

## 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  $\pm$ 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  $\pm$ 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 For fasted group, food had been withdrawn for exactly 24 hours before harvest.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  $\pm$ SD.

**Fig. S6.** Immunoblotting analyses of total lysates from primary hepatocytes transduced with GFP or C/EBP $\beta$  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/EBP $\beta$  and mTOR pathways. **(A)** C/EBP $\beta$  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/EBP $\beta$  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  $\pm$  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  $\pm$  SD.

Fig. S1.

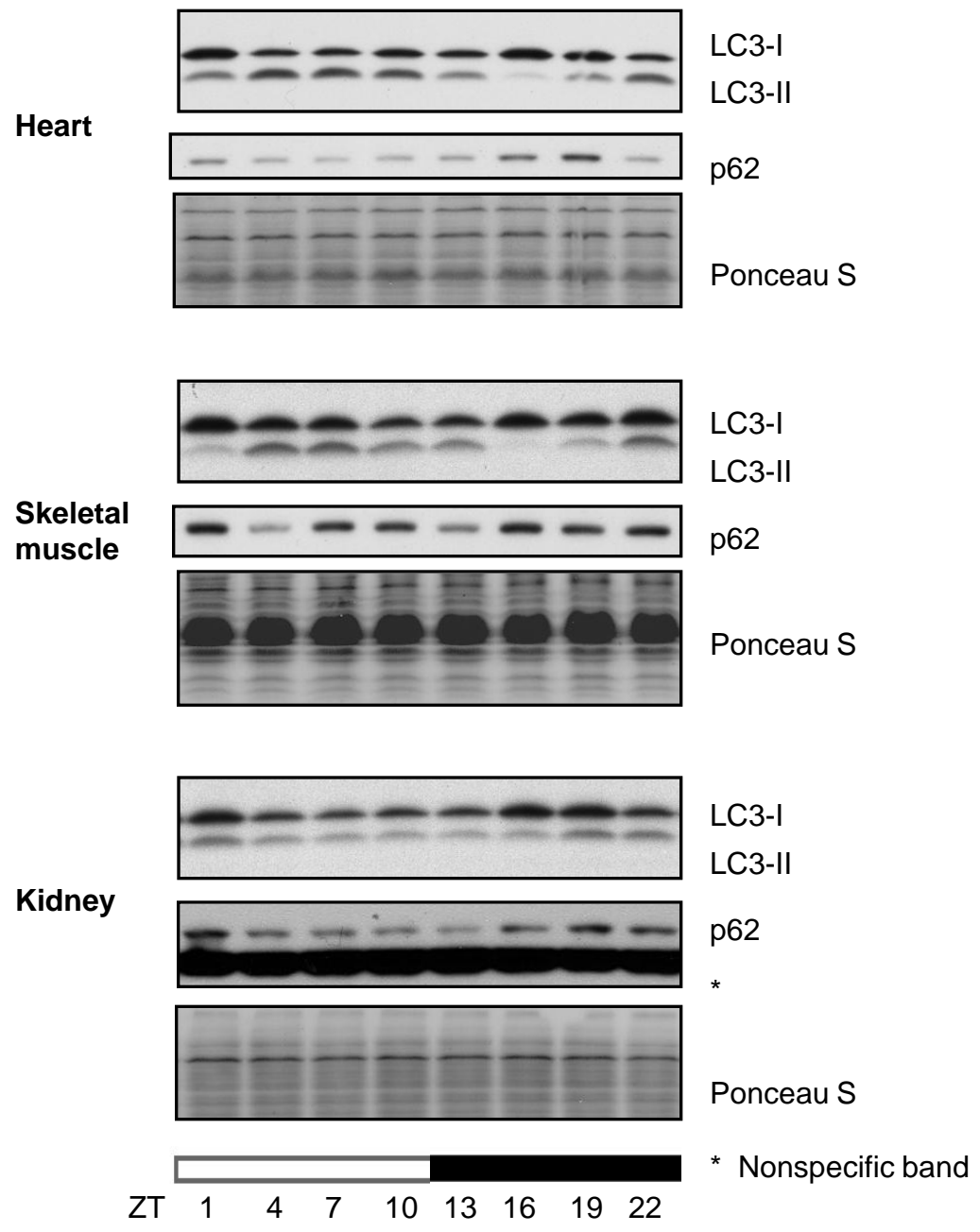
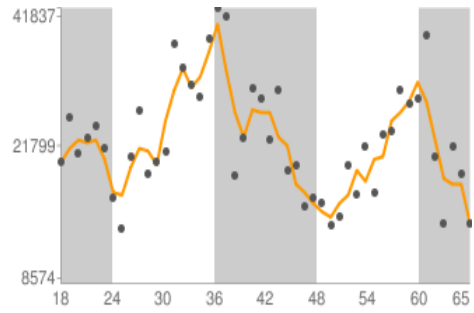
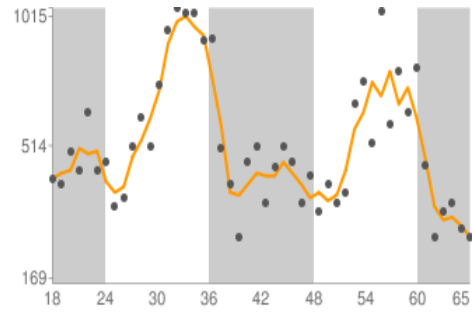


