

**Supplementary material**

**Distribution of Palinuridae and Scyllaridae phyllosoma larvae within the East Australian Current: a climate change hot spot**

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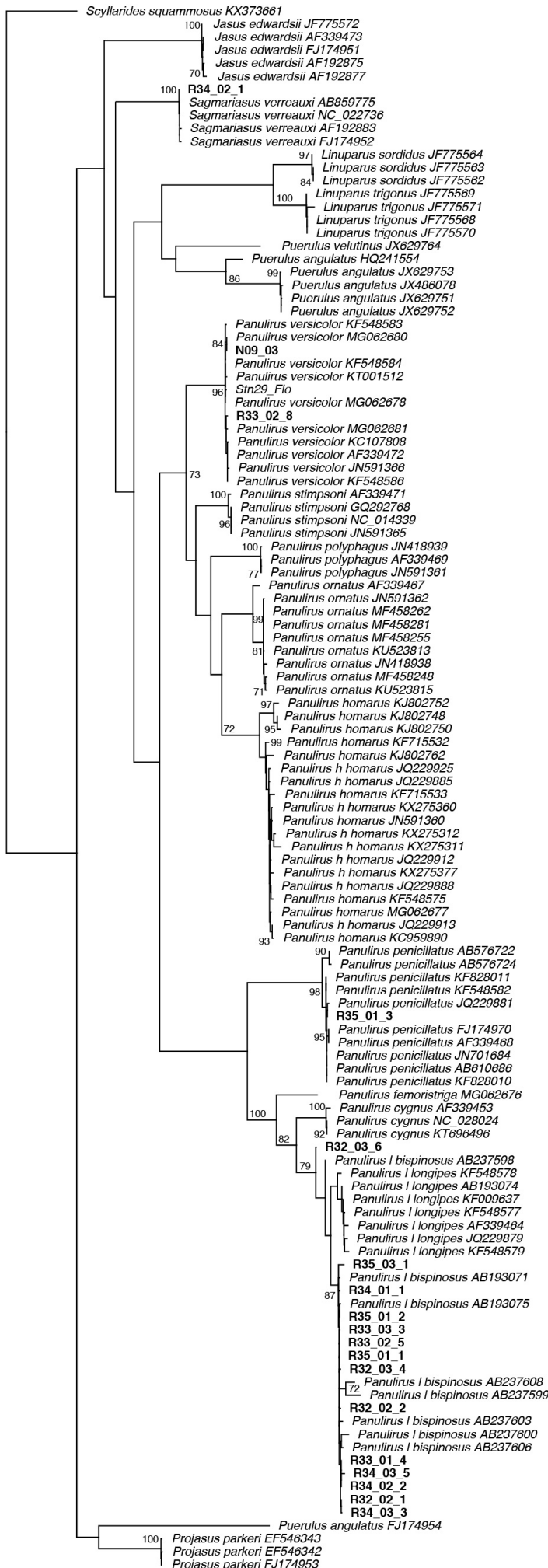
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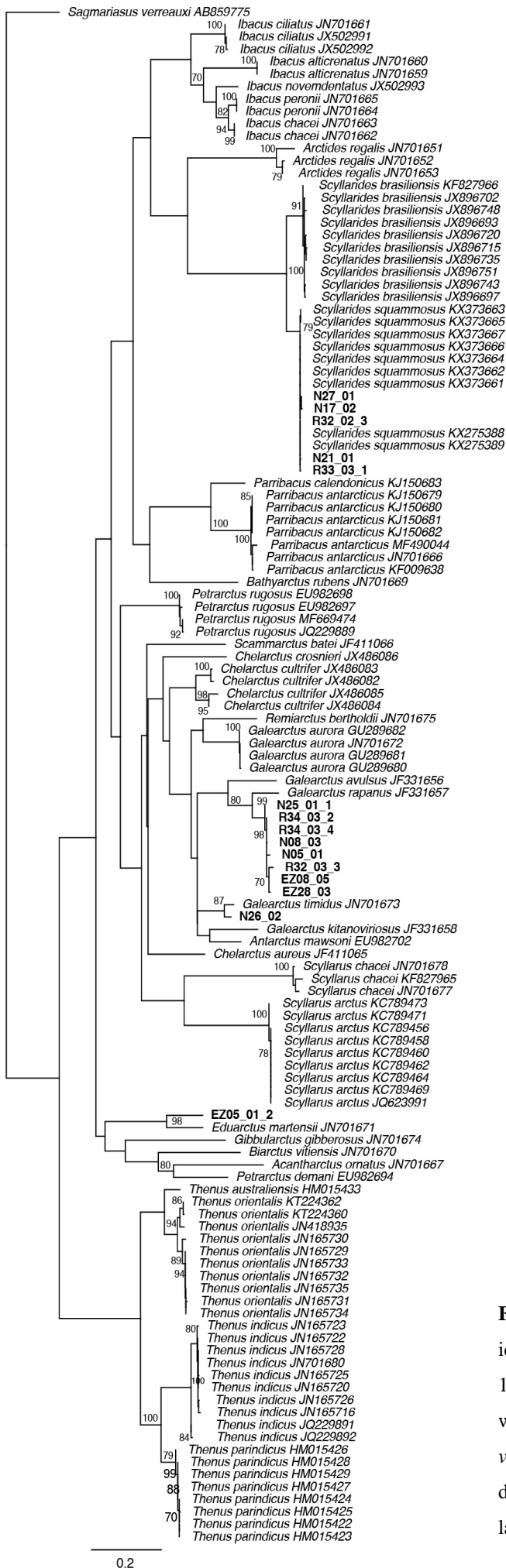
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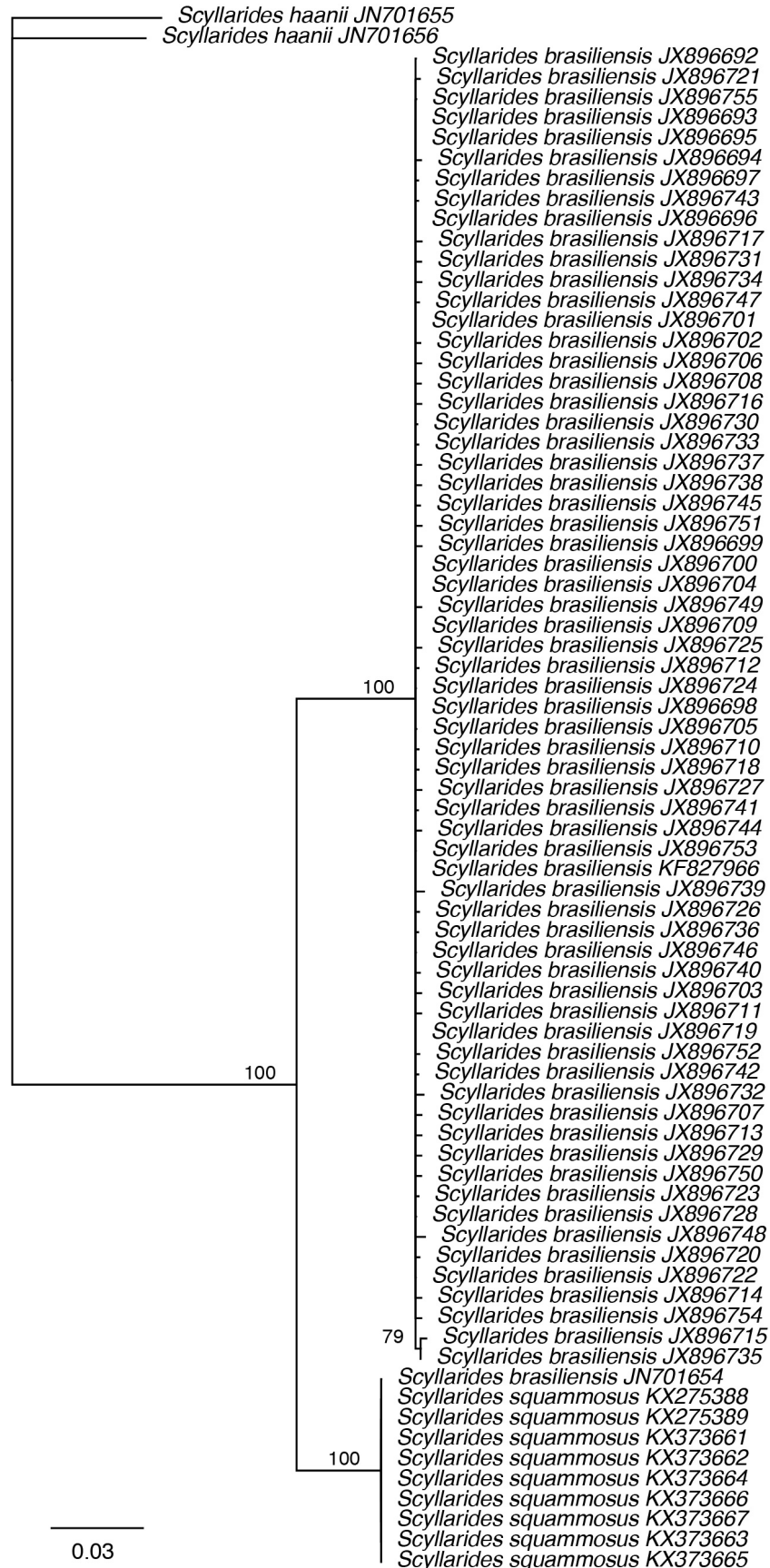
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**Fig. S1.** A palinurid maximum-likelihood species identification tree using all available COI sequences or the 10 most divergent COI sequences as references. The tree was built with a HKY substitution model and *Scyllarides squammosus* as the outgroup. Collected samples are denoted by letter and number combinations. Node labels represent bootstrap values from 1000 replicates.



**Fig. S2.** A scyllarid maximum-likelihood species identification tree using all available COI sequences or the 10 most divergent COI sequences as references. The tree was built with a HKY substitution model and *Sagmariasus verreauxi* as the outgroup. Collected samples are denoted by letter and number combinations. Node labels represent bootstrap values from 1000 replicates.



**Fig. S3.** A Neighbour Joining tree using all COI sequences available in GenBank for *Scyllarides brasiliensis*, *Scyllarides hanii* and *Scyllarides squamosus*. Note that JN701654 groups within the *S. squamosus* clade. Node labels represent consensus support over 1000 bootstraps.