# SUPPORTING INFORMATION

## S1. Methods

**S1.1 The extraction and purification of BLPs.** The extraction and purification of BLPs were done based on our previous studies.[1-3] In brief, the Chinese bayberry leaves were dried at 40°C for 12 h and then ground well into a powder by milling. The finely ground powder (1 kg) was extracted with 70% aqueous acetone (10 L) containing 0.1% (w/v) ascorbic acid at room temperature for 12 h. The extraction was performed two times. The acetone extracts were pooled and rotary-evaporated under vacuum at 40°C to remove acetone. The aqueous phase was recovered and washed with hexane and dichloromethane to remove nonpolar material, and then the organic solvents were evaporated under vacuum. The aqueous phase was lyophilized to dryness to obtain the crude bayberry leaf extracts (CBLPs). The CBLPs were adsorbed on an HPD-500 column and washed by 90% ethanol. The 90% ethanol elute was evaporated under vacuum and the aqueous phase was lyophilized to dryness to obtain the resin purified BLPs (RPBLPs). Then, the RPBLPs was loaded onto a Sephadex LH-20 column, and eluted stepwise with 50% methanol to elute pigments and sugars, 90% methanol to remove most flavonoids, and 70% acetone to obtain the purified BLPs.

**S1.2 Gut Microbiota Analysis.** The 16S rRNA gene comprising the V3-V4 regions was amplified. The following thermocycler protocol was used: 95 °C for 5 min, 25 cycles of 95 °C for 30 s, 50 °C for 30 s and 72 °C for 40 s, and a final extension at 72 °C for 7 min. The amplification was confirmed by 2% gel electrophoresis. High-throughput pyrosequencing of the PCR products was performed on an Illumina MiSeq platform at RiboBio Co, Ltd. (Guangzhou, China). Paired-end reads from the original DNA fragments were merged using FLASH (V1.2.8) and were assigned to each sample based on the unique barcodes. Operational taxonomic units (OTUs) were chosen at 97% nucleotide similarity level against Greengenes database.[4] Alpha diversity indexes (Chao1, Shannon, Simpson) were calculated using QIIME.[5] Heatmaps and Principal component analysis (PCA) was generated according to the abundance of OTUs using R (version 3.2.3). Hierarchical clustering analysis was calculated based on the data matrix of the Unweighted Pair Group Method with Arithmetic Mean (UPGMA). Prediction of functional genes of KEGG pathways was performed with Phylogenetic Investigation of Communities by Reconstruction of Unobserved States (PICRUSt).

Taxonomic biomarkers were performed using the linear discriminant analysis (LDA) effect size (LEfSe) analysis with an LDA score above 2 set as the threshold for significance.

**S1.3 Short-Chain Fatty Acids (SCFA) Analysis.** SCFA was analyzed using a 7890A gas chromatograph (GC) (Agilent Technologies, Palo Alto, CA, USA) with a HP-INNOWAX column (30 m × 0.25 mm, 0.25 μm) and flame ionization detector (Agilent Technologies, CA, USA). SCFA was extracted with a previous method with slight modification.[6] Cecal content (100 mg) was diluted with 700 μL of 0.1 M $H_2SO_4$ and homogenized on ice. Afterwards, the mixture was centrifuged at 10,000 g at 4 °C for 10 min. The supernatant was obtained and filtered through a 0.45 μm micropore filter and was transferred to a GC vial prior to injection into the GC instrument. $N_2$ was used as the carrier gas at the flow rate of 1.2 mL/min. The temperature of the injection port and the flame ionization detector was 240 °C. The oven temperature was maintained at 100 °C for 0.5 min and increased to 180 °C at 4 °C/min. The injection volume was 1 μL with 10:1 split. SCFA concentration of samples was calculated based on the retention time and the integrated peaks with the standard curves of acetate, propionate, butyrate, isobutyrate, valerate and isovalerate (Sigma-Aldrich, MO, USA).

**S2. Results**

**Table S1. Diet composition of chow diet (CD) and high fat diet (HFD)**

| **Nutrients (g/100g)** | **CD, Product #W59840608** |
|---|---|
| Crude fiber | 3.3 |
| Crude protein | 19.2 |
| Crude fat | 6.6 |
| Water | 9.9 |
| Ash | 5.8 |
| Potassium | 0.85 |
| Calcium | 1.11 |
| Total | 46.76g/100g |
| | |
| **Nutrients (g/100g)** | **HFD, Product #D12492** |

| | |
|---|---|
| Protein | 26.2 |
| Carbohydrate | 26.3 |
| Fat | 34.9 |
| Total | 87.4g/100g |
| **Ingredient (g)** | |
| Casein, 30 Mesh | 200 |
| L-Cystine | 3 |
| Maltodextrin 10 | 125 |
| Sucrose | 68.8 |
| Cellulose, BW200 | 50 |
| Soybean Oil | 25 |
| Lard | 245 |
| Mineral Mix S10026 | 10 |
| DiCalcium Phosphate | 13 |
| Calcium Carbonate | 5.5 |
| Potassium Citrate, 1 H2O | 16.5 |
| Vitamin Mix V10001 | 10 |
| Choline Bitartrate | 2 |
| FD&C Blue Dye #1 | 0.05 |
| Total | 773.85 |

