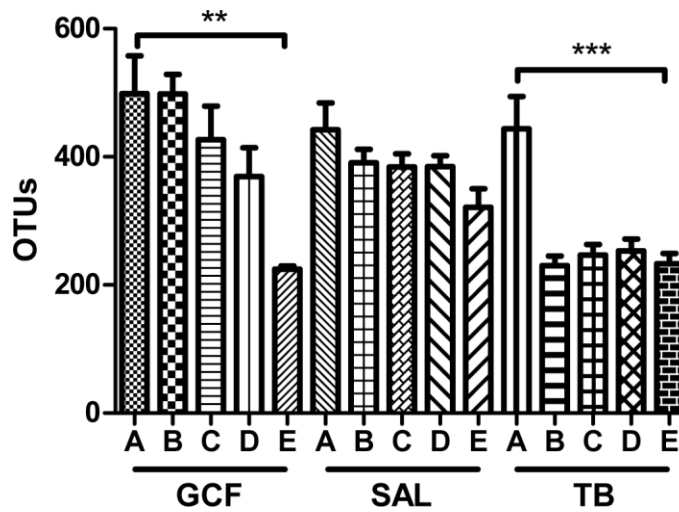Supplementary Figure 1. Rarefaction curve: the abscissa is the number of randomly selected sequences and the ordinate is the number of OTUs clustered based on the number of sequences. Each curve represents a sample, and the curve tends to be stable, indicating that the number of extracted sequences is enough to reflect the OTUs of the sample.
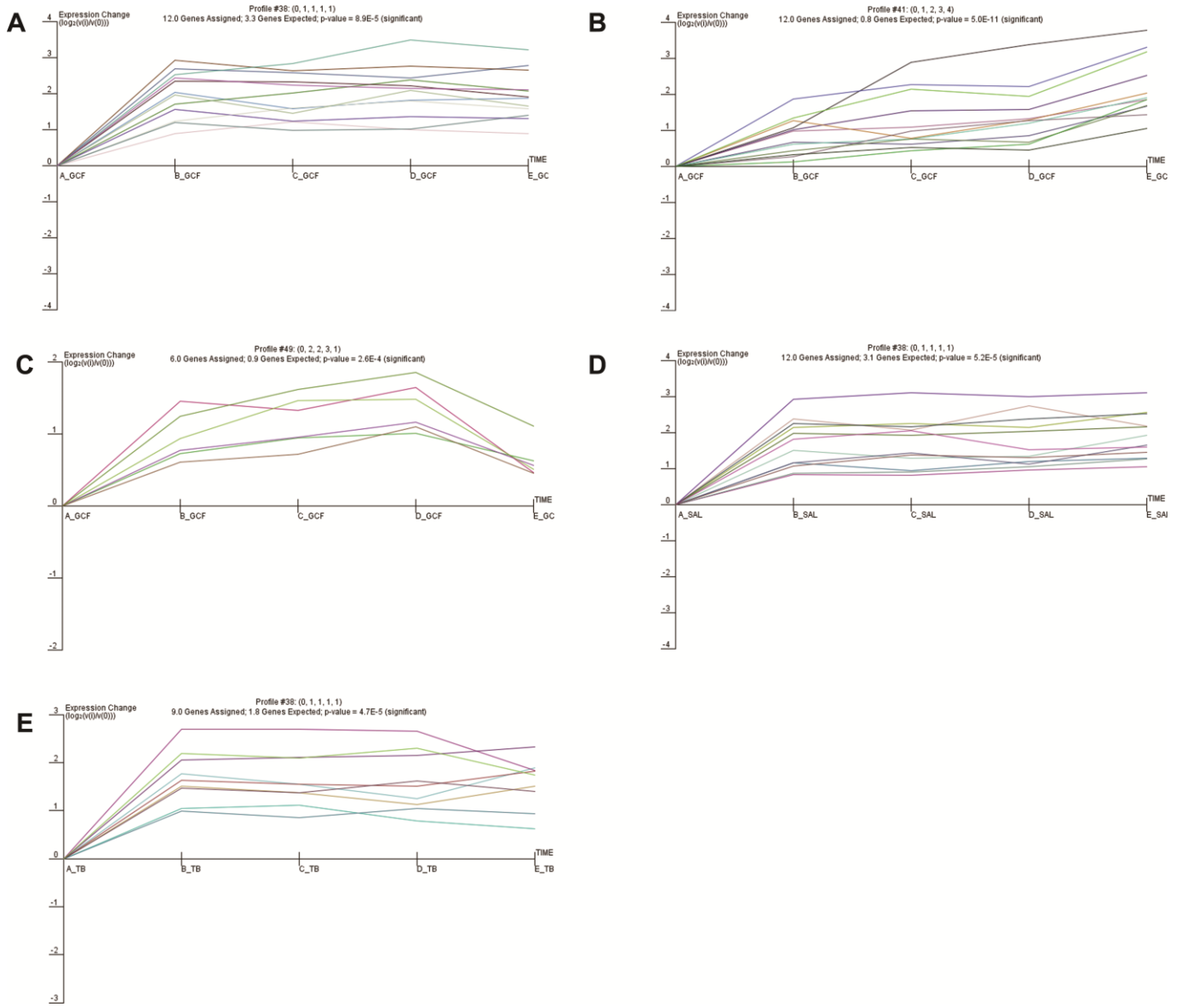

**Supplementary Figure 2. OTUs of the samples.**
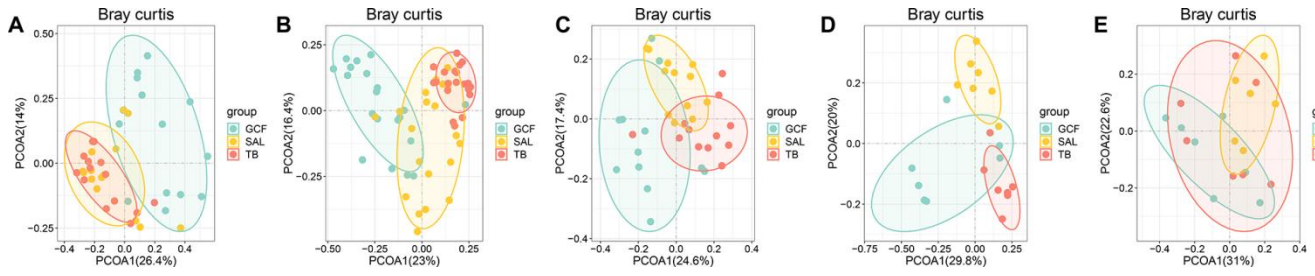
Supplementary Figure 3. The β-diversity indexes of bacteria over time differentiated in the three oral sites. (**A**–**E**) were age groups.
