

## Supplementary Information

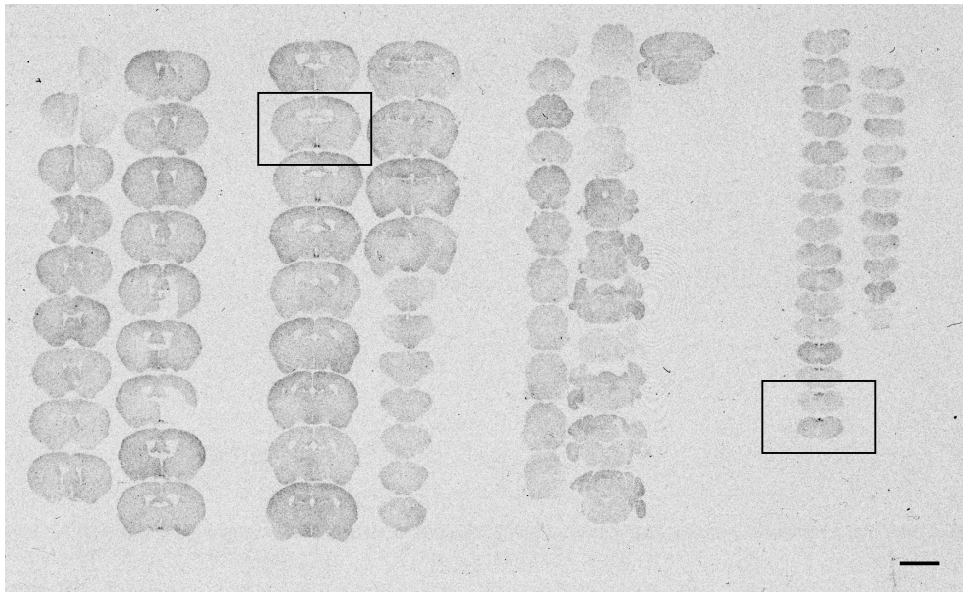
### **FGF21 regulates circadian behavior and metabolism by acting on the nervous system**

Angie L. Bookout<sup>1,2</sup>, Marleen H. M. de Groot<sup>3,4</sup>, Bryn M. Owen<sup>1</sup>, Syann Lee<sup>2</sup>, Laurent Gautron<sup>2</sup>, Heather L. Lawrence<sup>1</sup>, Xunshan Ding<sup>4</sup>, Joel K. Elmquist<sup>2</sup>, Joseph S. Takahashi<sup>3,4</sup>, David J. Mangelsdorf<sup>1,4\*</sup>, and Steven A. Kliewer<sup>1,5\*</sup>

<sup>1</sup>Department of Pharmacology; <sup>2</sup>Department of Internal Medicine, Division of Hypothalamic Research; <sup>3</sup>Department of Neuroscience; <sup>4</sup>Howard Hughes Medical Institute; <sup>5</sup>Department of Molecular Biology, University of Texas Southwestern Medical Center, Dallas TX 75390, USA

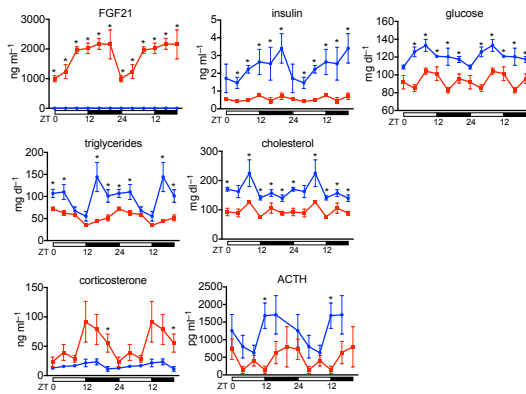
\*To whom correspondence should be addressed. Email:

[davo.mango@utsouthwestern.edu](mailto:davo.mango@utsouthwestern.edu); [steven.kliewer@utsouthwestern.edu](mailto:steven.kliewer@utsouthwestern.edu)

