**Table S1. Specific primers used for qRT-PCR analysis of gene expression**

| Gene | Forward (5′–3′) | Reverse (5′–3′) |
|---|---|---|
| ACC-1 | GATGAACCATCTCCGTTGGC | GACCCAATTATGAATCGGGAGT |
| FXR | GGCAGAATCTGGATTTGGAATCG | GCTGAACTTGAGGAAACGGG |
| PGC-1 | TATGGAGTGACATAGAGTGTGCT | CCACTTCAATCCACCCAGAAAG |
| PPAR-α | AGAGCCCCATCTGTCCTCTC | ACTGGTAGTCTGCAAAACCAAA |
| UCP-1 | AGGCTTCCAGTACCATTAGGT | CTGAGTGAGGCAAAGCTGATTT |
| SREBP-1c | TGGAGCTTTTGAGACTCAGGA | TCGATTAAGCAGGTGAGGTCG |
| FABP-1 | ATGAACTTCTCCGGCAAGTACC | CTGACACCCCCTTGATGTCC |
| HMGCR | AGCTTGCCCGAATTGTATGTG | TCTGTTGTGAACCATGTGACTT |
| PPAR-γ | TCGCTGATGCACTGCCTATG | GAGAGGTCCACAGAGCTGATT |
| FASN | GGAGGTGGTGATAGCCGGTAT | TGGGTAATCCATAGAGCCCAG |
| CD36 | ATGGGCTGTGATCGGAACTG | GTCTTCCCAATAAGCATGTCTC |
| SCD-1 | TTCTTGCGATACACTCTGGTGC | CGGGATTGAATGTTCTTGTCGT |
| ABCA1 | GCTTGTTGGCCTCAGTTAAGG | GTAGCTCAGGCGTACAGAGAT |
| ABCG1 | CTTTCCTACTCTGTACCCGAGG | CGGGGCATTCCATTGATAAGG |
| ZO-1 | ACCACCAACCCGAGAAGAC | CAGGAGTCATGGACGCACA |
| Claudin-1 | GGGGACAACATCGTGACCG | CCGGATAAAAAGAGTACGCTG |
| β-actin | CATGTACGTTGCTATCCAGGC | CTCCTTAATGTCACGCACGAT |

**Table S2. Amino acid composition of MEP**

| Amino acids | Relative amount (%) | Amino acids | Relative amount (%) |
|---|---|---|---|
| Aspartate (Asp) | 13.03 | Proline (Pro) | 6.28 |
| Threonine (Thr) | 5.59 | Tryptophan (Trp) | 2.29 |
| Serine (Ser) | 3.63 | Lysine (Lys) [a] | 7.15 |
| Glutamate (Glu) | 13.57 | Phenylalanine (Phe) [a] | 0.80 |
| Glycine (Gly) | 6.32 | Isoleucine (Ile) [a] | 6.05 |
| Alanine (Ala) | 7.18 | Leucine (Leu) [a] | 8.31 |
| Cysteine (Cys) | 1.17 | Valine (Val) [a] | 7.80 |
| Arginine (Arg) | 8.24 | Methionine (Met) [a] | 0.54 |
| Histidine (His) | 1.62 | | |

[a]: Represented essential amino acids.

