

Figure 1. PCoA show different pretreatment gut microbiome (n=14/15)

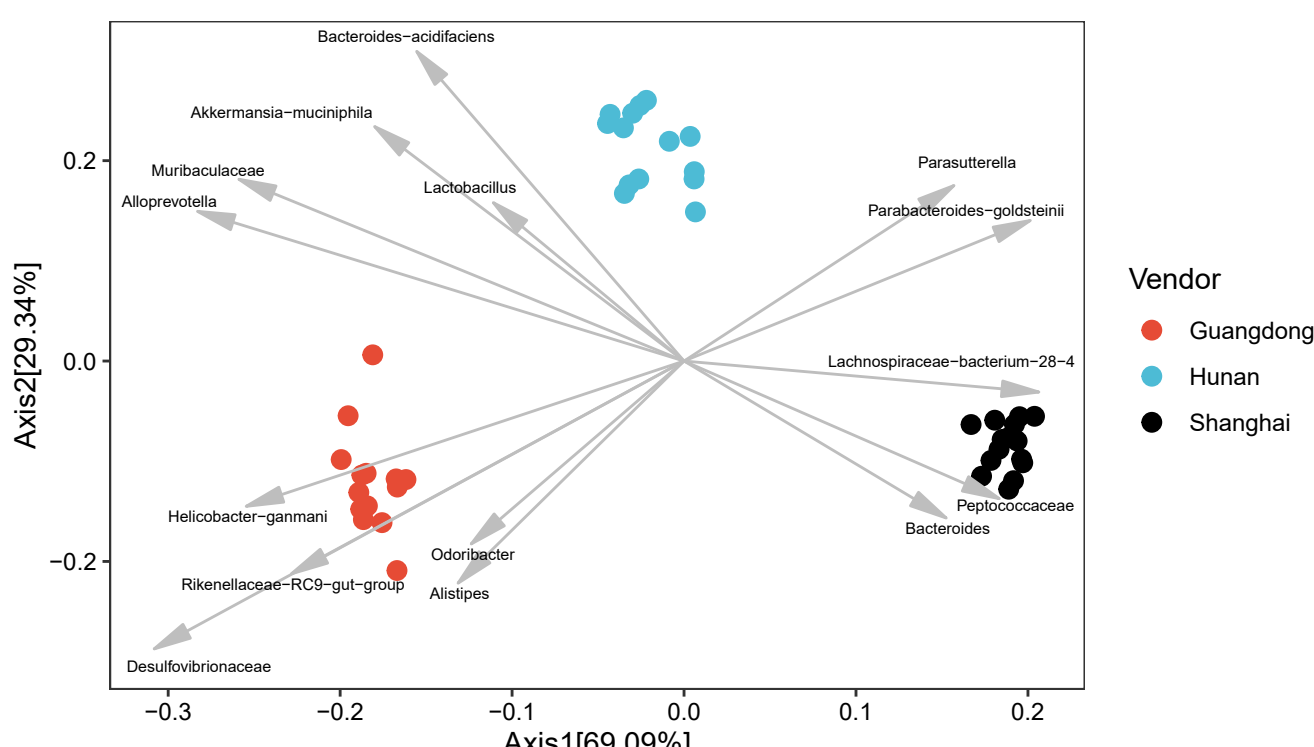
