Supporting Information for ORIGINAL ARTICLE

Supplementary materials and methods

Quantitative analysis of NOB

The levels of NOB in mice feces were quantitated by a liquid chromatography-tandem mass spectrometry system (LC-MS/MS). The feces were added 9-fold w/v of ultrapure water followed by ultrasonic extraction for 10 min. Next, the supernatant was harvested after centrifuging at 13,000 rpm and 4℃ for 10 min after adding methanol. The supernatant was then dried under nitrogen, and then resuspension in 100 mL methanol and centrifugation for 10 min at 13,000 rpm and 4℃. Chromatographic separation of samples was conducted on a TSQ Vantage triple quadrupole mass spectrometer and Prelude SPLC system (Thermo Fisher Scientific, USA). The mobile phase was isocratic elution, with the solvent compositions A solution being 5 mM ammonium acetate and 0.1% [v/v] formic acid, and B solution being methanol. For the column, a temperature of 40°C was established. TraceFinder software (version 3.3 sp1, Thermo Fisher Scientific, USA) was employed for data acquisition and analysis.

Supplementary tables and figures

Table S1. Primers for qPCR

	Left primer (5'-3')	Right primer (5'-3')
TNF-α	CCACCACGCTCTTCTGTCTAC	AGGGTCTGGGCCATAGAACT
IL-1β	GGTCAAAGGTTTGGAAGCAG	TGTGAAATGCCACCTTTTGA
IL-6	TGATGCACTTGCAGAAAACA	ACCAGAGGAAATTTTCAATAGGC
GAPDH	TGACCTCAACTACATGGTCTACA	CTTCCCATTCTCGGCCTTG

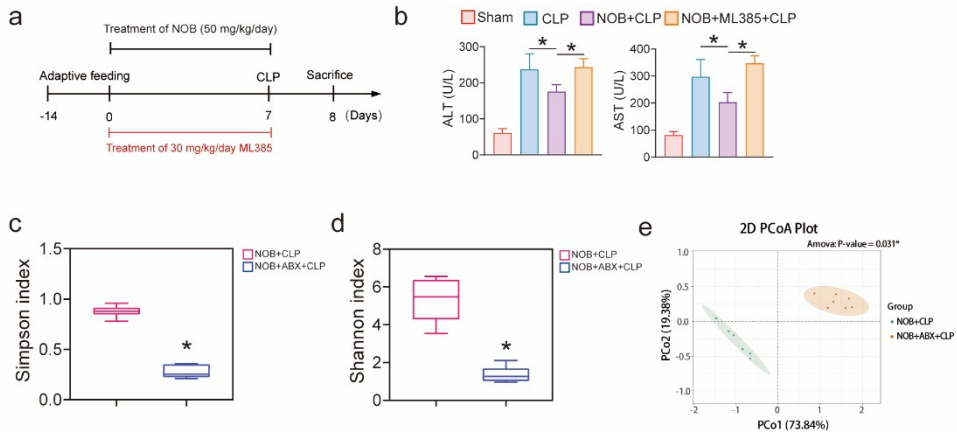

Figure S1 (**a**) Experimental design and timeline for effects of NOB and ML385 on SALI. (**b**) Relative plasma ALT and AST levels (n=4). (**c-d**) The Alpha diversity indices were accessed by Simpson and Shannon in gut microbiomes. (*n* = 6). (**e**) The β-diversity of intestinal bacteria showed by the weighted unifrac principal coordinates analysis (PCoA). (*n* = 6). **P* < 0.05.

