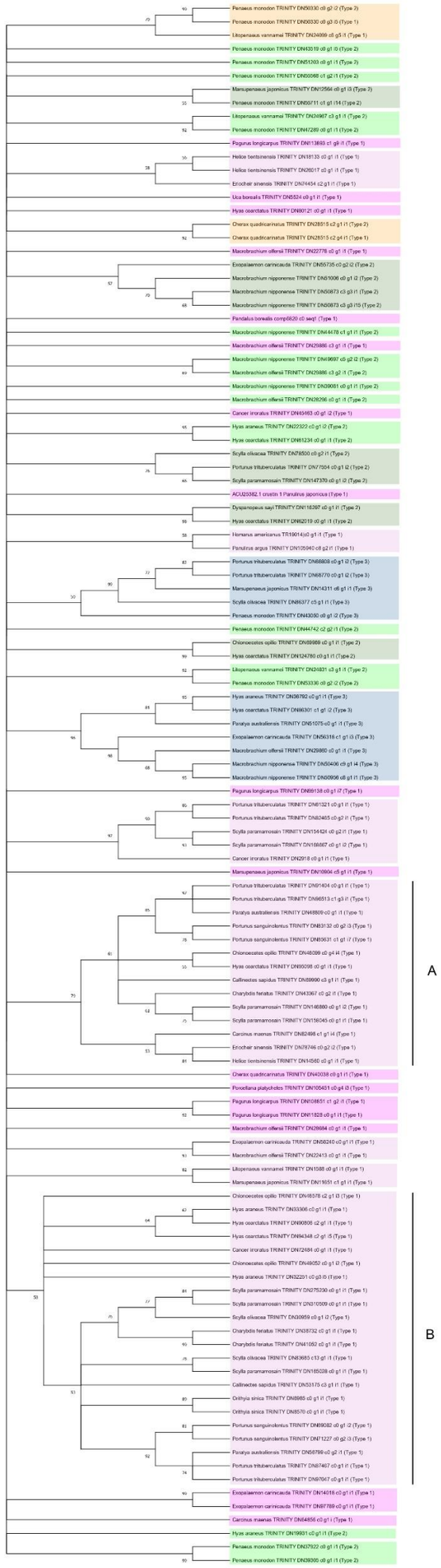
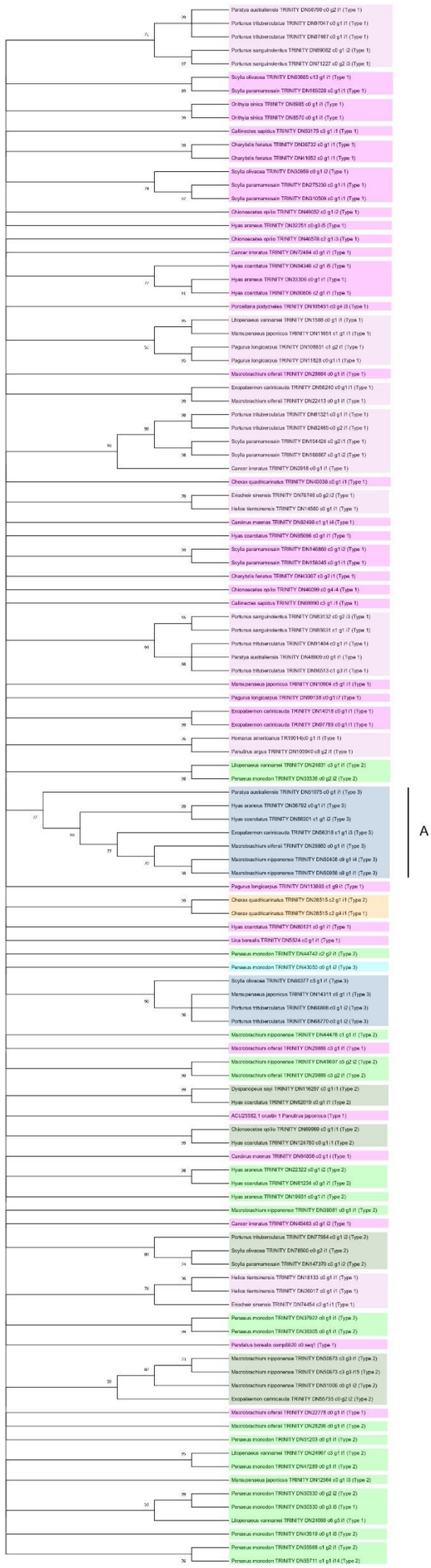
Supplementary Material

S 3.2 Legend of phylogenetic tree groupings.

