

## Supporting Information

S1 Text. Appendix A. Calculation of the  $2^{\Delta\Delta CT}$

$$\Delta\Delta CT = (CT(\text{target}, \text{untreated}) - CT(\text{ref}, \text{untreated})) - (CT(\text{target}, \text{treated}) - CT(\text{ref}, \text{treated}))$$

Where:

$CT(\text{target}, \text{untreated})$  = Ct value of the gene of interest in control sample (for convention time 7:30 in our study)

$CT(\text{ref}, \text{untreated})$  = Ct value of the geometric mean of the two control genes used in the control sample

$CT(\text{target}, \text{treated})$  = Ct value of the gene of interest at the different time points

$CT(\text{ref}, \text{treated})$  = Ct value of the geometric mean of the two control genes at the different time points

We also calculated the  $E^{\Delta\Delta CT}$

Where E represents the efficiency calculated as follow:

$$\text{Efficiency} = 2^{-1/\text{slope}}$$

## S1 Text. Appendix B. Calculation of the error propagation

The errors bars represented in Figure 5 (confidence limits) are calculated as follow for each single time point:

$$\mathbf{Error} = \sqrt{(\mathbf{Error}(\mathbf{control}))^2 + (\mathbf{Error}(\mathbf{treated}))^2}$$

Remember that the control sample is at 7:30 time point for convention. For simplicity we report just the equation for the calculation of the error propagation at one representative time point (T)

$$\mathbf{Error}(T) = \sqrt{(\mathbf{Error}(\mathbf{ref}))^2 + (\mathbf{Error}(\mathbf{target}))^2}$$

$$\mathbf{Error}(\mathbf{ref}) = (2 * \mathbf{geom. mean}(\mathbf{ref1}, 2)) * \sqrt{(\mathbf{arit. mean}(\mathbf{ref1}) * \mathbf{SE})^2 + (\mathbf{arit. mean}(\mathbf{ref2}) * \mathbf{SE})^2}$$

$$\mathbf{Error}(\mathbf{target}) = \mathbf{standard error of the aritm. mean} = \frac{\mathbf{Standard deviation}}{\sqrt{n}}$$

## S1 Text. Appendix C. Statistical analysis of RT-qPCR results

A one way ANOVA was used to assess significant differences among RNA expression at different time point. We used the  $2\Delta CT$  values as input for the statistical test. These were calculated as follow:

$$2\Delta CT = E^{((-1)*\Delta CT)}$$

$$\Delta CT = \text{Mean } CT(\text{target}_i) - \text{geom. mean } CT(\text{ref}_i1, 2)$$

Where E = Efficiency as reported in Section 1

$CT \text{ ref}_i1, 2$  = The CTs values of the  $i$  sample of cDNA for reference gene 1 and 2.

**S1 Text. Table A. Primers used for cloning**

<b>Genes</b>	<b>Primer</b>	<b>Position (bp)</b>	<b>Primer sequence (5' -&gt; 3')</b>	<b>Ann. Temp. (°C)</b>
<i>period</i>	<i>per-F1</i>	12-37	CCCAGAGTTAGTGGAGTAAAGGTGTG	56.7
	<i>per-R1</i>	1262-1241	TGTGGCAGATGACCCAGGTAGG	
	<i>per-F2</i>	315-337	TGGCGACAATGCTGATTTTAGTG	57.2
	<i>per-R2</i>	2103-2078	TGAGAGAGTCTGTGAGTGTGATAGCG	
	<i>per-F3</i>	2020-2039	AGCACCCATCCAGCCTTTTC	57.8
	<i>per-R3</i>	3260-3238	CGGTTTCATCTCAGAATCCTTTGG	
	<i>per-F4</i>	3058-3077	CGTCCACCACTAACCTGCG	56.1
	<i>per-R4</i>	4095-4073	CCTTGAGCCACCTATTGCCATAC	
	<i>per-F5</i>	3658-3678	AGATTACGACAGCCTGCCTGG	54.1
	<i>per-R5</i>	4850-4831	TCCGTTCTTTTTTTTCGCCC	
<i>timeless</i>	<i>tim-F2</i>	752-773	TCGGACAGTTGGTAGAGGTGCG	56.5
	<i>tim-R2</i>	2304-2283	TGTTTGAGGATTCGTCGTCGTG	
	<i>tim-F3</i>	168-192	GCACCATCAGAAGCCTCATAAAATG	56.4
	<i>tim-R3</i>	801-778	CAAGCGAATCAGCAACACAAATAG	
<i>clock</i>	<i>clk-F3</i>	122-149	AGTTTAGTGATAACCAGGGAGTAAGAGC	54.5
	<i>clk-R3</i>	393-372	CGGACAGTTCGTTGATGAGGAG	
<i>bmal1</i>	<i>bmal1-F1</i>	1-24	TCCTTCTCCTCTGATGGCTCTAAG	52.1
	<i>bmal1-R1</i>	222-200	TGTCAGTTTGTCAAGCTTCCGAG	
<i>α-act</i>	<i>a-act-F1</i>	300-322	CACTCCTTCTACAACGAACTGCG	58.1
	<i>a-act-R1</i>	1160-1141	GCACTTGCGGTGGACAATGC	
	<i>a-act-F3</i>	127-146	TATCCCCTCCATCGTCGGC	57.7
	<i>a-act-R3</i>	398-378	GGTCATCTTCTCACGGTTGGC	

