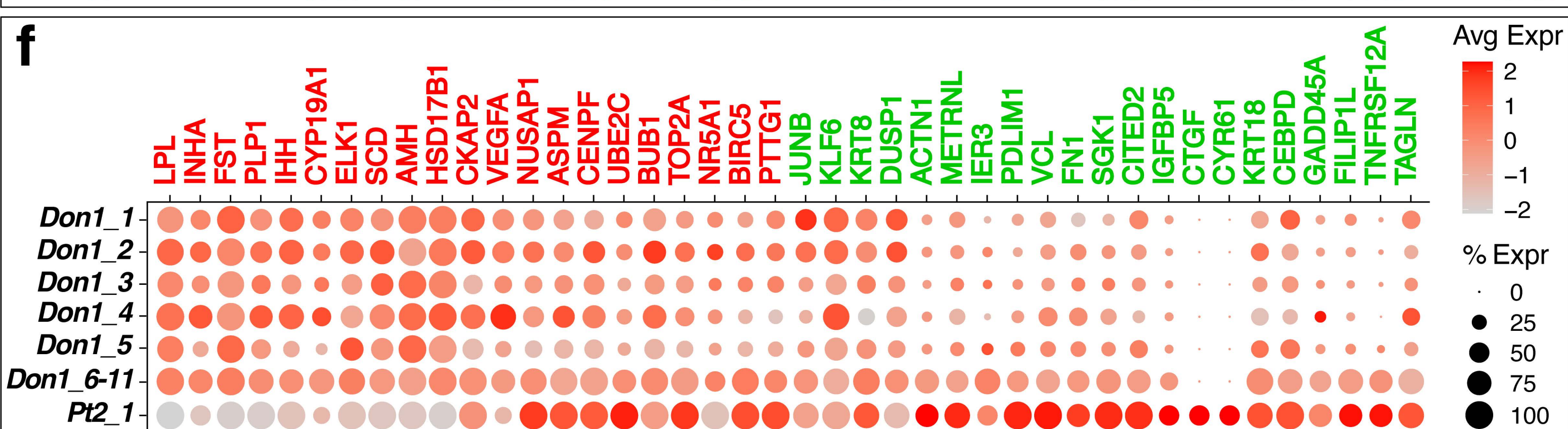
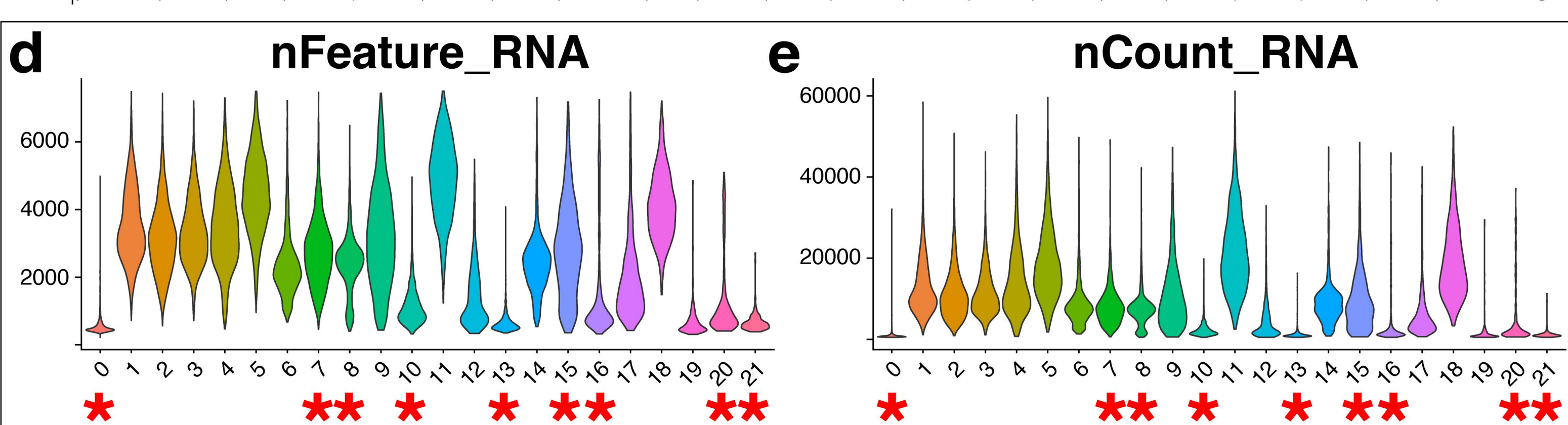
