



综合空间谱系揭示儿童腺样体肥大中的 过渡性微生物动态和菌群异质性

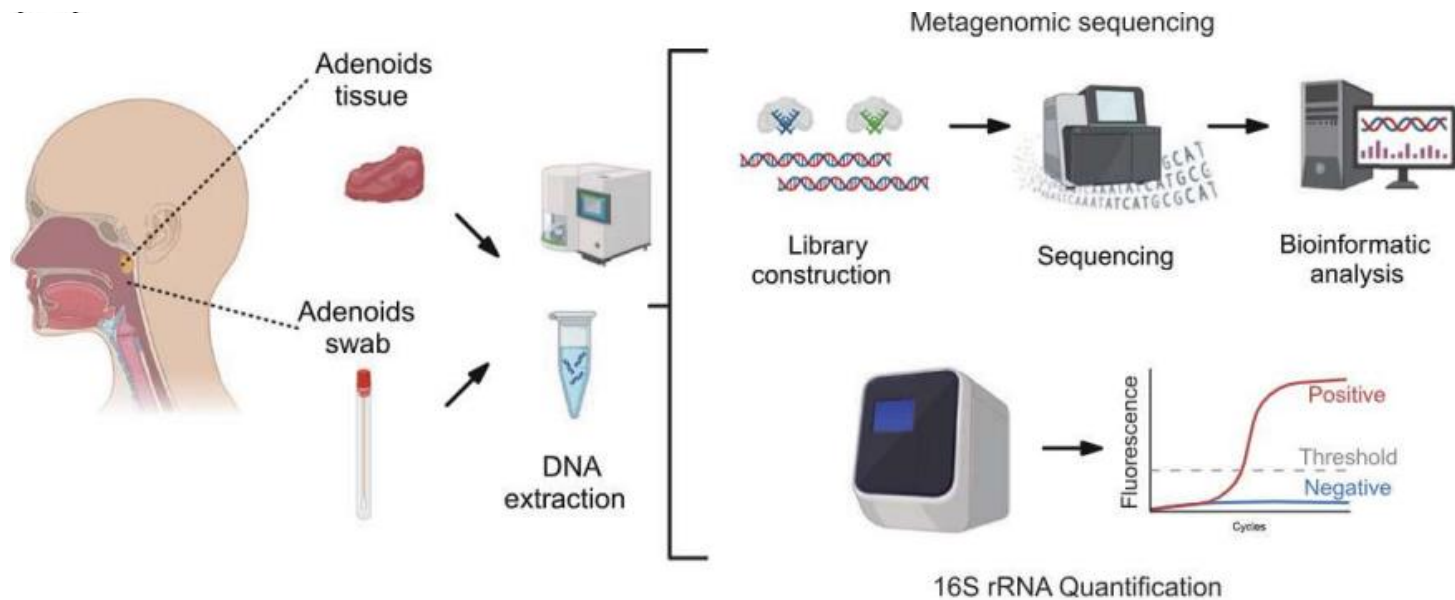
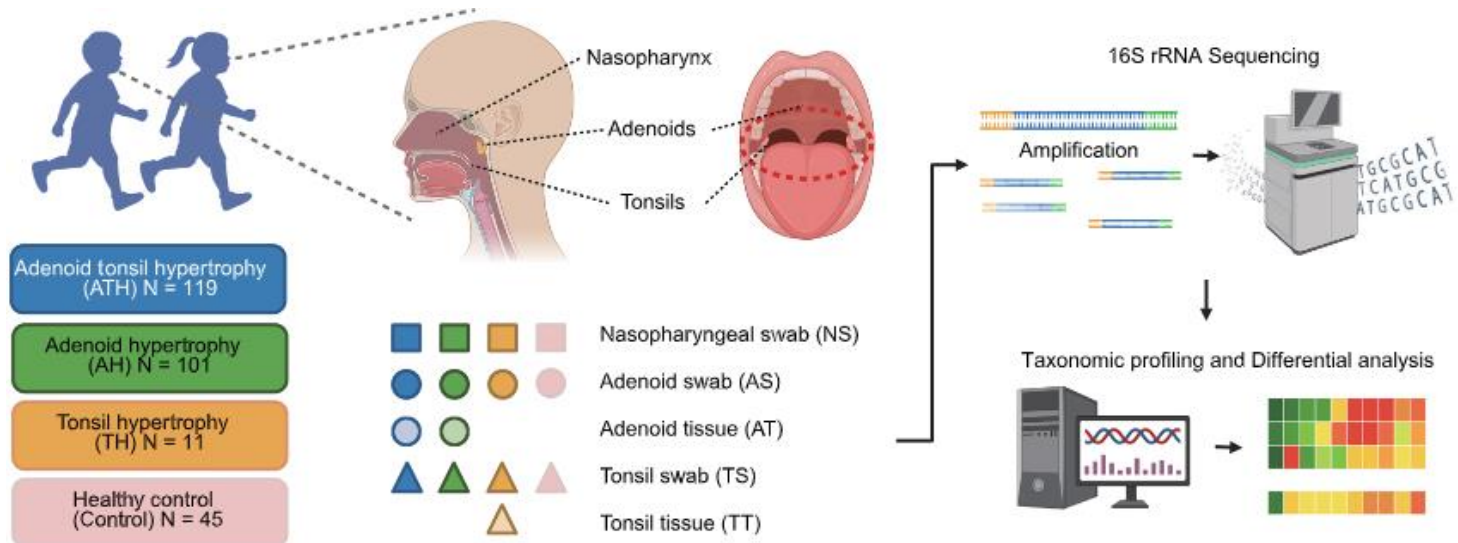
