

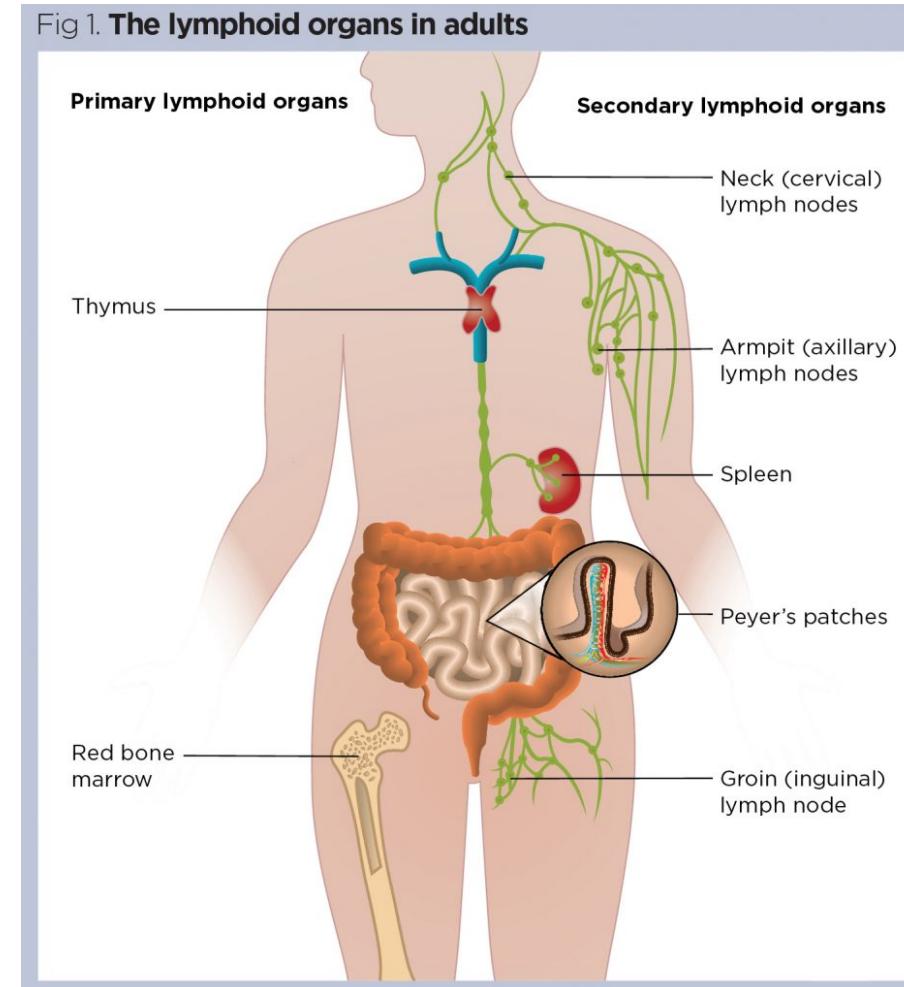
Single-cell transcriptional profiling of human thymic stroma uncovers novel cellular heterogeneity in the thymic medulla

Bautista et al.

NATURE COMMUNICATIONS | Feb 17;12(1):1096

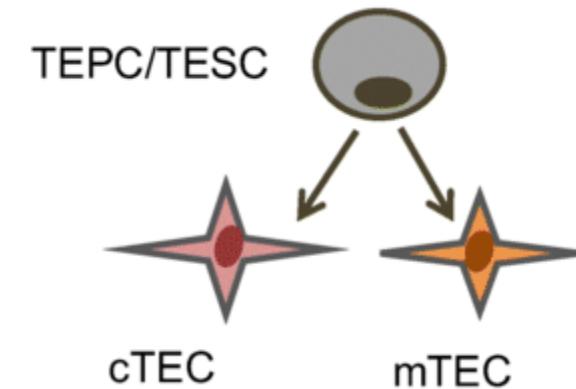
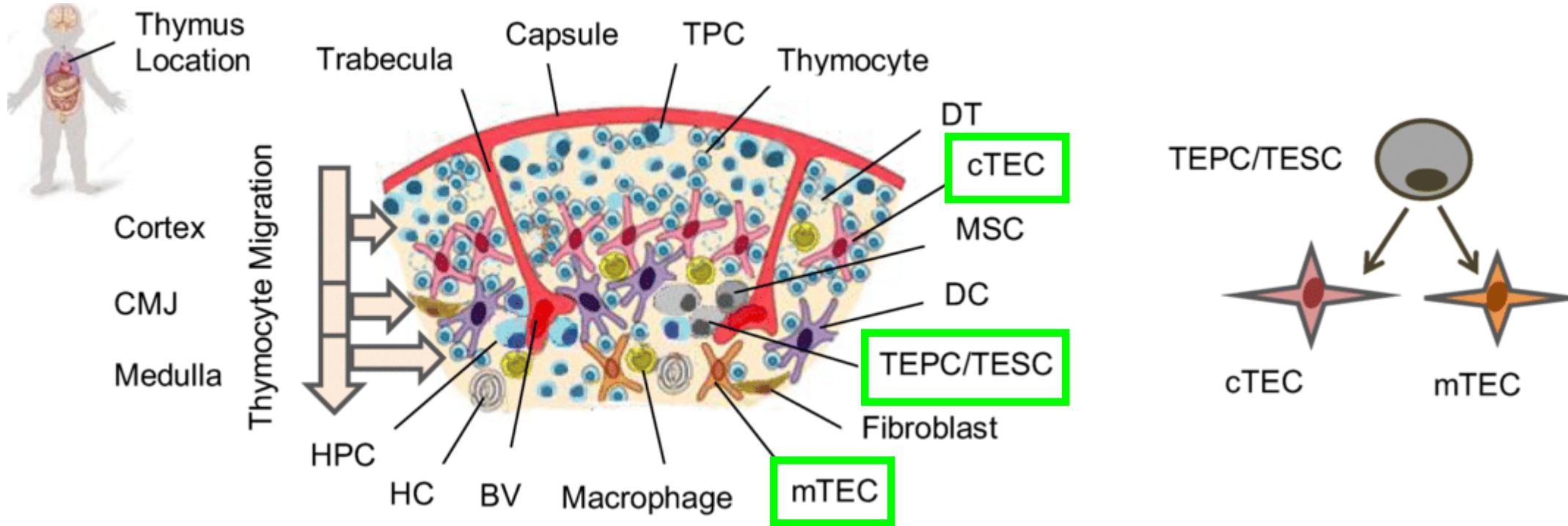
DOI: 10.1038/s41467-021-21346-6

