

Supplementary Figure 1. Phylogeny of Metazoan CRYPTOCHROMES. (*A*) Unrooted tree of 210 Metazoan protein sequences (RAxML, GAMMA-based Likelihood: log -118860.635040) illustrates that CRYs cluster to five distinct groups: CYCLOBUTANE PYRIMIDINE DIMER PHOTOLYASE (CPD-PL, orange), DASH (*Drosophila*, *Arabidopsis*, *Synechocystis*, *Human*)-type cryptochrome (green), mammalian and *Drosophila*-type of cryptochrome (CRY-m, grey; CRY-d, blue), and 6-4 DNA photolyase (6-4 PL, deep purple). (*B-D*) Depict details of particular tree regions with representative taxa. Positions of *P. apterus* CRYs are highlighted.

after-hours overtime

Supplementary Figure 2. Phylogeny of Metazoan JETLAG and FBXL3/21 proteins. (*A*) The unrooted tree containing representative metazoan FBXL proteins (mouse proteins are by grey names) with a detailed dataset of JETLAG (JET) and FBXL21/3 sequences (242 proteins in total, RAxML, GAMMA-based Likelihood: -108138.373258). (*B*) Detail of the tree depicting phylogeny of FBXL3 / FBXL21. (*C*) Phylogeny of JETLAG homologs and its related JET-like (FBXL15). (*D*) Alignment of FBXL3 and FBXL21, two vertebrate paralogs represented by the zebrafish (*Danio rerio*) and mouse (*Mus musculus*), compared to the ancestral sequence from *Petromyzon* and to FBXL3 representing major metazoan groups in which the protein was identified. The blue and red rectangles highlight the positions that are substituted in *after-hours* in the mouse FBXL3 [\(31\)](#page-54-0), highlighted by the light blue full circle, and *overtime* mutant in the mouse FBXL21 [\(13\)](#page-53-0), highlighted by magenta full circle, respectively.

Supplementary Figure 3. Phylogeny of Metazoan PERIOD proteins (PER). The unrooted tree containing representative Metazoan PER proteins (133 proteins in total, RAxML, GAMMA-based Likelihood: -185735.690583).

Supplementary Figure 4. Phylogeny of TIMELESS proteins indicates clear and unambiguous separation of TIM-d and TIM-m clusters. The tree was constructed from the protein alignment of 167 metazoan sequences using RAxML (GAMMA-based Likelihood: -245239.706545). The mammalian-type of TIM (TIM-m, in gold) was found in all representatives of Metazoan species (see table S1 for detail list), whereas the *Drosophila-*type TIM (TIM-d, in red) is present in the majority of insect species, Collembola (*Sminthurus*), Crustacea (*Daphnia*), Chelicerata, Mollusca, Hemichordata and Echinodermata. Positions of *P. apterus* TIM-m and TIM-d are highlighted by black arrows.

Supplementary Figure 5. Free-running period of RNAi animals with complex rhythmicity. (*A*) Summary of the gene silencing describing its impact on the behavioral rhythmicity shown as % of males demonstrating strong rhythmicity, complex rhythmicity, and arrhythmicity. fr #1 and fr #2 = non-overlapping dsRNA fragment 1 and 2, respectively. (*B*) Individual free-running period (τ) values are shown as a dot for each male with complex rhythmicity; red bars represent means \pm SEMs (calculated if >10 % individuals demonstrated rhythmicity). Columns depict the mean free-running period (τ) , standard error of mean (\pm SEM).

Supplementary Figure 6. *P. apterus* **activity after** *dbt* **(i***dbt***) and** *slimb* **(i***slimb***) knock-down shown as double- plotted actograms.** The activity of adult males was recorded at 25 ºC and lightdark cycles for five days. Then, males were released to constant-dark conditions (indicated by grey arrow). Typical examples of: (*A*) i*dbt* fr #1, (*B*) i*dbt* fr #2, (*C*) i*slimb* fr #1, (*D*) i*slimb* fr #2 knockdown are shown. fr #1 and fr #2 refer to non-overlapping dsRNA fragment 1 and 2, respectively.

