotypes, including a large group of laterally compressed reef fishes, fast-swimming open-ocean predators, bottom-dwelling flatfishes, seahorses, and pufferfishes. The evolutionary success of spiny-rayed fishes is the culmination of a post K-Pg adaptive radiation in which rates of lineage diversification were decoupled from periods of high phenotypic disparity.

Main

The Cretaceous-Paleogene (K-Pg) mass extinction fundamentally affected the evolutionary trajectory of terrestrial vertebrates, laying the foundation for spectacular radiations of eutherian mammals, neoavian birds, amphibians, and squamates[5-12]. In contrast, the impact of the K-Pg on marine vertebrate lineages is less clear. Most marine vertebrates are spiny-rayed fishes (Acanthomorpha), which collectively represent over a quarter of all living vertebrates[3]. It is hypothesized that the mass extinction of dominant Mesozoic plankton feeders following the K-Pg relieved acanthomorph fishes from previous predation and competitive pressures, enabling their occupation of vacated niches[13]. Paleogene fossils suggest a corresponding increase in acanthomorph taxonomic diversity and morphological disparity[14], and phylogenomic analyses have prompted the complementary proposal that the origins of many major acanthomorph lineages coincide with the K-Pg[4,15]. However, the acanthomorph fossil record is sparse in the 20 million years around the end-Cretaceous[16], and phylogenomic efforts to date have been limited by sampling designs that inadequately represents the group's staggering taxonomic richness[4,15]. These factors have hindered the resolution of the timing and patterns of acanthomorph diversification near the K-Pg; it remains uncertain if acanthomorph diversification in the Cenozoic was gradual or punctuated, and whether there is a coupling of phenotypic and lineage diversification that is considered a hallmark of adaptive radiation[17]. A well-resolved, time-calibrated, phylogeny that includes all major lineages is critical to understanding the evolutionary dynamics of spiny-rayed fishes in the wake of the K-Pg.

The largest challenge to acanthomorph evolutionary studies is inferring a phylogeny of its more than 19,450 species[3]. The resolution of relationships within the subclade Percomorpha, which contains more than 95% of all acanthomorph species, has been particularly difficult. During most of the twentieth century, inferences of acanthomorph and percomorph relationships relied on anatomical characters that resulted in largely unresolved phylogenetic hypotheses[18]. 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 pufferfishes[19]. 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 mullets[22]. 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 species[24] to explore the patterns of body shape diversification in spiny-rayed fishes across the K-Pg boundary.

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

In addition to yielding confident phylogenetic resolution among major lineages and taxonomic families, the maximum likelihood UCE phylogeny reveals novel relationships among some of the most scientifically interesting lineages of percomorph fishes (Figs. 1, 2, Supplementary Figs. 1-25). For example, Sanger sequencing studies led to the discovery that the enigmatic coral reef-dwelling engineer gobies (*Pholidichthys*) are the sister lineage of freshwater cichlids (Fig. 1, Supplementary Fig. 11)[1,21,22]. Whereas these Sanger analyses provided weak resolution beyond the monophyly of these two lineages, our UCE phylogeny resolves the freshwater tropical African and South American leaffishes (Polycentridae) as the sister lineage of the *Pholidichthys*-cichlid clade (BSS = 100%), providing an opportunity for insight into the evolution of the remarkable species richness and key morphological novelties found in cichlid fishes. We also confidently resolve the near-shore rocky reef dwelling False Scorpionfish (*Centrogenys vaigiensis*) as the sister lineage to a clade of more than 630 species of wrasses and parrotfishes (Labridae; BSS = 100%) (Fig. 2, Supplementary Fig. 21). This newly discovered relationship is not corroborated by the species tree analysis, but consistent with this discovery is that wrasses and *Centrogenys vaigiensis* share ancestral, highly modified components of the "labroid" pharyngeal jaw apparatus[22]. This result thereby reduces the number of independent evolutions of pharyngognathy, an advanced feeding mechanism that promotes trophic diversification by freeing the oral jaws from prey-processing functions[22]. The maximum likelihood phylogeny inferred from our UCE dataset provides an important framework for further exploration of the relationships among the most closely related lineages of acanthomorph and percomorph fishes.

Divergence time estimates for Acanthomorpha, inferred from relaxed molecular clock analyses calibrated with 43 well-justified fossil calibrations, allow for unprecedented resolution of the timing and tempo of family-level lineage diversification. The mean Bayesian posterior age estimates for stem lineages for 80% of living acanthomorph families post-date the K-Pg and are primarily distributed across the Paleocene through the early Miocene (~65 – 15 Mya) (Extended Data Fig. 2). This pattern contrasts with earlier hypotheses of an explosive origin of acanthomorph familial diversity following the K-Pg mass extinction[4,16]. Plotting the accumulation of acanthomorph family origination times reveals an extended period of lineage origination that persists for approximately 40 million years after the K-Pg (Fig. 2). Although most of the taxonomic families assigned to living acanthomorphs originated in the Paleogene, we detect no statistically supported mass extinctions or tree-wide shifts in lineage diversification rates, indicating an indiscernible effect of the K-Pg on acanthomorph lineage diversification (Extended Data Fig. 3). Moreover, stepping-stone simulations, used to evaluate the relative and absolute fit of competing diversification models to the observed time-calibrated phylogeny, strongly support a constant-rate birth-death model (Extended Data Table 1). Bayesian estimates of the evolutionary rates of individual acanthomorph lineages are similarly homogenous across the K-Pg and through the Cenozoic (Extended Data Fig. 4). We observe increases in speciation rates in only a few percomorph clades, such as branches in the phylogeny leading to Apogonidae (cardinalfishes), Pseudocrenilabrinae (most Middle Eastern and African cichlids), Chaetodontidae (butterflyfishes), the species-rich *Sebastes* (rockfishes), and Lycodinae (a lineage of eelpouts).

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

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

Our estimate of the timing of acanthomorph body shape diversification at the onset of the Paleogene refines inferences from the fossil record. Acanthomorph taxonomic diversity and morphological disparity was low in the Late Cretaceous prior to the K-Pg event, after which body shape disparity and taxonomic diversity became greatly elevated[14,16]. The timing of this diversification remained unclear due to a scarcity of deposits yielding abundant and well-preserved teleost skeletons between the Campanian-Maastricthian (~72 Mya) in the Late Cretaceous to the Paleocene-Eocene boundary (~56 Mya)[14,16]. Though isolated acanthomorph otoliths are known throughout this interval, they remain little studied relative to those from Eocene and younger deposits[26]. Our analyses provide the precision lacking in the fossil record, revealing that the disparity observed in early Cenozoic fossil acanthomorphs was likely the product of an extended period of phenotypic diversification that began approximately 60 Mya and lasted approximately 15-20 Myr. The initiation of a steady accumulation of living acanthomorph families and morphological disparity following the K-Pg extends through much of the acanthomorph fossil gap (Fig. 2), demonstrating that the rise of acanthomorph diversity in the early Eocene was not punctuated[16].

The prolonged expansion of morphological variation following the K-Pg was dominated by divergences in body elongation between clades (Extended Data Fig. 5a, Extended Data Fig. 6b,c), a phenotypic trait that has adaptive consequences. Body elongation is a primary axis of body shape variation in freshwater and marine fishes[24,27] that is often coupled with habitat transitions between pelagic, demersal and fully benthic habitats[28], including in the aftermath of the K-Pg extinction[23]. Our observations of diversification in body elongation shortly after the K-Pg is therefore likely correlated with niche divergence along the benthic-pelagic axis. This pattern of morphological diversification is consistent with the classic trend in phenotypic evolution during adaptive radiation[17], although it was not accompanied by changes in lineage diversification rate. Nonetheless, our results imply that conditions in the aftermath of the global K-Pg event promoted exceptional morphological diversification perhaps in response to the novel landscape of ecological opportunity that took shape during the Paleogene[13].

Our results provide a new perspective to the role of the K-Pg as a catalyst of vertebrate diversification by demonstrating that its effects on acanthomorph lineage diversification rates and disparity were decoupled. Although there is no indication that acanthomorph lineage diversification rates increased near the K-Pg, much less explosively (Extended Data Fig. 3), the time following the K-Pg undoubtedly played a critical role in increasing taxonomic diversity and shaping the ecomorphological disparity of the vast majority of living spiny-rayed fishes (Fig. 2 and Extended Data Fig. 2). The approximately 15-20 Myr period following the K-Pg brought about the origin of ecomorphological types that acted as a reservoir of diversity, setting the stage for more recent, phylogenetically or geographically localized radiations, including endothermic open-ocean tunas, Antarctic notothenioids, parrotfishes on modern coral reefs, and African Rift Lake cichlids[29-32]. Though the decoupling of lineage and phenotypic diversification in Acanthomorpha contradicts commonly invoked expectations of adaptive radiation[17], this pattern is evident in the evolutionary dynamics of other vertebrate adaptive radiations following the K-Pg, including birds and placental mammals[5,8,33,34]. Our findings illuminate the origin of phenotypic diversity that characterizes the dominance of acanthomorph fishes in modern marine habitats and broadens our understanding of adaptive radiation in species-rich vertebrate lineages following the K-Pg mass extinction event.

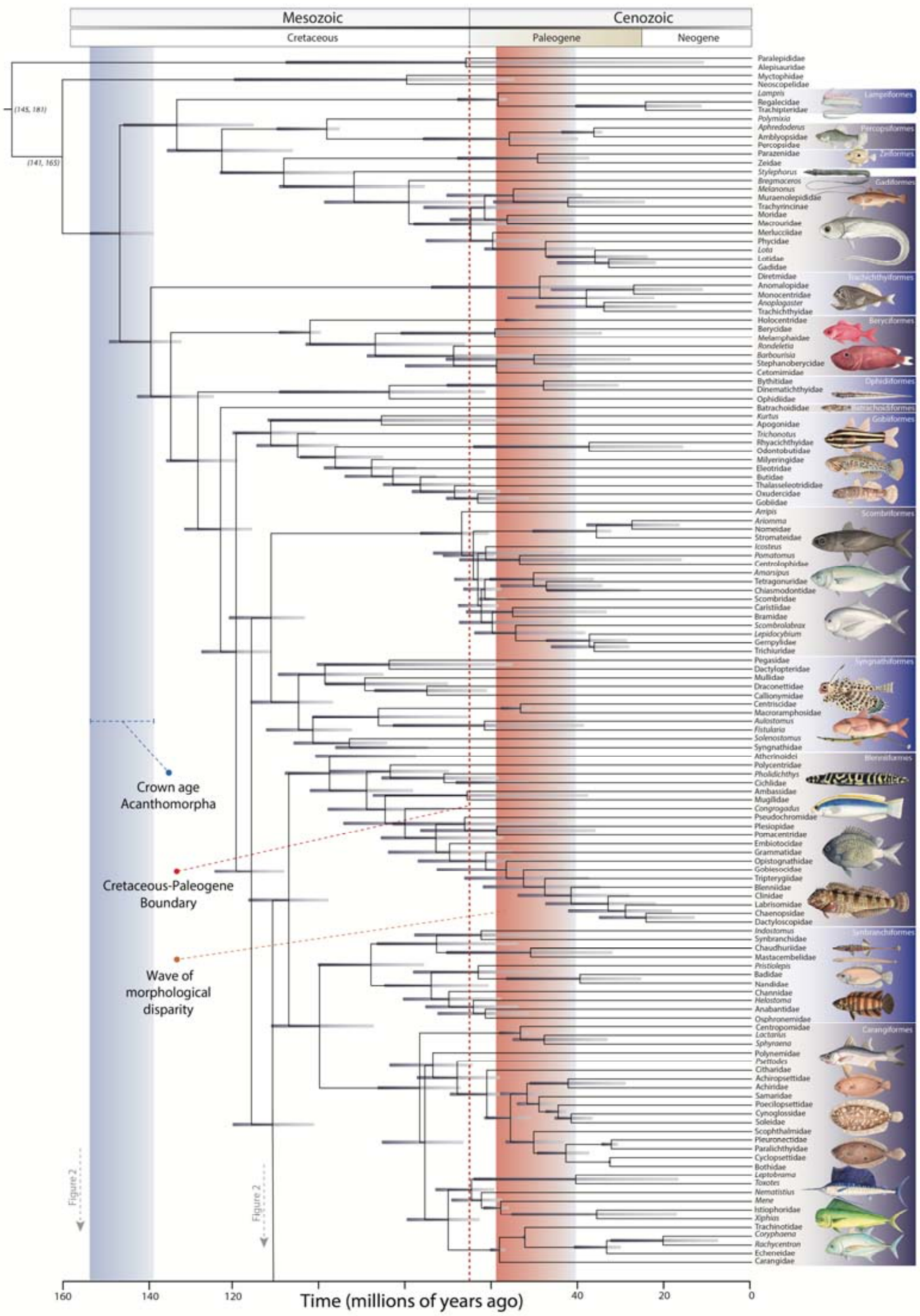

Fig. 1: Time-calibrated phylogeny of Acanthomorpha.

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

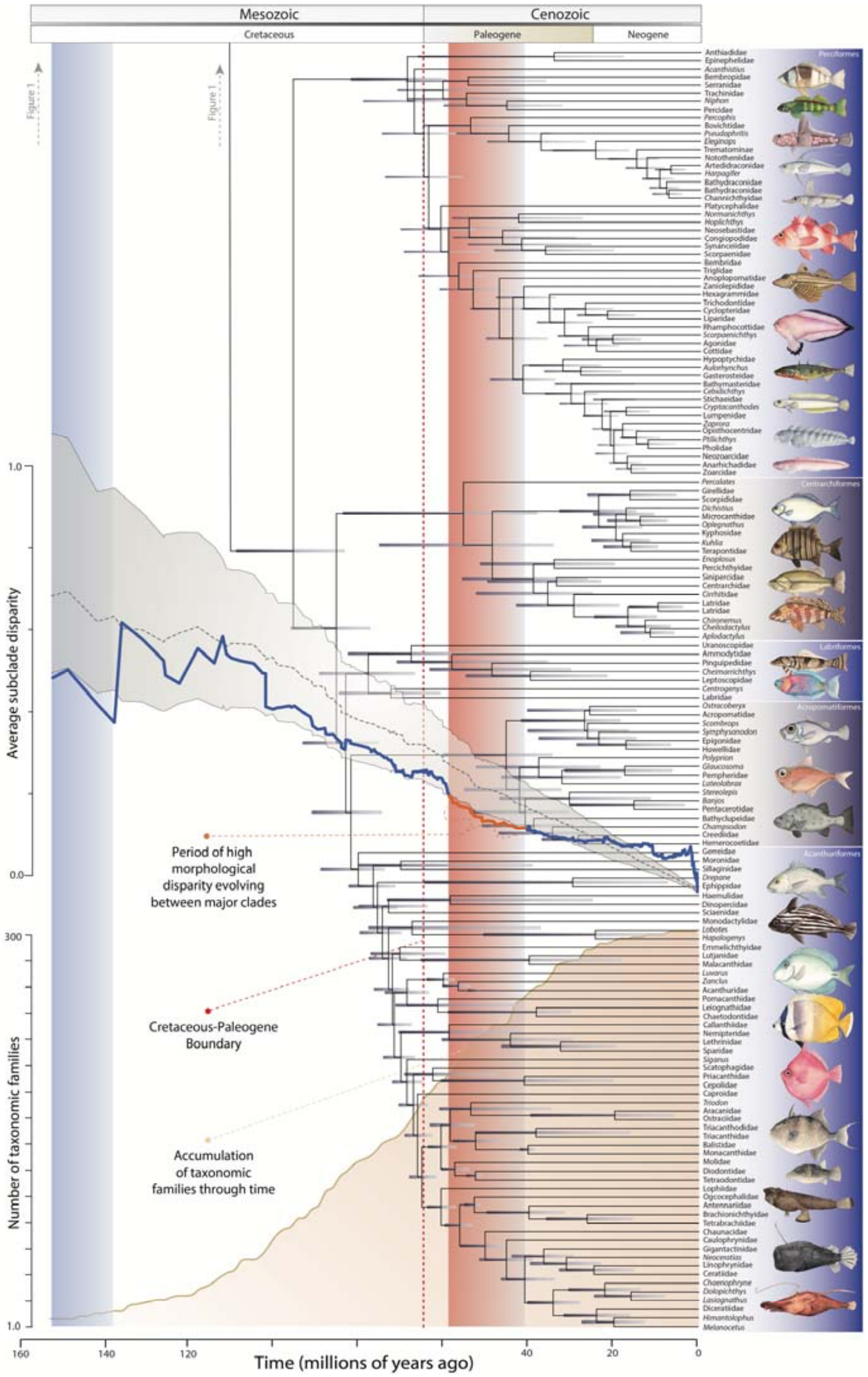

Fig. 2: Time-calibrated phylogeny and disparity and lineage accumulation through time for Acanthomorpha.

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

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Methods

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

Taxon sampling and procurement of sequence data

This study incorporates ultraconserved element (UCE) sequence data from 1,109 specimens, including nine outgroup taxa and 1,075 acanthomorph species spanning 308 recognized, taxonomic families in Acanthomorpha (Supplementary Table 1). We generated new sequence data from 647 specimens representing 628 species of acanthomorphs and six outgroups. We extracted DNA from muscle or fin tissue following the standard protocol for Qiagen's DNeasy Blood and Tissue kits. We prepared dual-indexed DNA libraries and targeted the 1,314 UCE loci enriched by the myBaits UCE Acanthomorph kit from Arbor Biosciences[4]. Enriched libraries were sequenced on Illumina HiSeq platforms in 2 × 150 bp paired-end runs. UCE data for 360 specimens came from five previous phylogenomic studies (Supplementary Table 1), and UCE sequences for 96 species were extracted from whole genome shotgun sequence data published in the NCBI GenBank[35,36]

Data processing and phylogenetic analyses

We used the PHYLUCE[35,36] computer package to process raw read data, conduct de novo assembly and construct alignments of UCE loci. We generated two separate alignments of UCE loci present in at least 75% of the samples: one consisting of all 1,109 specimens (1,084 species) and another including only a subset of the 702 species that overlapped with the taxon sampling of a previously published morphological dataset. The 1,084- and 702-taxon alignments consisted of 987 loci (383,250 bp) and 989 loci (499,957 bp), respectively.

Using these two 75% complete data matrices, we conducted multiple phylogenetic analyses using maximum likelihood methods in IQ-TREE v. 1.7[37] and RAxML-ng v. 0.9.0[38]. We topologically constrained the divergence time analyses represented in Figure 1 with phylogenies inferred in IQ-TREE using single-partition alignments of the 702 taxa and 1,084 taxa datasets. Both of these tree searches assumed the GTR+Gamma model of molecular evolution and used ultrafast bootstrap approximation to generate 1,000 bootstrap replicates and 1,000 replicates of the Shimodaira-Hasegawa approximate likelihood ratio test (SH-aLRT). We used the program TOPD_v4.6[39] to ensure the phylogenies inferred using different partitioning schemes and maximum likelihood programs presented similar tree topologies.

We also used IQ-TREE's ModelFinder Plus and ultrafast bootstrap approximation options to infer maximum likelihood gene trees for each UCE locus. In TreeShrink[40], we used a false positive tolerance rate parameter (alpha) of 0.05 to identify and remove potentially aberrant sequences from the single-gene alignments. We re-aligned filtered alignments using MAFFTv7.130b[41] and used them to repeat inference of gene trees in IQ-TREE. We employed the resulting gene trees to generate a summary species tree in ASTRAL-III v5.6.3[42].

We applied Bayesian methods to understand the degree of topological discordance along the backbone of the Acanthomorph tree. We inferred gene trees for UCE loci with Bayesian methods for an 82-taxon alignment that represented the major acanthomorph subclades and was generated using MAFFT. We ran these tree searches in MrBayes v. 3.2.7[43] for 2 million generations, assuming a GTR+Gamma model of molecular evolution. Using an alpha value of 1.0, we estimated genome-wide concordance factors in BUCKy[44] as a measure of the amount of topological discordance between these Bayesian gene trees.

Divergence time estimation

We estimate divergence times for the 702- and 1,084-taxa phylogenies in BEAST v.2.5[45-47] using reduced datasets of randomly subsampled UCE loci[29,48]. For both phylogenies, we repeated dating analyses on three different alignments of 30 loci. For each of these alignments, we accounted for site-specific variation in evolutionary patterns by selecting the best-fit partitioning schemes using PartitionFinder2 v. 2.1.1[49]. We performed at least three replicate analyses for each 30-locus dataset. We ran all BEAST analyses under a relaxed lognormal clock model and a birth-death tree model, using the IQ-TREE phylogenies inferred from the single-partition, 702-taxa and 1,084-taxa alignments as topological constraints. We used forty-three fossil constraints (detailed in the Supplementary Information) to assign minimum age priors and ran BEAST analyses for a minimum of 200 million generations after discarding a burnin of 200 million iterations. We used Tracer v.1.7.1[50] to assess convergence of parameters across replicate MCMC chains and ensure there were no directional trends in parameter estimates. For each set of random loci, we combined replicate analyses in LogCombiner and constructed maximum clade credibility (MCC) trees using TreeAnnotator in BEAST v1.8.4[51], with summarized node heights rescaled to reflect the posterior median heights. MCC trees for the 702-taxon datasets were summarized from 10,000 post-burnin, randomly sampled trees, while MCC trees for the 1,084-taxon datasets were summarized from 1,200 such trees.

Diversification rate analyses

We removed all outgroup and duplicate taxa from the 1,084 taxa maximum clade credibility tree displaying the highest effective sample size (ESS) and used this pruned tree for all diversification rate analyses. We used TESS[52] to conduct stepping-stone simulations that estimated the marginal likelihoods of eight birth-death models, allowing us to calculate Bayes Factors and assess the competing models' relative and absolute fits to the time-calibrated phylogeny of Acanthomorpha. We examined tree-wide speciation, extinction, and net-diversification rates using TESS's CoMET model. For this analysis, we accounted for our incomplete sampling, specified a uniform sampling strategy, and ran three replicate reversible-jump MCMC chains until ESS values were ≥200. CoMET runs were checked for within- and between-analysis convergence of the diversification rate parameters as described in the Supplementary Information. Using the same time-calibrated phylogeny, we also inferred rate heterogeneity across lineages using BAMM v.2.5.0[53]. BAMM analyses accounted for the incomplete taxon sampling of taxonomic families and other major representative clades and used empirically determined rate priors identified by the R package BAMMtools v.2.1.6[54]. We ran 23 MCMC chains with different combinations of parameters in BAMM, each for 100 million generations, and we identified the rate shifts along specific branches that were predicted by at least sixteen of these analyses.

Phylogenetic comparative methods

We pruned a body trait dataset of teleost fishes[24] to include maximum body depth, maximum fish width, head depth, lower-jaw length, mouth width, minimum caudal-peduncle depth, and minimum caudal-peduncle width for the 680 species that matched the species represented in the 702-taxon UCE phylogeny. To correct for body size, we regressed log-transformed trait values against log-transformed standard fish lengths and calculated phylogenetic residuals in PHYTOOLS[55]. We assessed disparity through time using GEIGER[56] and the time-calibrated IQ-TREE phylogeny. We repeated disparity through time analyses on 100 randomly sampled time trees from the posterior distribution generated in BEAST, and summarized the mean and 95% confidence interval for the 1.0 My time interval after the K-Pg during which average subclade disparity first dropped below the value simulated under Brownian evolution, as well as the proportion of trees through time that strayed from the Brownian prediction. We tested the sensitivity of disparity through time analyses to the exclusion of body shape traits and of major clades that arose immediately around the K-Pg boundary. Finally, we used PHYTOOLS to visualize body shape morphospace using principal component analysis (PCA) and to generate phenograms that visualize the evolutionary histories of the following seven major lineages: Carangiformes, Lophioidei, Perciformes, Scombriformes, “Squamipinnes” (the clade in Supplemental Fig. 23 defined by *Chaetodon kleinii* and *Luvarus imperialis*), Syngnathiformes and Tetraodontoidei.

Code availability

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

Data availability

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

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Author contributions

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

Ethics declarations

Competing interests

The authors declare no competing interests.

Additional information

Supplementary Information is available for this paper.

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Extended data table and figure legends

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

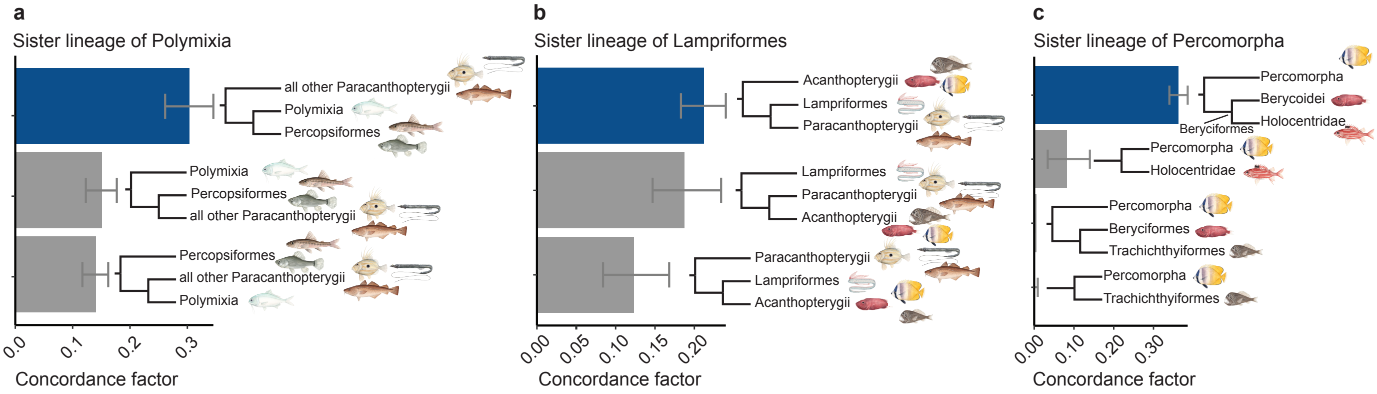
Extended Data Table 1: Pairwise comparisons of 8 birth-death (BD) branching process models.

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.)

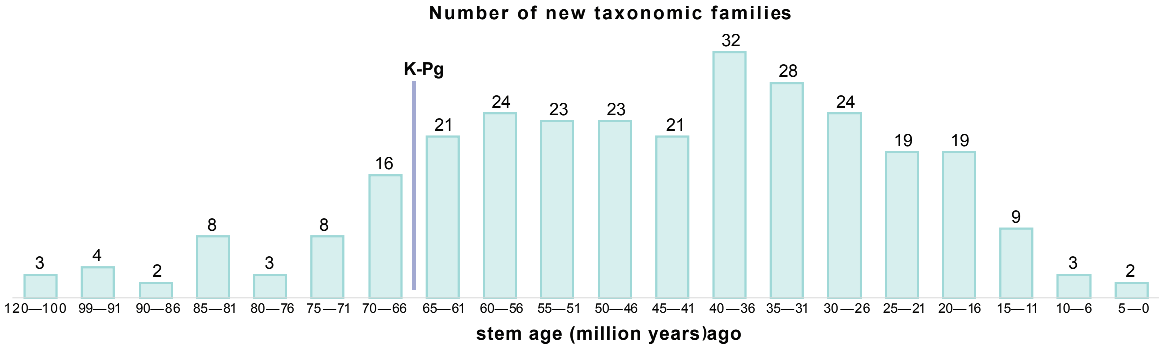
decreasing speciation rate with diversified sampling, 5.) constant diversification rate with a rate shift 50 Mya ("Episodic BD") with uniform sampling, 6.) constant diversification rate with a rate shift 50 Mya ("Episodic BD") with diversified sampling, 7.) constant speciation rate with a single mass 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 (2ln(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.



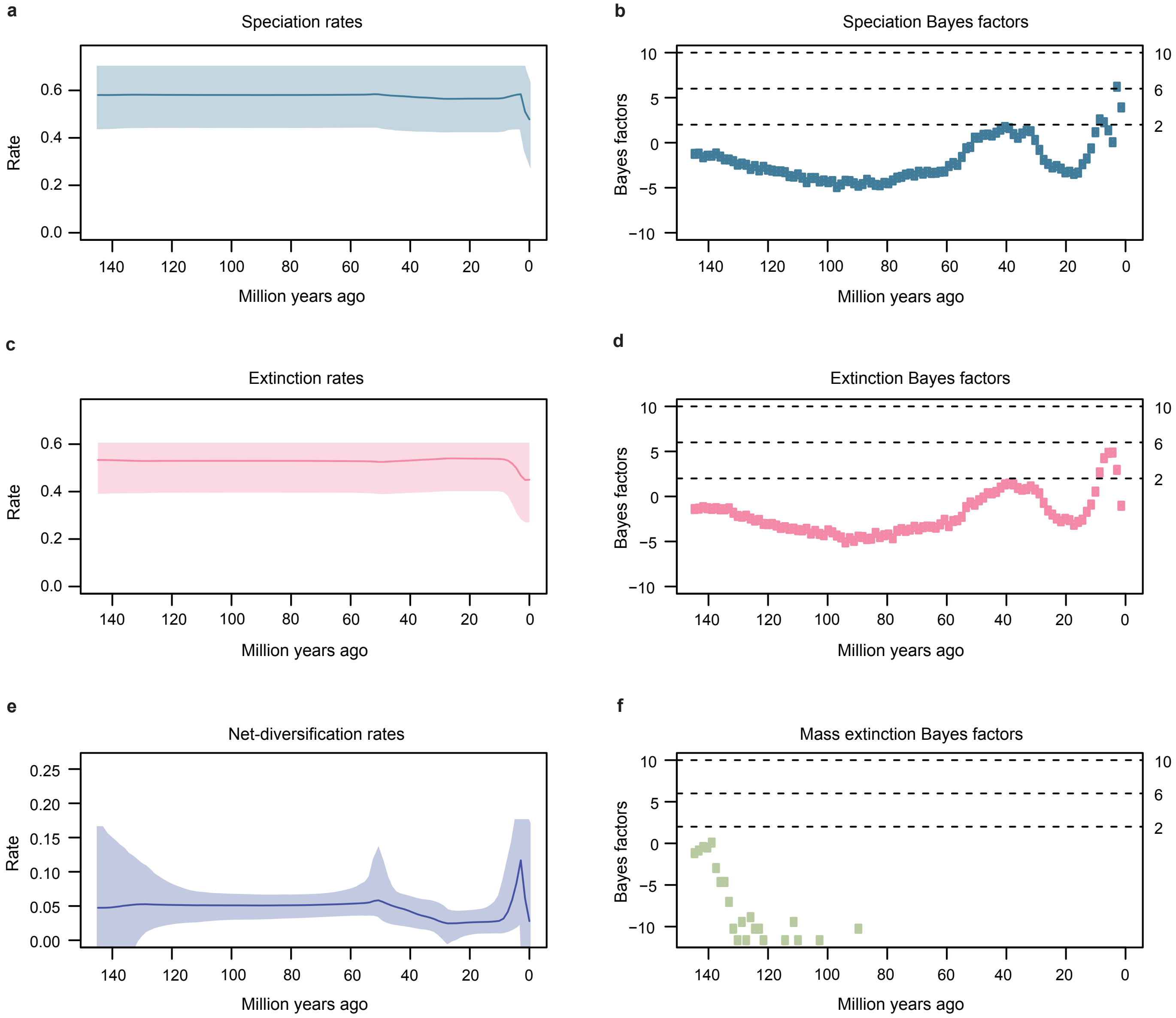
BUCKy-inferred genome-wide concordance factor estimates, with 95% confidence intervals, representing the proportion of gene trees exhibiting alternative topologies among major acanthomorph lineages. Blue bars reflect the concordance factor for the topology inferred in our concatenated analyses (see Figs. 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.



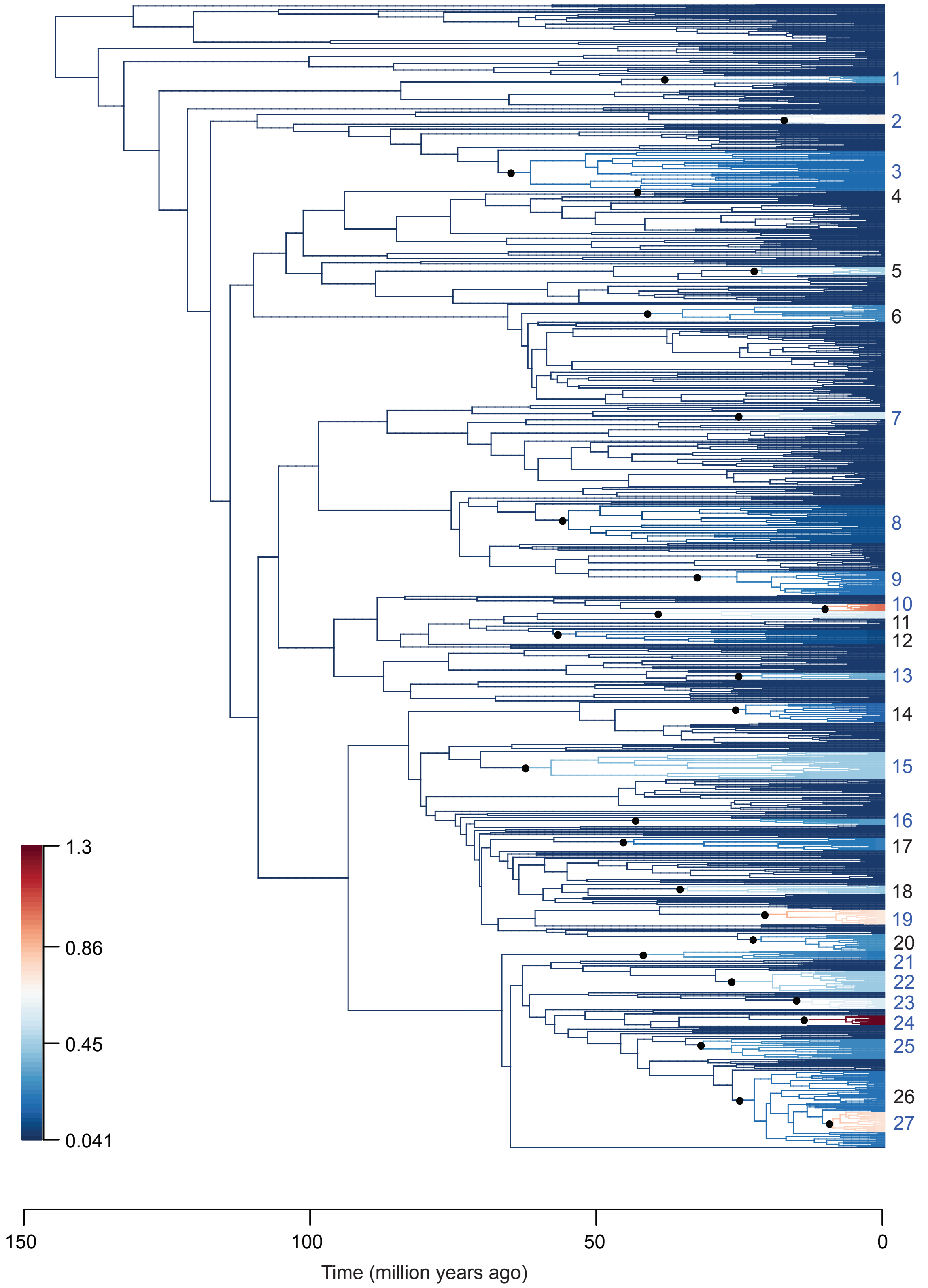
The bar plot of the estimated number of new taxonomic families originating during 5 million year bins. Note that the amounts of time represented by the first two bars are greater than the 5 million years represented by all other bars.

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



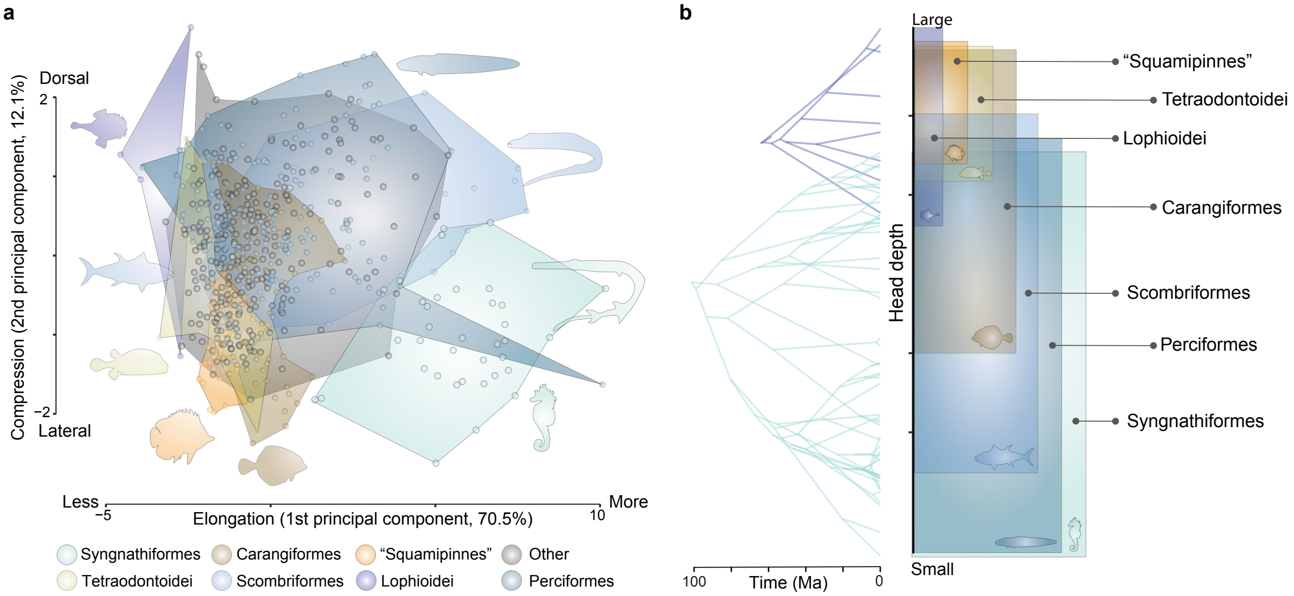
In **b, d,** and **e,** horizontal dashed lines and the right-hand y-axis mark statistical support cutoffs for rate shifts, with $2 \leq \text{BF} < 6$ considered to be low support, $6 \leq \text{BF} < 10$ considered to be moderate support and ≥ 10 considered to be high support. The rate shifts observed 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.



