Table S1. Preprocessing statistics and quality control of the raw data.

Sample	Raw Data		Valid Data		Valid%	Q20%	Q30%	GC%
	Read	Base	Read	Base				
HFD-OTP0	41290832	6.23G	40061706	5.52G	97.02	92.37	92.38	44.56
HFD-OTP4	52312648	7.90G	50232630	6.77G	96.02	96.93	91.48	44.74
HFD0	42965118	6.49G	39650996	5.39G	92.29	97.09	92.07	46.95
HFD4	51988192	7.85G	50420982	6.97G	96.99	97.40	92.41	43.04

Supplemental Figure Captions

Figure S1. Representative elution profiles of tea catechins, gallic acid, caffeine, theobromine and theophylline from oolong tea (1, gallic acid; 2, (-)-gallocatechin (GC); 3, theobromine; 4, EGC; 5, (-)-catechin (C); 6, theophylline; 7, EGCG; 8, caffeine; 9, EC; 10, (-)-gallocatechin-3-gallate (GCG); 11, EGCG3''Me; 12, ECG; 13, (-)-catechin gallate (CG)).

Figure S2. Effect of OTP on body weight in mice fed with HFD for four weeks.

* Indicates significant body weight differences ($P < 0.05$) between different treatments.

Figure S3. LEfSe identified the most differentially abundant taxa in the faecal microbiota of the HFD-induced obesity mouse model. Taxonomic cladogram obtained from LEfSe analysis of 16S rRNA sequencing. (Red) HFD-0 enriched taxa; (Green) HFD-4 enriched taxa; (Blue) HFD-OTP0 enriched taxa; (Purple) HFD-OTP4 enriched taxa (A). The brightness of each dot is proportional to its effect size.

Figure S4. Principal coordinate analysis plot of the faecal microbiota based on the unweighted UniFrac metric.

Figure S5. KEGG analysis of differentially expressed genes between HFD-OTP0 and HFD-OTP4.