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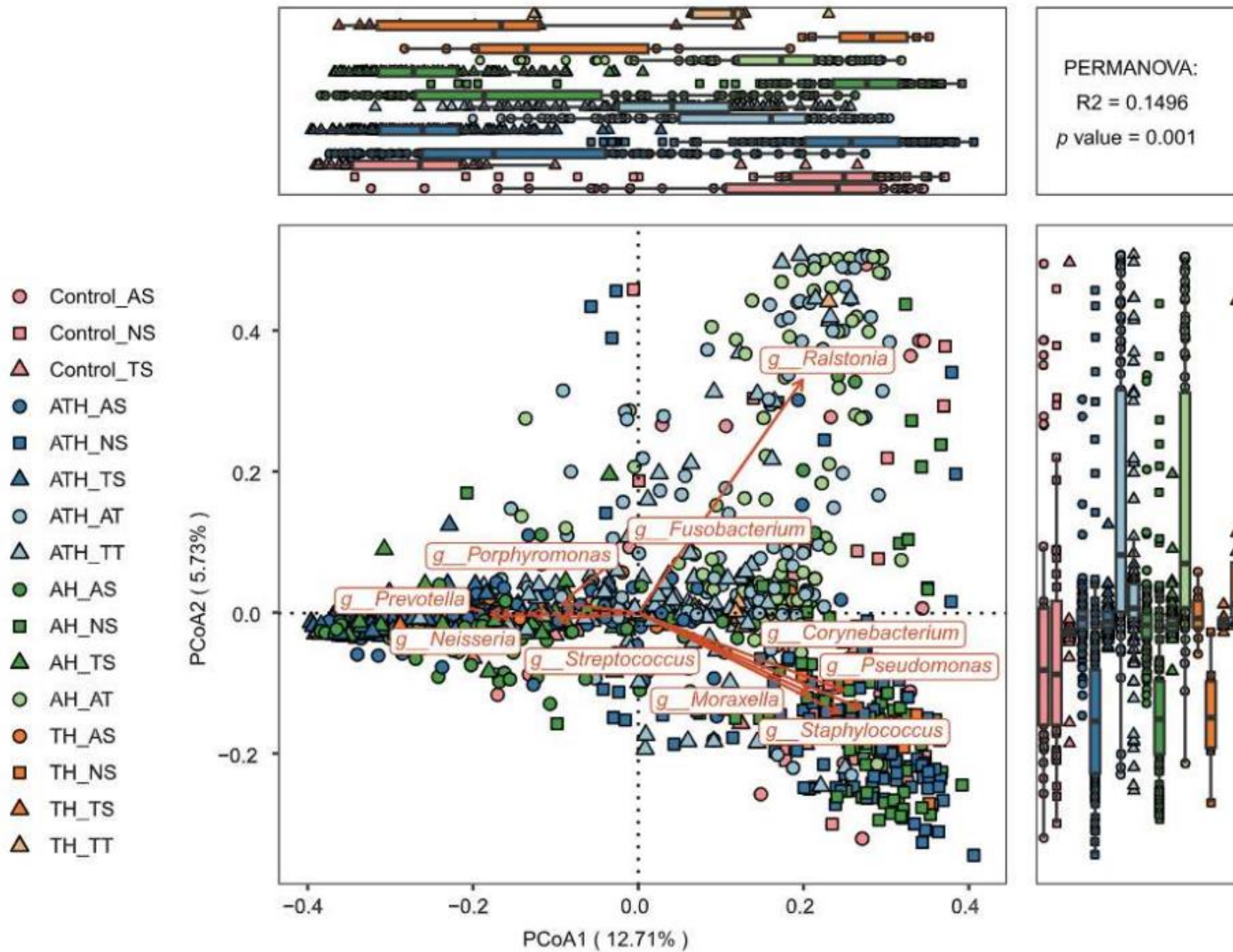


