

Figure S1. Gross findings of Sample 1 (adrenal gland from SIMC-Uro #12142 who underwent surgery for renal cell carcinoma).

(A) Gross findings of the adrenal gland and tumor after surgical removal. The portions circled by yellow arrows were used for single-cell RNA sequencing.

(B) Gross findings of the portions used for single-cell RNA sequencing.

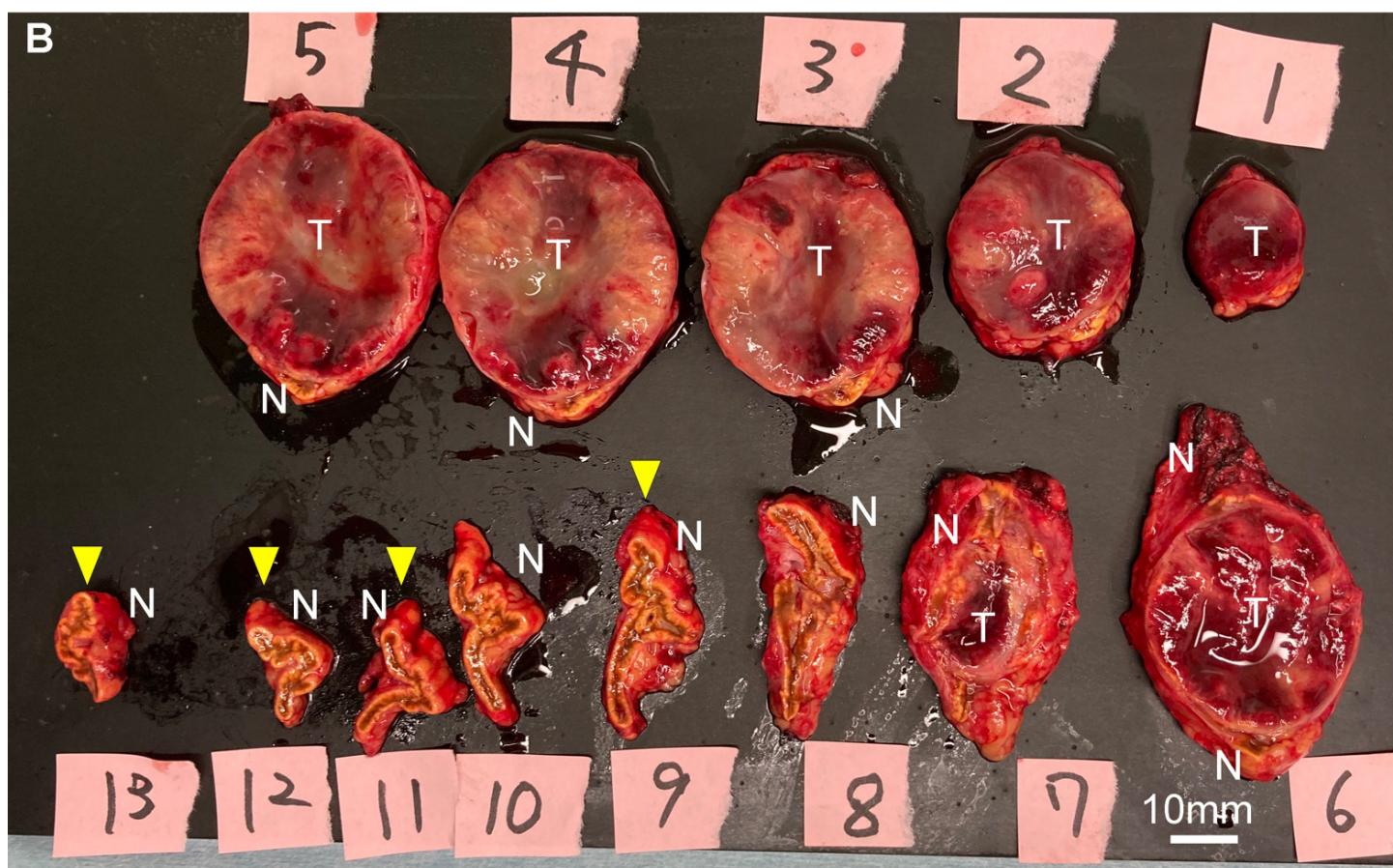
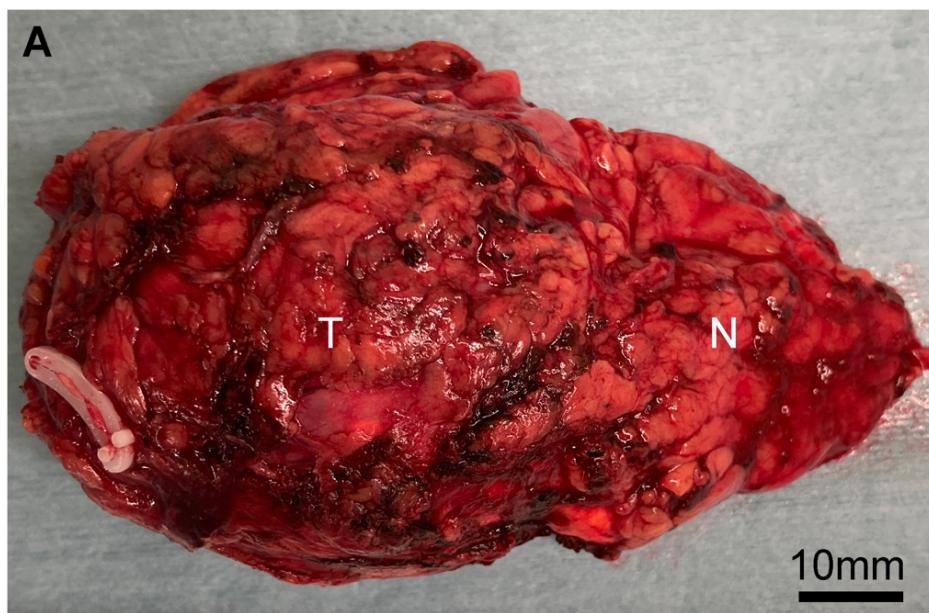


