

Fig. S1: Placement of all 33 fossil calibrations for percomorph outgroups and in Labridae.

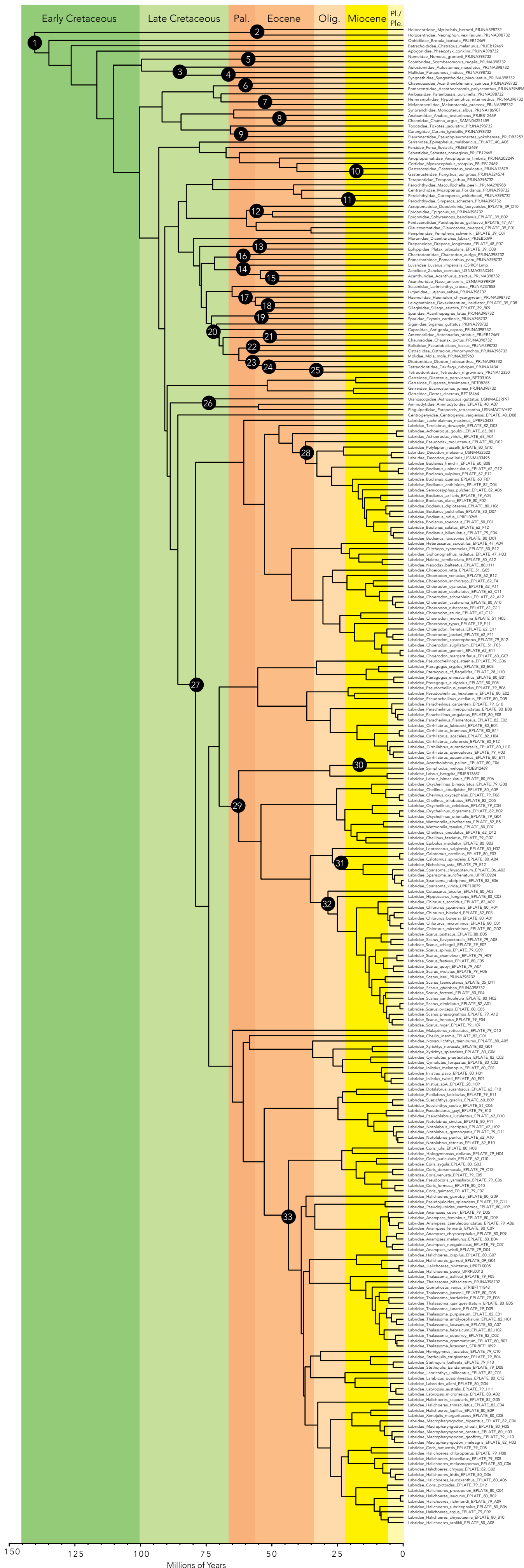




Fig. S3: Maximum Likelihood phylogeny Maximum Likelihood phylogeny estimated in IQ-Tree from 1084 concatenated nucleotide loci, with outlier genes removed based on GLS scores. SH-aLRT/UFBoot values are not shown for branches with maximum support (100/100).

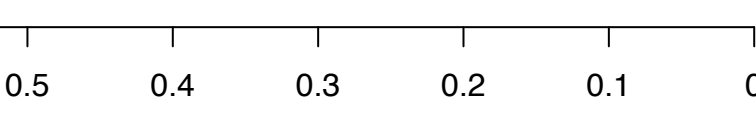
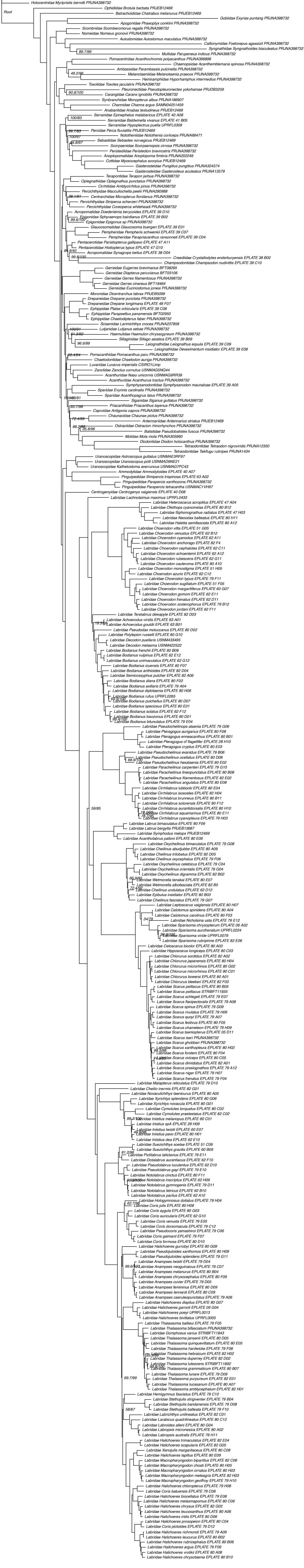


Fig. S4: Maximum Likelihood phylogeny estimated in IQ-Tree from all 1088 concatenated nucleotide loci, with third codon positions removed. SH-ALRT/UFBoot values are not shown for branches with maximum support (100/100).

