



Comprehensive spatial profiling reveals transitional microbiome dynamics and microbial heterogeneity in pediatric adenoid hypertrophy

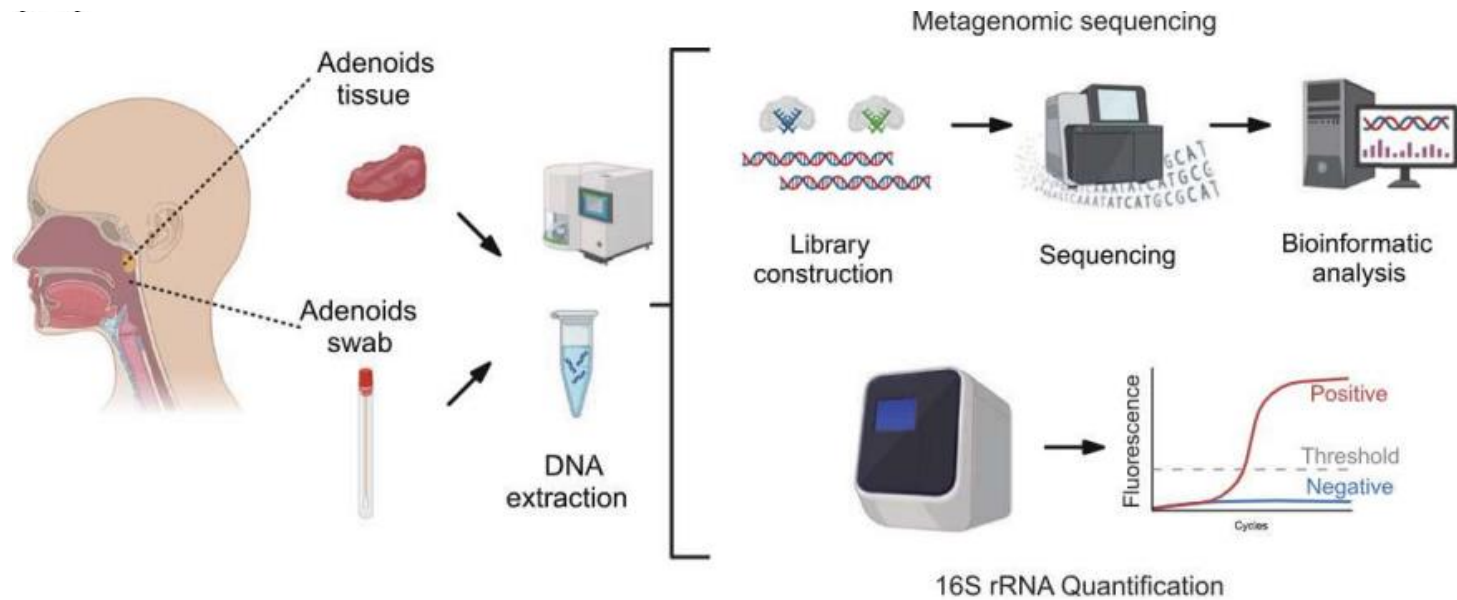
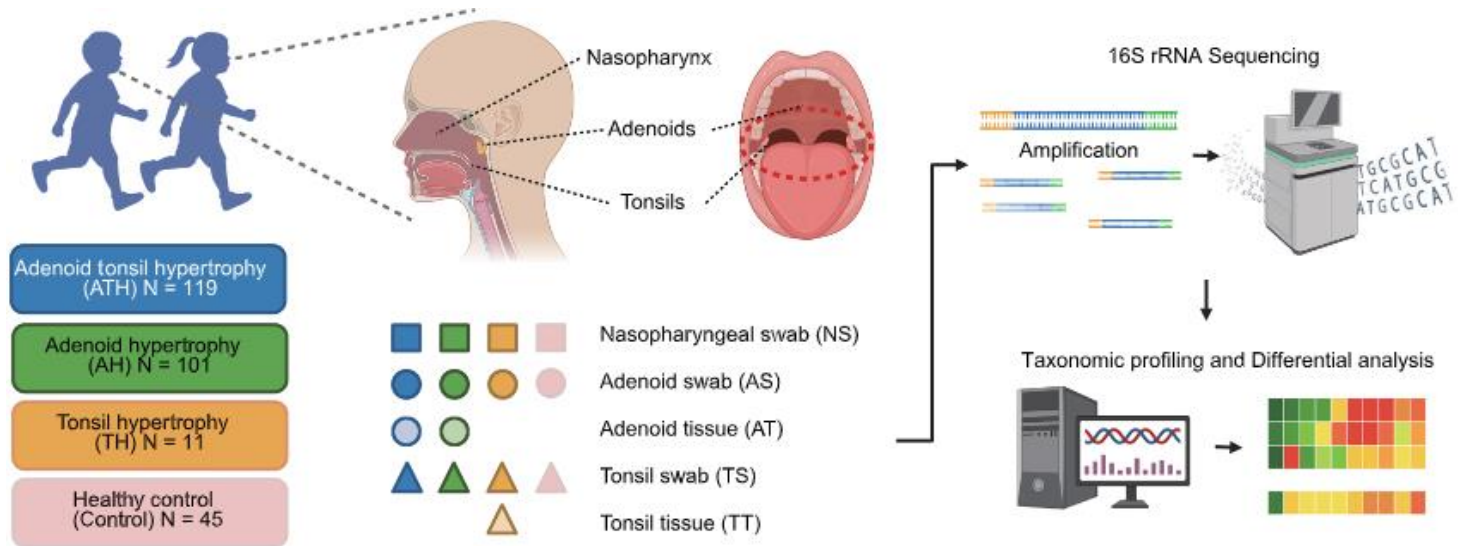
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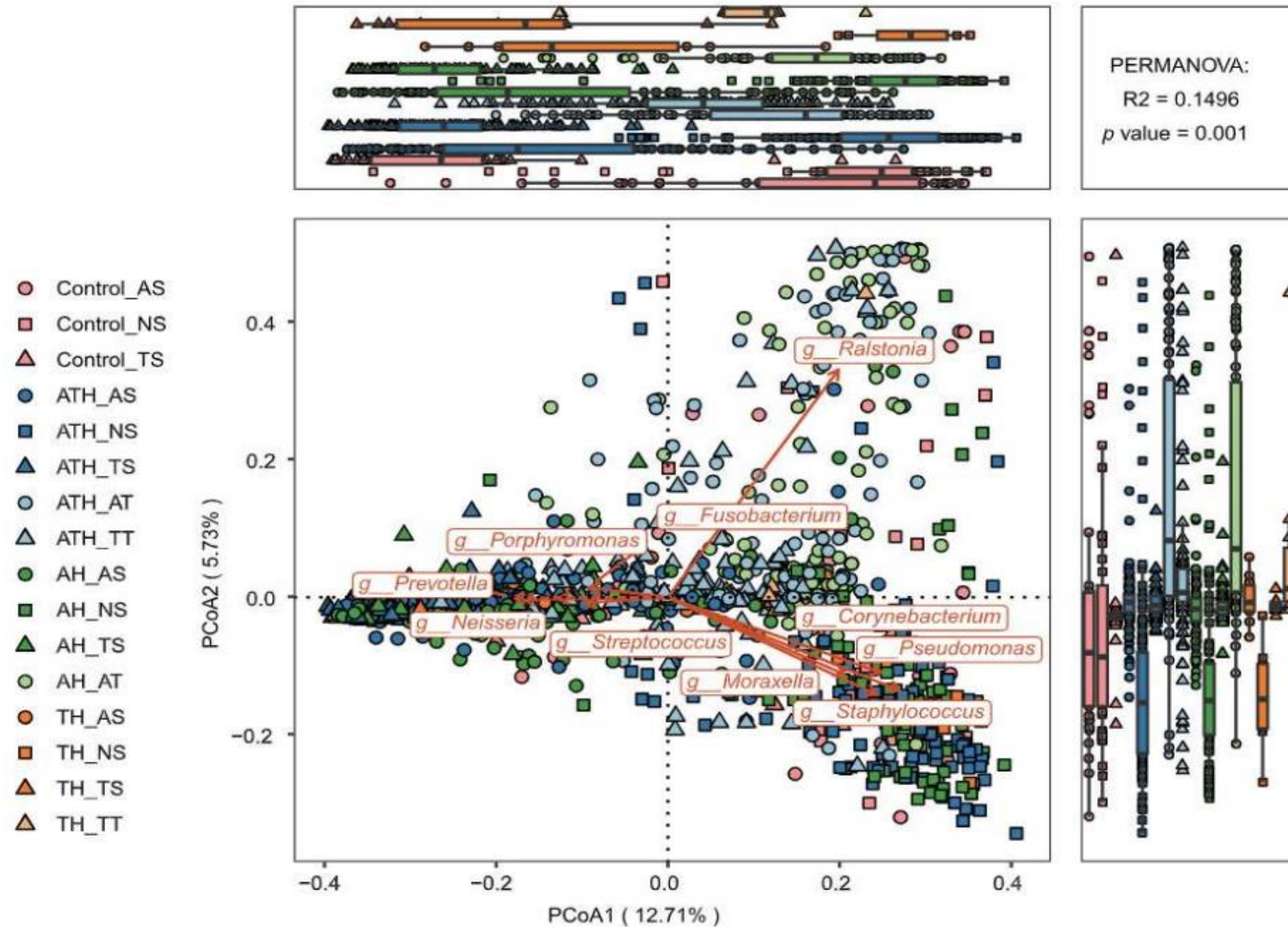


