

Figure S1. Example of methylation frequency estimation with Nanopolish (Simpson *et al.* 2017) along contig 1212. Upper panel shows individual reads colored by modification likelihood estimated by Nanopolish, with color ramp legend in right margin. Values above 0 indicate positive support for base modification/methylation. Lower panel shows modification frequency averaged from reads.

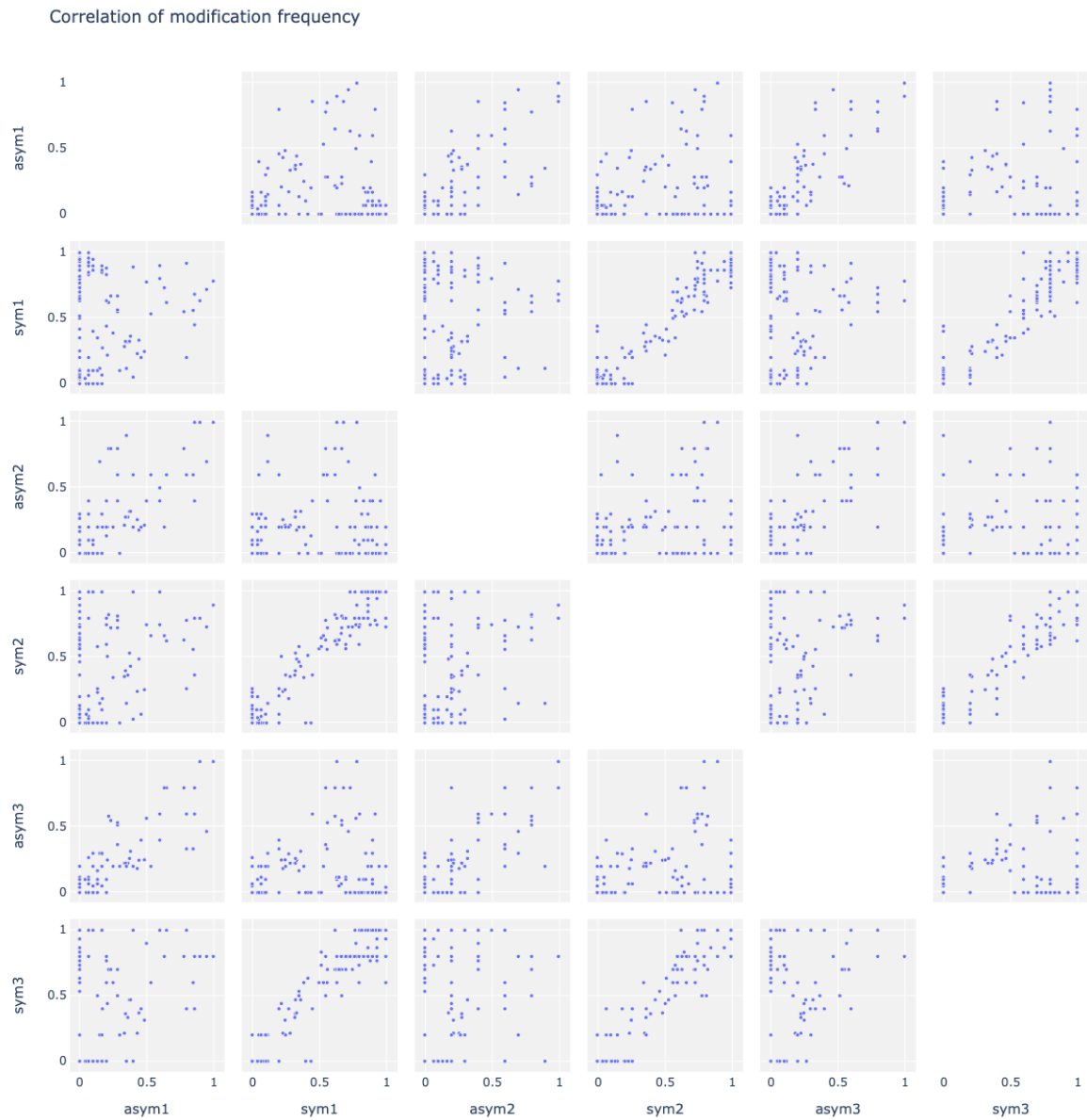


Figure S2. Correlation plots showing pairwise comparisons of modification frequency for each sample along the region of contig 1212 shown in Fig. 3C. Note that modification frequencies of symbiotic specimens ('sym') show strong positive correlations.

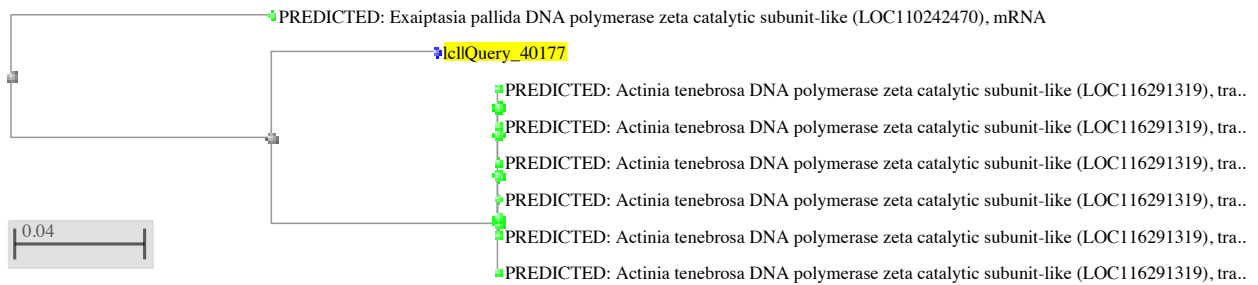


Figure S3. Neighbor-joining tree of NCBI megablast results with the 20 kb region of contig 1212 shown in Fig. 3C as the query sequence (highlighted in yellow). The closest matches were DNA polymerase zeta mRNA sequences from other sea anemone species.