S1 Text. Table B. Primers used for RT-qPCR

Genes	Primer name	Position on cDNA fragment	Primer sequence (5' -> 3')	Amplicon size (bp)	Efficiency (E)	R <sup>2</sup>
<i>NnPeriod</i>	per-F1	364-388	TGGAAGAAGTTGAAGGAGAAGACCG	151	2.2	0.969
	per-R1	515-493	CAATACTGCTGGCTGTTTCGCTG			
<i>NnTimeless</i>	tim-F1	256-280	GCCCTATCAGATTGACCTGGACAAG	154	1.9	0.969
	tim-R1	409-385	CATCACCCTCCCTCATAACCAAG			
<i>Nnclock</i>	clk-F1	33-57	TGGTGGTGGTGTGAAGTGGATTTAC	132	2.5	0.970
	clk-R1	164-142	CAGATTTGCCAGGTGATGTTTCG			
<i>Nnbmal1</i>	bmal1-F1	1-21	TCCTTCTCCTCTGATGGCTCT	108	2.2	0.968
	bmal1-R1	108-89	TTTATTCCAATCCCCAGCAG			
<i>Nna-act</i>	aAct-F2	414-438	GGTTATTGTCTCCCACACGCTATCC	136	2.0	0.979
	aAct-R2	549-527	TGATGTCACGAACGATTTCTCGC			
<i>Nn18S</i>	18S-F1	132-153	AGGGCGTTGGTCGTCGTTATTC	134	2.0	0.968
	18S-R1	265-246	CTTGTATTGGCGGGGGTTGC			

**S1 Text. Table C. List of candidate clock genes in *Nephrops norvegicus*.** Transcripts that can be considered as putative clock genes or genes related to the circadian system. **PPDE** (Posterior Probability of Differential Expression) represents the posterior probability of differential expression. **post FC (L/D)** represents the fold change of transcripts abundance between photophase/scotophase. Bold-highlighted transcripts result to be differentially expressed (PPDE > 0.95) across the two phases. (+) and (-) symbols indicate up- and down- regulation respectively during the light phase.

