

Fig. S1

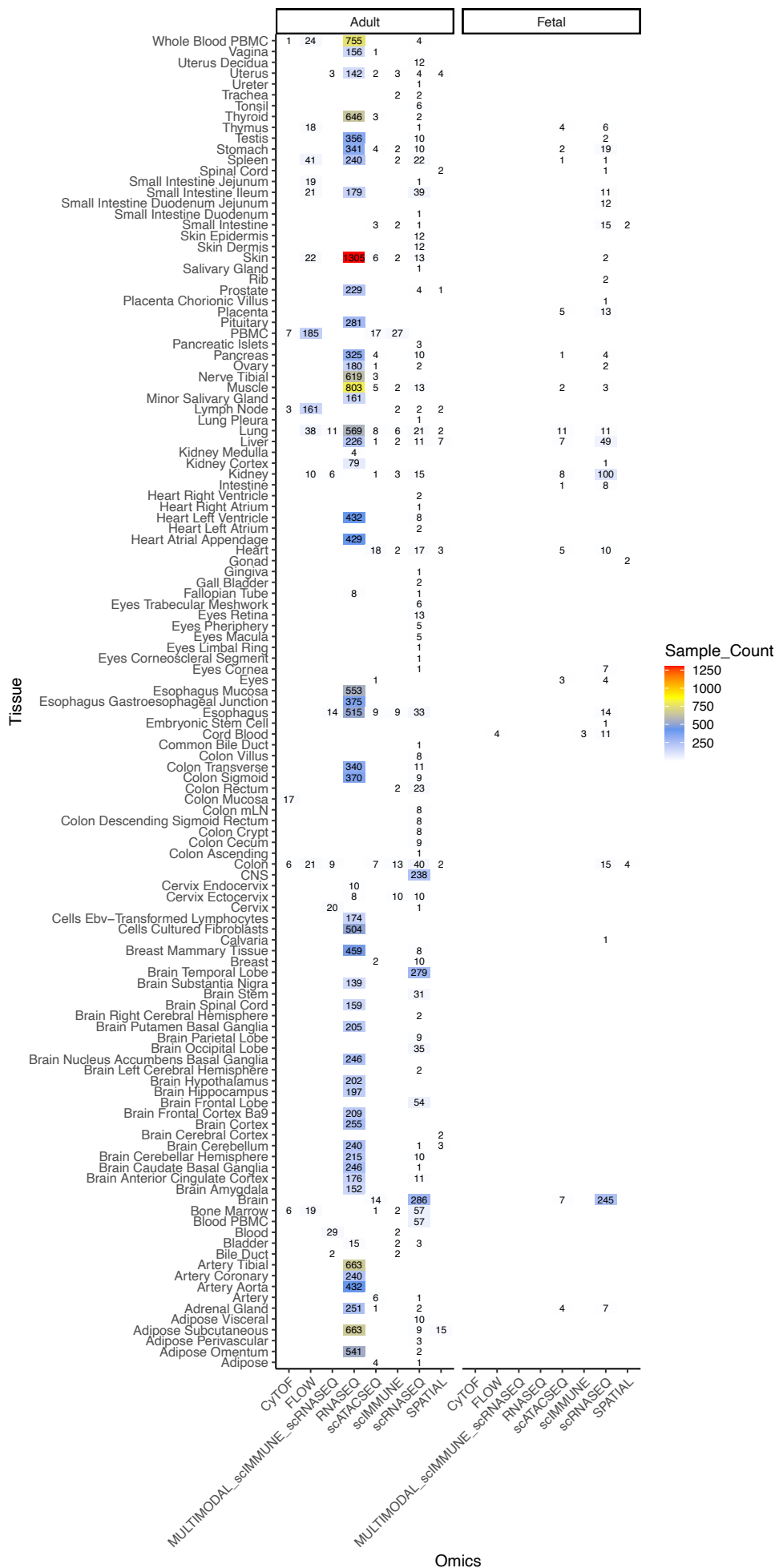
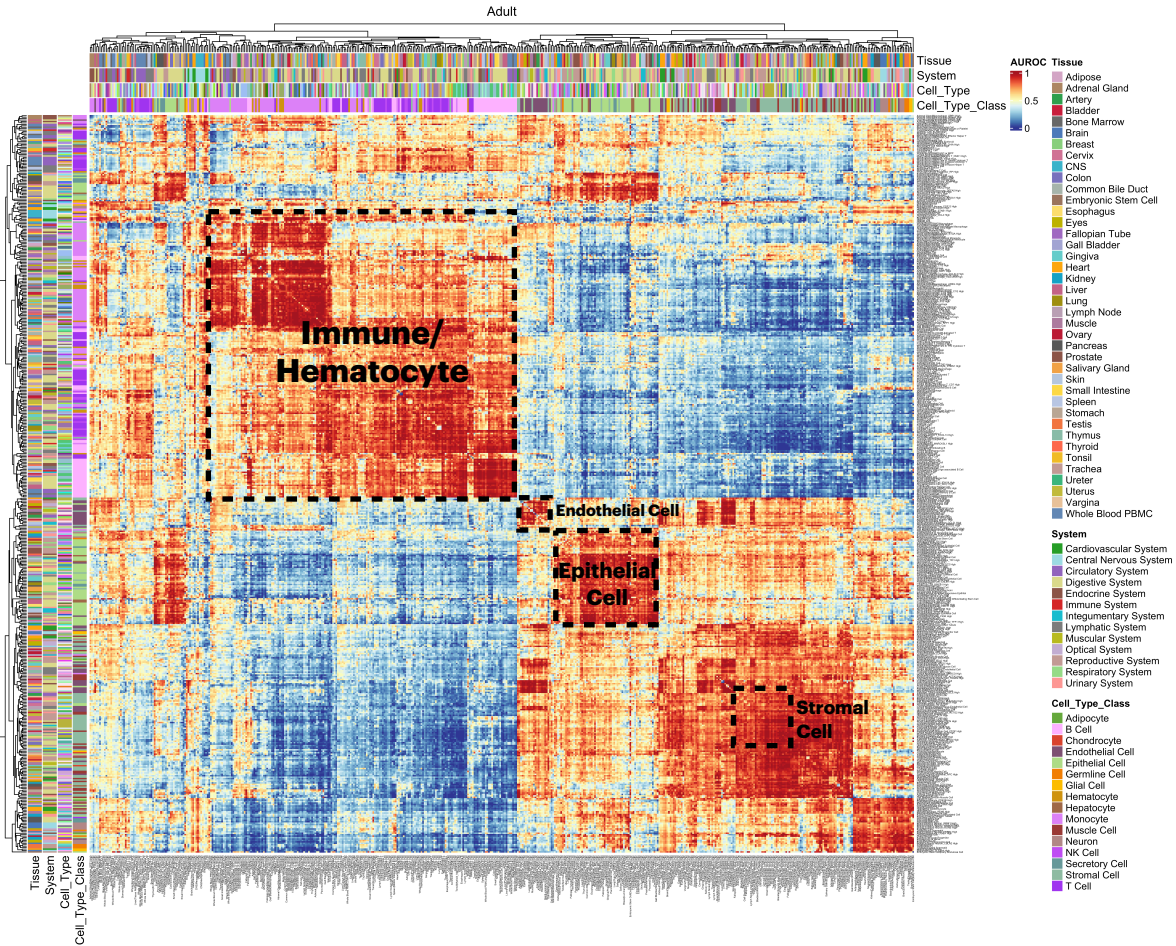


