

Table S1. Calories of feeds used in this study

	Normal diet	Low fiber diet	45% High fat diet
Protein (%)	21.03	24.38	20
Carbohydrate (%)	65.30	62.19	35
Fat (%)	13.67	13.43	45
Kcal/g	4.04	4.02	4.73

TableS2. Changes in body weight, feed intake, water intake and fecal parameters of mice at day 21.

Bioparameters	Treatments			
	Control	Low-fiber diet	High-fat diet	Loperamide
Body weight (g)	27.66±0.34	26.74±0.32	26.85±0.30	26.52±0.49
Food intake (g)	6.89±0.47	4.78±0.37*	4.03±0.31*	6.45±0.44
Water intake (g)	7.71±0.32	7.73±0.92	6.31±0.60	7.41±0.47
Fecal output g ⁻¹ of food (n)	18±0.60	8.80±1.45*	8.68±1.07*	17.51±1.06

*P<0.05

Different letters also indicate significant difference based on Duncan's multiple range test

Table S3. Average number of reads, operational taxonomic units, and structural genes for MiSeq and HiSeq

Samples	MiSeq		HiSeq	
	Reads	OTUs	Reads	Genes
CTL	35,322 (7,756) ^a	149 (20)	26,650,146 (1,164,704)	140,749 (35,318)
HFD	31,474 (5,768)	99 (9)	24,921,520 (437,432)	125,488 (9,837)
LFD	30,570 (5,937)	106 (5)	24,176,031 (1,160,224)	120,265 (22,184)
LPM	36,900 (3,128)	150 (19)	24,245,117 (2,163,476)	82,109 (3,437)

^a Standard deviation

Table S4. Abundance (TPM) and taxa of CTL contigs with higher differential abundance compared to HFD

Lowest common ancestor	buk	ptb	gabD	ACSM
<i>Lactobacillus</i>	0	0	20	0
<i>Lactobacillus johnsonii</i>	0	0	6	0
<i>Lactobacillus johnsonii</i> DPC 6026	0	0	9	0
<i>Lactobacillus reuteri</i> TD1	0	0	3	0
Bacteroidales	362	362	0	0
<i>Parabacteroides distasonis</i> ATCC 8503	65	65	0	0
Bacteria	51	51	0	0
<i>Roseburia hominis</i> A2-183	7	7	0	0
Gamma proteobacteria	7	7	0	0
Unclassified	420	399	38	9
Total	912	891	76	9

Table S5. Abundance (TPM) and taxa of HFD contigs with higher differential abundance compared to CTL

Lowest common ancestor	2.3.1.54	adhE	BDH	gctA	gctB	4.1.3.4	mhpF
<i>Lactococcus lactis</i> subsp. <i>cremoris</i> A76	0	0	72	0	0	0	0
<i>Lactococcus lactis</i> subsp. <i>cremoris</i> NZ9000	18	0	7	0	0	0	0
<i>Lachnoclostridium phytofermentans</i> ISDg	0	0	7	0	0	0	0
<i>Roseburia hominis</i> A2-183	79	71	0	0	0	0	0
<i>Lactococcus lactis</i>	0	29	0	0	0	0	0
Clostridiales	130	48	0	0	0	0	0
Bacteria	3	18	0	0	0	10	0
<i>Lactococcus lactis</i> subsp. <i>cremoris</i> MG1363	0	25	0	0	0	0	0
<i>Mycoplasma leachii</i> PG50	0	17	0	0	0	0	0
<i>Oscillibacter valericigenes</i> Sjm18-20	31	8	0	10	0	0	0
Bacteroidales	449	0	0	0	0	0	0
<i>Bacteroides</i>	286	0	0	0	0	0	0
<i>Thermobacillus composti</i> KWC4	36	0	0	0	0	0	0
<i>Lactococcus lactis</i> subsp. <i>cremoris</i> KW2	31	0	0	0	0	0	0
<i>Clostridium beijerinckii</i> NCIMB 8052	50	0	0	0	0	0	0
<i>Clostridium</i> sp. SY8519	40	0	0	0	0	0	0
Firmicutes	32	0	0	0	0	0	0
<i>Clostridium saccharoperbutylacetonicum</i> N1-4(HMT)	27	0	0	0	0	0	0
<i>Parabacteroides distasonis</i> ATCC 8503	14	0	0	0	0	0	0
Peptococcaceae	10	0	0	0	0	0	0
<i>Clostridium saccharobutylicum</i> DSM 13864	8	0	0	0	0	0	0
<i>Bacteroides thetaiotaomicron</i> VPI-5482	4	0	0	0	0	0	0
Unclassified	2105	1121	443	70	33	14	14
Total	3354	1339	528	80	33	24	14

Table S6. Abundance (TPM) and taxa of CTL contigs with higher differential abundance compared to LFD

Lowest common ancestor	buk	ptb	paaH	fabV	phbB
<i>Oscillibacter valericigenes Sjm18-20</i>	0	0	25	0	0
Bacteria	51	51	0	34	0
<i>Roseburia hominis A2-183</i>	7	7	15	0	0
Bacteroidales	362	362	0	0	0
<i>Parabacteroides distasonis ATCC 8503</i>	65	65	0	0	0
Gamma proteobacteria	7	7	0	0	0
Unclassified	421	400	460	118	4
Total	912	891	499	152	4

Table S7. Abundance (TPM) and taxa of LFD contigs with higher differential abundance compared to CTL

