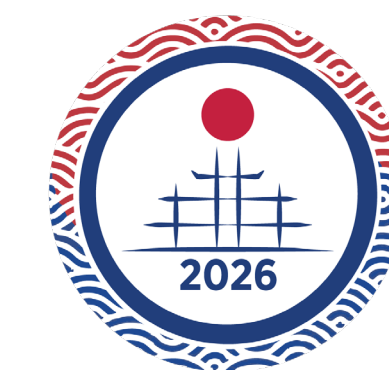




P1.034: Circulating Microbial DNA as Biomarkers for Early Lung Adenocarcinoma Detection

Zeyuan Zhao¹, Xuewang Jia¹, Zuoqing Song¹
¹Tianjin Medical University General Hospital, Tianjin/CN
Correspondence: thoracic_expert@aliyun.com



IASLC 2026 World
Conference on Lung Cancer
SEPTEMBER 12 - 15, 2026
SEOUL, REPUBLIC OF KOREA

INTRODUCTION

- Lung cancer remains the leading cause of cancer-related mortality worldwide, largely due to late-stage diagnosis.
- Although low-dose CT (LDCT) improves early detection, its clinical utility is limited by false-positive findings.
- Circulating microbial DNA (cmDNA) has emerged as a potential non-invasive liquid biopsy biomarker, but its role in early lung cancer detection remains unclear.
- This study aimed to characterize plasma cmDNA profiles across disease stages and evaluate their potential for detecting stage I lung adenocarcinoma.

METHODS

- Design:**
Discovery cohort (n = 61)
- Healthy controls: n = 20
 - Stage I lung adenocarcinoma: n = 21
 - Advanced-stage lung adenocarcinoma: n = 20

Plasma WGS
Plasma collection and whole-genome sequencing
All lung cancer cases were histologically confirmed as lung adenocarcinoma.

- cmDNA profiling**
- Microbial relative abundance
 - Bray-Curtis PCoA
 - LEfSe differential taxa analysis
 - KEGG pathway inference

Random forest classifier development

- Independent validation cohort (n = 120)**
- Healthy controls: n = 70
 - Stage I lung adenocarcinoma: n = 50

DISCUSSION AND CONCLUSION

CONCLUSION

- Plasma cmDNA exhibits distinct signatures in early-stage LUAD and shows promise as a non-invasive biomarker for early detection.

Actionable Take Away Message

- cmDNA alterations are detectable as early as stage I LUAD.
- The classifier achieved an AUC of 0.908 in the independent validation cohort.
- cmDNA may complement current approaches to early lung cancer detection.

Future Direction for Research

- Prospective, multicenter validation in larger and more diverse cohorts.
- Evaluate the incremental value of cmDNA combined with LDCT and clinical risk factors.
- Assess reproducibility across populations and sequencing workflows.

REFERENCES & ACKNOWLEDGEMENTS

REFERENCES

- Chen H, et al. *Cell Rep Med*. 2024;5(4):101499.
- Zhou H, et al. *Microorganisms*. 2023;11(3):582.
- de Koning HJ, et al. *N Engl J Med*. 2020;382(6):503-513.
- Nejman D, et al. *Science*. 2020;368(6494):973-980.

ACKNOWLEDGEMENTS & FUNDING

We thank all participants and the clinical, sequencing, and bioinformatics teams for their contributions.

Funding

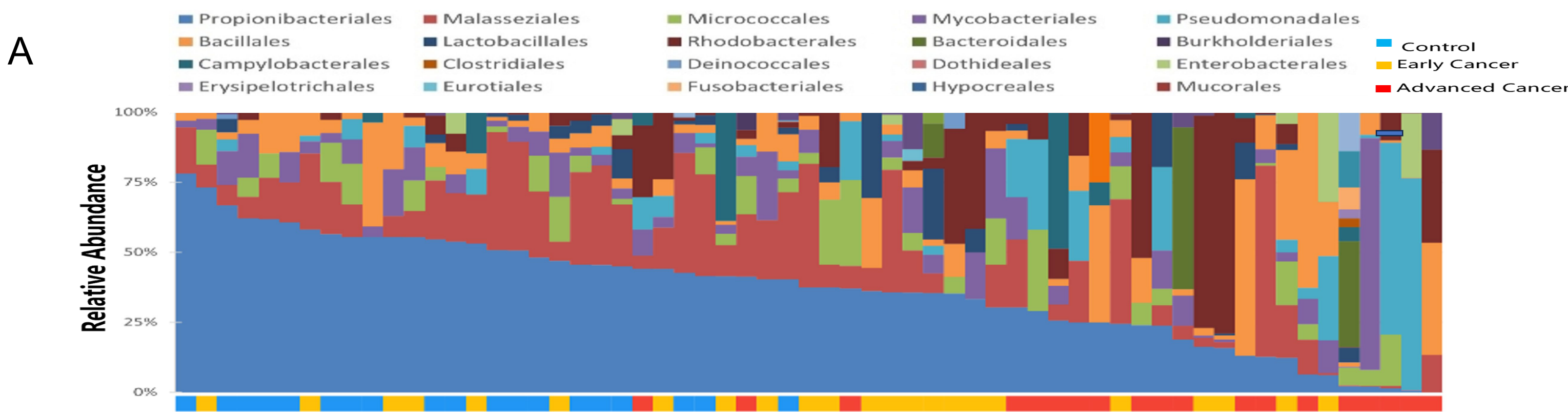
Supported by the Tianjin Binhai New Area Outstanding Science and Technology Talent Training Program (Grant No. KGY2025-22-YY).