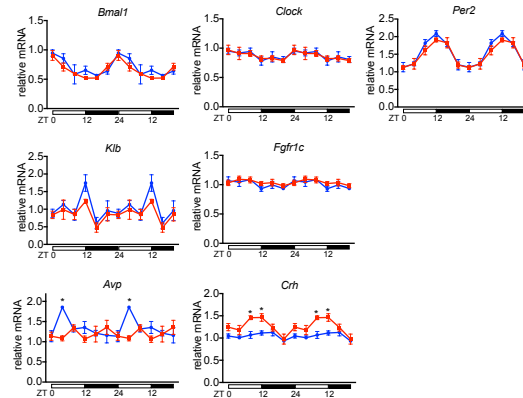


**Supplementary Figure 1**  $\beta$ -Klotho in situ hybridization across the mouse brain. Mouse brain coronal sections (25  $\mu$ m, 1:4 series) were subjected to free-floating in situ hybridization with a  $^{33}$ P-labeled antisense riboprobe for *Klb* and mounted onto slides in rostral (top left) to caudal (bottom right) order. Boxed areas indicate regions shown in **Figure 1**. Bar = 45 mm.

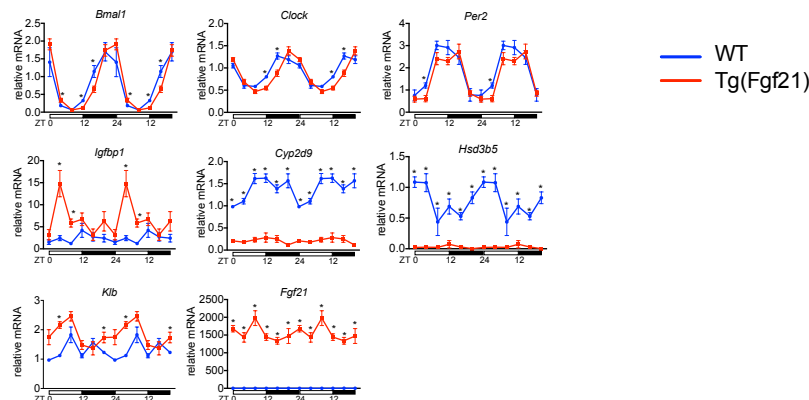