Background- primary lymphoid organs



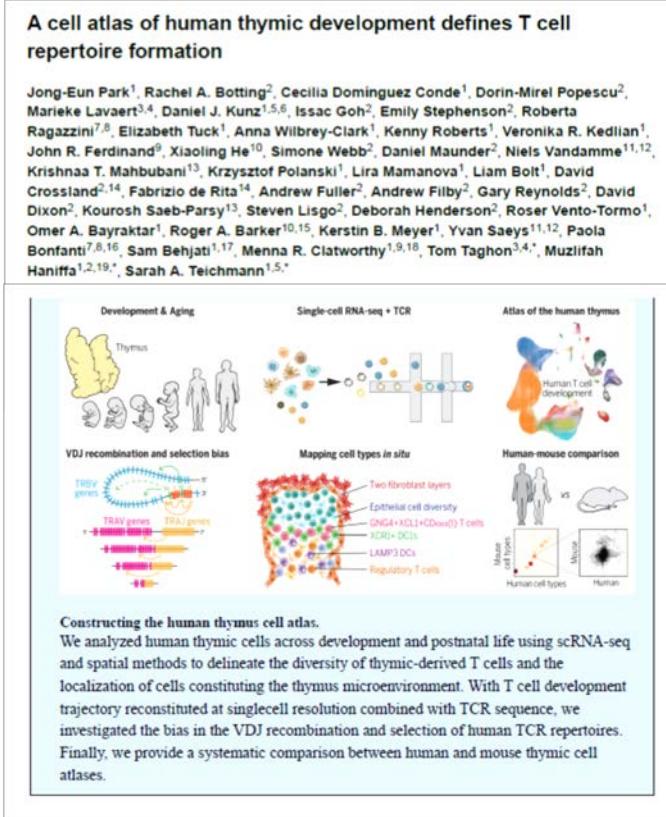
<https://www.nursingtimes.net/clinical-archive/immunology/the-lymphatic-system-2-structure-and-function-of-the-lymphoid-organs-26-10-2020/>

Background



Shchikin, V.P., Antica, M. Thymus Regeneration and Future Challenges. *Stem Cell Rev and Rep* 16, 239–250 (2020). <https://doi.org/10.1007/s12015-020-09955-y>

Background- Heterogeneity of the thymic medulla



LETTER

Single-cell mapping of the thymic stroma identifies IL-25-producing tuft epithelial cells

Chamara Bornstein^{1,4}, Shir Nevo^{1,4}, Amir Gilad^{1,4}, Noam Kadouri^{1,4}, Marie Pegorier^{1,4}, Françoise Gerbe³, Eyal David¹, Alice Machado², Anna Chuprin¹, Beata Toth⁴, Ori Goldberg¹, Shalev Izkowitz⁴, Naomi Taylor², Philippe Jay², Valerie S. Zimmerman³, Jakub Abramson^{1,2,*} & Ido Amit^{1,2,*}

T cell development and selection are coordinated in the thymus by a specialized niche of diverse stromal populations^{1–3}. Although much progress has been made over the years in identifying the functions of the different cell types in the thymic stroma, there is still a lack of a comprehensive characterization of their diversity and heterogeneity. Here we combined massively parallel single-cell RNA sequencing^{4–6}, spatial mapping, chromatic profiling and gene targeting to characterize the entire stromal compartment of the mouse thymus. We identify distinct cell types in the mouse thymic epithelial cells (TECs) showing the highest degree of heterogeneity. Our analysis highlights four major medullary TEC (mTEC I–IV) populations, with distinct molecular functions, epigenetic landscapes and lineage regulators. Specifically, mTEC IV constitutes a new and highly divergent TEC lineage with molecular characteristics of the gut chemoattractant epithelial tuft cells. Mice deficient in specific levels of tuft stromal critical genes show a dramatic reduction in the number of tuft stromal cells, which is associated with the loss of specific mTEC populations. Together, our results highlight the diversity and the specificity of the stromal compartments in the mouse thymus.

ARTICLE

<https://doi.org/10.1038/s41586-018-0346-1> OPEN
Diversity in medullary thymic epithelial cells controls the activity and availability of iNKT cells

Beth Lucas¹, Andrea J. White¹, Emilie J. Cosway¹, Sonia M. Parnell¹, Kieran D. James¹, Nick D. Jones¹, Izumi Ohigashii², Yousuke Takahama³, William E. Jenkinson¹ & Graham Anderson^{1,2*}

The thymus supports multiple αβ T cell lineages that are functionally distinct, but mechanisms that control this multifaceted development are poorly understood. Here we examine medullary thymic epithelial cell (mTEC) heterogeneity and its influence on CD1d-restricted iNKT cells. We find three distinct mTEC^{low} subsets distinguished by surface, intracellular and secreted molecules, and identify LTRR as a cell-autonomous controller of their development. Importantly, this mTEC heterogeneity enables the thymus to differentially control iNKT sublineages possessing distinct effector properties. mTEC expression of LTRR is essential for the development thymic tuft cells which regulate NKT2 via IL-25, while LTRR controls CD104⁺ CCL21⁺ mTEC^{low} that are capable of IL-15-transpresentation for regulating NKT1 and NKT17. Finally, mTECs regulate both iNKT-mediated activation of thymic dendrite cells, and iNKT availability in extrathymic sites. In conclusion, mTEC specialization controls intrathymic iNKT cell development and function, and determines iNKT pool size in peripheral tissues.

HHS Public Access

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Thymic tuft cells promote an IL4-enriched medulla and shape thymocyte development

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Lineage tracing and cell ablation identifies a post-Aire-expressing thymic epithelial cell population

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role in enforcing central tolerance (TSA) and deletion of self-reactive T cells. Aire (Aire), a transcriptional regulator, is a transmembrane protein that contains a domain of tissue-specific self-antigens (TSA). TSA expression depends in part on the presence of a transmembrane protein that is identified as the defective gene in the immunodeficiency disorder known as the Polyglandular Syndrome Type 1 (PSS1). While the molecular mechanisms by which Aire maintains tolerance are not fully elucidated, many individual studies have shown that Aire-dependent mechanisms play a role in maintaining tolerance. For example, Aire-dependent mechanisms include the prevention of T cell reactivity to self and the regulation of T cell differentiation. Additionally, Aire-dependent mechanisms include the prevention of T cell reactivity to self and the regulation of T cell differentiation.