Kaining Chen, Xin Wan, Wenli Guo, Huiwen Ke, Xu Mei, Yanqiu Chen, Wenhao Zhou, et al. 2026.
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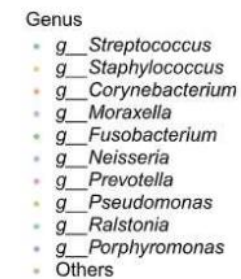
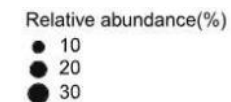
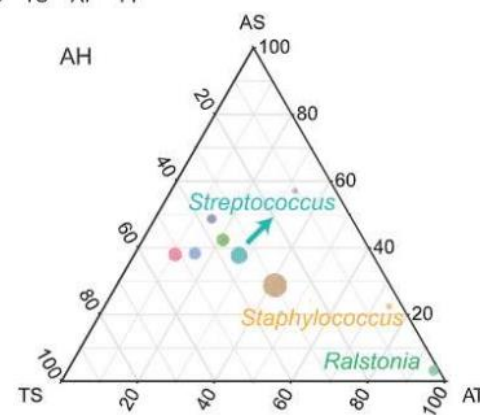
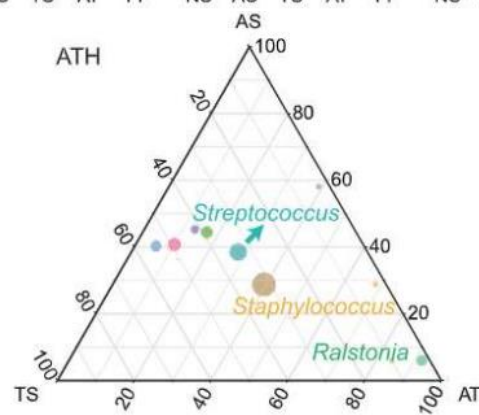
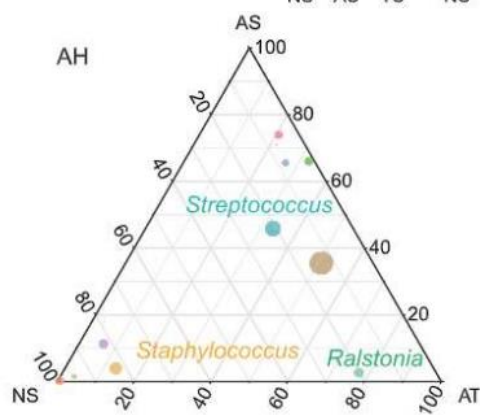
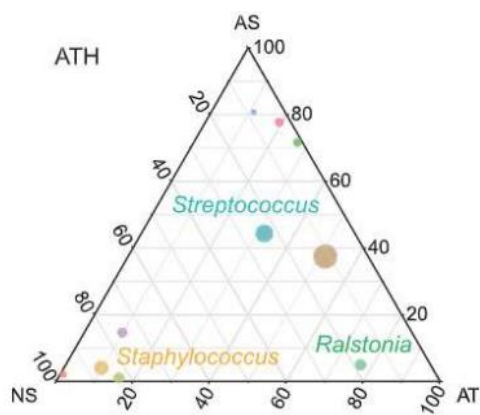
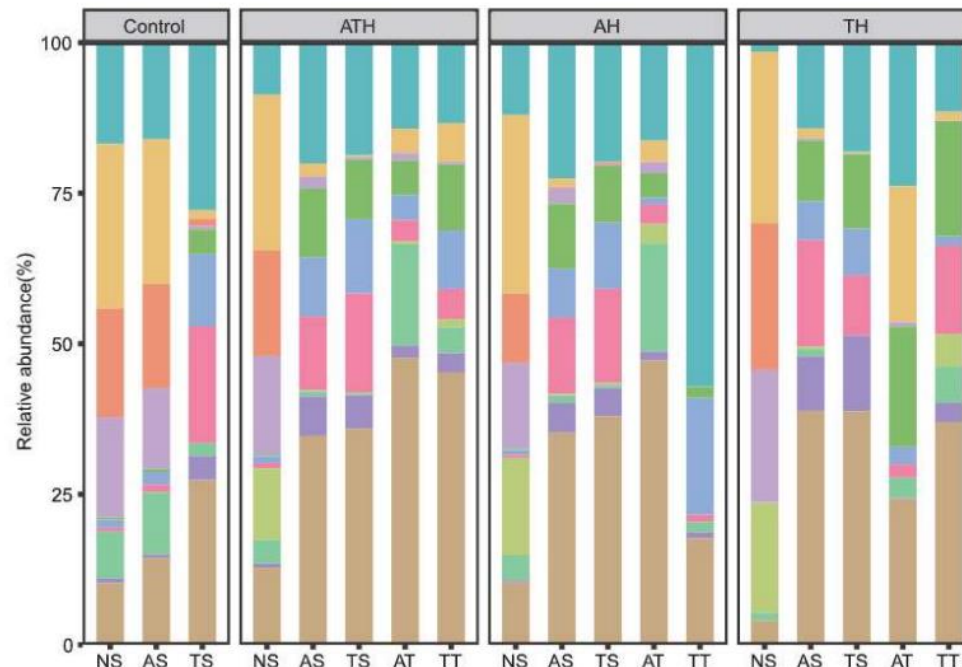
Research Design and Sample System



