Supplementary data

Supplemental tables

Supplemental Table 1. Ingredients and chemical composition of diets (as fed basis)

Ingredients（g/kg）	CON[3]	Fiber	SO	Fiber + SO
Corn	810	810	810	810
Soybean meal (44% CP)	155	155	155	155
Fish meal (65% CP)	10	10	10	10
L-Lys HCl (98%)	1.4	1.4	1.4	1.4
Choline chloride (50%)	1.5	1.5	1.5	1.5
Salt	4	4	4	4
Limestone	5.5	5.5	5.5	5.5
Monocalcium phosphate	7.6	7.6	7.6	7.6
Vitamin-mineral premix [1]	5	5	5	5
Soybean oil	0	0	100	100
Inulin (99%)	0	25	0	25
Cellulose (99%)	0	100	0	100
Total	1000	1125	1100	1225
Nutrient composition (g/kg)[2]				
Digestible energy (Mcal/kg)	3.30	2.93	3.79	3.41
Crude protein (CP)	140	124.44	127.27	114.29
Total lysine	7.62	6.77	6.91	6.20
Total tryptophan	1.45	1.29	1.32	1.18
Ether extract	32.1	28.53	29.18	26.20
Calcium	5.5	4.89	5.00	4.49
Total phosphorus	5.2	4.62	4.73	4.24
Soluble fiber	12	32.89	10.91	30.20
Insoluble fiber	112	188.44	101.82	173.06
Total fiber (soluble + insoluble)	124	221.33	112.73	203.27
Daily nutrient intake (g/d)				
Feed intake (g/d)	2400	2700	2640	2940
DE intake (MJ/d)	33.14	33.14	41.92	41.92
Total lysine intake (g/d)	18.28	18.28	18.28	18.28
Total tryptophan intake (g/d)	3.48	3.48	3.48	3.48

Total fiber intake (g/d)	297.6	597.6	297.6	597.6

[1]Vitamin-mineral premix provided the following per kilogram of basal diet: 8000 IU vitamin A, 800 IU vitamin D_3, 30 IU vitamin E, 4 mg vitamin K, 0.16 mg biotin, 2mg folacin, 25 mg niacin, 20 mg pantothenic acid, 10 mg riboflavin, 2 mg thiamin, 1 mg vitamin B6, 20 ug vitamin B12, 16 mg copper, 0.25 mg iodine, 125 mg iron, 30 mg manganese, 0.25 mg selenium, 125 mg zinc.

[2]Values of soluble fiber and insoluble fiber in low-energy low-fiber diet were analyzed data according to the enzymatic-gravimetric method AOAC 991.43.

[3]CON, control, daily intake of 2.4 kg basal diet; Fiber, CON diet plus extra 300 g/d inulin and cellulose at the ratio of 1:4; SO, CON plus extra 240 g/d soybean oil; Fiber + SO, CON diet plus 300 g/d inulin and cellulose (1:4) and 240 g/d soybean oil.

Supplemental Table 2. Oligonucleotide primers relative-Quantitative real-time PCR

Primers	Sequences (5' – 3')	Gene Bank No.
Bax	F: CGCATTGGAGATGAACTGGA R: CCAGTTGAAGTTGCCGTCAG	XM_003127290.5
Bcl-2	F: GCCTTTGTGGAGCTGTATGG R: CCCGTGGACTTCACTTATGG	XM_021099593.1
Caspase-3	F: GCCGAGGCACAGAATTGGACTG R: GCCAGGAATAGTAACCAGGTGCTG	NM_214131.1
TPH-1	F: TGGATCTGAACTGGATGCTG R: CGGTTCCCCAGGTCTTAATC	XM_021083266.1
5-HTR$_{1D}$	F: ATCCAGGGACCCTCCAAGTC R: AGTGTGGAGCTTCCTGGTCA	NM_214158.1
5-HTR$_{2A}$	F: TCTCTCACCACCCTGCTTCT R: TCTCTAGGGACACTGCCATGA	NM_214217.1
5-HTR$_{2B}$	F: CGCCTAACATGGTTGACTGTG R: TGGGCAGAGTTTTGTCCTTGT	NM_001164019.1
5-HTR$_{2C}$	F: TCCGTTTCTCGTCTAGCTGC R: TGGCCTACAGATGCTCATGG	NM_001286590.1
5-HTR$_{7}$	F: CCGTCAGGCAGAATGGCAAG R: TCGTCATTTACGTTCTGCGCC	NM_214085.1
β-actin	F: CCAGCACGATGAAGATCAAGA R: AATGCAACTAACAGTCCGCCTA	XM_003124280.5

TPH-1, Tryptophan hydroxylase 1; 5-HTR, 5-HT receptor.

