



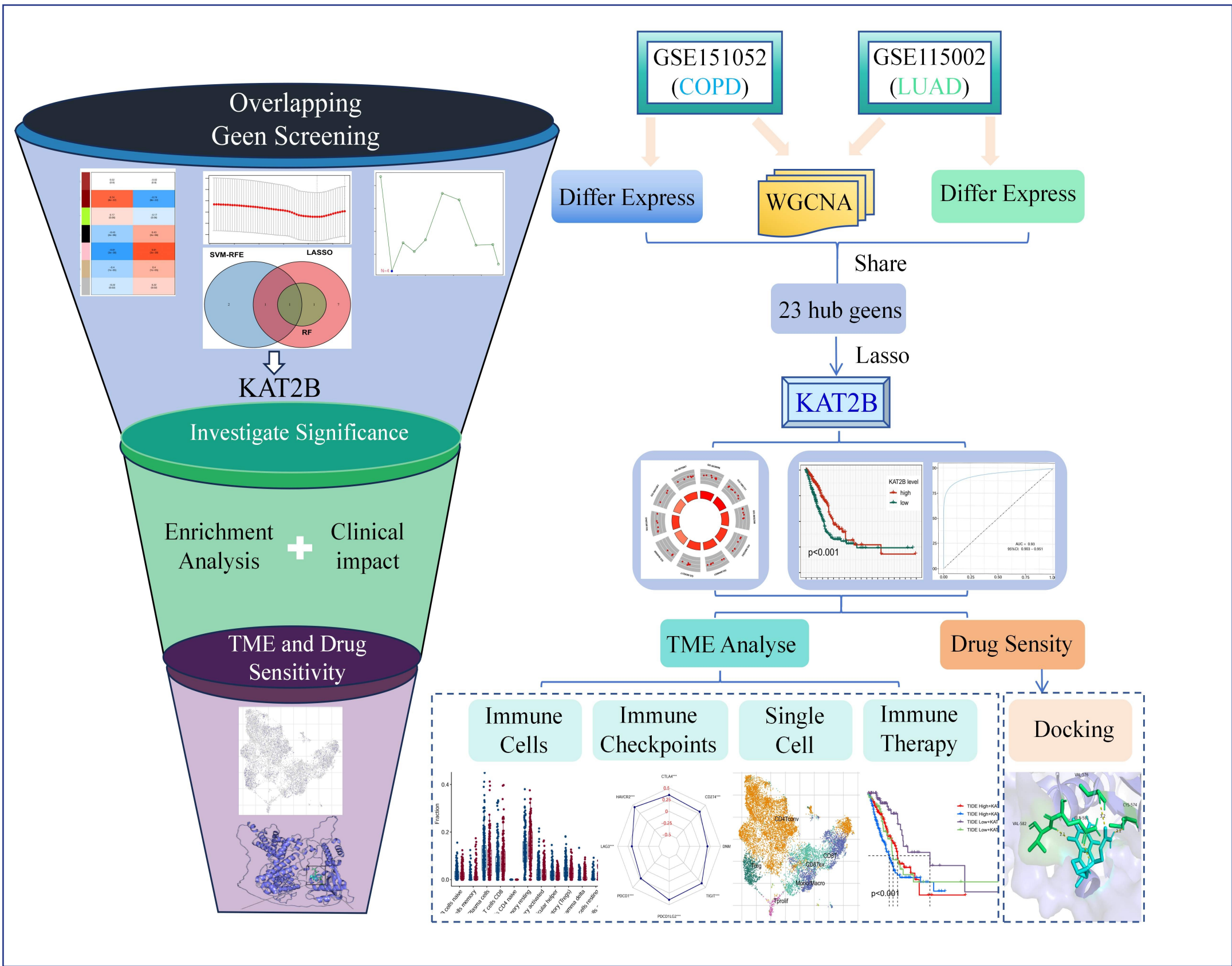
P3.086: Examination of overlapping gene profiles and molecular mechanisms in chronic obstructive pulmonary disease and lung adenocarcinoma

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INTRODUCTION



METHODS

Design:

Gene expression datasets associated with COPD and LUAD were obtained from the Gene Expression Omnibus (GEO) database, including GSE151052, GSE115002, GSE76925, and GSE140797. Weighted gene co-expression network analysis (WGCNA) was performed to identify disease-related gene modules. Shared genes between COPD and LUAD were determined through module intersection analysis. Functional enrichment analyses, including Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG), were conducted to explore biological functions and pathways. Machine learning algorithms, including least absolute shrinkage and selection operator (LASSO), support vector machine-recursive feature elimination (SVM-RFE), and random forest (RF), were used to identify key genes. The diagnostic and prognostic value of the core gene was evaluated using TCGA-LUAD data. Immune infiltration analysis was performed using ESTIMATE and CIBERSORT, and the relationship between the key gene and immune cells was further explored using single-cell sequencing and spatial transcriptomics data. In addition, immunotherapy response prediction and molecular docking analyses were conducted.

