**Table 1** Gradient elution process

| Time(min) | A: 0.2% formic acid solution | B: acetonitrile |
|-----------|------------------------------|-----------------|
| 0 | 95% | 5% |
| 20 | 80% | 20% |
| 25 | 5% | 95% |
| 34 | 5% | 95% |
| 35 | 95% | 5% |
| 45 | 95% | 5% |

**Table 2** Primer sequences for metabolic related genes

| Gene | Primer sequence |
|------|-----------------|
| *Tumor necrosis factor α, TNF-α* | Forward: ACCCTCACACTCACAAACCAC |
| | Reverse: ACAAGGTACAACCCATCGGC |
| *Interleukin- 6, IL-6* | Forward: ACAAAGCCAGAGTCCTTCAGAG |
| | Reverse: TGTGACTCCAGCTTATCTCTTG |
| *Interleukin-1β, IL-1β* | Forward: AAATGCCACCTTTTGACAGTGATG |
| | Reverse: GCAGCCCTTCATCTTTTGGG |
| *Claudin 1* | Forward: ACTCCTTGCTGAATCTGAACAGT |
| | Reverse: GGACACAAAGATTGCGATCAG |
| *Occludin* | Forward: CAGGATGGGAACCCTCACTA |
| | Reverse: ACAGGCCCTGCAGTAGGA |
| *ZO-1* | Forward：TTTGAGAGCAAGCCTTCTGC |
| | Reverse：AGCATCAGTTTCGGGTTTTC |
| *Nlrp3* | Forward：ACTTGCAGAAGCTGGGGTTG |
| | Reverse：AGTTTACAGTCCGGGTGCAG |
| *Caspase1* | Forward：CGTACACGTCTTGCCCTCAT |
| | Reverse：CTCTTTCACCATCTCCAGAGC |
| *36B4* | Forward：GGCTGACTTGGTTGCTTTGG |
| | Reverse：AGCAAAGGAAGAGTCGGAGG |
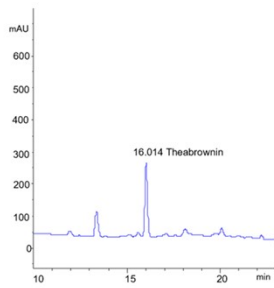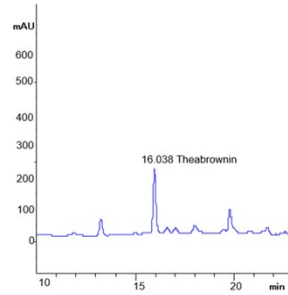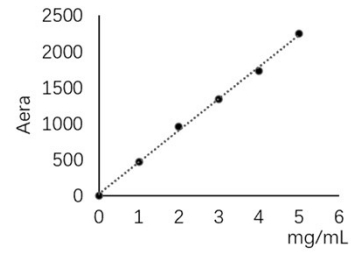
**Supplementary data Figure 1.** (A) HPLC analysis chromatogram of TB reference substance (B) HPLC analysis chromatogram of TB sample which was used for animal intervention. (C)The regression equation. The retention time of TB was 16 min. The standard curve was drawn with the concentration (mg/mL) as the abscissa (X) and the peak area as the ordinate (Y), and the calculated regression equation was $Y= 439.59X + 25.971$ and $R^2= 0.9978$ mice. TB sample peak area was plugged into the corresponding standard curve equation and the TB sample content was 90.57%.
