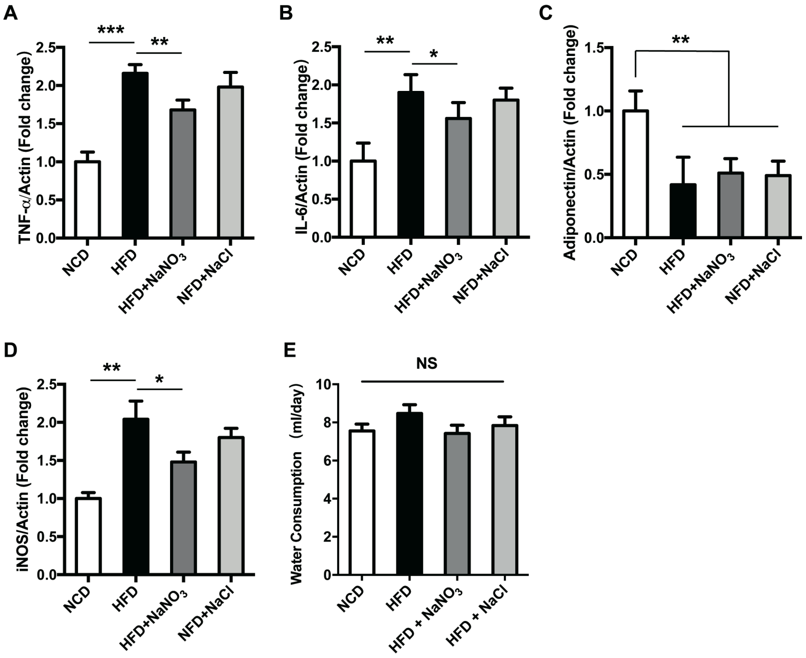
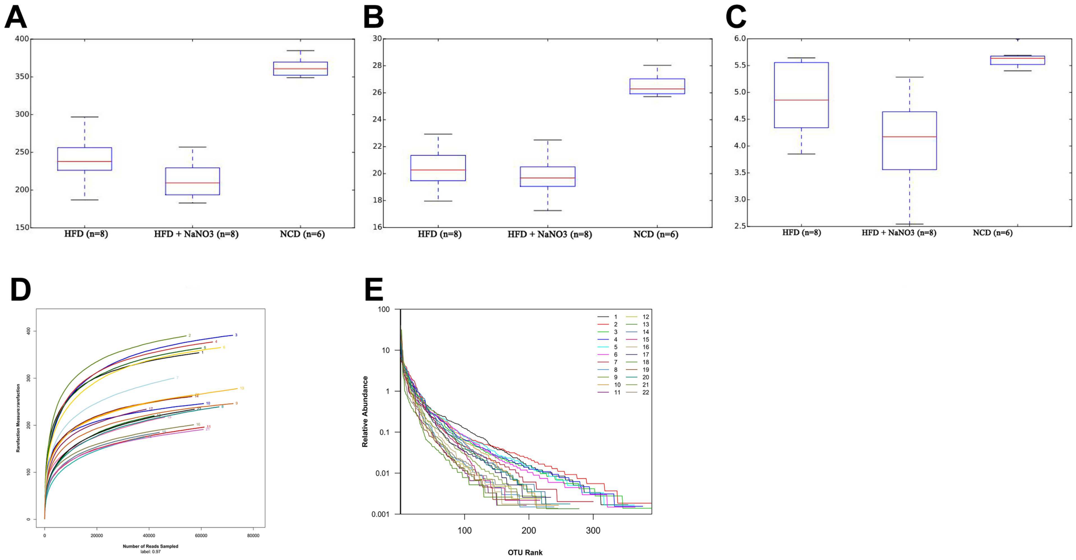
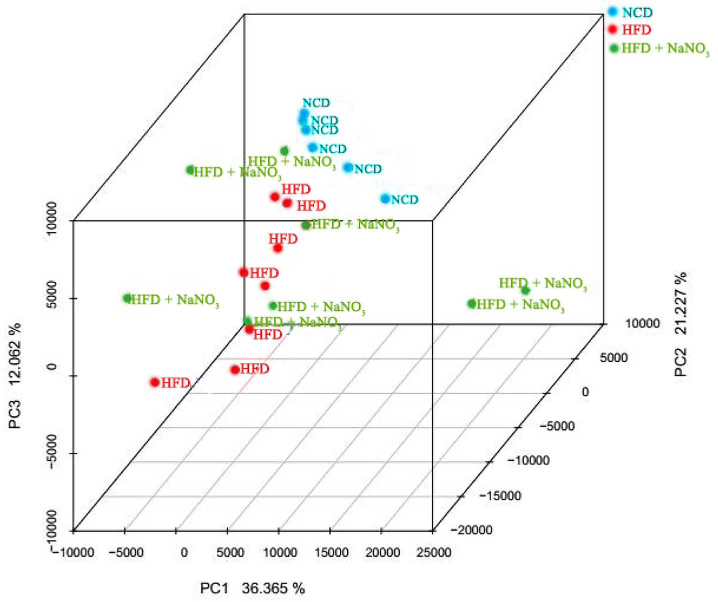


