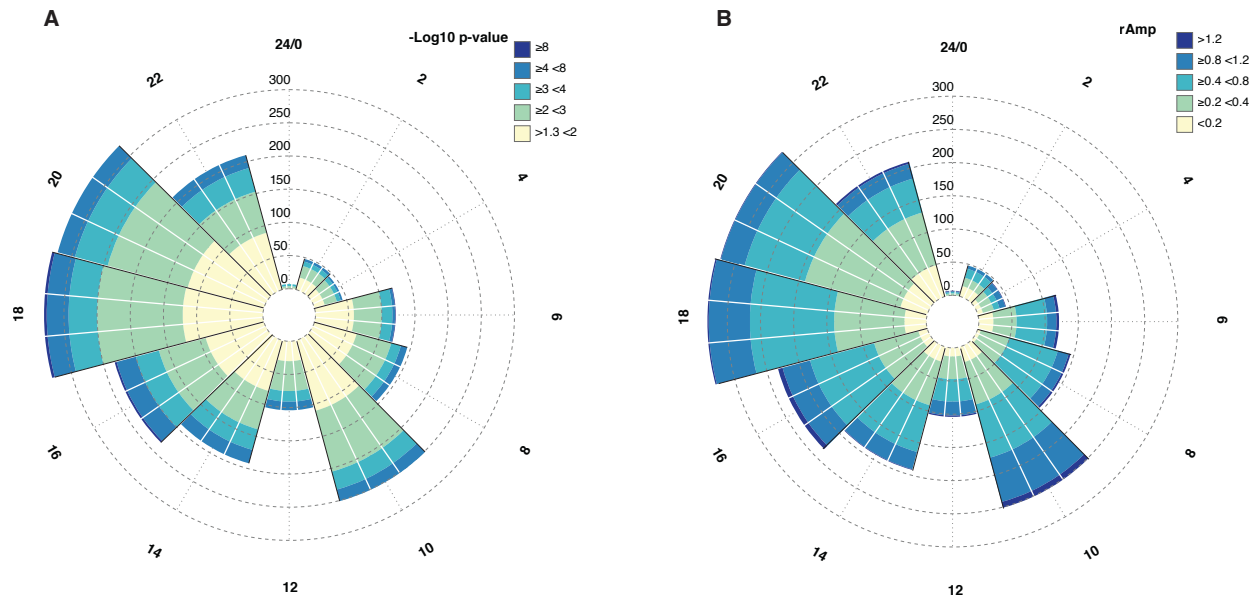


Supplemental Figures and Tables.

