## Legends for Supplemental Figures and Tables

**S1 Fig:** Water parameters during the experiment. Temperature and pH were measured daily; salinity, dissolved inorganic carbon (DIC) and alkalinity were measured weekly, beginning Week 2; all other parameters were calculated. Lines are mean values across tanks for each treatment.

**S2 Fig:** PCA biplot of principal components 3 and 4, constructed from RNA-Seq derived SNPs (n=331). Points represent individual crabs that are color-coded by OA treatment, which do not indicate clustering by treatment, and sizes represent the percent of SNPs that are missing in each individual.

**S3 Fig**: Correlation plots among SNP-derived PCA scores and gene expression-derived PCA scores along the first two principal components, with Pearson correlation coefficients and p-values calculated for each treatment.

**S4 Fig:** PCA biplot of principal components 3 and 4 constructed from all expressed genes.

**S5 Fig:** Network of biological processes (Gene Ontology terms, “GO”) that were

enriched in genes differentially expressed in moderate acidification (pH 7.8) compared to control conditions (pH 8.0), where green and red indicate processes enriched in upregulated and downregulated genes, respectively. The network was constructed using the GO hierarchical structure.

**S6 Fig:** Network of biological processes (Gene Ontology terms, “GO”) that were

enriched in genes differentially expressed in severe acidification (pH 7.5) compared to control conditions (pH 8.0), where green and red indicate processes enriched in upregulated and

downregulated genes, respectively. The network was constructed using the GO hierarchical structure.

**S7 Fig:** Network of biological processes (Gene Ontology terms, “GO”) that were

enriched in genes differentially expressed in severe acidification (pH 7.5) compared to moderate acidification (pH 7.8), where green and red indicate processes enriched in genes upregulated and downregulated in the severe treatment, respectively. The network was constructed using the GO

hierarchical structure.

**S1 Table:** Mean water parameters for each tank. Also available on GitHub: [Supplemental-Table-1\_Water-parameters-by-tank.csv](https://github.com/laurahspencer/red-king_RNASeq-2022/blob/main/manuscript/PLOS-Climate-submission/Supporting-Information/Supplemental-Table-1_Water-parameters-by-tank.csv)

**S2 Table:** Statistics for modules with eigengenes that correlated significantly with pCO2 concentration. Modules in purple (↓) and green (↑) indicate modules for which gene expression decreased and increased with pCO2, respectively. The percent of genes that were transposable elements are also included for each module. Modules are randomly assigned color names, and the letters correspond to Figure 5 panels in the main text.

**S3 Table:** Number of differentially expressed genes and enriched GO terms by pairwise treatment contrast. Colors and arrows indicate the number of DEGs and GO terms that were upregulated (↑) and downregulated (↓) in the more severe OA treatment, where ambient = pH 8.0, moderate = pH 7.8, and severe = pH 7.5.

**S4 Table**: Enriched Gene Ontology terms in gene modules associated with pCO2 treatment, which were identified using WGCNA. Also available on GitHub: [Supplemental-Table-3\_WGCNA-Enrichment-Results.csv](https://github.com/laurahspencer/red-king_RNASeq-2022/blob/main/manuscript/Supplemental/Supplemental-Table-3_WGCNA-Enrichment-Results.csv)

**S5 Table**: Enriched Gene Ontology terms in differentially expressed genes, which were identified using WGCNA. Also available on GitHub: [Supplemental-Table-4\_DEG-Enrichment-Results.csv](https://github.com/laurahspencer/red-king_RNASeq-2022/blob/main/manuscript/Supplemental/Supplemental-Table-4_DEG-Enrichment-Results.csv)

**S6 Table**: Enriched Gene Ontology terms in upregulated low-variance genes, which were identified using WGCNA. Also available on GitHub: [Supplemental-Table-5\_Upregulated-Low-CV-Enrichment-Results.csv](https://github.com/laurahspencer/red-king_RNASeq-2022/blob/main/manuscript/Supplemental/Supplemental-Table-5_Upregulated-Low-CV-Enrichment-Results.csv)

**S7 Table:** A list of the 68 unique transposable elements detected in gene expression data. See separate file or [Supplemental-Table-6\_Transposons.csv](https://github.com/laurahspencer/red-king_RNASeq-2022/blob/main/manuscript/Supplemental/Supplemental-Table-6_Transposons.csv)

**S8 Table**: Percent of genes differentially expressed among pairwise contrasts that map to transposable elements. Colors indicate genes that were more active in ambient (blue), moderate OA (orange), and severe OA (red) treatments in each pairwise comparison. Values below the dotted line indicate the % of upregulated genes with low within-treatment variation (CV < 3%) that were TEs.