Supplementary Figure S2. Maximum-Likelihood phylogenetic tree of the Ostreidae derived from 42 sequences of 28S (956 positions) obtained from GenBank. The analysis was conducted in MEGA6 [Tamura et al., 2013. *Mol Biol Evol* 30: 2725-2729] based on the Tamura-Nei model with a discrete Gamma distribution, and using *Hyotissa hyotis*, *H. imbricata* and *Neopycnodonte cochlear* as outgroup. Genbank accession numbers are provided after species names; bootstrap support (>70) over 100 replicates is reported The three main lineages are coloured as follows: Crassostreinae in violet; Saccostreinae in green; and Ostreinae in blue. * indicate sequences selected for the multi-locus combined analyses and ** indicate sequences added for the species-tree analysis.