

# Supplementary Information: The genetic basis for adaptation in giant sea anemones to their symbiosis with anemonefish and Symbiodiniaceae

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**Figure S1: Spearman's correlations for all species and all tissues**

The gene expression of jellyfish tentacles was highly distinct, with very low similarities between jellyfish and non-jellyfish samples

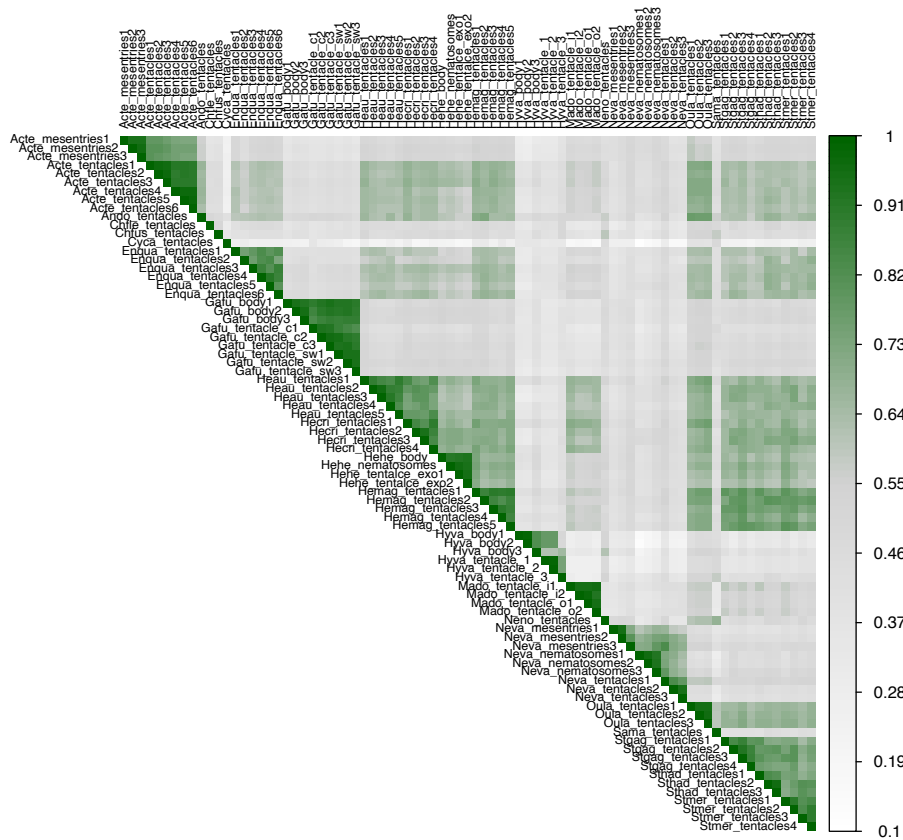
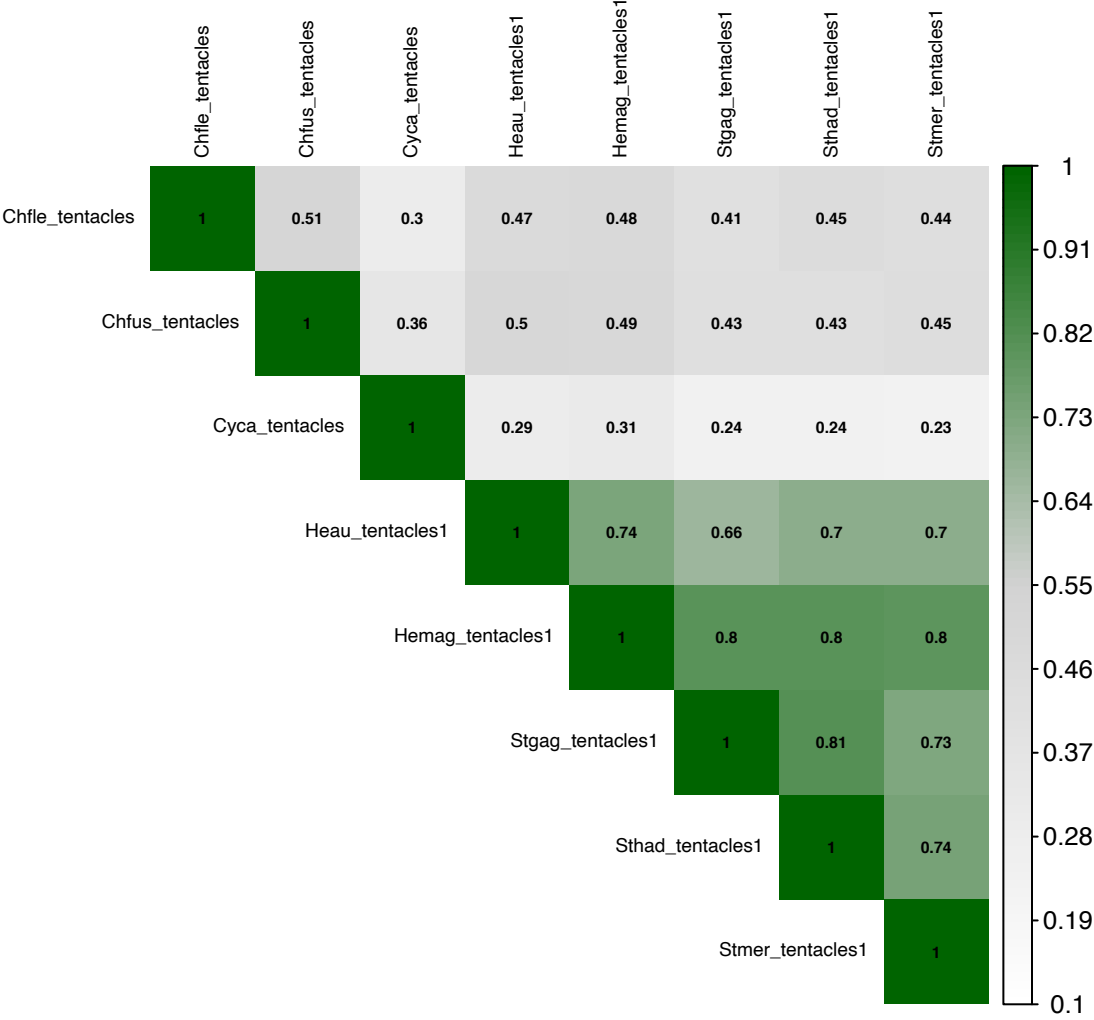


