

Fig. S1 The body weight and food consumption. (A) weekly body weight. (B) weekly food consumption. The results are presented as the mean \pm standard deviation (SD); $n = 5$ for each treatment. *Analysis of variance (ANOVA) was used, significant differences between groups were indicated ($P < 0.05$). Because FMT did not begin until the 6th week, the PD_FMT group was a separated replica of the PD group at the 5th week.

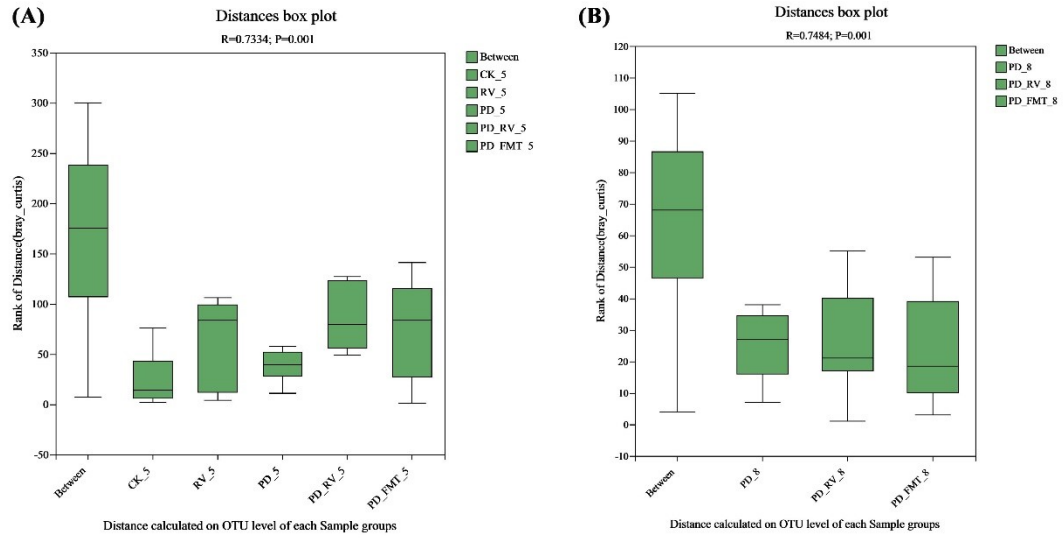


Fig.S2 Analysis of similarities (ANOSIM) at OTU levels at the 5th and 8th week.

