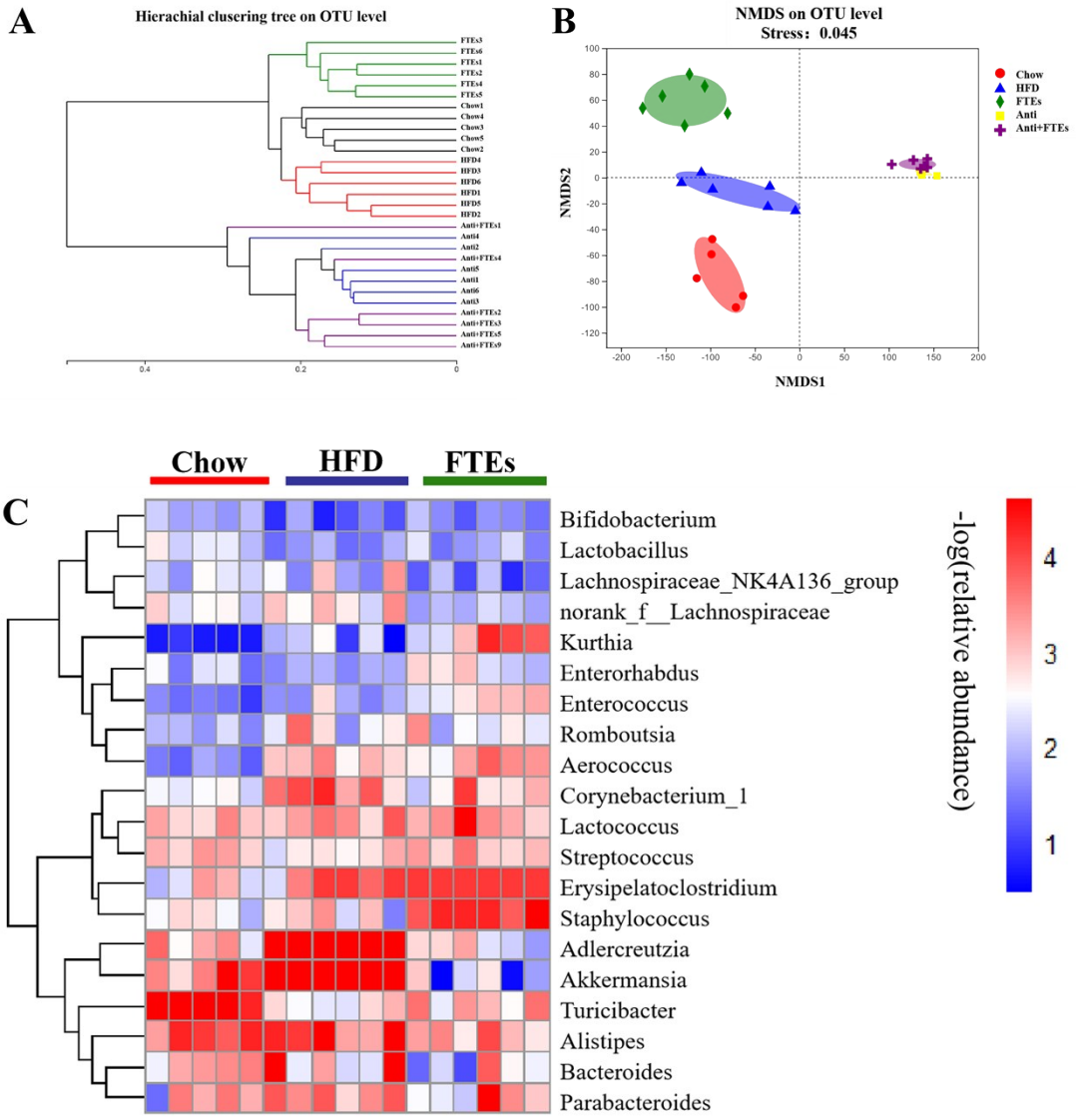


Table S1. Composition of the animal diet.

