



Fig. S1. Phylogeny of the Dikarya marine OTU-clusters. ML phylogeny calculated from an alignment of 94 sequences and 342 positions. Bootstrap values from both 1000 ML and 1000 Log-Det distance pseudo-replicates are shown when $\geq 50\%$. Blue squares next to each sequence indicates OTU-clusters which have >99% identity to a database sequence from a marine environment.