



Figure S2. Topology resulting from the Maximum Likelihood analysis of the Ostreidae Histone H3 dataset (entire tree). Numbers above the branches represent bootstrap support values, only values over 50 are shown. Scale bar indicates substitutions per site. Specimens sequenced in this study fall within an exclusive clade (indicated), no Histone H3 sequences for *Magallana bilineata*, *M. madrasensis* or *M. iredalei* exist within the NCBI nr database.