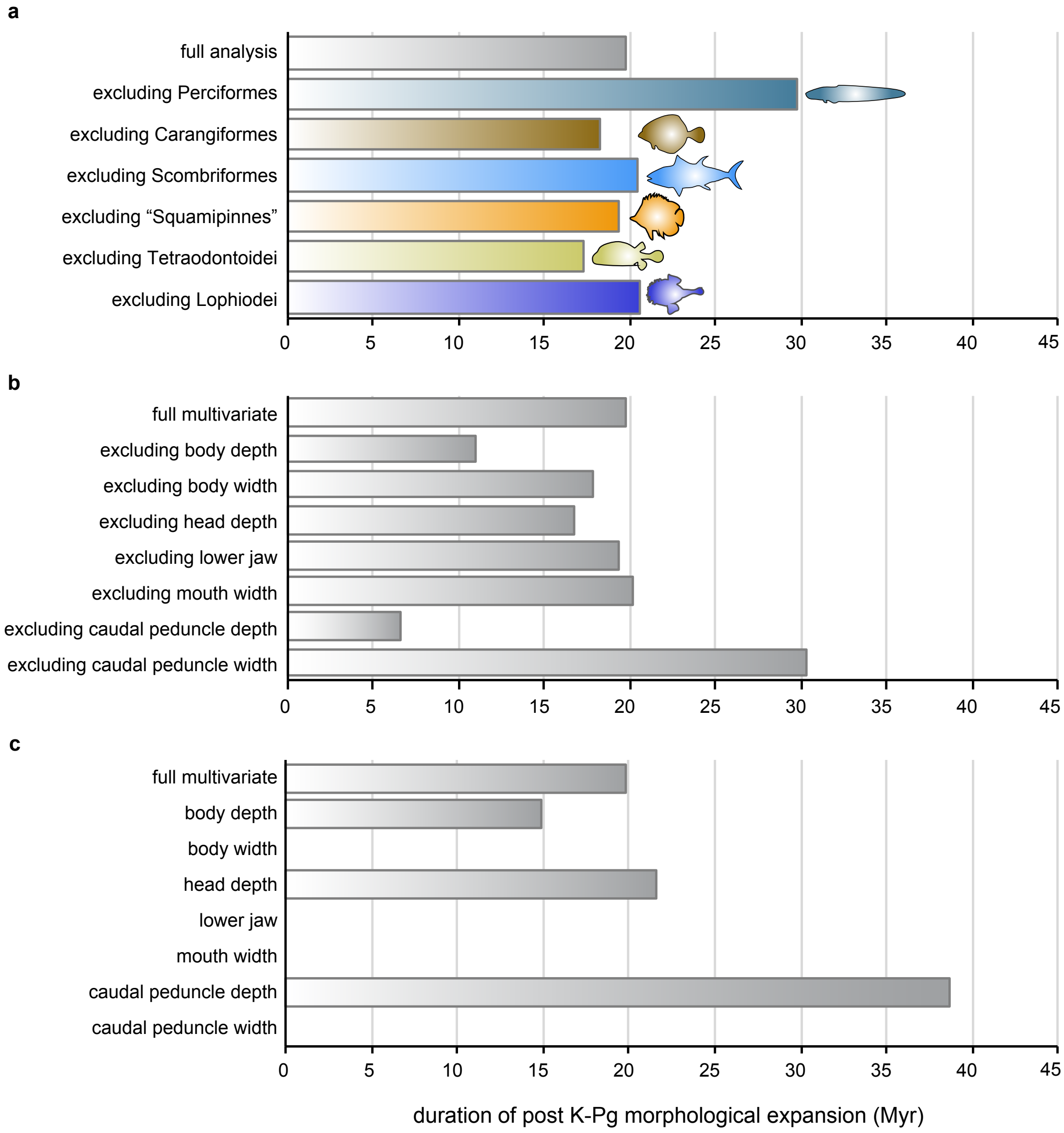
The configuration presented here is the maximum shift credibility (MSC) configuration for an analysis that expected 15 rate shifts under the prior. Darker pink colors depict relatively fast rates, while darker green colors depict relatively slow rates. Rate shifts along branches are denoted with filled, 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 Mulllidae), 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. Supplementary Methods

a. Taxon sampling

The phylogenetic analyses included UCE sequence data sampled from 1,109 specimens that include 1,084 species. For this study, we collected new UCE sequence data from 653 specimens. We retrieved UCE loci from the remaining 456 specimens at NCBI from previous studies of acanthomorph phylogeny[4,29,48,57,58] or from whole genomic data (Supplementary Table 1). This study included representatives of all currently recognized acanthomorph taxonomic orders, 307 of the 331 (92.7%) described taxonomic families of Acanthomorpha and 276 of the 290 (95.2%) families of Percomorpha[3]. Based on previous phylogenetic analyses[15,20], we sampled two species of Aulopiformes and seven species of Myctophiformes as outgroups for the phylogenetic analyses: *Notolepis coatsi*, *Alepisauraus ferox*, *Scopelengys tristis*, *Neoscopelus macrolepidotus*, *Neoscopelus microchir*, *Dasyscopelus selenops*, *Benthosema glaciale*, *Notoscopelus caudispinosus*, and *Ceratoscopelus warmingii*. We sampled phenotypic data from 680 of the 1,075-acanthomorph species sampled in the UCE inferred phylogeny. We inferred phylogenies from the UCE dataset for an inclusive taxon sampling of 1,084 species and for a set of 702 species that included the 680 for which corresponding morphological data was obtained. We refer to these UCE datasets and resulting phylogenies as the 1,084 and 702 species datasets and trees, respectively.

b. Library preparation, target enrichment, and sequencing

We isolated DNA from tissue biopsies using Qiagen DNeasy Blood and Tissue kits following the manufacturer's protocol. We used a Qubit fluorometer (Life Technologies) to quantify 1-2 uL of all DNA extractions. We sheared approximately 500 ng of genomic DNA from each sampled specimen using a QSonica Q800R3 sonicator to obtain fragment sizes between 300-600 bp. For library preparation and target enrichment of UCE loci, we followed protocols described in a previous study[4] using Kapa HyperPrep kits (Kapa Biosystems) and Illumina TruSeq iTru5 and iTru7 adapters for dual indexing of genomic libraries[59]. We used a bait set from Arbor Biosciences designed to target 1,314 UCE loci in acanthomorph fishes for target-enrichment of UCE loci[4]. Enriched libraries were sequenced using 150 bp paired-end sequencing on Illumina HiSeq platforms.

c. Assembly and alignment construction

To process raw read data, construct assemblies, identify UCE sequences, and construct alignments for each UCE locus, we used the PHYLUCE computer package[35,36], which uses parallel wrapper functions around external programs to perform tasks required to process high-throughput DNA sequence data. We used the illumiprocessor parallel wrapper program (https://github.com/faircloth-lab/illumiprocessor) to implement Trimmomatic[60], which removes adapter index sequences and low-quality bases from demultiplexed raw reads. We constructed assemblies for each sample using *trinity* v.r2013-02-25[61] and used the PHYLUCE program phyluce_assembly_match_contigs_to_loci.py to identify which assembled contigs represented UCE sequences by matching them to a FASTA file containing the UCE bait sequences.

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

We integrated these two data sets and used PHYLUCE programs to infer a separate set of alignments and phylogenies for the 702 species including the sampling of morphological data and the full 1,109 specimen sampling using the same protocols. We generated alignments for each UCE locus using MAFFT v7.130b[41] and trimmed with trimAL v1.4.rev[62]. For further downstream phylogenetic analyses, we retained UCE loci that included at least 75% of the total specimens in both the 1,084 and 702 species datasets.

d. Phylogenetic analyses

We inferred phylogenies for both the 1,084 and 702 species datasets using maximum likelihood methods as implemented in IQ-TREE v. 1.7[37] and RAxML-ng 0.9.0[38]. In IQ-TREE, we ran tree searches using ultrafast bootstrap approximation until 1,000 bootstrap replicates and 1,000 replicates of the Shimodaira-Hasegawa approximate likelihood ratio test (SH-aLRT) were generated[63]. Phylogenies inferred in IQ-TREE using the unpartitioned alignments described above served as the topological constraints for subsequent divergence time analyses. Maximum likelihood tree searches conducted in IQ-TREE used the ModelFinderPlus[64] option, which applies a relaxed hierarchical clustering search algorithm to determine partitioning schemes and models of molecular evolution.

Before conducting analyses in RAxML-ng v0.9.0[38] , we determined partitioning schemes using PartitionFinder2 v2.1.1[49], with units of partitioning based on individual UCE loci. We identified these partitioning schemes using a relaxed hierarchical clustering search algorithm with a maximum cluster size set to 1000 data blocks, the Bayesian Information Criterion method for partition model comparison, and GTR+Gamma as the model of molecular evolution. We removed all fully undetermined columns from our partitioned, concatenated alignment using RAxML-ng, compressed the alignment, and converted to binary. We performed maximum likelihood tree searches on these alignments using the extended majority rule criterion method implemented with the autoMRE command to continue bootstrapping until convergence.

We compared the tree topologies inferred in the concatenated analyses described above using the program TOPD_v4.6[39]. Phylogenies based on the 1,084 species dataset (IQ-TREE single-partition, IQ-TREE multiple partitions, and RAxML-ng multiple partitions) were compared to one another, and separate analyses compared the three phylogenies inferred from the 702 species dataset. We utilized TOPD to calculate partition metrics, i.e., TOPD's "Split" method[65], and path length metrics, i.e., TOPD's "Nodal" method[66]. We produced lists of taxa with different phylogenetic positions among the compared trees using TOPD's "Disagree" method, which removes a single taxon at each iteration and calculates the reduction in trees' split distance.

We inferred a summary species tree in ASTRAL-III v5.6.3[42], using maximum likelihood gene trees for each UCE locus generated with IQ-TREE v 1.6.12. For individual gene tree inference, we applied the ModelFinder Plus[64] option to determine the optimal model of molecular evolution as well as the ultrafast bootstrap approximation with a maximum of 10,000 bootstrap iterations. We used TreeShrink[40] to identify abnormally long branch lengths in the individual UCE gene trees and to minimize the impact of misspecified sequences. We used a false positive tolerance rate parameter (alpha) of 0.05 in our TreeShrink filtering to automate the removal of potentially aberrant sequences from the UCE alignment. We re-aligned the TreeShrink-pruned alignments using MAFFT v7.130b[41] and re-inferred gene trees using IQ-TREE, as above. We used these gene trees to infer a species tree in ASTRAL-III.

e. Concordance factor analyses

We used BUCKy[44] to estimate genome-wide concordance factors, which allows the evaluation of phylogenetic discordance among individual UCE gene trees. We compared alternative phylogenetic hypotheses among the major lineages of Acanthomorpha using these concordance factors. BUCKy estimates the frequency of topological partitions that occur in a sample of Bayesian gene tree posterior distributions and provides an estimate for their genome-wide frequency and 95% confidence intervals. Because the number of possible topological relationships among taxa increases non-linearly as the number of species included in the analysis increases, large taxonomic datasets are intractable for thorough concordance factor analyses with BUCKy. We therefore used a reduced taxonomic dataset of 82 species that represent each of the major subclades of Acanthomorpha to reduce computational burden. For this reduced dataset, we generated alignments of the 82 species using MAFFT (**Supplementary Table 1**). We used MrBayes v. 3.2.7[43] to infer a Bayesian gene tree distributions for each UCE locus. We ran MrBayes analyses with a GTR+Gamma molecular evolutionary model for 2 million generations, with trees sampled every 2,000 generations. Using the BUCKy program mbsum, we discarded the first 75% of sampled trees from the posterior sample of each UCE locus as burnin, summarized branching patterns in the remaining post-burnin posterior distribution, and used an alpha value of 1.0 for concordance factor estimation. These gene tree posterior distributions were then used for subsequent BUCKy estimation of concordance factors.

f. Divergence-time estimation

We estimated divergence times for both the 702 and 1,084 species phylogenies using BEAST v.2.5[45] following a protocol used in other UCE studies where BEAST analyses were run using reduced datasets of 30 UCE loci[29,48,67]. We constrained the phylogeny used in the BEAST runs using the IQ-TREE analyses of the 1,084 and 702 species datasets. For both the 1,084 and 702 species datasets, we performed BEAST analyses on three different sets of 30 loci, each randomly drawn without replacement from the entire set of ~1,000 UCE loci. Exploratory BEAST analyses using sets of 25 and 50 loci yielded similar divergence time estimates, justifying the moderately computationally expensive analyses using the 30 locus datasets. For each subset of 30 loci, we determined the optimum partitioning scheme using the relaxed hierarchical clustering algorithm in PartitionFinder2 v. 2.1.1[49]. For divergence dating analyses performed in BEAST, we employed a relaxed lognormal clock model and a birth-death tree model. We assigned minima for age priors using forty-three fossil occurrences, described below. For each 30-locus dataset, we ran at least three replicate analyses for a minimum of 200 million generations beyond a total burnin of 200 million generations. As MCMC chains progressed, we accepted suggestions provided by BEAST for improving operators' tuning parameter values. We used Tracer v.1.7.1 to observe effective sample size (ESS) values for posterior parameter estimates, to assess convergence among replicate MCMC chains, and to check for directional trends in parameter estimates[50]. Though the large size of the phylogenies created computational limits that resulted in moderate ESS values for some parameters, most parameter estimates reached ESS values well above 200. Some analyses were run up to 900 million generations in length to obtain adequate ESS values and ensure no directional trends in and unimodal distributions of parameter estimates. We used LogCombiner in BEAST v.1.8.4[51,68] to remove a burnin, and trees from each replicate run were randomly thinned. We thinned the sets of 1,084-species trees such that a total of 1,200 trees would remain across all runs, with an equal number of trees from each replicate contributing to the final summary trees. We randomly thinned the sets of 702-species trees such that 10,000 total trees remained across replicate runs. For each set of loci, we used LogCombiner to combine trees from replicate runs and TreeAnnotator in BEAST v.1.8.4 (Drummond et al. 2012) to estimate maximum clade credibility trees.

g. Diversification rate analyses

We performed diversification rate analyses on the time-calibrated 1,084-taxa phylogeny that was run for the most generations and therefore had the highest ESS values for posterior parameter estimates. Species diversity of acanthomorph lineages used to determine sampling fractions for all diversification rate analyses were based on numbers of species presented in Eschmeyer's Catalog of Fishes[3], which at the time of the analyses included 19,219 species of Acanthomorpha. We removed all outgroups and duplicate samples of the same species before performing diversification rate analyses, leaving a phylogeny consisting of 1,075 acanthomorph species and a sampling fraction of 0.056. We performed stepping-stone simulations within TESS[52] to estimate the marginal likelihoods of eight birth-death models and evaluate their fit to the acanthomorph time-calibrated phylogeny. Competing models included those with constant diversification rates, with episodically changing rates, or with decreasing speciation rates. Variants of the constant rate model with and without a mass extinction event were also tested to assess the potential impact of the K-Pg mass extinction on acanthomorph diversification. We tested variants of the competing models that accommodated the effects of incomplete taxon sampling by correcting for uniform (random) or diversified sampling methods.

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

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

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

We inferred global diversification rates and examined rate heterogeneity across clades using BAMM v.2.5.0[53]. Our analyses corrected for incomplete sampling by accounting for the sampling fractions of 304 major representative clades, most of which are taxonomic families, in accordance with the number of species described by Eschmeyer's Catalog of Fishes [3]. We also used the information on species diversity to appropriately adjust these clade-specific sampling fractions for non-monophyletic taxonomic groups. As in the TESS analyses, we set the global sampling fraction for all BAMM analyses to 0.056. We identified appropriate rate priors using the function setBAMMpriors in the R package BAMMtools v.2.1.6[69], accounting for incomplete taxon sampling.

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

h. Body shape trait data

We pruned a body trait dataset to the 680 species that matched those in the 702-species UCE phylogeny[24]. The body shape dataset included maximum body depth, maximum fish width, head depth, lower-jaw length, mouth width, minimum caudal-peduncle depth, and minimum caudal-peduncle width. We measured maximum body depth as the maximum linear distance from the dorsal to ventral margin of the body, anywhere in the region between the posterior edge of the operculum to the anterior portion of the caudal peduncle. We measured maximum fish width as the maximum width anywhere along the body. We measured head depth as the vertical distance from the dorsal to ventral margins of the head passing through the center of the eye. We measured lower jaw length as the linear distance from the anterior end of the lower jaw to the articular-quadrate joint. We measured mouth width as the linear distance between the left and right articular-quadrate joints. We measured minimum caudal peduncle depth as the minimum vertical distance from the dorsal to ventral margin of the caudal peduncle. We measured minimum caudal peduncle width as the narrowest point along the caudal peduncle. Lastly, we measured fish standard length as the linear distance from the anterior tip of the upper jaw to the posterior edge of the hypural plate or to the posterior end of the vertebral column (i.e., in species that lack a hypural plate). We accounted for size by regressing log-transformed lengths against log-transformed standard fish length and calculating phylogenetic residuals using the phyl.resid function implemented in PHYTOOLS[55]. We used this matrix of residuals for seven traits for phylogenetic comparative analyses using a multivariate framework.

i. Disparity through time analyses

We assessed disparity through time (DTT) using the dtt function implemented in GEIGER[56]. We incorporated uncertainty in divergence times by repeating analyses across 100 trees randomly sampled from the posterior distribution. Since we were specifically interested in patterns around and following the K-Pg boundary, we summarized disparity through time in 1 My intervals as the proportion of trees in which the observed subclade disparity fell below that expected from a Brownian motion process (*i.e.*, the expected pattern if the clade is undergoing adaptive radiation) (results in Supplementary Fig. 28). Focusing on the time following the K-Pg boundary, we statistically summarized the 1 My time interval during which the observed subclade disparity first dropped below that expected from a Brownian motion process (results in Supplementary Fig. 28). We tested the sensitivity of disparity through time analyses to body shape traits and to the inclusion of major clades by repeating all analyses to the exclusion of clades that arose immediately around the K-Pg boundary and to the exclusion of each trait, as well as repeating the analyses for each trait separately in a univariate framework (results in Extended Data Fig. 6). We also visualized the evolutionary histories of the following focal lineages using the phenogram function implemented in PHYTOOLS[55]: Carangiformes, Lophioidei, Perciformes, Scombriformes, "Squamipinnes" (here defined as the clade containing *Chaetodon kleinii* and *Luvarus imperialis*), Syngnathiformes, and Tetraodontoidei. We visualized body shape morphospace using principal component analysis (PCA) with the prcomp function. Since the traits had different variances, we scaled all traits prior to performing PCA.

2. Fossil calibrations for relaxed clock BEAST analyses

i. *Node*: Stem lineage Lampriformes, dating the most recent common ancestor (MRCA) of *Lampris guttatus* and *Stylephorus chordatus*, which is the MRCA of Lampriformes and all other paracanthopterygians. *First occurrence*: †*Aipichthys minor*. Sannine Limestone, Hadjula, Lebanon. *Resolution in phylogenetic analyses*: †*Aipichthys minor* is resolved as a lampriform stem lineage in parsimony analyses of morphological characters[70,71]. *Stratigraphy*: The Hadjula fish beds are located below reported occurrence of *Mantelliceras mantelli*, which defines the first complete ammonite zone of the Late Cretaceous. The top of the *Mantelliceras mantelli* Zone is dated at 98.0 Ma[72], from which we derive a minimum age for *Aipichthys*. *Minimum age*: 98.0 Ma. *Prior setting*: lognormal prior, minimum age 98.0 Ma, mean=1.0, S.D.=1.25, upper 95% CI: 119.0 Ma[48].

ii. *Node*: Stem lineage Polymixiiformes, dating the MRCA of *Polymixia lowei* and *Aphredoderus sayanus*, which subtends the MRCA of *Polymixia* and Percopsiformes. *First occurrence*: †*Homonotichthys dorsalis*. Lower Chalk of Sussex and Kent, UK[73]. *Resolution in phylogenetic analyses*: none. *Character states*: four full-sized branchiostegals; anterior branchiostegals reduced and forming support for chin barbel[16,73]. *Stratigraphy*: middle-upper Cenomanian, zone of *Holoaster subglobosus*, corresponding to the late Cenomanian[73-75]. The minimal age for †*Homonotichthys dorsalis* is provided by the age of Cenomanian-Turonian boundary, which is dated as 93.9 Ma[72]. *Absolute age estimate*: 93.6 Ma (28). *Prior setting*: lognormal prior, minimum age 93.6 Ma, mean = 1.06, S.D.=1.25, upper 95% CI: 116.35 Ma[4].

iii. *Node*: Stem lineage Aphredoderidae, dating the MRCA of *Aphredoderus sayanus* and *Typhlichthys subterraneus*, which subtends the MRCA of Aphredoderidae and Amblyopsidae. *First occurrence*: †*Trichophanes foliarum*. Florissant Formation, Colorado, USA[76]. *Resolution in phylogenetic analyses*: †*Trichophanes* and Aphredoderus form a clade in a maximum parsimony analysis of 47 morphological characters[77]. *Character states*: ventral margins of lachrymal and infraorbitals spiny; alveolar process of premaxilla divided into separate segments[76-78]. *Stratigraphy*: The upper Priabonian Florissant Roadcut is dated radiometrically using ^{40}Ar/^{39}Ar isotope ratios as 34.07 Ma[79]. *Absolute age estimate*: 34.1 Ma. *Prior setting*: lognormal prior, minimum age 34.1 Ma, mean=1.0, S.D.= 1.347, upper 95% CI: 59.0 Ma[20].

iv. *Node*: Stem lineage *Zenopsis*, dating the MRCA of *Zenopsis* and *Zeus*. *First occurrence*: †*Zenopsis clarus*, †*Z. tyleri*, and †*Z. hoernesi*. Lower Maikopian series, Psheka Horizon of the Belaya River, Caucasus[80], and Lower Dysodylic shales, Strujinoasa-Drăguşina and Piatra Neamţ, Romania[81]; Lower Dysodylic shales, Piatra Neamţ, Romania[81]; Laško (Tüffer), Slovenia[81]. *Resolution in phylogenetic analyses*: maximum parsimony analysis of 45 morphological characters resulted in a phylogeny where †*Zenopsis clarus*, †*Z. tyleri*, and †*Z. hoernesi,* and *Z. oblongus* are resolved in a clade[82]. *Character states*: slender lachrymal; pelvic-fin spines absent; buckler-like plates present along ventral midline of abdomen, and along dorsal ridge from middle of spinous to end of soft dorsal fin[82]. *Stratigraphy*: lower Rupelian [P18], lower Khadumian regional stage[83]. *Absolute age estimate*: 32.0 Ma[84]. *Prior setting*: lognormal prior, minimum age 32.0 Ma, mean=1.0, S.D.= 0.33, upper 95% CI: 36.7 Ma[20].

v. *Node*: Stem lineage Lampridae, dating the MRCA of *Lampris guttatus* and *Zu elongatus*, which is the MRCA of Lampriformes. *First occurrence*: †*Turkmene finitimus*. Danatinsk Suite, Uylya-Kushlyuk locality, Turkmenistan[85,86]. *Resolution in phylogenetic analysis*: none. *Character states*: first dorsal fin pterygiophore strongly reclined posteriorly; enlarged pectoral fins inserting high on flank; shoulder girdle broad ventrally, with expanded coracoid; long parapophyses absent from abdominal vertebrate[86]. *Stratigraphy*: uppermost Thanetian-lowermost Ypresian[87]. *Absolute age estimate*: 55.8 Ma[84]. *Prior setting*: lognormal prior, minimum age 55.8 Ma, mean=1.0, S.D.= 1.411, upper 95% CI: 83.5 Ma[20].

vi. *Node:* Stem lineage Holocentridae, dating the MRCA of *Myripristis violacea* and *Rondeletia loricata*, which subtends the MRCA of Holocentridae and Berycoidei. *First occurrence*: †*Stichocentrus liratus* from the Sannine Limestone, Hadjula, Lebanon[88]. *Resolution in phylogenetic analyses*: none. *Character states*: The penultimate anal-fin spine of †*Stichocentrus* is enlarged and represents a synapomorphy of holocentroids[16,89]. *Stratigraphy*: See discussion for Calibration i, †*Aipichthys minor*. *Absolute age estimate*: 98.0 Ma. *Prior* *setting*: lognormal prior, minimum age 98.0 Ma, mean=1.0, S.D.= 0.8, upper 95% CI: 108.0 Ma[48].

vii. *Node*: Stem lineage Myripristinae, dating the MRCA of *Myripristis violacea* and *Sargocentron coruscum*, which subtends the MRCA of Holocentridae. *First occurrence*: †*Eoholocentrum macrocephalum*, †*Berybolcensis leptacanthus*, and †*Tenuicentrum pattersoni*. Pesciara beds of 'Calcari nummulitici', Bolca, Italy[90-92]. *Resolution in phylogenetic analyses*: analysis of 72 morphological characters resolve †*Eoholocentrum*, †*Berybolcensis*, and †*Tenuicentrum* as stem-lineage Myripristinae[93]. *Character states*: tooth-bearing platform expanded and overhangs lateral side of dentary near symphysis; premaxillary tooth field curves dorsally toward ascending process at symphysis; edentulous ectopterygoid (†*Berybolcensis* and †*Tenuicentrum*); spinous procurrent caudal-fin rays reduced to four in the upper and three in the lower lobe (†*Berybolcensis* and †*Tenuicentrum*)[93]. *Stratigraphy*: upper Ypresian [NP14][94,95]. *Absolute age estimate*: 50 Ma[84]. *Prior setting*: lognormal prior, minimum age 50.0 Ma, mean=1.0, S.D.= 0.6, upper 95% CI: 57.3 Ma[20].

viii. *Node*: Crown lineage Syngnathiformes, dating the MRCA of *Pegasus volitans* and *Syngnathus scovelli*, which subtends the MRCA of Syngnathiformes. *First occurrence*: †*Gasterorhamphosus zuppichinii*. "Calcari di Melissano", Porto Selvaggio, Lecce province, Italy[96]. *Resolution in phylogenetic analyses*: none, but Orr[97] argues that †*Gasterorhamphosus* is a stem lineage of a clade containing Macrorhamphosidae and Centriscidae. *Character states*: anal-fin spine absent; enlarged dorsal-fin spine with serrated posterior margin; elongated tubular snout; pleural ribs absent; cleithrum bears enlarged posterodorsal process; rod-like anteroventral process of coracoid; pectoral rays simple[97,98]. *Stratigraphy*: uppermost Campanian-lowermost Maastrichtia[99]. *Absolute age estimate*: 69.71 Ma [48]. *Prior setting*: lognormal prior, minimum age 69.71 Ma, mean=1.0, S.D.= 0.785, upper 95% CI: 79.6 Ma[48].

ix. *Node*: Stem lineage Centriscidae, dating the MRCA of *Aeoliscus strigatus* and *Macroramphosus gracilis*, which subtends the MRCA of Centriscidae. *First occurrence*: †*Paramphisile weileri* and †*Paraeoliscus robinetae*. Pesciara beds of 'Calcari nummulitici', Bolca, Italy[100]. *Resolution in phylogenetic analyses*: none. *Character states*: caudal fin directed posteroventrally (†*Paraeoliscus*); dorsal spine jointed distally[97]. *Stratigraphy*: See discussion for Calibration viii †*Eoholocentrum macrocephalum*. *Absolute age estimate*: 50 Ma[84]. *Prior setting*: lognormal prior, minimum age 50.0 Ma, mean=1.0, S.D.= 0.6, upper 95% CI: 57.3 Ma[20].

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

xi. *Node*: stem lineage Stromateidae, dating the MRCA of *Pampus argenteus* and *Ariomma indica*, which subtends the MRCA Stromateidae and the clade that comprises *Ariomma* and Nomeidae. *First occurrence*: †*Pinichthys pulcher* from the Pshekha Horizon †*Planorbella* Beds, Lower Maikop Caucasus[104]. *Resolution in phylogenetic analyses*: none. *Character states*: †*Pinichthys* has a stellate, bony base of papillae in the region expected to bear pharyngeal sacs[105]. Synapomorphies of stromateiod displayed by †*Pinichthys* include: a continuous dorsal fin; a ventral articulation between the coracoid and ventral tip of the cleithrum; and an elongated first anal fin pterygiophore that is strongly reclined[106]. †*Pinichthys* differs from extant lineages of Stromateidae by having well-developed pelvic fins in adults and lacking extension of the first anal fin pterygiophore posterior to the first haemal spine[29]. †*Pinichthys* is interpreted as a stem-lineages stromateiod, which is consistent with previous interpretations[104] *Stratigraphy*: Details presented in Friedman et al.[29]. *Absolute age estimate*: 32.02 Ma. *Prior setting*: lognormal prior, minimum age 32.02 Ma, mean=1.0, S.D.= 1.2, upper 95% CI: 51.6 Ma[29].

xii. *Node*: stem lineage Chiasmodontidae, dating the MRCA of *Kali kerberti* and *Tetragonurus atlanticus*, which subtends the MRCA of Chiasmodontidae and *Tetragonurus*. *First occurrence*: †*Bannikovichthys paelignus* from the fish-bearing laminates of Toricella Paligna, Italy[107]. *Resolution in phylogenetic analyses*: none. *Character states*: The hypothesis that

†*Bannikovichthys* is related to living Chiasmodontidae is based on an absence of scales, elongated opercles, delicate ossification of the interopercle and subopercle, and enlarged hourglass-shaped radials[107]. The relationships of †*Bannikovichthys* among living chiasmodontids is uncertain, so it is conservatively treated as a stem-lineage taxon[29]. *Stratigraphy*: Details presented in Friedman et al.[29]. *Absolute age estimate*: 11.9 Ma. *Prior setting*: lognormal prior, minimum age 11.9 Ma, mean=1.0, S.D.= 1.454, upper 95% CI: 41.56 Ma[29].

xiii. *Node*: within crown of *Scomber*, dating the MRCA of *Scomber australasicus* and *Scomber japonicus*. *First occurrence*: *Scomber colias* from the Raz-el-Aïn, Oran, Algeria. *Resolution in phylogenetic analyses*: This fossil is attributed to the living species *Scomber colias*, which is resolved as the sister lineage of S. japonicus in a molecular phylogenetic analysis[108]. *Stratigraphy*: Details presented in Friedman et al.[29]. *Absolute age estimate*: 5.94 Ma. *Prior setting*: lognormal prior, minimum age 5.94 Ma, mean=1.0, S.D.= 1.255, upper 95% CI: 27.4 Ma[29].

xiv. *Node*: stem lineage *Scomber*, dating the MRCA of *Scomber australasicus* and *Rastrelliger kanagurta*. *First occurrence*: †*Scomber saadii* from the Padbeh Formation of Istehbanât, Iran[109]. *Resolution in phylogenetic analyses*: None. Character states: †*Scomber saadii* exhibits serrations on the teeth that is a synapomorphy of *Scomber*[108,110]. *Stratigraphy*: Details presented in Friedman et al.[29]. *Absolute age estimate*: 33.9 Ma. *Prior setting*: lognormal prior, minimum age 33.9 Ma, mean=1.0, S.D.= 1.02, upper 95% CI: 48.45 Ma[29].

xv. *Node*: stem lineage *Acanthocybium*, dating the MRCA of *Acanthocybium solandri* and *Scomberomorus maculatus*. *First occurrence*: †*Palaeocybium proosti* from the London Clay Formation, Isle of Sheppey, UK[111]. *Resolution in phylogenetic analysis*: none. *Character states*: †*Palaeocybium* and *Acanthocybium* share closely spaced teeth with blunt tips and the holotype specimen shows an elongate lower jaw that is similar to *Acanthocybium* and *Scomberomorus*[112-114]. Stratigraphy: Details presented in Friedman et al.[29]. *Absolute age estimate*: 50.5 Ma. *Prior setting*: lognormal prior, minimum age 50.5 Ma, mean=1.0, S.D.= 0.5, upper 95% CI: 56.72 Ma[29].

xvi. *Node*: stem lineage Sardini + Thunnini, dating the MRCA of *Scomberomorus maculatus* and *Euthynnus affinis*. *First occurrence*: †*Eocoelopoma portentosum* from the Danatinsk Formation, Turkmenistan[115]. *Resolution in phylogenetic analyses*: None. *Character states*: Details presented in Friedman et al.[29]. Stratigraphy: Details presented in Friedman et al.[29]. Absolute age estimate: 54.17 Ma. *Prior setting*: lognormal prior, minimum age 54.17 Ma, mean=1.0, S.D.= 0.698, upper 95% CI: 62.71 Ma[29].

xvii. *Node*: stem lineage *Thunnus*, dating the MRCA of *Thunnus orientalis* and *Auxis rochei*, which is the MRCA of Thunnini. *First occurrence*: †*Thunnus abchasicus* from the Kuma Horizon, Pshekha River, Caucasus[116]. *Resolution in phylogenetic* analyses: None. *Character states*: †*Thunnus abchasicus* exhibits several synapomorphies of *Thunnus* that include the presence of small oral teeth and the shortened preural vertebrae[116]. The presence of a spine in the second dorsal fin suggests that †*T. abchasicus* is a stem lineage *Thunnus*[115]. Stratigraphy: Details presented in Friedman et al.[29]. *Absolute age estimate*: 38.62 Ma. *Prior setting*: lognormal prior, minimum age 38.62 Ma, mean=1.0, S.D.= 0.91, upper 95% CI: 50.78 Ma[29].

xviii. *Node*: stem lineage *Promethichthys*, dating the MRCA of *Promethichthys prometheus* and *Diplospinus multistriatus*. *First occurrence*: †*Hemithyrsites maicopicus* from the Upper Maikop of the Kurdzhips River, Adygea, Caucasus[115]. *Resolution in phylogenetic analyses*: None. *Character states*: Derived traits shared by *Promethichthys* and †*Hemithyrsites maicopicus* include reduction of the pelvic fin to a single spine and the presence of two pairs of dorsal and anal finlets[115]. *Stratigraphy*: Details presented in Friedman et al.[29]. *Absolute age estimate*: 15.97 Ma. *Prior setting*: lognormal prior, minimum age 15.97 Ma, mean=1.0, S.D.= 0.986, upper 95% CI: 29.67 Ma[29].

xix. *Node*: Stem lineage Channidae, dating the MRCA of *Channa micropeltes* and *Helostoma temminckii,* which subtends the MRCA of Channidae and a clade containing Helostoma, Anabantidae, and Osphronemidae. *First occurrence*: †*Anchichanna kuldanensis* from the Ganda Kas Area, Kuldana Formation, Kala Chitta Hills, Pakistan[117]. *Resolution in phylogenetic analyses*: None. *Character states*: †*Anchichanna kuldanensis* exhibits the Channidae synapomorphy of the outer wall of the auditory bulla formed mainly by the prootic, but is likely a stem-lineage taxon because it does not share synapomorphies with either *Channa* or *Parachanna*[117]. *Stratigraphy*: The Kuldana Formation and other vertebrate fossil localities of the Kala Chitta Hills straddle the Ypresian-Lutetian boundary[118]. *Absolute age estimate*: 41.3 Ma. *Prior setting*: lognormal prior, minimum age 41.3 Ma, mean=1.0, S.D.= 1.31, upper 95% CI: 64.7 Ma[119].

xx. *Node*: Stem lineage Sphyraenidae, dating the MRCA of *Sphyraena jello* and *Lactarius lactarius*. *First occurrence*: †*Sphyraena bolcensis,* Pesciara beds of 'Calcari nummulitici', Bolca, Italy[120,121]. *Resolution in phylogenetic analyses*: None. *Character states*: three 'T'-shaped, sutured predorsals or spineless pterygiophores[122]; elongate gape; upper jaw non-protrusible; enlarged fangs on dentary, premaxilla, and palatine. *Stratigraphy*: upper Ypresian [NP14][94,95]. *Absolute age estimate*: 50.0 Ma[95]. *Prior setting*: lognormal prior, minimum age 50.0 Ma, mean=1.0, S.D.= 0.5999, upper 95% CI: 57.3 Ma[1].

xxi. *Node*: Stem lineage *Mene*, dating the MRCA of *Mene maculata* and *Xiphias gladius*. *First occurrence*: †*Mene purdyi*, 'Mancora Formation', Perú[123]; †*M. triangulum*, Danatinsk Suite, Uylya-Kushlyuk locality, Turkmenistan[85,87]; and †*Mene* sp., 'Stolle Klint clay', Ølst Formation, Denmark[124]. *Resolution in phylogenetic analyses*: None. *Character states*: frontal vault; many small infraorbitals; all anal fin rays short, with anteriormost rays plate like; anal fin spines absent; postcleithrum broad and contacts first anal fin pterygiophore; disc-like body with deep ventral keel; greatly elongated second anal fin ray[123]. *Stratigraphy*: uppermost Thanetian-lowermost Ypresian [NP14][87,124]. *Absolute age estimate*: 55.2 Ma[125]. *Prior setting*: lognormal prior, minimum age 55.2 Ma, mean=1.0, S.D.= 0.92, upper 95% CI: 67.5 Ma[1,48].

xxii. *Node*: Stem lineage Carangidae, dating the MRCA of *Caranx caninus* and *Trachinotus goodei*, which subtends the MRCA of the clade comprising Carangidae, *Coryphaena*, *Rachycentron*, Scomberoidinae, and Trachinotinae. *First occurrence*: †*Archaeus oblongus*. Danatinsk Suite, Uylya-Kushlyuk locality, Turkmenistan[85]. *Resolution in phylogenetic analyses*: None. *Character states*: broad gap between second and third anal-fin spines[126]. *Stratigraphy*: uppermost Thanetian-lowermost Ypresian[87]. *Absolute age estimate*: 55.8 Ma[84]. *Prior setting*: lognormal prior, minimum age 55.8 Ma, mean=1.0, S.D.= 0.661, upper 95% CI: 63.9 Ma[1].

xxiii. *Node*: Stem lineage Caranginae, dating the MRCA of *Caranx caninus* and *Seriola dumerili*, which subtends the MRCA of Carangidae. *First occurrence*: †*Eastmanalepes primaevus,* Pesciara beds of 'Calcari nummulitici', Bolca, Italy[127]. *Resolution in phylogenetic analyses*: None. *Character states*: lateral line scales modified as thick scutes[126,128]. *Stratigraphy*: upper Ypresian [NP14][94]. *Absolute age estimate*: 49.0 Ma[48]. *Prior setting*: lognormal prior, minimum age 49.0 Ma, mean=1.0, S.D.= 0.1, upper 95% CI: 52.2 Ma[1,48].