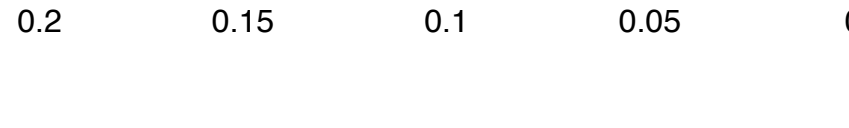


Fig. S5: Maximum Likelihood phylogeny estimated in IQ-Tree from 818 concatenated nucleotide loci, with a minimum of 150 taxa per locus. SH-aLRT/UFBoot values are not shown for branches with maximum support (100/100).

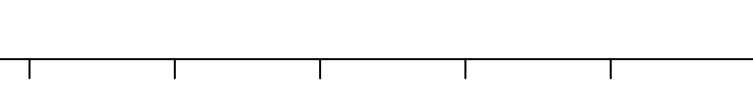
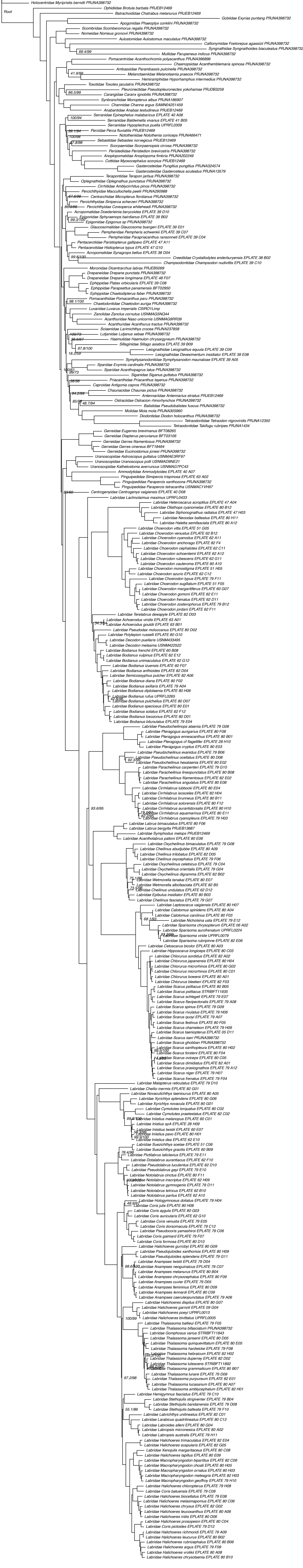
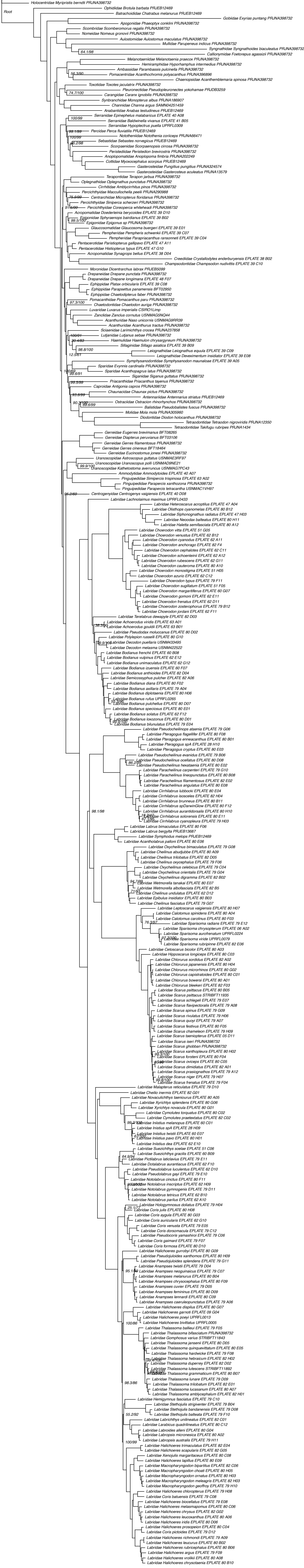