Fig. S1. Sample count in fetal and adult groups across tissues and omics types.

Fig. S2

A



B

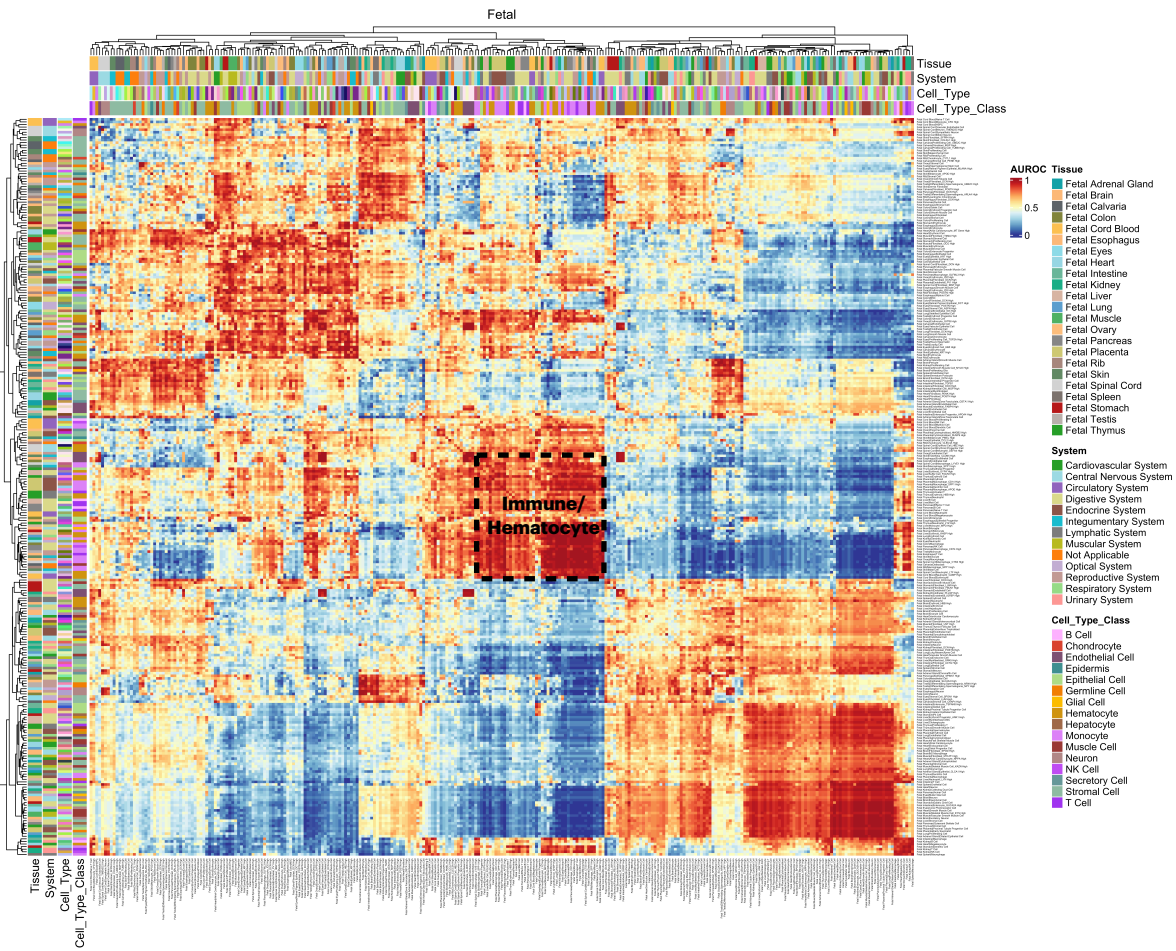
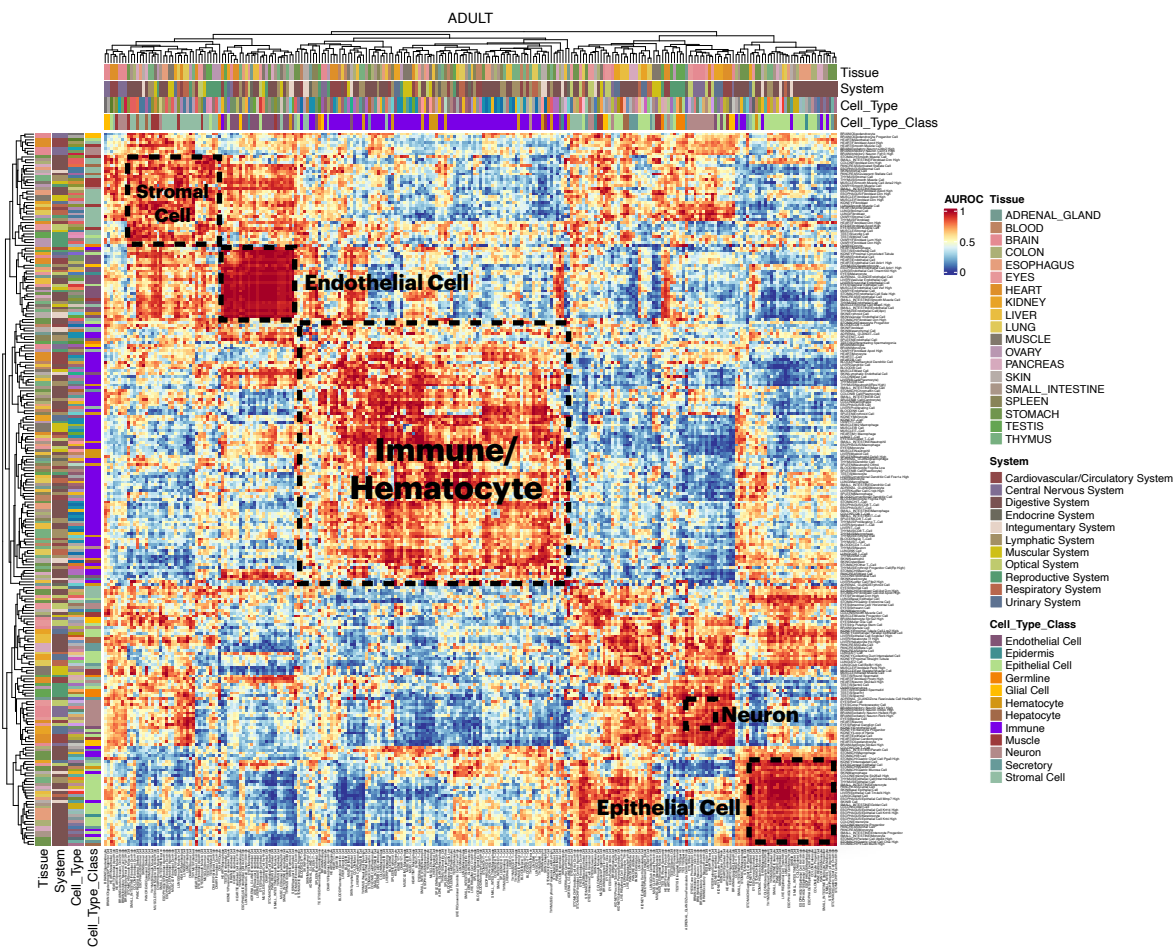


