

**Supplemental Table 1.** *Statistical evaluation (p-values) of rhythmicity of clock gene expression in neuronal and non-neuronal tissues during jet lag.*

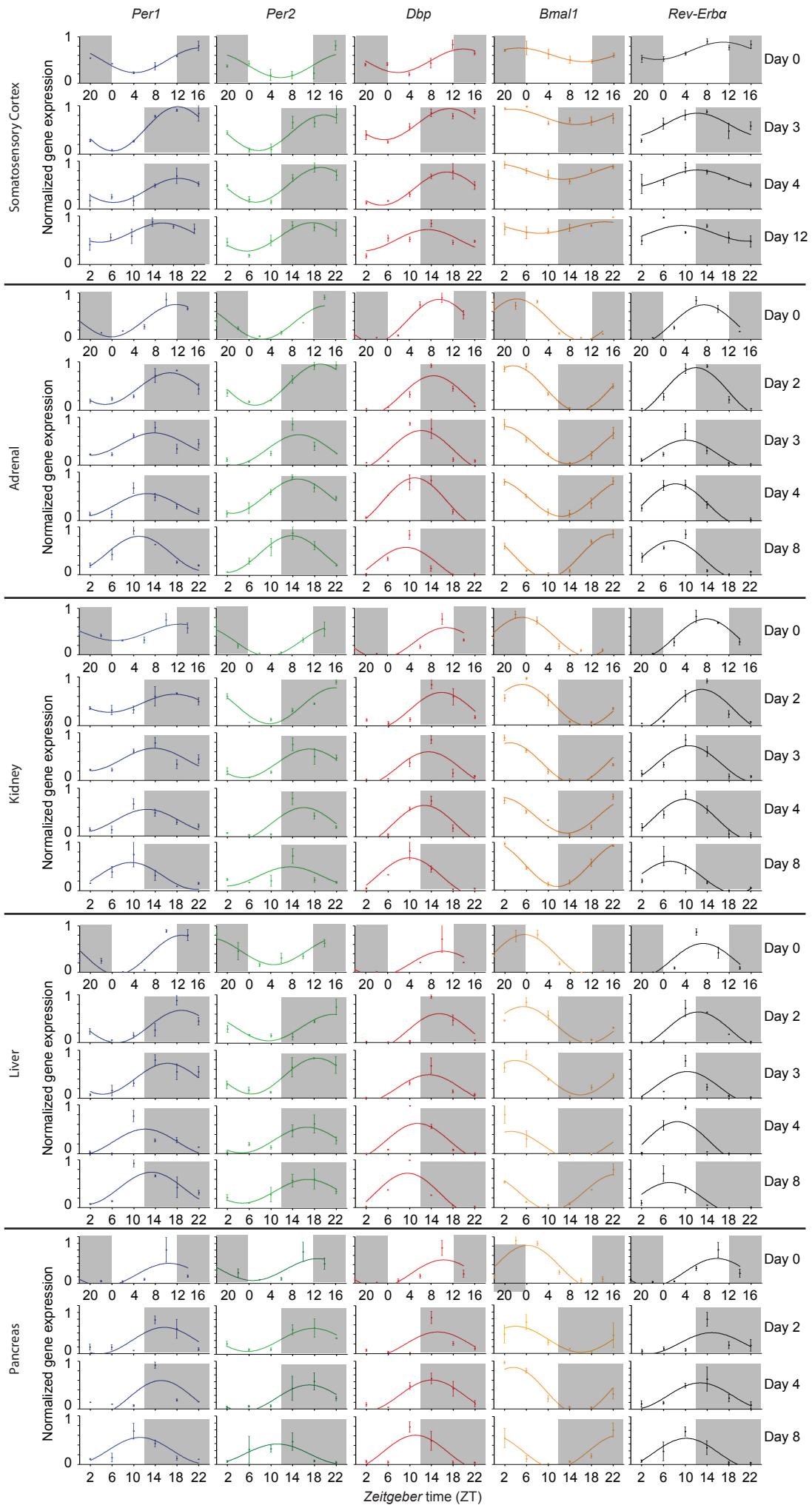
Rhythmic clock gene expression profiles in the SCN, the somatosensory cortex, the adrenal, the kidney, the liver and the pancreas were evaluated by sine wave curve fitting using the CircWave Batch Software (CircWave Batch V3.3;  $\alpha = 0.05$ ,  $\beta = 24$ ; Oster et al. 2006). Significance of rhythmicity is indicated by p-values before (day 0) and after 6 h shift of the photoperiod (days 2, 3, 4 and 8 or 12; see Methods for details).