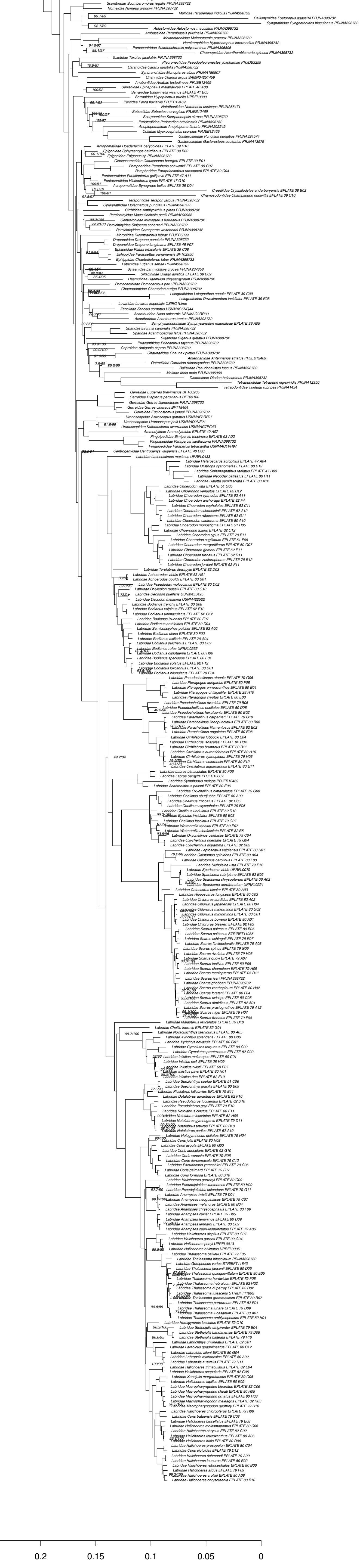


Fig. S7: Maximum Likelihood phylogeny estimated in IQ-Tree from 665 concatenated nucleotide loci, with a minimum of 200 taxa per locus. SH-aLRT/UFBoot values are not shown for branches with maximum support (100/100).



0.5 0.4 0.3 0.2 0.1 0

**Fig. S8: Maximum Likelihood phylogeny estimated in IQ-Tree from 665 concatenated nucleotide loci, with a minimum of 200 taxa per locus and third codon positions removed. SH-aLRT/UFBoot values are not shown for branches with maximum support (100/100).**



0.2 0.15 0.1 0.05 0



Fig. S9: Maximum Likelihood phylogeny estimated in IQ-Tree from 375 concatenated nucleotide loci, with a minimum of 250 taxa per locus. SH-aLRT/UFBoot values are not shown for branches with maximum support (100/100).

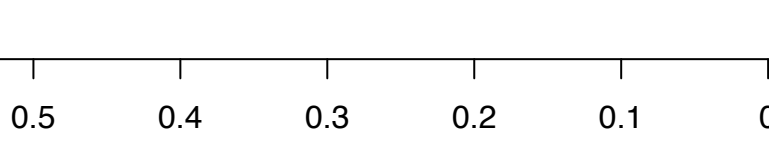
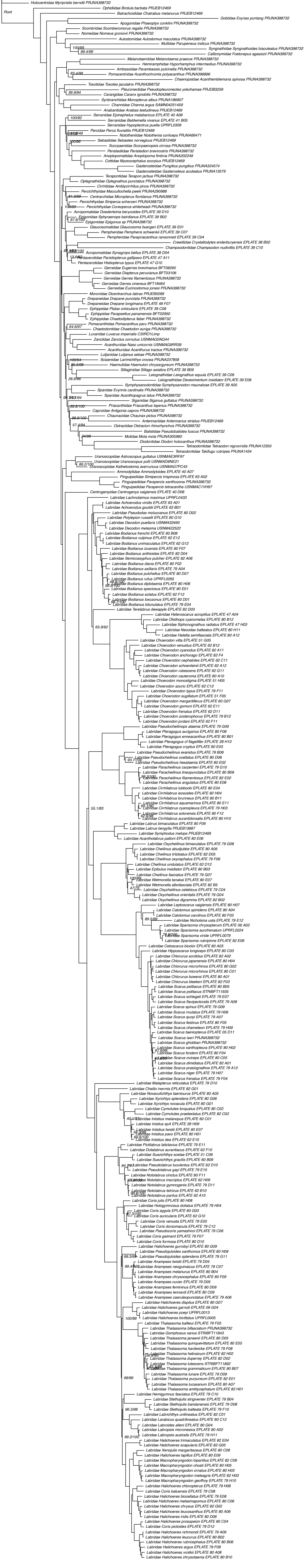




Fig. S11: Maximum Likelihood phylogeny estimated in IQ-Tree from all 1088 loci as amino acids. SH-aLRT/UFBoot values are not shown for branches with maximum support (100/100).

