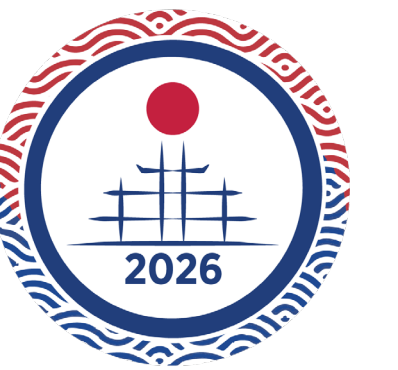




P2.016: Single-Cell and Spatial Transcriptomics Reveal Age-Specific Remodeling of the TME in Early-Stage Lung Adenocarcinoma

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INTRODUCTION

Introduction

- Early-onset lung cancer is increasing, but how host age shapes the tumor immune microenvironment (TME) remains unclear.

Objective

- To compare the TME between younger and older patients with early-stage lung adenocarcinoma using single-cell RNA sequencing and spatial transcriptomics.

METHODS

Design

- Patients with surgically resected T1 LUAD were classified into younger (≤ 30 years) and older (> 60 years) groups.
- Single-cell RNA sequencing and spatial transcriptomics were used to characterize age-related cellular and molecular differences in the TME.
- Age-specific signatures were further evaluated using independent public single-cell and bulk transcriptomic datasets.

DISCUSSION AND CONCLUSION

Actionable Take Away Message

- Host age is associated with distinct immune and stromal TME states in early-stage LUAD.
- Age-related TME signatures may support future biomarker development and patient stratification.

Future Direction for Research

- Validate key age-related TME signatures at the protein and spatial levels using multiplex immunofluorescence.
- Confirm these findings in larger cohorts and functionally investigate NR4A1+ CD8+ T cells and stromal interactions.

REFERENCES & ACKNOWLEDGEMENTS

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Artificial Intelligence (AI) Use Disclaimer

ChatGPT (OpenAI) was used solely for English-language editing and refinement of the poster text. All scientific content, data analysis, interpretation, and conclusions were independently reviewed and approved by the authors.

RESULTS

- Distinct TME states:** Integrated analysis revealed an immune-enriched TME in older patients and an immune-sparse TME in younger patients.
- Malignant epithelial evolution:** Tumor cells showed immune-pressure adaptation in older patients but more invasive programs in younger patients.