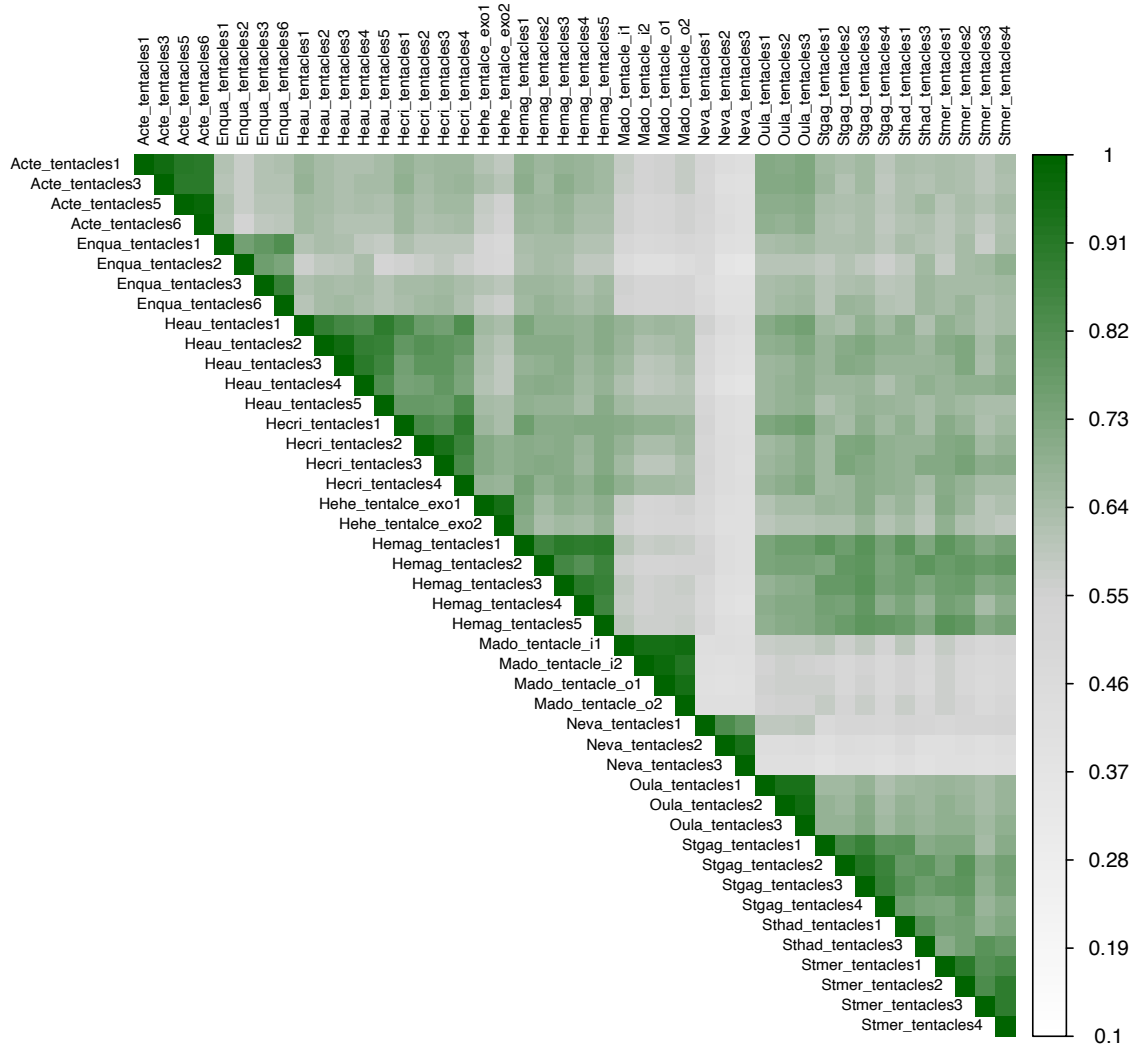
Figure S2: Spearmans correlations for non-actinaria and Heteractis-Stichodactyla