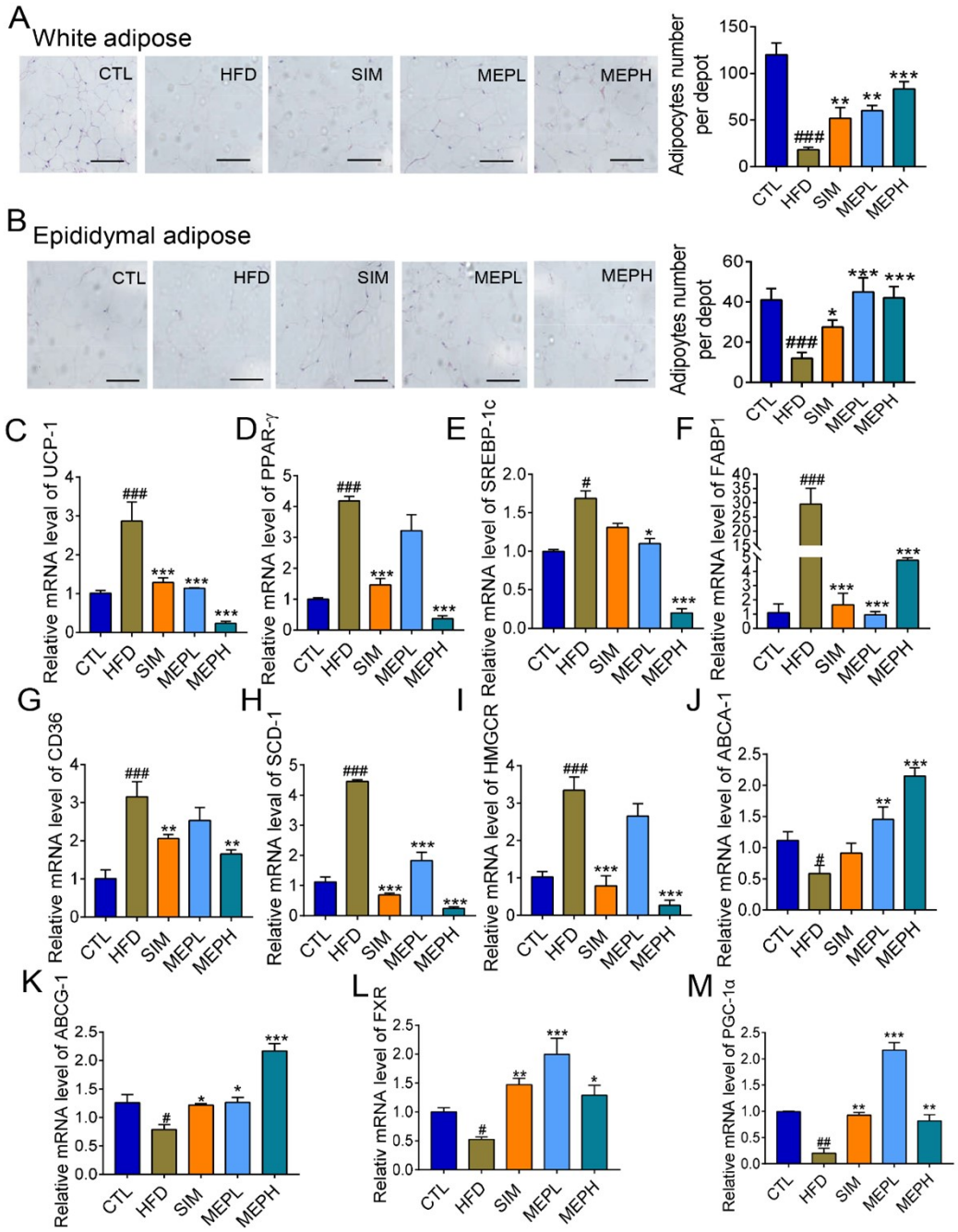


**Fig S1. MEP alleviated adipocyte proliferation and regulated the expression of lipid metabolism in mice with NAFLD.** H&E analysis of white adipose tissue (A) and epididymal adipose tissue (B), scale bar: 50 μm. The mRNA levels of UCP-1 (C), PPAR-γ (D), SREBP-1c (E), FABP1 (F), CD36 (G), SCD-1 (H), HMGCR (I), ABCA-1 (J), ABCG-1 (K), FXR (L) and PGC-1α (M) were detected. All values are presented as means ± SEM (n = 5). Significantly different (*P<0.05, **P<0.01, ***P<0.001) versus the HFD group. Significantly different (#P<0.05, ##P<0.01, ###P<0.001) versus the CTL group.

