SUPPLEMENTARY TABLE 7.   KEY RESOURCES TABLE

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Experimental models : Organisms/Strains		
C57Bl/6	Charles River	027
B6.129S4(Cg)-Arntltm1Weit/J (Bmal1$^{flox/flox}$)	The Jackson Laboratory	#:007668
LC1-Cre	(1)	N/A
Pax8-rtTA	(1)	N/A
Bmal1$^{flox/flox}$ LC1-Cre Pax8-rtTA	This paper	
Reagents		
Phosphate Buffer 10X pH 7.4	Gibco	70011-044
Doxycycline Hyclate	Applichem	A2951
Standard diet	Kliba-Nafag	3242
Data		
RNA-seq data	This paper	GSE216252
Proteomics data	This paper	PXD036803 (Proteomexchange.org)
Metabolomics data	This paper	doi: 10.5281/zenodo.7225427
Softwares and Algorithms		
GraphPad Prism	GraphPad Software, LCC	v9.4.0
Xcalibur	ThermoFisher Scientific	v4.2
MaxQuant	Max-Planck-Institute of Biochemistry	v.1.6.14.0
Perseus	(2)	1.6.5.0
IMOD	Electron microscopy facility University of Lausanne	v4.10.35
bcl2fastq2	Illumina, Inc.	v2.20
Cutadapt	https://doi.org/10.14806/ej.17.1.200	v1.8
fastq_screen	(3)	v0.11.1
reaper	(3)	v15-065
STAR	(4)	v2.5.3a

htseq-count	(4)	v0.9.1
R	https://www.r-project.org/	v4.0.3, v4.1.0
Bioconductor (R packages for bioinformatics)	https://bioconductor.org/, (5)	v3.12, v3.13
dryR	(6) https://github.com/naef-lab/dryR	v1.0.0
edgeR	(7) https://doi.org/10.18129/B9.bioc.edgeR	
STAR	(8) https://code.google.com/archive/p/rna-star/	v. 2.5.3a

1. Traykova-Brauch M, Schonig K, Greiner O, Miloud T, Jauch A, Bode M, et al. An efficient and versatile system for acute and chronic modulation of renal tubular function in transgenic mice. *Nat Med.* 2008;14(9):979-84.
2. Tyanova S, Temu T, Sinitcyn P, Carlson A, Hein MY, Geiger T, et al. The Perseus computational platform for comprehensive analysis of (prote)omics data. *Nat Methods.* 2016;13(9):731-40.
3. Wingett SW, and Andrews S. FastQ Screen: A tool for multi-genome mapping and quality control. *F1000Res.* 2018;7:1338.
4. Davis MP, van Dongen S, Abreu-Goodger C, Bartonicek N, and Enright AJ. Kraken: a set of tools for quality control and analysis of high-throughput sequence data. *Methods (San Diego, Calif).* 2013;63(1):41-9.
5. Huber W, Carey VJ, Gentleman R, Anders S, Carlson M, Carvalho BS, et al. Orchestrating high-throughput genomic analysis with Bioconductor. *Nat Methods.* 2015;12(2):115-21.
6. Weger BD, Gobet C, David FPA, Atger F, Martin E, Phillips NE, et al. Systematic analysis of differential rhythmic liver gene expression mediated by the circadian clock and feeding rhythms. *Proc Natl Acad Sci U S A.* 2021;118(3).
7. Robinson MD, McCarthy DJ, and Smyth GK. edgeR: a Bioconductor package for differential expression analysis of digital gene expression data. *Bioinformatics.* 2010;26(1):139-40.
8. Dobin A, Davis CA, Schlesinger F, Drenkow J, Zaleski C, Jha S, et al. STAR: ultrafast universal RNA-seq aligner. *Bioinformatics.* 2013;29(1):15-21.