Fig. S2.

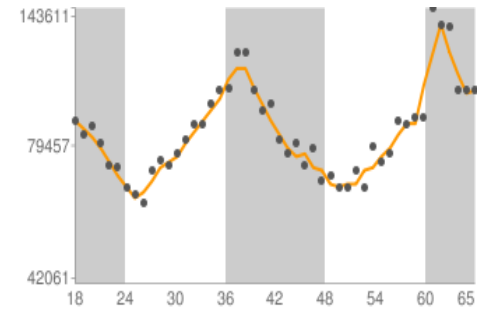
**C/EBP $\beta$**



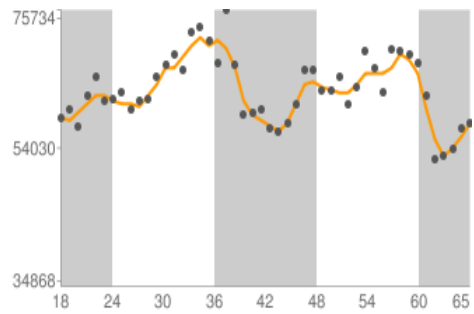
**Ulk1**



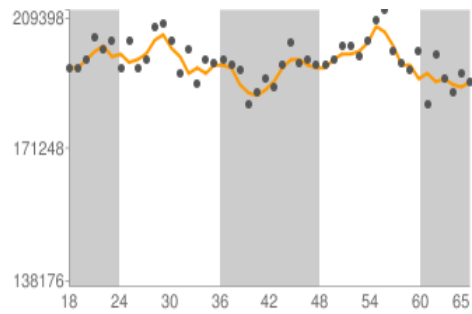
**Bnip3**



**LC3B**



**Cts1**



**Gabarap11**

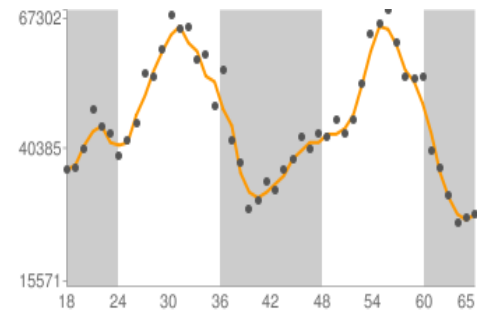


Fig. S3.