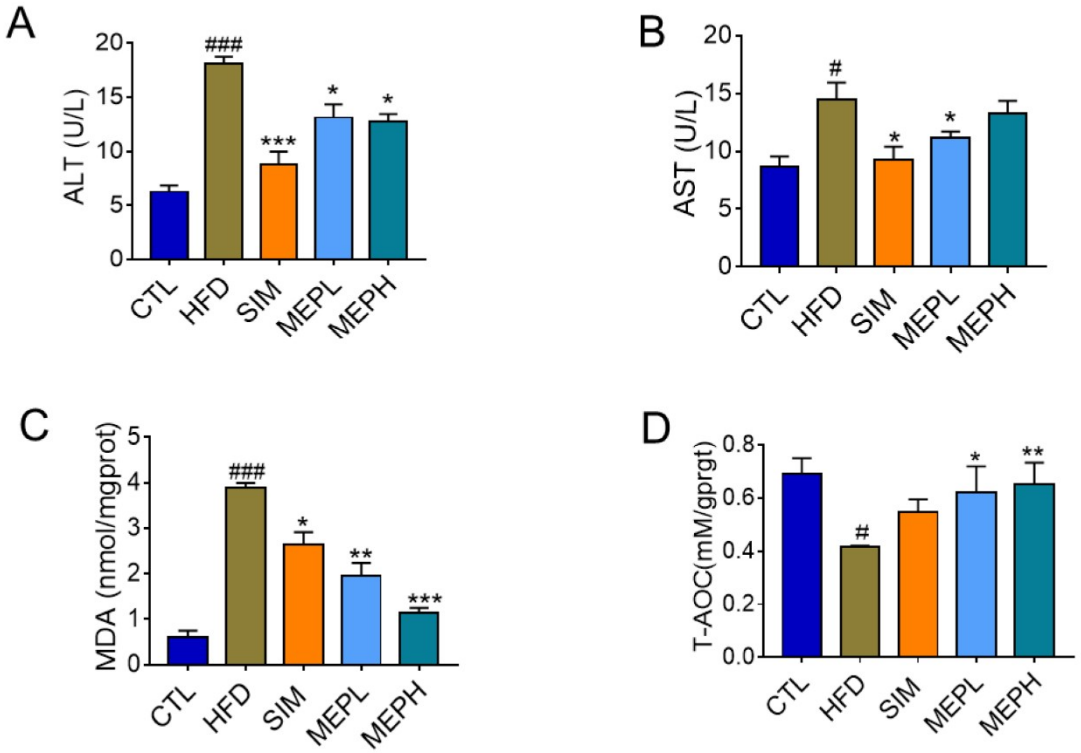


**Fig S2. MEP improved liver function *in vivo*.** The levels of ALT (A) and AST (B) in serum, and the levels of MDA (C) and T-AOC (D) in liver tissue were detected. All values of animal experiments are presented as means ± SEM (n = 5). Significantly different (*P<0.05, **P<0.01, ***P<0.001) versus the HFD group. Significantly different (#P<0.05, ###P<0.001) versus the CTL group.

