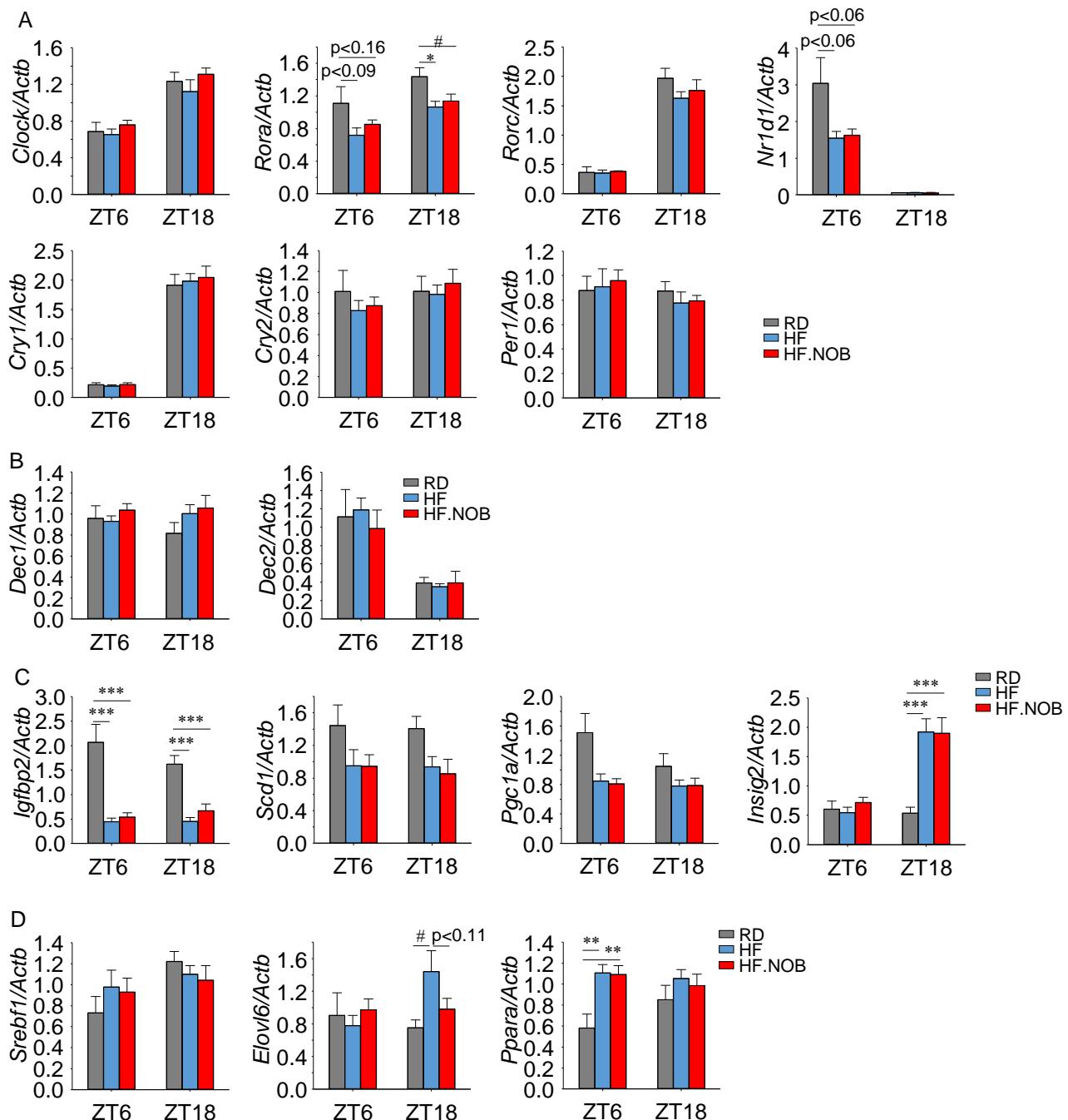
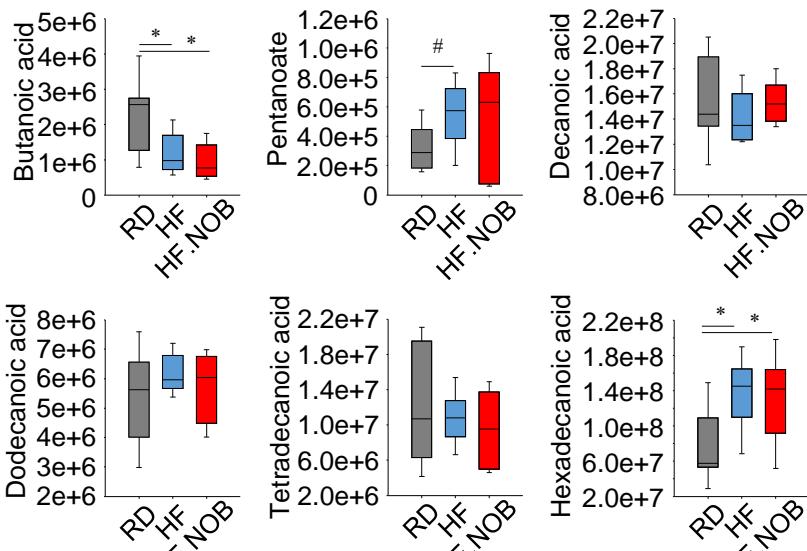


