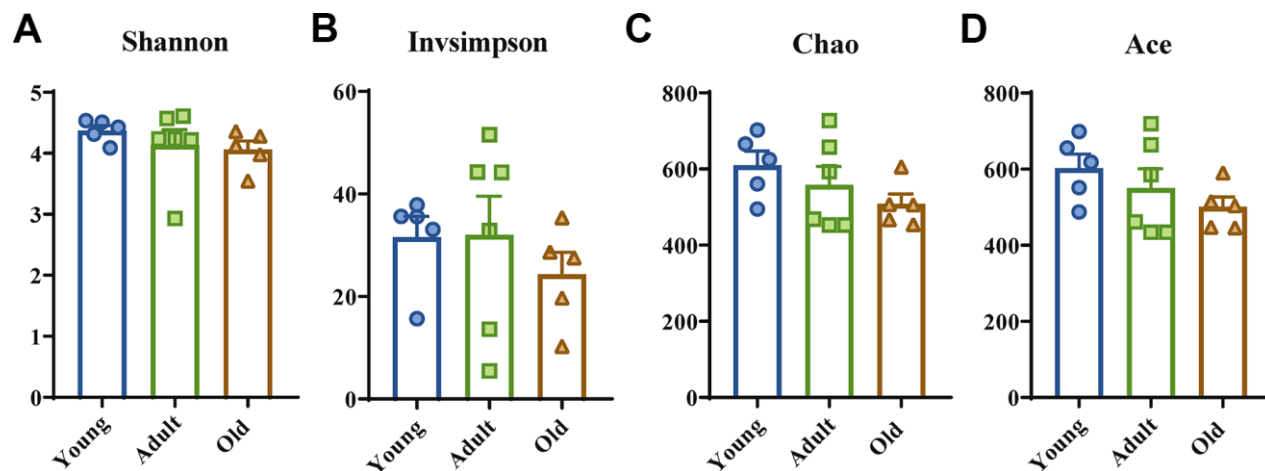
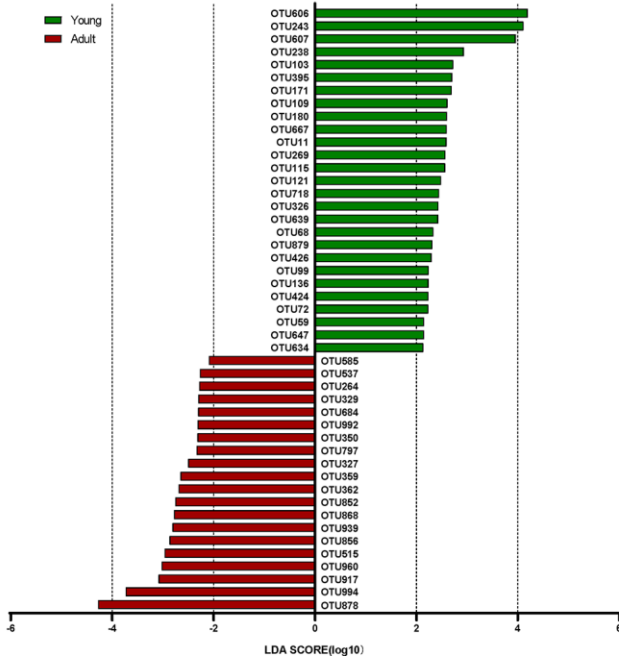
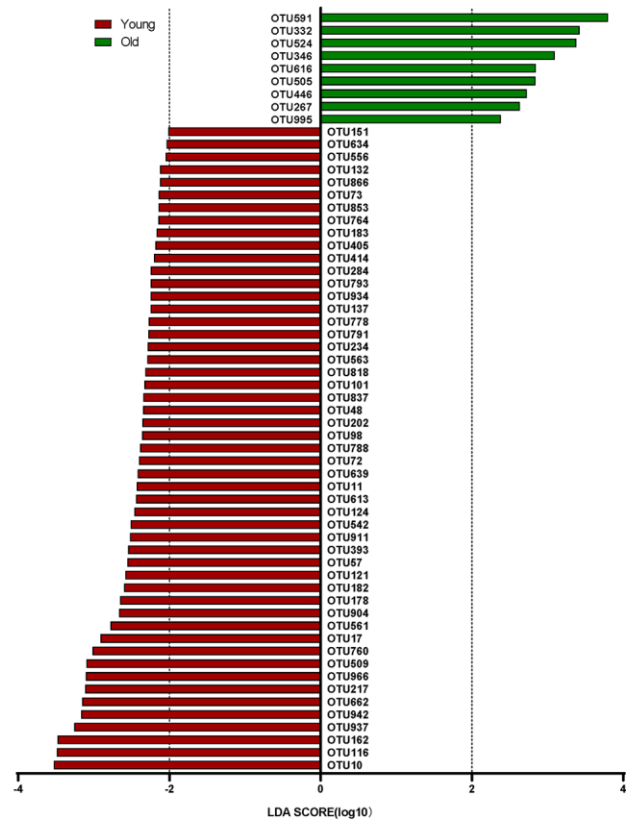
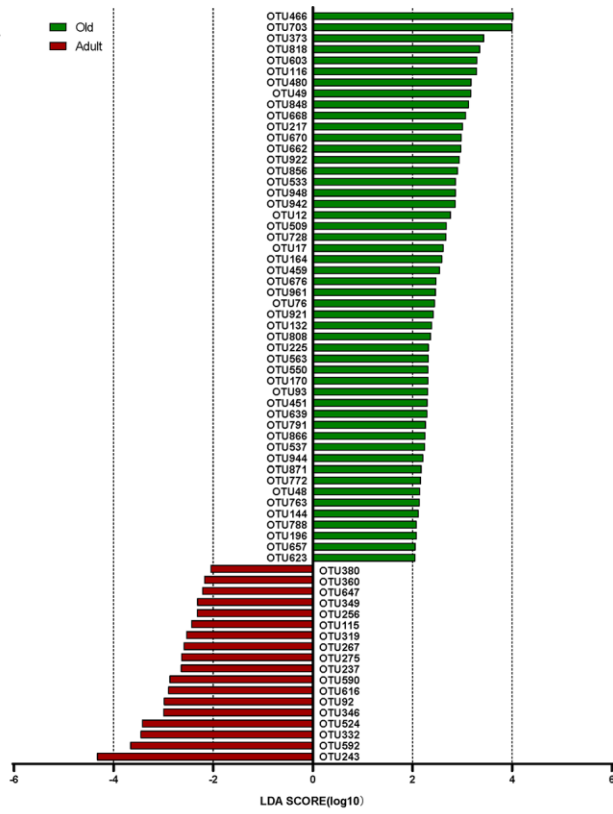


SUPPLEMENTARY FIGURES

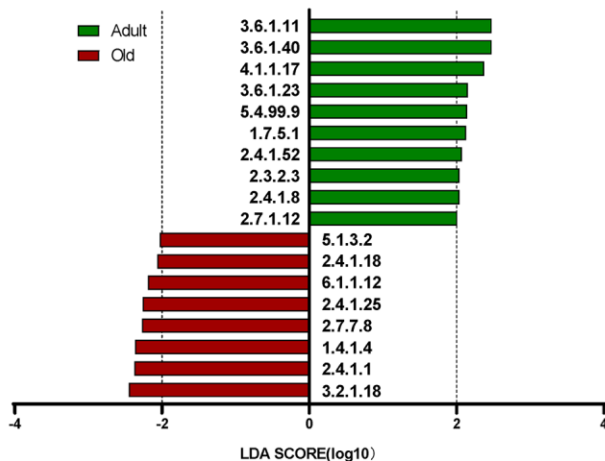
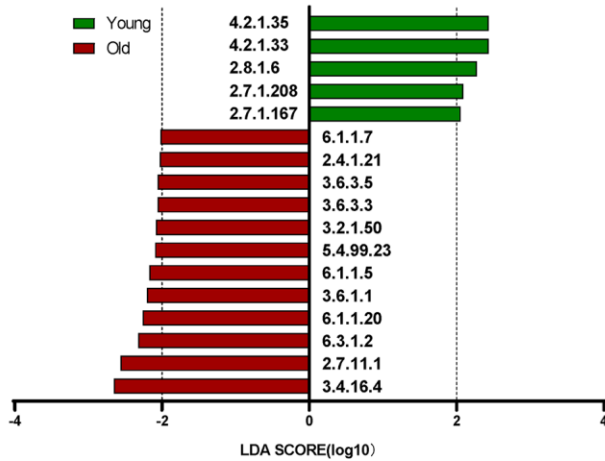
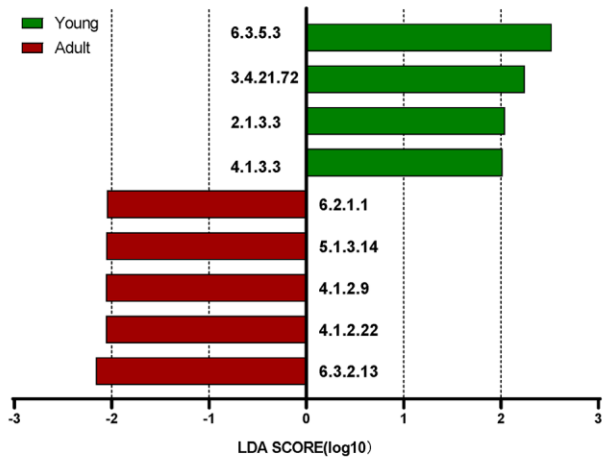