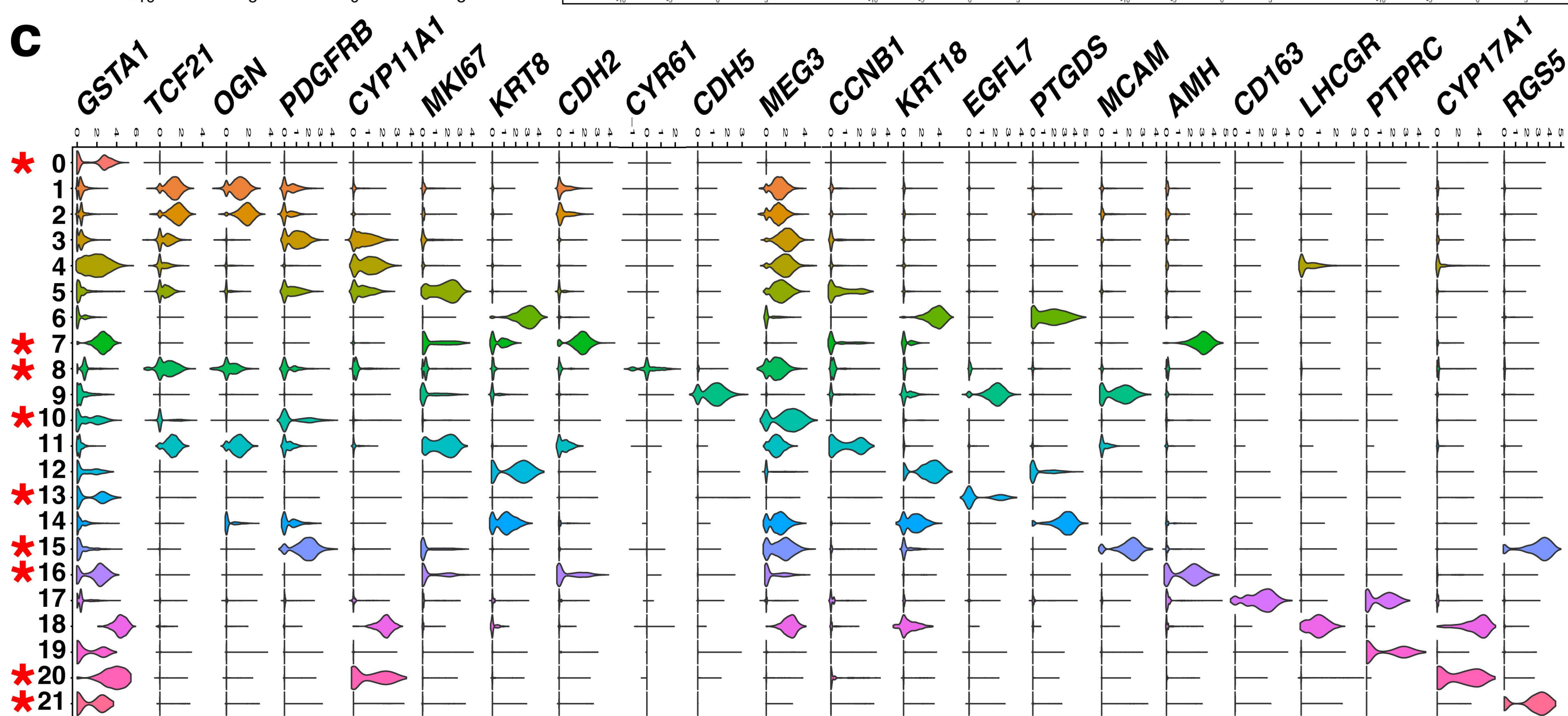
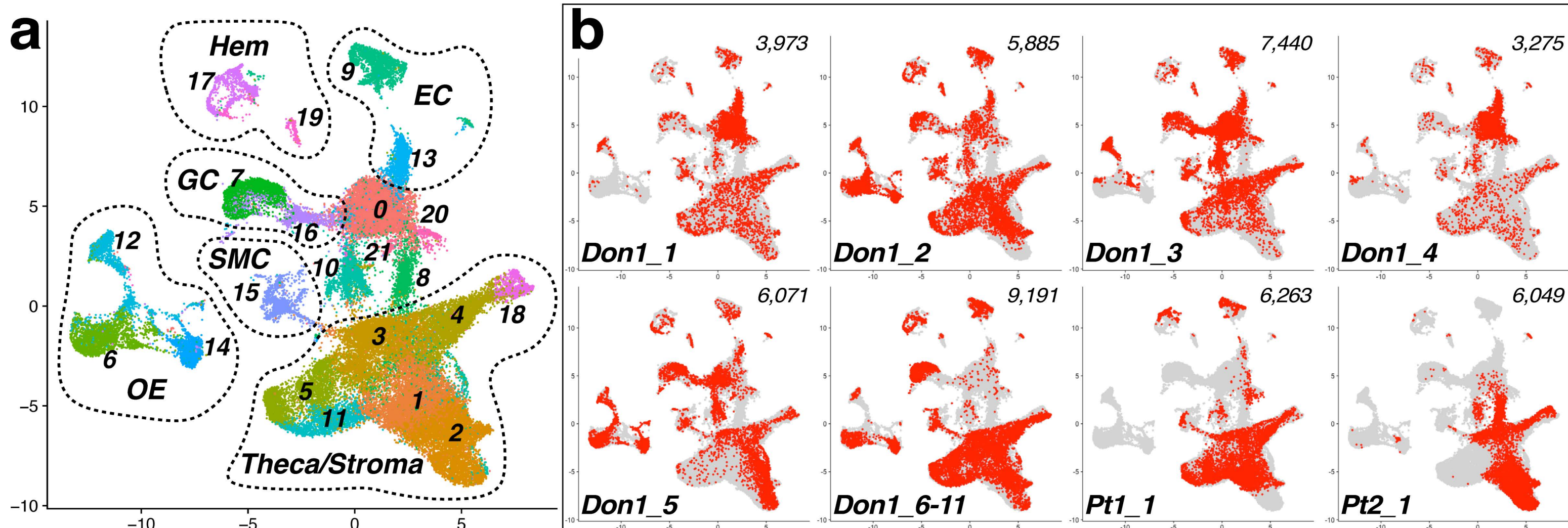