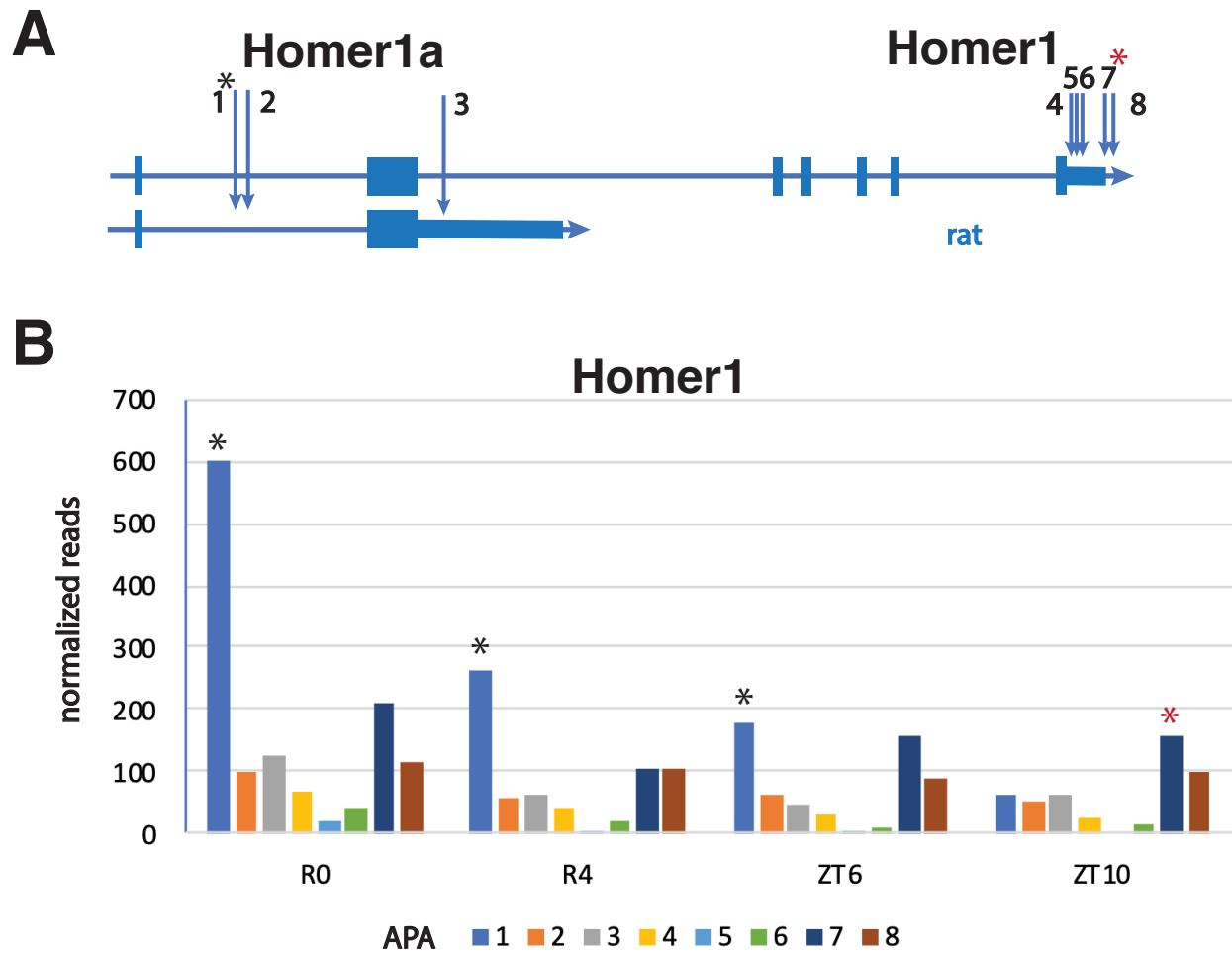
Supplemental Figure S1	Rose Plots
Supplemental Figure S2	Homer1 gene
Supplemental Table S3	GO & Pathways for diurnal APAs
Supplemental Table S4	GO & Pathways by phase
Supplemental Table S6	GO and Pathways for 12h cyclers

Legends for separate Tables:

Supplemental Table S1
Supplemental Table S2
Supplemental Table S5
Supplemental Table S7



Supplementary Figure S1. Rose plots showing the number of diurnal PASs clustered by phase of peak expression centered every 2 h from 2 to 24 h. The relative number of PASs are represented by the radius (length) of each segment. (A) Color represents a breakdown of the $-\log_{10}$ of p-values. (B) Color represents a breakdown of the relative amplitudes.



Supplementary Figure S2. A map of the distal half of the rat Homer1 gene including Homer1a and a chart of reads of the 8 APAs found. (A) Dark blue arrows indicate the positions of APA sites. APA #1, which creates a Homer1a isoform, had significant differential expression in the ZT6 vs R0 comparison. (B) Normalized read counts for each of the eight APAs plotted for R0, R4, ZT6 and ZT10. Note that APA #1 is the most abundant for the first three, whereas #7 is the most abundant at ZT10.

Supplemental Table S3. Gene Ontology and Pathway analyses of genes with ≥ 2 APAs and one or more diurnal APA site. Gene ontology terms and pathways identified by WebGestalt using the 1,173 genes with APAs that exhibited time-of-day oscillations and had two or more total APAs. GO and pathway descriptions are followed by the size (total number of genes that the term is comprised of), overlap (number of input genes matching the term), expect (number of input genes expected to match by chance), ratio (number of actual/expected matches), pValue (probability), FDR (false discovery rate; probability adjusted for multiple sampling), database (For GO analysis: BP, Biological process; CC, Cellular Component; MF, Molecular Function. For pathway analysis: KEGG, Kyoto Encyclopedia of Genes and Genomes; Panth, Panther; React, Reactome; Wiki, Wikipathway), input (gene symbols of input that match the GO or Pathway term).