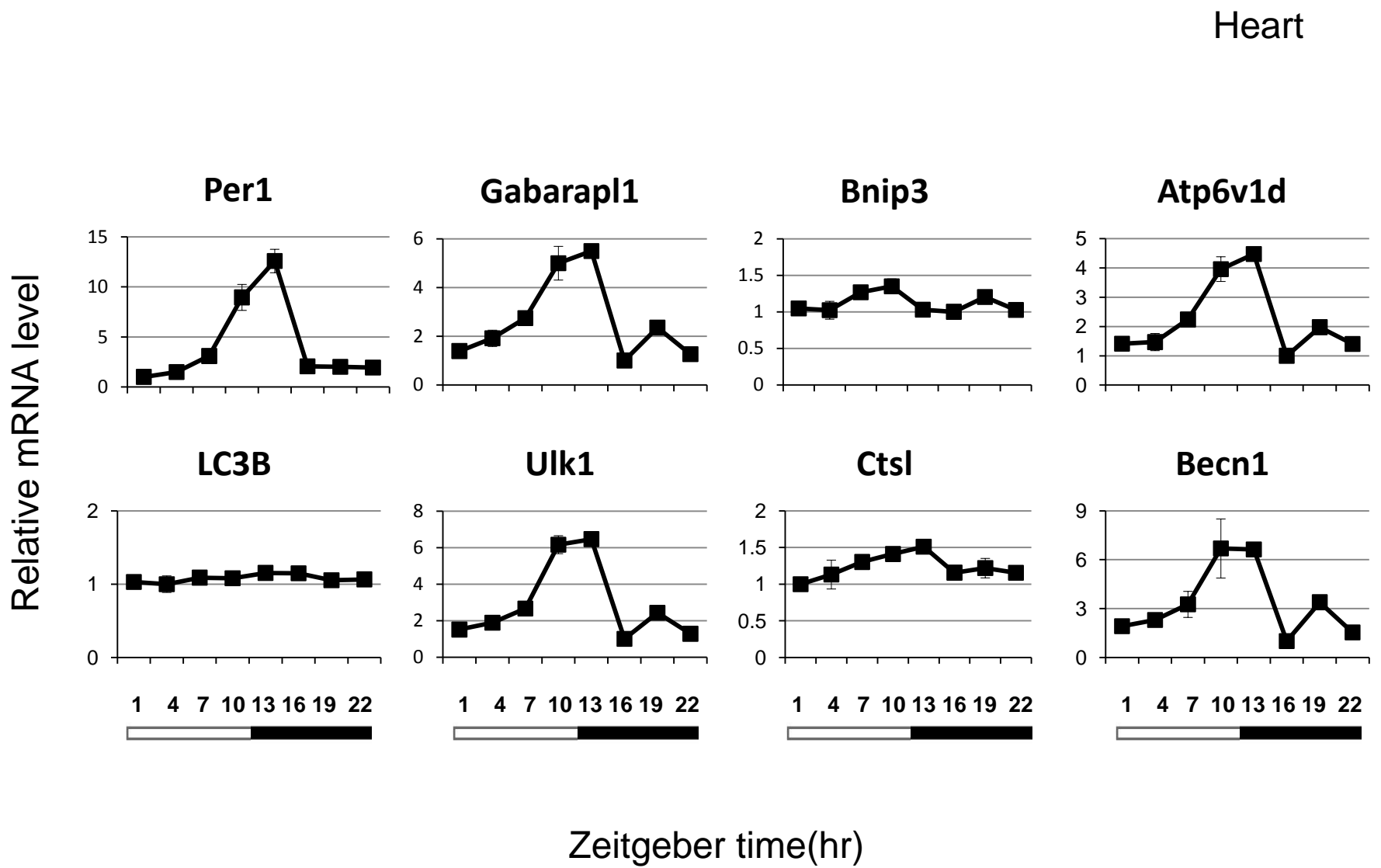


Fig. S4.

