

Supplementary materials

Supplemental Tables

Table S1. Assessment of disease activity index (DAI)

Body weight loss (%)	Stool	Bleeding	Score
<2%	Normal	No rectal bleeding	0
≥2%-<5%	Softer stool	Weak haemoccult	1
≥5%-<10%	Moderate diarrhoea	Visual blood in stool	2
≥10%-<15%	Diarrhoea	Fresh rectal bleeding	3
≥15%	-	-	4

Table S2. Assessment of macroscopic scores

Colon damage	score
No damage	0
Hyperemia without ulcers	1
Hyperemia and wall thickening without ulcers	2
One ulceration site without wall thickening	3
Two or more ulceration sites	4
0.5 cm extension of inflammation or major damage	5
1 cm extension of inflammation or severe damage	6-10

Table S3. Assessment of histopathological scores

Grade	Extent of inflammation	Infiltration neutrophils+ lympho- histiocytes	Extent of crypt damage	Crypt abscesses	Sub- mucosal oedema	Loss of goblet cells	Reactive epithelial hyperplasia
0	None	None	None	None	None	None	None
1	Mucosa	Focal	Basal one third	Focal	Focal	Focal	Focal
2	Mucosa+submucosa	Multifocal	Basal two thirds	Multifocal	Multifocal	Multifocal	Multifocal
3	Mucosa+submucosa+muscle layer	Diffuse	Entire crypt damage		Diffuse	Diffuse	Diffuse
4	Transmura		Crypt damage+ulceration				

Table S4. Primers used for RT-PCR analysis

Genes	Primer	sequence (5' →3')
IL-10	Forward primer	AGCCGGGAAGACAATAACTG
	Reverse primer	CATTTCCGATAAGGCTTGG
IL-12p40	Forward primer	CCTGGTTTGCCATCGTTTTG
	Reverse primer	TCAGAGTCTCGCCTCCTTTGTG
TNF- α	Forward primer	CCCTCACACTCAGATCATCTTCT
	Reverse primer	GCTACGACGTGGGCTACAG
IFN- γ	Forward primer	GGAACTGGCAAAGGATGGTGAC
	Reverse primer	GCTGGACCTGTGGGTTGTTGAC
IL-12	Forward primer	TTGAGTGCCAATTCGATGAT
	Reverse primer	TTGAGGGCTTGTTGAGATGA
IL-17A	Forward primer	GCTCCAGAAGGCCCTCAGACT
	Reverse primer	CCAGCTTTCCCTCCGCATTGA
IL-22	Forward primer	TCAGTGCTAAGGATCAGTGCT
	Reverse primer	TGATTGCTGAGTTTGGTCAGG
Chil3	Forward primer	ACCTGCCCCGTTTCAGTGCCAT
	Reverse primer	CCTTGGAATGTCTTTCTCCACAG
Chil1	Forward primer	AGCAGTATTTCTCCACCCTGAT
	Reverse primer	ACCTTTCCTGCTGACAAAGC
IL-6	Forward primer	TAGTCCTTCCCTACCCCAATTTCC
	Reverse primer	TTGGTCCTTAGCCACTCCTTC
IL-1 β	Forward primer	CTCACAAGCAGAGCACAAGC
	Reverse primer	TCCAGCCCATACTTTAGGAAGA
FATCD36	Forward primer	CCAGTGTATATGTAGGCTCATCCA
	Reverse primer	TGGCCTTACTTGGGATTGG
FABP4	Forward primer	AAGAAGTGGGAGTGGGCTTT
	Reverse primer	TCGACTTTCCATCCCACTTC
PPAR- α	Forward primer	ATGCCAGTACTGCCGTTTTTC
	Reverse primer	CCGAATCTTTCAGGTCGTGT
SCD1	Forward primer	CATCATTCTCATGGTCCTGCT
	Reverse primer	CCCATTTCGTACACGTCATTCT
LPL	Forward primer	AATTTGCTTTTCGATGTCTGAGAA
	Reverse primer	CAGAGTTTGACCGCCTTCC
ACSL1	Forward primer	TGGGGTGGAAATCATCAGCC
	Reverse primer	CACAGCATTACACACTCTACAACGG
ap2	Forward primer	CAGAAGTGGGATGGAAAGTCG
	Reverse primer	CGACTGACTATTGTAGTGTTTGA
ADIPO	Forward primer	ACATCCTGGCCACAATGGCACAC
	Reverse primer	GTCTCACCCCTTAGGACCAAGAAG
TGF- β	Forward primer	AACTATTGCTTCAGCTCCACAG
	Reverse primer	AGTTGGCATGGTAGCCCTTG
GAPDH	Forward primer	ACTCCACTCACGGCAAATTC
	Reverse primer	TCTCCATGGTGGTGAAGACA