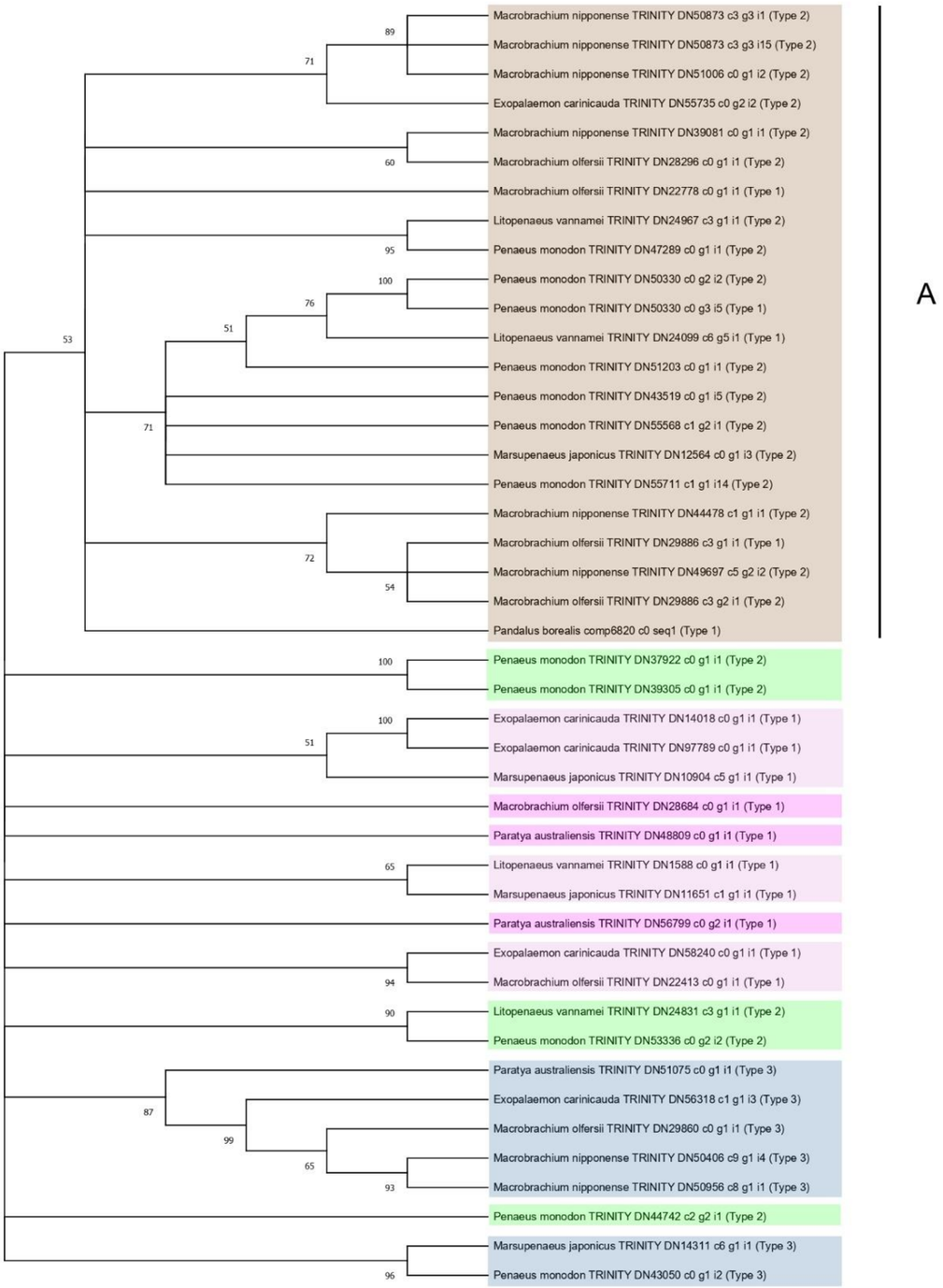
Index	Colour
Crustin type I clans that are homologous for genus	
Crustin type I clans that are heterogenous for genus	
Crustin type II clans that are homologous for genus	
Crustin type II clans that are heterogenous for genus	
Crustin type III clans that are homologous for genus	
Crustin type III clans that are heterogenous for genus	
Clans homologous for genus and heterogenous for crustin type	
Clans heterogenous for both genus and crustin type	



