

## Supplementary Figures

### Agalma analysis

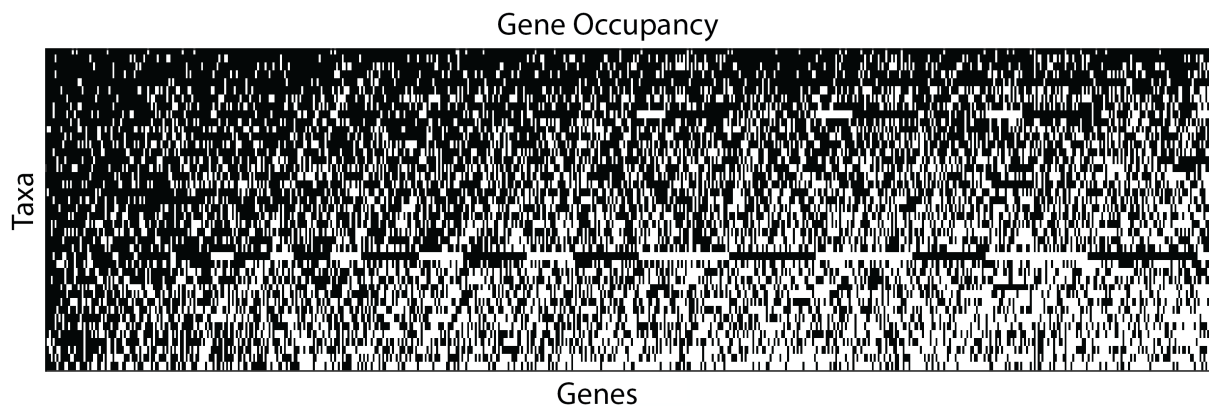


Figure S1: 60% gene occupancy matrix for 41 species across 1,071 genes. Genes and species are sorted by sampling, the best sampled shown in the upper left.

## SOWH analysis

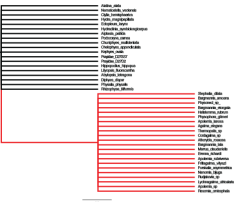

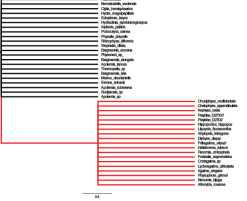
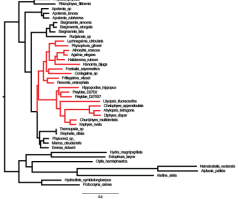
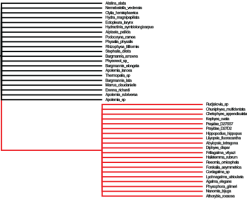
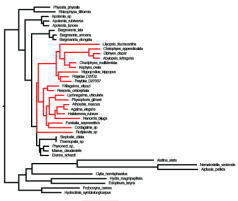
	constraint topology	best tree estimated under constraint	test statistic difference in lnL (observed data)	range of null distribution (simulated data)	p-value (confidence interval, n = 100)
monophyletic physonecks			7,867.81	-2.80*10 <sup>-5</sup> - 1.11	<0.01 (0 - 0.03)
monophyletic monoeccious (- <i>Rudjakova</i> sp.)			2,454.99	-3.10*10 <sup>-5</sup> - 2.54	<0.01 (0 - 0.03)
monophyletic monoeccious (+ <i>Rudjakova</i> sp.)			24,136.83	-0.19 - 2.01	<0.01 (0 - 0.03)

Figure S2: Constrained topologies specified in SOWH testing. Test statistic and p-value for each tree estimated under constraint are given.