1) Medullary thymic epithelial cells (mTECs) express Aire, which is required for guiding central tolerance, which is mediated by the presentation of tissue-specific self-antigens (TSA). TSA expression depends in part on the presence of a transmembrane protein that is identified as the defective gene in the immunodeficiency disorder known as the Polyglandular Syndrome Type 1 (PSS1). While the molecular mechanisms by which Aire maintains tolerance are not fully elucidated, many individual studies have shown that Aire-dependent mechanisms play a role in maintaining tolerance. For example, Aire-dependent mechanisms include the prevention of T cell reactivity to self and the regulation of T cell differentiation. Additionally, Aire-dependent mechanisms include the prevention of T cell reactivity to self and the regulation of T cell differentiation.

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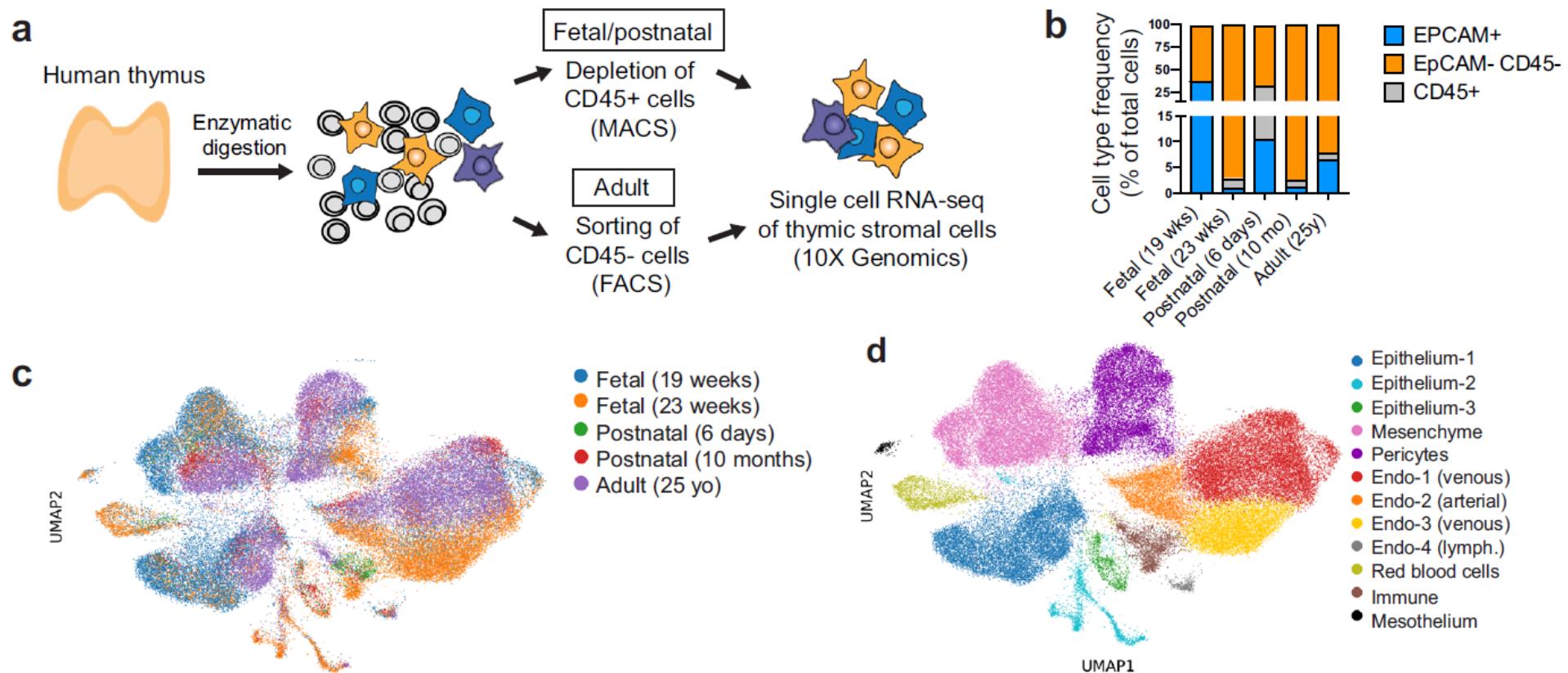
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Methods

- Human thymic tissue:
 - 19-23 gestational-week (legal, elective termination of pregnancy)
 - pediatric tissue (corrective cardiothoracic surgery)
 - Adult thymic tissue: organ acquisition for clinical transplantation
- Mice: Rosa26CAG-stopflox-tdTomato and Ascl1-creERT2, ADIG mice
- Tissue preparation: DNase, Liberase, gentle MACs (spleen program), ca. 1,5 h digestion,
- Stromal cell enrichment: FACS or magentic column (CD45, EPCAM/CD45)
- Single cell: 10x 3'v2 or 3, Novaseq 600, Cellranger v 2.0.0, 2.1.1, 3.0.2
 - Data analysis: Scanpy (v1.4.4, 1.6.0), quality: 200-500 features, <10% MT + features ≤3 cells
 - Total cells: 68008
 - Clustering: Leiden algorithm, res:main 0.7, sub 0.5
 - Park et al.: res: main 0.51, sub 0.25
 - Trajectory: RNA Velocity
- IF-stainings
- Immunohistochemistry
- Flow cytometry