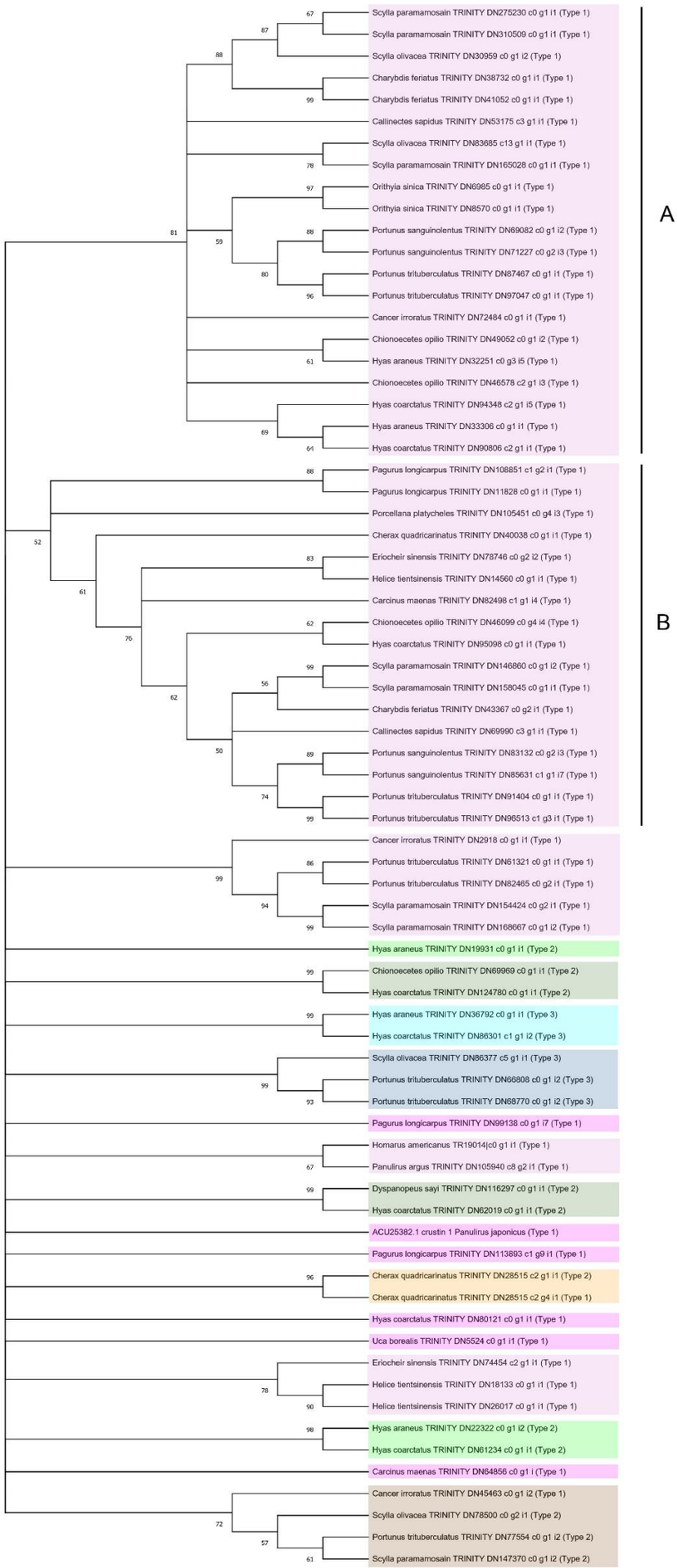
S 3.3 A bootstrap unrooted phylogeny of the crustin sequences aligned by Muscle and translated by ExPASy. The phylogeny was inferred using the Maximum Likelihood method and Whelan and Goldman model through MEGA X. The bootstrap consensus tree was inferred from 1000 replicates and branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed.