The following figure contrasts the difference in expression between jellyfish and giant sea anemones *Heteractis* and *Stichodactyla*



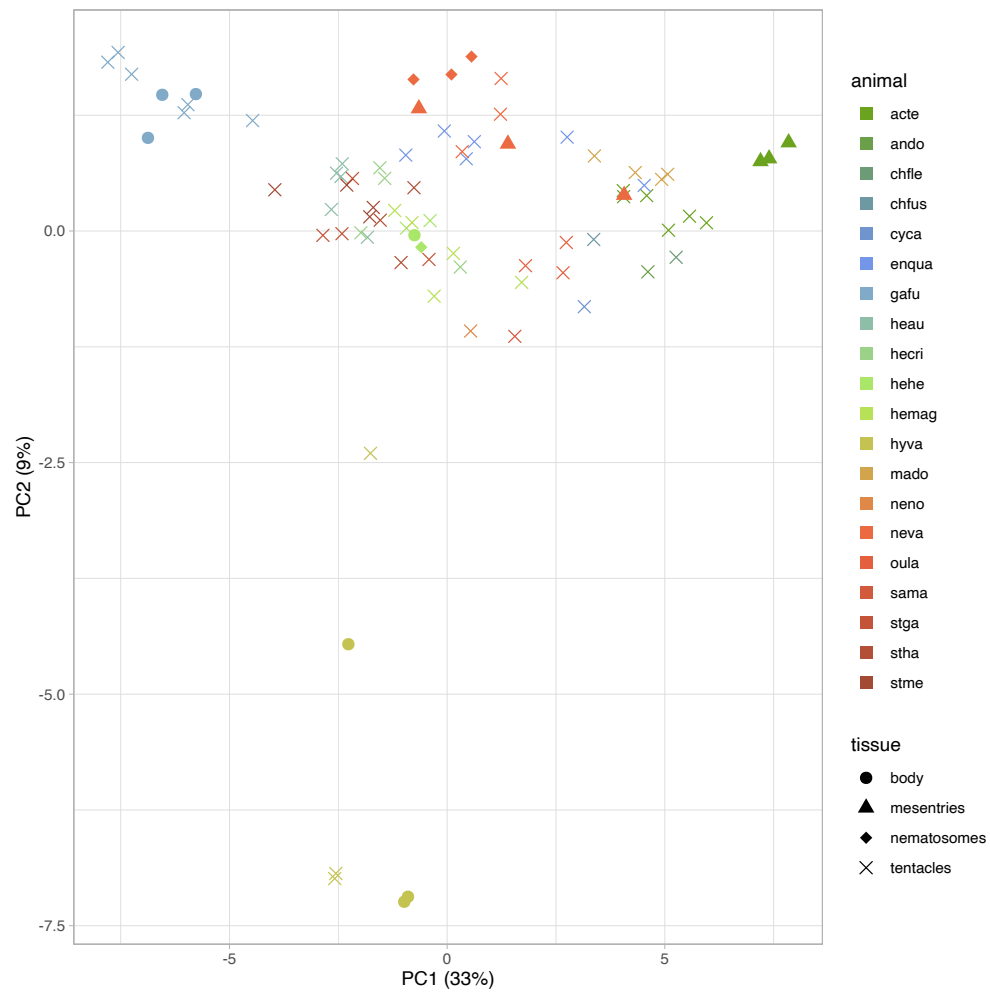
**Figure S3: Spearmans correlations for all actinaria tentacles**

Gene expression within actinaria was overall more similar than between actinaria and non-actinaria



**Figure S4: PCA for all cnidaria samples**

The PCA with all cnidarian samples is included in the supplementary information and showed the same overall trends as ones with only anthozoans.



**Figure S5: Spearmans correlations for random set of 47 genes**

We estimated correlations using a random assortment of 47 genes to check if this was the case. A random set of 47 genes showed less noisy correlation patterns (Fig S5), suggesting that the 47 genes in cluster 1 are highly variable due to biological factors and not sampling bias.

