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References


References


References


References


References


References


### Appendices

Supplementary Table S.1. Primers used for the genes under investigation in the qRTPCR experiment. The best Tblastx match and E value are shown for the EST sequence corresponding to the indicated accession number. The *Symbiodinium*-specific PCNA primers were designed on the same sequences used in Boldt et al. (2009).

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<th>Genes</th>
<th>Accession number</th>
<th>Best Tblastx match</th>
<th>E value</th>
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<th>Reverse primer</th>
<th>Amplicon size (bp)</th>
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Supplementary Table S.2. Ranking of the candidate ICGs according to their M and CV values (Hellemans et al. 2007) calculated between healthy-looking and severely bleached samples across the nine colonies used in qRTPCR experiment.

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### Supplementary Table S.3. MIQE checklist (Bustin et al. 2009).

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<th>MIQE checklist (Bustin et al. 2009)*</th>
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*Note: The MIQE checklist is a comprehensive guide for the preparation, optimization, and reporting of quantitative real-time PCR data. It includes detailed guidelines for experimental design, sample preparation, and data analysis. The checklist is designed to ensure reproducibility and transparency in the field of gene expression analysis. Each item is rated on a scale from 1 to 6, with 1 indicating a critical requirement and 6 indicating optional or additional information. This table is a simplified version for educational purposes.
Supplementary Fig. S.1. Consistent difference between average quantification cycles of healthy (dark grey) and bleached (light grey) samples in nine colonies, for the best performing ICGs: GAPDH, rpL9 and S7.
Supplementary Fig. S.2. Maximum likelihood tree of the USP domain sequences in animals. The numbers on the nodes indicate their support by a SH-like likelihood ratio test.
Supplementary Fig. S.3. Maximum likelihood tree of the USP domain sequences in animals. The numbers on the nodes indicate their bootstrap support.
Supplementary Fig. S.4. Bayesian tree of the USP domain sequences in all species. The numbers on each node represent the posterior probability.
Supplementary Fig. S.5. Maximum likelihood tree of the USP domain sequences in all species. The numbers on the nodes indicate their support by a SH-like likelihood ratio test.
Supplementary Fig. S.6. Maximum likelihood tree of the USP domain sequences in all species. The numbers on the nodes indicate their bootstrap support.
Supplementary Fig. S.7. Likelihood mapping assessing the monophyly of animal USPs. 79.1% of 10,000 random quartets are consistent with metazoan (a) and non-metazoan sequences (b) grouping separately.
Supplementary Fig. S.8. Multiple sequences alignment of USP domains. Vertical bars indicate an intron between two amino acid positions, left slanted bars indicate that a codon has 1 nucleotide in the 5’ exon and 2 nucleotides in the 3’ exon, right slanted bars indicate that a codon has 2 nucleotide in the 5’ exon and 1 nucleotide in the 3’ exon. The boxes above the alignment denote the approximate position of alpha helices (pink) and beta strands (blue) in the secondary structure of 1MJH. Asterisks under the alignment highlight the position of residues involved in ATP binding in 1MJH. The arrow under the alignment points at the position of the intron conserved between plants and animals.