Supplementary Figure S1. NOB reduces serum carnitine and acyl-carnitine levels. Serum metabolomic profiles of carnitine and acyl-carnitine levels (n=7-9). RD: regular diet; HF: high-fat diet; HF.NOB: high-fat diet with 0.1% NOB. * p<0.05, ** p<0.01, *** p<0.001, One-Way ANOVA; # p<0.05, ## p<0.001, t-test. Bar graphs represent Mean ± SEM. For box-whisker plots, box edges correspond to 25th and 75th percentiles, lines inside of box correspond to 50th percentiles and whiskers include extreme data points.

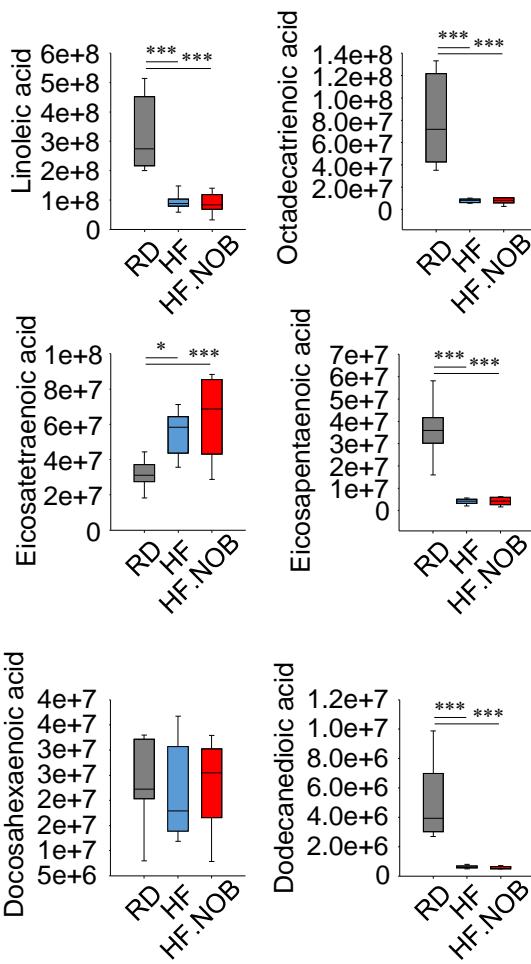


Supplementary Figure S2. NOB alters circadian and metabolic gene expression in the liver. (A) Core clock gene expression levels in the liver were analyzed by qPCR (n=7-11). (B) Core clock related Dec1 and Dec2 gene expression levels in the liver were analyzed by qPCR (n=7-11). (C) Fatty acid and lipid metabolism related genes in liver were analyzed by qPCR (n=7-11) (D) Clock output energy homeostasis related gene expression levels in the liver were analyzed by qPCR (n=7-11). RD: regular diet; HF: high-fat diet; HF.NOB: high-fat diet with 0.1% NOB. * p<0.05, ** p<0.01, *** p<0.001, One-Way ANOVA; # p<0.05, t-test. Bar graphs represent Mean ± SEM.