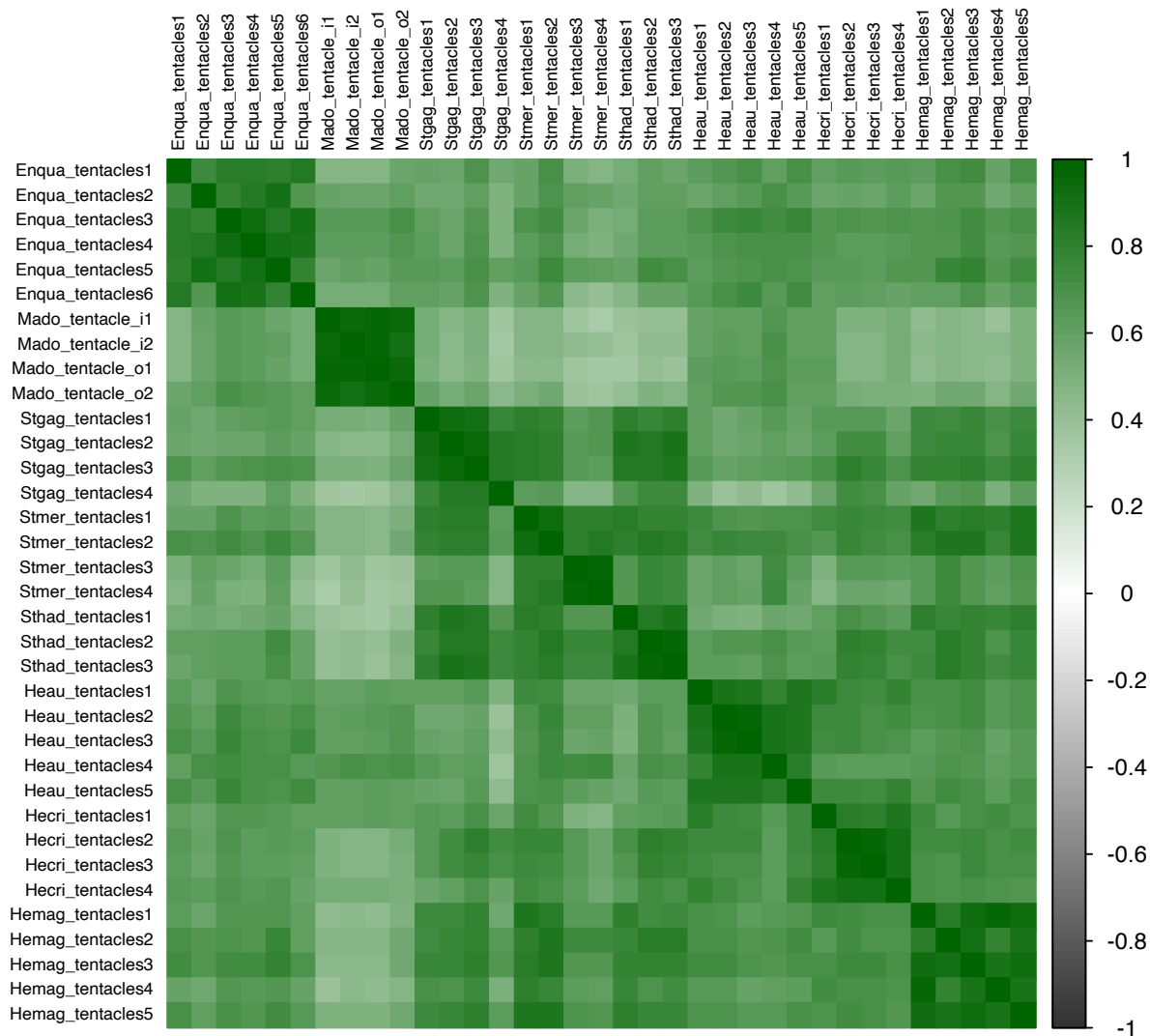
