



Baseline Immune, Microbial, and Metabolic Features Associated With HRAEs in ICI-treated Lung Cancer

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INTRODUCTION

Clinical problem

- HRAEs can interrupt ICI therapy.
- Reliable pre-treatment biomarkers remain lacking.
- The pre-ICI immune–microbial–metabolic background is poorly understood.

Study question

Are HRAEs linked to distinct baseline multi-omics profiles?

Central message: HRAEs may reflect baseline susceptibility.

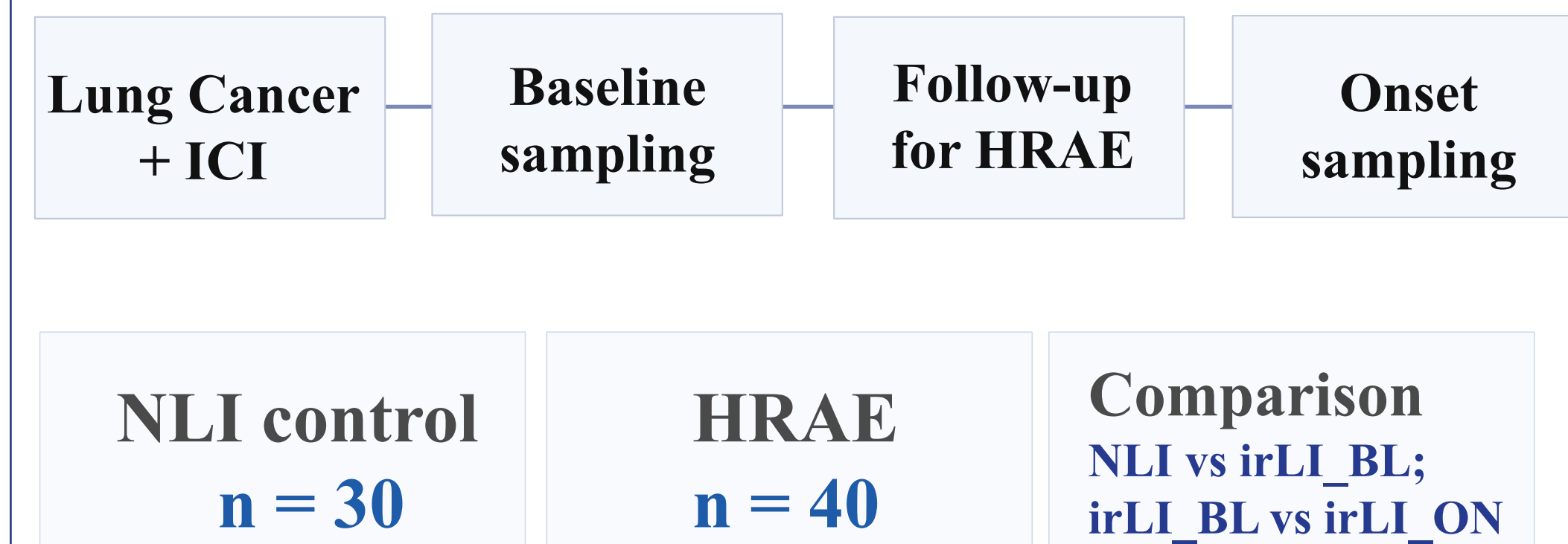
METHODS

Design:

Single-center retrospective observational study

Jan 2022–Jun 2025 | n = 70

Cohort and sampling



Data layers

- Immune profiling
- Shotgun metagenomics
- Untargeted metabolomics
- **Statistics:** group comparisons, PERMANOVA, logistic regression, ROC

DISCUSSION AND CONCLUSION

Take-home message

- HRAEs were associated with pre-existing host biological differences.
- Baseline multi-omics features support susceptibility-oriented risk stratification.
- Onset-stage changes suggest immune amplification rather than systemic restructuring.