Supplementary Figure 7. *Timeless-m* **silencing influences rhythmicity in** *P. apterus***.** (*A*) Summary of the rhythmicity during first 5 days of constant darkness (left) and second half of constant darkness (all recorded at 25 ºC). (*B-C*) Examples of double-plotted actograms of *tim-m* silenced males (i*tim-m*). The activity of adult males was recorded at 25 ºC and light-dark cycles for five days. Then, males were released to constant-dark conditions (indicated by grey arrow).

Supplementary Figure 8. Deletion in *tim-d* **⁰³ does not influence splicing of exon 7 and 8.** To clarify if the 11bp deletion and two in-frame substitutions might influence *tim-d* splicing, total RNA was isolated from the brains of *tim-d^{o3}* homozygous mutant animals, mRNA reverse transcribed, and the corresponding region of *tim-d* transcript PCR amplified. The chromatogram obtained from direct sequencing of *tim-d ⁰³* PCR product is shown in the first line of the alignment. The third line corresponds to the cDNA of the wild-type control with exon position highlighted underneath. Protein sequences are shown below *tim-d^{o3}* and *tim-d^{wt}*, respectively. The black box corresponds to the stop codon (coded by TGA).

Supplementary Figure 9. Overview of *P. apterus cryptochrome-m* **engineered mutants.** (*A*) DNA insertion of a sequence in *cry-m⁰⁴*mutant contains an in-frame stop codon. (*B*) Two-base pair deletion in *cry-m⁰⁵* mutant results in a frameshift. The stop codon is downstream of the presented region. (*C*) 27-base pair in-frame insertion results in additional 9 amino acids in CRY-m9in. (*D*) *cryptochrome-m* gene model (bottom) with highlighted exons and introns (note different scale for exons and introns). Corresponding wild-type protein is shown above the gene model with the highlighted position of mutations, protein domains, and the C-terminus (stop). Predicted CRY-m⁹ⁱⁿ mutant protein contains nine-amino acid insertion (see Supplementary Data Fig. 10 for protein alignment of this region with CRY proteins from different insect species). In contrast to *cry-m*9in, two other mutants, *cry-m*⁰⁴and *cry-m*⁰⁵, are *bona fide* loss-of-function mutants because the indels result in frameshifts leading to premature stop codons. Predicted protein sequences are shown at the top of the panel.

Supplementary Figure 10. *Cryptochrome-m* **engineered mutants target evolutionarily conserved region in CRY-m.** Representative CRY-m proteins were aligned with protein sequences of three *P. apterus* mutants. Two of them, CRY-m⁰⁴ and CRY-m⁰⁵ (No. 36 and No. 37, respectively), are terminated prematurely (indicated as a stop). The third mutant, CRY-m⁹ⁱⁿ (No. 35), contains an in-frame insertion of nine amino acids into the evolutionarily conserved CRY-m region.

Supplementary Figure 11. Overview of *P. apterus period* **engineered mutants.** (*A*) A two-base pair DNA deletion in *per⁰¹*mutant results in a frameshift and stop codon (depicted as an asterisk in black background). (*B*) Eight-base pair deletion in *per⁰⁷* mutant results in a frameshift. The stop codon is downstream of the presented region. (*C*) Two transcript isoforms differing by alternative transcription starts (ATG) and alternative retention of exon 7 are presented in *period* gene models (bottom) with highlighted exons and introns (note different scale for exons and introns). The open reading frames are identical for isoforms A and B from exon 8. Therefore, despite the different N terminal regions, mutations *per⁰¹* and *per⁰⁷* identically shorten the resulting mutant proteins. Corresponding wild-type protein is shown above the gene model with the highlighted position of mutations, protein domains, and the C-terminus (stop). Predicted protein sequences are shown at the top of the panel.

Supplementary Figure 12. A detailed summary of the free-running period () in the wild-type and genetic mutants. (*A*) Summary indicating number and phenotypes of measured mutant and heterozygous animals compared to their corresponding wild-type control siblings (labelled as 'ctrl*. cry-m*' and 'ctrl*. per, tim-d*', respectively). The statistical difference from the controls is shown as a p-value. (*B*) Individual τ values are plotted as a dot for each male, red bars depict means \pm SEMs (values shown in parenthesis if <10 % of individuals were rhythmic). (C) Individual τ values plotted for males that showed either multiple periodic components or the τ changed during the recording. (*D*) The strength of the rhythmicity in the 'strong rhythmicity' group is shown as the PN value and red bars depict mean. (*E*) The strength of the rhythmicity in the 'complex rhythmicity' group is shown as the PN value. Wild-type control siblings are plotted for each genotype separately in panels *A* and *E*).

