

Supplementary Information

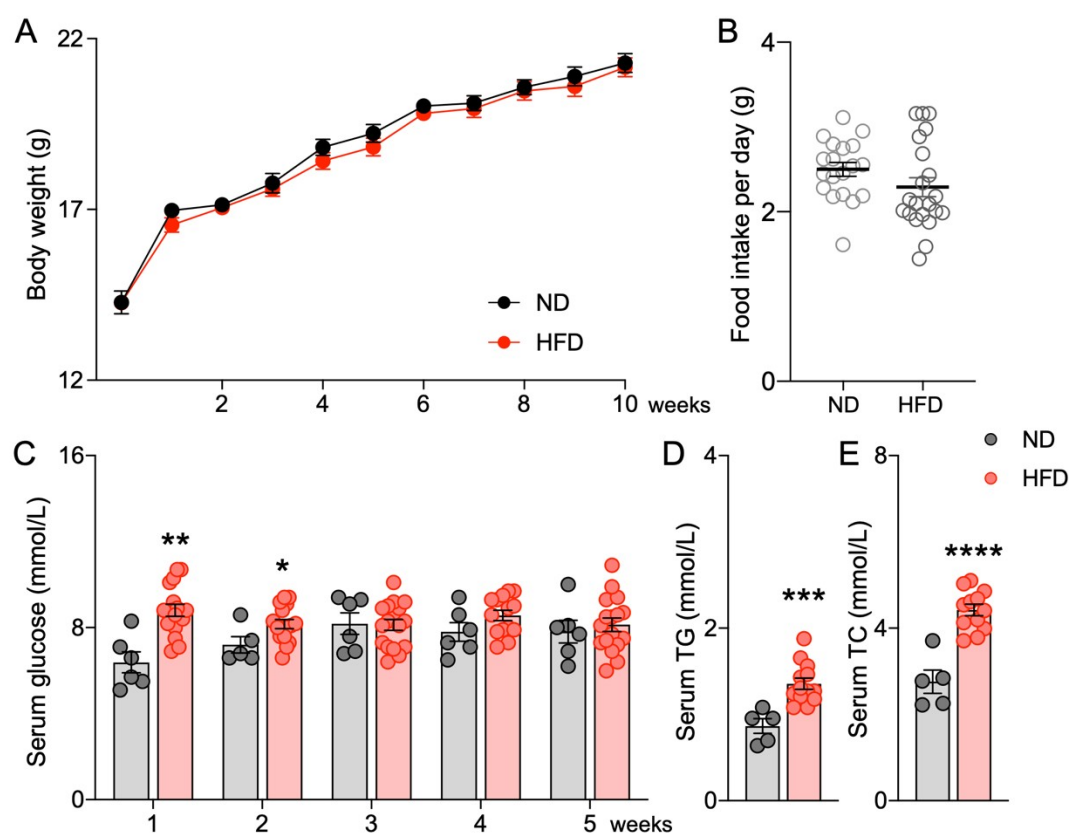


Figure S1. Study model of HFD before pregnancy. Body weight (A) and food intake (B) during the entire modeling period. (C) Serum glucose levels at 5 weeks after modeling. (D) Serum TG and TC levels at week 10 of modeling. The presented values were the means $\pm$ SEMs. * p <0.05, ** p <0.01, *** p <0.001, **** p <0.0001 versus the corresponding control.