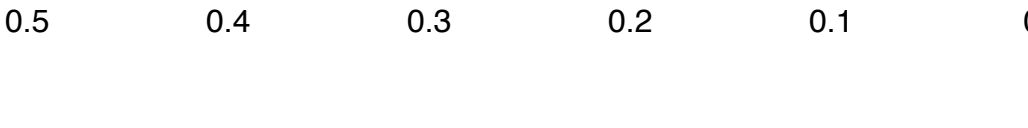
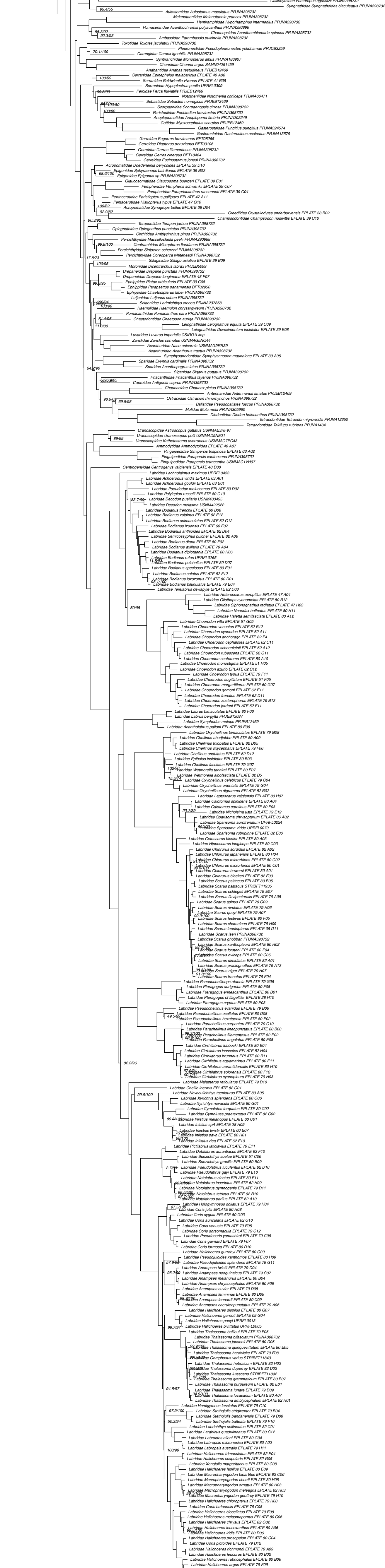


Fig. S12: Maximum Likelihood phylogeny estimated in IQ-Tree from 818 loci as amino acids. SH-aLRT/UFBoot values are not shown for branches with maximum support (100/100).

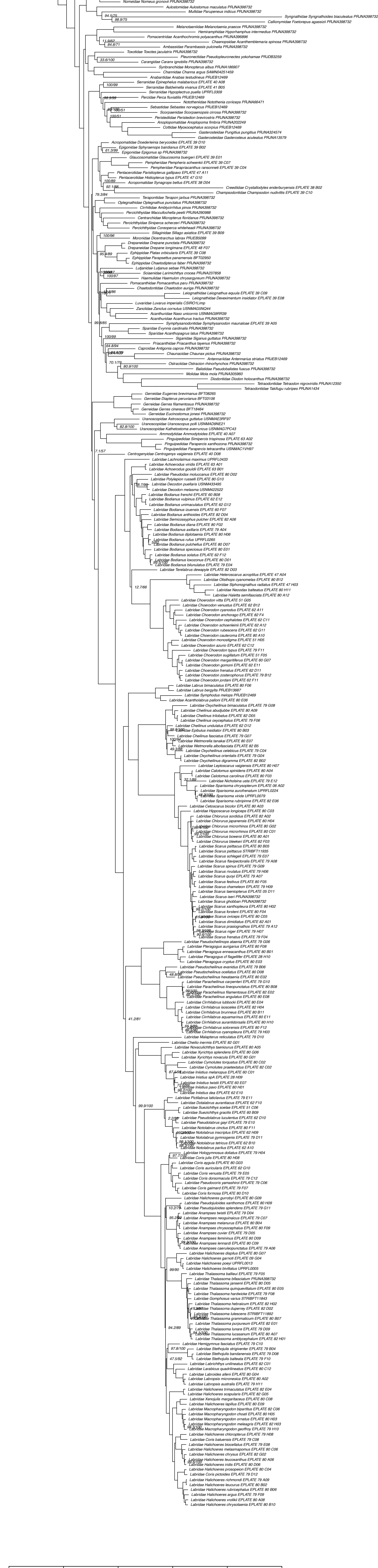


Fig. S13: Maximum Likelihood phylogeny estimated in IQ-Tree from 665 loci as amino acids. SH-aLRT/UFBoot values are not shown for branches with maximum support (100/100).



Fig. S14: Maximum Likelihood phylogeny estimated in IQ-Tree from 375 loci as amino acids. SH-aLRT/UFBoot values are not shown for branches with maximum support (100/100).