Transcript	Length (bp)	Match	Start	End	PPDE	Post FC (L/D)	Species	Access number
comp65743_c0_seq1	304	48 related 2	3	299	0.125	0.301	<i>Drosophila melanogaster</i>	FB FBgn0038402
comp8903_c0_seq1	165	5'-AMP-activated protein kinase catalytic subunit alpha-2	135	1646	0.293	0.177	<i>Pongo abelii</i>	UNIPROTKB Q5RD00
comp6931_c0_seq1	3892	Alpha-N-acetylglucosaminidase	3549	1936	0.012	1.474	<i>Homo sapiens</i>	UNIPROTKB P54802
comp6931_c0_seq2	3710	Alpha-N-acetylglucosaminidase	3255	1936	0.13	3.121	<i>Homo sapiens</i>	UNIPROTKB P54802
comp48442_c0_seq1	219	AT5G63860	2	193	0.083	0.462	<i>rabidopsis thaliana</i>	TAIR locus:2163986
comp1846_c0_seq1	6297	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	352	3969	0.378	6.492	<i>Rattus norvegicus</i>	RGD 619951
comp1846_c0_seq10	2755	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	54	1505	0.055	2.461	<i>Rattus norvegicus</i>	RGD 619951
comp1846_c0_seq11	2300	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	733	1050	0.144	0.265	<i>Rattus norvegicus</i>	RGD 619951
comp1846_c0_seq12	1899	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	137	649	0.472	5.6	<i>Rattus norvegicus</i>	RGD 619951
comp1846_c0_seq2	5387	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	352	4137	0.927	0.062	<i>Rattus norvegicus</i>	RGD 619951
comp1846_c0_seq5	3804	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	517	1476	0.097	2.804	<i>Rattus norvegicus</i>	RGD 619951
<b>comp1846_c0_seq6 (+)</b>	3665	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	54	1337	0.985	28.033	<i>Rattus norvegicus</i>	RGD 619951
comp1846_c0_seq8	2894	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	517	1644	0.048	0.848	<i>Rattus norvegicus</i>	RGD 619951
comp65830_c0_seq1	855	beta-transducin repeat containing	2	853	0.369	0.166	<i>Rattus norvegicus</i>	RGD 1359721
comp1689_c0_seq1	5472	cAMP-dependent protein kinase 1	670	1614	0.02	0.686	<i>Drosophila melanogaster</i>	FB FBgn0000273
comp1689_c0_seq2	5177	cAMP-dependent protein kinase 1	267	1319	0.006	0.926	<i>Drosophila melanogaster</i>	FB FBgn0000273
comp33327_c0_seq1	1296	cAMP-dependent protein kinase R2	1156	44	0.083	0.458	<i>Drosophila melanogaster</i>	FB FBgn0022382
comp78077_c0_seq1	983	Caveolin-1	947	459	0.197	3.621	<i>Ornithorhynchus anatinus</i>	UNIPROTKB Q07E02
comp30303_c0_seq1	535	CG2650	510	91	0.06	0.839	<i>Drosophila melanogaster</i>	FB FBgn0000092
comp1595_c0_seq13	3033	circadian trip	1616	426	0.826	0.097	<i>Drosophila melanogaster</i>	FB FBgn0260794
comp1595_c0_seq14	3021	circadian trip	1616	426	0.351	0.184	<i>Drosophila melanogaster</i>	FB FBgn0260794
comp23855_c0_seq2	445	Clock	122	33	0.096	0.574	<i>Drosophila melanogaster</i>	FB FBgn0023076
comp10496_c0_seq1	3957	clockwork orange	2893	2486	0.035	1.343	<i>Drosophila melanogaster</i>	FB FBgn0259938
comp10496_c0_seq2	3936	clockwork orange	2872	2465	0.035	0.906	<i>Drosophila melanogaster</i>	FB FBgn0259938
comp10496_c0_seq3	3242	clockwork orange	3049	2486	0.025	0.808	<i>Drosophila melanogaster</i>	FB FBgn0259938
comp10496_c0_seq4	3221	clockwork orange	3028	2465	0.029	0.789	<i>Drosophila melanogaster</i>	FB FBgn0259938