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

xxv. *Node*: Stem lineage Echeneidae, dating the MRCA of *Echeneis naucrates* and *Coryphaena hippurus*, which subtends the MRCA of clade containing Echeneidae, *Coryphaena*, *and Rachycentron*. *First occurrence*: unnamed Echeneidae undet. from the Frauenweiler clay pit, Germany[130]. *Resolution in phylogenetic analyses*: None. *Character states*: no supraneurals; multiple anal fin pterygiophores insert anterior to first haemal spine; spinous dorsal fin modified as adhesion disc[129,131]. *Stratigraphy*: See discussion in Harrington et al.[48]. *Absolute age estimate*: 29.62 Ma[48]. *Prior setting*: lognormal prior, minimum age 29.62 Ma, mean=1.0, S.D.= 0.87, upper 95% CI: 41.0 Ma[48].

xxvi. *Node*: Stem lineage *Scomberoides*, dating the MRCA of *Scomberoides lysan* and *Trachinotus goodei*, which subtends the MRCA of Scomberoidinae and Trachinotinae. *First occurrence*: *Scomberoides spinosus* from the Upper Maikop at Chernaya Rechka, Caucasus[87].

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

xxvii. *Node*: Stem lineage Citharidae, dating the MRCA of *Gymnachirus melas* and *Scophthalmus* rhombus, which subtends the MRCA of Citharidae and all other pleuronectoids except *Psettodes*. *First occurrence*: †*Eobothus minimus* from the Pesciara beds of 'Calcari nummulitici', Bolca, Italy[133,134]. *Resolution in phylogenetic analyses*: †*Eobothus* is the sister lineage of *Citharus*[133]. *Character states*: complete orbital asymmetry; dorsal fin extends above orbit; hook-shaped urohyal; parahypural not in articulation with pural centrum 1; long neural spine on preural centrum 2[133]. *Stratigraphy*: See discussion in Harrington et al. [48]. *Absolute age estimate*: 49.0 Ma[48]. *Prior setting*: lognormal prior, minimum age 49.0 Ma, mean=1.0, S.D.= 0.68, upper 95% CI: 57.3 Ma[48].

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

xxix. *Node:* Stem lineage Bothidae, dating the MRCA of *Bothus pantherinus* and *Cyclopsetta frimbriata*, which subtends the MRCA of the clade containing Bothidae and Cyclopsettidae. *First occurrence*: †*Oligobothus pristinus* from the Lower Dysodilic shales, Piatra Neamţ, Romania[137]. *Resolution in phylogenetic analyses*: None. *Character states*: myorhabdoi present[137]. *Stratigraphy*: See discussion in Harrington et al.[48]. *Absolute age estimate*: 29.62 Ma[48].

Prior setting: lognormal prior, minimum age 29.62 Ma, mean=1.0, S.D.= 0.06, upper 95% CI: 32.6 Ma[48].

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

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

xxxii. *Node:* Stem lineage Pseudocrenilabrinae, dating the MRCA of *Bathybates minor* and *Amphilophus citrinellus*, which subtends the MRCA of the clade that contains Pseudocrenilabrinae and Cichlinae. *First occurrence*: †*Mahengechromis plethos* from Mahenge, Tanzania[142]. *Resolution in phylogenetic analyses*: Several phylogenetic resolutions of †*Mahengechromis* place the taxon as either a crown lineage Cichlidae or crown lineage Pseudocrenilabrinae[142,143]. We follow Rabosky et al.[119] in conservatively treating †*Mahengechromis* as a stem-lineage Pseudocrenilabrinae. *Character states*: The identification of †*Mahengechromis* as a cichlid is supported by the morphology of the lower pharyngeal jaw, squamation, and meristics of vertebrae and median fins[142-144]. *Stratigraphy*: The Mahenge fossil deposits accumulated in a crater formed by intrusion of kimberlite and U-Pb of a zircon crystal dates the formation of the kimberlite at 45.83 +/-0.17 Ma[145]. Because the lacustrine sediments predate the kimberlite emplacement it was suggested the age of the fossil deposits are 0.2 to 0.1 Ma younger[145,146]. We use the conservative date of 45 Ma used in Rabosky et al.[119]. Absolute age estimate: 45.0 Ma. *Prior setting*: lognormal prior, minimum age 45.0 Ma, mean=1.0, S.D.= 1.29, upper 95% CI: 67.3 Ma.

xxxiii. *Node*: Crown lineage Exocetoidei, dating the MRCA of *Xenentodon cancila* and *Hemiramphus far*, which subtends the MRCA of Belonidae and Hemiramphidae. *First occurrence*: †*Rhamphexocoetus volans* from Pesciara beds of 'Calcari nummulitici', Bolca, Italy[147]. *Resolution in phylogenetic analyses*: None. *Character states*: lower jaw symphysis extended; ventral lobe of caudal fin enlarged relative to dorsal lobe; pectoral fins greatly expanded[148-150]. *Stratigraphy*: upper Ypresian [NP14][94,95]. *Absolute age estimate*: 49.0 Ma[4]. *Prior setting*: lognormal prior, minimum age 49.0 Ma, mean=1.0, S.D.= 1.49, upper 95% CI: 80.52 Ma[4].

xxxiv. *Node*: Stem lineage *Calotomus* (Labridae), dating the MRCA of *Calotomus spinidens* and *Sparisoma radians*. *First occurrence*: †*Calotomus preisli* from the Leitha Limestone, St. Margarethen, Austria[151]. Resolution in phylogenetic analyses: None. *Character states*: Presence of upper pharyngeal bones bearing 1 to 3 rows of teeth and presence of a lateral canine on the premaxilla are synapomorphies for Scarinae. A conical tooth on the medial face of the premaxilla is a synapomorphy of *Calotomus*[151]. *Stratigraphy*: The Leitha Limestone is constrained by calcareous nannofossils to the standard biozone NN6[151], which is entirely in the Serravallian stage of the Miocene. The top of NN6 is dated at 11.9 Ma[4]. Absolute age estimate: 11.9 Ma[4]. *Prior setting*: lognormal prior, minimum age 11.9 Ma, mean=1.0, S.D.= 1.501, upper 95% CI: 43.95 Ma[4].

xxxv. *Node*: Stem lineage Luvaridae, dating the MRCA of *Luvarus imperialis* and *Acanthurus bahianus*, which subtends the MRCA of *Luvarus* and the clade containing *Zanclus cornutus* and Acanthuridae. *First occurrence*: †*Avitoluvarus dianae*, †*A. mariannae*, †*Kushlukia permira*, and †*Luvarus necopinatus*. Danatinsk Suite, Uylya-Kushlyuk locality, Turkmenistan[152]. *Resolution in phylogenetic analyses*: a parsimony analysis of morphological characters resolves a clade that contains †*Avitoluvarus,* †*Kushlukia*, †*Luvarus necopinatus*, and *L. imperialis*, which is sister to a clade comprising *Zanclus* and Acanthuridae[152]. *Character states*: median pterygial truss surrounding most of body; two or fewer dorsal-fin spines; no anal-fin spines; distal end of first anal-fin pterygiophore greatly elongated anteriorly; hypurals 1-4 fused; caudal fins broadly overlap hypural(s); pelvic fin rudimentary in adults; teeth absent or greatly reduced[152]. *Stratigraphy*: uppermost Thanetian-lowermost Ypresian[87]. *Absolute age estimate*: 55.8 Ma[84]. *Prior setting*: lognormal prior, minimum age 55.8 Ma, mean=1.0, S.D.= 0.661, upper 95% CI: 63.9 Ma[20].

xxxvi. *Node*: Stem lineage Acanthurinae, dating the MRCA of *Acanthurus bahianus* and *Naso unicornis*, which subtends the MRCA of Acanthuridae. *First occurrence*: †*Proacanthurus tenius* from the ‘Pesciara beds of ‘Calcari nummulitici’, Bolca, Italy[153]. *Resolution in phylogenetic analyses*: None. *Character states*: caudal peduncle bears folding spine[153]. *Stratigraphy*: upper Ypresian [NP14][94]. *Absolute age estimate*: 50 Ma[94]. *Prior setting*: lognormal prior, minimum age 50.0 Ma, mean=1.0, S.D.= 0.6, upper 95% CI: 57.3 Ma[1].

xxxvii. *Node*: Stem lineage Siganidae, dating the MRCA of *Siganus spinus* and *Scatophagus argus*. *First occurrence*: †*Siganopygaeus rarus*. Danatinsk Suite, Uylya-Kushlyuk locality, Turkmenistan[154]. *Resolution in phylogenetic analyses*: parsimony analysis of morphological characters resolves four Eocene and Oligocene taxa, including †*Siganopygaeus*, as stem-lineage Siganidae[154]. *Character states*: two pelvic-fin spines; seven or more anal-fin spines; ten or fewer anal-fin rays[154]. *Stratigraphy*: uppermost Thanetian-lowermost Ypresian[87]. *Absolute age estimate*: 55.8 Ma[84]. *Prior setting*: lognormal prior, minimum age 55.8 Ma, mean=1.0, S.D.= 0.661, upper 95% CI: 63.9 Ma[20].

xxxviii. *Node*: Stem lineage of Chaetodontidae, dating the MRCA of *Chaetodon kleinii* and *Leiognathus equula*, which subtends the MRCA of the clade that contains Chaetodontidae and Leiognathidae. *First occurrence*: Chaetodontidae cf. *Chaetodon* (tholichthys-stage larvae) from the ‘Fish shales’, Frauenweiler clay pit, Germany[130,155]. *Resolution in phylogenetic analyses*: None. *Character states*: overlapping, sequential articulation between first dorsal fin pterygiophores, supraneurals, and supraoccipital crest; second infraorbital excluded from orbital margin; two sets of lateral processes on each side of first dorsal fin pterygiophore define a clear groove; distal head of second supraneural longer than that of first supraneural[155-157]. *Stratigraphy*: The 'Fish shales' lie within NP23[138]. *Absolute age estimate*: 29.62 Ma[4]. *Prior setting*: lognormal prior, minimum age 29.62 Ma, mean=1.0, S.D.= 1.498, upper 95% CI: 61.6 Ma[4].

xxxix. *Node*: Stem lineage *Chaetodon*, dating the MRCA of *Chaetodon kleinii* and *Prognathodes marcellae*. *First occurrence*: †*Chaetodon ficheuri* from the Saint-Denis du Sig, Raz-el-Aïn, Les Planteurs, and Eugène, Algeria[156]. *Resolution in phylogenetic analyses*: None. *Character states*: overlapping, sequential articulation between first dorsal fin pterygiophores, supraneurals, and supraoccipital crest; second infraorbital excluded from orbital margin; two sets of lateral processes on each side of first dorsal fin pterygiophore define a clear groove; distal head of second supraneural longer than that of first supraneural[156,157]. *Stratigraphy*: Messinian[158-160]. *Absolute age estimate*: 7.1 Ma. *Prior setting*: lognormal prior, minimum age 7.1 Ma, mean=0.26, S.D.= 0.2, upper 95% CI: 8.9 Ma[20].

xl. *Node*: Stem lineage *Gazza*, dating the MRCA of *Gazza minuta* and *Leiognathus equula*. *First occurrence*: †*Euleiognathus tottori* from the Iwami Formation, Tottori Group, Japan[161,162]. *Resolution in phylogenetic analyses*: none. *Character states*: long ascending processes of premaxillae; paddle-like expansions of neural and haemal spine of preural centrum 4; single supraneural; serrated anterior margins of fin spines; caniniform teeth[163]. The final character is unique to *Gazza* within leiognathids[161,164]. The nesting of *Gazza* within the phylogeny of Leiognathidae indicates caniniform teeth are derived within the clade[163,165,166]. See Gill and Michalski[167] who are sceptical that †*Euleiognathus is a* leiognathid. *Stratigraphy*: middle Miocene[161,162]. *Absolute age estimate*: 11.6 Ma[168]. *Prior setting*: lognormal prior, minimum age 11.6 Ma, mean=0.8, S.D.= 1.0, upper 95% CI: 23.1 Ma[20].

xli. *Node*: Stem lineage Diodontidae, dating the MRCA of *Diodon liturosus* and *Canthigaster rostrata*, which subtends the MRCA of Diodontidae and Tetraodontidae. *First occurrence*: †*Prodiodon tenuispinus*, †*P. erinaceus*, †*Heptadiodon echinus*, and †*Zignodon fornasieroae* from the Pesciara beds of 'Calcari nummulitici', Bolca, Italy[169]. *Resolution in phylogenetic analyses*: parsimony analysis of morphological characters resolves a clade containing

†*Prodiodon tenuispinus*, †*P. erinaceus*, †*Heptadiodon echinus*, †*Zignodon fornasieroae*, *Diodon holocanthus*, and *Chilomycterus schoepfi*[169]. *Character states*: premaxillae fused along midline; dentaries fused along midline; jaws massive[169]. *Stratigraphy*: upper Ypresian [NP14][94]. *Absolute age estimate*: 50 Ma[84]. *Prior setting*: lognormal prior, minimum age 50.0 Ma, mean=1.0, S.D.= 0.6, upper 95% CI: 57.3 Ma[20].

xlii. *Node*: Stem lineage of Balistidae, dating the MRCA of *Balistes capriscus* and *Aluterus monoceros*, which subtends the MRCA of Balistidae and Monacanthidae. *First occurrence*: †*Gornylistes prodigiosus* from the Kuma Horizon, Krasnodar Region, Caucasus[170]. *Resolution in phylogenetic analyses*: None. *Character states*: ventral shaft of second spine-bearing dorsal pterygiophore absent; supraneural strut present between abdominal neural spine and final spine-bearing dorsal pterygiophore; four anal-fin pterygiophores anterior to the haemal spine of the third caudal vertebra[169]. *Stratigraphy*: Bartonian [NP17] Kumian regional stage[83]. *Absolute age estimate*: 37.2 Ma[84]. *Prior setting*: lognormal prior, minimum age 37.2 Ma, mean=1.0, S.D.= 0.42, upper 95% CI: 42.6Ma[20].

xliii. *Node*: Stem lineage Antennarioidei, dating the MRCA of *Antennarius striatus* and *Ogcocephalus radiatus*. *First occurrence*: †*Eophryne bartutii* from the Pesciara beds of 'Calcari nummulitici', Bolca, Italy[171]. *Resolution in phylogenetic analyses*: None. †*Eophryne* was hypothesized to share common ancestry with Antennariidae based on overall morphological similarity[171]. The phylogenetic placement used for this calibration is conservatively applied to the more inclusive Antennarioidei. *Character states*: triradiate ectopterygoid; spatulate postmaxillary process of premaxilla[171-173]. *Stratigraphy*: upper Ypresian [NP14][94]. *Absolute age estimate*: 50 Ma[84]. *Prior setting*: lognormal prior, minimum age 50.0 Ma, mean=1.0, S.D.= 0.6, upper 95% CI: 57.3 Ma[1].

3. Supplementary results and discussion

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

The maximum likelihood analyses of the 702-taxon and 1,084-taxon UCE datasets confidently resolve the phylogenetic relationships of all sampled acanthomorph families. The phylogeny inferred from the IQ-TREE analysis of the multiple-partition, concatenated 1084-taxon dataset is represented in Supplementary Figs. 1-25. The results of the five other phylogenetic analyses are available on Dryad. Bootstrap support values across the entire IQ-TREE phylogeny are high, with most nodes being supported by 100% bootstrap support and only 27 of 1,107 nodes (2.4%) having values ≤95%. Tree topologies inferred using the different methods described in *Section 1d* are largely consistent according to comparisons conducted in TOPD-FMTS v.4.6[39] (see Supplementary Table 2). Robinson-Foulds metrics across all comparisons were low (≤0.033), as were nodal distances (≤1.046). Supplementary Table 2 lists the 19 species that differ in their phylogenetic relationships across the different analyses. Most of these species are found in areas of the tree that have been historically difficult to resolve, such as Anthiadidae, Carangidae and Apogonidae. Tree topologies inferred in IQ-TREE and RAxML using multiple-partition, 700-taxon alignments were identical.

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

The new UCE-inferred phylogeny provides an opportunity to reevaluate the classification of Percomorpha to identify inclusive taxonomic groupings that reflect phylogenetic relationships. An initial effort at building classifications based on molecular phylogenies attempted to preserve the ordinal ranks of the clades such as the Pleuronectiformes, Tetraodontiformes, Atheriniformes, and Synbranchiformes[174]. This classification proposed a delimitation of 33 taxonomic orders in Percomorpha that each contain an average of only 7.4 families and 492.9 species, and resulted in 10% of all percomorph families unassigned to a taxonomic order[174]. In Figs. 1 and 2, Supplementary Figs. 1-25, and Supplementary Table 3 we offer an alternative delimitation of 13 clades that we treat as taxonomic orders to accommodate the classification of all 290 percomorph families. In the proposed classification, each taxonomic order comprises an average 2,226.8 species and 18.2 families.

The names of the orders in the proposed percomorph classification are consistent with conventions in ichthyological systematics by establishing a link with one of the constituent taxonomic families and using the "–iformes" suffix[175,176]. For example, this delimitation of Blenniiformes includes the Blenniidae and 48 other families (e.g., cichlids, livebearers, and mullets) that were previously identified as a monophyletic group in molecular phylogenetic studies[1,4,15,21,22,177]. Previously named Ovalentaria[22], this diverse clade of percomorphs had been divided among seven orders[174], one of which, Mugiliformes, included a single family, Mugilidae (mullets).

b. Phylogeny of non-percomorph acanthomorphs

i. Monophyly and relationships of Paracanthopterygii

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

ii. Phylogenetic relationships of Lampriformes

The new UCE phylogeny of Acanthomorpha resolves Lampriformes as the sister lineage of Paracanthopterygii (Fig. 1), which agrees with a previous phylogenetic analysis of UCE loci[4]. Other studies offer conflicting phylogenetic positions for Lampriformes; a phylogenomic analysis of ~1,000 exons resolve lampriforms as the sister lineage of the Acanthopterygii[15], while morphological phylogenies place the lampriforms as the sister lineage of all other Acanthomorpha[18]. The Bayesian concordance factor analyses result in overlapping 95% credible intervals for the phylogeny that places lampriforms as sister to Paracanthopterygii and the phylogeny that resolves lampriforms as the sister lineage of all other acanthomorphs (Extended

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

iii. Phylogenetic relationships of Gadiformes

The new UCE phylogeny of Gadiformes is similar to a recent study that utilized DNA sequences from more than 14,000 portions of protein coding genes [179]. Results from the two analyses are congruent in resolving *Bregmaceros* (codlets) as the sister lineage of all other Gadiformes, but differ in three specific relationships. The UCE phylogeny resolves Muraenolepididae (eel cods) and Trachyrincidae (armored grenadiers) as sister lineages, but the exon phylogeny resolves *Melanonus* (pelagic cods) as the sister lineage of Muraenolepididae. The UCE phylogeny places Merlucciidae (merluccid hakes) as the sister lineage of an inclusive clade containing Phycidae (phycid hakes), Lotidae (hakes and burbots), and Gadidae (cods and haddocks), but the exon phylogeny resolves Merlucciidae as the sister lineage of a clade containing *Eulichthys polynemus* (Eucla cod), Muraenolepididae, *Melanonus*, Trachyrincidae, Moridae, *Macruronus* (blue grenadiers), *Lyconus* (Atlantic hakes), Bathygadidae (rattails), *Steindachneria argenta*, and Macrouridae. Lotidae is resolved as monophyletic in the exon phylogeny[179], but this lineage is paraphyletic in the UCE phylogeny with *Lota lota* (Burbot) resolved as the sister lineage of a clade containing *Brosme brosme* (Cusk), *Molva* (lings), and Gadidae (true cods) (Fig. 1, Supplementary Fig. 1).

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

Acanthopterygii includes Trachichthyiformes, Beryciformes, and Percomorpha (Fig. 1). The earliest molecular studies identified the sister lineage of percomorphs as either a monophyletic group consisting of Trachichthyiformes and Beryciformes[1,20] or the beryciform subclade Holocentridae (squirrelfishes)[21]. The UCE inferred phylogeny presented in this study and previous phylogenomic analyses resolve Trachichthyiformes as the sister lineage to all other acanthopterygians and Beryciformes, which includes Holocentridae, as the percomorph sister lineage[4,15,178,180] (Fig. 1, Supplementary Fig. 2). This topology is also the most supported hypothesis in the concordance factor analyses (Extended Data Fig. 1c). The alternative hypotheses, including the phylogeny that places Holocentridae as sister to Percomorpha, produced substantially lower Bayesian concordance factor scores with 95% credible intervals that do not overlap with the scores of the optimal phylogeny (Extended Data Fig. 1c). The UCE data presented here reject the hypothesis that Holocentridae is the sister lineage of Percomorpha.

c. Phylogenetic relationships of Percomorpha

Percomorphs are classified in an astounding 290 taxonomic families[181], which is more than living birds (252 families) and many more than mammals (167 families), squamates (58 families), amphibians (67 families), and turtles (11 families)[182-184]. By the middle of the 20th century the vast majority of percomorph families were delimited and considered monophyletic groups[175,185], but relationships among these delimited taxonomic families were woefully unresolved at the start of the 21st century[186,187]. This lack of phylogenetic resolution among the nearly 300 taxonomic families led to the now famous analogy that Percomorpha was the "bush at the top" of the teleost phylogeny[188]. Since the start of the 21st century, however, molecular studies have offered dramatic resolution of percomorph relationships[1,4,15,21]. The UCE phylogeny inferred in this study resolves the species sampled from 276 taxonomic families into one of twelve taxonomic orders that contain more than one family. All 12 of these inclusive lineages are monophyletic and strongly supported in the UCE phylogeny (Figs. 1,2, Supplementary Figs. 3-25). Relationships are consistent with previous efforts using Sanger sequenced loci and phylogenomic analyses, but no prior analysis included a high fraction (276 of 290) of the percomorph families.

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

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

Ophidiiformes (cusk eels) is resolved as the sister lineage to all other percomorphs (Fig. 1). Relationships within this species-rich lineage of mostly marine fishes are not well known and the delimitation of taxonomic families is in flux[189]. The UCE phylogeny resolves two clades in Ophidiiformes that correspond to the suborders Bythitoidei and Ophidioidei (Fig. 1, Supplementary Fig. 3). Within Bythitoidei, the families Dinematichthyidae (pygmy brotulas) and Bythitidae (livebearing brotulas) are both monophyletic (Supplementary Fig. 3). As discovered in previous studies[189-191], the formerly recognized taxonomic families Parabrotulidae and Aphyonidae are phylogenetically nested in Bythitidae (Supplementary Fig. 3). Historically, Ophidioidei contained Ophidiidae and Carapidae, but the UCE phylogeny (Fig. 1, Supplementary Fig. 3) as well as previous studies using whole mtDNA genome sequences and Sanger sequenced nuclear genes resolve Carapidae as phylogenetically nested within Ophidiidae[1,21,119,192], prompting the synonymization of the family Carapidae with Ophidiidae[174].

ii. Phylogenetic relationships of Batrachoididae

There is limited taxon sampling of Batrachoididae in the UCE phylogeny, but the subfamily Batrachoidinae (sampled with *Batrachoides pacifici* and *Opsanus tau*) is paraphyletic (Supplementary Fig. 3). Porichthyinae is paraphyletic in a phylogeny inferred from Sanger sequenced mitochondrial and nuclear genes[119].

iii. Phylogeny of Gobiiformes

One of the most surprising results from molecular analyses of percomorph phylogeny was the discovery that gobies, cardinalfishes (Apogonidae), and nurseryfishes (Kurtidae) resolve in a strongly supported monophyletic group[20,193,194]. Subsequent molecular studies resolved two competing hypotheses of relationships among the major lineages of Gobiiformes: 1) *Kurtus* and Apogonidae resolved as a clade, or 2) Apogonidae as the sister lineage of a clade containing *Trichonotus* (sand divers) and Gobioidei[1,4,21,194-198]. The UCE phylogeny in this study resolves two major lineages in Gobiiformes: the Apogonoidei that contains *Kurtus* and Apogonidae, and a clade containing *Trichonotus* and Gobioidei (Fig. 1, Supplementary Figs. 3,4). The relationships of the eight taxonomic families classified in Gobioidei are identical to phylogenies inferred using Sanger sequenced mtDNA and nuclear genes[197,198] (Fig. 1, Supplementary Fig. 4).

iv. Phylogenetic relationships of Scombriformes and Syngnathiformes

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

Tunas, barracudas, cutlassfishes and swordfishes were historically classified in Scombroidei. Early phylogenetic analyses of Sanger sequenced mtDNA and nuclear genes resolved species classified in the traditional delimitation of Scombroidei into two distantly related percomorph lineages[199]. Xiphiidae (swordfishes), Istiophoridae (billfishes) and Sphyraenidae (barracudas) were resolved in the clade Carangiformes along with flatfishes, jacks and archerfishes (Fig. 1)[48]. The remaining lineages of the historical Scombroidei— Scombridae (tunas), Gempylinae (snake mackerels), Trichiurinae (cultassfishes) and *Pomatomus saltatrix* (Bluefish)—are resolved in the clade Scombriformes that also includes the stromatioids, e.g., Stromateidae (butterfishes) and Chiasmodontidae (swallowers)[29]. Other lineages in Scombriformes include the enigmatic *Icosteus aenigmaticus* (Ragfish) and *Amarsipus carlsbergi* (Bagless Glassfish), both of which are deep-branching, monotypic lineages that long evaded phylogenetic resolution among percomorphs (Fig. 1, Supplementary Fig. 5). The UCE phylogeny resolves *Lepidocybium flavobrunneum* (Escolar) as the sister lineage of a clade containing Gempylidae and Trichiuridae (Fig. 1, Supplementary Fig. 6). *Lepidocybium flavobrunneum* is traditionally classified in Gempylidae, which is paraphyletic in the UCE phylogeny as the remaining gempylids are more closely related to species of Trichiuridae (Fig. 1, Supplementary Fig. 6). This relationship has previously been resolved in a phylogenetic analysis using morphological data[122].

Syngnathiformes as consisting of seahorses and pipefishes, flying gurnards, goatfishes, and dragonets was first resolved as a clade in phylogenetic analyses of Sanger sequenced mtDNA and nuclear genes[21,200]. Prior to the application of molecular phylogenetics, Callionymidae (dragonets) and Draconettidae (draconettids) were classified as closely related to

Gobiesocidae (clingfishes)[201-204]. As reflected in molecular phylogenies, Pietsch[98] proposed that Dactylopteridae (helmet gurnards) were closely related to other syngnathiform lineages, but they were classified by others with the sculpins, rockfishes and scorpionfishes in Scorpaeniformes. Mullidae (goatfishes) were long classified in the wastebasket taxon Perciformes[175,202,205] but thought to be closely related to Haemulidae (grunts) and Sparidae (porgies)[206]. The UCE phylogeny resolves two major lineages of Syngnathiformes: 1) a clade we delimit as Mulloidei that contains Pegasidae (seamoths), Dactylopteridae, Mullidae, Callionymidae, and Draconettidae and 2) a lineage we delimit as Syngnathoidei, consisting of Syngnathidae (pipefishes and seahorses), Solenostomidae (ghost pipefishes), Aulostomidae (trumpetfishes), Fistularidae (cornetfishes), Centriscidae (shrimpfishes) and Macroramphosidae (snipefishes) (Fig. 1, Supplementary Figs. 7-9).

v. Relationships among Blenniiformes, Synbranchiformes and Carangiformes

The UCE phylogeny resolves a strongly supported monophyletic group where Blenniiformes (e.g., blennies, cichlids, livebearers, and mullets) is the sister lineage of a clade containing Synbranchiformes (e.g., swamp eels, gouramies, snakeheads, and leaffishes) and Carangiformes (e.g., flatfishes, jacks and pompanos, billfishes, and barracudas). The discovery of this clade is one of the many dramatic results from molecular phylogenetics of percomorphs[1], as this large and inclusive group contains more than 7,300 species that are classified into 92 taxonomic families.

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

The monophyly of Blenniiformes—originally named Ovalentaria—resulted from a phylogenetic analysis of Sanger sequenced nuclear genes[22]. In the UCE phylogeny, Blenniiformes is monophyletic and contains two major clades: Atherinoidei (formerly Atherinomorpha) and all other lineages of Blenniiformes. Atherinoidei contains three major lineages: 1) Belonoidea (formerly Beloniformes, which includes needlefishes, medakas, halfbeaks, and flying fishes), 2) Cyprinodontoidea (formerly Cyprinodontiformes, which includes killifishes, rivulines, pupfishes, and livebearers), and 3) Atherinoidea (formerly Atheriniformes, which includes silversides and rainbowfishes). Phylogenomic analysis of our UCE dataset results in a well-resolved phylogeny of Atherinoidei, where every node along the backbone of the atherinoid tree is supported with a 100% bootstrap score (Fig. 1, Supplementary Fig. 10). Morphological phylogenies resolve Atherinoidea as the sister lineage of a clade containing Belonoidea and Cyprinodontoidea[149,207], but the UCE phylogeny resolves Atherinoidea and Belonoidea as sister lineages (Fig. 1, Supplementary Fig. 10).

Over the past 15 years, the number of taxonomic families recognized in Cyprinodontoidea (killifishes, rivulines, pupfishes, and livebearers) increased from 10 to 16[181,186]. The recognition of these six additional families resulted from phylogenetic analyses of Sanger sequenced mtDNA and nuclear genes that overturned the results of morphological studies[208-210] and demonstrated the non-monophyly of Cyprinodontidae (pupfishes) and Poeciliidae (livebearers). The UCE phylogeny (Fig. 1, Supplementary Fig. 10) is consistent with morphological phylogenetic analyses in the resolution of Rivulidae (New World rivulines), Aplocheilidae (Asian rivulines), and Nothobranchiidae (African rivulines) as a monophyletic group, as well as a clade containing Poeciliidae, Anablepidae (four-eyed fishes), *Valencia* (toothcarps), Procatopodidae (African lampeyes), Fundulidae (topminnows), Cyprinodontidae, *Profundulus* (Middle American killifishes), Goodeidae (goodeids), and *Cubanichthys* (Caribbean killifishes)[211,212]. Morphological and molecular phylogenetic studies show congruence on specific relationships within Cyprinodontoidea. For example, the morphological analysis by Costa[212] identified *Profundulus* and Goodeidae as a clade. This result is supported in the UCE phylogeny as well as studies from Sanger sequenced mtDNA and nuclear genes[208-210]. Among the notable differences between molecular and morphological phylogenies of cyprinodontoids is the resolution of Cyprinodontidae and Fundulidae as sister lineages (Fig. 1, Supplementary Fig. 10).

Belonoidea is monophyletic in the UCE phylogeny, but despite limited taxon sampling the families Zenarchopteridae and Hemiramphidae are found to be paraphyletic (Fig. 1, Supplementary Fig. 10). Five families of Belonoidea are recognized in Eschmeyer's Catalog of Fishes[181]. Phylogenies resulting from analyses of morphological characters and Sanger sequenced mtDNA nest Scomberesocidae (sauries) well within Belonidae (needlefishes) and resolve Hemiramphidae (halfbeaks) as paraphyletic relative to Exocoetidae (flyingfishes)[213,214]. In the UCE phylogeny, the hemiramphid *Oxyporhamphus micropterus* is more closely related to the sampled species of Exocoetidae than the other two sampled hemiramphids (Fig. 1, Supplementary Fig. 10), as previously inferred using morphological data[215]. The new phylogeny also resolves *Zenarchopterus dispar* as more closely related to the sampled belonid species *Xenentodon cancila* than to the other two sampled zenarchopterid species (Fig. 1, Supplementary Fig. 10).

There are 11 taxonomic families of Atherinoidea recognized in Eschmeyer's Catalog of Fishes[181], but Notocheiridae is well nested in Atherinopsidae in phylogenetic analyses of Sanger sequenced mtDNA and nuclear genes[216,217]. Of the ten other families, eight are sampled in the UCE phylogeny. Missing from the analysis is the monotypic Dentatherinidae (Mercer's tusked silverside) and Telmatherinidae (Celebes rainbowfishes). The UCE phylogeny is consistent with current classifications and previous molecular and morphological phylogenetic analyses in resolving Atherinopsidae (New World silversides) as the sister lineage of all other atherinoids[1,21,216,218] (Fig. 1, Supplementary Fig. 10). Another area of agreement in the UCE phylogeny and previous molecular analyses is the resolution of a clade containing the monogeneric Atherionidae (pricklenose silversides) and Phallostethidae (priapiumfishes)[217] (Fig. 1, Supplementary Fig. 10).

There are differences in the recognition of taxonomic families of Atherinoidea in Eschmeyer's Catalog of Fishes[181] and Nelson et al.[176] that involve lineages associated with Melanotaeniidae (rainbowfishes). Following Dyer and Chernoff[218], Nelson et al.[176] treat Bedotiidae (Madagascar rainbowfishes), Pseudomugilidae (blue eyes), and Telmatherinidae as subfamilies of Melanotaeniidae. This delimitation of Melanotaeniidae is not supported in the UCE phylogeny as Bedotiidae is resolved as the sister lineage of Atherinidae (Old World silversides) (Fig. 1, Supplementary Fig. 10). In previous analyses of Sanger sequenced mtDNA and nuclear genes, Melanotaeniidae is paraphyletic because the species *Cairinsichthys rhombosomoides* is resolved as the sister lineage of a clade containing all sampled species of Telmatherinidae and Pseudomugilidae[216,217]; however, in the UCE phylogeny Melanotaeniidae—sampled with *Cairinsichthys* and *Iriatherina werneri*—is monophyletic with strong node support (Fig. 1, Supplementary Fig. 10). The non-monophyly of Melanotaeniidae in previous phylogenetic analyses is likely driven by limited phylogenetic informativeness of Sanger sequenced genes to resolve relationships among Atherinoidea, as evidenced by the low bootstrap and Bayesian posterior node support values associated with these phylogenies[216,217].

vii. Blenniiformes: Phylogenetic relationships of Cichlidae, **Pholidichthys** *and Polycentridae*

Within Blenniiformes, the UCE phylogeny resolves a clade containing Cichlidae, *Pholidichthys* (engineer gobies) and Polycentridae (leaffishes) (Fig. 1, Supplementary Fig. 11). Before the advent of molecular phylogenetics, the morphology of the pharyngeal jaw apparatus was cited as evidence to group Cichlidae with Labridae (wrasses and parrotfishes), Embiotocidae (surfperches), and Pomacentridae (damselfishes) in a group named Labroidei[219-222]. Phylogenetic analyses of ten Sanger sequenced nuclear genes strongly resolved *Pholidichthys* (engineer gobies) and Cichlidae as sister lineages, but these analyses did not confidently identify a sister lineage of this clade within the Blenniiformes[1,22]. As recently delimited[223], Polycentridae contains five species classified among four genera distributed in freshwater habitats in Africa and South America: *Afronandus sheljuzhkoi* (Africa), *Polycentropsis abbreviata* (Africa), *Polycentrus* (two species in South America), and *Monocirrhus polyacanthus* (South America). The resolution of the freshwater Polycentridae as the sister lineage of the clade containing *Pholidichthys*-Cichlidae provides insight into the origin of freshwater blenniiform lineages and the biogeographic relationships of freshwater fishes in South America and Africa[224,225].

viii. Blenniiformes: Relationships of Mugilidae, Ambassidae, Pseudochromidae, Congrogadidae and Pomacentridae

The phylogenetic relationships of Mugilidae (mullets) have long vexed phylogenetic studies of acanthomorphs, leading Stiassny[226] to declare in a morphological phylogenetic study that "without mullets our lives would be a lot simpler." Morphological analysis of branchial musculature supported a hypothesis that Mugilidae and Atherinoidei (formerly Atherinomorpha) are sister lineages[227], but analysis of pelvic girdle morphology supported an affinity with other percomorph lineages[226]. The heterogeneity of relationships inferred from these two different anatomical systems appears explained in the results of molecular phylogenetic analyses with Mugilidae, Atherinoidei, or other "higher" percomorph lineages sensu Johnson and Patterson[18] resolved in Blenniiformes. In Sanger sequencing efforts, the sister lineage of Mugilidae within Blenniiformes varies between Plesiopidae (longfins) and Embiotocidae (surfperches), always with weak node support[1,22,177]. However, analysis of the UCE dataset and phylogenomic inferences based on exon data[15] both resolve Mugilidae and Ambassidae as sister lineages with strong node support (Fig. 1, Supplementary Fig. 11).

