Effects of Dicaffeoylquinic Acids from *Ilex kudingcha* on Lipid Metabolism and Intestinal Microbiota in High-Fat-Diet Fed Mice

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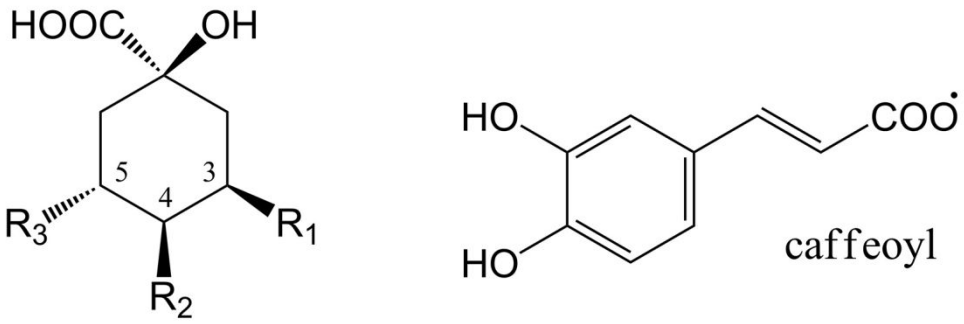
Table S1. Target genes and their primer sequences.

Target gene	Forward primer (5'-3')	Reverse primer (5'-3')
CPT1	CATCCACGCCATACTGCT	GACCTTGAAGTAACGGCCTC
PPARα	TCATCAAGAAGACCGAGTCC	CCTCTTCATCCCCAAGCGTA
PPARγ	GCTGAACGTGAAGCCCATCG	GGCGAACAGCTGAGAGGACT
SREBP-1c	GGCACTAAGTGCCCTCAACCT	GCCACATAGATCTCTGCCAGTGT
FAS	GGCACCTATGGCGAGGACTT	GCCCTCCCGTACACTCACTC
LXRα	TCAGAAGAACAGATCCGCTTG	CGCCTGTTACACTGTTGCT
GAPDH	AGGTCGGTGTGAACGGATTTG	TGTAGACCATGTAGTTGAGGTCA



Compounds	R1	R2	R3
3,4-diCQA	caffeoyl	caffeoyl	OH
3,5-diCQA	caffeoyl	OH	caffeoyl
4,5-diCQA	OH	caffeoyl	caffeoyl

Figure S1. Chemical structures of di-*O*-caffeoylquinic acids (diCQAs) (IUPAC nomenclature).