Figure S2. Gross findings of Sample 2 (adrenal gland from SIMC-Uro #12936 who underwent surgery for pheochromocytoma).

(A) Gross findings of the adrenal gland and tumor after surgical removal.

(B) Gross findings after sectioning the adrenal gland and tumor into several pieces. Sections indicated by yellow arrows were used for single-cell RNA sequencing.

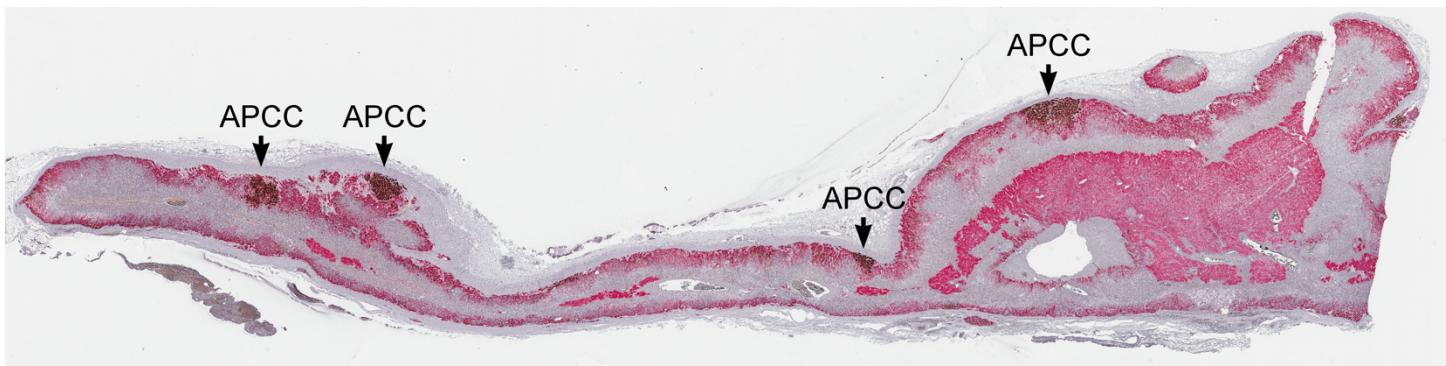


Figure S3. Double immunohistochemical staining for CYP11B2 (brown) and CD56 (red) on another adrenal sample.