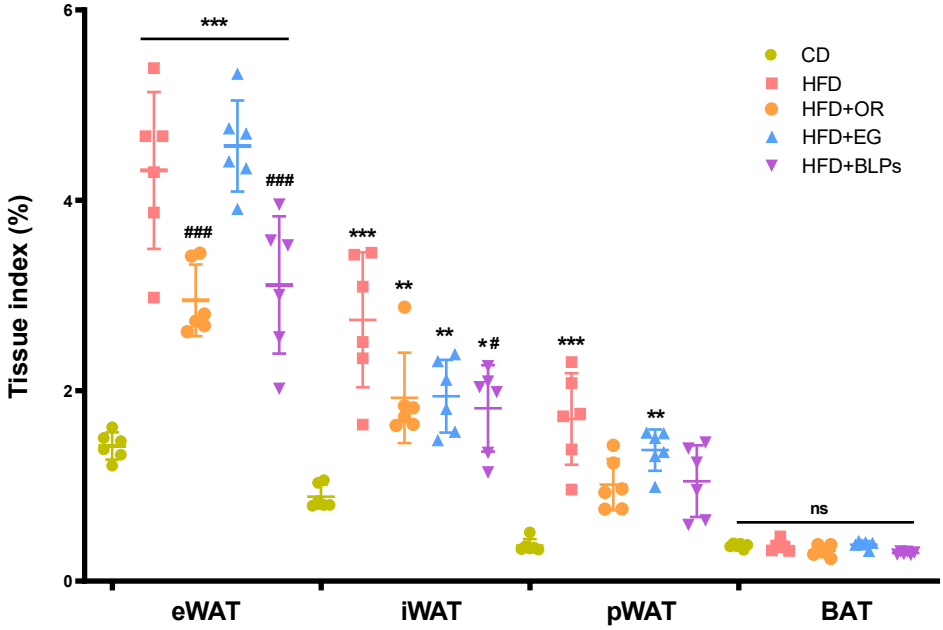


**Fig. S1** Tissue index of eWAT, iWAT, pWAT and BAT of mice. Results are expressed as mean ± SD (n = 6). (*)(**)(***) $p < 0.05$, 0.01, 0.001, compared with the CD group and (#)(##)(###) $p < 0.05$, 0.01, 0.001, compared with the HFD group. Multiple comparisons were performed by one-way analysis of variance (ANOVA) followed by Turkey's test.

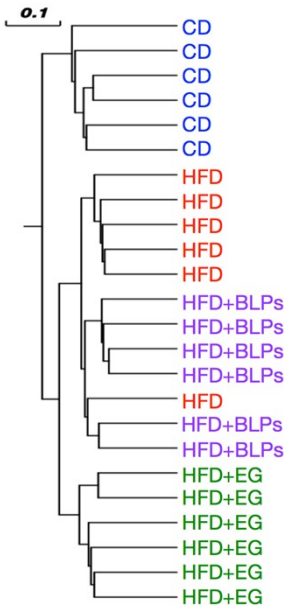


**Fig. S2** Hierarchical clustering analysis of cecal microbiota of mice from different groups was calculated based on the data matrix of UPGMA. The distance of a vertical line indicates the differences of various samples.