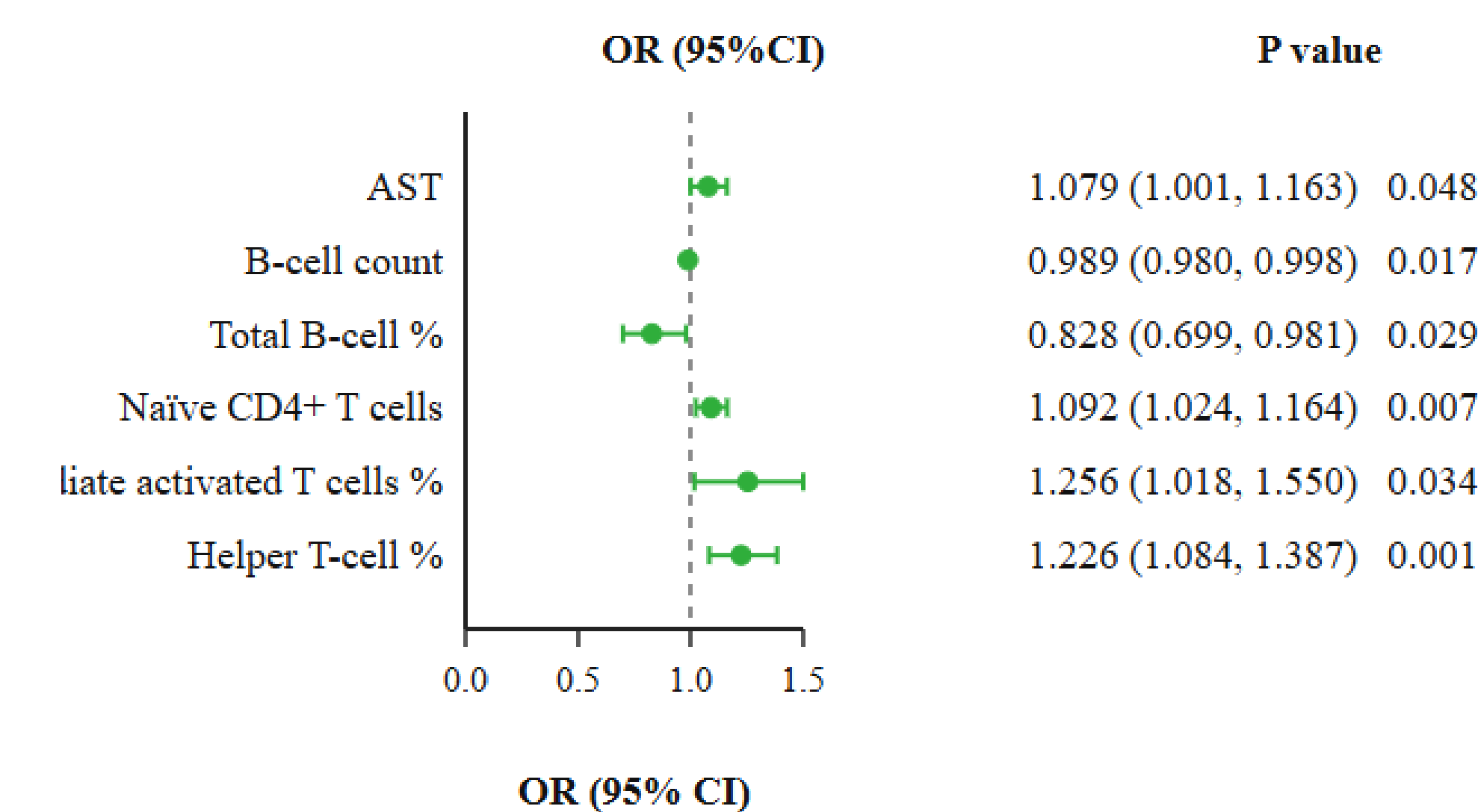
Future Direction

- Prospective multi-center validation
- Pre-treatment risk model development

