

S5 Fig. Principal component analysis using an unsupervised analysis of all gene transcripts. Treatment groupings are similar to those observed in the heatmaps for differentially expressed gene patterns (Fig. 3). A) For copper rockfish, PC2 (12.9%) and PC3 (11.6%) separated $p\text{CO}_2$ treatments into the two highest and lowest $p\text{CO}_2$ treatments. The variance explained by PC1 (13.8%) did not differ greatly from PC2 and PC3. B) For blue rockfish, PC1 (18.3%) and PC2 (13.8%) separated the control and extreme $p\text{CO}_2$ treatments and clustered the moderate treatments.