Supplemental Table 3. The growth performance and age at puberty of gilts fed different energy and dietary fiber levels

Items	CON	Fiber	SO	Fiber + SO	*P*-Value		
					SO	Fiber	SO×Fiber
BW, kg							
Initial	91.7±1.5	91.6±1.5	91.7±1.3	91.7±1.2	0.958	0.974	0.956
At puberty	116.1±4.4	117.4±4.7	115.9±1.9	118.1±2.3	0.939	0.637	0.906
On the 19th day of 4th estrus	155.3±4.7	156.3±4.4	172.6±2.7	175.1±2.7	<0.001	0.652	0.835
ADG, g/d	0.51±0.02	0.50±0.02	0.72±0.02	0.72±0.02	<0.001	0.739	0.841
Backfat thickness, mm							
Initial	9.88±0.43	9.81±0.21	9.88±0.30	9.94±0.24	0.839	1.000	0.839
At puberty	11.94±0.58	11.62±0.28	14.00±0.40	13.56±0.24	<0.001	0.356	0.877
On the 19th day of 4th estrus	16.06±0.78	16.38±0.72	23.50±0.96	20.81±1.03	<0.001	0.190	0.101
Backfat gain	6.19±0.45	6.56±0.64	13.62±0.97	10.88±1.14	<0.001	0.171	0.075
Age, day							
Initial	161.8±0.2	161.2±0.2	161.5±0.2	161.5±0.2	1.000	0.168	0.168
At puberty	207.9±7.4	210.0±8.5	193.2±1.2	197.5±3.5	0.032	0.599	0.861
On the 19th day of 4th estrus	286.4±7.1	291.5±8.6	273.5±1.6	277.8±3.6	0.033	0.436	0.942

Value are expressed as means ± S.E. (n = 8 for each treatment). Within a row, means without a common letter indicate significant difference between diet groups ($P < 0.05$). CON, control, daily intake of 2.4 kg basal diet; Fiber, CON diet plus extra 300 g/d inulin and cellulose at the ratio of 1:4; SO, CON plus extra 240 g/d soybean oil; Fiber + SO, CON diet plus 300 g/d inulin and cellulose (1:4) and 240 g/d soybean oil. BW, body weight; ADG, average daily gain.

Supplemental Table 4. The plasma metabolites in gilts fed different energy and dietary fiber levels

Items					*P*-Value		
	CON	Fiber	SO	Fiber + SO	Fiber	SO	CON
TG, mmol/L	0.29±0.03	0.28±0.03	0.42±0.04	0.33±0.03	0.010	0.142	0.219
NEFA, mmol/L	0.08±0.01^{c}	0.08±0.01^{c}	0.20±0.02^{a}	0.15±0.01^{b}	<0.001	0.061	0.039
TC, mmol/L	1.90±0.14	1.82±0.06	2.24±0.07	1.98±0.08	0.013	0.088	0.315
LDL-C, mmol/L	0.88±0.08	0.79±0.02	0.92±0.06	0.80±0.06	0.714	0.100	0.800
HDL-C, mmol/L	0.84±0.08	0.83±0.03	0.84±0.06	0.92±0.06	0.501	0.625	0.507

