Circatidal control of gene expression in the deep-sea hot vent shrimp *Rimicaris leurokolos*

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Abstract

Biological clocks are a ubiquitous feature of all life, enabling the use of natural environmental cycles to track time. Although studies on circadian rhythms have contributed greatly to the knowledge of chronobiology, biological rhythms in dark biospheres such as the deep sea remain poorly understood. Lacking day-night cycles, the deep sea allows organisms to adapt to other temporal effects such as geophysical cycles, which remain unknown. Here, based on a laboratory free-running experiment, we reveal potentially endogenous rhythms in gene expression of the deep-sea hydrothermal vent shrimp *Rimicaris leurokolos*. Oscillations with ~12-hour periods, likely reflecting tidal influence, greatly prevail over others in the temporal transcriptome. The tidal transcripts exhibit an antiphased expression pattern divided into two internally synchronized clusters, correlated with wide-ranging biological processes that occur in the nucleus and cytoplasm, respectively. Exhibiting robust tidal transcriptional expression but relatively weak rhythmicity in circadian clock genes, *R. leurokolos* likely depends on a circatidal clock consisting of at least some components independent of the circadian clocks. In addition, comparing the tidal transcripts with the ~12-hour ultradian rhythms genes in fruit fly and mouse shows large similarity, indicating the likely scenario of broad impact of tide on the ~12-hour oscillations across the metazoan. These findings not only provide new insights into the temporal adaptations in deep-sea organisms but also highlight deep-sea hydrothermal vent organisms as intriguing models for chronobiological, particularly 12-hour ultradian rhythms, studies.

Introduction

As an adaptation to natural periodic environmental changes, biological clocks have been evolving in all kingdoms of life to keep track of time[1-3]. Numerous organisms anticipate daily changes including light, temperature, and food availability, resulting in persistent rhythms dominated by circadian periodicity of ~24 hours at behavioral, physiological, and molecular levels[4-6]. To achieve this, animals rely on their internal circadian clock systems like transcription-translation feedback loops (TTFLs) that can be entrained to match the environmental cycles[7]. In dark biospheres such as the underground and deep-sea habitats, however, the absence of sunlight veils organisms there from the direct effects of everlasting day-night transitions. How organisms living in the dark schedule their activities through time, as an adaptation to darkness, remains obscure[8, 9].

The deep ocean, the largest but the least studied habitat on Earth[10], is of great interest for chronobiology research due to its distinct ecological environment[11]. With increasing depth the intensity, spectral composition, and degree of polarization of sunlight decrease dramatically, and are eventually absorbed and scattered completely at approximately 1000 m[12]. From the ecological perspective, it is more appropriate for deep-sea organisms to synchronize their biological rhythms with other zeitgebers (e.g., geophysical cycles) instead of the light cycle[11, 13]. Indeed, various environmental fluctuations related to tidal cycles have been observed in the deep, especially in hydrothermal vent ecosystems[14-17]. Vent faunas rely strongly on their local environment, and survive on organic compounds produced by chemosynthetic microbes through chemosynthesis utilizing dissolved chemicals in the vent fluids[18]. Therefore, vent animals are likely to be affected by spatial and temporal variations in environmental factors modulated by tides. Several previous studies have reported potential tide-related rhythms of behavior and community dynamics in deep-sea organisms from chemosynthetic ecosystems[13, 19-21], and a recent study revealed tidal cycles dominated the gene expression of the deep-sea vent mussel *Bathymodiolus azoricus* through periodic *in situ* sampling across 24.8 hours[22]. Although these evidences suggest that vent organisms exhibit biological rhythms in the wild, whether they need endogenous rhythms or clocks to accommodate and anticipate local environmental changes to maximize their fitness is still poorly understood.

In the Iheya North hydrothermal vent field of the Okinawa Trough (126°53.80’E, 27°47.45’N; 982m depth), the alvinocaridid shrimp *Rimicaris leurokolos* (formerly *Shinkaicaris leurokolos*[23]) lives in close proximity to the vigorously venting orifice

(0.2–0.8 m and occasionally less than 0.2 m from the vent[24]) where the hot plume and cold surrounding seawater mix spontaneously and dramatically[25] (Fig. 1a, b). This differs from bathymodioline mussels that inhabit more peripheral areas of vent fields (0.8–2.5 m and mostly greater than 2.5 m from the vent orifice[24]). In the central areas where *R. leurokolos* occurs, however, environmental factors fluctuate frequently at the seconds-minutes scale due to the vigorous mixing between hot vent fluid and cold surrounding seawater, possibly masking any detectable tidal effects in terms of temperature and chemistry. Considering the trade-off between tolerance and escape response[26-28], perhaps an internal clock could help *R. leurokolos* respond to occasional events[29] (e.g., temperature anomalies). Therefore, we hypothesised that *R. leurokolos* could schedule its activities either by direct response to environmental changes or by an endogenous clock.

The 24-hour circadian rhythms are important for the temporal adaptations to the day-night cycles in terrestrial and shallow-water animals. Although circadian patterns are dominant in terrestrial animals, recent studies revealed robust ultradian rhythms such as ~12-hour cycling gene expression[30-33]. These rhythms were found cell autonomous, driven by a 12-hour pacemaker independent from the circadian clock. As many homologous genes were found rhythmic with a period of ~12 hours both in terrestrial and marine animals, a hypothesis was then proposed that the circatidal rhythms in marine animals and ~12-hour rhythms in terrestrial animals are evolutionarily conserved. However, for the shallow-water or terrestrial species, the ~12-hour rhythms are likely becoming indistinguishable under the mixture of the ~24-hour circadian rhythms[34]. It is better to examine the ~12-hour rhythms in a system that is lacking of day-night cycles.

Here, through a laboratory free-running experiment across 72 hours, we addressed the biological rhythms of gene expression in the vent shrimp *R. leurokolos* and tested if it can maintain rhythmicity under constant conditions. Our work reveals free-running rhythms dominated by 12-hour tidal patterns in the transcriptome of *R. leurokolos*, which are likely driven by an unidentified endogenous clock including but not limited to circatidal components. The possible zeitgebers are constrained, excluding light, temperature, and fluid chemistry. By comparing the tidal rhythms, we found that the tidal rhythmicity is seemingly stronger in *R. leurokolos* than in *B. azoricus*, a mussel living relatively distant from the vent. In addition, *R. leurokolos* shares many common genes and biological processes in the tidal rhythms with the ~12-hour rhythms in sea

anemones, fruit flies, and mammals, suggesting the evolutionary conservation of ~12-hour gene expression across a broad range of phyla.

Results and discussion

Transcriptome analysis of deep-sea vent shrimp *R. leurokolos*

We reanalysed a published long-term temperature measurement (Mean ± SD = 4.4 ± 0.1□) recorded at the periphery of the Iheya North vent field where bathymodioline mussels typically occur[35], and found a steady semidiurnal tidal cycle with a periodicity of 12.4 hours (Fig. 1c). Despite that, the periodic cues might be weakened or disrupted near the vent chimney where *R. leurokolos* shrimps inhabit. In fact, the temperature measured in the *R. leurokolos* colony rapidly fluctuated between 7.63 to 17.74°C in approximately 2.5 minutes (Mean ± SD = 10.16 ± 1.71°C), and other environmental factors co-vary in the same period[36] (Fig. 1d, Supplementary Data 1). The seconds-minutes scale fluctuations likely mask any detectable periodic signals such as tidal cycles, making it hard for *R. leurokolos* to predict the local environmental changes. Nevertheless, reproduction in *Rimicaris* shrimps showed periodic patterns and was found unlinked to seasonal variations in surface production[37], suggesting the presence of potential temporal adaptations in the deep-sea organisms such as an endogenous biological clock.

To study the potential endogenous rhythms in *R. leurokolos*, we carried out a free-running experiment under constant conditions (totally darkness and 4□) across 72 hours and assembled a *de novo* transcriptome using a total of 57 shrimps sampled at 4-hour intervals. We worked on the whole cephalothorax due to the uncertainty of localization of the central clock in crustaceans[38]. Although temporal gene expression could vary in different tissues, the cephalothorax transcriptome supported us in detecting rhythmicity within the overall gene expression. The reference *de novo* transcriptome comprised 313,108 contigs with an N50 of 720 bases and contained 90,755 predicted open reading frames (ORFs), which showed 92% completeness (S:83.8%, D:8.2%) with the BUSCO score. Candidate protein-coding transcripts with low expression were filtered out, leaving 23,905 transcripts with a 60.4% annotation rate for rhythmic analyses. A principal components analysis (PCA) of normalized gene expression showed a rough trend from the start of sampling (0 hours) to the end (72 hours, Supplementary Fig. 1a). Performing the Mann-Kendall trend test on the raw dataset, we found that 10,273 transcripts (i.e., 42.97% of the transcriptome) had a significant monotonic trend (P-value < 0.05). The trend was then removed using CEEMDAN[39] to produce a steady baseline and enhance the strength of rhythm detection methods[40]

(Supplementary Fig. 1b). In the PCA results plotted using detrended gene expression, the trend disappeared and sample points from different sampling times clustered together (Fig. 1e), indicating a minimal external effect on the experiment as the shrimps were seemingly experiencing the same conditions.