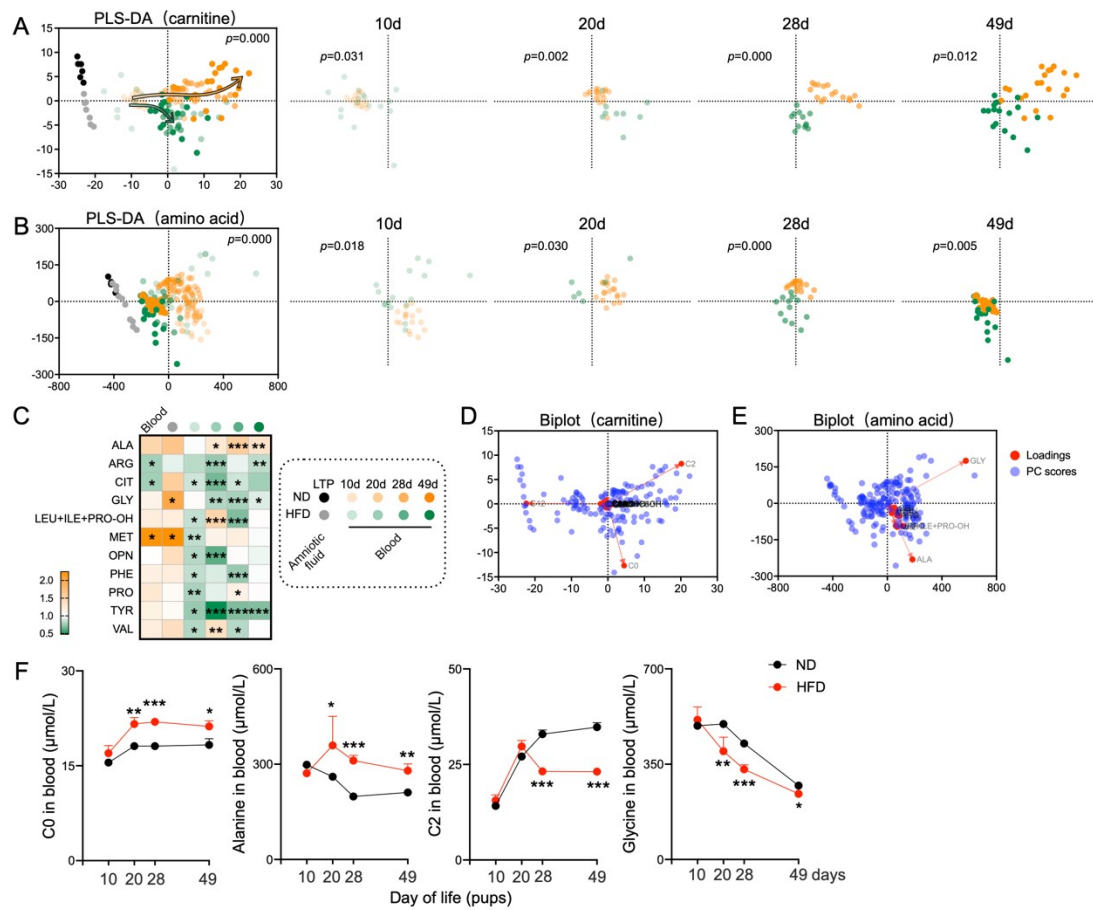


Figure S2. Effects of Maternal HFD before pregnancy on carnitine and amino acids metabolism in dam and offspring. PLS-DA score plots (A, B) and corresponding coefficient loading plots (D, E) of carnitine and amino acids. (C) Heat map of normalized mean values of amino acids in amniotic fluid and blood. (D) The levels of C0, alanine, C2, glycine in blood. The presented values were the means $\pm$ SEMs. * $p<0.05$, ** $p<0.01$, *** $p<0.001$ versus the corresponding control.

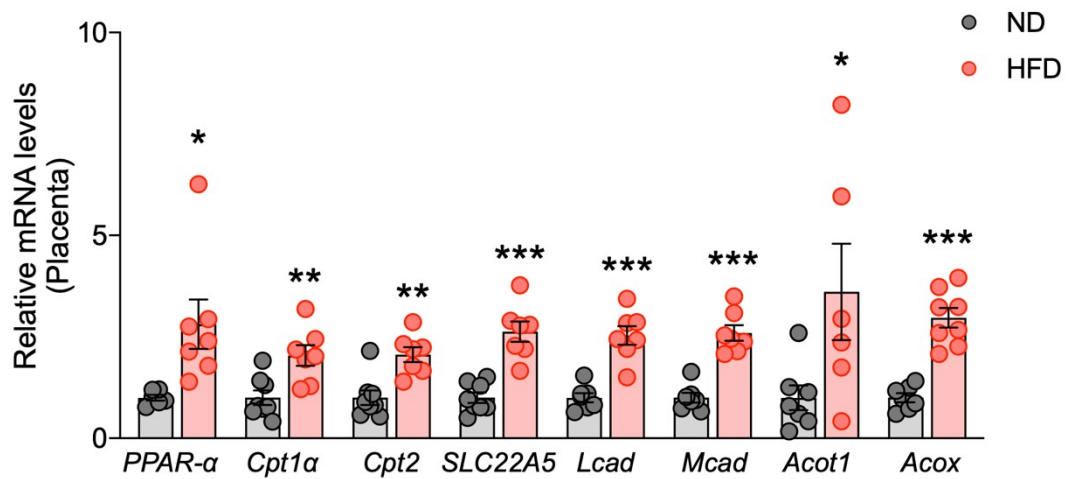


Figure S3. Maternal HFD exposure altered the expression of genes related to fatty acid β -oxidation in the placenta. The presented values were the means $\pm$ SEMs. * p <0.05, ** p <0.01, *** p <0.001 versus the corresponding control.