Kaining Chen, Xin Wan, Wenli Guo, Huiwen Ke, Xu Mei, Yanqiu Chen, Wenhao Zhou, et al. 2026.
Comprehensive spatial profiling reveals transitional microbiome dynamics and microbial heterogeneity in pediatric adenoid hypertrophy. *iMetaOmics* 3: e70101. <https://doi.org/10.1002/imo2.70101>

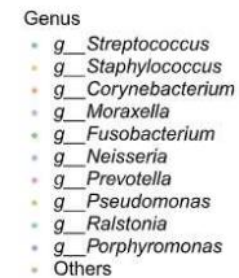
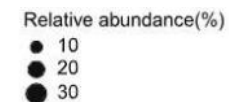
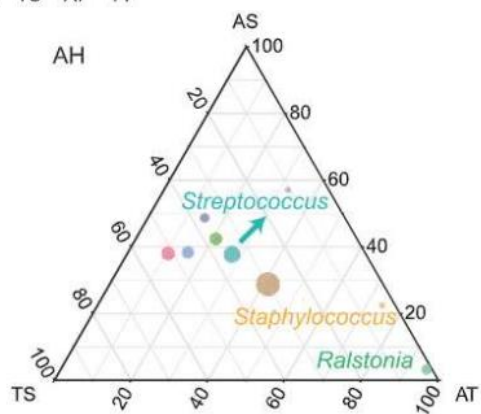
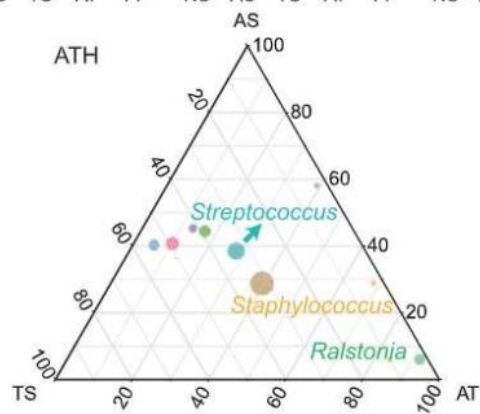
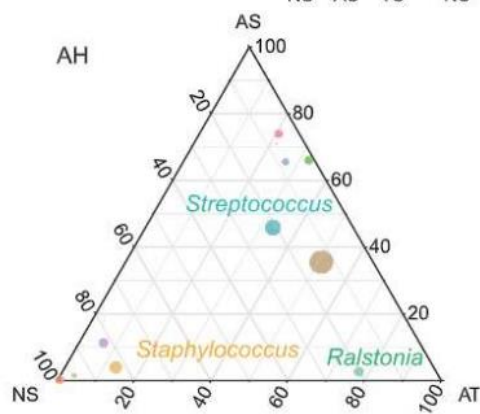
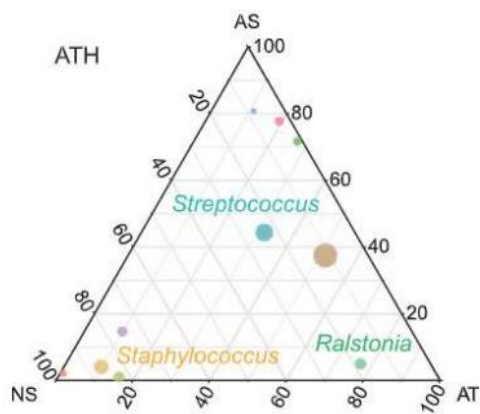
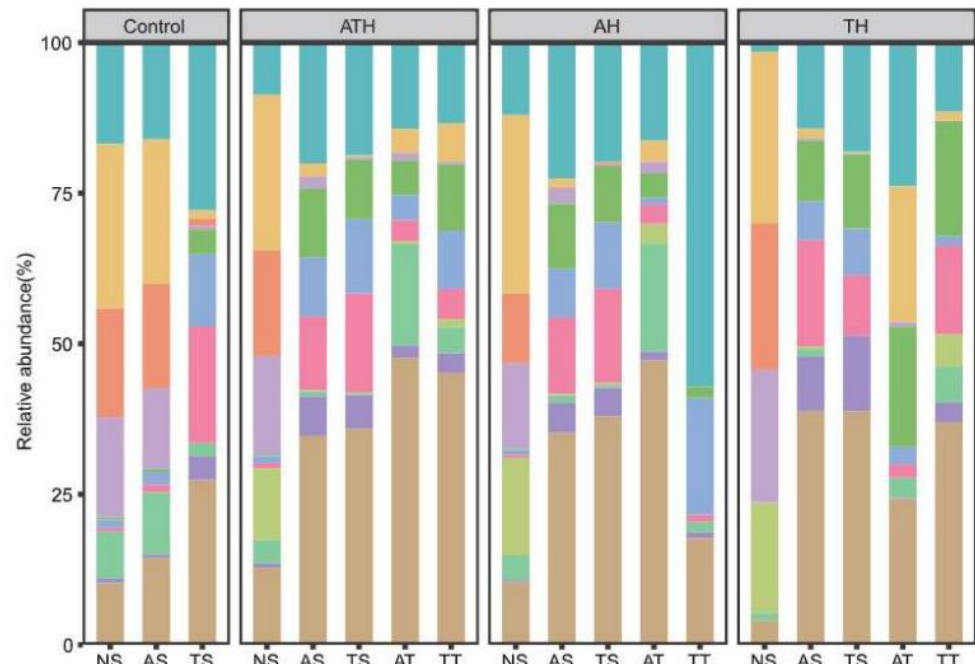
研究设计与样本体系



