Table S1 The composition of the diets (per 100g).

Diet	High fat diet	Normal chow diet
Carbohydrate (g)	26.4	63.5
Protein (g)	24.7	17.4
Fat (g)	34.1	4.0
Energy (kcal/g)	5.1	3.6
Energy from carbohydrate (%)	20.6	70.6
Energy from protein (%)	19.4	19.4
Energy from fat (%)	60.0	10.0

Table S2 The primer sequences of the related gene in quantified by RT-qPCR.

Target Name		Primer
β-actin	F	CTCCTGAGCGCAAGTACTCT
	R	TACTCCTGCTTGCTGATCCAC
GPX	F	AGCCAGCTACTGAGGTCTGA
	R	CAGCATTTAGGAGGCAAGCA
PPAR-α	F	ATGAACAAAGACGGGATGCT
	R	CTTGGGTTCCATGATGTCACAG
PPAR-γ	F	TTCTGGCCCACCAACTTCG
	R	AAATGCTGGAGAAATCAACTGTG
SREBP-1c	F	CTATGGAGGGCATGAAACCCGAA
	R	CGGGCTCAGAGTCACTACCAC
ACAT	F	AAGTCTACATGGGCAATGTCA
	R	TCATTCCTGAAGCACAAACCTT
FAB4	F	GGGATGGAAAGTCGACCACA
	R	AAGTCACGCCTTTCATAACACA
FAS	F	ACTAATAGCATCTCCGAGAGT
	R	GGGCCTCCTTGATATAATCCTT
PGC-1α	F	TCATCACCTACCGTTACACC
	R	AAGTCAGTTTCGTTCGACC
LPL	F	AGATGCCCTACAAAGTGTTCC
	R	GTGCCGTACAGAGAAATCTCG
HMGR	F	GCTGGAATTATGAGTGCCCTA
	R	TACCCAGAATGTACTTGGACCC
LCAT	F	GTAACCACACACGGCCTGTC
	R	GTCTTACGGTAGCACATCCAGT
UCP1	F	TGCCAGGACAGTACCCAAG
	R	AAAAGAAGCCACAAACCCTT
Z0-1	F	GACGAAGAAGTGCATGACCC
	R	GCTTGCACTCCTATCCCTT
occludin	F	ATAATGGGAGTGAACCCGAC
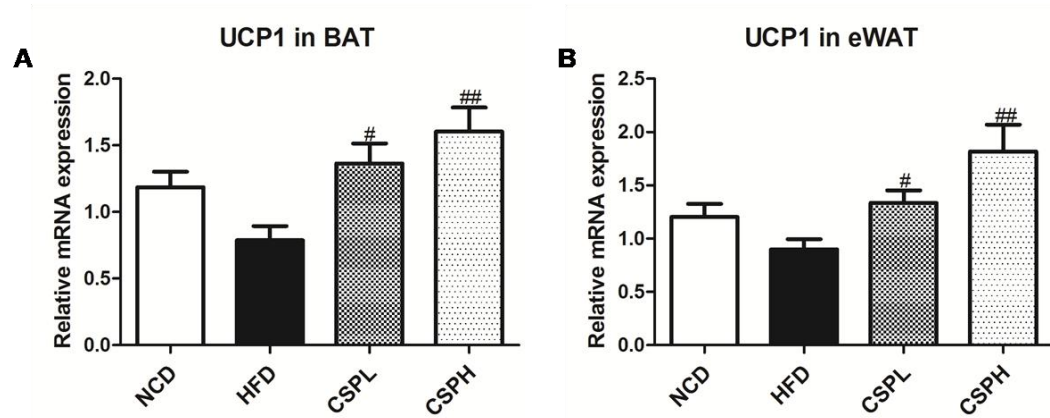
Fig S1. CSP supplementation upregulated the gene expression of UCP1 in BAT and eWAT. (A) UCP1 in BAT; (B) UCP1 in eWAT. Data are expressed as the mean ± SEM (n=6). # $P<0.05$, ## $p<0.01$,### $p<0.001$ compared with HFD.