Fig. S2. Correlations between cell types based on gene expression signatures revealed distinct cell type class clusters.

(A-B) Heatmap showing the correlations of the cell types from adult (A) and fetal (B) cell types based on the expression of their top upregulated genes. The intensity of the heatmap shows the AUROC level between cell types. Colour blocks on the top of the heatmap represent tissues (first row from the top), biological systems (second row), cell types (third row) and cell type classes (fourth row).

Fig. S3

A



B

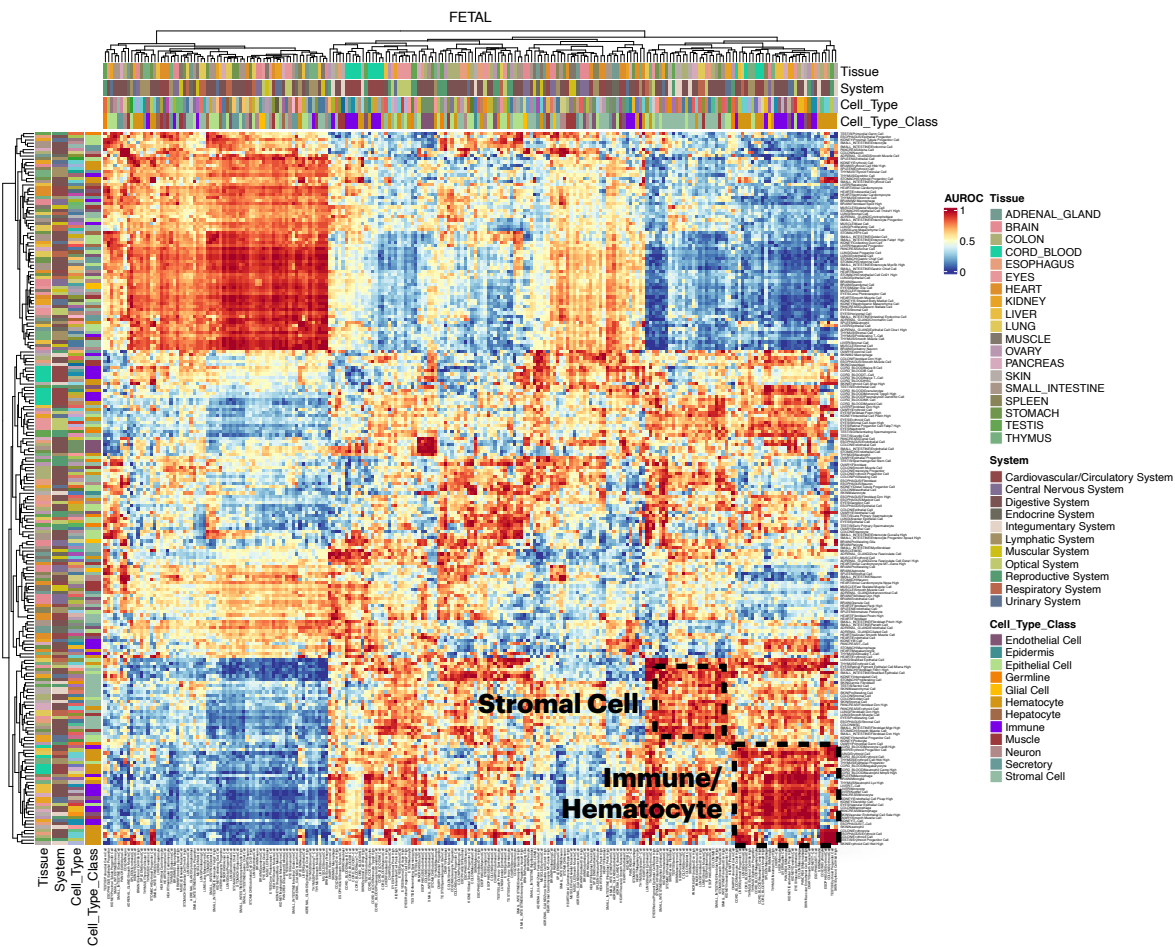


Fig. S3. Correlations between cell types based on TF signatures revealed similar clustering patterns.

(A-B) Heatmap showing the correlations of the cell types from adult (A) and fetal (B) cell types based on the expression of the TF signatures of each cell type. The intensity of the heatmap shows the AUROC level between cell types. Colour blocks on the top of the heatmap represent tissues (first row from the top), biological systems (second row), cell types (third row) and cell type classes (fourth row).