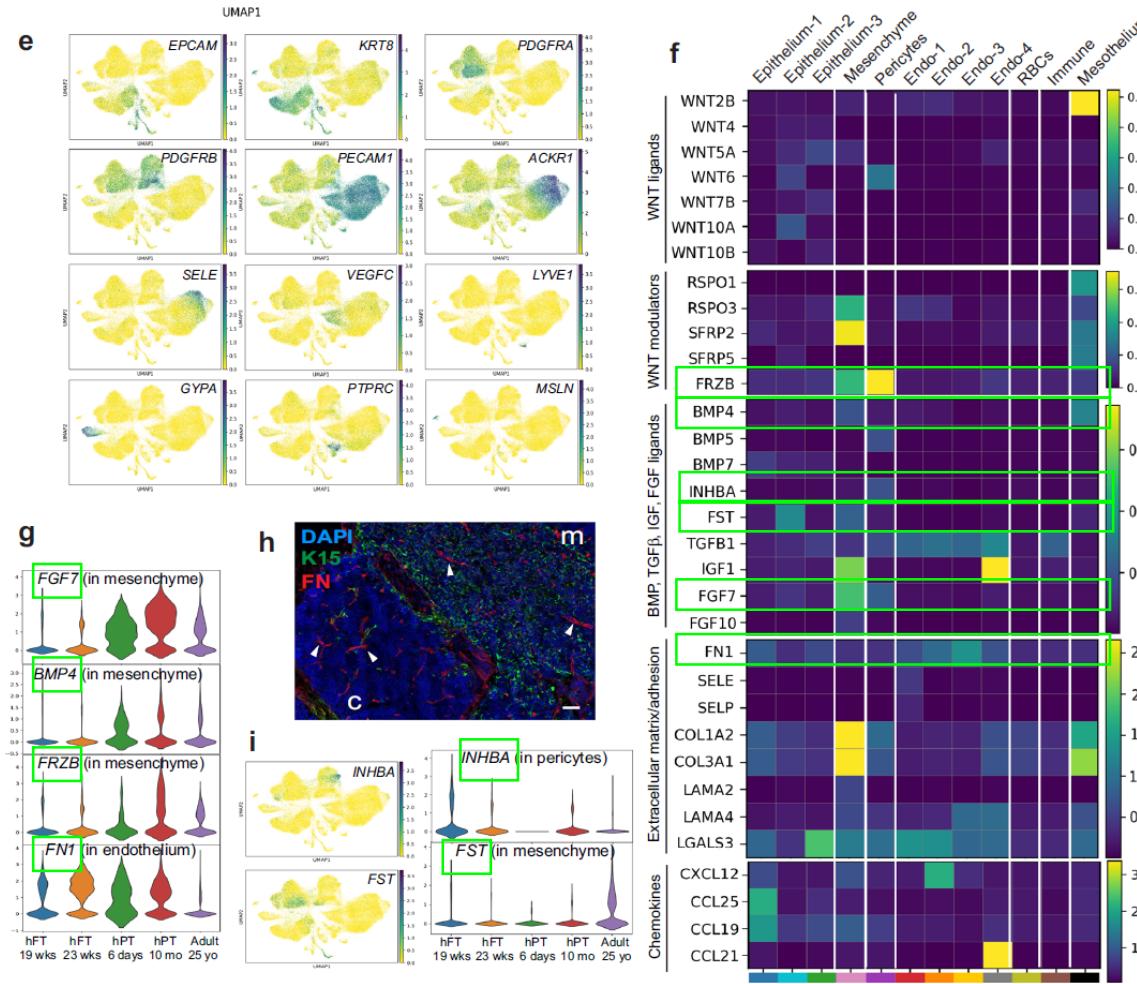
Results

Single-cell profiling of stromal cells from human thymus



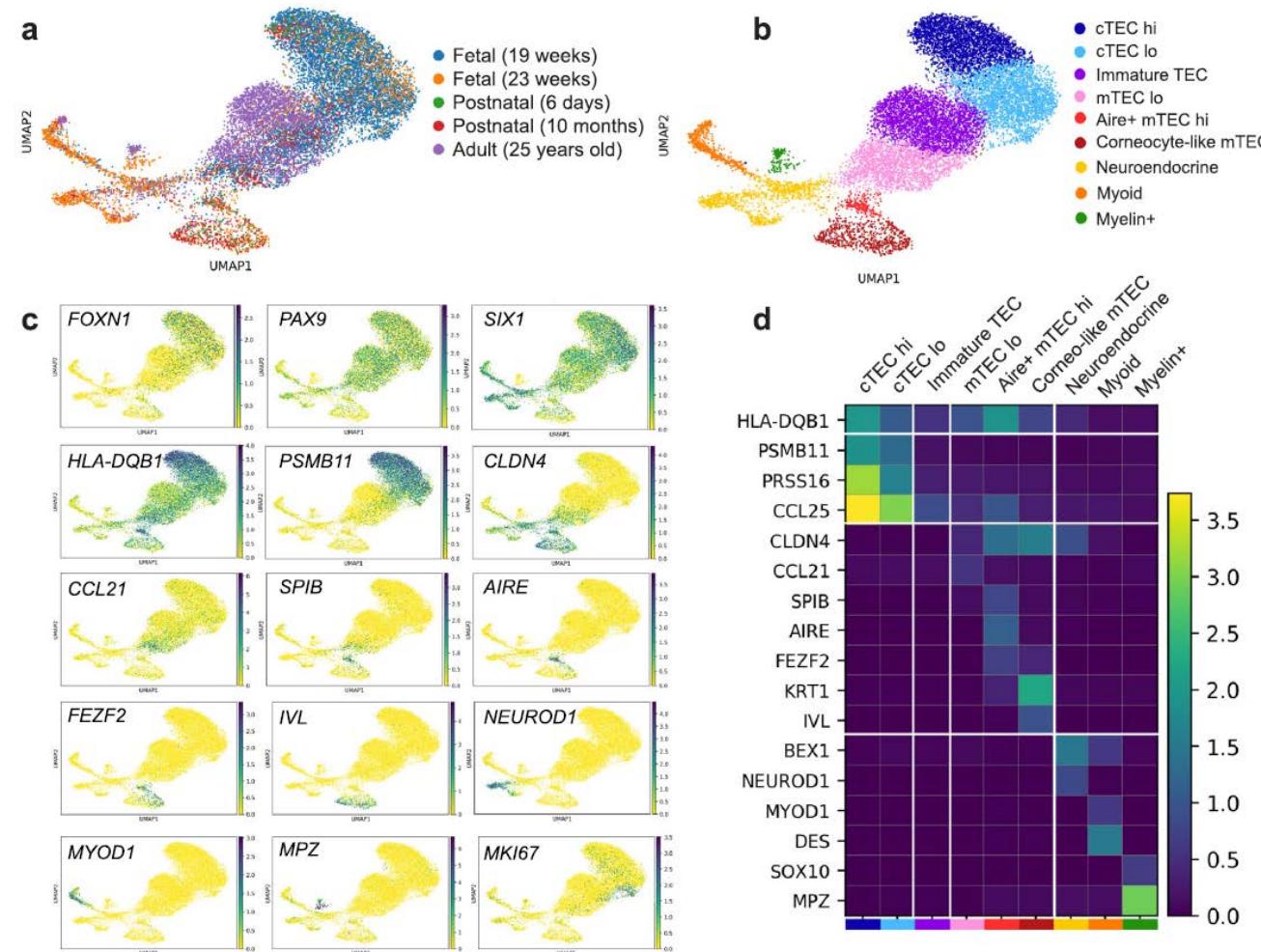
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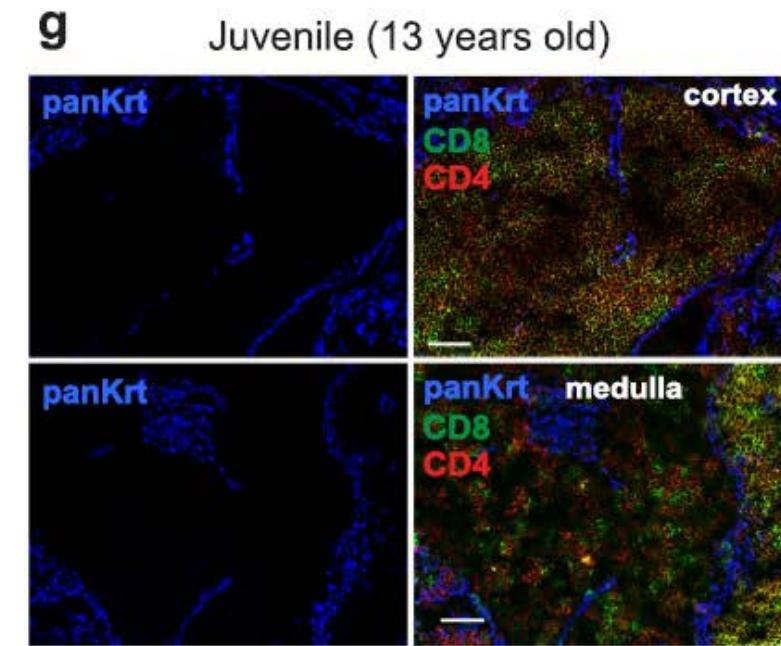
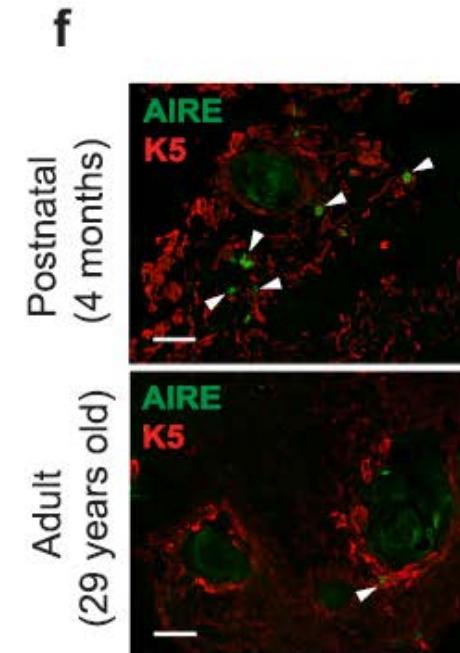
