

## Supplementary Materials

### Supplementary Material 1:

**Table S1.** Calculated disease activity index (DAI) score.

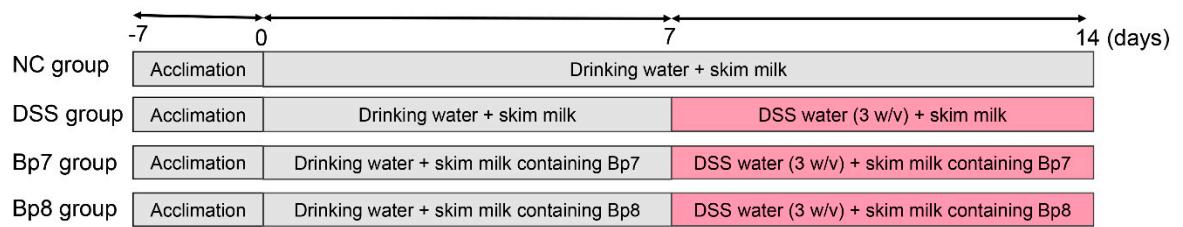
Score	Weight loss (%)	Stool consistency	Stool bleeding
0	no loss	normal	occult blood test-negative
1	1.0-5.0	soft but formed	occult blood test-positive
2	5.0-10.0	soft	slight
3	10.0-15.0	slight diarrhea	blood traces in stool
4	more than 15.0	watery diarrhea	gross rectal bleeding

## Supplementary Material 2:

**Table S2.** Primer sequences for quantitative real-time PCR

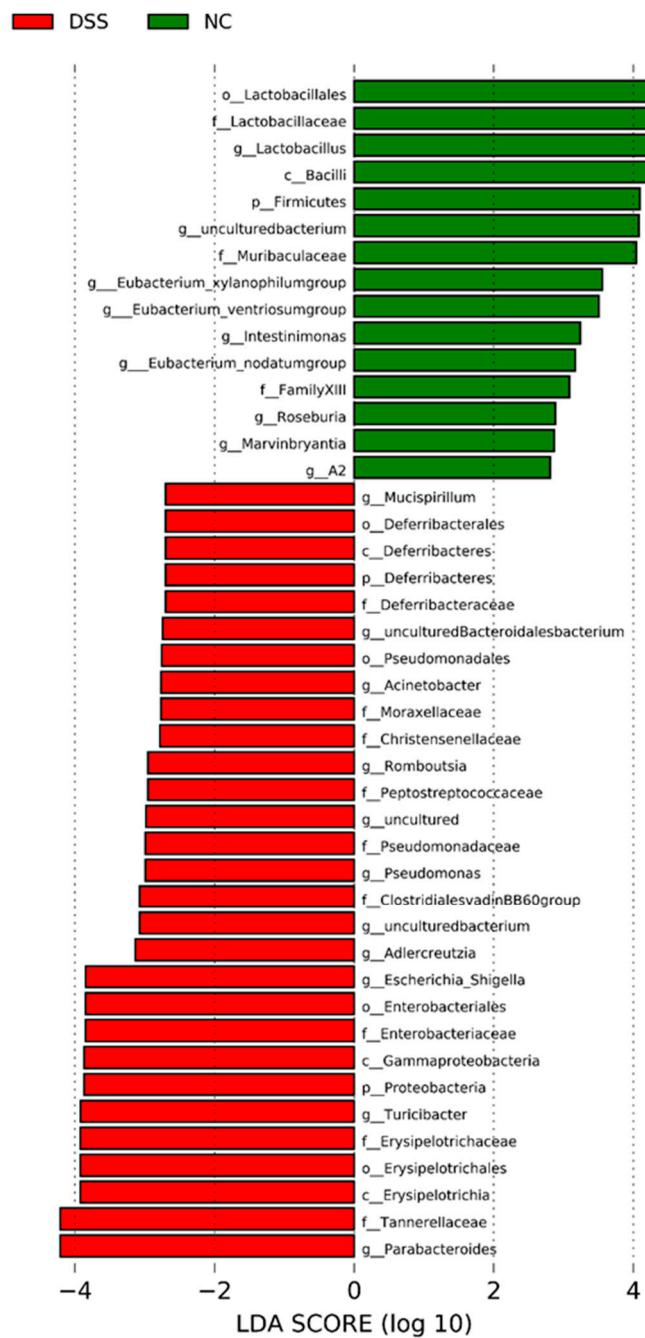
Gene	Forward primer (5'-3')	Reverse primer (5'-3')
STAT3	GAGGAGGCATTCGGAAAG	TCGTTGGTGTACACAGAT
PPAR $\gamma$	TGGGTGAAACTCTGGGAGAT	CCATAGTGGAAGCCTGATGC
NF- $\kappa$ B	CGCCCCTTATCGACCACC	CCTCTCCAAGAGTCGTCCA
COX2	GAAGTCTTGGTCTGGTGCCTG	GTCTGCTGGTTGGAATAGTTG
iNOS	CTTGGAGCGAGTTGTGGATTGTC	TAGGTGAGGGCTTGGCTGAGT
Nrf2	CCTCCGCTGCCATCAGTCAGT	TCGGCTGGGACTCGTGTCA
MyD88	GCATGGTGGTGGTTGTTCTG	GAATCAGTCGCTTCTGTTGG
Occludin	CCGGCCGCCAAGGTTCA	GCTGATGTCACTGGTCACCTA
Claudin-1	GGCTTCTCTGGATGGATCG	CCCCAGCAGGATGCCAATTA
ZO-1	GCCTTGAACTTGACCTCTGC	GAAATCGTGCTGATGTGCCA
GAPDH	AGGTCGGTGTGAACGGATTG	GGGGTCGTTGATGGCAACA