In phylogenetic studies of Sanger sequenced mtDNA and nuclear genes, Pseudochromidae (dottybacks) is resolved as paraphyletic relative to Plesiopidae (roundheads) and Pomacentridae (damselfishes)[1,21]. In the UCE phylogeny, Pseudochromidae is paraphyletic because Congrogadidae (eelblennies) is resolved as the sister lineage of a clade containing the remaining species of Pseudochromidae, Plesiopidae, Pomacentridae, Grammatidae (basslets), Opistognathidae (jawfsihes), Gobiesocidae (clingfishes), and Blennioidei (blennies) (Fig. 1, Supplementary Fig. 11).

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

The UCE phylogeny is congruent with trees inferred using exon data and Sanger sequenced mtDNA and nuclear genes in resolving a clade containing Grammatidae, Opistognathidae, Gobiesocidae, and Blennioidei[1,15,21], but differs in resolving Embiotocidae (surfperches) as the sister lineage of this clade (Fig. 1, Supplementary Fig. 11). Grammatidae and Opistognathidae are successive outgroups to a clade containing Gobiesocidae and Blennioidei (Fig. 1, Supplementary Fig. 11). In the UCE phylogeny, the relationships among the families of Blennioidei—Tripterygiidae (triplefin blennies), Dactyloscopidae (sand stargazers), Blenniidae (combtooth blennies), Clinidae (kelp blennies), Labrisomidae (labrisomid blennies), and Chaenopsidae (tube blennies)—are nearly identical to those inferred from Sanger sequenced mtDNA and nuclear genes[1,21] (Fig. 1, Supplementary Fig. 11). However, a study with the largest sampling of blennioid species indicates that Labrisomidae and Chaenopsidae are both paraphyletic[228].

x. Phylogenetic relationships of Synbranchiformes

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

One of the many surprises to emerge from the molecular phylogenies of percomorphs was the resolution of *Indostomus* (armored sticklebacks) as nested within Synbranchoidei[1,177,192,229,230]. Traditionally, *Indostomus* was classified with seahorses, shrimpfish, and sticklebacks in the polyphyletic Gasterosteiformes based on the presence of dermal bony plates along the side of the body, a reduced cranial skeleton, and a small mouth size[186]. Analysis of developmental ontogeny of several morphological traits led to the conclusion that *Indostomus* is closely related to sticklebacks (Gasterosteidae)[231]. However, *Indostomus* and sticklebacks are distantly related in all molecular phylogenies and Gasterosteidae is classified here in Perciformes. Aside from the resolution of *Indostomus* as a synbranchoid, specifically as the sister lineage of Synbranchidae (swamp eels), the UCE phylogeny of Synbranchoidei is identical to relationships inferred from morphology where Synbranchidae is resolved as the sister lineage of a clade containing Chaudhuriidae (earthworm eels) and Mastacembelidae (freshwater spiny eels)[232] (Fig. 1, Supplementary Fig. 12).

Anabantoidei—delimited here as including Nandidae (Asian leaffishes), Badidae (chameleonfishes), Pristolepididae (Malayan leaffishes), Channidae (snakeheads), Helostomatidae (Kissing Gourami), Anabantidae (climbing gouramies), and Osphronemidae (gouramies and fighting fishes)—is monophyletic in the UCE phylogeny and characterized by the unique possession of teeth on the parasphenoid[223,233:9-12]. The UCE phylogeny resolves a clade containing Pristolepididae, Nandidae, and Badidae (Fig. 1, Supplementary Figs. 12, 13), which is supported with a unique morphology of the ventral gill arch musculature where the *rectus ventralis IV* has an additional insertion on the ceratobranchial 5[223,234]. The clade containing Badidae and Nandidae is supported with two morphological traits: 1) a distally divided haemal spine on the second preural centrum and 2) the restriction of the attachments cells in eggs to the ventral side of the yolk sac[223: Figs. 2d-f, 4]. Previous classifications grouped Pristolepididae and Badidae in Nandidae[186]. Given that the current delimitation of Nandidae and Pristolepididae each contain a single genus and Badidae includes two genera, future classifications can reduce monogeneric families and limit redundant taxonomic group names by classifying all these lineages in Nandidae.

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

xi. Phylogenetic relationships of Carangiformes

The UCE phylogeny is broadly congruent with other studies using UCEs[48], but differs in the relationships of *Lates*, *Centropomus* (snooks), and *Sphyraena* (barracudas) (Fig. 1, Supplementary Fig. 14). Analyses of Sanger sequenced nuclear genes consistently supported the monophyly of Carangiformes[1,21,235,236], but did not strongly support the relationships among the major carangiform clades. The UCE phylogeny includes a clade containing Centropomidae (sampled with *Lates* and *Centropomus*), *Lactarius lactarius* (False Trevally), and *Sphyraena*. Previous analyses using UCEs also resolved Centropomidae as monophyletic[48], but placed *Sphyraena* as the sister lineage of all other Carangiformes. A phylogenetic analysis of Carangiformes based on a dataset that combines a smaller number of UCE loci with discretely coded morphological characters resolves Centropomidae as paraphyletic with *Lates* and *Psammoperca*, forming a clade that is sister to a lineage containing *Centropomus*, *Lactarius* and *Sphyraena*[237].

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

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

xii. Eupercaria: relationships among Perciformes, Centrarchiformes, Labriformes, Acropomatiformes and Acanthuriformes

Phylogenetic analyses of Sanger sequenced loci led to the resolution of Eupercaria, an inclusive clade that contains more than 37% of species and 53% of all taxonomic families in Percomorpha[174]. While earlier studies resolved a clade containing Perciformes, Centrarchiformes, Labriformes, Acropomatiformes, and Acanthuriformes, phylogenies inferred from Sanger sequenced genes provided little resolution for the relationships among the major lineages of Eupercaria[1,21]. Analysis of the UCE dataset results in a phylogeny where Eupercaria is resolved as a clade with strong support for the relationships among the major lineages; Perciformes, Centrarchiformes, and Labriformes are found to be successive outgroups to a clade containing Acropomatiformes and Acanthuriformes. All of the nodes along the backbone of the eupercarian phylogeny are supported with bootstrap values of 100% except the clade containing Acropomatiformes and Acanthuriformes (BSS = 99%) (Fig. 2, Supplementary Fig. 22). The phylogenomic analyses of the UCE loci resolve this substantial issue of the teleost phylogeny, which was once identified as the new bush on the top of the percomorph phylogeny[21].

xiii. Phylogenetic relationships of Perciformes

Prior to the application of molecular data to investigate the phylogenetic relationships of teleosts, the vast majority of percomorphs were classified in the catchall taxon Perciformes. In addition to perciforms, percomorphs included morphologically unique and disparate lineages such as Pleuronectiformes (flatfishes), Tetraodontiformes (pufferfishes), and Gasterosteiformes (sticklebacks and seahorses). Any lineage of percomorph that was not as morphologically distinctive as a flatfish or seahorse was classified in Perciformes. At the end of the 20th century Perciformes contained more than 10,000 species and 160 taxonomic families[186]. Phylogenetic analyses of molecular datasets revealed that the perciform wastebasket contained lineages that spanned much of the backbone of the Percomorpha phylogeny. The UCE phylogeny offers a confirmation for the disassembly of Perciformes that involves the migration of more than 100 taxonomic families into nearly all other major lineages of Percomorpha.

An entirely different concept and delimitation of Perciformes emerged from molecular phylogenetic studies[1,19,21,177,187,193,238-241]. No longer a taxonomic wastebasket, Perciformes (as delimited here) contains more than 3,200 species that are classified among at least 53 taxonomic families and comprises a diverse array of lineages that not only were previously classified as perciforms, but also as scorpaeniforms and gasterosteiforms[3,176]. In addition to the namesake Percidae (perches, walleyes, and darters), the newer concept of Perciformes resulting from molecular phylogenetic analyses includes seabasses, scorpionfishes, rockfishes, sculpins, searobins, weaverfishes, notothenioids, eelpouts, sticklebacks, flatheads, and many others (Supplementary Table 3).

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

In addition to the non-monophyly of the traditional Serranidae, the molecular phylogeny of Perciformes provides several strongly supported relationships that were not anticipated from inferences using morphological characters[18,205,244]. The UCE phylogeny is congruent with earlier analyses using Sanger sequenced loci but provides greater resolution and node support than obtained in earlier efforts. The commercially and scientifically important freshwater lineage Percidae is resolved in a clade that contains the marine *Niphon spinosus* and Trachinidae (weaverfishes), a lineage we refer to as Percoidei (Fig. 2, Supplementary Fig. 16, Supplementary Table 3). Notothenioidei includes the well-known Antarctic adaptive radiation as well as *Percophis brasiliensis* (Brazilian Flathead), which is distributed in the Atlantic Ocean from the coast of southern Brazil to central Argentina[245]. Notothenioidei is strongly resolved as the sister lineage of a new delimitation of Scorpaenoidei that includes almost all the lineages traditionally classified in Scorpaeniformes such as Platycephalidae (flatheads), Scorpaenidae (scorpionfishes and rockfishes), Triglidae (searobins), Bembridae (deepwater flatheads), Platycephalidae (flatheads), Hoplichthyidae (ghost flatheads), Hexagrammidae (greenlings), Trichodontidae (sandfishes), Cyclopteridae (lumpfishes), Liparidae (snailfishes), and Cottidae (sculpins). In addition to these classic scorpaeniform lineages the new delimitation of Scorpaenoidei includes

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

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

Gasterosteoidea and Zoarcoidea resolve as sister lineages with strong node support, which is a result supported in earlier phylogenetic analyses of Sanger sequenced mtDNA and nuclear genes[1,21]. Within Zoarcoidea the Bathymasteridae (ronquils) are resolved as the sister lineage of all other zoarcoids. In an earlier study using Sanger sequenced loci, Bathymasteridae was resolved as paraphyletic[1], but the UCE phylogenetic analyses sample all three bathymasterid genera and strongly support the lineage as a monophyletic group (Supplementary Fig. 18). *Scytalina cerdale* (Graveldiver) is nested well within Stichaeidae (Supplementary Fig. 18) while *Gymnoclinus cristulatus* (Trident Prickleback) is distantly related to other stichaeids (Supplementary Fig. 19), resolving as the sister lineage of Neozoarcidae. Previous phylogenetic analyses of morphology and Sanger sequenced mtDNA and nuclear genes resolve Stichaeidae as paraphyletic[247-249]. The zoarcoid lineages *Cryptacanthodes* (wrymouths), Lumpenidae (pricklebacks), *Zaprora silenus* (Prowfish), Opisthocentridae (ocellated blennies), *Ptilichthys goodei* (Quillfish), Pholidae (gunnels), *Gymnoclinus*, Neozoarcidae, Anarhichadidae (wolffishes), and Zoarcidae (eelpouts) resolve as a strongly supported clade that is the sister lineage of the paraphyletic Stichaeidae (Fig. 2, Supplementary Figs. 18,19).

xiii. Phylogenetic relationships of Centrarchiformes

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

The classification of Centrarchiformes is dynamic and unsettled, reflected in part by a high proportion of families that contain a single genus. Molecular phylogenies consistently resolve two sets of traditionally delimited centrarchiform families as non-monophyletic. First, the two species of *Percalates* were traditionally classified as Percichthyidae[244], but resolve as the sister lineage of all other centrachiforms[1,21,174,236,250]. There is no described taxonomic family to accommodate the classification of *Percalates*. Second, the classification of families within Cirrhitoidea was dramatically realigned as a result of molecular phylogenetic analyses. Traditionally, Cheilodactylidae (morwongs) contained three to five genera and approximately 20 species[202,252]. Previous phylogenetic analyses of mtDNA genes, morphological characters, and UCE data resolved Cheilodactylidae as polyphyletic, with all but two of the species traditionally classified as cheilodactylids nested within a paraphyletic Latridae[253-255]. The findings of these phylogenetic analyses resulted in a transfer of these species to Latridae from Cheilodactylidae. The new UCE phylogeny is consistent with these previous results, but differs from the phylogeny presented in Ludt et al.[255] in resolving *Aplodactylus* rather than *Chironemus* as the sister lineage of *Cheilodactylus* (Fig. 2, Supplementary Fig. 20).

xiv. Phylogenetic relationships of Labriformes

The UCE phylogeny strongly resolves a clade we delimit as Labriformes which contains two major lineages: Uranoscopoidei and Labroidei (Supplementary Fig. 21). As resolved in previous phylogenies inferred from Sanger sequenced nuclear genes[198], Uranoscopoidei contains Uranoscopidae (stargazers), Ammodytidae (sandlances), and Pinguipedidae (sandperches) as successive sister lineages to a clade containing the enigmatic *Cheimarrichthys fosteri* (Torrentfish) and Leptoscopidae (southern sandfishes) (Fig. 2, Supplementary Fig. 21). Morphological studies place *Cheimarrichthys* as closely related to Pinguipedidae or as the sister lineage of all "trachinoids," which include all the lineages delimited here as Uranoscopoidei[256-258]. The hypothesis that *Cheimarrichthys* and Pinguipedidae share common ancestry was rejected through the discovery that *Cheimarrichthys* shares more derived morphological character states with Leptoscopidae than any other "trachinoid" or uranoscopoid lineage[259]. Reflective of their shared common ancestry, *Cheimarrichthys* and Leptoscopidae have a similar geographic distribution; *Cheimarrichthys* is an anadromous species widely distributed among the rivers of New Zealand and leptoscopids are distributed along the Pacific and Indian coasts of Australia and New Zealand [260,261].

Labroidei includes the sister lineages *Centrogenys vaigiensis* (False Scorpionfish) and Labridae (wrasses and parrotfishes) (Fig. 2, Supplementary Fig. 21). As discussed above regarding Blenniiformes, the species rich marine Labridae and the freshwater Cichlidae were hypothesized as closely related based on the morphology of the modified "labroid" pharyngeal jaw apparatus[219-221], which is now known to have originated multiple times in Percomorpha[22]. Previous molecular phylogenetic analyses using Sanger sequenced nuclear genes demonstrated that labrids and cichlids are not closely related despite both having modified "labroid" pharyngeal jaws, but these early molecular studies resulted in an ambiguous and poorly supported resolution of the species rich Labridae[1,22]. The resolution of Labridae and *Centrogenys vaigiensis* as sister lineages in the UCE phylogeny is interesting as both lineages have all three components of the modified labroid pharyngeal jaw apparatus[22].

xv. Phylogenetic relationships of Acropomatiformes

The discovery of Acropomatiformes resulted entirely from phylogenetic analyses of Sanger sequenced mtDNA and nuclear and genes[1,198,236,245] and was never intimated through the study of morphology[205,244]. The lineage is an odd assortment of deep sea and near shore percomorph lineages that were previously classified in the wastebasket version of Perciformes and the demonstrably polyphyletic Trachinoidei[1,198,245]. While molecular studies consistently resolve Acropomatiformes as a clade, its monophyly is not strongly supported with Bayesian posteriors or bootstrap values and relationships within the clade differ dramatically across studies[1,198,236,245,262].

The UCE phylogeny resolves Acropomatiformes as monophyletic with 100% bootstrap support (Fig. 2, Supplementary Fig. 22). All but two nodes within Acropomatiformes are present in 100% of the bootstrap replicates. First, the clade containing *Bathyclupea* (deepsea herrings), *Champsodon* (gapers), Creediidae (sandburrowers), and Hemerocoetidae (signalfishes) is supported with a bootstrap score of 97%. Second, the clade containing *Scombrops* (gnomefishes), Symphysanodontidae (slopefishes), Epigonidae (deepwater cardinalfishes), and Howellidae (oceanic basslets) is supported with a 99% bootstrap score (Fig. 2, Supplementary Fig. 22). The relationships among acropomatiforms in the UCE tree are quite different from any previous study and include the non-monophyly of Polyprionidae (wreckfishes) as *Polyprion* is resolved as the sister lineage of a clade containing *Glaucosoma* (pearl perches), Pempheridae (sweepers), and *Lateolabrax* (Asian seaperches) while *Stereolepis* is the sister lineage of a clade containing *Banjos* (banjofishes) and Pentacerotidae (armorheads). The resolution of Howellidae and Epigonidae as sister lineages in the UCE phylogeny is interesting in the context of four osteological traits shared between these two lineages and the possibility of additional shared traits in Howellidae and other acropomatiform lineages[263]. Future phylogenetic studies will round out the sampling of Acropomatiformes by including *Dinolestes lewini* (Long-finned Pike), Malakichthyidae (temperate ocean-basses), and Synagropidae (splitfin ocean-basses) to take advantage of the strong phylogenetic resolution provided by the UCE loci for this clade.

xvi. Phylogenetic relationships of Acanthuriformes

The first wave of molecular phylogenetic analyses of percomorphs was based on whole mitochondrial genomes and small sets of Sanger sequenced mitochondrial and nuclear genes. The major lineages of percomorphs and their composition began to emerge because of these molecular phylogenetic analyses. The monophyly of the major percomorph lineages and their relationships to one another are well resolved in the UCE phylogeny and we delimit these inclusive clades as taxonomic orders (e.g., Gobiiformes, Scombriformes, and Perciformes). Hampering these earliest molecular phylogenetic studies of percomorphs was a lack of phylogenetic resolution for relationships within and between major lineages of Eupercaria which include Perciformes, Centrarchiformes, Acropomatiformes, and what Smith et al.[25] delimit as Acanthuriformes. The lack of phylogenetic resolution was particularly acute in Acanthuriformes, a lineage that includes more than 2,320 species classified in 56 taxonomic families. The phylogenies resulting from earlier molecular studies resolved taxonomic families within Acanthuriformes as monophyletic with high bootstrap support [e.g., Chaetodontidae (butterflyfishes), Acanthuridae (surgeonfishes), and Sparidae (porgies)], but had very poor support for relationships among these lineages[1,21,25].

Acanthuriformes is monophyletic in the UCE phylogeny with strong bootstrap node support; however, six nodes along the backbone of the acanthuriform phylogeny have bootstrap scores ranging from 70% to 94% (Fig. 2, Supplementary Figs. 22-24). Despite this lower support for a small portion of the acanthuriform phylogeny, the UCE tree provides insight into several issues not resolved in earlier molecular studies of percomorph phylogenetics. First, Gerreidae (morjarras), which long evaded phylogenetic resolution, is the sister lineage of all other Acanthuriformes (Fig. 2, Supplementary Fig. 22). Second, Moronidae (temperate basses) and Sillaginidae (whitings) are resolved here as sister lineages (Fig. 2, Supplementary Fig. 22). Though they were resolved as a closely related in earlier molecular studies[1], Lutjanidae and Haemulidae are distantly related in the UCE phylogeny (Fig. 2, Supplementary Fig. 22,23). Finally, ten lineages identified as *incertae sedis* within Eupercaria by Betancur-R et al.[174] are phylogenetically resolved with moderate to high bootstrap support in Acanthuriformes (Fig. 2, Supplementary Figs. 22-24).

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

While the discovery that Lophioidei and Tetraodontoidei are closely related was based on phylogenetic analyses of molecular data, subsequent investigation of their morphology identified several soft tissue characters that are likely synapomorphies of a lophioid-tetraodontoid clade[265]. It has also been discovered that the larvae of these two lineages exhibit unique morphology and pigmentation[266]. Congruent with earlier studies, the UCE tree resolves an inclusive lineage containing *Siganus* (rabbitfishes), Scatophagidae (scats), Priacanthidae (bigeyes), Cepolidae (bandfishes), and Caproidae (boarfishes) as the sister lineage of the Lophioidei-Tetraodontoidei clade. These nodes in the UCE phylogeny are all characterized by high bootstrap support values (Fig. 2, Supplementary Figs. 24,25).

xvii. Acanthuriformes: phylogenetic relationships of Tetraodontoidei

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

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

xviii. Acanthuriformes: phylogenetic relationships of Lophioidei

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

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

d. ASTRAL-III species tree analysis

The ASTRAL-III inferred summary species tree is similar to the phylogeny inferred from the concatenated data analyses (Figs. 1,2, Supplementary Figs. 1-25) in resolving Lampriformes as the sister lineage of a monophyletic Paracanthopterygii, monophyly of Acanthopterygii, and very similar relationships among the major lineages of Percomorpha (Supplementary Fig. 26). The non-collapsed species tree is available on Dryad. The ASTRAL-III species tree differs from the concatenated-dataset, maximum likelihood phylogeny in the inference of Trachichthyiformes and Beryciformes as a clade that is sister to Percomorpha, the gadiform *Bregmaceros* as the sister lineage of a clade containing *Stylephorus* and all other gadiforms, the placement of *Centrogenys*, and the non-monophyly of Acropomatiformes and Labriformes. The ASTRAL-III species tree also does not resolve Gerreidae as the sister lineage of all other Acanthuriformes. In general, the phylogenetic placement of major eupercarian clades in the tree estimated under the multi-species coalescent model differs from the topology of the concatenated-dataset, maximum likelihood trees, but nodal support values were significantly stronger for the backbone relationships inferred using maximum likelihood methods (Supplementary Figs. 1-26).

e. Divergence-time estimates

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

Our age estimates are largely in agreement with those presented in previous phylogenomic analyses of ~1,000 UCE loci[4] and ~1,100 exons[15] (Supplementary Fig. 29). For most major clades, our analyses inferred slightly older stem ages, but with 95% highest posterior densities that overlap with the dates reported in previous studies (Supplementary Fig. 29). However, our analyses inferred comparably younger stem lineage ages for *Polymixia*, Percopsiformes, and clades within Eupercaria[4,15]. Our stem lineage age estimates are significantly older for Gobiiformes and the Syngnathiformes-Scombriformes clade[4]. Perhaps as a result of incongruent phylogenetic topologies, our analyses inferred younger stem age estimates for Acanthuriformes than estimated in the phylogenomic analysis of exon data[15].

We similarly estimate crown lineage ages for major clades with 95% highest posterior densities that largely overlap with previous phylogenomic analyses[4,15]. Exceptions include the crown age estimates of Acanthuriformes, Syngnathiformes and Scombriformes, Trachichthyiformes, Beryciformes, Gobiiformes, Syngnathiformes and Blenniiformes. Many of the discrepancies in crown ages likely result from differences among inferred phylogenetic trees (especially within Eupercaria), or from the relatively sparse taxon sampling in previous phylogenomic studies[4,15].

f. Diversification rate analyses

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

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

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

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

The fact that many of the rate shifts identified by BAMM occur along tipwards branches may indicate that the species richness of Acanthomorpha is driven by relatively recent, more phylogenetically or geographically localized radiations instead of a burst of diversification after the K-Pg. This pattern does not seem to be unique to acanthomorphs; numerous radiations have shown to have a similar pattern of constant diversification across the K-Pg boundary despite bursts in the origin of disparity in morphological and ecological traits[7]. Nevertheless, there is a chance that this pattern is the by-product of analytical corrections for incomplete sampling. Such corrections may reduce the statistical power to infer shifts in diversification rates and increase the probability of Type II error when rate variation is present[286]. It is also known that Bayesian methods of diversification rate estimation, including BAMM and TESS, penalize parameter-rich diversification models and favor less-complex models even under liberal priors. Given the infinite number of possible diversification scenarios that could result in the observed phylogeny[287], it is therefore possible that TESS estimated a constant-rate model to best fit our data because of its simplicity rather than its accuracy.

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Supplementary Table 1: Binomial names and higher taxonomic classification of species included in the phylogeny, institutional voucher information for specimens (if applicable), and NCBI SRA BioSample accession numbers. The sixth column ('Morphology Analyses') denotes whether species were included in the body shape analyses, and the seventh column ('Concordance Analyses') denotes if samples were included in the BUCKy concordance factor analyses. NCBI BioSample numbers denoted with an asterisk (*) indicate samples 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	*Alepisaurus ferox*	YPM ICH 25657	SAMN05915027	✓	
Aulopiformes	Paralepididae	*Notolepis coatsi*	YPM ICH 022576		✓	
Myctophiformes	Myctophidae	*Benthosema glaciale*	See NCBI SRA	SAMEA4028768*	✓	
Myctophiformes	Myctophidae	*Ceratoscopelus warmingii*	SIO 0510-09-28	SAMN05915048	✓	
Myctophiformes	Myctophidae	*Dasyscopelus selenops*	YPM ICH 25697		✓	✓
Myctophiformes	Myctophidae	*Notoscopelus caudispinosus*	YPM ICH 028430		✓	
Myctophiformes	Neoscopelidae	*Neoscopelus macrolepidotus*	ASIZP 0913636		✓	
Myctophiformes	Neoscopelidae	*Neoscopelus microchir*	ASIZO 0910701		✓	✓
Myctophiformes	Neoscopelidae	*Scopelengys tristis*	UW 115136		✓	
Lampriformes	*Lampris*	*Lampris guttatus*	SIO 04-195	SAMN05915079	✓	✓
Lampriformes	Regalecidae	*Regalecus glesne*	YPM ICH 26237	SAMN05915116		
Lampriformes	Trachipteridae	*Zu elongatus*	NMNZ P.042029/TS3	SAMN05915140	✓	✓
Polymixiiformes	*Polymixia*	*Polymixia lowei*	YPM ICH 025498	SAMN05915104	✓	✓
Percopsiformes		*Aphredoderus sayanus*	YPM ICH 25183	SAMN05915031	✓	✓
Percopsiformes	Amblyopsidae	*Typhlichthys subterraneus*	See NCBI SRA	SAMEA4028771*	✓	
Percopsiformes	Percopsidae	*Percopsis omiscomycus*	YPM ICH 017307	SAMN05915097		✓
Percopsiformes	Percopsidae	*Percopsis transmontana*	See NCBI SRA	SAMEA4028770*		
Zeiformes	Parazenidae	*Cyttopsis rosea*	See NCBI SRA	SAMEA4028773*	✓	✓
Zeiformes	Zeidae	*Zenopsis conchifera*	MCZ 155779	SAMN05915138	✓	
Zeiformes	Zeidae	*Zeus faber*	NSMT 62233	SAMN05915139	✓	✓
Stylephoriformes		*Stylephorus chordatus*	YPM ICH 25672	SAMN05915127	✓	✓
Gadiformes	*Bregmaceros*	*Bregmaceros cantori*	See NCBI SRA	SAMEA4028775*	✓	✓
Gadiformes	*Melanonus*	*Melanonus zugmayeri*	See NCBI SRA	SAMEA4028779*	✓	
Gadiformes	Muraenolepididae	*Muraenolepis marmoratus*	See NCBI SRA	SAMEA4028780*		
Gadiformes	Trachyrincidae	*Trachyrincus murrayi*	See NCBI SRA	SAMEA4028782*		
Gadiformes	Trachyrincidae	*Trachyrincus scabrus*	See NCBI SRA	SAMEA4028781*		
Gadiformes	Moridae	*Laemonema laureysi*	See NCBI SRA	SAMEA4028784*	✓	
Gadiformes	Moridae	*Mora moro*	See NCBI SRA	SAMEA4028783*	✓	

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

Beryciformes	Holocentridae	*Sargocentron coruscum*	YPM ICH 23957	SAMN05915119	✓	
Beryciformes	Berycidae	*Beryx decadactylus*	YFTC 13731, n.v.			✓
Beryciformes	Berycidae	*Beryx splendens*	See NCBI SRA	SAMEA4028808*	✓	
Beryciformes	Berycidae	*Centroberyx druzhinini*	ASIZD 0911026		✓	
Beryciformes	Melamphaidae	*Melamphaes longivelis*	YPM ICH 028501		✓	
Beryciformes	Melamphaidae	*Poromitra gibbsi*	YPM ICH 028486		✓	
Beryciformes	Melamphaidae	*Scopelogadus beanii*	YPM ICH 028434		✓	
Beryciformes	*Rondeletia*	*Rondeletia bicolor*	YPM ICH 027515		✓	
Beryciformes	*Rondeletia*	*Rondeletia loricata*	YPM ICH 25674	SAMN05915117	✓	
Beryciformes	Cetomimidae	*Ataxolepis apus*	YPM ICH 025531			
Beryciformes	Cetomimidae	*Cetostoma regani*	YPM ICH 028287		✓	
Beryciformes	Cetomimidae	*Ditropichthys storeri*	YPM ICH 028280		✓	
Beryciformes	Cetomimidae	*Mirapinna esau*	YFTC 26026, n.v.			
Beryciformes		*Barbourisia rufa*	YPM ICH 010068		✓	✓
Beryciformes	Stephanoberycidae	*Acanthochaenus luetkenii*	YFTC 24122, n.v.		✓	
Beryciformes	Stephanoberycidae	*Acanthochaenus luetkenii*	YFTC 24124, n.v.			
Beryciformes	Stephanoberycidae	*Malacosarcus macrostoma*	USNM 400019			
Ophidiiformes	Dinematichthyidae	*Diancistrus jeffjohnsoni*	YFTC 32439, n.v.		✓	
Ophidiiformes	Dinematichthyidae	*Dinematichthys iluocoeteoides*	USNM 334123			✓
Ophidiiformes	Dinematichthyidae	*Diancistrus tongaensis*	USNM 374200		✓	
Ophidiiformes	Dinematichthyidae	*Ogilbia cayorum*	ZMUC P771463			
Ophidiiformes	Dinematichthyidae	*Ogilbichthys* sp.	USNM 349073			
Ophidiiformes	Dinematichthyidae	*Typhliasina pearsei*	ZMUC P771455			
Ophidiiformes	Bythitidae	*Aphyonus gelatinosus*	ZMUB/MAR 3880			
Ophidiiformes	Bythitidae	*Bidenichthys capensis*	KU 6466			
Ophidiiformes	Bythitidae	*Brosmophyciops pautzkei*	SAIAB 86260			
Ophidiiformes	Bythitidae	*Cataetyx messieri*	ZMUC P771617		✓	
Ophidiiformes	Bythitidae	*Diplacanthopoma brachysoma*	MCZ 155341			
Ophidiiformes	Bythitidae	*Megacataetyx niki*	NMNZ P.41257			
Ophidiiformes	Bythitidae	*Parabrotula tanseimaru*	CBM 10557	SAMN18716611*		
Ophidiiformes	Ophidiidae	*Acanthonus armatus*	MNHN 2004-1311			
Ophidiiformes	Ophidiidae	*Apagesoma australe*	ZMUC P771525			
Ophidiiformes	Ophidiidae	*Bassogigas walkeri*	SIO 08-109			✓
Ophidiiformes	Ophidiidae	*Brotula barbata*	See NCBI SRA	SAMEA4028811*	✓	
Ophidiiformes	Ophidiidae	*Carapus acus*	See NCBI SRA	SAMEA4028813*		
Ophidiiformes	Ophidiidae	*Carapus bermudensis*	KU 18739	SAMN05915045		
Ophidiiformes	Ophidiidae	*Chilara taylori*	KU 28277		✓	
Ophidiiformes	Ophidiidae	*Dannevigia tusca*	YFTC 32428, n.v.			
Ophidiiformes	Ophidiidae	*Dicrolene intronigra*	KU 3677		✓	

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

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

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

Scombriformes	Tetragonuridae	*Tetragonurus pacificus*	SNFR 15336	SAMN13222523	
Scombriformes	Chiasmodontidae	*Chiasmodon niger*	YPM ICH 25663	SAMN05915052	✓
Scombriformes	Chiasmodontidae	*Dysalotus alcocki*	YPM ICH 025665	SAMN13222451	✓
Scombriformes	Chiasmodontidae	*Dysalotus oligoscolus*	YPM ICH 025654	SAMN13222452	
Scombriformes	Chiasmodontidae	*Kali kerberti*	UW 115135	SAMN05915076	✓
Scombriformes	Chiasmodontidae	*Kali macrodon*	YPM ICH 027772	SAMN13222468	✓
Scombriformes	Chiasmodontidae	*Kali macrura*	KU 8140	SAMN13222469	
Scombriformes	Chiasmodontidae	*Pseudoscopelus altipinnis*	YPM ICH 027632	SAMN13222498	
Scombriformes	Chiasmodontidae	*Pseudoscopelus astronesthidens*	KU 6518	SAMN13222499	
Scombriformes	Chiasmodontidae	*Pseudoscopelus obtusifrons*	YPM ICH 027787	SAMN13222501	
Scombriformes	Chiasmodontidae	*Pseudoscopelus odontoglossum*	YPM ICH 027854	SAMN13222500	
Scombriformes	Chiasmodontidae	*Pseudoscopelus scutatus*	YPM ICH 025805	SAMN13222503	
Scombriformes	Scombridae	*Acanthocybium solandri*	KU 5425	SAMN13222425	✓
Scombriformes	Scombridae	*Auxis rochei*	CBM 14077	SAMN13222436	✓
Scombriformes	Scombridae	*Auxis thazard*	CBM 12877	SAMN13222437	
Scombriformes	Scombridae	*Euthynnus affinis*	CBM 12671	SAMN13222455	✓
Scombriformes	Scombridae	*Gasterochisma melampus*	NSMT 93197	SAMN13222462	
Scombriformes	Scombridae	*Gymnosarda unicolor*	NSMT 62530	SAMN13222464	✓
Scombriformes	Scombridae	*Katsuwonus pelamis*	CBM 12672	SAMN13222471	✓
Scombriformes	Scombridae	*Rastrelliger kanagurta*	NSMT 76071	SAMN13222505	✓
Scombriformes	Scombridae	*Scomber australasicus*	CBM 12636		✓
Scombriformes	Scombridae	*Scomber japonicus*	CBM 12641	SAMN13222509	✓
Scombriformes	Scombridae	*Scomber scombrus*	YPM ICH 020681	SAMN05915123	✓
Scombriformes	Scombridae	*Scomberomorus maculatus*	Pers. Coll.: P.Wainwright, PW1207	SAMN05915124	✓
Scombriformes	Scombridae	*Scomberomorus niphonius*	CBM 14469	SAMN13222512	
Scombriformes	Scombridae	*Scomberomorus regalis*	KU 30178		✓
Scombriformes	Scombridae	*Thunnus orientalis*	NSMT-P 93077		✓
Scombriformes	Scombridae	*Thunnus tonggol*	SNFR 16558		
Scombriformes	Caristiidae	*Caristius macropus*	UW 113533	SAMN13222445	
Scombriformes	Caristiidae	*Paracaristius maderensis*	YPM ICH 027617	SAMN13222486	
Scombriformes	Caristiidae	*Paracaristius nudarcus*	YPM ICH 25618		
Scombriformes	Bramidae	*Brama caribbea*	YPM ICH 025808	SAMN13222442	✓
Scombriformes	Bramidae	*Brama dussumieri*	CBM 15373	SAMN13222443	✓
Scombriformes	Bramidae	*Brama japonica*	SIO 01-183	SAMN05915040	✓
Scombriformes	Bramidae	*Eumegistus illustris*	n.v. tissue only	SAMN13222454	
Scombriformes	Bramidae	*Pterycombus brama*	KU 8137	SAMN13222504	✓
Scombriformes	Bramidae	*Pterycombus petersii*	OCF-P 20071225		✓

