

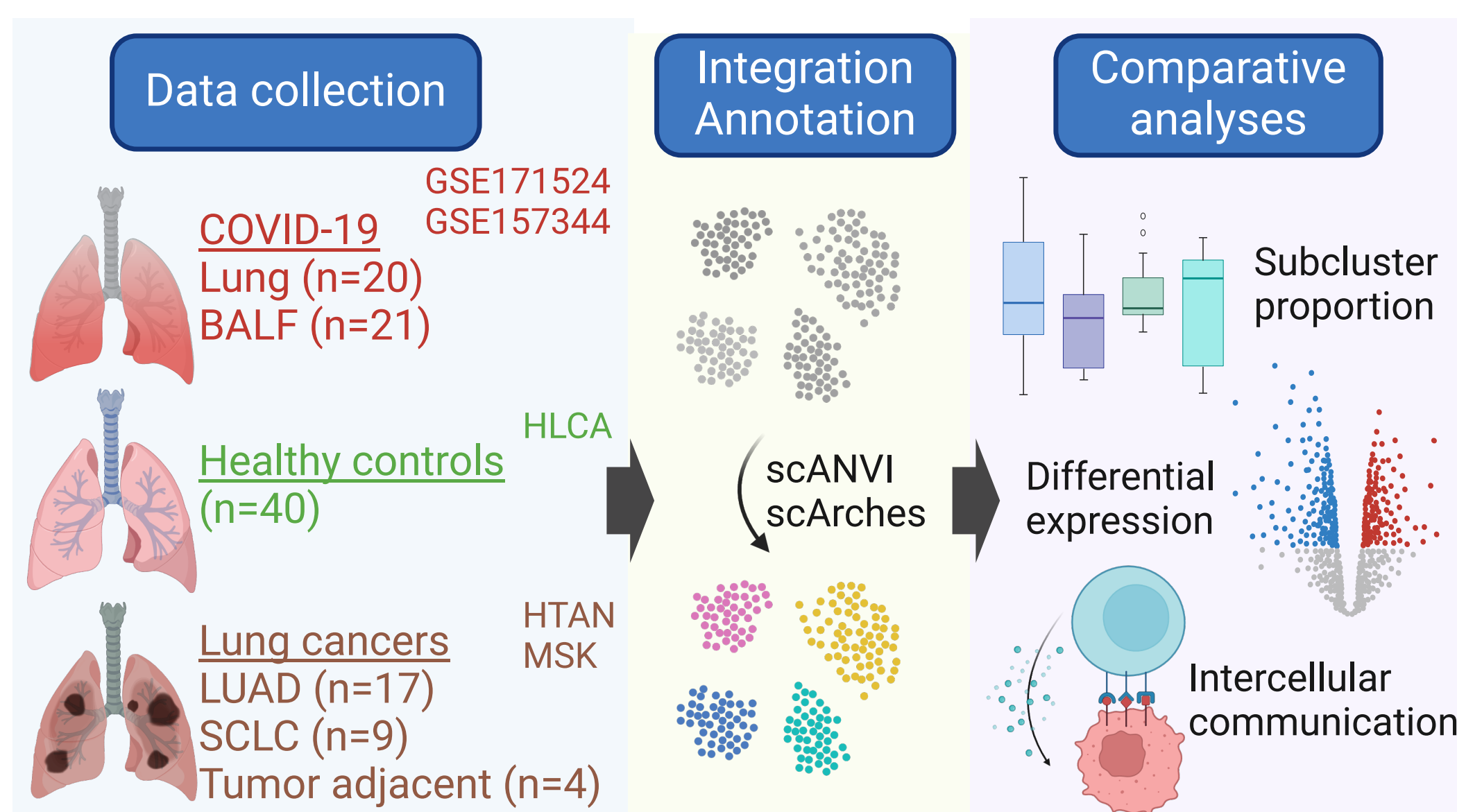
# Single-cell transcriptomics reveals pre-existing COVID-19 vulnerability factors in lung cancer patients

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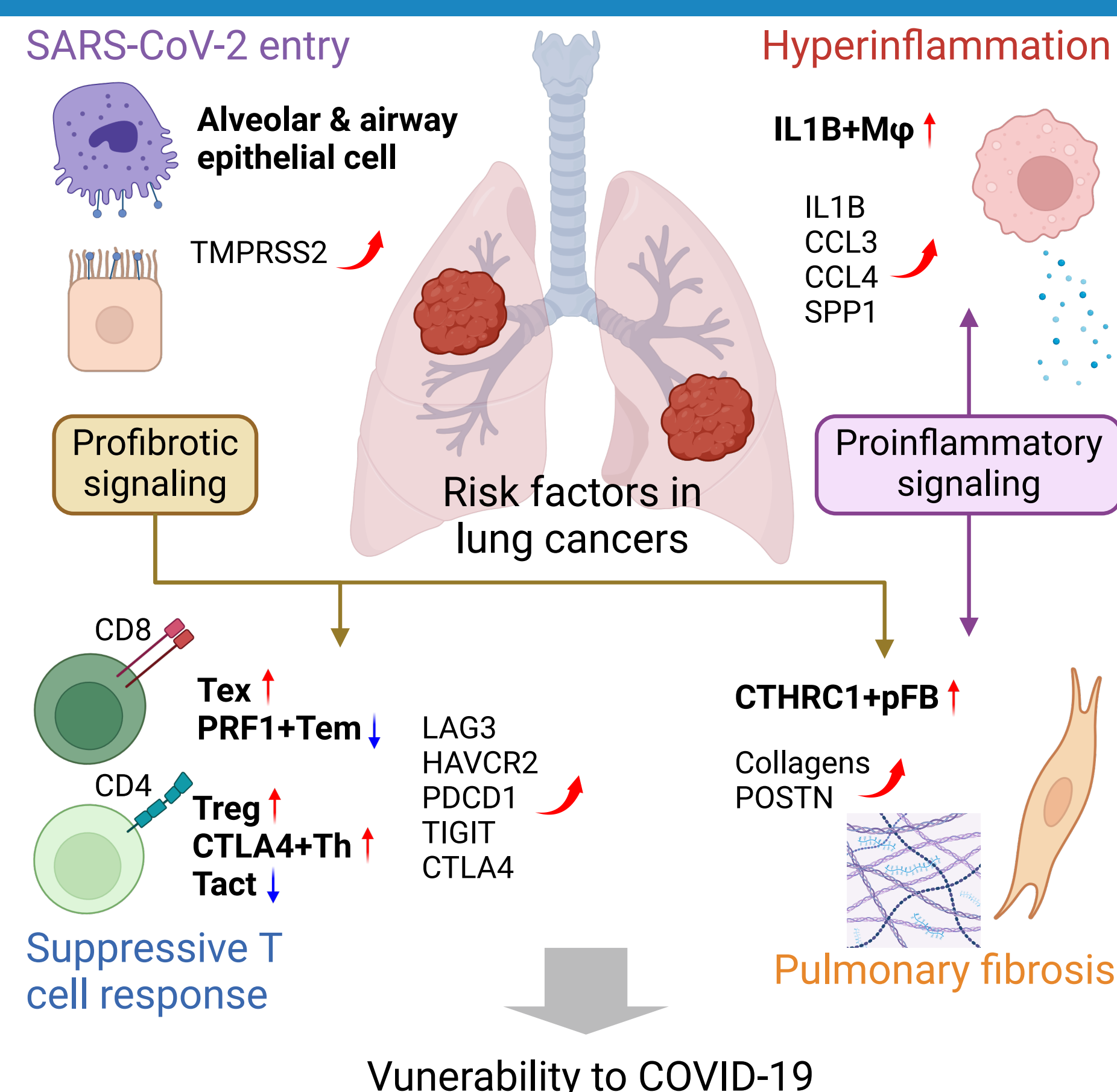
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## Introduction & Methods

COVID-19 and cancer are leading threats to human health and patients may develop both diseases simultaneously. Previous studies have revealed that cancer patients are particularly vulnerable to COVID-19 and often experience worse outcomes. However, the molecular mechanisms underlying the associations remain poorly understood. We aim to investigate potential mechanisms using scRNA-seq.