tissue	Per1	Per2	Dbp	Bmal1	Rev-Erba	day
SCN (ISH)	<0.0001	<0.0001	<0.0001	0.0006	<0.0001	day0
	<0.0001	0.0004				day2
	0.0003	0.0430	<0.0001	0.0067	0.0032	day3
	0.0009	0.0007	0.0035	<0.0001	0.0015	day4
	0.0021	<0.0001	<0.0001	0.0002	0.0025	day12
Somatosensory Cortex (ISH)	0.0001	0.0316	0.0023	0.0229	0.0485	day0
						day2
	<0.0001	0.0013	0.0001	0.0100	0.0010	day3
	0.0039	0.0001	0.0006	0.0035	0.0030	day4
	0.0096	0.0006	0.0305	0.0481	0.0498	day12
Adrenal (qPCR)	0.0343	0.0003	<0.0001	0.0001	<0.0001	day0
	0.0001	<0.0001	0.0004	<0.0001	0.0002	day2
	0.0233	0.0042	0.0089	<0.0001	0.0034	day3
	0.0424	<0.0001	0.0077	0.0001	0.0021	day4
	0.0020	0.0005	0.0012	<0.0001	0.0001	day8
Kidney (qPCR)	0.0210	0.0021	0.0014	<0.0001	<0.0001	day0
	0.0160	<0.0001	0.0025	<0.0001	0.0004	day2
	0.0125	0.0030	0.0028	<0.0001	0.0002	day3
	0.0004	0.0123	0.0013	0.0010	0.0037	day4
	0.0063	0.0413	0.0033	<0.0001	0.0014	day8
Liver (qPCR)	0.0030	0.0181	0.0088	<0.0001	0.0003	day0
	0.0001	0.0013	0.0075	0.0001	0.0028	day2
	0.0029	0.0002	0.0118	0.0035	0.0053	day3
	0.0359	0.0386	0.0440	0.0213	0.0015	day4
	0.0008	0.0214	0.0044	<0.0001	0.0007	day8
Pankreas (qPCR)	0.0324	0.0082	0.0199	0.0114	0.0001	day0
	0.0341	0.0019	0.0272	0.0028	0.0454	day2
	0.0244	0.0406	0.0063	0.0018	0.0164	day4
	0.0096	0.0185	0.0041	0.0292	0.0039	day8

**Supplemental Table 2.** Results of a *statistical analysis of PS<sub>50</sub> values.*

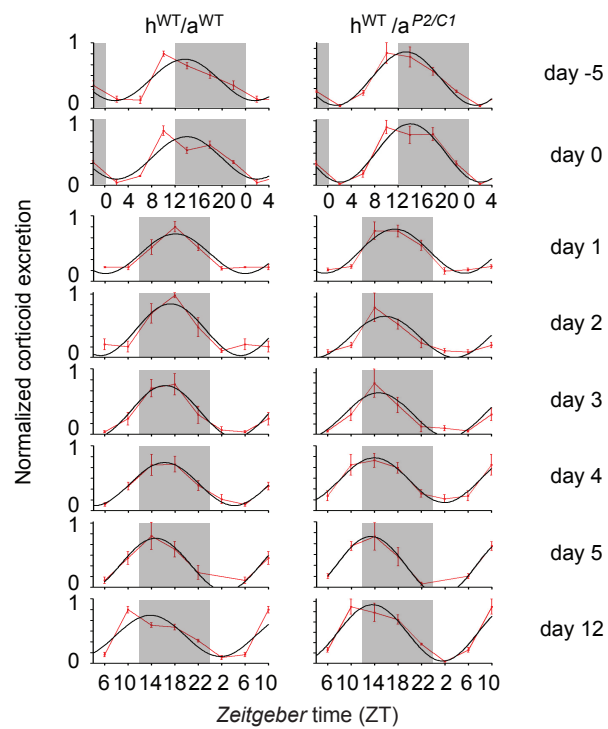
Differences between the rate of gene expression adjustments to a 6 h phase advance in the different tissues examined were analyzed using F-test evaluation using the GraphPad software. Significance of rhythmicity is indicated by p-values and the corresponding F-values. (see Methods for details).