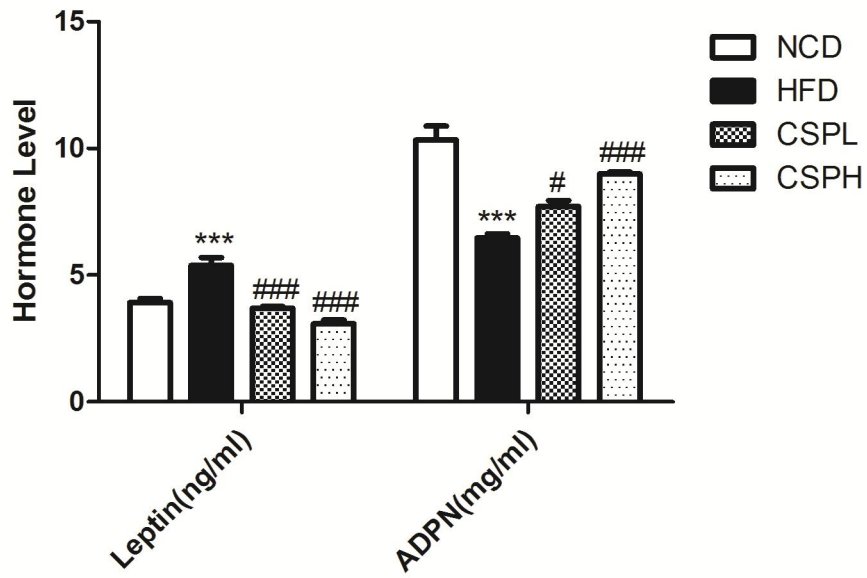
Fig S2. CSP supplementation ameliorated serum hormone level of leptin and ADPN in HFD-fed mice.Data are expressed as the mean ± SEM (n=6). * $P<0.05$, ** $P<0.01$, *** $P<0.001$ compared with NCD; # $P<0.05$, ## $p<0.01$, ### $p<0.001$ compared with HFD.
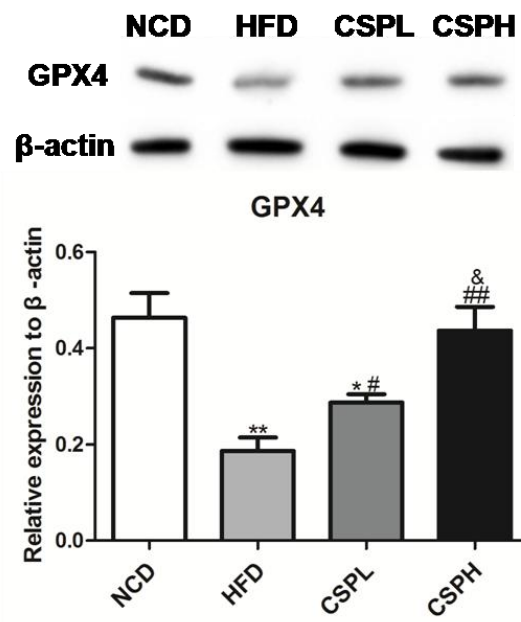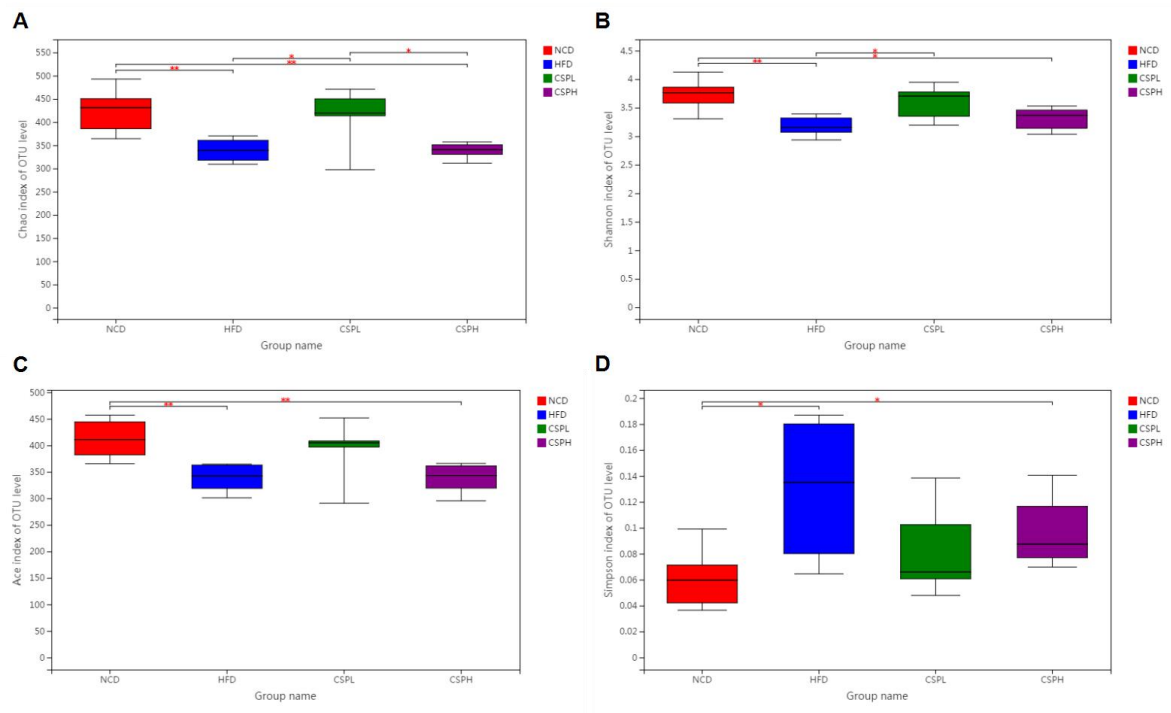