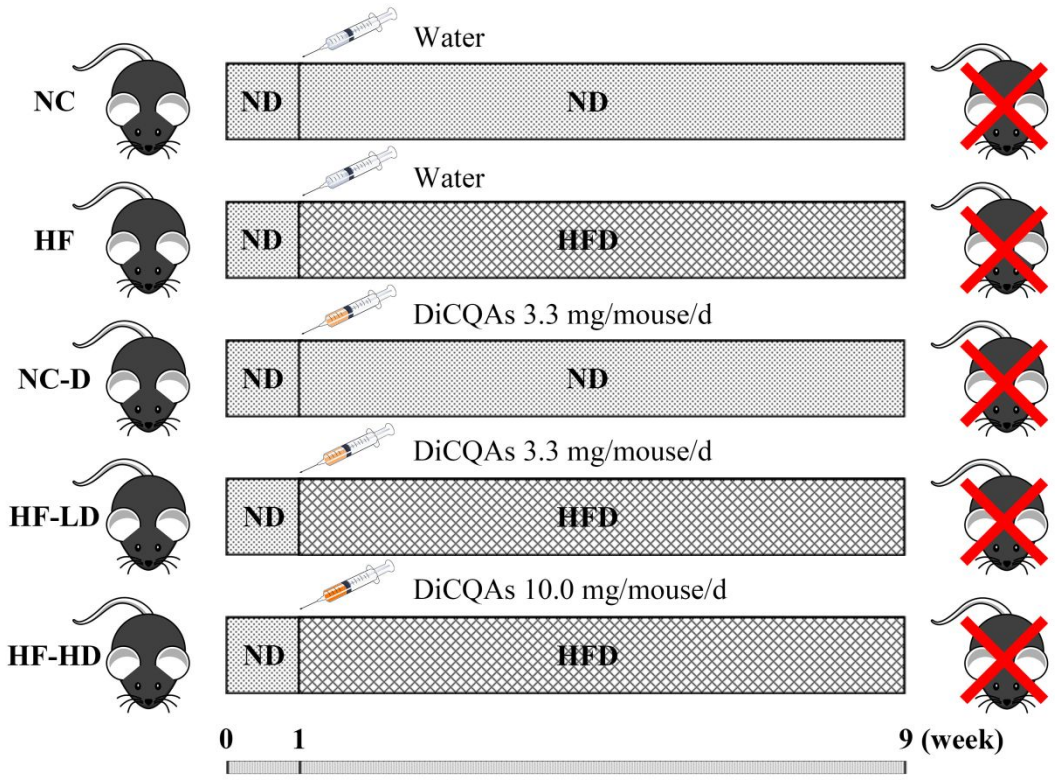


Figure S2. Pilot procedure of the feeding and treatment of the mice (ND, normal diet; HFD, high-fat diet).