	GO description	size	overlap	expect	ratio	pValue	FDR	database	input
Phase 2	neuron to neuron synapse	322	11	1.87	5.88	2.30E-06	2.20E-03	CC	Syt11;Sh3gl2;Pak3;Erc2;Grik2;Nrgn;Syt7;Dlgap2;Nlgn1;Grin2b;Cnksr2
Phase 2	glutamatergic synapse	368	11	2.14	5.14	8.27E-06	3.04E-03	CC	Cnr1;Sh3gl2;Pak3;Ywhae;Grik2;Nrgn;Ephb1;Syt7;Nlgn1;Grin2b;Cnksr2
Phase 2	monoamine transport	85	6	0.49	12.14	9.54E-06	3.04E-03	BP	Agt;Prkcb;Syt11;Cnr1;Syt7;Gpm6b
Phase 2	synaptic membrane	396	11	2.30	4.78	1.65E-05	3.94E-03	CC	Gabrg3;Syt11;Cnr1;Erc2;Grik2;Nrgn;Syt7;Dlgap2;Nlgn1;Grin2b;Cnksr2
Phase 2	amine transport	105	6	0.61	9.83	3.20E-05	6.13E-03	BP	Agt;Prkcb;Syt11;Cnr1;Syt7;Grin2b
Phase 2	axon part	389	10	2.26	4.42	7.93E-05	1.24E-02	CC	Slc32a1;Dpysl3;Syt11;Cnr1;Ywhae;Erc2;Grik2;Syt7;Grin2b;Kif1b
Phase 2	scaffold protein binding	41	4	0.24	16.79	9.05E-05	1.24E-02	MF	Ywhae;Nlgn1;Grin2b;Kif1b
Phase 2	postsynaptic specialization	327	9	1.90	4.74	1.11E-04	1.24E-02	CC	Syt11;Pak3;Erc2;Grik2;Nrgn;Dlgap2;Nlgn1;Grin2b;Cnksr2
Phase 2	divalent inorganic cation homeostasis	409	10	2.38	4.21	1.20E-04	1.24E-02	BP	Pdzd8;Agt;Vapb;Cnr1;Cacna1i;Sppl3;jph4;Ywhae;Grik2;Grin2b
Phase 2	regulation of membrane potential	334	9	1.94	4.64	1.30E-04	1.24E-02	BP	Gabrg3;Cnr1;Cacna1i;Ywhae;Grik2;Nlgn1;Grin2b;Gnaq;Kcnh7
Phase 2	organic hydroxy compound transport	199	7	1.16	6.05	1.52E-04	1.32E-02	BP	Agt;Prkcb;Syt11;Slco1c1;Cnr1;Syt7;Gpm6b
Phase 2	regulation of response to drug	94	5	0.55	9.15	2.12E-04	1.69E-02	BP	Agt;Prkcb;Syt11;Cnr1;Syt7
Phase 2	ammonium transport	98	5	0.57	8.78	2.58E-04	1.90E-02	BP	Prkcb;Syt11;Cnr1;Syt7;Gpm6b
Phase 2	cellular metal ion homeostasis	455	10	2.64	3.78	2.85E-04	1.94E-02	BP	Pdzd8;Agt;Vapb;Cnr1;Cacna1i;Sppl3;jph4;Ywhae;Grik2;Grin2b
Phase 2	regulation of trans-synaptic signaling	375	9	2.18	4.13	3.09E-04	1.97E-02	BP	Agt;Cnr1;jph4;Grik2;Nrgn;Ephb1;Syt7;Nlgn1;Grin2b
Phase 2	synaptic vesicle cycle	163	6	0.95	6.33	3.63E-04	2.17E-02	BP	Slc32a1;Syt11;Cnr1;Sh3gl2;Syt7;Nlgn1
Phase 2	GABA-ergic synapse	66	4	0.38	10.43	5.77E-04	3.25E-02	CC	Slc32a1;Gabrg3;Cnr1;Syt7
Phase 2	drug transport	182	6	1.06	5.67	6.51E-04	3.46E-02	BP	Agt;Slc32a1;Prkcb;Syt11;Cnr1;Syt7
Phase 2	neuron projection terminus	185	6	1.08	5.58	7.09E-04	3.57E-02	CC	Slc32a1;Syt11;Erc2;Grik2;Syt7;Grin2b
	GO description	size	overlap	expect	ratio	pValue	FDR	database	input
Phase 10	localization within membrane	130	9	1.06	8.48	1.11E-06	1.06E-03	BP	Nptx1;Arhgap44;Glrbc;Gsn;Efnb2;Myo5b;Erbin;Lrrc7;Kalrn
Phase 10	protein-containing complex localization	177	9	1.45	6.22	1.40E-05	6.69E-03	BP	Nptx1;Arhgap44;Pa2g4;Ttc21a;Efnb2;Myo5b;Erbin;Lrrc7;Kalrn