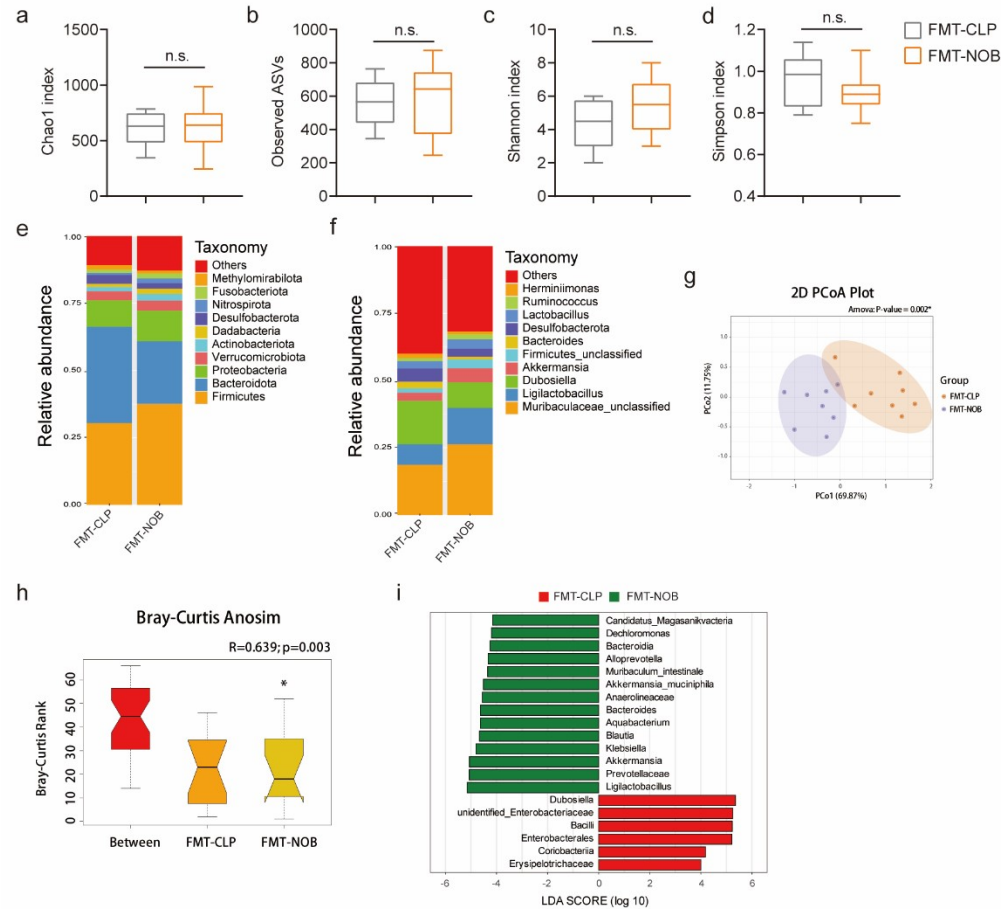

Fig. S2 Gut microbiota structure in FMT-treated mice. (a-d) Alpha diversity indices were accessed by Chao 1, observed OTUs, Shannon, and Simpson in

gut microbiomes. (e-f) Relative abundance of the gut bacteria at the phylum and genus level in each group. (g) The β-diversity of intestinal bacteria showed by the weighted uniFrac principal coordinates analysis (PCoA). (h) Anosim analysis on weighted UniFrac distances in feces. (i) Histogram of linear discriminant analysis (LDA) represented the enriched bacteria between the FMT-CLP and FMT-NOB groups, n=8. Data are expressed as the mean±SEM. *P<0.05, and n.s. indicates nonsignificant.

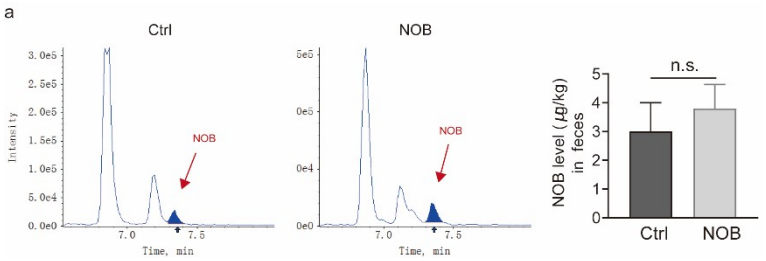

Fig.S3 NOB levels in feces from mice treated with or without NOB for 7 days by targeted liquid chromatography-tandem mass spectrometry analysis (LC-MS/MS). n=5. Data are expressed as the mean±SEM. The n.s. indicates nonsignificant.