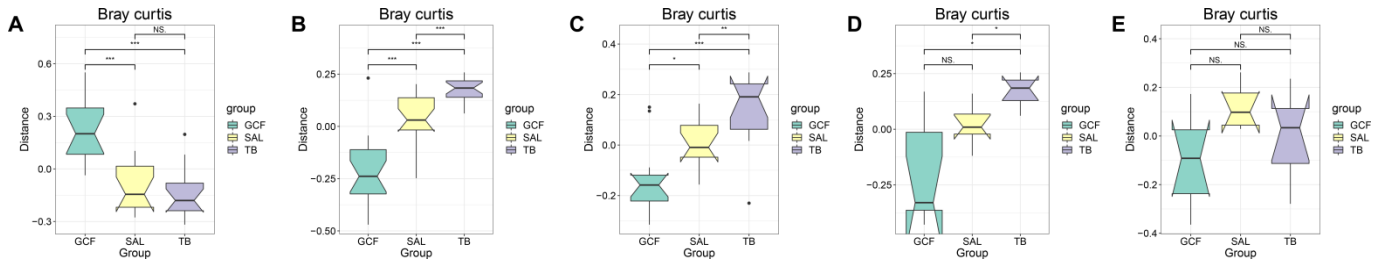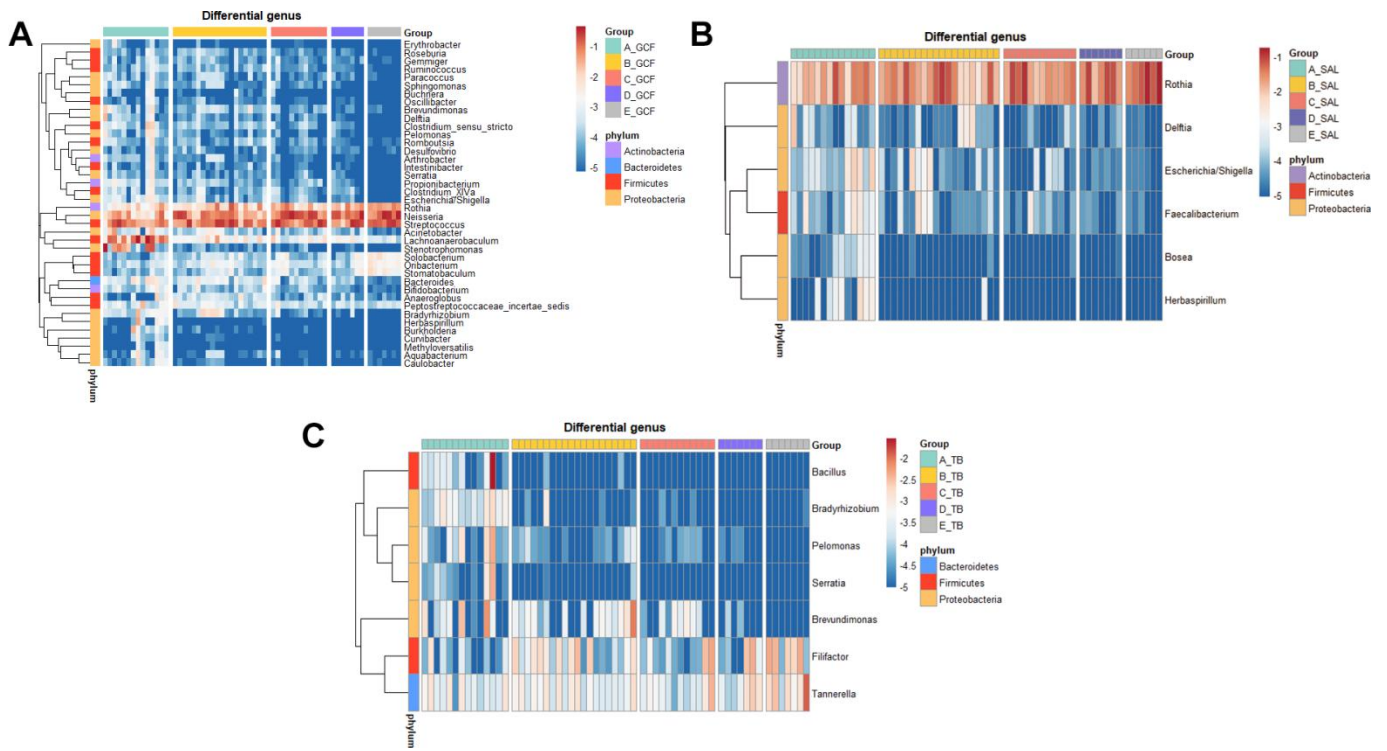

Supplementary Figure 4. The first principal component analysis of microbial changes with age in various oral sites. (**A**–**E**) were age groups.
