

Single-cell RNA sequencing identifies pathogenic characteristics of T cells in eosinophilic esophagitis

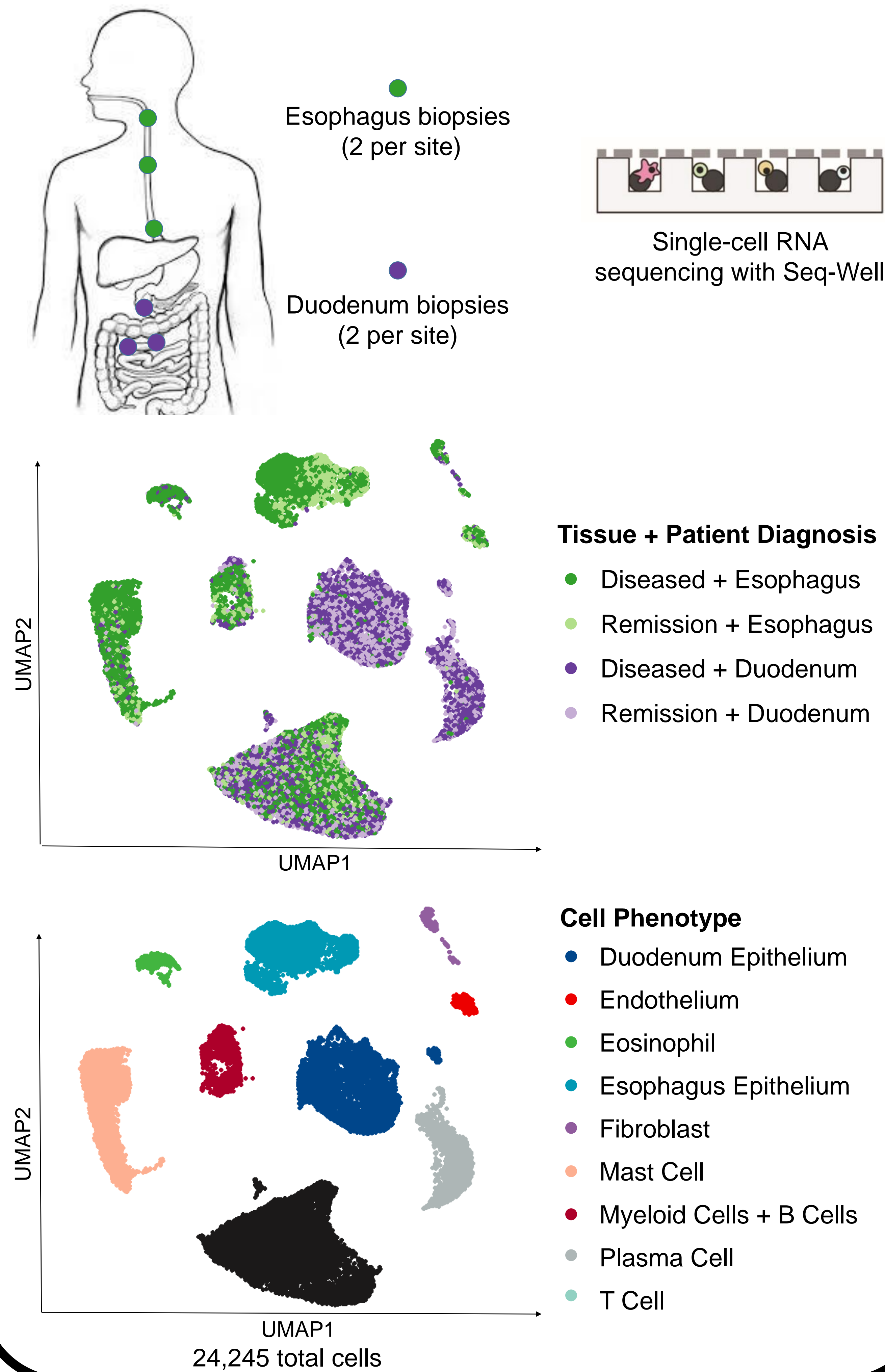
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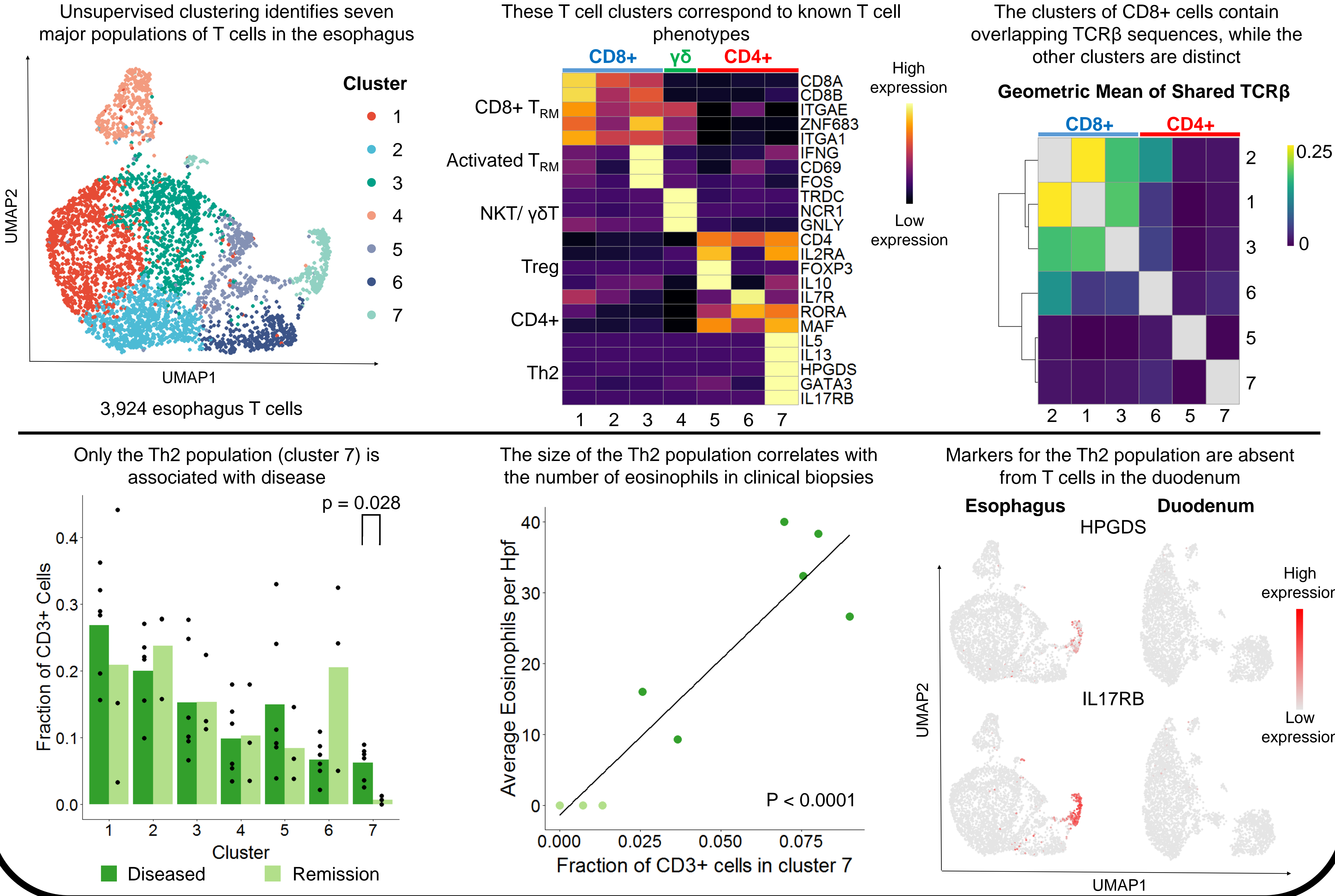
Background