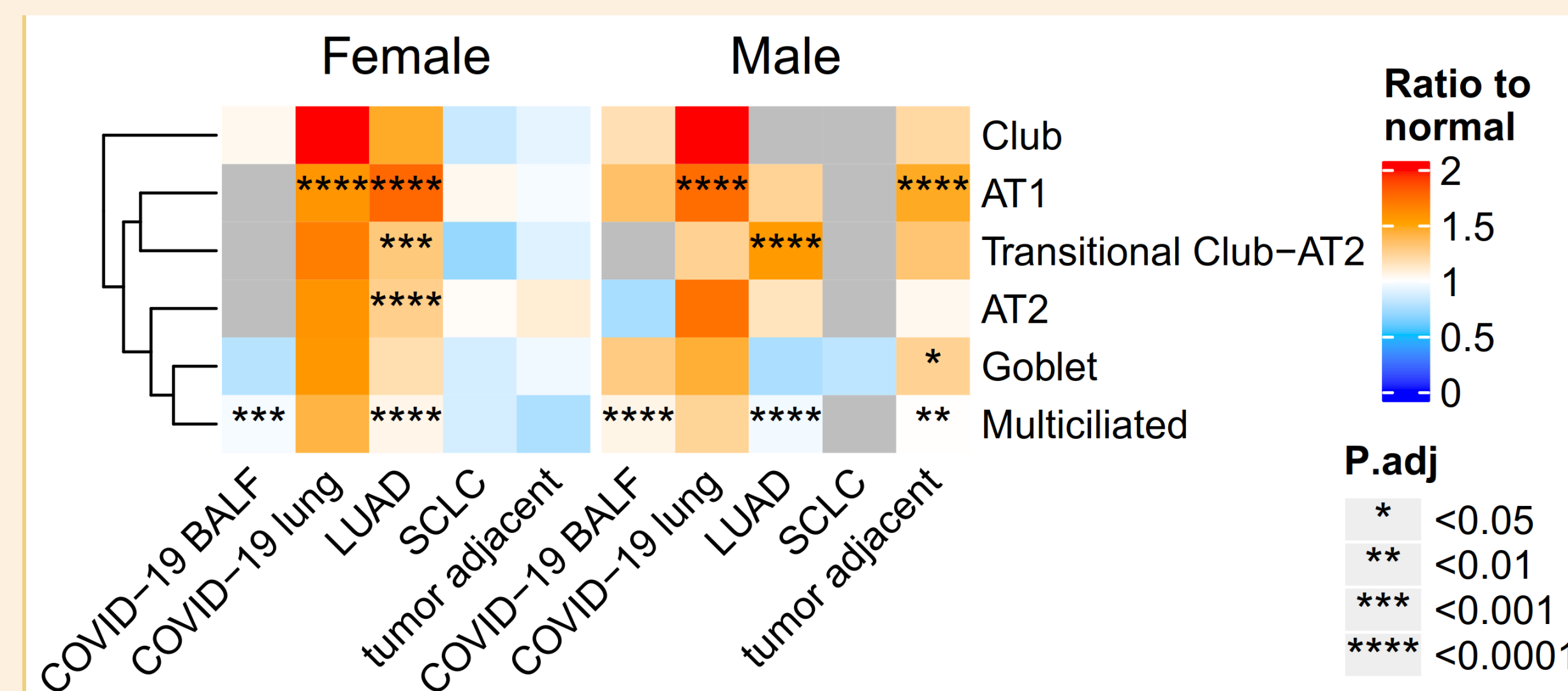
## Conclusion



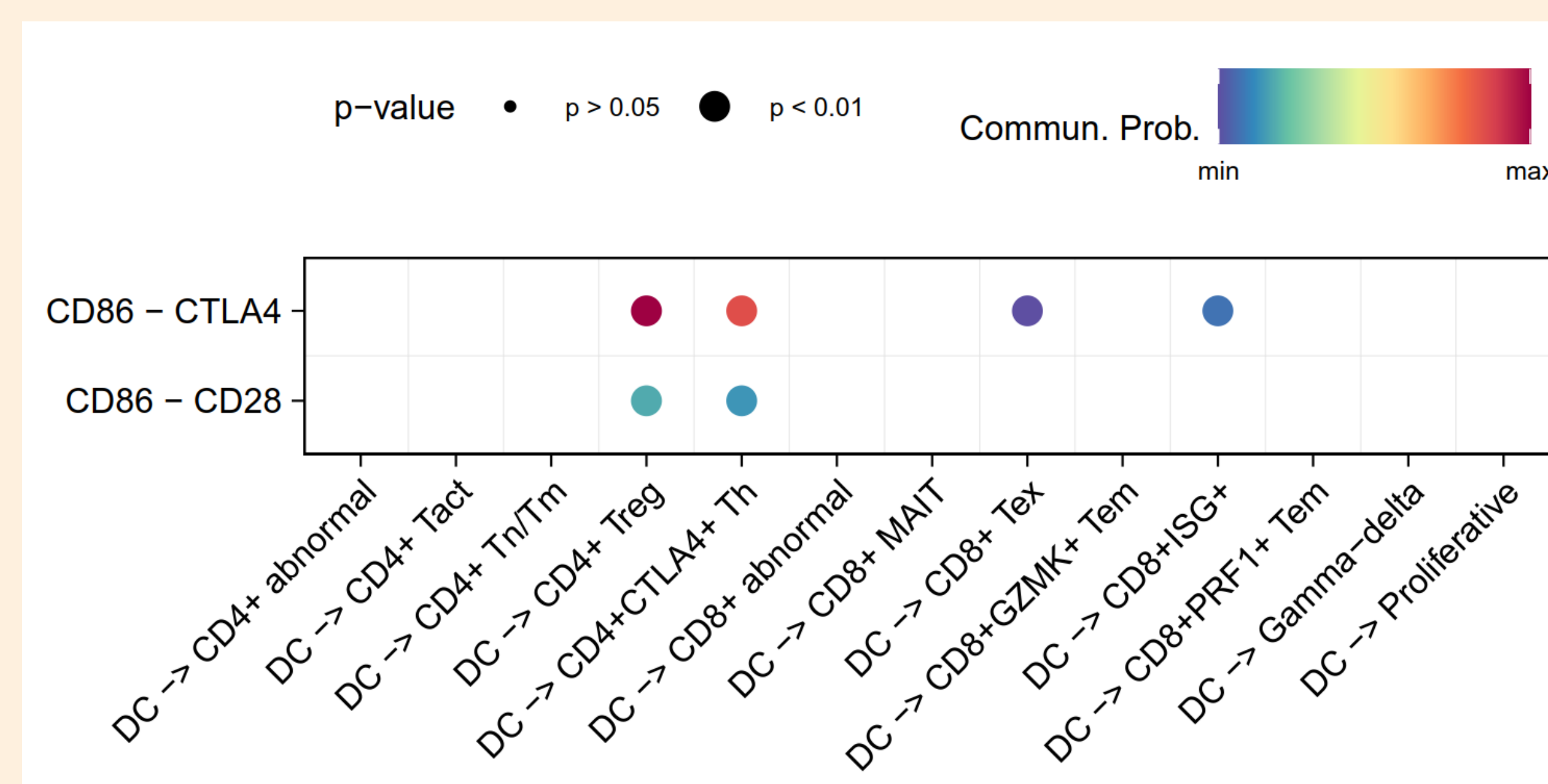
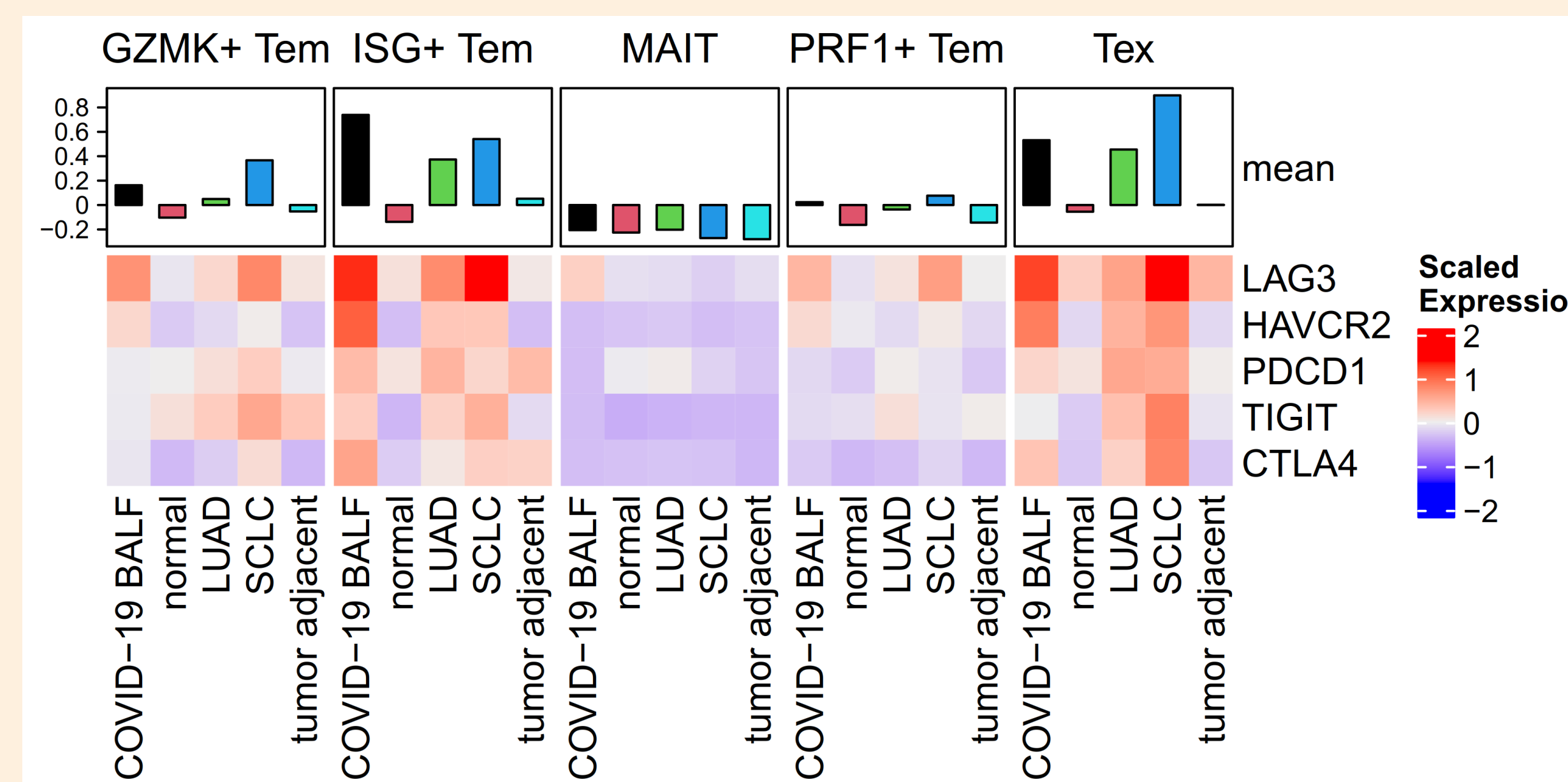
## Acknowledgement