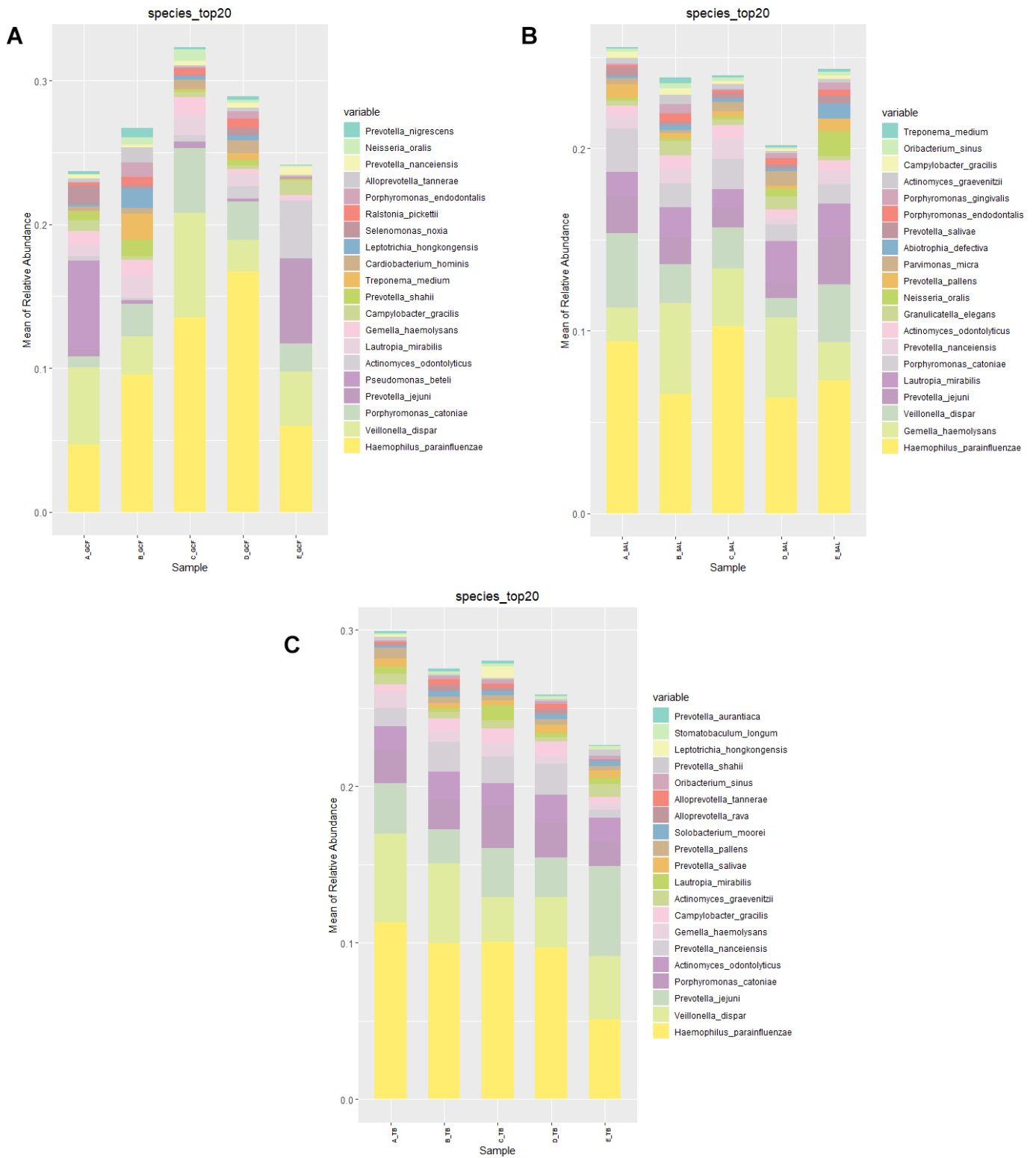
Supplementary Figure 5. The bacteria contained in the module changed over time. (**A**–**C**) were GCF moduals; (**D**), SAL module; (**E**), TB module.
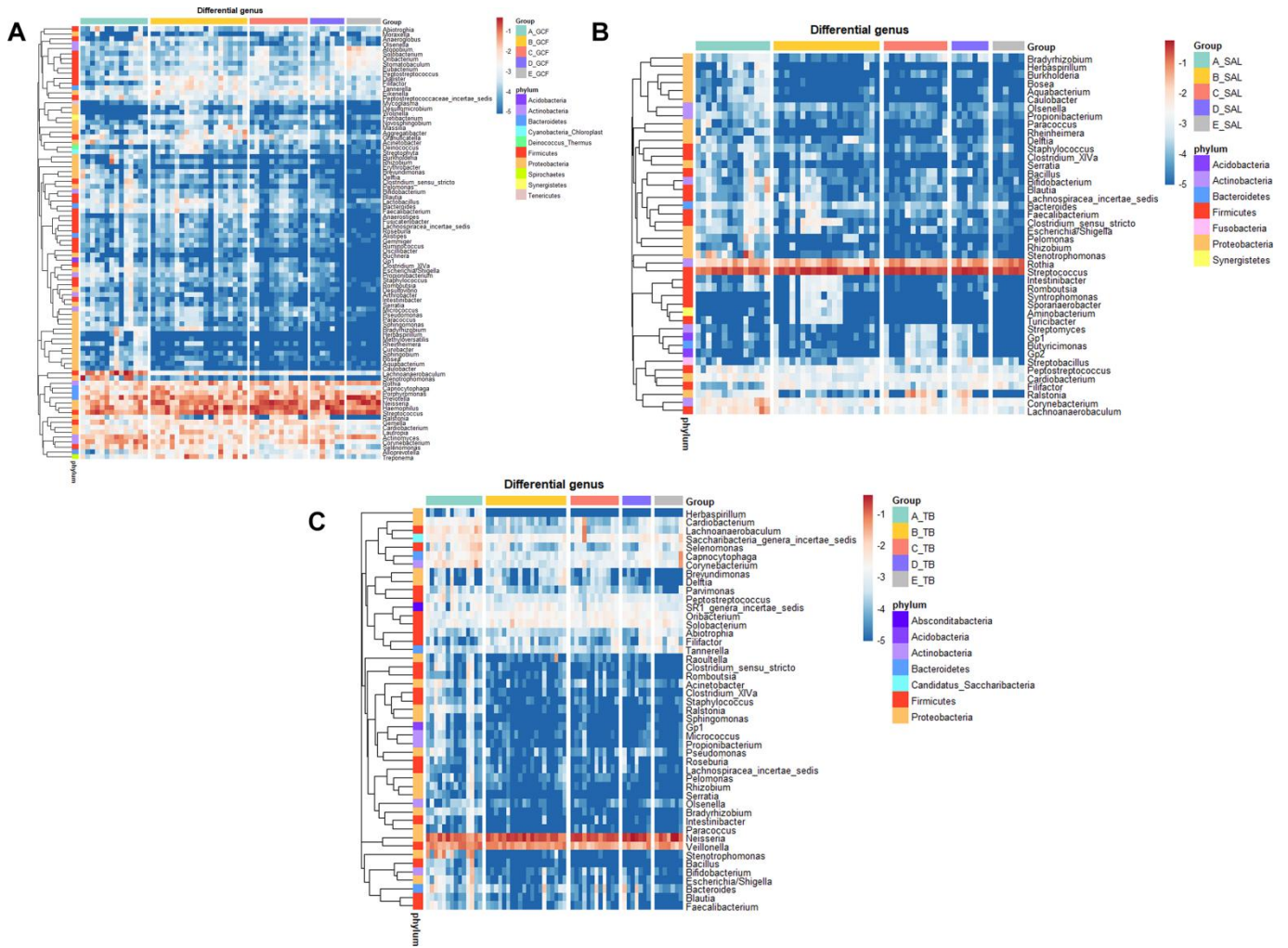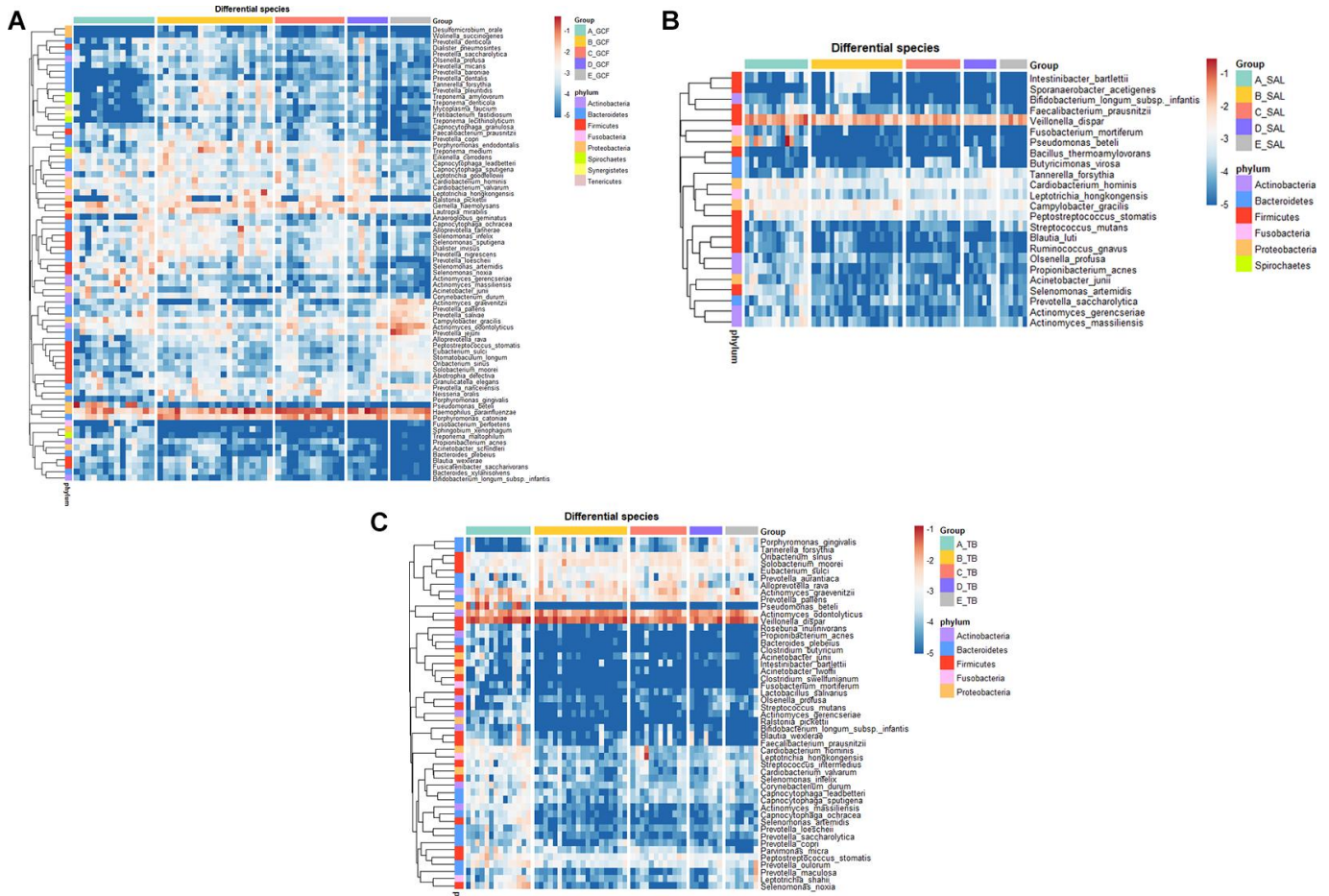
Supplementary Figure 6. The genus that had marked