

Transcriptional effects of temperature acclimation and circadian rhythms in Arctic char (*Salvelinus alpinus*)

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Background

- Regional temperature shifts can exceed the magnitude experienced over the last 21,000 years by the end of this century, challenging the adaptability of stenothermal species.
- Warming is the most rapid in high latitudes, which are characterized by a strong seasonal variation in temperature and day-length.
- The molecular mechanisms generating pronounced seasonal rhythms in arctic fish behavior and physiology are poorly understood ^a.
- Arctic char is a cold-water adapted salmonid with anadromous, resident and landlocked forms (fig 1).

Aims

- I. Explore circadian variation in the transcription of metabolic genes.
- II. Address temporal variation in the response to increased temperature.

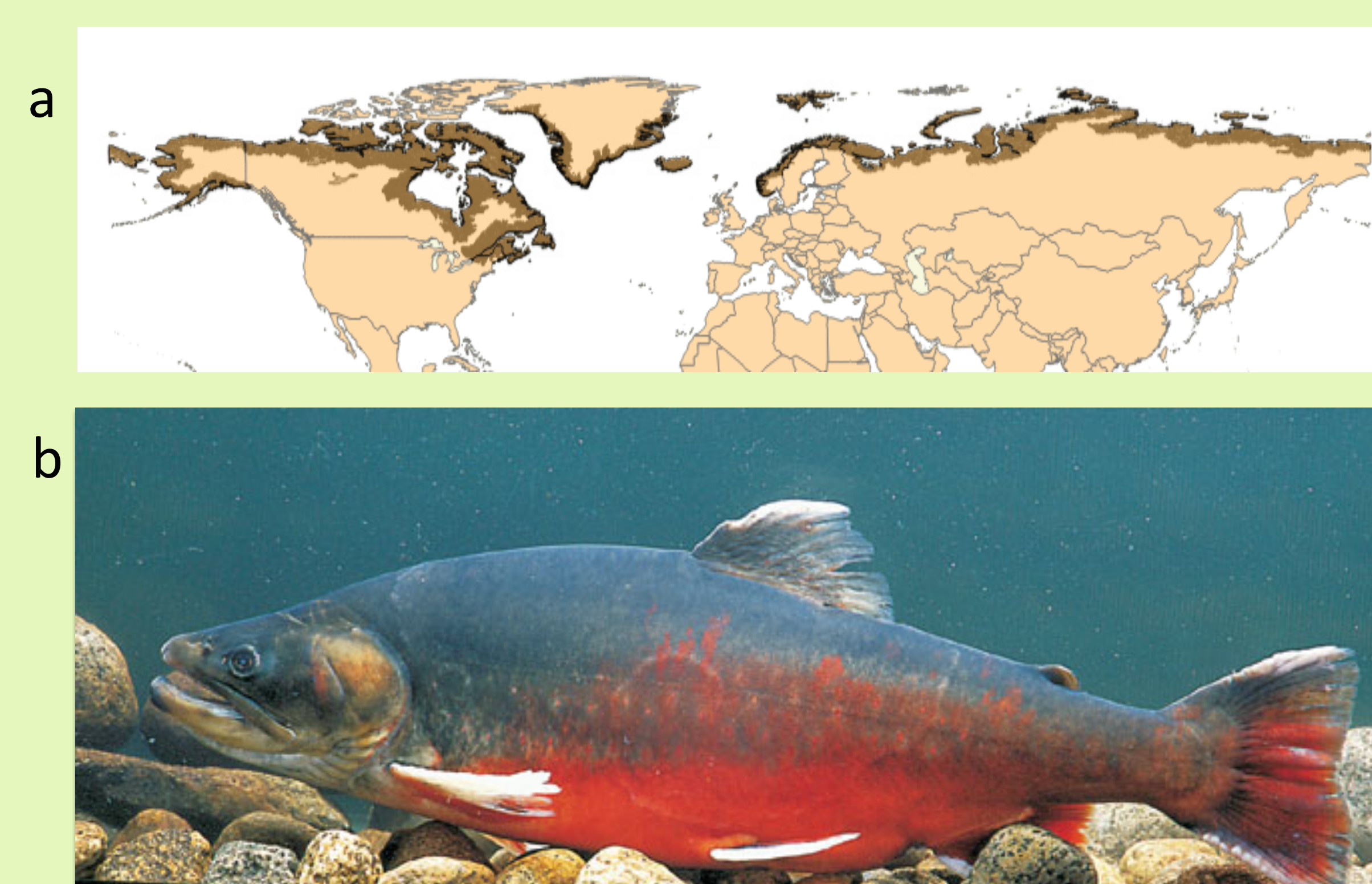
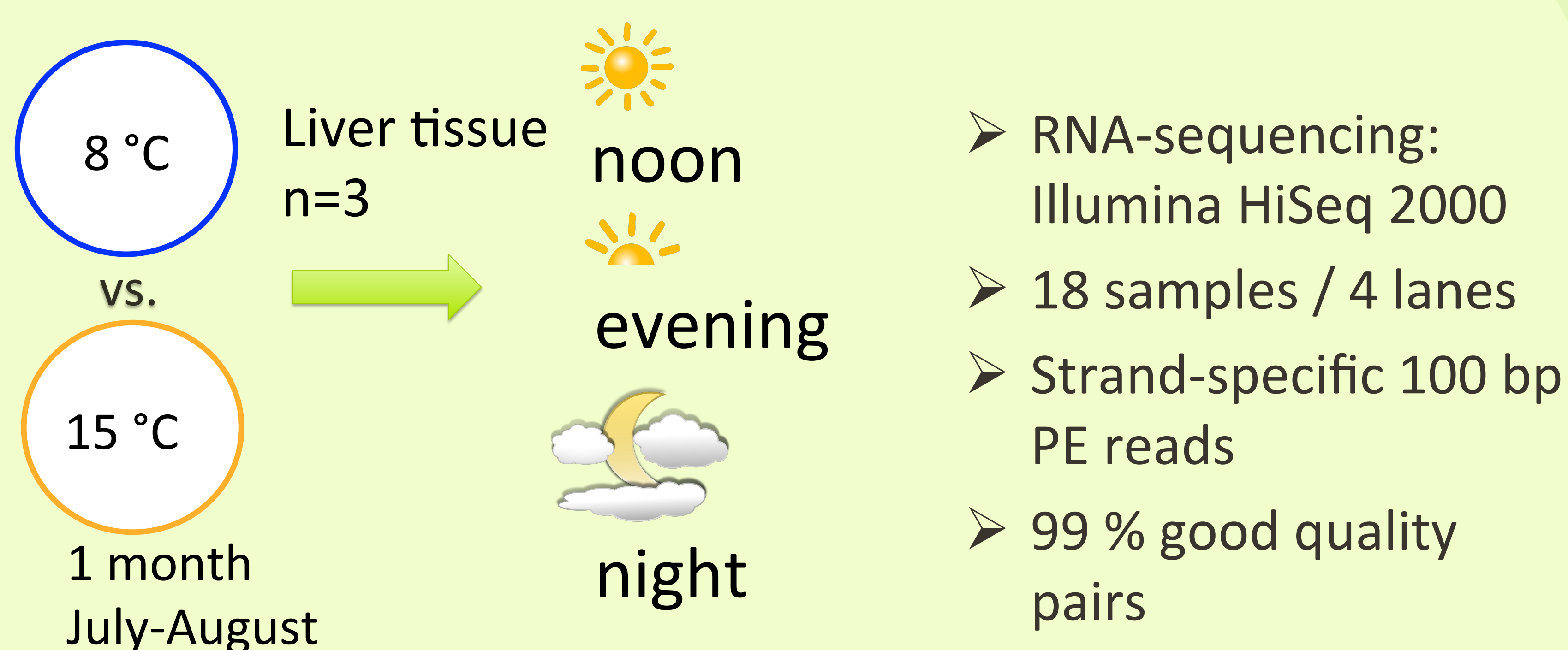


Fig. 1. a) Arctic char has circumpolar distribution. b) adult male Arctic char in breeding color.

Experiment and Results



Paired reads were quality-trimmed with trimmomatic and assembled into transcripts with Trinity (Table 1). Count data for transcript clusters was obtained with Corset software. Sample distance (fig.2) and differential expression analysis was performed with count data. Clusters with Benjamini-Hochberg adjusted FDR <0.05 and $\text{abs}(\log_2 \text{fold-change}) > 1$ between temperatures, within time points, were defined as differentially expressed (fig. 3).

Table 1. Metrics for the reference assembly.

