Figure S1. Food intake, serum ALT and AST, and hematoxylin and eosin staining of the intestine of the 6 groups of mice. (A) Food intake. (B) Serum ALT and (C) serum AST. (D) Hematoxylin and eosin staining of the intestines of the six groups. Scale bar, 80 μm. NFD-CON control mice fed with NFD; NFD-AL, mice fed with NFD and treated with a low dose of DADS; NFD-AH mice fed with NFD and treated with a high dose of DADS; HFD-CON, control mice fed with HFD; HFD-AL, mice fed with HFD and treated with a low dose of DADS; HFD-AH, mice fed with HFD and treated with a high dose of DADS. NFD, normal food diet; HFD, high fat diet; DADS, diallyl disulfide; ALT, alanine aminotransferase; AST, aspartate aminotransferase.

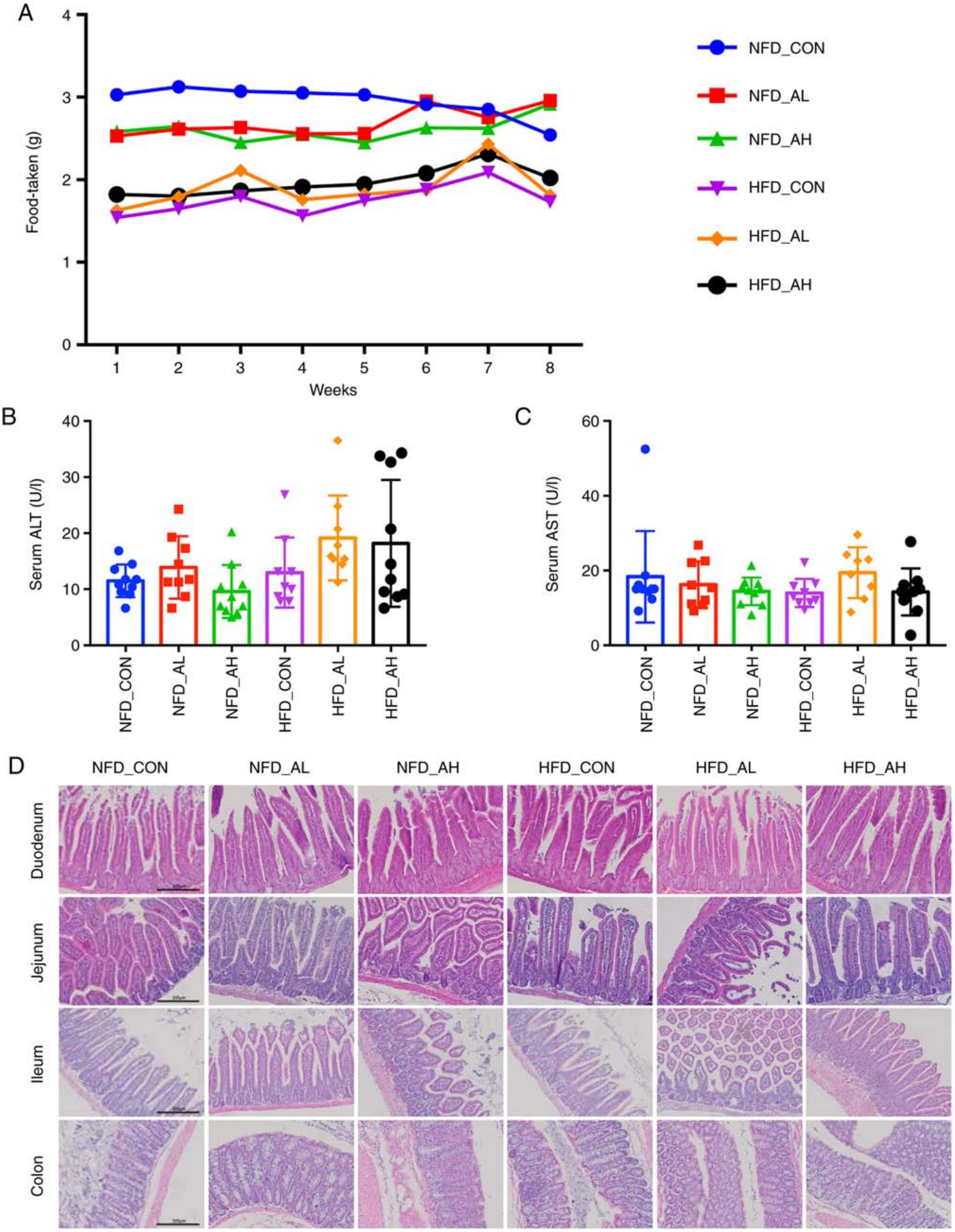

Figure S2. Expression of lipid metabolism-associated genes in the liver of the mice in the NFD groups. (A) mRNA expression levels of lipin 1, hepatic lipase, PNPLA2 and PGC-1α. (B) mRNA expression levels of HNF4α, CYP7A1 and FXR. (C) mRNA expression levels of Abcg5, CD36 and LDLR. $^{*}P<0.05$, $^{**}P<0.01$, $^{***}P<0.001$ vs. NFD-CON.

