

Supplementary

Table S1. Primers for qPCR.

Gene	Accession number	Forward primer (5'→3')	Reverse primer (5'→3')
ACACA	NM_022193	GCCAGCAGAATTTGTTACTC	ATAAGACCACCGCCGGATAG
ACLY	NM_016987	TGGACTTTGACTACGTGTGC	AAGACAGGGATCAGGATTTTC
ACOX1	NM_017340	TGATGAAATACGCCAGGTG	CCCATACGTCAGTTGTTAC
ADIPOQ	NM_144744.3	CGCTTATGTGTATCGCTCAG	GTCCCGGAATGTTGCAGTAG
APOE	NM_138828	TGAACCGCTTCTGGGATTAC	TGTGTGACTTGGGAGCTCTG
BMAL1	NM_024362	TTTGTAGATCAGAGGGCGAC	GTACCTAGAAGTTCTGTGG
CD36	NM_031561.2	GAAGCACTGAAGAATCTGAAGAG	TCCAACACCAAGTAAGACCATC
CLOCK	NM_001289832	AGTTAGGGCTGAAAGACGGC	TTCCAGTGCTTCTTGAGAC
CPT1a	NM_031559	GGGATTAAGTTCTGCTATG	AAGATGTGTGAGGAAGGTGG
CRY1	NM_198750	CACTATGCTCACGGAGACAG	CCCATGGAGCTTCTTCTTTG
CYP7A1	NM_012942	TGTGTGAGGGACCAGGTCTCT	AGCTCAAAGGTTGGAGGA
DBP	NM_001289982	CTCTAGGGACACACCCAGTCTT	AGGCTTCAATTCCTCCTCTGAGA
DEC1	NM_053328	GAAACCATTGGACTCAGCTC	TTTCCCAGGGCCTTCTGATC
DGAT1	NM_053437.2	TGTTCCGCCTTTGGGCATTG	GGGCATCATAGTTGAGCACG
E4BP4	NM_053727.2	ACTGGCATCACAAAGAACTG	AGACCACCTCTGCGGATAAG
ELOVL6	NM_134383	ACCCGAACTAGGTGATACG	CCCAGCTACCATGTCTTTG
FAS	NM_017332	CCAAGCAGGCACACACAATG	GATACCTCCGTCGACAATAG
FBP1	NM_012558	TGTATAGCGTTCAGTCTCTCC	GGGTGCTGATATCCGTTTCCG
GCK	NM_001270849	AGAAGATCATCGGTGGGAAG	TTAAGCAGCACAAAGTCGTAC
GPAM	NM_017274	ACACCATCCCTGACATCCTG	TAACGCCTCTTGCCACACTC
G6PC	NM_013098	TCCGGTGCTTGAATGTCGTC	TCTGGAGGCTGGCATTGTAG
HMGCR	NM_013134	TGCACAGACTCCTCAGACGTG	TTCGTCAAACACCAGCTTCC
HSL	NM_012859	TCCCAGGAAGAGGCTGAAAC	CCAGCAGAGGAGACATGAAG
LPL	NM_012598.2	TCCGGGCCAGCAACATTATC	GCCACATCATTTCCACCAG
LXR α	NM_031627	TCCGAGATCTGGGATGTCCA	TGCCATGCAAGGGTCTCTTT
ME	NM_012600	CTTGTTGCCACCCTGCATTG	TAAGCACACTGTAGAAGAGC
MTP	NM_001107727.1	GAGAGGTCCGATTTACAAC	ATAGGTAGTGACAGAGTGG
PER1	NM_001034125	CTTCGGGAGCTCAAACCTCG	TATTCCTGGTTAGCCTGCAC
PEPCK	NM_198780	AACTGTTGGCTGGCTCTCAC	TCTGCTCTTGGTAATGATG
PFKL	NM_013190	TGAGCATAGACAAGGGTTTC	CCGAGTTCCATGTGAGTTCC
PGC-1 α	NM_031347	TCCTTTAACTCTCCGTGTCG	GATCTTGACCTGGAATATGG
PGC-1 β	NM_176075	AAGAGCACTGGACCTAGACC	GCTTGTTGACATCCCCTTTC
PKLR	NM_012624	CTGAGCGTATCCTGAAATGC	AAATAGGGTGTAACTGGGTC
PPAR α	NM_013196	TTCGGCTAAAGCTGGCGTAC	ACTGGCATTFTTCCGGTTC
PPAR δ	NM_013141	AAGCCATCCAGGACACCATC	CACTCTCCGTCTTCTTCAGC
PPAR γ	NM_001145366	CTGTGGACCTCTCTGTGATG	CCGTGGTAAAGGGTTTGATG
REV-ERB α	NM_147210	CCTTTGAGGTGCTGATGGTG	ACATGACTGTCTGGTCCTTC
18S ribosomal RNA	NR_046237	CGCCGCTAGAGGTGAAATTC	TTGGCAAATGCTTTCCGCTC
SCD1	NM_139192	ATCTCCAGTTCTACACGAC	GGCACCTTCTCATCTTCTC
SREBP1	NM_001276707	GGAGCCATGGATTGCACATT	AGGAAGGCTTCCAGAGAGGA
SREBP2	NM_001033694.2	ACGGTGTGATTGTCTTGAGC	TTTGGCGAGGTCTAGGTCTG