Phase 10	regulation of postsynaptic membrane neurotransmission	73	6	0.60	10.06	2.81E-05	8.95E-03	BP	Nptx1;Arhgap44;Efnb2;Erbin;Lrrc7;Kalrn
Phase 10	glutamatergic synapse	368	12	3.01	3.99	4.49E-05	1.07E-02	CC	Nptx1;Arhgap44;Grik1;Efnb2;Cacna1c;Myo5b;Erbin;Fmpd4;Cttnbp2;Grm8;Lrrc7;Kalrn
Phase 10	protein localization to synapse	60	5	0.49	10.20	1.26E-04	2.41E-02	BP	Nptx1;Arhgap44;Erbin;Lrrc7;Kalrn
Phase 10	endosomal transport	148	7	1.21	5.79	2.06E-04	3.29E-02	BP	Arhgap44;Rab7b;Leprpt;Ykt6;Myo5b;Erbin;Lrrc7
	GO description	size	overlap	expect	ratio	pValue	FDR	database	input
Phase 18	Signaling by VEGF	80	10	1.58	6.32	3.69E-06	6.83E-03	React	Actb;Ptik2b;Src;Nck2;Nras;Prr5;Mapk1;Ftl1;Pik3r1;Mapk14
Phase 18	Signaling by Receptor Tyrosine Kinases	304	19	6.01	3.16	9.48E-06	7.88E-03	React	Actb;Tec;Ptik2b;Src;Frs2;Atf1;Nck2;Ptpn11;Nras;Prr5;Mapk1;Mapkap1;Spre1;Atp6v1c1;Ptkrc;Ftl1;Pik3r1;Mapk14;Ntrk2
Phase 18	VEGFA-VEGFR2 Pathway	73	9	1.44	6.24	1.28E-05	7.88E-03	React	Actb;Ptik2b;Src;Nck2;Nras;Prr5;Mapk1;Pik3r1;Mapk14
Phase 18	Signaling by NTRKs	59	8	1.17	6.86	1.92E-05	8.91E-03	React	Src;Frs2;Atf1;Nras;Mapk1;Pik3r1;Mapk14;Ntrk2
Phase 18	Signaling by FGFR1	45	7	0.89	7.87	2.58E-05	9.56E-03	React	Src;Frs2;Ptpn11;Nras;Mapk1;Spre1;Pik3r1
Phase 18	Estrogen signaling pathway	133	11	2.63	4.18	6.46E-05	1.99E-02	KEGG	Krt26;Src;Adcy8;Nras;Plcb1;Hsp90b1;Mapk1;Fkbp4;Fkbp5;Pik3r1;Gnao1
Phase 18	response to carbohydrate	252	17	5.36	3.17	2.80E-05	2.36E-02	BP	Ptk2b;Casp3;Hmgcr;Adcy8;Cdk16;Hmgbl1;Ufm1;Mfn1;Plcb1;Giul;Smad4;Ppargc1a;Pde8b;Mef2c;Slc8a1;Wdr35;Pik3r1
Phase 18	neuron to neuron synapse	322	19	6.85	2.77	6.03E-05	2.36E-02	CC	Eef2k;Actb;Ptik2b;Dnajb1;Src;Iqsec3;Plekha5;Sh2d5;Adcy8;Nck2;Shisa7;Kcnh1;Dlg3;Mapk1;Cdh2;Synj2bp;Scn8a;Grm5;Ntrk2
Phase 18	postsynaptic specialization	327	19	6.96	2.73	7.41E-05	2.36E-02	CC	Eef2k;Actb;Ptik2b;Dnajb1;Src;Iqsec3;Plekha5;Sh2d5;Adcy8;Nck2;Shisa7;Kcnh1;Dlg3;Mapk1;Cdh2;Synj2bp;Scn8a;Grm5;Ntrk2
Phase 18	Downstream signal transduction	24	5	0.47	10.54	9.05E-05	2.39E-02	React	Src;Nck2;Ptpn11;Nras;Pik3r1
Phase 18	Thyroid hormone signaling pathway	118	10	2.33	4.29	1.13E-04	2.52E-02	KEGG	Actb;Med27;Src;Hdac1;Fxyd2;Nras;Plcb1;Slc2a1;Mapk1;Pik3r1
Phase 18	Signaling by FGFR4	40	6	0.79	7.59	1.22E-04	2.52E-02	React	Src;Frs2;Ptpn11;Nras;Mapk1;Pik3r1
Phase 18	Signaling by FGFR3	41	6	0.81	7.40	1.41E-04	2.55E-02	React	Src;Frs2;Ptpn11;Nras;Mapk1;Pik3r1
Phase 18	Signaling by EGFR	27	5	0.53	9.37	1.64E-04	2.55E-02	React	Src;Ptpn11;Nras;Ptkrc;Pik3r1
Phase 18	EGFR1 Signaling Pathway	173	12	3.42	3.51	1.65E-04	2.55E-02	Wiki	Ralb;Ptik2b;Src;Hdac1;Asap1;Atf1;Nck2;Ptpn11;Nras;Mapk1;Pik3r1;Mapk14
Phase 18	GAB1 signalosome	7	3	0.14	21.68	2.52E-04	3.20E-02	React	Src;Ptpn11;Pik3r1