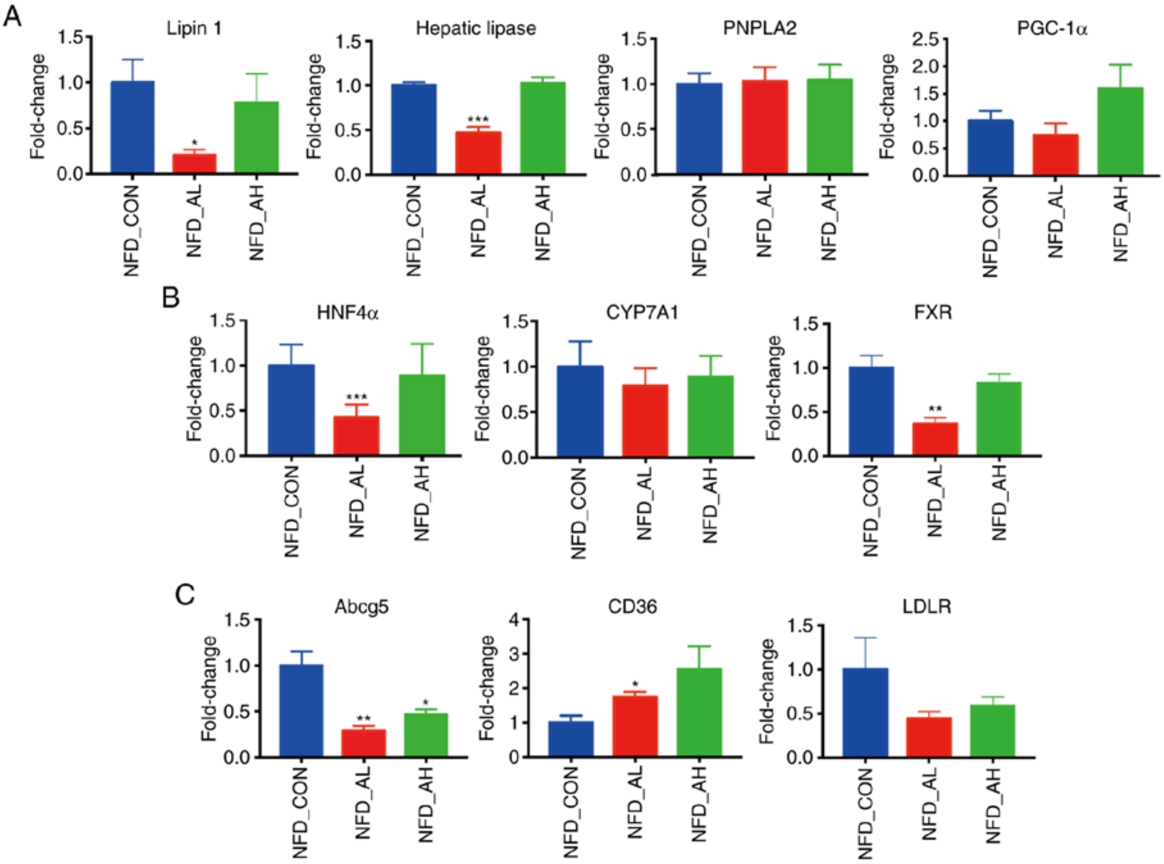

Figure S2. Continued. (D) mRNA expression levels of ACCα1, Accβ1, Fasn, DGAT1, DGAT2, ELOVL5, SREBP-1, SREBP-2, HMGCoAR, PPARγ and SCD1. (E) mRNA expression levels of FGF4α, FGF15 and FGF21. $^{*}P<0.05$, $^{**}P<0.01$, $^{***}P<0.001$ vs. NFD-CON. NFD-CON, control mice fed with NFD; NFD-AL, mice fed with NFD and treated with a low dose of DADS; NFD-AH, mice fed with NFD and treated with a high dose of DADS. NFD, normal food diet; DADS, diallyl disulfide; PNPLA2, patatin-like phospholipase domain-containing protein 2; PGC-1α, peroxisome proliferator-activated receptor γ coactivator-1α; HNF4α, hepatocyte nuclear factor 4α; CYP7A1, cholesterol 7-α hydroxylase gene; FXR, farnesoid X receptor; Abcg5, adenosine triphosphate-binding cassette subfamily G members 5; LDLR, low density lipoprotein receptor; ACCα1, acetyl-CoA carboxylase α1; Accβ1, acetyl-CoA carboxylase β1; Fasn, fatty acid synthase; DGAT1, diacylglycerol acyltransferase 1; DGAT2, diacylglycerol acyltransferase 2; ELOVL5, elongases of very long-chain fatty acids 5; SREBP-1, sterol regulatory element-binding protein-1; SREBP-2, sterol regulatory element-binding protein-2; HMGCoAR, hydroxy-methyl-glutaryl coenzyme A reductase; PPARγ, peroxisome proliferator-activated receptor γ; SCD1, Stearoyl-CoA desaturase-1; FGF4α, fibroblast growth factor 4α; FGF15, fibroblast growth factor 15; FGF21, fibroblast growth factor 21.

