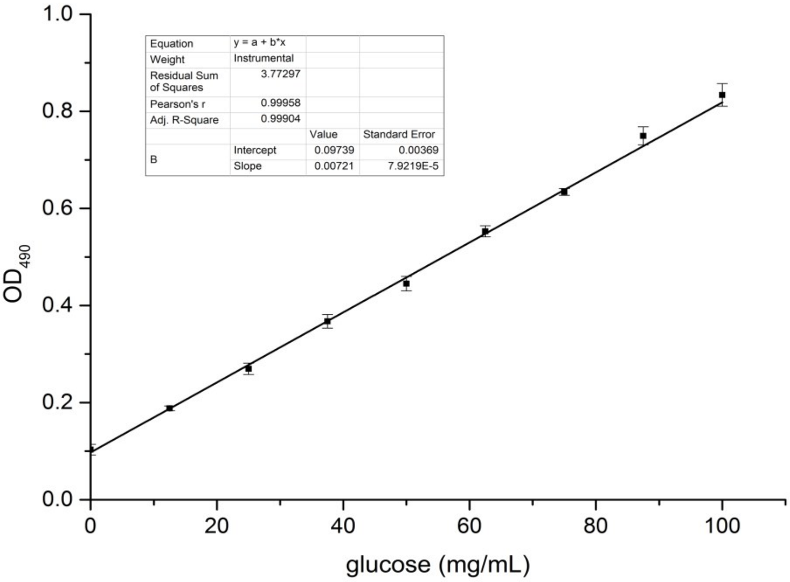
Table S1 Quantitative-PCR primer information

Phylum	Primer sequence (5′-3′)	Tm (°C)	Amplicon length (bp)
Bacteroidetes	Forward: GTTTAATTCGATGATACGCGAG Reverse: TTAASCCGACACCTCACGG	60	122
Firmicutes	Forward: GGAGYATGTGGTTTAATTCGAAGCA Reverse: AGCTGACGACAACCATGCAC	60	126
Actinobacteria	Forward: TGTAGCGGTGGAATGCGC Reverse: AATTAAGCCACATGCTCCGCT	60	227
Delta- and Gamma proteobacteria	Forward: GCTAACGCATTAAGTRYCCCG Reverse: GCCATGCRGCACCTGTCT	60	189
Candidatus Saccharibacteria	Forward: AAGAGAACTGTGCCTTCGG Reverse: GCGTAAGGGAAATACTGACC	60	187
Tenericutes	Forward: ATGTGTAGCGGTAAAATGCGTAA Reverse: CMTACTTGCGTACGTACTACT	60	200

Fig. S1 The crude exopolysaccharide (EPS) produced by *L. helveticus* KLDS1.8701.



Equation	y = a + b*x		
Weight	Instrumental		
Residual Sum of Squares	3.77297		
Pearson's r	0.99958		
Adj. R-Square	0.99904		
		Value	Standard Error
B	Intercept	0.09739	0.00369
	Slope	0.00721	7.9219E-5

Fig. S2 The calibration curve of glucose used for the phenol-sulfuric acid method.

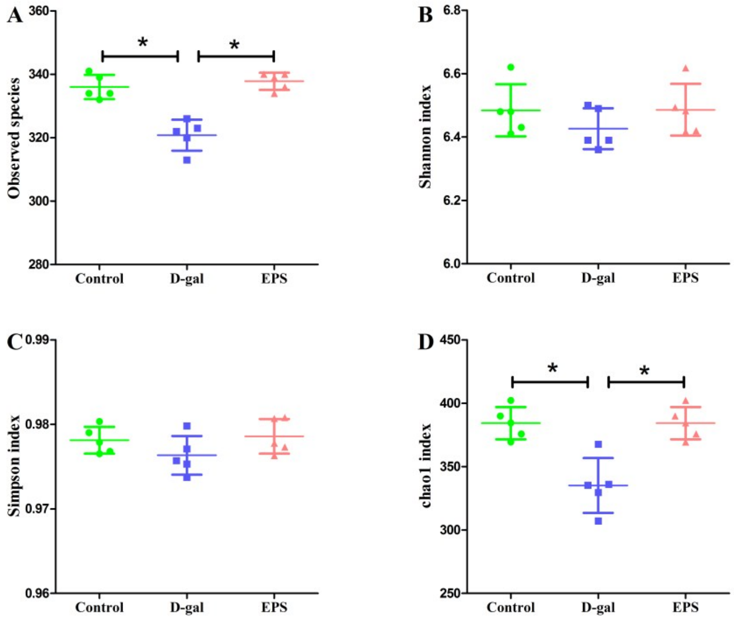


Fig. S3 Influences of EPS supplementation on gut microbiota α-diversity. (**A**) Observed-species index; (**B**) Shannon index; (**C**) Simpson index; and (**D**) chao 1 index. All data are expressed as mean ± SD. * $p < 0.05$: significantly different compared with D-gal model mice.

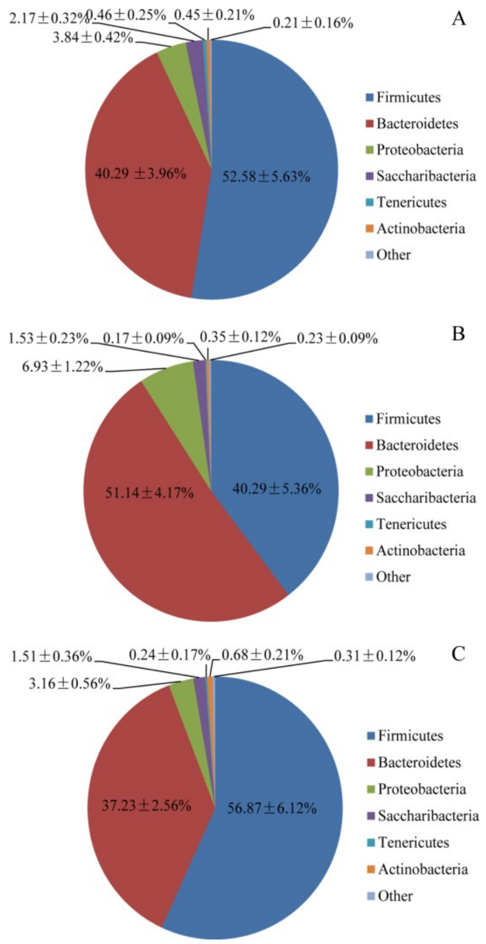


Fig. S4 qPCR analyses of the phylum level in the cecal contents among all groups. (**A**) The control group; (**B**) The D-gal group; and (**C**) The EPS group. All data are expressed as mean ± SD.