



**Figure S1.** Hypothalamic gene expression in transgenic compared to WT mice. (A) The distributions (number of probes) of normalized fold change ( $\text{Log}_2$ ) in expression of all detected hypothalamic probes between  $\text{Per}3^{4/4}$  compared to WT (black line) and  $\text{Per}3^{5/5}$  compared to WT (red line). The percentage of these detected probes that were significantly differentially expressed are also indicated with the right-hand axis (black bars =  $\text{Per}3^{4/4}$ , red bars =  $\text{Per}3^{5/5}$ ). (B) Horizontal bars (black =  $\text{Per}3^{4/4}$ , red =  $\text{Per}3^{5/5}$ ) indicate the up- and down-regulated fold changes ( $\text{Log}_2$ ) in the differential expression (compared to WT) of five genes associated with sleep homeostasis (top), and a core set of circadian clock genes (bottom). The vertical grey dashed lines in panels A and B indicate the maximal fold change observed in the clock gene transcripts, which were all non-significant. (C) Gene ontology analysis of biological process, molecular function, and cellular component terms that were associated with differentially expressed hypothalamic genes in  $\text{Per}3^{5/5}$  compared with WT (number of observed probes contributing to each term, enrichment score, percentage of differentially expressed genes contributing to each term and adjusted P value are indicated). Gene ontology analysis did not reveal significant terms for the differential expression in the  $\text{Per}3^{4/4}$  mice due to the smaller number of probes analyzed.

ProbeName	GeneSymbol	Per3 <sup>4/4</sup> vs.Per3 <sup>5/5</sup>	WT vs Per3 <sup>4/4</sup> and/or Per3 <sup>5/5</sup>	Per3 <sup>5/5</sup>	Per3 <sup>4/4</sup>	WT
A_52_P267651	<i>Arntl</i>			-0.12898	0.10941	-0.04331
A_51_P272553	<i>Bhlhe40</i>			-0.01092	-0.04802	0.04374
A_51_P451176	<i>Bhlhe41</i>		P = 0.0052	0.16994	0.06284	-0.31015
A_52_P618912	<i>Bhlhe41</i>			0.26348	0.07570	-0.23859
A_52_P161365	<i>Clock</i>			0.11360	-0.15249	-0.01458
A_52_P279391	<i>Clock</i>			0.11598	-0.07711	0.00522
A_52_P334670	<i>Clock</i>		P = 0.0262	0.05596	-0.14214	0.29667
A_52_P334677	<i>Clock</i>			-0.05199	-0.14977	0.20162
A_51_P302204	<i>Cry1</i>			-0.25761	0.06965	-0.06256
A_52_P420500	<i>Cry1</i>		P = 0.0458	-0.68362	-0.50719	0.31876
A_51_P135542	<i>Cry2</i>		P = 0.0055	0.00655	0.08840	-0.49925
A_52_P248378	<i>Cry2</i>		P = 0.0434	0.06761	0.06106	-0.16752
A_51_P136277	<i>Csnk1d</i>		P = 0.0245	0.09405	0.32989	-0.33567
A_51_P359813	<i>Csnk1d</i>			-0.12066	-0.04088	0.10839
A_52_P11576	<i>Csnk1d</i>			0.11080	0.18629	-0.16877
A_52_P477369	<i>Csnk1d</i>		P = 0.0161	0.22056	0.36733	-0.37472
A_51_P429197	<i>Csnk1e</i>			0.16857	-0.02134	-0.01003
A_52_P542419	<i>Csnk1e</i>			-0.00284	0.04857	0.00023
A_51_P180492	<i>Dbp</i>		P = 0.0102	0.02481	0.08902	-0.29256
A_52_P534749	<i>Npas2</i>		P = 0.6067	-0.00435	-0.06607	-0.17249
A_51_P223776	<i>Nr1d1</i>		P = 0.0245	0.08307	0.12696	-0.46491
A_52_P130952	<i>Nr1d1</i>			0.11137	0.30631	-0.36408
A_52_P130961	<i>Nr1d1</i>			-0.41301	0.11641	-0.34571
A_52_P303891	<i>Nr1d2</i>		P = 0.0363	-0.08817	-0.09040	0.23406
A_52_P79889	<i>Per1</i>			0.09700	0.02805	-0.01378
A_51_P282760	<i>Per2</i>			-0.09000	-0.02738	0.09985
A_52_P536869	<i>Per2</i>			-0.12907	0.32956	-0.13785
A_51_P258493	<i>Per3</i>		P = 0.0372	0.25613	-0.03558	-0.21079
A_51_P477779	<i>Rora</i>			0.15948	-0.09179	0.16905
A_52_P652442	<i>Rora</i>			0.23779	-0.04323	0.01108
A_52_P652950	<i>Rora</i>			0.35369	-0.05030	0.04104