Skeletal muscle

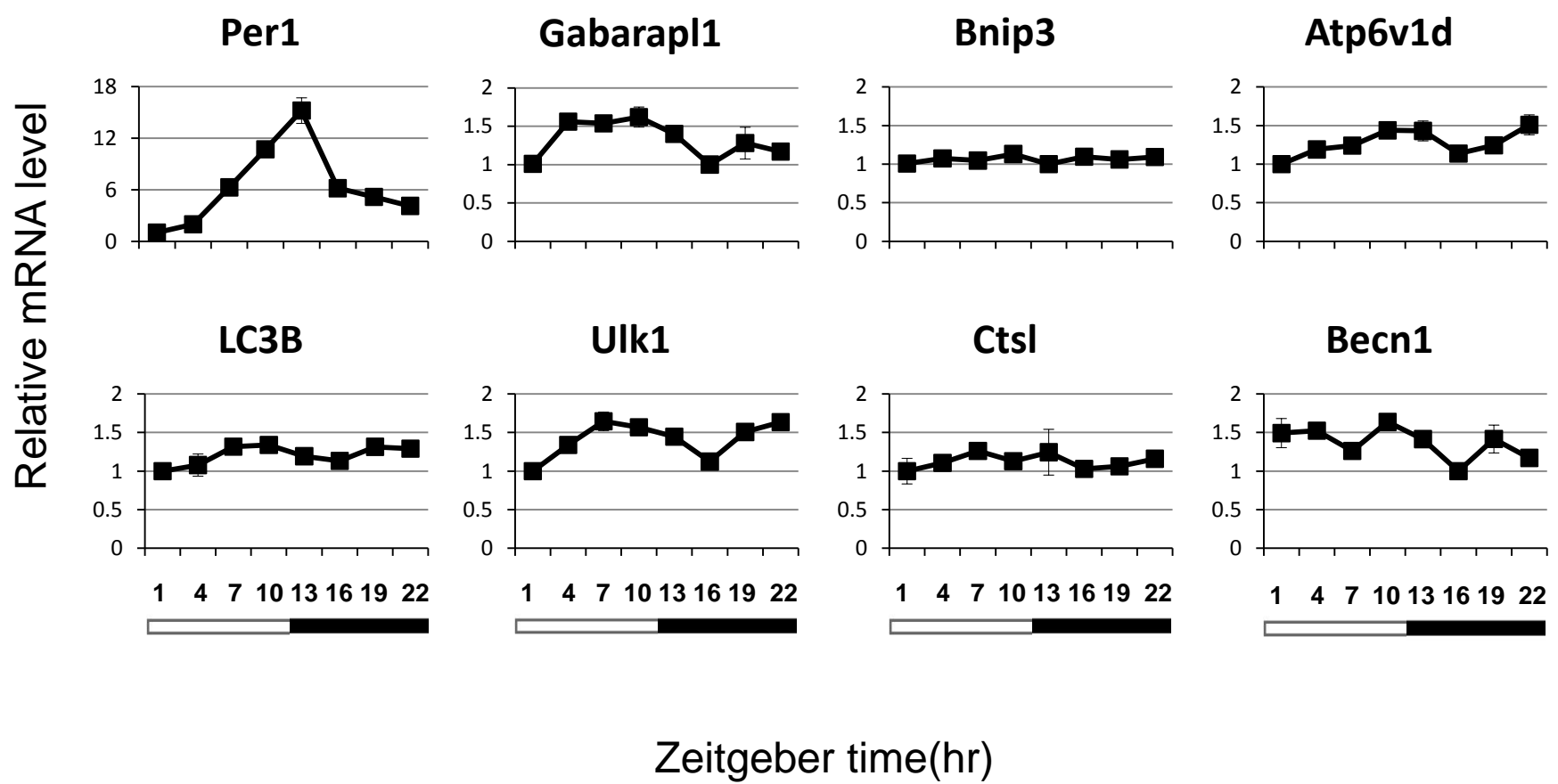


Fig. S5.