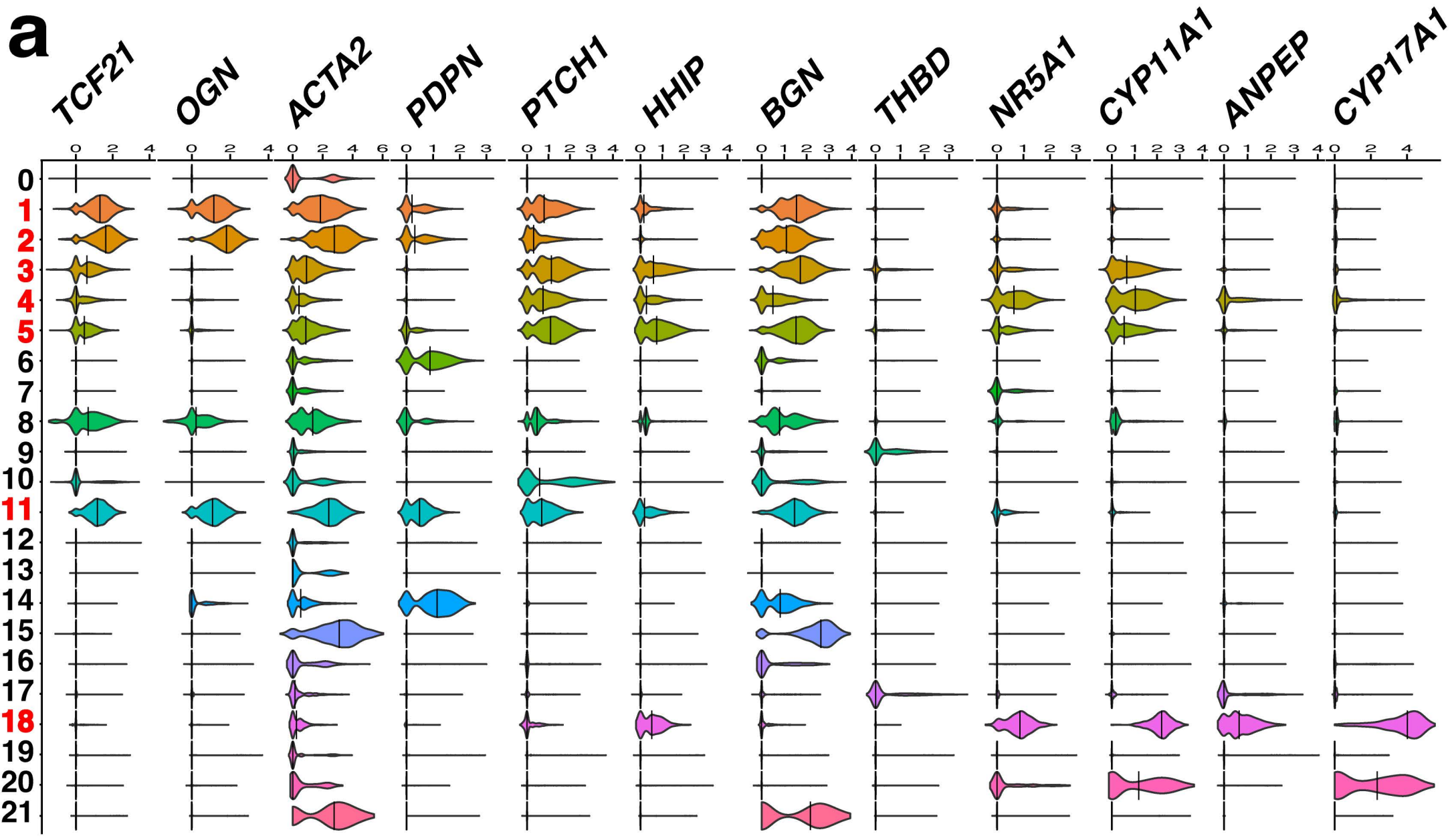
