

Final Figures:

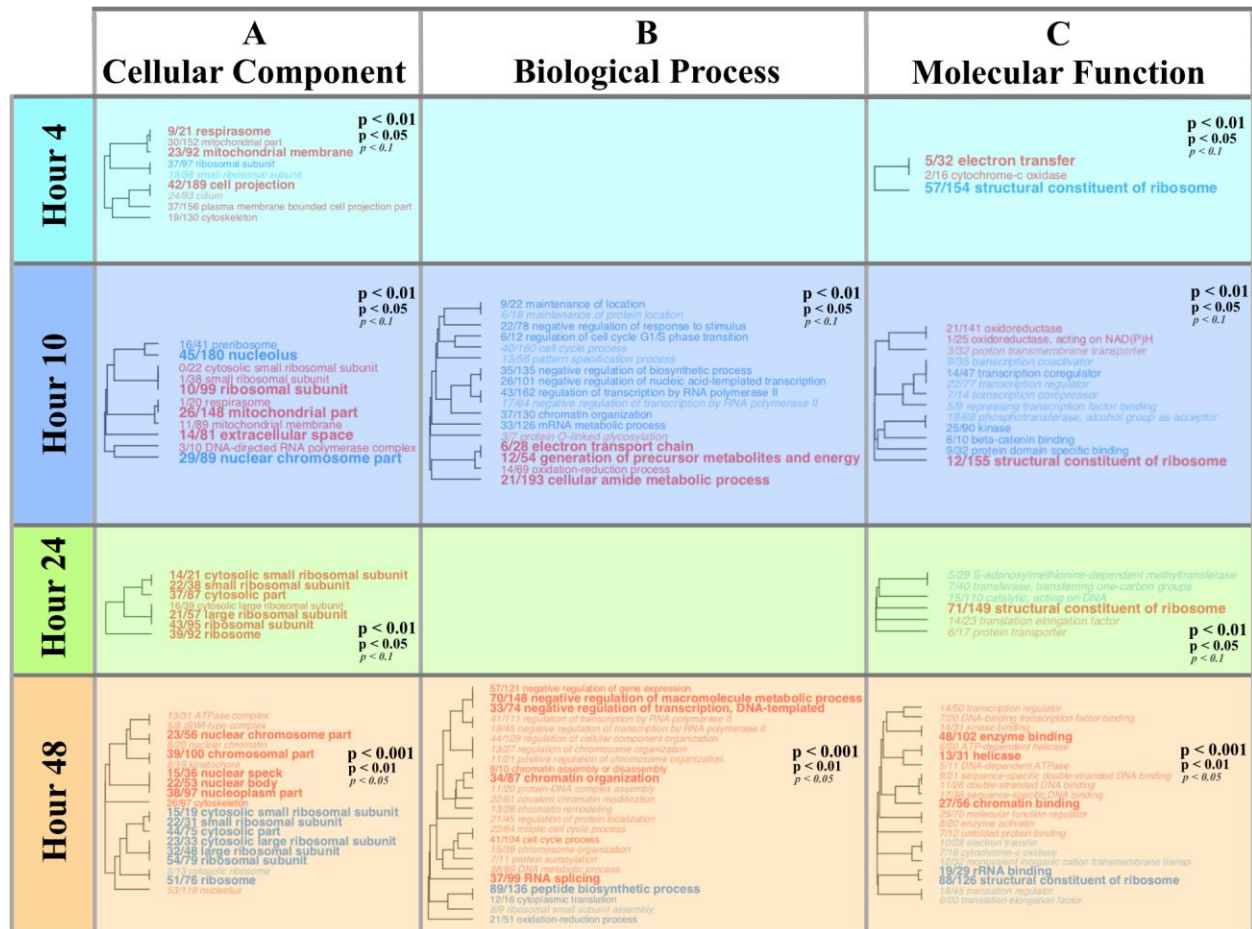


Figure 1 | Significantly enriched gene ontology (GO) categories for the pairwise comparison between pH 7.5 and pH 8.0. Mann-Whitney U (MWU) tests were conducted based on ranking of signed log p-values and the results were plotted as dendrograms with an indication of genes shared between categories. Enrichment by 'cellular component', 'biological process' and 'molecular function' are shown for hours 4, 10, 24, and 48. Overrepresented categories relative to pH 8.0 are colored as red and underrepresented categories are colored as blue. A blank grid indicates that there were no significantly enriched categories for that division at that hour.