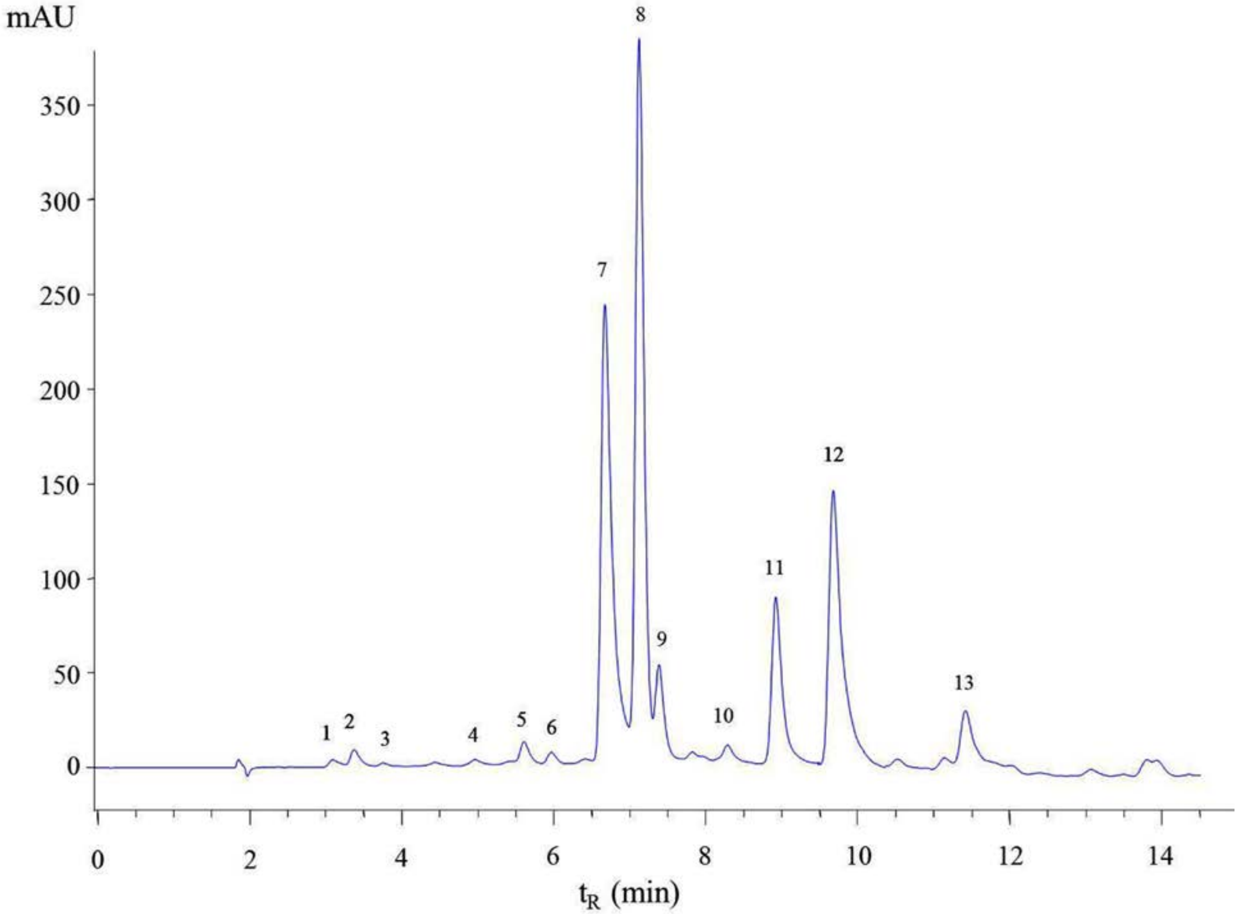

mAU
350
300
250
200
150
100
50
0
1
2
3
4
5
6
7
8
9
10
11
12
13
0
2
4
6
8
10
12
14
t_R (min)