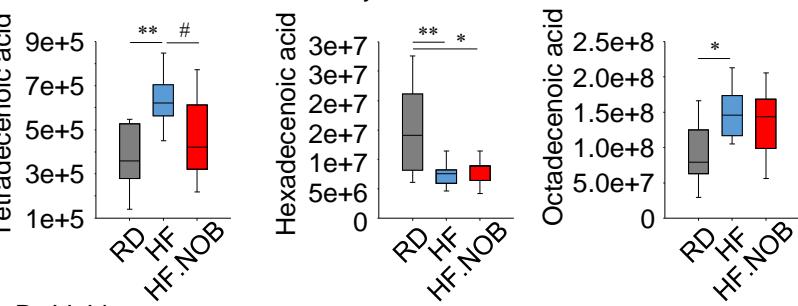
A Saturated fatty acid



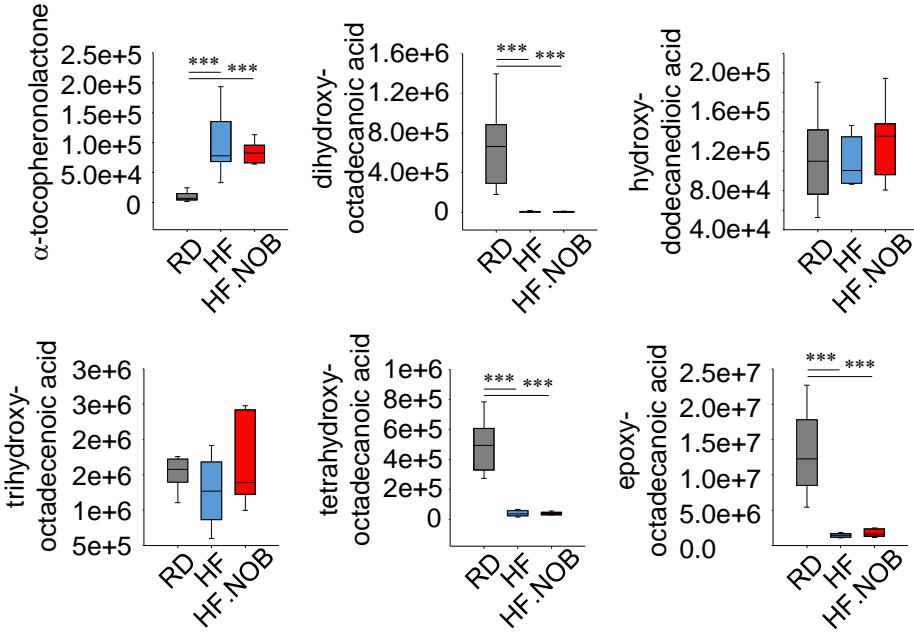
C Poly-unsaturated Fatty Acids



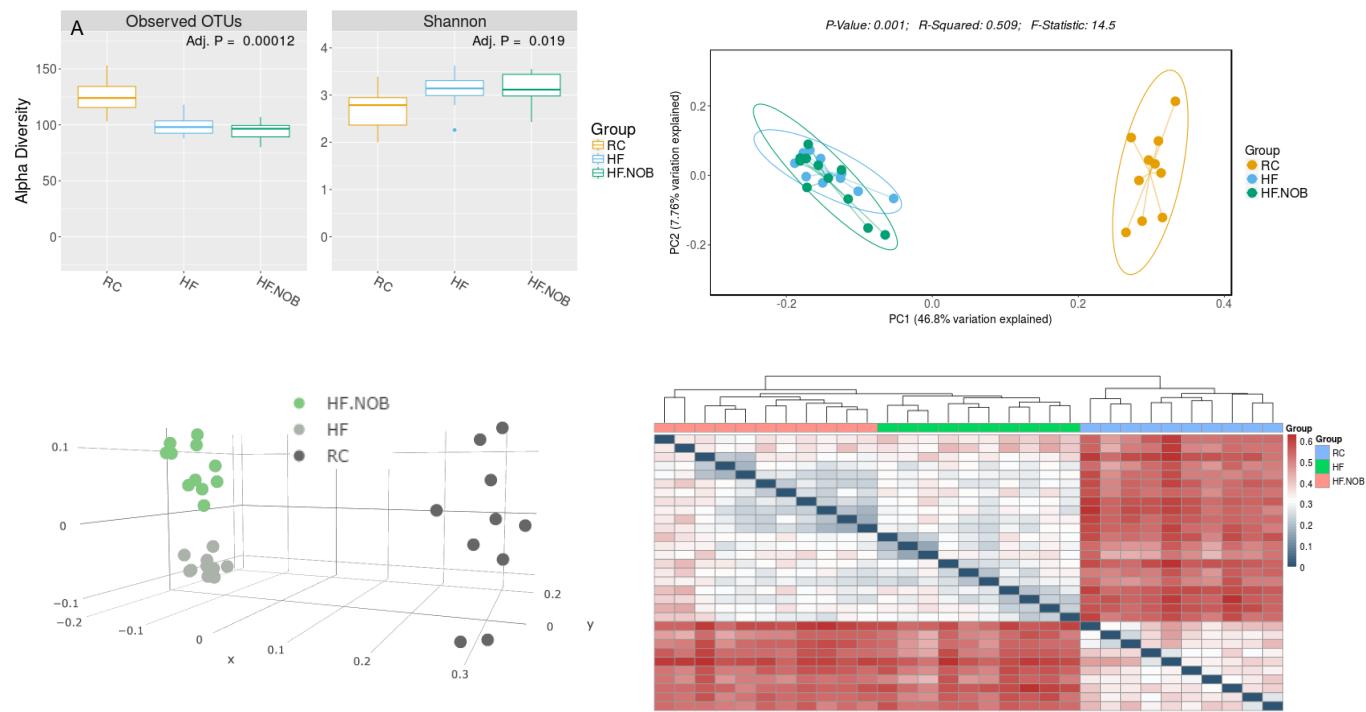
B Monounsaturated Fatty Acids



D Lipids



Supplementary Figure S3. NOB does not influence fatty acid and lipid excretion. (A) Saturated fatty acid, (B) mono-unsaturated fatty acid, (C) poly-unsaturated fatty acid and (D) other lipid profiles in fecal samples measured by metabolomics ($n=10-12$). RD: regular diet; HF: high-fat diet; HF.NOB: high-fat diet with 0.1% NOB. * $p<0.05$, ** $p<0.01$, *** $p<0.001$, One-Way ANOVA; # $p<0.05$, t-test. For box-whisker plots, box edges correspond to 25th and 75th percentiles, lines inside of box correspond to 50th percentiles and whiskers include extreme data points.



Supplementary Figure S4. NOB remodels gut microbiota and protects liver from inflammatory damage. Taxa abundance distribution at the genus level via 16S rRNA sequencing. Left top: box plot; right top: 2D ordination; left bottom: 3D ordination; right bottom: hierarchical plots. Panels indicate the comparison among all 3 sample groups, namely RD, HF and HF.NOB groups (n=10-12).

Supplementary Table S1: qPCR Primer sequences for the genes listed, 5' to 3'.