# Stochastic Character maps

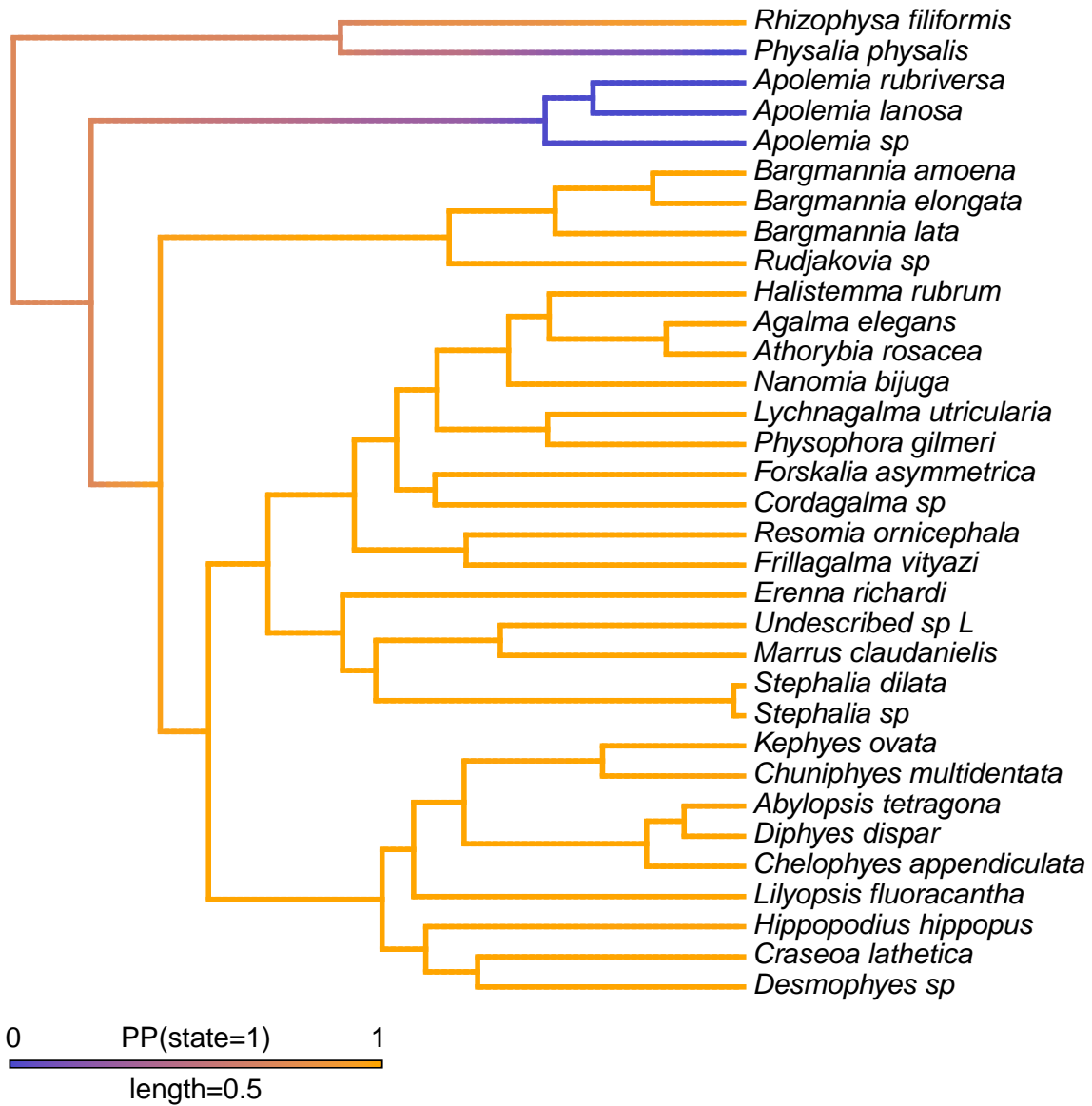


Figure S3: Stochastic character map of presence of tentilla with *Physalia* included as not bearing tentilla.