Spatial heterogeneity: The bacterial community structure changes with the location

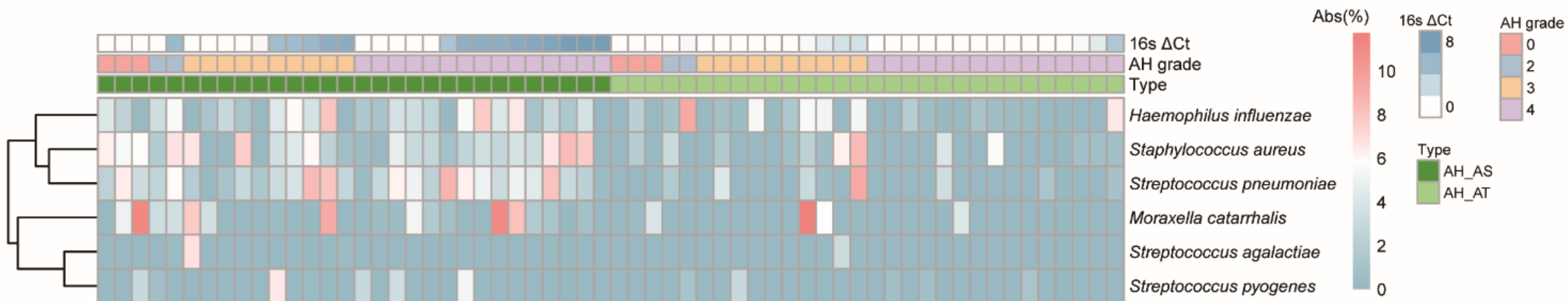
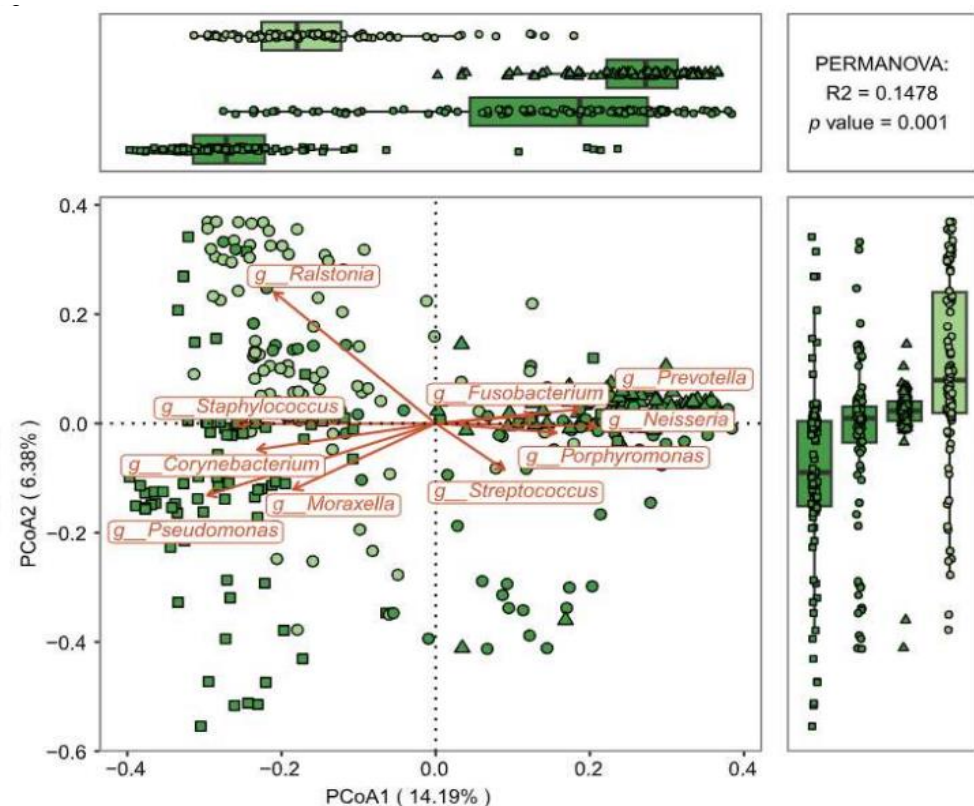
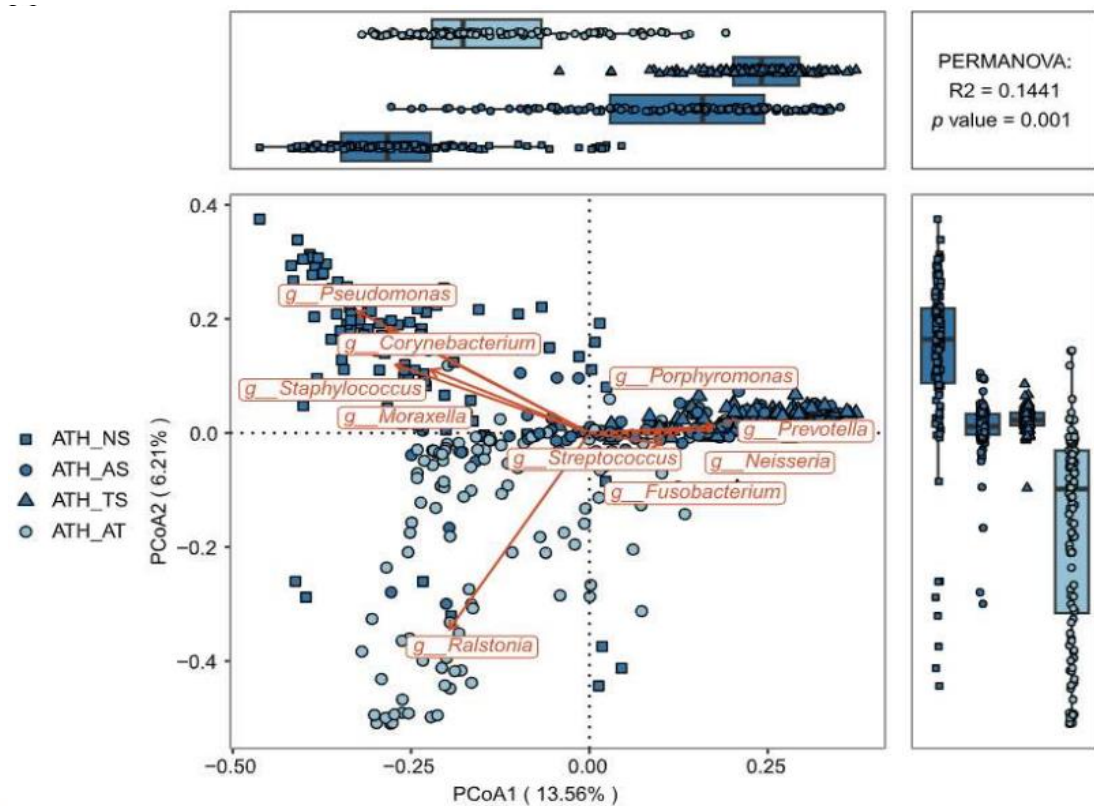


