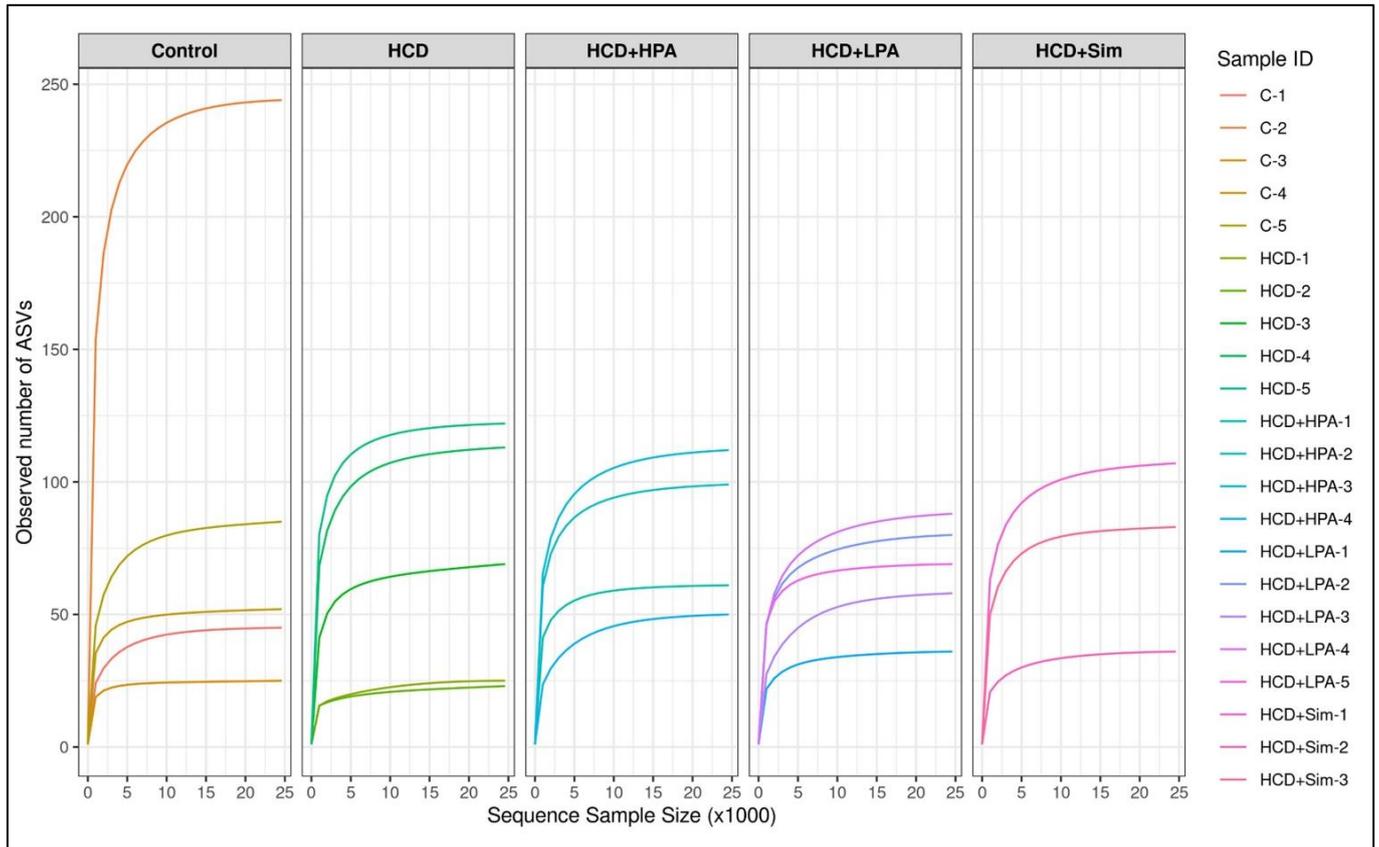


Supplementary data



Supplementary S1. Rarefaction analysis of 16S rRNA gene sequences obtained from rat fecal samples. The approximate saturation of microbial richness of all samples was 24,671 sequencing depths, as estimated by the rarefaction curves. Each line represented individual fecal sample.