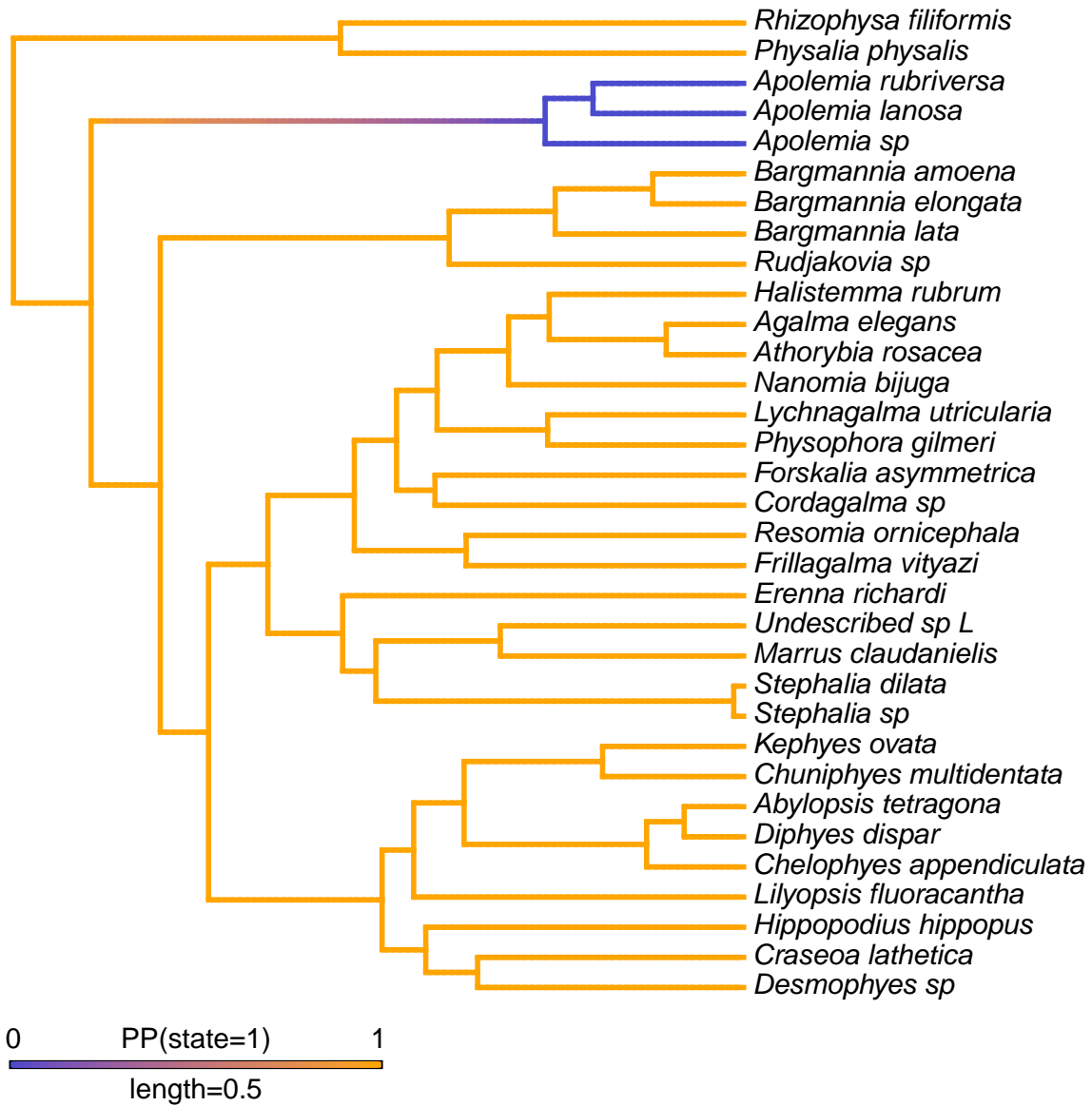


Figure S4: Stochastic character map of presence of tentilla with *Physalia* included as bearing tentilla.