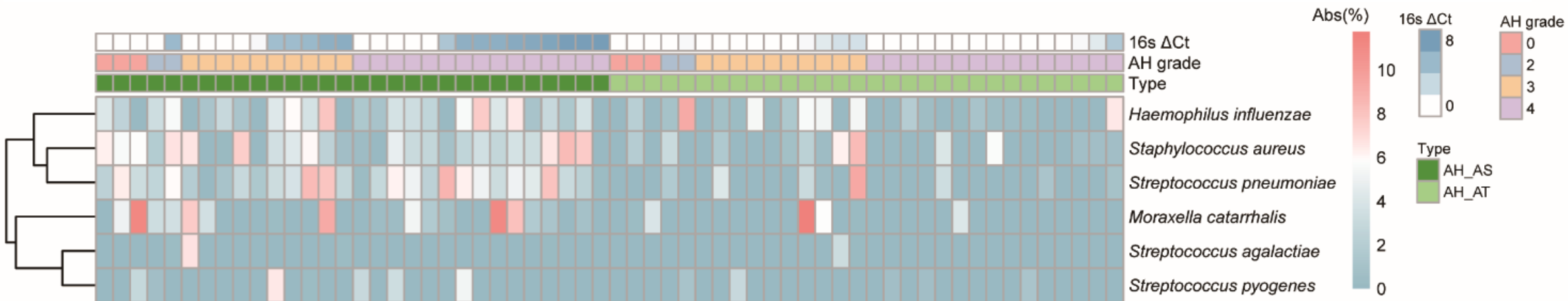
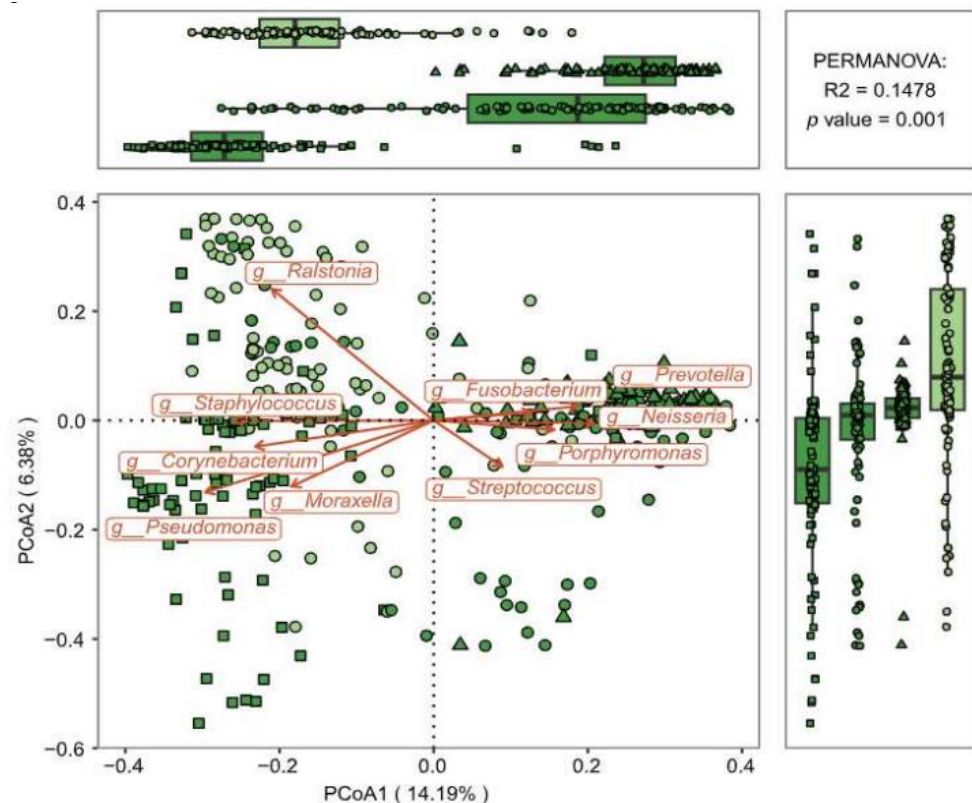