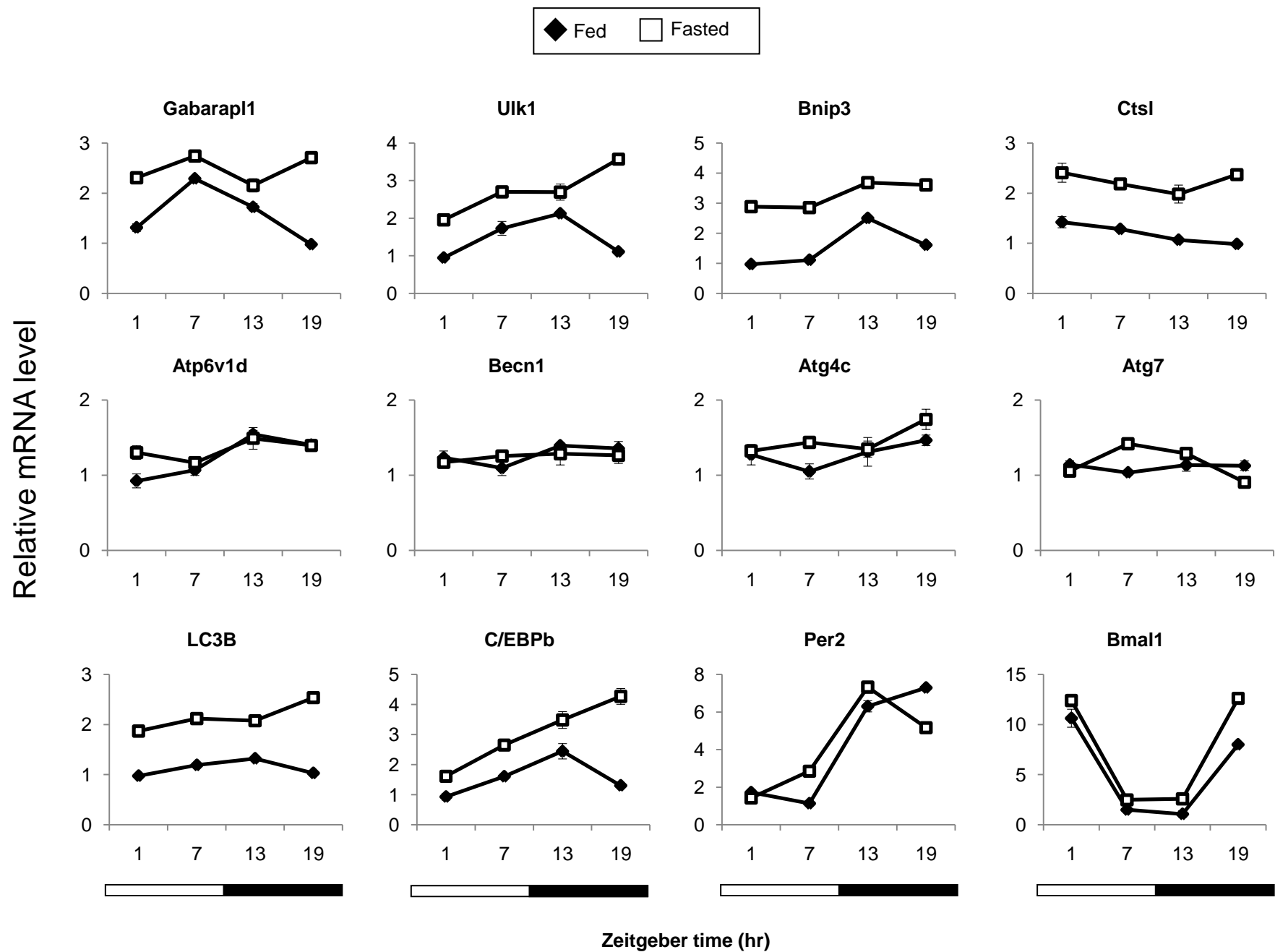


Fig. S6.

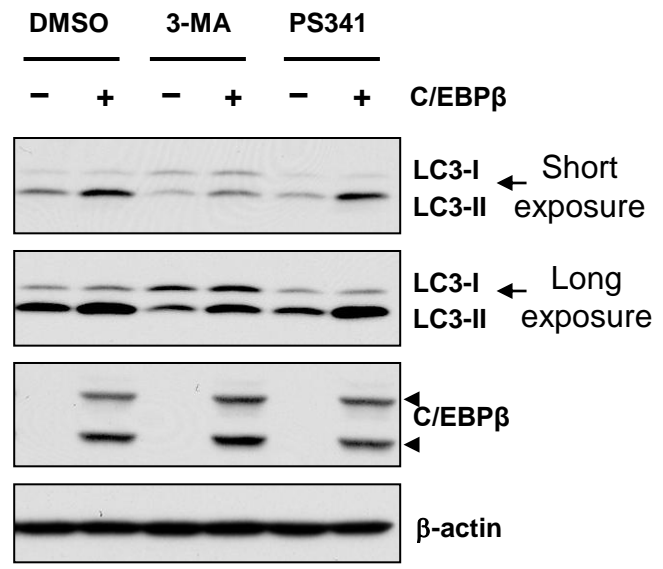
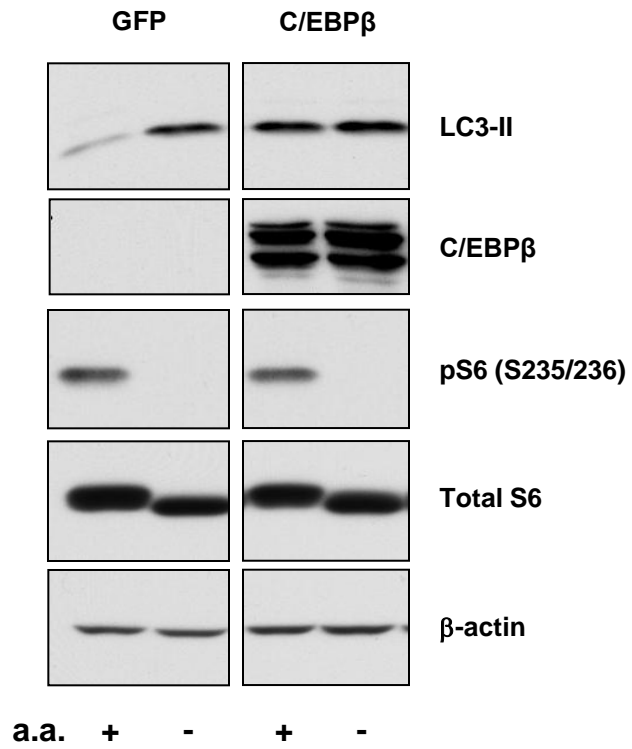




