

Appendix tables

Appendix Table 1 Primer sequence

Target Gene	Primer Sequence (5'→3')	Product Length, bp	Accession No.
TNF-a	Forward (F): GAAACACACGAGACGCTGAAGT	95	NM_012675.3
	Reverse (R): TCCAGTGAGTTCCGAAAGCC		
IL-1 β	F: CCTCGTGCTGTCTGACCCAT	114	NM_031512.2
	R: TTGTCGTTGCTTGTCTCTCCTT		
IL-10	F: CCAGTCAGCCAGACCCACA	108	NM_012854.2
	R: GGAATCTGTCAGCAGTATGTTGTC		
GPR43	F: GGCACCGAGAACCAAATCAC	100	NM_001005877.1
	R: CGAAAAAGAGGACCAGGCAC		
CCL5	F: GAGGGTCTCTCCATTCTGATCC	107	NM_031116.3
	R: CCAGGAATGAGTGGGAGTAGG		
ZO-1	F: GAGTGGAGAACTGTCAGGCATT	124	NM_001106266.1
	R: ACTGGCTGGTATTTTTAACGGA		
Occludin	F: GATGCTGGTTGCTGGAGAAGT	103	NM_031329.2
	R: TTCCCAGACGAGAGTCCAAAG		
β -actin	F: AGATGTGGATCAGCAAGCAGG	108	NM_031144.3
	R: TCAAAGAAAGGGTGTAAAACGC		
GAPDH	F: AAGAAGGTGGTGAAGCAGGC	119	NM_017008.4
	R: CCAGCATCAAAGGTGGAAGAA		

Appendix Table 2 Bacteria distributions of feces from rats in the Control and HFD groups
(4-week HFD)

	Species	Control	HFD	
Phylum	<i>Firmicutes</i>	47.02% ± 1.73%	37.89% ± 7.09%	
	<i>Bacteroidetes</i>	50.76% ± 1.62%	51.07% ± 7.60%	
	<i>Proteobacteria</i>	1.71% ± 0.26%	5.57% ± 1.15%**	
	<i>Actinobacteria</i>	0.16% ± 0.03%	5.29% ± 1.65%*	
Genus	<i>Bacteroides</i>	5.59% ± 1.89%	25.92% ± 4.20%**	
	<i>Alloprevotella</i>	7.88% ± 2.10%	4.22% ± 1.18%	
	<i>Ruminococcaceae_UCG_014</i>	8.88% ± 1.24%	0.04% ± 0.01%**	
	<i>Blautia</i>	0.65% ± 0.29%	7.67% ± 2.87%*	
	<i>Ruminococcus_1</i>	6.33% ± 1.20%	0.04% ± 0.01%**	
	<i>Lactobacillus</i>	5.54% ± 1.75%	0.57% ± 0.20%*	
	<i>Prevotellaceae_UCG_001</i>	4.29% ± 0.85%	1.34% ± 0.56%*	
	<i>Collinsella</i>	0.01% ± 0.006%	4.55% ± 1.63%*	
	<i>Parabacteroides</i>	0.61% ± 0.19%	3.29% ± 1.08%*	
	<i>Romboutsia</i>	0.67% ± 0.06%	3.04% ± 0.72%*	
	<i>Parasutterella</i>	0.79% ± 0.09%	3.26% ± 0.54%**	
	<i>Fusicatenibacter</i>	0.01% ± 0.005%	3.86% ± 2.26%	
	<i>Turicibacter</i>	0.35% ± 0.08%	3.09% ± 0.97%*	
	<i>[Eubacterium]_coprostanoligenes_group</i>	3.11% ± 0.63%	0.12% ± 0.05%**	
	p			
		<i>[Ruminococcus]_gnavus_group</i>	0.00% ± 0.00%	2.95% ± 0.71%*

Data are expressed as the mean ± SEM (n = 5), *P < 0.05, **P < 0.01 versus the control group.

Appendix Table 3 Bacteria distributions of feces from rats in the Control, HFD, and NFP groups
(9-week HFD)

	Species	Control	HFD	NFP	
Phylum	<i>Firmicutes</i>	44.08% ± 3.20%	32.74% ± 3.77%	40.94% ± 4.59%	
	<i>Bacteroidetes</i>	49.44% ± 3.09%	55.28% ± 5.35%	50.25% ± 4.10%	
	<i>Proteobacteria</i>	5.03% ± 0.84%	5.09% ± 1.40%	4.65% ± 0.54%	
	<i>Actinobacteria</i>	0.24% ± 0.06%	5.92% ± 1.69%*	3.59% ± 0.76%*	
Genus	<i>Prevotella_9</i>	0.05% ± 0.02%	31.89% ± 7.18%**	21.26% ± 3.43%**#	
	<i>Bacteroides</i>	4.60% ± 0.32%	11.37% ± 3.03%*	4.33% ± 0.98%#	
	<i>Alloprevotella</i>	5.69% ± 1.68%	3.32% ± 0.70%	4.16% ± 1.67%	
	<i>Lactobacillus</i>	7.68% ± 1.87%	0.94% ± 0.33%**	5.25% ± 1.65%#	
	<i>Blautia</i>	0.95% ± 0.35%	4.46% ± 0.41%**	4.32% ± 0.87%*	
	<i>Collinsella</i>	0.06% ± 0.02%	5.68% ± 1.67%**	3.39% ± 0.97%*	
	<i>Romboutsia</i>	1.22% ± 0.13%	3.03% ± 0.53%*	4.29% ± 0.84%*	
	<i>Ruminococcaceae_UCG_014</i>	4.95% ± 0.96%	0.82% ± 0.24%**	1.69% ± 0.37%*	
	<i>Parasutterella</i>	2.97% ± 0.75%	0.81% ± 0.13%*	1.55% ± 0.45%	
	<i>Lachnospiraceae_NK4A136_group</i>	5.02% ± 1.02%	0.04% ± 0.02%**	0.42% ± 0.24%**	
	<i>Rikenellaceae_RC9_gut_group</i>	4.67% ± 0.65%	0.007% ± 0.003%**	0.16% ± 0.08%**	
	<i>Allobaculum</i>	0.21% ± 0.09%	0.73% ± 0.17%	1.82% ± 0.35%**#	
	<i>Turicibacter</i>	0.21% ± 0.07%	2.93% ± 0.33%**	1.32% ± 0.35%#	
	<i>[Eubacterium]_coprostanoligenes_grou</i>	0.93% ± 0.17%	0.52% ± 0.22%	2.38% ± 0.73%#	
	p				
		<i>Ruminococcus_1</i>	1.73% ± 0.21%	0.17% ± 0.09%**	1.36% ± 0.38%#

Data are expressed as the mean ± SEM (n = 6). *P < 0.05, **P < 0.01 versus the control group, #P < 0.05 versus the HFD group.