General biological rhythms in the temporal transcriptome of *R. leurokolos*

We first used the eigenvalue/pencil[30] and ECHO[41] algorithms to carry out unbiased identification of any potential periodic oscillations in the gene expression of *R. leurokolos*. The results uncovered similar rhythmicity that most cycling transcripts were identified as ultradian rhythms, which oscillated in the tidal range of 10-14 hours, while much fewer cycling transcripts oscillated in the daily range of 22-26 hours (Fig. 2a). The eigenvalue/pencil algorithm was able to identify superimposed oscillations from one cycling transcript. For cycling transcripts with multiple components composed of tidal and daily oscillations, the amplitude of the tidal component is significantly larger (Fig. 2b), suggesting a stronger rhythmicity. Despite the high sensitivity of detecting weak ultradian rhythms, the eigenvalue/pencil method could have high positive false rates[31]. To validate the results, we then detected cycling transcripts with two robust nonparametric algorithms, RAIN[42] and empirical JTK_CYCLE[43] (eJTK). Searching for cycling transcripts (FDR < 0.05) with periods in the range of 8-28 hours at regular intervals of 4 hours, we found the number of rhythmic transcripts identified by RAIN and eJTK both reached a peak at the 12-hour period that corresponded to a tidal cycle (Supplementary Fig. 2a). Interestingly, ECHO shared many common cycling transcripts with RAIN (60.8% of transcripts) and eJTK (65.8% of transcripts) but detected numerous extra tidal transcripts, likely due to the inclusiveness of identifying different harmonics of oscillating elements[44]. Combining the results of these three methods, we identified a total of 8,122 rhythmic transcripts (33.98% of the transcriptome) in the tidal range (Fig. 2c), versus 1,230 rhythmic transcripts (5.15% of the transcriptome) in the daily range (Fig. 2d). The list of rhythmic transcripts is provided in Supplementary Data 2.

Notably, there was an overlap of 600 rhythmic transcripts between the tidal oscillated group and the daily oscillated group (Supplementary Fig. 2b). Ostensibly, 24-hour daily patterns could not only reflect circadian effects but also generate in parallel with mixed semidiurnal tidal cycles (see Supplementary Fig. 2c), diurnal tidal cycles, and inertial oscillations (about 26.4-hour period at the sampling latitude). Here, influences of the latter two can be excluded according to the Lomb-Scargle periodogram analysis

performed before (Fig. 1c). Nearly 60% of the overlapped transcripts obtained lower adjusted *P*-values when identified as tidal oscillations rather than daily oscillations, reflecting higher statistical significance in the tidal component (Supplementary Fig. 2d). Furthermore, we calculated the root mean square (RMS) amplitude of tidal and daily components and the result showed that most transcripts had larger amplitude in tidal oscillations, indicating the tidal cycles contribute more biologically relevant effects to the overlapping rhythmic transcripts (Supplementary Fig. 2e). This was in line with the comparison of RMS amplitude between rhythmic transcripts in the tidal and daily range (Fig. 2e). Therefore, in the temporal transcriptome of *R. leurokolos*, the proportion of rhythmic transcripts dominated by approximately 24-hour daily cycles is considerably less than the value obtained statistically, and the former is likely close to the proportion (2.6% of the transcriptome) reported in the previous study on deep-sea vent mussels[22].

These results demonstrate sustainable endogenous rhythmic gene expression in *R. leurokolos* under constant conditions. The temporal transcriptome is dominated by the approximately 12-hour tidal rhythms, which greatly prevail over other oscillations with different periods, especially the 24-hour daily transcripts that are likely unrelated to the circadian rhythms.

Patterns of tidal gene expression in *R. leurokolos*

To uncover the biological rhythms ticking in the deep, we then focused on the dominant tidal rhythms in the temporal transcriptome of *R. leurokolos*. Our 72-hour duration of sampling covered approximately six tidal cycles, allowing us to test the stability and robustness of rhythmicity in the tidal gene expression[45]. To capture the amplitude changes over time, we fitted the gene expression to an extended fixed-amplitude model using ECHO[41] and categorized the results into different oscillation types based on the value of the amplitude change coefficient (see Materials and methods for details). For convenience of analysis, we concentrated on the tidal transcripts identified by the ECHO algorithm (Benjamini-Hochberg corrected *P*-values < 0.05). The analysis revealed five types of oscillation groups, of which two (overexpressed type and repressed type) were considered arrhythmic due to the sharp increase or decrease in amplitude, respectively. For the rest of the tidal rhythmic transcripts, the harmonic group with stable amplitudes comprised 23.57% (n = 1,499 of 6,361) of transcripts and the forced group with amplified amplitudes comprised 24.65% (n = 1,568 of 6,361) of transcripts, whereas 51.78% (n = 3,294 of 6,361) of transcripts with reduced amplitudes were included in the damped group (Fig. 3a).

Although there was a significantly amplified or reduced amplitude in at least 75% of tidal rhythmic transcripts, the period and phase of most tidal cycles were seemingly fixed. Interestingly, the whole tidal transcriptome exhibited an antiphased expression pattern with many transcripts reaching the peak at the same time. We then divided the tidal transcriptome into two clusters by gene expression using K-Means clustering (Supplementary Fig. 3a, b). Clusters 1 and 2 showed a generally antithetical gene expression pattern over time, and the phases were almost complementary in the tidal cycle (Fig. 3b, c). This bimodal expression pattern is widely observed in the circadian rhythms of terrestrial organisms that experience transcriptional 'rush hours' preceding dawn and dusk, which is considered to assist in making preparations for the impending change in lighting[5, 6, 46]. Likewise, *R. leurokolos* could schedule its peak of tidal gene expression around high tide and low tide to provide intrinsic fitness, as observed in other marine organisms[47-49].

The rhythmicity of 3,837 transcripts in cluster 1 was relatively stable with almost equivalent amounts of modest forced, harmonic, and damped oscillations, whereas the 2,524 transcripts in cluster 2 were nearly occupied by damped oscillations that decreased obviously in amplitude, particularly during the second half of experiment (Fig. 3c). Indeed, there was seemingly a strong correlation between trend directions and oscillation types (Supplementary Fig. 3c). In other words, a tidal transcript with a decreasing expression trend was more likely to have a reduced amplitude, and vice versa. This likelihood was extremely high in cluster 2 where over 94% of tidal transcripts with a downward trend were also damped. Since we isolated *R. leurokolos* shrimps from the hydrothermal vent and cultivated them in the lab under constant conditions for 72 hours, there were unsurprisingly considerable changes in the gene expression over time corresponding to transcriptional responses to potential stresses such as decompression. Therefore, the amplitude likely decreases as a byproduct of declining gene expression levels, especially for most transcripts in cluster 2. Although desynchronization between different tissues of *R. leurokolos* could lead to arrhythmic gene expression in our free-running study, we still detected a considerable number of rhythmic transcripts with highly synchronized expression, suggesting the effect of desynchronization was likely not significant.

Wide range of biological processes related to tidal cycles in *R. leurokolos*

The tidal rhythmic transcripts could be categorized by gene expression, oscillation types,

and original trends, all of which included several subgroups that likely reflected similar or different biological relevance. To search for potential biological functions modulated by tidal rhythms, we performed functional enrichment analyses over the tidal transcriptome based on these three classification schemes using clusterProfiler[50]. Gene ontology (GO) and KEGG pathway analyses revealed that tidal rhythms generally affected various biological processes such as DNA repair, regulation of transcription, translation, transport, organelle organization, and citrate cycle (Fig 3d, Supplementary Fig. 4). There was an expected high correlation between the biological functions of classified subgroups. For example, terms enriched in cluster 2 were more or less the same as those in the damped or downward subgroup. Notably, rhythmic processes related to the nucleus such as chromatin organization, DNA biosynthetic process, and transcription were uniquely enriched in cluster 1; whereas rhythmic processes supported by the cytoplasm such as translation, protein folding, vesicle-mediated transport, and oxidative phosphorylation were highly enriched in cluster 2. Thus, it is likely that *R. leurokolos* shrimps can organize various rhythmic biological processes in terms of spatial and temporal expression patterns to coordinate their internal physiology, regardless of the presence of clear zeitgebers.

In hydrothermal vents, particularly near the fluid orifice where *R. leurokolos* inhabits, hot, anoxic fluids with abundant potentially toxic chemical substances (e.g., hydrogen sulfide) mix dramatically with the cold surrounding seawater, resulting in an extreme and variable environment. Vent organisms have evolved various adaptive strategies at morphological, physiological, and biochemical levels[18]. We hypothesized that intrinsic rhythms could help vent animals schedule their activities to cope with the harsh environment, and as expected, we found many transcripts related to various cellular stress response processes were tidally oscillated. These tidal oscillations include sulfide:quinone oxidoreductase (SQR), 3-mercaptopyruvate sulfurtransferase (3-MST) and sulfotransferases (SULTs) genes that play a key role in sulfur metabolism[51] (Fig. 4a), together with catalase (CAT), superoxide dismutase (SOD), glutathione S-transferase (GST), glutathione peroxidase (GPx), and several enzymes from the Cytochrome P450 family, which are involved in the reactive oxygen species (ROS) homeostasis and cellular detoxification[52, 53] (Fig. 4b). In addition, tidal genes influence other cellular processes such as heat and hypoxia response (Fig. 4c), including heat shock proteins (HSPs), hypoxia up-regulated protein 1 (HYOU1), hypoxia-inducible factor 1-alpha inhibitor (FIH-1), egl nine homolog 1 (EGLN1). Most of these transcripts showed damped rhythmic expression over time under constant conditions, suggesting

that *in situ* environmental cues were necessary for the maintenance and synchronization of rhythmic processes related to stress responses. In contrast, most tidal genes involved in the innate immune response of decapods, such as cathepsin L, relish, akirin 2, prophenoloxidase-activating factor (PPAFs), and a homolog of *Rimicaris exculata* C-type lectin 1, showed steady or amplified expression over time[54, 55] (Fig. 4d). The results reveal broad tidal regulation of gene expression in the cellular response to various environmental stresses, suggesting an adaptive advantage for *R. leurokolos* living in harsh, fluctuating environments.

