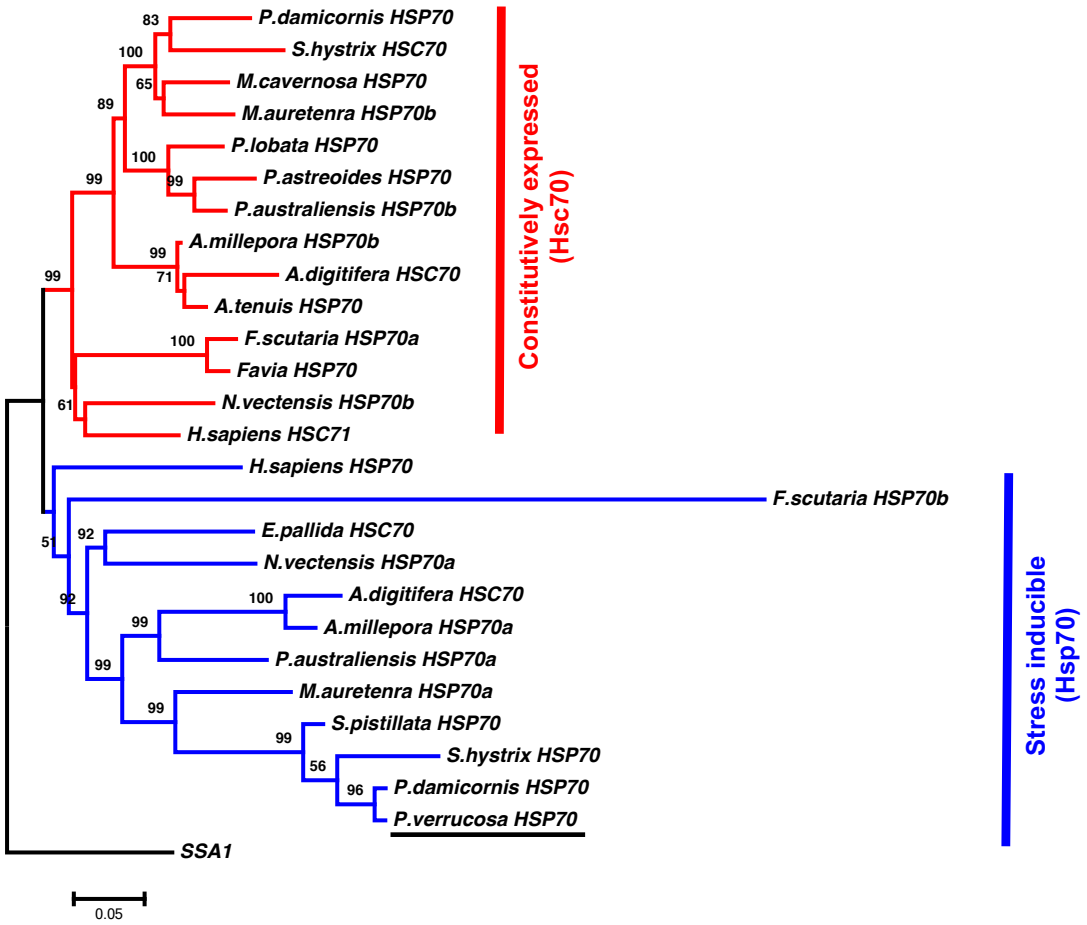
S2 Figure. Phylogenetic relationships among Hsp70 deduced amino acid sequences of corals. Multiple sequence alignment was generated with the MEGA software ver 6 [1] and the MUSCLE algorithm [2]. The tree was constructed by the Maximum Likelihood algorithm using PAUP* [3]. Bootstrap confidence values for the sequence groupings are indicated in the tree (N = 1000). The appropriate model parameters for the maximum-likelihood analysis were determined using a likelihood-ratio test with jModelTest [4]. The *P. verrucosa* Hsp70 sequence employed in this study is highlighted. The human Hsp70 (Human_HSP70, GenBank Ac. Numb. P17066) and Hsc70 (Human_HSC71, GenBank Ac. Numb. AAH19816) sequences were included in the alignment for comparison. SSA1 from *Saccharomyces cerevisae* was used as outgroup (GenBank Ac. Numb. P10591). Acronym explanations, accession numbers, and sequence features for coral protein sequences are reported in S1 Table.



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