## Oral glucose tolerance test, insulin tolerance test and the insulin resistance index

Blood samples were collected and the glucose was measured using a glucometer (Sannuo Biological Transmission Co., Ltd. Changsha, China). The oral glucose tolerance test: the mice were fasting for a whole night, and then orally administered glucose solution (2 g/kg body weight) at week 10. Their glucose was determined at 0, 15, 30, 60, 90 and 120 min after glucose administration. The insulin tolerance test: After fasting 6 h, the mice were intraperitoneally injected with insulin (0.5 U/kg body weight, Novolin R, Novo Nordisk) at week 11. Glucose was determined at 0, 15, 30, 60, 90 and, 120 min after insulin injection. The total glucose areas under the curve (AUC) were calculated using the trapezoidal rule. The insulin was tested using ELISA (Xin Le Biotechnology Co., Ltd. Shanghai, China).

HOMA-IR = (fasting insulin levels × fasting blood glucose)/22

## Blood serum analysis

The serum levels of triglyceride (TG), total cholesterol (TC), LDL cholesterol (LDL-C), aspartate aminotransferase (AST), alanine aminotransferase (ALT), C-reactive protein (CRP) and creatinine (CRE) were determined using Hitachi-7180 automatic biochemical analyzer (Tokyo, Japan). The serum levels of adiponectin, LPS, interleukin-1β (IL-1β), interleukin-6 (IL-6), tumor necrosis factor-alpha (TNF-α) were tested using ELISA (Xin Le Biotechnology Co., Ltd. Shanghai, China).

## Morphology of the liver and epididymal fat

After mice were sacrificed, the liver and epididymal fat were subsequently fixed in 4% paraformaldehyde overnight at 4°C, and then embedded in paraffin for hematoxylin and eosin (H&E) staining analysis. The stained area was viewed and photographed using a microscope (Olympus Corporation, Tokyo, Japan) under the objective.

## Quantitative PCR analysis

Total RNA was extracted from liver and epididymal fat using RNAiso Plus reagent (TaKaRa, Dalian, China). Two µL RNA after an evaluation of quality determined using a Micro-Spectrophotometer Nano-200 was used to synthesize cDNA with the Fast King RT Kit (With gDNase, TIANGEN, Beijing, China). Two µL of the diluted cDNA (1:10) was done quantitative PCR using SYBR Green BioEasy Master mix (BIOER, Hangzhou, China) and a CFX96 Touch™ Real-Time PCR Detection System (Bio-Rad). The sequences of the primers used for Real Time qPCR of this study are shown in Table S2. The level of mRNA expression was normalized with housekeeping gene *β-actin*, and data analysis was using the $2^{-\Delta\Delta Ct}$ method.

**Short-chain fatty acid concentration of feces**

Two hundred mg fecal samples were homogenized with 2 mL distilled water and centrifuged at 4°C at 10000 ×g for 10 min. Taken 1 mL supernatants and acidified by adding 200 µL 50% $H_2SO_4$ (v/v). After vortexing and standing for 5 min, 1 mL diethyl ether was added, and the mixed solution was incubated at 4°C for 30 min, and then the samples were centrifuged at 4°C (10000 ×g, 10 min). The organic phase was filtered using a 0.22 µm nylon filter and collected for gas chromatography analysis (GC-2014C, Shimadzu Corporation, Japan; 30 m × 0.25 µm × 0.25 µm RTX-wax column; flame ionization detector). The initial temperature was 50°C for 1 min, then increased 120°C at 15°C/min, 170°C at 5°C/min, 240°C at 15°C/min, and then held at 3 min. The injector temperature was 250°C and the detector temperature was 270°C.

Table S1 The chemical sensors corresponding to different types of volatile substances in electronic nose

| **Sensor name** | **Sensor sensitives** |
|---|---|
| W1C | Sensitive to aromatic organic compounds |
| W5S | Sensitive to nitrogen oxides |
| W3C | Sensitive to ammonia and aromatic compounds |
| W6S | Sensitive to hydrogen |
| W5C | Sensitive to alkanes, aromatic compounds, and nonpolar organic compounds |
| W1S | Sensitive to methane |
| W1W | Sensitive to sulfides and terpenes |
| W2S | Sensitive to alcohol and partially sensitive to aromatic compounds |
| W2W | Sensitive to aromatic compounds and organic sulfides |
| W3S | Sensitive to alkanes |

