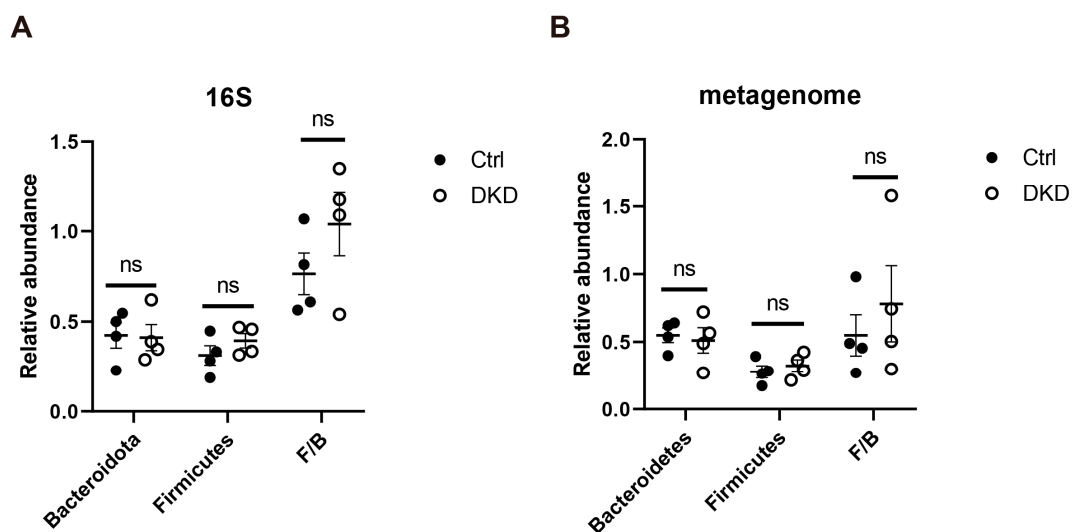


Supplemental information



Supplemental Figure S1 At the phylum level, there was no significant difference in relative abundance of Bacteroidetes and Firmicutes between Ctrl and DKD groups

Supplemental Table S1

Body weight, blood glucose levels, UACR in the mice of Ctrl and DKD groups.

Supplemental Table S2A and B

Relative abundance of microorganisms in each sample at each classification level (domain, phylum, class, order, family, genus, species) obtained from 16S rDNA sequencing analysis (A) and metagenomes (B).

Supplemental Table S3

The annotated results of metagenomic sequences in COG, KEGG, CAZy and CARD databases.

Supplemental Table S4

This list can be used for GSVA analysis and display relationship between AMR and corresponding antibiotic resistance modified from recorded in the CARD.

Supplemental Table S5

This data contains compound characteristics, quantitative results, and information on differences between groups for each substance detected in metabonomics.