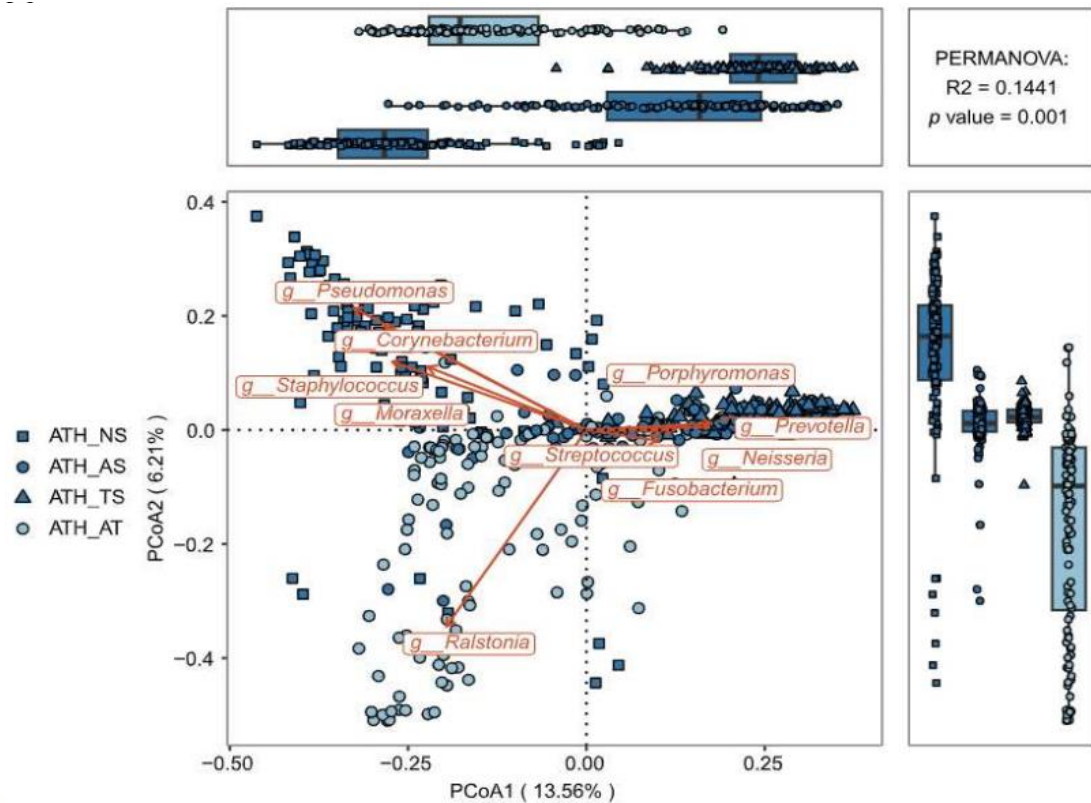
空间异质性：菌群结构随部位改变



