Analysis of the circadian transcriptome of the Antarctic krill *Euphausia superba*

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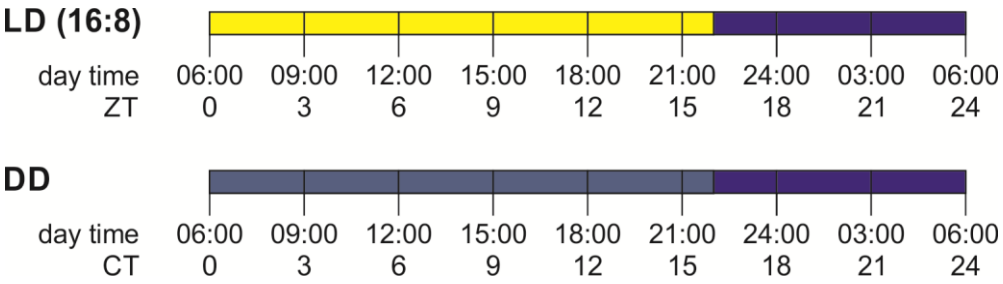
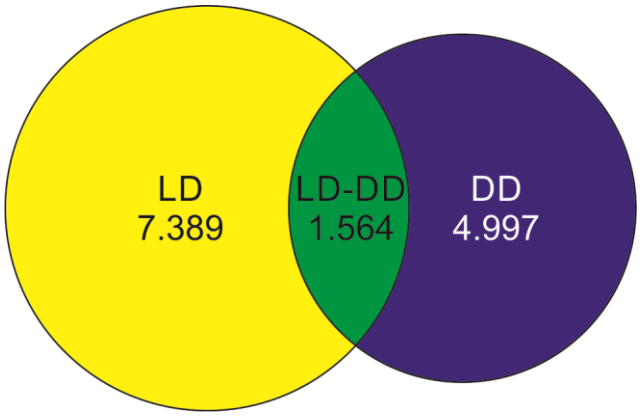
SUPPLEMENTARY FIGURES



Supplementary Figure 1. Experimental design.

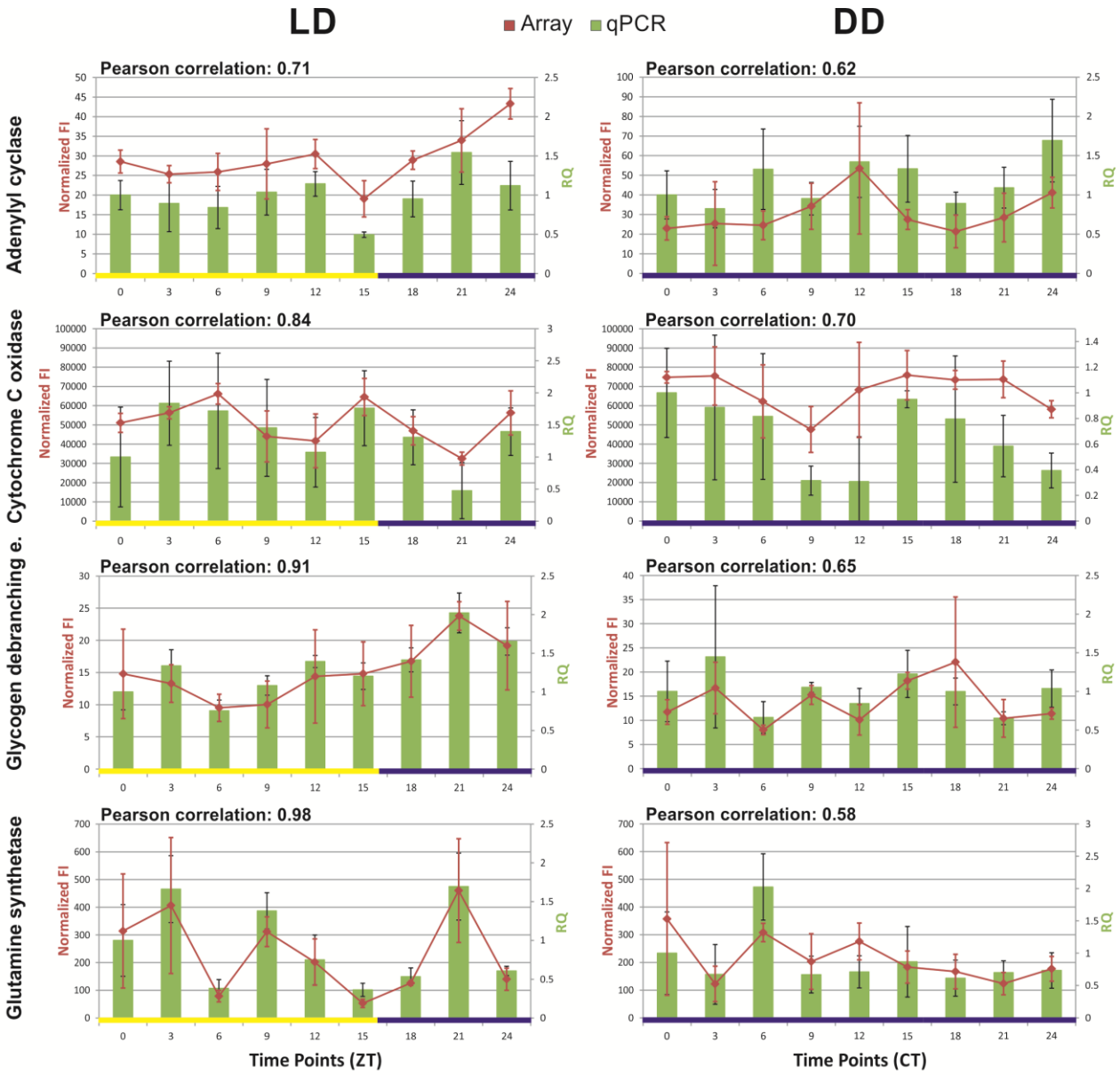
In order to define the gene expression profiles, specimens were collected at regular intervals throughout the 24-hour cycle in a light:dark (LD) regime of 16 hours light and 8 hours darkness followed by constant darkness (DD). Yellow and blue bars refer to light and dark periods, respectively.