Phase 18	Ras signaling pathway	238	14	4.71	2.98	2.73E-04	3.20E-02	KEGG	Ets2;Ralb;Gng4;Efn3;Pla2g12a;Stk4;Ptpn11;Rgl1;Nras;Mapk1;Afdn;Ftl1;Pik3r1;Ntrk2
Phase 18	Signaling by Interleukins	238	14	4.71	2.98	2.73E-04	3.20E-02	React	Psmb3;Tec;Ptik2b;Casp3;Atf1;Ptpn11;Psm5d5;I1rap;Mapk1;Brwd1;Irk1;Pik3r1;Mapk14;Skp1
Phase 18	Relaxin signaling pathway	132	10	2.61	3.83	2.86E-04	3.20E-02	KEGG	Gng4;Src;Adcy8;Nras;Plcb1;Mapk1;Col1a2;Pik3r1;Mapk14;Gnao1
Phase 18	Rap1 signaling pathway	213	13	4.21	3.09	3.16E-04	3.20E-02	KEGG	Actb;Ralb;Efn3;Src;Adcy8;Nras;Plcb1;Mapk1;Afdn;Ftl1;Pik3r1;Mapk14;Gnao1
Phase 18	Gap junction	88	8	1.74	4.60	3.41E-04	3.20E-02	KEGG	Tubb2b;Gucyl1a1;Src;Adcy8;Nras;Plcb1;Mapk1;Grm5
Phase 18	Myometrial Relaxation and Contraction Pathways	135	10	2.67	3.75	3.42E-04	3.20E-02	Wiki	Grk5;Ets2;Actb;Gng4;Gucyl1a1;Pkiq;Adcy8;Atf1;Grk4;Slc8a1
Phase 18	mRNA Processing	112	9	2.21	4.06	3.71E-04	3.20E-02	Wiki	Prrt1;Nxf1;Prpf4;Sf3a3;Srsf7;Dicer1;Snrpb;Sfpq;Papola
Phase 18	Signaling by SCF-KIT	32	5	0.63	7.90	3.77E-04	3.20E-02	React	Tec;Src;Ptpn11;Nras;Pik3r1
Phase 18	Signaling by NTRK1 (TRKA)	49	6	0.97	6.19	3.85E-04	3.20E-02	React	Frs2;Atf1;Nras;Mapk1;Pik3r1;Mapk14
Phase 18	Cohesin Loading onto Chromatin	8	3	0.16	18.97	3.97E-04	3.20E-02	React	Stag1;Pds5b;Stag2
Phase 18	PIP3 activates AKT signaling	193	12	3.82	3.14	4.53E-04	3.49E-02	React	Psmb3;Src;Hdac1;Frs2;Ptpn11;Psm5d5;Prr5;I1rap;Mapk1;Mapkap1;Irk1;Pik3r1
Phase 18	Signaling by FGFR	71	7	1.40	4.99	4.90E-04	3.59E-02	React	Src;Frs2;Ptpn11;Nras;Mapk1;Spre1;Pik3r1
Phase 18	RET signaling	34	5	0.67	7.44	5.04E-04	3.59E-02	React	Dok4;Src;Frs2;Ptpn11;Pik3r1
Phase 18	Establishment of Sister Chromatid Cohesion	9	3	0.18	16.86	5.87E-04	4.02E-02	React	Stag1;Pds5b;Stag2
Phase 18	IL-6 Signaling Pathway	96	8	1.90	4.21	6.15E-04	4.07E-02	Wiki	Tec;Ptik2b;Casp3;Hdac1;Ptpn11;Mapk1;Pik3r1;Mapk14
Phase 18	forebrain development	295	17	6.28	2.71	1.96E-04	4.38E-02	BP	Rtn4r1;Arpc5;Casp3;Dnajb1;Src;Hdac1;Plcb1;Slc2a1;Ext1;Ran;Ppargc1a;Mef2c;Slc8a1;Kif1a;Gnao1;Zeb2;Ntrk2
Phase 18	positive regulation of nervous system development	447	22	9.51	2.31	2.29E-04	4.38E-02	BP	Eef2k;Ptik2b;Tubb2b;Hdac1;Adam17;Sox11;Atf1;Trpc6;Jade2;Hmgbl1;Mfn1;Gprc5b;I1rap;Kidins220;Enpp2;Mef2c;Plas2;Brinp1;Grm5;Zeb2;Ntrk2;Nrxn1
Phase 18	IL-2 Signaling Pathway	76	7	1.50	4.66	7.40E-04	4.73E-02	Wiki	Ets2;Ptik2b;Ptpn11;Plcb1;Mapk1;Pik3r1;Mapk14
Phase 18	Mitotic Telophase/Cytokinesis	10	3	0.20	15.17	8.26E-04	4.95E-02	React	Stag1;Pds5b;Stag2
Phase 18	Neurotrophin signaling pathway	125	9	2.47	3.64	8.28E-04	4.95E-02	KEGG	Frs2;Ptpn11;Nras;Mapk1;Kidins220;Irk1;Pik3r1;Mapk14;Ntrk2