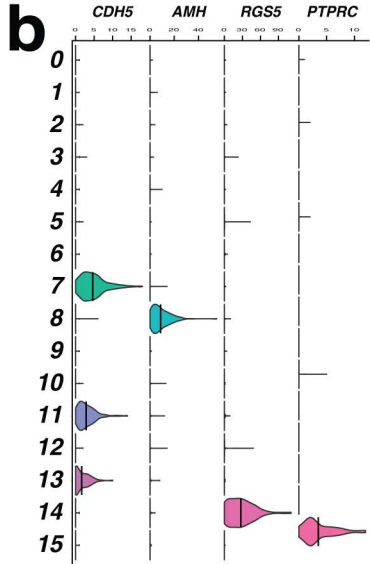
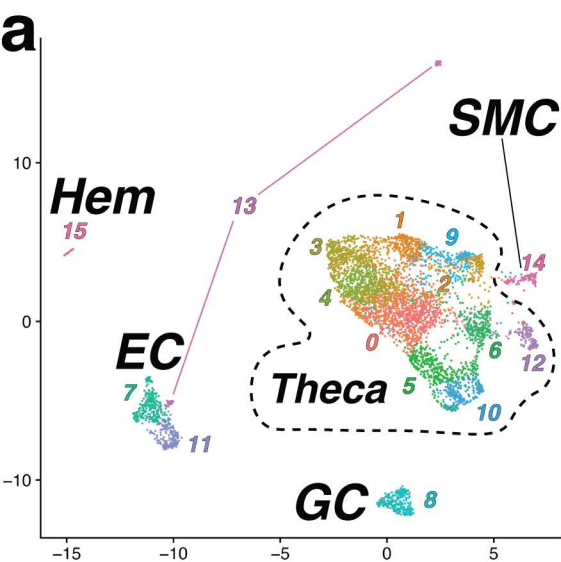