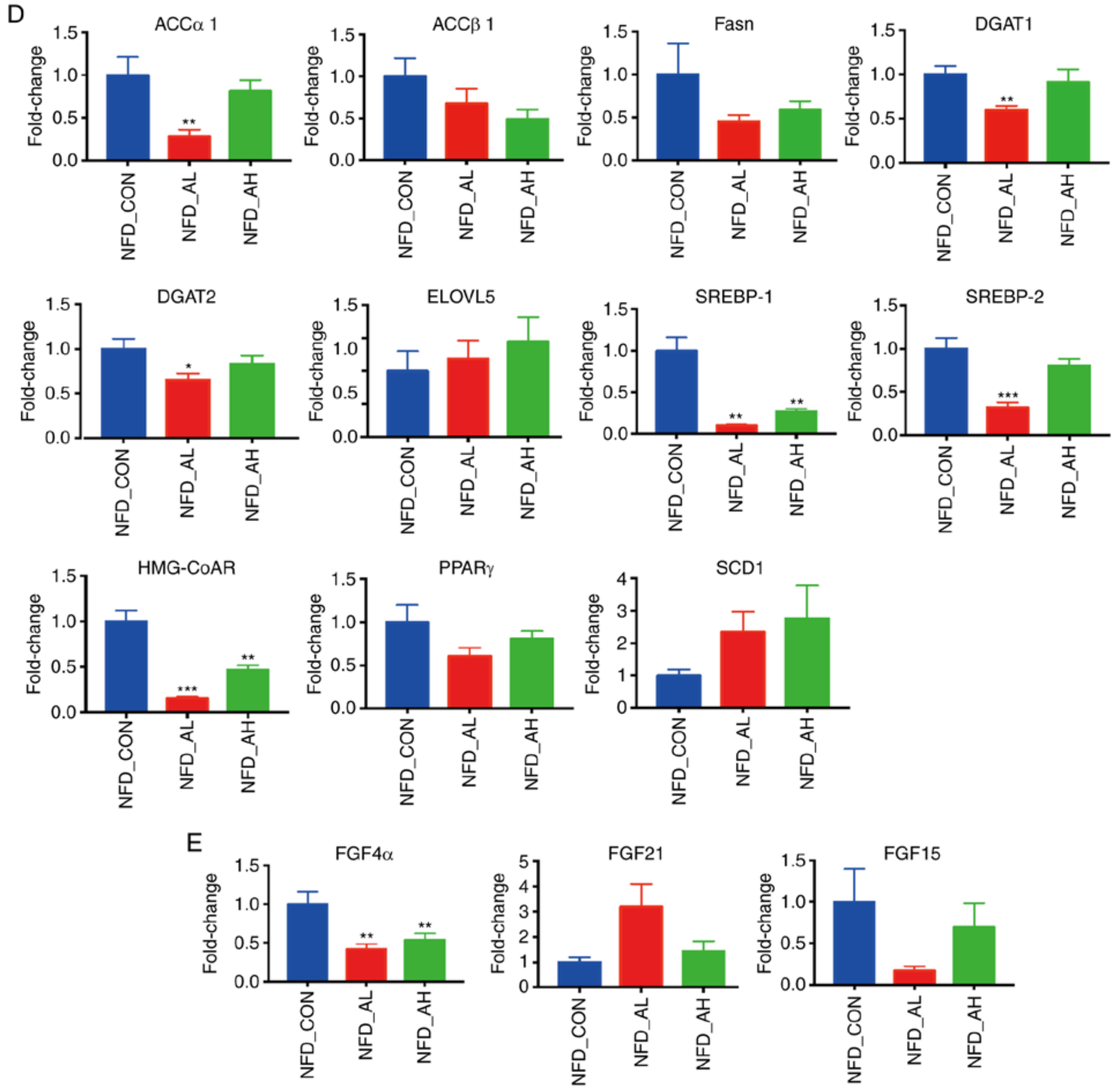

Figure S3. Shannon rarefaction curves and Venn diagram of different groups. (A) Shannon rarefaction curves of the different groups. (B-D) Venn diagrams of the different groups. NFD-CON, control mice fed with NFD; NFD-AL, mice fed with NFD and treated with low a dose of DADS; NFD-AH, mice fed with NFD and treated with a high dose of DADS; HFD-CON, control mice fed with HFD; HFD-AL, mice fed with HFD and treated with a low dose of DADS; HFD-AH, mice fed with HFD and treated with a high dose of DADS. NFD, normal food diet; HFD, high fat diet; DADS, diallyl disulfide.