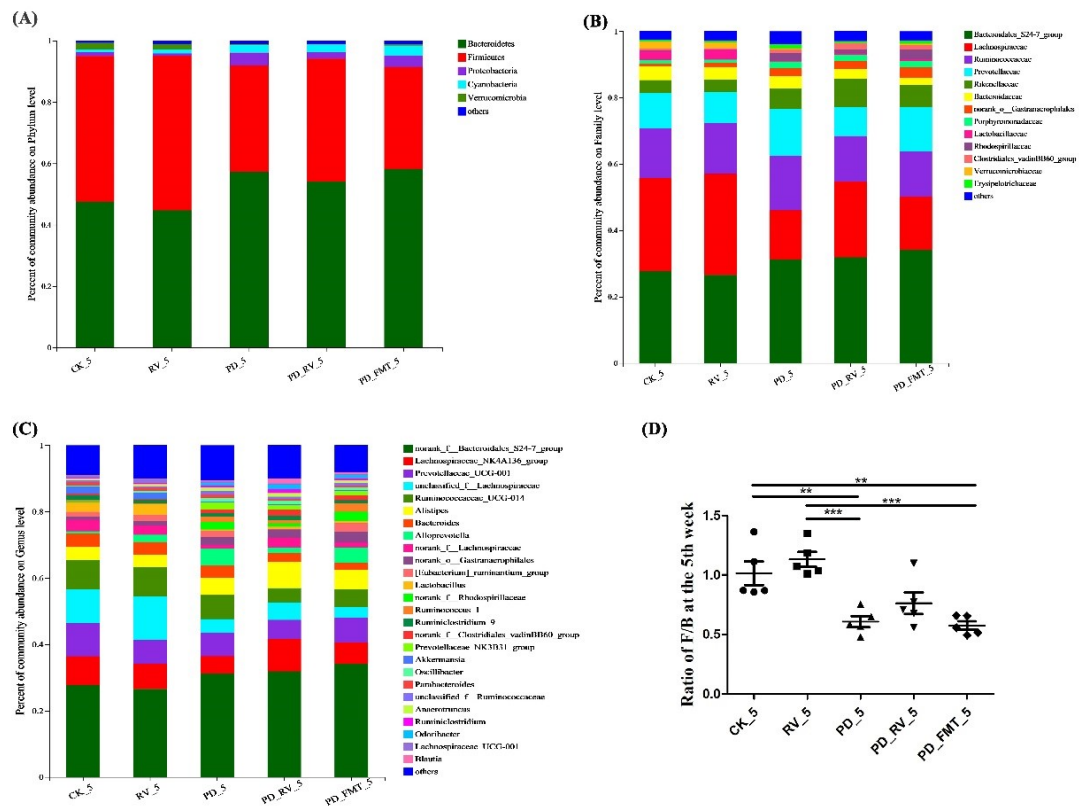


Fig. S3 The bacterial community composition at the 5th week. Bar chart of bacteria that exceeded 1% of the total at phylum (A), family (B), and genus (C) levels. (D) The Fimicutes/Bacteroidetes (F/B) ratio. The results are presented as the mean \pm standard deviation (SD); $n = 5$ for each treatment. *Analysis of variance (ANOVA) was used, significant differences between groups were indicated ($P < 0.05$). Because FMT did not

begin until the 6th week, the PD_FMT group was a separated replica of the PD group at the 5th week.