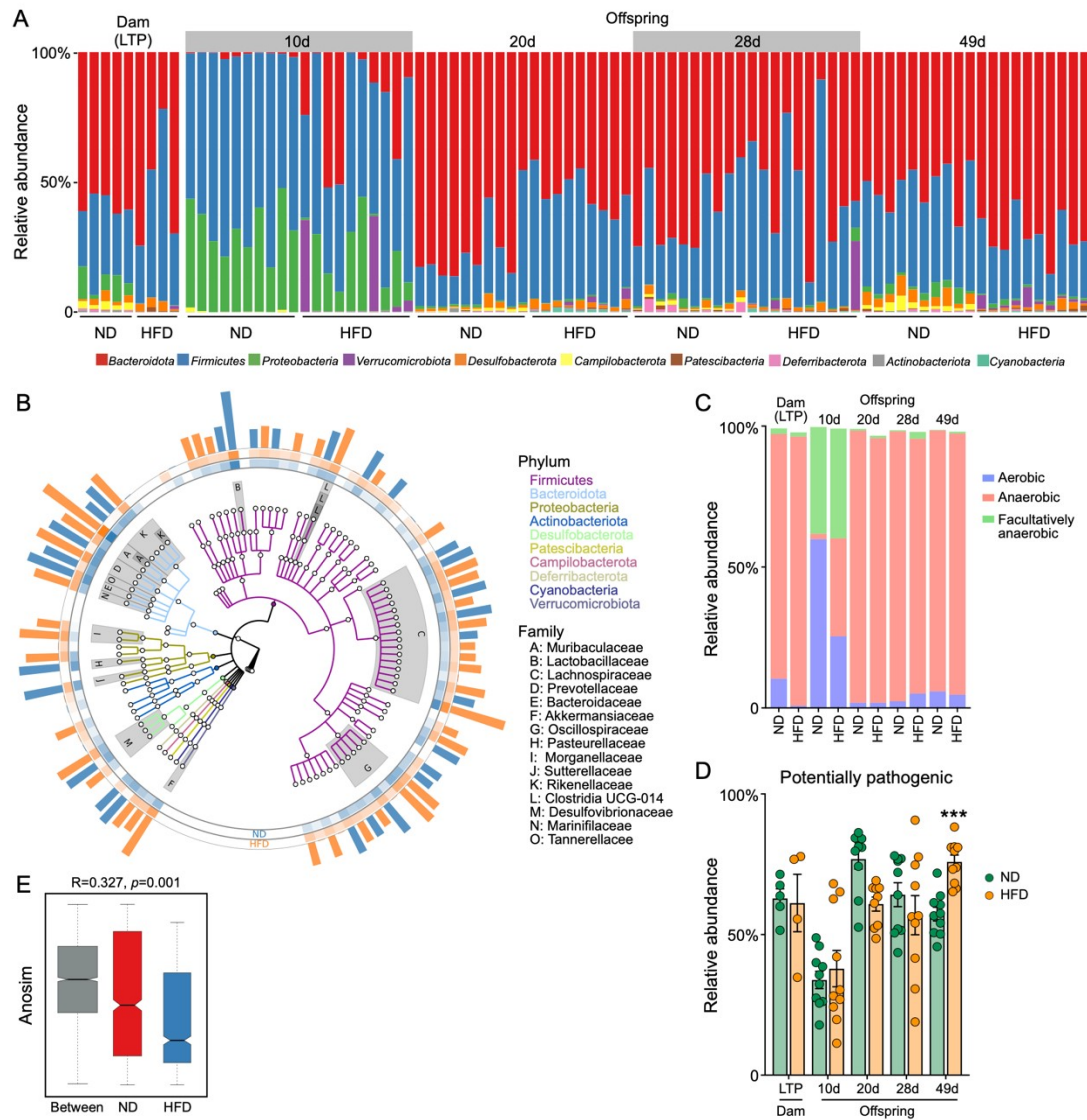


Figure S4. Effects of Maternal HFD before pregnancy on gut microbiota in dam and offspring. (A) The gut microbiota composition profiles at the phylum level (each color represents one bacterial phylum). (B) Community distribution map of evolutionary tree samples. (C) The relative abundance of aerobic, anaerobic and facultatively anaerobic bacteria. (D) The relative abundance of potentially pathogenic bacteria. (E) Anosim analysis. The presented values were the means $\pm$ SEMs. *** $p < 0.001$ versus the corresponding control.

