

## **Contrasting transcriptome response to thermal stress in two key zooplankton species, *Calanus finmarchicus* and *C. glacialis***

**Irina Smolina<sup>\*</sup>, Spyros Kollias, Eva F. Møller, Penelope Lindeque, Arvind Y.M. Sundaram, Jorge M.O. Fernandes, Galice Hoarau**

\* Corresponding author: ism@uin.no

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Supplement 1 Content:

Fig. S1. Experimental set-up for thermal stress of *Calanus finmarchicus* and *C. glacialis* at four temperatures and two durations.

Fig. S2. Grazing by *Calanus finmarchicus* and *C. glacialis* during short-term thermal experiment measured as fecal pellet production.

Fig. S3. Number of reads in *Calanus finmarchicus* (a) and *C. glacialis* (b) libraries.

Fig. S4. Functional classifications of annotated transcripts in *Calanus finmarchicus* and *C. glacialis* for GO categories of biological processes.

Fig. S5. Variation of log<sub>2</sub> fold changes of expression values assessed by RNAseq and qPCR.

Fig. S6. Stability of putative reference genes for *C. finmarchicus* (a) and *C. glacialis* (b) during thermal stress.

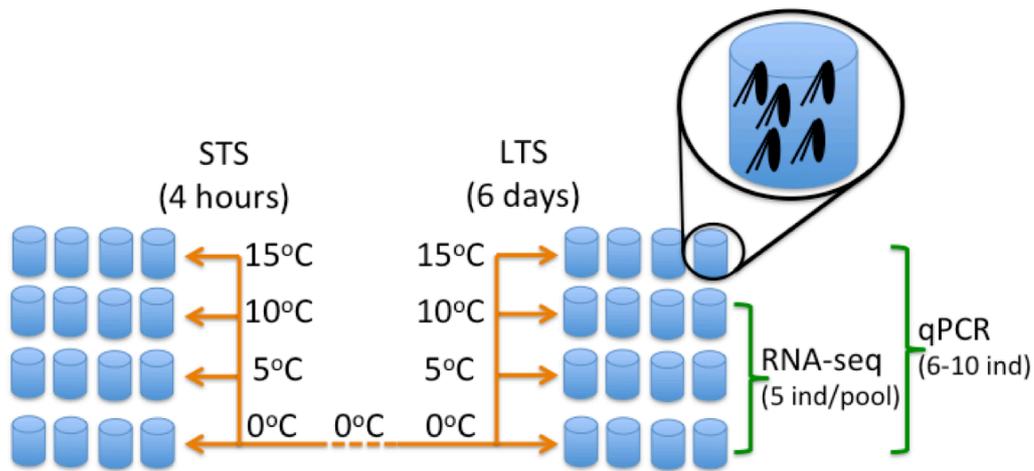


Fig. S1. Experimental set-up for thermal stress of *Calanus finmarchicus* and *C. glacialis* at four temperatures and two durations. Total number of individuals per treatment is 20. Physiological response was measured from all live copepods, while 5 individuals per treatment were taken for RNA-seq, and between 6 and 10 individuals per treatment were used for qPCR. For more details see 'Materials and methods' in the main article. Key: STS, short-term thermal stress; LTS, long-term thermal stress.

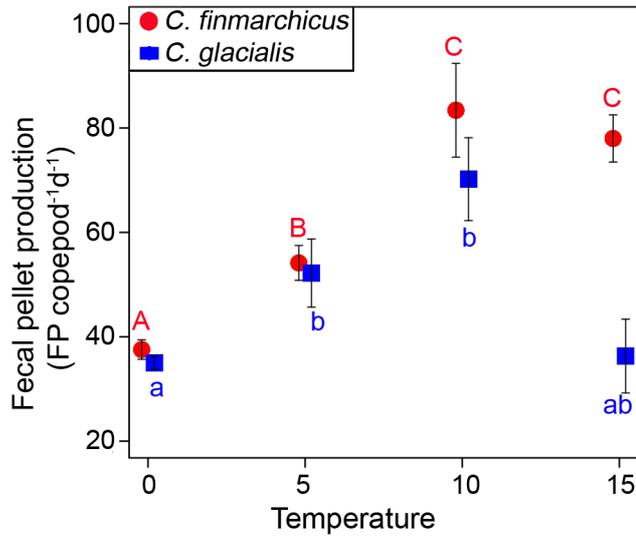


Fig. S2. Grazing by *Calanus finmarchicus* and *C. glacialis* during short-term thermal experiment measured as fecal pellet production (fecal pellet copepod<sup>-1</sup> day<sup>-1</sup>) (mean  $\pm$  standard error). Significant difference ( $p < 0.05$ ) of fecal pellet production values between temperatures ( $^{\circ}\text{C}$ ) is indicated by different letters: uppercase for *C. finmarchicus* and lowercase for *C. glacialis*.