Mounting evidence suggests the presence of cross-talking between circadian clocks and the cell cycle[56, 57]. Here, we found the annotation of many tidal transcripts was related to the cell cycle. The transition between G1 and S is controlled and regulated by key genes involved in the checkpoint pathways, of which several were tidally oscillating in the transcriptome, including cyclin D2, tumor suppressor protein p53, c-Myc binding protein 2 (MYCBP2), retinoblastoma-like protein 1 (RBL1), transcription factor E2F2 and E2F5, TIMELESS-interaction protein (TIPIN), and E3 ubiquitin-protein ligase MDM2[56-59] (Supplementary Fig. 5a). In addition, major components of the RAD9-RAD1-HUS1 clamp complex that play pivotal roles in DNA repair oscillate in the tidal range[60] (Supplementary Fig. 5b). As crucial elements of the spindle assembly checkpoint (SAC), genes such as mitotic arrest deficient 2 (MAD2), serine/threonine-protein kinase BUB1 and BUB3 that regulate chromosome separation were also found to be tidally cycling[61] (Supplementary Fig. 5c). Taken together, tidal rhythms appear to generally regulate the progression of the cell cycle in *R. leurokolos* to cope with DNA damage derived from periodic intrinsic and environmental stresses.

Possible molecular basis and zeitgebers of biological rhythms in *R. leurokolos*

We reveal broad rhythmic gene expression of *R. leurokolos* under constant conditions, and many of the oscillations show a high stability of rhythmicity over several cycles, indicating the possible presence of endogenous oscillators that govern the dominant tidal rhythms in *R. leurokolos*. Based on circatidal locomotor and gene expression rhythms observed in various coastal and marine animals, two much-debated major hypotheses have been proposed to explain the molecular mechanisms underlying circatidal rhythms[62]. Generally, the circatidal rhythms could rely on either (a) an independent circatidal oscillator (a unimodal 12.4-hour clock[63] or two coupled unimodal antiphase 24.8-hour clocks[64]) that are not associated with the circadian clock or (b) a single bimodal clock that could transform rhythms between circatidal and circadian

patterns depending on the dominant zeitgeber[65].

We searched for and identified *R. leurokolos* homologs of the canonical circadian clock genes that form the molecular oscillator in the fruitfly *Drosophila melanogaster*, including Clock, Period (PER), Timeless (TIM), Cryptochrome (CRY), Clockwork orange (CWO), Double-time (DBT, also known as casein kinase 1ε), Vrille (VRI), and PDP1ε[7] (Supplementary Fig. 6a-d, Supplementary Data 3). These well-conserved core clock components form a negative feedback loop containing transcriptional repressors Period and Timeless and transcriptional activators Clock and Bmal/Cycle. However, no Bmal/Cycle transcript was identified in *R. leurokolos* and the Clock transcript exhibited extremely low expression that rendered it unfeasible for rhythm analysis. Indeed, all *R. leurokolos* clock gene homologs lacked obvious 24-hour rhythmicity (Fig. 5a-g). Although there was a possibility that some clock genes oscillated in certain tissues, and were detected as disorganized because of the desynchronization of expression from multiple tissues, we found a relatively low number of 24-hour oscillated transcripts in the temporal transcriptome of *R. leurokolos*. This may provide intrinsic fitness for these hydrothermal vent shrimps that are likely completely isolated from the surface as adults[37]. Moreover, most clock genes showed a lack of rhythmicity in the tidal range as well. Although the transcriptional repressor Period and Double-time, a kinase that phosphorylates the period protein[66], were statistically oscillated in the tidal range, the Period transcript showed an opposite expression with the Timeless transcript in the second half of the free-running experiment (Fig. 5a, b), which was abnormal for the circadian clock regulated by the TTFL mechanism. Since a robust endogenous clock is required to be free-running with a self-sustained period for maintaining the rhythmicity of tidal oscillations in *R. leurokolos*, we hypothesize that there is a circatidal clock with at least part of independent molecular components from the circadian clocks. Separate circadian and circatidal clocks were also reported in the intertidal isopod *Eurydice pulchra*[67] and mangrove cricket *Apteronemobius asahinai*[68]. Nevertheless, the core clock genes still encode functional proteins with conserved domains (Supplementary Fig. 6e), and we cannot exclude the possibility that some core circadian clock genes are necessary for tidal rhythms[69, 70], even though they lose free-running transcription rhythmicity. These circadian clock genes may also be useful during the larval dispersal stage of the shrimp, which may take place in the photic zone[71].

Although *R. leurokolos* shrimps likely generate tidal rhythms using an endogenous circatidal clock, it is still difficult to understand and test how they synchronized their

intrinsic rhythms given the highly variable environmental factors in their habitat. Temperature is likely not an appropriate zeitgeber due to the dramatic fluctuation with frequency at the seconds-minutes scale, which tends to disturb the entrainment cycles. Moreover, the molecular heat stress response was observed to be rarely mobilized in the natural populations of alvinocaridid shrimps[28]. They choose to live in the thermal preferendum (10 to 25°C) most of the time and at the molecular level, are likely not sensitive to natural temperature changes[26]. As a phenotypic adaptation to the dark deep ocean, *Rimicaris* shrimps evolved a 'dorsal eye' instead of the externally differentiated eye[72]. Despite the lack of image-forming optics, this specialized organ is thought to be capable of detecting extremely dim light from the vent[73]. We then searched for phototransduction genes in *R. leurokolos*, including two main protein families, opsins and cryptochromes. We found a lack of light receptive-type cryptochrome transcript in *R. leurokolos*, but one transcript of transcriptional repressor-type cryptochrome involved in the regulation of the circadian clock showed a disordered expression (Fig. 5c). For opsins, three transcripts were identified, including two middle wavelength-sensitive (MWS) opsins and one long wavelength-sensitive (LWS) opsin (Supplementary Fig. 7). All three opsin transcripts were statistically arrhythmic, and quantitative PCR (qPCR) was performed to validate the results (Fig. 5h-k). Therefore, potential light sources at vents, including thermal radiation from the chimney and possible non-thermal emission mechanisms[74], are more likely to serve as a constant direction indicator to locate chimneys and therefore vent fluid, rather than acting as a principal zeitgeber for *R. leurokolos*. Given temperature and chemistry fluctuate dynamically, we suggest that food source[75, 76], pressure[77, 78], or even soundscape cues from the surface[79, 80] could be potentially useful zeitgebers for the deep-sea hydrothermal vent shrimp *R. leurokolos*.

Rhythmicity comparison of two vent species living in different microenvironments

A previous study on the Atlantic deep-sea hydrothermal vent mussel *Bathymodiolus azoricus* revealed *in situ* biological rhythms predominated by tidal gene expression[22], and here we report dominant free-running tidal rhythms in another vent species, *R. leurokolos*. Despite the different geographic localities of the two species, they both show similar biological rhythm patterns and exhibit robust rhythms related to the responses to environmental stresses such as DNA damage, and thermal, immune, and oxidative stress, suggesting a generally temporal adaptation to the harsh deep-sea hydrothermal environments. From an ecological perspective, the plasticity of biological systems permits organisms to adjust their rhythms to cope with different environmental

stresses[81]. For example, in the intertidal zone, high-shore animals exhibited more pronounced behavioral and transcriptional oscillations than the low-shore ones[47, 82]. In hydrothermal vents, local geochemical environments are important factors determining the micro-distribution of faunal assemblages, promoting vent organisms to evolve different adaptation strategies[83]. A long-term *in situ* monitoring revealed high stability in a *B. azoricus* mussel assemblage, and the temperature fluctuated mildly in both larger mussels (Mean ± SD = 6.2 ± 1.5□) and smaller mussels[83] (5.0 ± 0.1□). However, *R. leurokolos* lives near the vent chimney, where the hot plume and cold surrounding seawater mix spontaneously, and the temperature fluctuates more dynamically at the seconds-minutes scale (Mean ± SD = 10.16 ± 1.71°C). Therefore, these two vent organisms likely evolved different strategies in biological rhythms to cope with their microenvironment variations.

To minimize the influence of rhythm analysis, we applied our transcriptome analysis and rhythm detection pipeline to the published *in situ* gene expression dataset of vent mussel *B. azoricus*[22]. Our analysis generated a total of 31,813 transcripts for rhythm detection analysis, which was near the number of contigs assembled in the published study (n = 34,196). As expected, rhythmic oscillations in the tidal range predominated the *in situ* temporal transcriptome of *B. azoricus*. Compared to *R. leurokolos*, however, the proportion of tidal transcripts in the transcriptome was lower in *B. azoricus* regardless of the detection algorithm used (Supplementary Fig. 8a, b). Indeed, considering that rhythmic gene expression was organ-specific[5], the result was disputable as we detected overall rhythmicity within mixed tissues of *R. leurokolos*, whereas the study on *B. azoricus* only worked on gills. We further examined and compared the strength of tidal rhythms in the two species by calculating the rhythmicity index (RI) using the autocorrelation analysis, and the results suggested the general rhythmicity of tidal gene expression was greater in *R. leurokolos* (Supplementary Fig. 8c). This is unexpected since it should be easier for *B. azoricus*, living in a relatively distant area from the vent orifice with stable diffuse flow, to detect environmental factors influenced by tidal cycles. A possible explanation is that *R. leurokolos* needs to depend on a strong pacemaker to predict environmental fluctuations and prepare for transcriptional regulation, whereas *B. azoricus* could schedule the transcription by either relying on an endogenous clock or responding directly to the tidal-modulated environmental cues[22].

To our best knowledge, organisms living in unpredictable and changeable environments tend to evolve weak rhythmicity for intrinsic fitness. For example, the plateau pika

Ochotona curzoniae inhabiting the Qinghai-Tibet Plateau, an extreme area with drastic daily weather changes, shows extremely weak behavioral and psychological rhythms as the result of disrupted endogenous circadian clocks[84]. Why *R. leurokolos* inhabiting a more dynamic environment shows more robust rhythmicity compared to *B. azoricus* is an intriguing topic warranting future studies, although this could also be related to intrinsic differences between mussels and shrimps, as well as the influence of chemosymbiosis on the host[85].