Fig. S4

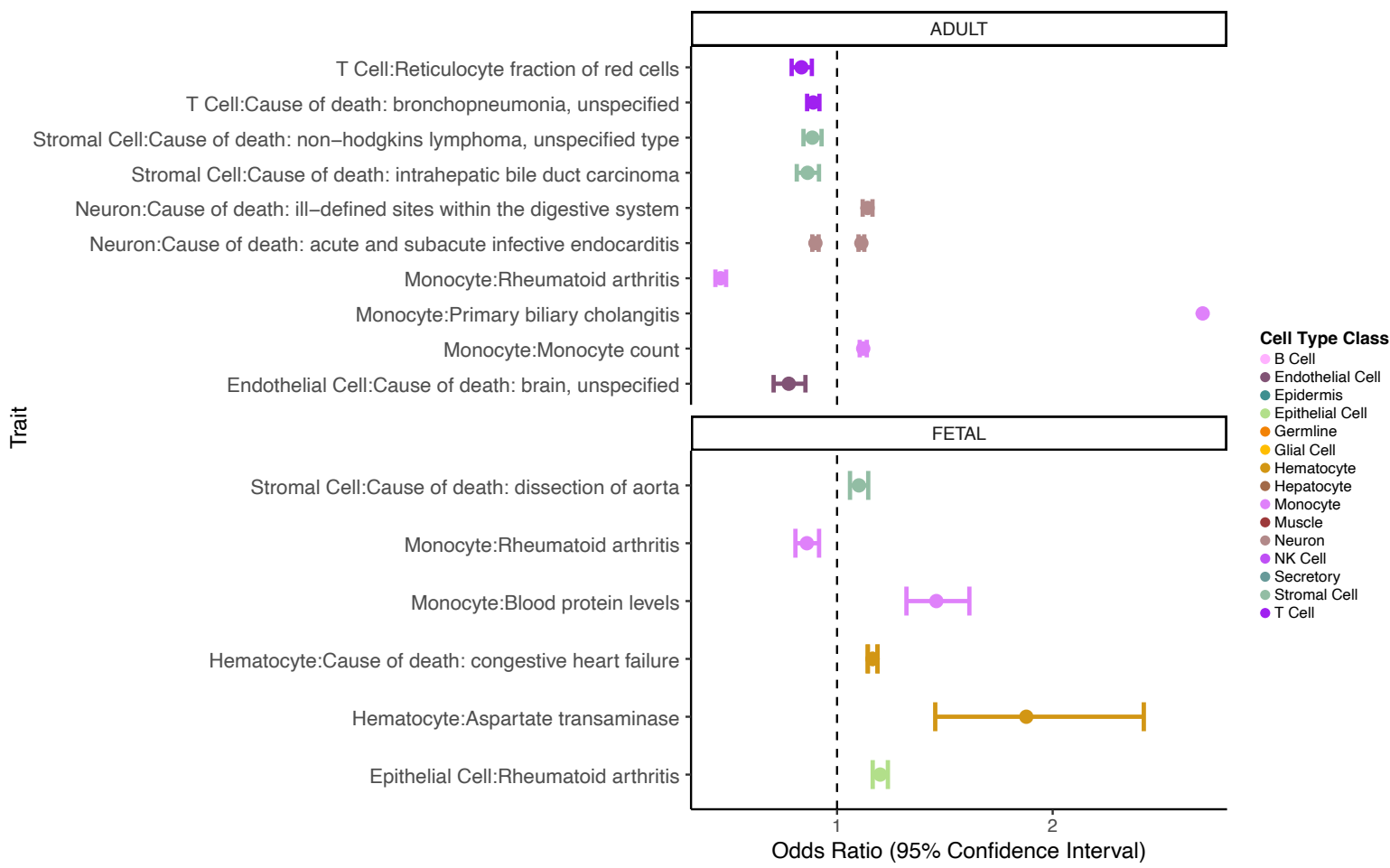


Fig. S4. Phenotype or disease trait associations. Forest plot showing the associations of phenotype or disease traits in selected cell type classes of scRNA-seq data for both adult and fetal tissues. The X-axis displays the odds ratio of each trait, and the colors of the points represent cell type classes.

Fig. S5

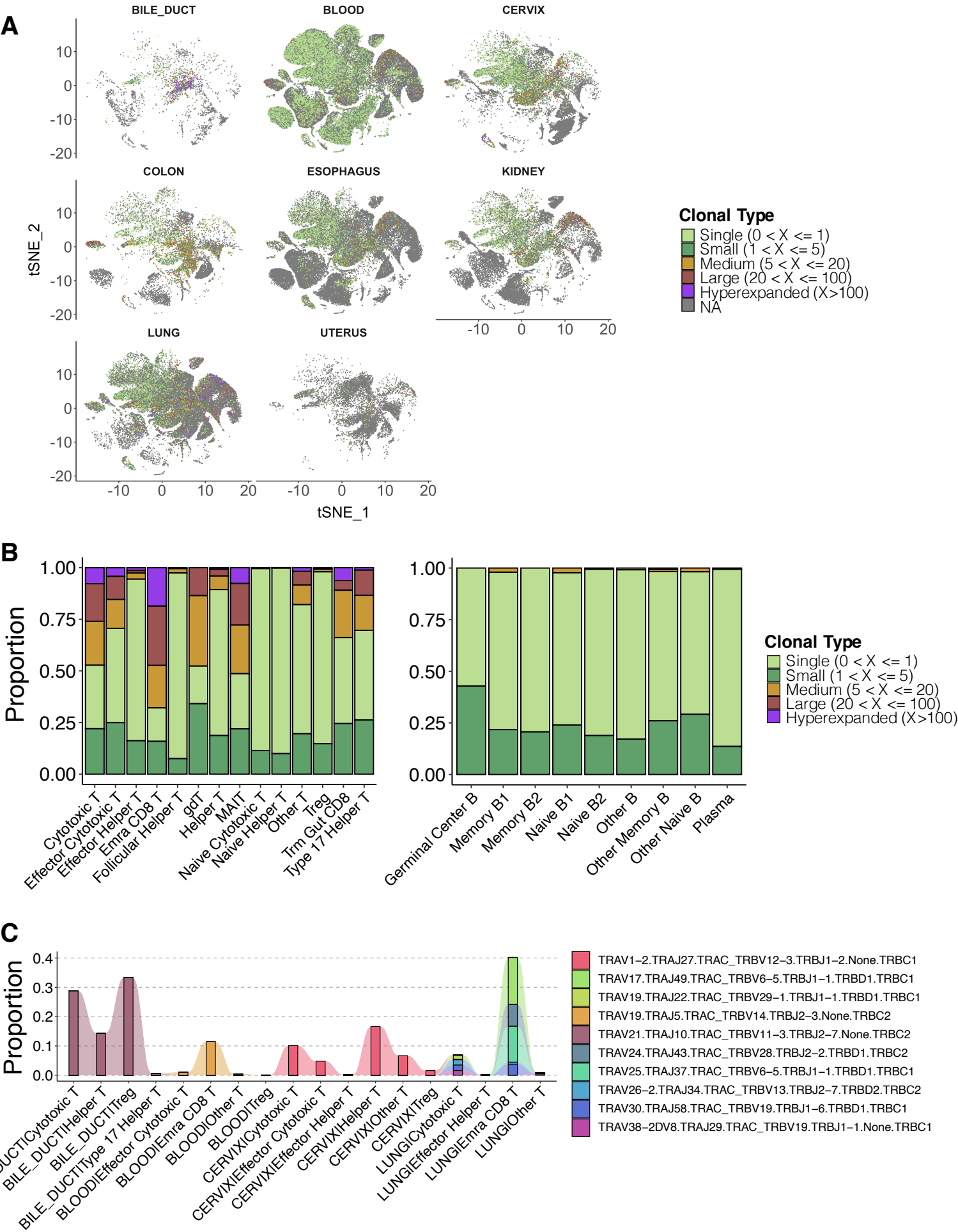


Fig. S5. Landscape of clonal expansion patterns across tissues.

(A) tSNE of the tissues from the multi-modal tissues of the scImmune-profiling data. Colors indicate clonal type expansion groups of the cells. Cells not present in the T or B repertoires are colored gray (NA group). Tissues with too few cells present in the T or B repertoires were filtered (i.e., bile duct and kidney) in the main analysis.

(B) Stacked bar plots revealing the overall clonal expansion landscapes of the T and B-cell repertoires. Colors represent clonal type groups.

(C) Alluvial plot showing the top clonal types in T-cell repertoires and their proportions shared across tissues containing these clonotypes. Colors represent clonotypes.

