

## **Description of Additional Supplementary Files**

**Supplementary Data 1. Marker genes for all stromal cell clusters.** Marker genes were identified by testing for differential expression of a subgroup against all other cells using a t-test with overestimated variance implemented in the `tl.rank_genes_groups` function of Scanpy.

**Supplementary Data 2. Marker genes for epithelial clusters.** Marker genes were identified by testing for differential expression of a subgroup against all other cells using a t-test with overestimated variance implemented in the `tl.rank_genes_groups` function of Scanpy.

**Supplementary Data 3. Marker genes for immature TECs.** Marker genes were identified by testing for differential expression of a subgroup against all other cells using a t-test with overestimated variance implemented in the `tl.rank_genes_groups` function of Scanpy.

**Supplementary Data 4. Marker genes for medullary epithelial clusters.** Marker genes were identified by testing for differential expression of a subgroup against all other cells using a t-test with overestimated variance implemented in the `tl.rank_genes_groups` function of Scanpy.

**Supplementary Data 5. Genes differentially expressed in tuft cells vs ionocytes.** Characteristic gene signatures were identified by testing for differential expression of a subgroup against all other cells using a t-test with overestimated variance implemented in the `tl.rank_genes_groups` function of Scanpy.

**Supplementary Data 6. Genes with expression that positively correlate with a high TSA score in AIRE+ and corneocyte-like mTECs.** A Spearman correlation coefficient with associated p-value was calculated using the `spearmanr` function from the SciPy statistical package. The list was filtered to keep genes expressed in at least five cells that had positive correlation coefficients  $>0.15$  and p values  $< 0.25$ .