Supplementary Table S1

Score	Weight loss	Stool consistency	Blood stool
0	0%	normal	no blood
1	1-5%	loose stool	
2	5-10%	watery diarrhea	presence of blood
3	10-20%	slimy diarrhea, little blood	
4	>20%	severe watery diarrhea with blood	gross bleeding

Scoring system for Disease Activity Index

Supplementary Table S2

Primer sequence

ID	Name	Sequence
NM_008084.2	GAPDH-F	CCTCGTCCCGTAGACAAAATG
	GAPDH-R	TGAGGTCAATGAAGGGGTCGT
NM_013605.2	Muc1-F	GGTGCTGGTCTGTATTTTGGTT
	Muc1-R	TAGGGTATTCACTCATAGGATGGTAG
NM_023566.4	Muc2-F	GGCTCGGAACTCCAGAAAGAAG
	Muc2-R	CTCGGCAGTCAGACGCAAAG
XM_030254765.1	Muc3-F	GCAGAAGGGCGATAAGTGGT
	Muc3-R	CTGAAGCGGATGGAGAACACG
NM_080457.4	Muc4-F	TGCCTACCAAGTTCACCCCC
	Muc4-R	CTTTGTCCAATAGTTCTGTTTCCC
NM_009386.2	ZO-1-F	GGGAAAACCCGAAACTGATG
	ZO-1-R	GCTGTACTGTGAGGGCAACG
NM_031168.2	IL-6-F	CCCCAATTTCCAATGCTCTCC
	IL-6-R	CGCACTAGGTTTGCCGAGTA
NM_001278601.1	TNF-α-F	CCCTCACACTCACAAACCACC
	TNF-α-R	CTTTGAGATCCATGCCGTTG
NM_008361.4	IL-1β-F	GCATCCAGCTTCAAATCTCGC
	IL-1β-R	TGTTCATCTCGGAGCCTGTAGTG
NM_010548.2	IL-10-F	TGCCAAGCCTTATCGGAAATG
	IL-10-R	AAATCACTCTTCACCTGCTCCAC
NM_013650.2	S100A8-F	AGTGTCCTCAGTTTGTGCAGAATAT
	S100A8-R	TTTTATCACCATCGCAAGGAACTC
NM_009921.2	Camp-F	GGCAGCTACCTGAGCAATGTG
	Camp-R	TTCTTGAACCGAAAGGGCTG

Supplementary Table S3. The correlation among different genera and UC related indexes

	Genera	SCFAs	Gut barrier proteins	cytokines	Organ index	Colon length and body weight	Significance of the correlation with DAI	Regulators
Group A: The genera positively correlated with DAI and enhanced in DSS groups	*Parabacteroides*	Butyric acid↓,Valeric acid↓, Isobutyric acid↓, Isovaleric acid↓	Muc1↓, Muc3↓, Muc4↓, ZO-1↓, Muc2↓	IL-6↑, IL-1β↑, TNF-α↑, IL-10↓	Spleen↑, Liver↑, Kidney↑	Colon length↓, body weight↓	+***	LRS, FMT
	Escherichia/Shigella	Valeric acid↓, Butyric acid↓, Propionic acid↓, Isovaleric acid↓	ZO-1↓, Muc1↓, Muc2↓	IL-1β↑, IL-6↑, IL-10↓	Kidney↑, liver↑	Colon length↓	+*	LRS, FMT
	Oscilibacter	Butyric acid↓,Valeric acid↓	Muc1↓, Muc2↓, Muc3↓	IL-6↑, TNF-α↑, IL-1β↑, IL-10↓	Spleen↑, Liver↑	Colon length↓, body weight↓	+***	LRS
	Clostridium XIVa	Isovaleric acid↓, Valeric acid↓, Acetic acid↓, Propionic acid↓	Muc2↓	TNF-α↑，IL-6↑, IL-1β↑,IL-10↓	Spleen↑, Liver↑, Kidney↑	/	+**	LRS
	Butyricimonas	Butyric acid↓,Valeric acid↓,	Muc1↓, Muc3↓, ZO-1↓	IL-6↑, TNF-α↑	Kidney↑, liver↑	body weight↓	+**	FMT
	Klebsiella	Butyric acid↓, Propionic acid↓,	ZO-1↓	IL-1β↑, IL-6↑, IL-10↓	Kidney↑, liver↑	/	+*	FMT
	Bacteroides		Muc1↓	IL-1β↑			+*	FMT
	Mucispirillum		Muc3↓, Muc2↓, MUC4↓	IL-6↑, TNF-α↑, IL-1β↑	Spleen↑, liver↑	Colon lenghth↓, body weight↓	+**	/
	Bifidobacterium	Isobutyric acid↑,	ZO-1↑	IL-10↑	Kidney↓, liver↓	/	/	LRS, FMT