### a Plasma Analytes



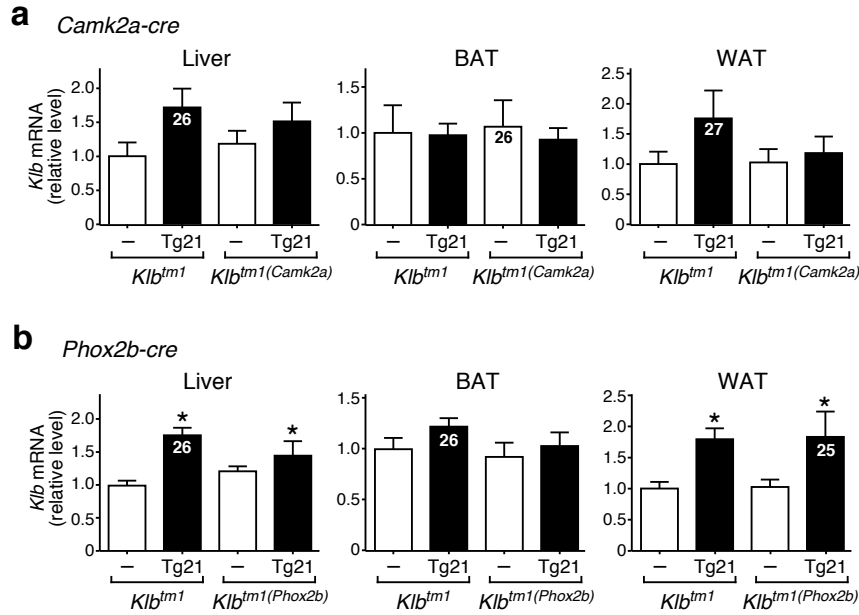
### b Hypothalamus Gene Expression



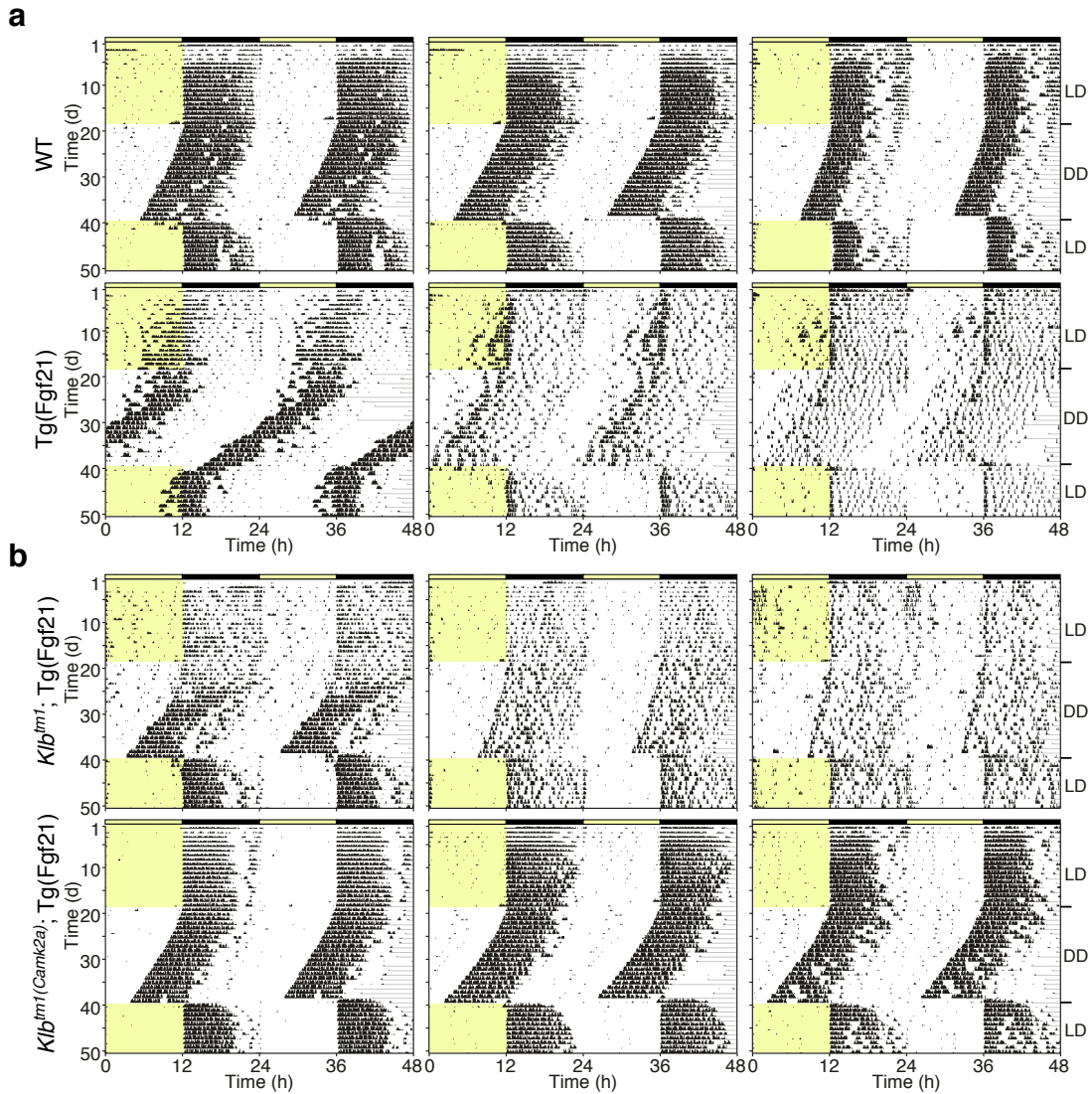
### c Liver Gene Expression



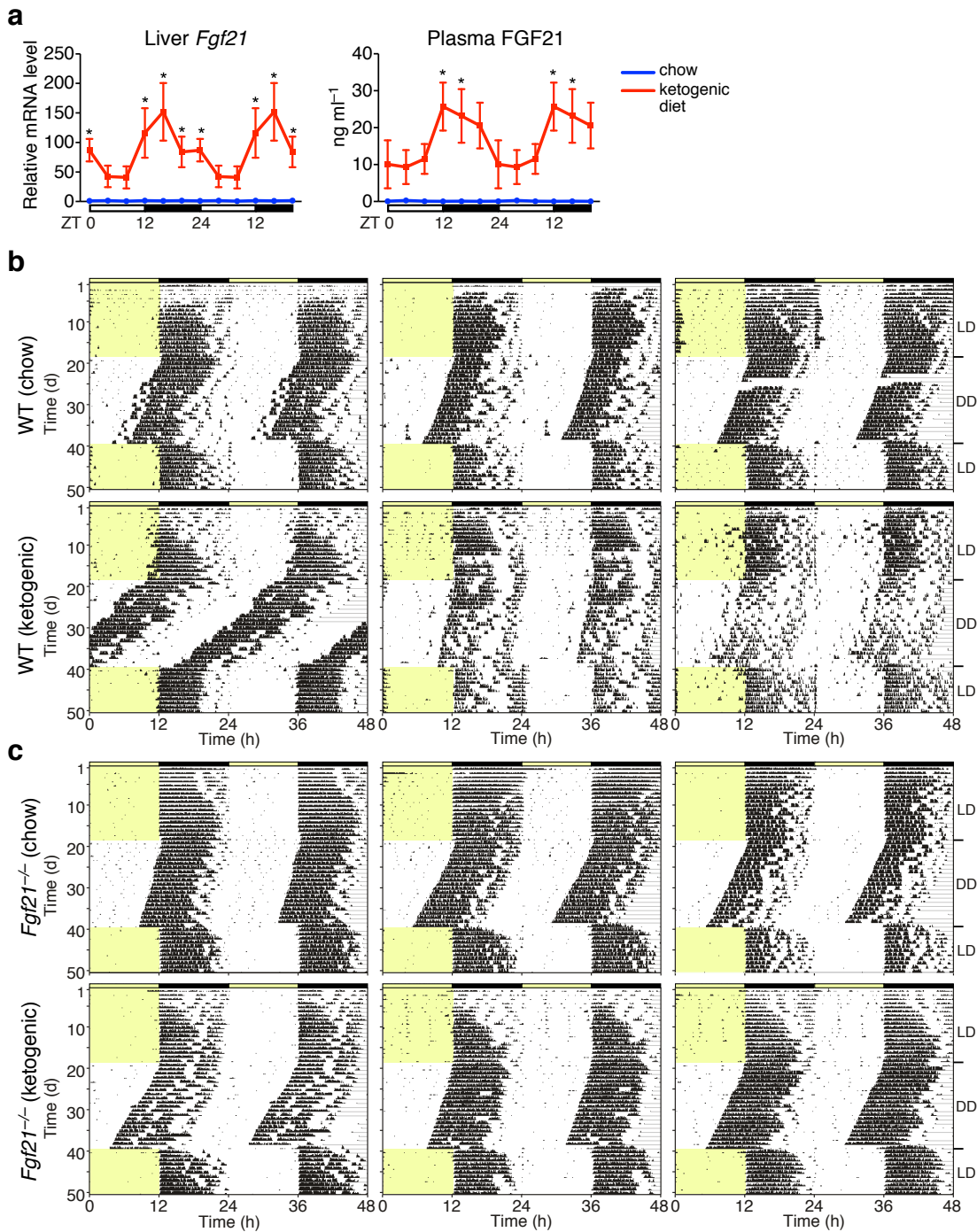
**Supplementary Figure 2** Circadian profiles of gene expression and plasma analytes in Tg(Fgf21) mice. Male wild-type (WT) or Tg(FGF21) mice were sacrificed every 4 h over a 24 h period, beginning at the start of the light phase (ZT0). **(a)** Plasma hormones and metabolites. **(b)** Hypothalamic clock, FGF21 receptor, and neuropeptide gene expression. Arginine vasopressin (*Avp*); Corticotropin releasing hormone (*Crh*). **(c)** Liver clock, growth hormone pathway, and FGF21 signaling pathway gene expression. Values on the x-axes are double-plotted; data represent mean  $\pm$  SEM,  $n = 3-6$ . Asterisks indicate significant differences ( $P < 0.05$ ) between WT and Tg(Fgf21).