Supplementary Figure 1. Gut microbial characteristics of monkeys at the α -diversity analysis. Comparing the microbial composition of three groups based on α -diversity analysis. (A–D) In these four indexes (Shannon, Invsimpson, Chao and Ace), there is no significant difference among the three groups (Young, n=5; Adult, n=6; Old, n=5).

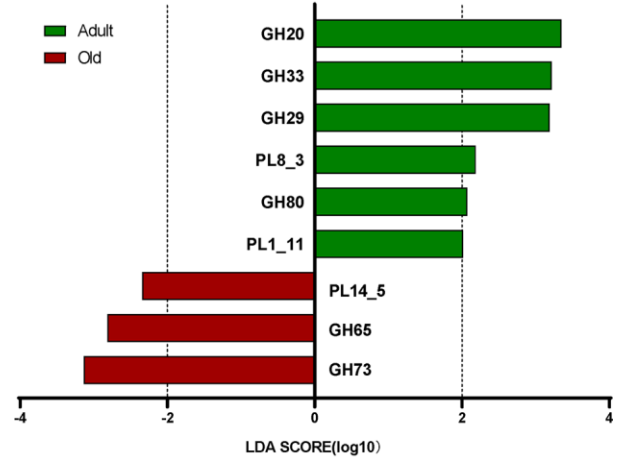