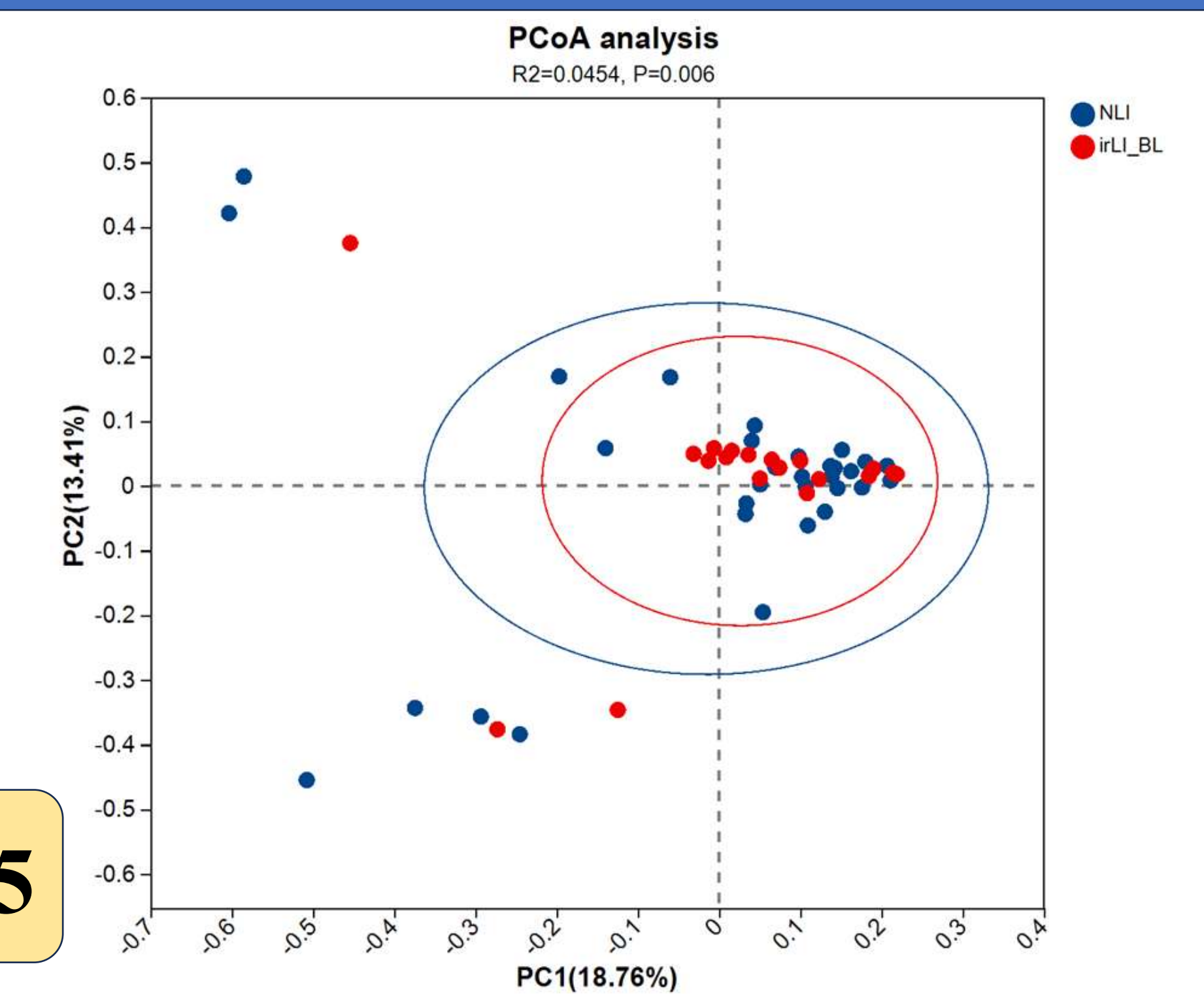
RESULTS

Key finding: Baseline immune, microbial, and metabolic differences preceded ICI initiation.