Niche preference of dominant genera

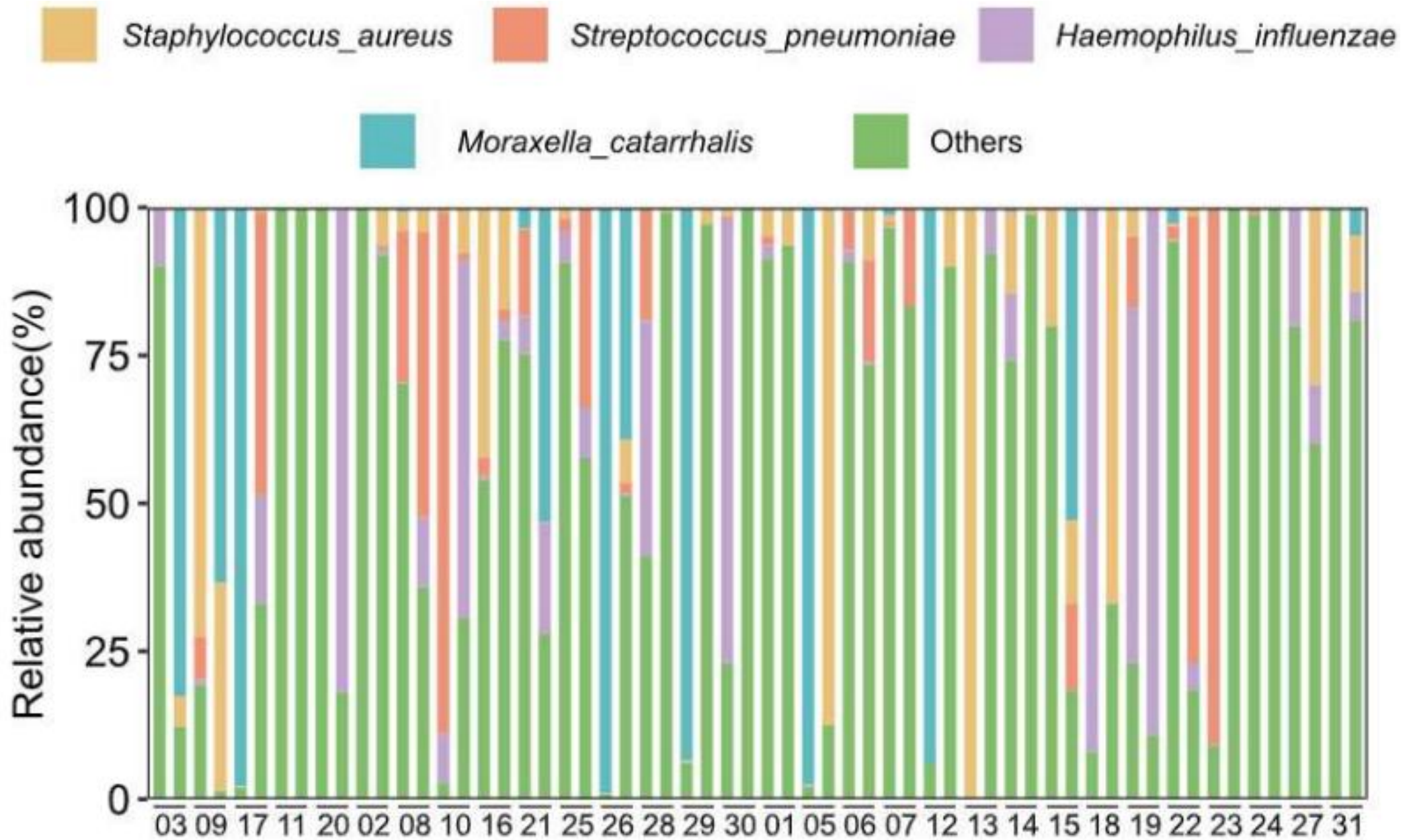




Adenoid tissue: transitional ecological niche