Ingredients	Chow diet (D12450H)	High-fat diet (D12451)
Casein	18.96%	23.31%
L-Cystine	0.28%	0.35%
Corn Starch	42.86%	8.48%
Maltodextrin 10	7.11%	11.65%
Sucrose	16.38%	20.14%
Cellulose, BW200	0.47%	5.83%
Soybean oil	2.37%	2.91%
Lard	1.90%	20.68%
Mineral Mix	0.95%	1.17%

Vitamin Mix	0.95%	1.17%
Choline Bitartrate	0.19%	0.23%
DiCalcium Phosphate	1.23%	1.57%
Calcium Crabonate	0.52%	0.64%
Potassium Citrate,1 H_20	1.56%	1.92%
Total calories (kcal/g)	3.85	4.73

Table S2. The relative abundance of gut microbiota in genus level between HFD and Anti groups.

Name	HFD（%）	Anti（%）
p__Bacteroidetes, g__Alistipes	0.0224±0.0277	0**
p__Firmicutes, g__Erysipelatoclostridium	0.1012±0.2211	0*
p__Firmicutes, g__Lachnospiraceae_NK4A136_group	1.2911±1.3494	0.0013±0.0032**
p__Firmicutes, g__Enterococcus	1.7343±0.9913	0.0018±0.0022**
p__Actinobacteria, g__Enterorhabdus	1.7484±0.7628	0**
p__Firmicutes, g__Lactobacillus	2.7300±1.5076	0.0189±0.0425**
p__Firmicutes, g__Kurthia	7.8084±13.0511	0**
p__Actinobacteria, g__Bifidobacterium	8.2843±6.4787	0.0009±0.0022**
p__Firmicutes, g__Faecalibaculum	18.1254±4.6443	0.0004±0.0011
p__Bacteroidetes, g__unclassified_o__Bacteroidales	0	0.0150±0.0129**
p__Proteobacteria, g__Parasutterella	0.0004±0.0011	14.8707±6.2449**
p__Proteobacteria, g__Escherichia-Shigella	0.0026±0.0024	8.6522±5.4739**
p__Proteobacteria, g__Citrobacter	0.0040±0.0040	27.1351±6.8712**
p__Proteobacteria, g__Klebsiella	0.0040±0.0072	3.6478±2.7194**
p__Bacteroidetes, g__Parabacteroides	0.0374±0.0538	41.9350±14.2825**

Data were expressed as mean ± SD, and statistical analysis by Wilcoxon rank sum test, *$p < 0.05$, **$p < 0.01$.

Supplementary Figure Captions

Figure S1. Effect of FTES on obese mice. (A-C) The weight of epididymis fat, mesenteric fat and retroperitoneal fat. (D-E) Concentrations of LDL-C, HDL-C in serum. (F) The level of blood glycemia in oral glucose tolerance test. Data were expressed as mean ± SD, and statistically analyzed by One-way ANOVA, *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$; ns, not significant.

Figure S2. Effect of FTES on antibiotic treated mice. (A-C) The weight of epididymis fat, mesenteric fat and retroperitoneal fat. (D-E) Concentrations of LDL-C, HDL-C in serum. (F) The level of blood glycemia in oral glucose tolerance test. Data were expressed as mean ± SD, and statistically analyzed by Student's t test, *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$; ns, not significant.

Figure S3. (A) Food intake, (B) water intake, (C) OTU rank-abundance curves, (D) Partial least squares-discriminate analysis (PLS-DA) on OUT level. Data were expressed as mean ± SD, and statistically analyzed by One-way ANOVA. Different letters a, b represent significant difference, $p < 0.05$.

Figure S4. (A) Hierarchical cluster analysis by Spearson-Approx method. (B) Non-metric multidimensional scaling (NMDS) on OUT level. (C) The heatmap of differential genera among Chow, HFD and FTES groups, which were analysised by the Wilcoxon rank sum test ($p < 0.05$).