Table S2. Sequences of the primers used for quantitative Real-Time PCR

| Target gene | Forward primer (5'→3') | Revere primer (5'→3') | Product Size (bp) | Accession number |
|---|---|---|---|---|
| **TNF-α** | CCCTCACACTCAGATCATCTTCT | GCTACGACGTGGGCTACAG | 61 | NM_013693.3 |
| **IL-1β** | CCTGCAGCTGGAGAGTGTGGAT | TGCTCTGCTTGTGAGGTGCTG | 150 | NM_008361.4 |
| **IL-6** | GGCCTTCCCTACTTCACAAG | ATTTCCACGATTTCCCAGAG | 126 | NM_001314054.1 |
| **FAS** | GGAGGTGGTGATAGCCGGTAT | TGGGTAATCCATAGAGCCCAG | 140 | NM_007988.3 |
| **Fabp2** | TTCTCAGAGCCTGGAGCAAC | GATGACGAATGAGCCTGGCA | 86 | NM_007980.3 |
| **CD36** | CAGATGACGTGGCAAAGAAC | TGGCTCCATTGGGCTGTA | 144 | NM_001159558.1 |
| **PPARγ** | CGCTGATGCACTGCCTATG | ATGCGAGTGGTCTTCCATCA | 124 | NM_011146.3 |
| **MCP-1** | CAGGTCCCTGTCATGCTTCT | CCCATTCCTTCTTGGGGTCA | 121 | NM_011333.3 |
| **Srebp-1c** | GATCAAAGAGGAGCCAGTGC | TAGATGGTGGCTGCTGAGTG | 191 | NM_001358315.1 |
| **β-actin** | GGACTGTTACTGAGCTGCGTT | CGCCTTCACCGTTCCAGTT | 209 | NM_007393.5 |

Table S3. OAV analysis of aroma characteristics of different teas

| **Compounds** | **Odor detection thresholds** | **OAV** | |
|---|---|---|---|
| | | **FBT** | **MFBT** |
| Acetic acid | 180 | 0.0131 | - |
| Tetradecanoic acid | 10.0 | 0.0653 | - |
| n-Hexadecanoic acid | >10 | - | <0.4294 |
| Benzene | 2 | - | 0.1160 |
| Toluene | 1 | 0.6720 | 0.4340 |
| o-Xylene | 0.45023 | 1.9546 | - |
| Naphthalene, 1-methyl- | 0.02 | 63.6000 | - |
| Naphthalene, 2-methyl- | 0.01 | - | 27.9000 |
| Hexanoic acid, methyl ester | 0.087 | - | 2.6782 |
| methyl salicylate | 40 | - | 0.0165 |
| 2-Heptanone | 10 | 0.3958 | 0.1708 |
| 5-Hepten-2-one, 6-methyl- | 0.05 | 66.1400 | 81.0200 |
| 2-Octanone | 0.0145 | - | 16.6897 |
| Cyclohexanone, 2,2,6-trimethyl- | 0.1 | - | 19.7300 |
| Isophorone | 11.9 | - | 0.0715 |
| 3-Buten-2-one, 4-(2,6,6-trimethyl-1-cyclohexen-1-yl)- | 0.0084 | - | 156.7857 |
| Propanal, 2-methyl- | 0.018 | - | 41.1667 |
| Butanal, 3-methyl- | 1.1 | - | 4.0136 |
| Butanal, 2-methyl- | 0.0125 | - | 396.1600 |
| Pentanal | 0.012 | - | 50.0833 |
| Hexanal | 5 | 1.7144 | 1.8476 |
| Benzaldehyde | 0.33 | 5.3394 | 10.0364 |
| Benzeneacetaldehyde | 0.06 | - | 41.1833 |
| 2-Octenal, (E)- | 0.003 | 223.3333 | - |
| Nonanal | 0.02 | 418.9500 | - |
| Decanal | 0.03 | 86.0667 | 13.2333 |
| 1-Cyclohexene-1-carboxaldehyde, 2,6,6-trimethyl- | 0.003 | - | 396.3333 |
| 1,3-Butanediol | 10-20 | 0.0234-0.1172 | - |
| 1-Octanol | 0.13 | 7.5231 | 2.7846 |
| trans-Linalool oxide (furanoid) | 0.32 | 13.0750 | 7.5844 |
| Linalool | 6 | - | 0.6598 |
| Furan, 2-methyl- | 27 | | 0.0274 |
| Furan, 2-ethyl- | 8 | 0.1264 | 0.3663 |
| Furan, 2-pentyl- | 0.1 | 16.5100 | 25.4500 |
| D-Limonene | 10 | - | 0.0467 |