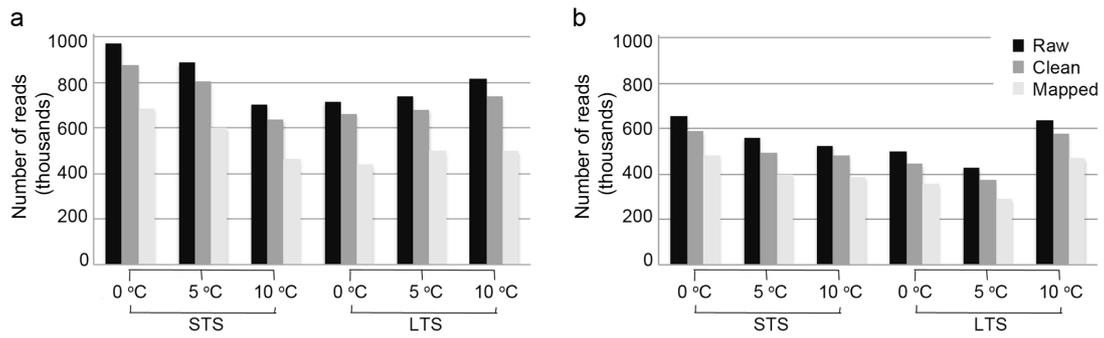


Fig. S3. Number of reads in *Calanus finmarchicus* (a) and *C. glacialis* (b) libraries. Key: STS, short-term thermal stress (4 h); LTS, long-term thermal stress (6 d); Raw: total sequenced reads; Clean: reads with a Phred quality score above 17, longer than 35 bp and decontaminated for ERCC RNA Spike-In reads; Mapped: reads uniquely mapped to the assembly.

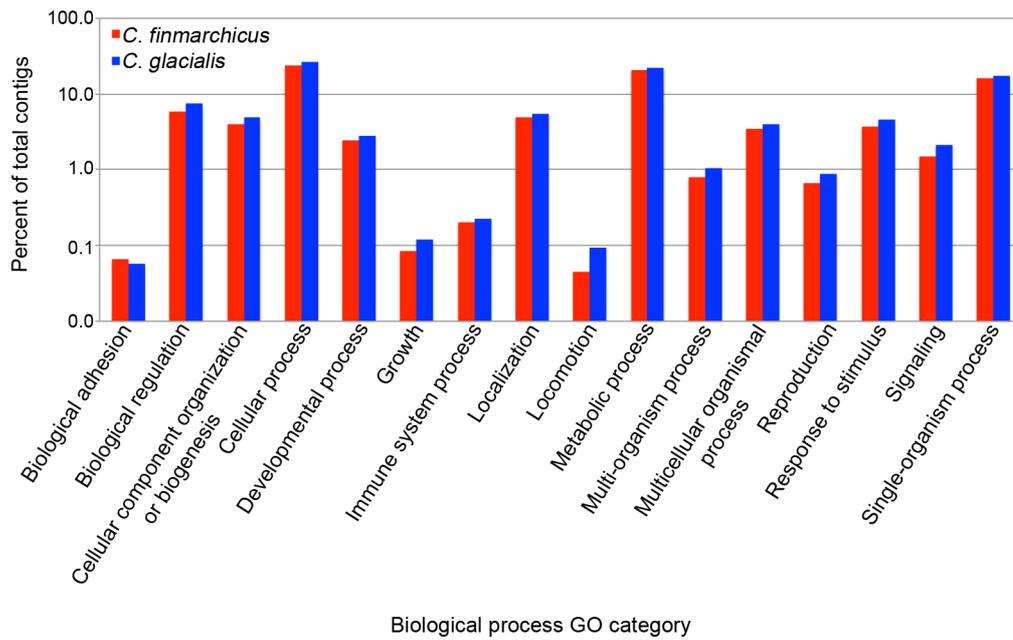


Fig. S4. Functional classifications of annotated transcripts in *Calanus finmarchicus* and *C. glacialis* for GO categories of biological processes.