Supplemental table S1A: Clock gene expression in hypothalamic samples

ProbeName	GeneSymbol	Per3 <sup>4/4</sup> vs.Per3 <sup>5/5</sup>	WT vs Per3 <sup>4/4</sup> and/or Per3 <sup>5/5</sup>	Per3 <sup>5/5</sup>	Per3 <sup>4/4</sup>	WT
A_52_P267651	<i>Arntl</i>			-0.06289	0.14908	-0.01202
A_51_P272553	<i>Bhlhe40</i>			-0.02212	-0.07854	-0.06550
A_51_P451176	<i>Bhlhe41</i>		P = 0.0032	0.18719	0.05677	-0.24150
A_52_P618912	<i>Bhlhe41</i>			0.09504	0.14551	-0.26483
A_52_P161365	<i>Clock</i>			0.08955	-0.02715	0.05125
A_52_P279391	<i>Clock</i>			0.07064	-0.15654	-0.07816
A_52_P334670	<i>Clock</i>			0.05231	-0.09172	0.21352
A_52_P334677	<i>Clock</i>		P = 0.0377	-0.02105	-0.19695	0.10035
A_51_P302204	<i>Cry1</i>			-0.05304	0.16666	-0.09487
A_52_P420500	<i>Cry1</i>		P = 0.0071	-0.53089	-0.47892	0.57222
A_51_P135542	<i>Cry2</i>		P = 0.0017	0.26195	0.13782	-0.45281
A_52_P248378	<i>Cry2</i>		P = 0.0078	0.08495	0.18414	-0.16797
A_51_P136277	<i>Csnk1d</i>		P = 0.0094	0.01389	0.27917	-0.39669
A_51_P359813	<i>Csnk1d</i>			-0.01190	-0.04583	-0.01672
A_52_P11576	<i>Csnk1d</i>		P = 0.0019	0.01862	0.20343	-0.43821
A_52_P477369	<i>Csnk1d</i>		P = 0.0015	0.02986	0.20707	-0.64890
A_51_P429197	<i>Csnk1e</i>			0.15034	-0.05504	0.00226
A_52_P542419	<i>Csnk1e</i>			-0.02476	-0.03711	-0.01421
A_51_P180492	<i>Dbp</i>			0.09361	0.10192	-0.18879
A_52_P79889	<i>Npas2</i>		P = 0.0418	0.13054	0.03951	-0.21103
A_51_P223776	<i>Nr1d1</i>			0.17853	0.19377	-0.22922
A_52_P130952	<i>Nr1d1</i>			-0.01569	0.24713	-0.35349
A_52_P130961	<i>Nr1d1</i>			-0.22156	0.01417	-0.34439
A_52_P303891	<i>Nr1d2</i>		P = 0.0109	0.00165	-0.09362	0.13994
A_52_P79889	<i>Per1</i>		P = 0.0412	0.14551	0.04336	-0.12888
A_51_P282760	<i>Per2</i>			0.10941	-0.02899	-0.01415
A_52_P536869	<i>Per2</i>			0.03497	0.22631	-0.15680
A_51_P258493	<i>Per3</i>		P = 0.008	0.22901	-0.04939	-0.45997
A_51_P477779	<i>Rora</i>			0.00057	-0.16541	0.01888
A_52_P652442	<i>Rora</i>			0.05234	-0.04869	-0.05583
A_52_P652950	<i>Rora</i>			0.10809	-0.05947	-0.07725

Supplemental table S1B: Clock gene expression in cortical samples

<i>Per3</i> <sup>4/4</sup>		<i>Per3</i> <sup>5/5</sup>	
Gene/Probe	Fold change	Gene/Probe	Fold change
<i>Ccl21a</i>	-3.39	<i>Lct</i>	-3.38
<i>Gdpd3</i>	2.76	A_52_P788961	2.81
<i>Lcn12</i>	-2.32	<i>Grn</i>	-2.38
<i>Pttg1</i>	2.31	8430429K09Rik	2.25
<i>Prl</i>	-2.18	<i>Dsp</i>	-2.20
<i>Dyrk4</i>	-2.17	<i>Neurod6</i>	-1.98
LOC674214	-1.95	<i>Sln</i>	-1.96
<i>Slx1b</i>	-1.81	A_51_P311235	-1.90
<i>Ugt2b38</i>	-1.78	<i>Agxt</i>	-1.87
<i>Apoc4</i>	1.77	<i>Hamp</i>	-1.62
<i>Tsix</i>	1.68	<i>Neurod2</i>	-1.62
<i>Gm3893</i>	-1.56	<i>Thbs4</i>	-1.61
<i>Wfdc2</i>	1.27	<i>Ccl21a</i>	-1.57
A930018M24Rik	-1.23	<i>Fam105a</i>	1.54
AU023762	-1.19	<i>Grin2a</i>	-1.53
<i>Gh</i>	-1.19	A_52_P348256	-1.52
<i>Sln</i>	1.13	<i>Egr3</i>	-1.49
A_52_P36261	1.10	<i>Thbs4</i>	-1.49
<i>Myh1</i>	1.10	<i>Spink8</i>	-1.47
<i>Folr1</i>	1.06	9430091E24Rik	-1.43
<i>Sult1c2</i>	0.99	<i>Wipf3</i>	-1.42
<i>Tmem72</i>	0.93	<i>Fabp1</i>	-1.39
A_51_P417257	-0.93	<i>Mup5</i>	-1.38
<i>Chi3l4</i>	-0.89	2310002F09Rik	-1.36
<i>Tns1</i>	-0.89	<i>Tnfrsf25</i>	-1.36
<i>Cd38</i>	0.88	<i>Kcne2</i>	-1.33
<i>Myh4</i>	0.88	<i>Itpka</i>	-1.33
<i>Defb22</i>	-0.87	<i>Hormad1</i>	-1.32
<i>Mpl</i>	-0.84	<i>Egr4</i>	-1.30
<i>Eif2a</i>	-0.83	<i>Dusp18</i>	1.24

Table S2: Top 30 fold change probes for each genotype compared to WT in the hypothalamus during the ultradian light-dark cycle.