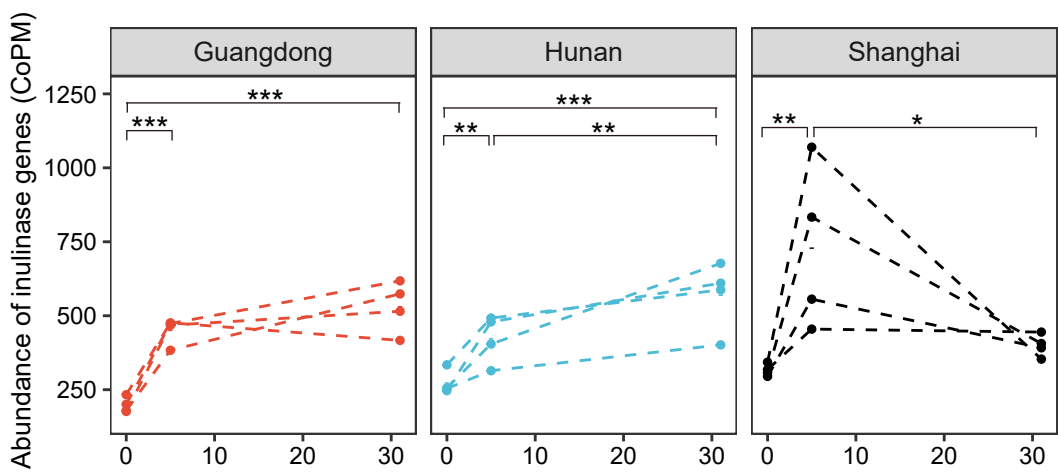
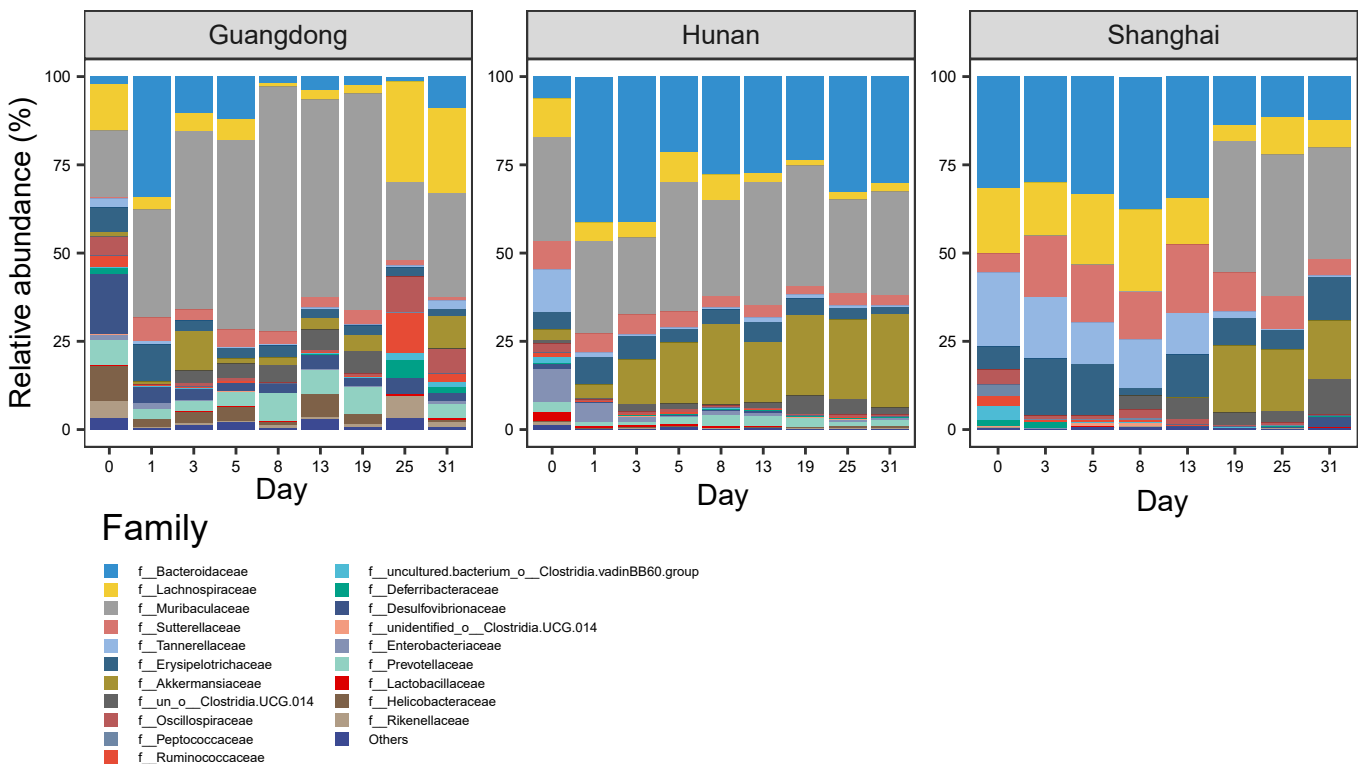