Table S5. Differentially expressed genes on PPAR- α signaling pathway regulated by LncRNA

Transcript ID	Gene ID	Gene name	DSS+rSj16 FPKM	DSS+PBS FPKM	Log2 (fold change)	p value	q value	Target gene ID	Target gene name
ENSMUST00000131787	ENSMUSG00000086841	2410006 H16Rik	52.3918	75.0075	-0.517695	0.00225	0.040104	ENSMUSG00000018796	ACSL1
ENSMUST00000181446	ENSMUSG00000096972	Gm2688 3	10.4392	14.9587	-0.51898	0.00255	0.0442766	ENSMUSG00000015568	LPL

Table S6. Differentially expressed genes on PPAR- α signaling pathway regulated by miRNA

Gene name	DSS+rSj16 FPKM	DSS+PBS FPKM	Log2 (fold change)	p value	q value	Target gene ID	Target gene name
mmu-miR-374c-3p	448.0110169	934.7574171	-1.0611	1.68E-40	5.27E-39	ENSMUSG00000018796	ACSL1
mmu-miR-335-3p	33.03882562	78.16471299	-1.2424	0.0000126	0.00015008	ENSMUSG00000022878	ADIPO

Supplemental Figures

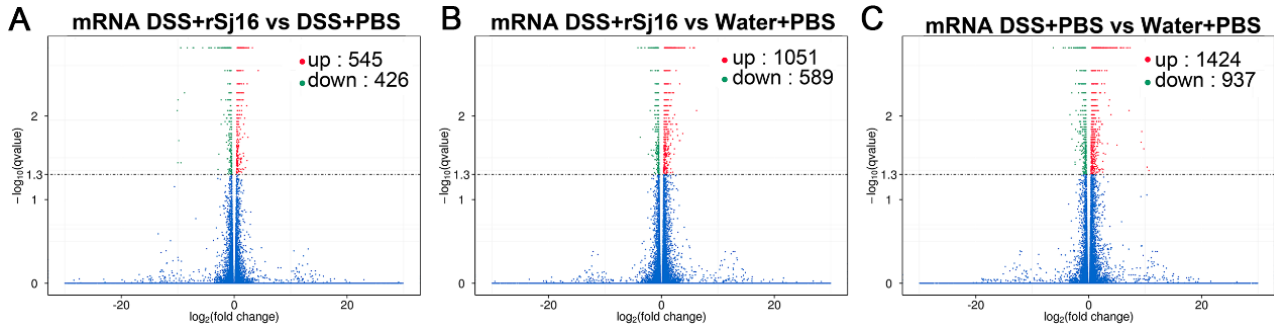


Figure S1 Volcano diagrams of mRNAs comparative gene expression analysis. **(A)** DSS + rSj16 group compare with DSS+PBS group revealed 971 (545 up and 426 down) statistically significantly differentially expressed genes. **(B)** DSS+ rSj16 group compare with Water + PBS group revealed 2,361 genes (1051 up and 589 down) statistically significantly differentially expressed genes. **(C)** 1640 genes (1424 up and 937 down) differentially expressed genes were found between DSS + PBS group and Water + PBS group.