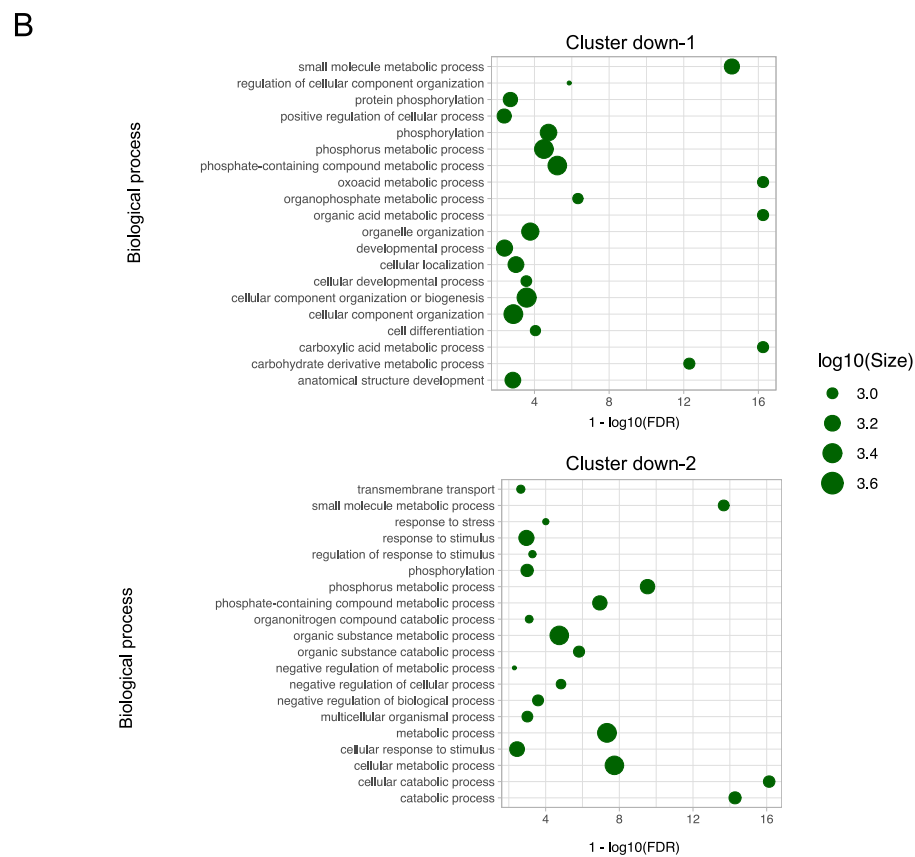
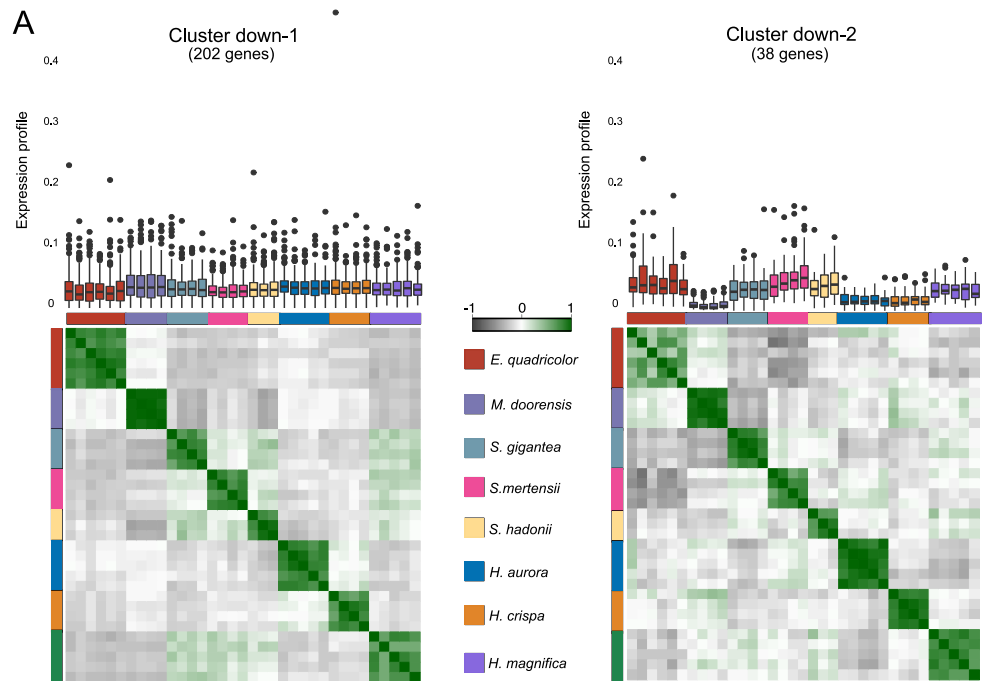