- Eosinophilic esophagitis (EoE) is an allergen-triggered condition in which eosinophils are recruited to the esophagus, causing inflammation.
- Like other allergic diseases, treatment for EoE relies primarily on antigen avoidance.
- The mechanisms through which the local microenvironment supports inflammation in EoE remain largely unknown.
- To better understand the tissue ecosystem of EoE, we utilized single-cell RNA sequencing to perform a single-cell genomics analysis of the types and functions of cells manifest within esophagus and duodenum biopsies from patients with EoE.

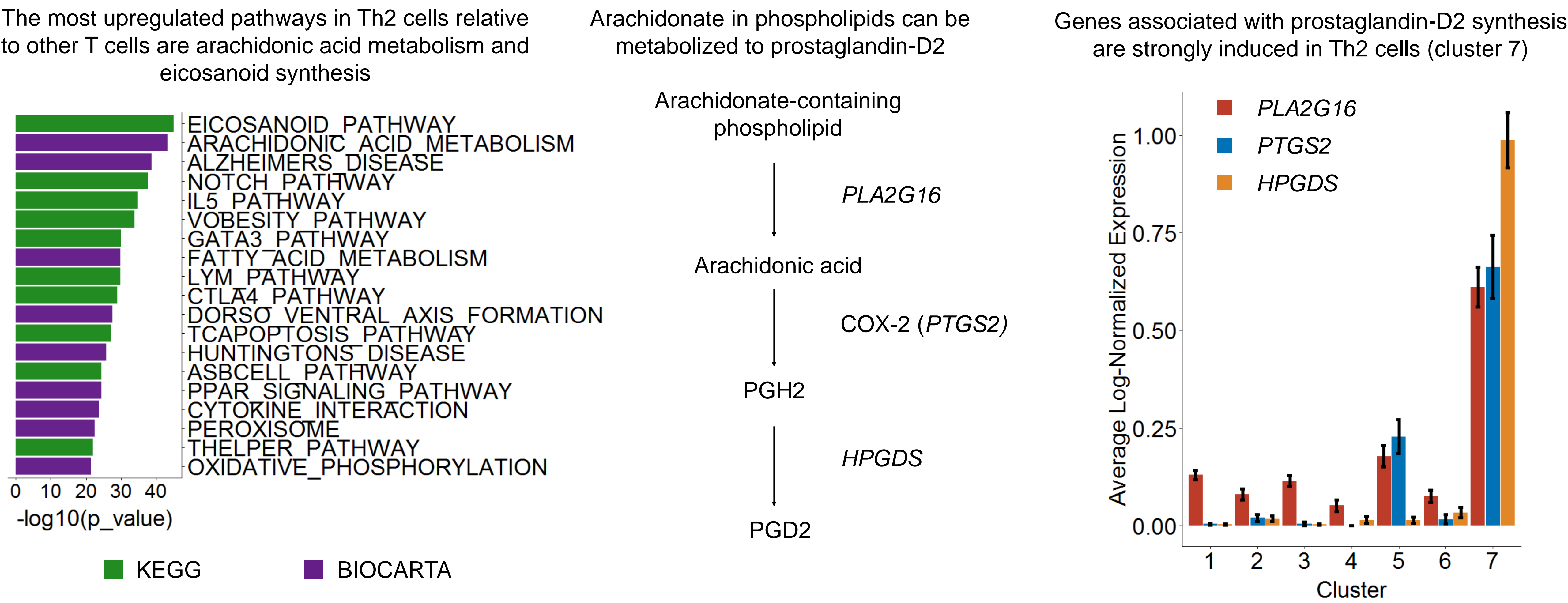
Approach: Single-cell RNA sequencing of esophagus and duodenum biopsies



Th2 cells are enriched in the esophagus of diseased patients



Metabolic characteristics of Th2 cells suggest synthesis of prostaglandin-D2



Summary

- We present a single-cell genomics analysis of 24,245 cells from the esophagus and duodenum biopsies of patients with EoE.
- We identify a clonal population of Th2 cells in the esophagus biopsies of diseased patients that expresses common Th2 mediators and whose size correlates with the number of eosinophils detected in tissue biopsies.
- Gene signatures corresponding to eicosanoid synthesis and arachidonic acid metabolism are upregulated in Th2 cells, suggesting that prostaglandin-D2 synthesis by Th2 cells contributes to eosinophil recruitment and inflammation in EoE.

Acknowledgements

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