Supplementary Figure 2. Circadian expression signatures.

A weighted Venn diagram showing the relative portion of genes with sinusoidal expression patterns (RAIN) in LD and DD (see Table S1 and S2). The intersection represents putative clock-controlled genes with an oscillatory expression both in LD and DD (see Table S3).


LD
Array
qPCR
DD
6-4 photolyase
Arrestin
Nina-C
Casein kinase ε
Slimb
Pearson correlation: 0.93
Pearson correlation: 0.73
Pearson correlation: 0.86
Pearson correlation: 0.94
Pearson correlation: 0.74
Pearson correlation: 0.72
Pearson correlation: 0.83
Pearson correlation: 0.71
Pearson correlation: 0.76
Pearson correlation: 0.73
Normalized FI
RQ



Supplementary Figure 3. Validation of microarray expression values by qRT-PCR.

mRNA expression levels are represented by histograms. Normalized qRT-PCR data are expressed as fold changes (RQ) relative to the average expression for ZT0 and CT0. Yellow and blue bars refer to light and dark periods, respectively. *Ubiquitin carboxyl-terminal hydrolase 46* and *RNA polymerase I-specific transcription initiation factor RRN3 isoform 1* were used as endogenous controls. The microarray expression profiles of each gene are shown as line graphs (red) while qRT-PCR results are reported as histograms. Pearson correlation was calculated to estimate the association between microarray data and qRT-PCR results ($r > 0.6$ is considered as statistically significant).

SUPPLEMENTARY TABLES

>require(rain)

>data<-read.table(file)

>result<-rain(data, period=18, period.delta=6, deltat=3, nr.series=3, method='independent')

Supplementary Table 7. List of commands used to identify genes showing rhythmic expression profiles during the 24 hours in microarray data by using RAIN.

Description	Forward Primer (5'-3')	Reverse Primer (5'-3')
6-4 photolyase	CTTGGAACGCACCACTCTCT	CACGATTCTACGTGGGTAGTCC
arrestin homolog	AGCTAGTTCACCCAGACCCA	ACGGCGGAGGTTCTTGAAAT
casein kinase 1 epsilon	TATTGTCTCGTCGGCTTGC	TGGGTATTTGGATCCTACAACAT
neither inactivation nor afterpotential protein C	AACTGAAGTTGCAATAAAGGATCA	TGCCTCCACCATATGTAGTCC
slimb	GCTGCCACAGATGCTTCA	TGCCTCCACCATATGTAGTCC
cytochrome c oxidase subunit I	GCAATAAGCGAATGGTTGACC	GATACTCAGACTACCCAGATGC
glycogen debranching enzyme	TGCAAATGAGTCTCCATGGC	TGTGCAGTAGACGATCAAGG
glutamine synthetase	TGTATCTTCCTCCAGGATGGC	ATACATGGCCTGGCATTTGC
adenylyl cyclase	AGCAACACCAGCAGTTTAGG	TTCATGGTCACCACATACGG
clock	GCTGCAGCAAATGATAATGC	TGCCATATTGGGCCATAACT
cryptochrome 2	TCATGAACCATGGACTGCAC	GGTGGACACGACTTCAACAA
period	GCAGCTATGCCCAACTTTAATC	GGACTAGCAACAGGGACATTTT
ubiquitin carboxyl-terminal hydrolase 46	AAATCGTCAGAAACGGGCTA	TTAGCGGTTATGGAACATTACG
RNA polymerase I-specific transcription initiation factor RRN3 isoform 1	CTTGGACGGGGTAGTTCCTA	TGTGATGTTTACCTCCGCAGT

Supplementary Table 8. Primers used in quantitative qRT-PCR.