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

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

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

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

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

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

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

Anabantiformes	Nandidae	*Nandus* cf. *oxyrhynchus*	Pers. Coll.: W.L.Smith 488	✓	
Anabantiformes	Channidae	*Channa andrao*	Pers. Coll.: J.Day		
Anabantiformes	Channidae	*Channa argus*	CBM 12593		
Anabantiformes	Channidae	*Channa aurantimaculata*	Pers. Coll.: J.Day		
Anabantiformes	Channidae	*Channa bleheri*	Pers. Coll.: J.Day		
Anabantiformes	Channidae	*Channa gachua*	Pers. Coll.: J.Day	✓	
Anabantiformes	Channidae	*Channa lucius*	UF 236121		
Anabantiformes	Channidae	*Channa marulius*	UF 237264	✓	
Anabantiformes	Channidae	*Channa micropeltes*	Pers. Coll.: W.L.Smith 355	✓	
Anabantiformes	Channidae	*Channa striata*	UF 173357	✓	
Anabantiformes	Channidae	*Parachanna insignis*	CUMV 96133		
Anabantiformes	Channidae	*Parachanna obscura*	CUMV 96491		
Anabantiformes		*Helostoma temminckii*	Pers. Coll.: W.L.Smith 36	✓	
Anabantiformes	Anabantidae	*Anabas testudineus*	UF 237404	✓	
Anabantiformes	Anabantidae	*Ctenopoma acutirostre*	CUMV 93049	✓	
Anabantiformes	Anabantidae	*Ctenopoma gabonense*	CUMV 87803		
Anabantiformes	Anabantidae	*Ctenopoma kingsleyae*	CUMV 91505	✓	
Anabantiformes	Anabantidae	*Ctenopoma maculatum*	CUMV 92275		
Anabantiformes	Anabantidae	*Ctenopoma multispine*	CUMV 91229		
Anabantiformes	Anabantidae	*Ctenopoma muriei*	CUMV 94531	✓	
Anabantiformes	Anabantidae	*Ctenopoma nigropannosum*	CUMV 96662	✓	
Anabantiformes	Anabantidae	*Ctenopoma ocellatum*	Pers. Coll.: W.L.Smith 279		
Anabantiformes	Anabantidae	*Microctenopoma ansorgii*	YPM ICH 025197	✓	
Anabantiformes	Anabantidae	*Microctenopoma fasciolatum*	YPM ICH 32030		
Anabantiformes	Anabantidae	*Microctenopoma nanum*	CUMV 93021	✓	
Anabantiformes	Anabantidae	*Microctenopoma pekkolai*	CUMV 94529		
Anabantiformes	Anabantidae	*Microctenopoma uelense*	CUMV 91502		
Anabantiformes	Anabantidae	*Sandelia bainsii*	SAIAB 199798		
Anabantiformes	Anabantidae	*Sandelia capensis*	SAIAB 186085	✓	
Anabantiformes	Anabantidae	*Sandelia capensis*	SAIAB 186114		
Anabantiformes	Anabantidae	*Sandelia capensis*	SAIAB 186029		
Anabantiformes	Osphronemidae	*Belontia hasselti*	UF 165962	✓	
Anabantiformes	Osphronemidae	*Betta albimarginata*	Pers. Coll.: J.Day		
Anabantiformes	Osphronemidae	*Betta macrostoma*	Pers. Coll.: J.Day	✓	
Anabantiformes	Osphronemidae	*Betta mandor*	YPM ICH 34720		
Anabantiformes	Osphronemidae	*Betta splendens*	Pers. Coll.: J.Day	✓	
Anabantiformes	Osphronemidae	*Ctenops nobilis*	YPM ICH 33735		✓
Anabantiformes	Osphronemidae	*Luciocephalus aura*	UF 167012		

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

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

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

Carangiformes	Carangidae	*Chloroscombrus orqueta*	KU 8495	SAMN05915053	✓	
Carangiformes	Carangidae	*Decapterus maruadsi*	KU 8984	SAMN05785334	✓	
Carangiformes	Carangidae	*Gnathanodon speciosus*	LSUMZ 17993		✓	
Carangiformes	Carangidae	*Hemicaranx bicolor*	MNHN 1913-0110		✓	
Carangiformes	Carangidae	*Megalaspis cordyla*	KU 4705	SAMN05785347	✓	
Carangiformes	Carangidae	*Parastromateus niger*	LSUMZ 17039		✓	
Carangiformes	Carangidae	*Selaroides leptolepis*	LSUMZ 14065		✓	
Carangiformes	Carangidae	*Selene peruviana*	SIO 07-88L			
Carangiformes	Carangidae	*Selene vomer*	LSUMZ 14271		✓	
Carangiformes	Carangidae	*Seriola dumerili*	Pers. Coll.: P.Wainwright, PW2629		✓	
Carangiformes	Carangidae	*Seriola dumerili*	SAIAB ACEP-09-314			
Carangiformes	Carangidae	*Seriola zonata*	KU 1188	SAMN05915125	✓	
Carangiformes	Carangidae	*Trachurus trachurus*	KU 8077	SAMN05785370	✓	
Perciformes	Epinephelidae	*Cephalopholis argus*	CAS CAG01	SAMN05915047	✓	✓
Perciformes	Epinephelidae	*Cephalopholis cruentata*	YPM ICH 24718		✓	
Perciformes	Epinephelidae	*Diploprion drachi*	Pers. Coll.: G. Bernardi		✓	
Perciformes	Epinephelidae	*Jeboehlkia gladifer*	AMNH CUR13192			✓
Perciformes	Epinephelidae	*Liopropoma rubre*	YPM ICH 24752		✓	
Perciformes	Epinephelidae	*Rypticus subbifrenatus*	YPM ICH 24697		✓	
Perciformes	Anthiadidae	*Acanthistius cinctus*	KER 427		✓	✓
Perciformes	Anthiadidae	*Pseudanthias squamipinnis*	Pers. Coll.: M.Alfaro, Alfaro-969	SAMN05915109	✓	✓
Perciformes	Anthiadidae	*Trachypoma macracanthus*	KER 433			
Perciformes	Bembropidae	*Bembrops anatirostris*	YFTC 14558, n.v.		✓	
Perciformes	Bembropidae	*Chrionema furunoi*	NSMT-P 78494			
Perciformes	Serranidae	*Chelidoperca hirundinacea*	NSMT-P115036			
Perciformes	Serranidae	*Hypoplectrus puella*	Pers. Coll.: M.Alfaro, Alfaro-1010.1	SAMN05915074	✓	
Perciformes	Serranidae	*Serranus tigrinus*	Pers. Coll.: P.Wainwright, PW1343: mea207		✓	✓
Perciformes	Trachinidae	*Echiichthys vipera*	YFTC 24258, n.v.			
Perciformes	Trachinidae	*Trachinus radiatus*	n.v.		✓	
Perciformes		*Niphon spinosus*	SIO 00-174		✓	✓
Perciformes	Percidae	*Allohistium cinereum*	UT 91.7531		✓	
Perciformes	Percidae	*Ammocrypta beanii*	INHS 38611		✓	
Perciformes	Percidae	*Ammocrypta pellucida*	YPM ICH 017573		✓	
Perciformes	Percidae	*Crystallaria asprella*	YFTC 686, n.v.		✓	
Perciformes	Percidae	*Etheostoma baileyi*	UT 91.7240		✓	
Perciformes	Percidae	*Etheostoma basilare*	n.v. whole fish in tissue tube		✓	
Perciformes	Percidae	*Etheostoma blennius*	YPM ICH 024144			

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

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

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

Perciformes	Lumpenidae	*Leptoclinus maculatus*	UW 49369	✓	
Perciformes	Lumpenidae	*Leptoclinus maculatus*	UW 151205		✓
Perciformes	Lumpenidae	*Lumpenella longirostris*	UW 151000	✓	
Perciformes	Lumpenidae	*Lumpenus sagitta*	UW 150616	✓	
Perciformes	Lumpenidae	*Poroclinus rothrocki*	UW 150577	✓	
Perciformes		*Zaprora silenus*	UW 152655	✓	
Perciformes		*Zaprora silenus*	UW 150107		
Perciformes	Opisthocentridae	*Askoldia variegata*	UW 44508		
Perciformes	Opisthocentridae	*Opisthocentrus ocellatus*	UW 44935	✓	
Perciformes	Opisthocentridae	*Opisthocentrus tenuis*	UW 47877	✓	
Perciformes	Opisthocentridae	*Opisthocentrus zonope*	UW 47885	✓	
Perciformes	Opisthocentridae	*Pholidapus dybowskii*	UW 47882		
Perciformes		*Ptilichthys goodei*	Pers. Coll.: P.Wainwright, PCW 2416	✓	
Perciformes	Pholidae	*Apodichthys flavidus*	UW 151663	✓	
Perciformes	Pholidae	*Pholis clemensi*	UW 47872		
Perciformes	Pholidae	*Pholis laeta*	UW 43793		
Perciformes	Pholidae	*Pholis ornata*	Pers. Coll.: P.Wainwright, PW244: B27	✓	
Perciformes	Pholidae	*Pholis ornata*	UW 151676		
Perciformes	Pholidae	*Rhodymenichthys dolichogaster*	UW 44516	✓	
Perciformes		*Gymnoclinus cristulatus*	UW 44509		
Perciformes	Neozoarcidae	*Neozoarces steindachneri*	UW 47875		
Perciformes	Anarhichadidae	*Anarhichas orientalis*	UW 150194	✓	
Perciformes	Anarhichadidae	*Anarhichas orientalis*	UW 111905		
Perciformes	Anarhichadidae	*Anarrhichthys ocellatus*	UW 49014		
Perciformes	Zoarcidae	*Bothrocara brunneum*	UW 150525	✓	
Perciformes	Zoarcidae	*Bothrocara molle*	UW 111363	✓	
Perciformes	Zoarcidae	*Bothrocara pusillum*	UW 151315	✓	
Perciformes	Zoarcidae	*Bothrocara zestum*	UW 150975		
Perciformes	Zoarcidae	*Gymnelus viridis*	UW 150119	✓	
Perciformes	Zoarcidae	*Lycenchelys camchatica*	UW 119335	✓	
Perciformes	Zoarcidae	*Lycenchelys crotalinus*	UW 118611	✓	
Perciformes	Zoarcidae	*Lycodapus fierasfer*	UW 115137	✓	
Perciformes	Zoarcidae	*Lycodapus mandibularis*	UW 152155	✓	
Perciformes	Zoarcidae	*Lycodes akuugun*	UW 117198		
Perciformes	Zoarcidae	*Lycodes beringi*	UW 150976	✓	
Perciformes	Zoarcidae	*Lycodes brevipes*	UW 151235	✓	
Perciformes	Zoarcidae	*Lycodes concolor*	UW 150529	✓	
Perciformes	Zoarcidae	*Lycodes cortezianus*	UW 115164	✓	
Perciformes	Zoarcidae	*Lycodes diapterus*	YFTC 13952, n.v.	✓	

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

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

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

Acropomatiformes	Hemerocoetidae	*Enigmapercis* sp.	NSMT-P 114722		✓	
Acropomatiformes	Hemerocoetidae	*Osopsaron formosensis*	NSMT-P 77318			✓
Acropomatiformes	Hemerocoetidae	*Pteropsaron evolans*	NSMT-P 77317			
Eupercifomes	Gerreidae	*Eucinostomus jonesii*	YPM ICH 24864		✓	✓
Eupercifomes	Gerreidae	*Gerres cinereus*	YPM ICH 24843		✓	
Eupercifomes	Moronidae	*Dicentrarchus labrax*	Pers. Coll.: F.J. Sanchez Vazques, U. of Murica		✓	
Eupercifomes	Moronidae	*Morone saxatilis*	YPM ICH 018448		✓	
Eupercifomes	Sillaginidae	*Sillago chondropus*	Pers. Coll.: W.L.Smith			
Eupercifomes	Sillaginidae	*Sillago sihama*	SAIAB 77085		✓	
Eupercifomes	*Drepane*	*Drepane punctata*	ROM 69918		✓	
Eupercifomes	Ephippidae	*Platax orbicularis*	SAIAB 77666		✓	
Eupercifomes	Dinopercidae	*Dinoperca petersi*	SAIAB 81789		✓	
Eupercifomes	Haemulidae	*Haemulon album*	CAS HAL01	SAMN05915068	✓	
Eupercifomes	Haemulidae	*Haemulon flavolineatum*	CAS HFG04	SAMN05915069	✓	
Eupercifomes	Haemulidae	*Haemulon parra*	CAS HPA01	SAMN05915070	✓	
Eupercifomes	Sciaenidae	*Collichthys lucidus*	See NCBI SRA	SAMN10225518*	✓	
Eupercifomes	Sciaenidae	*Larimichthys crocea*	See NCBI SRA	SAMN10434301*	✓	
Eupercifomes	Sciaenidae	*Micropogonias undulatus*	YPM ICH 023546	SAMN05915083	✓	
Eupercifomes	Sciaenidae	*Miichthys miiuy*	See NCBI SRA	SAMN02486174*	✓	
Eupercifomes	Sciaenidae	*Nibea albiflora*	See NCBI SRA	SAMEA1067819*	✓	
Eupercifomes	Sciaenidae	*Pareques acuminatus*	CAS PAC20	SAMN05915094	✓	
Eupercifomes	Monodactylidae	*Monodactylus sebae*	YPM ICH 020540		✓	
Eupercifomes	Lobotidae	*Hapalogenys dampieriensis*	NMV Z 6535			
Eupercifomes	Lobotidae	*Lobotes surinamensis*	Pers. Coll.: P.Wainwright, PW2610		✓	
Eupercifomes	Emmelichthyidae	*Erythrocles schlegelii*	KU 7270		✓	
Eupercifomes	Lutjanidae	*Lutjanus goreensis*	CAS LGO01	SAMN05915081	✓	
Eupercifomes	Malacanthidae	*Caulolatilus princeps*	SIO 08-66		✓	
Eupercifomes	Malacanthidae	*Malacanthus plumieri*	Pers. Coll.: P.Wainwright, PW1198		✓	
Eupercifomes	Pomacanthidae	*Centropyge flavissima*	YPM ICH 026532		✓	
Eupercifomes	Pomacanthidae	*Chaetodontoplus melanosoma*	Pers. Coll.: P.Wainwright, PW643		✓	✓
Eupercifomes	Pomacanthidae	*Holocanthus passer*	Pers. Coll.: P.Wainwright, PW642		✓	✓
Eupercifomes	Pomacanthidae	*Pomacanthus paru*	CAS PPA01	SAMN05915105	✓	
Eupercifomes	Leiognathidae	*Gazza minuta*	YFTC 18187, n.v.		✓	✓
Eupercifomes	Leiognathidae	*Karalla daura*	LSUMZ 8791		✓	
Eupercifomes	Leiognathidae	*Leiognathus equula*	LSUMZ 8683		✓	✓
Eupercifomes	Leiognathidae	*Secutor nuconius*	LSUMZ 8682		✓	
Eupercifomes	Chaetodontidae	*Chaetodon kleinii*	Pers. Coll.: P.Wainwright, PW2291B	SAMN05915049	✓	
Eupercifomes	Chaetodontidae	*Chaetodon leucopleura*	See NCBI SRA	SAMN09765312		

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

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

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

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

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

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

	702-taxon trees	**1,084-taxon trees**		
	Multiple-partition vs IQ-TREEsingle*	IQ-TREEsingle* vs IQ-TREEmulti†	IQ-TREEsingle* vs RAxML	IQ-TREEmulti† vs RAxML
	Acanthistius cinctus *Arripis trutta* *Chloroscombrus orqueta* *Icosteus aenigmaticus* *Lycodes concolor* *Pomatomus saltatrix* *Pseudanthias squamipinnis* *Selaroides leptolepis* *Sillago sihama*	*Acanthistius cinctus* *Acanthurus triostegus* *Icosteus aenigmaticus*	*Acanthistius cinctus* *Acanthurus triostegus* *Apogon affinis* *Astrapogon stellatus* *Cryptopsaras couesii* *Ectodus descampsii* *Haplotaxodon microlepis* *Icosteus aenigmaticus* *Nomorhamphus celebensis* *Phaeoptyx pigmentaria* *Xenentodon cancila* *Zenarchopterus dispar*	*Apogon affinis* *Astrapogon stellatus* *Cryptopsaras couesii* *Ectodus descampsii* *Haplotaxodon microlepis* *Nomorhamphus celebensis* *Phaeoptyx pigmentaria* *Xenentodon cancila* *Zenarchopterus dispar*
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

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

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

Columns list taxa with different phylogenetic positions among the compared trees. Robinson-Foulds split distances, the number of disagreeing splits, and nodal distances are provided at the bottom of each column. All RAxML-ng analyses were performed on multiple-partition alignments that were partitioned with PartionFinder2. The topologies of the 702-taxon trees inferred using multiple-partition alignments in IQ-TREE and RAxML-ng were identical.

Supplementary Table 3: Classification of Acanthomorpha. The number of species in each taxonomic order is offered in the second column. Though every family is classified in an order, not every family is classified in a 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
			Hispidoberycidae
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
			Ariommatidae
			Arripidae
			Bramidae
			Caristiidae
			Centrolophidae
			Chiasmodontidae
			Gempylidae
			Icosteidae
			Lepidocybidae
			Nomeidae
			Pomatomidae
			Scombridae
			Scombrolabracidae
			Stromateidae
			Tetragonuridae
			Trichiuridae
Syngnathiformes (=Syngnatharia)	674		
		Syngnathoidei	Aulostomidae
		Syngnathoidei	Centriscidae
		Syngnathoidei	Macroramphosidae
		Syngnathoidei	Fistularidae
		Syngnathoidei	Solenostomidae
		Syngnathoidei	Syngnathidae
		Syngnathoidei	Pegasidae
		Callionymoidei	Callionymidae
		Callionymoidei	Draconettidae
			Mullidae
			Dactylopteridae
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	Indostomidae
		Synbranchoidei	Synbranchidae
		Synbranchoidei	Chaudhuriidae
		Synbranchoidei	Mastacembelidae
		Anabantoidei	Anabantidae
		Anabantoidei	Helostomatidae
		Anabantoidei	Osphronemidae
		Anabantoidei	Channidae
		Anabantoidei	Badidae
		Anabantoidei	Nandidae
		Anabantoidei	Pristolepididae
Carangiformes	1,100		
(=Carangaria)			
		Carangoidei-Carangoidea	Carangidae
		Carangoidei-Carangoidea	Trachinotidae
		Carangoidei-Carangoidea	Coryphaenidae
		Carangoidei-Carangoidea	Echeneidae
		Carangoidei-Carangoidea	Rachycentridae
		Carangoidei-Xiphioidea	Istiophoridae
		Carangoidei-Xiphioidea	Xiphiidae
		Carangoidei	Leptobramidae
		Carangoidei	Menidae
		Carangoidei	Nemastiidae
		Carangoidei	Toxotidae
		Pleuronectoidei	Psettodidae
		Pleuronectoidei-Pleuronectoidea	Achiridae

		Pleuronectoidei-Pleuronectoidea	Achiropsettidae
		Pleuronectoidei-Pleuronectoidea	Bothidae
		Pleuronectoidei-Pleuronectoidea	Citharidae
		Pleuronectoidei-Pleuronectoidea	Cyclopsettidae
		Pleuronectoidei-Pleuronectoidea	Cynoglossidae
		Pleuronectoidei-Pleuronectoidea	Oncopteridae
		Pleuronectoidei-Pleuronectoidea	Paralichthyidae
		Pleuronectoidei-Pleuronectoidea	Paralichthodidae
		Pleuronectoidei-Pleuronectoidea	Pleuronectidae
		Pleuronectoidei-Pleuronectoidea	Poecilopsettidae
		Pleuronectoidei-Pleuronectoidea	Rhombosoleidae
		Pleuronectoidei-Pleuronectoidea	Samaridae
		Pleuronectoidei-Pleuronectoidea	Scophthalmidae
		Pleuronectoidei-Pleuronectoidea	Soleidae
			Centropomidae
			Lactariidae
			Polynemidae
			Sphyraenidae
Perciformes	3,192		
		Percoidei	Percidae
		Percoidei	Trachinidae
		Percoidei	Niphonidae
			Epinephelidae
			Grammistidae
			Liopropomatidae
			Serranidae
			Anthiadidae
			Bembropidae
		Notothenioidei	Percophidae
		Notothenioidei	Bovichtidae
		Notothenioidei	Pseudaphritidae
		Notothenioidei	Eleginopsidae
		Notothenioidei	Artedidraconidae
		Notothenioidei	Bathydraconidae
		Notothenioidei	Channichthyidae
		Notothenioidei	Harpagiferidae
		Notothenioidei	Nototheniidae
		Scorpaenoidei	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	Scytalinidae
		Scorpaenoidei	Stichaeidae
		Scorpaenoidei	Zaproridae
		Scorpaenoidei	Eulophiidae
		Scorpaenoidei	Opisthocentridae
		Scorpaenoidei	Lumpenidae
		Scorpaenoidei	Neozoarcidae
		Scorpaenoidei	Zoarcidae
		Scorpaenoidei	Aulorhynchidae
		Scorpaenoidei	Gasterosteidae
		Scorpaenoidei	Hypoptychidae
Centrarchiformes	299		
			Aplodactylidae
			Centrarchidae

			Cheilodactylidae
			Chironemidae
			Cirrhitidae
			Dichistiidae
			Enoplosidae
			Girellidae
			Kuhliidae
			Kyphosidae
			Microcanthidae
			Scorpididae
			Latridae
			Oplegnathidae
			Percichthyidae
			Sinipercidae
			Terapontidae
Labriformes	757		
		Labroidei	Labridae
		Labroidei	Centrogenyidae
		Uranoscopoidei	Uranoscopidae
		Uranoscopoidei	Cheimarrichthyidae
		Uranoscopoidei	Pinguipedidae
		Uranoscopoidei	Ammodytidae
		Uranoscopoidei	Leptoscopidae
Acropomatiformes	308		
			Acropomatidae
			Banjosidae
			Bathyclupeidae
			Champsodontidae
			Creediidae
			Dinolestidae
			Epigonidae
			Glaucosomatidae
			Hemerocoetidae
			Howellidae
			Lateolabracidae
			Leptoscopidae
			Malakichthyidae
			Ostracoberycidae

			Pempheridae
			Pentacerotidae
			Polyprionidae
			Stereolepidae
			Scombropidae
			Synagropidae
			Symphysanodontidae
Acanthuriformes	2,350		
		Acanthuroidei	Acanthuridae
		Acanthuroidei	Zanclidae
		Acanthuroidei	Luvaridae
			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

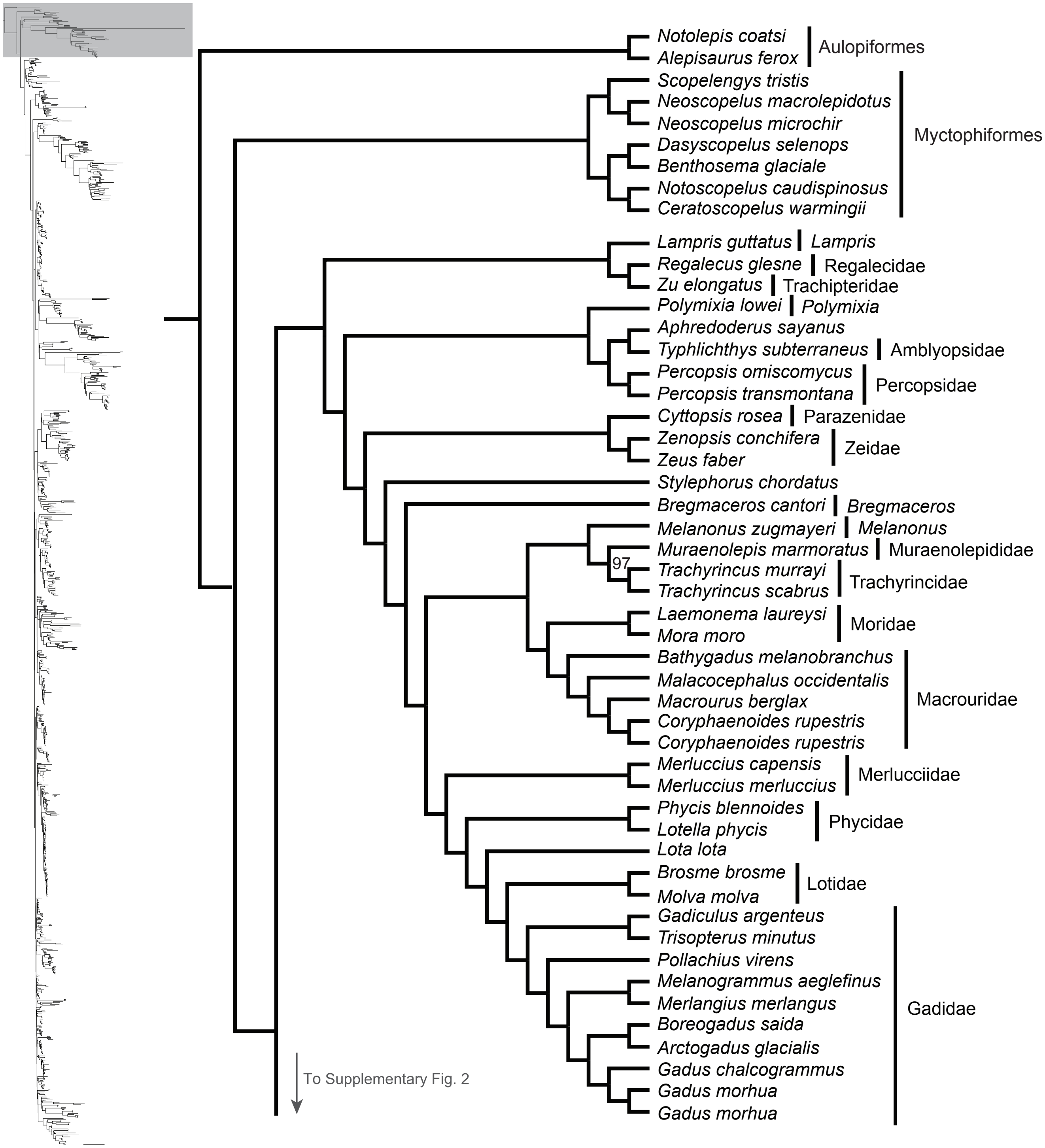
Supplementary Table 4: Divergence date estimates in millions of years (Mya) and 95% Highest Posterior Densities (HPD) for major acanthomorph clades, generated using six alignments of 30 UCE loci in BEAST. Estimates from the 702-taxon and 1,084-taxon time trees are both represented. All stem and crown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

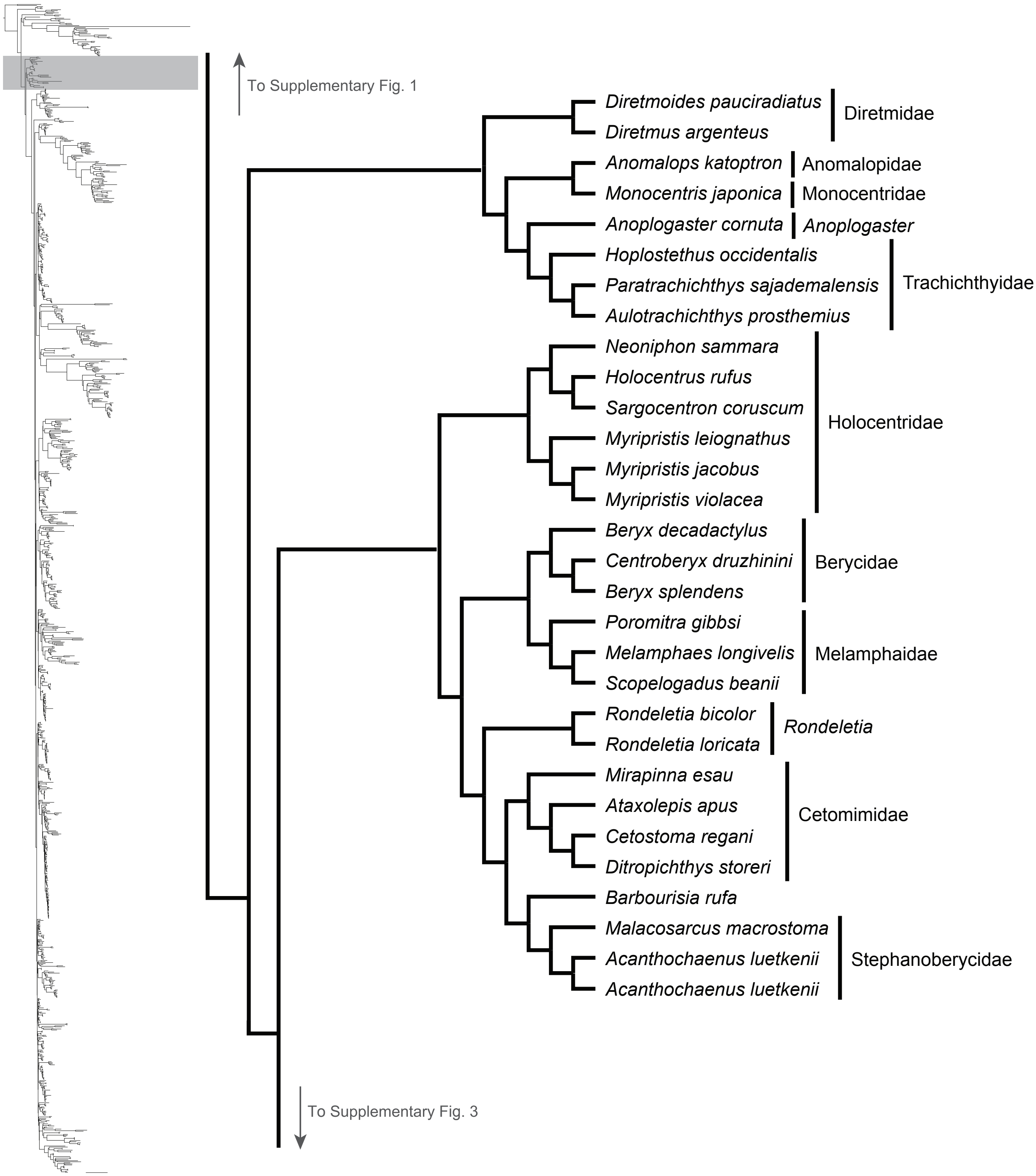
		30 loci set B	110.65	[97.59, 119.08]	104.49	[93.39, 114.84]
		30 loci set C	111.82	[101.46, 120.96]	105.30	[92.93, 115.32]
	702	30 loci set D	109.82	[99.69, 119.86]	102.66	[91.04, 112.38]
		30 loci set E	109.64	[98.89, 119.71]	101.48	[88.91, 111.90]
		30 loci set F	107.73	[87.68, 122.92]	98.93	[80.57, 113.81]
Scombriformes	1,084	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]
	702	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]
Blenniiformes	1,084	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]
	702	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]
Synbranchiformes	1,084	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]
	702	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]
Carangiformes	1,084	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]
	702	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]
Perciformes	1,084	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]
	702	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]
Centrarchiformes	1,084	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]
	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]
Labriformes	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]
	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]
Acropomatiformes	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]
	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]
Acanthuriformes	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]
	702	30 loci set D	78.83	[71.72, 87.89]	76.39	[69.95, 84.70]
		30 loci set E	77.45	[70.87, 85.19]	75.97	[69.71, 83.28]
		30 loci set F	80.07	[70.93, 89.84]	78.16	[69.59, 87.49]
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]



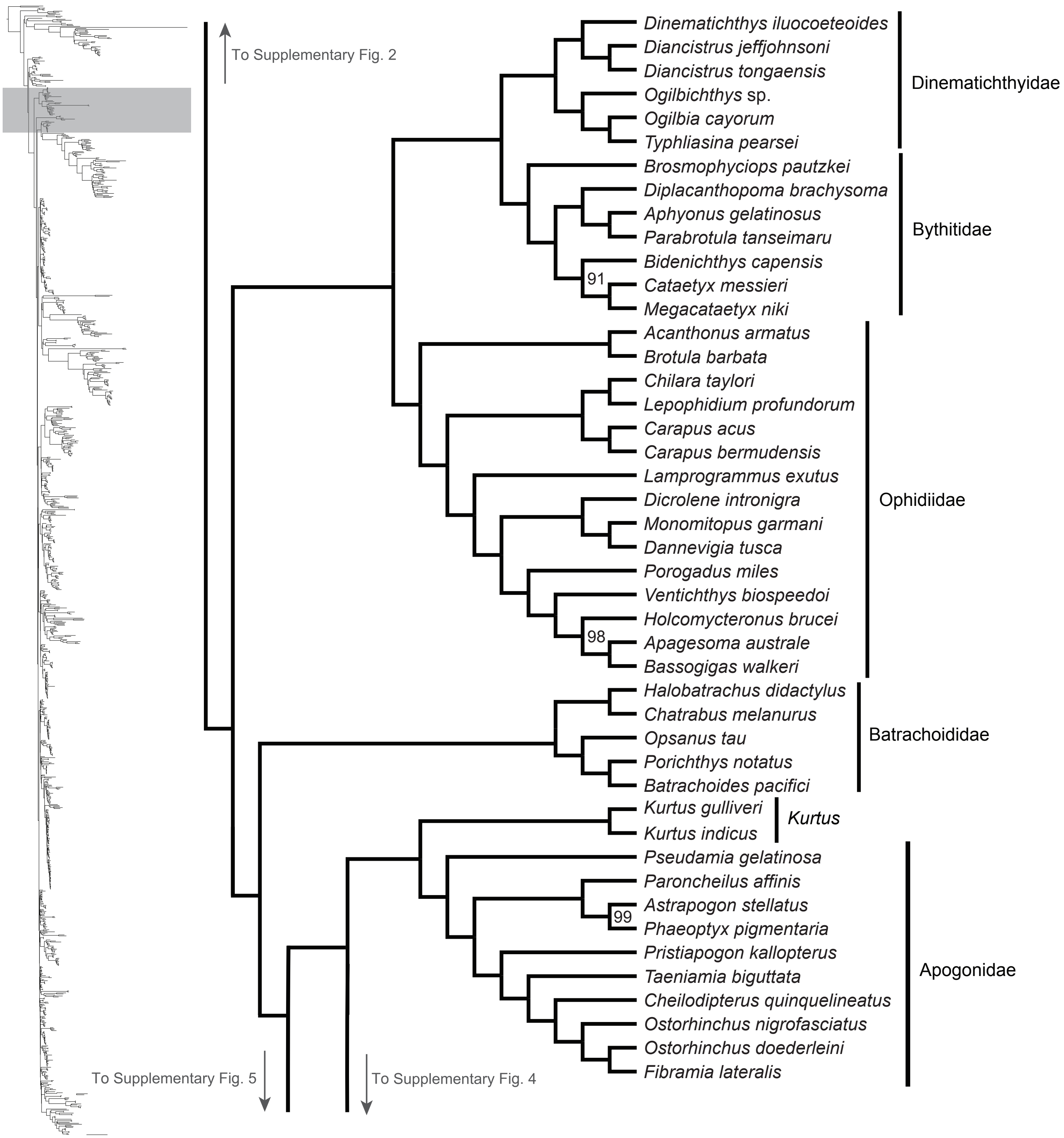
Supplementary Fig. 1: Maximum likelihood phylogeny inferred in IQ-TREE.

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.



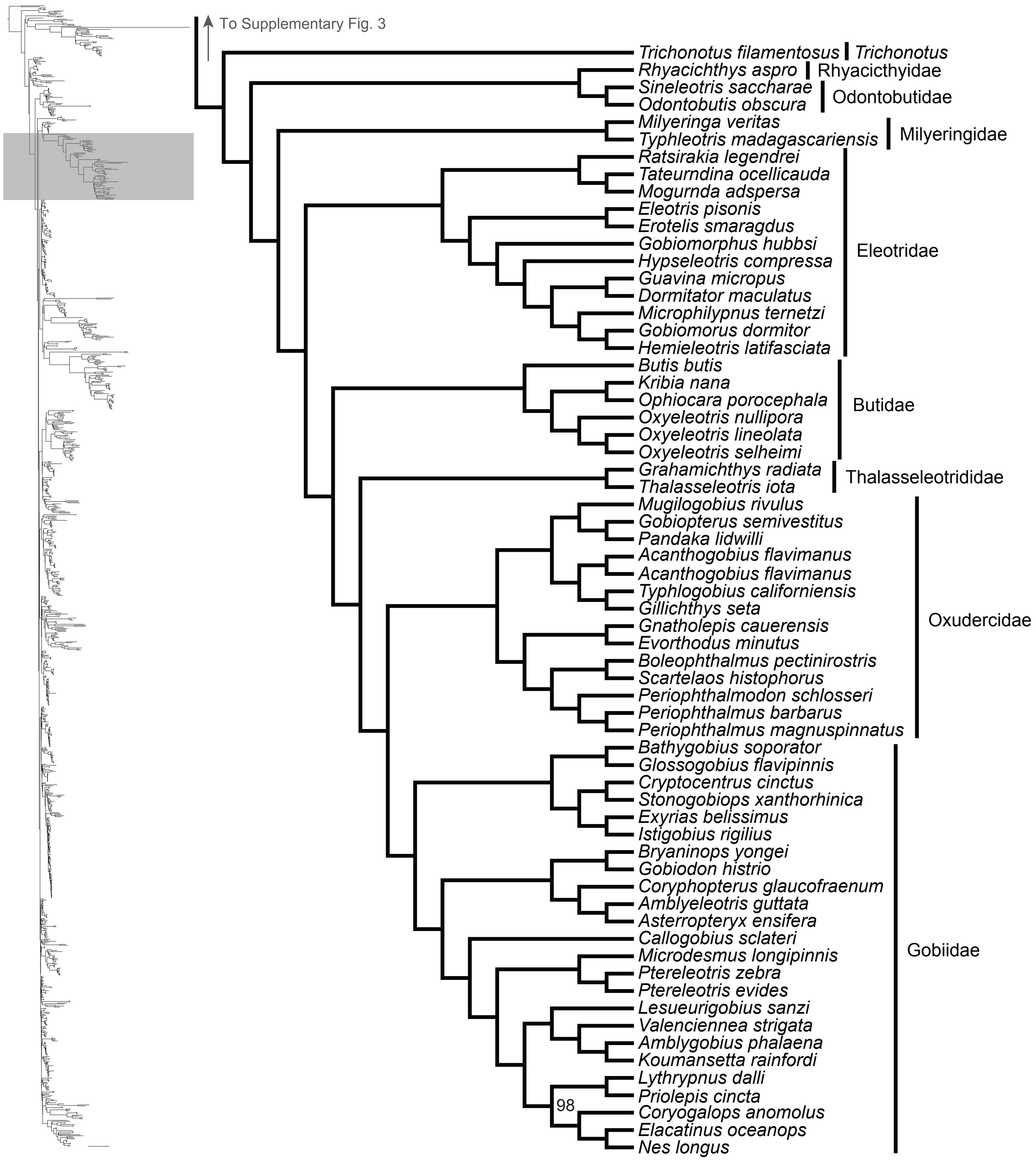
Supplementary Fig. 2: Maximum likelihood phylogeny inferred in IQ-TREE.