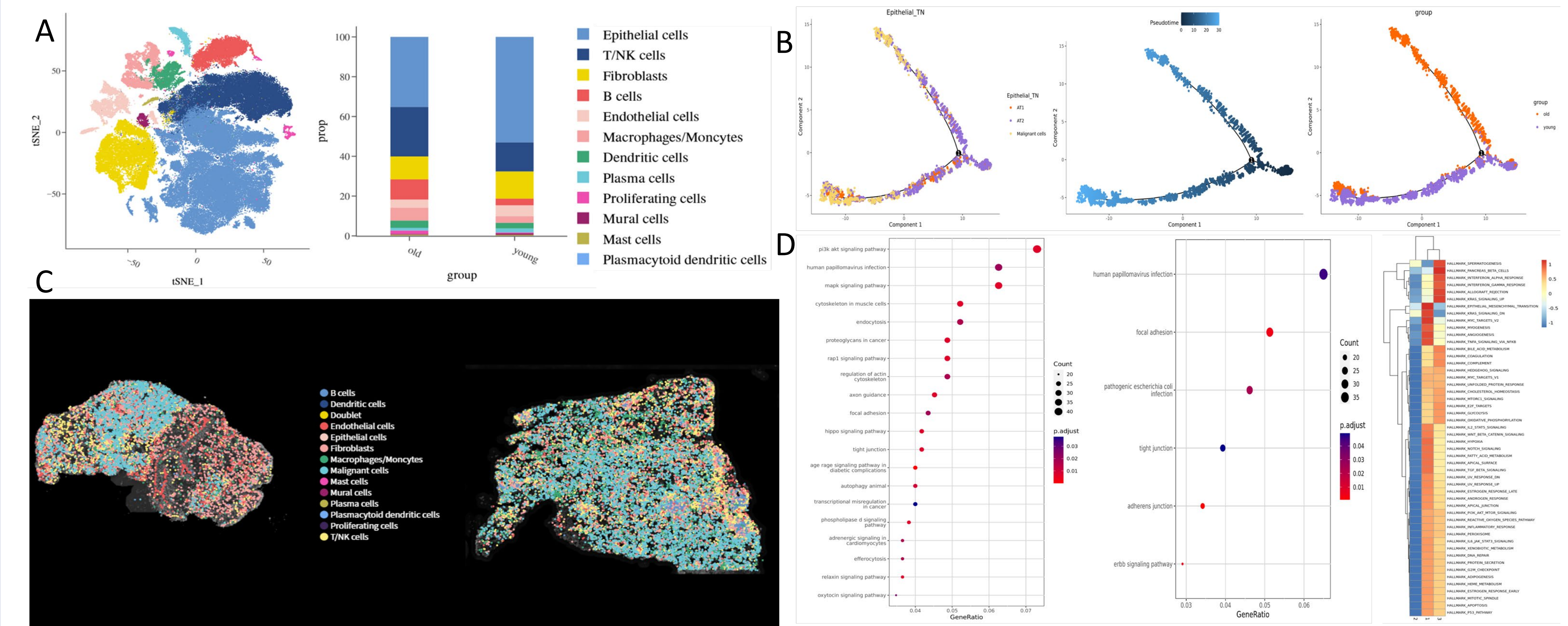


Figure 1. Age-associated TME remodeling in early-stage LUAD. (A) t-SNE map and cell-type proportions by age group. (B) Monocle 2 trajectories of AT1, AT2, and malignant epithelial cells, colored by cell type, pseudotime, and age group. (C) Spatial distributions of major cell types in representative younger (left) and older (right) tumors. (D) KEGG enrichment of genes upregulated in younger and older malignant cells, and GSEA of age-associated pathways.

- T-cell heterogeneity:** A transcriptionally quiescent NR4A1+ CD8+ T-cell subset was enriched in younger patients.
- Cellular interactions:** Cell-cell communication was immune-regulation-dominant in older patients and stroma-driven in younger patients.

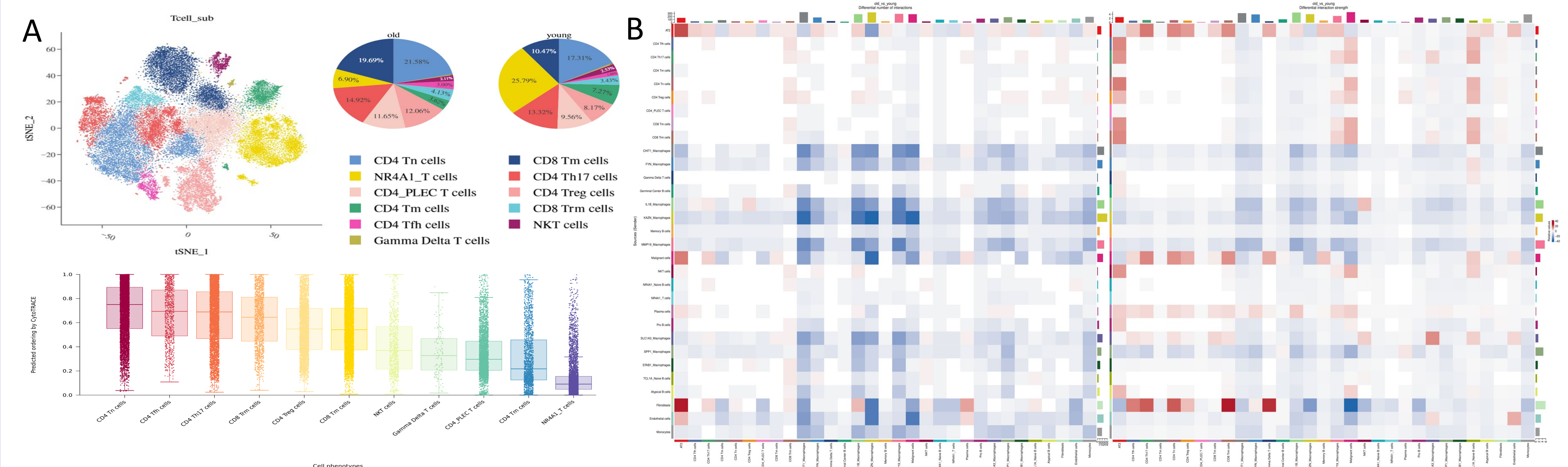


Figure 2. Age-associated T-cell states and intercellular communication in early-stage LUAD. (A) t-SNE map of T-cell subsets, their relative proportions by age group, and stemness scores. (B) Comparison of cell-cell communication networks between younger and older patients.