The potential evolutionary conservation between marine tidal rhythms and terrestrial 12-hour rhythms

We show that the deep-sea vent shrimp *R. leurokolos* exhibits robust endogenous rhythms related to tidal effects instead of daily cycles, making it a useful model for testing the hypothesis that marine tidal rhythms and 12-hour rhythms of terrestrial animals share conserved features. To investigate this, we compared the tidal gene expression of *R. leurokolos* with published ~12-hour rhythms in the BMAL1 knockout mouse liver[30] and *Drosophila* S2 cells[32], two systems without canonical circadian clock gene expressions. A total of 406 single-copy orthologous genes were identified as showing ~12-hour rhythms in these three species. The vent shrimp *Rimicaris* shared more genes with the fruit fly *Drosophila* compared with the mouse *Mus* (54 genes vs 36 genes), suggesting a phylogenetic relationship. We also found 21 genes with a period of ~12-hour rhythms in all three species (Fig. 6a). These genes were enriched in the processes of DNA replication, regulation of transcription, ribosome biogenesis, protein folding, and trans-Golgi network, which are also highly enriched in the ~12-hour rhythms of human beings[33] (Fig. 6b). The heat shock protein 70 cochaperone DNAJA1, which were also reported in 12-hour rhythms of mammals[33] and tidal rhythms of the sea anemone *Aiptasia diaphana*[85], also showed a robust free-running tidal rhythm in *R. leurokolos* (Fig. 4b). These results support the evolutionary conservation of ~12-hour gene expression related to the processes of central dogma information flow in both terrestrial and marine animals across a broad range of phyla, indicating the ~12-hour rhythms in animals overall likely initially evolved for adjusting to the tidal cycle.

Conclusion

In this study, our analyses provide evidence for endogenous biological rhythms in the deep-sea hydrothermal vent shrimps *Rimicaris leurokolos* through a 72-hour free-running experiment and constrain the possible zeitgeber for biological clocks ticking in the deep, shedding light on biological rhythms in the light-absent biosphere

(Fig. 7). We propose that rhythms with a period of 24 hours driven by the conventional circadian clock largely decrease or even disappear in adult deep-sea hydrothermal vent fauna. Instead, rhythmic gene expression coordinated with approximately 12-hour tidal cycles, which are likely controlled by an independent circatidal clock, evolved as a temporal adaptation to the environmental fluctuations in hydrothermal ecosystems. Independent of solar energy but being influenced by tidal cycles, organisms in the deep sea may be powerful models for chronobiologists to decipher the evolution and molecular mechanisms of circatidal clocks and ~12-hour rhythms, important across a wide range of living organisms.

Materials and methods

Environmental temperature monitoring

The local fluctuations in the temperature of a *Rimicaris leurokolos* colony on the NBC chimney (126°53.80'E, 27°47.45'N; 982 m deep) of the Original Site, Iheya North vent field were measured using a RINKO dissolved oxygen and temperature sensor (JFE Advantech Co., Ltd.) during dive #1610 of the remotely operated vehicle (ROV) *Hyper-Dolphin* on-board R/V *KAIYO* cruise KY14-01 for 162 seconds, and data were recorded every second. Published temperature data in a peripheral area of the original site, Iheya North vent field far away from active chimneys, which were recorded continuously every 10 min from the 4th of September 2010 to the 20th of August 2011, were re-analyzed[35]. We used the Lomb-Scargle periodogram to detect periodicity in the temperature time series. The raw data of environmental records are provided as Supplementary Data 1.

Sampling procedure and experiment design

A total of 184 adult individuals of *Rimicaris leurokolos* were collected by a suction sampler from the top of the NBC chimney at the Original Site, Iheya North hydrothermal field (126°53.80'E, 27°47.45'N; 982 m depth) during dive #1613 of ROV *Hyper-Dolphin* on-board R/V *KAIYO* in the cruise KY14-01. Once on-board the ship, 154 live shrimps were immediately transferred into a lightproof seawater container in a dark cold room set to 4°C for the subsequent free-running experiment. After 2.5 hours, five *R. leurokolos* individuals were collected by a meshed scoop, dissected, and fixed every 4 hours for a total duration of 72 hours. The cephalothorax and abdominal segments of each individual were preserved in RNAlater (Invitrogen), kept at 4°C overnight, and then stored at -80°C until RNA extraction. During the sampling, we did not provide any food source as the previous laboratory study on behaviors of vent shrimps revealed that the introduction of food largely increased the activities of these shrimps[76]. As a possible

zeitgeber[86], an external food source gives an opportunity for shrimps to synchronize their activities and even gene expression at a certain time, which should be avoided in the free-running experiment. Despite that, *R. leurokolos* may feed on bacteria attached to other individuals. We did not find any dead shrimp during the free-running experiment, which might reflect the health conditions of *R. leurokolos*.

RNA extraction and sequencing

Total RNA was extracted using TRIzol reagent (ThermoFisher) following the manufacturer's protocol. The quality of RNA was examined by 1% agarose gel electrophoresis. The mRNA from each shrimp cephalothorax was enriched by Oligo-dT probes and further reverse transcribed to first-strand cDNA for library construction. All cDNA libraries were sequenced on an Illumina NovaSeq 6000 platform with 150 bp paired-end mode.

***De novo* transcriptome assembly**

A total of 57 RNA-Seq samples were generated from *R. leurokolos* during 72 hours of sampling at 4-hour intervals with three replicates per time point. Raw reads were firstly trimmed using Trimmomatic version 0.39[87] (set parameters: LEADING:10 TRAILING:10 SLIDINGWINDOW:4:15 MINLEN:50) in the paired-end mode, and then potentially associated bacteria contamination reads were removed with Kraken2 version 2.0.8-beta[88]. In the absence of an available genome reference of *R. leurokolos*, *de novo* assembly was performed with Trinity version 2.11.0[89] (set jaccard clip option). The transcripts with the highest expressed isoforms were kept. Salmon version 1.4.0[90] was used to quantify the expression of each assembled transcript. Benchmarking Universal Single-Copy Orthologs (BUSCO) version 5.0.0[91] was employed to evaluate the transcriptome completeness against the "metazoa_odb10" ortholog database.

Gene quantification and annotation

The Trimmed Means of M values (TMM) cross-sample normalization method[92] was applied to remove the sequencing variations and potential "batch effects" among samples using the abundance_estimates_to_matrix.pl script in the Trinity toolkit. The coding sequences were translated into proteins using TransDecoder version 5.5.0 (https://github.com/TransDecoder/TransDecoder) and only the single best open reading frame (ORF) was retained for each transcript. In addition, lowly expressed transcripts with 0 counts in at least 38 samples (i.e. two-thirds of all 57 samples) were filtered out, leaving 23,905 transcripts for subsequent analyses. The predicted proteins were

annotated by searching the candidate protein sequences against the NCBI non-redundant (NR) database using BLASTP with DIAMOND version 2.0.13[93] with ultra-sensitive mode and E-value threshold of 1×10^{-5}, the Kyoto Encyclopedia of Genes and Genomes (KEGG) database via KEGG Automatic Annotation Server (KAAS), and the Gene Ontology (GO) via BLAST2GO version 6.0[94]. The gene enrichment analyses were performed with ClusterProfiler version 4.2.2[50].

Gene expression analyses

The principle components analysis (PCA) was performed using the plotPCA function in R package DESeq2 version 1.34.0[95]. Permutational multivariate analysis of variance (PERMANOVA) and analysis of similarities (ANOSIM) were applied to test the statistical significance of the PCA results. The potential monotonic trends in the raw gene expression of all transcripts were determined with the Mann-Kendall trend test, and we pinpointed two overall clusters of transcripts that had either an upward trend (S score > 0 and *P*-value < 0.05) or a downward trend (S score < 0 and *P*-value < 0.05). To remove the trend and produce a steady baseline for subsequent rhythm analyses, we used CEEMDAN[39], an adaptive decomposition method designed for non-stationary and non-linear time series signals. The ceemdan detrend was performed with the R package Rlibeemd[96] (set parameters: num_imfs = 0; noise_strength = 0.4; S_number = 0; num_siftings = 50; ensemble_size = 250).

Rhythm detection analyses

Without benchmarking approaches for genome-scale analyses of biological rhythms[97, 98], we implemented the rhythmic analyses exploratorily under the considerations as follows: (a) choose the appropriate rhythm detection algorithms; (b) generate an overview of rhythmicity in our gene expression dataset using unbiased methods that can detect a wide range of periods; (c) detect the rhythmicity for each transcript using specialized methods with certain periods.