S 3.4 A bootstrap unrooted phylogeny of the crustin sequences WAP domain aligned by Muscle and translated by ExPASy. The phylogeny was inferred using the Maximum Likelihood method and Whelan and Goldman model through MEGA X. The bootstrap consensus tree was inferred from 1000 replicates and branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed.

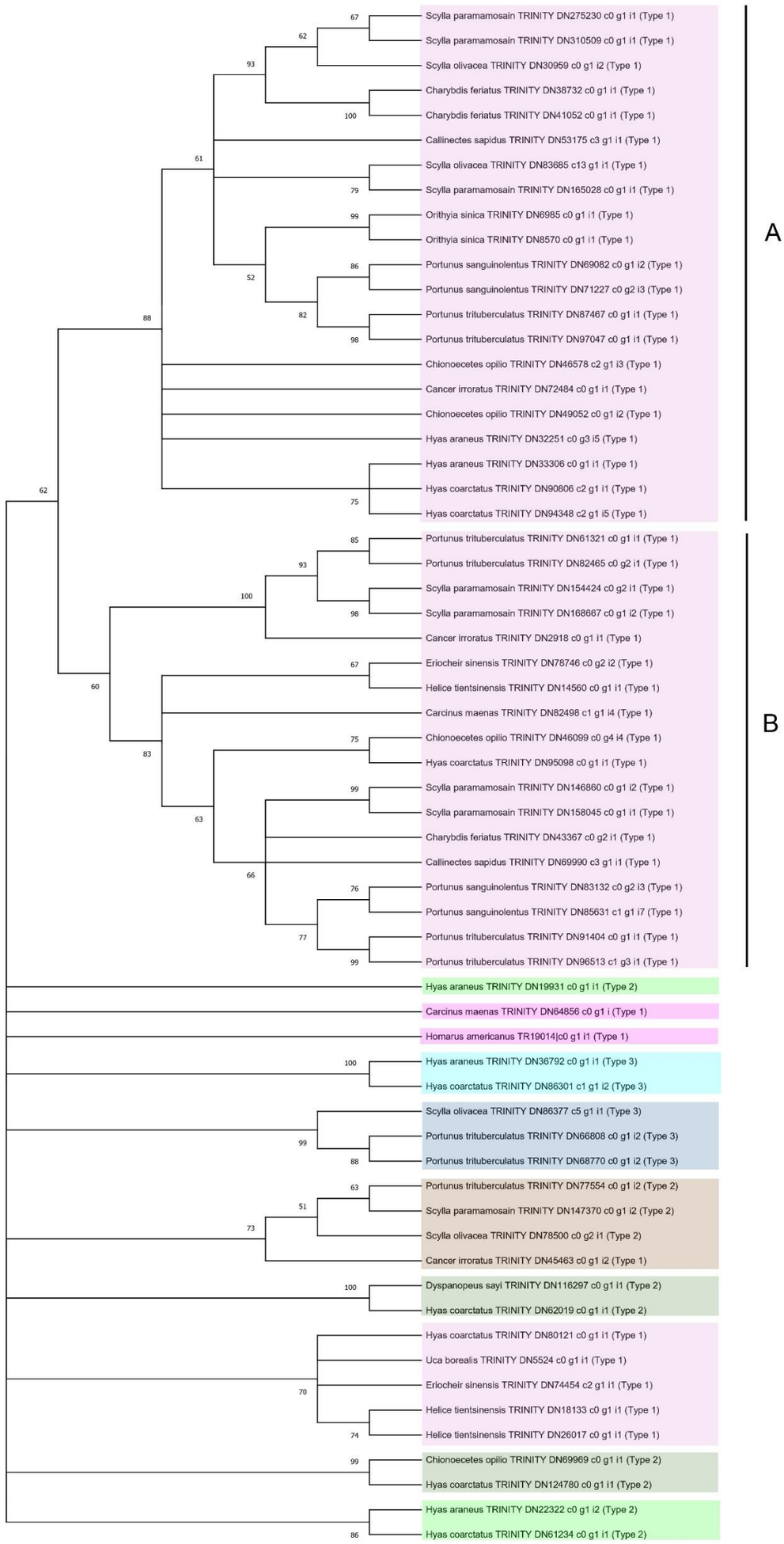


S 3.5 A bootstrap unrooted phylogeny of the crustin sequences from shrimp species aligned by Muscle and translated by ExPASy. The phylogeny was inferred using the Maximum Likelihood method