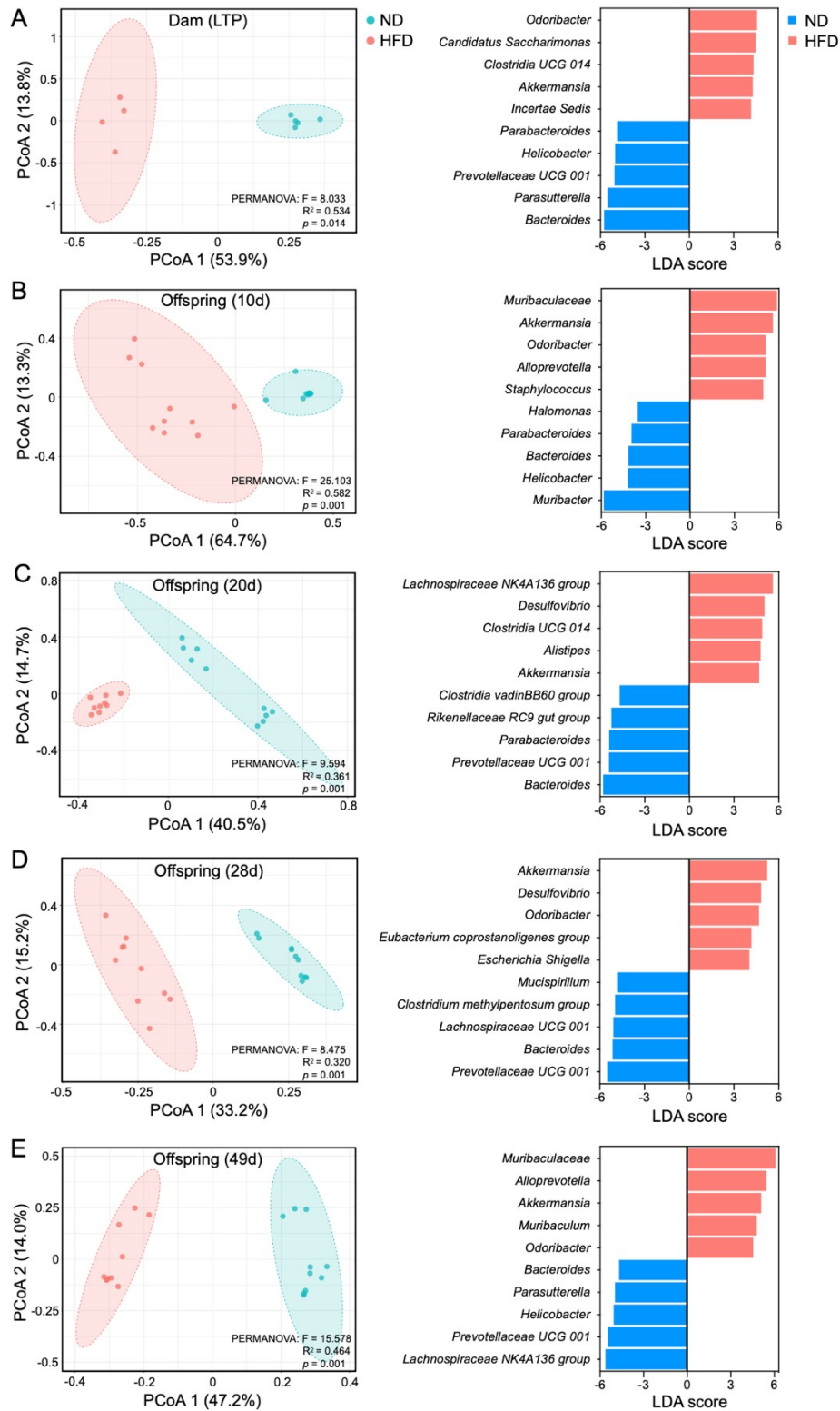


Figure S5. Maternal HFD before pregnancy altered the composition of gut microbiota in dam and offspring. (A-E) Bray-Curtis based PCoA estimates and LefSe analysis of microbiota. LDA score=TOP 5, and $p < 0.05$