For *R. leurokolos*, we knew nothing about its biological rhythm, and no golden-standard circadian or non-circadian genes were available for evaluating the detection power (such as AUC values and ROC curves) of different algorithms[99, 100]. Thus, we assessed various rhythm detection methods based on our experiment design (for details see Supplementary Table 1). Overall, we chose four rhythm detection algorithms in this study, the mathematic method eigenvalue/pencil[30] (carried out with customized scripts), the Extended Circadian Harmonic Oscillator application[41] (ECHO), and two non-parametric

statistical methods RAIN[42] and empirical JTK_CYCLE[43] (eJTK), which were designed to detect asymmetric waveforms. For eigenvalue/pencil and ECHO, rhythmic transcripts with the periodicity of 10-14 hours and 22-26 hours were considered as tidal and daily oscillated[48]. Oscillations with the largest amplitude in one transcript for eigenvalue/pencil were considered the dominant oscillation[31]. For RAIN and eJTK, rhythmic transcripts with a period of 12 hours and 24 hours were considered tidal and daily cycling. Multiple-testing was carried out to adjust *P*-values using the Benjamini-Hochberg method for RAIN and ECHO, and an empirical method based on the gamma distribution for combining dependent *P*-values for eJTK. Transcripts with an FDR ≤ 0.05 were considered statistically rhythmic. The root mean square (RMS) amplitude and Rhythmicity Index (RI) of rhythmic transcripts were calculated by LimoRhyde2[101] and autocorrelation analysis, respectively. Significance of amplitude and detected *P*-values between tidal and daily oscillations was examined with the unpaired Student's *t*-test, while the paired Student's *t*-test was conducted on the tidal and daily components of rhythmic transcripts. We also used ECHO to fit data with an extended fixed amplitude model and categorize the oscillation type using amplitude change coefficient (γ) as forced ($-0.15 < \gamma < -0.03$; amplified amplitude), harmonic ($-0.03 \leq \gamma \leq 0.03$; steady amplitude), damped ($0.03 < \gamma < 0.15$; reduced amplitude), overexpressed ($\gamma \leq -0.15$), and repressed ($\gamma > 0.15$), of which the latter two are considered arrhythmic[41]. The significance of overlaps between rhythmic transcripts with different original trends and oscillation types was examined using Fisher's exact test (Supplementary Table 2). The results of rhythm detection analyses are listed in Supplementary Data 2.

For the clustering of tidal transcripts presented in Fig. 3, we assessed four different clustering methods with different numbers of clusters by validation measures using the R package clVaild version 0.7[102] and found the kmeans method with two clusters was estimated to be the most optimal one. Heatmaps were drawn with ComplexHeatmap version 2.10.0[103] on Z-score normalized expression. All analyses and plots were performed in R version 4.1.1, except for eJTK which was performed with Python version 2.7.

Identification of putative circadian clock genes

We searched for putative circadian clock genes in our *de novo* assembled transcriptome using the proteic Basic Local Alignment Search Tool (BLASTP) carried out by DIAMOND with a series of known core clock and clock-associated genes as queries (Supplementary Data 3). For candidate circadian clock transcripts, sequences were

scanned against the coding regions and conserved functional domains using the InterProScan tools[104]. To determine the sequence homology of candidate transcripts, we further conducted the phylogenetic analysis. The amino acid sequences were first aligned using MAFFT version 7.490[105] and then trimmed using trimAl version 1.4.1 with the '-automated1' option[106]. The maximum-likelihood trees were then constructed using the IQ-Tree version 2.1.3[107] with the ultrafast bootstrap approximation (UFBoot) and ModelFinder for examining the best-fit model. Overall, we reconstructed four phylogenetic trees by using the Q.insect+Γ4 model for the Clock and Bmal/Cycle tree, the Q.insect+I+Γ4 model for the Period tree and the Timeless/Timeout tree, and the LG+R4 model for the Photolyase/Cryptochrome tree. In the identified circadian clock genes, the Clock transcript exhibited extremely low expression and was thus excluded from the rhythm detection. Visualization of all phylogenetic trees was performed with ggtree version 3.8.2[108].

Quantitative PCR (qPCR) and phylogenetic analysis of opsin genes

To validate the gene expression levels deduced in the sequencing-based transcriptome analysis, we also performed qPCR analysis on one target gene (*opsin*) and one gene (*tubulin*) that serves as the internal standard in qPCR. In brief, the extracted RNA was treated with DNAse I (Invitrogen), and sequentially reverse-transcribed into single-strand cDNA by using the high-capacity cDNA reverse transcription kit (Applied Biosystems). QPCR was performed on A LightCycler 480 instrument II (Roche), and the relative gene expression level was analyzed based on the $2^{-\Delta\Delta Ct}$ method.

The primer sequences for qPCR analysis are listed below:

>Tubulin_F
AACACGGCATTGAACCAACC
>Tubulin_R
CTATCCATTGTCCCCGGCTC
>Opsin_F
GCATCCTCGACTCCTGTAGC
>Opsin_R
CACGCATGGCTTTTTCGTGA

As it was unclear about the maximum absorption of identified opsin genes, a phylogenetic analysis was used to show the genealogy of the opsins of *R. leurokolos* together with other arthropod opsins. We collected a total of 94 opsin sequences from

arthropods (including crustaceans, chelicerates, and insects), together with 5 vertebrate opsin clade sequences as an outgroup (Supplementary Data 4). The phylogenetic analysis was performed with the same procedure in the identification of candidate circadian clock genes. The maximum-likelihood phylogeny was finally built using IQ-Tree with 1000 replicates of the ultrafast bootstrap and LG+F+Γ5 model as the suggested best-fit model[107].

Conserved rhythmic orthologs analysis

The 12-hour rhythmic gene expression data of mouse liver and *Drosophila* S2 cell used in this study were published previously[30, 32]. Together with the *de novo* transcriptome of *R. leurokolos* assembled in this study, the protein sequences from mouse genome assembly GCF_000001635 and fruit fly genome assembly GCF_000001215 were used to construct orthogroups using Orthofinder version 2.5.4[109] with default settings. The conserved rhythmic analysis was performed with the single-copy orthologous genes (Supplementary Data 5). Gene enrichment analysis and pathway network enrichment analysis of conserved single-copy orthologous genes are performed with clusterProfiler version 4.2.2 and aPEAR version 1.0.0[110], respectively.

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Competing interests

The authors declare that they have no competing interests.

Data and materials availability

Raw RNA-Seq data are available on NCBI as BioProject PRJNA993859. The *de novo* reference transcriptome of *Rimicaris leurokolos* is available in figshare (https://doi.org/10.6084/m9.figshare.23667327.v2). All original codes used in this work are available at GitHub (https://github.com/belphe/Shinkaicaris).

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Figure Legends

Fig 1. Deep-sea chronobiology study on the hydrothermal vent shrimp *Rimicaris leurokolos*. a *R. leurokolos* shrimps (in the green circle) live in the central zone where hydrothermal fluids mix with cold surrounding seawater spontaneously. **b** This work was performed with the *R. leurokolos* colony from the top of the active NBC mound at the Iheya North vent field, Okinawa Trough (126°53.80'E, 27°47.45'N; 982 m depth). **c** Time series of published temperature data covering 351 days recorded at the peripheral area of our sampling site. Lomb-Scargle (LS) periodogram analysis reveals a strong semidiurnal tidal cycle dominated by the M2 tidal constituent, the possible 26.4-hour inertial oscillation is extremely weak. **d** Time series of *in situ* temperature and dissolved oxygen records during 162 seconds when the sensor was placed in the *R. leurokolos* colony showing frequent environmental fluctuations with high variability. **e** Principal components analysis (PCA) plot showing the detrended transcriptomic data from the free-running experiment samples (n = 57). Significance of inter-group differences was examined by the PERMANOVA (*P*-value = 0.376) and ANOSIM (*P*-value = 0.958) analysis both on Bray-Curtis dissimilarities.

Fig 2. The *R. leurokolos* temporal transcriptome was dominated by tidal oscillations under constant conditions. a Distribution of the periods of oscillations identified by the eigenvalue/pencil method and the ECHO application. Oscillations with a period range of 10-14 hours and 22-26 hours are regarded as tidal and daily cycling, respectively. **b** Paired *t*-test plot of amplitude for the rhythmic transcripts with both tidal and daily components. **c, d** Venn diagrams detailing the number of rhythmic transcripts (FDR < 0.05) identified by ECHO, RAIN, and eJTK in the tidal range (**c**) and daily range (**d**). **e** Raincloud plot of the root mean square (RMS) amplitude for 12-hour tidal transcripts and 24-hour daily transcripts. The stars indicated the level of significance: **** *P*-value < 0.0001.

Fig 3. Free-running tidal transcriptomic patterns of *R. leurokolos*. a Density distribution based on amplitude change coefficient (γ) of tidal transcripts detected by ECHO. Oscillation types are categorized as forced ($-0.15 < \gamma < -0.03$; amplified amplitude), harmonic ($-0.03 \leq \gamma \leq 0.03$; steady amplitude), damped ($0.03 < \gamma < 0.15$; reduced amplitude), overexpressed ($\gamma \leq -0.15$), and repressed ($\gamma > 0.15$), and the latter two are considered arrhythmic. **b** Rose chart showing phase distribution comparison of tidal transcripts in cluster 1 and cluster 2. For each oscillation, the phase is divided by period length and then times 360 (degrees) to normalize phases of transcripts with

different period lengths. **c** Heatmap showing highly synchronized gene expression of tidal transcripts (ECHO FDR < 0.05). Each row represents a transcript with three individuals per time point. Transcripts are clustered and ordered by phases, oscillation type, and monotonic trend. Expression of each gene is Z-score normalized. **d** Bubble diagram showing significantly enriched gene ontology (GO) terms related to biological processes of tidal subgroups categorized by three classification schemes (from left to right: cluster, oscillation type, trend). Cross symbols represent a lack of enriched terms in the corresponding subgroup.

