



Additional file 7. EPDR phylogenetic analysis with reduced taxa (maximum likelihood). This analysis produces higher support for the presence of the two major EPDR clades. The values within the central circle of the tree indicate a maximum likelihood bootstrap value of 65 and a Bayesian posterior probability of 96% for the division into two clades. Colouring of the branches corresponds to the phylogenetic groups to which the species belong, and follows the scheme established in Figure 1. The scale bar reflects the number of substitutions per site. Species abbreviations: Apec=*Asterina pectinifera*, Apla=*Acanthaster planci*, Aque=*Amphimedon queenslandica*, Bbel=*Branchiostoma belcheri*, Cowc=*Capsaspora owczarzakii*, Ctel=*Capitella teleta*, Drer=*Danio rerio*, Hasi=*Haliotis asinina*, Hsap=*Homo sapiens*, Lgig=*Lottia gigantea*, Mbre=*Monosiga brevicollis*, Mmus=*Mus musculus*, Nvec=*Nematostella vectensis*, Ocar=*Oscarella carmela*, Omyk=*Oncorhynchus mykiss*, Pmin=*Patiria miniata*, Scil=*Sycon ciliatum*, Skow=*Saccoglossus kowalevskii*, Spur=*Strongylocentrotus purpuratus*, Tnig=*Tetraodon nigroviridis*, Trub=*Takifugu rubripes*, Xtro=*Xenopus tropicalis*.