DISCUSSION AND CONCLUSION

Actionable Take Away Message

- KAT2B was identified as a key shared gene linking COPD and LUAD and was closely associated with immune regulation, tumor microenvironment characteristics, and therapeutic responses.

Future Direction for Research

- These findings suggest that KAT2B may serve as a potential biomarker and therapeutic target for patients with COPD complicated by LUAD.

REFERENCES & ACKNOWLEDGEMENTS

The most critical references:

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Use the QR code to view the full list of references.



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Artificial Intelligence (AI) Use Disclaimer

*This study did not use artificial intelligence or related tools during the research process.

RESULTS

- Kaplan-Meier analysis revealed that the KAT2B high-expression group exhibited significantly better overall survival ($P < 0.001$). KAT2B possesses both excellent diagnostic value and favorable prognostic implications.
- Diagnostic performance: The ROC curve yielded an AUC of 0.931, enabling efficient discrimination between LUAD and normal tissues, indicating that KAT2B is a potential diagnostic biomarker.
- KAT2B profoundly modulates the tumor immune microenvironment, predicts immunotherapy response, and correlates with chemotherapeutic drug sensitivity.
- It is significantly positively correlated with immune checkpoint molecules including CTLA4, PDCD1, TIGIT, and LAG3. Single-cell and spatial transcriptomics further confirmed that KAT2B is mainly expressed in immune cells such as CD8⁺ T cells, CD4⁺ T cells, monocytes/macrophages, Tregs, and B cells.