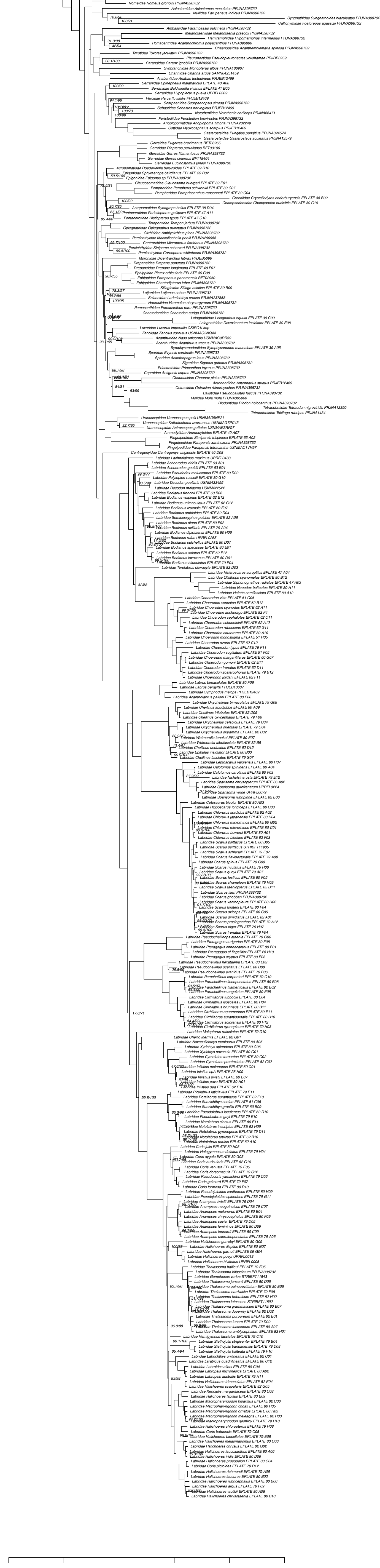


Fig. S15: Multispecies coalescent tree computed in ASTRAL-III from 1088 loci. Local posterior probabilities are not shown on branches with maximum support (1.0).







Fig. S17: Multispecies coalescent tree computed in ASTRAL-III from 818 loci. Local posterior probabilities are not shown on branches with maximum support (1.0).

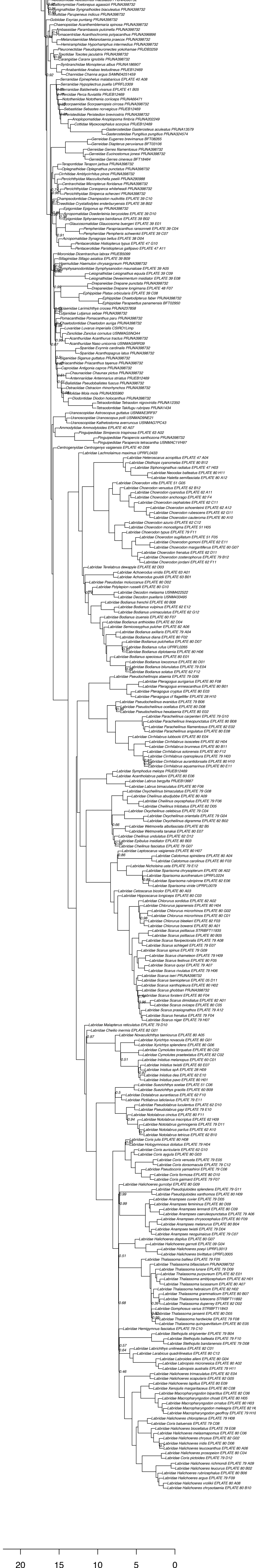
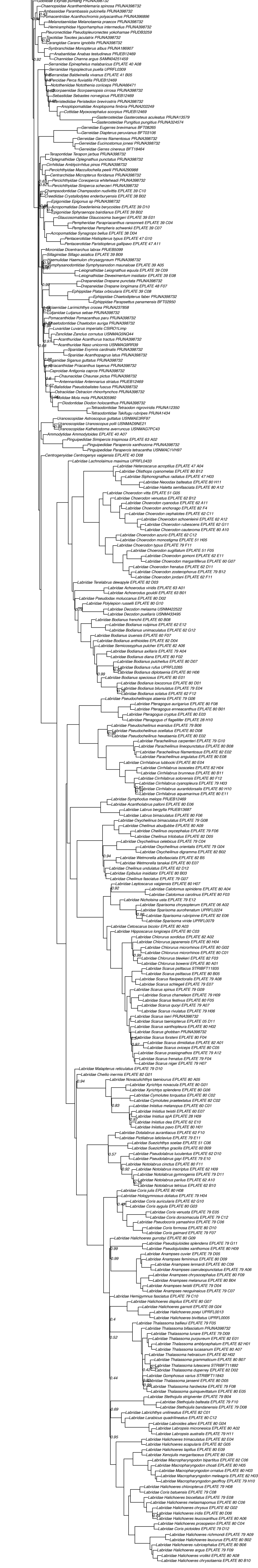


Fig. S18: Multispecies coalescent tree computed in ASTRAL-III from 665 loci. Local posterior probabilities are not shown on branches with maximum support (1.0).



20 15 10 5 0

Fig. S19: Multispecies coalescent tree computed in ASTRAL-III from 375 loci.