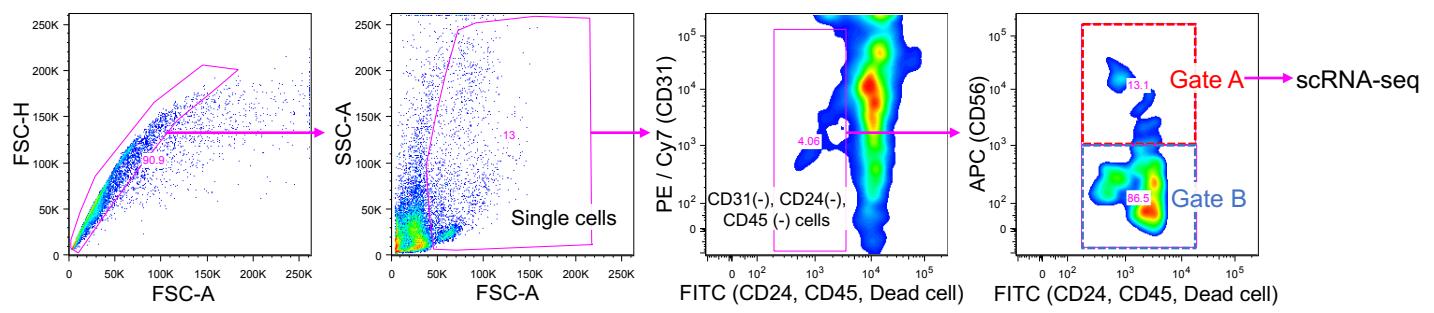
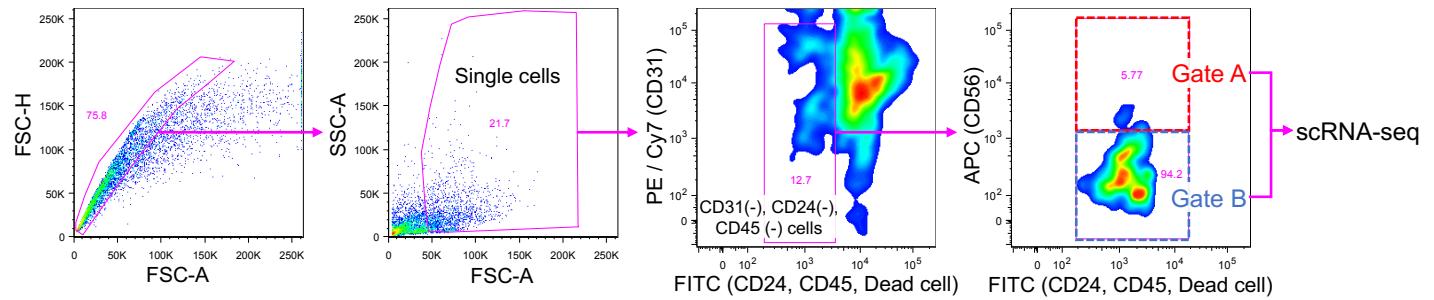
A**B**

Figure S4. Fluorescence-activated cell sorter (FACS) gating strategy for enriching adrenocortical cells (A, Sample 1; B, Sample 2).