Figure S5. Fecal transplantation improved lipid metabolism in high-fat diet fed mice. (A) The weight of liver, mesenteric fat and retroperitoneal fat. (B) Serum concentrations of TC, LDL-C, HDL-C. (C) Food and water intake. (D) Alpha diversity was presented as the index of Chao, Shannon. Data were expressed as mean ± SD, and statistically analyzed by One-way ANOVA, *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$; ns, not significant.

Figure S6. Heatmap showing significantly different metabolites between the HFD group and Chow group or FTES group based on Student's t test ($p < 0.05$).

Figure S7. Differential metabolites and enriched metabolic pathways after treated by FTES in negative ion model. (A) Heatmap showing significantly different metabolites between the HFD group and FTES group based on Student's t test. (B) Metabolome view maps of the significantly different metabolites-related metabolic pathways between the HFD group FTES group. Pathway impact for topology analysis and *p*-value for enrichment analysis were performed using MetaboAnalyst 4.0. The size and color of each circle represent the pathway impact value and *p*-value, respectively.

Figure S1.

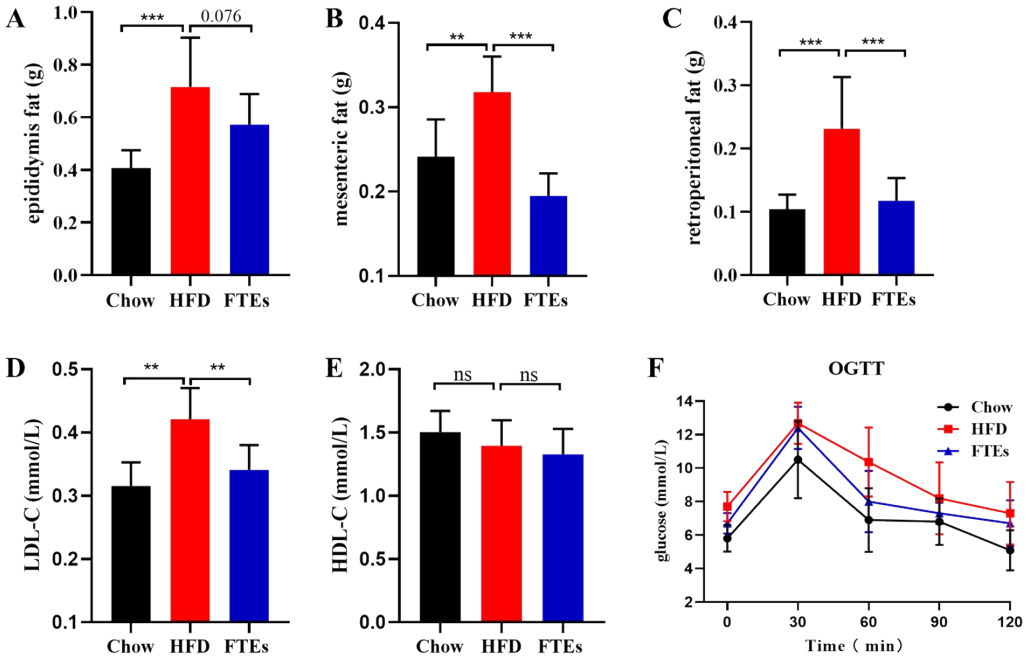

A
epididymis fat (g)
1.0
0.8
0.6
0.4
0.2
0.0
***
0.076
Chow HFD FTEs
B
mesenteric fat (g)
0.4
0.3
0.2
0.1
**
***
Chow HFD FTEs
C
retroperitoneal fat (g)
0.4
0.3
0.2
0.1
0.0
***
***
Chow HFD FTEs
D
LDL-C (mmol/L)
0.5
0.4
0.3
0.2
0.1
**
**
Chow HFD FTEs
E
HDL-C (mmol/L)
2.0
1.5
1.0
0.5
0.0
ns
ns
Chow HFD FTEs
F
OGTT
glucose (mmol/L)
14
12
10
8
6
4
2
0
30
60
90
120
Time (min)
Chow
HFD
FTEs

Figure S2.