Fig. S6

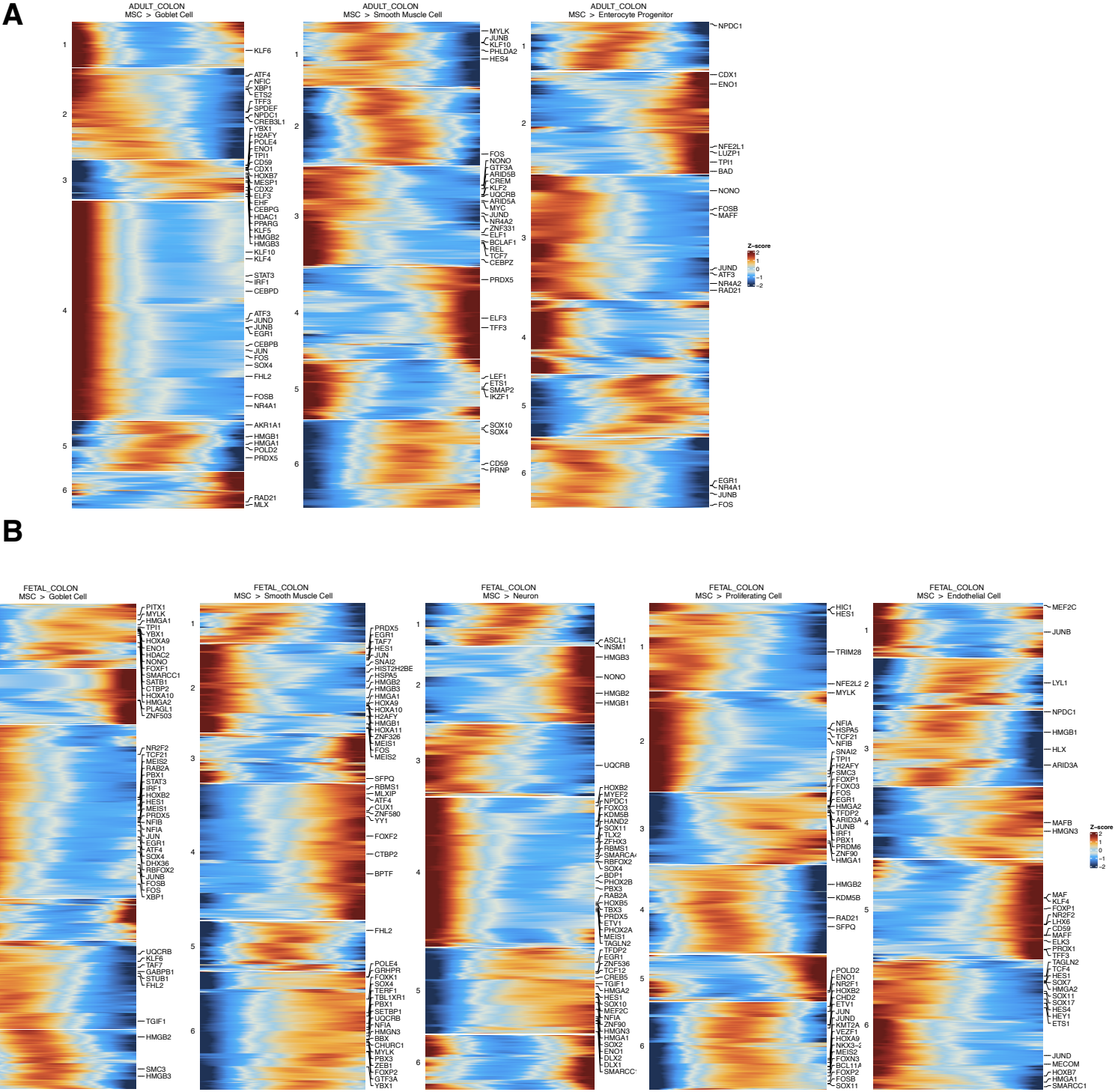
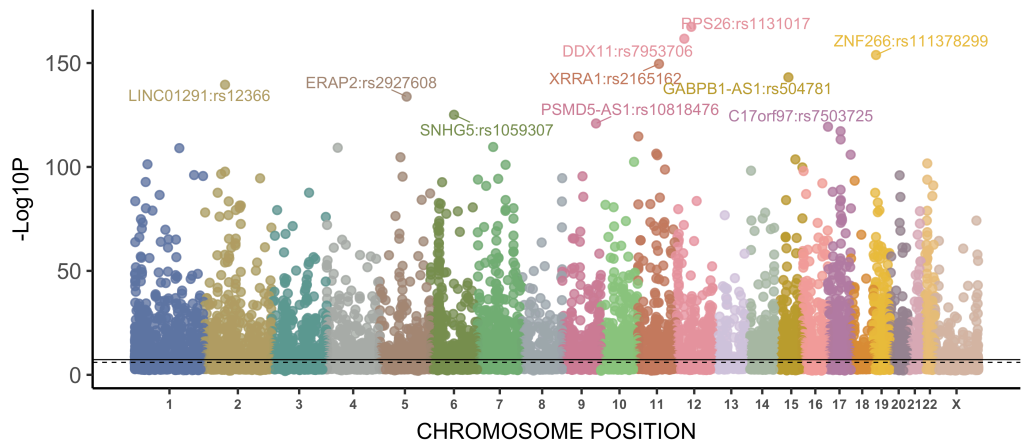


Fig. S6. Pseudotime heatmaps of MSC lineage cell types in the adult and fetal colon.

