Figure S1. Bioinformatic pipeline for processing Symbiodiniaceae rDNA sequences. The flowchart shows the major steps implemented in analyzing the data and constructing the web-based database portal (http://sym-its2.marinegenomics.cn). These include: data mining, merging and dereplication, construction of HMM of ITS2-proximal stems, identification and delineation of ITS2 sequences, and compilation of the reference core and extended databases.