Group B: The genera positively correlated with SCFAs and enhanced in LRS or FMT groups		Isovaleric acid↑, Propionic acid↑, Valeric acid↑						
	Akkermansia	Valeric acid↑						LRS, FMT
	Olsenella	Acetic acid↑	Muc2↑	IL-10↑	/	/	/	LRS, FMT
	Bilophila	/	/	/	/	/	/	LRS,FMT
	Flavonifrator	Isovaleric acid↑ Propionic acid↑	/	/	/	/	/	LRS
	Parasutterella	Isobutyric acid↑ Isovaleric acid↑, Propionic acid↑, Valeric acid↑	/	IL-10↑	/	/	/	LRS
	Bamesiella	Isovaleric acid↑	Muc4↓	IL-10↑	/	/	/	/
Group C: The genera negatively correlated with DAI	*Prevotella*	Caproic acid↑,Butyric acid↑	Muc1↑, Muc3↑, MUC4↑	IL-6↓, TNF-α↓, IL-1β↓	Spleen↓, Kidney↓	Body weight↑,colon length↑	-***	FMT
	Enterorhabdus	/	Muc3↑, Muc4↑	IL-6↓, TNF-α↓,IL-1β↓	Spleen↓, liver↓	Colon length↑, body weight↑	-*	FMT
	Parvibacter	/	Muc3↑, Muc4↑	IL-6↓, TNF-α↓, IL-1β↓	Spleen↓	Colon length↑, body weight↑	-*	FMT
	Staphylococcus	/	/	/	/	/	/	/

	Saccharibacteria genera incertae sedis	Caproic acid↑	Muc3↑, Muc2↑	IL-6↓, TNF-α↓	Spleen↓	Colon length↑, body weight↑	-*	/
	Alloprevotella	Caproic acid↑	Muc3↑, Muc2↑, Muc4↑	IL-6↓, TNF-α↓,IL-1β↓	Spleen↓	Colon length↑, body weight↑	-*	/
Group D: The genera positively correlated with antipeptide	*Ruminococcus*	Butyric acid↑, Isobutyric acid↑, acetic acid↓	Muc1↑, Muc4↑	/	/	/	/	LRS
	Romboutsia	Butyric acid↑	Muc1↑, Muc4↑	/	/	/	/	/
	Butyricicoccus	Acetic acid↓	/	/	/	/	/	/
	Lactobacillus	Isovaleric acid↑	ZO-1↑	/	/	/	/	/