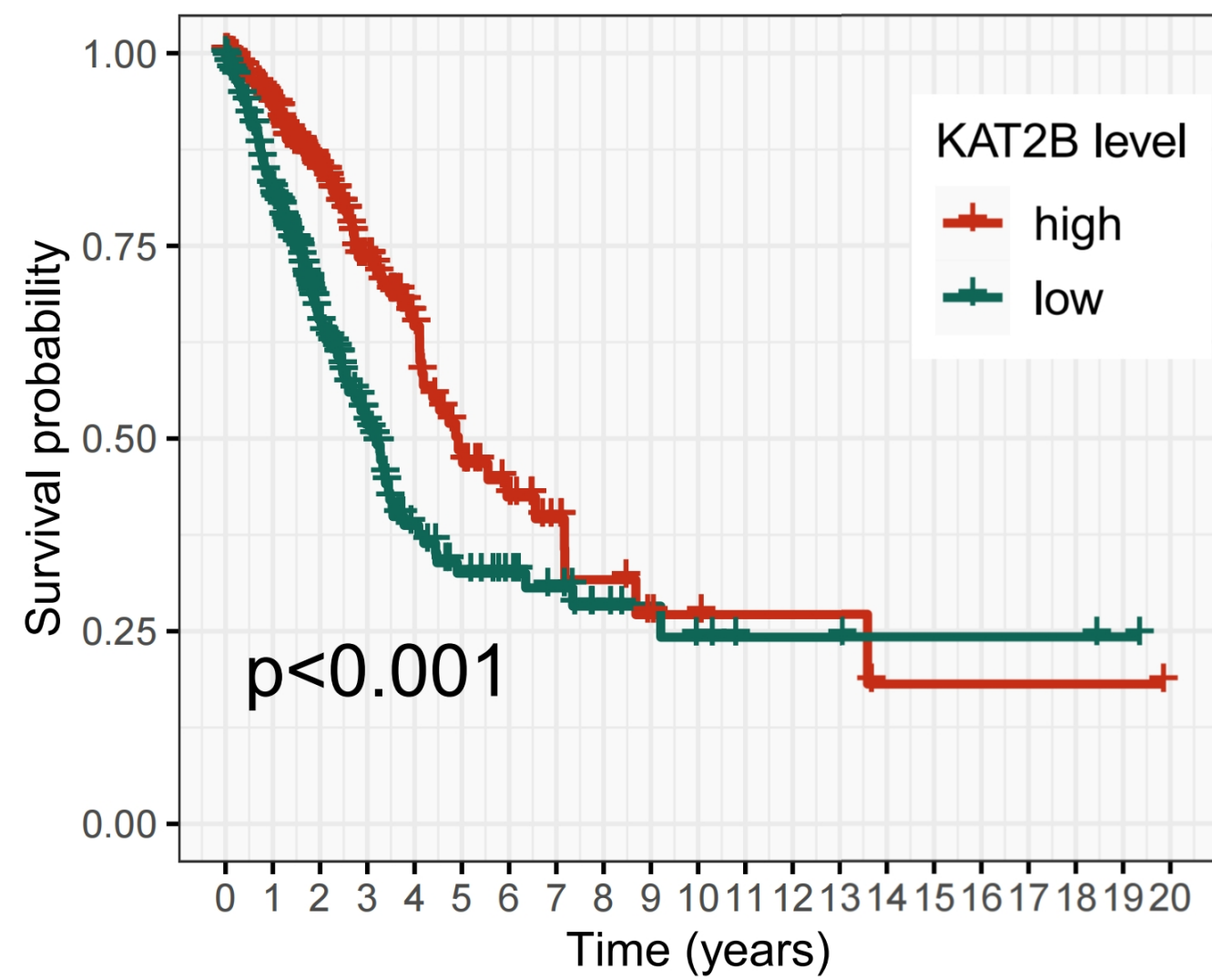


Figure 1: Prognostic value of KAT2B

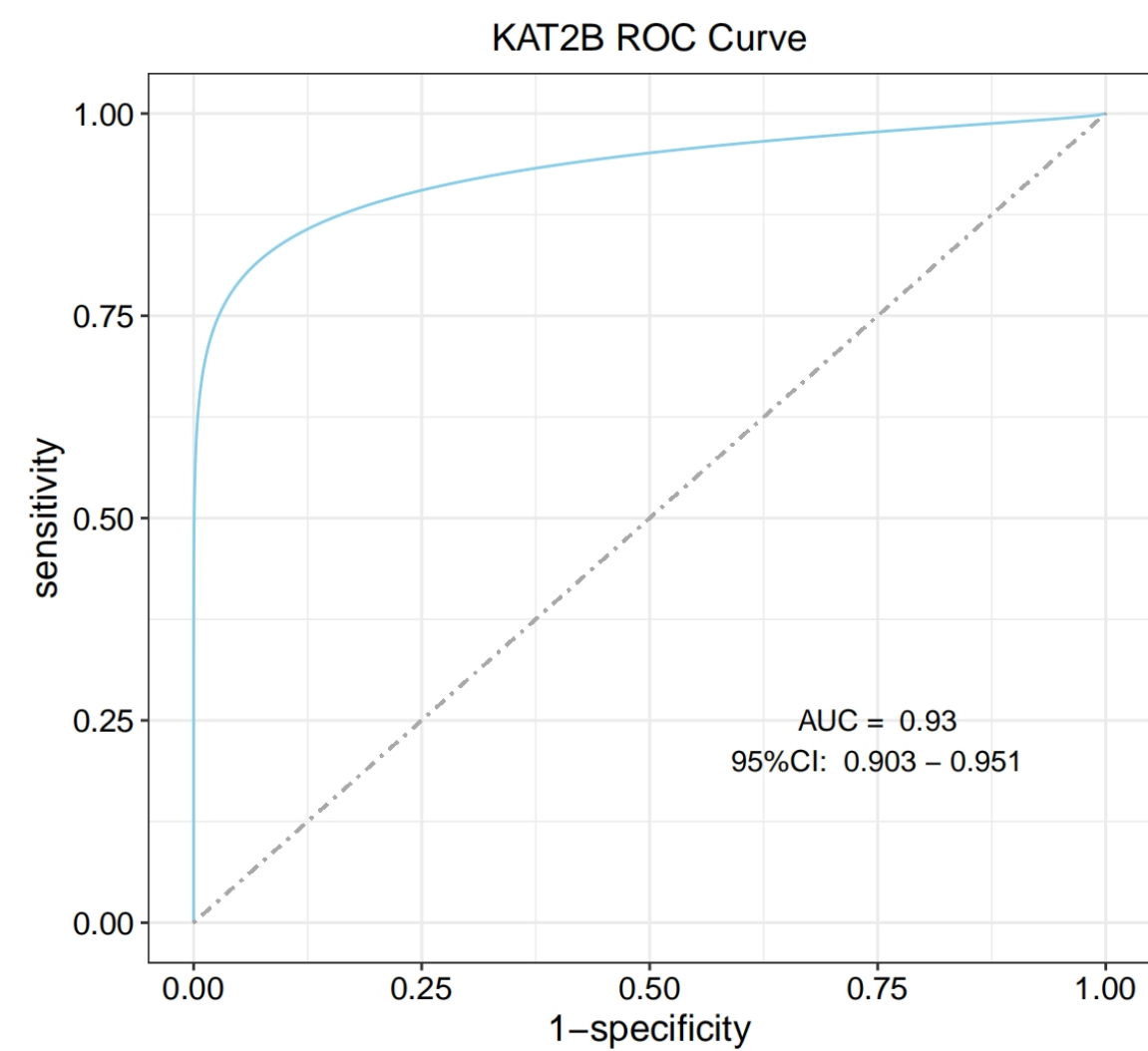