Supplementary Figure 13. TIM-d domains and protein alignment, part A. *P. apterus* TIM-d 03 mutant protein sequence and six *P. apterus* wt TIM-d isoforms were aligned to *Drosophila* TIM-d (NP_001334730.1). Dashes (-) indicate gaps in the alignment, amino acids are color-coded according to their biochemical properties, and asterisks correspond to positions of a stop codons, which in mutant results in a premature termination of the TIM-d⁰³ protein. Major functional domains were highlighted under *Drosophila* TIM-d together with important residues (indicated by grey arrows), whose mutations in *Drosophila* produce altered τ [\(33-36\)](#page-54-1). L-TIM indicates N-terminal protein extension resulting from alternative translation start in *ls-tim* allele [\(37,](#page-55-0) [38\)](#page-55-1). All major functional domains and key residues of TIM-d seem to be conserved in *P. apterus.*

Supplementary Figure 14. TIM-d domains and protein alignment, part B. The second part of the protein alignment depicting six *P. apterus* wt TIM-d isoforms aligned to *Drosophila* TIM-d (NP_001334730.1). Dashes (-) indicate gaps in the alignment, and amino acids are color-coded according to their biochemical properties. Major functional domains were highlighted under *Drosophila* TIM-d together with important residues (indicated by grey arrows), whose mutations in *Drosophila* produce altered τ [\(33,](#page-54-1) [36,](#page-55-2) [39,](#page-55-3) [40\)](#page-55-4). All major functional domains and key residues of TIM-d seem to be conserved in *P. apterus.*

Supplementary Figure 15. Examples of *P. apterus* **locomotor activity shown as doubleplotted actogram.** The activity of adult males was recorded at 25 ºC and light-dark cycles for five days. Then, males were released to constant-dark conditions (indicated by grey arrow). (*A*) Typical examples of arrhythmic *cry-m⁰⁴* homozygotes, (*B*) *cry-m⁰⁴* homozygotes with multiple periodic components, or the τ changed during the recording, (C) $\lim_{\sigma \to 0}$ homozygotes, and (D) wild-type males are shown.

suspicious. (*A*) Unrooted tree containing representative Metazoan CRYs, two *Arabidopsis thaliana* CRY proteins, *Bemisia tabaci* XP_018906320, and CRY proteins from plants and Ascomycota (Fungi) (66 protein sequences in total, RAxML, GAMMA-based Likelihood: - 49344.467111). *B. tabaci* branches within DASH group, however, (*B*) Detailed inspection points to its clear relatedness to plant and fungal CRYs. Although horizontal gene transfer from plant or fungi to *Bemisia* cannot be excluded, the cross-contamination seems to be the most parsimonious explanation for the origin of the sequence.

Supplementary Materials and Methods

Animal model

Linden bugs, *Pyrrhocoris apterus*, were reared at 25 ± 0.5 °C under diapausepreventing long photoperiod of 18 h light and 6 h dark with access to linden seeds (*Tilia cordata*) and water *ad libitum*. The majority of experiments (RNA interference, CRISPR/Cas9 gene-editing of *per* and *tim-d* genes) were performed on Roana strain, whereas Oldrichovec strain was used for *cry-m* gene editing. See [\(1\)](#page-53-1) for details of the strain's origin.

Circadian clock gene discovery in *Pyrrhocoris apterus*

Circadian clock gene homologs were identified in *P. apterus* in-house Illuminabased brain transcriptomes using the BLAST algorithm in the Geneious Prime 21.0.3 program (Biomatters, New Zealand, https://www.geneious.com/). As queries, protein sequences of circadian clock genes from *Drosophila melanogaster* and mouse were used. The full-length sequences were confirmed, and alternatively-spliced isoforms were identified in full-cDNA sequences obtained by Oxford Nanopore Technology (Oxford Nanopore, Oxford, UK) from male and female brains. These curated transcriptomic data were further compared to the in-house *P. apterus* genome draft to define exons and introns. Sequences used in this study were uploaded to GenBank (see Table S3 for accession numbers). The entire *P. apterus* genome and transcriptome will be published elsewhere. Putative functional domains in PER, TIM-d, and CRY-m were predicted on the homology to already established domains in *D. melanogaster* and mouse orthologs.