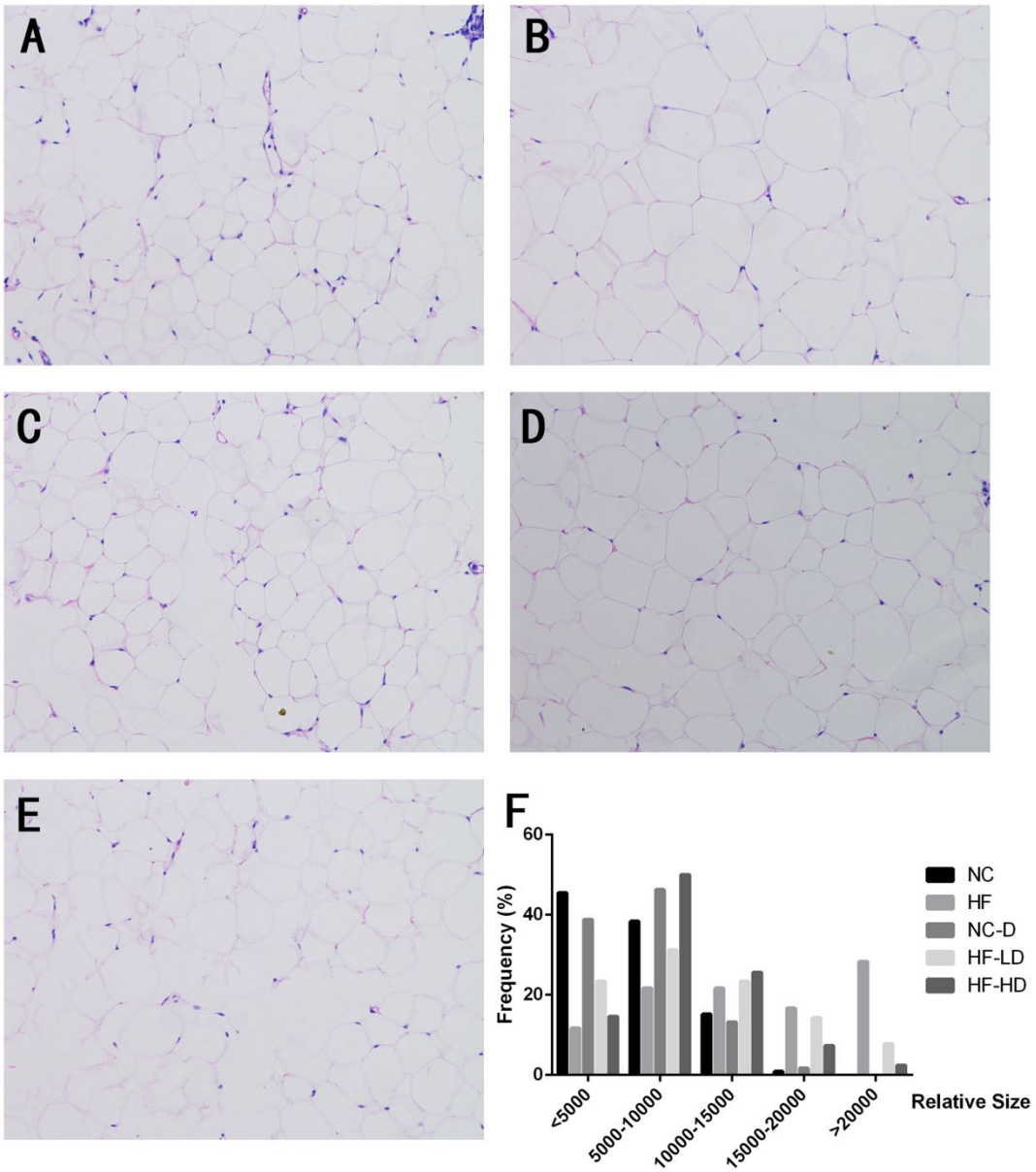


Figure S3. Morphological observations of adipose tissue of mice in NC (A), HF (B), NC-D (C), HF-LD (D) and HF-HD (E) group (× 200, hematoxylin-eosin staining), and the distribution of adipocyte size of the mice in each group (F).

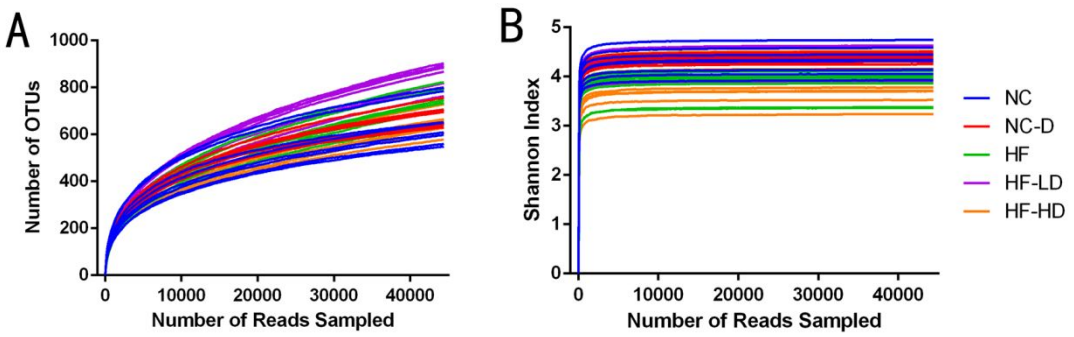


Figure S4. Rarefaction curves (A) and Shannon curves (B) of mice fecal samples (NC: blue, NC-D: red, HF: green, HF-LD: purple, HF-HD: orange).

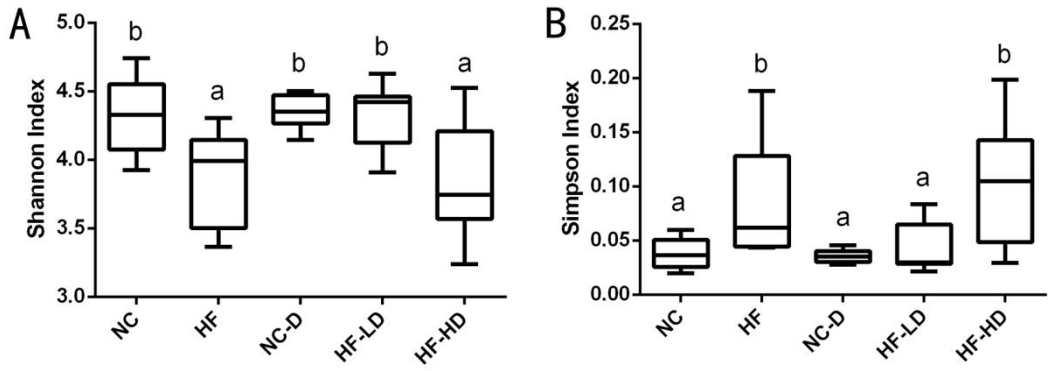


Figure S5. Shannon index (A) and Simpson index (B) of mice gut microbiota (a Different letters mean the significant difference between the groups, $p < 0.05$).