Figure 2: Diagnostic value of KAT2B

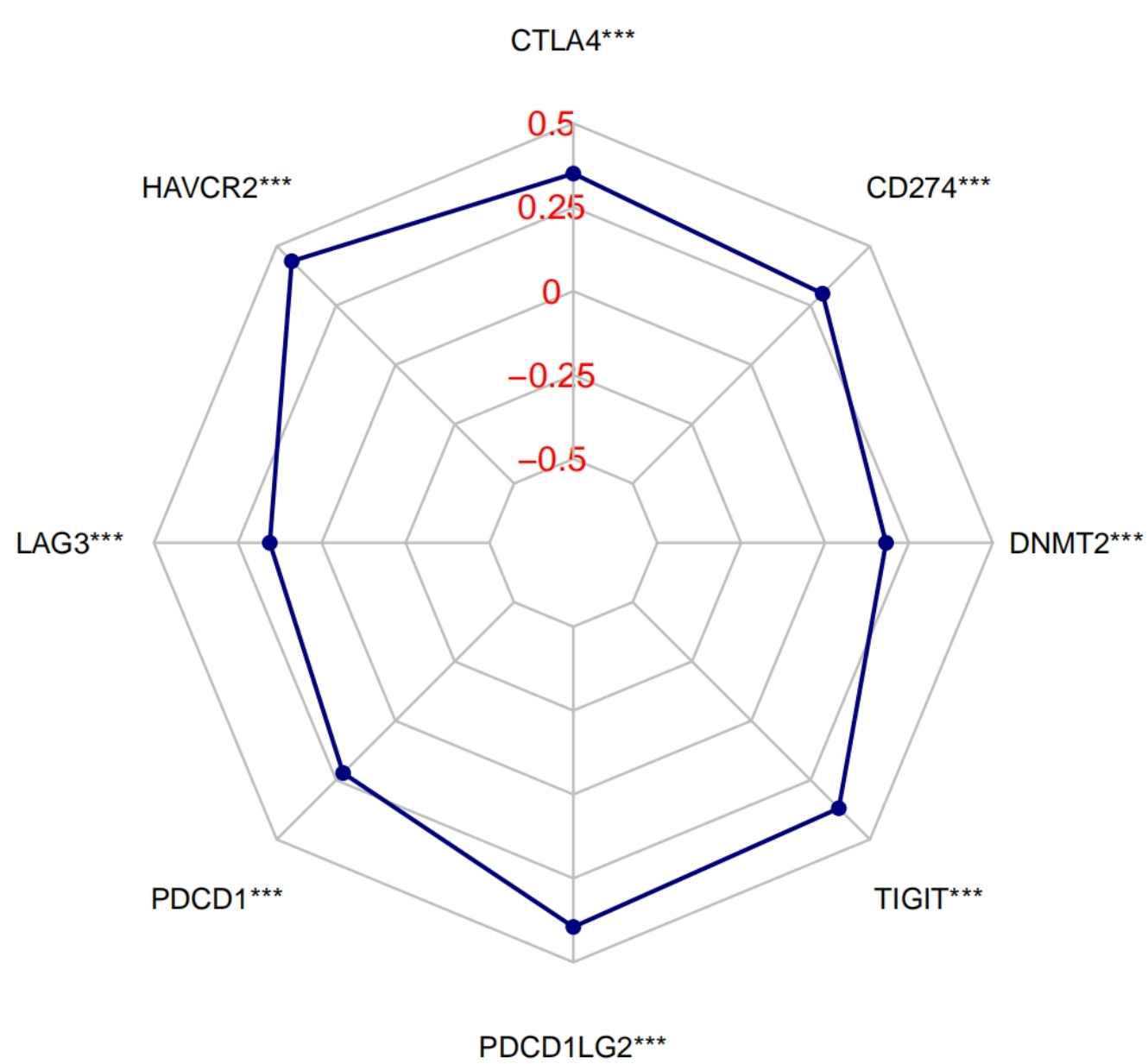


Figure 3: Correlation