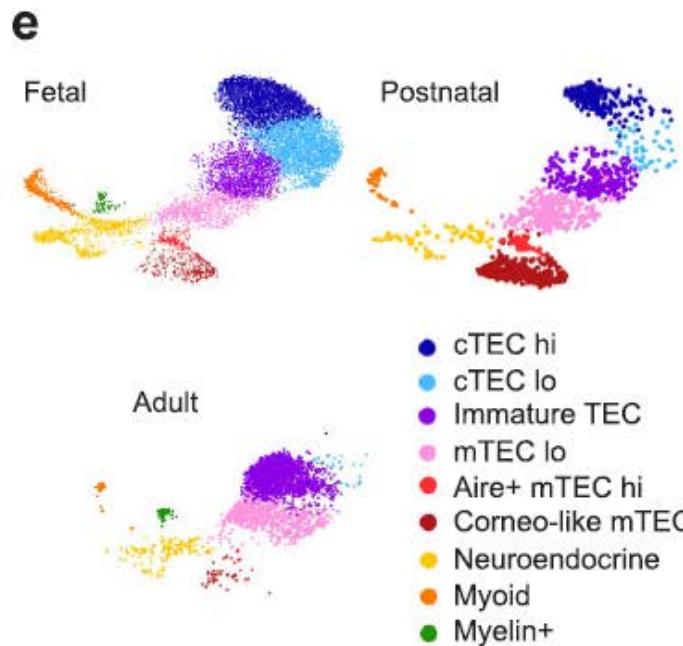
Results

Profiling of human thymic epithelial cells at different stages



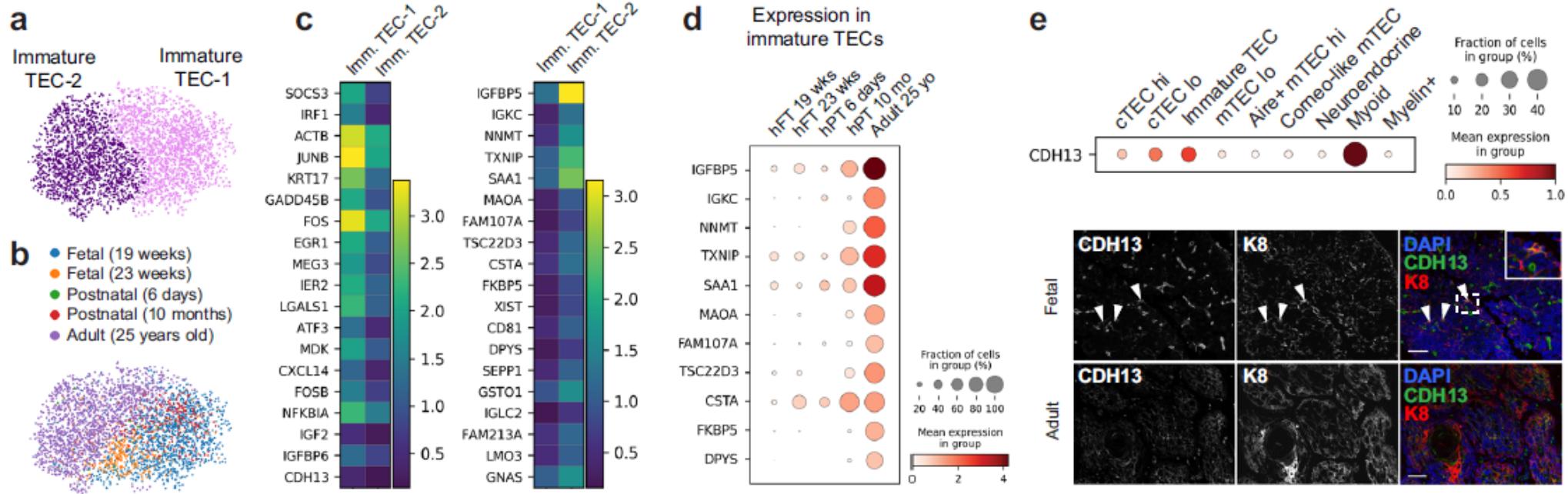
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Profiling of human thymic epithelial cells at different stages