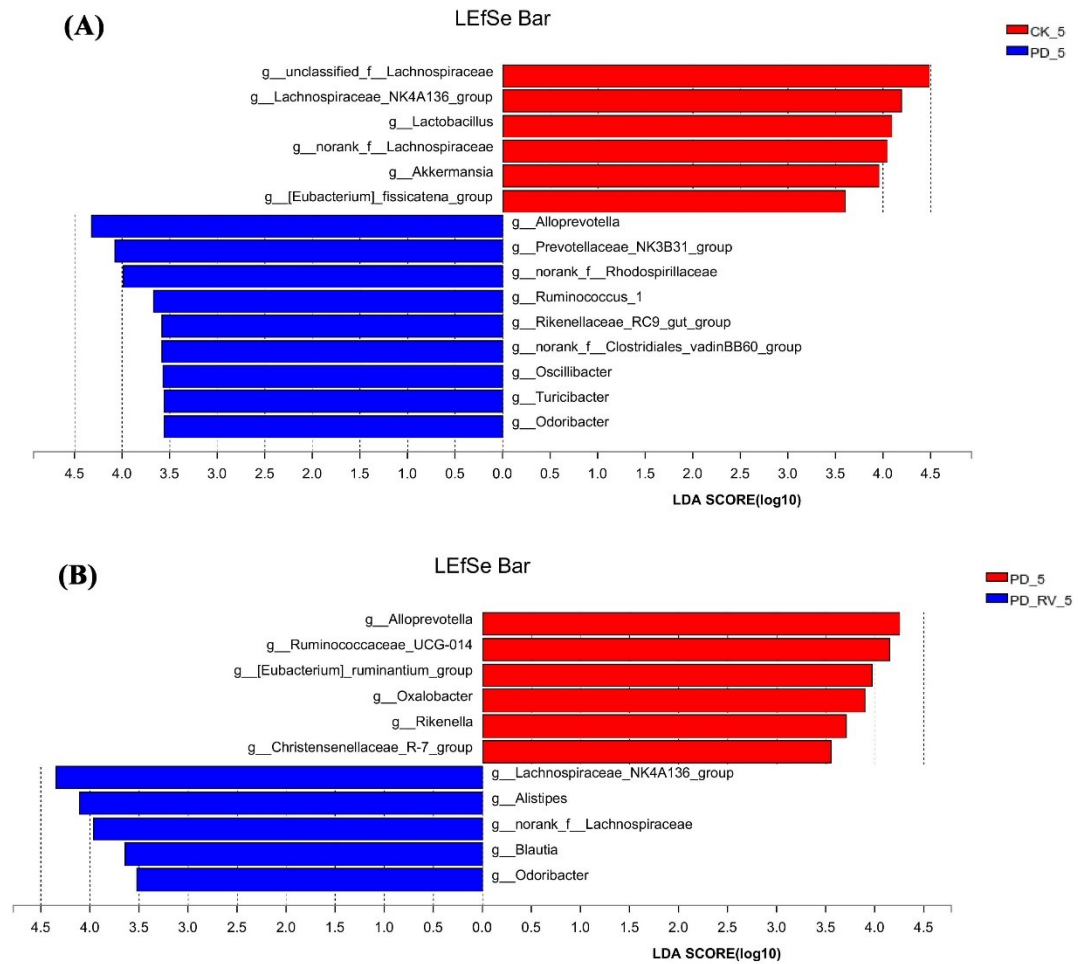


Fig. S4 The LfSe analysis between groups at the 5th week. Non-parametric factorial Kruskal–Wallis (KW) sum-rank test was used. $n = 5$ for each treatment.

Table S1. Primers used in the real-time PCR assays.

Gene	Primer Sequences (5'-3')
TNF- α	
Forward	CCCTCACACTCAGATCATCTTCT
Reverse	GCTACGACGTGGGCTACAG
IL-6	
Forward	TAGTCCTTCTACCCCAATTTCC
Reverse	TTGGTCCTTAGCCACTCCTTC
IL-1 β	
Forward	GCAACTGTTCTGAACTCAACT
Reverse	ATCTTTTGGGGTCCGTCAACT
GAPDH	
Forward	TCTGGAAAGCTGTGGCGTGAT
Reverse	GCCAGTGAGCTTCCCGTTCAG
Total bacteria	
341F	CCTACGGGAGGCAGCAG
518R	ATTACCGCGGCTGCTGG
Butyrate producing bacteria	
Bco-F	GCIGAICATTTACITGGAAYWSITGGCAYATG
Bco-R	CCTGCCTTTGCAATRTCIACRAANGC

Table S2. Relative abundance of Genera > 1% in different groups at 5th week.

Relative abundances (%)	CK	RV	PD	PD_RV	PD_FMT
norank_f_Bacteroidales_S24-7_group	27.64±1.92	26.52±1.99	31.15±2.98	31.86±5.67	34.05±3.88*
Lachnospiraceae_NK4A136_group	8.76±1.86	7.63±2.74	5.28±1.05*	9.81±2.87 [#]	6.45±1.58
Prevotellaceae_UCG-001	9.94±1.79	7.17±1.71	7.11±1.88	5.69±0.74*	7.46±5.56
unclassified_f_Lachnospiraceae	10.26±3.17	13.18±3.14	4.07±0.54*	5.32±0.46* [#]	3.30±1.32
Ruminococcaceae_UCG-014	8.80±1.96	8.83±3.84	7.25±2.43	4.28±2.43*	5.24±1.49*
<i>Alistipes</i>	3.90±0.38	3.71±1.40	5.20±1.29	7.85±2.81*	5.95±2.64
<i>Bacteroides</i>	4.12±1.17	3.79±1.06	3.72±1.39	2.80±0.95	2.07±0.91*
<i>Alloprevotella</i>	0.64±0.32	2.18±1.03	5.03±0.89*	1.57±0.41* [#]	4.71±2.46*
norank_f_Lachnospiraceae	3.51±2.18	2.83±1.02	1.08±0.40*	3.03±1.35	1.56±0.66*
norank_o_Gastranaerophilales	0.88±0.67	1.30±0.92	2.41±1.57	2.42±1.72	3.22±0.64*
[Eubacterium]_ruminantium_group	1.48±1.30	1.96±2.18	2.00±0.59	0.22±0.18	2.56±1.46
<i>Lactobacillus</i>	2.72±2.17	3.04±3.11	0.31±0.12*	0.58±0.41*	0.63±0.30*