and Whelan and Goldman model through MEGA X. The bootstrap consensus tree was inferred from 1000 replicates and branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed.

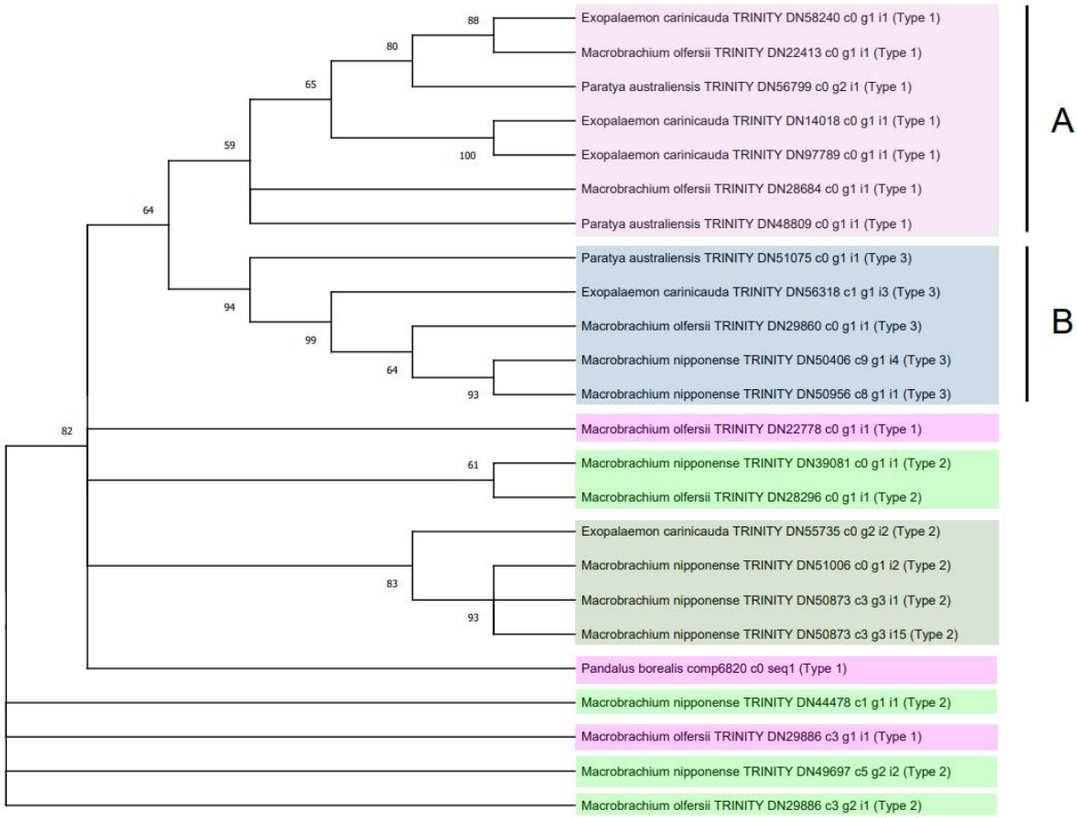


S 3.6 A bootstrap unrooted phylogeny of the crustin sequences from non-shrimp species aligned by Muscle and translated by ExPASy. The phylogeny was inferred using the Maximum Likelihood method and Whelan and Goldman model through MEGA X. The bootstrap consensus tree was inferred from 1000 replicates and branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed.