between KAT2B and checkpoints

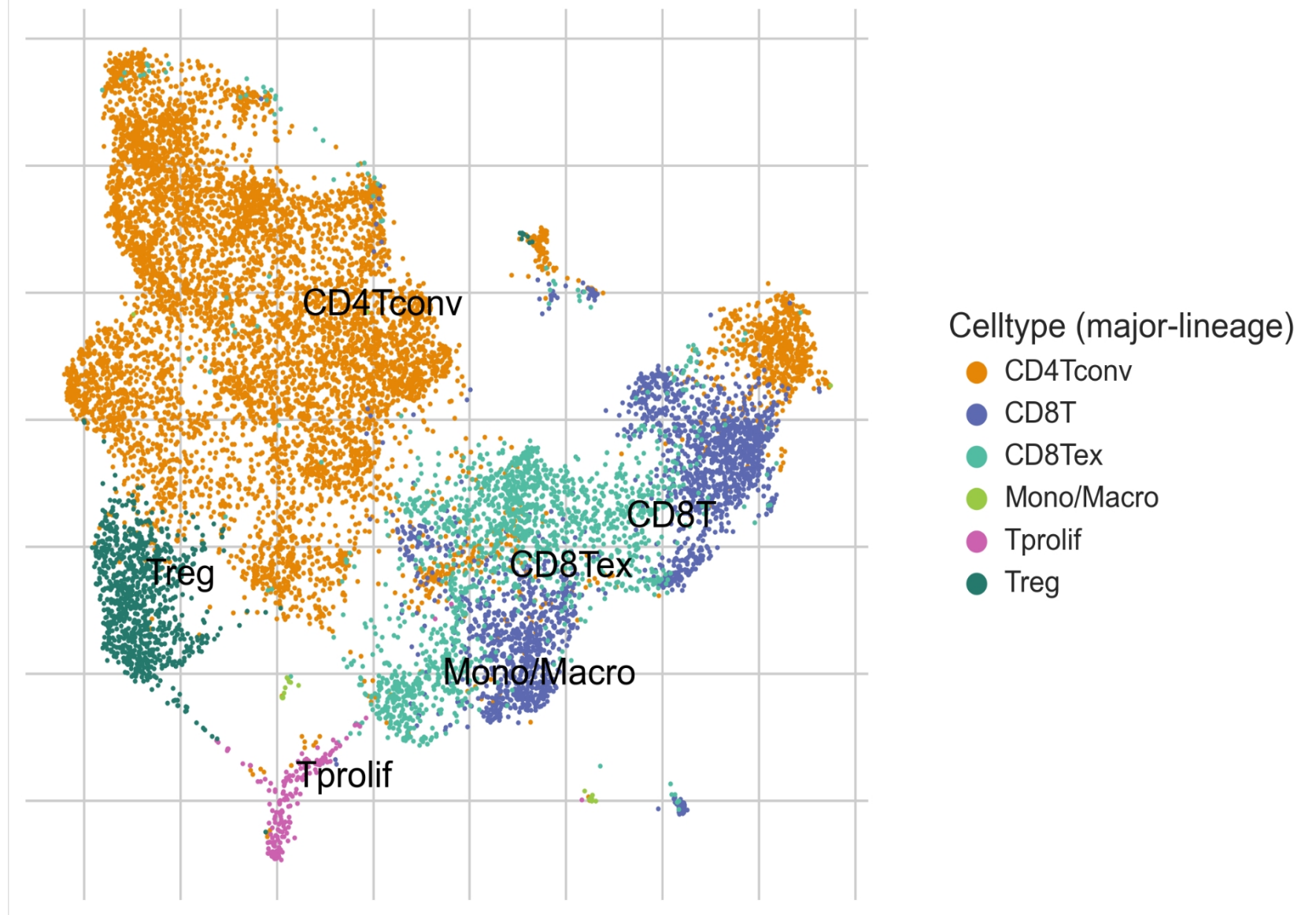


Figure 4: KAT2B is expressed in immune cells