Supporting Information

Masri et al. 10.1073/pnas.1217632110

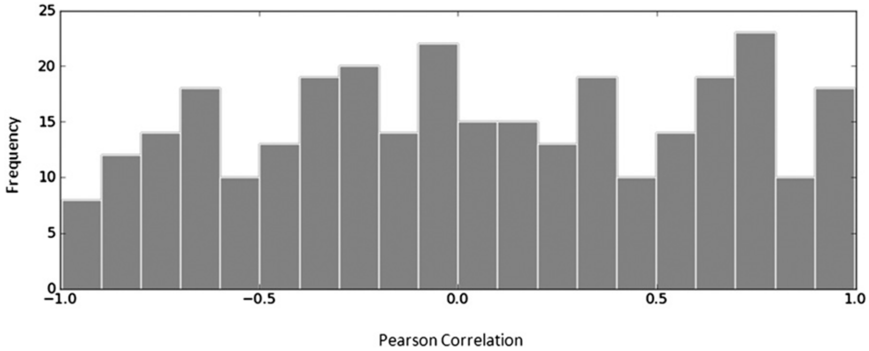

Fig. S1. Correlation between WT and *Clock*$^{-/-}$ acetylation profiles. Pearson's correlation was calculated for acetylation profiles comparing WT and *Clock*$^{-/-}$ livers. Correlation coefficients are shown in the histogram ranging from –1 (inversely correlated) to 1 (positively correlated). A correlation of 0 indicates no correlation in acetylation profiles.

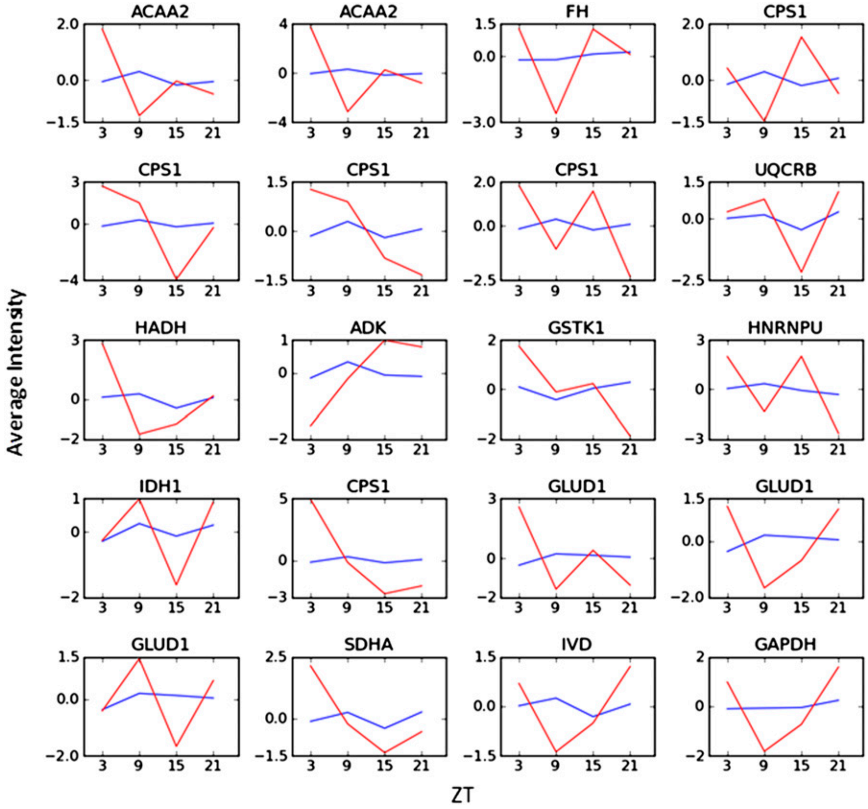

Fig. S2. Acetylated peptides versus unmodified peptide abundance. A graphical representation displays average intensity profiles of unmodified peptides versus acetylated peptide intensity, identified by MS from the same protein. Acetylation profiles are shown in red and unmodified peptide profiles are shown in blue. Data are shown over the four ZTs: 3, 9, 15, and 21.

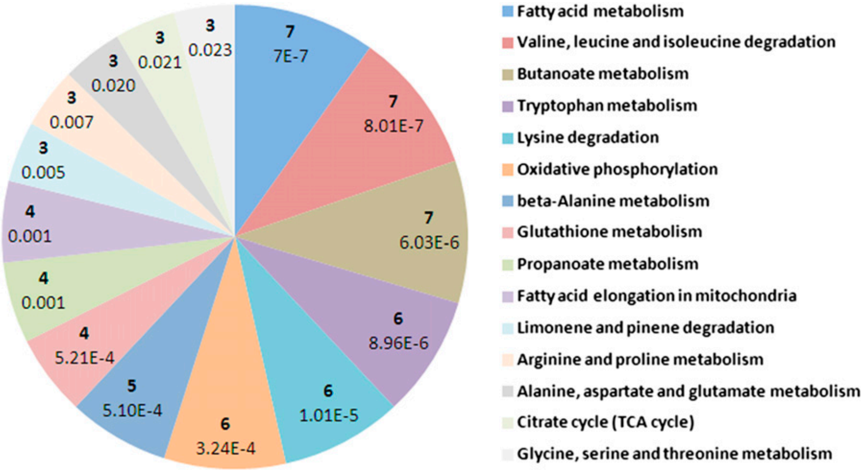

Fig. S3. KEGG pathway analysis for enzymes differentially acetylated at one ZT. KEGG pathway analysis was done using DAVID to identify significant biological pathways enriched in our hits. Hits that were disrupted only at one ZT were used for DAVID analysis. This list includes 47 hits, although 43 were identified by DAVID as belonging in a biological pathway. Some hits do overlap in more than one pathway. Significant biological pathways are shown in the pie chart, with number of hits and *P* value also indicated.

Other Supporting Information Files

Table S1 (XLSX)
Table S2 (XLSX)