Table S1**Table S1** The primer sequence pairs used in the real-time quantitative PCR reactions

Gene name	Full name	Primer sequence
<i>18s</i>		Forward 5'-CGAACGTCTGCCCTATCAACTT-3' Reverse 5'-CCGGAATCGAACCCTGATT-3'
<i>16s</i>		Forward 5'-ACTCCTACGGGAGGCAGCAG-3' Reverse 5'-ATTACCGCGGCTGCTGG-3'
<i>Acc</i>	Acetyl-CoA carboxylase	Forward 5'-TAACAGAATCGACACTGGCTGGCT-3' Reverse 5'-ATGCTGTTCTCAGGCTCACATCT-3'
<i>Acl</i>	Atp citrate lyase	Forward 5'-AGGAAGTGCCACCTCCAACAGT-3' Reverse 5'-CGCTCATCACAGATGCTGGTCA-3'
<i>Acot-1</i>	Acyl-CoA thioesterase 1	Forward 5'-CTGGCGCATGCAGGATC-3' Reverse 5'-GGCACTTTTCTTGATAGCTCC-3'
<i>Acox</i>	Acyl-CoA oxidase	Forward 5'-GCCCCAACTGTGACTTCCATT-3' Reverse 5'-GGCATGTAACCCGTCAGCACT-3'
<i>Claudin-1</i>	<i>Claudin-1</i>	Forward 5'-GTTTGCAGAGACCCCATCAC-3' Reverse 5'-AGAAGCCAGGATGAAACCCA-3'
<i>Cpt1a</i>	Carnitine palmitoyltransferase-1 α	Forward 5'-CGCACGGAAGGAAAATGG-3' Reverse 5'-TGTGCCCAATATTCTG-3'
<i>Cpt2</i>	Carnitine palmitoyltransferase-2	Forward 5'-CAGCACAGCATCGTACCCA-3' Reverse 5'-TCCCAATGCCGTTCTCAAAT-3'
<i>Dgat1</i>	Diacylglycerol acyltransferase1	Forward 5'-GACGGCTACTGGGATCTGA-3' Reverse 5'-TCACCACACACCAATTCAGG-3'
<i>Dgat2</i>	Diacylglycerol acyltransferase2	Forward 5'-CGCAGCGAAAACAAGAATAA-3' Reverse 5'-GAAGATGTCTTGAGGGGCTG-3'
<i>Fabp1</i>	Fatty acid-binding protein 1	Forward 5'-GTCAGCTGTGGAAAGGAAGC-3' Reverse 5'-GTCTCCAGTTCGCACTCCTC-3'
<i>Fas</i>	Fatty acid synthase	Forward 5'-GCAGCAAGTGTCCACCAACAA-3' Reverse 5'-CTCATCGGAGCGCAGGATAGA-3'
<i>Fatp2</i>	Fatty acid transport protein 2	Forward 5'-GGAACCACAGGTCTTCCAAA-3' Reverse 5'-TAAAGTAGCCCCAACCCACGA-3'
<i>Gpat</i>	Glyceraldehyde 3-phosphate acyltransferase	Forward 5'-CAACACCATCCCCGACATC-3' Reverse 5'-GTGACCTTCGATTATGCGATCA-3'
<i>HMG-CoA synthase</i>	3-Hydroxy-3-methyl-glutaryl-CoA synthase	Forward 5'-TGTGGCACCGGATGTCTTT-3' Reverse 5'-GACCAGATACCACGTTCTTCAA-3'
<i>HMG-CoA reductase</i>	3-Hydroxy-3-methyl-glutaryl-CoA reductase	Forward 5'-TGTGGTTTGTGAAGCCGTCAT-3' Reverse 5'-CGTCAACCATAGCTTCCGTAGTT-3'
<i>Klf4</i>	Kruppel-like factor 4	Forward 5'-AGAGGAGCCCCAAGCCAAAGAGG-3' Reverse 5'-CCACAGCCGTCCAGTCACAGT-3'
<i>Lcad</i>	Long-chain acyl-CoA dehydrogenase	Forward 5'-TCTTTTCCTCGGAGCATGACA-3' Reverse 5'-GACCTCTCTACTCACTTCTCCAG-3'