1. Baseline immune susceptibility



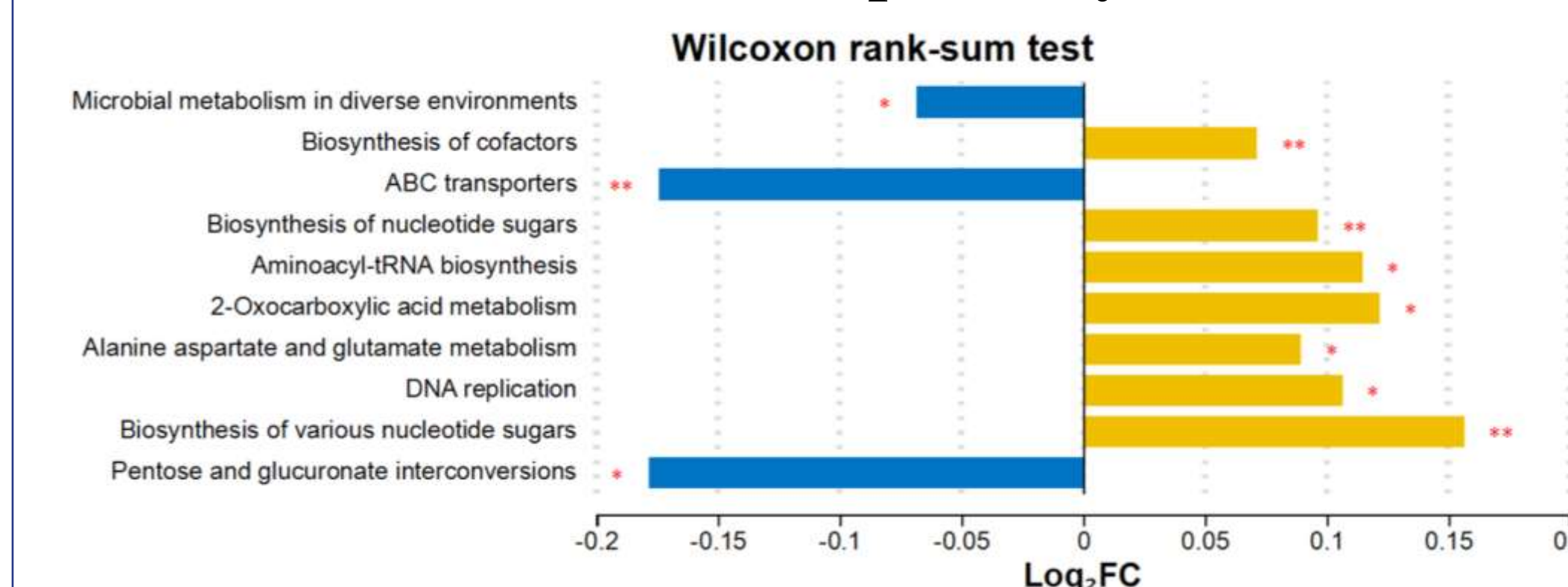
2. Gut microbiome structure



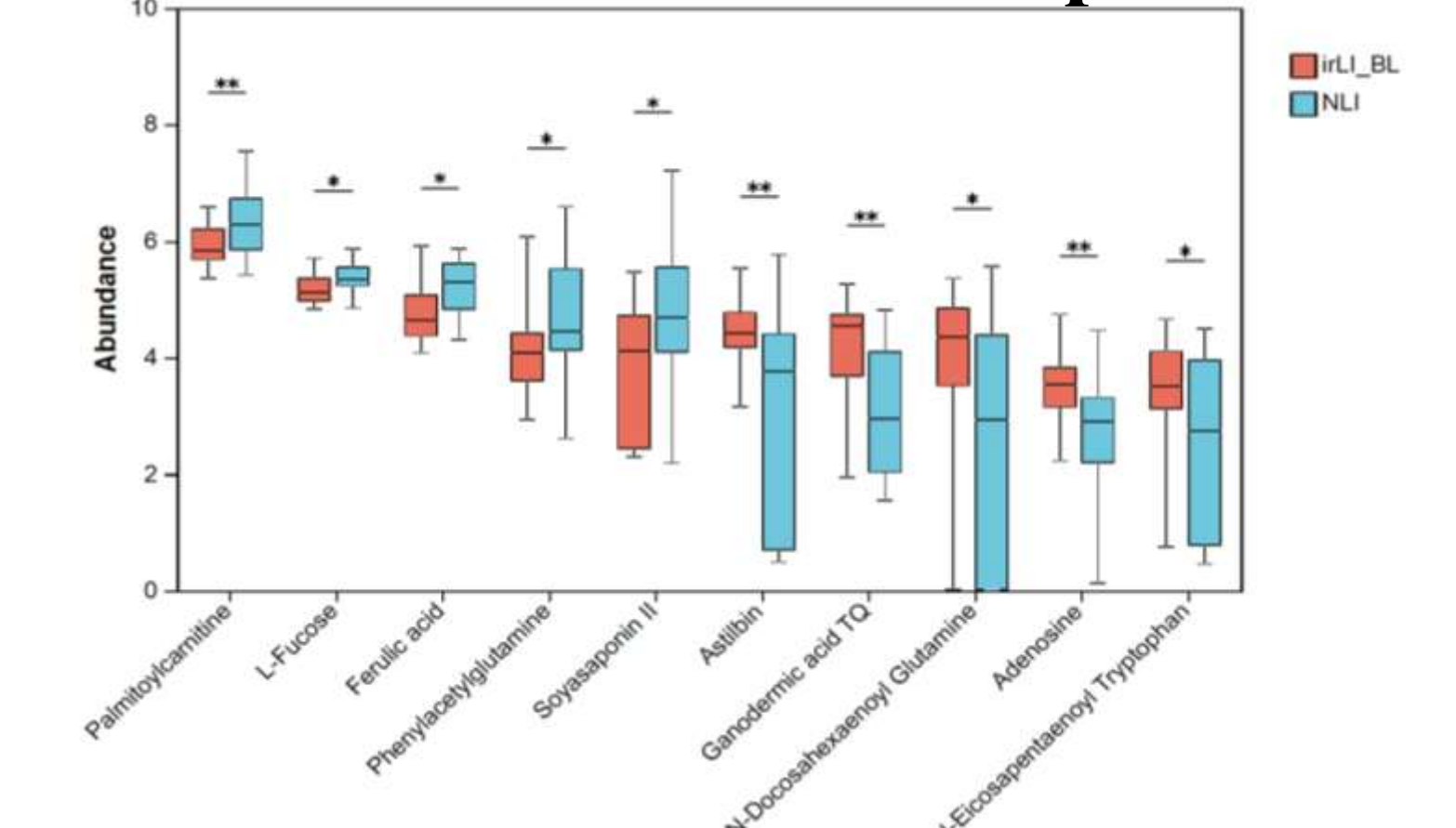