norank_f_Rhodospirillaceae	0.28±0.16	0.16±0.07	2.25±0.79*	1.06±0.87	2.78±1.69*
<i>Ruminococcus_1</i>	0.53±0.37	0.26±0.21	1.60±0.43	1.01±0.57	2.62±1.95*
<i>Ruminiclostridium_9</i>	1.39±0.27	1.02±0.14	0.98±0.27	1.23±0.26	0.85±0.16
norank_f_Clostridiales_vadinBB60_group	0.47±0.22	0.25±0.07	1.14±0.43*	1.80±0.68*	1.47±0.81*
Prevotellaceae_NK3B31_group	0.00±0.00	0.00±0.00	2.09±1.22	1.51±0.65	1.29±0.93
<i>Akkermansia</i>	2.14±1.28	1.83±1.97	0.30±0.24*	0.15±0.15*	0.37±0.26*
<i>Oscillibacter</i>	0.50±0.22	0.62±0.21	1.18±0.28*	1.07±0.26	0.94±0.25*
<i>Parabacteroides</i>	1.01±0.10	0.90±0.33	1.03±0.41	0.48±0.20	0.63±0.26
unclassified_f_Ruminococcaceae	0.55±0.18	0.50±0.08	1.10±0.77	0.75±0.20	0.79±0.26
<i>Anaerotruncus</i>	0.39±0.19	0.58±0.17	0.91±0.38	0.73±0.20	0.64±0.11
<i>Ruminiclostridium</i>	0.38±0.13	0.31±0.11	0.68±0.21	1.16±0.47*	0.73±0.19
<i>Odoribacter</i>	0.00±0.00	0.00±0.00	0.70±0.15*	1.34±0.28*#	1.03±0.33*
<i>Parasutterella</i>	0.86±0.39	0.51±0.13	0.63±0.14	0.47±0.20	0.55±0.22
norank_f_Ruminococcaceae	0.28±0.16	0.68±0.19	0.64±0.25	0.94±0.30	0.47±0.07
Lachnospiraceae_UCG-001	0.66±0.35	1.28±0.87	0.47±0.54	0.45±0.28	0.14±0.05
<i>Roseburia</i>	0.50±0.53	0.55±0.31	0.61±0.41	0.82±0.21	0.40±0.26
<i>Blautia</i>	0.22±0.09	0.16±0.06	0.40±0.42	1.37±0.34*#	0.68±0.30
Rikenellaceae_RC9_gut_group	0.00±0.00	0.00±0.00	0.81±0.37*	0.69±0.47*	0.73±0.34*
<i>Ruminiclostridium_6</i>	0.17±0.16	0.94±0.57*	0.08±0.06	0.50±0.16*	0.04±0.01
<i>Turicibacter</i>	0.01±0.02	0.01±0.01	0.80±0.41*	0.39±0.24*#	0.41±0.25
<i>Bilophila</i>	0.15±0.11	0.14±0.07	0.43±0.26	0.54±0.28	0.25±0.07
[Eubacterium]_fissicatena_group	0.78±0.50	0.43±0.45	0.03±0.03*	0.00±0.00*	0.01±0.01*
<i>Butyricicoccus</i>	0.08±0.04	0.20±0.08	0.21±0.09	0.54±0.30	0.17±0.16
<i>Escherichia-Shigella</i>	0.01±0.00	0.00±0.00	0.78±0.39*	0.00±0.00#	0.83±0.42*
<i>Ruminococcus_2</i>	0.41±0.46	0.22±0.38	0.00±0.00*	0.00±0.00*	0.00±0.00*
others	5.61±0.78	6.30±0.85	5.53±0.57	5.22±0.43	5.02±0.27

Note: The results are presented as mean ± SD; $n = 5$. * $P < 0.05$ compared with the CK group, # $P < 0.05$ compared with the PD group. Because FMT was not started until 6th week, the PD_FMT group was the replica of the PD group at 5th week.