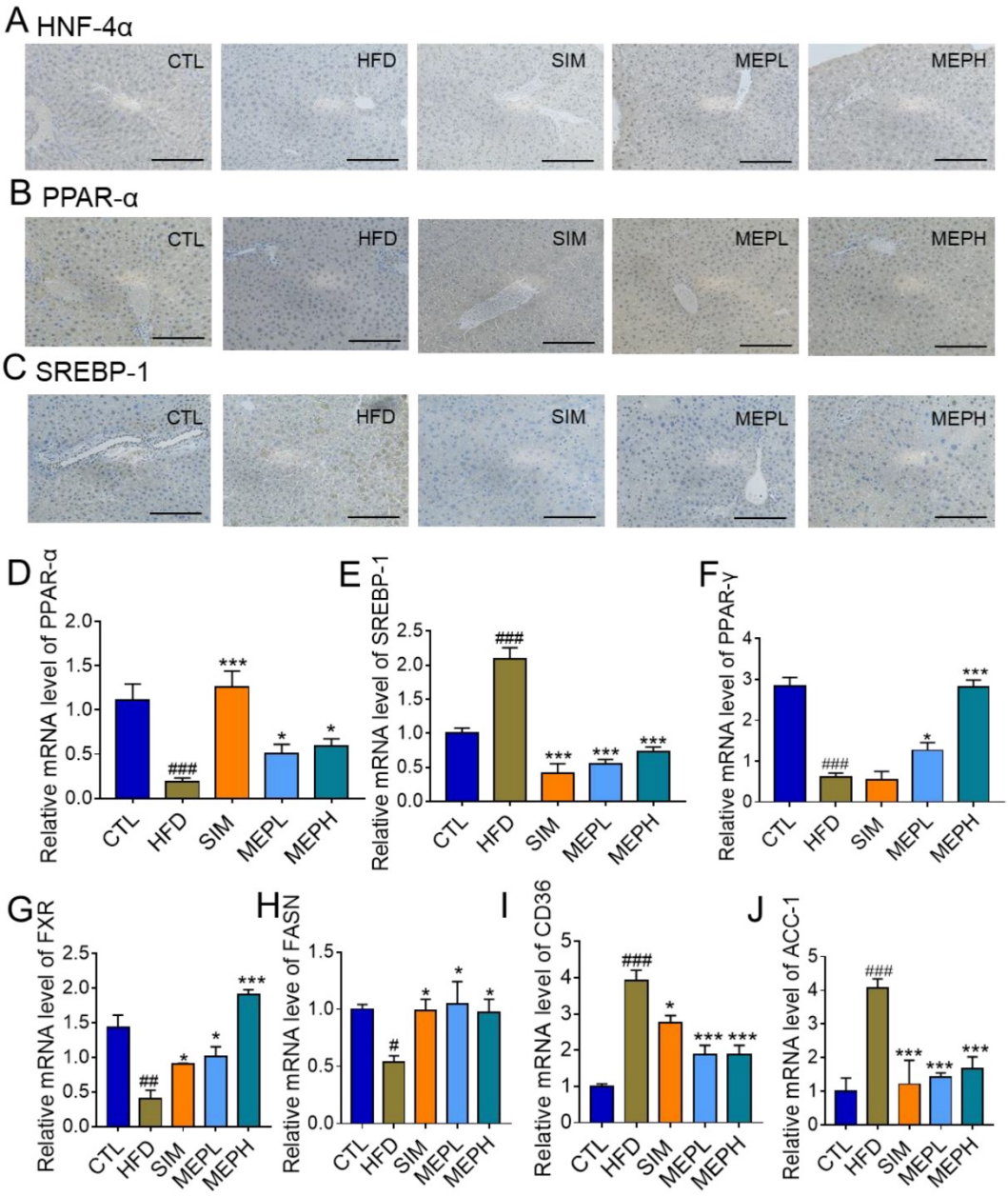


**Fig S3. MEP regulated lipid metabolism in liver cells of NAFLD mice.** Immunohistochemical analysis of HNF-4α (A), PPAR-α (B) and SREBP (C) were showed. The mRNA levels of PPAR-α (D), SREBP (E), PPAR-γ (F), FXR (G), FASN (H), CD36 (I) and ACC-1 (J) were detected. All values are presented as means ± SEM (n = 5). Significantly different (*P<0.05, **P<0.01, ***P<0.001) versus the HFD group. Significantly different (#P<0.05, ##P<0.01, ###P<0.001) versus the CTL group. Scale bar: 50 μm.