Supplementary Figure S1

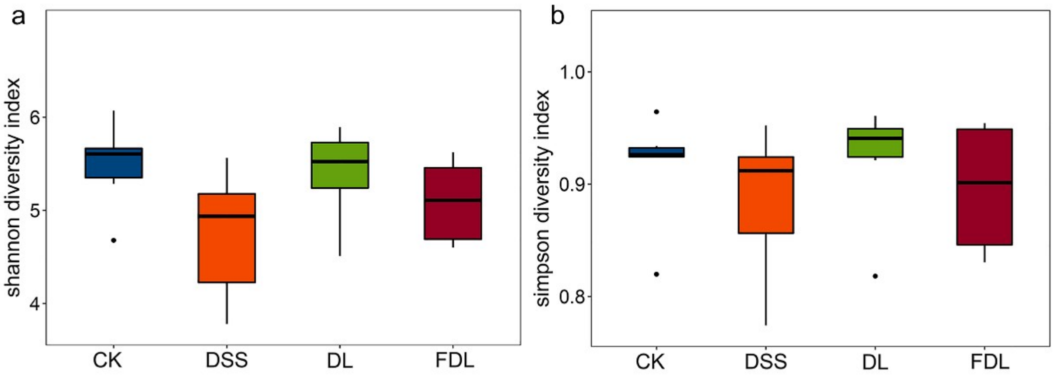

Figure S1. Alpha diversity boxplot index of Shannon **(a)** and Simpson diversity **(b)**. *CK: 0.9% saline; DSS: 3% dextran sodium sulfate+0.9% saline; DL: 3% dextran sodium sulfate +10^9 cfu/mL *Lactobacillus rhamnosus* SHA113; FDL: 3% dextran sodium sulfate+ mixed antibiotic (1 g/L metronidazole, 1 g/L vancomycin, 2 g/L streptomycin) +0.125 g/mL feces.

Supplementary Figure S2

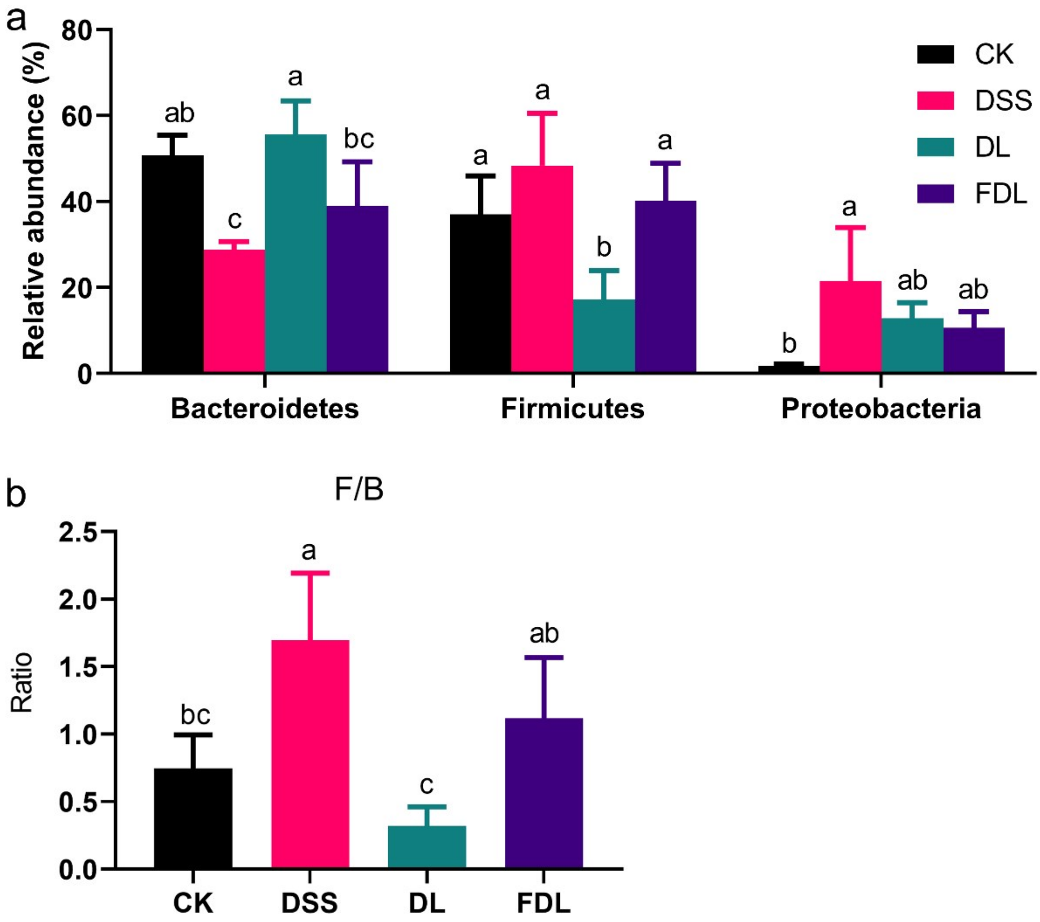

Figure S2. Gut microbiota composition in different groups (Phylum level) **(a)** Difference analysis of Bacteroidetes, Firmicutes and Proteobacteria. **(b)** Firmicutes/Bacteroides (F/B) *CK: 0.9% saline; DSS: 3% dextran sodium sulfate+0.9% saline; DL: 3% dextran sodium sulfate +10^9 cfu/mL *Lactobacillus rhamnosus* SHA113; FDL: 3% dextran sodium sulfate+ mixed antibiotic (1 g/L metronidazole, 1 g/L vancomycin, 2 g/L streptomycin) +0.125 g/mL feces