Fig S3. CSP supplementation enhanced the protein level of selenoensyme-GPX4 in liver. Data are expressed as the mean ± SEM (n=4). * P<0.05, ** P<0.01, compared with NCD; # P<0.05, ## p<0.01, compared with HFD; & p<0.05 compared with CSPL

Fig S4. Effect of CSP on alpha diversity of gut microbiota in normal mice and inobesity mice without or with CSP treatment. (A–D) Alpha diversity was evaluated by (A) Chao1 index; (B) Shannon index; (C) Ace index, (C) Simpson index. Data are presented as mean ± SD. Differences were analyzed by student's T-test. and denoted as follows: * *P*<0.05, ** *P*<0.01, *** *P*<0.001.
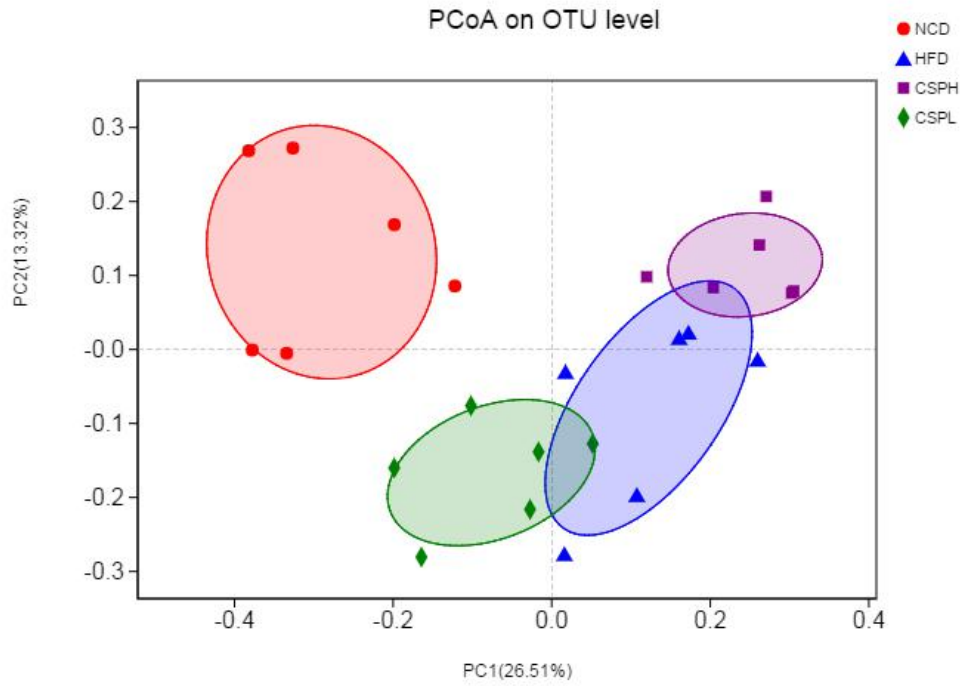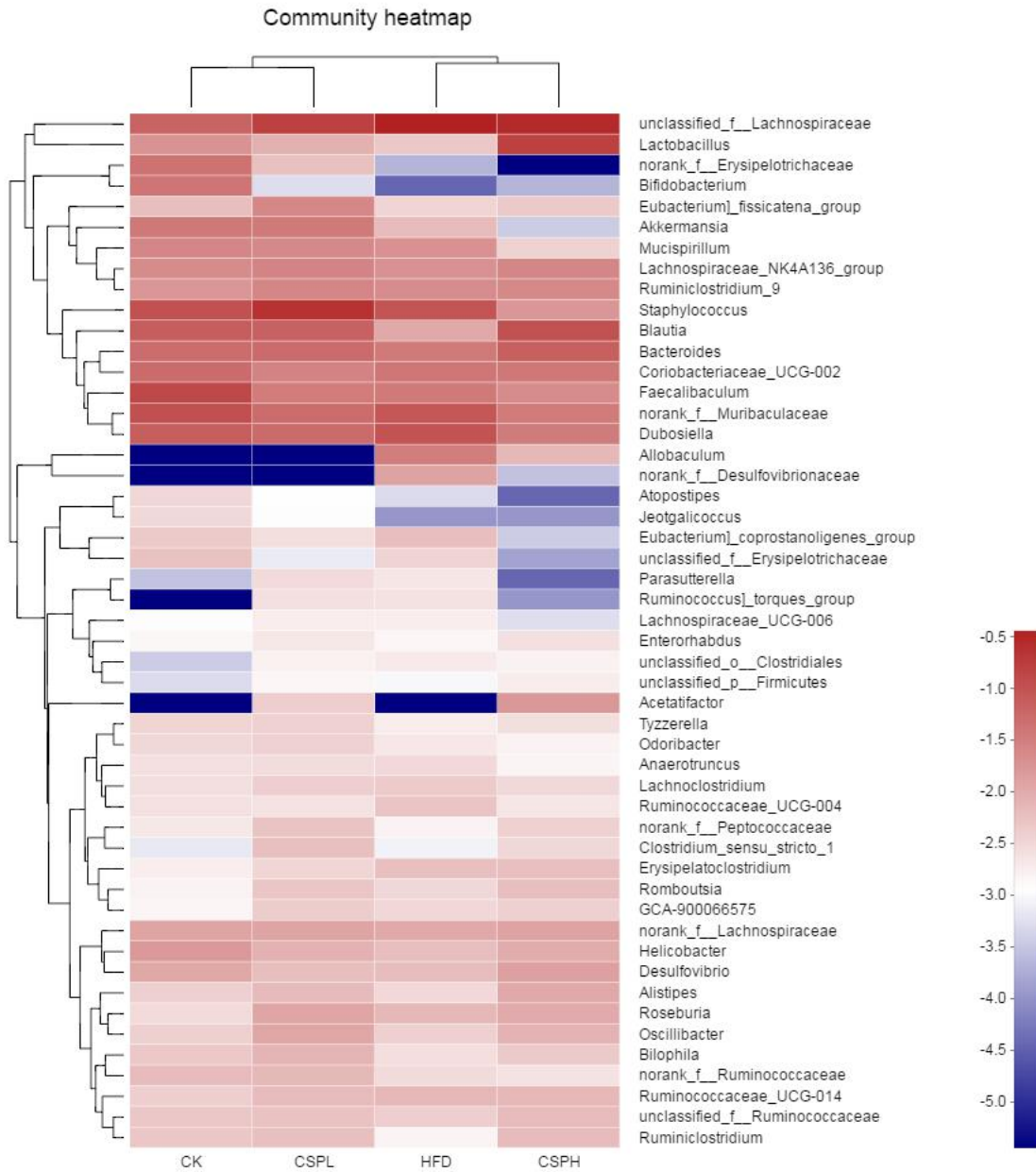
Fig S5. Principal coordinate analysis (PCoA) on OTU level based on Bray-Curtis dissimilarity.