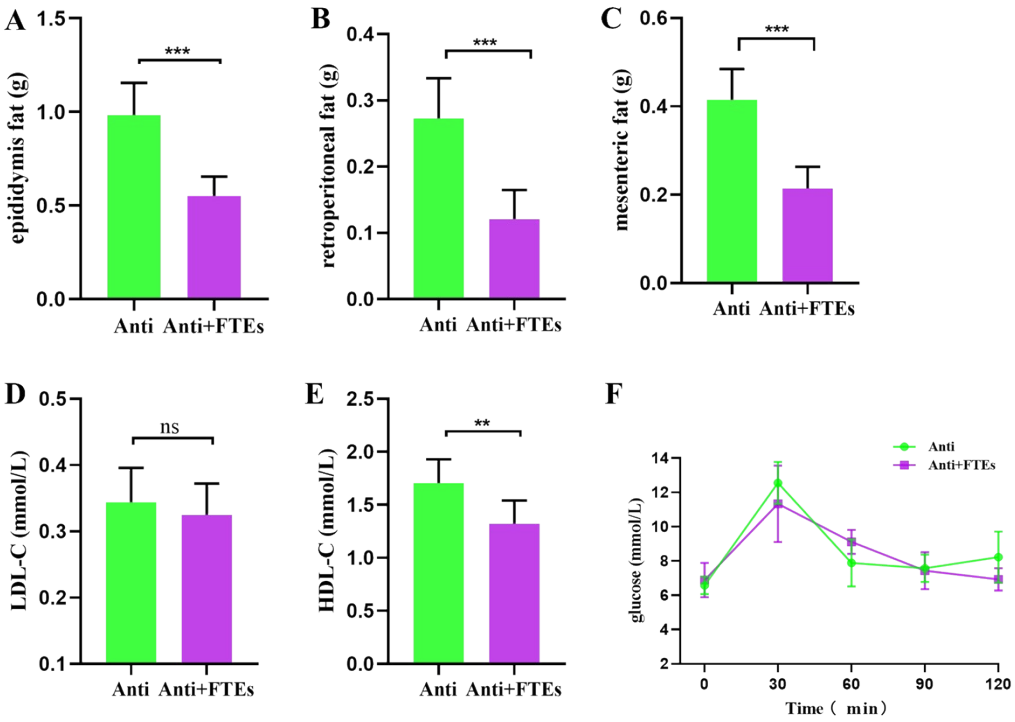

A
epididymis fat (g)
1.5
1.0
0.5
0.0
***
Anti
Anti+FTEs
B
retroperitoneal fat (g)
0.4
0.3
0.2
0.1
0.0
***
Anti
Anti+FTEs
C
mesenteric fat (g)
0.6
0.4
0.2
0.0
***
Anti
Anti+FTEs
D
LDL-C (mmol/L)
0.5
0.4
0.3
0.2
0.1
ns
Anti
Anti+FTEs
E
HDL-C (mmol/L)
2.5
2.0
1.5
1.0
0.5
0.0
**
Anti
Anti+FTEs
F
glucose (mmol/L)
14
12
10
8
6
4
2
0
30
60
90
120
Time (min)
Anti
Anti+FTEs

Figure S3.