variation with age. (**A**) GCF; (**B**) SAL; (**C**) TB.

Supplementary Figure 7. The genus that underwent gradual changes with age. (**A**) GCF; (**B**) SAL; (**C**) TB.
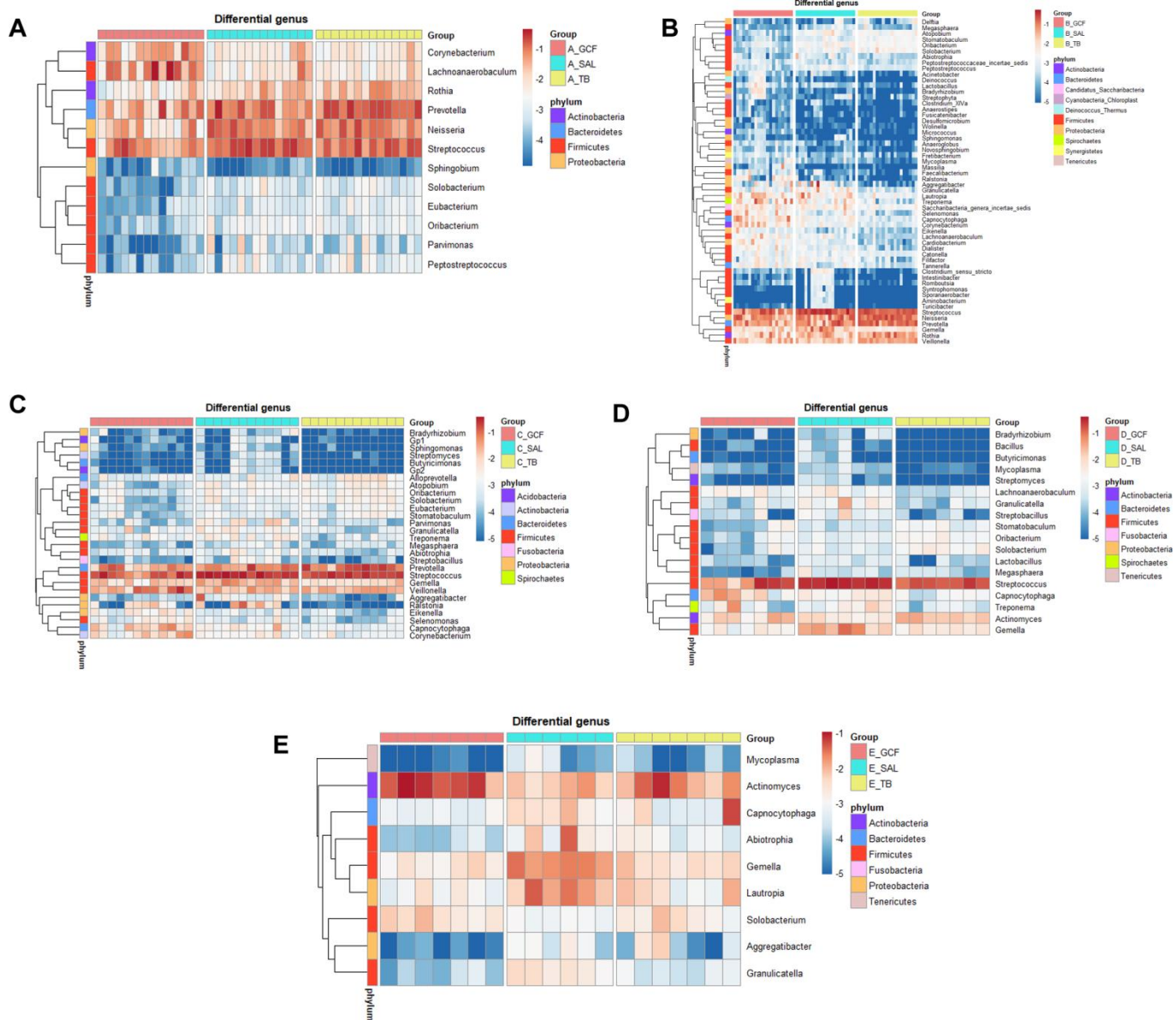
Supplementary Figure 8. The composition of microbiota at the species level. (**A**) GCF; (**B**) SAL; (**C**) TB.