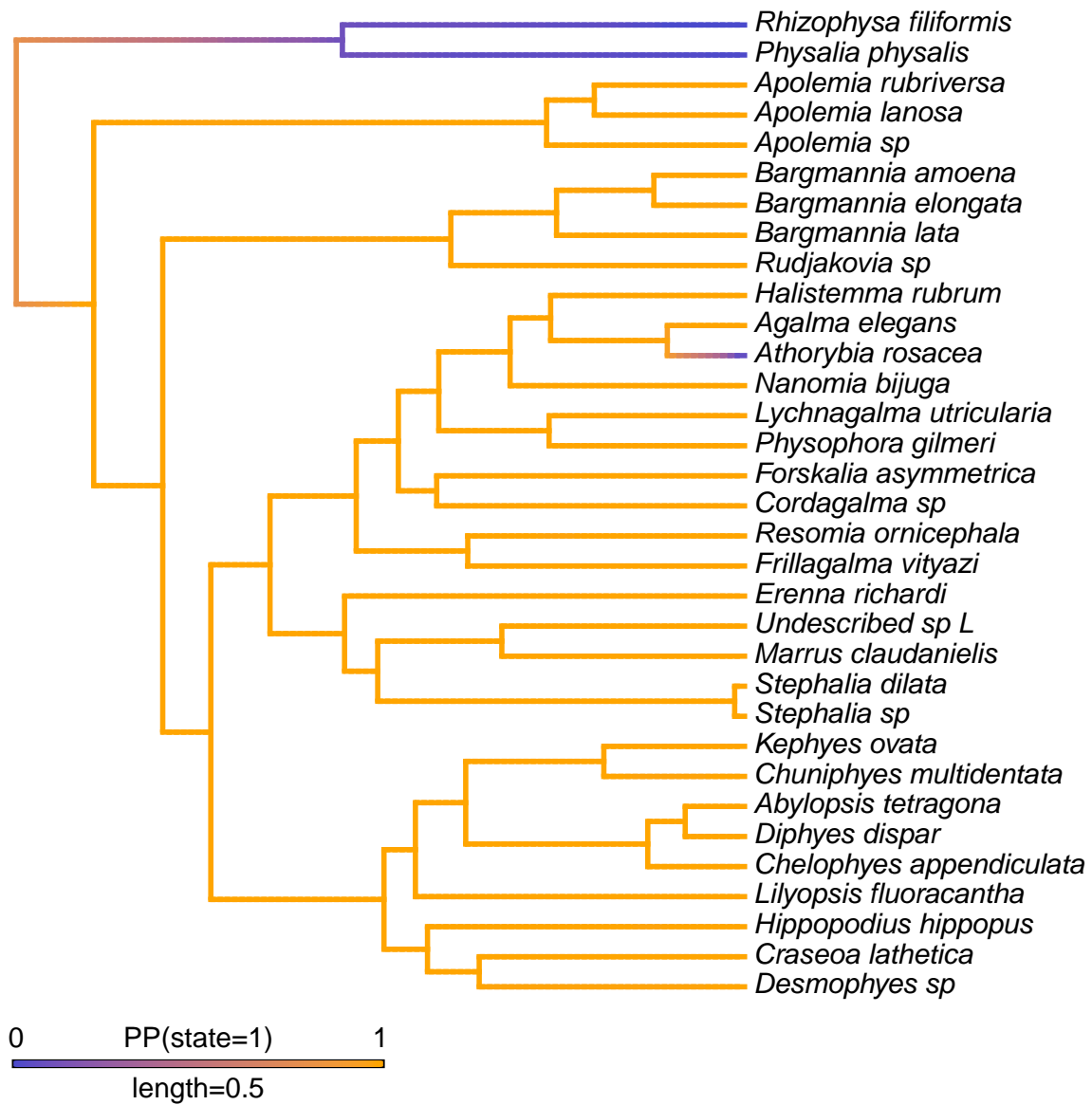


Figure S5: Stochastic character map of presence of nectosome.