a



Supplemental Table 1. Description of ovarian tissues sources and use.

Sample Designation	Tissue Source	Age (years)	Medical History/Cause of death	Material	Usage (Library name)	Figures
Don1	Tissue donor	31	Stroke	Single cell preparations from isolated antral follicles (fresh)	scRNASeq (Don1_1, Don1_2, Don1_3, Don1_4, Don1_5, Don_6-11)	Supp Fig 1a-f, Fig 1a-b, Fig 2a
				Frozen sections of fixed fresh tissue	Immunolabeling	Fig 2b-d, Fig 2g-l, Fig3a-d, Fig 3f, Fig 4a
					RNA in situ hybridization	Fig 1d-g
Pt1	Fertility Preservation	21	Acute lymphocytic leukemia	Single cell preparations from isolated antral follicles (fresh)	scRNASeq (Pt1_1)	Supp Fig 1a-f, Fig 1a-c, Fig 2a
Pt2	Fertility Preservation	24	Chronic myeloid leukemia	Single cell preparations from isolated antral follicles (fresh)	scRNASeq (Pt2_1)	Supp Fig 1a-f, Fig 1a-c, Fig 2a
Pt3	Fertility Preservation	23	Acute myeloid leukemia	Single cell preparations from isolated antral follicles (fresh)	snRNASeq/scATACSeq (Pt3_1)	Fig 5a-f
Don2	Tissue donor	28	Stroke	Frozen sections of xenotransplanted fixed cortical tissue	Xenotransplantation for proliferation studies (n=4 tissue pieces, n=2 mice)	Fig 4b-h
				Frozen sections of fixed fresh tissue	RNA in situ hybridization	Fig 3e, Fig 3g
					Immunolabeling	Fig 2e-f

Supplementary Material

Supplemental Figure 1. Single cell distribution and Quality Control of global scRNASeq

analysis. (a) UMAP plot of all cell populations submitted for scRNASeq with grouping of cell clusters into six main follicular populations; SMC = Smooth muscle cell, GC = Granulosa cell, OE = Ovarian epithelium, Hem = Hematopoietic, EC = Endothelial cell. (b) Distribution of cells on the aggregate UMAP plot from each library preparation showing the sample designation and cell number retained for final analysis. (c) Violin plots showing expression of representative markers used to identify main follicular populations by Seurat cluster; clusters with low features and/or counts are designated by red asterisks. (d-e) Violin plots showing number of RNA features (d) and RNA counts (e) per Seurat cluster. (f) Dot plot showing expression levels of genes associated with an atretic GC phenotype within the identified GCs from each library. Genes in red are downregulated in atretic follicles, while genes in green are upregulated in atretic follicles.

Supplemental Figure 2. Expression level of marker panel genes in theca and non-TCs from the

ovary. (a) Violin plots of transcripts that were used to define unique theca sub-types (Fig 2a) showing expression levels across all cell clusters isolated from follicles (SuppFig 1a). Clusters that were included in the theca/stroma group are highlighted in red.

Supplemental Figure 3. (a-b) UMAP plot (a) showing predicted Seurat clusters based on snRNASeq and scATACSeq profiles of isolated cells, with violin plots of common gene expression (b) used to identify main populations designated in (a).

Supplemental Table 1. Description of ovarian tissue sources and use.

Supplemental Data 1. List of significantly differentially expressed transcripts by Seurat

cluster. Genes differentially expressed by $\text{LogFC} \geq 0.25$ globally among Seurat clusters from either the “All cells” comparison (SuppFig 1) or the curated sub-analysis of theca/stroma cells (Fig 1 and 2) are listed.

Supplemental Data 2. Values used for quantification of cell proliferation in EdU/CldU treated, xenograft-bearing mice.