De novo transcriptome assembly	
Trinity transcripts	335 244
Trinity 'genes'	200 141
Open reading frames	77 324
Unique BLASTp hits	19 132
>80 % full-length BLASTp hits	9 479
BUSCO Coverage/Fragments ^b	80 % / 5 %

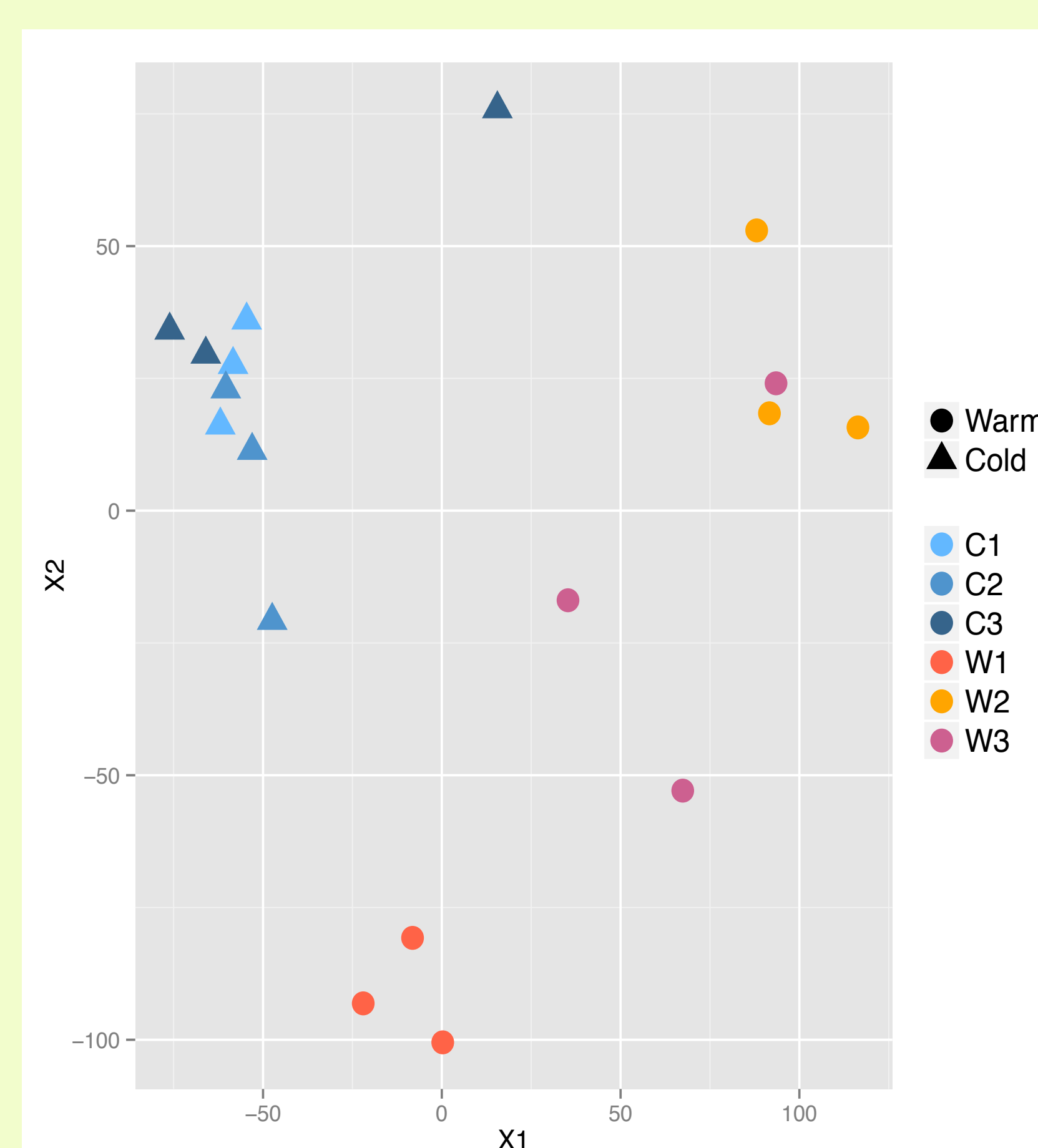


Fig. 2. MDS plot of sample distances based on regularized transformed \log_2 read counts (rlog). Time points indicated by numbers 1= noon, 2= evening, 3= night.