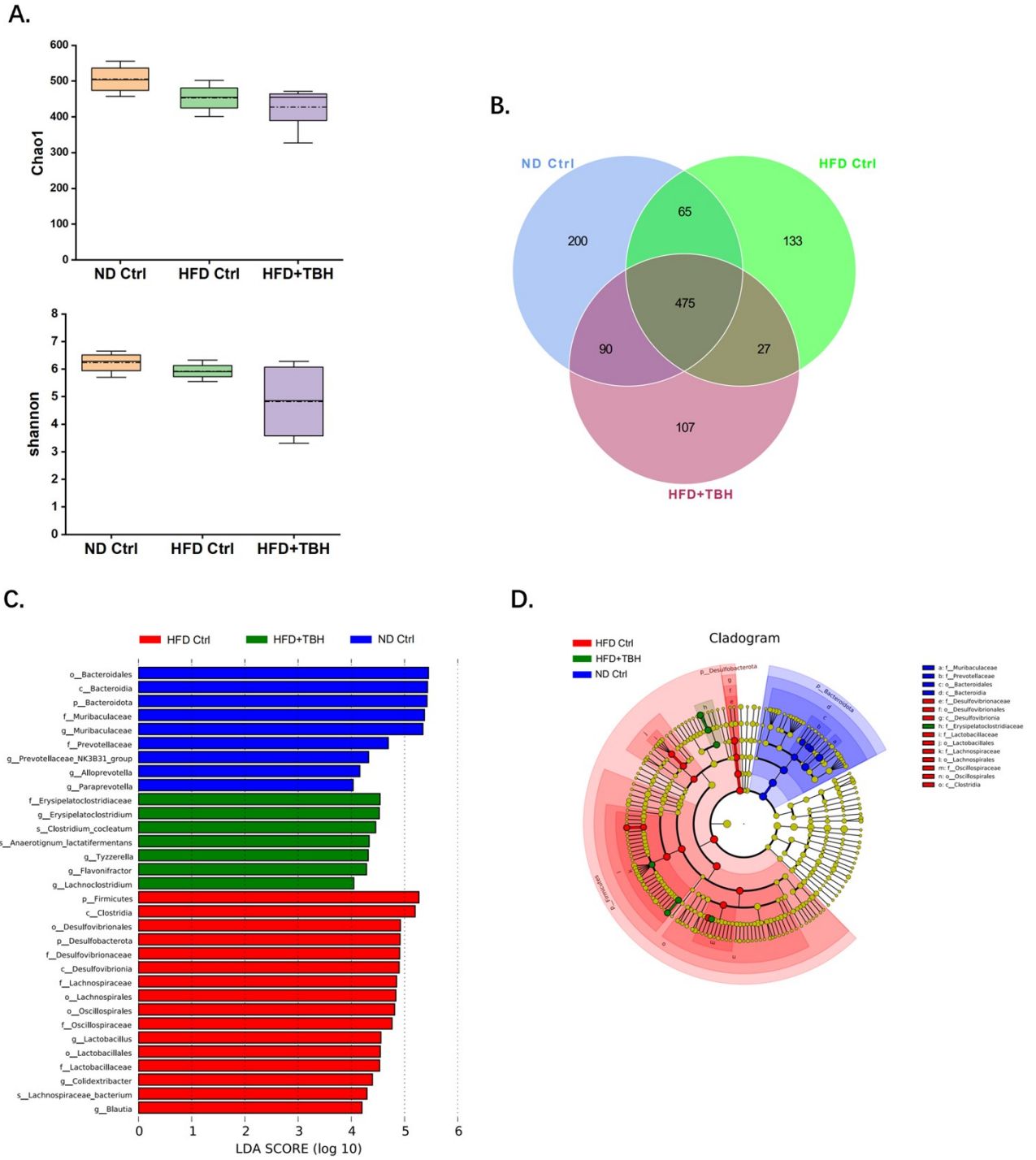
**Supplementary data Figure 2.** TB from Fu Brick tea altered the composition of gut microbiota in HFD-fed mice. (A) Chao1 index and Shannon index. (B) Venn diagram. (C) LDA score. (D) Cladogram. The data are mean ± s.d. (error bars). n=4 mice per group.
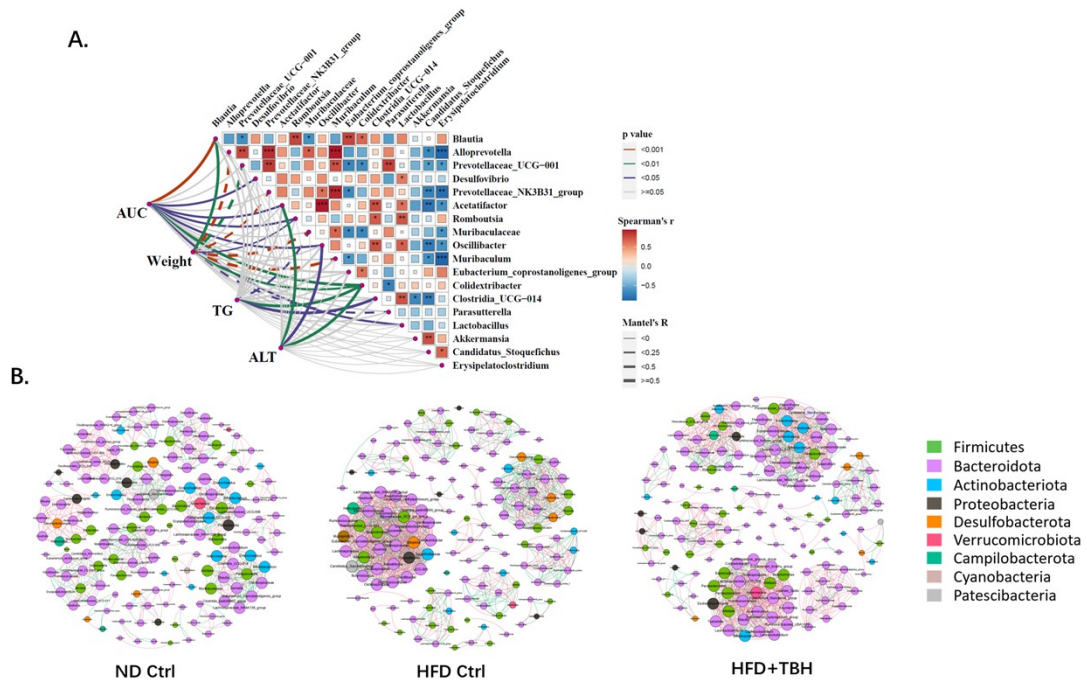
**Supplementary data Figure 3**. The correlation between metabolic phenotype and the abundance of gut microbiota. The feces of ND-fed Ctrl mice, HFD-fed Ctrl mice, and HFD-fed treated with high dose of TB mice were collected, and 16S RNA sequencing was performed to analyze the species composition and abundance of the gut microbiota. (A) Correlation analysis of relevant phenotypic indicators to gut microbial indicators. The thickness and color of the lines represent the correlation level and p value level, respectively. The solid lines represent positive correlation and dash lines represent negative