

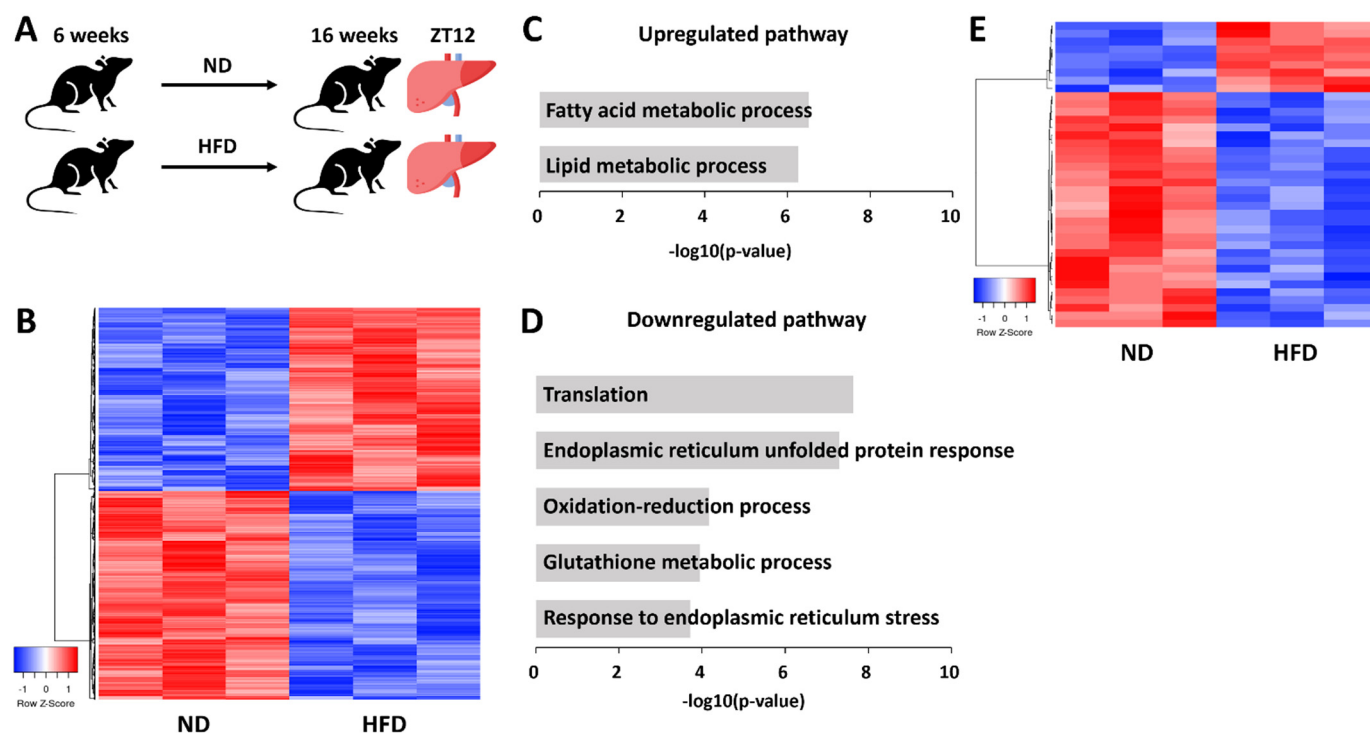
Supplemental Table S1. Compositions of diets and calorie % from total energy

Ingredients (g/kg)	LPD	ND	HPD
Casein	50.03	200.08	330.63
L-Cystine	0.75	3.00	4.51
Corn Starch	600.39	397.16	315.60
Maltodextrin	100.07	132.05	100.19
Sucrose	51.03	100.04	51.10
Cellulose	50.03	50.02	50.10
Soybean oil	90.06	70.03	90.17
Lard	0.00	0.00	0.00
Kcal %			
Protein	5.0	20.3	33.0
Carbohydrate	75.0	63.9	47.0
Fat	20.0	15.8	20.0
Energy (kcal/gm)	4.1	4.0	4.1