Lowest common ancestor	2.3.1.54	BDH	atoD	paaF	gctA	gctB
<i>Roseburia hominis</i> A2-183	56	26	0	0	27	27
<i>Bacteroides</i>	1085	0	0	0	0	0
<i>Clostridium saccharobutylicum</i> DSM 13864	115	0	0	0	0	0
<i>Bacteroidales</i>	34	0	0	0	0	0
<i>Clostridium lentocellum</i> DSM 5427	13	0	0	0	0	0
<i>Mageeibacillus indolicus</i> UPII9-5	81	0	0	0	0	0
<i>Parabacteroides distasonis</i> ATCC 8503	11	0	0	0	0	0
Bacteria	10	0	0	26	0	0
<i>Lactobacillus salivarius</i> CECT 5713	22	0	0	0	0	0
<i>Bifidobacterium</i>	4	0	0	0	0	0
<i>Oscillibacter valericigenes</i> Sjm18-20	13	0	0	0	10	0
Clostridiales	114	0	0	0	0	0
<i>Akkermansia muciniphila</i> ATCC BAA-835	25	0	0	0	0	0
Firmicutes	50	0	0	0	0	0
<i>Streptococcus equi</i> subsp. zooepidemicus	12	0	0	0	0	0
<i>Rhodanobacter denitrificans</i>	19	0	0	0	0	0
<i>Bacillus cytotoxicus</i> NVH 391-98	13	0	0	0	0	0
<i>Symbiobacterium thermophilum</i> IAM 14863	0	0	11	0	0	0
<i>Bacteroides vulgatus</i> ATCC 8482	84	0	0	0	0	0
<i>Escherichia coli</i> APEC O78	21	0	0	0	0	0
<i>Escherichia coli</i> SE11	17	0	0	0	0	0
<i>Escherichia coli</i> W	16	0	0	0	0	0
Lactobacillaceae	12	0	0	0	0	0
<i>Bacteroides fragilis</i> NCTC 9343	9	0	0	0	0	0
<i>Streptococcus anginosus</i> C238	9	0	0	0	0	0
<i>Fusobacterium nucleatum</i>	8	0	0	0	0	0
Enterobacteriaceae	6	0	0	0	0	0
<i>[Clostridium] saccharolyticum</i> WMI	5	0	0	0	0	0
<i>Escherichia coli</i>	0	0	0	15	0	0
Unclassified	2077	285	205	41	29	28
Total	3940	311	216	81	66	55

Table S8. Abundance (TPM) and taxa of CTL contigs with higher differential abundance compared to LPM

Lowest common ancestor	adh E	ACA DS	paa H	crt	ydi F	ACS M	mhp F	ECH S1	phb B	ato D
<i>[Eubacterium] eligens ATCC 27750</i>	66	0	0	0	0	9	0	0	0	0
<i>Candidatus Arthromitus sp. SFB-rat-Yit</i>	5	0	0	0	0	0	0	0	0	0
<i>Ruminococcus albus 7 = DSM 20455</i>	3	0	0	0	0	0	0	0	0	0
<i>Roseburia hominis A2-183</i>	19	32	15	26	0	0	0	0	0	0
<i>Oscillibacter valericigenes Sjm18-20</i>	0	15	25	0	8	0	0	0	0	0
<i>Lactobacillus</i>	30	0	0	0	0	0	0	0	0	0
<i>[Clostridium] stercorarium subsp. stercorarium DSM 8532</i>	9	0	0	0	0	0	0	0	0	0
<i>Candidatus Arthromitus sp. SFB-mouse-Japan</i>	4	0	0	0	0	0	0	0	0	0
<i>Bacteroides</i>	0	26	0	0	0	0	0	0	0	0
Bacteria	6	14	0	0	0	0	0	0	0	0
<i>Thermanaerovibrio acidaminovorans DSM 6589</i>	6	0	0	0	0	0	0	0	0	0
Firmicutes	6	0	0	0	0	0	0	0	0	0
<i>Lactobacillus johnsonii NCC 533</i>	5	0	0	0	0	0	0	0	0	0
Clostridiales	4	0	0	0	0	0	0	0	0	0
<i>Clostridium sp. SY8519</i>	0	6	0	0	0	0	0	0	0	0
Unclassified	435	422	459	38 1	4	0	9	5	4	3
Total	599	515	499	40 7	11	9	9	5	4	3

Table S9. Abundance and taxa of LPM contigs with higher differential abundance compared to CTL

Lowest common ancestor	ptb	buk	gabD	2.3.3.10
<i>Lactobacillus</i>	0	0	47	37
<i>Lactobacillus johnsonii</i> N6.2	0	0	0	12
<i>Lactobacillus reuteri</i> TD1	0	0	14	4
<i>Lactobacillus johnsonii</i>	0	0	72	12
<i>Arcobacter nitrofigilis</i> DSM 7299	0	0	4	0
<i>Bacteroides</i>	642	642	0	0
<i>Roseburia hominis</i> A2-183	10	10	0	0
<i>Lactobacillus reuteri</i>	0	0	0	6
Bacteroidales	242	242	0	0
<i>Alistipes</i>	8	8	0	0
<i>Mycobacterium smegmatis</i> JS623	0	6	0	0
<i>Lactobacillus johnsonii</i> DPC 6026	0	0	0	10
<i>Lactobacillus johnsonii</i> NCC 533	0	0	22	0
<i>Lactobacillus ruminis</i> ATCC 27782	28	28	0	0
unclassified	544	523	6	0
total	1475	1460	165	82