NLI vs irLI_BL: P= 0.006, R² = 0.045

3. Fecal metabolomics

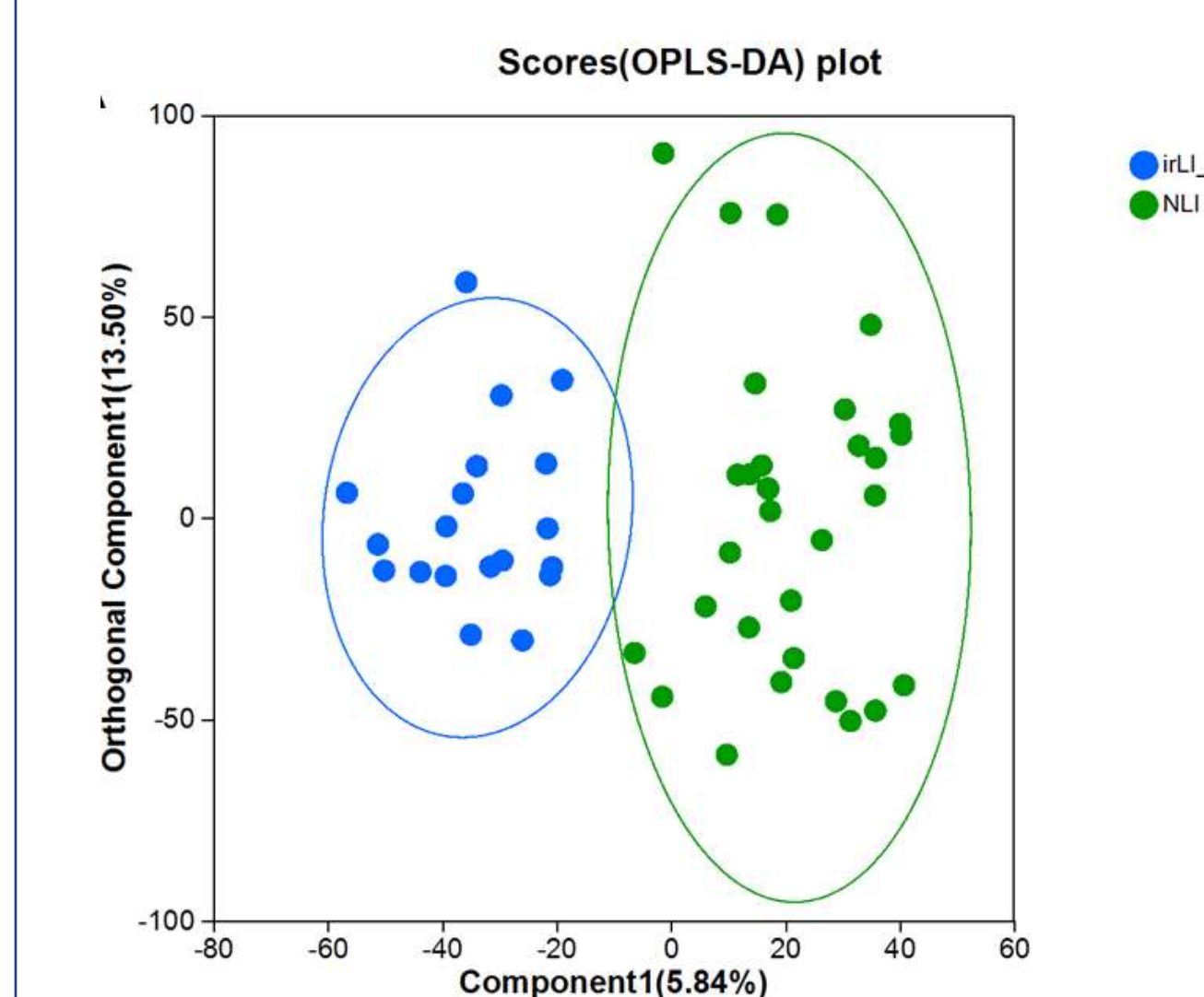
Baseline functional pathway shifts