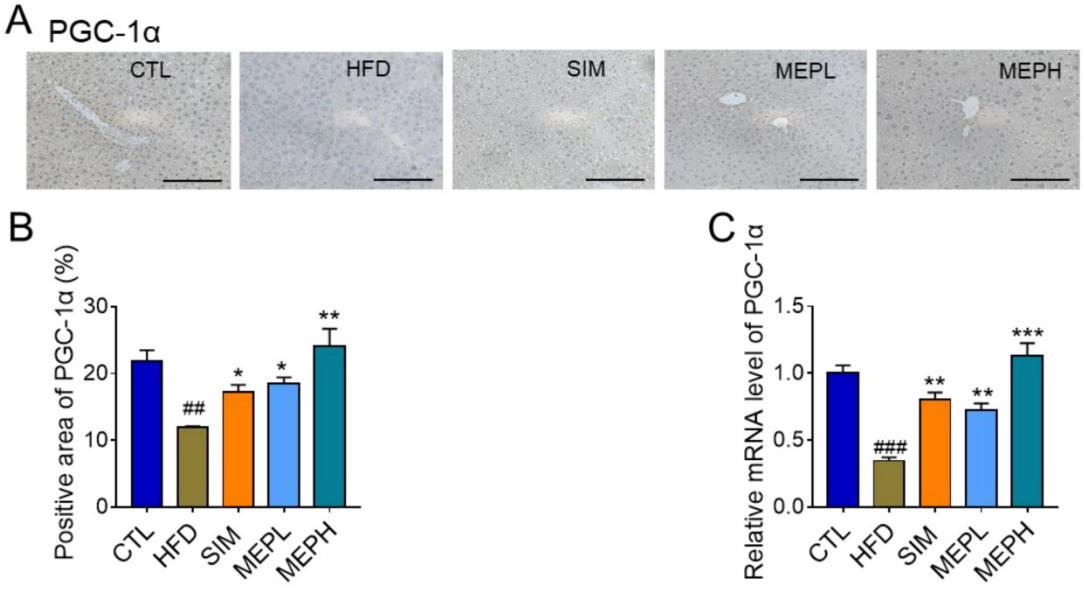


**Fig S4. MEP regulated PGC-1α level in liver of NAFLD mice.** Immunohistochemical analysis of PGC-1α (A) was showed, and the positive staining areas of PGC-1α (B). The mRNA level of PGC-1α was detected (C). All values of animal experiments are presented as means ± SEM (n = 5). Significantly different (*P<0.05, **P<0.01, ***P<0.001) versus the HFD group. Significantly different (##P<0.01, ###P<0.001) versus the CTL group. Scale bar: 50 μm.

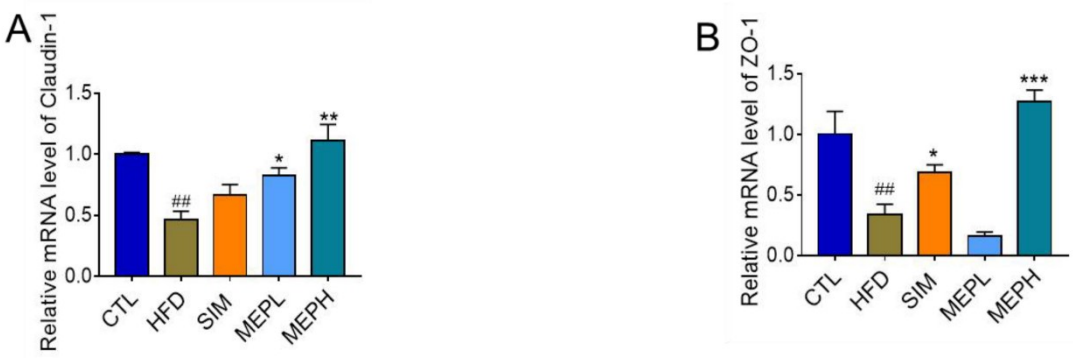


**Fig S5. MEP restored the mRNA levels of Claudin-1 (A) and ZO-1 (B) in NAFLD mice.** All values are presented as means ± SEM (n = 5). Significantly different (*P<0.05, **P<0.01, ***P<0.001) versus the HFD group. Significantly different (##P<0.01) versus the CTL group.

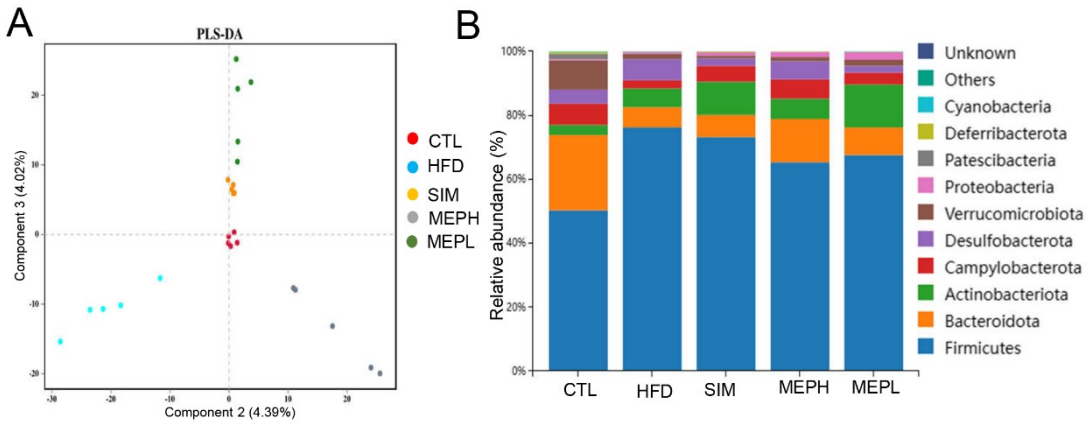


**Fig S6. PLS-DA of 16S rRNA genes (A). Composition of gut microbiota in phylum level (B).**