Figure 4. Metagenomic analysis show different inulinase gene abundances between short- and long-term intervention (n=4)



A Cox mixed-effects model was applied to gene abundances using mice as a random effect, and pairwise Tukey's tests were made with the general linear hypothesis test (glht) function, correcting P values for multiple comparisons by the single-step method (default procedure in multcomp).

Figure 2. 16S analysis show dynamics of the microbial composition at family level



Dynamics of the top 15 orders (absolute abundance)

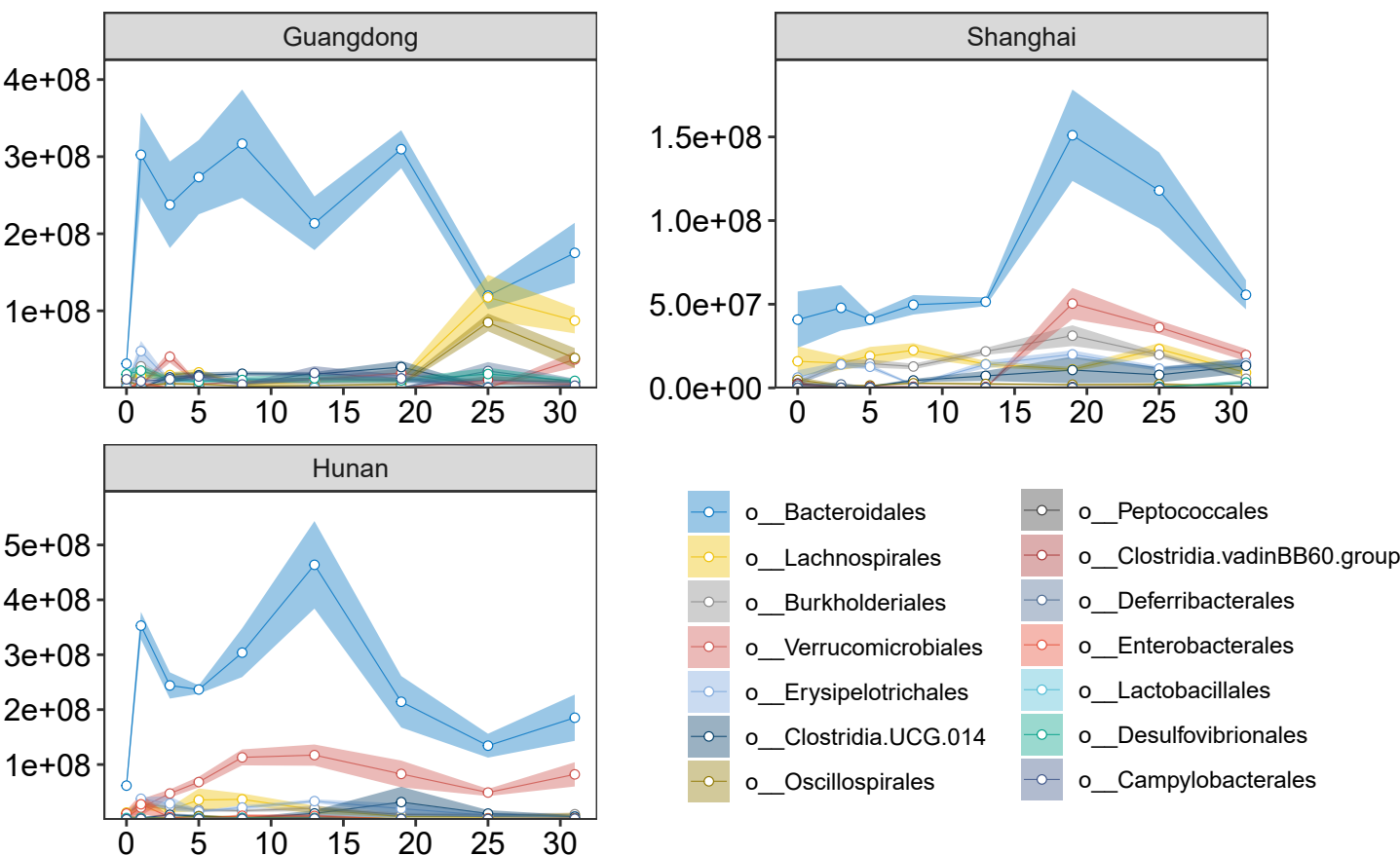
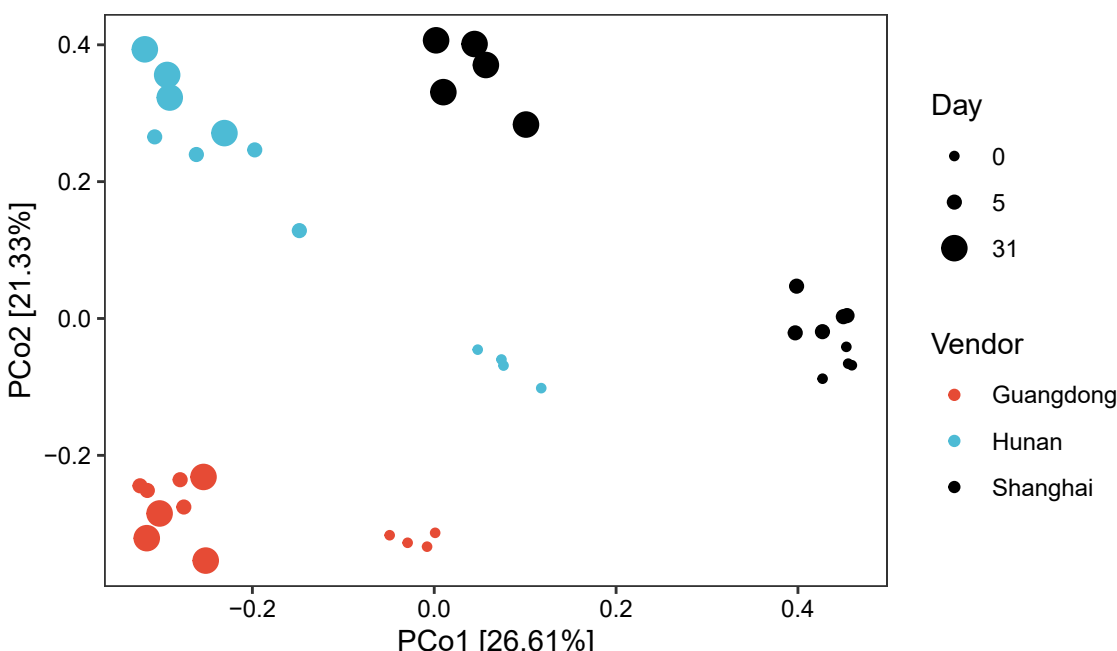


Figure2. PCoA show the different microbial function composition (all vendors, bray-curtis)



PCoA of the metagenome gene abundance (bray-curtis, PERMANOVA test between day 5 and 31)