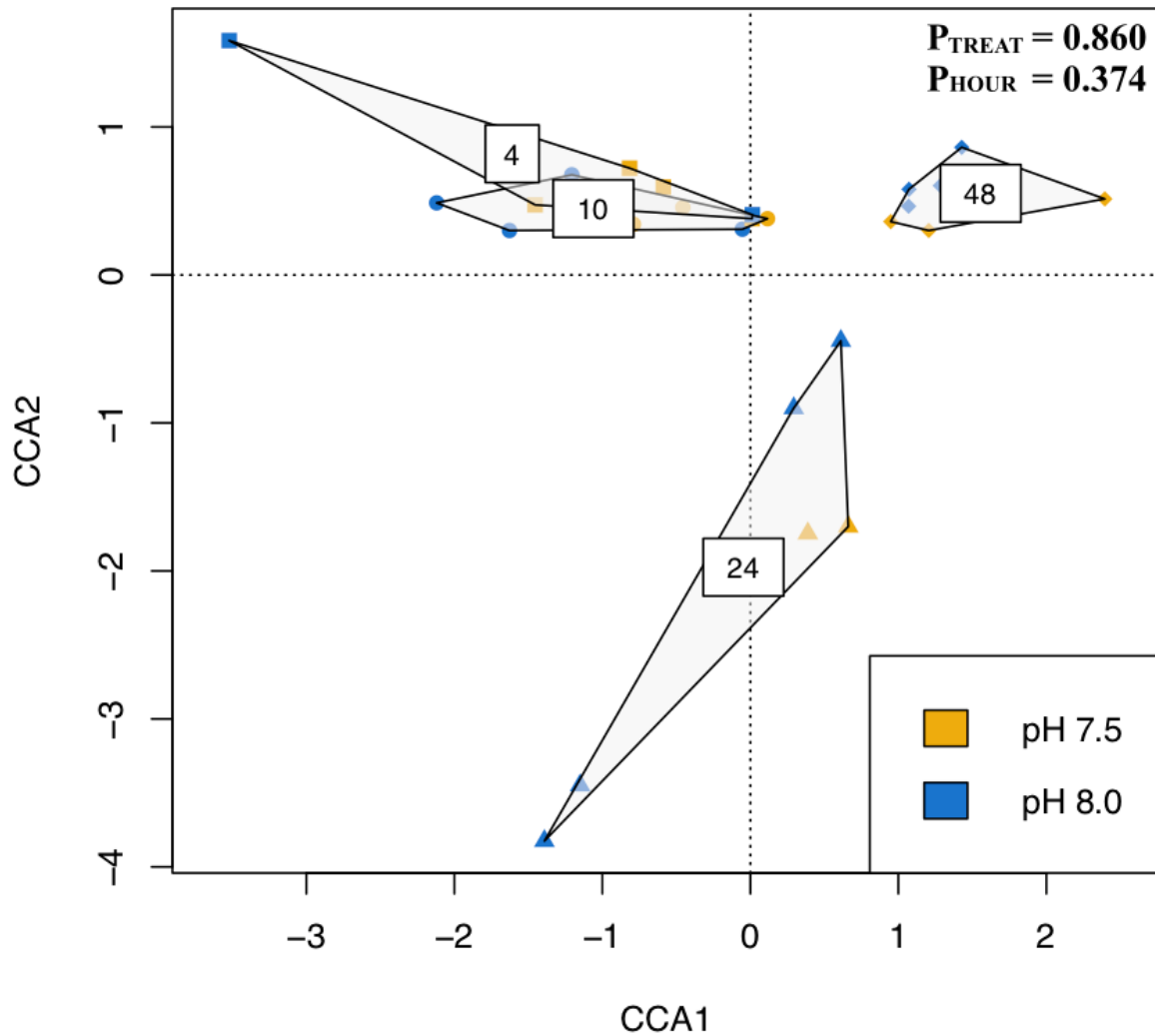


Figure 2 | Canonical Correspondence Analysis (CCA) of all r-log transformed isogroups clustered by time point and experimental treatment. Responses of *C. fornicata* larvae across different hours ($p = 0.374$) and pH treatments ($p = 0.860$) were found to not be significant. Colors indicate pH treatment condition: blue = pH 8.0, yellow = pH 7.5.