Supplemental Table S2. Primer sequences for qRT-PCRs

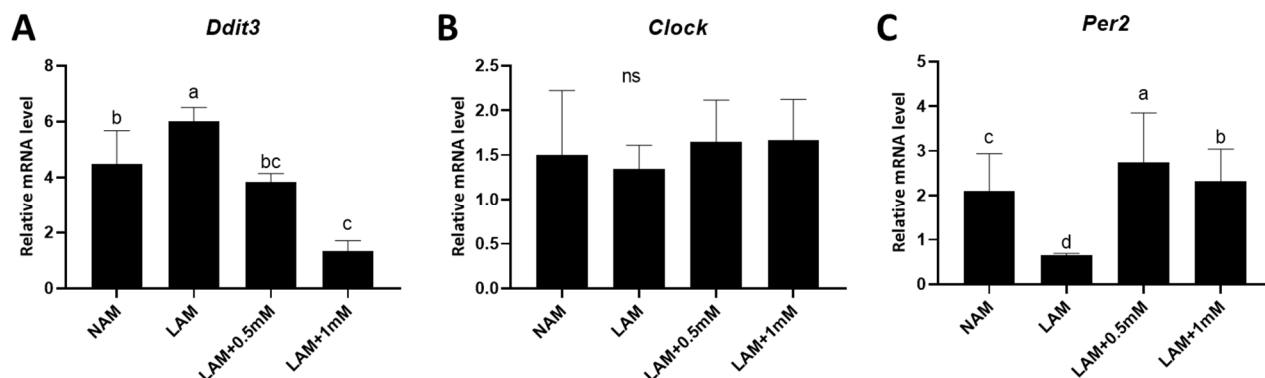
Gene name	Gene accession number	Species	Primer sequence (5'-3')	
<i>Tbp</i>	NM_013684.3	Mouse	Forward	GACCAGAACAACAGCCTTCC
			Reverse	GAGTAAGTCCTGTGCCGTAAG
<i>Clock</i>	NM_001289826.1	Mouse	Forward	GCAGCTTCCTTCAGTTCAGC
			Reverse	GAAAGGCAGCAGAGAGGATG
<i>Bmal1</i>	NM_007489.4	Mouse	Forward	CCCGCTGAACATCACAAGTA
			Reverse	TGAGCCTGCCCTGGTAATAG
<i>Per2</i>	NM_011066.3	Mouse	Forward	GAAGGAGGACCAGGAGAAGC
			Reverse	TGCCTTCTCCTCACTCTCG
<i>Per3</i>	NM_011067.3	Mouse	Forward	TCATGACATAACCAGGTGCCC
			Reverse	CTGTGTGGCTGTGGATCCA
<i>Cry1</i>	NM_007771.3	Mouse	Forward	CAGACTCACTCACTCAAGCAAGG
			Reverse	TCAGTTACTGCTCTGCCGCTGGAC
<i>Dbp</i>	NM_016974.3	Mouse	Forward	AATGACCTTTGAACCTGATCCCGCT
			Reverse	GCTCCAGTACTTCTCATCCTTCTGT
<i>Nampt</i>	NM_021524.2	Mouse	Forward	GGCGCTTTGCTACAGAAGTT
			Reverse	TTTGTTGGGATCAGCAACTG
<i>Fgf21</i>	NM_020013.4	Mouse	Forward	CAAATCCTGGGTGTCAAAGC
			Reverse	ATGGGCCTCAGACTGGTACA
<i>Pck1</i>	NM_011044.2	Mouse	Forward	ATGAAGTTTGATGCCCAAGG
			Reverse	CGTTGGTGAAGATGGTGT TTT
<i>Gcg</i>	NM_008100.4	Mouse	Forward	CCAGGTGGTCATGTCTTCTG
			Reverse	GCATTGTGTAACCCAACGATT
<i>Irs1</i>	NM_010570.4	Mouse	Forward	AAGACGTGAGGTCTTGTTG
			Reverse	GCCAGAGGATCGTCAATAGC
<i>Gck</i>	NM_001287386.1	Mouse	Forward	TGGTGGATGAGAGCTCAGTG
			Reverse	CCTCTCCGTGGAACAGAAGA
<i>G6pdx</i>	NM_008062.3	Mouse	Forward	GGTGTAACCTCCAGGGCTCA
			Reverse	CACCACTGCTGCACAAGATT
<i>Fasn</i>	NM_007988.3	Mouse	Forward	GTTGGGGGTGTCTTCAACCT
			Reverse	CAGCTCAGGGCAGGCTTC
<i>Acc1</i>	NM_133360.3	Mouse	Forward	AGTGGCTGGAGAAGCAACTG
			Reverse	GAGATGTGCTGGGTCAATGTG
<i>Atgl</i>	NM_001163689.1	Mouse	Forward	TACTGTGGCCTCATTCCTCC
			Reverse	GGGACACTGTGATGGTATTC
<i>Pgcl1a</i>	NM_008904.3	Mouse	Forward	TTACACCTGTGACGCTTTTCG
			Reverse	GTGGAAGCAGGGTCAAAATC
<i>Cpt1a</i>	NM_013495.2	Mouse	Forward	TGCCTCTATGTGGTGTCCAA
			Reverse	AAACAGTTCCACCTGCTGCT
<i>Pparg</i>	NM_001127330.3	Mouse	Forward	GCCCTTTGGTGACTTTATGG
			Reverse	CATCTTCTGGAGCACCTTGG
<i>Atf4</i>	NM_009716.3	Mouse	Forward	CCACCATGGCGTATTAGAGG
			Reverse	CTTCGCTGTTCAAGGAAGCTC
<i>Atf6</i>	NM_001081304.1	Mouse	Forward	TACCACCCACAACAAGACCA
			Reverse	TGATGATCCCGGAGATAAAGG
<i>Ddit3</i>	NM_007837.4	Mouse	Forward	GGAGGTCCTGTCCTCAGATG
			Reverse	GGACGCAGGGTCAAGAGTAG
<i>Ppp1r15a</i>	NM_008654.2	Mouse	Forward	CGGCTCAGATTGTTCAAAGC
			Reverse	CAGCAAGGAAATGGACTGTG