**Supplementary Figure 3** *Klb* expression is intact in peripheral tissues of the *Klb* brain knockout models. Male mice of indicated genotypes without (–) or with (Tg21) the Tg(Fgf21) insertion were sacrificed ZT8. *Klb* mRNA was quantified in liver and brown and white adipose of (a) *Camk2a-cre* and (b) *Phox2b-cre* models. Data represent mean ± SEM,  $n = 5–9$ . Ct values shown inside bars. Asterisks indicate significant differences ( $P < 0.05$ ) between Tg21 and (–) control mice.

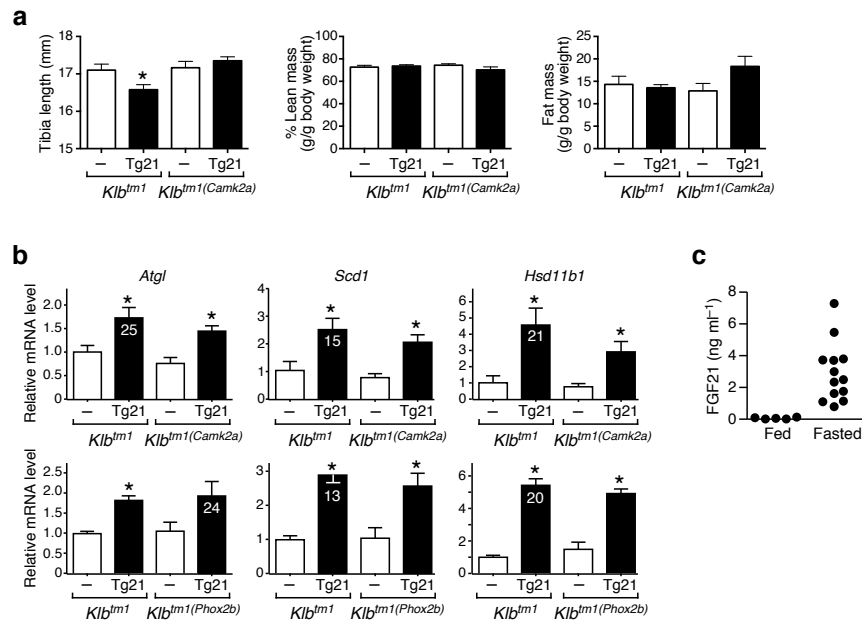


**Supplementary Figure 4** Representative actograms for Tg(Fgf21) mice. Representative actograms are shown double-plotted for three individual **(a)** wild-type (WT) or Tg(Fgf21) male mice, and **(b)**  $Klib^{tm1}::Tg(Fgf21)$  or  $Klib^{tm1(Camk2a)}::Tg(Fgf21)$  male mice (bottom). Time on x-axis refers to zeitgeber time (ZT) 0 at lights on. Yellow indicates light phase (LD, 12 hours light/12 hours dark; DD, constant darkness).



**Supplementary Figure 5** Ketogenic diet mimics transgenic FGF21 overexpression in regulating circadian behavior. **(a)** Hepatic FGF21 mRNA and plasma protein levels in male wild-type mice fed chow or ketogenic diet for 6 weeks. Mice were sacrificed every

4 h over a 24 h period, beginning at the start of the light phase (ZT0). Values on the x-axes are double-plotted; data represent mean  $\pm$  SEM,  $n = 4$ . Asterisks indicate significant differences ( $P < 0.05$ ) between diets. **(b, c)** Representative actograms are shown double-plotted for three individual wild-type males **(b)** fed standard chow or ketogenic diet, and *Fgf21*<sup>-/-</sup> males **(c)** fed standard chow or ketogenic diet. Time on x-axis refers to zeitgeber time (ZT) 0 at lights on. Yellow indicates light phase (LD, 12 hours light/12 hours dark; DD, constant darkness).



