**Supplementary data**

Table S1 Ingredients of the high fat and low fat diet.

|  |  |  |
| --- | --- | --- |
| Item | High fat diet | Low fat diet |
| Casein L-cystine, g | 276 | 194 |
| Carbohydrate dextrin sucrose, g | 250 | 0 |
| Corn starch, g | 0 | 673 |
| Lard, g | 341 | 0 |
| Soybean oil, g | 0 | 40 |
| Fiber (Cellulose), g | 68 | 48 |
| Mineral and vitamin mixture, g | 65 | 45 |
| Antioxidant (TBHQ), g | 0.07 | 0.01 |
| Total, g | 1000 | 1000 |
| Energy，kcal/g | 5.1 | 3.6 |
| % kcal from Protein | 19% | 19% |
| % kcal from Carbohydrate | 21% | 71% |
| % kcal from Fat | 60% | 10% |

Table S2 Primer sequences used for qRT-PCR

|  |  |  |  |
| --- | --- | --- | --- |
| Name |  | Sequences 5’-3’1 | Source |
| UCP-1 | F2 | GGCCCTTGTAAACAACAAAATAC | Li, *et al.*, 2022 [3] |
|  | R | GGCAACAAGAGCTGACAGTAAAT |
| PPARα | F | CGTCACGGAGCTCACAGAAT | Clifford, et al., 2021 [4] |
| R | ACTCGCGTGTGATAAAGCCA |
| Mafg | F | GACCCCCAATAAAGGAAACAA |
|  | R | TCAACTCTCGCACCGACA |
| Scd1 | F | CCGGAGACCCCTTAGATCGA |
|  | R | TAGCCTGTAAAAGATTTCTGCAAACC |
| Lpin1 | F | CCTTCTATGCTGCTTTTGGGAACC |
|  | R | GTGATCGACCACTTCGCAGAGC |
| Dgat2 | F | GGCGCTACTTCCGAGACTAC |
|  | R | TGGTCAGCAGGTTGTGTGTC |
| Srebp1c | F | GGAGCCATGGATTGCACATT |
|  | R | GGCCCGGGAAGTCACTGT |
| Pgc1α | F | AAACTTGCTAGCGGTTCTCAC |
|  | R | GGCAATCCGTCTTCATCCAC |
| PPARγ | F | GCCCTTTGGTGACTTTATGG |
|  | R | CAGCAGGTTGTCTTGGATGT |
| β-actin | F | GTTGGTTGGAGCAAACATC |  |
|  | R | CTTATTTCATGGATACTTGGAATG |  |

1 Primer sequences are displayed in the 5’ to 3’ direction.

2 F, forward primer; R, reverse primer.

Table S3 The dimension of particle of inulin with different polymerized degree

|  |  |  |
| --- | --- | --- |
| No. | Diameter of inulin powder, μm | |
| Low polymerized degree | High polymerized degree |
| 1 | 77.733 | 24.765 |
| 2 | 76.126 | 23.112 |
| 3 | 68.653 | 24.753 |
| 4 | 74.019 | 20.138 |
| 5 | 96.099 | 19.567 |
| 6 | 79.508 | 29.68 |
| 7 | 86.551 | 10.415 |
| 8 | 159.816 | 19.453 |
| 9 | 106.815 | 11.609 |
| 10 | 104.564 | 21.958 |
| 11 | 104.666 | 20.198 |
| 12 | 67.165 | 10.415 |
| 13 | 132.868 | 21.307 |
| 14 | 66.848 | 12.798 |
| 15 | 74.823 | 19.377 |
| 16 | 66.509 | 14.608 |
| 17 | 74.019 | 8.313 |
| 18 | 59.057 | 9.969 |
| 19 | 42.517 | 12.964 |
| 20 | 50.78 | 7.579 |
| 21 | 52.807 | 19.839 |
| 22 | 76.907 | 11.035 |
| 23 | 41.053 | 14.445 |
| Average | 79.996 | 16.882 |

Table S4 The detailed wavenumber of FTIR spectra of inulin with different degree of polymerization

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Low degree of polymerization inulin | | |  | High degree of polymerization inulin | | |
| Peak position, cm-1 | Intensity | interpretation |  | Peak position, cm-1 | Intensity | interpretation |
| 599.22 | 0.138 | OH out-of-pla[1]ne bend |  | 598.40 | 0.176 | OH out-of-plane bend |
| 781.48 | 0.0634 | -(CH2)- rocking |  | 821.70 | 0.114 | 2-ketose |
| 824.84 | 0.096 | 2-ketose[2] |  | 934.06 | 0.344 | OH bending |
| 868.18 | 0.0779 | OH bending |  | 1027.59 | 0.787 | C-O-C stretching |
| 931.45 | 0.196 | OH bending |  | 1133.10 | 0.562 | C-O stretching |
| 1028.74 | 0.572 | C-O-C stretching |  | 1459.03 | 0.321 | C-H bending |
| 1109.68 | 0.402 | C-O stretching |  | 1648.40 | 0.136 | OH bending |
| 1269.26 | 0.204 | C-O stretching |  | 2934.59 | 0.362 | C-H stretching |
| 1340.12 | 0.211 | C-H bending |  | 3385.30 | 0.671 | O-H stretching |
| 1457.07 | 0.251 | C-H bending |  |  |  |  |
| 1646.91 | 0.106 | OH bending |  |  |  |  |
| 2934.90 | 0.285 | C-H stretching |  |  |  |  |
| 3386.55 | 0.58 | O-H stretching |  |  |  |  |