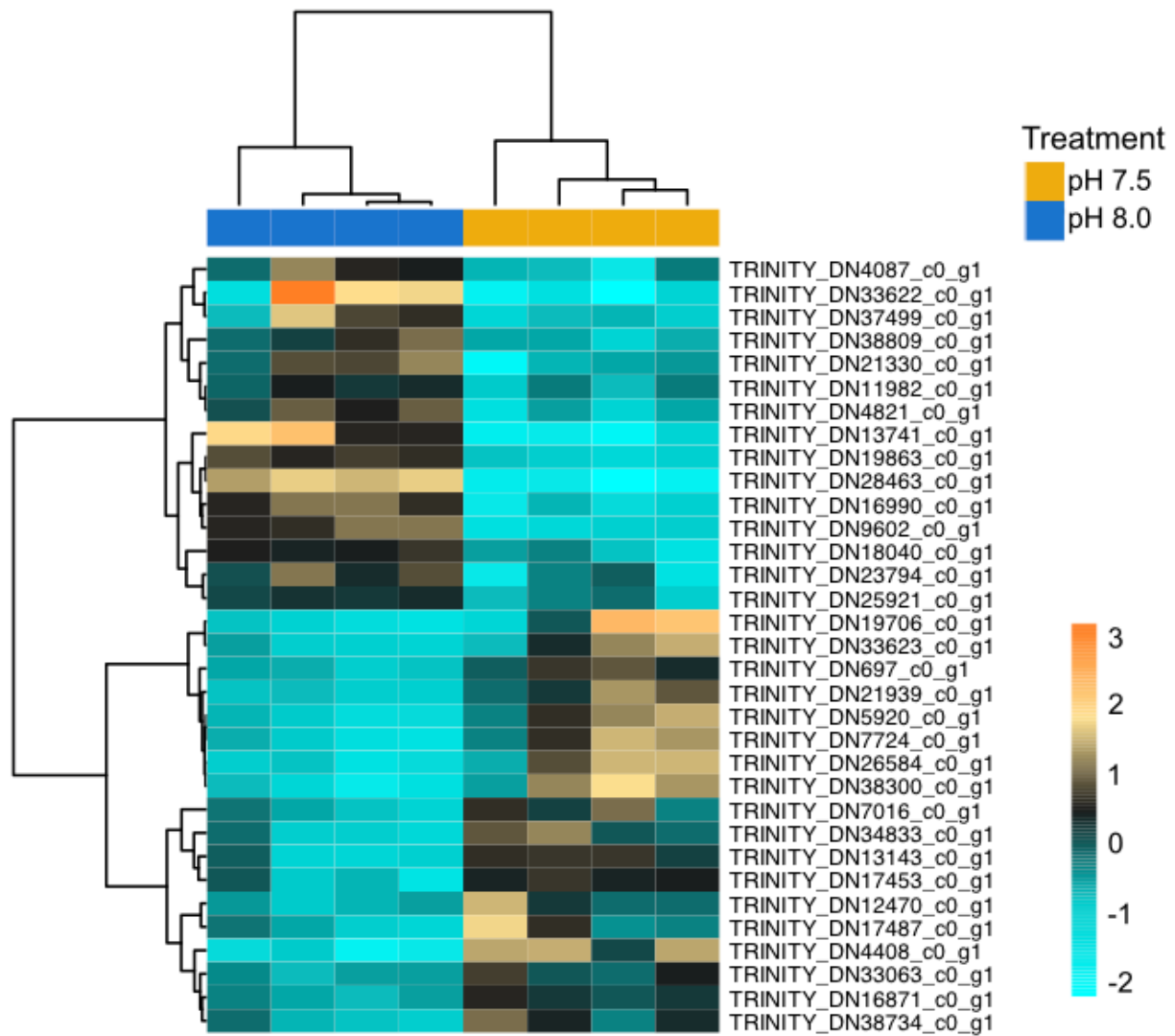


Figure 3 | Heatmap of top DEGs (FDR-adjusted = 0.1) in common between pH 7.5 samples relative to pH 8.0 samples at hour 48. Columns are indicative of independent libraries and rows represent genes. Colors show fold changes for the genes relative to the mean of the genes. Hierarchical clustering of samples and genes are based on Pearson's correlation.