## Supplementary

Table S1 The effects of probiotics on mouse body weight

Groups	Primary weight (g)	Terminal weight (g)	Margin (g)	P values
High-dose group	21.2±0.5	39.6±1.5	18.4±1.6	0.250*
Middle-dose group	21.1±0.5	40.3±2.1	19.2±2.1	0.835*
Low-dose group	21.2±0.6	39.6±1.8	18.4±1.7	0.245*
CCG	21.2±0.5	41.0±2.5	19.8±2.5	1.000*
NCG	21.1±0.7	41.1±2.0	19.9±1.8	

<sup>\*,</sup> compared to NCG. CCG, constipation control group; NCG, negative (healthy) control group.

Table S2 Results of pre- and post-treatment routine blood tests

Routine blood tests	L. plantarum Lp3a (n=59)	Placebo (n=58)	P value
White blood cell (109/L)			
Before trial	6.35±1.44	6.48±1.30	0.604*
After trial	6.55±1.52	6.52±1.55	0.934*
Comparison within group (t, P)	-1.456, 0.151 <sup>#</sup>	-0.303, 0.763#	
Red blood cell (10 <sup>12</sup> /L)			
Before trial	4.49±0.28	4.54±0.29	0.332*
After trial	4.50±0.29	4.54±0.35	0.448*
Comparison within group (t, P)	-0.200, 0.842#	-0.044, 0.965#	
Hemoglobin (g/L)			
Before trial	137.37±12.56	134.71±11.79	0.239*
After trial	136.42±13.00	133.88±13.64	0.304*
Comparison within group (t, P)	0.537, 0.593#	0.435, 0.665#	
Blood platelet (10 <sup>9</sup> /L)			
Before trial	193.59±53.63	190.97±51.73	0.788*
After trial	191.15±52.65	189.12±53.85	0.837*
Comparison within group (t, P)	0.391, 0.698#	0.332, 0.741#	

 $<sup>^{\</sup>star}$ , data compared by independent t-test.  $^{\#}$ , data compared by paired t-test.

Table S3 Results of pre- and post-treatment biochemical parameters

Biochemical parameters	L. plantarum Lp3a (n=59)	Placebo (n=58)	P value
Alanine aminotransferase (U/L)			
Before trial	26.39±4.81	26.53±4.81	0.871*
After trial	26.49±5.18	26.62±5.65	0.898*
Comparison within group (t, P)	-0.177, 0.860#	-0.152, 0.879 <sup>#</sup>	
Aspartate aminotransferase (U/L)			
Before trial	26.76±4.25	27.21±4.96	0.574*
After trial	26.63±3.70	27.29±4.79	0.401*
Comparison within group (t, P)	0.293, 0.771#	-0.114, 0.910#	
Blood urea nitrogen (mmol/L)			
Before trial	5.24±0.89	5.20±1.04	0.813*
After trial	5.31±0.63	5.33±0.74	0.848*
Comparison within group (t, P)	-0.617, 0.540 <sup>#</sup>	1.203, 0.234#	
Creatinine (umol/L)			
Before trial	68.85±15.30	72.33±14.84	0.214*
After trial	70.92±14.54	72.91±15.34	0.471*
Comparison within group (t, P)	-1.417, 0.162 <sup>#</sup>	-0.401, 0.690#	
Albumin (g/L)			
Before trial	42.34±3.79	41.97±3.40	0.580*
After trial	42.20±3.34	42.84±3.68	0.322*
Comparison within group (t, P)	0.261, 0.795#	-1.602, 0.115 <sup>#</sup>	
Total serum protein (g/L)			
Before trial	69.59±4.54	70.35±3.82	0.330*
After trial	70.50±4.94	70.16±3.75	0.675*
Comparison within group (t, P)	-1.188, 0.240#	0.271, 0.788#	
Total cholesterol (mmol/L)			
Before trial	4.79±0.49	4.82±0.41	0.727*
After trial	4.82±0.45	4.72±0.38	0.195*
Comparison within group (t, P)	-0.402, 0.689#	1.463, 0.149#	
Triglyceride (mmol/L)			
Before trial	1.22±0.37	1.21±0.32	0.865*
After trial	1.26±0.34	1.19±0.37	0.292*
Comparison within group (t, P)	-0.942, 0.350#	0.319, 0.751#	
Fast blood glucose (mmol/L)			
Before trial	4.96±0.52	4.91±0.46	0.590*
After trial	4.86±0.41	4.82±0.40	0.330*
Comparison within group (t, P)	0.830, 0.410#	1.260, 0.213#	

<sup>\*,</sup> data compared by independent *t*-test.\*, data compared by paired *t*-test.

Table S4 Vital signs before and after treatment

Vital signs	L. plantarum Lp3a (n=59)	Placebo (n=58)	P value
Heartbeat (time/min)			
Before trial	74.69±5.69	75.00±5.53	0.769*
After trial	75.32±5.23	75.31±5.27	0.990*
Comparison within group (t, P)	-1.112, 0.271#	-0.523, 0.603#	
Systolic pressure (mmHg)			
Before trial	129.32±5.83	131.03±5.44	0.103*
After trial	130.51±3.68	130.60±4.30	0.898*
Comparison within group (t, P)	-1.606, 0.114#	0.556, 0.573#	
Diastolic pressure (mmHg)			
Before trial	88.98±6.00	90.17±5.21	0.255*
After trial	88.73±5.99	90.26±5.08	0.139*
Comparison within group (t, P)	0.258, 0.797#	-0.109, 0.914#	

<sup>\*,</sup> data compared by independent *t*-test. \*, data compared by paired *t*-test.

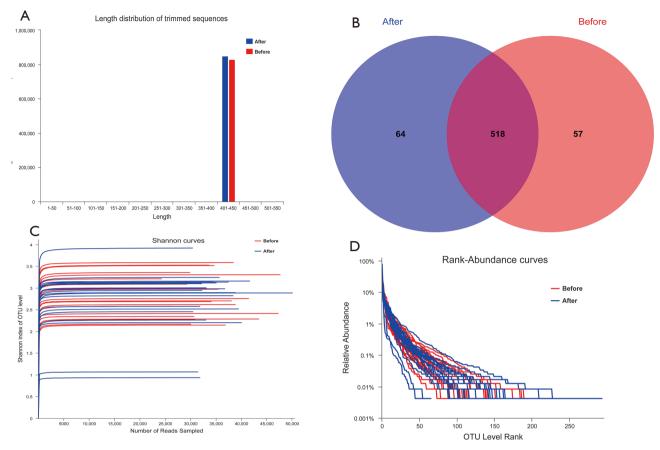


Figure S1 16S rRNA sequencing analysis of the pre- and post-treatment fecal microbiome samples: (A) Sequence lengths varied from 401 to 450 bp in the pre- and post-treatment samples; (B) Genes clusters for 575 Operational Taxonomic Units (OTUs) in the pre-treatment and 582 OTUs in the post-treatment samples, of which 518 OTUs were common; (C) Shannon index of the rarefaction curves for the pre- and post-treatment fecal samples demonstrating species richness, diversity, and evenness; (D) Rank-abundance curves for the pre- and post-treatment fecal samples demonstrating species richness, diversity, and evenness.