Table S4 Go groups and KEGG pathways of the fecal microbial community

| | **Name** | **C** † | **M** | **FBT** | **MFBT** |
|---|---|---|---|---|---|
| Go terms | General function prediction only | 0.113710467 | 0.116098964 | 0.118503906 | 0.117254245 |
| | Carbohydrate transport and metabolism | 0.084216909 | 0.081390349 | 0.087845443 | 0.090216656 |
| | Cell wall/membrane/envelope biogenesis | 0.078210978 | 0.06958315 | 0.067785466 | 0.06850963 |
| | Amino acid transport and metabolism | 0.075418128 | 0.079374974 | 0.078411264 | 0.077216959 |
| | Transcription | 0.072885619 | 0.077720007 | 0.082652813 | 0.083362492 |
| | Translation, ribosomal structure and biogenesis | 0.071404088 | 0.06606493 | 0.067583518 | 0.066132259 |
| | Replication, recombination and repair | 0.067067294 | 0.066305609 | 0.069298966 | 0.067585301 |
| | Function unknown | 0.064256264 | 0.066735186 | 0.068486 | 0.06885251 |
| | Energy production and conversion | 0.05811516 | 0.056685547 | 0.052412073 | 0.052546627 |
| | Signal transduction mechanisms | 0.050526764 | 0.063425676 | 0.057785771 | 0.057507998 |
| | Inorganic ion transport and metabolism | 0.046298273 | 0.043778241 | 0.04209692 | 0.043806594 |
| | Coenzyme transport and metabolism | 0.043459092 | 0.041979707 | 0.038615766 | 0.039132923 |
| | Posttranslational modification, protein turnover, chaperones | 0.034327324 | 0.032012892 | 0.030950259 | 0.03113896 |
| | Nucleotide transport and metabolism | 0.031309332 | 0.029149045 | 0.031196057 | 0.030210787 |
| | Defense mechanisms | 0.029421443 | 0.029438721 | 0.032593564 | 0.031607976 |
| | Lipid transport and metabolism | 0.024022337 | 0.021368399 | 0.020969088 | 0.021715226 |
| | Intracellular trafficking, secretion, and vesicular transport | 0.021657631 | 0.019392593 | 0.017531665 | 0.018374765 |
| | Cell cycle control, cell division, chromosome partitioning | 0.013234919 | 0.013282356 | 0.013824437 | 0.013299603 |
| | Cell motility | 0.010937049 | 0.015853881 | 0.012154624 | 0.011681039 |

| | | | | | |
|---|---|---|---|---|---|
| | Secondary metabolites biosynthesis, transport and catabolism | 0.0092763 | 0.010038628 | 0.009059319 | 0.009552615 |
| | Chromatin structure and dynamics | 9.08E-05 | 0.000197598 | 0.000105821 | 0.000116379 |
| | Cytoskeleton | 7.90E-05 | 7.10E-05 | 8.75E-05 | 0.000102488 |
| | RNA processing and modification | 7.48E-05 | 5.26E-05 | 4.97E-05 | 7.59E-05 |
| | Extracellular structures | 1.63E-08 | 1.79E-08 | 5.65E-08 | 6.74E-08 |
| KEGG pathway | Carbohydrate metabolism | 0.150377 | 0.15177 | 0.157306 | 0.159428 |
| | Global and overview maps | 0.137685 | 0.135496 | 0.134312 | 0.135548 |
| | Amino acid metabolism | 0.110041 | 0.10812 | 0.10853 | 0.108848 |
| | Energy metabolism | 0.072048 | 0.0701 | 0.069133 | 0.069338 |
| | Metabolism of cofactors and vitamins | 0.06606 | 0.064904 | 0.061181 | 0.061449 |
| | Nucleotide metabolism | 0.060034 | 0.057624 | 0.059945 | 0.058854 |
| | Translation | 0.056855 | 0.056007 | 0.057903 | 0.056339 |
| | Replication and repair | 0.048466 | 0.046363 | 0.049156 | 0.048088 |
| | Membrane transport | 0.040192 | 0.052548 | 0.055165 | 0.052718 |
| | Lipid metabolism | 0.032912 | 0.030964 | 0.031176 | 0.032458 |
| | Glycan biosynthesis and metabolism | 0.032874 | 0.024979 | 0.024672 | 0.025695 |
| | Signal transduction | 0.027462 | 0.033116 | 0.028668 | 0.028576 |
| | Folding, sorting and degradation | 0.022027 | 0.021419 | 0.021276 | 0.021307 |
| | Metabolism of other amino acids | 0.021787 | 0.020542 | 0.021319 | 0.021387 |
| | Metabolism of terpenoids and polyketides | 0.018733 | 0.018362 | 0.019261 | 0.018892 |
| | Xenobiotics biodegradation and metabolism | 0.015636 | 0.017327 | 0.016741 | 0.017426 |
| | Biosynthesis of other secondary metabolites | 0.014312 | 0.013377 | 0.013398 | 0.013608 |
| | Cell motility | 0.012535 | 0.021004 | 0.015552 | 0.01429 |
| | Drug resistance | 0.008761 | 0.007556 | 0.007608 | 0.00763 |
| | Infectious diseases: Bacterial | 0.007957 | 0.008284 | 0.00797 | 0.007599 |
| | Cancers: Overview | 0.007822 | 0.007408 | 0.007775 | 0.007892 |
| | Cell growth and death | 0.007743 | 0.00749 | 0.00731 | 0.007223 |
| | Transport and catabolism | 0.006946 | 0.004547 | 0.004374 | 0.00484 |
| | Endocrine system | 0.004884 | 0.004855 | 0.004673 | 0.004778 |

