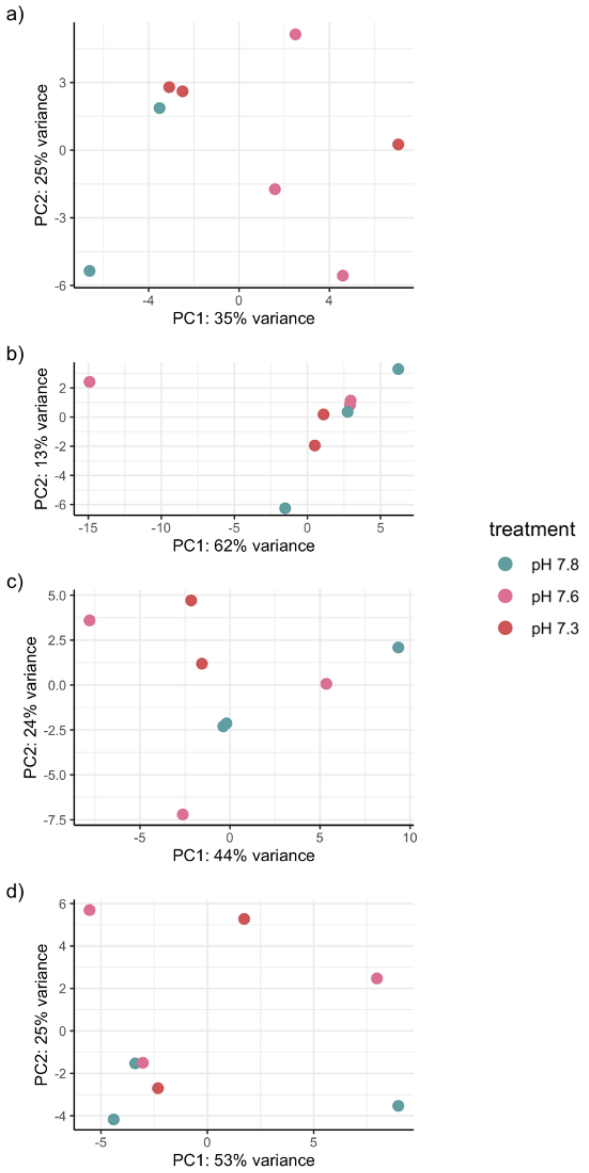


**Fig. S1.** Principal coordinates analysis using the top 500 genes with the highest expression variation between samples out of all genes passing a low counts filter, wherein a gene must have a count of 10 or greater in at least 7 out of 8 samples (pOverA ~0.875, 10) in A) fertilized eggs, B) cleaving embryos, C) prawn chips, and D) early gastrulae based on sample-to-sample distance computed from genes passing a low counts filter, wherein a gene must have a count of 10 or greater in at least 7 out of 8 samples (pOverA ~0.875, 10).

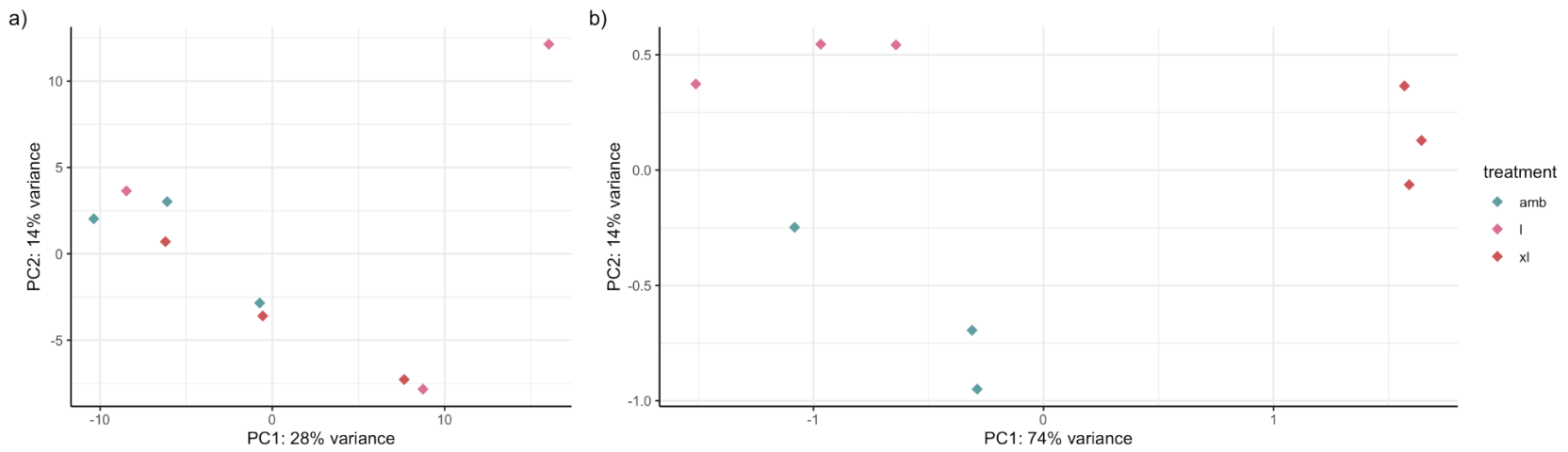


**Fig. S2.** Principal coordinates analyses of the symbiont genes in the planula samples. a) A principal coordinates analysis based on sample-to-sample distance computed from the top 500 genes with the highest expression variation between samples out of the 1,365 genes passing a low counts filter, wherein a gene must have a count of 10 or greater in at least 7 out of 8 samples (pOverA ~0.875, 10). b) A principal coordinates analysis based on sample-to-sample distance computed from the 29 symbiont genes differentially expressed in planula developing in different pH environments.

**Table S1.** Discrete measurements for temperature, salinity, and OA chemistry corresponding to Table 1.

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**Table S2.** Differential gene expression and k-means clustering (k=2) results for planula larvae exposed to pH 7.8 (Ambient), 7.6 (Low), and 7.3 (Xlow).

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**Table S3.** Gene ontology and KEGG enrichment summary statistics of the differentially-expressed genes in planula larvae exposed to pH 7.8 (Ambient), 7.6 (Low), and 7.3 (Xlow). Results were obtained using GOseq. Cluster refers to K-means cluster, with C1 (Up) being genes up-regulated under pH 7.6 and C2 (Down) being genes down-regulated under pH 7.6 compared to Ambient. Gene ontology enrichment results include associated GOslim data and identifiers retireved from the obo database.

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**Table S4.** Differential gene expression of symbionts in planula larvae exposed to pH 7.8 (Ambient), 7.6 (Low), and 7.3 (Xlow) and their Blastx local alignment search results to the NCBI non-redundant database.

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