comp1618_c0_seq1	3239	Cryptochrome-1	197	1666	0.008	0.592	<i>Homo sapiens</i>	UNIPROT Q16526
comp25352_c0_seq1	1976	curled	231	1316	0.058	1.981	<i>Drosophila melanogaster</i>	FB FBgn0261808
comp25352_c0_seq2	1786	curled	83	1126	0.053	1.197	<i>Drosophila melanogaster</i>	FB FBgn0261808
comp25352_c0_seq3	1429	curled	302	769	0.065	0.817	<i>Drosophila melanogaster</i>	FB FBgn0261808
comp25352_c0_seq4	980	curled	231	854	0.842	0.066	<i>Drosophila melanogaster</i>	FB FBgn0261808
comp54873_c0_seq1	222	cycle	55	222	0.083	0.462	<i>Drosophila melanogaster</i>	FB FBgn0023094
comp1099_c0_seq1	7845	discs large 1	1033	3504	0.006	0.536	<i>Drosophila melanogaster</i>	FB FBgn0001624
comp1099_c0_seq2	7827	discs large 1	1033	3486	0.008	1.25	<i>Drosophila melanogaster</i>	FB FBgn0001624
comp21486_c0_seq1	706	discs large 1	379	134	0.512	0.154	<i>Drosophila melanogaster</i>	FB FBgn0001624
comp16468_c0_seq1	6864	Dopa decarboxylase	6738	5344	0.019	0.753	<i>Drosophila melanogaster</i>	FB FBgn0000422
comp16468_c0_seq3	3218	Dopa decarboxylase	3092	1698	0.046	0.703	<i>Drosophila melanogaster</i>	FB FBgn0000422
comp49424_c0_seq1	527	Dopamine transporter	526	14	0.104	0.446	<i>Drosophila melanogaster</i>	FB FBgn0034136
comp69404_c0_seq1	229	Dopamine transporter	21	155	0.083	0.462	<i>Drosophila melanogaster</i>	FB FBgn0034136
comp73842_c0_seq1	482	Dopamine transporter	480	4	0.178	0.223	<i>Drosophila melanogaster</i>	FB FBgn0034136
comp27457_c0_seq1	3891	Dttg protein	439	837	0.038	0.76	<i>Drosophila sp.</i>	UNIPROT P91608
comp27457_c0_seq2	3828	Dttg protein	439	915	0.038	0.822	<i>Drosophila sp.</i>	UNIPROT P91608
comp11431_c0_seq1	4284	dunce	267	2375	0.094	0.574	<i>Drosophila melanogaster</i>	FB FBgn0000479
comp11431_c0_seq2	4263	dunce	267	2354	0.066	0.528	<i>Drosophila melanogaster</i>	FB FBgn0000479
comp11431_c0_seq3	4260	dunce	267	2351	0.189	0.293	<i>Drosophila melanogaster</i>	FB FBgn0000479
comp11431_c0_seq4	4239	dunce	267	2330	0.116	0.285	<i>Drosophila melanogaster</i>	FB FBgn0000479
comp11431_c0_seq5	3575	dunce	116	1666	0.05	1.279	<i>Drosophila melanogaster</i>	FB FBgn0000479
comp11431_c0_seq6	3554	dunce	116	1645	0.027	1.438	<i>Drosophila melanogaster</i>	FB FBgn0000479
comp12887_c0_seq1	1705	dusky	1464	676	0.02	1.611	<i>Drosophila melanogaster</i>	FB FBgn0004511
comp89314_c0_seq1	408	dusky	102	365	0.12	0.405	<i>Drosophila melanogaster</i>	FB FBgn0004511
<b>comp9690_c0_seq16 (-)</b>	2331	ebony	596	2200	0.957	0.042	<i>Drosophila melanogaster</i>	FB FBgn0000527
comp9690_c0_seq22	1692	ebony	432	1061	0.151	0.256	<i>Drosophila melanogaster</i>	FB FBgn0000527
comp9690_c0_seq27	802	ebony	76	171	0.927	0.060	<i>Drosophila melanogaster</i>	FB FBgn0000527
comp9690_c0_seq6	3245	ebony	1738	3114	0.033	1.079	<i>Drosophila melanogaster</i>	FB FBgn0000527
comp9690_c0_seq8	3022	ebony	432	2891	0.036	0.449	<i>Drosophila melanogaster</i>	FB FBgn0000527
comp9690_c0_seq9	2739	ebony	1277	2608	0.155	0.345	<i>Drosophila melanogaster</i>	FB FBgn0000527
comp43073_c0_seq1	731	Ecdysone receptor	452	75	0.643	0.104	<i>Drosophila melanogaster</i>	FB FBgn0000546
comp45891_c0_seq1	264	Ecdysone receptor	263	159	0.083	0.462	<i>Drosophila melanogaster</i>	FB FBgn0000546
comp50197_c0_seq1	448	Ecdysone receptor	1	420	0.102	0.525	<i>Drosophila melanogaster</i>	FB FBgn0000546