AI USE DISCLOSURE

DeepSeek was used for language editing. All scientific content, data interpretation, and conclusions were independently reviewed and approved by the authors.

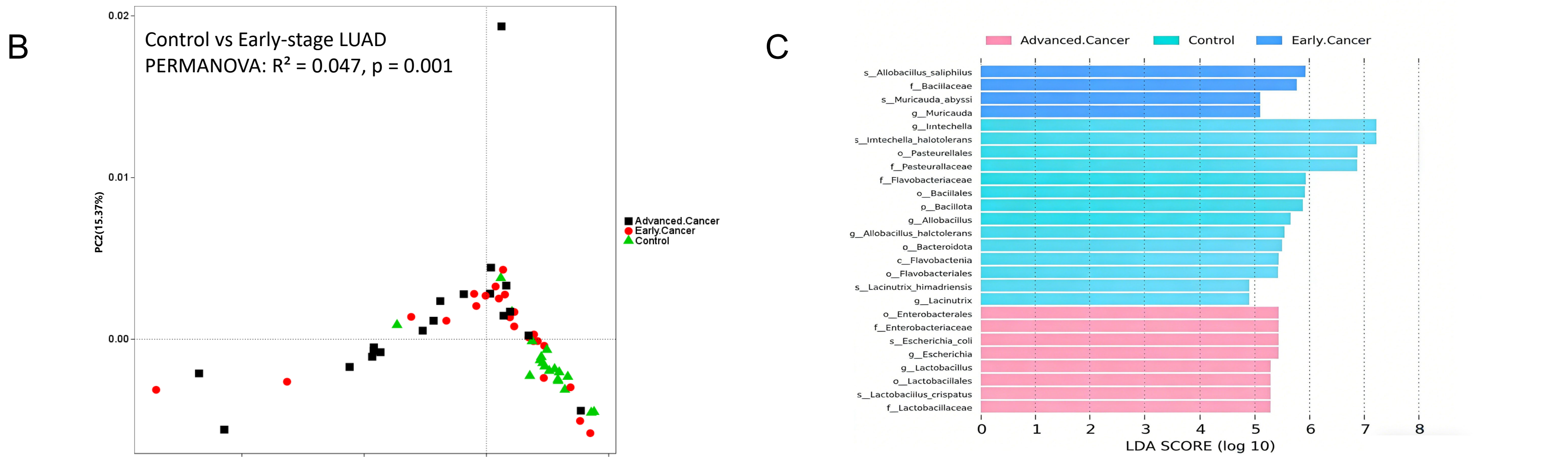
RESULTS

Figure A Stage-dependent alterations in circulating microbial DNA



Plasma cmDNA composition showed stage-dependent alterations across healthy controls, stage I LUAD, and advanced-stage LUAD.

