FIGURE S1. COI Maximum Likelihood tree reconstructed using GARLI 2.0. Numbers adjacent to nodes show the bootstrap support values. The scale indicates the number of substitution per site. Reference sequences from GenBank belonging to all the known Aurelia species are in bold.
FIGURE S2. 28S Maximum Likelihood tree reconstructed using GARLI 2.0. Numbers adjacent to nodes show the bootstrap support values. The scale indicates the number of substitution per site. Reference sequences from GenBank belonging to other known Aurelia species available in GenBank are in bold.