Supplementary Table S4. Gene Ontology and Pathway analysis of diurnal PASs from genes with ≥ 2 total PASs grouped by phase of peak expression.

GO and pathway analyses were performed using the Over-representation Analysis function of the online web tool WebGestalt. Phase of peak expression and GO or pathway description is followed by the size (total number of genes that the term is comprised of), overlap (number of input genes matching the term), expect (number of input genes expected to match by chance), ratio (number of actual/expected matches), pValue (probability), FDR (false discovery rate; probability adjusted for multiple sampling), database (For GO analysis: BP, Biological process; CC, Cellular Component; MF, Molecular Function. For pathway analysis: KEGG, Kyoto Encyclopedia of Genes and Genomes; Panth, Panther; React, Reactome; Wiki, Wikipathway), input (gene symbols of input that match the GO or Pathway term).

Supplementary Table S6. Results of GO and Pathway analysis for 12 h cycling APAs. Gene ontology and pathway analyses were performed on 12 h cycling PASs from genes with ≥ 2 total APA sites using the over-representation analysis function of the online web tool WebGestalt. The GO or pathway description is followed by the size (total number of genes that the term is comprised of), overlap (number of input genes matching the term), expect (number of input genes expected to match by chance), ratio (number of actual/expected matches), pValue (probability), FDR (false discovery rate; probability adjusted for multiple sampling), database (For GO analysis: BP, Biological process; CC, Cellular Component; MF, Molecular Function. For pathway analysis: KEGG, Kyoto Encyclopedia of Genes and Genomes; Panth, Panther; React, Reactome; Wiki, Wikipathway), input (gene symbols of input that match the GO or Pathway term).