comp59204_c0_seq1	513	F-box and WD repeat domain containing 11	7	513	0.077	0.934	<i>Rattus norvegicus</i>	RGD 1309121
comp8570_c0_seq1	3139	glass	1887	925	0.057	0.289	<i>Drosophila melanogaster</i>	FB FBgn0004618
comp11966_c0_seq1	820	Heat shock protein 83	2	820	0.029	0.774	<i>Drosophila melanogaster</i>	FB FBgn0001233
comp19340_c0_seq1	2213	jetlag	2174	1398	0.026	1.072	<i>Drosophila melanogaster</i>	FB FBgn0031652
comp83131_c0_seq1	291	KaiRIA	1	291	0.089	2.289	<i>Drosophila melanogaster</i>	FB FBgn0028422
comp4180_c0_seq3	4236	Large proline-rich protein BAG6	1313	87	0.059	0.51	<i>Ornithorhynchus anatinus</i>	UNIPROTKB A7X5R6
comp10165_c0_seq1	1259	lark	1258	575	0.059	1.76	<i>Drosophila melanogaster</i>	FB FBgn0011640
comp10165_c0_seq2	1227	lark	1226	543	0.062	2.021	<i>Drosophila melanogaster</i>	FB FBgn0011640
comp10165_c0_seq3	1185	lark	1123	575	0.143	0.377	<i>Drosophila melanogaster</i>	FB FBgn0011640
comp10165_c0_seq4	1153	lark	1091	543	0.251	0.251	<i>Drosophila melanogaster</i>	FB FBgn0011640
comp10165_c0_seq5	1095	lark	1094	498	0.154	3.774	<i>Drosophila melanogaster</i>	FB FBgn0011640
comp10165_c0_seq6	1063	lark	1062	466	0.09	1.742	<i>Drosophila melanogaster</i>	FB FBgn0011640
comp10165_c0_seq7	1021	lark	959	498	0.822	12.99	<i>Drosophila melanogaster</i>	FB FBgn0011640
comp10165_c0_seq8	989	lark	927	466	0.074	0.448	<i>Drosophila melanogaster</i>	FB FBgn0011640
comp10165_c0_seq9	335	lark	334	212	0.089	0.378	<i>Drosophila melanogaster</i>	FB FBgn0011640
comp1808_c0_seq1	1440	lark	101	688	0.008	0.853	<i>Drosophila melanogaster</i>	FB FBgn0011640
comp1808_c0_seq2	902	lark	101	301	0.024	1.298	<i>Drosophila melanogaster</i>	FB FBgn0011640
comp29701_c0_seq1	1374	lark	1112	639	0.036	0.988	<i>Drosophila melanogaster</i>	FB FBgn0011640
comp6509_c0_seq1	1127	lark	471	115	0.059	1.997	<i>Drosophila melanogaster</i>	FB FBgn0011640
comp6509_c0_seq2	959	lark	303	1	0.032	0.792	<i>Drosophila melanogaster</i>	FB FBgn0011640
comp6509_c0_seq3	747	lark	471	115	0.332	0.157	<i>Drosophila melanogaster</i>	FB FBgn0011640
comp6509_c0_seq4	579	lark	303	1	0.138	2.73	<i>Drosophila melanogaster</i>	FB FBgn0011640
comp3068_c0_seq1	3907	minibrain	1730	2935	0.323	0.18	<i>Drosophila melanogaster</i>	FB FBgn0259168
comp3068_c0_seq2	3864	minibrain	1730	2935	0.051	0.895	<i>Drosophila melanogaster</i>	FB FBgn0259168
comp5354_c0_seq1	3603	Myocyte enhancer factor 2	71	1216	0.024	0.794	<i>Drosophila melanogaster</i>	FB FBgn0011656
comp5354_c0_seq2	3591	Myocyte enhancer factor 2	71	1237	0.011	0.866	<i>Drosophila melanogaster</i>	FB FBgn0011656
comp34215_c0_seq1	967	narrow abdomen	2	484	0.073	0.591	<i>Drosophila melanogaster</i>	FB FBgn0002917
comp66820_c0_seq1	451	narrow abdomen	451	2	0.307	0.147	<i>Drosophila melanogaster</i>	FB FBgn0002917
comp85336_c0_seq1	285	narrow abdomen	37	285	0.125	0.301	<i>Drosophila melanogaster</i>	FB FBgn0002917
comp96661_c0_seq1	223	narrow abdomen	221	3	0.083	0.462	<i>Drosophila melanogaster</i>	FB FBgn0002917
comp97497_c0_seq1	329	narrow abdomen	2	328	0.083	0.462	<i>Drosophila melanogaster</i>	FB FBgn0002917
comp8495_c0_seq1	8857	Neurofibromin 1	65	7399	0.079	0.587	<i>Drosophila melanogaster</i>	FB FBgn0015269
comp8495_c0_seq2	8845	Neurofibromin 1	65	7387	0.046	0.721	<i>Drosophila melanogaster</i>	FB FBgn0015269