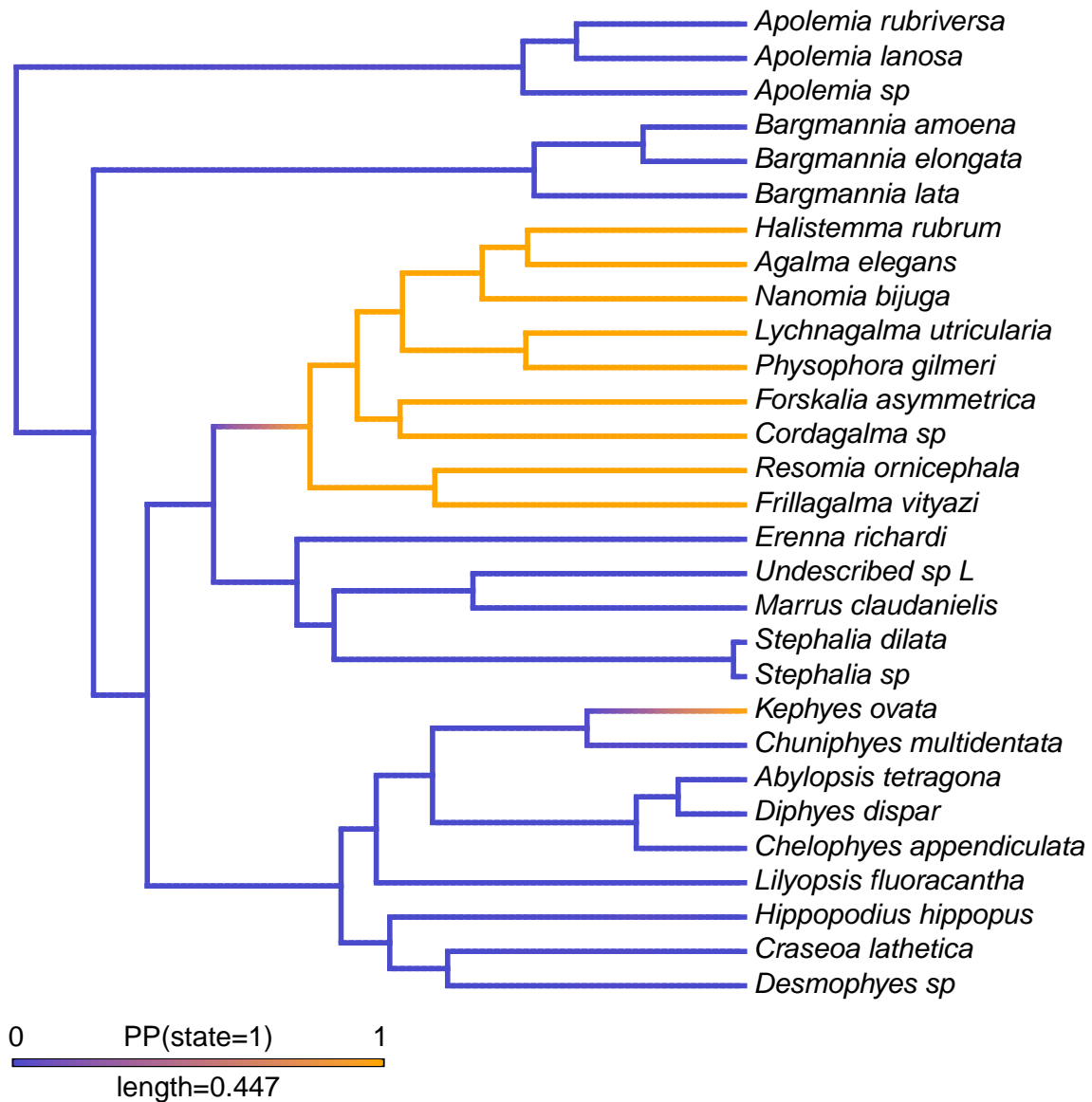


Figure S6: Stochastic character map of presence of a descending mantle canal in the nectophores. Cystonects and Athorybia were excluded as they do not have a nectosome.