**Supplementary Figure 6** Brain-specific effects of FGF21 on growth morphometry and adipose gene expression. **(a)** Tibia length, lean mass, and fat mass from male mice of indicated genotypes without (-) or with (Tg21) the Tg(Fgf21) insertion ( $n = 4-7$ ). Animals were sacrificed at ZT8. **(b)** White adipose tissue gene expression in brain deletion of *Klb*. Male mice ( $n = 5-9$ ) of indicated genotypes were sacrificed at ZT8. Ct values shown inside bars. Data represent mean  $\pm$  SEM. Asterisks indicate significant differences ( $P < 0.05$ ) between Tg21 and (-) control mice. **(c)** Plasma FGF21 levels in individual 12-week old male C57BL/6J mice at ZT3 fed ad libitum or fasted for 24 h.



**Supplementary Table 1** Metabolic parameters from *Klb<sup>tml(Camk2a)</sup>::Tg(Fgf21)* and *Klb<sup>tml(Phox2b)</sup>::Tg(Fgf21)* mice.

	<i>Klb<sup>tml</sup></i>	<i>Klb<sup>tml</sup>::</i> Tg(Fgf21)	<i>Klb<sup>tml(Camk2a)</sup></i>	<i>Klb<sup>tml(Camk2a)</sup>::</i> Tg(Fgf21)
<i>n</i>	5	7	5	7
glucose (mg dl <sup>-1</sup> )	130.9 ± 4.72	126.8 ± 4.69	140.8 ± 9.82	118.9 ± 3.86
βhydroxybutyrate (μM)	66.29 ± 8.63	205.4 ± 44.96*	29.68 ± 9.65	45.38 ± 6.053
cholesterol (mg dl <sup>-1</sup> )	146.1 ± 13.32	112 ± 6.32*	161.1 ± 15.94	153.7 ± 8.67
triglycerides (mg d <sup>-1</sup> )	50.18 ± 12.72	42.13 ± 5.96	55.9 ± 7.24	67.42 ± 13.74
FGF21 (ng ml <sup>-1</sup> )	0.54 ± 0.09	657.4 ± 117.5*	0.75 ± 0.15	737.3 ± 167.4*

	<i>Klb<sup>tml</sup></i>	<i>Klb<sup>tml</sup>::</i> Tg(Fgf21)	<i>Klb<sup>tml(Phox2b)</sup></i>	<i>Klb<sup>tml(Phox2b)</sup>::</i> Tg(Fgf21)
<i>n</i>	9	9	5	8
glucose (mg dl <sup>-1</sup> )	131.6 ± 3.74	119.3 ± 8.67	147.1 ± 5.19	112.4 ± 15.48
cholesterol (mg dl <sup>-1</sup> )	136.6 ± 10.44	104.3 ± 6.20*	128.1 ± 15.30	126.5 ± 5.82
triglycerides (mg dl <sup>-1</sup> )	46.44 ± 4.08	49.08 ± 9.62	59.38 ± 6.59	41.33 ± 6.19
FGF21 (ng m <sup>-1</sup> )	0.41 ± 0.70	784.6 ± 111.1*	1.45 ± 0.85	933.5 ± 228.9*

Data are presented as mean ± SEM. Asterisks indicate significant differences ( $P < 0.05$ ) compared to controls without Tg(Fgf21). FGF21 measurement was taken at ZT3.

**Supplementary Table 2** Circadian wheel running parameters in *Klb<sup>tm1(Cank2a)</sup>::Tg(Fgf21)* mice.

	Wild-type chow	Tg(Fgf21) chow
<i>n</i>	16	28
total activity (revs/day × 10 <sup>4</sup> )	2.62 ± 0.17	1.91 ± 0.19*
% light activity	3.20 ± 0.71	13.94 ± 2.95*
% dark activity	96.80 ± 0.71	86.06 ± 2.95*
period (h)	23.62 ± 0.03	23.57 ± 0.04
amplitude (%)	17.79 ± 1.49	12.14 ± 1.50*
phase (h)	0.24 ± 0.07	-0.96 ± 0.37*