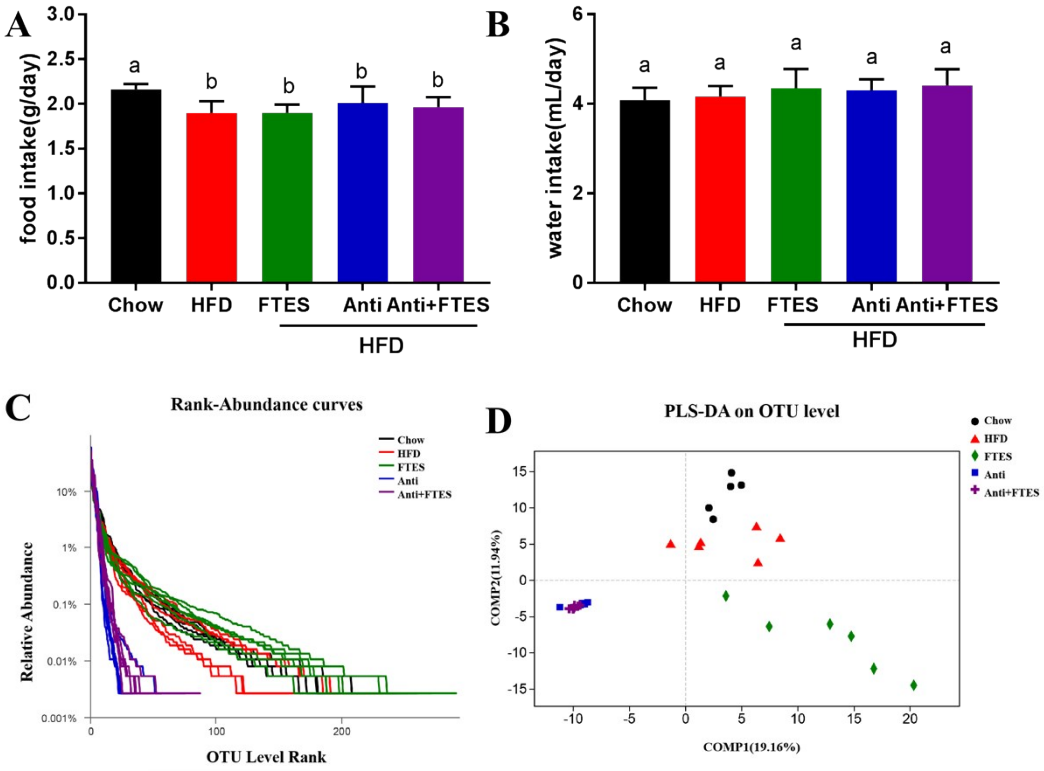

A
food intake(g/day)
3.0
2.5
2.0
1.5
1.0
0.5
0.0
a
b
b
b
b
Chow
HFD
FTES
Anti
Anti+FTES
HFD
B
water intake(mL/day)
6
4
2
0
a
a
a
a
a
Chow
HFD
FTES
Anti
Anti+FTES
HFD
C
Rank-Abundance curves
Chow
HFD
FTES
Anti
Anti+FTES
Relative Abundance
10%
1%
0.1%
0.01%
0.001%
0
100
200
OTU Level Rank
D
PLS-DA on OTU level
Chow
HFD
FTES
Anti
Anti+FTES
COMP2(11.94%)
15
10
5
0
-5
-10
-15
-10
-5
0
5
10
15
20
COMP1(19.16%)

Figure S4.