<i>LDL-R</i>	Low-density lipoprotein receptor	Forward 5'-GGAAAATGCATCGCTAGCAAGT-3' Reverse 5'-ATTGGACTGACAGGTGACAGACA-3'
<i>Mcad</i>	Medium-chain acyl-CoA dehydrogenase	Forward 5'-GAGCCTGGGAACCTCGGCTTGA-3' Reverse 5'-GCCAAGGCCACCGCAACTTT-3'
<i>Mtp</i>	Microsomal triglyceride transfer protein	Forward 5'-CACTCAGGCAATTCGAGACA-3' Reverse 5'-TATCGCTTTCTGGCTGAGGT-3'
<i>Muc2</i>	Mucin 2	Forward 5'-GCTGACGAGTGGTTGGTGAATG-3' Reverse 5'-GATGAGGTGGCAGACAGGAGAC-3'
<i>Ppar-α</i>	Peroxisome proliferator-activated receptor α	Forward 5'-CCTCAGGGTACCACTACGGAGT-3' Reverse 5'-GCCGAATAGTTCGCCGAA-3'
<i>Ppar-γ</i>	Peroxisome proliferator-activated receptor γ	Forward 5'-TTCGCTGATGCACTGCCTATG-3' Reverse 5'-CGAAGTTGGTGGGCCAGAA-3'
<i>Scd1</i>	Stearoyl-CoA desaturase-1	Forward 5'-TCCCTCCGGAAATGAACGAGAGAA-3' Reverse 5'-AGTGCAGCAGGACCATGAGAATGA-3'
<i>SLC22A5</i>	Organic Cation/Carnitine Transporter OCTN2 (Slc22a5)	Forward 5'-TGGATTGGGGCATCTGTCC-3' Reverse 5'-GAGAGGGAAAAAGACCT-3'
<i>SR-B1</i>	Scavenger receptor class B type	Forward 5'-CCCTTCGTGCATTTTCTCAAC-3' Reverse 5'-CATCCCAACAAACAGGCCA-3'
<i>Srebp1c</i>	Sterol regulating element binding protein 1c	Forward 5'-TATGGAGGGCATGAAACCCGAAGT-3' Reverse 5'-TTGACCTGGCTATCCTCAAAGGCT-3'
<i>ZO-1</i>	Zonula occludens-1	Forward 5'-AAGAATATGGTCTTCGATTGGC-3' Reverse 5'-ATTTTCTGTCACAGTACCATTATCTTC-3'

Table S2**TABLE S2** Effects of HFD before pregnancy on the α -diversity in gut microbiota

		ND	HFD
Shannon	F ₀ -LTP	6.58 ± 0.20	6.75 ± 0.26
	F ₁ -10d	1.76 ± 0.13	3.93 ± 0.27***
	F ₁ -20d	6.02 ± 0.24	7.08 ± 0.08***
	F ₁ -28d	7.05 ± 0.14	6.24 ± 0.27*
	F ₁ -49d	7.03 ± 0.09	6.6 ± 0.13*
Simpson	F ₀ -LTP	0.97 ± 0.00	0.97 ± 0.00
	F ₁ -10d	0.55 ± 0.04	0.82 ± 0.02***
	F ₁ -20d	0.94 ± 0.02	0.98 ± 0.00*
	F ₁ -28d	0.97 ± 0.00	0.95 ± 0.01
	F ₁ -49d	0.97 ± 0.00	0.97 ± 0.00
Chao1	F ₀ -LTP	1554.17 ± 88.81	1539.72 ± 173.16
	F ₁ -10d	245.34 ± 28.77	695.57 ± 80.90***
	F ₁ -20d	1223.19 ± 87.70	1825.77 ± 47.83***
	F ₁ -28d	1708.67 ± 59.53	1340.77 ± 128.11*
	F ₁ -49d	1847.90 ± 39.84	1771.16 ± 55.51
ACE	F ₀ -LTP	1567.67 ± 92.43	1577.78 ± 150.46
	F ₁ -10d	269.81 ± 32.36	732.88 ± 90.97***
	F ₁ -20d	1245.01 ± 90.46	1809.73 ± 35.61***
	F ₁ -28d	1719.91 ± 49.65	1382.68 ± 123.22*
	F ₁ -49d	1837.89 ± 36.16	1790.65 ± 51.50

The presented values are the means ± SEMs. An asterisk indicates a significant difference (* at $p < 0.05$, ** at $p < 0.01$, *** at $p < 0.001$) between the ND and HFD group.