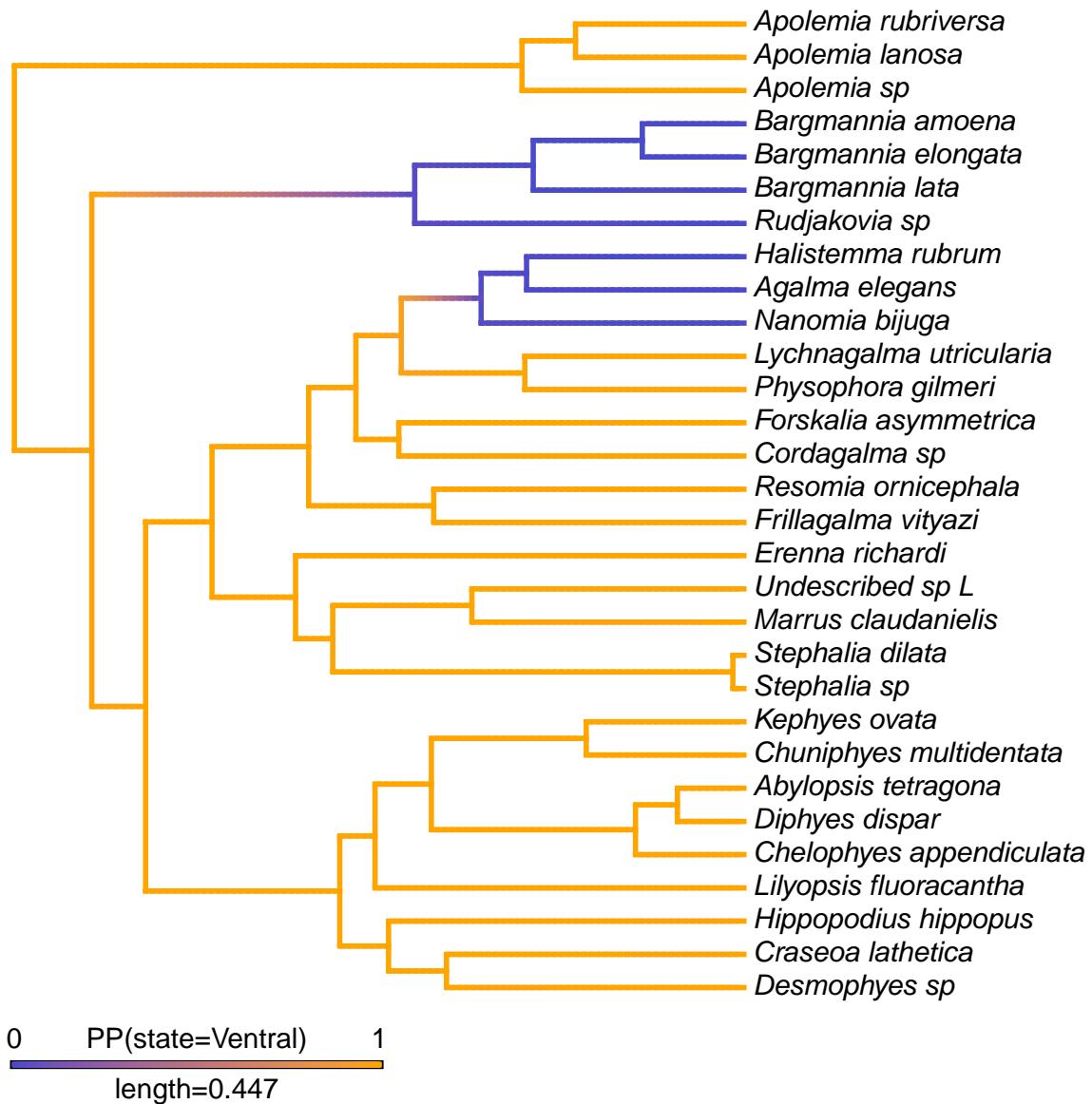


Figure S7: Stochastic character map for the evolution of the position of the nectosome. Cystonects were excluded as they do not have a nectosome.