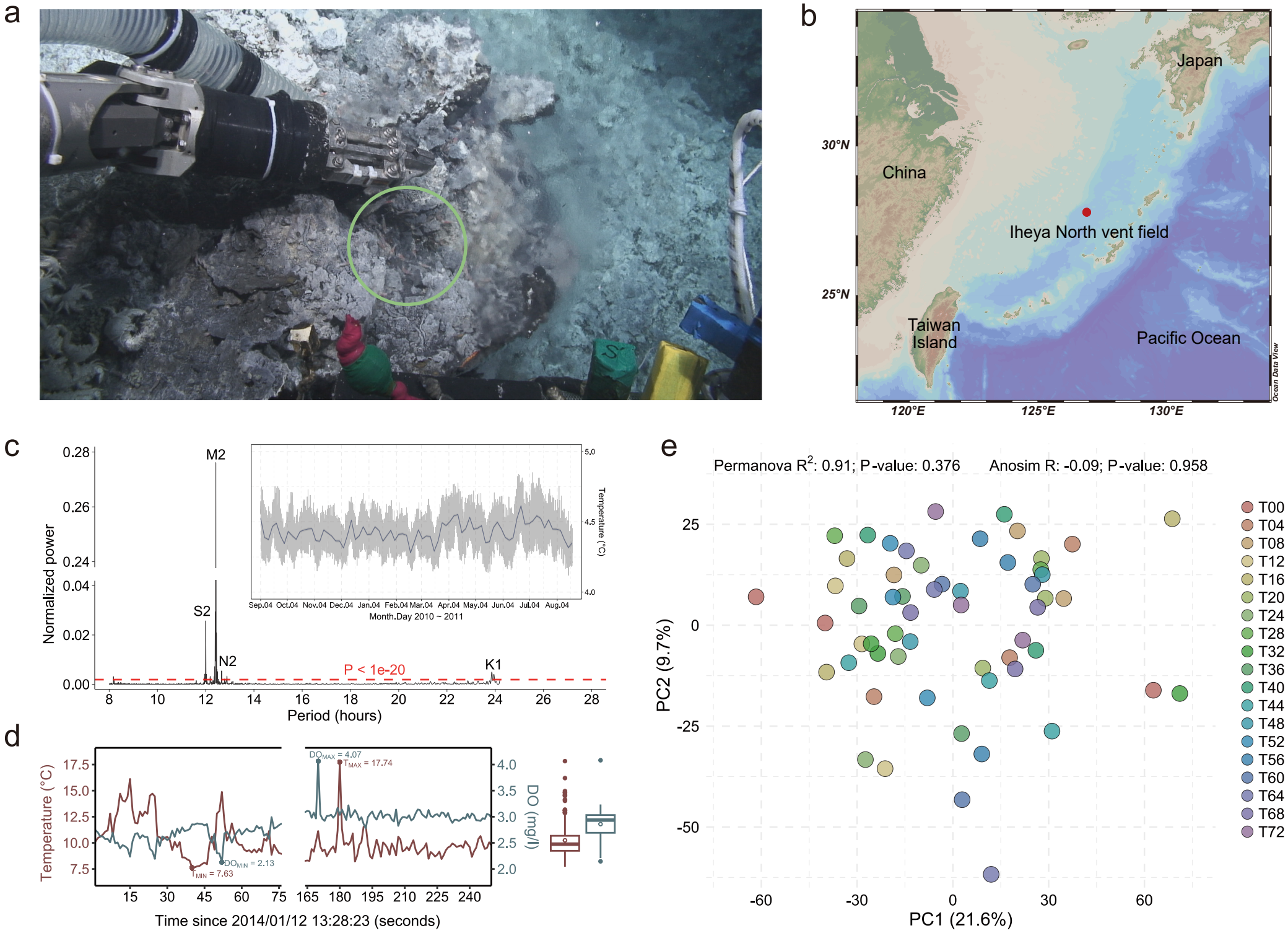
Fig 4. Expression profiles of examples of tidal transcripts of interest. The listed tidal genes are potentially involved in various cellular stress response processes, including **a** sulfur metabolism, **b** response to heat or hypoxia, **c** antioxidation and detoxification, and **d** innate immune response. Data points are displayed as mean values ± SEM (n = 3 biological replicates per time point). Normalized expression curves are fitted via the generalized additive model (GAM). Minimum *P*-values of each tidal transcript identified by RAIN, eJTK, and ECHO are presented in the plot.

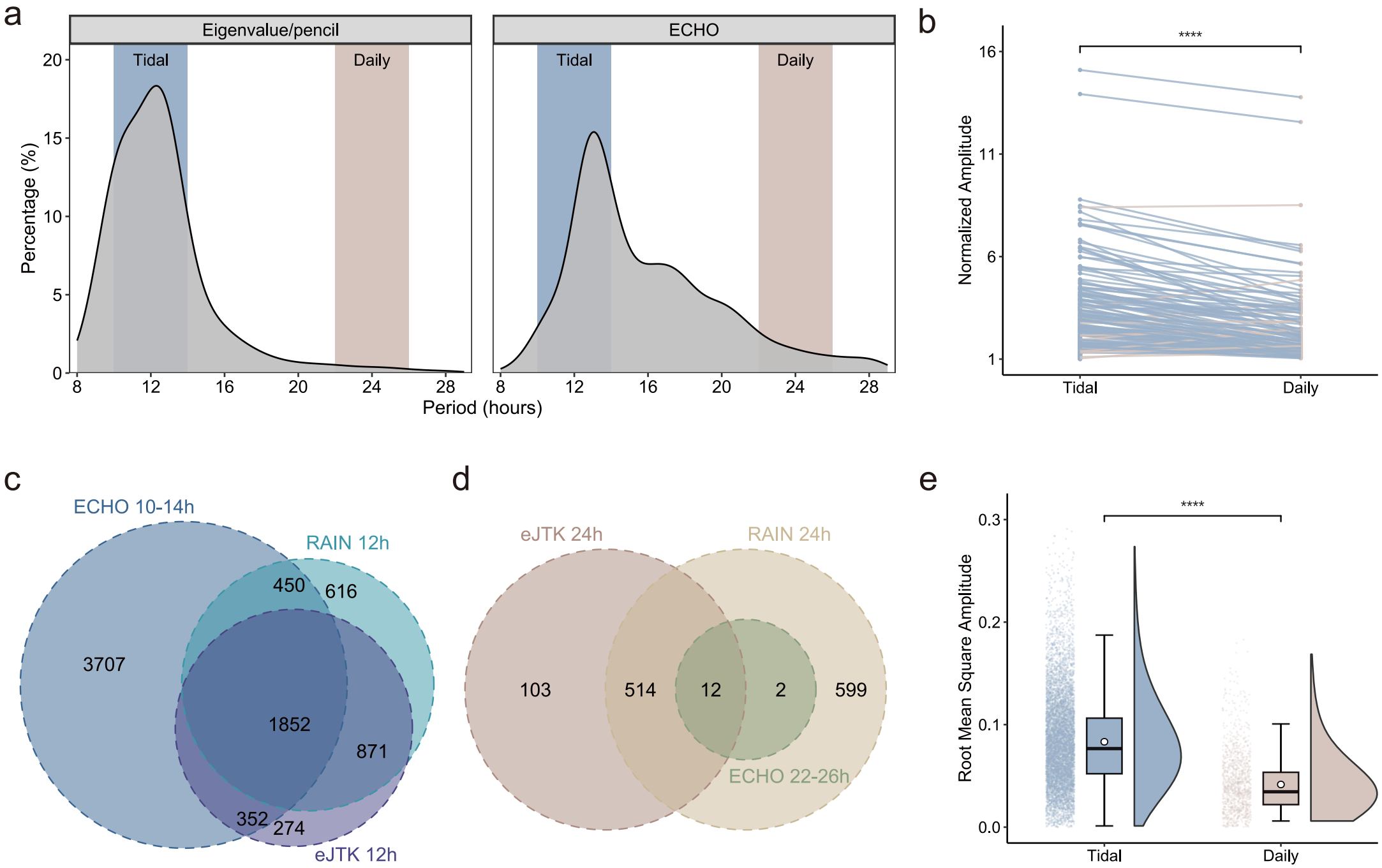
Fig 5. Expression profiles of core circadian clock genes and opsin genes. a-g Temporal expression of *R. leurokolos* homologs of candidate circadian clock genes for (**a**) PER, (**b**) TIM, (**c**) CRY2, (**d**) CWO, (**e**) DBT, (**f**) VRI, (**g**) PDP1ε. **h-j** Temporal expression of three identified opsin genes, including (H) one long-wavelength-sensitive (LWS) opsin and (**i, j**) two middle-wavelength-sensitive (MWS) opsins. (**k**) Opsin expression profile validated by quantitative PCR (qPCR). For RNA-Seq data, data points are displayed as mean values ± SEM (n = 3 biological replicates per time point). For qPCR data, normalized expression curves are fitted via the generalized additive model (GAM). Minimum *P*-values of results from tidal or daily detection of each transcript are presented in the plot. Significant levels of oscillations are indicated with stars: * FDR < 0.05.

