



Figure S2. Maximum likelihood phylogenetic analysis of the *Pinctada maxima* FoxJ1 protein. Percent bootstrap values greater than 70 are displayed on the relevant branches. NCBI accession numbers are provided for each sequence, except for the *L. gigantea* sequence where the gene model number is provided (Simakov et al. 2013). The scale bar indicates the branch length for 0.5 amino acid substitutions.