Electronic Supplementary Material (ESI) for Food & Function.

Table S1 Sequences of the primers used for quantitative Real-time PCR

Target gene	Forward primer (5'→3')	Revere primer (3'→5')
Occludin	CCCCAATGTTGAAGAGTGGGTTA	CACACTCAAGGTCAGAGGAATCT
Claudin-1	TAATTGGCATCCTGCTGGGG	CTGGCCAAATTCATACCTGGC
ZO-1	GAGCAGGCTTTGGAGGAGAC	TGGGACAAAAGTCCGGGAAG
TNF-α	CACAGAAAGCATGATCCGCG	CCATTTGGGAACTTCTCATCCC
IL-1β	GATGAAGGGCTGCTTCCAAAC	CTGCGAGATTTGAAGCTGGATG
IL-6	AGTTCCTCTCTGCAAGAGACTTC	AGTCTCCTCTCCGGACTTGT
IL-γ	ATGAACGCTACACACTGCATC	CCATCCTTTTGCCAGTTCCTC
IL-17a	TGGACTCTCCACCGCAATGAAG	GCTTTCCCTCCGCATTGACAC
Cxcl1	TGCACCCAAACCGAAGTCAT	ACTTGGGGACACCTTTTAGCAT
Cxcl2	GAGGGTGAGTTGGGAACTAGC	TTCCATGAAAGCCATCCGACT
Cxcl3	TGAGGCAGTATTCCTTGGCTG	ACCGGCATGACCTTGTTTGT
Cxcl5	TCCTCAGTCATAGCCGCAAC	TAGCTTTCTTTTTGTCACTGCCC
Ccl7	CCCTGGGAAGCTGTTATCTTCA	CTCGACCCACTTCTGATGGG
GAPDH	AGGTCGGTGTGAACGGATTTG	TGTAGACCATGTAGTTGAGGTCA

Table S2. The abundance of 12 genera with significant differences among the three groups

Genus	Group		
	Ctrl	Model	CCM
Lactobacillus	0.247±0.06* i)	0.139±0.022	0.139±0.088*
Bifidobacterium	0.125±0.069**	0.033±0.010	0.021±0.022
Akkermansia	0.034±0.026*	0.000±0.000	0.045±0.029*
Parabacteroides	0.002±0.001	0.003±0.002	0.008±0.006*
Clostridium_sensu_stricto_1	0.018±0.007	0.019±0.010	0.035±0.013*
Bacteroides	0.007±0.003	0.011±0.005	0.025±0.016^{b*}
Parasutterella	0.005±0.003	0.008±0.004	0.002±0.001*
Ruminococcaceae_UCG-013	0.002±0.002	0.006±0.005	0.011±0.003*
Candidatus_Saccharimonas	0.009±0.006*	0.036±0.022	0.020±0.010
Ruminococcaceae_UCG-014	0.020±0.007*	0.045±0.019	0.036±0.015
Turicibacter	0.056±0.042**	0.164±0.063	0.087±0.011*
uncultured_bacterium_o_Mollicutes_RF39	0.002±0.002***	0.010±0.003	0.004±0.003**

i) All data were expressed as the mean ± SD (n=5 mice/group). Significant differences among different groups were determined by one-way analysis of variance (ANOVA), followed by Tukey's test for multiple comparisons. The value of $p < 0.05$ was considered statistically significant (* $p<0.05$, ** $p<0.01$ and *** $p<0.001$ compared to the Model group).

Supplementary Figure

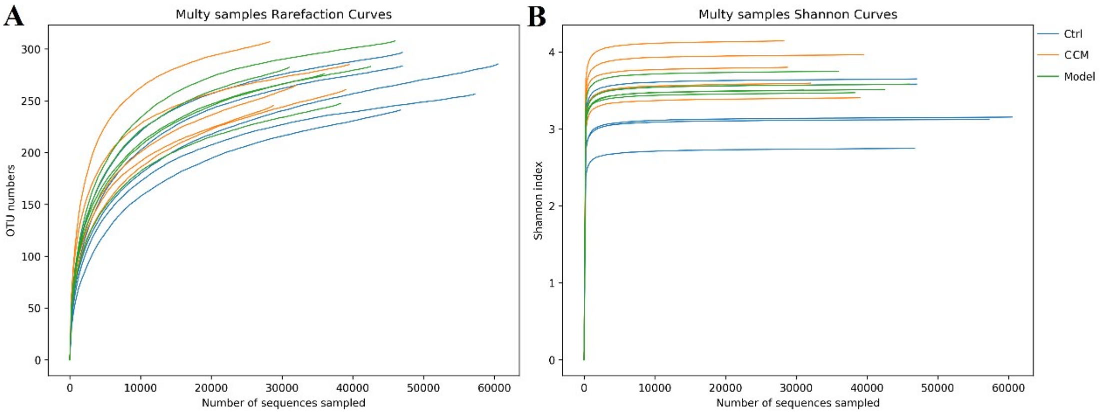

Fig. S1 (A) Rarefaction and (B) Shannon curves of intestinal microbiota.