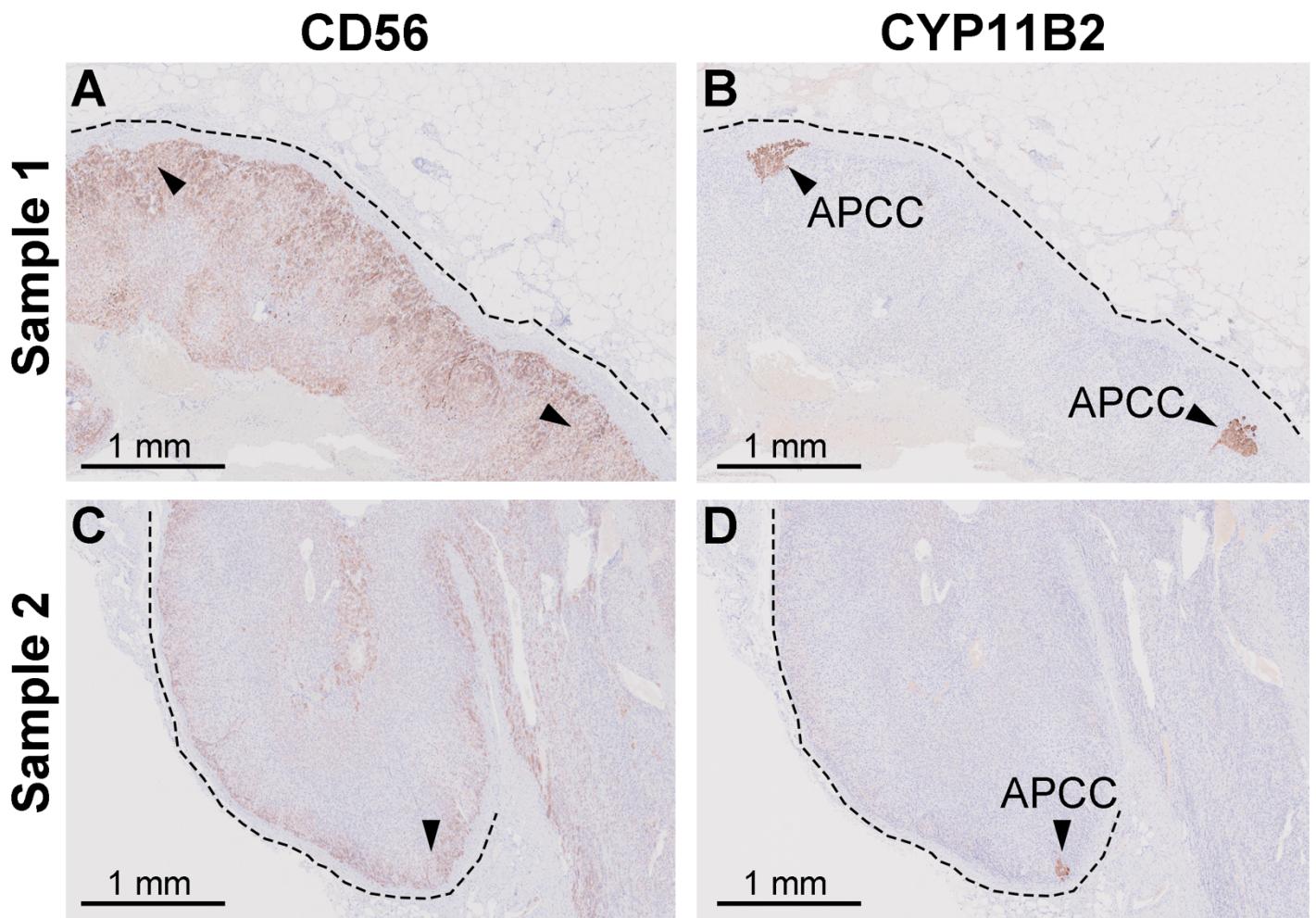


Figure S5. Immunohistochemical staining for CD56 and CYP11B2 on the serial section of Samples 1 and 2. (A) CD56 on Sample 1, (B) CYP11B2 on Sample 1, (C) CD56 on Sample 2, (D) CYP11B2 on Sample 2. Dotted line indicates the outline of the adrenal gland and black arrows indicate APCCs.