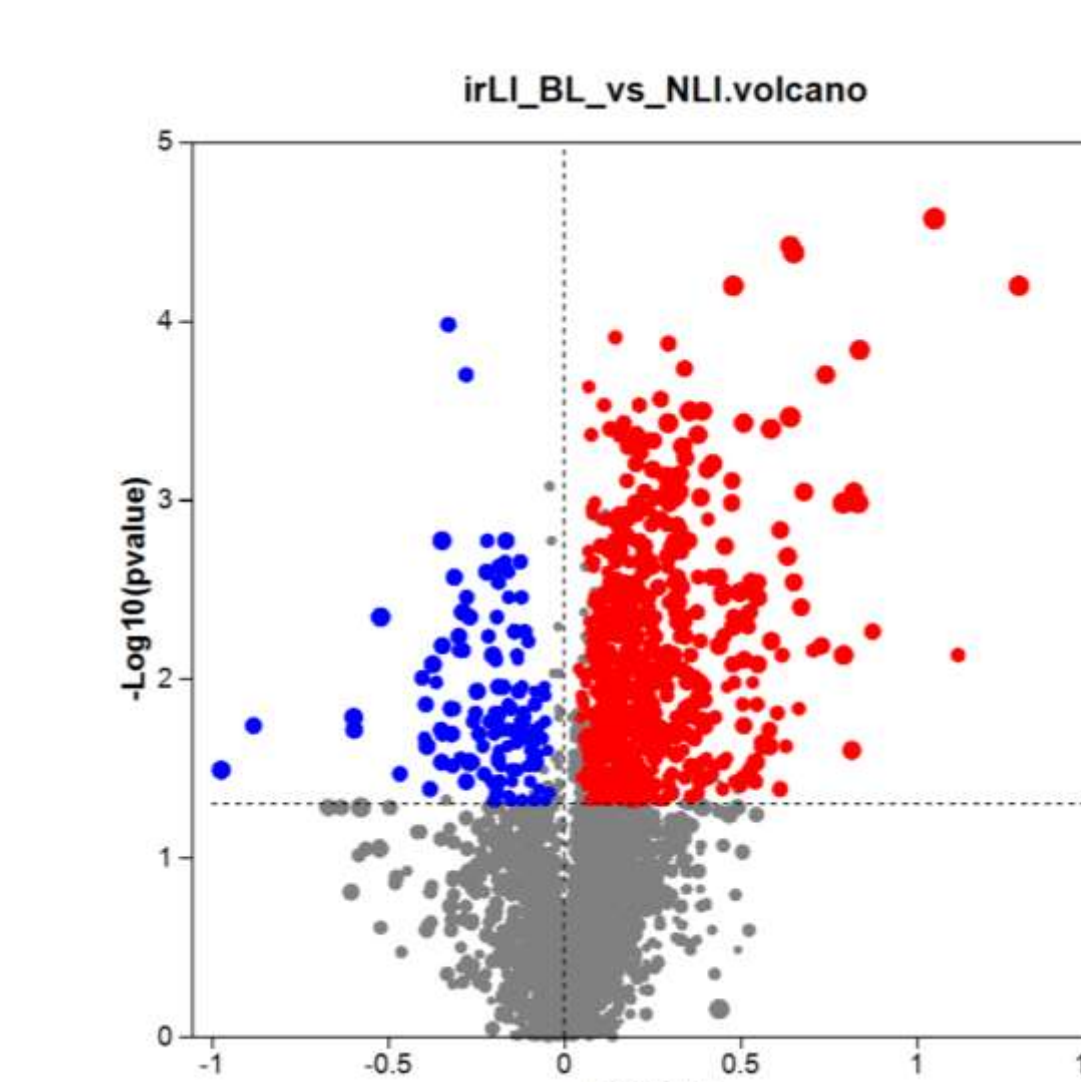
Differential metabolite profiles



Metabolomic profile separation



Differential feature overview



KEGG pathway enrichment