Table S3. Relative abundance of Genera > 1% in different groups at 8th week.

Relative abundance(%)	PD	PD_RV	PD_FMT
norank_f__Bacteroidales_S24-7_group	24.80±3.19	33.80±13.47	27.28±4.98
Lachnospiraceae_NK4A136_group	10.14±4.63	8.97 ±1.78	9.52±3.33
unclassified_f__Lachnospiraceae	8.39 ±1.34	9.07±5.49	7.80 ±3.21
<i>Alistipes</i>	4.20 ±1.56	10.87±3.83*	7.92 ±1.71*
Prevotellaceae_UCG-001	4.02±0.84	3.36 ±1.20	9.43 ±5.11
Ruminococcaceae_UCG-014	10.28±3.27	2.12±0.74*	2.25 ±1.50*
norank_f__Lachnospiraceae	4.12 ±1.45	4.49 ±1.47	3.05 ±1.46
<i>Alloprevotella</i>	2.32 ±0.48	2.06 ±1.30	3.52 ±3.04
<i>Bacteroides</i>	5.19 ±2.46	1.04 ±0.29*	1.57 ±0.81*
<i>Lactobacillus</i>	4.15 ±3.42	0.81 ±0.54*	0.90 ±0.63*
norank_o__Gastranaerophilales	0.72 ±0.45	0.66 ±0.51	4.37 ±1.95*
norank_f__Clostridiales_vadinBB60_group	0.32 ±0.23	2.16 ±0.86*	1.81 ±0.25*
<i>Ruminiclostridium_9</i>	1.31 ±0.63	1.51 ±0.79	1.35 ±0.55
<i>Ruminiclostridium</i>	0.65 ±0.31	1.72 ±0.37*	1.68 ±0.77*
<i>Blautia</i>	0.31±0.24	1.07 ±0.43*	1.91 ±1.59*
<i>Akkermansia</i>	2.29 ±0.88	0.83±0.49*	0.23 ±0.11*
<i>Oscillibacter</i>	0.82 ±0.40	1.24±0.39	1.08 ±0.51
norank_f__Ruminococcaceae	0.63 ±0.38	1.36±0.52	0.80 ±0.36
<i>Anaerotruncus</i>	0.65 ±0.30	1.20 ±0.43	0.85 ±0.17
<i>Odoribacter</i>	0.00 ±0.00	1.18 ±0.37*	1.20 ±0.10*
<i>Mucispirillum</i>	1.03 ±0.61	0.73 ±0.65	0.61 ±0.56
Prevotellaceae_NK3B31_group	0.00 ±0.00	1.19 ±0.75*	1.16 ±0.64*
<i>Roseburia</i>	0.85±0.52	0.47 ±0.29	0.82 ±0.28
Lachnospiraceae_UCG-001	0.93±0.26	0.26 ±0.05*	0.33 ±0.13*
[Eubacterium]_ruminantium_group	0.83 ±0.83	0.10 ±0.06	0.49±0.70
norank_f__Rhodospirillaceae	0.07 ±0.03	0.15±0.04	0.88 ±0.63
Rikenellaceae_RC9_gut_group	0.00 ±0.00	0.25±0.13*	0.80 ±0.16*
<i>Parabacteroides</i>	0.66 ±0.63	0.13 ±0.10	0.15 ±0.07
<i>Enterococcus</i>	0.00±0.00	0.21±0.42*	0.00±0.00 [#]
others	9.32 ±0.22	7.00 ±1.57	6.34±0.87

Note: The results are presented as mean ± SD; $n = 5$. * $P < 0.05$ compared with the PD group, [#] $P < 0.05$ compared with the PD_RV group.