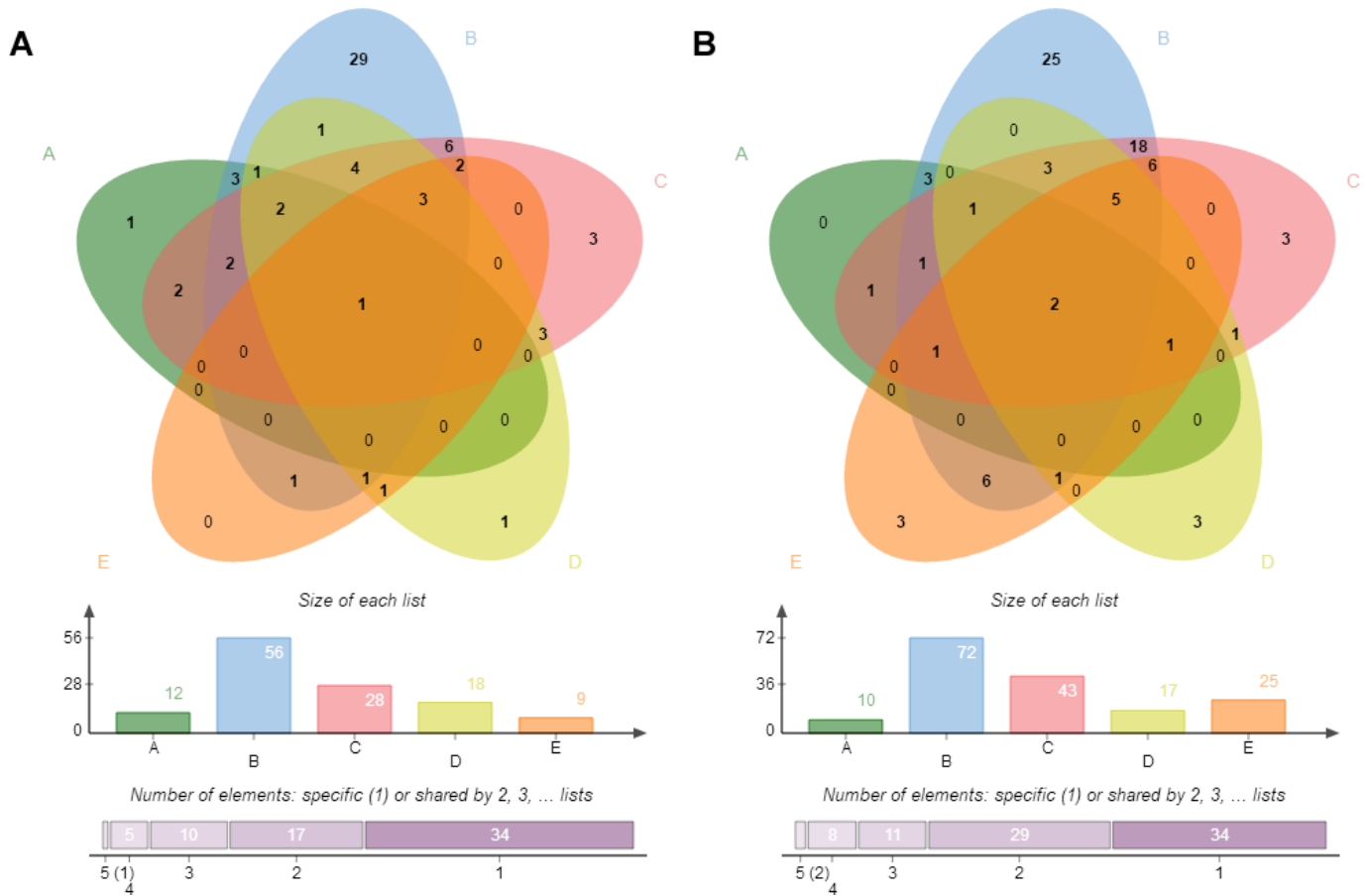
Supplementary Figure 9. The species that underwent significant changes. (**A**) GCF; (**B**) SAL; (**C**) TB.

Supplementary Figure 10. The species with gradual variations with trend. (**A**) GCF; (**B**) SAL; (**C**) TB.

Supplementary Figure 11. The genera differently distributed in the GCF, SAL and TB sites of oral cavity. (**A–E**), age groups.