| | | | | | |
|---|---|---|---|---|---|
| | Nervous system | 0.003344 | 0.003573 | 0.003716 | 0.003691 |
| | Neurodegenerative diseases | 0.002423 | 0.002052 | 0.001852 | 0.001981 |
| | Transcription | 0.002373 | 0.002466 | 0.002587 | 0.002501 |
| | Endocrine and metabolic diseases | 0.00185 | 0.001553 | 0.001605 | 0.00163 |
| | Environmental adaptation | 0.001818 | 0.002192 | 0.001991 | 0.001933 |
| | Immune system | 0.001339 | 0.001296 | 0.001355 | 0.00134 |
| | Cancers: Specific types | 0.000782 | 0.000964 | 0.001008 | 0.000926 |
| | Immune diseases | 0.000659 | 0.000598 | 0.000649 | 0.000624 |
| | Digestive system | 0.000504 | 0.000366 | 0.000257 | 0.000297 |
| | Excretory system | 0.000436 | 0.000222 | 0.000225 | 0.000323 |
| | Infectious diseases: Parasitic | 0.000166 | 0.000152 | 0.000142 | 0.000218 |
| | Circulatory system | 0.000107 | 7.33E-05 | 6.21E-05 | 7.26E-05 |
| | Substance dependence | 3.65E-05 | 0.000318 | 0.000136 | 0.000238 |
| | Infectious diseases: Viral | 1.31E-05 | 1.37E-05 | 1.24E-05 | 1.34E-05 |

[†] C, mice fed with standard diet; M, mice fed with high-fat diet and 10% fructose in drinking water (HFFD); FBT, mice fed with HFFD and FBT; MFBT, mice fed with HFFD and MFBT.

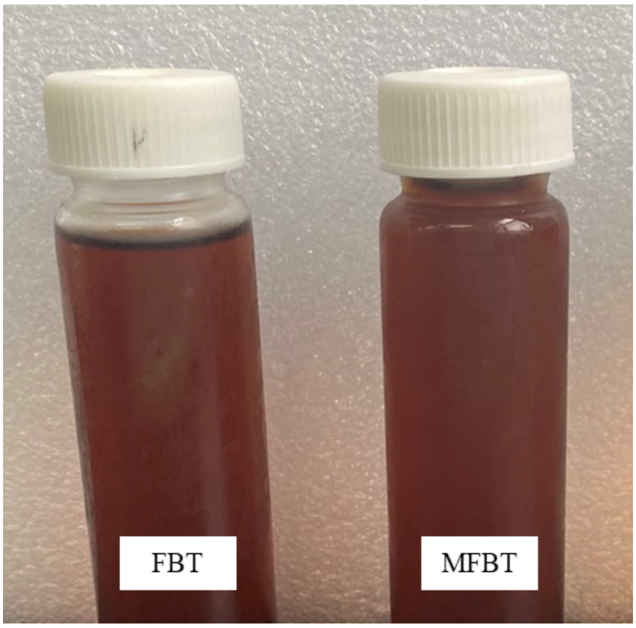

Fig. S1. The color of the FBT and MFBT.