RNA interference (RNAi)

RNAi was performed as in [\(2-5\)](#page-53-2). Briefly, two non-overlapping fragments located within the open reading frame of each gene were amplified using PCR (see Table S4 for the exact position of each fragment), cloned into pGEM-T Easy (Promega), and inserts were verified by Sanger sequencing. Templates for dsRNA *in-vitro* synthesis were prepared from pGEM-T Easy clones by PCR using M13 forward and pGEM-RNAi reverse 5'- TAATACGACTCACTATAGGGGACACTATAGAATACT-3' primer replacing SP6 to T7 promoter. Double-stranded RNA was synthesized using MEGAscript T7 transcription kit (Ambion/ThermoFisher) following the manufacturer's protocol. As a negative control, 178 bp long *beta-galactosidase* (*lacZ*) dsRNA was used. Adult males received 2 µl of dsRNA at a concentration of 4 mg/ml in Ringer's solution.

CRISPR/Cas9 gene editing

Details of *P. apterus* gene editing are described in [\(6\)](#page-53-3), here is just a brief overview: 0-12 h after egg laying embryos were injected with gRNA/Cas9 mix. Early experiments (*cry-m* editing) were performed with *Cas9* mRNA, whereas the later experiments (*per* and *tim-d* editing) relied on CAS9 protein (CP01 from PNA Bio). After 8-9 days, hatched larvae were transferred to a Petri dish supplied with water and linden seeds and allowed to grow until adulthood (G0 adults). Adults were mated to wild-type and, after first batches of eggs were laid, their gonads were dissected. PCR heteroduplex mobility assay was used to assess levels of mosaicism in gonads, and only the offspring from animals with the highest level of mosaicism were kept. In the next generation, individuals with successfully modified genes were identified from antennal-squish PCR.

Seven to nine generations of backcrosses to wt strain (~one year of backcrossing) were used to outcross possible off-target modifications. To further dissect the impact of the engineered mutation from an off-target effect and the bottleneck effect of these backcrosses, the following protocol was applied: heterozygotes were crossed together, and their adult male progeny (which consisted of the mixture of wt, heterozygotes, and homozygotes) were used to perform locomotor activity run. After the run ended and analyses of the behavior were performed, individuals were genotyped by PCR.

Locomotor activity recording and analysis

In all experiments, adult males were used for locomotor activity analysis. Bugs were individually housed in the test tubes (2.5 cm diameter, 15 cm in length) supplemented *ad libitum* with dry linden seeds and water and placed in the Locomotor Activity Monitors (LAM 25, TriKinetics Inc., Waltham, MA, USA). All activity measurements were performed in the Cooled Incubator MIR-154 (Sanyo/Panasonic, Japan) equipped with a built-in electronic timer, where bugs were synchronized for 5 days in LD conditions (18 h light, 6 h darkness) at 25 °C, followed by at least 10 days in constant darkness (DD) at 25 °C. The locomotor activity of *P. apterus* was recorded automatically in 5-min bins.

Males injected with dsRNA and their controls (intact males and males injected with *lacZ* dsRNA) were immediately placed in the Locomotor Activity Monitors. To evaluate the impact of CRISPR/Cas9-induced mutations, 2-5 day after adult ecdysis male siblings (wt, heterozygotes, and homozygotes; see the 'CRISPR/Cas9 gene editing' section for details) were run in parallel.

To determine rhythmicity and τ in the constant darkness, the Lomb-Scargle periodogram in ActogramJ plugin of ImageJ [\(7\)](#page-53-4) was employed to analyze activity from 10 consecutive days in DD. In the case of *tim-m* knockdowns, we also analyzed days 1-5 and days 6-10 separately. All actograms were further inspected by an independent investigator, who was not aware of the genotype. To describe *P. apterus* behavior in DD, three categories were defined following the description in [\(1\)](#page-53-1): 1) strong rhythm, if the PN value of the periodogram (significance level of the periodogram) crossed significance threshold and actogram passed visual inspection test; 2) complex rhythm, if multiple periodic components were identified, or if the τ changed during the recording; 3) arrhythmic, if the PN value did not reach significance threshold or actogram did not pass visual inspection test.