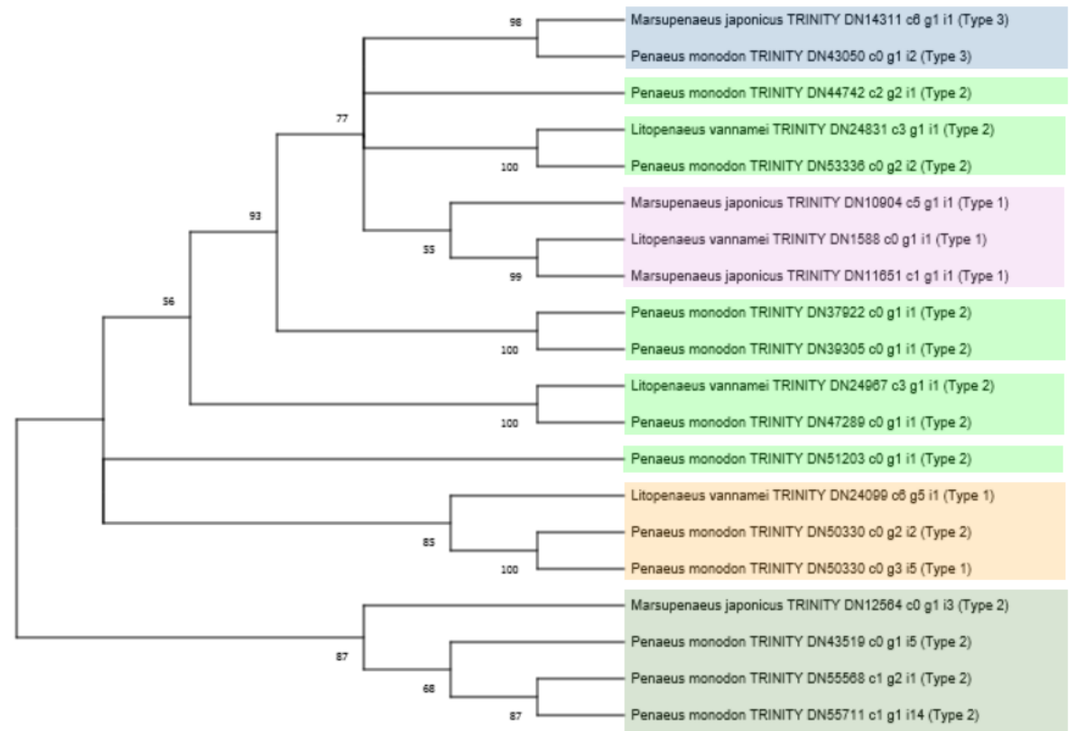
S 3.7 A bootstrap unrooted phylogeny of the crustin sequences from the infraorder Anomura aligned by Muscle and translated by ExPASy. The phylogeny was inferred using the Maximum Likelihood method and Whelan and Goldman model through MEGA X. The bootstrap consensus tree was inferred from 1000 replicates and branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed.



S 3.8 A bootstrap unrooted phylogeny of the crustin sequences from the infraorder Brachyura aligned by Muscle and translated by ExPASy. The phylogeny was inferred using the Maximum Likelihood method and Whelan and Goldman model through MEGA X. The bootstrap consensus tree was inferred from 1000 replicates and branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed.



S 3.9 A bootstrap unrooted phylogeny of the crustin sequences from the infraorder Caridea aligned by Muscle and translated by ExPASy. The phylogeny was inferred using the Maximum Likelihood method and Whelan and Goldman model through MEGA X. The bootstrap consensus tree was inferred from 1000 replicates and branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed.



S 3.10 A bootstrap unrooted phylogeny of the crustin sequences from the infraorder Dendrobranchiata aligned by Muscle and translated by ExPASy. The phylogeny was inferred using the Maximum Likelihood method and Whelan and Goldman model through MEGA X. The bootstrap consensus tree was inferred from 1000 replicates and branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed.