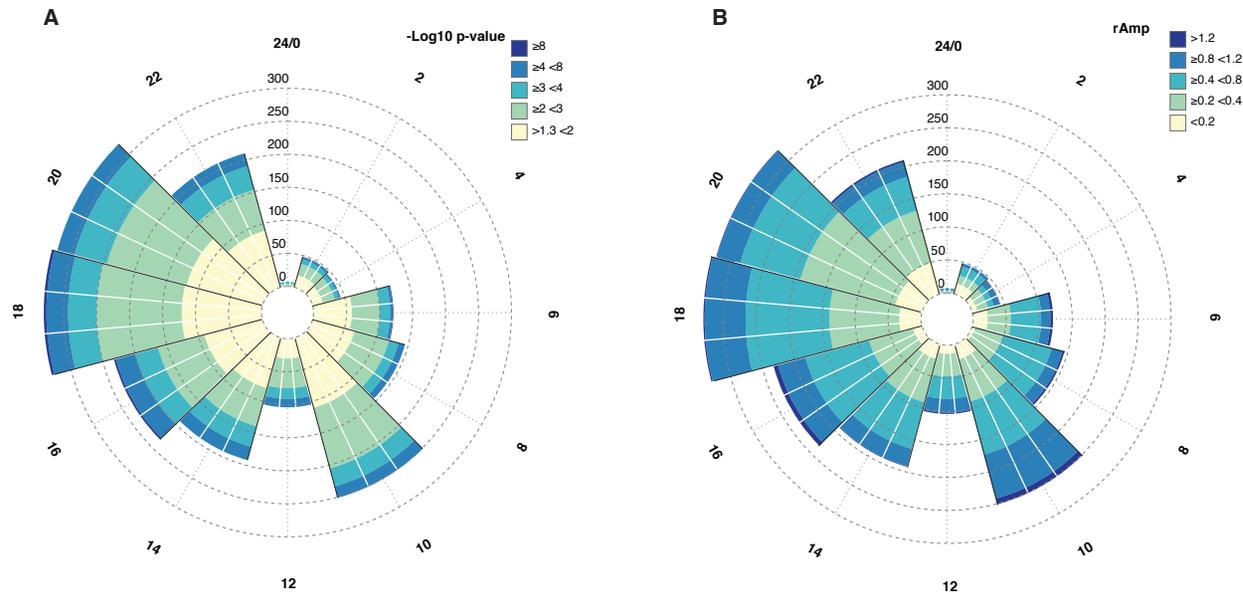


Supplemental Figures and Tables.

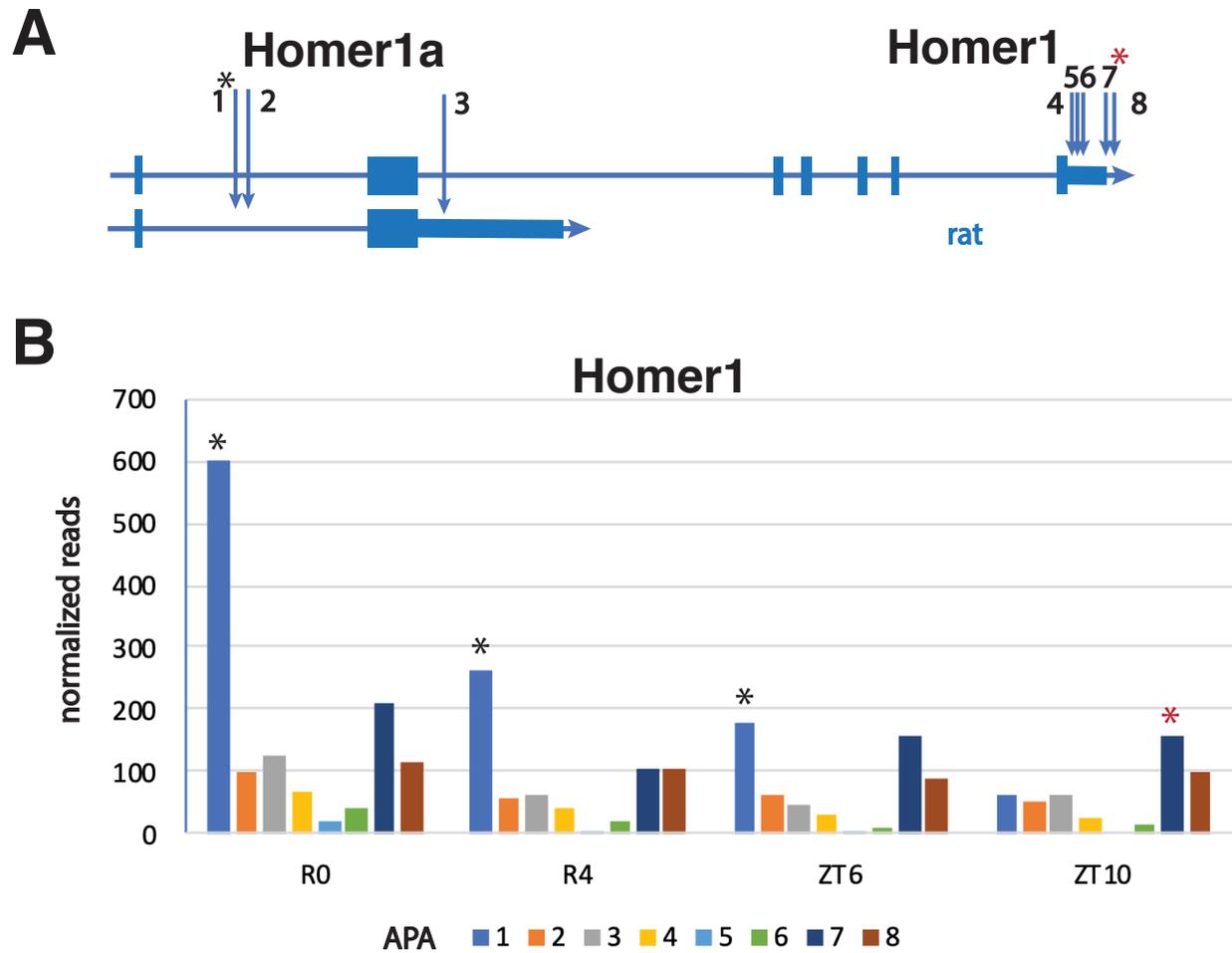
Supplemental Figure S1	Rose Plots
Supplemental Figure S2	Homer1 gene
Supplemental Table S3	GO & Pathways for diurnal APAs
Supplemental Table S4	GO & Pathways by phase
Supplemental Table S6	GO and Pathways for 12h cyclers

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;Ca2;Spp1;Spp3;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;Ca2;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;Sloc1c1;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;Ca2;Spp1;Spp3;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;Glr3;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;Ca2;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;Lepr;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;Gul;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;Pkg;Adcy8;Atf1;Grk4;Slc8a1
Phase 18	mRNA Processing	112	9	2.21	4.06	3.71E-04	3.20E-02	Wiki	Prrm1;Nxf1;Prpf4;Sf3a3;Srsf7;Dicer1;Snrpb;Sfpqa;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).

GO description	size	overlap	expect	ratio	pValue	FDR	database	input
glutamatergic synapse	368	46	14.22	3.23	1.47E-12	1.38E-09	CC	Cabp1, Ppp2r2a, Homer3, Dnrl, Linc, Wnt7a, Ppns, Myh10, Ppp1cc, Cpbp, Cbh11, Gucy1b1, Lrrm3, Trk, Fyn, LRRMT1, Ngn, Nedd5f4, Dlg4, Ywhae, Dlg1, Atp2b4, Dnm3, Gria2, Caorb4, Pcbp, Pknox2, Ngn5, Syt7, Grin1, Ctnnb2, Gird3, Rab11a, Ngn1, Pascin1, Gm8, Gm2b, Rms1, Tenm2, Atp2b2, Homer1, Mapk10, Ppp3ka, Kalm, Hlraip1, Dlgap1
regulation of trans-synaptic signaling	375	46	14.49	3.17	2.89E-12	1.38E-09	BP	Cabp1, Homer3, Dnrl, Kcnj2, Egr7, Linc, Wnt7a, Gm2b, Iqec2, Atp2b2, Cbh11, Gucy1b1, Syngt1, Atp2b2, Mapk10, Fyn, Sncg, LRRMT1, Caim1, Ngn, Nedd5f4, Crelb, Hmrl2, Pkn, Abat, Dlg4, Gria2, Caorb4, Pknox2, Ngn5, Ctrp1, Syt7, Fgfr14, Grin1, Gird3, Rab11a, Ngn1, Gm8, Gm2b, Rms1, Homer1, Ppp3ka, Ngn1
regulation of neuron projection development	422	43	16.31	2.64	5.57E-09	1.78E-06	BP	Hmnp9f, Pcpa3, Fcrl2, Dnrl, Isl1, Linc, Wnt7a, Klf4, Wsh3c, Dmck1, Ppns, Sncg, Rorb, Rorb2, Rbz1, Mln1, Ppp1r5, Sncg, Mec, Trk2, Dend5a, Camsap2, Trk, Fyn, Bim, Fkbp4, Ngn, Nedd5f4, Pafah1b1, Dlg4, Dnm3, Fgfr14, Atp2b2, Pknox2, Ngn1, Pascin1, Gm8, Gm2b, Rms1, Homer1, Ppp3ka, Kalm, Hlraip1
excitatory synapse	396	41	15.30	2.68	1.01E-09	1.91E-06	CC	Homer3, Dnrl, Linc, Lncx, Ppns, Gabra3, Atad1, Sncg, Syt11, Lrrm1, Linc, Wnt7a, Mec, Gabra1, LRRMT1, Ngn, Pknox, Kcnk1, Dlg4, Dlg1, Atp2b4, Dnm3, Gria2, Sdk1a1, Faim2, Ngn, ErbB4, Syt7, Grin1, Gird3, Cadm1, Ngn1, Pascin1, Gm8, Gm2b, Rms1, Tenm2, Atp2b2, Homer1, Hlraip1, Dlgap1, Ngn1
synapse organization	54	14	2.09	6.71	1.08E-08	1.91E-06	CC	Dnrl, Linc, Syt11, Mec, LRRMT1, Dlg4, Pcbp, Gm1, Gird3, Ngn1, Gm2b, Ngn1, Atp2b2, Homer1
postsynaptic specialization	327	36	12.64	2.97	1.23E-08	1.91E-06	BP	Angf9f7, Dnrl, Linc, Lncx, Wnt7a, Ppns, Sncg, Syt11, Mln1, Ppp1r5, Rorb2, Rbz1, Mln1, Ppp1r5, Lrrm3, Sncg, Mec, Trk2, Dend5a, Camsap2, Trk, Fyn, Bim, Fkbp4, Ngn, Nedd5f4, Pafah1b1, Dlg4, Dnm3, Fgfr14, Atp2b2, Pknox2, Ngn1, Pascin1, Gm8, Gm2b, Rms1, Homer1, Ppp3ka, Ngn1
neuron projection organization	68	15	2.63	5.71	3.47E-08	4.15E-06	BP	Dnrl, Linc, Wnt7a, Sncg, Mln1, Fyn, Abcd2, Pafah1b1, Dlg4, Dnm3, Fgfr14, Atp2b2, Homer1
neuron to neuron synapse	322	34	12.44	2.73	3.96E-08	1.06E-05	CC	Cabp1, Homer3, Dnrl, Linc, Lncx, Wnt7a, Sncg, Syt11, Lrrm3, Sncg, LRRMT1, Ngn, Pknox, Kcnk1, Trk, Fyn, Ngn, Pknox, Dlg4, Dnm3, Gria2, Ngn, ErbB4, Syt7, Grin1, Gird3, Cadm1, Ngn1, Pascin1, Gm8, Gm2b, Atp2b2, Homer1, Kalm, Hlraip1, Dlgap1
regulation of synapse structure or activity	201	25	7.77	3.22	2.39E-07	2.28E-05	BP	Dnrl, Linc, Lncx, Wnt7a, Ppns, Sncg, Myh10, Mln1, Lrrm3, Linc, Fgfr14, Fyn, LRRMT1, Nedd5f4, Pafah1b1, Dnm3, Gm1, Ctnnb2, Gird3, App, Ngn1, Homer1, Kalm, Hlraip1, Ngn1
desirable development	189	24	7.30	3.29	2.82E-07	2.46E-05	BP	Fcrl2, Dnrl, Linc, Wnt7a, Ppns, Sncg, Mln1, Mec, Trk2, Camsap2, Trk, Fyn, Nedd5f4, Pafah1b1, Dlg4, Dnm3, Hmnp9f, Epha5, Pknox2, Ngn1, Pascin1, Ppp3ka, Kalm
cell part morphogenesis	428	39	16.54	2.36	5.64E-07	4.49E-05	BP	Coxc1c, Fcrl2, Dnrl, Wnt7a, Ppns, Sncg, Myh10, Mln1, Lrrm3, Linc, Fgfr14, Fyn, LRRMT1, Nedd5f4, Pafah1b1, Dnm3, Gm1, Ctnnb2, Gird3, App, Ngn1, Homer1, Kalm, Hlraip1, Ngn1
PDZ domain binding	88	15	3.40	4.41	1.22E-06	8.97E-05	MF	Linc, Kcnp1, Cbp1, Pknox2, Gm1, Ndel, Pkn, Dlg4, Dlg1, Atp2b4, Gria2, Gird3, Cadm1, Ngn1, Atp2b2
glutamate receptor signaling pathway	78	14	3.01	4.64	1.45E-06	9.93E-05	BP	Homer3, Gria2, Fyn, Dlg4, Ppp3ka, Gria2, Gm1, Gria2, App, Ngn1, Gm8, Gm2b, Homer1, Kalm
neuron spine	152	22	7.03	3.13	2.05E-06	1.31E-04	CC	Dnrl, Kcnk2, Linc, Lncx, Ppp1cc, Syt11, Atp2b2, Fcrl2, Nedd5f4, Dmck1, Sdk1a1, Pknox2, Ngn1, Gm1, Ctnnb2, App, Ngn1, Gm2b, Tenm2, Homer1, Ppp3ka
protein localization to synapse	60	12	2.32	5.18	2.50E-06	1.41E-04	BP	Iqec2, Kc1, LRRMT1, Dlg4, Dlg1, Rab11a, Ngn1, Homer1, Mapk10, Kalm, Dlgap1, Ngn1
localization within membrane	130	18	5.02	3.58	2.51E-06	1.41E-04	BP	Dnrl, Iqec2, Gm, Lfng4, Nedd5f4, Dlg4, Dlg1, Dnm3, Cbh13, Hm122, Rab11a, Ngn1, Pascin1, Gm8, Gm2b, Kalm, Ngn1
axon part	389	35	15.03	2.33	2.91E-06	1.54E-04	CC	Btcl1a, Angf9f7, Dnrl, Sncg, Dmck1, Atp2b2a1, Syt11, Kc1c, Syngt1, Tubbb4, Trak2, Fkbp4, Sncg, Kcnk1, Pafah1b1, Dlg4, Ywhae, Dlg1, Knaab1, Gk2, Pcbp, Syt7, Grin1, App, Pascin1, Ofm1, Gm2b, Tenm2, Sgfp1, Usp9b, Snc2a
positive regulation of nervous system development	447	38	17.27	2.20	4.23E-06	2.13E-04	BP	Olig1, Fcrl2, Dnrl, Impact, Isl1, Wnt7a, Smad9, Wsh3c, Sock1, Dmck1, Tcf12, Ppp3cc, Brip2, Rbz1, Mln1, Ppp1r5, Lrrm3, Sncg, Mec, Trk2, Fyn, LRRMT1, Ngn, Pafah1b1, Dlg4, Fgfr14, Pknox2, Atp2b2, Homer1, Ppp3ka, Ngn1, Hmnp9f, Ngn1, Hlraip1, Ngn1
regulation of vesicle-mediated transport	363	33	14.03	2.35	4.50E-06	2.15E-04	BP	Hmnp9f, Wnt7a, Gm2b, Atp2b2, Trk, Rab29, Rbz1, Syt11, Sncg, Rorb2, Gm1, Acsl1, Atp2b2, Homer1
glutamate receptor binding	54	11	2.09	5.27	5.44E-06	2.48E-04	MF	Cabp1, Homer3, Fyn, Calm1, Dlg4, Dnm3, Gm1, Gird3, Atp2b2, Homer1
presynapse	489	40	18.90	2.12	6.02E-06	2.61E-04	CC	Sncg, Wnt7a, Ppns, Atp2b2a1, Ppp1cc, Cpbp, Gucy1b1, Syt11, Rab29, Syngt1, Atp2b2, Wdr7, Trk, Sncg, Sdc1c, Calm1, Ngn, Pknox, Kcnk1, Dlg4, Dlg1, Atp2b4, Dnm3, Gria2, Caorb4, Pcbp, Syt7, Grin1, Ctnnb2, App, Ngn1, Gm8, Gm2b, Rms1, Atp2b2, Sgfp1, Kalm, Ngn1
protein localization to membrane	371	32	14.34	2.23	3.84E-05	7.65E-04	BP	Zdhhc14, Dnrl, Bcl2, Linc, Iqec2, Nkx2, Tbc, Ar19, Rab29, Gm, Lfng4, Pevk1, Acsl1, Rabep1, Trk, Fyn, Mpp5, Calm1, Dlg4, Dlg1, Gk2, Dpp6, Hm122, Dlg, Rab11a, Ngn1, Pascin1, Gm8, Gm2b, Mapk10, Kcnp4, Kalm, Ngn1
kinasin binding	34	8	1.31	6.09	3.51E-05	1.36E-03	MF	Jamk1d1, Rab29, Trk, Sncg, Kcnp1, Dlg4, Dlg1, Atp2b2
negative regulation of cellular component organi	491	38	18.97	2.20	3.56E-05	1.36E-03	BP	Kcnc1, Iqec2, Tsc2, Cops1, Pcdh1, Impact, Gm, Pkn, Rab29, Rbz1, Syt11, Mln1, Sncg, Mnat1, Tubbb4, Trk2, Dend5a, Camsap2, Fyn, Pknox1, B2m, Fkbp4, Sncg, LRRMT1, Evi, Pkn, Pafah1b1, Trm3f7, Dlg4, Dnm3, Ppp3ka, Tmem67, Ngn1, Ngn, Ctsfp1, Ppp3ka
cell cycle phase transition	254	24	9.82	2.45	4.92E-05	1.81E-03	BP	Pknox1, Ppp3cc, Anapc1, Smad9f, Klf4, Zfp361, LOC10308028, Usp7, Ppp3r2a, Cc2c12, Nac12, Mnat1, Fcrl2, Umecl, Emsa, Calm1, Atp2b4, Caorb4, Cc2c7, Rab11a, Hmnp9f, App, Ctsfp2, Ppp3ka
vesicle-mediated transport in synapse	177	19	6.84	2.78	5.45E-05	1.93E-03	BP	Btcl1a, Wnt7a, Syt11, Atp2b2, Sncg, Sdc1c, Calm1, Nedd5f4, Dmck1, Caorb4, Pcbp, Syt7, Rab29, Rab11a, Ngn1, Pascin1, Gm8, Rms1, Mapk10
cell surface receptor signaling pathway involved i	361	30	13.95	2.15	6.70E-05	2.15E-03	BP	Pknox1, Dnrl, Linc, Wnt7a, Ppns, Sncg, Myh10, Mln1, Lrrm3, Linc, Fgfr14, Fyn, LRRMT1, Nedd5f4, Pafah1b1, Dnm3, Gm1, Ctnnb2, Gird3, App, Ngn1, Homer1, Kalm, Hlraip1, Dlgap1, Ngn1
cell morphogenesis involved in differentiation	462	35	17.85	1.96	1.11E-04	8.66E-03	BP	Tfoc1, Ccnc1, Fcrl2, Dnrl, Isl1, Egr7, Linc, Wnt7a, Dmck1, Ppns, Sncg, Mln1, Mec, Trk2, Trk, Fyn, Nedd5f4, Crelb, Pafah1b1, Dlg4, Dnm3, Hmnp9f, Epha5, Pknox2, Ngn1, Ofm1, Tenm2, Usp9b, Ppp3ka, Kalm
phosphoprotein binding	62	10	2.40	4.17	1.20E-04	3.81E-03	MF	Ccnc1, Linc, Atp2b2, Mapk10, Fkbp4, Sncg, Pafah1b1, Ywhae, Ccnc1a1, Rf1
Schaffer collateral - CA1 synapse	60	10	2.43	4.11	1.37E-04	4.23E-03	CC	Linc, Wnt7a, Iqec2, Cbh11, Syt11, Atp2b2, Fyn, Ngn, Rab11a, Ppp3ka
protein-containing complex localization	177	18	6.84	2.63	1.70E-04	5.09E-03	BP	Dnrl, Iqec2, Hm140, Egr7, Ywhae, Fkbp4, Nedd5f4, Dlg4, Dnm3, Hm122, Wdr35, Dync2h1, Rab11a, Ngn1, Pascin1, Mapk10, Kalm
endocytosis	418	32	16.15	1.98	1.80E-04	5.23E-03	BP	Hmnp9f, Linc, Ccnc1a1, Myo10, Abat1, Tbc, Rf1, Syt11, Sncg, Gm, Mln1, Rab29, Rabep1, Mlnk1, Gk1, B2m, Sncg, LRRMT1, Capi1, Calm1, Nedd5f4, Dlg4, Dnm3, Cbh13, Syt7, App, Ngn1, Pascin1, Hmnp9f, Sgfp1, Ppp3ka
membrane organization	438	33	16.93	1.95	1.93E-04	5.42E-03	BP	Spacc1, Cdh1epl1, Dnrl, Knaab1, Tgbr9f1, Wsh3c, Sock1, Dmck1, Tcf12, Ppp3cc, Brip2, Rbz1, Mln1, Ppp1r5, Sncg, Mec, Trk2, Fyn, Ngn, Pafah1b1, Dlg4, Fgfr14, Pknox2, Atp2b2, Homer1, Ppp3ka, Ngn1, Hmnp9f, Ngn1, Sgfp1, Mapk10, Ngn1
positive regulation of cell development	448	33	17.31	1.91	2.91E-04	7.63E-03	BP	Olig1, Fcrl2, Dnrl, Impact, Isl1, Wnt7a, Smad9, Wsh3c, Sock1, Dmck1, Tcf12, Ppp3cc, Brip2, Rbz1, Mln1, Ppp1r5, Sncg, Mec, Trk2, Fyn, Ngn, Pafah1b1, Dlg4, Fgfr14, Pknox2, Atp2b2, Homer1, Ppp3ka, Ngn1, Hmnp9f, Ngn1, Tcf4, Hlraip1, Ngn1
cytoplasmic region	338	27	13.06	2.07	2.92E-04	7.63E-03	CC	Btcl1a, Angf9f7, Dnrl, Sgfp1, Myo10, Hm140, Gucy1b1, Gm, Gabarap1, Sdk1a1, Tubbb4, Trak2, Acvra1, Mapk10, Gk4, Sncg, Capi1, Pafah1b1, Dlg4, Knaab1, Gk2, Pcbp, Wdr35, Dync2h1, Ctnnb2, Rms1, Mdnk
neuron projection terminus	185	18	7.15	2.52	2.96E-04	7.63E-03	BP	Sncg, Dmck1, Atp2b2a1, Syngt1, Syt11, Syngt1, Sncg, Pknox, Kcnk1, Dlg4, Gk2, Pcbp, Syt7, Grin1, App, Pascin1, Gm8, Gm2b, Sgfp1
positive regulation of cell projection organization	321	26	12.40	2.10	3.04E-04	7.63E-03	BP	Ccnc1, Dnrl, Linc, Pknox2, Nedd5f4, Dmck1, Rbz1, Mln1, Ppp1r5, Sncg, Mec, Trk2, Fyn, Ngn, Pafah1b1, Dlg4, Dnm3, Fgfr14, Pknox2, Atp2b2, Homer1, Ppp3ka, Ngn1, Hmnp9f, Ngn1, Tcf4, Hlraip1, Ngn1
negative regulation of nervous system developme	235	21	9.08	2.31	3.11E-04	7.63E-03	BP	Hmnp9f, Olig1, Fcrl2, Pknox2, Fcrl2, Wnt7a, Sock1a1, Ppns, Rab29, Rbz1, Trk2, Dend5a, B2m, Fkbp4, Pafah1b1, Dnm3, Hm122, App, Ngn1, Ngn, Ppp3ka
response to ammonium ion	141	15	5.45	2.75	3.60E-04	8.60E-03	BP	Pknox1, Ppp3r2a, Gria2, Gria2, Gabra1, Kcnp1, Mapk10, Sncg, Abat, Rga4, Hmnp9f, Fgfr14, Gm2b, Ccnc1a1, Homer1
actin-based cell projection	144	15	5.56	2.70	4.51E-04	1.02E-03	CC	Mom1a, Usp1, Dnrl, Bcl2, Klf8, Sncg, Ccnc2, Rom3, Ycam1, Nedd5f4, Pafah1b1, Dlg4, App, Ngn1, Tenm2
regulation of cell morphogenesis	348	27	13.45	2.01	4.63E-04	1.02E-03	BP	Ccnc1, Fcrl2, Dnrl, Isl1, Linc, Wnt7a, Dmck1, Ppns, Sncg, Mln1, Mec, Trk2, Trk, Fyn, Nedd5f4, Pafah1b1, Dlg4, Dnm3, Pknox2, Atp2b2, Homer1, Ppp3ka, Ngn1, Ofm1, Hmnp9f, Ngn1, Ppp3ka
site of polarized growth	160	16	6.18	2.59	4.67E-04	1.02E-03	CC	Angf9f7, Dnrl, Sncg, Trk2, Fkbp4, Sncg, LRRMT1, Calm1, Pafah1b1, Ywhae, Pcbp, App, Ofm1, Tenm2, Usp9b
regulation of postsynaptic membrane neurotrani	73	10	2.82	3.54	4.73E-04	1.02E-03	BP	Iqec2, Nedd5f4, Dlg4, Ywhae, Dlg1, Dnm3, Rab11a, Pascin1, Mapk10, Kalm
forebrain development	295	24	11.40	2.11	4.82E-04	1.02E-03	BP	Kcnc1, Olig1, Jamk1p1, Fcrl2, Ndel1, Bcl2, Wnt7a, Acvra1, Sdk1a1, Zeb1, Fyn, Ccnc1, Kcnk1, Pafah1b1, Atp2b4, Ppp3ka, Fgfr14, Sdk1a1, Ngn, ErbB4, Dlg1, App, Epha5, Gm2b
actinodin binding	130	14	5.02	2.79	4.95E-04	1.02E-03	MF	Kcnc1, Myo10, Atp2b2, Rbz1, Ccnc1, Camsap2, Gm2b, Atp2b4, Pknox2, Ngn1, Syt7, Rab29, Ppp3ka
synaptic vesicle cycle	163	16	6.30	2.54	5.73E-04	1.17E-03	BP	Wnt7a, Syt11, Atp2b2, Sncg, Sdc1c, Calm1, Dnm3, Caorb4, Pcbp, Syt7, Fgfr14, Rab29, Ngn1, Pascin1, Gm8, Rms1
negative regulation of cell differentiation	470	33	18.16	1.82	6.80E-04	1.35E-02	BP	Hmnp9f, Ccnc1, Olig1, Ccnc1, Pcpa3, Fcrl2, Wnt7a, Tgbr9f1, Zfp361, Iqec2, Sock1a1, Rorb2, Linc, Ppns, Rab29, Rbz1, Trk2, Dend5a, Pknox2, Ngn1, Pascin1, Gm8, Rms1, Tenm2, Atp2b2, Homer1, Ppp3ka, Ngn1
axon development	305	24	11.79	2.04	7.74E-04	1.50E-02	BP	Hmnp9f, Dnrl, Isl1, Egr7, Wnt7a, Klf4, Dmck1, Ppns, Cbh11, Trk2, Camsap2, Evi, Ngn, Ccnc1, Pafah1b1, Rab11a, App, Epha5, Ofm1, Pp1, Tem2, Usp9b, Kalm
central nervous system neuron differentiation	106	12	4.10	2.93	7.87E-04	1.50E-02	BP	Olig1, Fcrl2, Wnt7a, Cbh11, Mec, Pafah1b1, Fgfr14, Faim2, ErbB4, Gird3, Mlgap2, Rora
protein localization to nucleus	186	17	7.19	2.37	8.89E-04	1.64E-02	BP	Ccnc1a1, Ccnc1, Sncg, Hmck1, Nedd5f4, Ngn1, Mln1, Mec, Trk2, Fyn, Nedd5f4, Pafah1b1, Dlg4, Dnm3, Hmnp9f, Epha5, Pknox2, Ngn1, Ofm1, Dlg, Ppp3ka
mitochondrial envelope	497	34	19.21	1.77	8.92E-04	1.64E-02	CC	Aaga1a, Ccnc1, Sdc1a1a1, Ndub6f, Hk1, Mlnk1, Ccnc1, Hk1, SDC2a1a1, SDC1a1a1, Miro3a1, Sock1a1, Ndub6f, Gk, Trmmp9f, Ppp3cc, Sdc2a1a1, Gird3, Mlnk1, Ccnc1, Abcd1b, Usp9b, Acsl1, Usp9c, Arh2b, Sfnk1, Sncg, Usp9b, Calm1, Mlnk1a1, Mlnk1a1, Atp2b2, Ngn1, Dlg, Acsl1
GABA-ergic synapse	66	9	2.55	3.53	9.30E-04	1.68E-02	CC	Angf9f7, Gabra3, Gabra1, LRRMT1, Ngn, Cbh13, Syt7, Gm8, Atp2b2
negative regulation of transport	350	26	13.52	1.92	1.11E-03	1.97E-02	BP	Dnrl, Cabp1, Pknox1, Sncg, Sncg, Hmck1, Syt11, Sncg, Egr2, Sncg, Ppns, Ppns, Ppns, Sncg, LRRMT1, Calm1, Nedd5f4, Pknox2, Dlg4, Ywhae, Dlg1, Knaab1, Dlg1, Rab29, Hmnp9f, Ppp3ka, Hlraip1
regulation of membrane potential	334	25	12.91	1.94	1.24E-03	2.08E-02	BP	Dnrl, Wnt7a, Gabra1, Ccnc1a1, Samsl, Gabra1, Sncg, Pknox, Kcnk1, Abat, Dlg4, Ywhae, Ngn1, Gk1, Caorb4, Sdk1a1, Fgfr14, Gm1, App, Ngn1, Gm2b, Rms1, Ppp3ka, Snc2a, Ngn1
cellular response to inorganic substance	192	17	7.42	2.29	1.25E-03	2.08E-02	BP	Gucy1b1, Syt11, Gm, Mec, Samsl, Mapk10, B2m, Sncg, Ccnc1, Pknox, Hmnp9f, Ppp3ka, Syt7, Gm1, App, Ngn1, Gm2b
phosphatase binding	143	14	5.53	2.53	1.27E-03	2.08E-02	MF	Ppp3r1, Ppp3r2a, LOC10308028, Ppp1cc, Iqec1, Iqec1, Mapk10, Emsa, Dlg4, Dlg1, Atp2b4, Pknox2, Cc2c7, Grin1
endocytic vesicle	112	12	4.33	2.77	1.28E-03	2.08E-02	CC	Hmnp9f, Myo10, Rab29, Syt11, Sncg, Gm, Rab29, Rabep1, Evi, Syt7, Rab11a, Ngn1
endomembrane system organization	262	21	10.12	2.07	1.29E-03	2.08E-02	BP	Ccnc1a1, Rab29, Ccnc1, Syt11, Gm, Rab29, Rabep1, Mapk10, Camsap2, Mlgap1, Abcd2, Ccnc1, Pafah1b1, Turlap2, Syt7, Pknox2, Rab11a, Tmem67, Pascin1, Ctsfp1, Sgfp1
synaptic transmission, glutamatergic	83	10	3.21	3.32	1.31E-03	2.09E-02	BP	Iqec2, Abat1, Pkn, Gria2, Ccnc1, Gm2b, Ngn1, Gm8, Homer1, Ngn1
hindbrain development	128	13	4.95	2.63	1.34E-03	2.11E-02	BP	Kcnc1, Egr7, Wnt7a, Dmck1, Acvra1, Kcnk1, Abat, Hmnp9f, Ppp3ka, Faim2, Gird3, Ngn, Rora
transferase complex, transferring phosphorus cor	195	17	7.54	2.26	1.49E-03	2.29E-02	CC	Ccnc1, Ccnc1, Pknox1, Fcrl2, Tgbr9f1, Pkn, Linc, Tgfr14, Acvra1, Pknox1, Gird3a1, Mnat1, Pknox1, Pknox1, Pknox1
protein localization to cilium	34	6	1.31	4.57	1.73E-03	2.62E-02	BP	Tbc, Ar19, Hm140, Rabep1, Hm122, Wdr35
transcription factor binding	478	32	18.47	1.73	1.78E-03	2.66E-02	MF	Kcnc1, Dnrl, Hm140, Rabep1, Hm122, Wdr35
dephosphorylation	346	25	13.37	1.87	2.01E-03	2.96E-02	BP	Ppp3r1, Ppp3r2a

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.