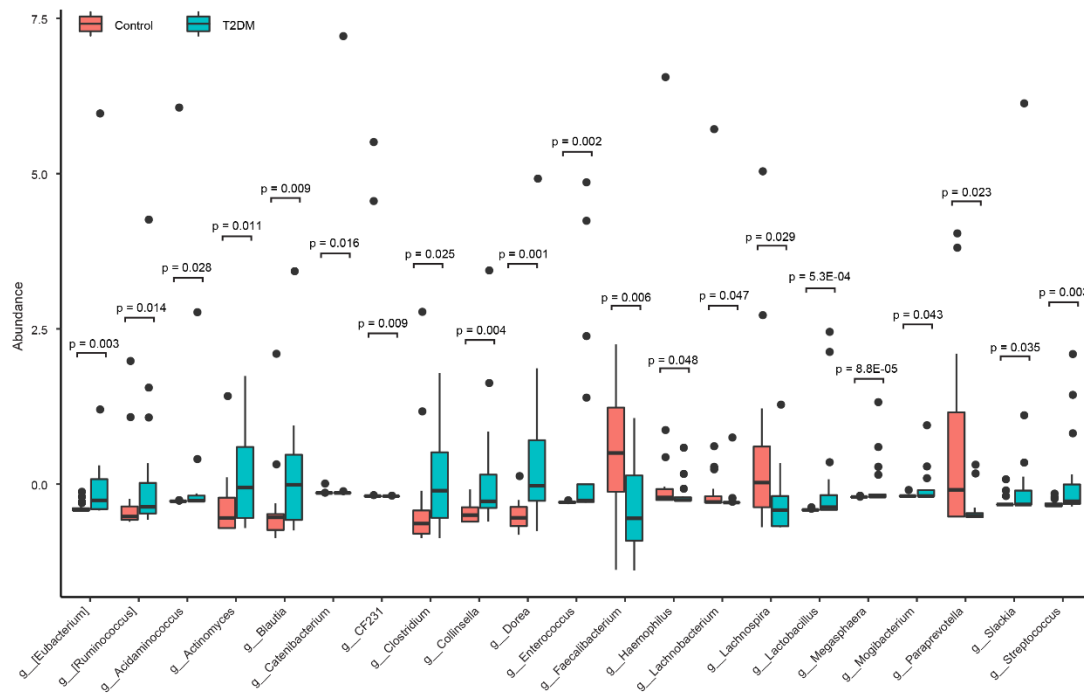
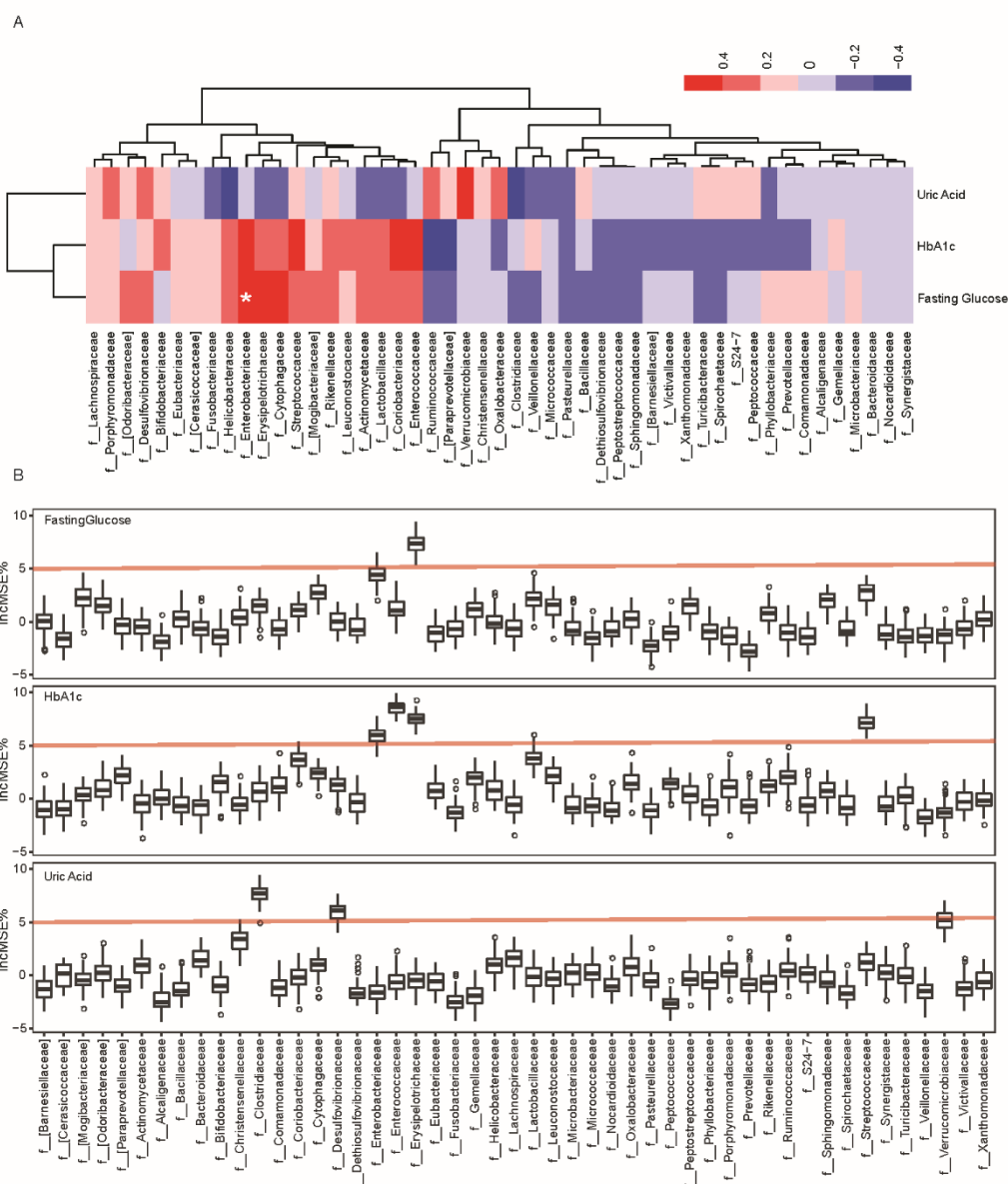


