Supplementary Methods (S1-2)

1. 16S rDNA Sequencing. Total microbial genomic DNA was extracted from the mice colonic contents in the CK and FO + JZXJ-7 groups using the QIAamp DNA tool kit (QIAGEN, Germany). The DNA concentration and purity were monitored on a 1% agarose gel and diluted to 1ng/μL to produce amplicons. Next, the 16S V3-V4 rRNA gene was amplified using primers 341F (CCTACGGNGGCWGCAG) and 806R (GGACTACHVGGGTATCTAAT). Subsequently, the products were extracted from 2% agarose gels and purified using the AxyPrep DNA gel extraction kit (Axygen Biosciences, MA, USA) according to the manufacturer's instructions, and quantified via the ABI Step One Plus real-time PCR system (Life Technologies, MA, USA). Sequencing was performed on an Illumina HiSeq 4000 platform (San Diego, CA, USA) by GUHE Info. Technology Co. (Hangzhou, China) with a MiSeq reagent kit v2 (Illumina, CA, USA).

The UPARSE software was used to perform operational taxonomic unit (OTU) clustering of 16S rRNA gene sequences based on 97% similarity. Alpha diversity of samples was calculated by QIME analysis of OTUs using Chao1, Shannon, Simpson, and coverage indices. The OTUs of each sample was used to determine beta diversity. The similarity between samples was calculated using the unweighted pairwise group method of arithmetic averaging (UPGMA) which were represented in principal component analysis and principal coordinate analysis (PCoA). The Stamp software was used to examine differences in taxonomic abundance of individuals. The Linear

discriminant analysis effect size (LEfSe) was used to quantify biomarkers between CK and FO + JZXJ-7 groups.

2. Metabolomic Analysis. Untargeted metabolomics analysis of the colonic contents was conducted. Briefly, a section of the colon (~100 mg) of the CK or FO + JZXJ-7 group was accurately weighed and mixed with 1 mL of pre-cooled 50% methanol (v:v) and homogenized at 3,000 g for 10 min using a homogenizer (Bertin Technologies, France). After removing the organic solvent, the samples were characterized by liquid chromatograph mass spectrometry (LC-MS) with an Acquity LC system (Waters, MA, USA) and a Q Exactive High resolution/precision mass spectrometer (Thermo Scientific, MA, USA). Raw data were processed by the XCMS, CAMERA, and metaX toolbox implemented by the R software. The online KEGG and HMDB databases and the metabolite fragment spectrum library were used to annotate the samples by matching the exact molecular mass data (m/z) of the samples with the metabolites in the database. The KEGG database[2] was used to analyze the metabolic pathways of differential metabolites. The intensity of the peak data was processed by metaX software. Differences in metabolite concentrations between CK and FO + JZXJ-7 groups were analyzed by Student *t* test. The *p* values between CK and FO + JZXJ-7 groups were corrected for multiple tests by False Discovery Rate (FDR, Benjamini-Hochberg) and supervised partial least squares discriminant analysis (PLS-DA). Different variables were discriminated by metaX.