Supplementary Figure 1. (A, B, C) The gene expression of TNF-α and IL-6 and adiponectin in inguinal adipose tissue. Inflammatory cytokines expression was higher in HFD fed mice and lowered by nitrate supplement. (D) The gene expression of iNOS in intestinal epithelial showed higher in HFD group and lowered by nitrate supplement. (E) The water consumption was monitored every week and calculated as mean consumption each day. The result of drinking intake was without differences among groups.

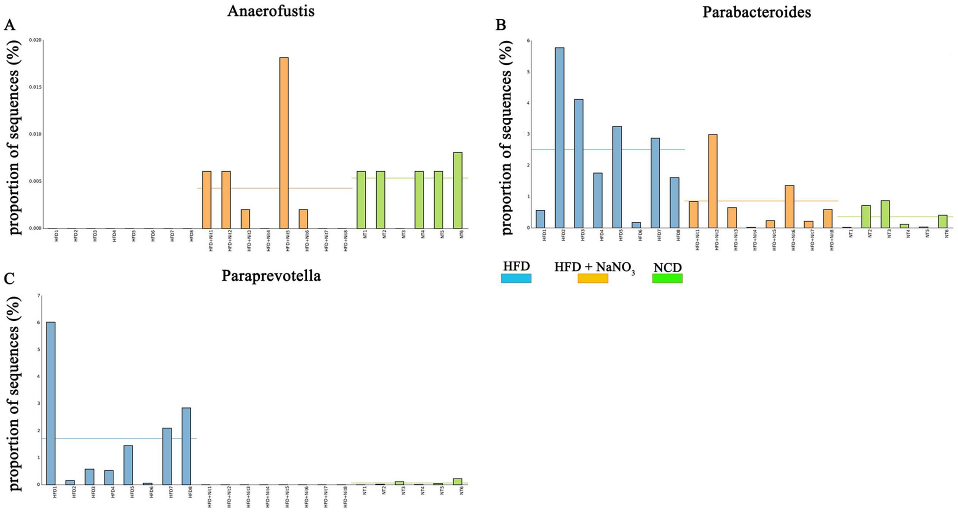


Supplementary Figure 2. The alpha diversity of gut microbiome among three groups.

(A, B) Both the observed species and Pd whole tree presented that the gut microbiome in the HFD group and the HFD + NaNO3 group were decreased than that in the NCD group. While no significant difference was found. (C) The Shannon index showed microbial diversity. The between-group variance in the HFD group and HFD + NaNO3 group were much larger than that in the NCD group. (D) The Rarefaction curve was to compare the abundance of different data and whether the sequencing data was reasonable. Our results showed that the samples collected and analyzed in our study were qualified. (E) The rank-abundance curve was to show the abundance and uniformity of samples. The results presented that the samples in our study were similar and qualified.



Supplementary Figure 3. Three-dimensional principal co-ordinates analysis (3D-PCA) of gut microbiome among three groups. Distribution exhibited the similarity or difference among groups in a visualized way corresponding with what showed in Figure 6B.



Supplementary Figure 4. Differential bacteria among three groups at the genus level by LDA Effect Size (LEfSe) Analysis. The graph showed specific differential bacteria including Anaerofustis, Parabacteroides, and Paraprevotella. And abundance from each specimen was presented.