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.



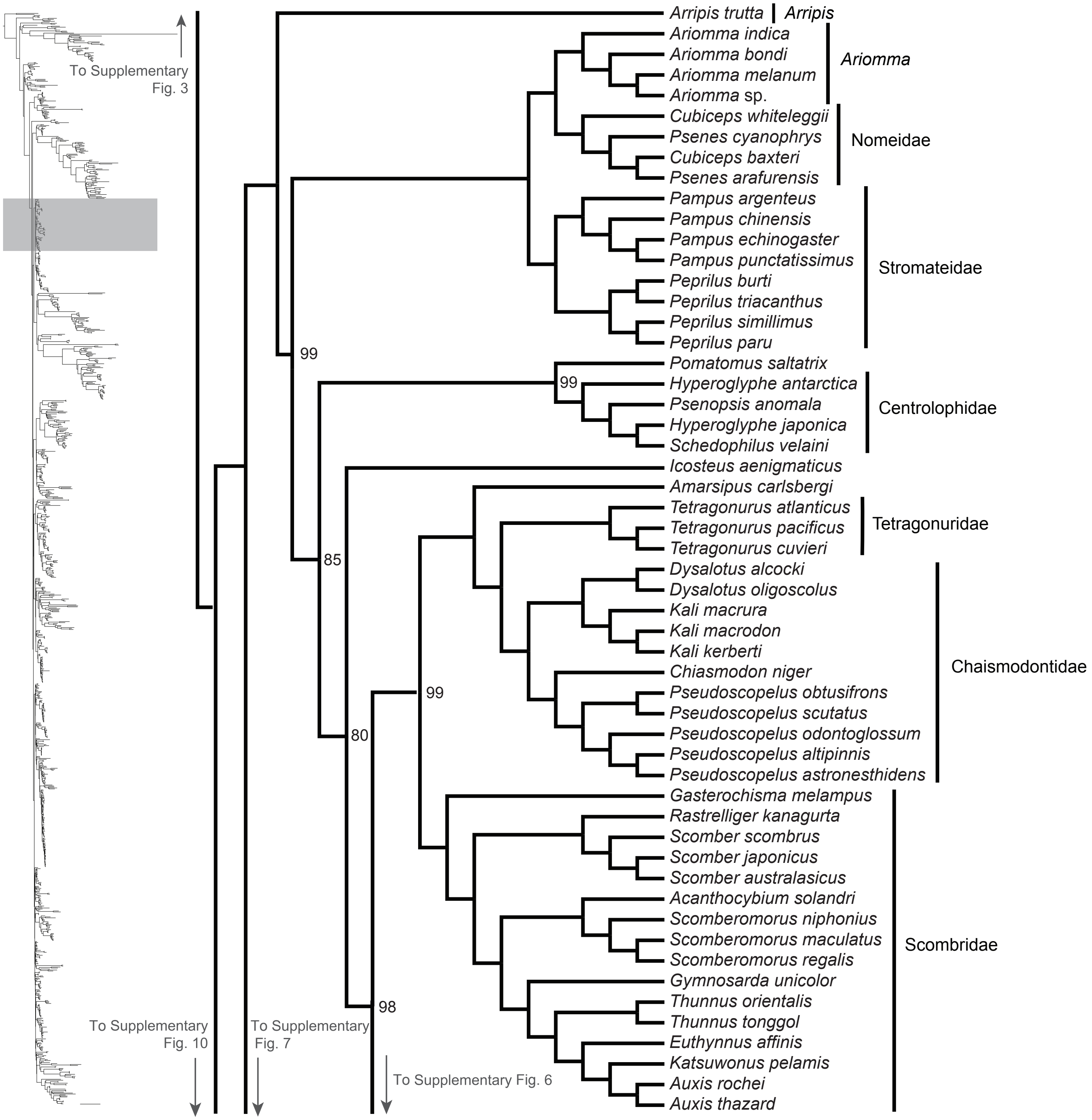
Supplementary Fig. 3: Maximum likelihood phylogeny inferred in IQ-TREE.

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.



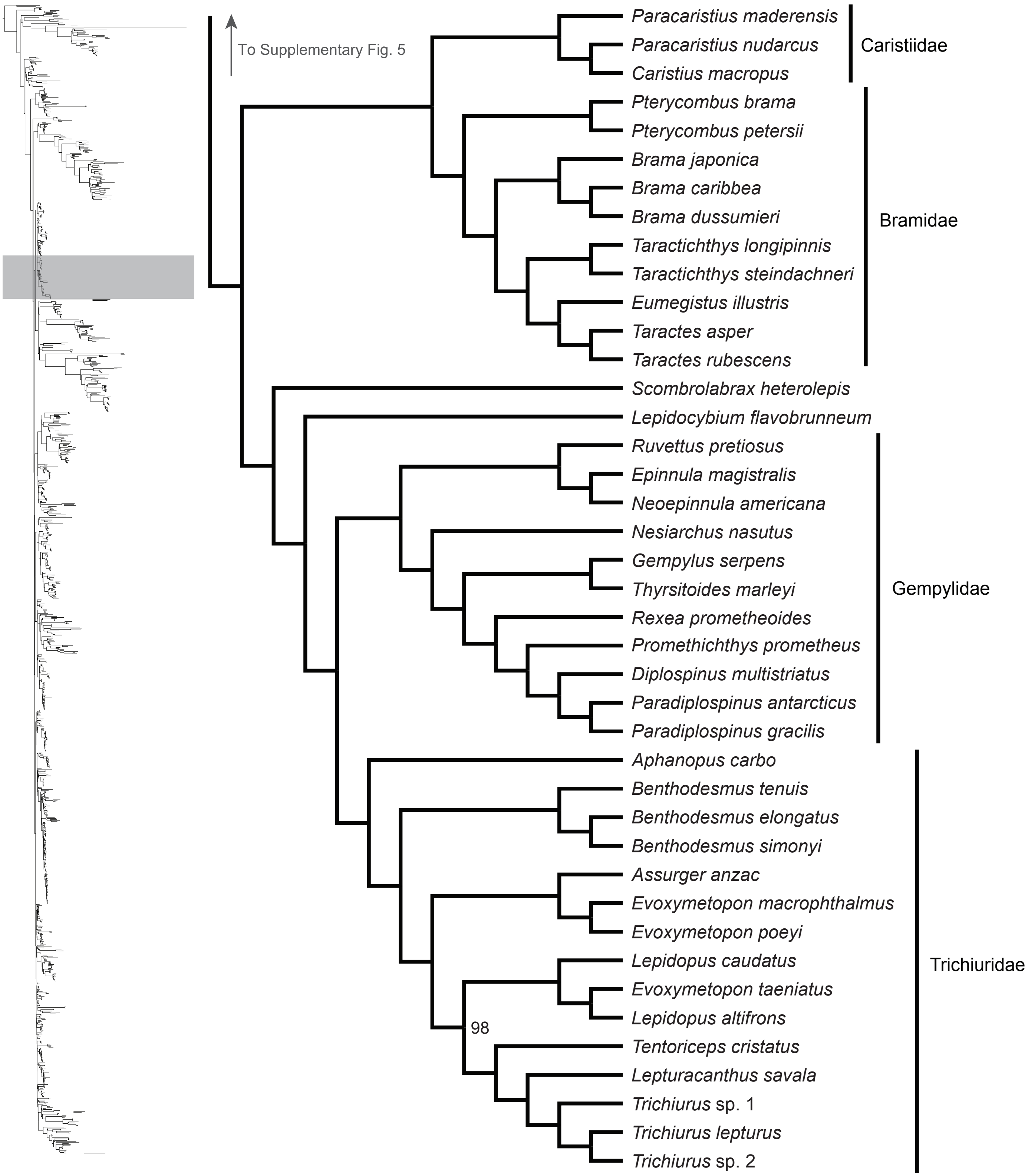
Supplementary Fig. 4: Maximum likelihood phylogeny inferred in IQ-TREE.

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.



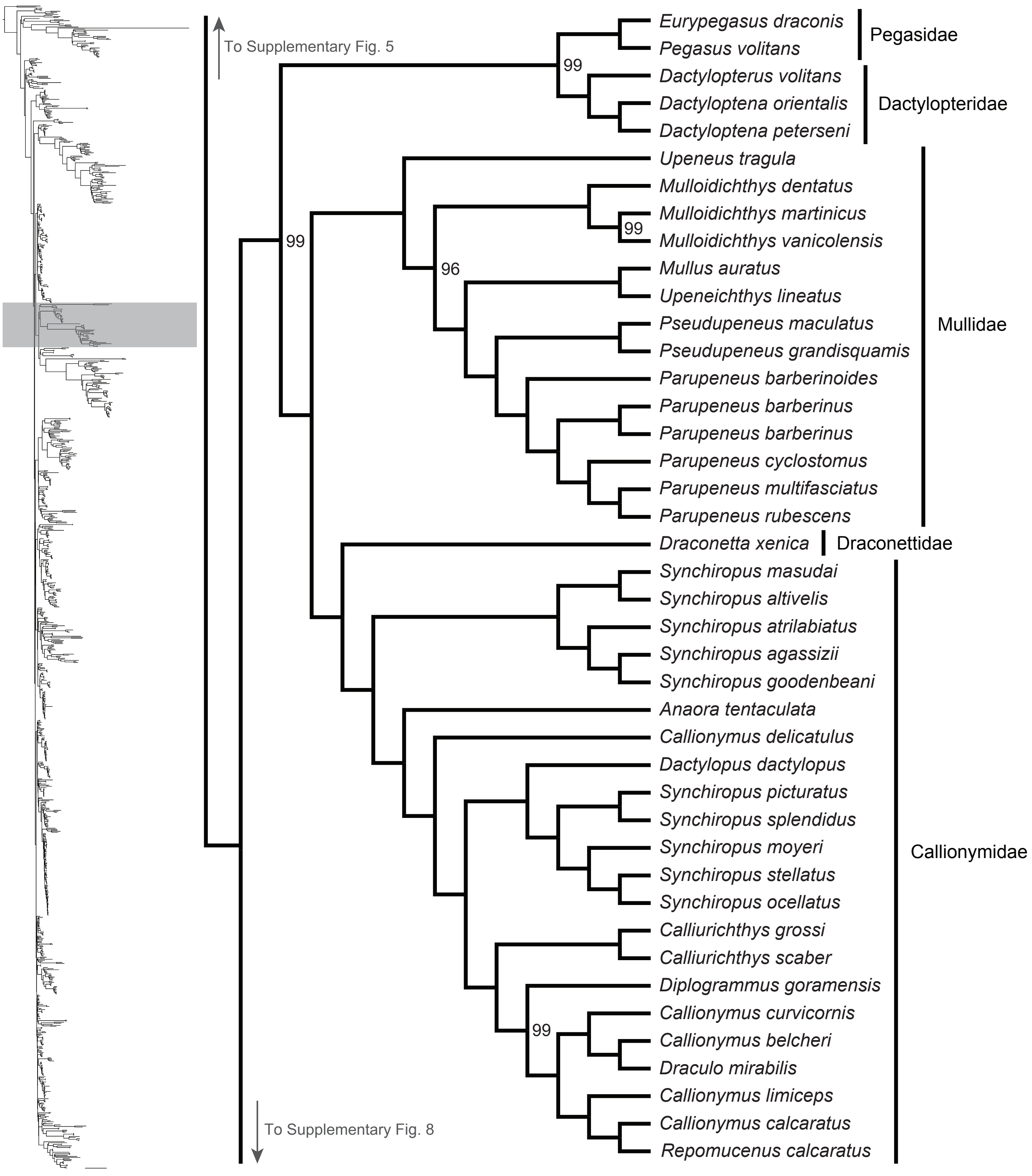
Supplementary Fig. 5: Maximum likelihood phylogeny inferred in IQ-TREE.

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 monogeneric taxa.



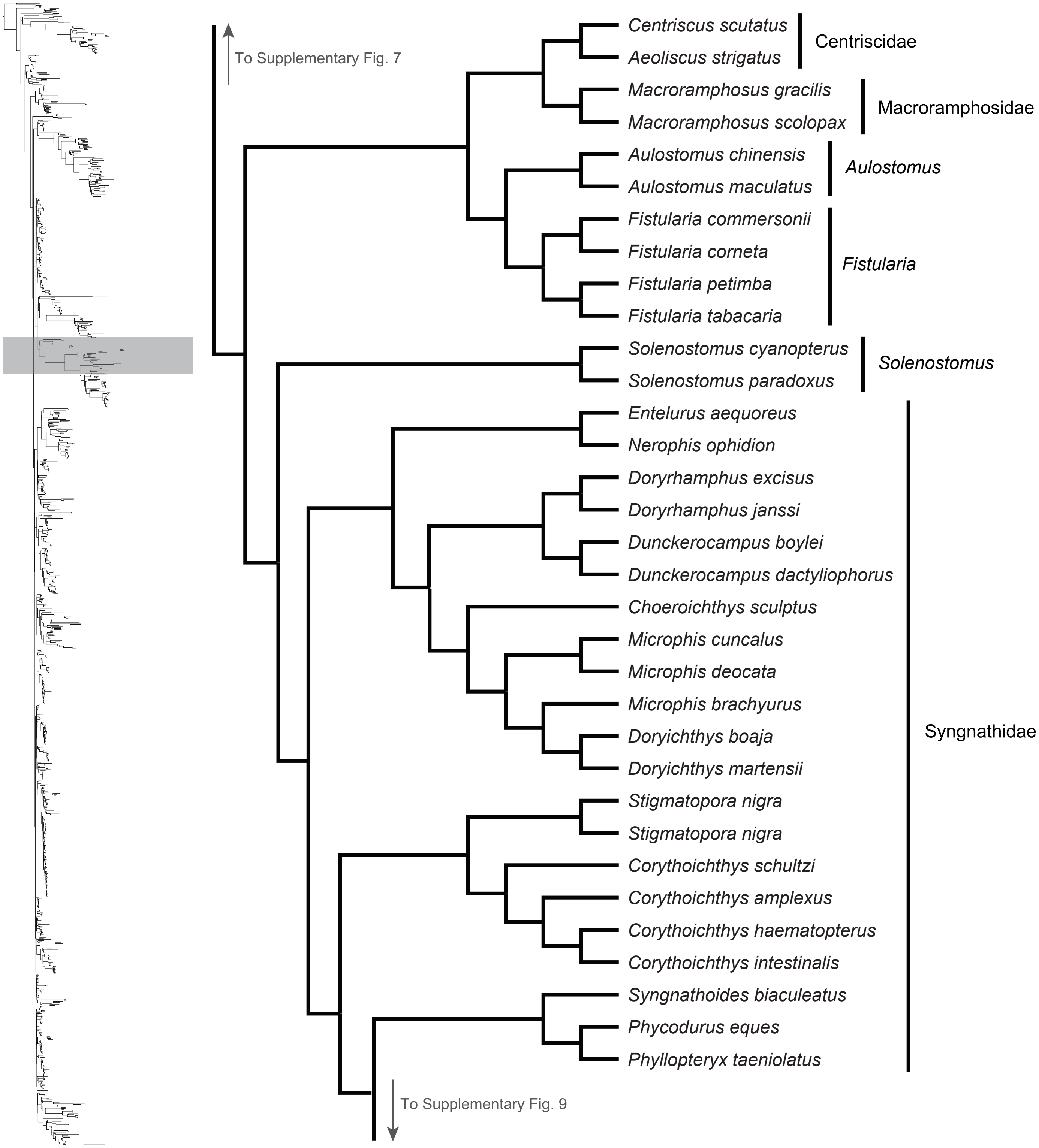
Supplementary Fig. 6: Maximum likelihood phylogeny inferred in IQ-TREE.

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.

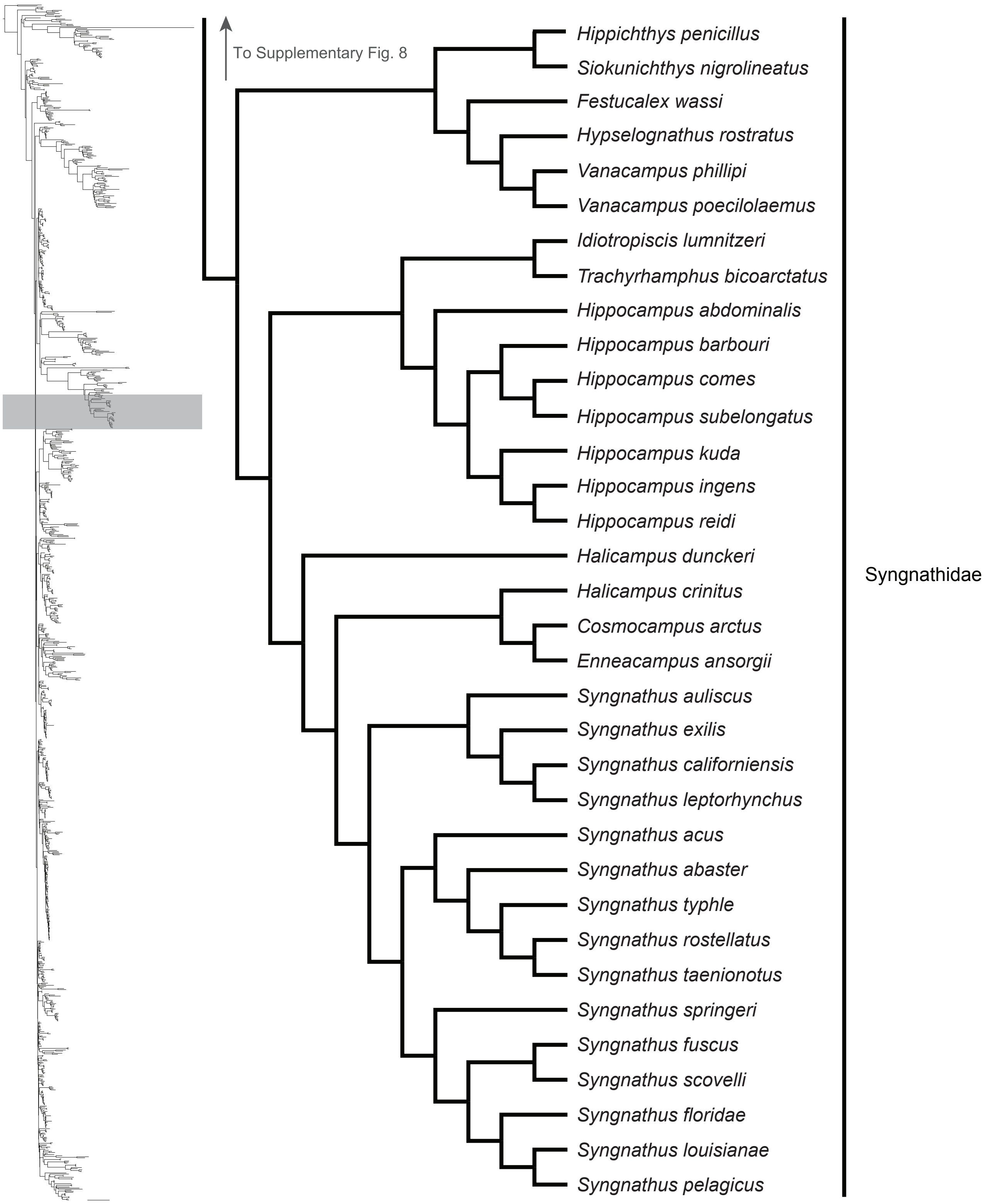


Supplementary Fig. 7: Maximum likelihood phylogeny inferred in IQ-TREE.

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.

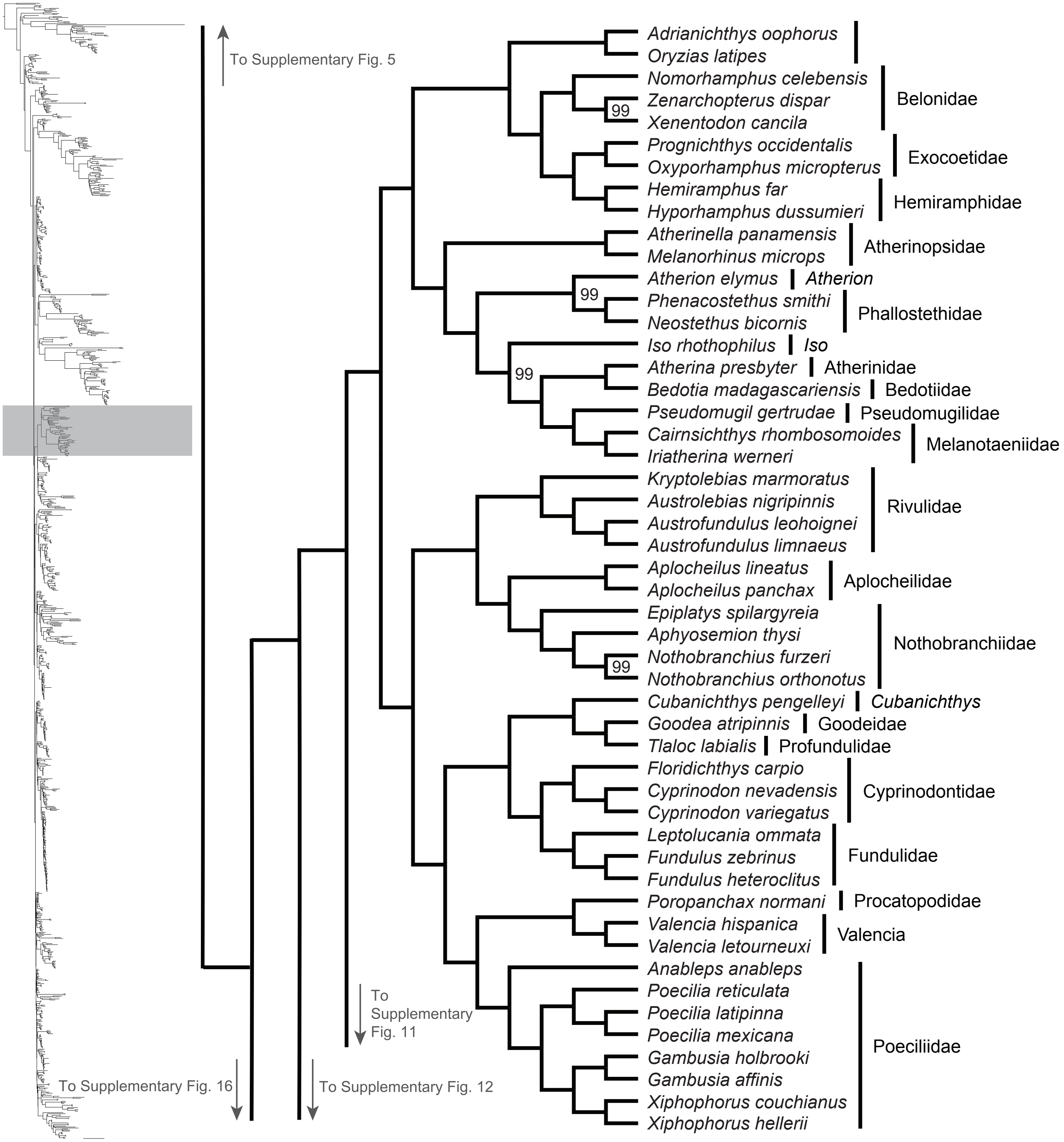


Supplementary Fig. 8: Maximum likelihood phylogeny inferred in IQ-TREE.
A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. All nodes have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars.

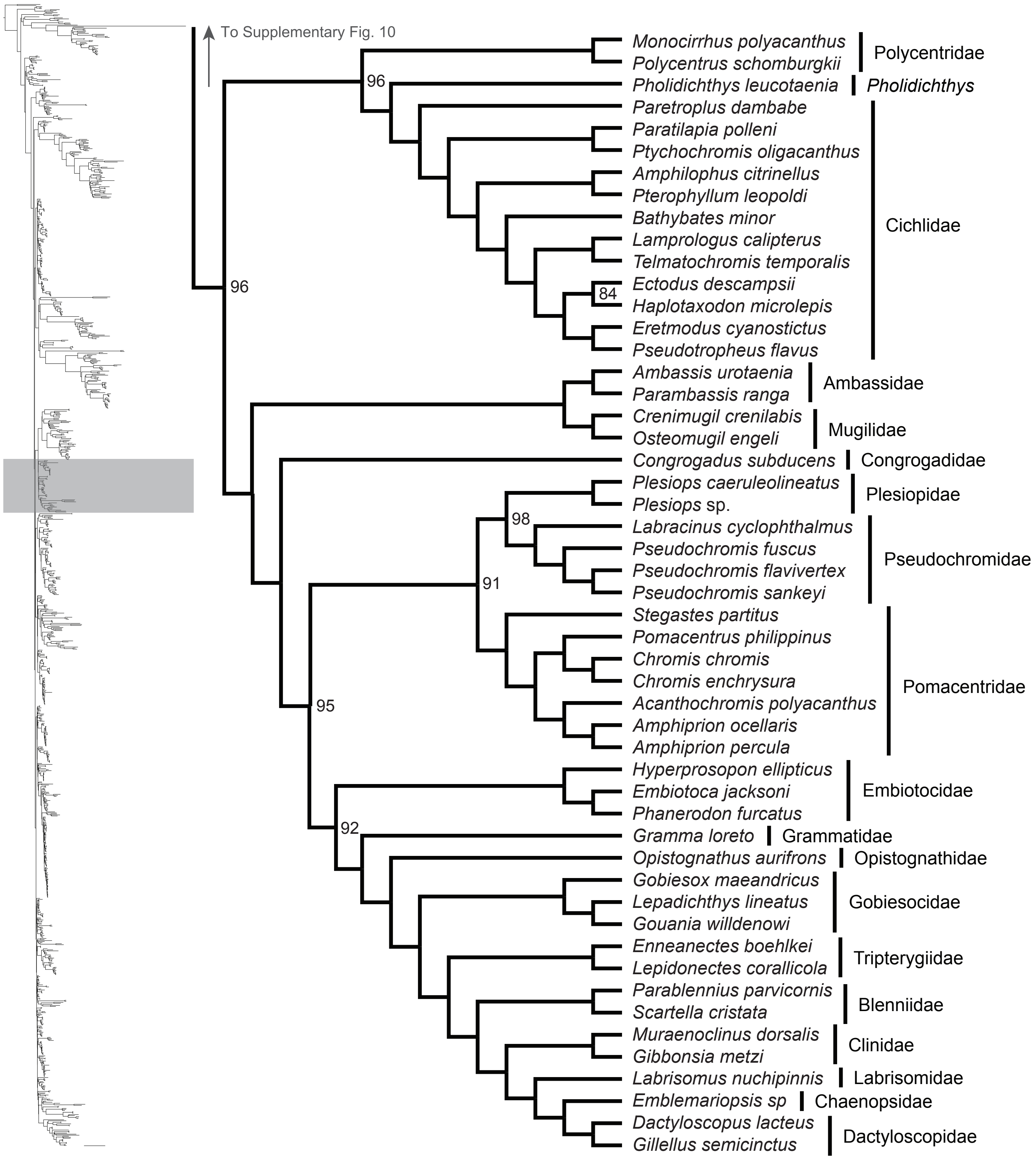


Supplementary Fig. 9: Maximum likelihood phylogeny inferred in IQ-TREE.

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.

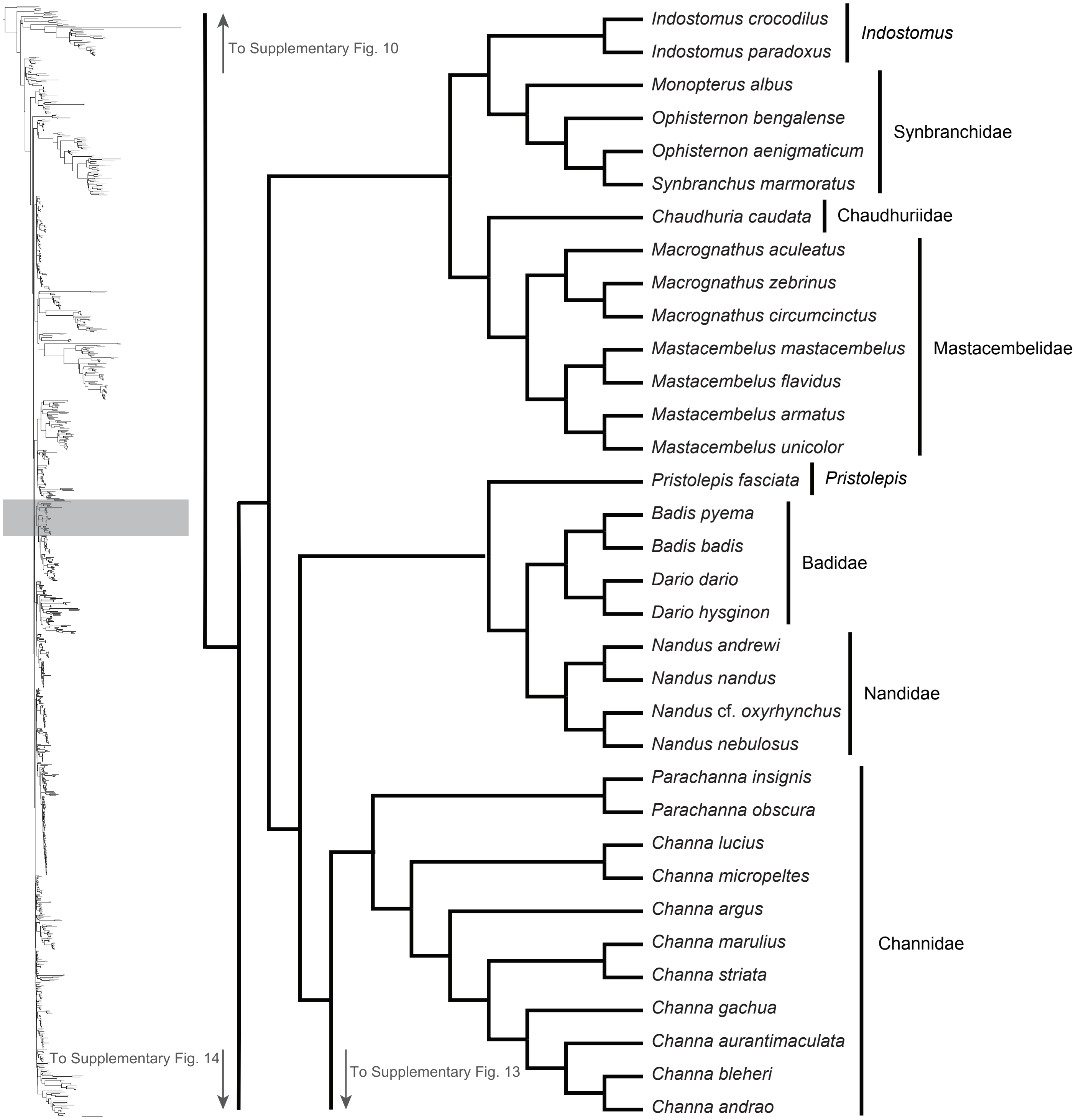


Supplementary Fig. 10: Maximum likelihood phylogeny inferred in IQ-TREE.
A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars.

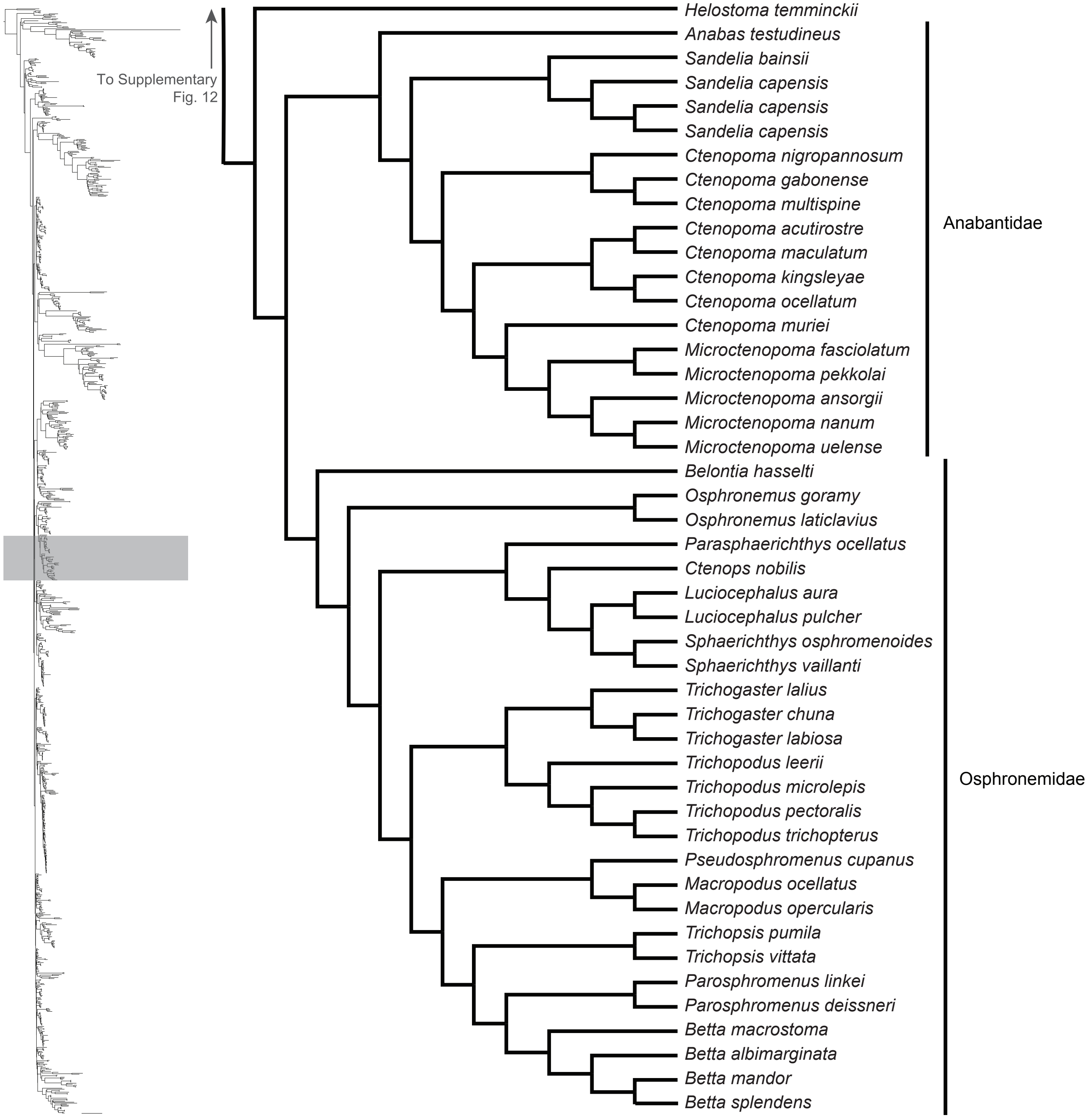


Supplementary Fig. 11: Maximum likelihood phylogeny inferred in IQ-TREE.

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.

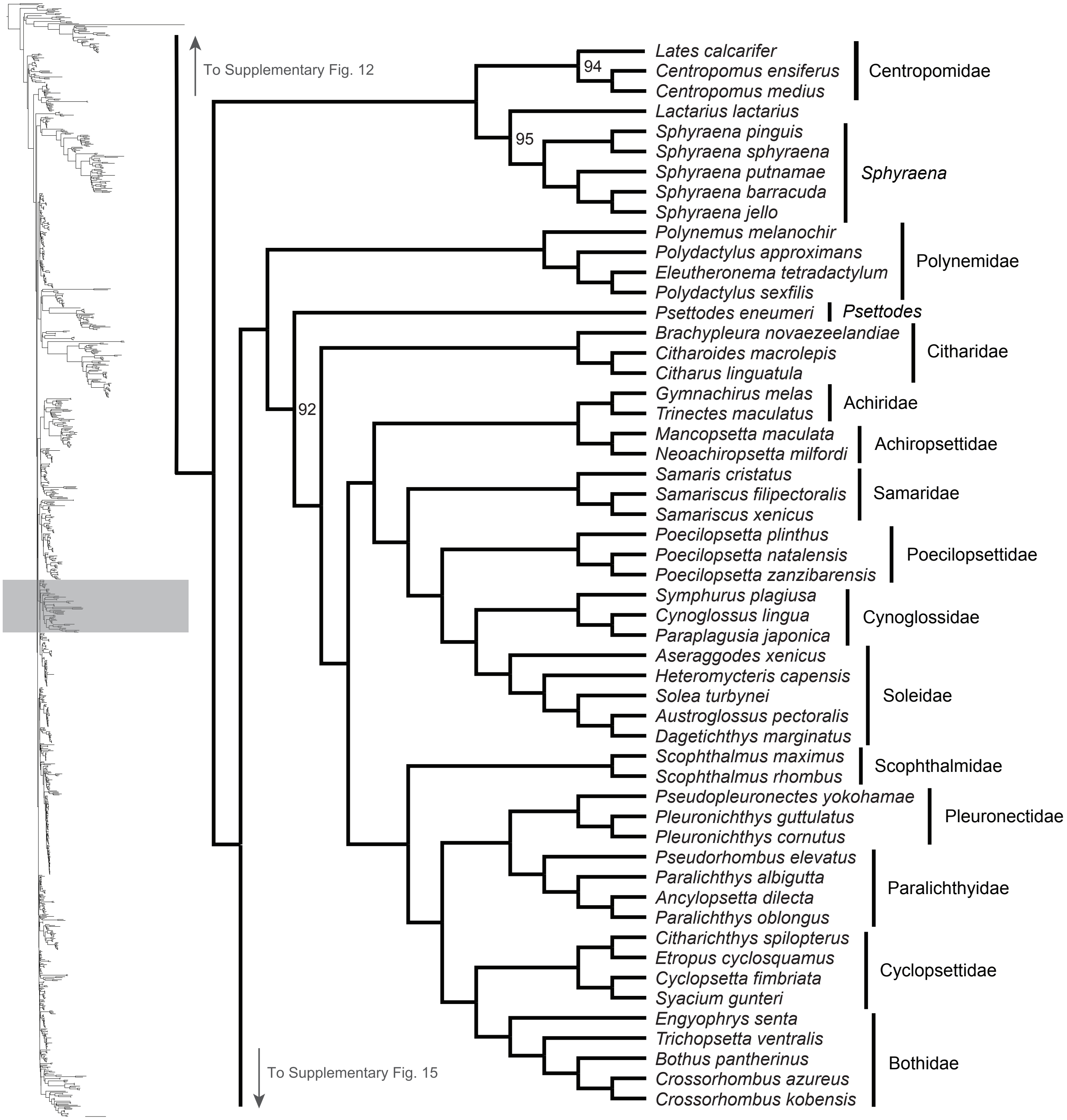


Supplementary Fig. 12: Maximum likelihood phylogeny inferred in IQ-TREE.
A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. All nodes have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars.