Fig. S7.

**A**



**B**

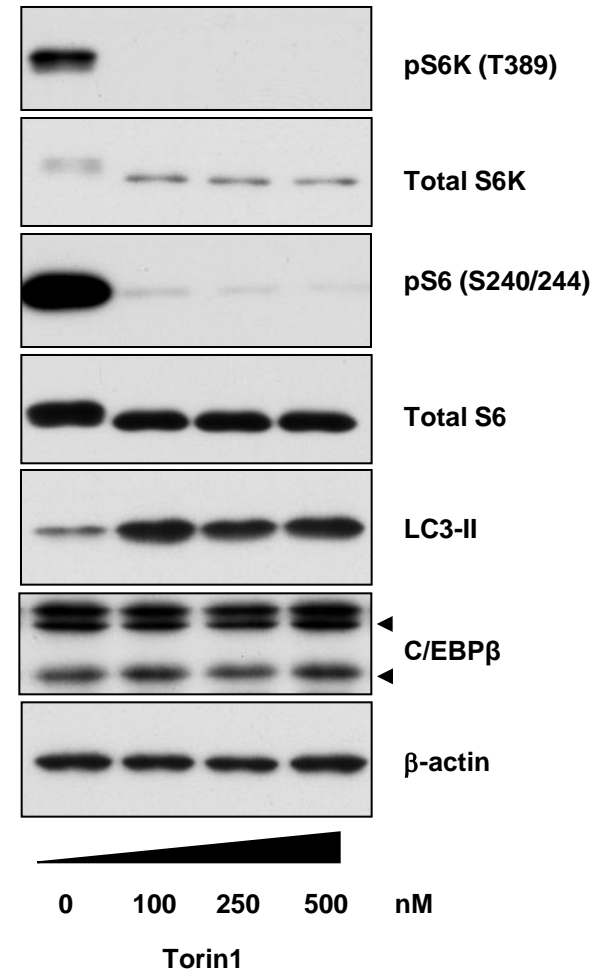


Fig. S8.