Fig. S1

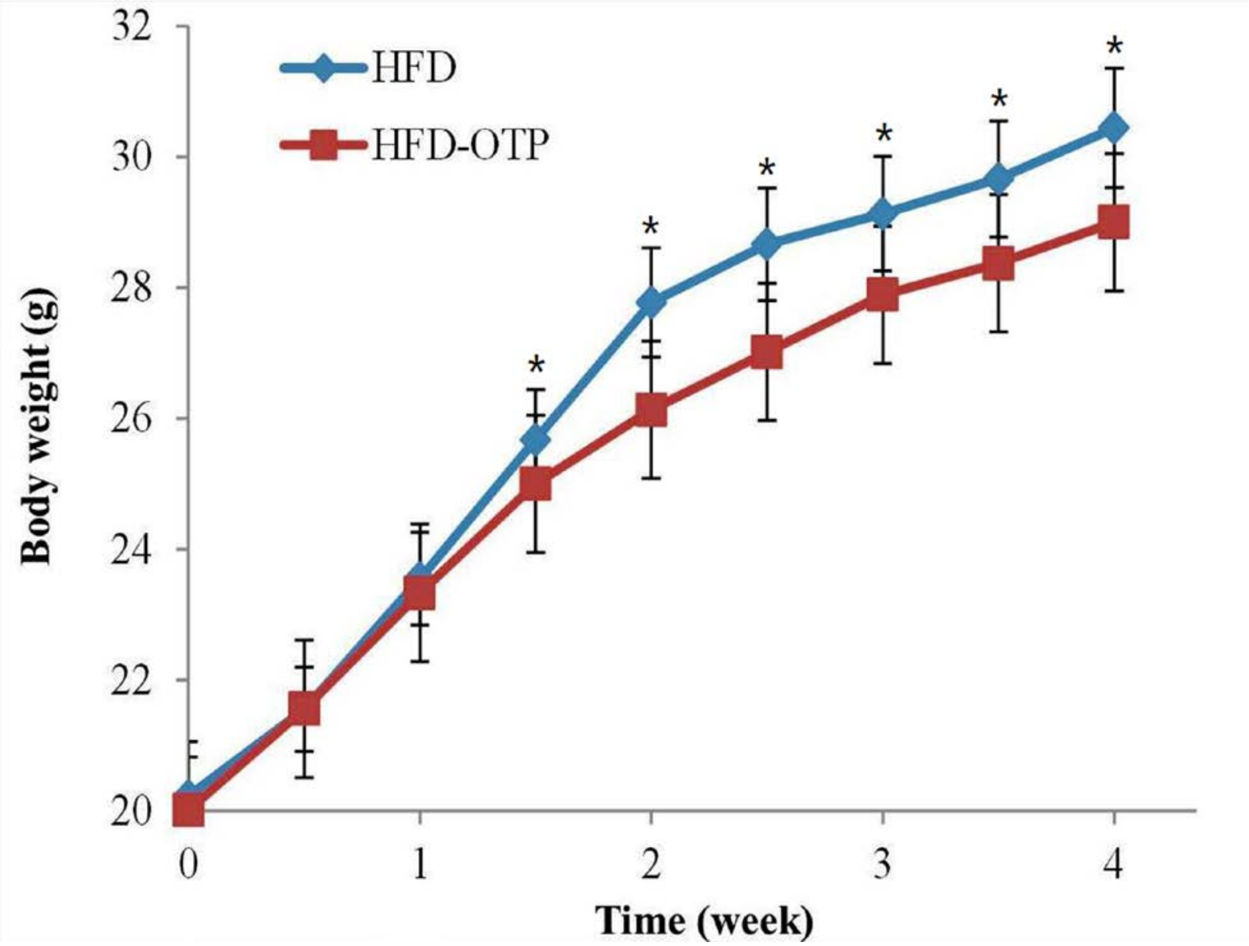


Fig. S2