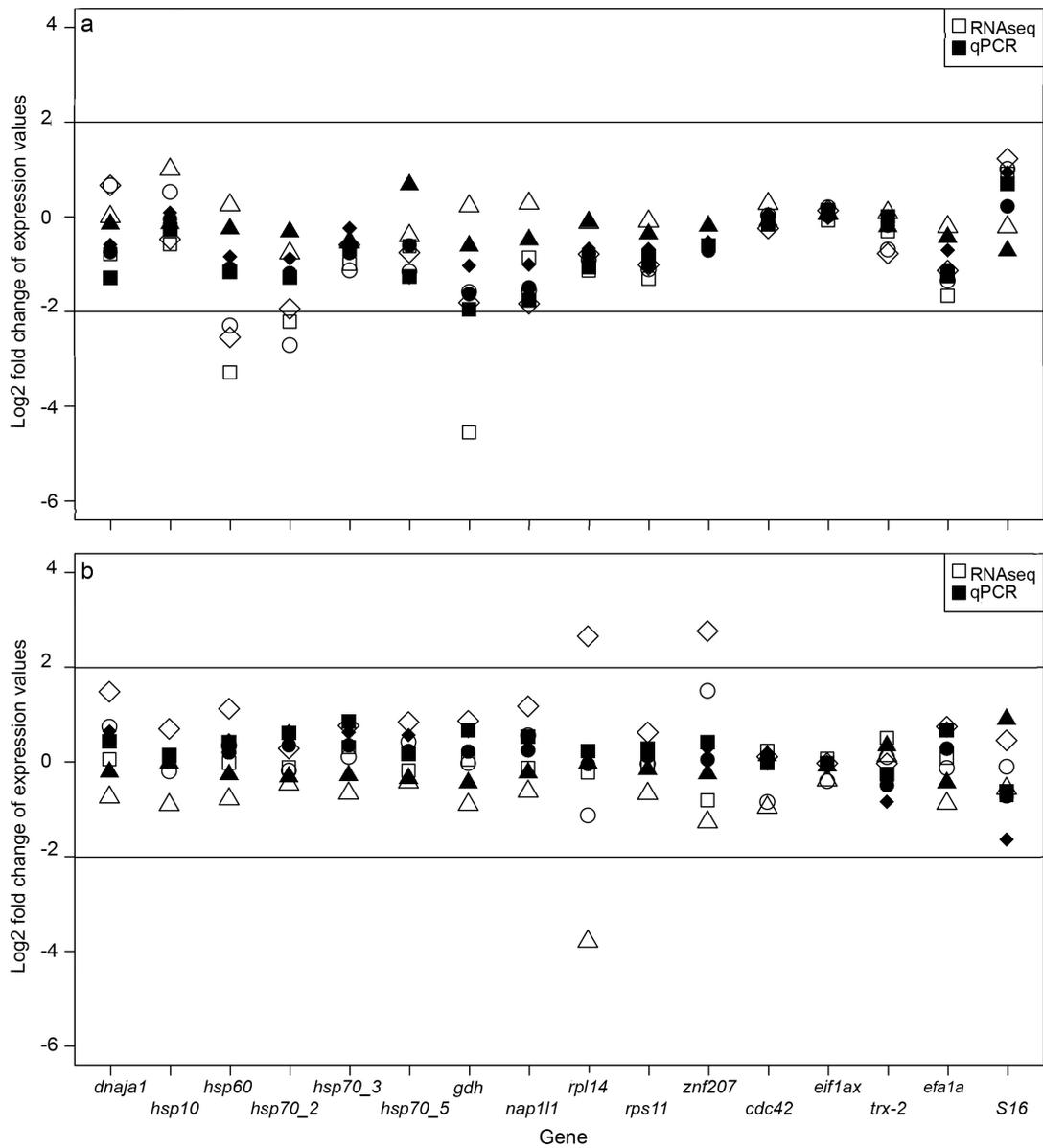


Fig. S5. Variation of log<sub>2</sub> fold changes of expression values assessed by RNaseq (white) and qPCR (black) in comparisons: STS versus SLS (■), 0 °C versus 5 °C (●), 0 °C versus 5 °C (▲), 5 °C versus 10 °C (◆) for each gene in *C. finmarchicus* (a) and *C. glacialis* (b).

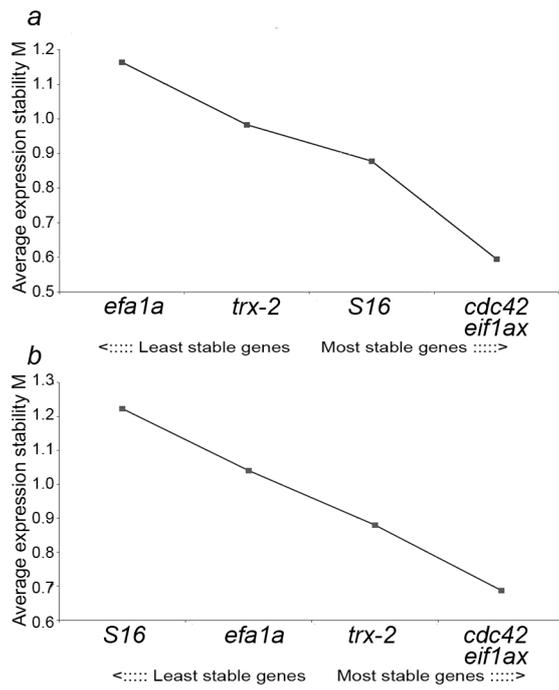


Fig. S6. Stability of putative reference genes for *C. finmarchicus* (a) and *C. glacialis* (b) during thermal stress.