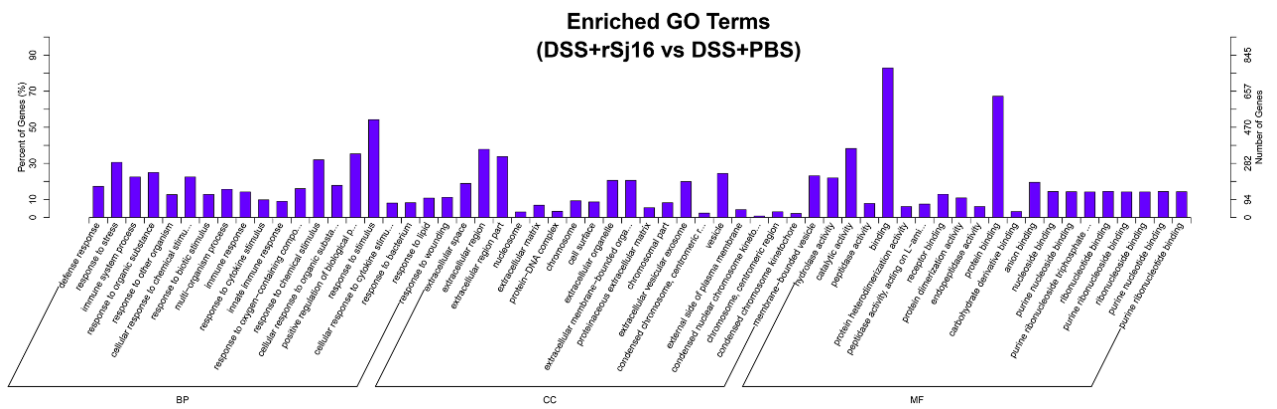


Figure S2 The differentially expressed genes of DSS + rSj16 group compare with DSS+PBS group were analyzed by GO. BP means biological process, CC means cellular component and MF means molecular function.

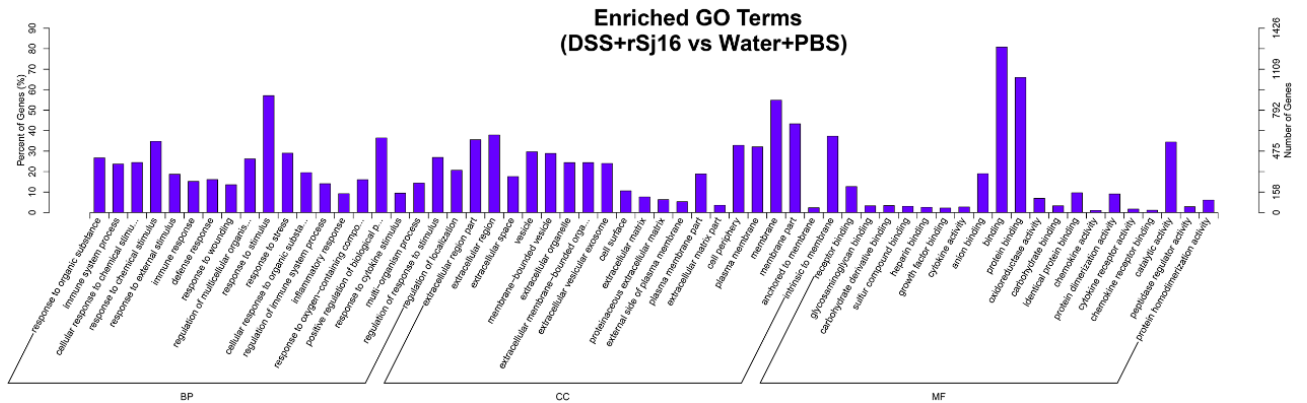


Figure S3 The differentially expressed genes of DSS + rSj16 group compare with Water+PBS group were analyzed by GO. BP means biological process, CC means cellular component and MF means molecular function.

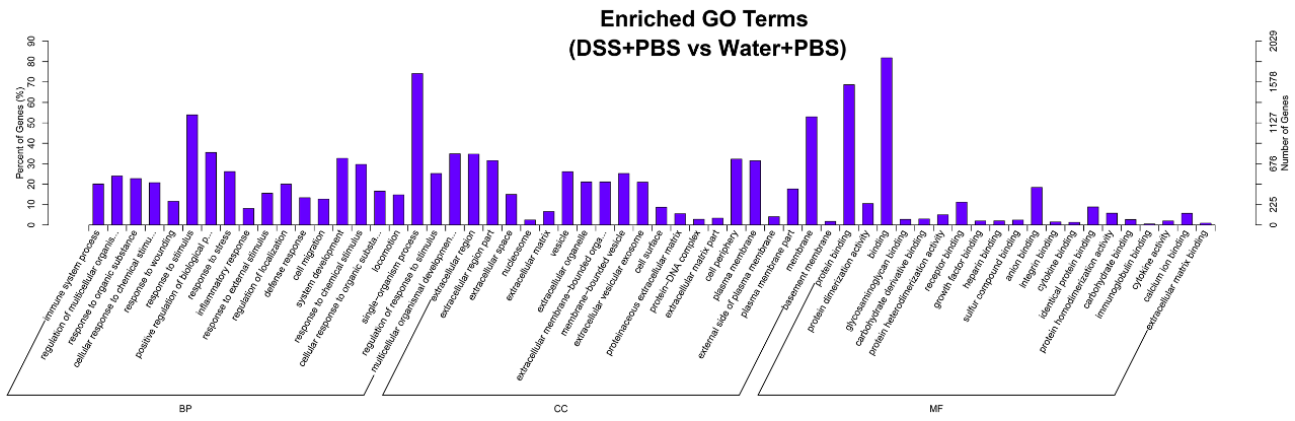


Figure S4 The differentially expressed genes of DSS + PBS group compare with Water+PBS group were analyzed by GO. BP means biological process, CC means cellular component and MF means molecular function.