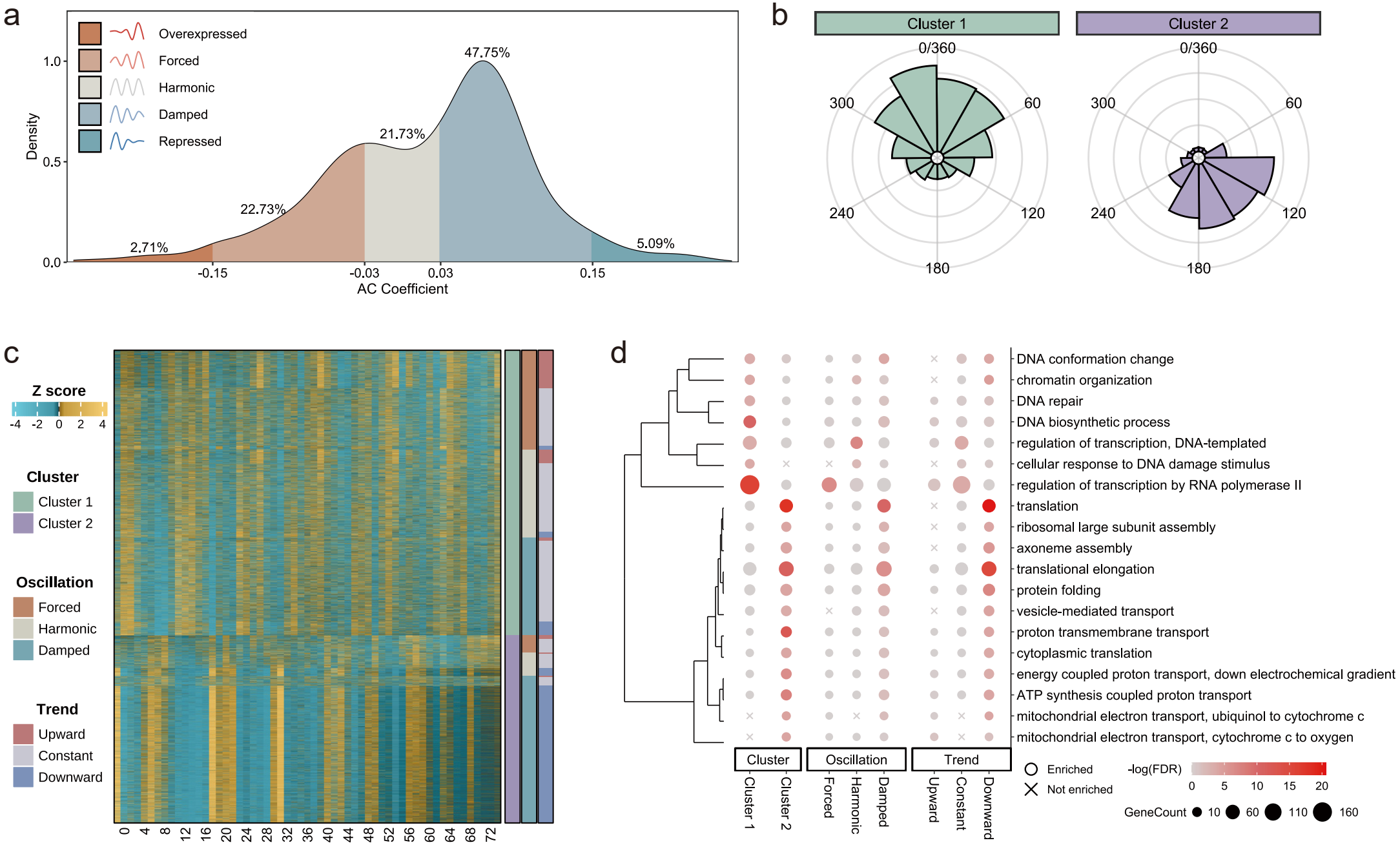
Fig 6. Homologous genes with a period of 12-hour rhythms between *R. leurokolos*, *Mus musculus*, and *Drosophila melanogaster*. a Venn diagram showing the comparison of ~12-hour rhythms of single-copy orthologous genes between three species. **b** Pathway enrichment network showing biological functions of 21 conserved ~12-hour genes in three species.

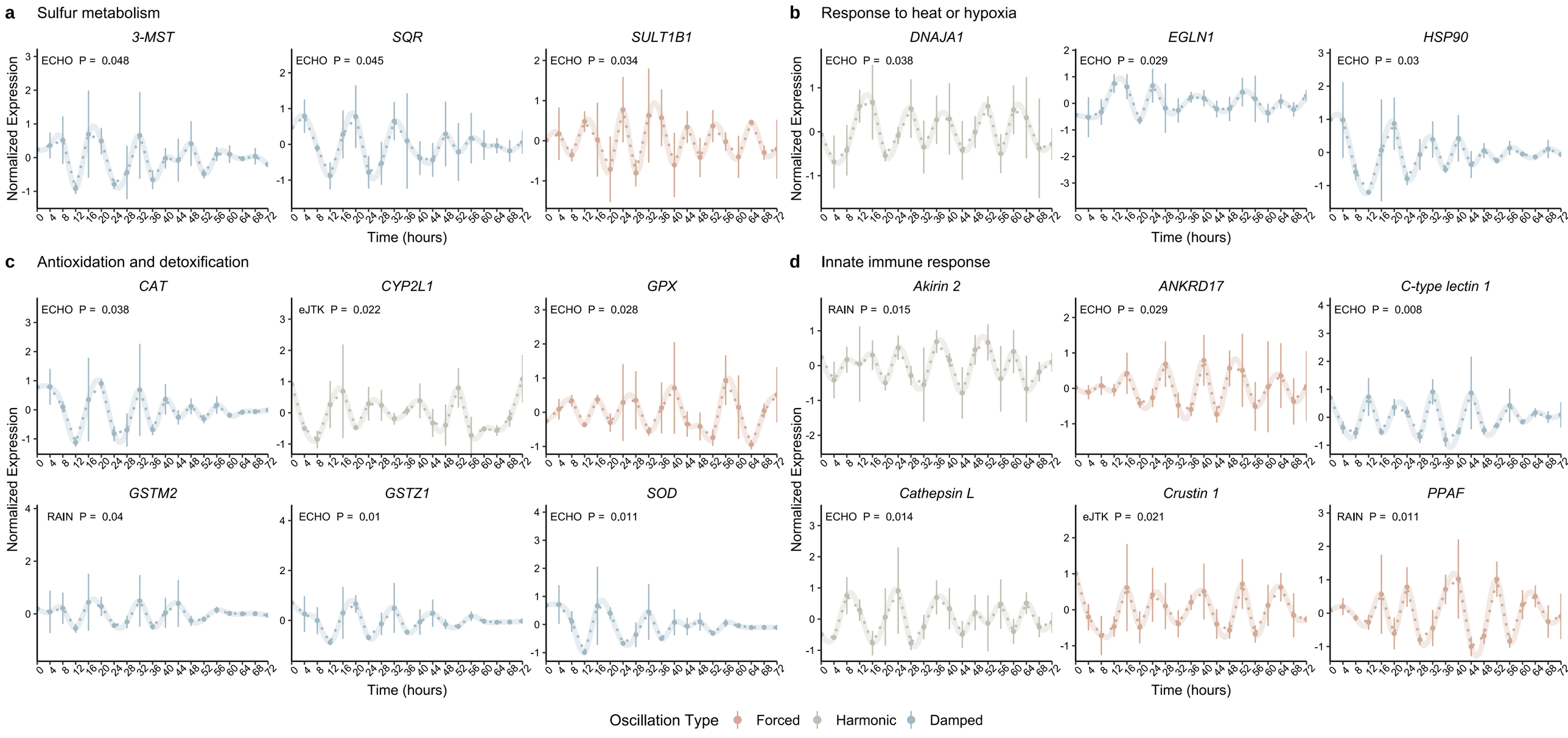
Fig 7. A new perspective of biological rhythms in the dark biosphere. Terrestrial

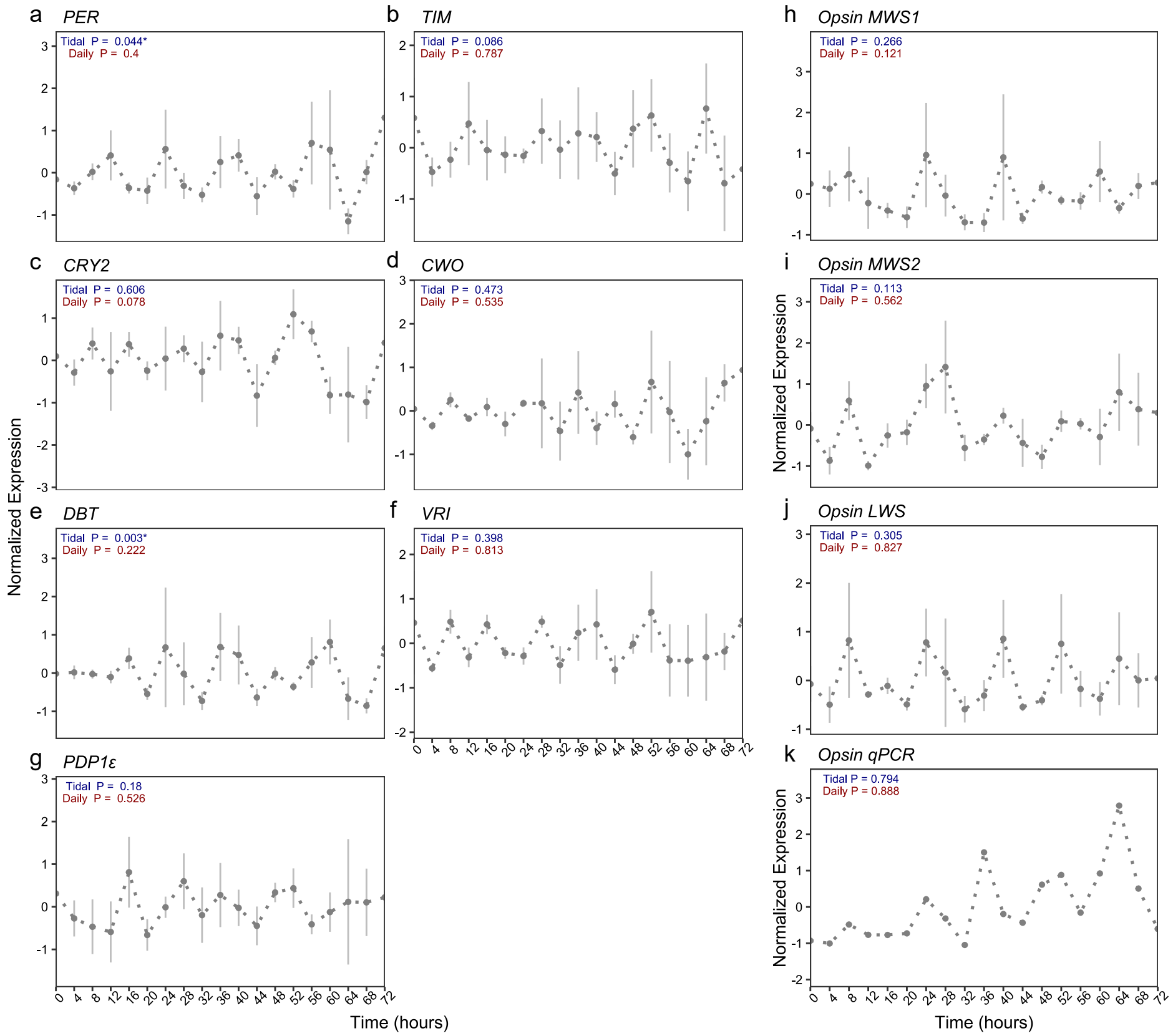
and shallow-water organisms largely rely on circadian clocks for anticipating periodic environmental changes such as the day-night transition. Terrestrial organisms such as human beings exhibit robust ~24-hour rhythms driven by the circadian clock. The intertidal mussel *Mytilus californianus* shows both circatidal and circadian rhythms, while the latter is the dominant one. The copepod *Calanus finmarchicus* also shows behavioral rhythms in diel vertical migration (DVM). However, a different scenario can be found in the dark biosphere. Living away from direct sunlight, subterranean mole rats scarcely depend on circadian rhythms for survival, and the endogenous circadian system is understood to be in the process of regression, even though still present. In this work, we found that in addition to the vent mussel *B. azoricus*, the vent shrimp *R. leurokolos* shows endogenous 12-hour rhythms in gene expression, as well as relatively weak 24-hour rhythms that are likely unrelated to the circadian clock, likely reflecting important effects of tidal cycles on deep-sea vent organisms.