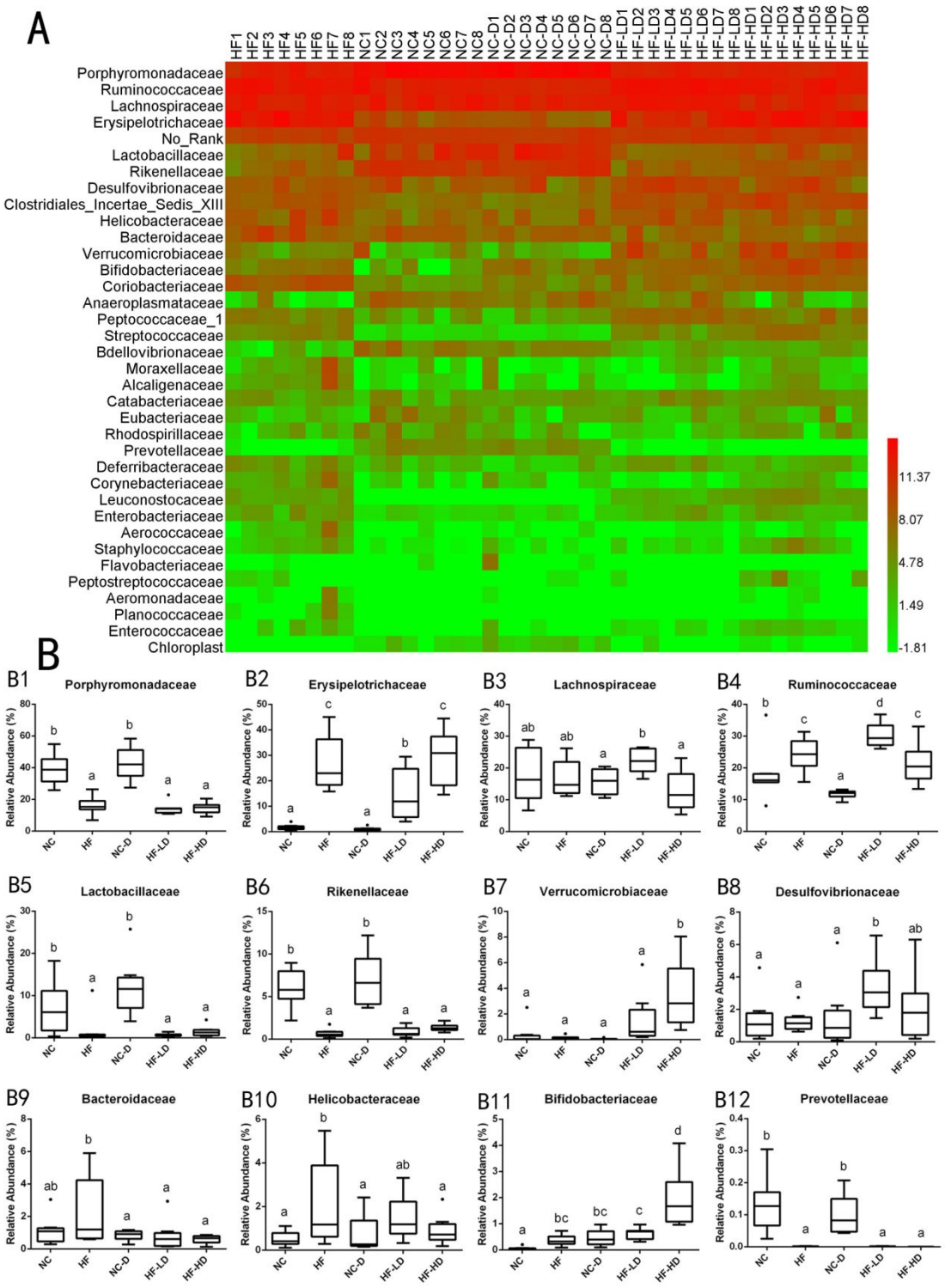


Figure S6. Gut microbial compositions of mice at family level (Heatmap (A) and Barplot (B) of relative abundance of representative families).