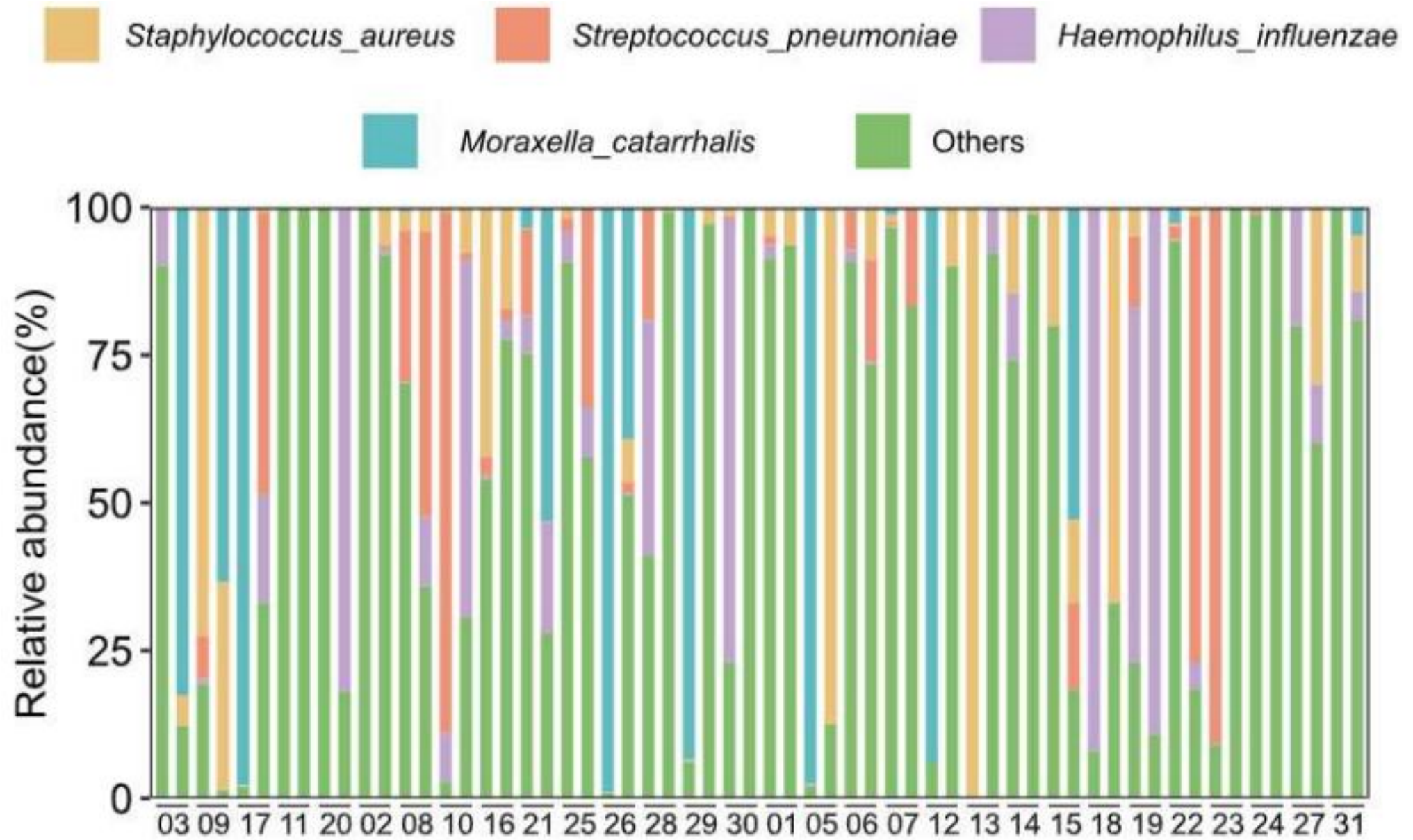
优势菌属的生态位偏好



腺样体组织: 过渡态生态位



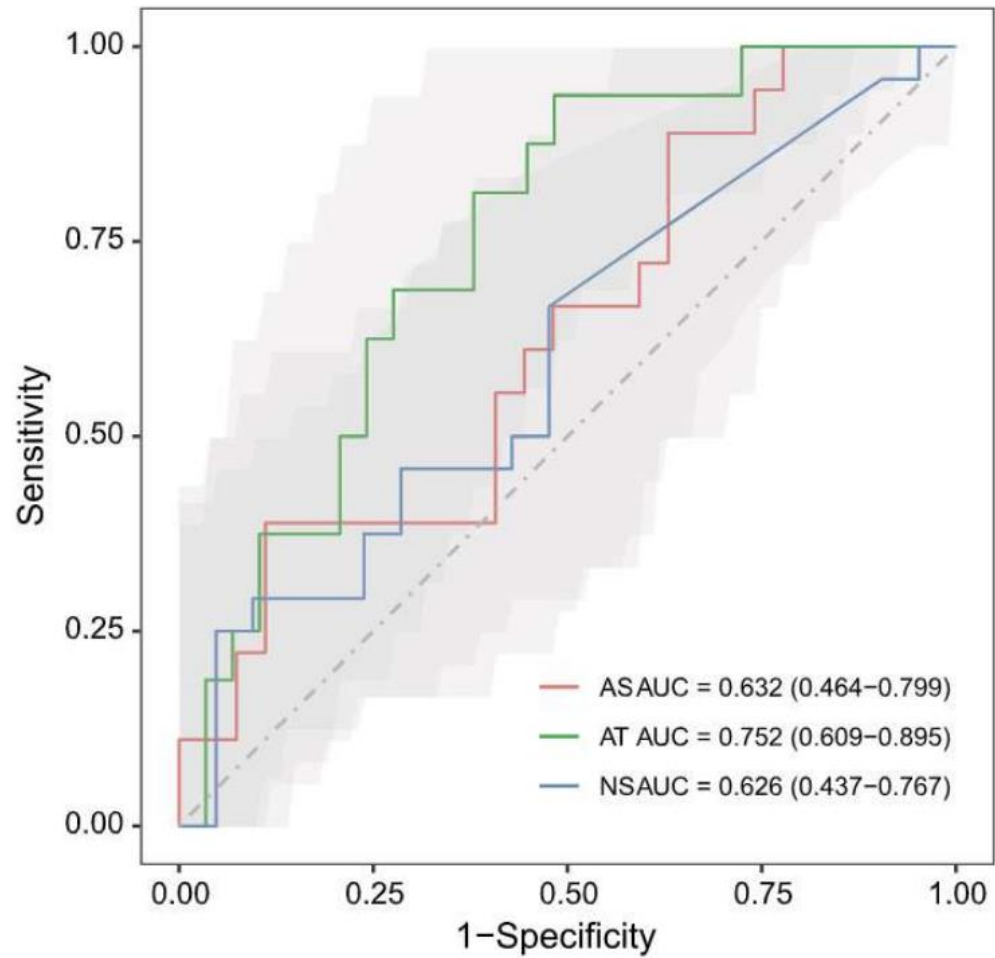
物种级验证:关键菌种的迁移/持续存在



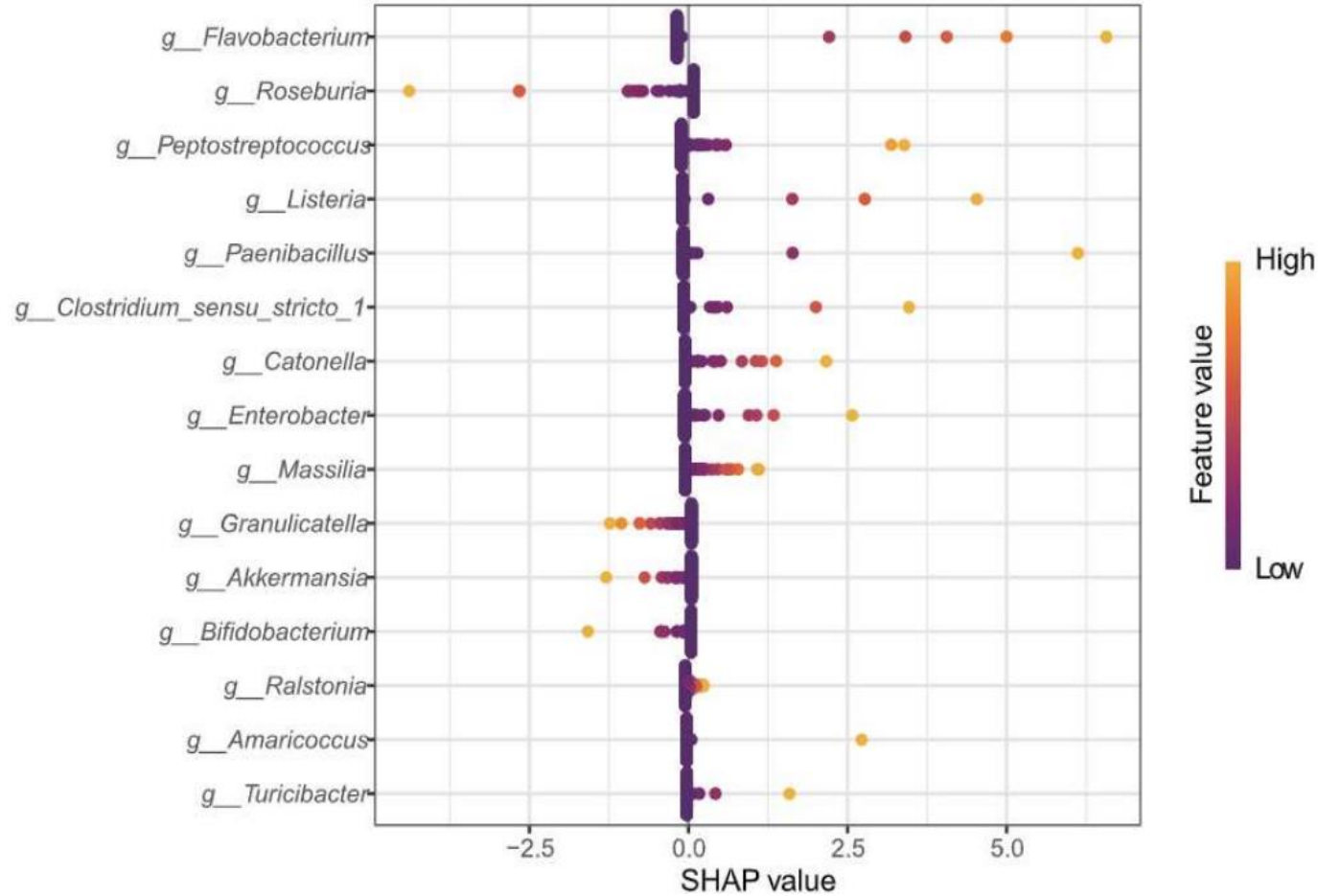


疾病严重程度预测：腺样体组织优于表面拭子