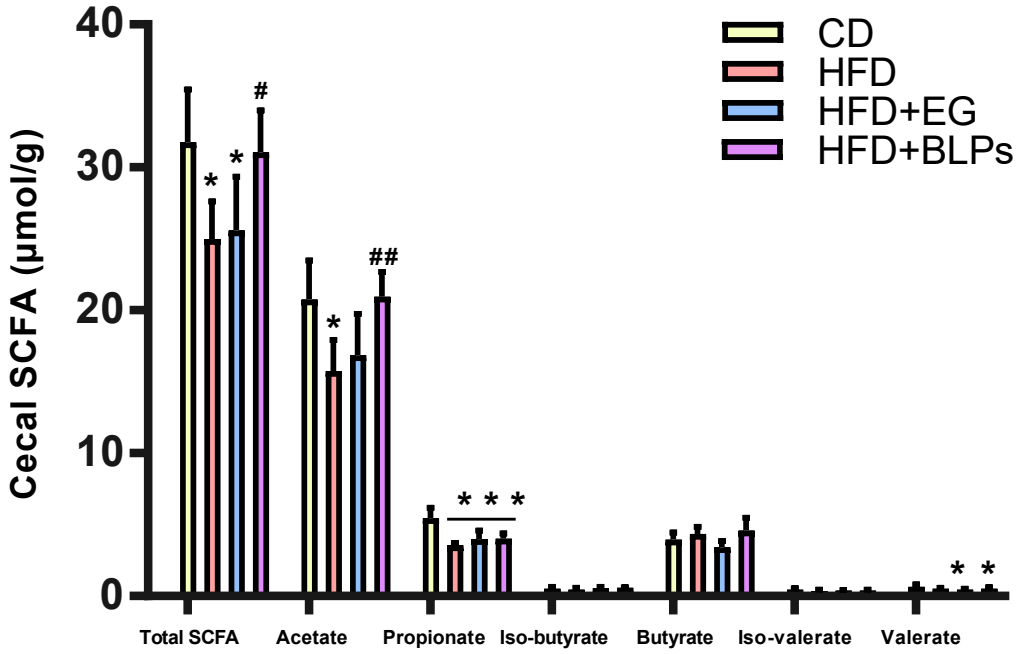


**Fig. S3 Production of SCFA in the ceca of mice.** Cecal contents of mice were extracted and analyzed by GC based on the standard curves of acetate, propionate, iso-butyrate, butyrate, iso-valerate and valerate. Results are expressed as mean ± SD (n = 6). (*)(**)(***) $p < 0.05, 0.01, 0.001$, compared with the CD group and (#)(##)(###) $p < 0.05, 0.01, 0.001$, compared with the HFD group. Multiple comparisons were performed by one-way analysis of variance (ANOVA) followed by Turkey's test.

**Table S2. α-diversity of mice fed with CD, HFD, HFD+EG and HFD+BLPs**

| □ | CD | HFD | HFD+EG | HFD+BLPs |
|---|---|---|---|---|
| Chao 1 | 1215.96±57.65 | 993.28.67±31.75$^{***}$ | 1059.88±50.83$^{**}$ | 1048.26±29.02$^{**}$ |
| Shannon | 6.88±0.21 | 5.47±0.17$^{***}$ | 6.36±0.37$^{*\#\#\#}$ | 6.01±0.09$^{***\#}$ |
| Simpson | 0.97±0.02 | 0.93±0.01$^{***}$ | 0.96±0.02$^{\#}$ | 0.94±0.01$^{**}$ |
| Observed Species | 857±68 | 734±28$^{**}$ | 737±71$^{**}$ | 751±32$^{*}$ |
| Goods Coverage | 0.997 | 0.997 | 0.997 | 0.997 |

Results are expressed as mean ± SD (n=6). (*)(**)(***) $p < 0.05, 0.01, 0.001$, compared with the CD group and (#)(##)(###) $p < 0.05, 0.01, 0.001$, compared with the HFD group. Multiple comparisons were performed by one-way analysis of variance (ANOVA) followed by Turkey's test.

**Table S3. PCR primers used in the present study**

| Gene | Sequence (5' to 3') | |
|---|---|---|
| ACC | Forward | AGCAGATCCGCAGCTTG |
| | Reverse | ACCTCTGCTCGCTGAGTGC |
| CPT1a | Forward | CTCCGCTCGCTCATTCCG |
| | Reverse | TGTGAACTGGAAGGCCACAG |
| FAS | Forward | TTCCAAGACGAAAATGATGC |
| | Reverse | AATTGTGGGATCAGGAGAGC |
| GAPDH | Forward | GCATCCACTGGTGCTGCC |
| | Reverse | TCATCATACTTGGCAGGTTTC |
| HMGCR | Forward | ATTCTGGCAGTCAGTGGGAACT |
| | Reverse | CCTCGTCCTTCGATCCAATTTA |
| IL-6 | Forward | CCGGAGAGGAGACTTCAC |
| | Reverse | TCCACGATTTCCCAGAGA |
| Occludin | Forward | ATGTCCGGCCGATGCTCTC |
| | Reverse | TTTGGCTGCTCTTGGGTCTGTAT |
| PPARα | Forward | TCACGCATGTGAAGGCTGT |
| | Reverse | AATCTTGCAGCTCCGATCACA |
| SREBP-1c | Forward | CCGAGATGTGCGAACTGGA |
| | Reverse | ATAGGGGGCGTCAAACAGG |
| TNF-α | Forward | GCCAACGGCATGGATCTCAA |
| | Reverse | TCTTGACGGCAGAGAGGAGG |
| ZO-1 | Forward | ACCCGAAACTGATGCTGTGGATAG |
| | Reverse | AAATGGCCGGGCAGAACTTGTGTA |

**References:**


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2. Y. Fu, L. P. Qiao, Y. M. Cao, X. Z. Zhou, Y. Liu and X. Q. Ye, *Plos One*, 2014, **9**.
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