comp8495_c0_seq3	8686	Neurofibromin 1	65	7399	0.046	0.48	<i>Drosophila melanogaster</i>	FB FBgn0015269
comp8495_c0_seq4	8674	Neurofibromin 1	65	7387	0.02	0.616	<i>Drosophila melanogaster</i>	FB FBgn0015269
<b>Comp841_c0_seq1 (-)</b>	4029	no receptor potential A	474	3737	0.973	0.036	<i>Drosophila melanogaster</i>	FB FBgn0262738
comp8804_c0_seq1	2651	numb	281	1441	0.076	1.612	<i>Drosophila melanogaster</i>	FB FBgn0002973
comp8804_c0_seq2	2614	numb	244	1404	0.058	1.576	<i>Drosophila melanogaster</i>	FB FBgn0002973
comp8804_c0_seq3	2585	numb	281	1375	0.052	0.555	<i>Drosophila melanogaster</i>	FB FBgn0002973
comp8804_c0_seq4	2573	numb	203	1363	0.103	1.857	<i>Drosophila melanogaster</i>	FB FBgn0002973
comp8804_c0_seq5	2548	numb	244	1338	0.031	0.658	<i>Drosophila melanogaster</i>	FB FBgn0002973
comp8804_c0_seq6	2507	numb	203	1297	0.072	0.674	<i>Drosophila melanogaster</i>	FB FBgn0002973
comp2789_c0_seq1	4961	period	4220	2901	0.032	0.384	<i>Drosophila melanogaster</i>	FB FBgn0003068
comp24010_c0_seq1	1436	Pigment-dispersing factor receptor	81	1259	0.034	0.838	<i>Drosophila melanogaster</i>	FB FBgn0260753
comp33631_c0_seq1	4066	Pigment-dispersing factor receptor	722	2005	0.038	0.554	<i>Drosophila melanogaster</i>	FB FBgn0260753
comp2319_c0_seq1	621	Prokineticin-2	425	177	0.661	7.021	<i>Bos taurus</i>	UNIPROTKB Q863H5
comp2319_c0_seq2	578	Prokineticin-2	382	134	0.085	3.765	<i>Bos taurus</i>	UNIPROTKB Q863H5
comp17940_c0_seq1	1678	Protein lin-52 homolog	315	551	0.745	0.107	<i>Oncorhynchus mykiss</i>	UNIPROTKB Q6X4M3
comp17940_c0_seq2	1573	Protein lin-52 homolog	105	446	0.037	1.177	<i>Oncorhynchus mykiss</i>	UNIPROTKB Q6X4M3
comp17014_c0_seq1	700	Protein quiver	274	576	0.241	0.271	<i>Drosophila mojavensis</i>	UNIPROTKB B4KR21
comp17014_c0_seq2	492	Protein quiver	277	492	0.109	0.317	<i>Drosophila mojavensis</i>	UNIPROTKB B4KR21
comp43724_c0_seq1	2037	Protein timeless homolog	1732	161	0.043	1.556	<i>Homo sapiens</i>	UNIPROTKB Q9UNS1
comp10628_c0_seq1	2883	quasimodo	459	1292	0.03	2.77	<i>Drosophila melanogaster</i>	FB FBgn0028622
comp62503_c0_seq1	366	Rhythmically expressed gene 5	226	336	0.176	3.444	<i>Drosophila melanogaster</i>	FB FBgn0015801
comp54599_c0_seq1	573	RNA-binding protein 4B	572	279	0.086	0.58	<i>Sus scrofa</i>	UNIPROTKB F1RUT7
comp573_c0_seq1	3368	RNA-binding protein 4B	129	371	0.015	1.059	<i>Sus scrofa</i>	UNIPROTKB F1RUT7
comp573_c0_seq2	3044	RNA-binding protein 4B	129	371	0.011	1.192	<i>Sus scrofa</i>	UNIPROTKB F1RUT7
comp573_c0_seq3	2925	RNA-binding protein 4B	129	371	0.012	1.752	<i>Sus scrofa</i>	UNIPROTKB F1RUT7
comp573_c0_seq4	2601	RNA-binding protein 4B	129	371	0.007	1.118	<i>Sus scrofa</i>	UNIPROTKB F1RUT7
comp24954_c0_seq1	3152	roundabout	362	2737	0.05	1.021	<i>Drosophila melanogaster</i>	FB FBgn0005631
comp24954_c0_seq2	3134	roundabout	362	2764	0.046	1.53	<i>Drosophila melanogaster</i>	FB FBgn0005631
comp24954_c0_seq3	2854	roundabout	46	2439	0.336	0.226	<i>Drosophila melanogaster</i>	FB FBgn0005631
comp24954_c0_seq4	2836	roundabout	46	2466	0.077	0.531	<i>Drosophila melanogaster</i>	FB FBgn0005631
comp26721_c0_seq1	7012	roundabout	442	2991	0.018	1.442	<i>Drosophila melanogaster</i>	FB FBgn0005631
comp26721_c0_seq2	5448	roundabout	3	1445	0.060	2.015	<i>Drosophila melanogaster</i>	FB FBgn0005631
comp45935_c0_seq1	1373	roundabout	1362	130	0.214	0.266	<i>Drosophila melanogaster</i>	FB FBgn0005631