Supplementary Figure S3

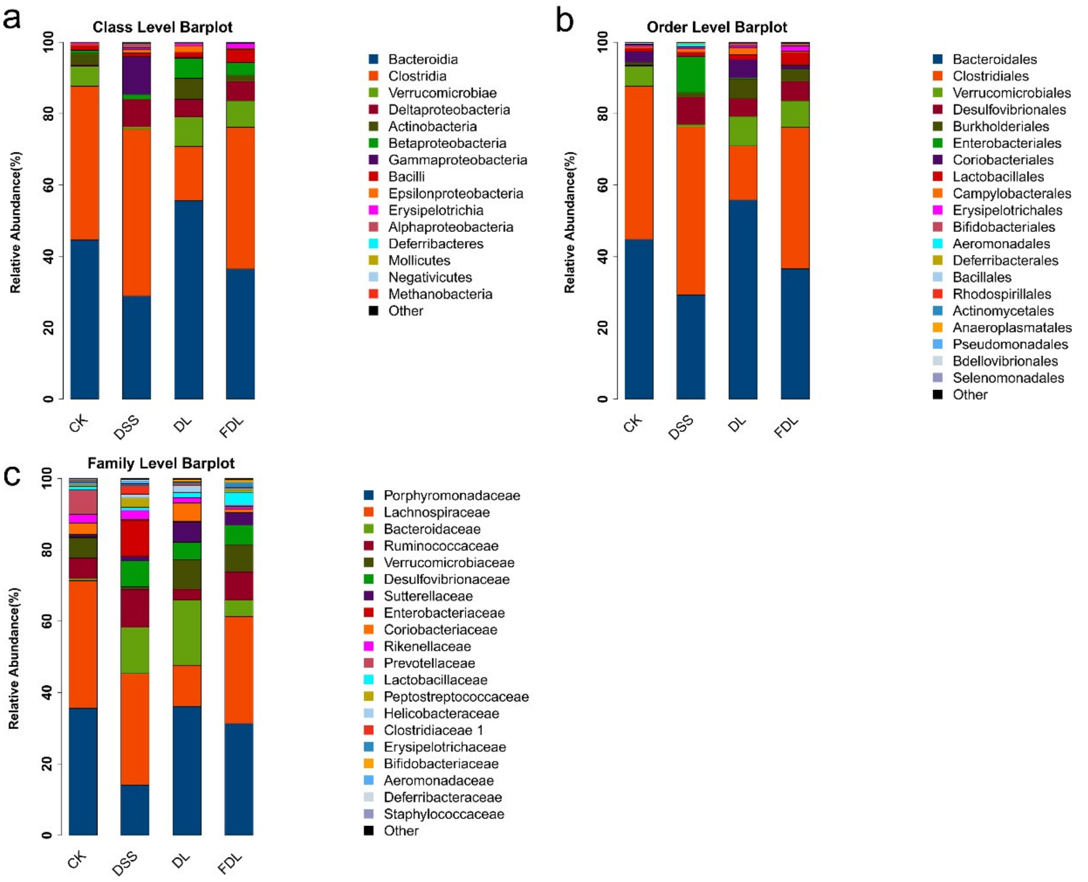

Figure S3. Bar plots of the taxonomic composition showing relative abundance at the Class level **(a),** Order level **(b)** and Family level **(c).** *CK: 0.9% saline; DSS: 3% dextran sodium sulfate+0.9% saline; DL: 3% dextran sodium sulfate +10^9 cfu/mL *Lactobacillus rhamnosus* SHA113; FDL: 3% dextran sodium sulfate+ mixed antibiotic (1 g/L metronidazole, 1 g/L vancomycin, 2 g/L streptomycin) +0.125 g/mL feces