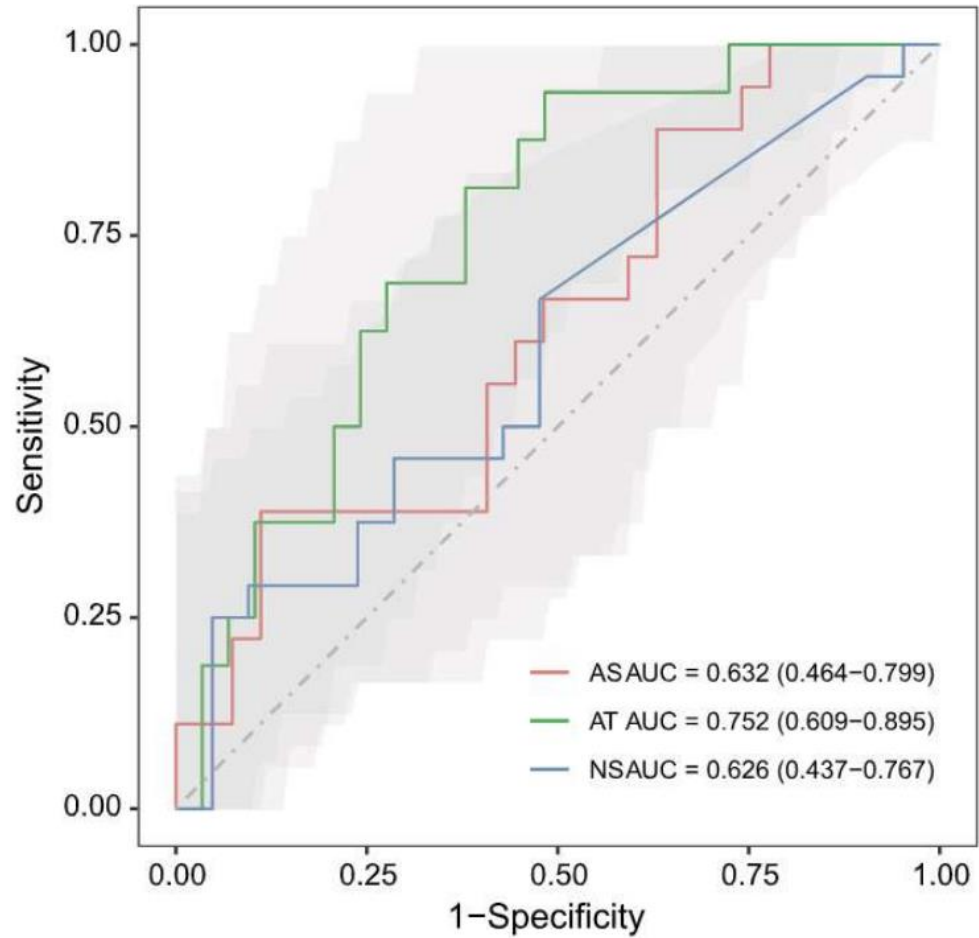
Species-level validation: Migration/continuity of key bacterial strains