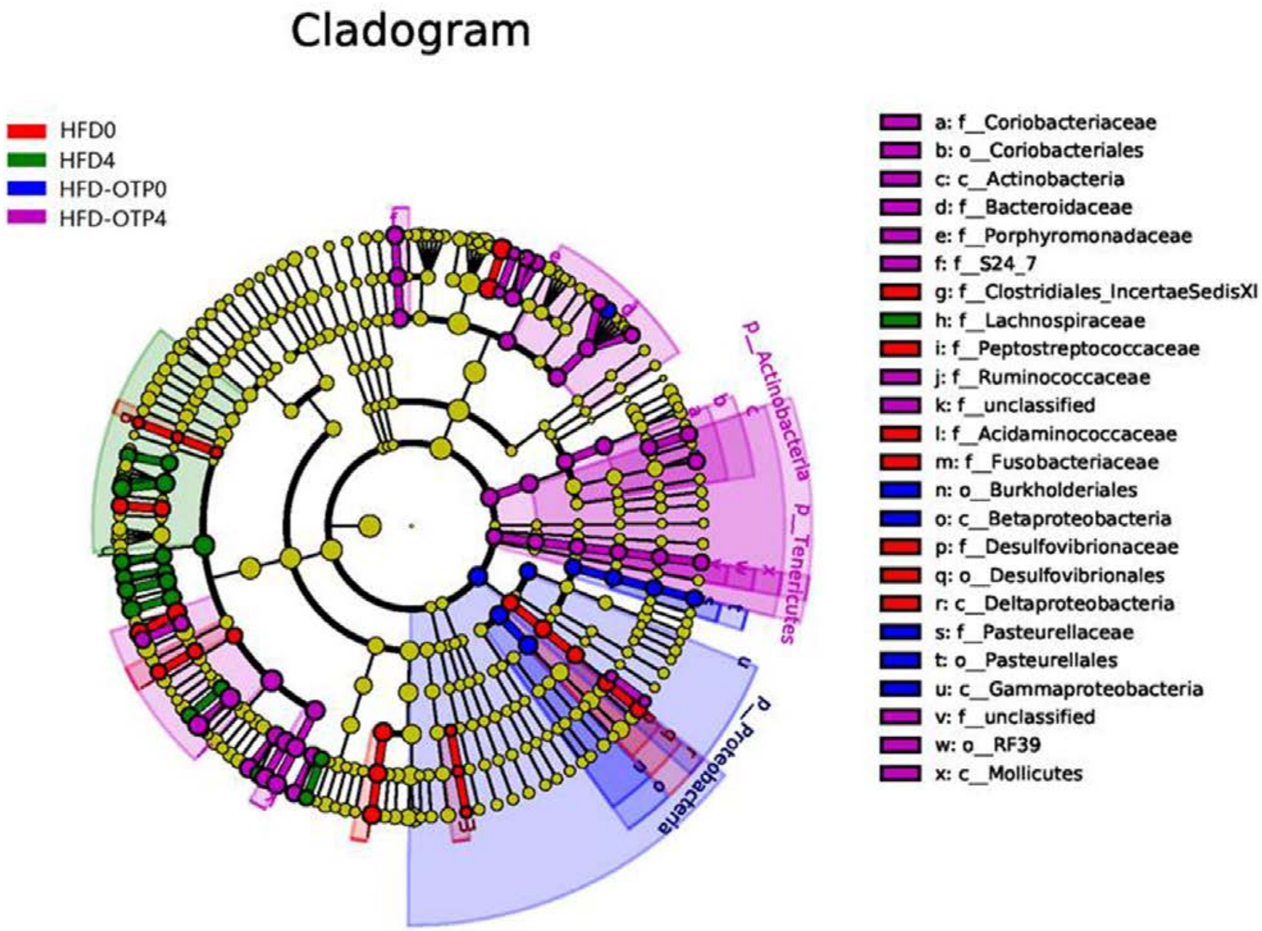
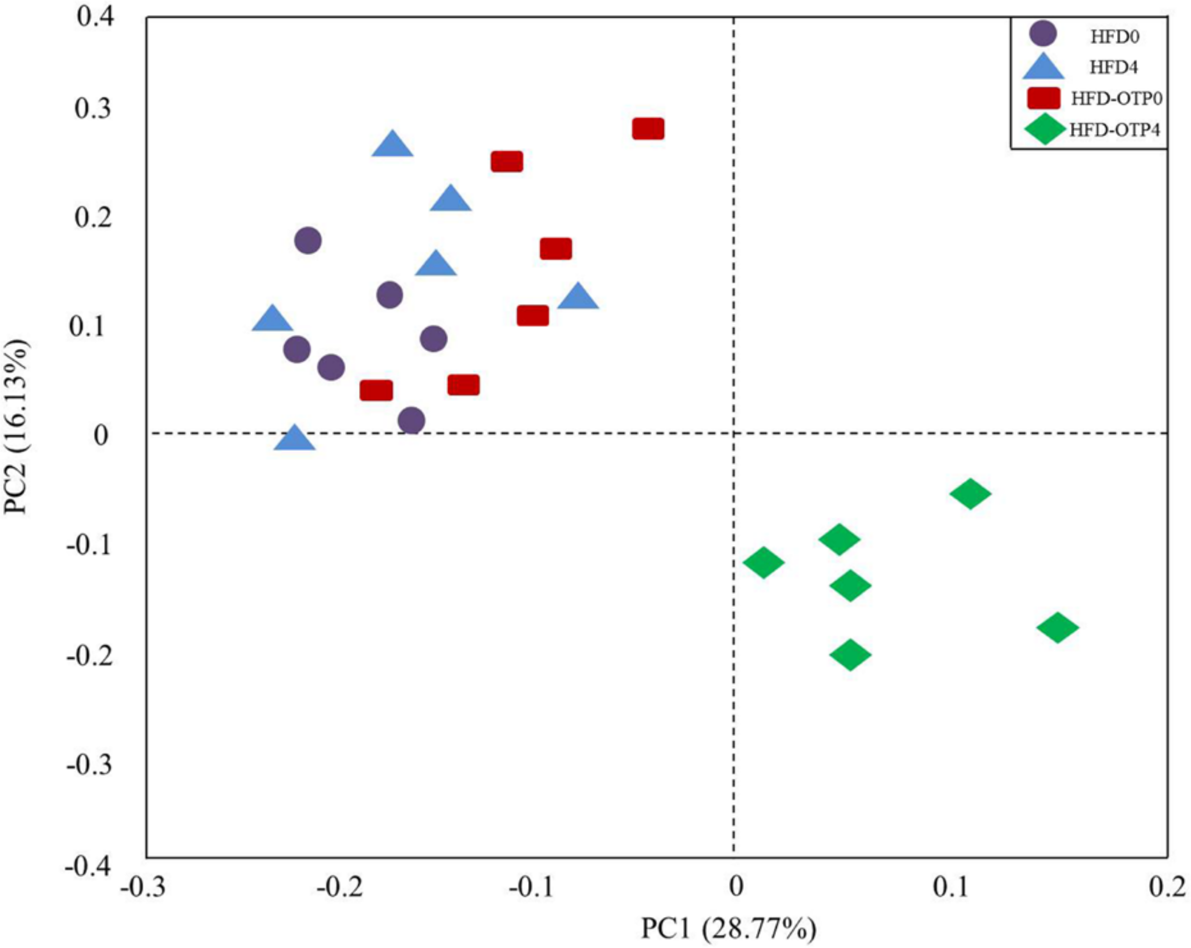