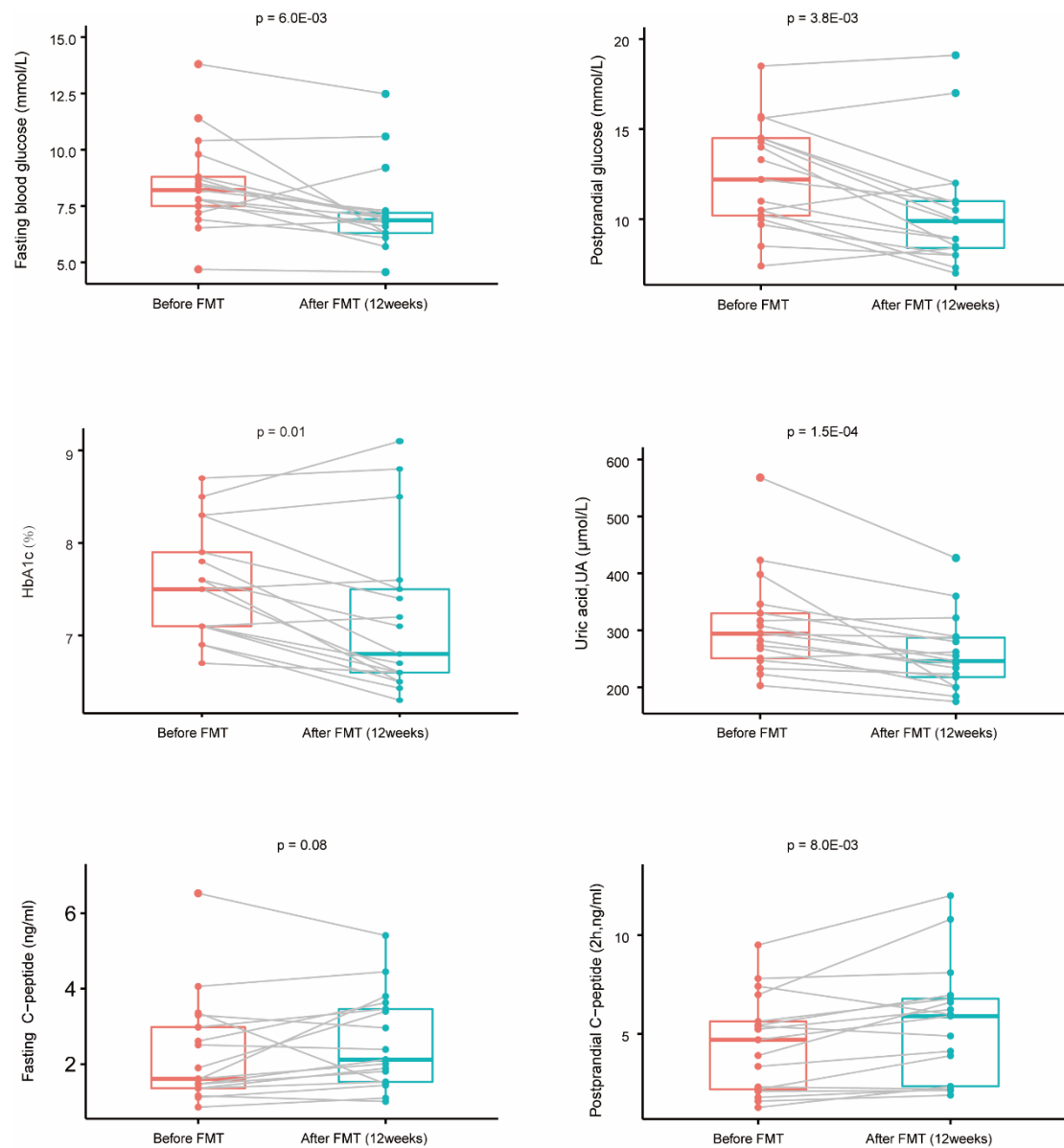
Supplementary Figure 1. No difference in alpha-diversity (Chao, Shannon, Simpson and ACE index) between control and T2DM samples. The p-values were obtained by Mann-Whitney rank-sum test. Boxes represent the median and interquartile ranges between the first and third quartiles. The dots represent outliers.



Supplementary Figure 2. Box-plot of relative abundance of 21 genera that showed the significant difference between T2DM and control. The p-values were obtained by Mann-Whitney rank-sum test. Boxes represent the median and interquartile ranges between the first and third quartiles. The dots represent outliers.



Supplementary Figure 3. The relationship between the family-level bacterial abundance and clinical factors. A. Heatmap of the Spearman's correlation coefficients between the family-level bacterial abundance and clinical factors using both T2DM and control samples. * $p < 0.05$. **B.** Random forest analysis to assess the association between the family-level bacterial abundance and clinical factors. Significant level is indicated in red line.



Supplementary Figure 4. Changes in clinical factors after FMT treatment. The p-values were obtained by Mann-Whitney paired test. Boxes represent the median and interquartile ranges between the first and third quartiles.