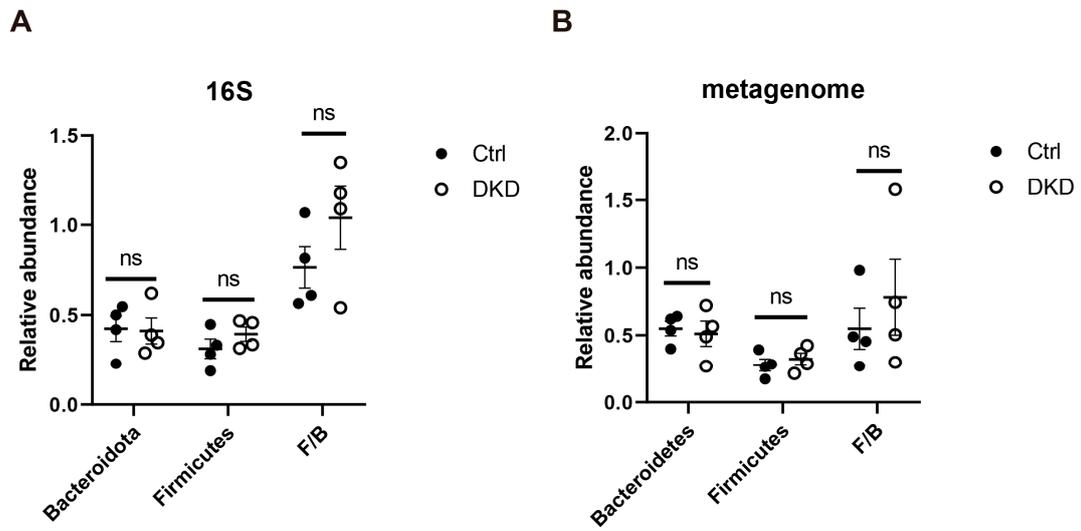


## Supplemental information



**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.