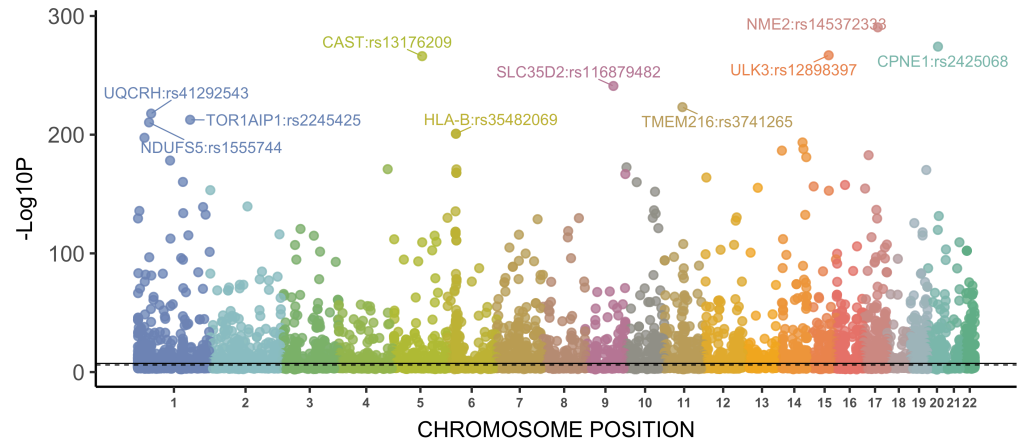
(A-B) Pseudotime trajectory of each cell type in the MSC lineage of adult (A) and fetal (B) colons. The color represents the cell type, and the violin plots represent the density of cells across pseudotime.

Fig. S7

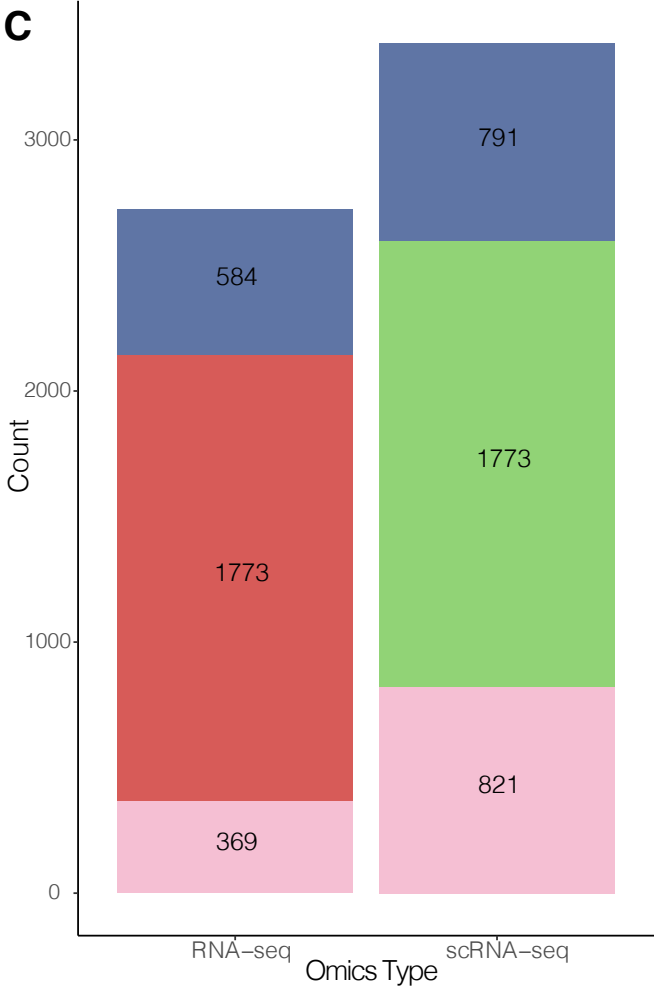
A



B



C



D

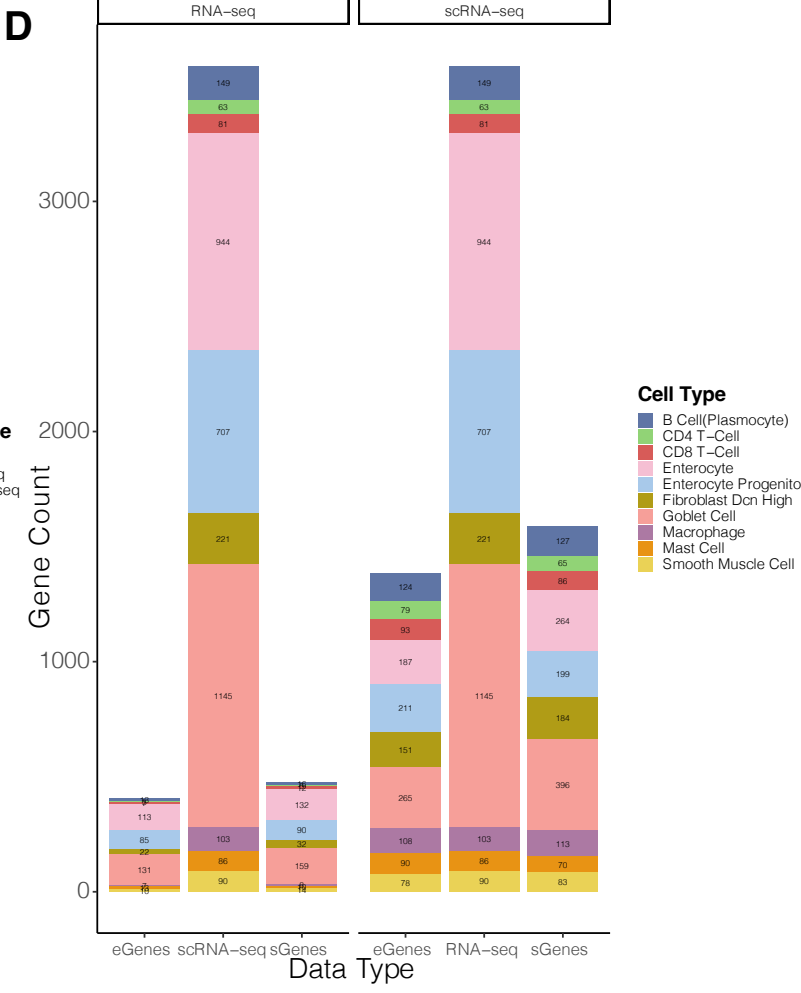


Fig. S7. Comparison of DE gene overlaps between bulk RNA-seq, scRNA-seq and WGS.

