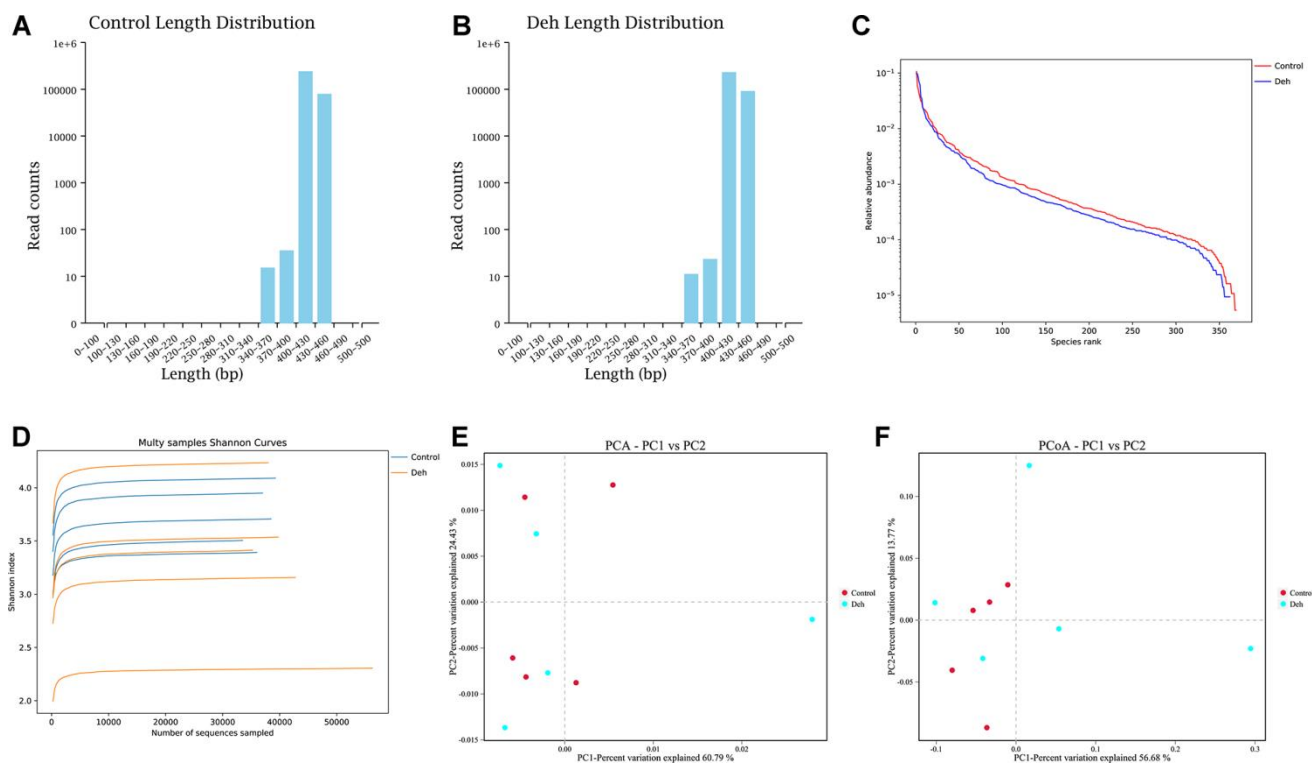
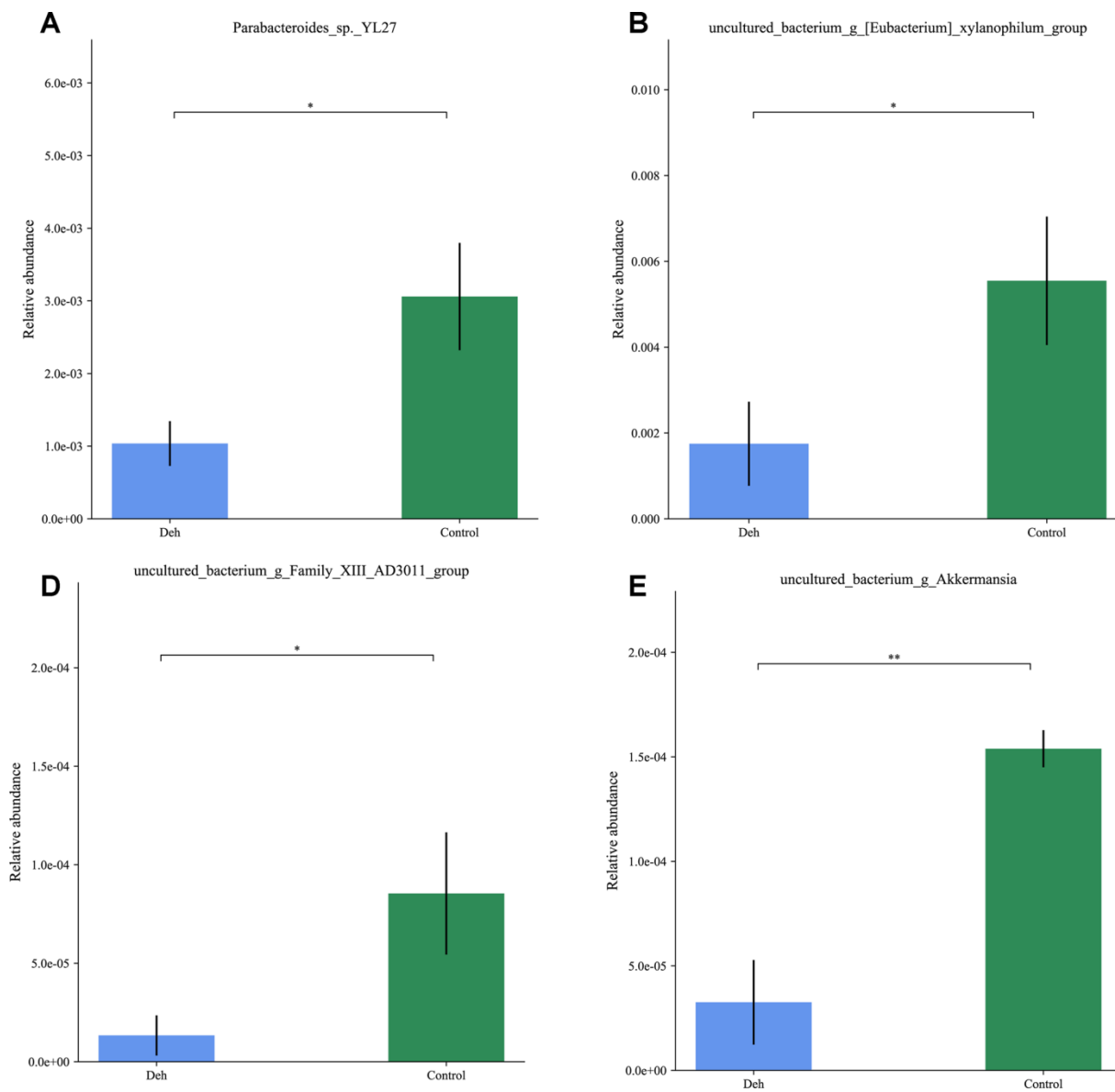


## SUPPLEMENTARY FIGURES



**Supplementary Figure 1. The quality of microbiome sequencing in mice feces. (A, B)** Length distribution in Control and Deh. **(C)** Relative abundance in Control and Deh. **(D)** Shannon index in Control and Den. **(E, F)** PCA and PCoA analysis between Control and Deh.



**Supplementary Figure 2. Effect of dehydroandrographolide on low abundance flora. (A–D)** At the species level, Parabacteroides sp. YL27, [Eubacterium] xylanophilum group, Family XIII AD3011 group and Akkermansia in Deh and Control group. Values are presented as the mean ± SD (\* $p < 0.05$ , \*\* $p < 0.001$ , \*\*\* $p < 0.001$  and \*\*\*\* $p < 0.0001$ ).