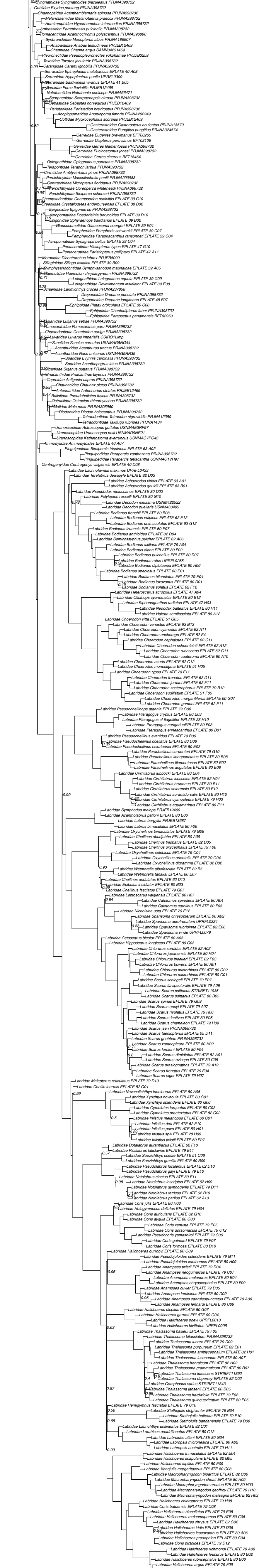
Local posterior probabilities are not shown on branches with maximum support (1.0).



20 15 10 5 0



**Fig. S21: Multispecies coalescent tree computed in ASTRAL-III from 818 loci.**  
**Branches with <33% bootstrap support in gene trees have been collapsed.**  
**Local posterior probabilities are not shown on branches with maximum support (1.0).**





**Fig. S23: Multispecies coalescent tree computed in ASTRAL-III from 375 loci.**  
**Branches with <33% bootstrap support in gene trees have been collapsed.**  
**Local posterior probabilities are not shown on branches with maximum support (1.0).**

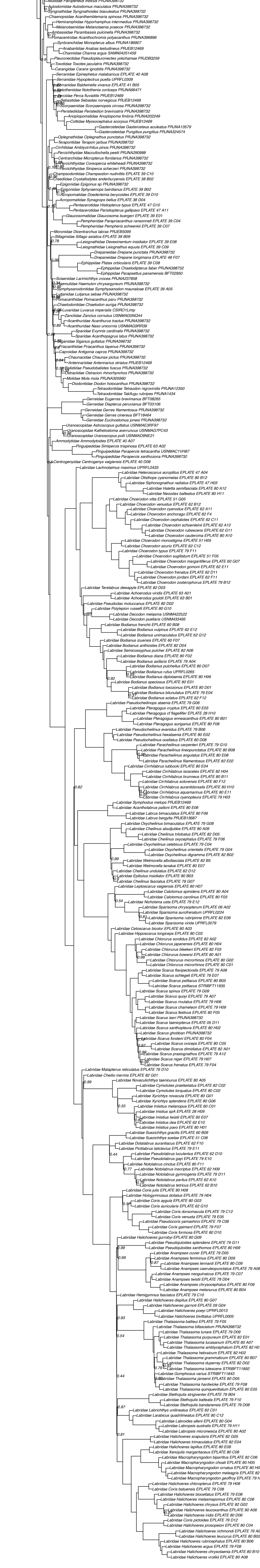


Fig. S24: Analysis of 40 taxa and 1088 loci under the GHOST model.

