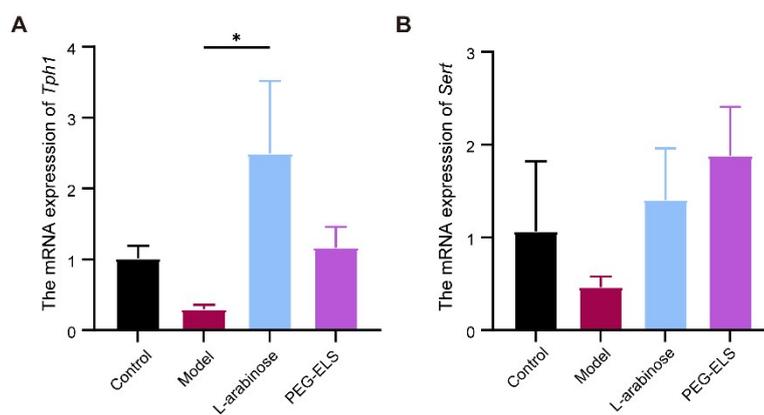


Supplementary data

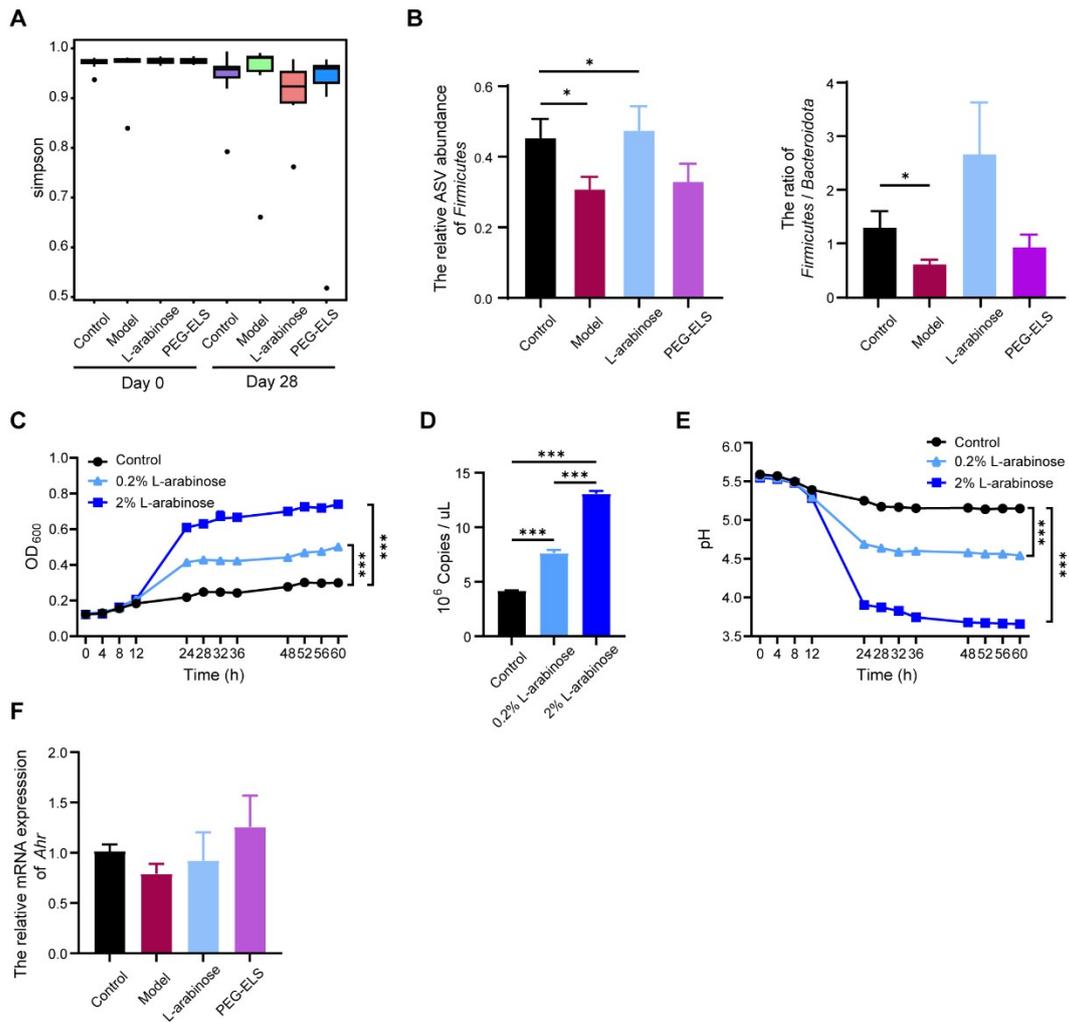
Supplementary Table.1 Primer sequence

Gene	Primer sequence
<i>mTph1</i>	F: AACAAAGACCATTCTCCGAAAG
<i>mTph1</i>	R: TGTAACAGGCTCACATGATTCTC
<i>mSert</i>	F: TATCCAATGGGTACTCCGCAG
<i>mSert</i>	R: CCGTTCCCCTTGGTGAATCT
<i>mActin</i>	F: ACCACACCTTCTACAATGAG
<i>mActin</i>	R: ACGACCAGAGGCATACAG
<i>mAhr</i>	F: AGCCGGTGCAGAAAACAGTAA
<i>mAhr</i>	R: AGGCGGTCTAACTCTGTGTTC

Supplementary figures



Supplementary Figure 1. Relative mRNA expression levels of *Tph1* and *Sert* in ileum of experimental mice (n = 4-6). * $P < 0.05$ vs Control.



Supplementary Figure. 2. L-arabinose regulated gut microbiota and relevant genes expression of constipated mice. (A) Statistical analysis of Alpha Diversity-Simpson index of intestinal bacteria in mice of Day 0 and Day 28 (n = 7-10). (B) Analysis on the difference of the relative ASV abundance of *Firmicutes* and the ratio of *Firmicutes/Bacteroidota* in each group of mice of Day 28 (n=7-10). (C) Changes of absorption at 600 nm of *Lactobacillus plantarum* TWK10 culture media in each group within 60 h (n = 3). (D) qPCR results of *Lactobacillus plantarum* TWK10 amount in each group at 60 h. (n = 3). (E) Changes of pH value of *Lactobacillus plantarum* TWK10 culture media in each group within 60 h (n = 3). (F) Relative expression levels of *Ahr* genes in ileum of experimental mice (n = 4-6). * $P < 0.05$, *** $P < 0.001$ vs Control.