Supplemental Figure S1. Results of secondary analysis of public microarray data indicating altered UPR response and expression of circadian genes in mouse liver in high fat diet (HFD) group.



(A) Experimental design of GSE52333. (B) Heatmap presenting expression of DEGs ($p < 0.01$) in HFD group versus normal diet (ND) group. (C) Upregulated pathway in results of gene ontology analysis with p -value < 0.01 and FDR < 0.05 . (D) Downregulated pathway in results of gene ontology analysis with p -value < 0.01 and FDR < 0.05 . (E) Heatmap presenting genes involved in Gene Ontology term "Circadian rhythm" (GO:0007623) among DEGs. Among 691 DEGs, 39 circadian genes were differentially expressed with significance ($p < 0.01$). In (B) and (E), each column represents a sample, and each row represents a gene. Red and blue color indicates up-regulated genes and down-regulated genes, respectively.

Supplemental Figure S2. Impacts of amino acids deprivation and ER stress inhibition with 4-PBA on *Ddit3*, *Clock*, and *Per2* expression in AML12 cells



AML12 cells were maintained in normal amino acids media (NAM, 100% amino acids) or low amino acids media (LAM, 25% amino acids) with or without 4-PBA, which is blocker of ER stress. Treatment with 4-PBA was conducted at a final concentration of 0.5 or 1 mM. After 48 hours, cells were harvested for the measurement of *Ddit3* (A), *Clock* (B), and *Per2* (C) expression. N=2 biological replicates. Data are presented as the means $\pm$ standard errors. A mixed model with least squares and Tukey's *post hoc* test were used for statistical analysis, indicated by different letters. A p-value < 0.05 was considered statistically significant.