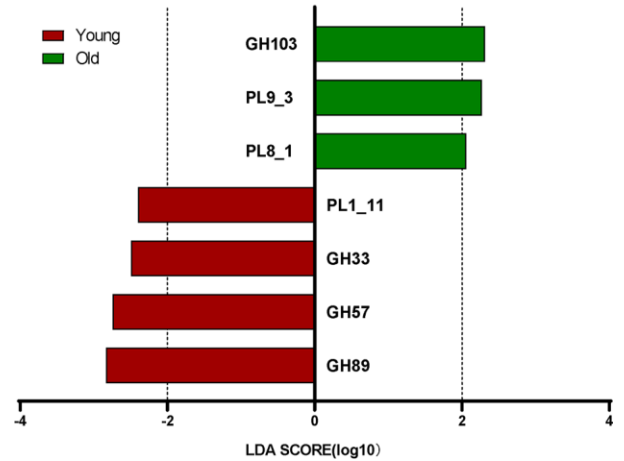
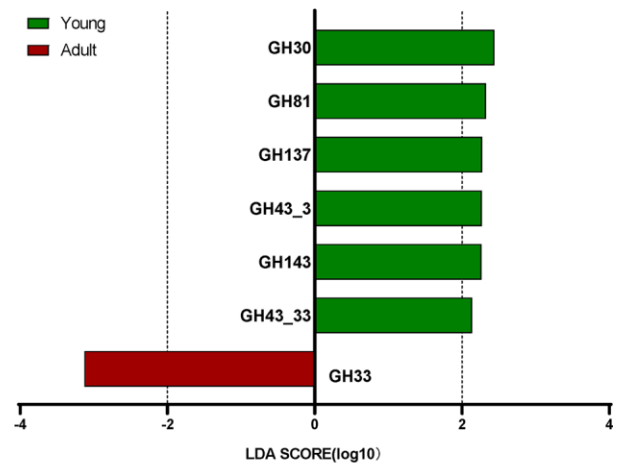
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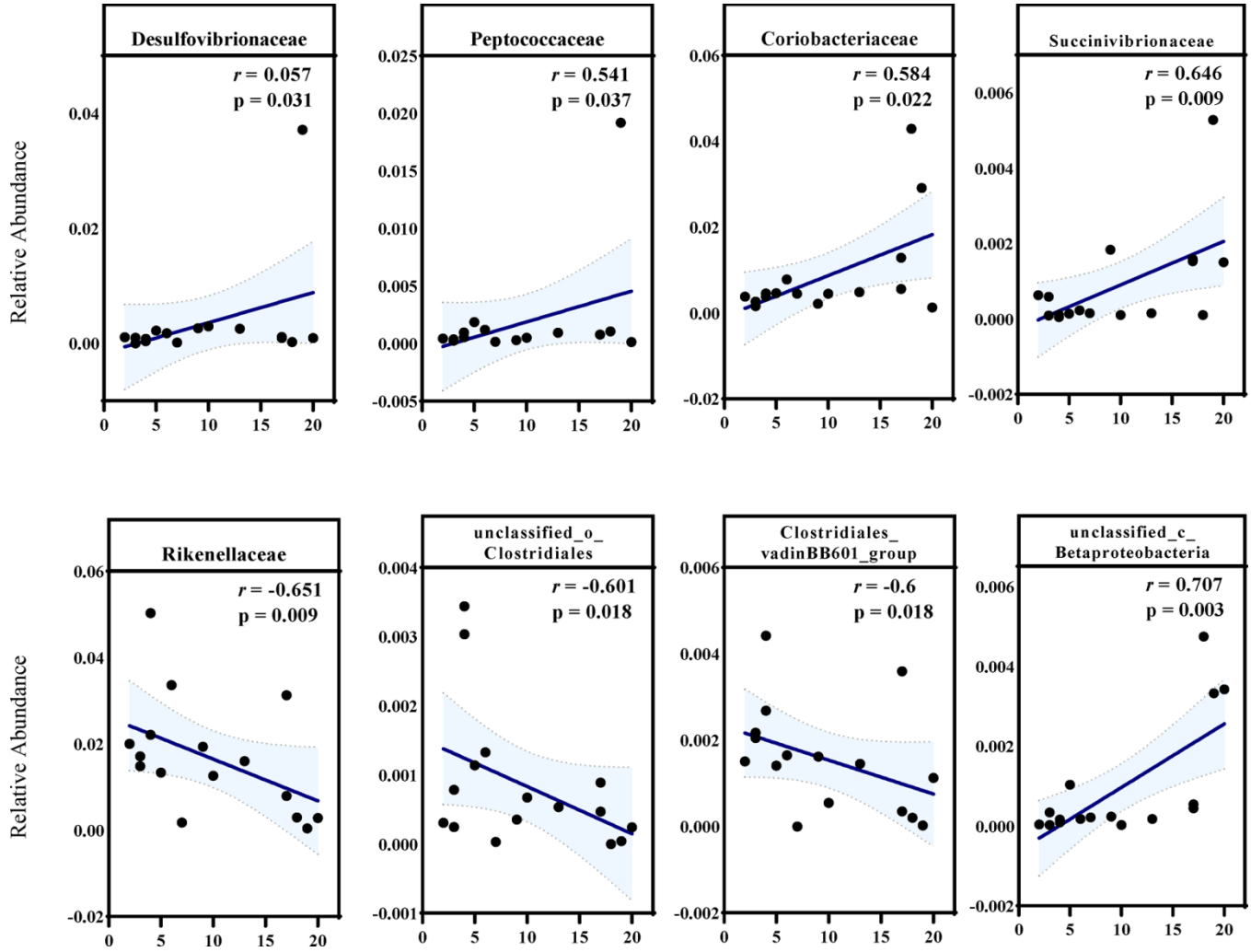
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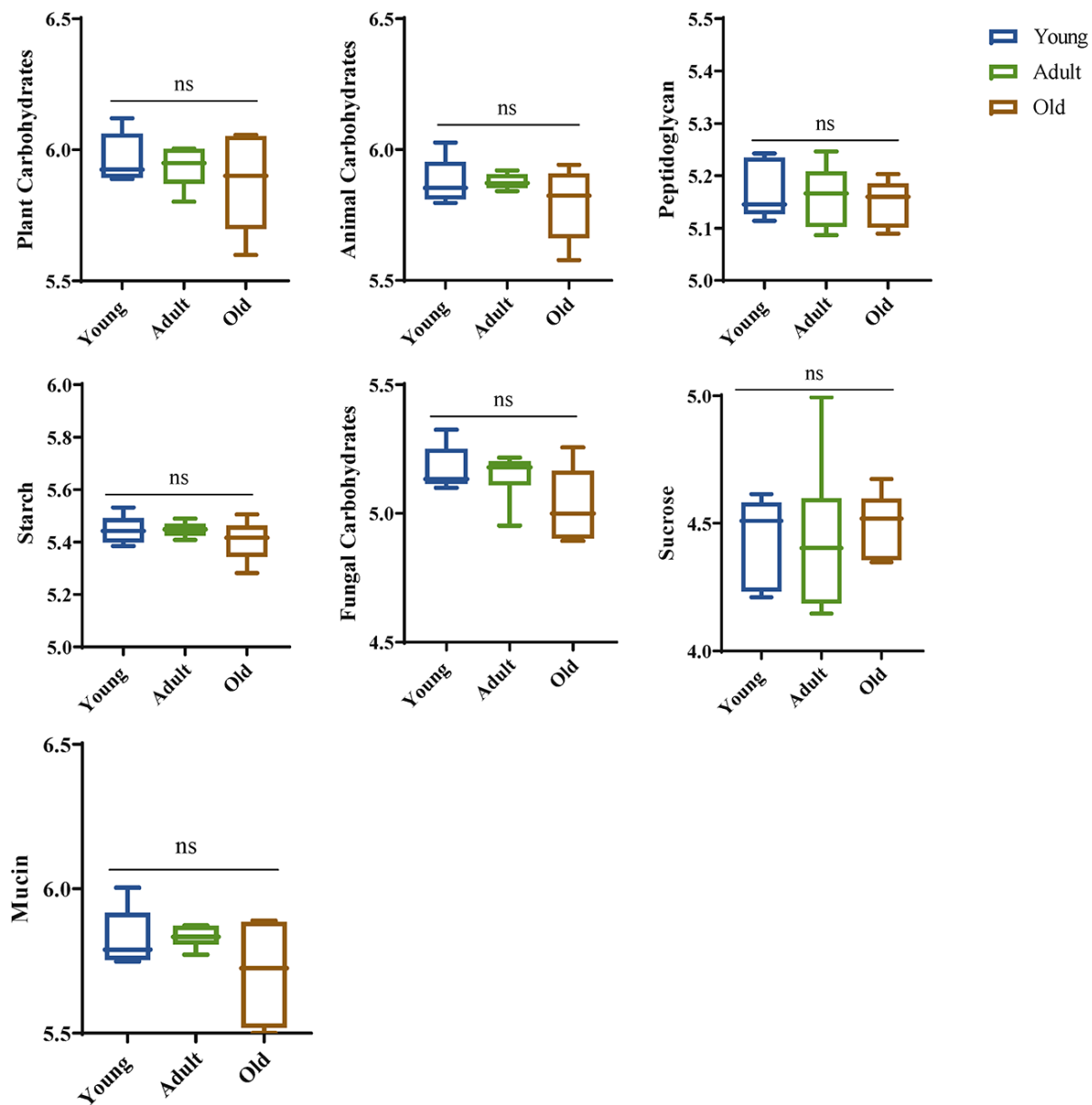
C



Supplementary Figure 2. The OTU and microbial functions differentially represented among three groups. OUT (A), KEGG enzymes (B) and CAZymes (C) differentially represented among the three age groups identified by Linear discriminant analysis (LDA) Effect Size (LEfSe) (LDA>2.0,p<0.05).



Supplementary Figure 3. The change trend of differential microbes at the family level related to age. The correlation was tested by Pearson correlation analyses and adjusted by partial correlation analysis for excluding the confounders for controlling the False Discovery Rate (FDR).



Supplementary Figure 4. Microbial functions in CAZymes among three groups. Representation of CAZymes in metagenomic data sets related to multiple classes of polysaccharides are plotted by their respective distributions.