



Figure S3. Concatenated phylogenetic analysis combining markers 16S, COI, ITS1 and 28S, reconstructing relationships between 28 *Aurelia* species hypotheses under maximum likelihood as the optimality criterion. Colored circles represent bootstrap resampling frequencies and SH-aLRT (black = ≥ 95 , grey = ≥ 75 , absent = < 75). When both of these values were not in the same range the lowest one was considered. Scale bar represents the number of nucleotide substitutions per site. Tables S4-S5 contains further details on sequences used to reconstruct this phylogeny and single-marker phylogenies are presented in Figs. S4-S7.