Supplementary Figure S4

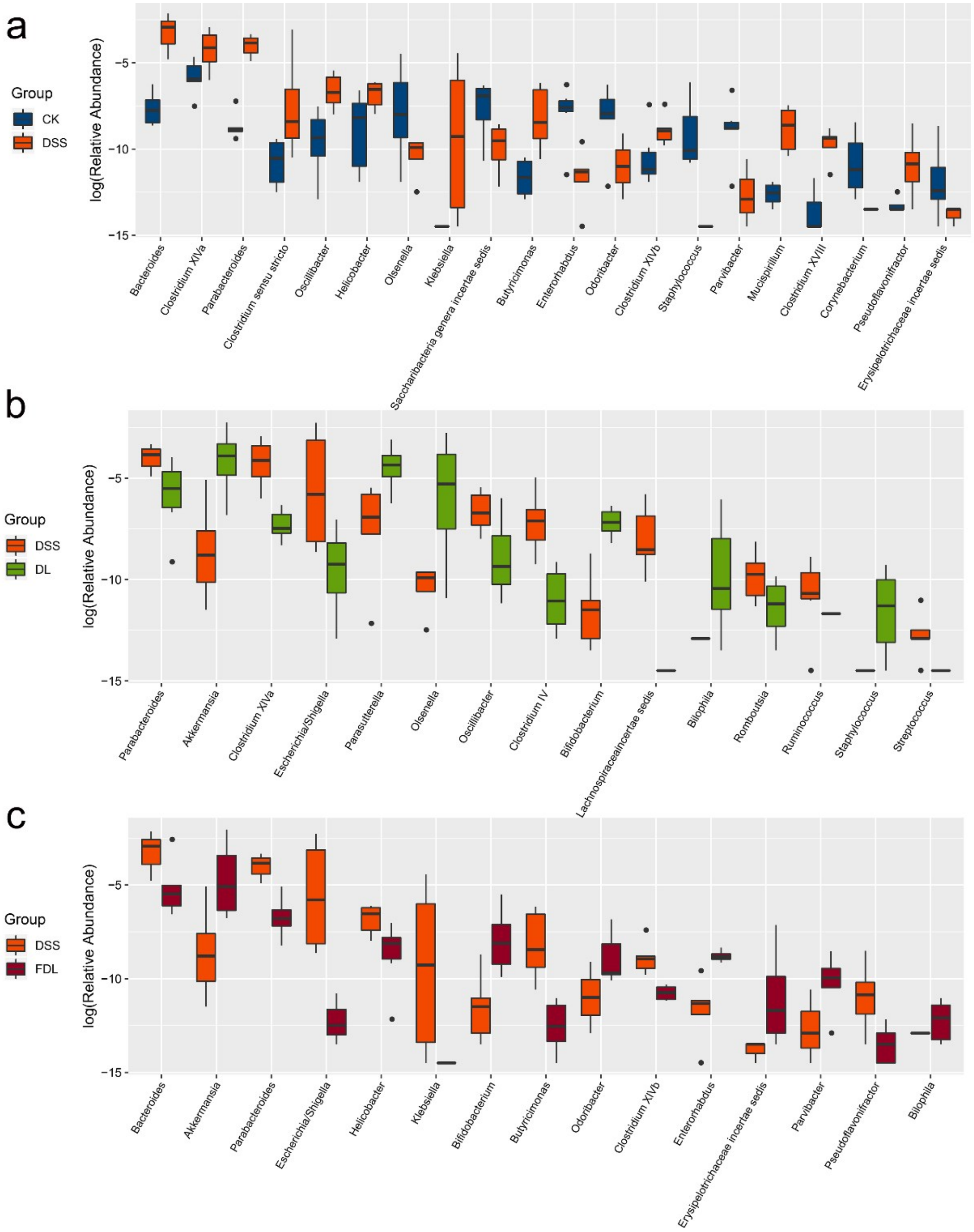

Figure S4 Differential bacteria (*P*< 0.05) at genus level in DSS group (compared with CK group), DL and FDL group (compared with DSS group). *CK: 0.9% saline; DSS: 3% dextran sodium sulfate+0.9% saline; DL: 3% dextran sodium sulfate +10^9 cfu/mL *Lactobacillus rhamnosus* SHA113; FDL: 3% dextran sodium sulfate+ mixed antibiotic (1 g/L metronidazole, 1 g/L vancomycin, 2 g/L streptomycin) +0.125 g/mL feces