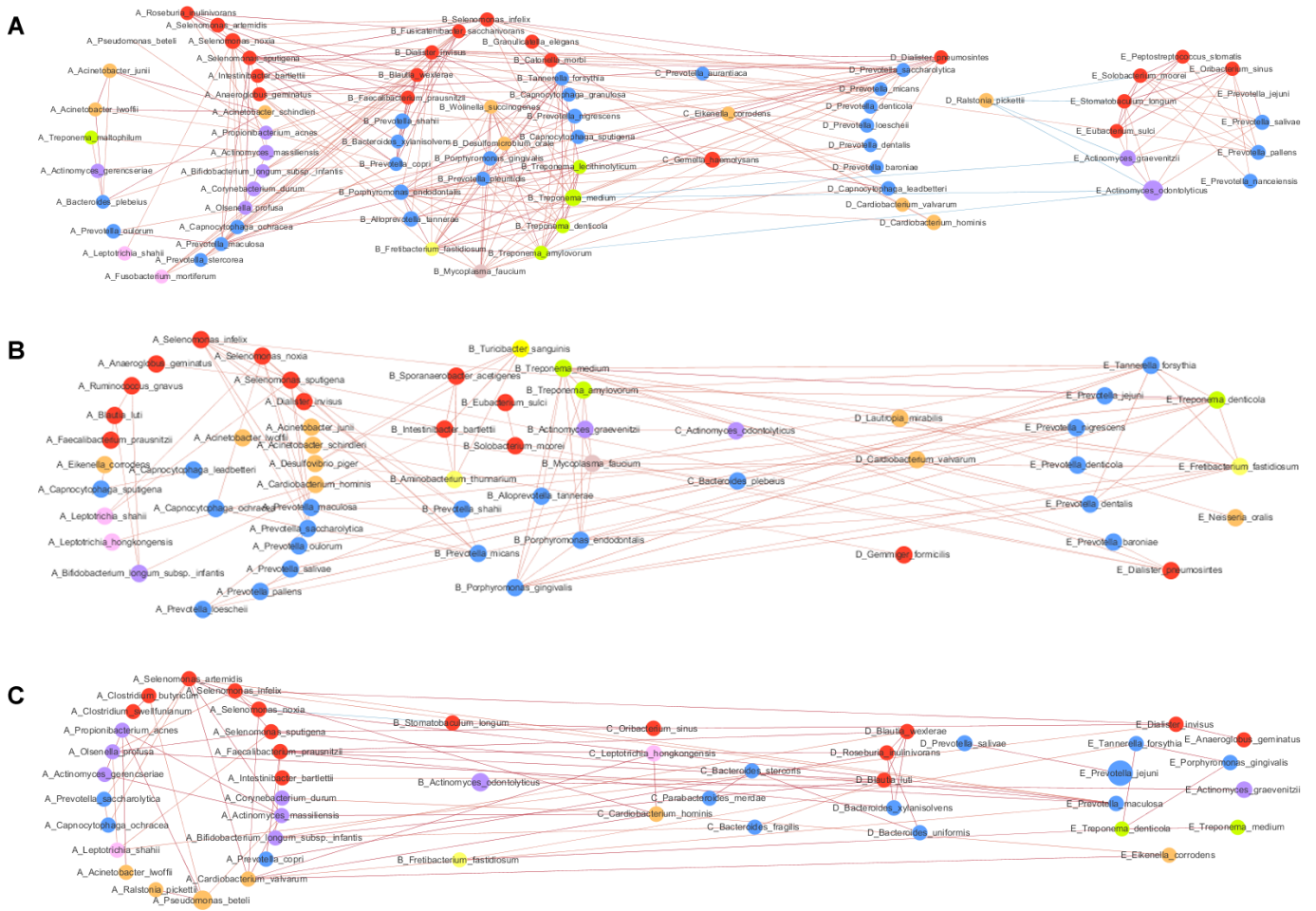
Supplementary Figure 12. The differential genus and species shared by the three sites of oral cavity at various ages. (**A**), at the genus level; (**B**), at the species level.

Supplementary Figure 13. The species differently distributed among the GCF, SAL and TB sites of oral cavity. (**A–E**), age groups.