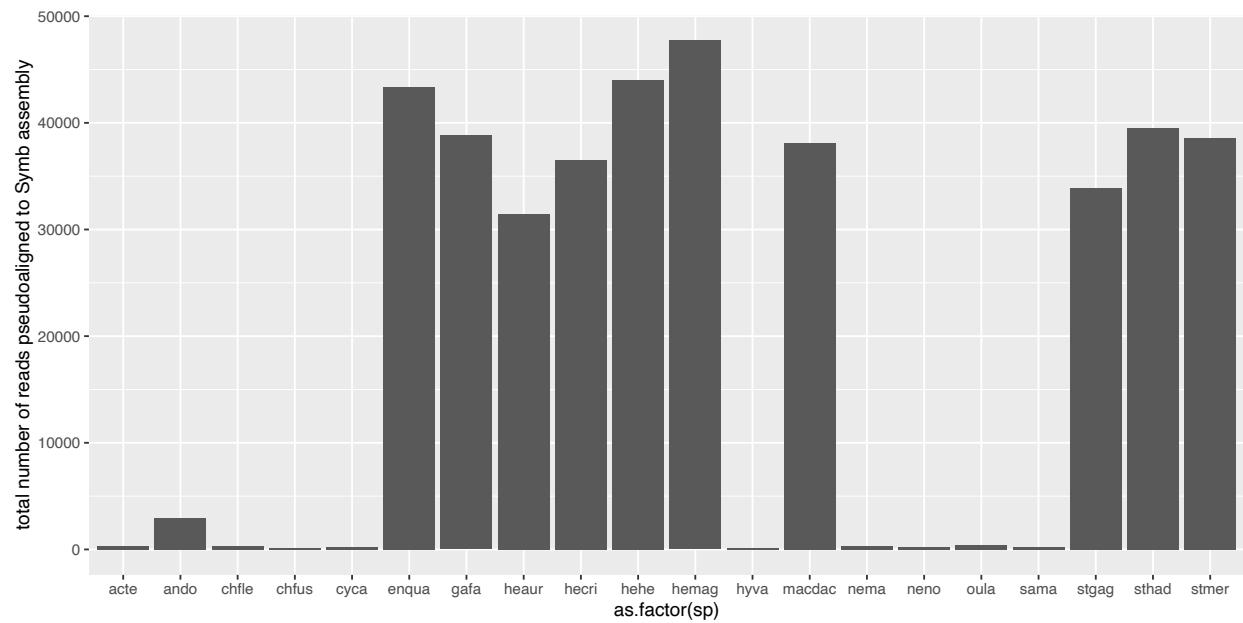