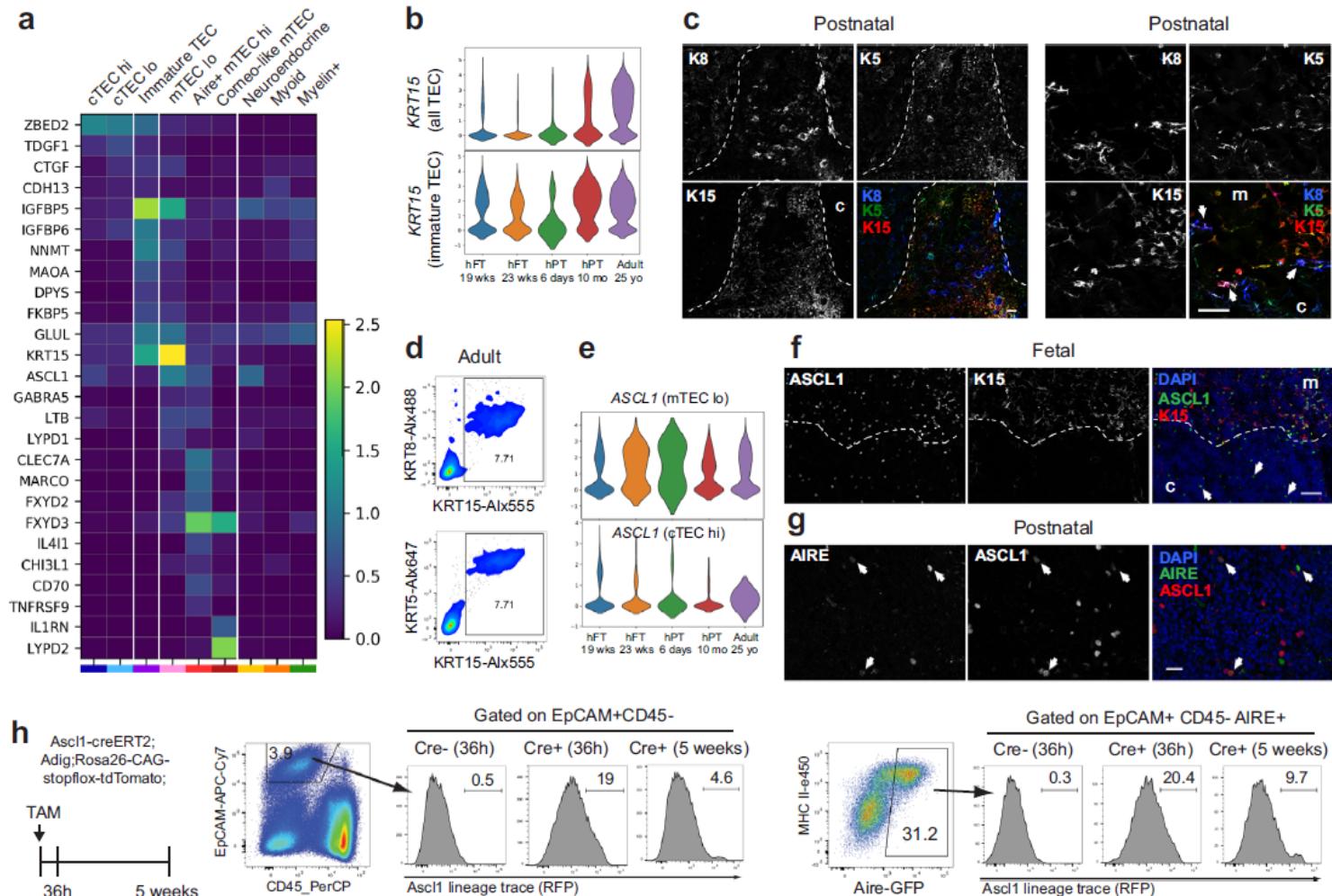
Results

Analysis of immature TECs



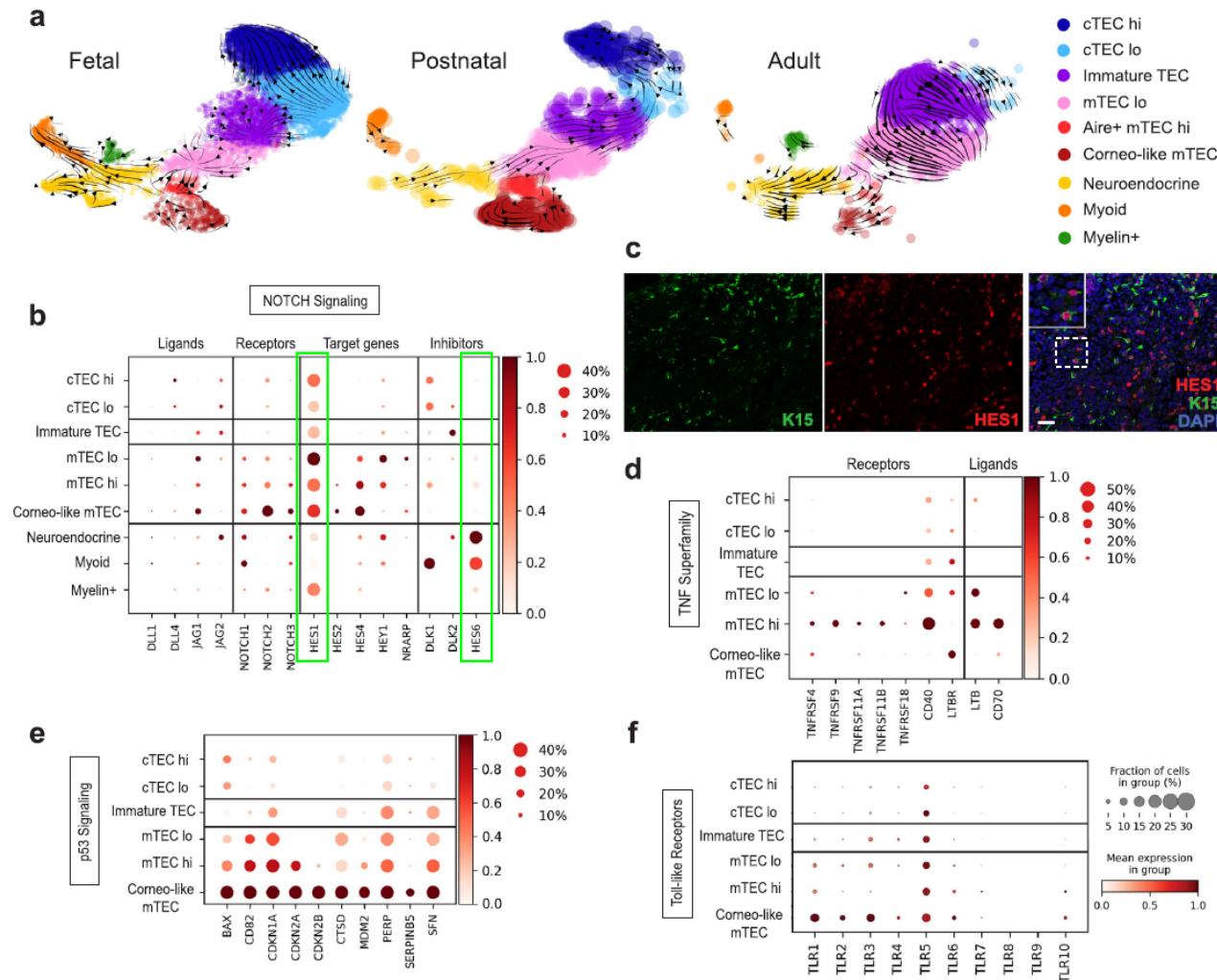
Results

Identification of new TEC markers



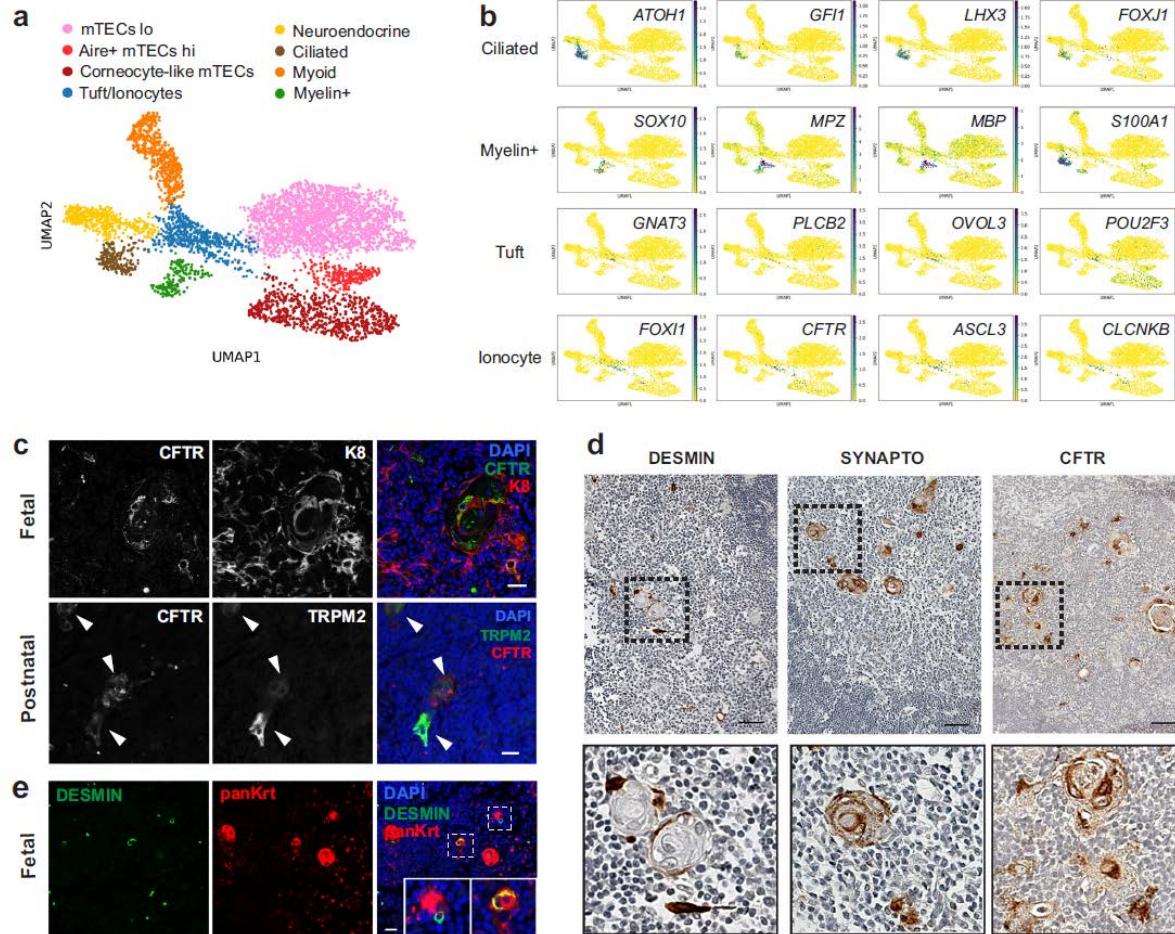
Results

Lineage decisions within the thymic epithelial compartment



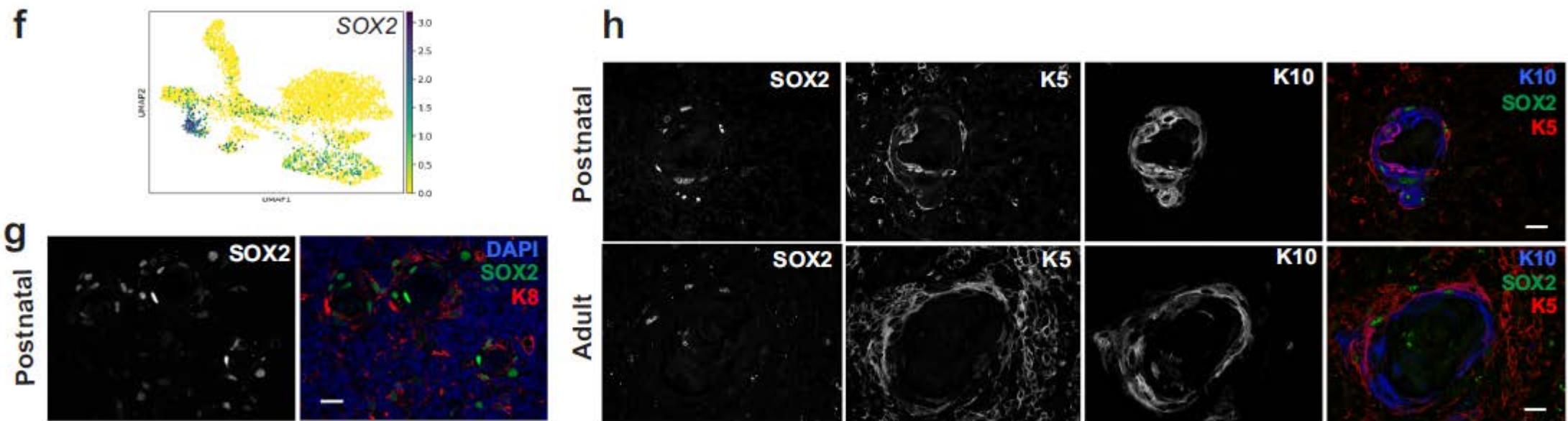
Results

Tuft cells, ionocytes, ciliated cells, and myelin-expressing cells are present in the human thymic medulla