Table S5 The significantly differences of cecal microbiota at different taxonomic levels in mice of different treatment groups

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Microbiota | | Relative Abundance | | | | | |
| LFD | HFD+HDI | HFD+LDI | HFD | SEM | *P* value |
| **Phylum** | |  |  |  |  |  |  |
|  | Verrucomicrobiota | 0.0055 b | 0.2406 a | 0.0781 b | 0.0001 b | 0.00007 | 0.009 |
|  | Fusobacteriota | 0.00069 a | 0.00033 ab | 0.000003 b | 0.000074 b | 0.02265 | 0.005 |
|  | Firmicutes/Bacteroidota | 1.0939 | 2.2978 | 1.6823 | 2.8711 | 0.28637 | 0.136 |
| **Family** | |  |  |  |  |  |  |
|  | Akkermansiaceae | 0.005464 b | 0.240579 a | 0.078111 b | 0.000128 b | 0.0227 | 0.021 |
|  | Fusobacteriaceae | 0.000688 a | 0.000326 ab | 0.000003 b | 0.000074 b | 0.0001 | 0.034 |
| **Genus** | |  |  |  |  |  |  |
|  | Akkermansia | 0.005464 b | 0.240579 a | 0.078111 b | 0.000128 b | 0.022651 | 0.013 |
|  | Bilophila | 0.000115 b | 0.000269 b | 0.002074 a | 0.000068 b | 0.000188 | 0.045 |
|  | Candidatus\_Soleaferrea | 0.000053 b | 0 b | 0 b | 0.000348 a | 0.00002 | 0.006 |
|  | Cetobacterium | 0.000688 a | 0.000326 ab | 0.000003 b | 0.000074 b | 0.00007 | 0.033 |
|  | Colidextribacter | 0.022275 b | 0.016398 b | 0.018153 b | 0.083236 a | 0.00821 | 0.033 |
|  | GCA\_900066575 | 0.001825 b | 0.009164 ab | 0.001404 b | 0.024647 a | 0.002837 | 0.0499 |
|  | Harryflintia | 0.000513 a | 0.000027 b | 0 b | 0.000509 a | 0.00008 | 0.045 |
|  | Incertae\_Sedis | 0.000409 ab | 0.001214 ab | 0.002867 a | 0.000174 b | 0.000334 | 0.043 |
|  | Negativibacillus | 0 b | 0 b | 0 b | 0.000373 ab | 0.00002 | 0.014 |
|  | unclassified\_Christensenellaceae | 0.000223 b | 0.000053 b | 0.000025 b | 0.001333 ab | 0.00015 | 0.049 |
|  | unclassified\_Clostridia | 0.000267 b | 0.000631 ab | 0.001613 a | 0.000197 b | 0.000192 | 0.045 |
|  | unclassified\_Erysipelotrichaceae | 0.003598 a | 0 b | 0.000524 b | 0.002224 ab | 0.000512 | 0.044 |
|  | unclassified\_Lachnospiraceae | 0.080019 a | 0.091354 a | 0.219439 b | 0.198044 b | 0.023523 | 0.039 |
| **Species** | |  |  |  |  |  |  |
|  | Ruminococcaceae\_bacterium\_GD6 | 0.000053 b | 0 b | 0 b | 0.000348 a | 0.00002 | 0.008 |
|  | unclassified\_Akkermansia | 0.005464 b | 0.240579 a | 0.078111 b | 0.000128 b | 0.022651 | 0.017 |
|  | unclassified\_Cetobacterium | 0.000688 a | 0.000326 ab | 0.000003 b | 0.000074 b | 0.00007 | 0.041 |
|  | unclassified\_Colidextribacter | 0.020313 b | 0.016105 b | 0.018083 b | 0.078622 a | 0.007593 | 0.034 |
|  | unclassified\_Lachnospiraceae\_FCS020\_group | 0.000063 a | 0.000943 b | 0.000628 ab | 0.000296 a | 0.000126 | 0.0498 |
|  | unclassified\_Negativibacillus | 0 b | 0 b | 0 b | 0.000373 a | 0.00002 | 0.017 |

Within each row, means without a common letter differ significantly at *P* < 0.05.

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Figure S1 Rarefaction curves (A) and rank abundance plots (B) of cecal microbiota for all samples across different treatment groups. Abbreviations: HFD, high-fat diet treatment group mice; HFDHD, high-fat diet and high-degree polymerization inulin treatment group; HFDLD, high-fat diet and low-degree polymerization inulin treatment group; LFD, low-fat diet treatment group.

A group of colorful candlestick chart

Description automatically generated with medium confidence

Figure S2 Analysis of similarities (ANOSIM) at the operational taxonomic unit (OTU) level (A), phylum level (B), family level (C), and genus level (D). An R value greater than 0 indicates no significant variations within treatment groups, while a *P* value less than 0.05 suggests significant differences among treatment groups regarding β diversity. HFD, high-fat diet treatment group mice; HFDHD, high-fat diet and high-degree polymerization inulin treatment group; HFDLD, high-fat diet and low-degree polymerization inulin treatment group; LFD, low-fat diet treatment group.

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