Supplementary Figure Legends

**Fig. S1.** Rhythmic induction of autophagy in the heart, skeletal muscle and kidney. Immunoblots of total tissue lysates using indicated antibodies. Ponceau S staining serves as loading control.

**Fig. S2.** Graphs of autophagy gene expression generated using dataset provided at: http://wasabi.itmat.upenn.edu/circa (Hughes et al. 2009). Note that transcriptional profiling was performed every hour for a total of 48 hrs in livers from mice kept under constant darkness.

**Fig. S3.** Rhythmic expression of autophagy genes in the heart. Shown is qPCR analysis of Per1 and autophagy genes at different time points. Data represent mean ± SD. ZT0 and 12 represent the onset of light and dark cycles, respectively.

**Fig. S4.** Daily expression of autophagy genes in skeletal muscle. Shown is qPCR analysis of Per1 and autophagy genes at different time points. Data represent mean ± SD. ZT0 and 12 represent the onset of light and dark cycles, respectively.

**Fig. S5.** qPCR analysis of hepatic autophagy and core clock gene expression in fed (filled diamond) or 24-hour fasted mice (open square) at different time points. For fasted group, food had been withdrawn for exactly 24 hours before harvest. Pooled samples from 3-4 mice were used per data point. Data represent mean ± SD.

**Fig. S6.** Immunoblotting analyses of total lysates from primary hepatocytes transduced with GFP or C/EBPβ adenoviruses in the presence of vehicle, 3-MA, or PS341. Immunoblots with different exposure time were shown to illustrate LC3-I and LC3-II in cells. Pooled samples from triplicates were used for each condition.

**Fig. S7.** Interaction between C/EBPβ and mTOR pathways. (A) C/EBPβ overexpression does not alter nutrient regulation of mTOR, as indicated by S6 phosphorylation. The lanes shown were from same original immunoblots. (B) Inhibition of mTOR activity by Torin1 does not alter C/EBPβ expression in primary hepatocytes.
**Fig. S8.** qPCR analysis of hepatic autophagy and core clock gene expression at ZT1 and ZT13 in mouse fed during dark (NF) or light (DF) phase following the switch of feeding time. Pooled samples from 3-5 mice were used for each data point. Data represent mean ± SD.

**Fig. S9.** qPCR analysis of hepatic autophagy and clock genes in control (filled diamond) and liver-specific Bmal1 knockout (open square) mice. Pooled samples from 3-5 mice were used for each data point. Data represent mean ± SD.
Fig. S1.

Heart

Skeletal muscle

Kidney

LC3-I
LC3-II
p62
Ponceau S

ZT 1 4 7 10 13 16 19 22

* Nonspecific band
Fig. S2.
Fig. S3.

Zeitgeber time (hr)

Relative mRNA level

Heart

Per1
Gabarapl1
Bnip3
Atp6v1d
LC3B
Ulk1
Ctsl
Becn1
Fig. S4.

Skeletal muscle

Relative mRNA level

Zeitgeber time (hr)

Per1
Gabarapl1
Bnip3
Atp6v1d

LC3B
Ulk1
Ctsl
Becn1
Fig. S5.

Graphs showing relative mRNA levels over Zeitgeber time (hr) for various genes:
- Gabarapl1
- Ulk1
- Bnip3
- Ctsl
- Atp6v1d
- Becn1
- Atg4c
- Atg7
- LC3B
- C/EBPb
- Per2
- Bmal1

Legend:
- Fed
- Fasted
Fig. S6.

[Diagram showing Western blot analysis of C/EBPβ, LC3-I, LC3-II, and β-actin under different conditions (DMSO, 3-MA, PS341) with short and long exposure.]
Fig. S7.
Fig. S8.

- **Reverba**
  - NF: 1, 13
  - DF: 1, 13

- **Ulk1**
  - NF: 1, 13
  - DF: 1, 13

- **Atp6v1d**
  - NF: 1, 13
  - DF: 1, 13

- **Bnip3l**
  - NF: 1, 13
  - DF: 1, 13
Fig. S9.

Relative mRNA level over Zeitgeber time (hr) for Dbp, Per2, and Reverbα with controls (diamonds) and Bmal1 LKO (squares).

- **Dbp**: Peaks at Zeitgeber times 7 and 19.
- **Per2**: Peaks at Zeitgeber times 10 and 19.
- **Reverbα**: Peaks at Zeitgeber times 4 and 19.

Legend:
- ◆ Control
- □ Bmal1 LKO
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<th>Forward primer</th>
<th>Reverse primer</th>
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