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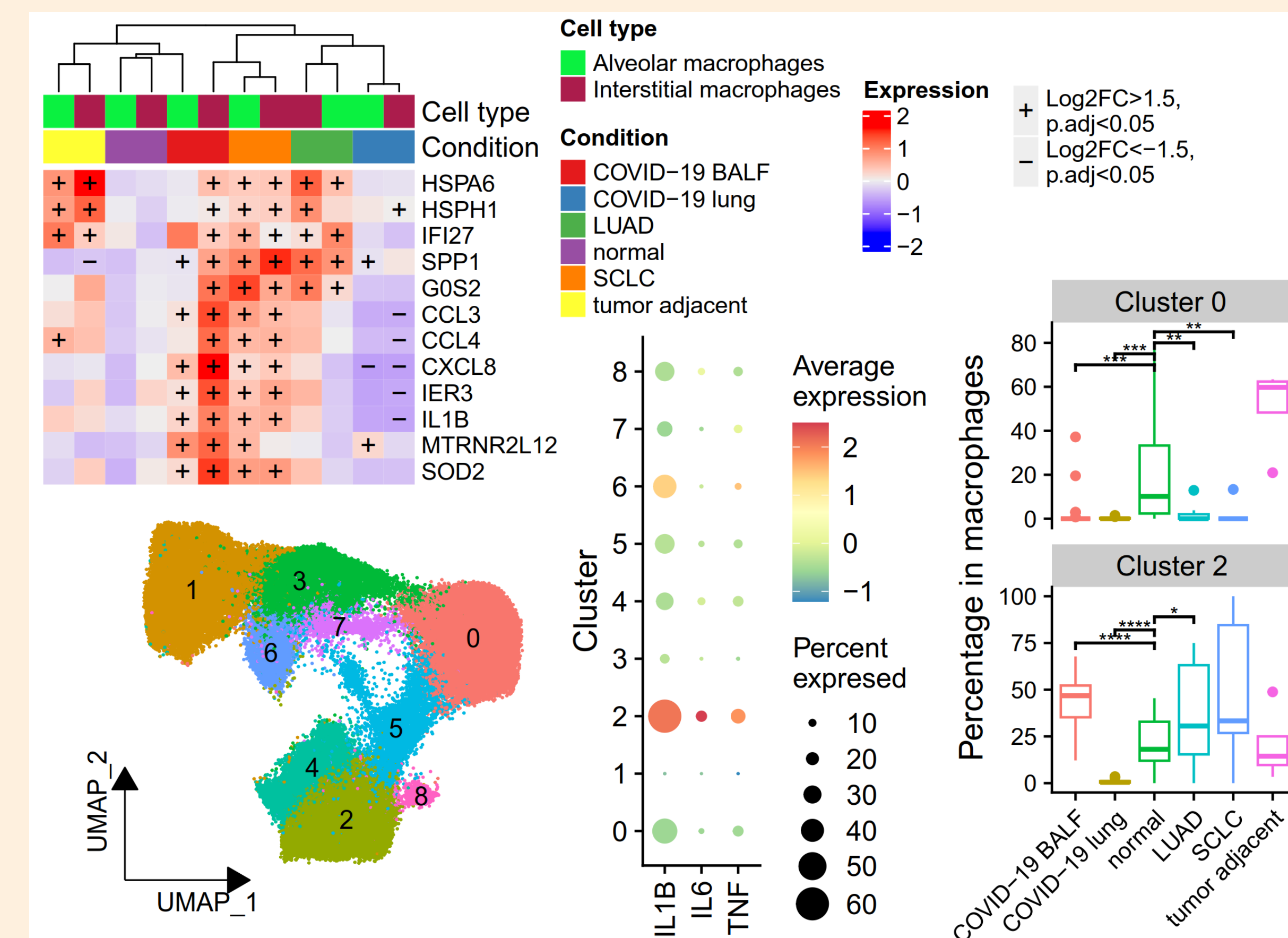
## Results



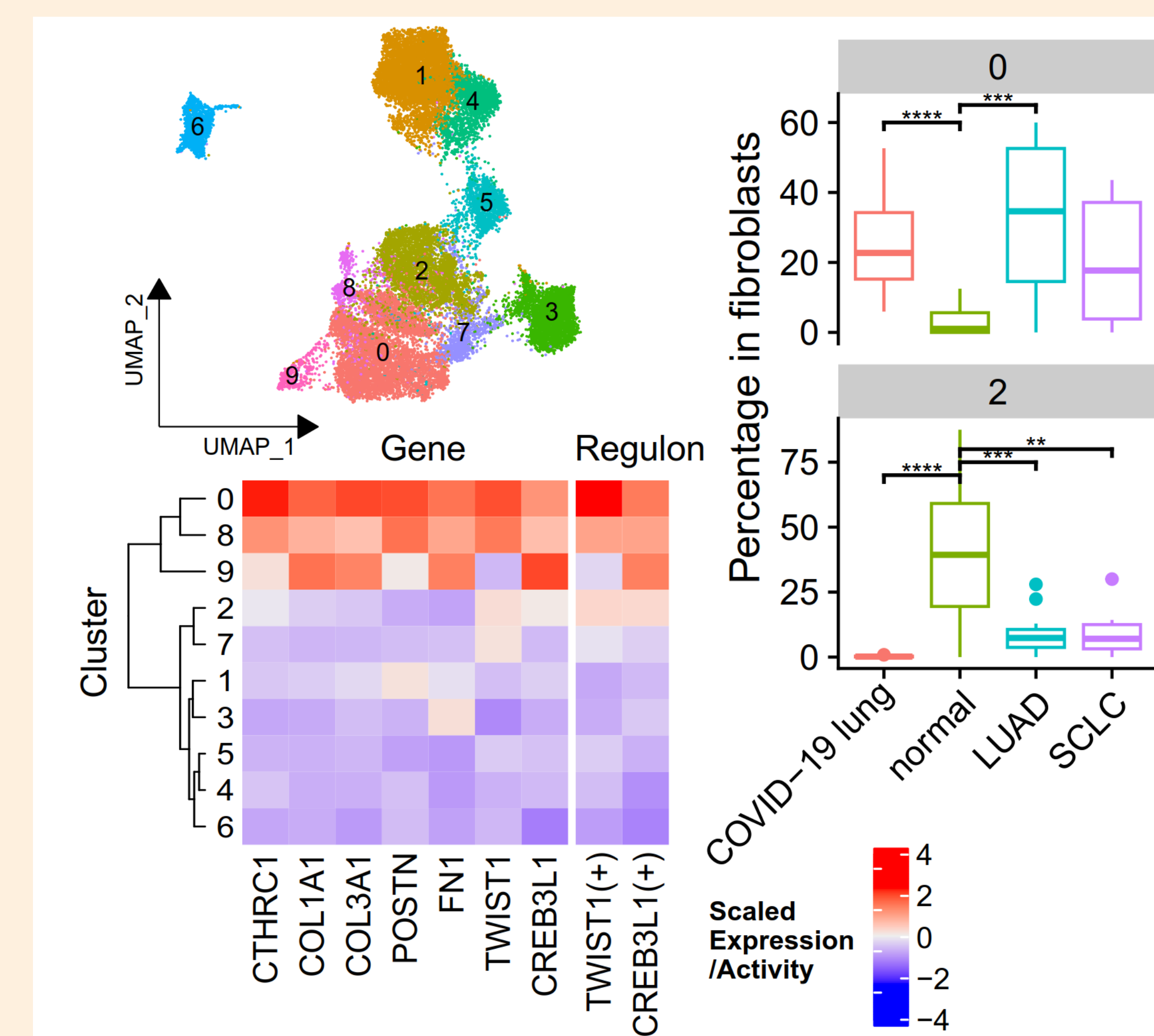
Upregulated TMPRSS2 expression in epithelial cells in LUAD -> increased risk of viral entry



Upregulated coinhibitory receptors on T cells, and inhibitory signaling through CTLA4-CD86 in COVID-19 and lung cancers -> increased risk of ineffective antiviral response



Upregulated proinflammatory gene expression in macrophages in COVID-19 and lung cancers -> increased risk of hyperinflammation and tissue damage



Increased proportion of pathological profibrotic fibroblasts, with high expression of collagens, peropstin, and TGFβ-induced transcription factors in COVID-19 and lung cancers -> increased risk of pulmonary fibrosis