	Forward	Reverse
<i>Actb</i>	TTGTCCCCCCAACTTGATGT	CCTGGCTGCCTAACACCT
<i>Arntl</i>	CCACCTCAGAGCCATTGATACA	GAGCAGGTTAGTCCACTTGTCT
<i>Npas2</i>	CAACAGACGGCAGCATCATCT	TTCTGATCCATGACATCCGC
<i>Clock</i>	CCTTCAGCAGTCAGTCCATAAAC	AGACATCGCTGGCTGTGTTAA
<i>Per1</i>	CCCAGCTTACCTGCAGAAG	ATGGTCGAAAGGAAGCCTCT
<i>Per2</i>	ATGCTGCCATCCACAAGA	GCGGAATCGAATGGGAGAAT
<i>Cry1</i>	CTGGCGTGGAAAGTCATCGT	CTGTCGCCATTGAGTTCTATG
<i>Cry2</i>	TGTCCCTCCTGTGTGGAAGA	GCTCCAGCTTGGCTTGA
<i>Rora</i>	GCACCTGACCGAAGACGAAA	GAGCGATCCGCTGACATCA
<i>Rorc</i>	TCAGCGCCCTGTGTTTTTC	GAGAACCAGGGCCGTGTA
<i>Nr1d1</i>	CATGGTGCTACTGTGTAAGGTGTGT	CACAGCGTGCACCCATAG
<i>Dec1</i>	GCAAGGAAACTTACAAACTGCC	CAATGCACTCGTTAACCGGT
<i>Dec2</i>	ATTGCTTACAGAATGGGGAGCG	AAAGCGCGCGAGGTATTGCAAGAC
<i>Cidec</i>	ATGGACTACGCCATGAAGTCT	CGGTGCTAACACGACAGGG
<i>Ppara</i>	AGAGCCCCATCTGCTCTC	ACTGGTAGTCTGAAAACCAA
<i>Pparc</i>	CGAGGACATCCAAGACAAC	TGTGACGATCTGCCTGAG
<i>Sreb1f</i>	CTGGCTGAGGGGGATGA	TACGGGCCACAAGAAGTAGA
<i>Sreb2</i>	CACAATATCATTGAAAAGCGCTACCGGTCC	TTTTTCTGATTGGCCAGCTTCAGCACCATG
<i>Hmgcs1</i>	AACTGGTGCAAGAAATCTCTAGC	GGTTGAATAGCTCAGAACTAGCC
<i>Hmgcs2</i>	ATACCAACCAACGCCCTGTTATGG	GTCCACATATTGGGCTGGAAA
<i>Hmgcr</i>	TCTTGGAATGCCCTGTGATT	GGGTTACGGGGTTGGTTAT
<i>Igfbp2</i>	CAGACGCTACGCTGCTATCC	CCCTCAGAGTGGCGTCATCA
<i>Scd1</i>	CATCATTCTCATGGCTCTGCT	CCCATTCTGACACGTCTATT
<i>Pgc1a</i>	TATGGAGTGACATAGAGTGTGCT	CCACTTCAATCCACCCACAAAG
<i>Insig2</i>	TAAATCACGCCAGTGCTAAAGT	GGTGACAACGGTTGCTAAGAAAG
<i>Elovl6</i>	GAAAAGCAGTCAACGAGAACG	AGATGCCGACCACCAAAGATA
<i>Cyp7a1</i>	GAACCTCCTTGGACAACGGG	GGAGTTGTGATGAAGTGGACAT
<i>Cyp7b1</i>	GGAGGCCACGACCCCTAGATG	GCCATGCCAAGATAAGGAAGC
<i>Cyp27a1</i>	CCAGGCACAGGAGAGTACG	GGGCAAGTGCAGCACATAG
<i>Cyp8b1</i>	TGCAAAAGAACTGGTGCTCAA	CGAACCTTAGGCCCTAGCAT
<i>Tnfa</i>	GCCTCTCTCATTCCTGCTTG	CTGATGAGAGGGAGGCCATT
<i>Il6</i>	ACAACCACGGCCTCCCTACTT	CACGATTCCCAGAGAACATGTG