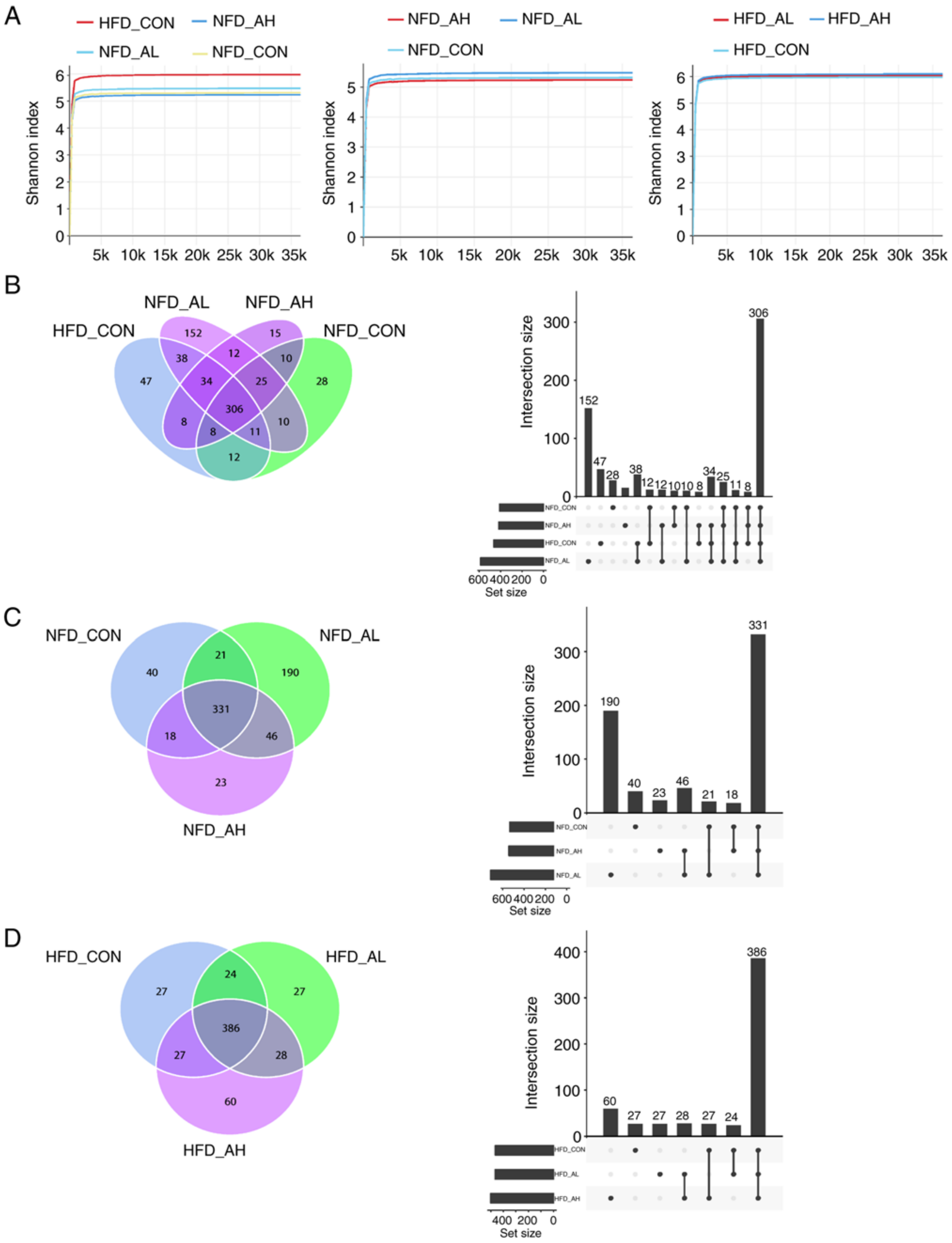

Figure S4. Unifrac analyses and relative composition of the gut microbiota in the 6 groups. (A and B) Unifrac analyses. (C and D) Relative composition of the gut microbiota at the bacterial phylum level. (E and F) Relative composition of the gut microbiota at the bacterial order level. *P<0.05 vs. NFD_CON, $^\#$P<0.05 vs. HFD_CON. NFD-CON, control mice fed with NFD; NFD-AL, mice fed with NFD and treated with low a dose of DADS; NFD-AH, mice fed with NFD and treated with a high dose of DADS; HFD-CON, control mice fed with HFD; HFD-AL, mice fed with HFD and treated with a low dose of DADS; HFD-AH, mice fed with HFD and treated with a high dose of DADS. NFD, normal food diet; HFD, high fat diet; DADS, diallyl disulfide.