The statistical analysis of the differences in τ was performed using Kruskal–Wallis test with Dunn's post-hoc test using Prism 7 (GraphPad Software, La Jolla, CA, USA). RNAi males were compared to corresponding controls, intact and ds*lacZ*, whereas homozygous mutants were compared to their heterozygous and wt siblings (see the CRISPR/Cas9 gene-editing section for explanation).

Phylogenetic analyses

A systematic search for circadian clock genes in Metazoa was performed in GenBank (NCBI) protein and genomic databases, and in transcriptome shotgun assemblies (TSA) using BLAST-P and tBLASTn algorithms, respectively, with taxon limits for searches in particular lineages at the level of orders, suborders, infraorders, and species. In some cases, the genome or whole-genome shotgun contigs (wgs) were explored. As queries, protein sequences of circadian clock genes from *D. melanogaster*,

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mouse, and *P. apterus* were used. To identify precisely the type of CRY (-m, -d, 6-4 photolyase, CPD photolyase, or DASH) [\(8-11\)](#page-53-5), TIM (-d or -m) [\(12\)](#page-53-6), and PER (PER1, PER2, or PER3), protein sequences were aligned using MAFFT algorithm [\(13\)](#page-53-0) in Geneious Prime 21.0.3 (Biomatters, New Zealand), unambiguously aligned regions were trimmed and phylogenetic analysis was performed using RAxML version 8.2.11 [\(14\)](#page-53-7) in Geneious Prime 21.0.3 (Biomatters, New Zealand). Final figure illustration additions, such as the description of taxa, were performed in Illustrator CS5 (Adobe).

The Metazoan phylogeny shown in Fig. 2 is a consensus of recent molecular phylogenomic studies; namely those focused on insects [\(15\)](#page-53-8), chelicerates, and arthropods [\(16\)](#page-53-9), mollusks [\(17\)](#page-54-2), vertebrates [\(18\)](#page-54-3), protostomian/deuterostomian split [\(19\)](#page-54-4). Within the richest group, insects, phylogenomic studies focused on Polyneoptera [\(20\)](#page-54-5), Blattodea [\(21\)](#page-54-6), hemipteroid assembly [\(22\)](#page-54-7), Hymenoptera [\(23\)](#page-54-8), Coleoptera [\(24\)](#page-54-9), and Lepidoptera [\(25\)](#page-54-10), were used as a reference for the corresponding part of the tree depicting the metazoan phylogeny.

Extended description of the Circadian Clock Gene Phylogeny

Phylogeny and evolution of circadian clock genes in Metazoa

The remarkable recent progress in Metazoan phylogenomics, the amount of TSA data, and a growing number of sequenced genomes allowed us to explore the circadian clock genes systematically across all major Metazoan groups. Here, we focus on lineagespecific gene losses which are well supported from multiple species, whole-genome assemblies, and deep sequencing of the entire transcriptomes. These losses are also highlighted in Fig. 2 of the study and summarized in Table S2.

PERIOD

PER protein-coding sequences were identified in all Metazoan species with the exception of one basal deuterostomian lineage consisting of Echinodermata and Hemichordata. The phylum Echinodermata, with starfish, sea urchins, and sea cucumbers, contains several species with well-sequenced genomes, including the purple sea urchin *Strongylocentrotus purpuratus* [\(26\)](#page-54-11) and the crown-of-thorns starfish *Acanthaster planci* [\(27\)](#page-54-12). The genome of hemichordates is also available [\(28\)](#page-54-13). Given the reasonable quality of these genomes, and the solid amount of TSA data, the absence of *per* in those two phyla is the most parsimonious explanation. Gene multiplication was observed in all vertebrates leading to three *period* gene paralogs, albeit reduced to only two of them in some lineages.

TIMELESS

Two TIM paralogs, TIM-d (the *Drosophila*-type) and TIM-m (the mammalian-type) exist in Metazoa [\(12\)](#page-53-6). The phylogenetic analysis undoubtedly separated them into two clusters (Fig. S3). TIM-m is present in all analyzed organisms consistently with its essential role in development [\(29,](#page-54-14) [30\)](#page-54-15). TIM-d is present in both Deuterostomia and Protostomia, however, three apparent gene losses were identified in: (*i*) Chordata, a lineage containing the lancelet *Branchiostoma* (Cephalochordata), the lamprey *Petromyzon* (Cyclostomata), and vertebrates; (*ii*) termites, with the exception of one basal termite species *Porotermes*; and (*iii*) Hymenoptera, an order containing wasps, bees, ants, and bumblebees. In all three cases, the gene loss is supported by multiple well-assembled genomes.