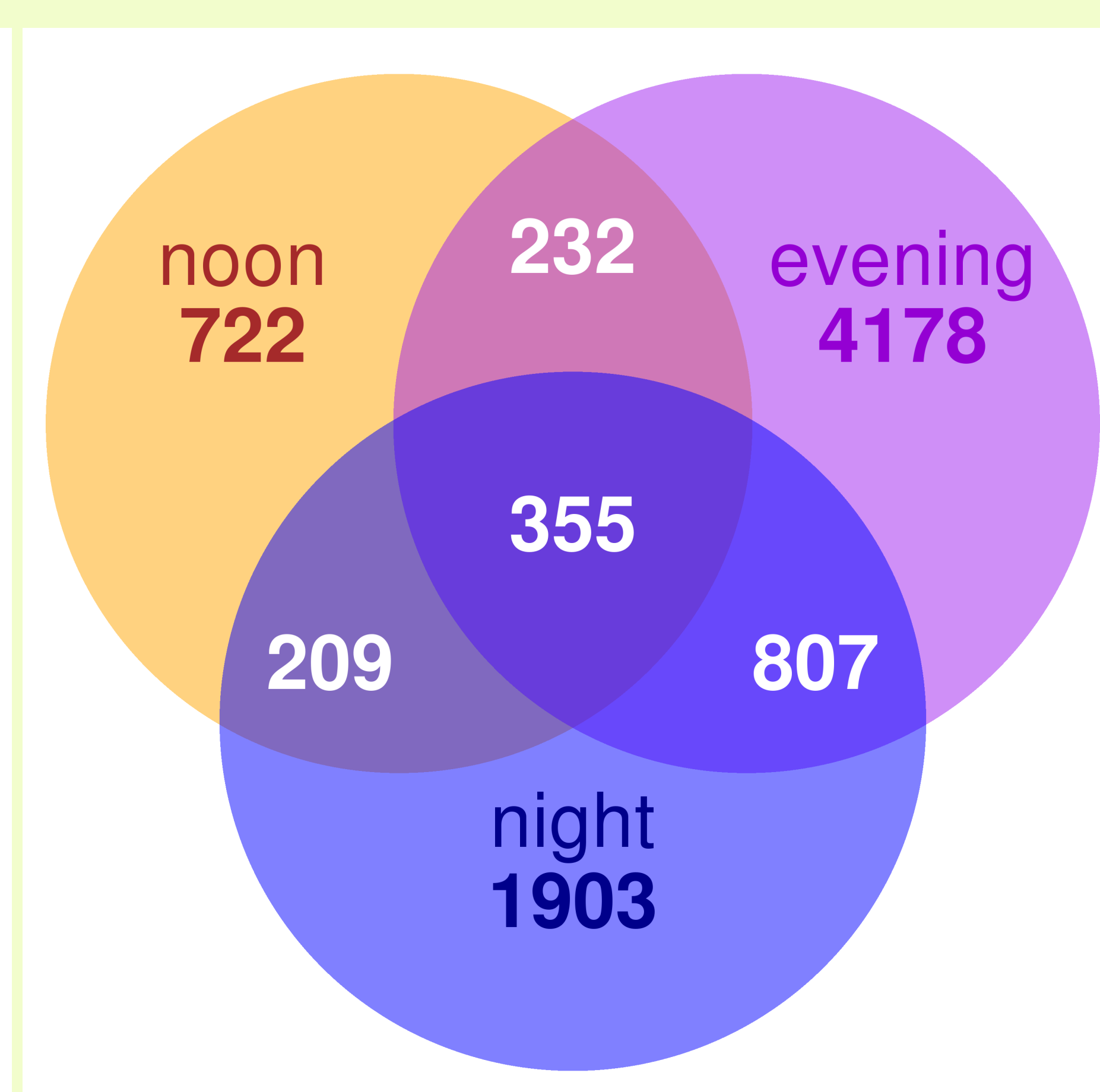


Fig. 3. A Venn diagram representing the number of differentially expressed and shared transcript clusters between temperatures at different time points.

Conclusions

- I. Circadian variation in transcription in liver tissue is temperature-dependent.
 - Possible adaptation to a seasonal environment.
- II. Targeting temperature responsive genes benefits from accounting for circadian rhythms.
- III. Transcript annotation will be the next step in creating an extensive genomic resource for Arctic char research.

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References:

^a Jorgensen & Johnsen, *Marine Genomics* 14, 2014

^b Simão et al. *Bioinformatics*, online Jun 9 2015

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