comp60778_c0_seq1	488	roundabout	2	394	0.116	0.449	<i>Drosophila melanogaster</i>	FB FBgn0005631
comp67560_c0_seq1	506	roundabout	340	486	0.636	0.079	<i>Drosophila melanogaster</i>	FB FBgn0005631
comp45706_c0_seq1	482	Serotonin receptor 1A	3	386	0.687	0.073	<i>Drosophila melanogaster</i>	FB FBgn0004168
comp90243_c0_seq1	327	Serotonin receptor 1A	325	86	0.089	2.289	<i>Drosophila melanogaster</i>	FB FBgn0004168
comp96775_c0_seq1	235	Shaker	234	1	0.083	0.462	<i>Drosophila melanogaster</i>	FB FBgn0003380
comp19976_c0_seq1	1351	slowpoke	1053	910	0.808	0.096	<i>Drosophila melanogaster</i>	FB FBgn0003429
comp29144_c0_seq1	219	slowpoke	218	87	0.089	1.655	<i>Drosophila melanogaster</i>	FB FBgn0003429
comp62466_c0_seq1	411	slowpoke	275	409	0.125	0.301	<i>Drosophila melanogaster</i>	FB FBgn0003429
comp4789_c0_seq1	2620	timeless	2545	1181	0.16	0.243	<i>Drosophila melanogaster</i>	FB FBgn0014396
comp4789_c0_seq2	2526	timeless	2451	1087	0.322	0.169	<i>Drosophila melanogaster</i>	FB FBgn0014396
comp6413_c0_seq1	2451	timeless	1551	196	0.489	0.13	<i>Drosophila melanogaster</i>	FB FBgn0014396
<b>comp6413_c0_seq2 (-)</b>	1966	timeless	1551	196	0.997	0.019	<i>Drosophila melanogaster</i>	FB FBgn0014396
comp39652_c0_seq1	1137	TIMELESS (Uncharacterized protein)	1135	458	0.042	0.959	<i>Sus scrofa</i>	UNIPROTKB F1SLB6
comp67299_c0_seq1	309	timeout	42	260	0.083	0.462	<i>Drosophila melanogaster</i>	FB FBgn0038118
comp7837_c0_seq1	1531	vrille	470	832	0.012	0.945	<i>Drosophila melanogaster</i>	FB FBgn0016076

---

**S1 Text. Table D. List of representative transcripts that showed the highest levels of abundance during photophase and scotophase.** Transcripts were ordered by rank, together with the information related to their annotation (symbol of the hit, species, Go function and access number of the hit). PPDE (Posterior Probability of Differential Expression) represents the posterior probability of differential expression. post FC (L/D) represents the fold change of transcripts abundance between photophase/scotophase.