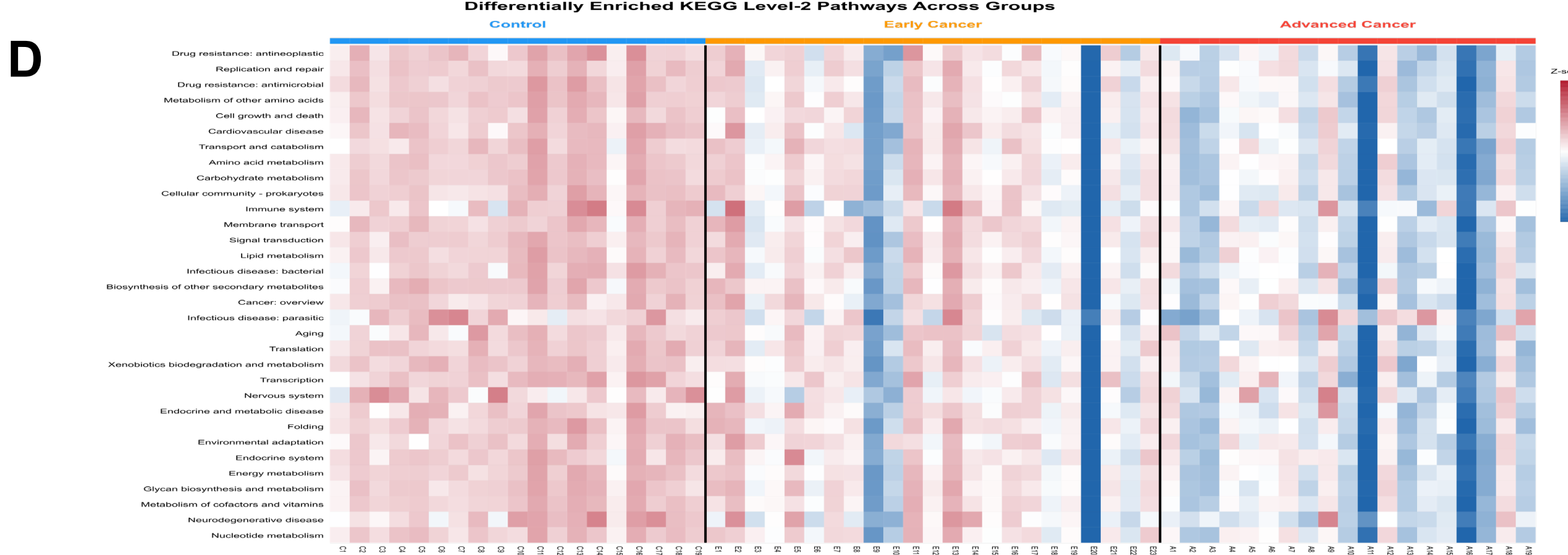
Figure B-C Early-stage LUAD exhibits distinct circulating microbial signatures



PCoA demonstrated modest but significant separation between healthy controls and stage I LUAD.

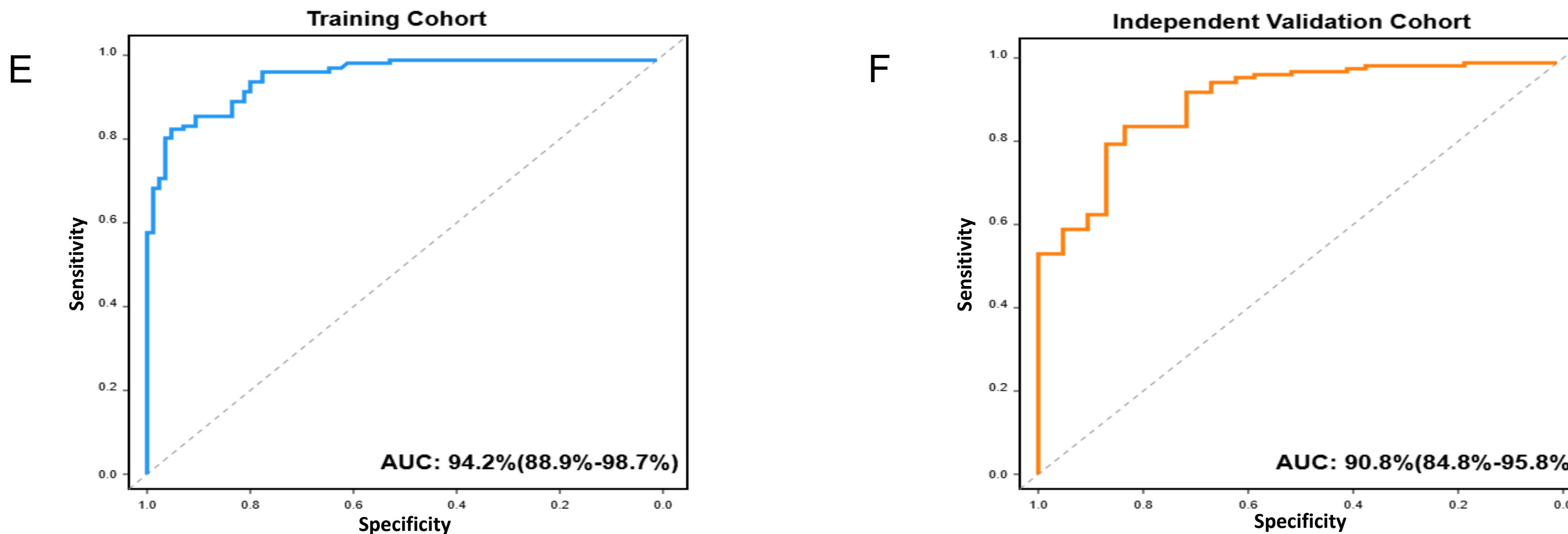
LEfSe identified distinct microbial taxa associated with controls, early-stage disease, and advanced-stage LUAD.

Figure D Functional alterations accompany cmDNA compositional changes



KEGG pathway inference revealed alterations in metabolic and immune-related microbial functions across disease stages.

Figure E-F cmDNA-based classifier shows strong discrimination for early-stage LUAD



Strong discrimination was observed in both the discovery and independent validation cohorts.