(A) Chromosomal positions of the top 10 eGenes in colon transverse bulk RNA-seq data. Gene names and their SNP rsid are shown.

(B) Chromosomal positions of the top 10 sGenes in colon transverse bulk RNA-seq data. Gene names and their SNP rsid are shown.

(C) Stacked bar plot showing the number of shared DE genes of the bulk RNA-seq data and the scRNA-seq data with the genes of the top eQTLs and sQTLs. The color represents the omics type.

(D) Stacked bar plot showing the number of shared DE genes across the bulk RNA-seq data, the scRNA-seq data, genes of the top eQTLs and sQTLs. Colors represent the cell types to which the genes belonged with reference to the DE genes of the cell types in the scRNA-seq data.

Fig. S8

scATAC-Seq Workflow

SCA V1.0.0

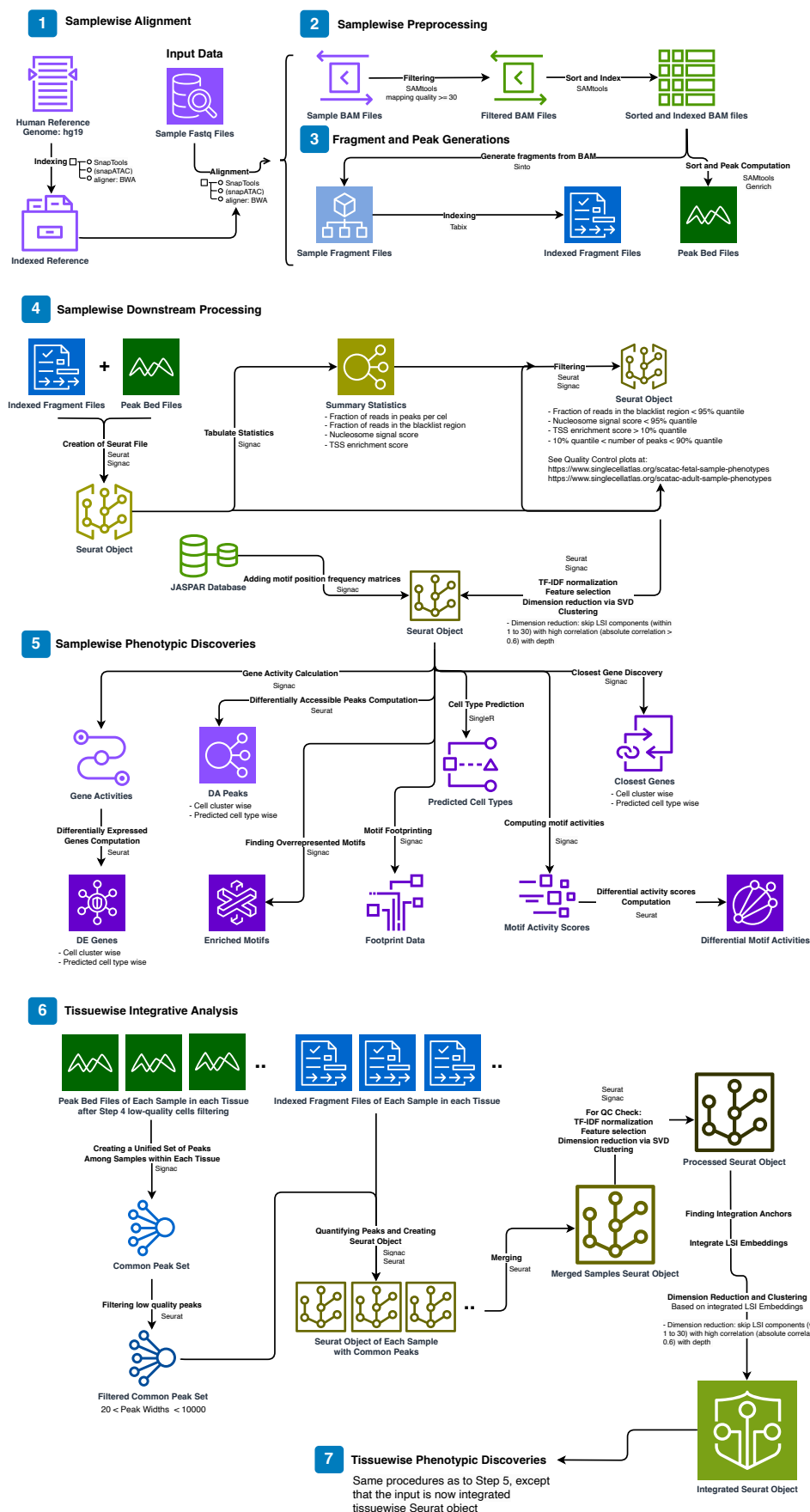


Fig. S8. Comprehensive workflow for scATAC-Seq data analyses in SCA V1.0.0.