

S3 Figure. Maximum likelihood phylogenetic tree that was built with PHYML [76] implemented in GENEIOUS PRO. The HKY substitution model [80] with a gamma correction $\alpha = 1.015$ and a proportion of invariant sites p-inv. = 0.691 was selected as the optimal model among those available in PHYML, according to JMODELTEST2. The robustness of branches was tested with 100 bootstraps, and a COI sequence of *Balanus eburneus* was used as an out-group for this maximum likelihood analysis.