	<i>Klb<sup>tm1</sup>::Tg(Fgf21)</i>	<i>Klb<sup>tm1(Cank2a)</sup>::Tg(Fgf21)</i>
<i>n</i>	11	12
total activity (revs/day × 10 <sup>4</sup> )	0.97 ± 0.22	2.60 ± 0.16*
% light activity	15.26 ± 3.72	1.87 ± 0.36*
% dark activity	84.74 ± 3.72	98.13 ± 0.36*
period (h)	23.58 ± 0.05	23.54 ± 0.02
amplitude (%)	7.82 ± 2.03	17.31 ± 1.29*
phase (h)	0.13 ± 0.16	0.35 ± 0.06

Data are presented as mean ± SEM. Asterisks indicate significant differences ( $P < 0.05$ ) compared to wild-type or *Klb<sup>tm1</sup>::Tg(Fgf21)* controls.

**Supplementary Table 3** Circadian wheel running parameters and plasma FGF21 in wild-type versus *Fgf21<sup>-/-</sup>* mice.

	Wild-type chow	Wild-type ketogenic	<i>Fgf21<sup>-/-</sup></i> chow	<i>Fgf21<sup>-/-</sup></i> ketogenic
<i>n</i>	6	24	18	23
total activity (revs/day × 10 <sup>4</sup> )	3.39 ± 0.18	1.86 ± 0.12*	2.87 ± 0.20	2.14 ± 0.12*
% light activity	3.48 ± 1.54	8.78 ± 1.47*	1.81 ± 0.53†	3.84 ± 0.76
% dark activity	96.52 ± 1.54	91.23 ± 1.47*	98.19 ± 0.53†	96.16 ± 0.76
period (h)	23.69 ± 0.02	23.62 ± 0.04	23.62 ± 0.03	23.64 ± 0.05
amplitude (%)	17.32 ± 2.37	15.41 ± 1.41	19.77 ± 1.06	19.43 ± 1.48
phase (h)	0.38 ± 0.20	-0.53 ± 0.24	0.52 ± 0.06	0.03 ± 0.16*
Plasma FGF21 (ng ml <sup>-1</sup> )	0.44 ± 0.0	21.92 ± 5.45*	undetectable	undetectable

Data are presented as mean ± SEM. Asterisks indicate significant differences ( $P < 0.05$ ) compared to chow-fed mice. Daggers indicate significant differences ( $P < 0.05$ ) compared to all other groups. FGF21 measurement was taken at ZT8.

**Supplementary Table 4** List of nuclei collected for expression profiling.

Nucleus	Paxinos & Franklin Atlas <sup>31</sup> Level	Full Name
CTX	40-41	cortex
Thal AD	39-40	anterodorsal thalamic nucleus
OVLT	27	vascular organ of lamina terminalis
MnPO	27	median preoptic nucleus
SCN	34-38	suprachiasmatic nucleus
PVH	37-41	paraventricular hypothalamic nucleus
RCN	39-40	retrochiasmatic nucleus
LHA1	39	lateral hypothalamic area to paraventricular hypothalamic nucleus
dmVMH	42-46	dorsomedial ventromedial hypothalamic nucleus
vVMH	42-46	ventrolateral ventromedial hypothalamic nucleus
ARC	42-46	arcuate nucleus
cDMH	47-48	compact dorsomedial hypothalamic nucleus
vDMH	47-48	ventral dorsomedial hypothalamic nucleus
LHA2	47	lateral hypothalamic area to dorsomedial hypothalamic nucleus plus perifornical area
PH	51	posterior hypothalamic area
PMV	51-53	pre mammillary nucleus, ventral part
VTA	61	caudal ventral tegmental area
mPBN	74-75	medial parabrachial nucleus
lPBN	74-75	lateral parabrachial nucleus
AP	92-93	area postrema
DMV (X)	92-93	dorsal motor nucleus of the vagus (Xth cranial nerve)
NTS	92-93	nucleus tractus solitarius
nodose		left nodose ganglion; cell body of vagal sensory neurons
DRG		mid-lower thoracic dorsal root ganglia (T7-T12)