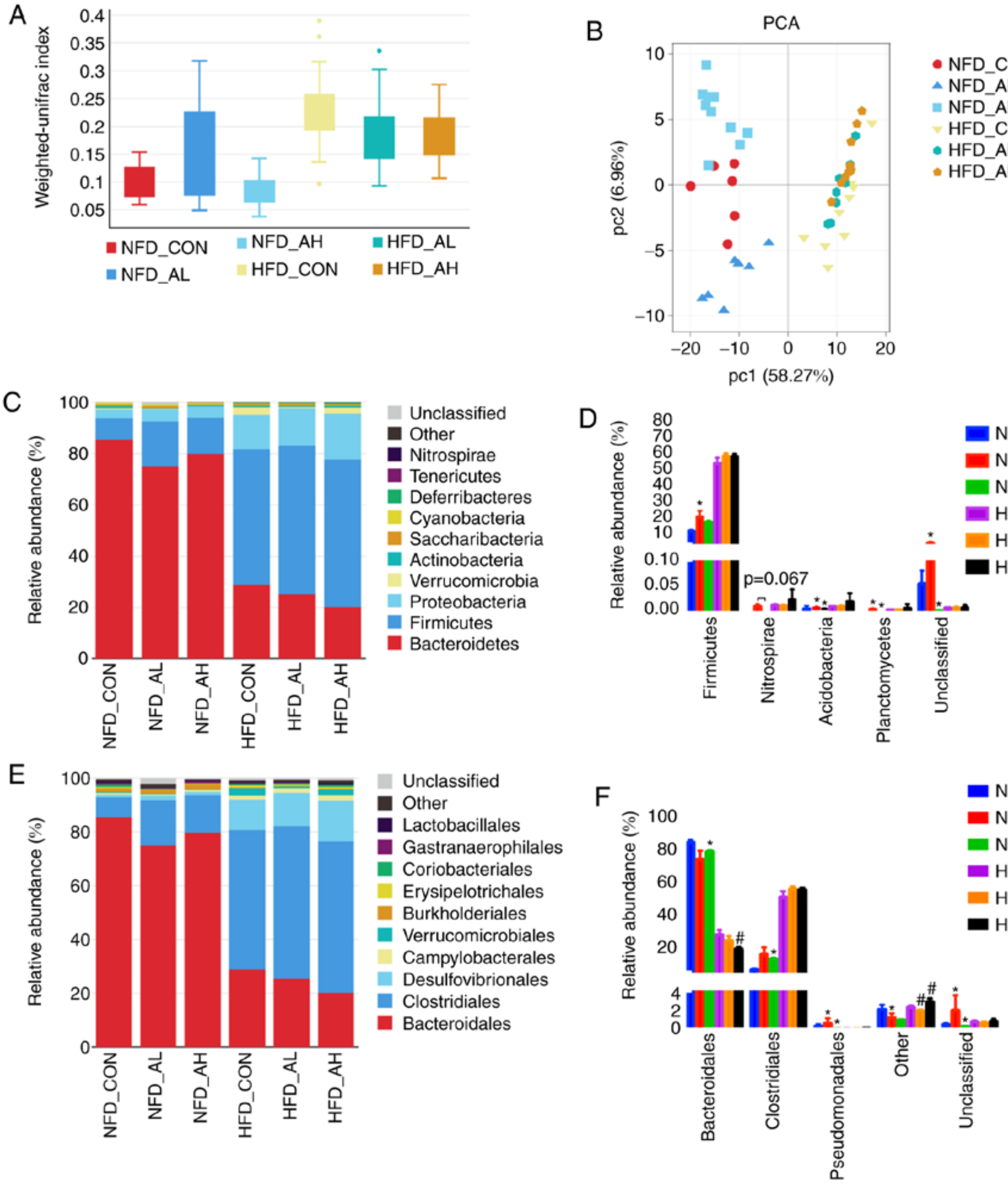

Figure S5. LEFse analysis of the different groups. (A and B) LEFse analysis of the NFD-CON, HFD-CON, HFD-AL and HFD-AH groups, red represents the bacteria specific for the HFD_AH group, green represents the bacteria specific for the HFD_AL group, blue represents the bacteria specific for the HFD_CON group and purple represents the bacteria specific for NFD_CON group. (C) Presentation of KEGG assignments of the altered pathways in the 6 groups. Red represents upregulation, and blue represents downregulation. (D and E) Association between fat, liver TG and TC, and the bacterial taxa. In D, different colors and shapes represent the bacteria of different groups. In E, different colors and shapes represent different factors. NFD-CON, control mice fed with NFD; NFD-AL, mice fed with NFD and treated with low a dose of DADS; NFD-AH, mice fed with NFD and treated with a high dose of DADS; HFD-CON, control mice fed with HFD; HFD-AL, mice fed with HFD and treated with a low dose of DADS; HFD-AH, mice fed with HFD and treated with a high dose of DADS. NFD, normal food diet; HFD, high fat diet; DADS, diallyl disulfide; TG, triglyceride; TC, total cholesterol; KEGG, Kyoto Encyclopedia of Genes and Genomes.

