

**Supplementary Figure S1.** Four *Indothais* specimens (BD1, BD2, BD3 and PB/OR), which were morphologically identified as *I. malayensis*, were used. Sequences of *I. javanica* and *I. malayensis* reported in a previous study (Claremont et al., 2012) were obtained from GenBank database. Similarly, sequences of *Rapana bezoar* from another study (Barco et al., 2010) was used as outgroups. All sequences were aligned using ClustalW via MEGA X (Kumar et al., 2018). Columns with gaps or missing data were excluded from the analysis. Thus, a total of 658, 548, 666 and 1422 bp of COI, 12S rRNA, 16S rRNA and 28S rRNA sequences were analysed, respectively. MEGA X was used to construct trees using Neighbor Joining algorithm with the evolutionary distances calculated using Kimura 2-parameter method. Bootstrap test was also conducted with 1000 replicates, and the bootstrap percentage values are shown at the tree nodes.