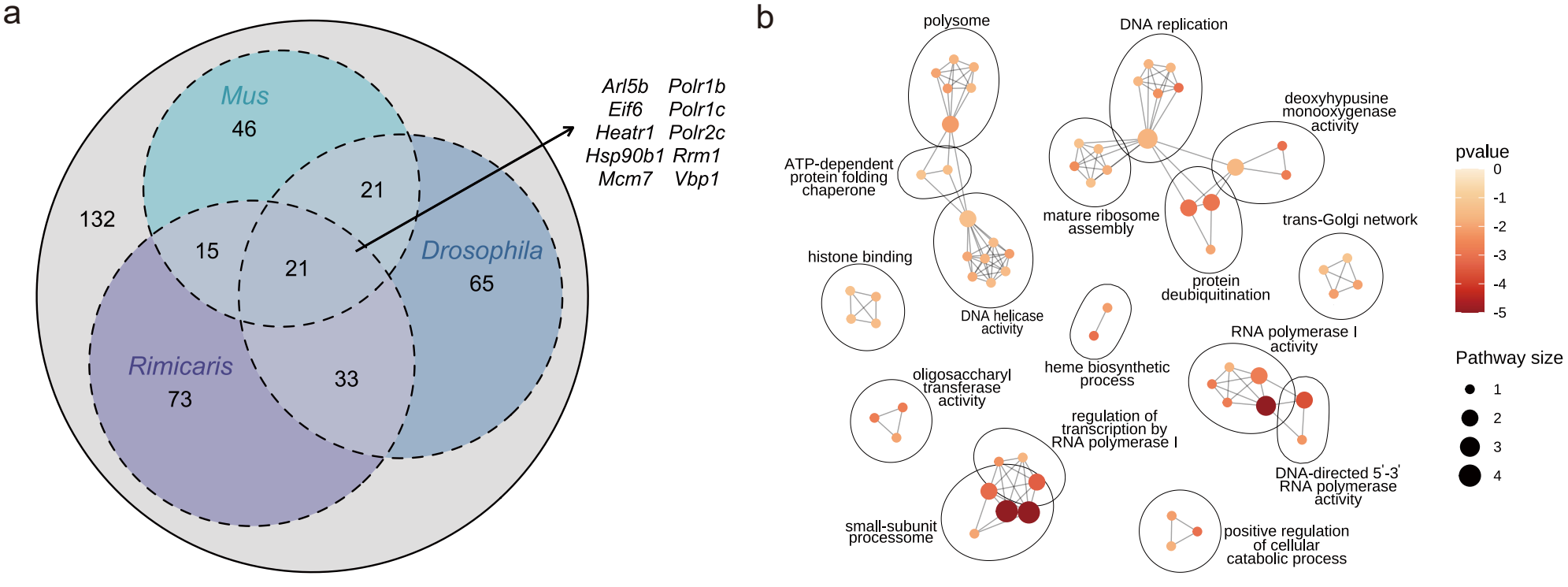

a
b
Japan
30°N
China
Iheya North vent field
25°N
Taiwan Island
Pacific Ocean
Ocean Data View
120°E
125°E
130°E
c
M2
S2
N2
K1
P < 1e-20
Normalized power
Period (hours)
Temperature (°C)
Month.Day 2010 ~ 2011
d
Temperature (°C)
DO (mg/l)
DO_MAX = 4.07
T_MAX = 17.74
DO_MIN = 2.13
T_MIN = 7.63
Time since 2014/01/12 13:28:23 (seconds)
e
Permanova R2: 0.91; P-value: 0.376
Anosim R: -0.09; P-value: 0.958
PC1 (21.6%)
PC2 (9.7%)
T00
T04
T08
T12
T16
T20
T24
T28
T32
T36
T40
T44
T48
T52
T56
T60
T64
T68
T72


a
Eigenvalue/pencil
ECHO
Tidal
Daily
Percentage (%)
Period (hours)
b
****
Normalized Amplitude
Tidal
Daily
c
ECHO 10-14h
RAIN 12h
eJTK 12h
3707
450
616
1852
871
352
274
d
eJTK 24h
RAIN 24h
ECHO 22-26h
103
514
12
2
599
e
****
Root Mean Square Amplitude
Tidal
Daily


a
Overexpressed
Forced
Harmonic
Damped
Repressed
Density
1.0
0.5
0.0
47.75%
21.73%
22.73%
2.71%
5.09%
-0.15
-0.03
0.03
0.15
AC Coefficient
b
Cluster 1
Cluster 2
0/360
60
120
180
240
300
c
Z score
-4 -2 0 2 4
Cluster
Cluster 1
Cluster 2
Oscillation
Forced
Harmonic
Damped
Trend
Upward
Constant
Downward
0 4 8 12 16 20 24 28 32 36 40 44 48 52 56 60 64 68 72
d
DNA conformation change
chromatin organization
DNA repair
DNA biosynthetic process
regulation of transcription, DNA-templated
cellular response to DNA damage stimulus
regulation of transcription by RNA polymerase II
translation
ribosomal large subunit assembly
axoneme assembly
translational elongation
protein folding
vesicle-mediated transport
proton transmembrane transport
cytoplasmic translation
energy coupled proton transport, down electrochemical gradient
ATP synthesis coupled proton transport
mitochondrial electron transport, ubiquinol to cytochrome c
mitochondrial electron transport, cytochrome c to oxygen
Cluster
Oscillation
Trend
Cluster 1
Cluster 2
Forced
Harmonic
Damped
Upward
Constant
Downward
Enriched
Not enriched
-log(FDR)
0 5 10 15 20
GeneCount
10 60 110 160


a
Sulfur metabolism
3-MST
ECHO P = 0.048
SQR
ECHO P = 0.045
SULT1B1
ECHO P = 0.034
b
Response to heat or hypoxia
DNAJA1
ECHO P = 0.038
EGLN1
ECHO P = 0.029
HSP90
ECHO P = 0.03
c
Antioxidation and detoxification
CAT
ECHO P = 0.038
CYP2L1
eJTK P = 0.022
GPX
ECHO P = 0.028
GSTM2
RAIN P = 0.04
GSTZ1
ECHO P = 0.01
SOD
ECHO P = 0.011
d
Innate immune response
Akirin 2
RAIN P = 0.015
ANKRD17
ECHO P = 0.029
C-type lectin 1
ECHO P = 0.008
Cathepsin L
ECHO P = 0.014
Crustin 1
eJTK P = 0.021
PPAF
RAIN P = 0.011
Normalized Expression
Time (hours)
Oscillation Type
Forced
Harmonic
Damped


a
PER
Tidal P = 0.044*
Daily P = 0.4
b
TIM
Tidal P = 0.086
Daily P = 0.787
h
Opsin MWS1
Tidal P = 0.266
Daily P = 0.121
c
CRY2
Tidal P = 0.606
Daily P = 0.078
d
CWO
Tidal P = 0.473
Daily P = 0.535
i
Opsin MWS2
Tidal P = 0.113
Daily P = 0.562
e
DBT
Tidal P = 0.003*
Daily P = 0.222
f
VRI
Tidal P = 0.398
Daily P = 0.813
j
Opsin LWS
Tidal P = 0.305
Daily P = 0.827
g
PDP1ε
Tidal P = 0.18
Daily P = 0.526
k
Opsin qPCR
Tidal P = 0.794
Daily P = 0.888
Normalized Expression
Time (hours)


a
Mus
46
Drosophila
65
Rimicaris
73
132
21
15
21
33
Arl5b Polr1b
Eif6 Polr1c
Heatr1 Polr2c
Hsp90b1 Rrm1
Mcm7 Vbp1
b
polysome
DNA replication
deoxyhypusine monooxygenase activity
ATP-dependent protein folding chaperone
mature ribosome assembly
trans-Golgi network
histone binding
protein deubiquitination
DNA helicase activity
RNA polymerase I activity
heme biosynthetic process
oligosaccharyl transferase activity
regulation of transcription by RNA polymerase I
DNA-directed 5'-3' RNA polymerase activity
small-subunit processome
positive regulation of cellular catabolic process
pvalue
0
-1
-2
-3
-4
-5
Pathway size
1
2
3
4