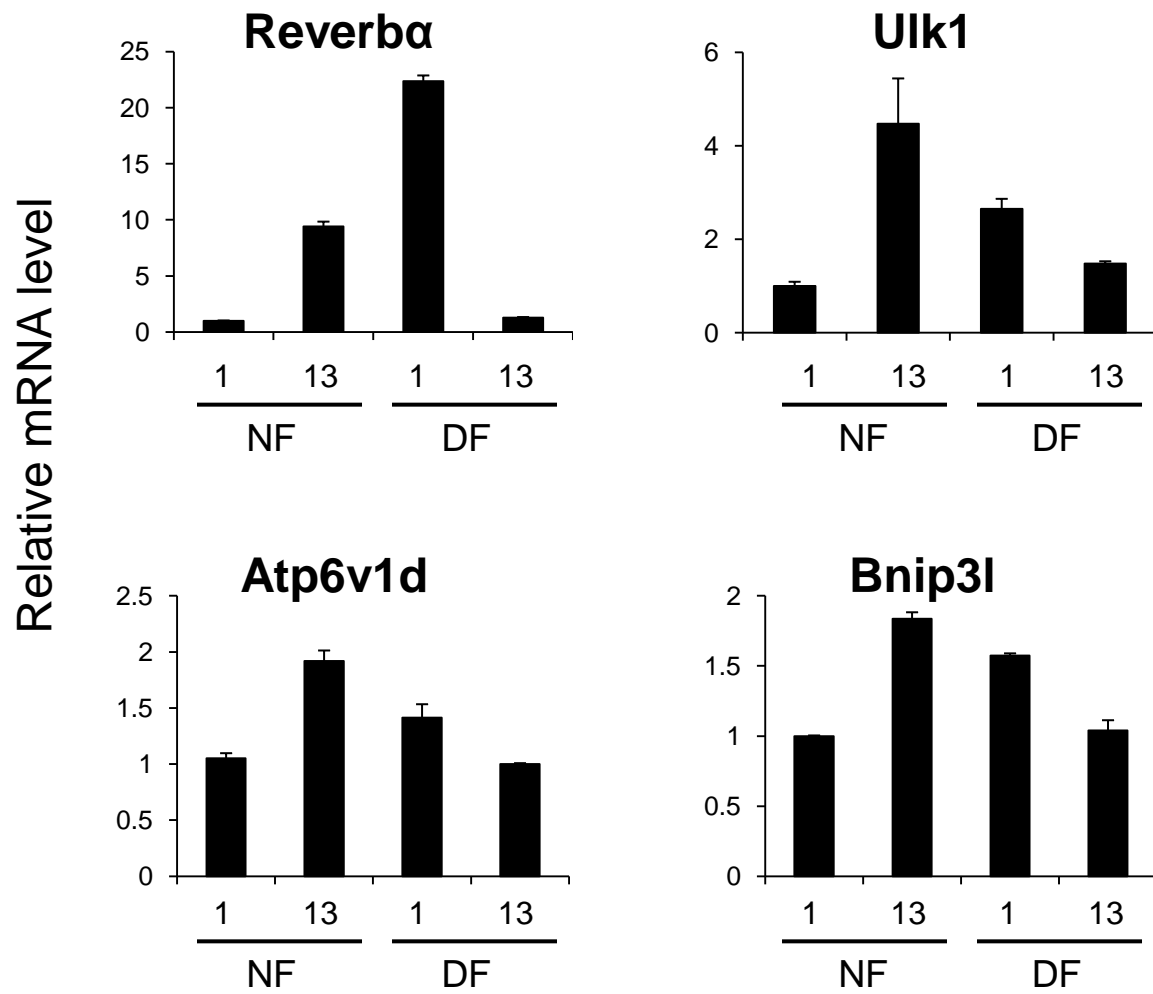
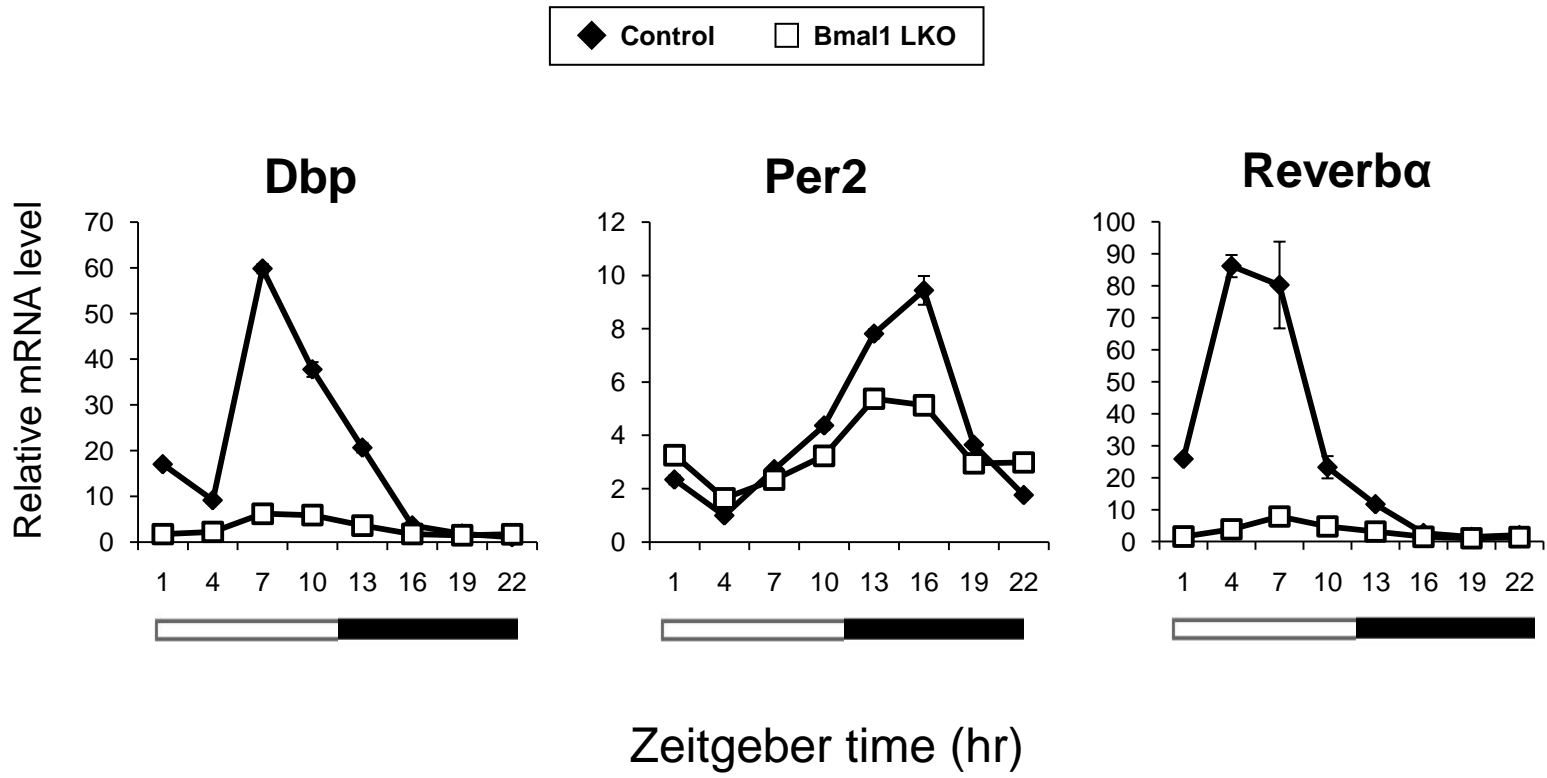