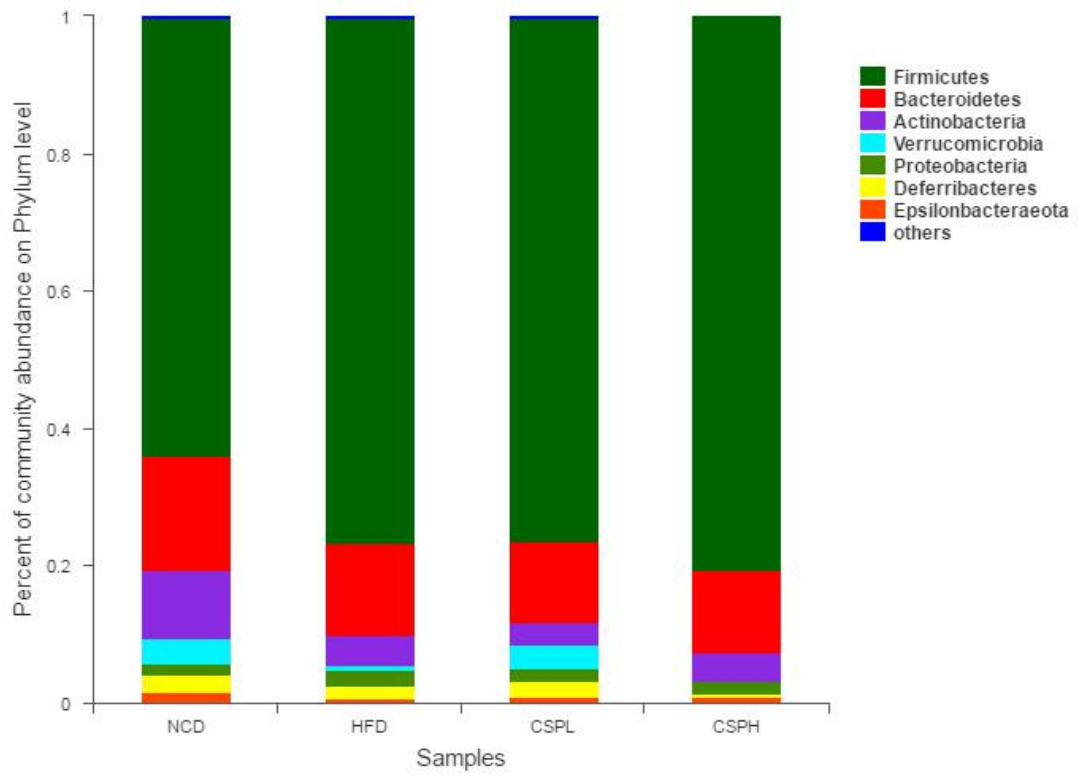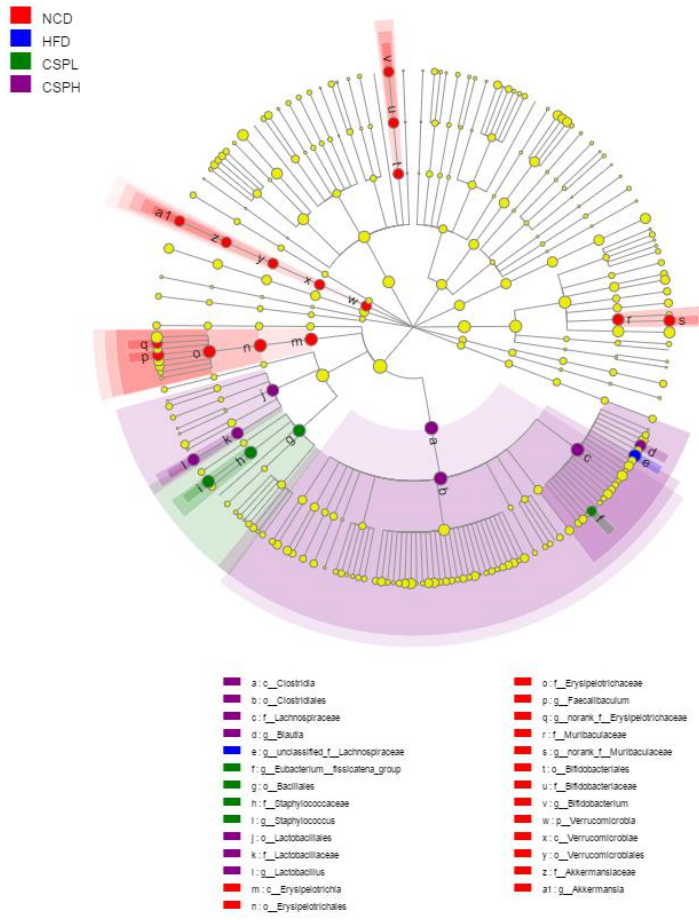
Fig S6. The relative abundance of gut microbiota at the phylum level.

Fig S7. Heat map analysis of the top 35 abundance of gut microbe at genus level.

Fig S8. Cladogram generated from LEfSe analysis with various levels.