Figure S6: Coseq analysis for downregulated orthologs



### Figure S7: Symbiodiniaceae abundance

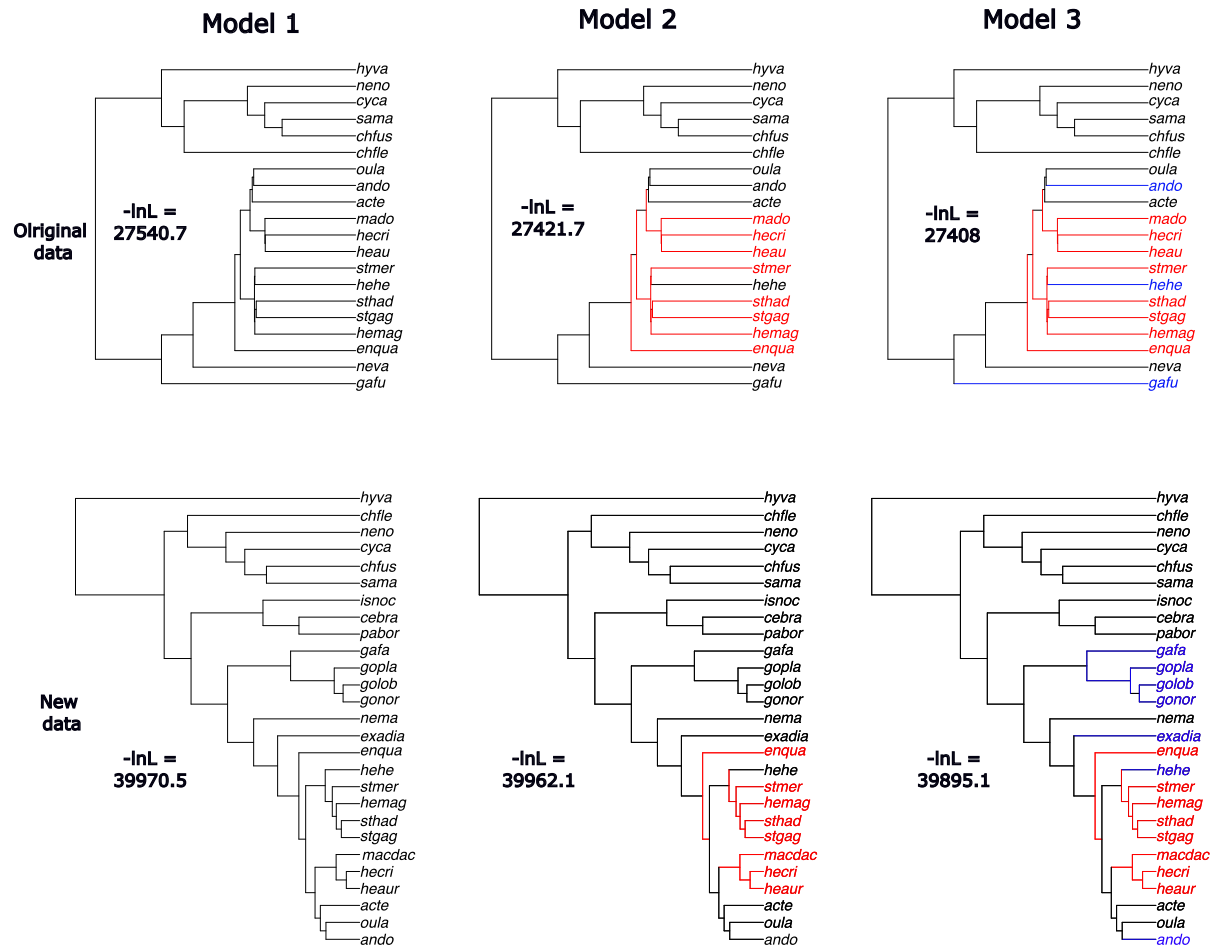
We used a pseudoalignment approach to determine the Symbiodiniaceae content in our species. The following figure shows the total number of reads pseudoaligned to the composite Symbiodiniaceae transcriptome.



## Figure S8: Additional CAGEE analysis

In our original analysis, the multi-rate model has significantly better fit. However an argument against our results could be the fact that we sample few species that host only Symbiodiniaceae. To address this, we carried the CAGEE analysis using tentacle transcriptomes from additional three coral species and one anemone, all of which harbour only Symbiodiniaceae. Furthermore, we also include three species of anemones that do not host either anemonefish or Symbiodiniaceae. Using this dataset, we not only confirm our previous trend - where the multi-rate model has the best fit - but we also observe that the multi-rate model has substantially better fit than any of the alternative models.

Hence, the inclusion of additional data not only corroborates our initial results, but it also provides more robust evidence supporting the evolutionary rate heterogeneity in gene expression within our dataset.



Additional species names:

pabor - *Pachyercanthus borealis*. isnoc - *Isarachnathus nocturnus*. cebra - *Ceriantheomorpha brasiliensis*. exadia - *Ecaiptasia diaphana*. golob - *Goniophora lobata*. gopla - *Goniopora planulata*. gonor - *Goniopora norfolkensis*