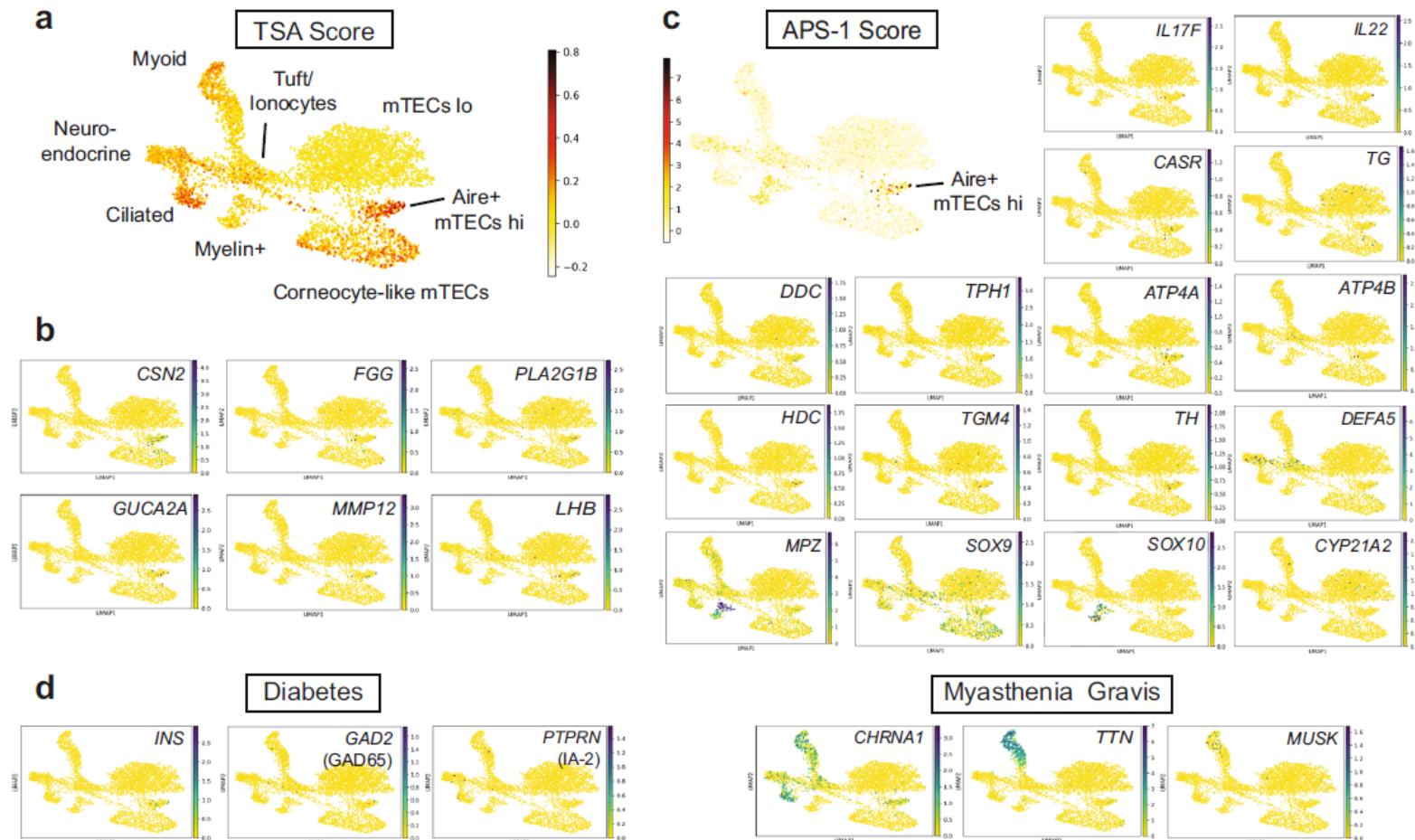
Results

Tuft cells, ionocytes, ciliated cells, and myelin-expressing cells are present in the human thymic medulla



Results

Characterization of tissue-specific antigen expression by human TECs





Discussion

- Ionocytes, Ciliated cells, Schwann cells,
- Crosstalk between TECs and stroma: WNT-pathway (FOXN1), activin A...
- similar progenitors of ionocytes, neuroendocrine and tuft cells
- Notch signaling -> TEC specification (HES6 inhibition of HES1)
- APS-1 antigens are AIRE-dependent
- Myoid cells as the main source of muscle antigens in the human thymic medulla

Conclusion

- Reference transcriptomic maps for TEC
- Evidence of greater heterogeneity among medullary TECs
- Platform to study the expression of disease-relevant antigens
- Insight on the relevance of the heterogeneity to induce immune tolerance and human autoimmune disease