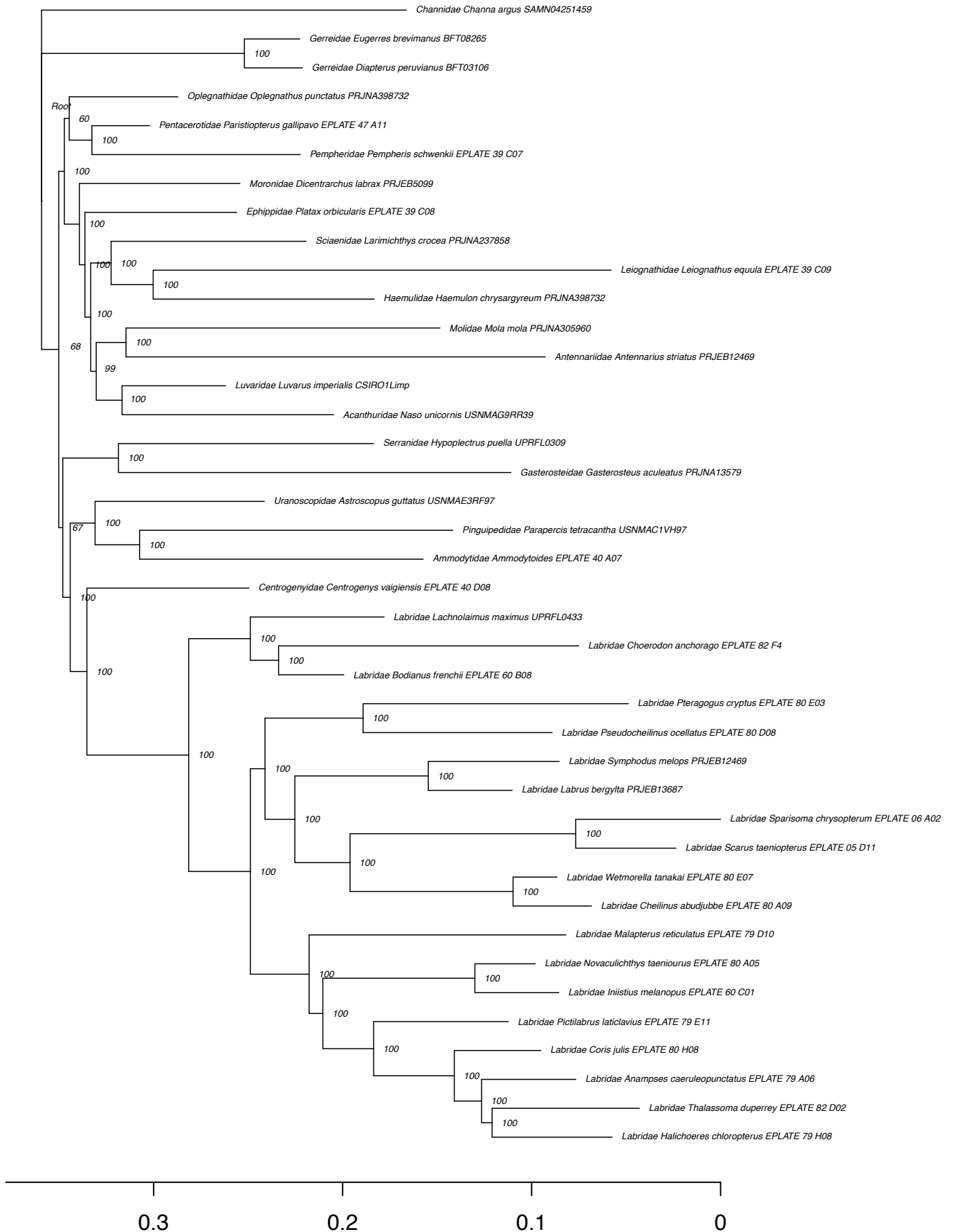




Fig. S25: Analysis of 40 labrid taxa and 1088 loci under the GHOST model.