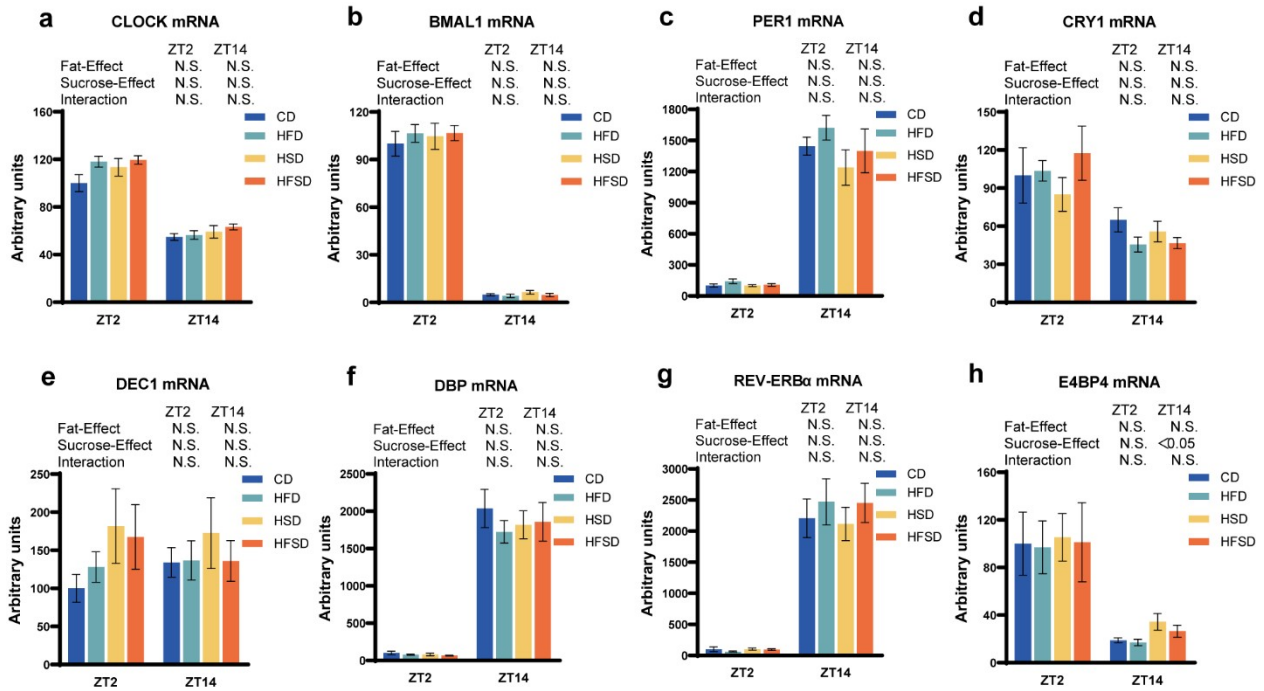


Figure S1. High-sucrose and high-fat diet did not change the hepatic clock gene in rats. Expression patterns of the genes (a) CLOCK, (b) BMAL1, (c) PER1, (d) CRY1, (e) DEC1, (f) DBP, (g) REV-RBP α , (h) E4BP4 as relative to the ApoE mRNA levels. CD: control starch diet group; HFD: high-fat diet group; HSD: high-sucrose diet group; HFSD: high-sucrose/fat diet group. ZT: Zeitgeber time. ZT2 is 2 hours after lights on, and ZT14 is 2 hours after lights off. All values are means \pm SEM, n=6 of each group timepoint. The statistical results of two-way ANOVA are indicated. “<0.05” denotes statistical significance ($P < 0.05$) for the factors or their interaction. N.S.: not significant.