Tissue	Reference gene	Statistical value	Gene				
			<i>Per1</i>	<i>Per2</i>	<i>Dbp</i>	<i>Bmal1</i>	<i>Rev-Erba</i>
SCN Figure 2C	<i>Per1</i>	p-value	-	0.7367	<0.0001	0.0003	0.0052
		F-value	-	0.1155 [1,26]	23.03 [1,23]	17.76 [1,23]	9.541 [1,23]
	<i>Per2</i>	p-value	0.7367	-	<0.0001	<0.0001	0,0001
		F-value	0.1155 [1,26]	-	29.23 [1,23]	29.32 [1,23]	21.28 [1,23]
Liver	<i>(Activity)</i>	p-value	<0.0001	<0.0001	0.3222	0.4494	0.9129
		F-value	23.43 [1,173]	37.65 [1,173]	0.98 [1,170]	0.57 [1,170]	0.01 [1,170]
Somatosensory cortex Figure 3A	<i>Per2</i>	p-value	0.5724	-	0.007	0.004	0.032
		F-value	0.33 [1,20]	-	8.92 [1,20]	10.61 [1,20]	5.29 [1,20]
Adrenal Figure 3B	<i>Per2</i>	p-value	0.313	-	0.042	0.037	0,0001
		F-value	1.05 [1,26]	-	4.58 [1,26]	4.84 [1,26]	5.29 [1,20]
Kidney Figure 3C	<i>Per2</i>	p-value	0.292	-	0.306	0.007	0.249
		F-value	1.15 [1,26]	-	1.08 [1,26]	8.34 [1,26]	1.38 [1,26]
Liver Figure 3D	<i>Per2</i>	p-value	0.048	-	0.015	<0.0001	0.1231
		F-value	4.27 [1,26]	-	6.82 [1,26]	38.28 [1,26]	2.54 [1,26]
Pancreas Figure 3E	<i>Per2</i>	p-value	0.941	-	0.976	0.515	0.029
		F-value	0.006 [1,20]	-	0.0009 [1,20]	0.44 [1,20]	5.50 [1,20]
	<i>Rev-Erba</i>	p-value	0.067	0.029	0.041	0.364	-
		F-value	3.70 [1,20]	5.50 [1,20]	4.71 [1,20]	0.86 [1,20]	-



**Supplemental Figure 1.** *Resetting of clock genes during jet lag in peripheral oscillators.*

Shown are diurnal mRNA profiles of different clock genes (3 animals per timepoint; average  $\pm$  SEM) at days 0, 2, 3, 4 and 8 or 12 after the LD shift. Experimental data were fitted with sine waves. Light and dark phases are marked by white and grey shading. *Zeitgeber* times are indicated on the abscissa of days 0, 8 or 12.



**Supplemental Figure 2.** Adrenal control of resetting of corticosterone excretion during jet lag.

Diurnal normalized corticosterone profiles of sham-operated mice (host<sup>WT</sup>/adrenal<sup>WT</sup> [h<sup>WT</sup>/a<sup>WT</sup>]) and wild-type mice harboring *Per2/Cry1* mutant adrenals (host<sup>WT</sup>/adrenal<sup>Per2/Cry1</sup> [h<sup>WT</sup>/a<sup>P2/C1</sup>]) (5 animals per time point; average  $\pm$  SEM) at day -5, 0, 5 and 12 after the LD shift and the sine wave fits (black). Light and dark phases are marked in white and grey shadings. *Zeitgeber* times are indicated at the bottom of day 0 and 12.