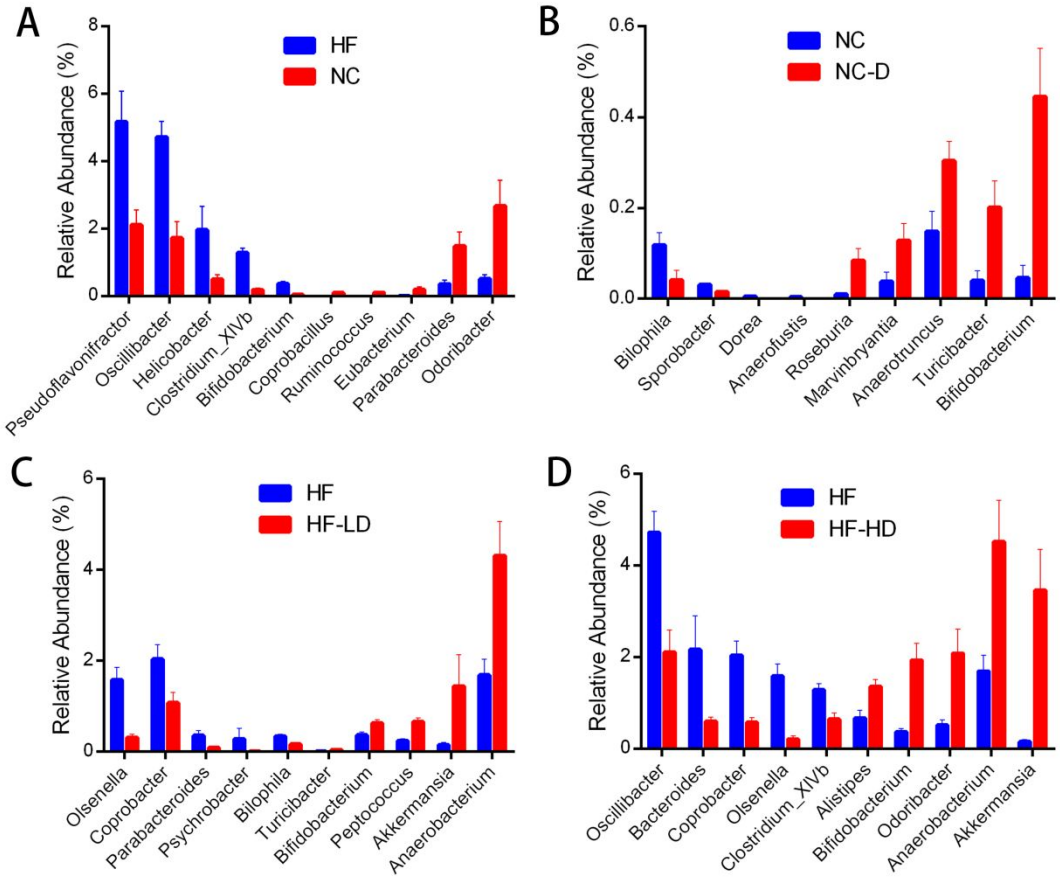


Figure S7. Matastats of differentially abundant features at genus level.

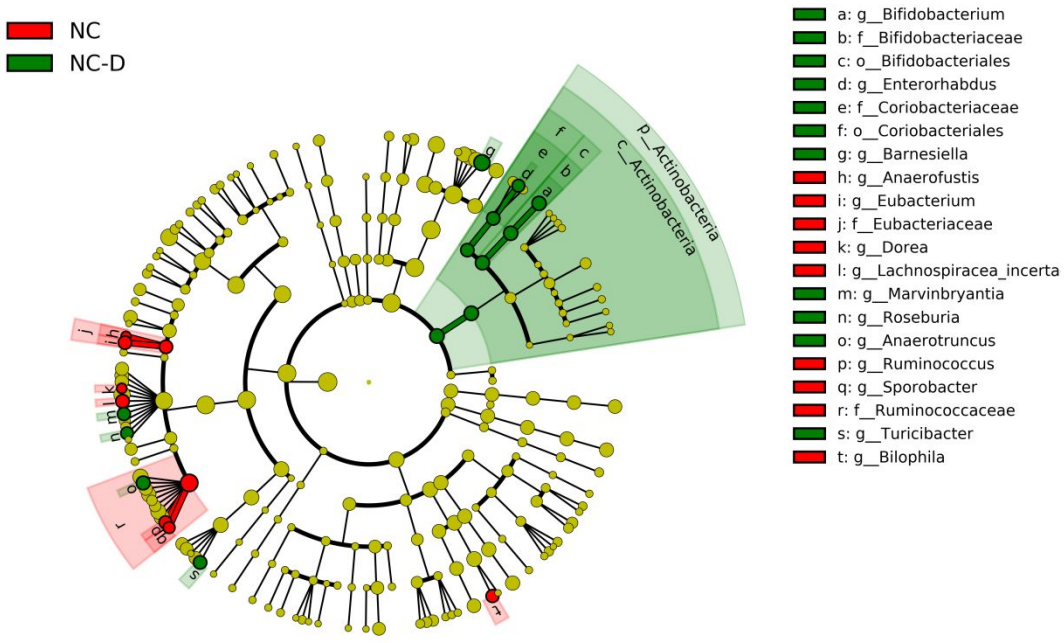


Figure S8. LEfSe of microbial communities affected by diCQAs in normal diet fed mice.