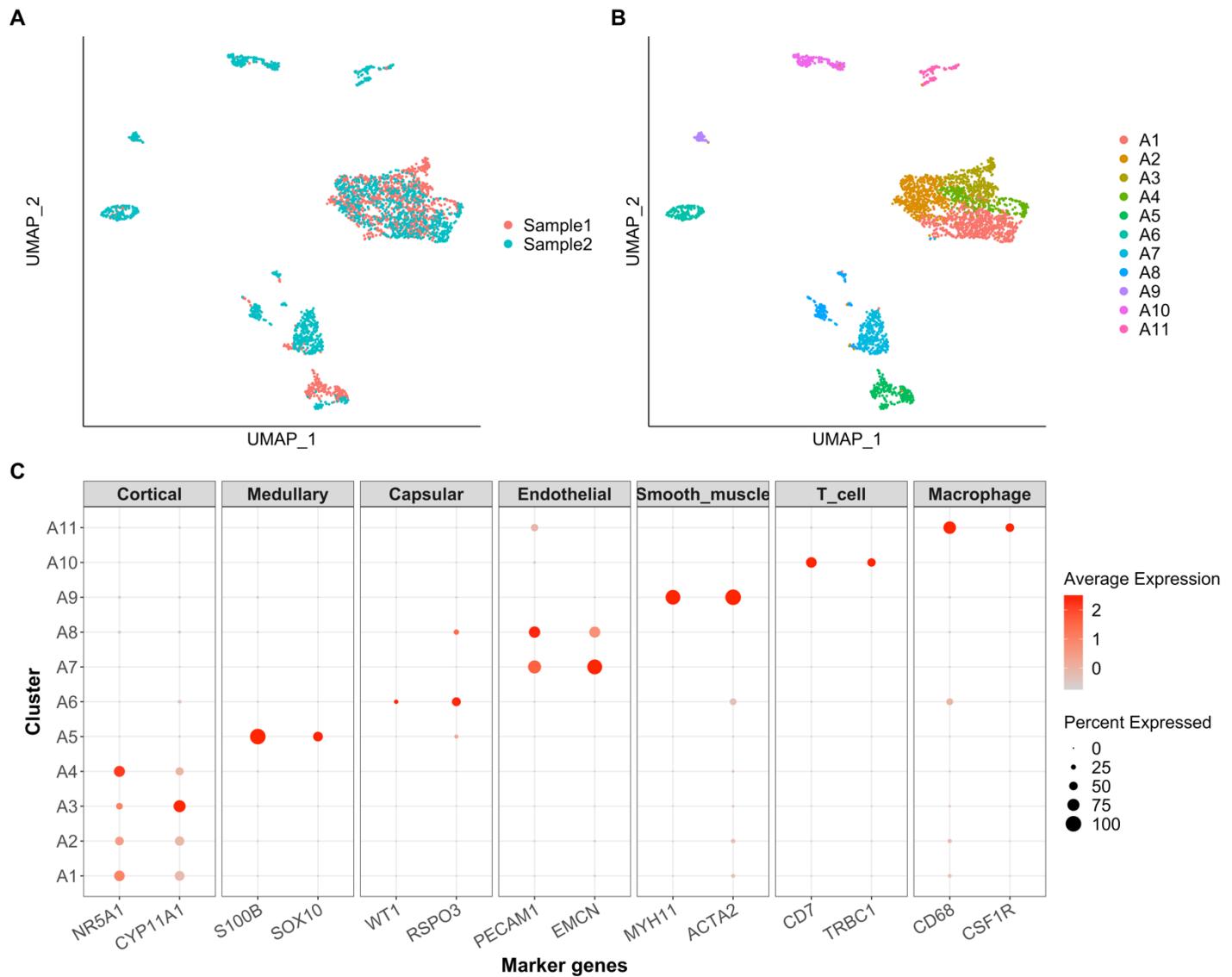