Rank	Transcript	PPDE	Post FC (L/D)	Symbol	Species	GO Function	Access number
<b>PHOTOPHASE</b>							
1	comp188_c2_seq4	1.000000000	6.48E+03	---	---	---	no hit
2	comp2506_c0_seq2	1.000000000	4.55E+03	CG42327	<i>Drosophila melanogaster</i>	protein tyrosine phosphatase activity	FB FBgn0259227
3	comp415_c0_seq7	1.000000000	3.69E+03	---	<i>Sus scrofa</i>	tight junction evidence	UNIPROTKB F1SMP5
4	comp968_c1_seq4	1.000000000	2.72E+03	capulet	<i>Drosophila melanogaster</i>	adenylate cyclase binding evidence	FB FBgn0261458
5	comp1479_c0_seq10	1.000000000	2.15E+03	---	---	---	no hit
6	comp3626_c0_seq8	0.999999999	1.32E+03	---	---	---	no hit
<b>SCOTOPHASE</b>							
1	comp310_c0_seq2	1.000000000	1.20E-04	---	---	---	no hit
2	comp1372_c1_seq3	1.000000000	1.99E-04	bent	<i>Drosophila melanogaster</i>	structural constituent of cytoskeleton	FB FBgn0005666
3	comp439_c0_seq2	1.000000000	2.22E-04	---	---	---	no hit
4	comp259_c0_seq13	1.000000000	2.31E-04	mhc	<i>Drosophila melanogaster</i>	striated muscle contraction	FB FBgn0086783
5	comp1307_c0_seq2	1.000000000	2.86E-04	MSF3	<i>Drosophila melanogaster</i>	high affinity inorganic phosphate	FB FBgn0031307
6	comp1154_c0_seq2	1.000000000	2.98E-04	---	---	---	no hit
7	comp802_c0_seq2	1.000000000	3.30E-04	Beta-carotene dioxygenase 1	<i>Gallus gallus</i>	retinoid metabolic process	UNIPROTKB Q91993
8	comp712_c4_seq4	1.000000000	3.31E-04	---	---	---	no hit
9	comp1364_c1_seq2	0.999999999	3.95E-04	cdk16	<i>Danio rerio</i>	transferring phosphorus-containing groups	ZFIN ZDB-GENE-030131-2939
10	comp676_c0_seq2	0.999999999	4.06E-04	FK506-binding protein 2	<i>Drosophila melanogaster</i>	FK506 binding evidence	FB FBgn0013954
11	comp1372_c1_seq1	0.999999998	4.83E-04	bent	<i>Drosophila melanogaster</i>	structural constituent of cytoskeleton	FB FBgn0005666
12	comp2261_c0_seq2	0.999999998	5.10E-04	---	---	---	no hit
13	comp157_c0_seq4	0.999999998	5.23E-04	Rrh	<i>Mus musculus</i>	retinal pigment epithelium rhodopsin homolog	MGI MGI:1097709
14	comp2004_c0_seq4	0.999999997	5.60E-04	CG6296	<i>Drosophila melanogaster</i>	triglyceride lipase activity	FB FBgn0039470
15	comp259_c0_seq19	0.999999997	5.62E-04	myosin heavy chain	<i>Drosophila melanogaster</i>	striated muscle contraction	FB FBgn0086783

S1 Text. Table E. Blastx of the contig annotated to *cryptochrome*

Genes	Species	Phylum - Class -Order	Definition	Identity	Gaps	Accession
	<i>Euphausia superba</i>	Arthropoda - Malacostraca - Euphasiacea	cryptochrome	441/539	3/539	CAQ86665
<i>cryptochrome</i>	<i>Eurydice pulchra</i>	Arthropoda - Malacostraca - Isopoda	cryptochrome 2	421/541	4/541	AGV28717
	<i>Talitrus saltator</i>	Arthropoda - Malacostraca - Amphipoda	cryptochrome 2	396/499	0/499	AFV96168

**S1 Text. Table F. Conserved domains of canonical clock genes in *Nephrops norvegicus***

<b>Protein</b>	<b>Conserved domain</b>	<b>Position (aa)</b>	<b>Aminoacid sequence</b>
	PAS domain	229-296	AAFLLKSFKSTRGFTVAISVQDGTVLQVSPAITDVLGFPKDMMLIGQSFIDFVYPKDSINLSSKIIHGLN
PERIOD	PAS domain	373-442	ESITYVPEETPAMGFSFIRHSASCNFSEYDPEAIPYLGHL PQDLTGNSVFD CYHXEDLPLLKAVYEGMVR
	PAC motif	450-493	SKPYRFRTFNNGSYVTLQTEWLFCVNPWTKRIDSIIIGQHRVLKGP
BMAL1	bHLH	41-74	SEIEKRRRDKMNTYIMELSSIIPVCTSRKLDKLT