correlation. (B) Co-occurrence Network of gut microbiota in ND Ctrl, HFD Ctrl, and HFD+TBH mice. Each node represents an ASV. The size of a node depends on its degree. The color of nodes is rendered at the phylum level, and the edges between the nodes indicate the correlation between species. The red lines represent positive correlation and green lines represent negative correlation. n=4 mice per group.
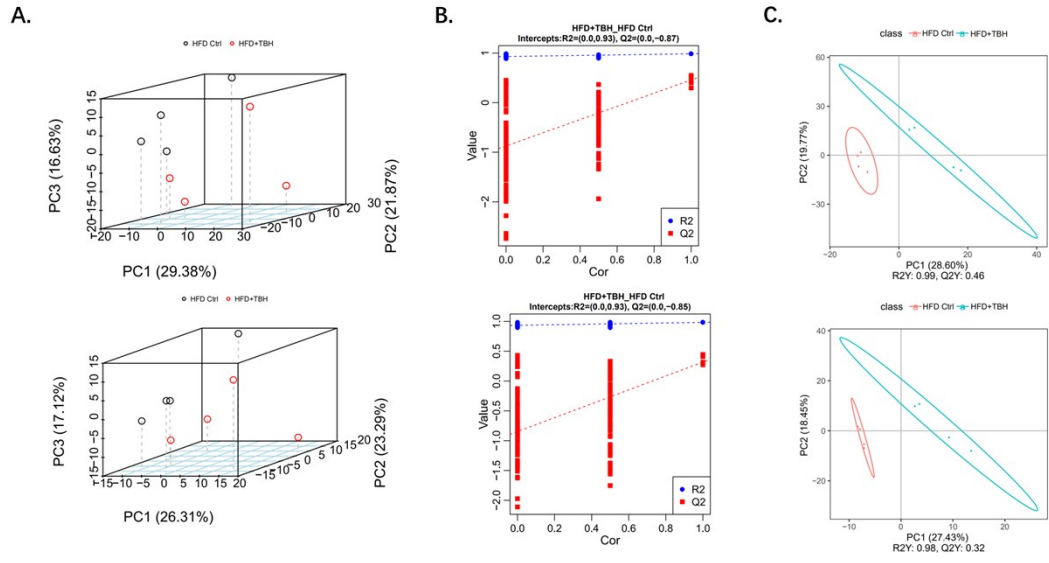
**Supplementary data Figure 4.** The effects of Fuzhuan theabrownin on the gut microbiota metabolites in HFD-fed mice. (A) Principal Component Analysis (PCA) (the upper frame is the positive ion mode; the lower frame is the negative ion mode). (B) PLS-DA to obtain a dispersion point plot (the upper frame is the positive ion mode; the lower frame is the negative ion mode). (C) Sort the verification plot (the upper frame is the positive ion mode; the lower frame is the negative ion mode). n=4 mice per group.