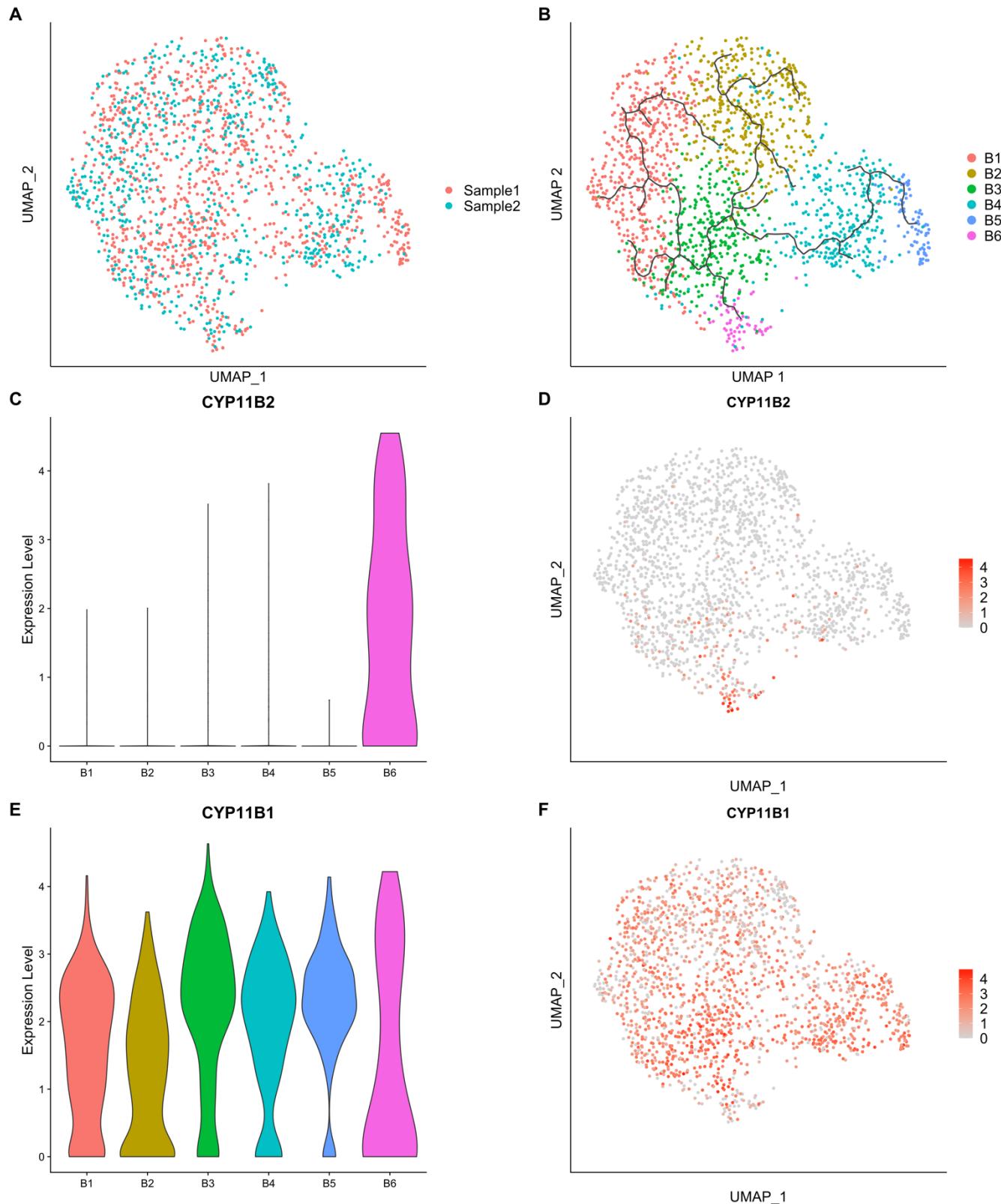