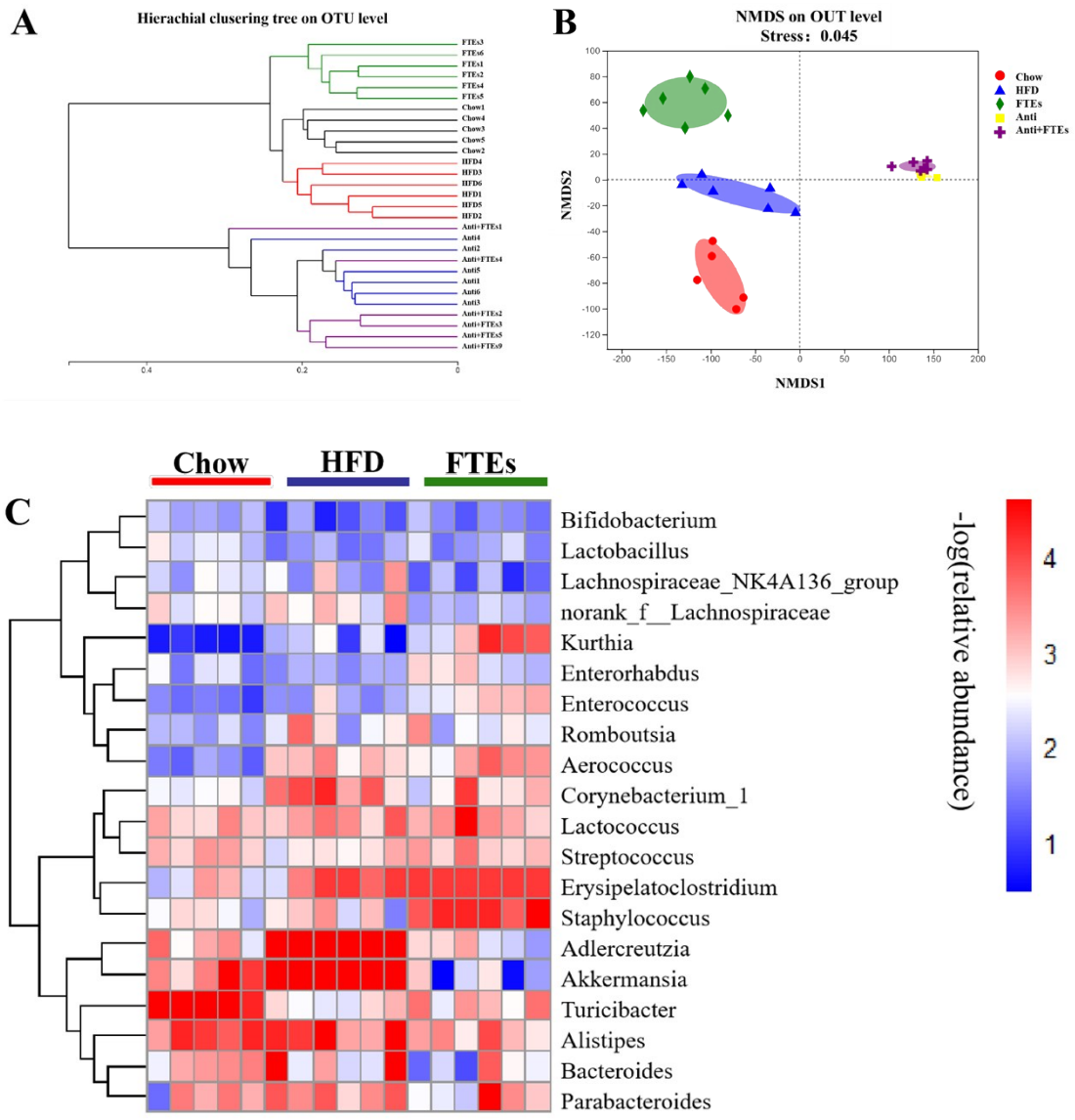

A
Hierachial clusering tree on OTU level
FTEs3
FTEs6
FTEs1
FTEs2
FTEs4
FTEs5
Chow1
Chow4
Chow3
Chow5
Chow2
HFD4
HFD3
HFD6
HFD1
HFD5
HFD2
Anti+FTEs1
Anti4
Anti2
Anti+FTEs4
Anti5
Anti1
Anti6
Anti3
Anti+FTEs2
Anti+FTEs3
Anti+FTEs5
Anti+FTEs9
0.4
0.2
0
B
NMDS on OUT level
Stress：0.045
Chow
HFD
FTEs
Anti
Anti+FTEs
NMDS2
NMDS1
C
Chow
HFD
FTEs
Bifidobacterium
Lactobacillus
Lachnospiraceae_NK4A136_group
norank_f__Lachnospiraceae
Kurthia
Enterorhabdus
Enterococcus
Romboutsia
Aerococcus
Corynebacterium_1
Lactococcus
Streptococcus
Erysipelatoclostridium
Staphylococcus
Adlercreutzia
Akkermansia
Turicibacter
Alistipes
Bacteroides
Parabacteroides
-log(relative abundance)
4
3
2
1

Figure S5.