JETLAG (JET)

JET, a protein responsible for degradation of TIM-d and CRY-d is reliably identifiable in Protostomia, where it was lost several times in (*i*) Cimicomorpha and Pentatomorpha, two large heteropteran groups, (*ii*) in aphids, (*iii*) Psocodea, a group containing lice, (*iv*) Hymenoptera, (*v*) Neuropterida, and (*vi*) crown Coleoptera, including the red flour beetle *Tribolium castaneum*. In Deuterostomia, we identified FBXL15 as proteins similar in sequence to JET and branching at the base of the protostomian JET cluster, thus, we refer to them as JET-like.

FBXL 3/21 proteins

FBXL3 and FBXL21 are two closely related CRY-m-interacting vertebrate paralogs [\(13,](#page-53-0) [31,](#page-54-0) [32\)](#page-54-16) that result from genome duplication, which took place in the ancestor of all known vertebrates. Thus, the original protein-coding gene is described as *FBXL3/21*. *FBXL3/21* was lost in: (*i*) mollusks and annelids, (*ii*) hemipteroid assembly (Heteroptera, Auchenorrhyncha, Sternorrhyncha), that is a large group containing true bugs, cicadas, planthoppers, aphids, psyllids, etc., (*iii*) Psocodea, (*iv*) and Holometabola except for Hymenoptera, where the sequence is well conserved (Fig. S2 panels B and D).

CRYPTOCHROMES

Metazoan CRYPTOCHROMES and PHOTOLYASES can be organized into five groups: CRY-d known as the *Drosophila*-type, CRY-m known from the mammalian clock, 6-4 PHOTOLYASE (6-4 PL), CPD PHOTOLYASE (CPD-PL), which is also known in *Drosophila* as PHOTOREPAIR, and DASH (*Drosophila*, *Arabidopsis*, *Synechocystis*, *Human*)-type CRY. Although the sequences can reliably be assigned to a specific group

reflecting its origin, the phylogenetic relationship does not guarantee the protein still possesses specific biochemical properties.

CRY-d was lost: (*i*) in all chordates (but is present in basal deuterostomian lineage, Echinodermata and Hemichordata), (*ii*) in the subset of Blattodea containing all termites and three roach families: Cryptocercidae, Lamproblattidae, and Blattidae. (*iii*) In Cimicomorpha and Pentatomorpha, two large heteropteran groups, (*iv*) parasitic lice, (*v*) Hymenoptera, and (*vi*) crown Coleoptera (beetles).

CRY-m was only lost in Cyclorrhapha, a crown group of Diptera.

6-4 PL forms a sister group to CRY-m and was lost in: (*i*) mammals, (*ii*) Cephalopoda (squids, octopuses), (*iii*) all Blattodea (cockroaches and termites), (*iv*) all Heteroptera, (*v*) parasitic lice, (*vi*) Hymenoptera, and (*vii*) crown Coleoptera. 6-4 PL was independently duplicated in the lancelet *Branchiostoma* and vertebrates, where it was reduced to one copy in birds and lost in mammals.

CPD PL was lost in: (*i*) placental mammals, (*ii*) termites and sister group Cryptocercidae, (*iii*) parasitic lice, (*iv*) and crown Coleoptera.

DASH was lost in: (*i*) mammals, (*ii*) cephalopods, (*iii*) chelicerates, (*iv*) and all insects. Although we were able to find a DASH-like sequence in *Bemisia*. However, its detailed phylogenetic reconstruction indicates the sequence is branching among DASH of plants and fungi, thus we probably witness sample contamination, which is in a plantsucking insect fairly conceivable option. However, we cannot rule out a horizontal gene transfer at this point, albeit it is an unlikely explanation.

P. apterus timeless gene structure and its alternatively spliced isoforms

In P. apterus tim-d, the deletion was engineered within the 7th exon, resulting in a frameshift followed by a premature stop codon. The only alternative splicing of *tim-d* was detected in downstream exons 9, 17, and 18 (Fig. 4A and Figs. S13 and S14), with the engineered deletion itself not affecting the splicing of exons 7 and 8 (Fig. S8). Therefore, *tim-d ⁰³* encodes only the initial one-third of the TIM-d protein lacking the evolutionarily conserved PER-interaction regions, nuclear localization signal, and several key amino acid residues downstream (Fig. 4A, Figs. S13 and S14). These features, essential for its proper function in *Drosophila*, are remarkably conserved also in *P. apterus* TIM-d.