Supplementary Figure 14. The species differently distributed among the GCF, SAL and TB sites of oral cavity in various age groups. (**A–E**), age groups.
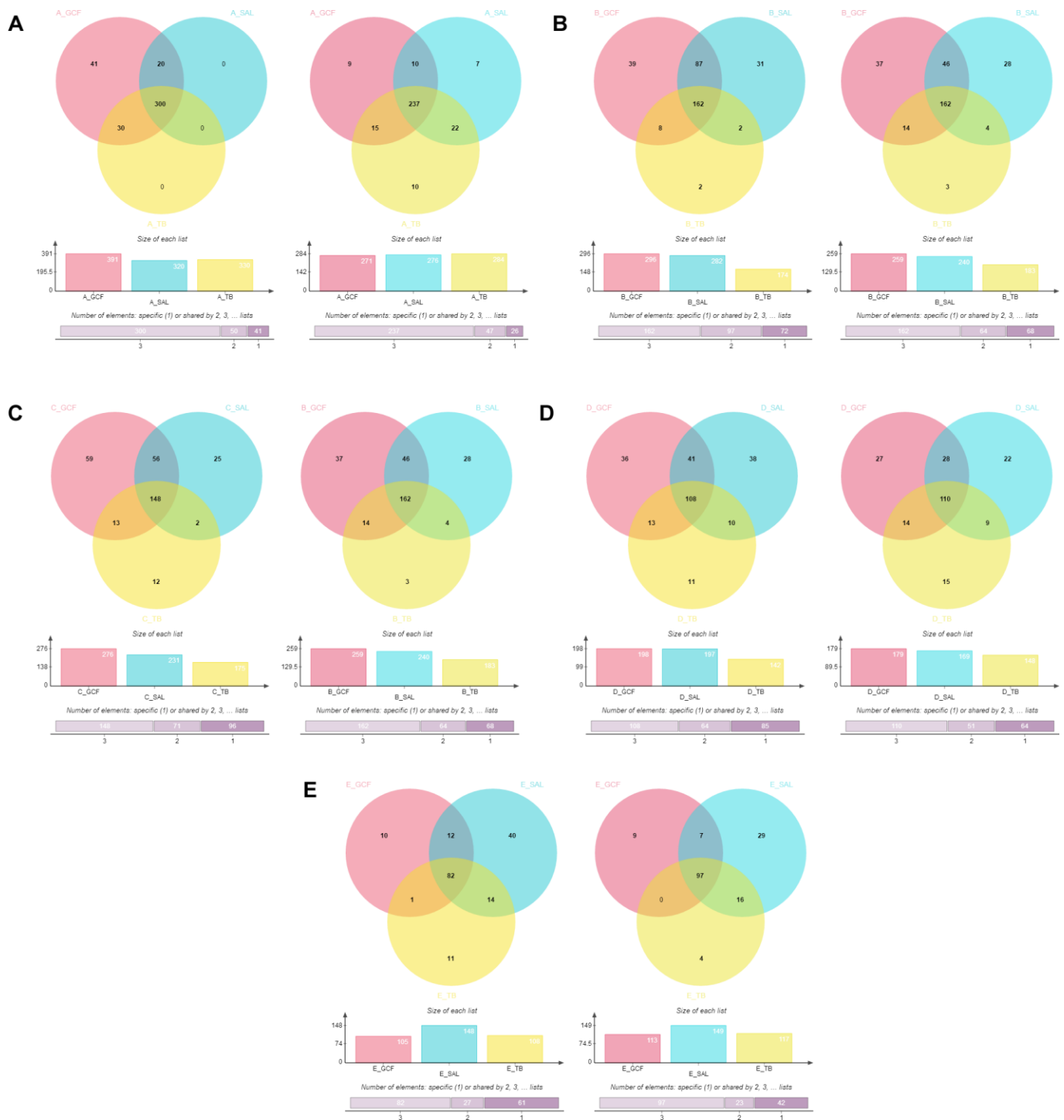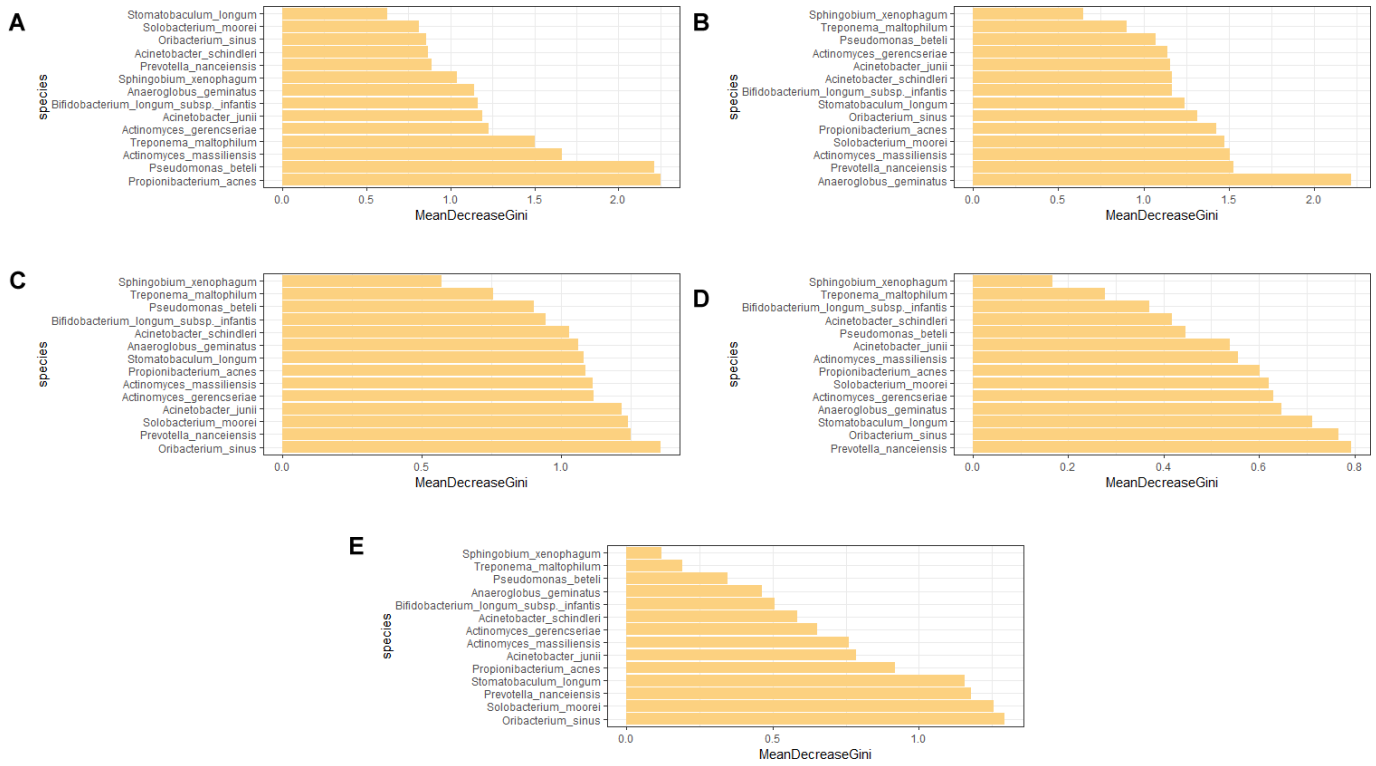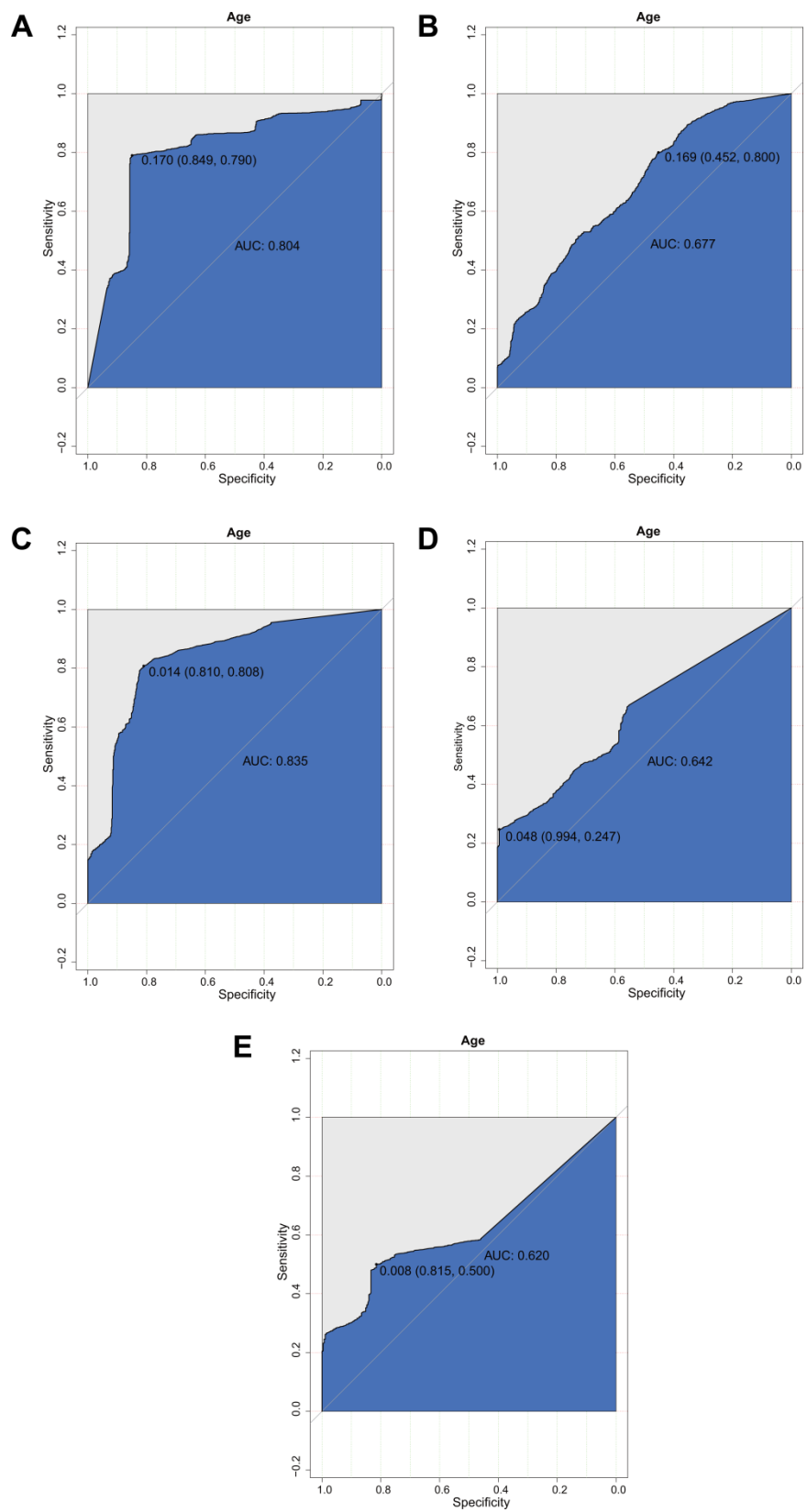
Supplementary Figure 15. The "core microbiome" of the three sites of oral cavity with age at the genus and species levels. (**A–E**), age groups.