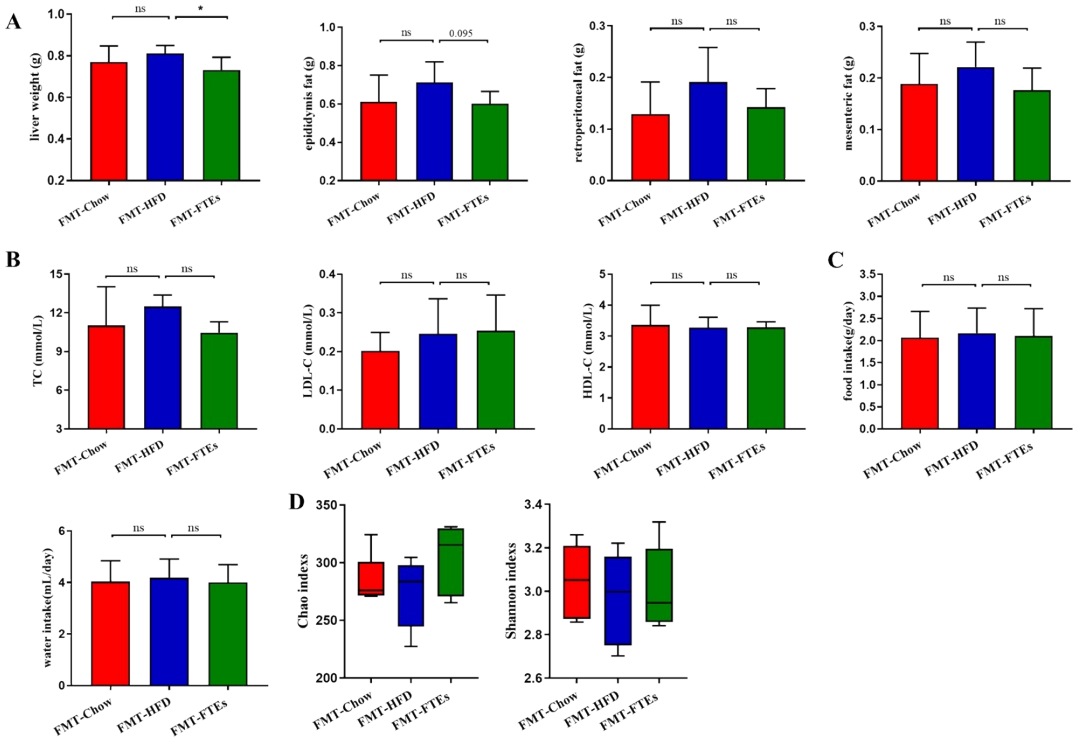

A
liver weight (g)
epididymis fat (g)
retroperitoneal fat (g)
mesenteric fat (g)
B
TC (mmol/L)
LDL-C (mmol/L)
HDL-C (mmol/L)
C
food intake(g/day)
water intake(mL/day)
D
Chao index
Shannon index
ns
*
0.095
FMT-Chow
FMT-HFD
FMT-FTEs

Figure S6.