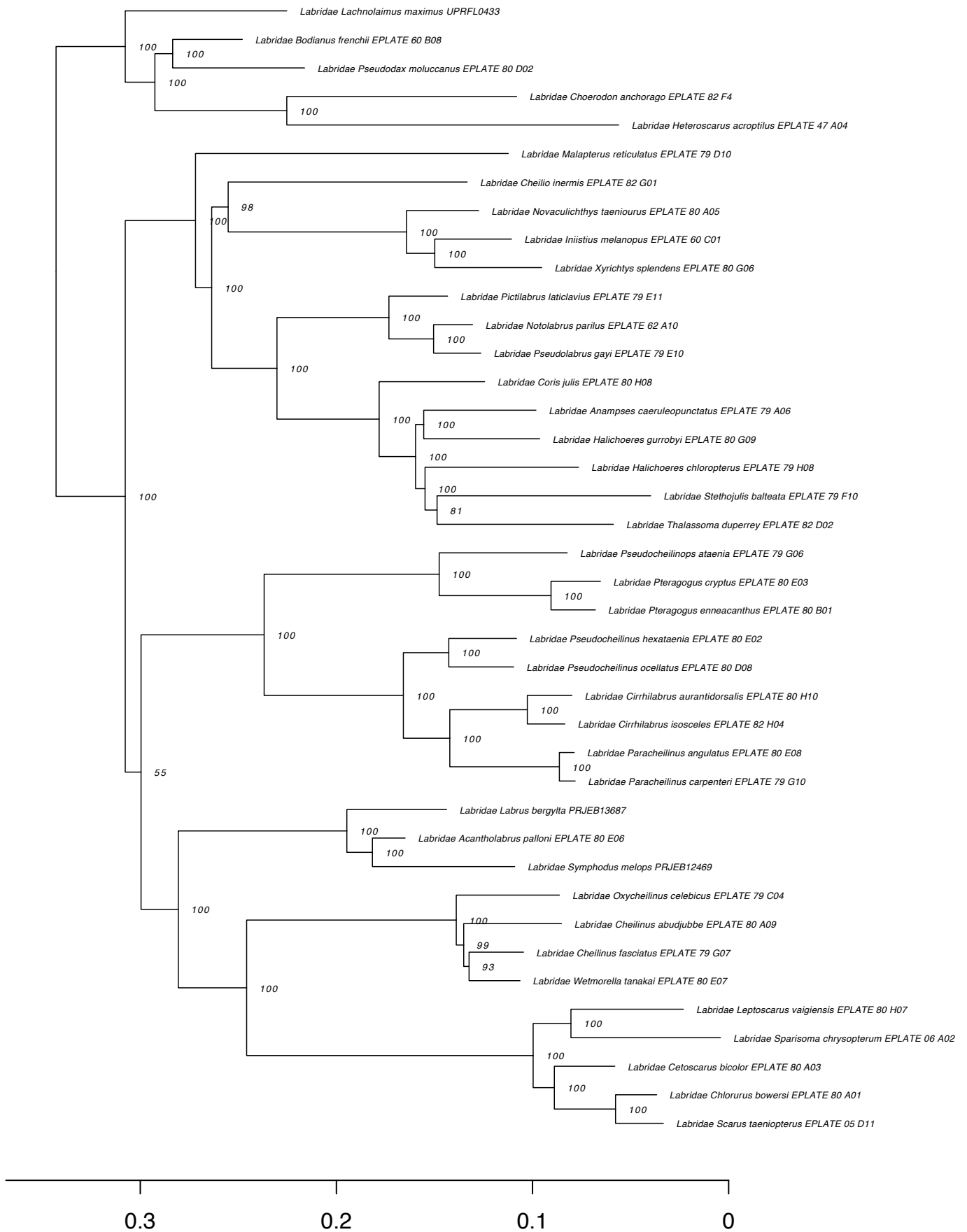
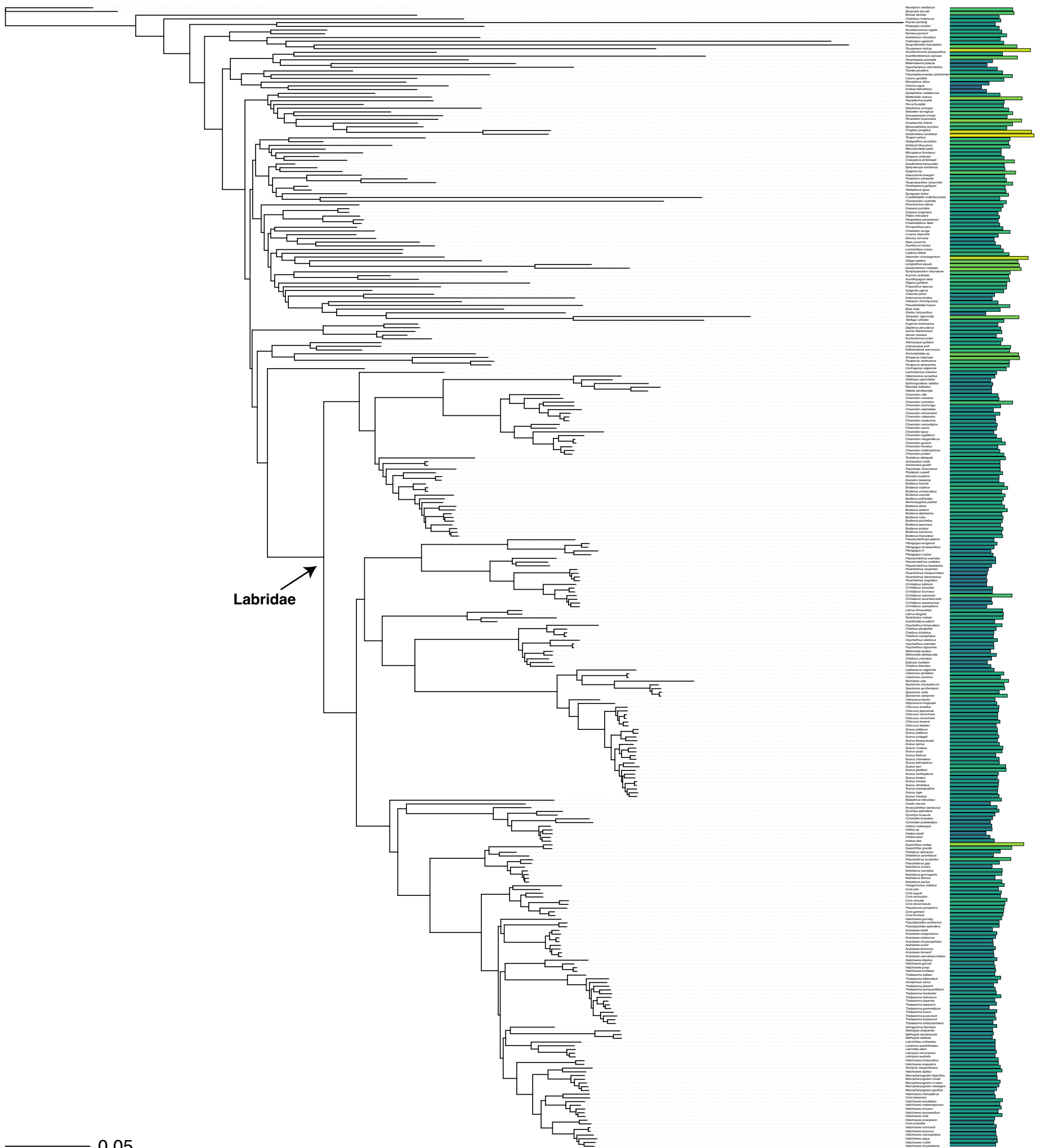


Figure S26: GC content for all genes across the phylogeny.



0.05

48 60

48 52 56 60



**Figure S28: Violin plots of GC content for all codon positions, and excluding the third codon position.**