Supplementary Figure 16. Correlation analysis of the oral microbiota at the species level. (**A**) GCF; (**B**) SAL; (**C**) TB.
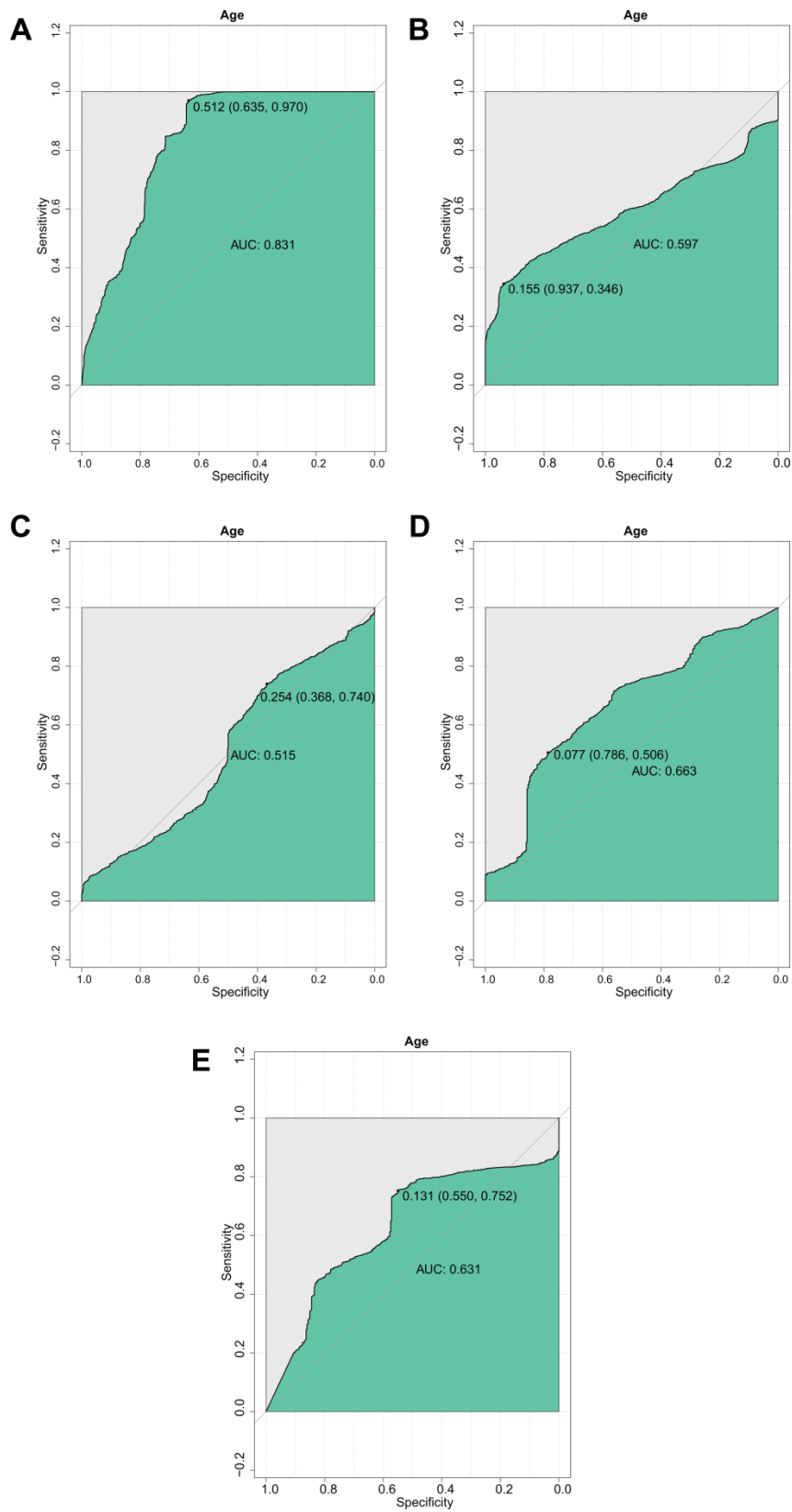
Supplementary Figure 17. Evaluation of the differential bacterial species of GCF with the random forest model.

Supplementary Figure 18. Accuracy rate of using SAL bacteria for distinguishment.

Supplementary Figure 19. Accuracy rate of using TB bacteria for distinguishment.