Cladogram
HFD0
HFD4
HFD-OTP0
HFD-OTP4
a: f__Coriobacteriaceae
b: o__Coriobacteriales
c: c__Actinobacteria
d: f__Bacteroidaceae
e: f__Porphyromonadaceae
f: f__S24_7
g: f__Clostridiales_IncertaeSedisXI
h: f__Lachnospiraceae
i: f__Peptostreptococcaceae
j: f__Ruminococcaceae
k: f__unclassified
l: f__Acidaminococcaceae
m: f__Fusobacteriaceae
n: o__Burkholderiales
o: c__Betaproteobacteria
p: f__Desulfovibrionaceae
q: o__Desulfovibrionales
r: c__Deltaproteobacteria
s: f__Pasteurellaceae
t: o__Pasteurellales
u: c__Gammaproteobacteria
v: f__unclassified
w: o__RF39
x: c__Mollicutes
p__Actinobacteria
p__Tenericutes
p__Proteobacteria

Fig. S3



0.4
0.3
0.2
0.1
0
-0.1
-0.2
-0.3
-0.4
-0.3
-0.2
-0.1
0
0.1
0.2
PC1 (28.77%)
PC2 (16.13%)
HFD0
HFD4
HFD-OTP0
HFD-OTP4

Fig. S4

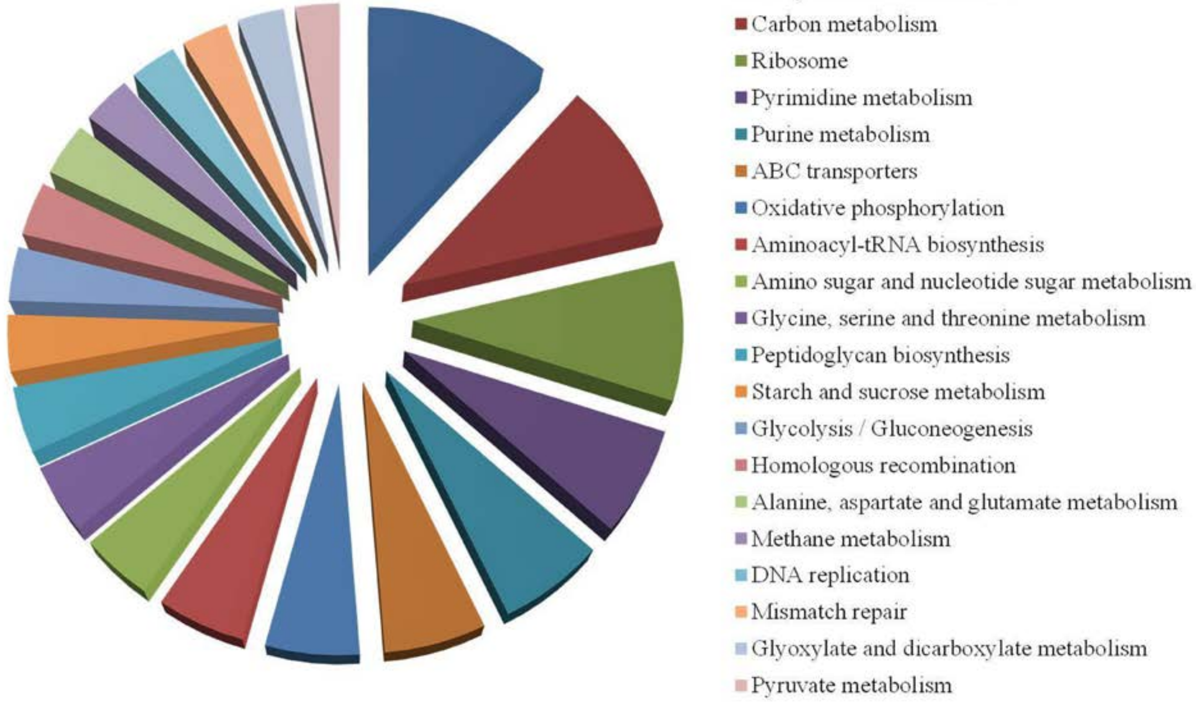

Biosynthesis of amino acids
Carbon metabolism
Ribosome
Pyrimidine metabolism
Purine metabolism
ABC transporters
Oxidative phosphorylation
Aminoacyl-tRNA biosynthesis
Amino sugar and nucleotide sugar metabolism
Glycine, serine and threonine metabolism
Peptidoglycan biosynthesis
Starch and sucrose metabolism
Glycolysis / Gluconeogenesis
Homologous recombination
Alanine, aspartate and glutamate metabolism
Methane metabolism
DNA replication
Mismatch repair
Glyoxylate and dicarboxylate metabolism
Pyruvate metabolism

Fig. S5