

File description:

1. *Calanus finmarchicus* reference transcriptome annotation. The 96,090 transcripts have been annotated against the SwissProt protein database (www.uniprot.org) identifying 28,616 transcripts with significant similarity to known proteins (E-value cutoff = 10^{-3}) and 10,334 transcripts with significant GO annotations (E-value cut-off = 10^{-6} ; <http://geneontology.org/>).
File name: [cfin_96k_annotSwissProt+GO.txt](#)
2. *Calanus finmarchicus* mapping data (Bowtie2)-raw counts. Relative expression as raw counts for all mapped reads from the 16 RNASeq libraries (E-field1, E-field2, E-field3, E-field4, L-field1, L-field2, L-field3, L-field4, E-culture1, E-culture2, E-culture3, E-culture4, L-culture1, L-culture2, L-culture3, L-culture4) mapped against the *C. finmarchicus* reference transcriptome (n=96,090).
File name: [cfin_96k_bowtieCounts.txt](#)
3. *Calanus finmarchicus* mapping data (Bowtie2)-RPKM. Normalized relative expression as RPKM (reads per kilobase of transcript length per million mapped reads) for all mapped reads from the 16 RNASeq libraries (E-field1, E-field2, E-field3, E-field4, L-field1, L-field2, L-field3, L-field4, E-culture1, E-culture2, E-culture3, E-culture4, L-culture1, L-culture2, L-culture3, L-culture4) mapped against the *C. finmarchicus* reference transcriptome (n=96,090).
File name: [cfin_96k_bowtieRPKM.txt](#)
4. *Calanus finmarchicus* mapping data (Bowtie2)-LogRPKM. Log transformed (\log_2) relative expression RPKM for all mapped reads from the 16 RNASeq libraries (E-field1, E-field2, E-field3, E-field4, L-field1, L-field2, L-field3, L-field4, E-culture1, E-culture2, E-culture3, E-culture4, L-culture1, L-culture2, L-culture3, L-culture4) mapped against the *C. finmarchicus* reference transcriptome (n=96,090). Relative expression data (RPKM) was log transformed (\log_2) after adding a pseudocount of 1 to the RPKM value for each transcript (i.e. $\log_2[\text{RPKM}+1]$).
File name: [cfin_96k_bowtieLogRPKM.txt](#)
5. *Calanus finmarchicus* mapping data (Bowtie2)-Zscore. Z-score of relative expression RPKM for all mapped reads from the 16 RNASeq libraries (E-field1, E-field2, E-field3, E-field4, L-field1, L-field2, L-field3, L-field4, E-culture1, E-culture2, E-culture3, E-culture4, L-culture1, L-culture2, L-culture3, L-culture4) mapped against the *C. finmarchicus* reference transcriptome (n=96,090). Z-score was calculated from the log normalized relative expression.
File name: [cfin_96k_bowtieZscore.txt](#)
6. Differentially expressed genes in *C. finmarchicus* and WGCNA. List of the 11,503 differentially expressed genes identified using a generalized linear model (GLM) across the samples. For each transcript relative expression ($\log_2[\text{RPKM}+1]$) and their WGCNA module identified in the network correlation analysis are listed.
File name: [cfin_DEGs+moduleMap_log2RPKM.txt](#)
7. Lipid metabolic process and fatty acid biosynthesis process GO terms. List of GO terms searched in the annotated *C. finmarchicus* reference transcriptome. The target GO terms 'lipid metabolic process' [GO0006629] and 'fatty acid biosynthesis process' [GO0006633] and their descendants were obtained using *AmiGO* software GO Online SQL Environment

(GOOSE)(October, 2019: <http://amigo2.berkeleybop.org/goose/cgi-bin/goose>). Transcripts annotated to any of the GO terms in this list have been included in the ‘lipid metabolism’ and ‘fatty acid biosynthesis’ filter.

[File name: Filter-GOOSE-LipidMet&FAbiosy.txt](#)

8. Oogenesis GO terms. List of GO terms searched in the annotated *C. finmarchicus* reference transcriptome. The target GO term ‘oogenesis_[GO0048477] and its descendants were obtained using *AmiGO* software GO Online SQL Environment (GOOSE)(October, 2019: <http://amigo2.berkeleybop.org/goose/cgi-bin/goose>). Transcripts annotated to any of the GO terms in this list have been included in the ‘oogenesis’ filter.

[File name: Filter-GOOSE-Oogenesis.txt](#)

9. RNA metabolic process GO terms. List of GO terms searched in the annotated *C. finmarchicus* reference transcriptome. The target GO term ‘RNA metabolic process [GO:0016070] and its descendants were obtained using *AmiGO* software GO Online SQL Environment (GOOSE)(October, 2019: <http://amigo2.berkeleybop.org/goose/cgi-bin/goose>). Transcripts annotated to any of the GO terms in this list have been included in the ‘RNA metabolism’ filter.

[File name: Filter-GOOSE-RNAmetabolicProcess.txt](#)

10. **Interactive version of Fig.6 showing z-scores of DEGs involved in oogenesis.** Differentially expressed genes between field and culture and early and late CV copepodids annotated with the ‘oogenesis’ (GO:0048477) GO term and its child terms (n=479). Color-coding for each gene indicates the magnitude of expression as z-scores of each individual sample. Relative expression of each sample is given in a separate column (ordered by group) as labeled at the top. Genes (rows) were ordered by hierarchical clustering.

[File name: Fig6-Oogenesis-DEGs_heatmaply.html](#)

11. **Interactive version of Fig.7 showing z-scores of DEGs involved in fatty acid biosynthesis.** Differentially expressed genes between field and culture and early and late CV copepodids annotated with the GO term ‘fatty acid biosynthetic process’(GO:0006633) or its child terms (n=65). Color-coding for each gene indicates the magnitude of expression as z-scores of each individual sample. Relative expression of each sample is given in a separate column (ordered by group) as labeled at the top. Genes (rows) were ordered by hierarchical clustering.

[File name: Fig7-FAbiosynthesis-DEGs_heatmaply.html](#)

12. **Interactive version of Fig. 8 showing z-scores of DEGs involved in RNA metabolism.** Differentially expressed genes between field and culture and early and late CV copepodids annotated with the GO term ‘RNA metabolic process’ (GO: 0016070) or its child terms (n=335). Color-coding for each gene indicates the magnitude of expression as z-scores of each individual sample. Relative expression of each sample is given in a separate column (ordered by group) as labeled at the top. Genes (rows) were ordered by hierarchical clustering.

[File name: Fig8-RNAmet-DEGs_heatmaply.html](#)

13. **Interactive version of Fig. 9b showing z-scores of filtered genes based on evidence for involvement in diapause preparation**

[File name: Fig9b_heatmaply.html](#)

14. **Interactive version of Fig. 9d showing z-scores of filtered transcripts having z-scores in all culture samples higher than any in the field samples.**

[File name: Fig9f_heatmaply.html](#)

15. **Interactive version of Fig. 9f showing z-scores of filtered** transcripts having z-scores in all field samples higher than any in the culture samples

[File name: Fig9f_heatmaply.html](#)

16. **mtCOI target sequences.** FASTA file sequences for mitochondrial COI for *Calanus finmarchicus*, *Calanus glacialis* and *Calanus helgolandicus*. For each sequence NCBI Accession number is provided

[File name: mtCOI-sequences](#)