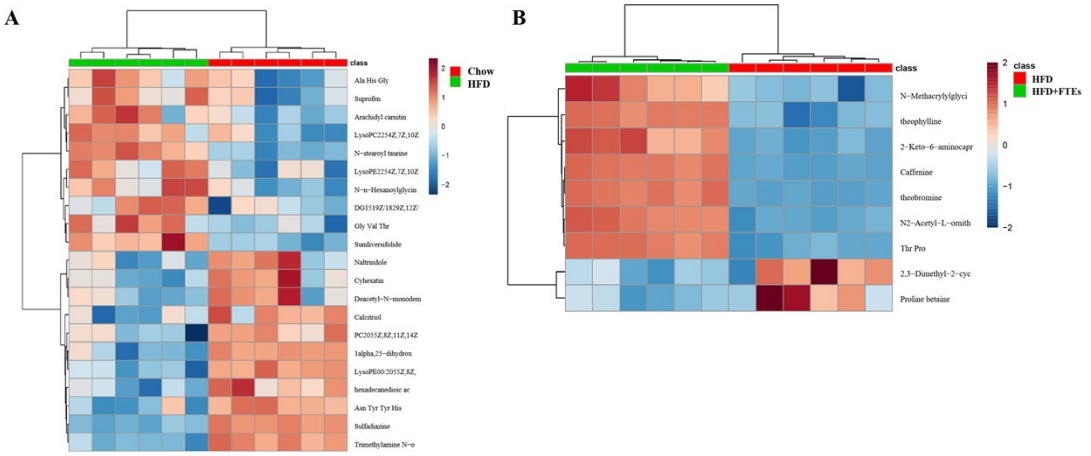
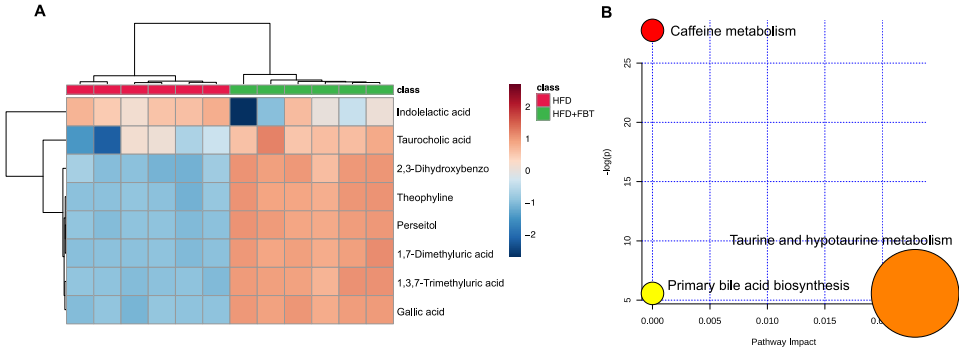

A
class
Chow
HFD
Ala His Gly
Suprofen
Arachidyl carnitin
LysoPC22:5(4Z,7Z,10Z
N-stearoyl taurine
LysoPE22:5(4Z,7Z,10Z
N-n-Hexanoylglycin
DG(15:0/18:2(9Z,12Z/
Gly Val Thr
Sundiversifolide
Naltrindole
Cyhexatin
Deacetyl-N-monodem
Calcitriol
PC(20:5(5Z,8Z,11Z,14Z
1alpha,25-dihydrox
LysoPE(0:0/20:5(5Z,8Z,
hexadecanedioic ac
Asn Tyr Tyr His
Sulfadiazine
Trimethylamine N-o
B
class
HFD
HFD+FTEs
N-Methacrylylglyci
theophylline
2-Keto-6-aminocapr
Caffeine
theobromine
N2-Acetyl-L-ornith
Thr Pro
2,3-Dimethyl-2-cyc
Proline betaine

Figure S7


A
class
Indolelactic acid
Taurocholic acid
2,3-Dihydroxybenzo
Theophyline
Perseitol
1,7-Dimethyluric acid
1,3,7-Trimethyluric acid
Gallic acid
class
HFD
HFD+FBT
2
1
0
−1
−2
B
Caffeine metabolism
Taurine and hypotaurine metabolism
Primary bile acid biosynthesis
-log(p)
25
20
15
10
5
0.000
0.005
0.010
0.015
Pathway Impact