Supplementary Table S1. All nuclear PASs with raw read numbers. PAS_ID is a unique identifier for each PAS. Gene Symbol, Chromosome are listed, as well as Strand according to the convention of each chromosome. Start and End refer to the nucleotide (n.t.) positions of the 3' ends of the most extreme reads within each PAS cluster. Span is the length of the cluster and peak is the mode or most common 3' end in the cluster. The number of PASs per gene is listed. When a PAS maps to a major, known PAS, "mPAS" is indicated. Some PASs have gene biotype and transcript IDs associated with them. Total refers to the sum of the reads for all samples. Subsequent columns contain the number of reads for individual samples.

Supplementary Table S2. All diurnal PASs with meta2d calculations. PAS_ID is a unique identifier for each PAS. Gene Symbol, Chromosome are listed, as well as Strand according to the convention of each chromosome. Start and End refer to n.t. positions of the 3' ends of the most extreme reads within each PAS cluster. Span is the length of the cluster and peak is the mode or most common 3' endpoint in the cluster. The number of PASs per gene is listed. When a PAS maps to a major, known PAS, "mPAS" is indicated. Some PASs have gene biotype and transcript IDs associated with them. Total refers to the sum of the reads for all samples. Subsequent columns contain meta2d calculations for the p-value, median p-value of 5 trials, Benjamini/Hochberg adjusted p-value and its median, peak phase and its average, read number baseline, and relative amplitude (amplitude/baseline) and its average. The following columns contain calculated p-value, BH.Q, period, phase, and amplitude from each of the separate algorithms -ARS, JTK and L-S.

Supplementary Table S5. All 12 h cycling PASs with meta2d calculations. PAS_ID is a unique identifier for each PAS. Gene Symbol, Chromosome are listed, as well as Strand according to the convention of each chromosome. Start and end refer to n.t. positions of the 3' ends of the most extreme reads within each PAS cluster. Span is the length of the cluster and peak is the mode or most common 3' endpoint in the cluster. The number of PASs per gene is listed. When a PAS maps to a major, known PAS, "mPAS" is indicated. Some PASs have Gene Biotype and Transcript IDs associated with them. Total refers to the sum of the reads for all samples. Subsequent columns contain meta2d calculations for p-value, median p-value of 5 trials, Benjamini/Hochberg adjusted p-value and its median, peak phase and its average, read number baseline, and relative amplitude (amplitude/baseline) and its average. The following columns contain calculated p-value, BH.Q, period, phase, and amplitude from each of the separate algorithms -ARS, JTK and L-S.

Supplementary Table S7. Differentially expressed PASs after SD and during recovery. Comparisons are of ZT6 vs R0 (first sheet), ZT8 vs R2 (second sheet), ZT10 vs R4 (third sheet) and ZT14 vs R8 (forth sheet). We removed high variation from the first principal component systematically (~5000 PASs), resulting in improved variance estimates for low read counts. Prcomp (in R) was used to perform principal component analysis (PCA) and to find eigenvectors by way of singular value decomposition. DESeq-2 with "Apeglm" Shrinkage and the Wald Test were used to generate test statistics in R software. The FDRtool was used to determine the Local FDR. Each row has data for a different PAS. Columns show PAS_ID, a unique identifier for each PAS. Gene Symbol, Chromosome are listed, as well as Strand according to the convention of each chromosome. Start and end refer to n.t. positions of the 3' ends of the most extreme reads within each PAS cluster. Span is the length of the cluster and peak is the mode or most common 3' endpoint in the cluster. The number of PASs per gene is listed. When a PAS maps to a major, known PAS, "mPAS" is indicated. Some PASs have Gene Biotype and Transcript IDs associated with them. Total refers to the sum of the reads for all samples. Output columns include baseMean, log2FoldChange, the associated SE lfcSE, pvalue and adjusted p-value padj.