Supplementary Table 1. Circadian clock gene homologs identified in Metazoa (graphically

depicted in Fig. 2)

transcriptome, or TSA *CPD photolyase* -- Not found in the genome, transcriptome, or TSA $DASH$ *timeless-d* XP_008192983 *timeless-m* XP_008201051 *period* XP_015835617 *jetlag* $\vert -\vert$ - Not found in the genome, transcriptome, or TSA *FBXL3/21* -- Not found in the genome, transcriptome, or TSA *Onthophagus taurus* Metazoa; Arthropoda; Insecta; Holometabola; Coleoptera; Polyphaga; Scarabaeidae c *ryptochrome-d cryptochromem* XP_022918997 *6-4 photolyase* -- *CPD photolyase* -- *DASH* - *timeless-d* XP_022903307 *timeless-m* XP_022919507 *period* XP_022899891 *jetlag* -- \qquad -- Not found in TSA *FBXL3/21* -- Not found in TSA *Agrilus planipennis* Metazoa; Arthropoda; Insecta; Holometabola; Coleoptera; Polyphaga; Buprestidae *cryptochrome-d* XP_025837056 *cryptochromem* XP_018331212 *6-4 photolyase* XP_018321940 *CPD photolyase* XP_018319593 *DASH* --
 timeless-d G *timeless-d* GDOC01018042 *timeless-m* XP_018327682 *period* XP_025836066 *jetlag* XP_018321770 *FBXL3/21* -- Not found in the TSA *Pogonus chalceus* Metazoa; Arthropoda; Insecta; Holometabola; Coleoptera; Adephaga; Carabidae *cryptochrome-d* JU432971 *cryptochromem* JU410080 *6-4 photolyase* JU430199 *CPD photolyase* JU423416 $DASH$ *timeless-d* JU426733; JU418895 2 partial fragments *timeless-m* JU429343 *period* JU419193 *jetlag* JU405152

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jetlag -- \vert -- Not found in the **TSA** *FBXL3/21* -- Not found in the TSA *Columbicola columbae* Metazoa; Arthropoda; Insecta; Paraneoptera; Psocodea; Phthiraptera; Philopteridae *cryptochrome-d* - *cryptochromem* GCWB01035766 *6-4 photolyase* -- *CPD photolyase* -- *DASH* -*timeless-d* GCWB01033489 *timeless-m* GCWB01038026 *period* GCWB01036402 *jetlag* $\vert -\vert$ -- Not found in the TSA *FBXL3/21* -- Not found in the TSA *Pediculus humanus* Metazoa; Arthropoda; Insecta; Paraneoptera; Psocodea; Phthiraptera; Pediculidae c *ryptochrome-d cryptochromem* XP_002430545 *6-4 photolyase* -- *CPD photolyase* -- *DASH* - *timeless-d* EEB19683 *timeless-m* EEB13198 *period* XP_002426301 *jetlag* -- Not found in the genome, transcriptome, or **TSA** *FBXL3/21* -- Not found in the genome, transcriptome, or TSA *Frankliniella occidentalis* Metazoa; Arthropoda; Insecta; Paraneoptera; Thysanoptera; Thripidae *cryptochrome-d* GCYR01014055 *cryptochromem* GAXD01023628 *6-4 photolyase* GCYR01020055 *CPD photolyase* | KAE8748624 $DASH$ *timeless-d* XP_026280944 *timeless-m* XP_026294102 *period* XP_026278055 *jetlag* XP_026275107 *FBXL3/21* XP_026283316 *Orothrips kelloggi* Metazoa; Arthropoda; Insecta; Paraneoptera; Thysanoptera; Aelothripidae *cryptochrome-d* GCXT01021188 *cryptochromem* GCXT01026378 *6-4 photolyase* GCXT01023161 *CPD photolyase* GCXT01015659 $DASH$ *timeless-d* GCXT01027714