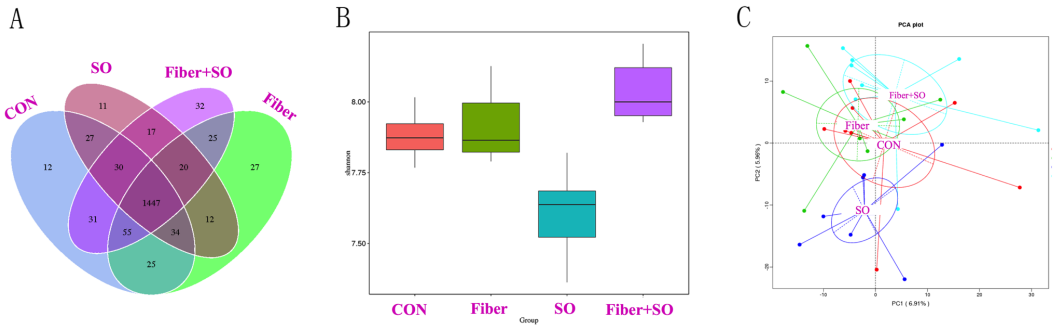
Value are expressed as means ± S.E. (n = 8 for each treatment). Within a row, means without a common letter indicate significant difference between diet groups (P < 0.05). TG = Triglycerides; NEFA = Non-esterified fatty acid; TC = Total cholesterol; LDL-C = Low density lipoprotein cholesterol; HDL-C = High density lipoprotein cholesterol. CON, control, daily intake of 2.4 kg basal diet; Fiber, CON diet plus extra 300 g/d inulin and cellulose at the ratio of 1:4; SO, CON plus extra 240 g/d soybean oil; Fiber + SO, CON diet plus 300 g/d inulin and cellulose (1:4) and 240 g/d soybean oil.

Supplemental Table 5. Raw reads, Tags and OTUs number of four groups

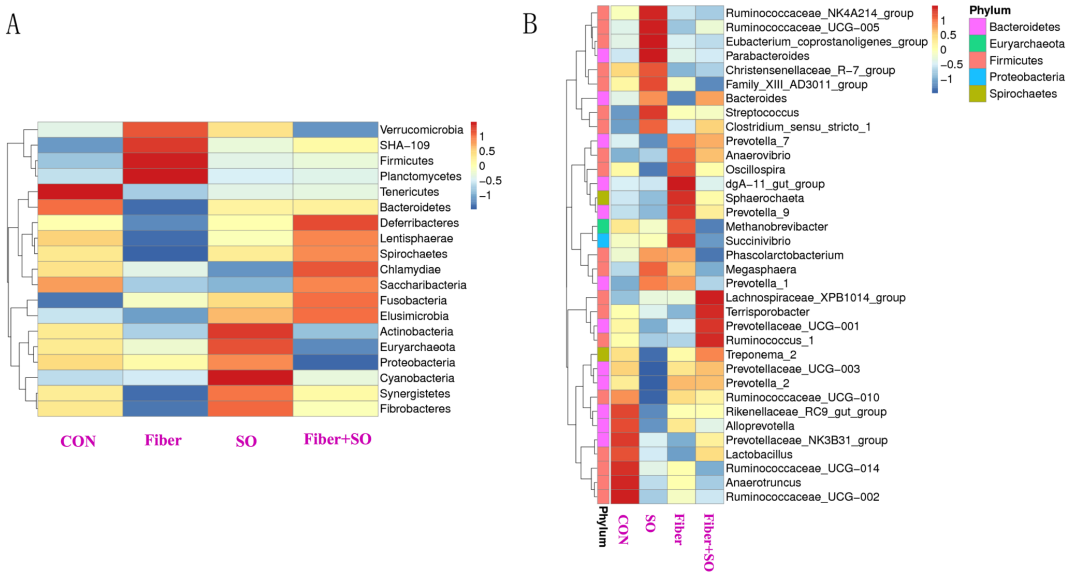
Group	Raw reads	Raw Tags	Effective Tags	OTUs
CON	657587	644468	587325	10324
Fiber	611616	599458	549913	10243
SO	623286	610544	553307	9795
Fiber+SO	652774	639509	586986	10439
Total	2545263	2493979	2277531	40801

Values are expressed as a sum, n = 8 for each group. OTUs, Operational Taxonomic Units. CON, control, daily intake of 2.4 kg basal diet; Fiber, CON diet plus extra 300 g/d inulin and cellulose at the ratio of 1:4; SO, CON plus extra 240 g/d soybean oil; Fiber + SO, CON diet plus 300 g/d inulin and cellulose (1:4) and 240 g/d soybean oil.

Supplemental Figures



Supplemental Figure 1. Venn diagrams and Microbiota alpha diversity and beta diversity comparison among four groups. (A) Venn diagrams were generated to describe the common and unique OTUs among treatments. (B) Shannon index analyses. (C) Principal Component Analysis. Gilts were regarded as the experimental units, n = 8 for each treatment. CON, control, daily intake of 2.4 kg basal diet; Fiber, CON diet plus extra 300 g/d inulin and cellulose at the ratio of 1:4; SO, CON plus extra 240 g/d soybean oil; Fiber + SO, CON diet plus 300 g/d inulin and cellulose (1:4) and 240 g/d soybean oil.