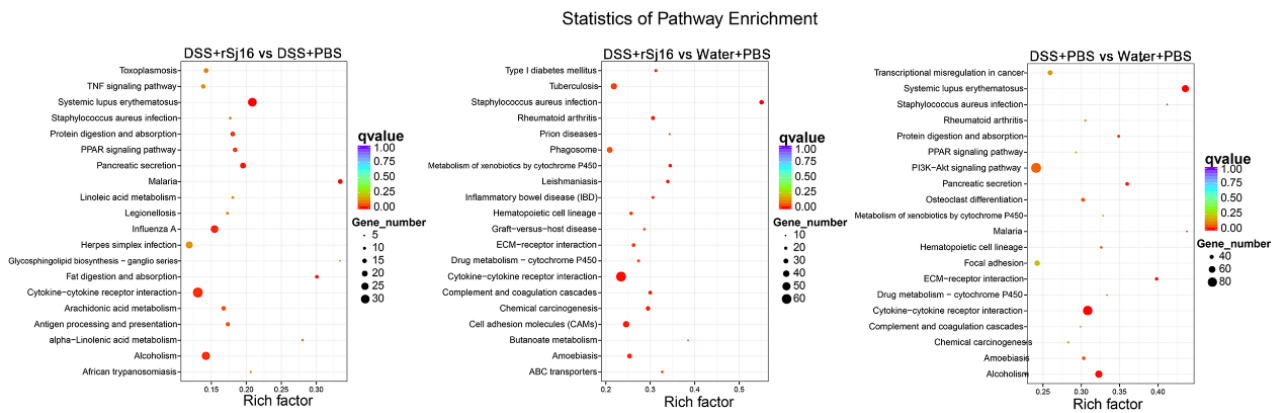


Figure S5 Differentially expressed genes were analyzed by KEGG enrichment analysis.

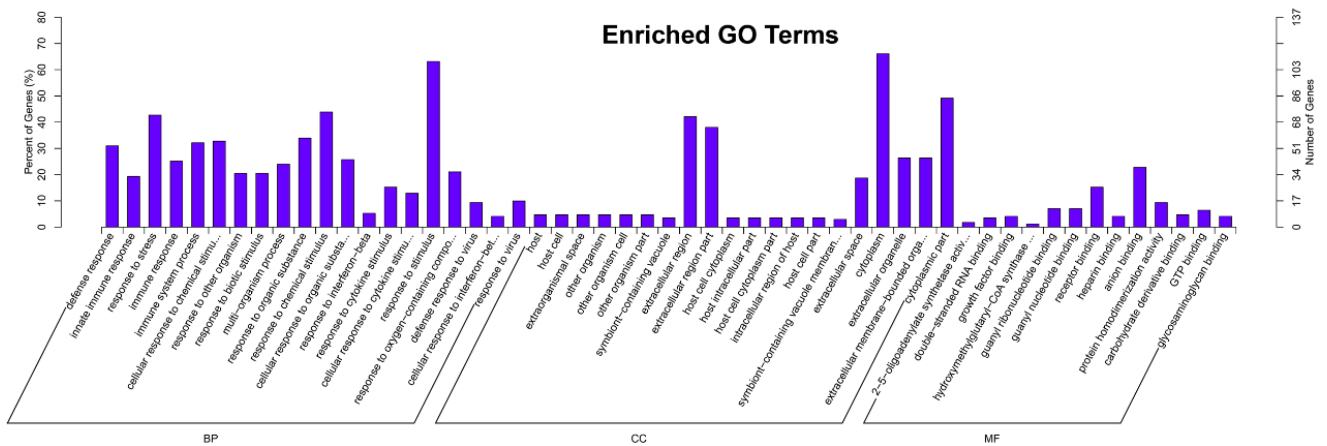


Figure S6 200 most obvious differentially expressed genes were subjected to analyzed by GO.