

Key

A/B/C... : crab IO

: ambient water temp

: elevated water temp

All samples taken from Tanner crab (*Chionoecetes bairdi*) infected with the parasitic dinoflagellate *Hematodinium* spp.

Treatment Group	Day 0	Day 2	Day 17
Ambient	<div>A B C</div>	<div>A B C</div>	<div>A B C</div>
Elevated	<div>G H I</div>	<div>G H I</div>	

No samples - all dead

Annotated *C. bairdi* / *Hematodinium* transcriptome

Build index w/ kallisto

Pseudalign w/ kallisto, obtain counts for each library

Build matrices for each pairwise comparison

Analyze with DESeq2, obtain p-values and p-adj for each transcript

List of DEGs

UniProt database w/ GO terms

Table of gene IDs and GO terms

CSV of gene IDs and p-values

Gene ontology (GO) enrichment analysis with GO-MWU

Table showing differential expression by pathway

For DEGs, get TPM counts for all libraries

Comparative network analysis

Will be using either:

- ASCA (ANOVA Simultaneous Component Analysis)
- WGCNA (Weighted Component Network Analysis)

Separate *C. bairdi* and *Hematodinium* genes with BLAST

Individually look at differentially-expressed *Hematodinium* genes

NCBI database of all Alveolata sequences

* = end point

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