Supplemental Figure 2. Heatmap of abundance of the fecal microbiota composition at the phylum level (A) and the genus level (B). The darker the color, the higher the relative abundance in a row. Gilts were regarded as the experimental units, n = 8 for each treatment. CON, control, daily intake of 2.4 kg basal diet; Fiber, CON diet plus extra 300 g/d inulin and cellulose at the ratio of 1:4; SO, CON plus extra 240 g/d soybean oil; Fiber + SO, CON diet plus 300 g/d inulin and cellulose (1:4) and 240 g/d soybean oil.

Supplemental methods

Microbial analysis

Total bacterial DNA of feces samples were extracted using the MO BIO PowerFecal® DNA Isolation Kit (Catalog No. 12830-50, MO BIO Laboratories, Inc) according to the manufacturer's protocols. Before sequencing, the concentration and purity of the extracted genomic DNA were measured. The integrity of the extracted genomic DNA was determined by electrophoresis on a 1% (w/v) agarose gel. The concentration and purity of the extracted genomic DNA were measured. According to the concentration, DNA was diluted to1ng/μL using sterile water. The DNA samples were sent to Novogene Bioinformatics Technology (Beijing, China) to perform amplicon pyrosequencing on the Illumina HiSeq PE250 platforms. The V4 hypervariable region of the 16S rRNA gene was amplified using 515F and 806R primer (5′-GTGCCAGCMGCCGCGGTAA-3′ and 5′-GGACTACHVGGGTWTCTAAT-3′, respectively). Raw Paired-end reads obtained by Illumina HiSeq sequencing were spliced. The splicing sequences were called raw tags. Quality filtering on the raw tags were performed under specific filtering conditions to obtain the high-quality clean tags (Bokulich et al., 2013) according to the QIIME(V1.7.0, http://qiime.org/index.html) (Caporaso et al., 2010) quality controlled process. And then chimeric filtering to get Effective Tags as shown in Supplemental Table S3. The effective tags were mapped to OTUs using Uparse software (v7.0.1001 http://drive5.com/uparse/) at 97% sequence similarity. Representative sequence for each OUT was screened for further annotation. The Ribosomal Database Project (RDP) classifier Version 2.2 was used to assign a taxonomic rank to each representative sequence. OTUs abundance information were normalized using a standard of sequence number corresponding to the sample with the least sequences. Subsequent analysis of alpha diversity and beta diversity were all performed basing on this output normalized data. The relative abundance of each OTU was examined at different taxonomic levels. At the phylum level, as the sum of the top 10 phyla with relative abundance exceeded 98%, we selected the top 10 phyla for statistical analysis with the control group as the reference. At the genus level, we selected genera with relative abundance of more than 0.2% in at least one sample for statistical analysis.

Serotonin and melatonin analysis

The serotonin concentrations in serum on day 18 of the fourth estrous cycle were analyzed at five different time points (7:00, 9:00, 10:00, 12:00 and 14:00). The grinded proximal colon and ovary tissues within liquid nitrogen were weighed (about 100 mg) and homogenized on ice in EP tubes containing cell lysis buffer (1mL) (RIPA P0013B Beyotime Biotechnology, China) with 1mM proteinase inhibitor PMSF and 0.1% ascorbic acid using ULTRA-TURRAX machine (T10 basic, IKA, Germany) at a speed of 30000 rpm for 40s. Samples were centrifuged at 12,000 g for 30 min at 4 °C and the supernatants were collected. Serotonin levels were detected in clear supernatant of proximal colon tissues and ovary tissues, serum and follicular fluid by ELISA according to the manufacturer instructions (DLD DIAGNOSTIKA GMBH, Hamburg, Germany). The data of proximal colon tissues and ovary tissues were normalized with tissue weight.

Melatonin concentrations in the serum and follicular fluids were measured with a

melatonin ELISA kit (IBL #RE54021) from Hamburg, Germany. The regular method provided by the kit, activating columns with HPLC-grade methanol with centrifugation (1 min at 120 x g) followed by evaporation of the sample with a SpeedVac concentrator. Detection limit for melatonin in this assay is 1.6 pg/mL. Melatonin content was calculated against standard values provided by the manufacturer using the 4-parameter logistic curve.