Figure S6. Clustering of adrenal cells.

- (A) Distribution of two samples on adrenal cells shown in the UMAP plot. Dots: single cells. Colors: samples.
- (B) UMAP plot showing the identified clusters of adrenal cells. Dots: single cells. Colors: identified clusters.
- (C) Dot plot showing the expression of marker genes for each cluster of adrenal cells. Dot color: the average expression level across all cells within the cluster. Dot size: the percentage of cells within the cell population expressing the gene.



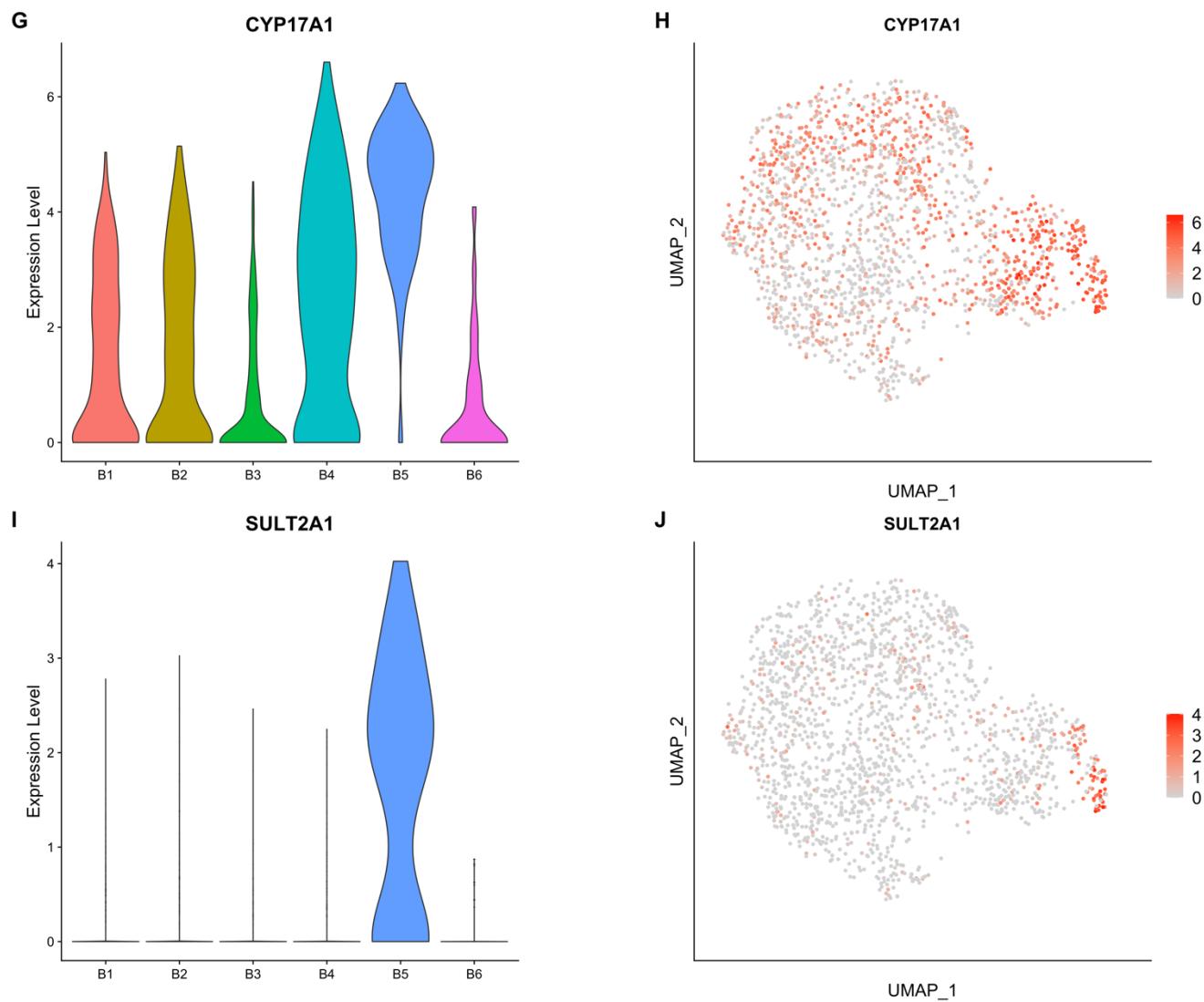


Figure S7. Clustering of adrenocortical cells.

- (A) Distribution of two samples on adrenocortical cells shown in the UMAP plot. Dots: single cells. Colors: samples.
- (B) The result of trajectory analysis of adrenocortical cells projected onto UMAP plot. Dots: single cells. Dot colors: clusters. Blackline: predicted trajectory.
- (C) Violine plot showing the expression level of *CYP11B2* for each cluster of adrenocortical cells.
- (D) Scatterplots showing the expression level of *CYP11B2* projected onto the UMAP plot. Dots: single cells. Dot color: gene expression level.
- (E) Violine plot showing the expression level of *CYP11B1* for each cluster of adrenocortical cells.
- (F) Scatterplots showing the expression level of *CYP11B1* projected onto the UMAP plot. Dots: single cells. Dot color: gene expression level.

- (G) Violin plot showing the expression level of *CYP17A1* for each cluster of adrenocortical cells.
- (H) Scatterplots showing the expression level of *CYP17A1* projected onto the UMAP plot. Dots: single cells. Dot color: gene expression level.
- (I) Violin plot showing the expression level of *SULT2A1* for each cluster of adrenocortical cells.
- (J) Scatterplots showing the expression level of *SULT2A1* projected onto the UMAP plot. Dots: single cells. Dot color: gene expression level.