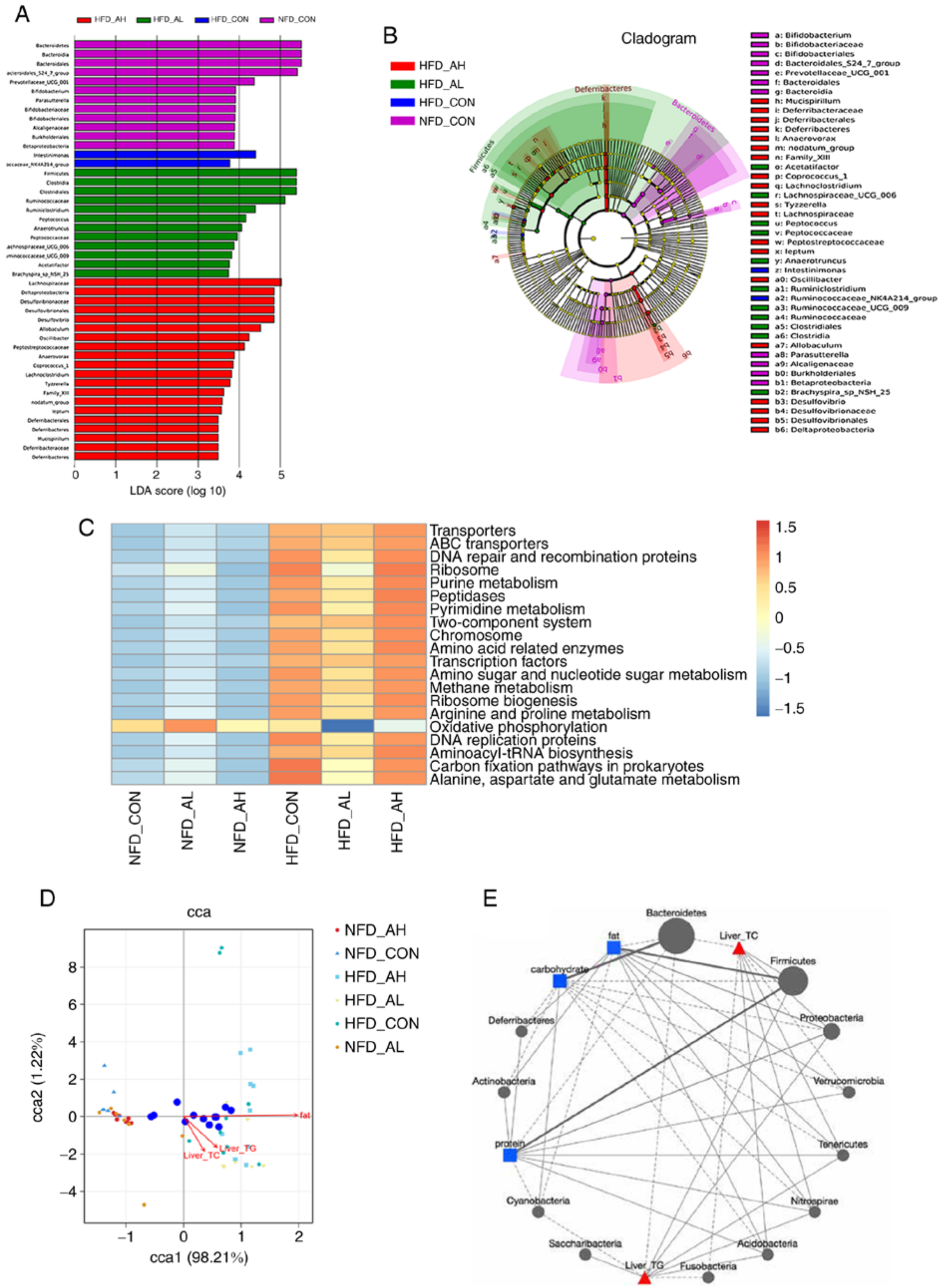

Table SI. Primer sequences of genes.

Genes	Forward (5' to 3')	Reverse (5' to 3')
Lipin1	CCCTGTATTTCCCCAAGAATGG	ATCTTTGGTGATCTCTCTGTGG
Hepatic lipase	CTACAAACACATTGCAGAGCAT	GTTGCAAGGAGTCAATGAAGAG
PNPLA2	CAGAGATGGACTTCGATTCCTT	CAGGTGCTCTAGAATTCGATCT
PGC-1α	GGATATACTTTACGCAGGTCGA	CGTCTGAGTTGGTATCTAGGTC
HNF4α	TGAGGAAGAACCACATGTACTC	GTAACGACACTGGTTCCTCTTA
CYP7A1	GGGATTGCTGTGGTAGTGAGC	GGTTATGGAATCAACCCGTTGT
FXR	TGGGTACAAGGGAGAGACTG	CCCTGTCTCCACAGACAACA
Abcg5	CATTGAAAGAGCACGATACCTG	AGATTCTGAACGAGACGCATAA
CD36	CTTTGAAAGAACTCTTGTGGGG	GTCTGTGCCATTAATCATGTCG
LDLR	CAGAAGTCGACACTGTACTGAC	AAGATGGACAGGAACCTCATAC
ACCα1	GGCCAGTGATATGCTGAGAT	AGGGTCAAGTGCTGCTCCA
ACCβ1	GATGACAGTGTCAGTGGTTCAG	CTTGTCTGCTTCCATTAGCTTC