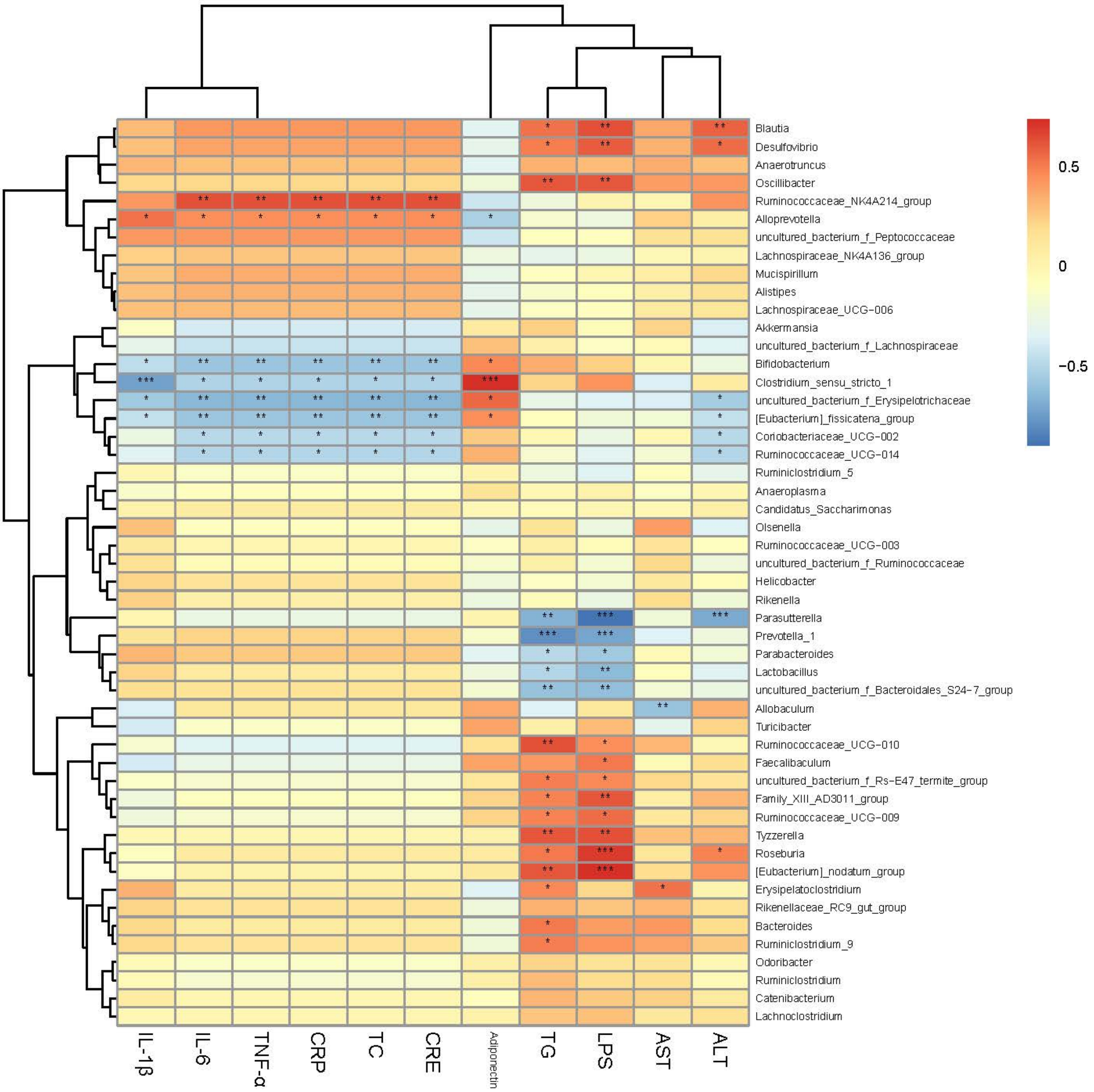

Fig. S2. Correlation analysis between obesity-related parameters and gut microbiota at the genus level. The color ranges from blue to red, indicating the change in correlation from negative to positive. $^{*}$, $^{**}$, and $^{***}$ represent $0.01< P \leq 0.05$, $0.001 < P \leq 0.01$, and $P \leq 0.001$, respectively.