

Legends for the Supplementary Datasets

1. **Supplementary Data 1.** Metadata profile of 252 samples included in this study.
2. **Supplementary Data 2.** Metagenomic sequencing data quality control metrics across 252 samples.
3. **Supplementary Data 3.** Gamma diversity of different sampling types across months
4. **Supplementary Data 4.** Genera with significant ($P < 0.05$) differential abundances between the RES sample and the Non-RES sampling type.
5. **Supplementary Data 5.** Family with significant ($P < 0.05$) differential abundances between the RES sample and the Non-RES sampling type.
6. **Supplementary Data 6.** Pathway with significant ($P < 0.05$) differential abundances between the RES sample and the Non-RES sampling type.
7. **Supplementary Data 7.** Associations between environmental factors and microbiome alpha-diversity through Generalized Linear Model.
8. **Supplementary Data 8.** Associations between environmental factors and resistome alpha-diversity through Generalized Linear Model.
9. **Supplementary Data 9.** Associations between significant environmental factors in the Generalized Linear Model and microbiome alpha-diversity through the Generalized Additive Model.
10. **Supplementary Data 10.** Annual international aviation metrics of Gaoqi Airport at Xiamen (2017–2024)
11. **Supplementary Data 11.** Associations between significant environmental factors in the Generalized Linear Model and resistome alpha-diversity through the Generalized Additive Model.
12. **Supplementary Data 12.** Source of publicly available metagenomic studies analyzed for comparative assessment of ARG prevalence across environmental niches.
13. **Supplementary Data 13.** Genomic structure patterns of mobile ARG patterns present in four sampling types.
14. **Supplementary Data 14.** Environment parameters across 128 WTP samples from six regional facilities.