Fasn	TAAAGCATGACCTCGTGATGAA	GAAGTTCAGTGAGGCGTAGTAG
DGAT1	CCGATTCTTCCAAGGGAACTAT	ATCGTAGTTGAGCACGTAGTAG
DGAT2	GAAGTCAGCAAGAAGTTTCCTG	CACCACGATGATGATAGCATTG
ELOVL5	CTTCAGTTTGTGCTGACAATCA	AAGAGAGCAATCAGGGAAATCA
SREBP-1	GCTACCGGTCTTCTATCAATGA	CGCAAGACAGCAGATTTATTCA
SREBP-2	TTTTACTGAAGTAGAGCGGGTC	CATGCATGGCTCTACAGGTATA
HMG-CoAR	GGTGCAAAGTTCCTTAGTGATG	GAATAGACACACCACGTTCATG
PPARγ	ATTCTGGCCCACCAACTTCGG	TGGAAGCCTGATGCTTTATCCCCA
SCD1	AACATTCAATCCCGGGAGAATA	GAAACTTTCTTCCGGTCGTAAG
FGF4α	GGTACGTGGACGGAGGAGTGAG	AGAGGCGGAGGCTGAGGTTG
FGF15	CTGTGTCAGATGAAGATCCACT	CAAATTTCGTTCGTTTTGGTCC
FGF21	AAGACACTGAAGCCCACCTG	CACCCAGGATTTGAATGACC
GAPDH	GCATCCACTGGTGCTGCC	TCATCATACTTGGCAGGTTTC

Table SII. Diversity estimation of the 16S rRNA gene library of the DADS and HFD treated mice from the sequencing.