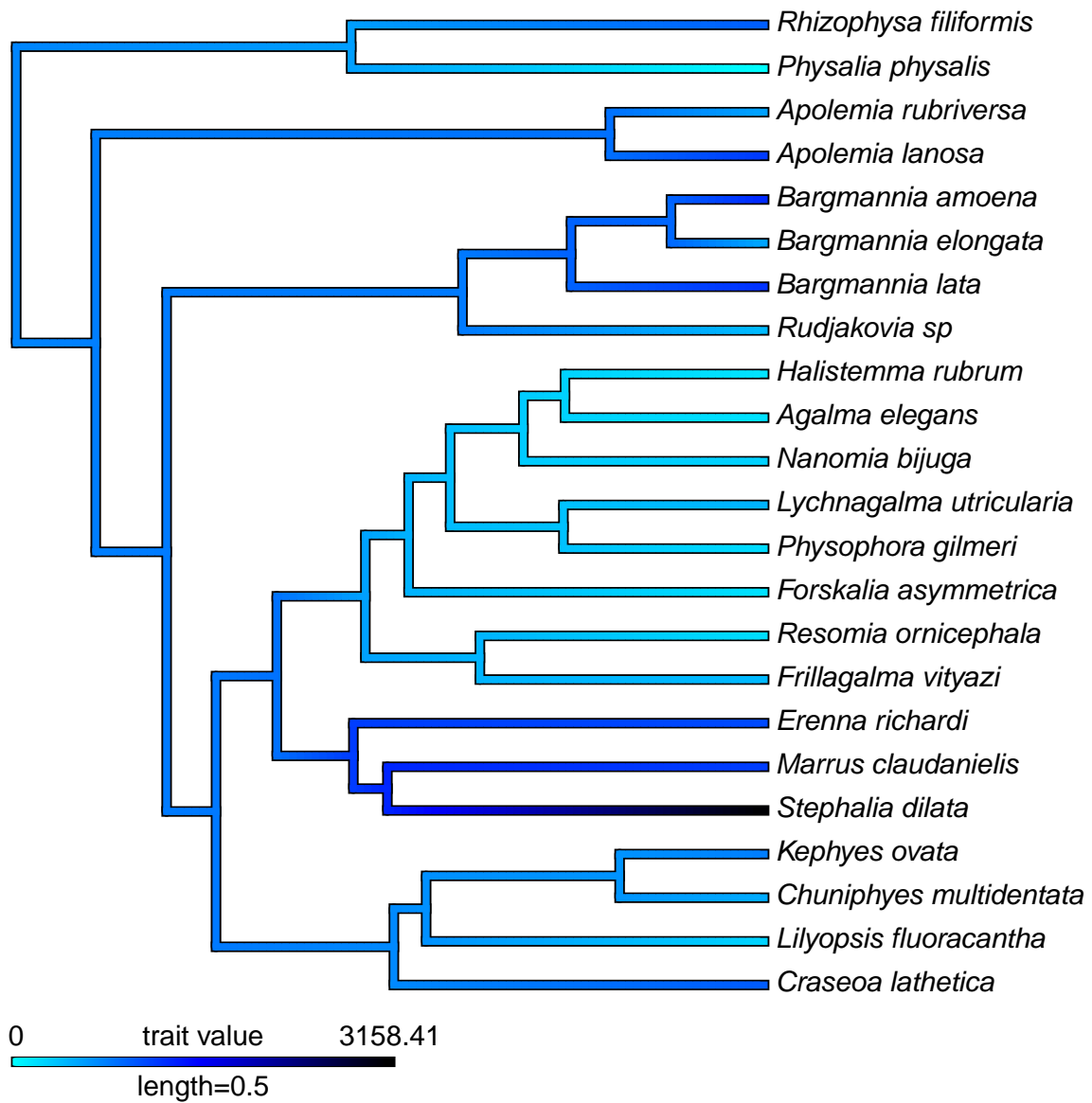


Figure S8: Brownian Motion character map of median depth of species observed with an MBARI ROV



