

**Table S1.** List of primer sequences used in the RT-PCR.

<b>Genes</b>	<b>Primers</b>	<b>Primer Sequences (5'-3')</b>
Ptprs	F	CCAAGAACCGCTATGCCAAC
	R	ACACCATCCGCCAGAAGTC
Slc6a4	F	ACCAGCAGACAAGGCAGAG
	R	GCCAATGACAGACAGGAGGA
Defb1	F	GGCATTCTCACAAGTCTTGGA
	R	AGTTGGGCTTATCTGGTTTACA
Tafa4	F	GCAATAAGAACCGCATAGAGGA
	R	GGCACCACCACTTCTCAATC
Serpina3k	F	CAGACTTCCAGCAGCCTACT
	R	AATTCACCAGCACCATCAATGT
Cfd	F	GGACGGATGACGACTCTGT
	R	GGACCCAACGAGGCATTCT
Usp44	F	GGACAGCAGATGAACGAAGG
	R	CAGACCACATGACTTGGAACA
CD69	F	AGGCTTGTACGAGAAGTTGGA
	R	TGGTTGTGGTGGAGAAGAAGT
Trim27	F	AGCATGAGTACCGCCTGTT
	R	TGTGTCTCCAATGTCCTGTAAG
Lamc2	F	CGCCTGGATGACCTCAAGA
	R	CGTAGTGCTCAGAAGAATGGAT

Traf3	F	ACACAGGCTTGCTGGAGTC
	R	CGCTTGTAGTCACGGATCTTC
GAPDH	F	TCAAGCTCATTTCCTGGTATGAC
	R	GGATAGGGCCTCTCTTGCTC

**Table S2.** Alpha diversity index of bacterial 16S rRNA gene sequences.

Items	DSS	DSS+LOW	DSS+MID	DSS+HIG	SEM	<i>p</i> -value
Shannon	3.794	3.824	3.911	3.720	0.0632	0.781
Simpson	0.0511	0.0472	0.0431	0.0507	0.00361	0.865
ACE	343	320	320	332	6.840	0.591
Chao	351	325	319	339	7.488	0.421

**Table S3.** The results of raw reads after quality control.

Sample	Raw eads	Clean reads	Clean bases(G)	Error rate(%)	Q20( %)	Q30( %)	GC content (%)
DSS+MI	811983	7880550	11.82	0.03	97.92	94.11	54.65
D1	36	0					
DSS+MI	909030	8802094	13.2	0.03	97.94	94.12	53.71
D2	36	6					

DSS+MI D3	1.05E+ 08	1.01E+0 8	15.17	0.03	97.63	93.52	52.8
DSS+MI D4	819886 24	7974798 6	11.96	0.02	98.15	94.72	52.61
DSS+MI D5	841204 20	8050420 2	12.08	0.03	97.65	93.56	49.83
DSS+MI D6	1.07E+ 08	1.05E+0 8	15.73	0.03	97.72	93.67	51.05
DSS1	1.03E+ 08	9974451 4	14.96	0.03	97.76	93.72	50.42
DSS2	1.06E+ 08	1.02E+0 8	15.27	0.03	97.83	93.91	50.46
DSS3	1.05E+ 08	1.01E+0 8	15.14	0.03	97.62	93.51	52.94
DSS4	817371 70	7933855 6	11.9	0.03	97.92	94.24	61.29
DSS5	935756 22	9005432 0	13.51	0.03	97.78	93.74	49.47
DSS6	842636 02	8066247 6	12.1	0.03	97.93	94.3	59.12