Groups	Total tags	OTUs	Chao	Ace	Shannon	Simpson
NFD_CON-1	59,580	358	436.12	411.37	5.41	0.95
NFD_CON-2	73,924	368	437.38	436.37	4.72	0.90
NFD_CON-3	81,442	404	489.00	482.17	4.98	0.93
NFD_CON-4	74,654	408	471.00	459.13	5.65	0.96
NFD_CON-5	62,723	359	432.09	416.30	5.40	0.95
NFD_CON-6	70,823	358	401.97	399.88	5.73	0.96
NFD_AL-1	59,628	349	434.02	436.16	4.85	0.91
NFD_AL-2	58,944	430	546.92	514.09	5.11	0.92
NFD_AL-3	57,641	449	591.74	574.49	5.65	0.95
NFD_AL-4	71,157	423	587.36	555.81	5.44	0.96
NFD_AL-5	80,814	498	591.14	567.27	5.73	0.95
NFD_AL-6	77,122	541	644.11	635.15	6.31	0.97
NFD-AL-7	49,562	349	408.29	397.16	5.24	0.94
NFD_AH-1	50,020	368	415.88	429.67	5.45	0.95
NFD_AH-2	66,806	397	468.15	455.89	5.04	0.92
NFD_AH-3	60,537	399	436.13	436.20	5.65	0.96
NFD_AH-4	80,508	391	480.02	479.11	5.04	0.93
NFD_AH-5	66,724	400	448.07	448.13	5.14	0.93
NFD-AH-6	93,466	426	479.33	468.25	5.17	0.93
NFD_AH-7	64,386	412	493.28	471.90	5.24	0.94
NFD_AH-8	67,041	443	505.57	495.66	5.51	0.95
NFD_AH-9	78,870	419	486.53	475.29	5.04	0.92
NFD_AH-10	83,566	392	436.63	443.71	5.09	0.92
HFD_CON-1	69,724	453	571.32	565.14	5.52	0.95
HFD-CON-2	57,756	479	576.23	559.72	6.58	0.98
HFD-CON-3	64,033	476	578.10	560.40	5.79	0.95
HFD_CON-4	72,607	487	578.54	556.38	6.19	0.97
HFD_CON-5	66,040	445	552.76	529.25	5.73	0.96
HFD_CON-6	66,457	437	547.25	555.91	6.37	0.98
HFD_CON-7	56,954	458	553.23	545.70	6.13	0.97
HFD_CON-8	63,061	457	524.23	519.92	5.60	0.92
HFD_CON-9	64,366	437	495.09	496.89	5.96	0.96
HFD_AL-1	43,696	451	553.10	535.41	6.42	0.97
HFD_AL-2	63,623	480	557.29	575.66	5.60	0.94
HFD_AL-3	60,243	487	566.73	579.19	6.09	0.96
HFD_AL-4	77,522	485	557.85	576.20	5.75	0.95
HFD_AL-5	63,648	486	590.34	568.64	6.09	0.96
HFD_AL-6	96,448	486	594.02	580.74	5.87	0.96
HFD_AL-7	57,478	466	549.00	536.34	6.31	0.97
HFD_AL-8	63,360	513	598.00	583.60	6.63	0.98
HFD_AL-9	57,146	473	638.09	589.43	6.17	0.97
HFD_AH-1	57,586	434	493.00	470.78	6.07	0.95
HFD-AH-2	72,798	444	513.39	479.95	5.92	0.94
HFD_AH-3	64,143	432	475.50	472.60	5.76	0.94
HFD_AH-4	79,085	574	635.42	609.77	6.21	0.96
HFD_AH-5	84,149	455	510.03	490.35	5.91	0.94
HFD_AH-6	66,166	428	481.93	485.54	6.18	0.97
HFD_AH-7	67,278	404	441.12	442.80	6.27	0.97
HFD_AH-8	66,941	420	453.28	456.50	6.13	0.97
HFD_AH-9	53,865	386	442.00	439.34	5.92	0.96

NFD_CON, the control mice fed with NFD; NFD_AL, the mice fed with NFD and treated with low dosed DADS; NFD_AH, the mice fed with NFD and treated with high dosed DADS; HFD_CON, the control mice fed with HFD; HFD_AL, the mice fed with HFD and treated with low dosed DADS; HFD_AH, the mice fed with HFD and treated with high dosed DADS.