ROC curve



Feature contribution from SHAP analysis (AT)

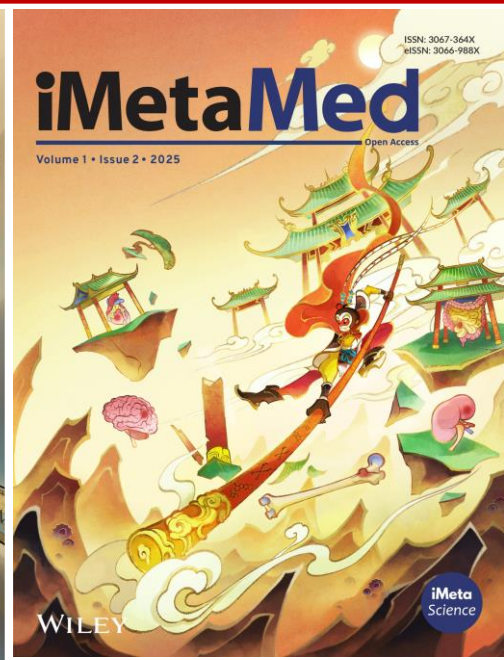
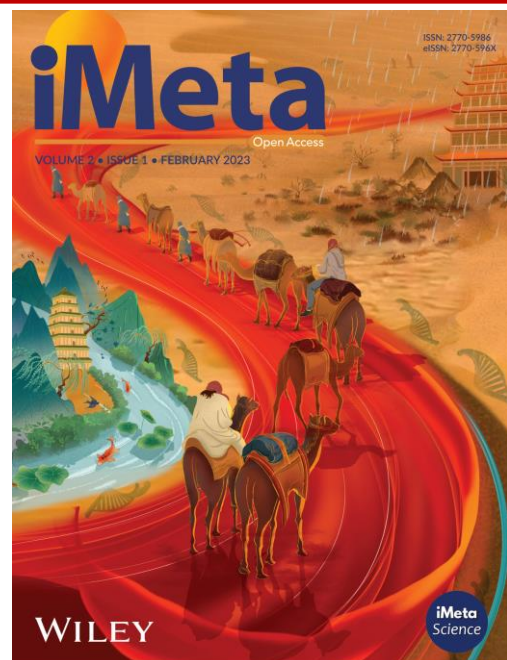


- 本研究建立了儿童AH/ATH上呼吸道-腺样体-扁桃体的空间微生物图谱;
- 取样部位对菌群结构具有显著影响, 腺样体组织呈现过渡性菌群动态和组织特异性富集;
- 多平台验证提示关键菌种可在表面与深部组织间持续存在, 可能参与慢性炎症维持;
- 腺样体组织微生物组成对AH严重程度具有更好的预测价值, 为未来多组学整合和微生态干预提供基础。

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