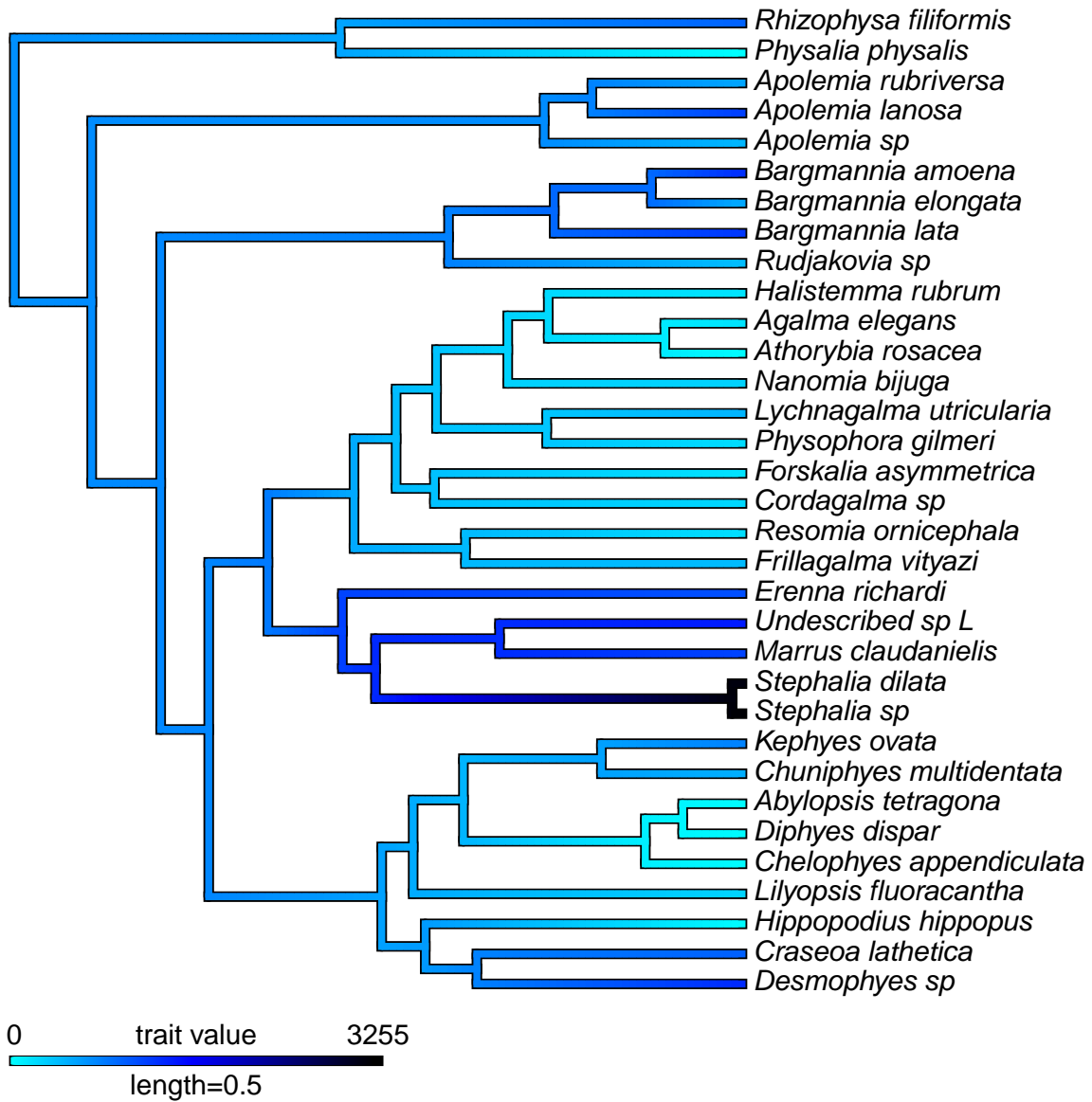


Figure S9: Brownian Motion character map of median depth of species including blue water diving observations.