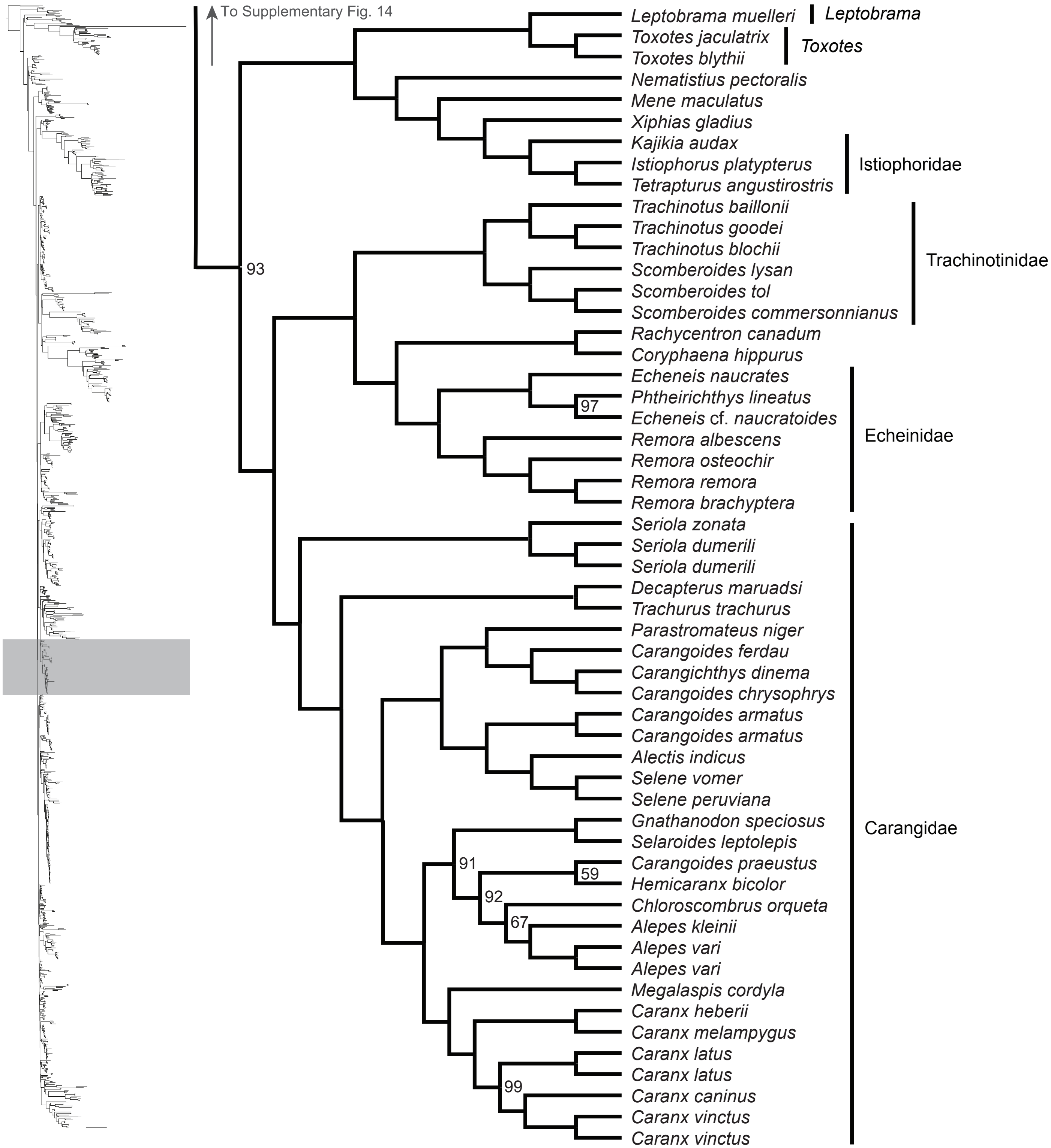


Supplementary Fig. 13: Maximum likelihood phylogeny inferred in IQ-TREE.

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 monogeneric taxa.

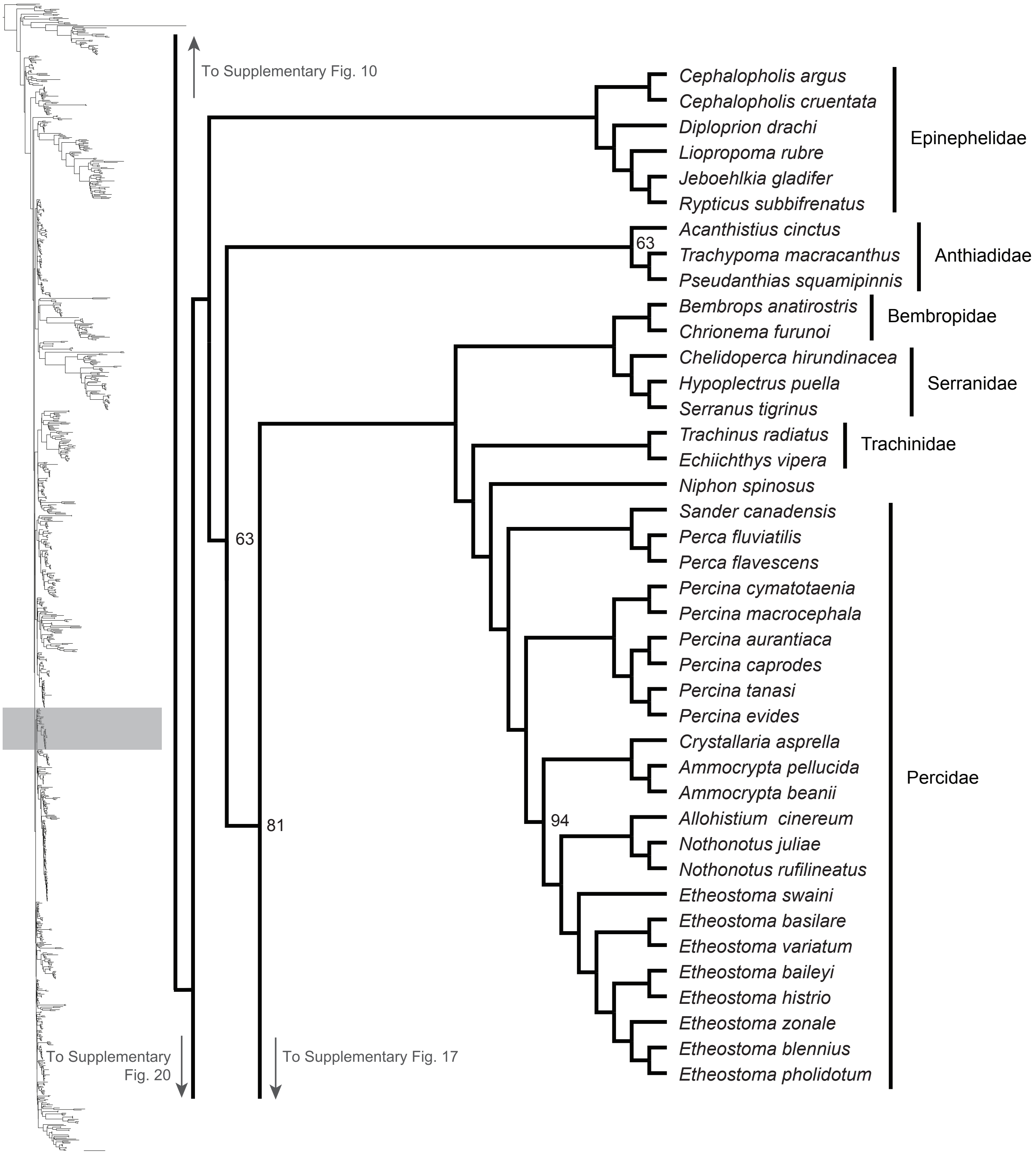


Supplementary Fig. 14: Maximum likelihood phylogeny inferred in IQ-TREE.
A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap 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.

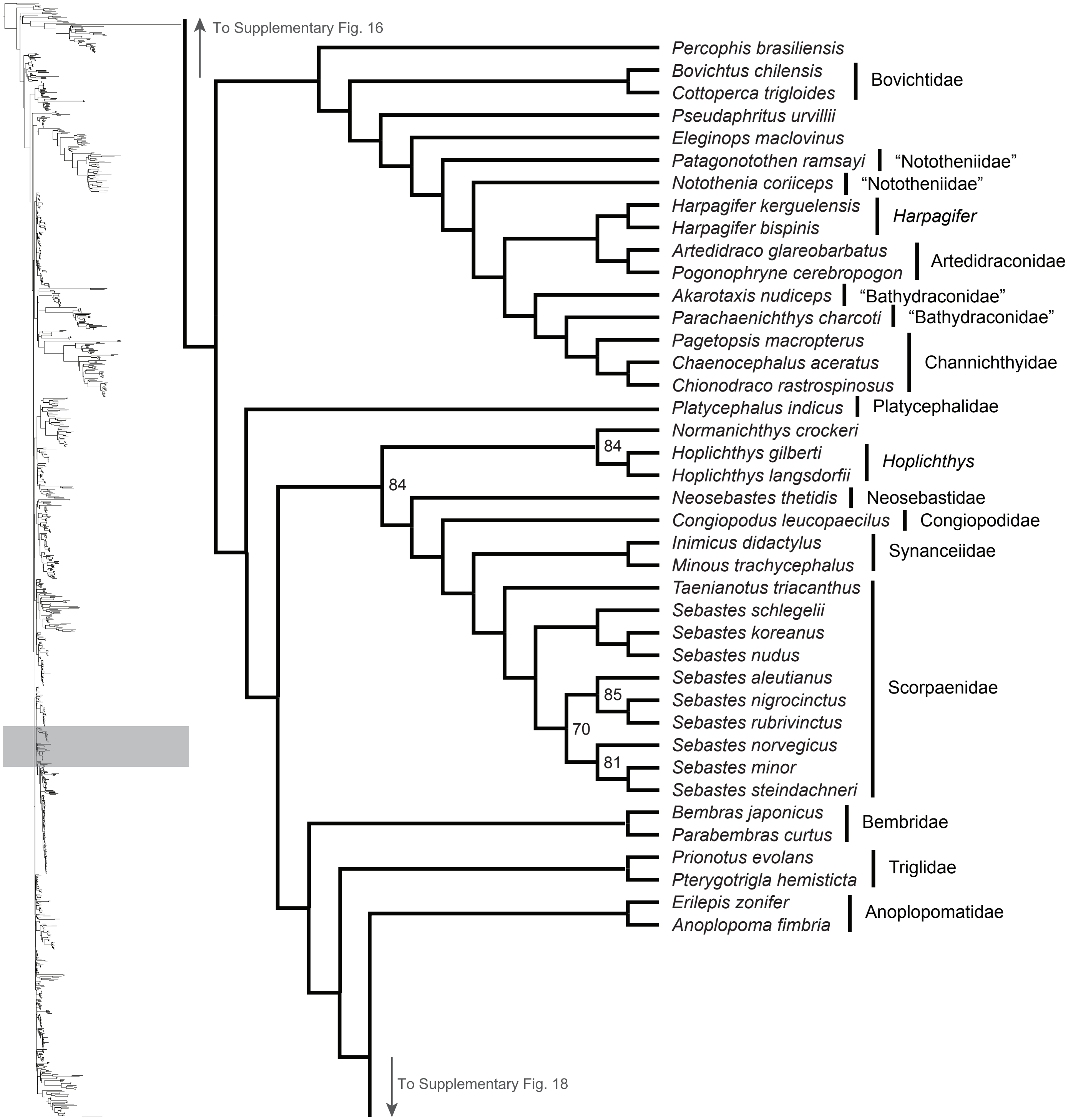


Supplementary Fig. 15: Maximum likelihood phylogeny inferred in IQ-TREE.

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.

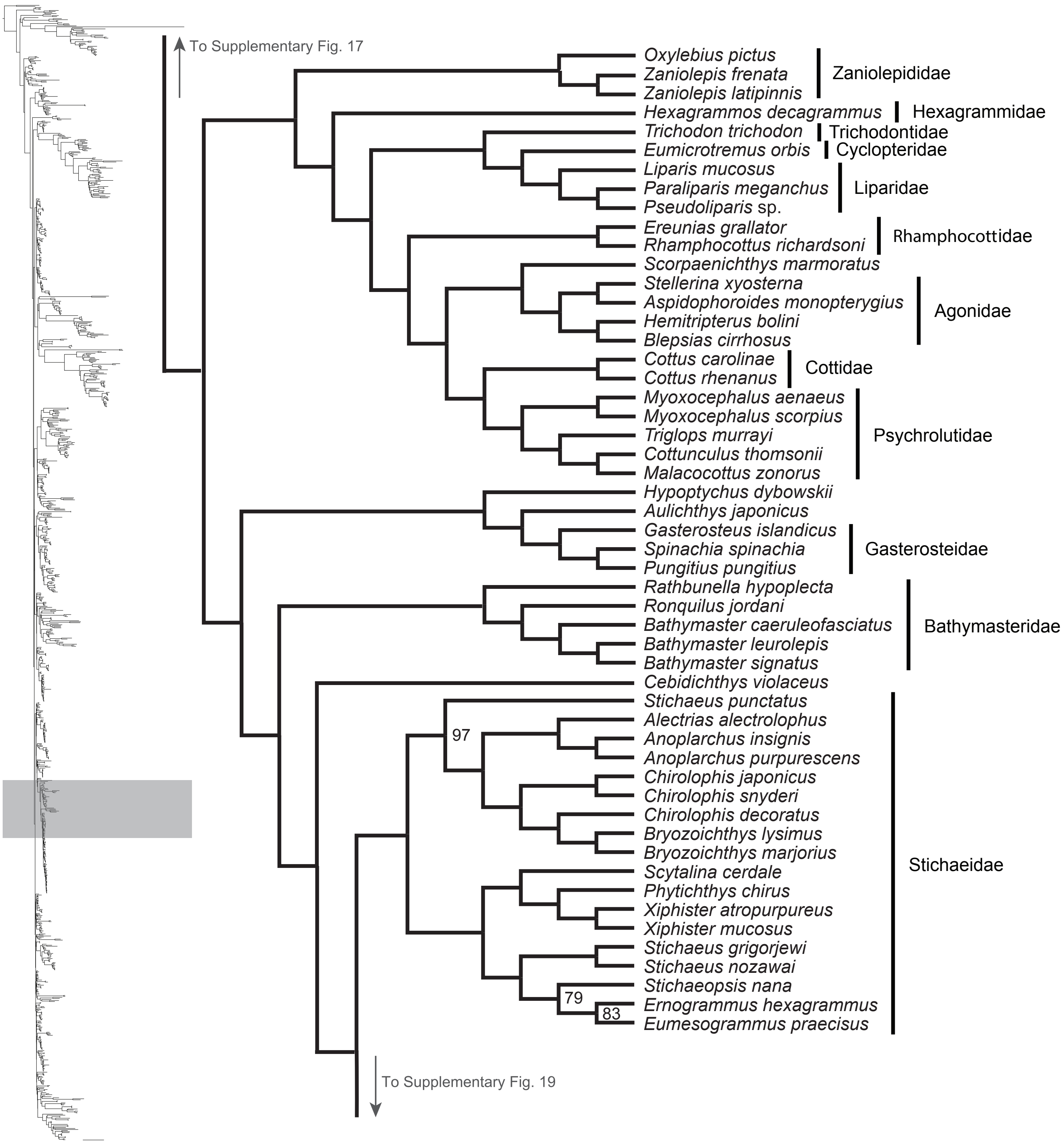


Supplementary Fig. 16: Maximum likelihood phylogeny inferred in IQ-TREE.
A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap 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.



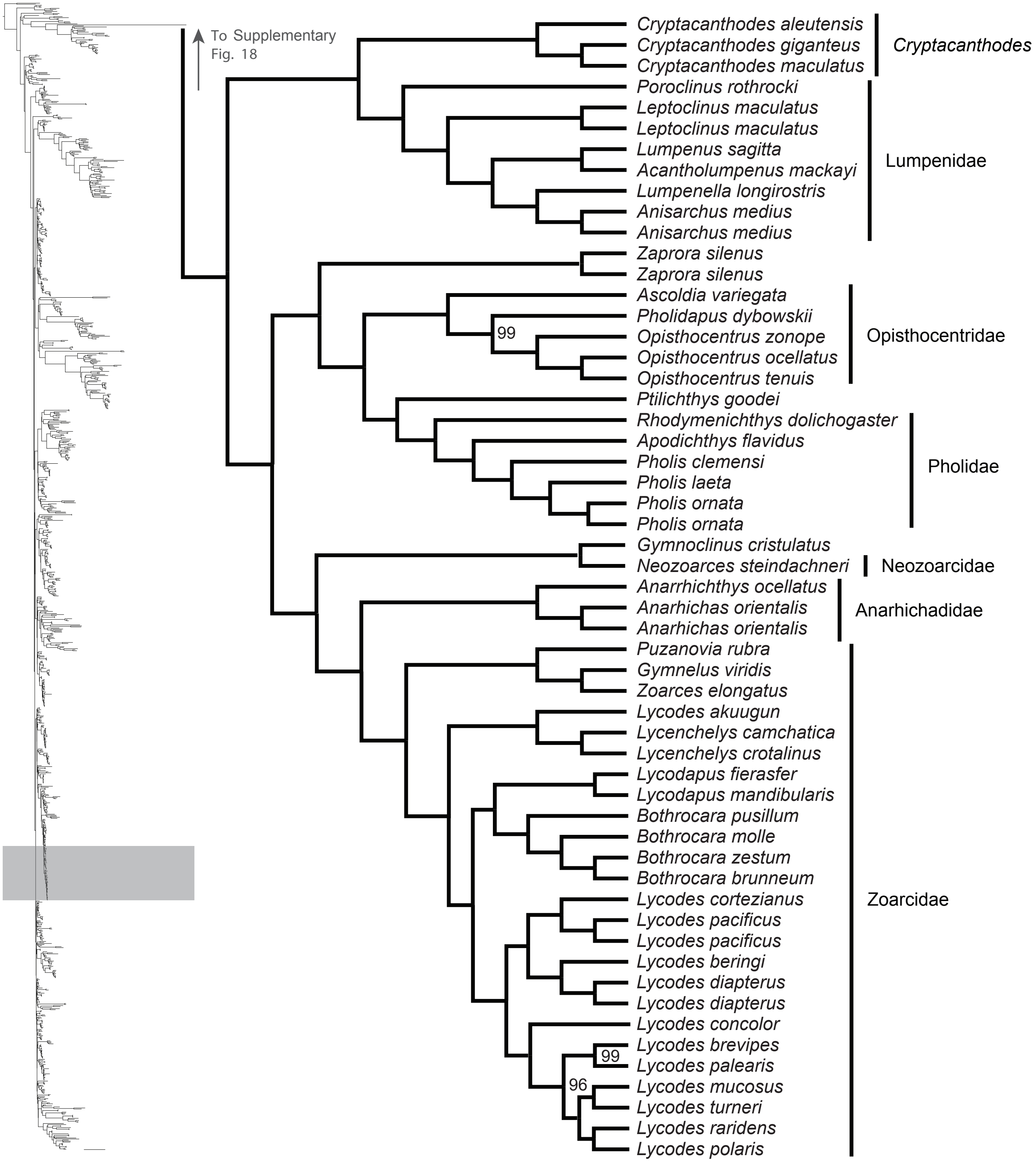
Supplementary Fig. 17: Maximum likelihood phylogeny inferred in IQ-TREE.

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 monogeneric taxa.

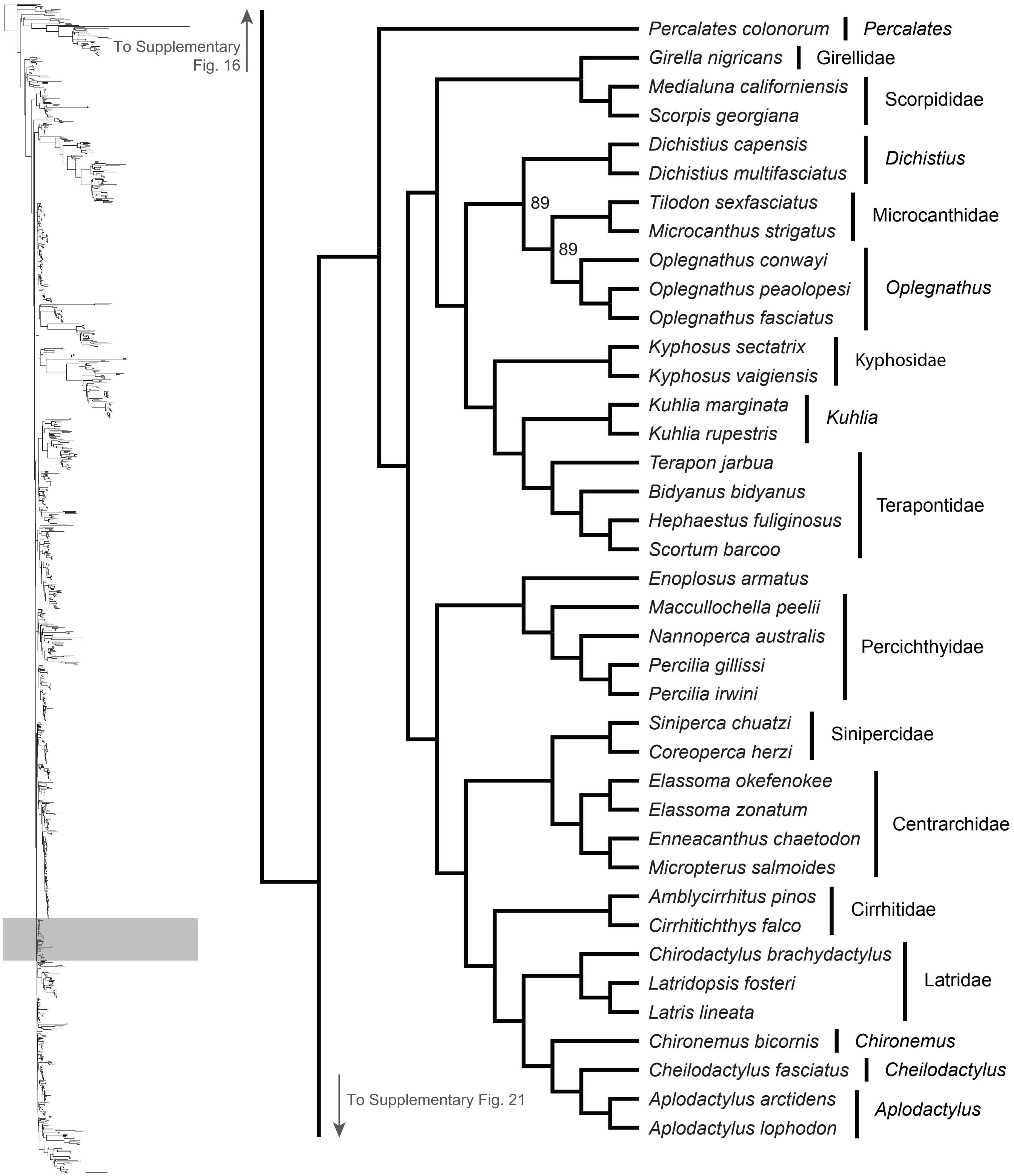


Supplementary Fig. 18: Maximum likelihood phylogeny inferred in IQ-TREE.

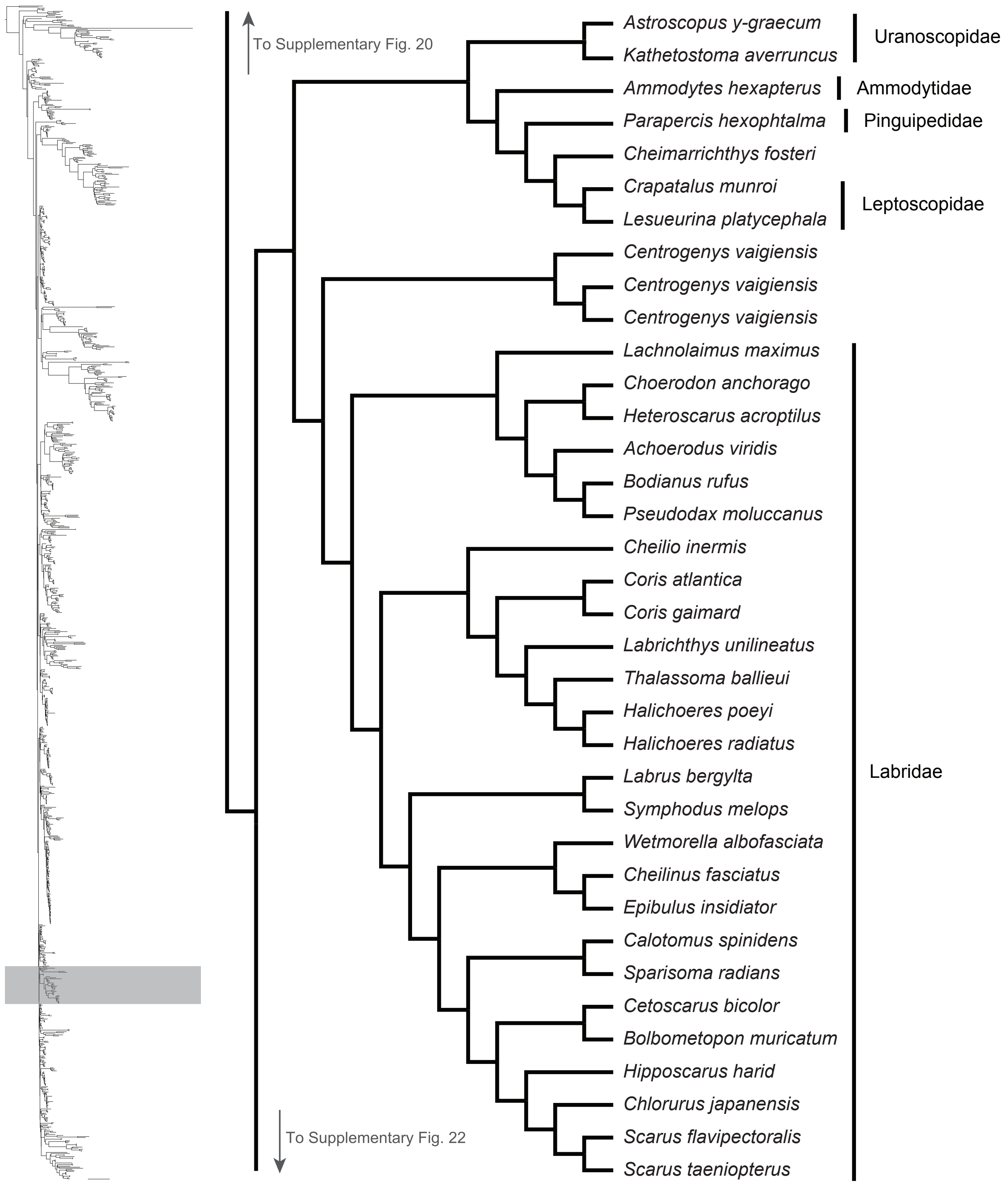
A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of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



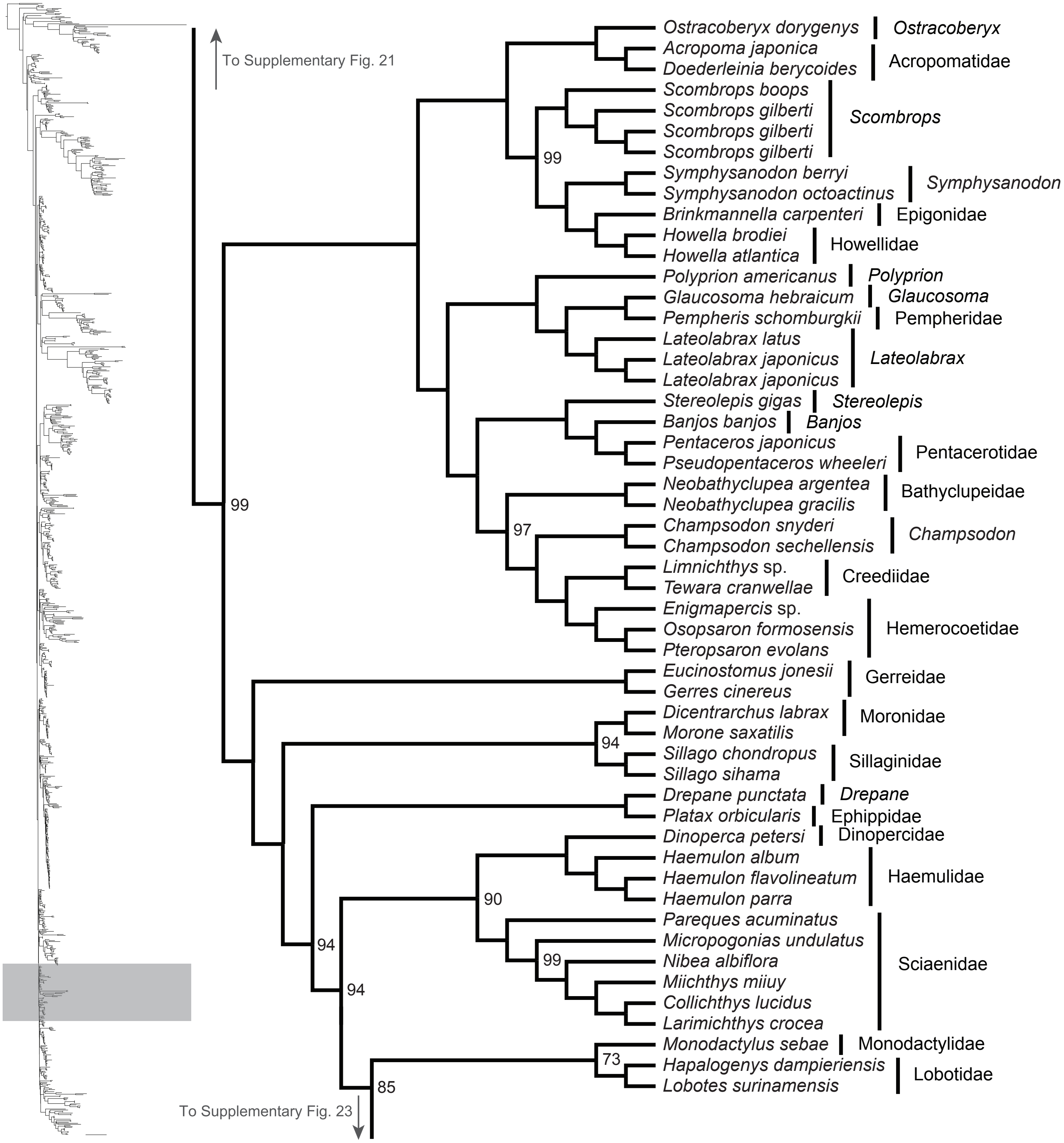
Supplementary Fig. 19: Maximum likelihood phylogeny inferred in IQ-TREE.
A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap 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.

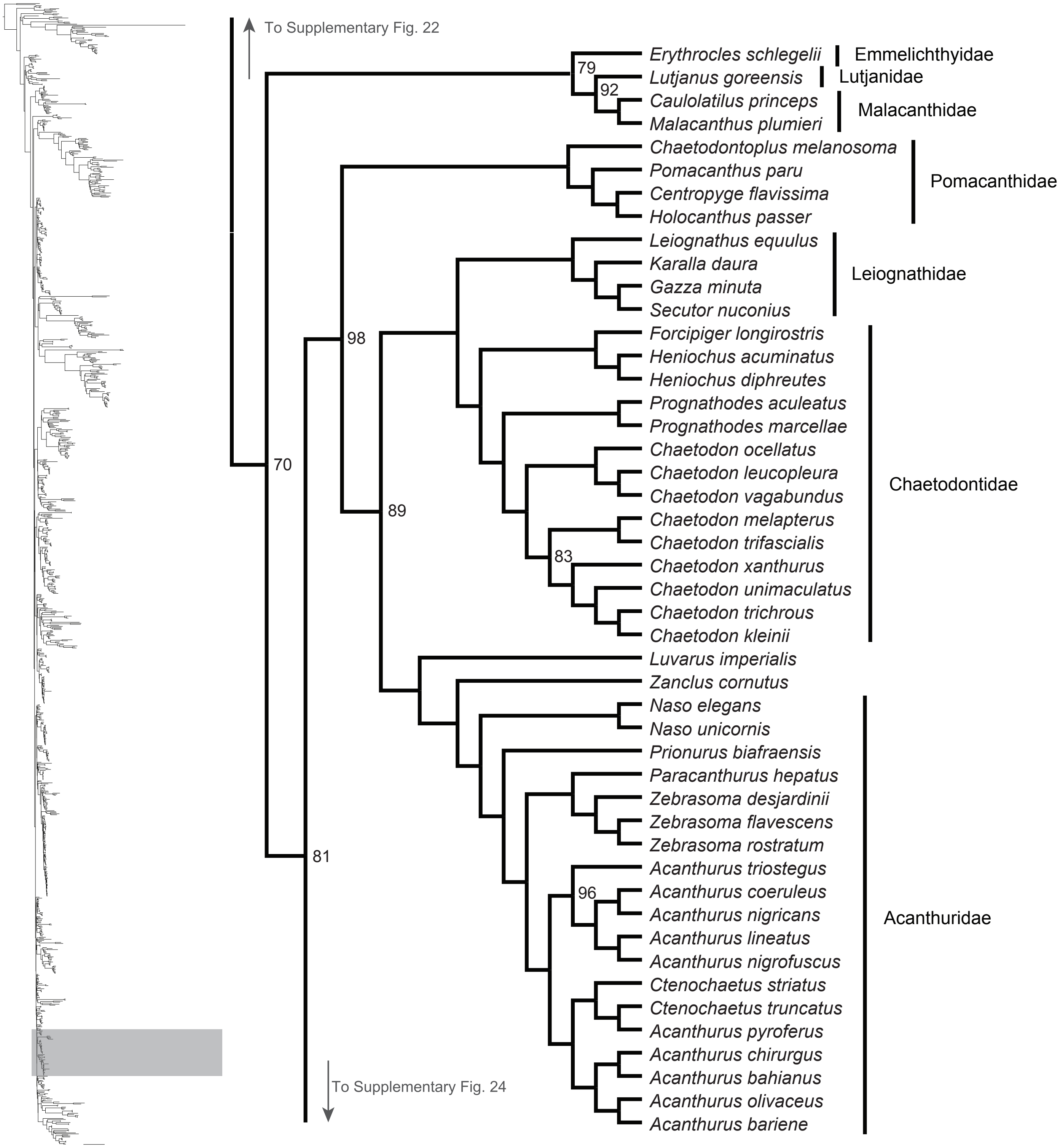


Supplementary Fig. 21: Maximum likelihood phylogeny inferred in IQ-TREE.
A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. All nodes have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of the vertical black bars. Any tips left unassigned to a higher taxon are monotypic or monogeneric taxa.