### Supplementary Material 3:



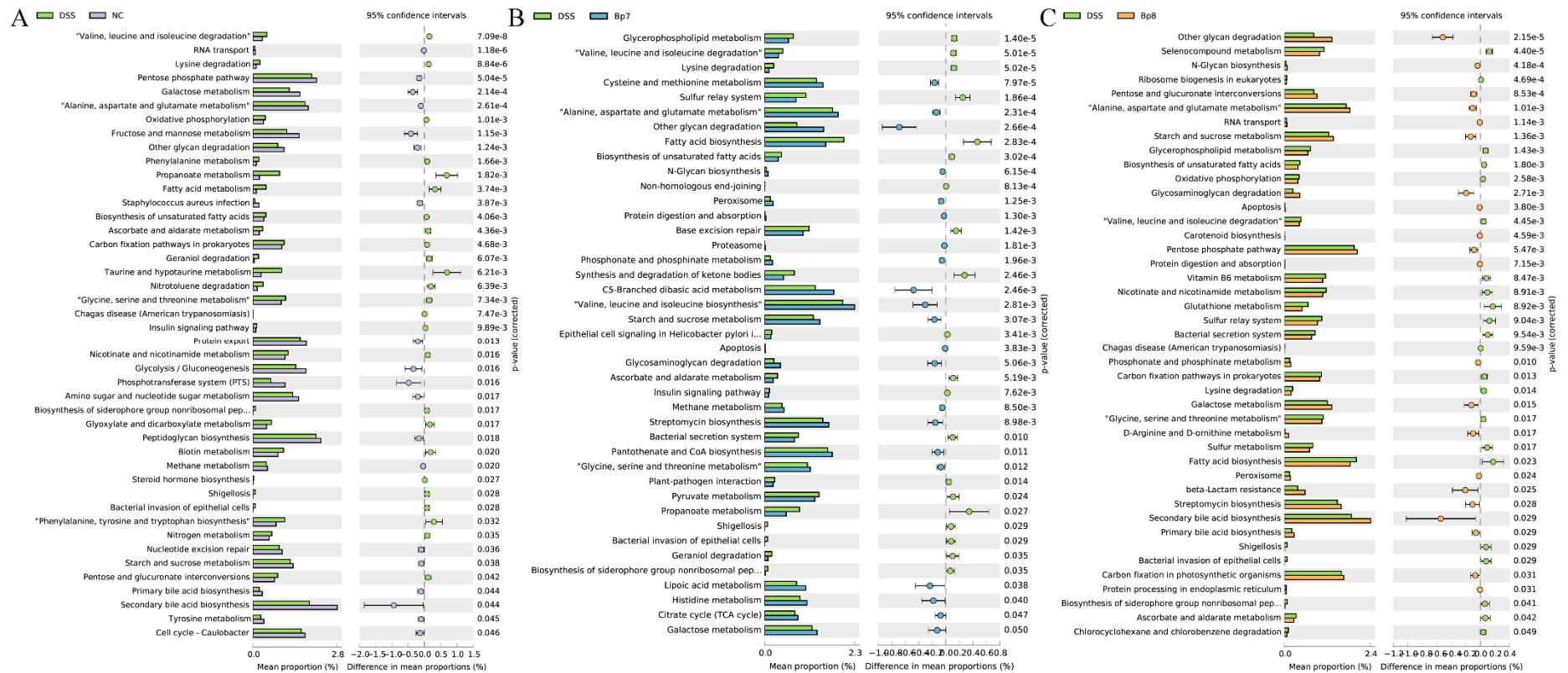
**Figure S1** The flow chart of animal experiment.

## Supplementary Material 4:



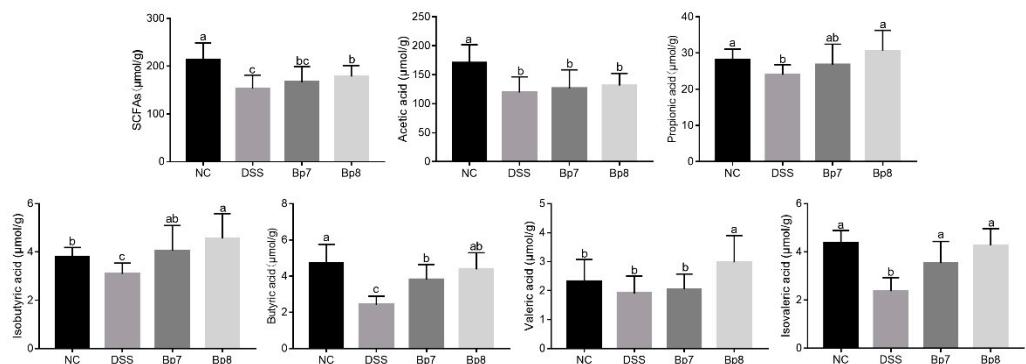
**Figure S2.** LEfSe identified the gut microbiota phylotypes with a statistically significant difference in abundance between NC and DSS groups.

## Supplementary Material 5:



**Figure S3.** Predicted metabolic functions for the altered genes of intestinal microbiota. Metabolic pathways of NC vs DSS (A), Bp7 vs DSS (B) and Bp8 vs DSS (C).

## Supplementary Material 6:



**Figure S4.** Influence of Bp7 and Bp8 intervention on the cecal SCFAs concentrations. Values are showed as the mean  $\pm$  SD (n = 8). The different letters represent significant differences between different experimental groups ( $P < 0.05$ ).