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Metazoa; Mollusca; Cephalopoda; Octopoda; Octopodidae *6-4 photolyase* -- not in TSA of any Cephalopoda (taxid:6605) *CPD photolyase* XP_029648244 *DASH* \qquad -- \qquad not in TSA of any Cephalopoda (taxid:6605) *timeless-d* XP_029642111 *timeless-m* XP_029654177 *period* XP_029633045 *jetlag* JR436235 *FBXL3/21* -- Not found in the TSA *Sepia esculenta* Metazoa; Mollusca; Cephalopoda; Sepiida; Sepiidae *cryptochrome-d* GGQU01009236 *cryptochromem* GGQU01028147 *6-4 photolyase* -- not in TSA of any Cephalopoda (taxid:6605) *CPD photolyase* GGQU01005854 *DASH* \qquad -- \qquad not in TSA of any Cephalopoda (taxid:6605) *timeless-d* GGQU01018501 *timeless-m* GGQU01119589 *period* | GGQU01013326 *jetlag* GGQU01008949 *FBXL3/21* -- Not found in the TSA *Strongylocentrotus purpuratus* Metazoa; Echinodermata; Echinoidea; Camarodonta; Strongylocentrotidae *cryptochrome-d* XP_030843606 *cryptochromem* XP_785873 *6-4 photolyase* XP_030853363 *CPD photolyase* XP_030838243 *DASH* XP_030855350
 timeless-d XP_011666280 *timeless-d* XP_011666280 *timeless-m* XP_784350 *period* \qquad -- \qquad Absent in the TSA, proteins, and genome *jetlag-related* XP_030835612 *FBXL3/21* XP_011668197 *Acanthaster planci* Metazoa; Echinodermata; Asteroidea; Valvatida; Acanthasteridae *cryptochrome-d* XP_022112080 *cryptochromem* XP_022093922 *6-4 photolyase* XP_022085333 *CPD photolyase* XP_022095977 *DASH* XP_022106989 *timeless-d* XP_022095151 *timeless-m* XP_022107896 *period* -- Absent in the TSA, proteins, and genome

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timeless-d -- Absent in the genome, transcriptome and TSA *timeless-m* NP_001265529 *period1* XP_005172684 *period2* AAI63549 *period3* AAI62472 *jetlag-related* NP_998107 *FBXL3/21* NP_001005773; XP_693270 2 paralogs *Xenopus laevis* Metazoa; Chordata; Vertebrata; Tetrapoda; Amphibia; Anura; Pipidae *cryptochrome-d* -- Absent in the genome, transcriptome, and TSA *cryptochromem* AAK94667; AAK94665 2 paralogs *6-4 photolyase* NP_001088990; NP_001081421 2 paralogs *CPD photolyase* NP_001089127 *DASH* NP_001084438 *timeless-d* -- Absent in the genome, transcriptome, and TSA *timeless-m* XP_018105525 *period1* XP_018106090 *period2* NP_001081098 *period3* XP_018081638; XP_018083480 *jetlag-related* NP_001079747 *FBXL3/21* XP_018105395; XP_018107511 *Anolis carolinensis* Metazoa; Chordata; Vertebrata; Tetrapoda; Sauria; Lepidosauria; Squamata; Dactyloidae *cryptochrome-d* -- Absent in the genome *cryptochromem* XP_003220970; XP_003214689 2 paralogs *6-4 photolyase* XP_008108122; XP_003225762 2 paralogs *CPD photolyase* XP_003227011 *DASH* XP 008110409 *timeless-d* -- Absent in the genome *timeless-m* XP_016846705 *period1* XP_008117781 *period2* XP_008104509 $period3$ *jetlag-related* XP_003223176 *FBXL3/21* XP_008113732; XP_003218703 *Taeniopygia guttata* Metazoa; Chordata; Vertebrata; Tetrapoda; Sauria; Archelosauria; *cryptochrome-d* -- Absent in the genome *cryptochromem* XP_030130159; XP_030118992 2 paralogs *6-4 photolyase* XP_012426408 *CPD photolyase* | XP 030136454 *DASH* XP_030120072

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Supplementary Table 2. Summary on genes absence in entire metazoan lineages

Supplementary Table 3. Circadian clock gene homologs and closely related genes identified in the Linden bug, *Pyrrhocoris apterus*

Supplementary Table 4. Primers used to clone cDNA templates used for dsRNA synthesis

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