Fig. S9.



**TABLE. S1. qPCR primer list.**

	<b>Forward primer</b>	<b>Reverse primer</b>
Gabarapl1	GCCGGTCATCGTGGAGAA	TGGATCCTCTTCCGGATTAAGA
Bnip3	TTCCACTAGCACCTTCTGATGA	GAACACCGCATTTACAGAACAA
Bnip3l	CGTTCCTTCCTCGTCTTCCA	TGTGGTGAAGGGCTGTCACA
Ctsl	TCTCACGCTCAAGGCAATCA	TCCGTCCTTCGCTTCATAGG
Atp6v1d	ATTGAACGCACCCTTGCCAT	TCTCCGCCGCTCCAAGT
Ulk1	AGCCCAGTTTCCAGGTGATCT	GTACGGCCGTGGCTCTCTAG
p62	CTCATCTTTCCAACCCCTTT	AGGACGTGGGCTCCAGTTC
Becn1	GTGCGCTACGCCAGATC	CAAGCGACCCAGTCTGAAATTA
LC3A	CGACCAGCACCCAGTAAGA	TGACCAACTCGCTCATGTTAACA
LC3B	AGTGGAAGATGTCCGGCTCAT	TCAGGCACCAGGAACTTGGT
Atg4c	GTGGCCGTCTTTGGCTTACA	CCGGATGCCTTGCTTCTTC
Atg7	TTCTGGTCTCCTTGCTCAAACA	AATTCCTCAAAGGCCATCCA
Gabarapl1_ChIP	GGCACTTTTCCAACCTCCAGA	TCCCTCCCCTTCAAGTTTCT
Bnip3l_ChIP	TGGAAGCCATCCCTCTTATG	GTCACAGGGCCAGATGAAGT
Bnip3_ChIP	TGACCCATAGTTCCCAATC	CGTGCATAGAGACAGCGAGA
Ctsl_ChIP	AAAATGTGCAGGGTGGAGAG	TGTCCTCCGCTCTGTCTTCT