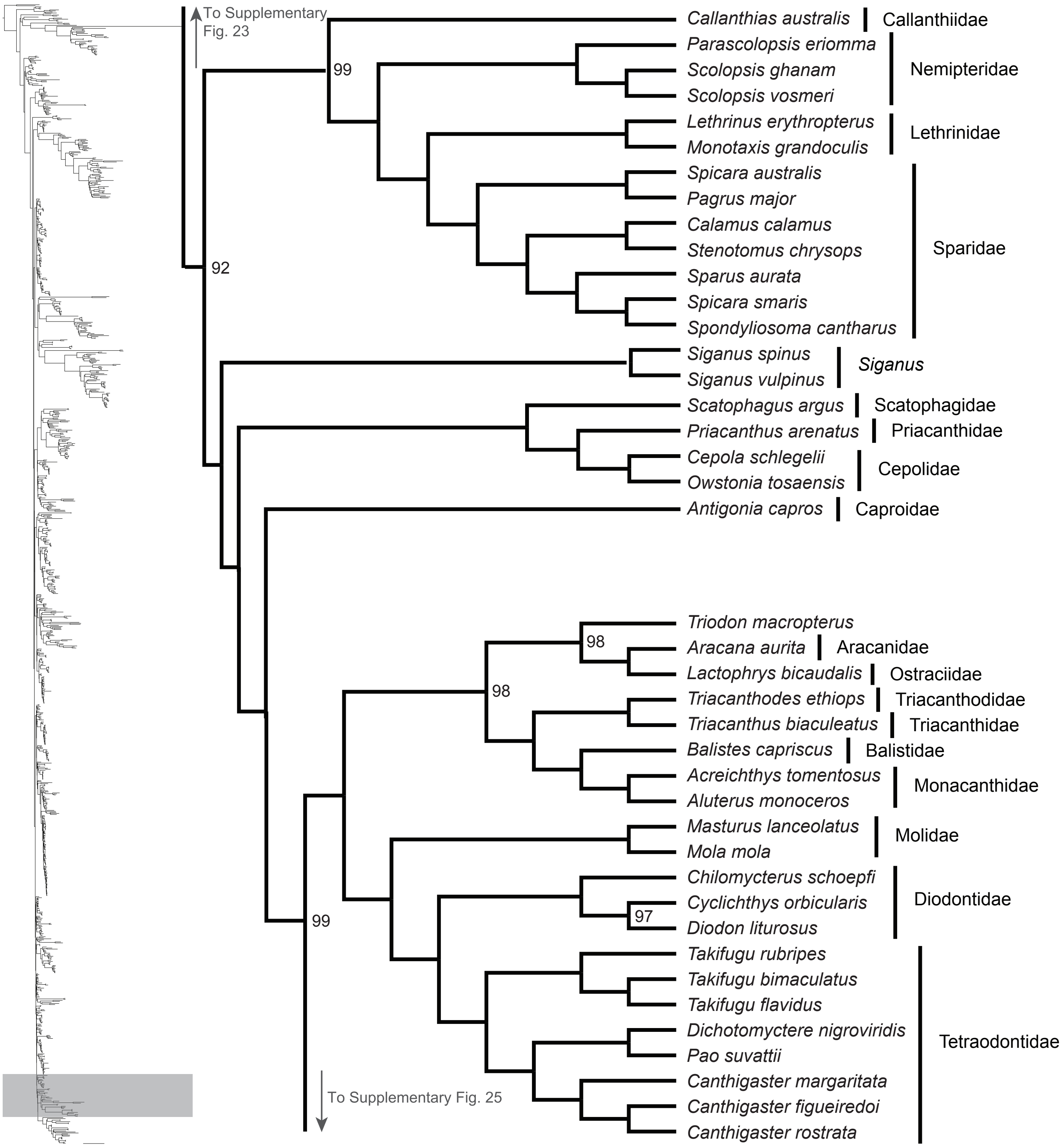


Supplementary Fig. 22: Maximum likelihood phylogeny inferred in IQ-TREE.

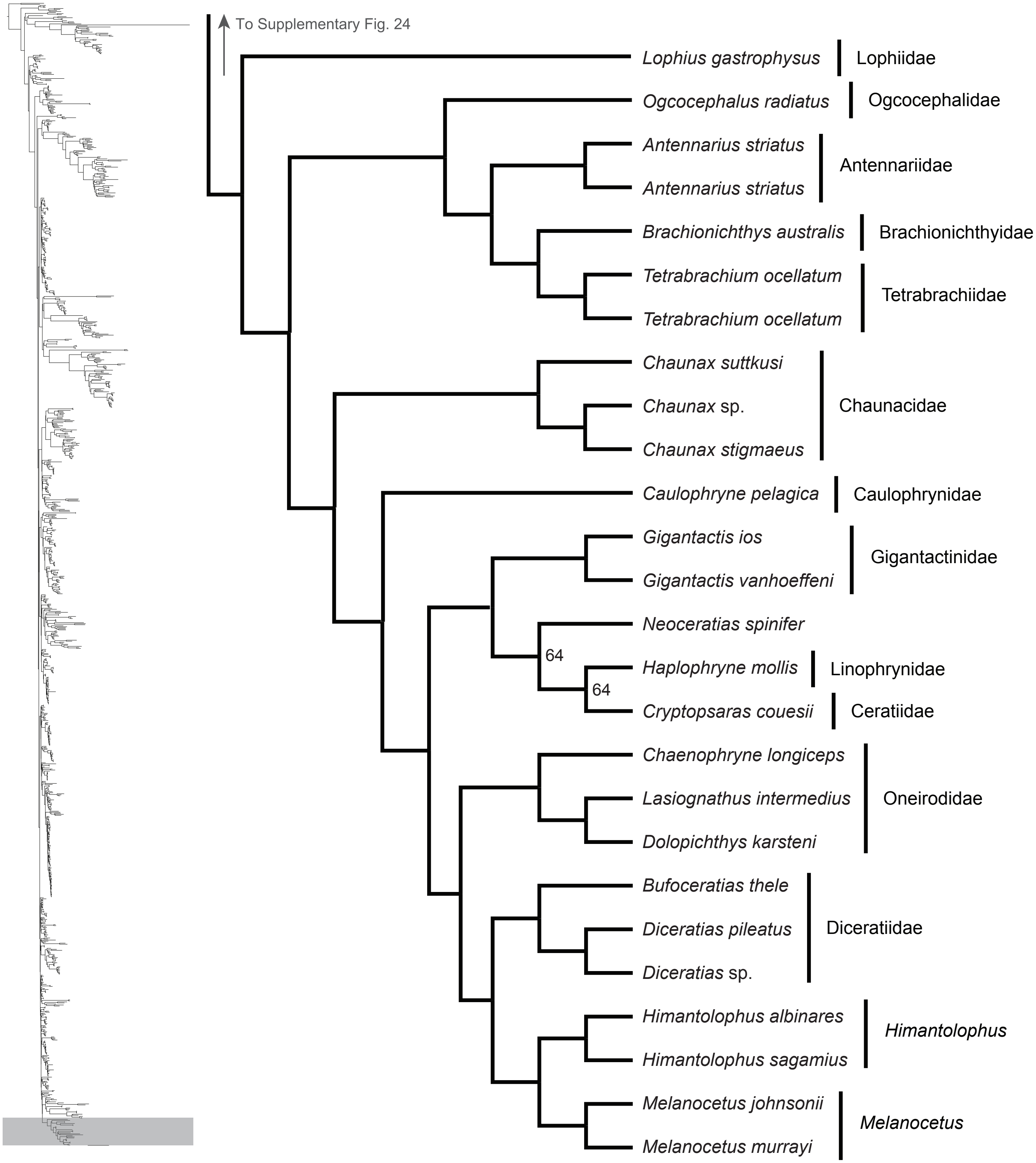
A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap support. Orders, families or genera for taxa are listed to the right of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



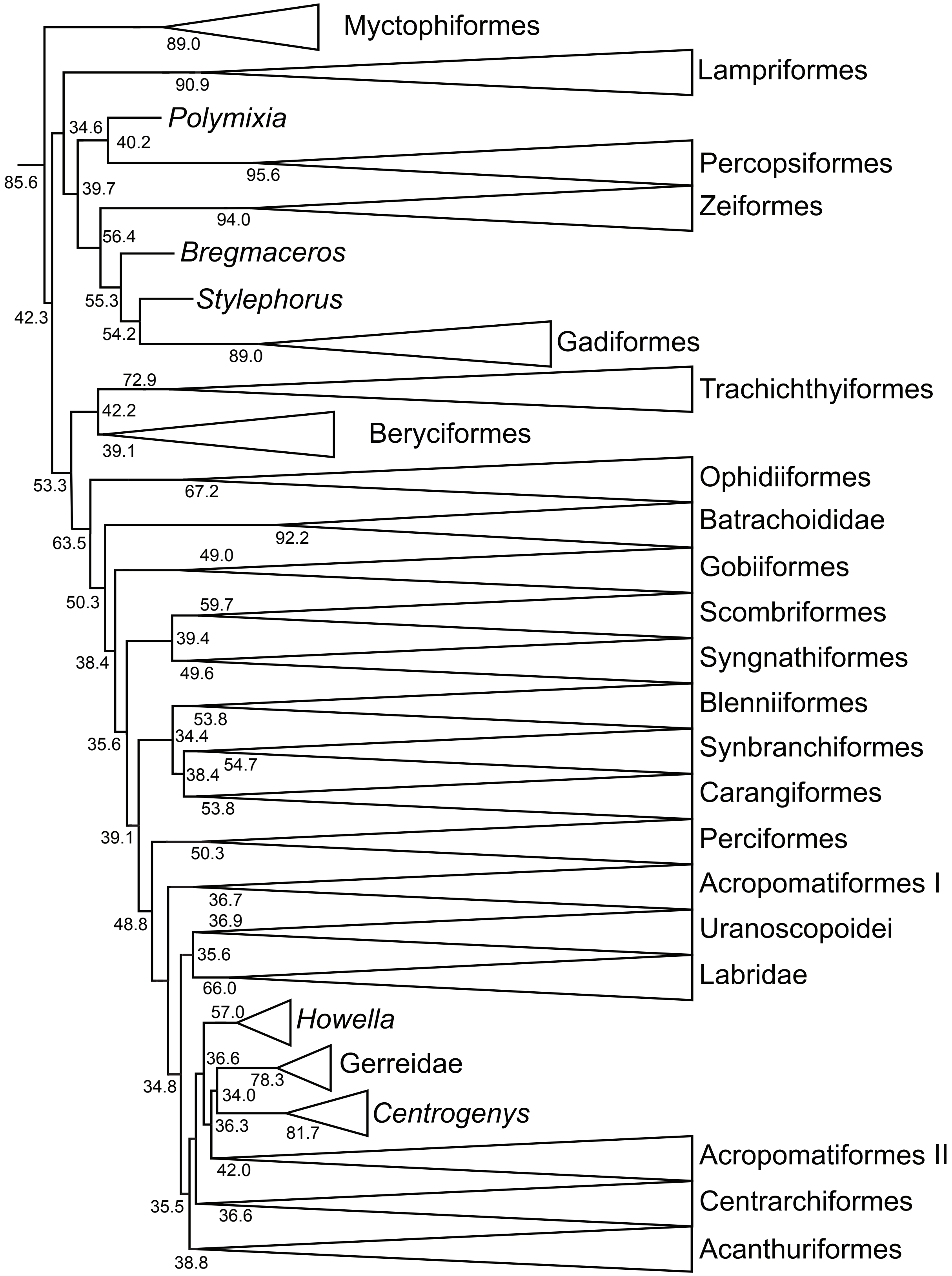
Supplementary Fig. 23: Maximum likelihood phylogeny inferred in IQ-TREE. A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap 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.

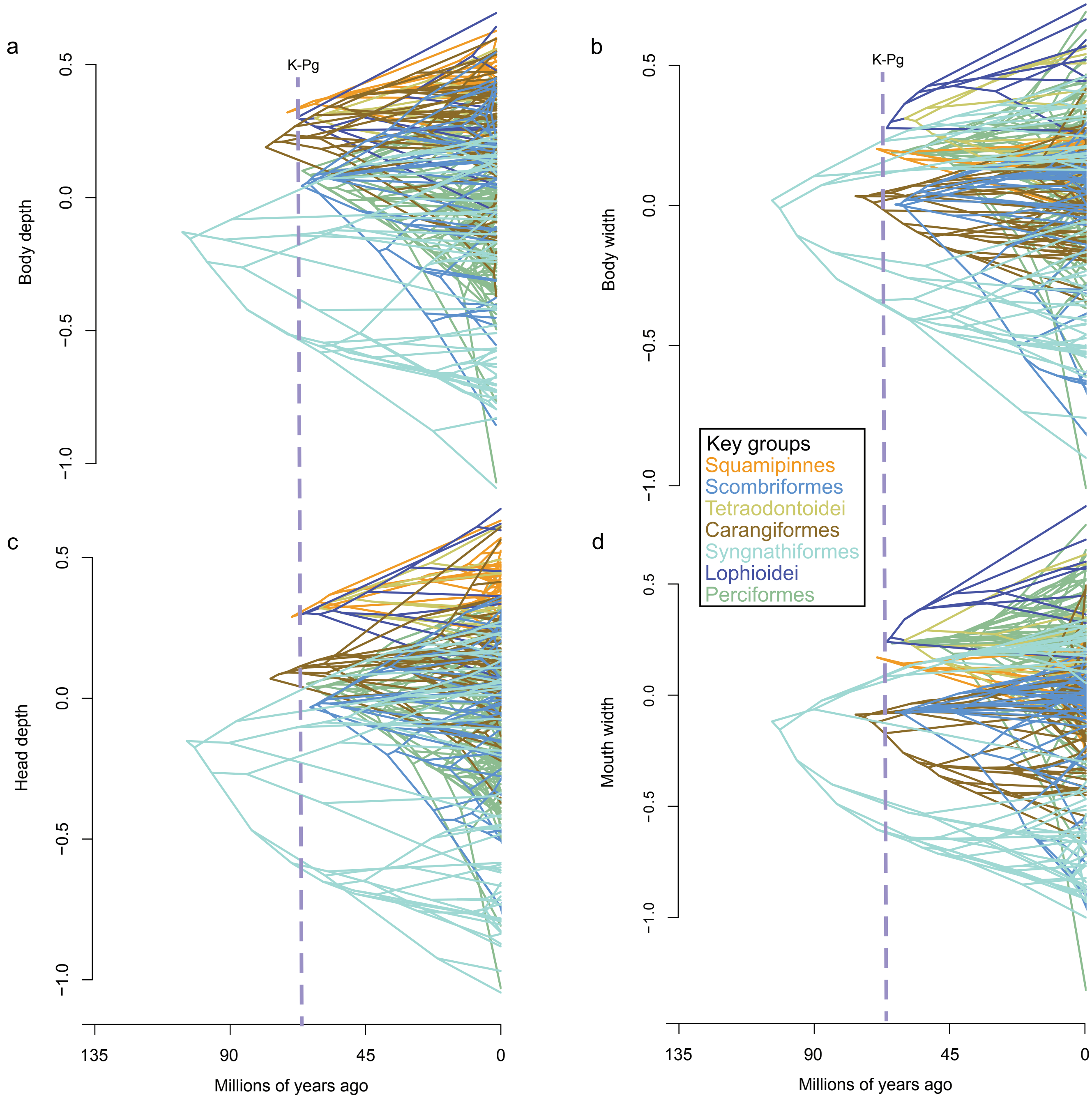


Supplementary Fig. 25: Maximum likelihood phylogeny inferred in IQ-TREE.
A guide tree on the left marks (with a gray rectangle), the region of the acanthomorph tree represented in the figure. Numbers at nodes reflect bootstrap support values. All nodes without a numerical annotation have 100% bootstrap 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.



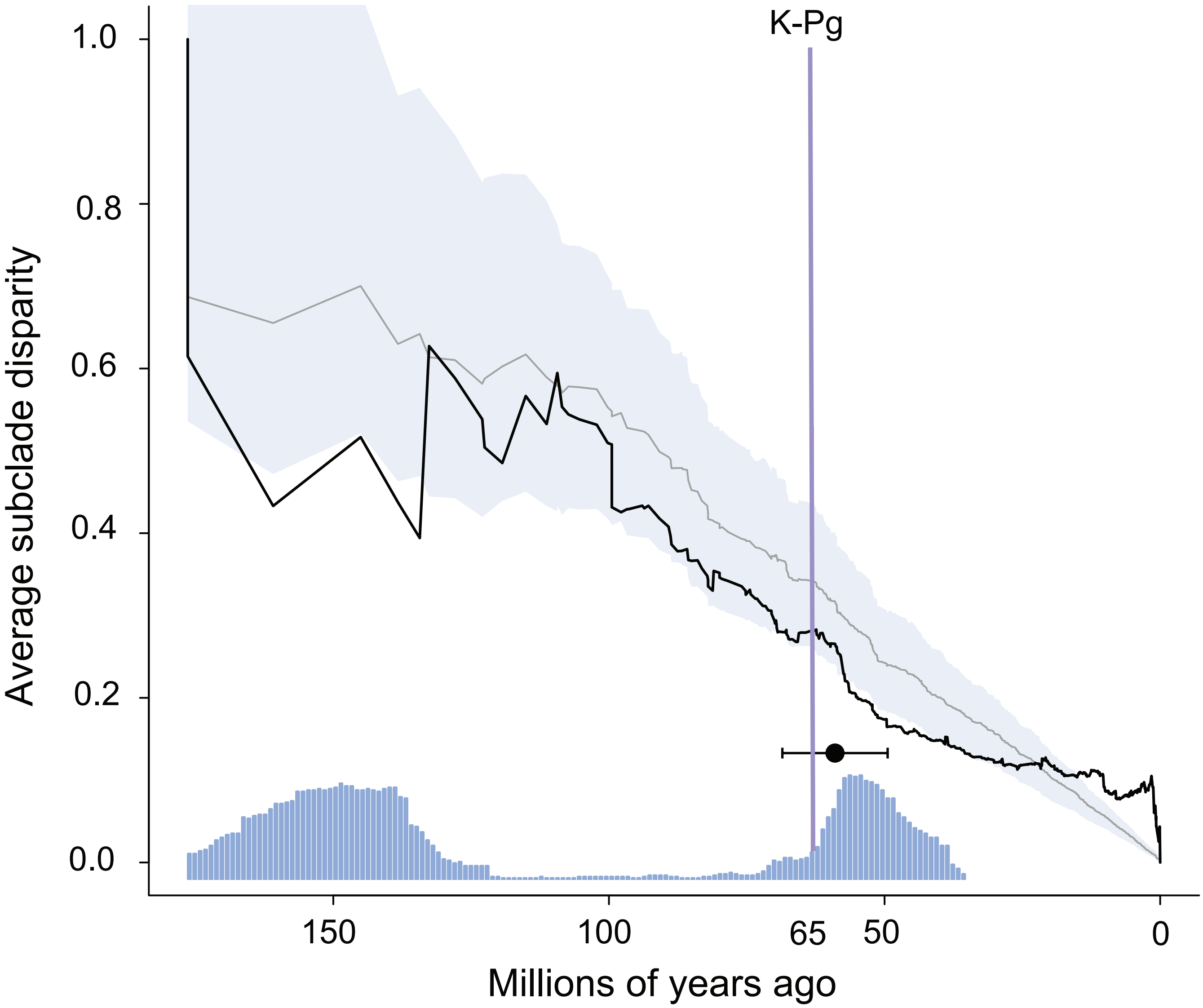
Supplementary Fig. 26: ASTRAL-III inferred species tree.

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.

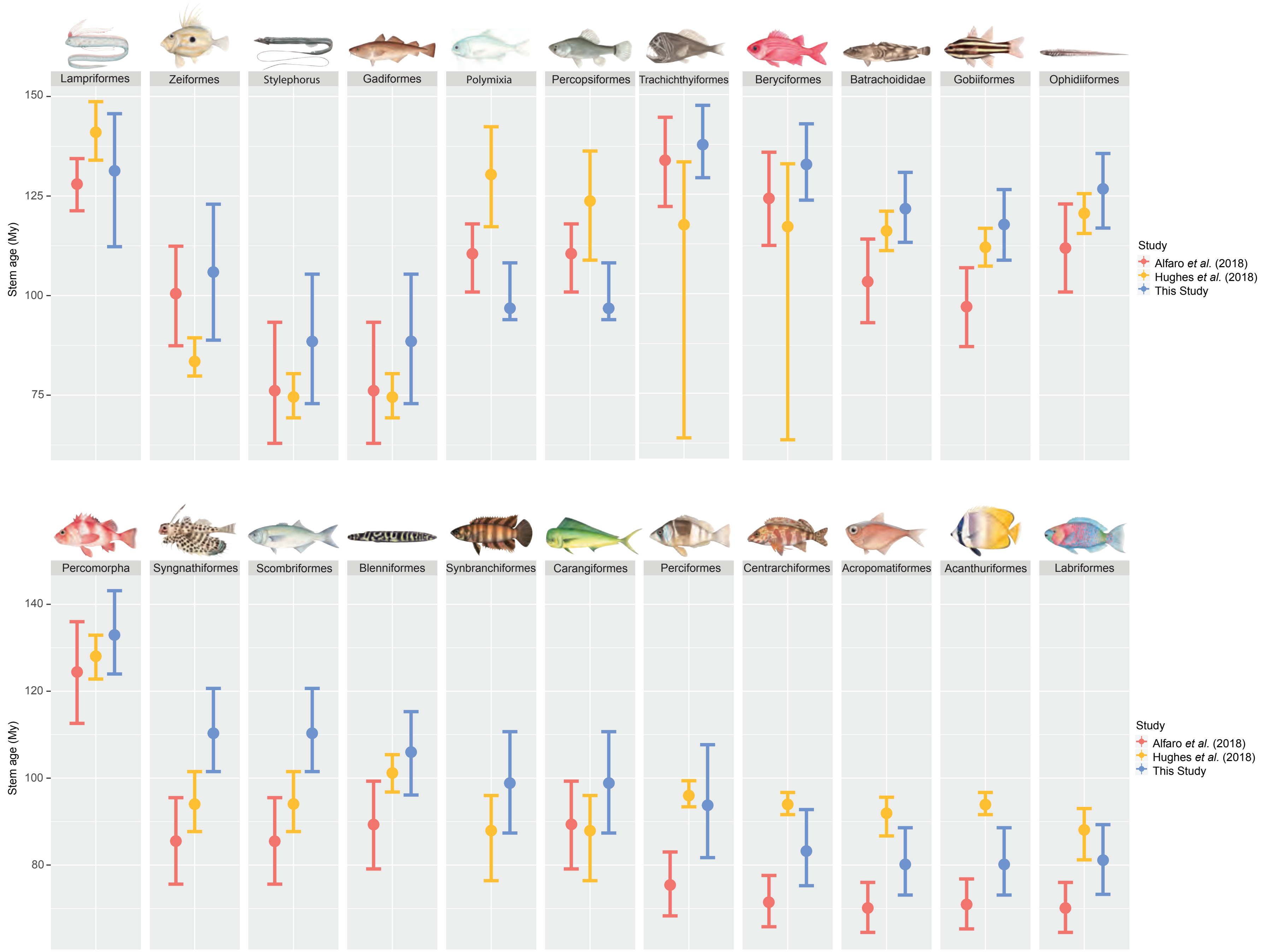


Supplementary Fig. 27: Phenograms depicting the evolutionary history of four phenotypic traits (body depth and width, and head depth and width) across seven major lineages that arose around the K-Pg.

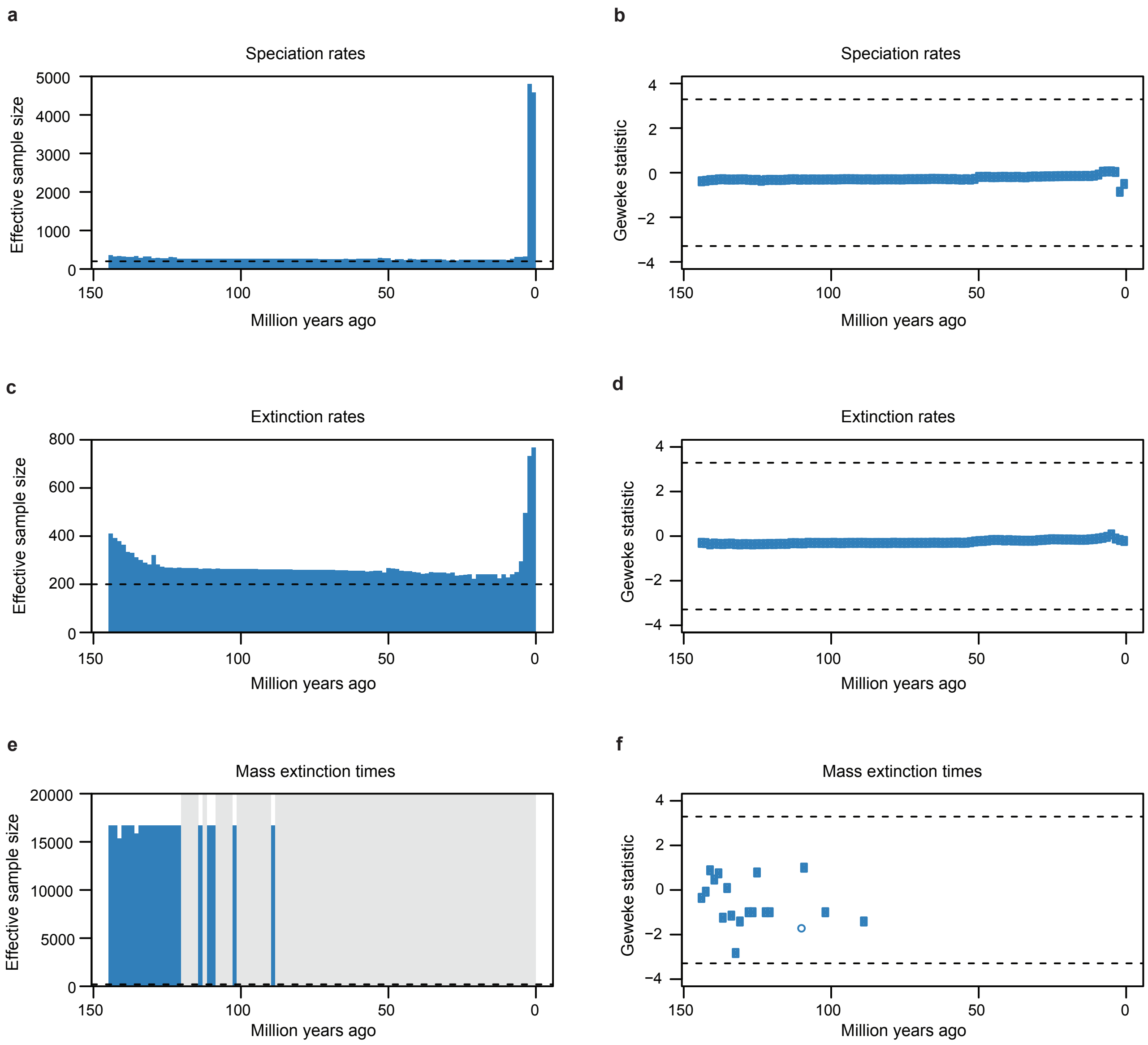
The vertical dashed line marks the K-Pg boundary.



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 (±95% CI) of the initial time point at which the observed disparity dropped below that expected from BM following the K-Pg.

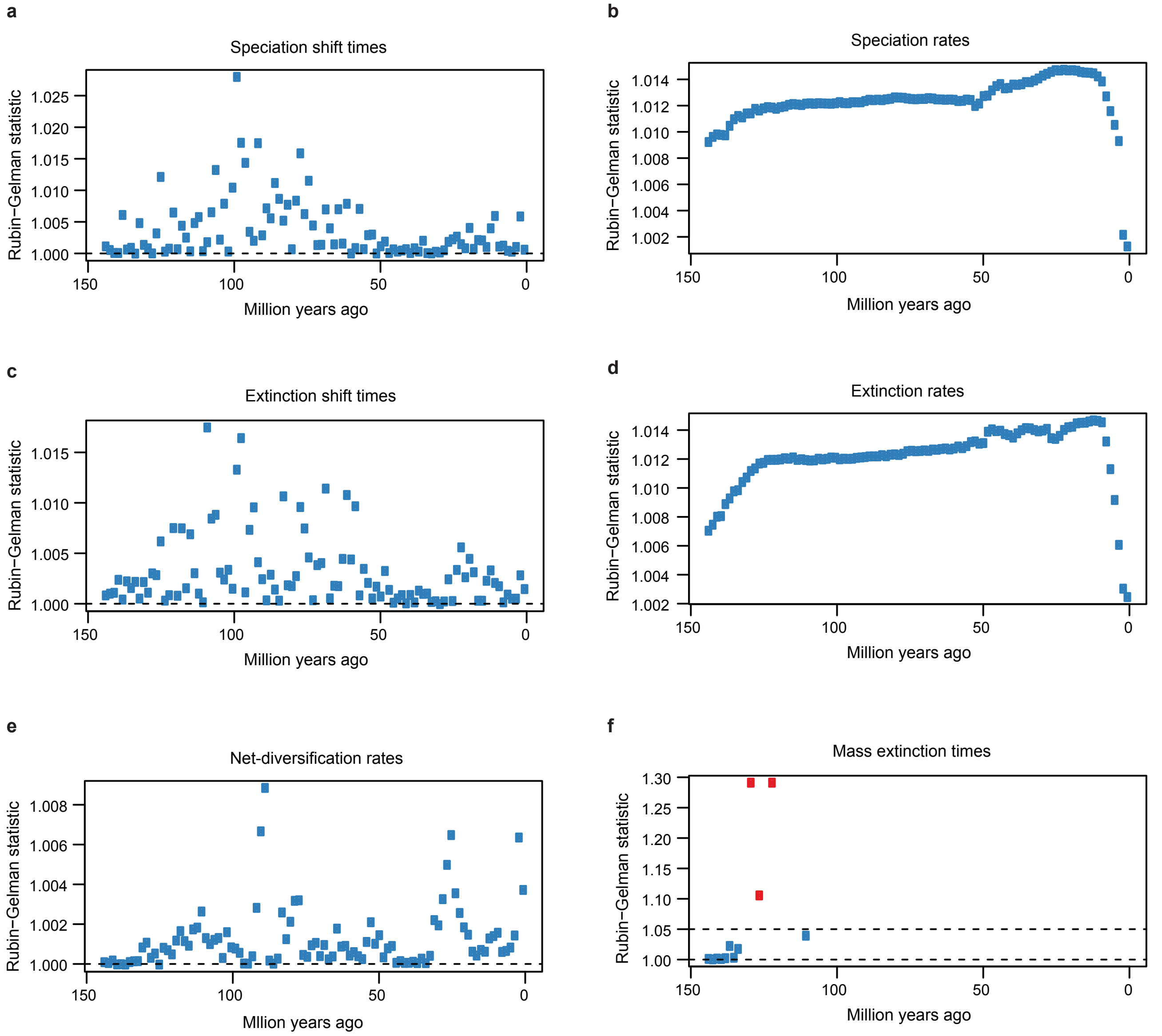


Supplementary Fig. 29: Median stem age estimates and 95% Highest Posterior Densities (HPD) for 22 major acanthomorph clades, as reported in the following 3 phylogenomic studies: Alfaro et al. (2018), Hughes et al. (2018) and this study.
Estimates for this study are the raw node heights reported in the 1,084-taxa 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.

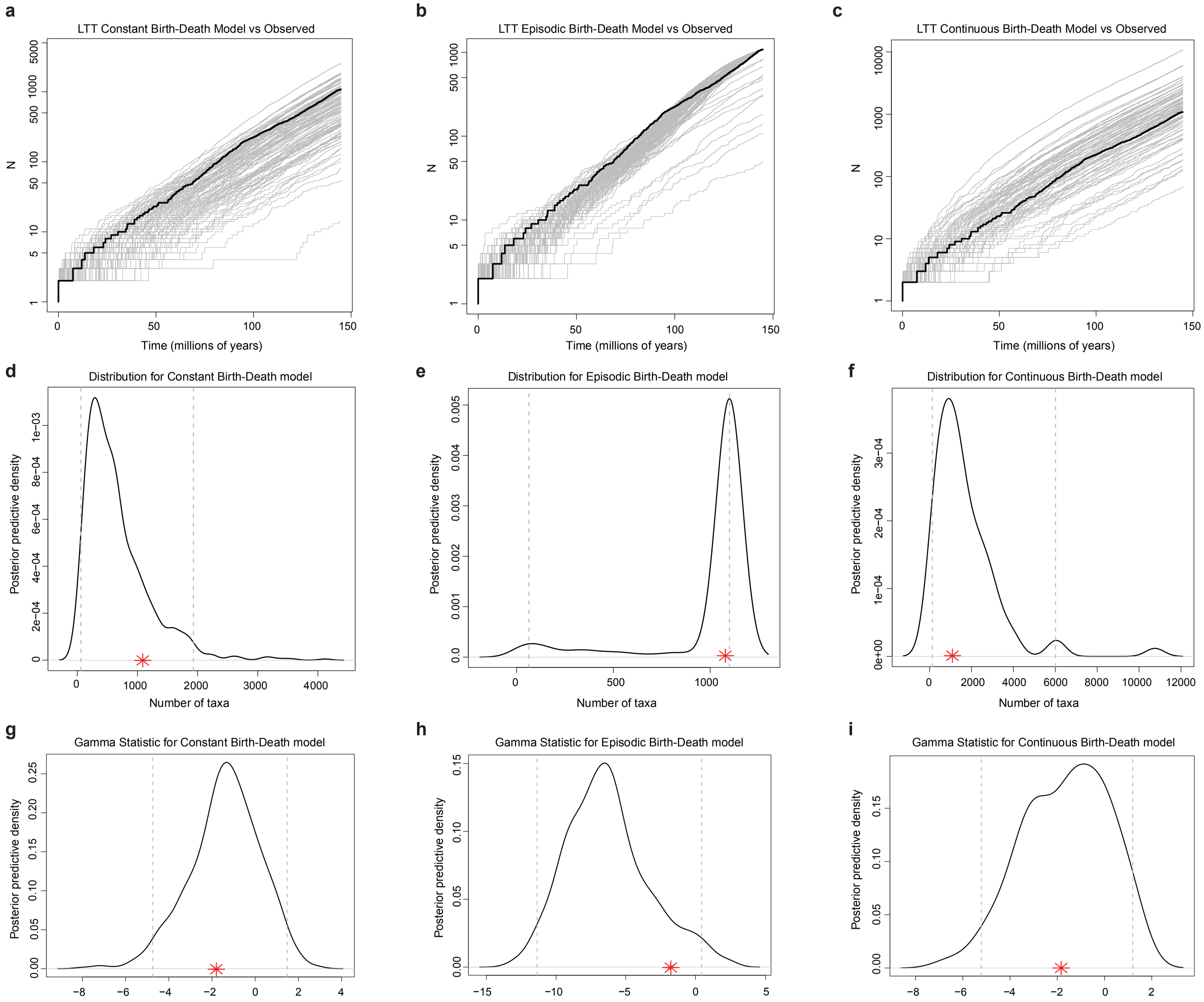


Supplementary Fig. 30: Effective sample sizes (ESS) of parameters and Geweke diagnostics reflect within-chain convergence in the TESS-CoMET analysis depicted in Extended Data Fig.3.

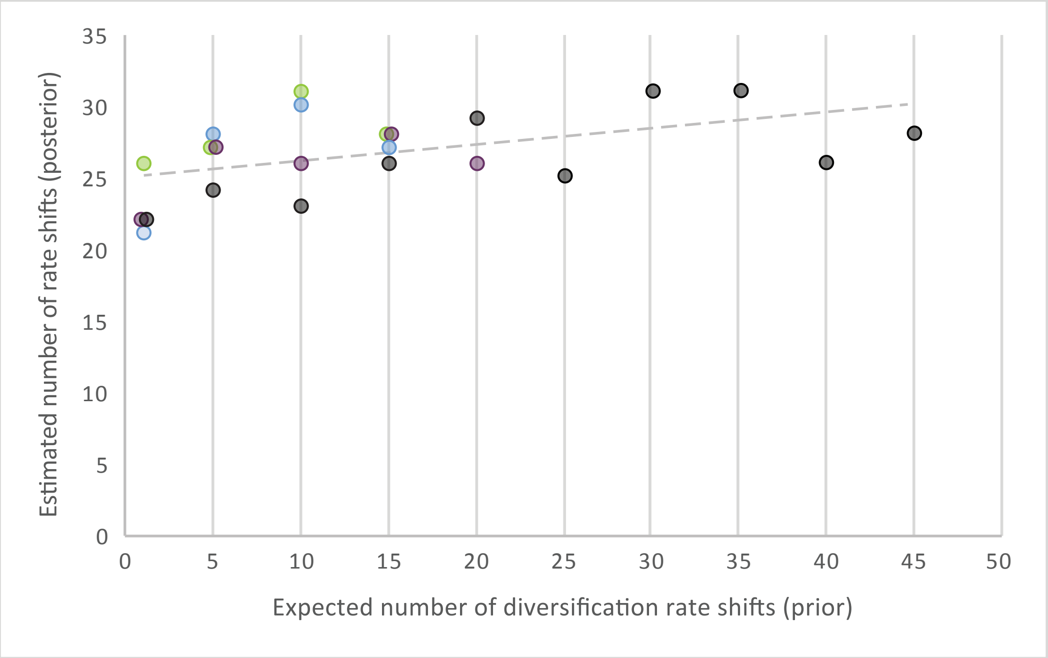
Blue bars and dots reflect that the run successfully converged for the parameter at a given time interval. Horizontal dashed lines reflect canonical, acceptable threshold values or 95% confidence intervals for the two diagnostics (ESS ≥ 200 for a, c, and e; $P > 0.05$ for b, d, and f). a, Effective sample 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-squared= 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 deltaT of 0.05, purple corresponds to 4 MCMC chains in the analysis with a deltaT of 0.1, blue corresponds to 2 MCMC chains in the analysis with a deltaT of 0.05, and green corresponds to 2 MCMC chains in the analysis with a deltaT of 0.1.