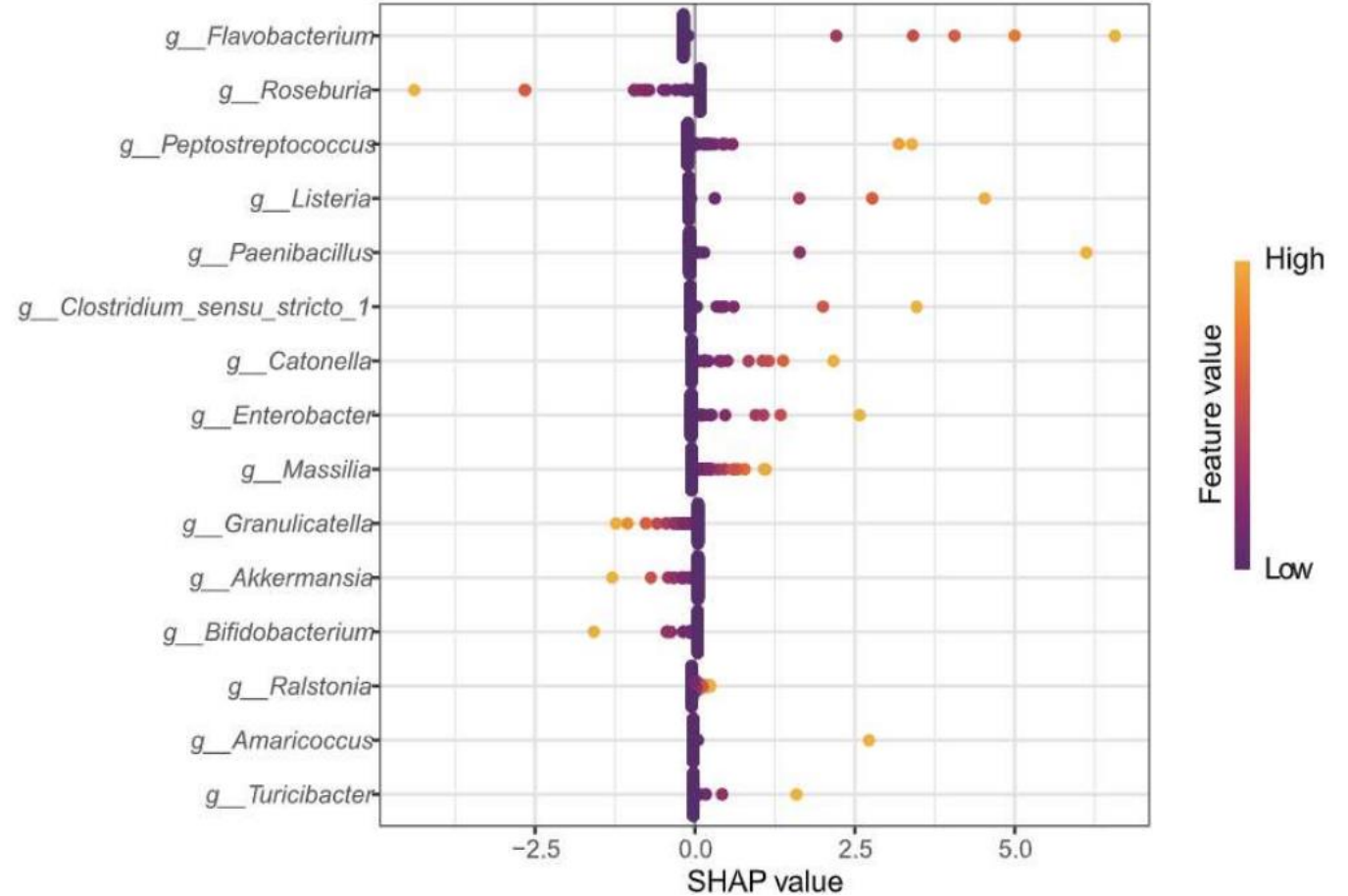


Disease severity prediction: Adenoid tissue is superior to surface swabs

ROC curve



Feature contribution from SHAP analysis (AT)





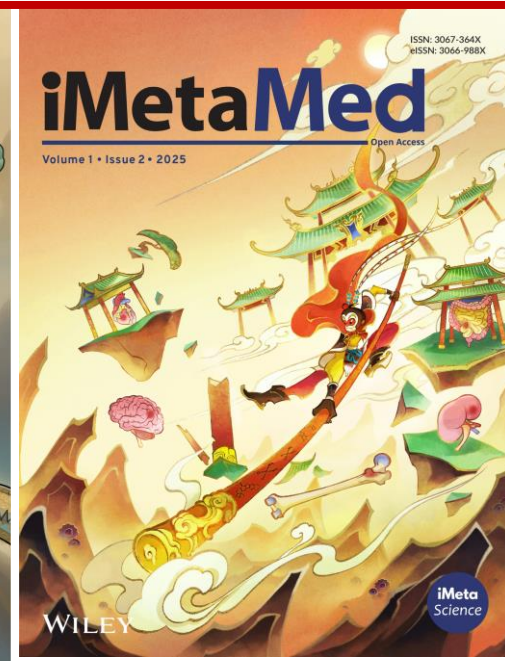
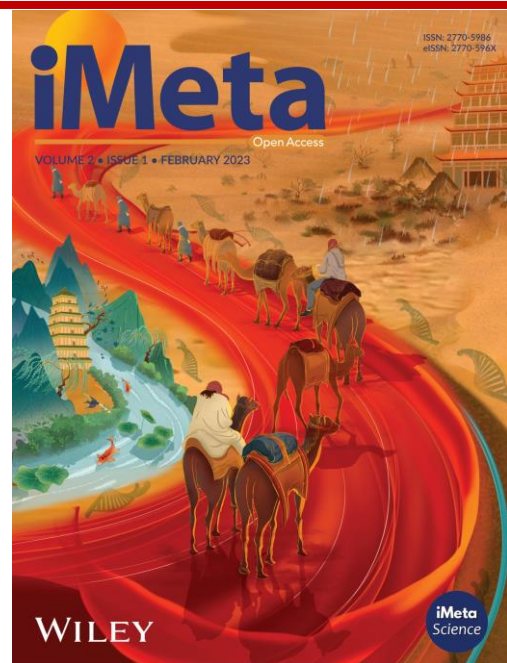
Summary

- ❑ This study establishes a spatial microbiome atlas of the upper respiratory tract, adenoids, and tonsils in pediatric AH/ATH.
- ❑ Sampling site significantly influences microbial structure; adenoid tissue displays transitional microbiota dynamics and tissue-specific enrichment.
- ❑ Multi-platform validation indicates that key bacterial species can persist between surface and deep tissue compartments, potentially contributing to chronic inflammation.
- ❑ The adenoid tissue microbiome has better predictive value for AH severity, providing a foundation for future multi-omics integration and microbiome-targeted interventions.

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