

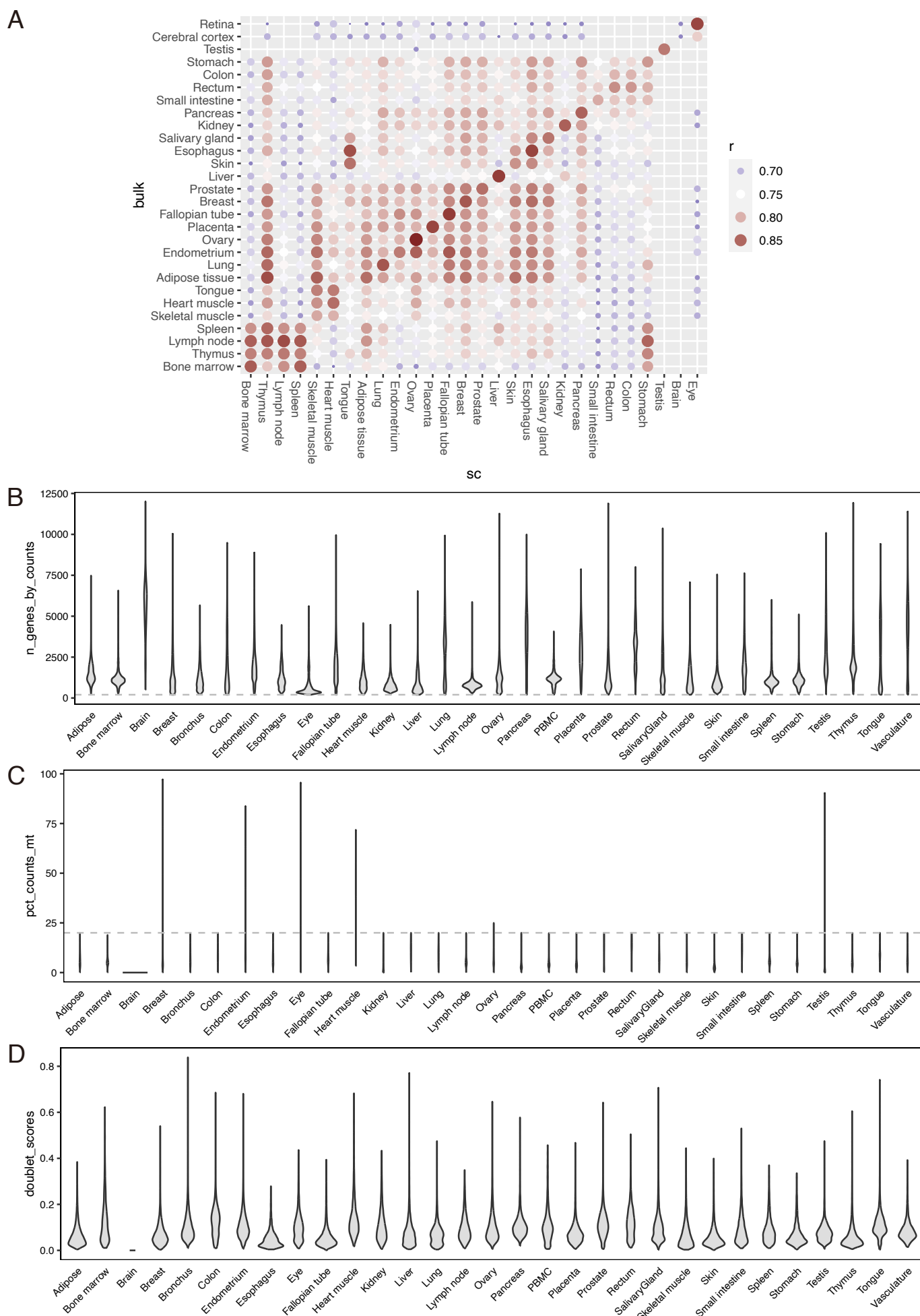


Fig S1. Quality control for single cell transcriptomics data, related to Figure 1.

(A) The bubble heatmap shows the spearman correlation between matched pseudo bulk and bulk transcriptomics of 25 tissues. Violin plots show the quality of cells for each tissue and organ in aspect of (B) number of genes by counts, (C) mitochondrial gene percentage (D) estimated doublet scores.

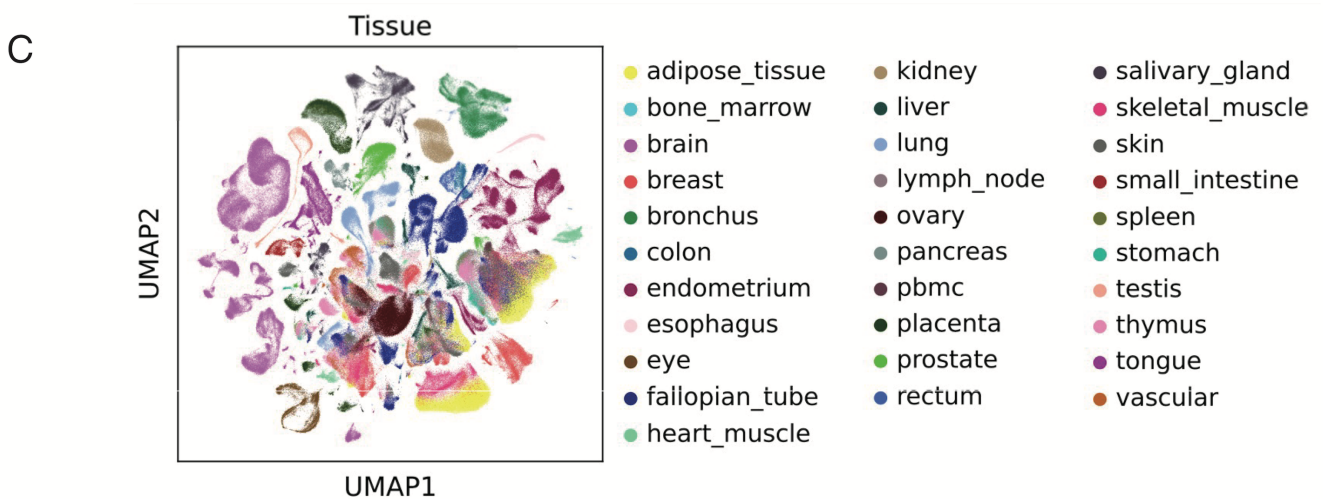
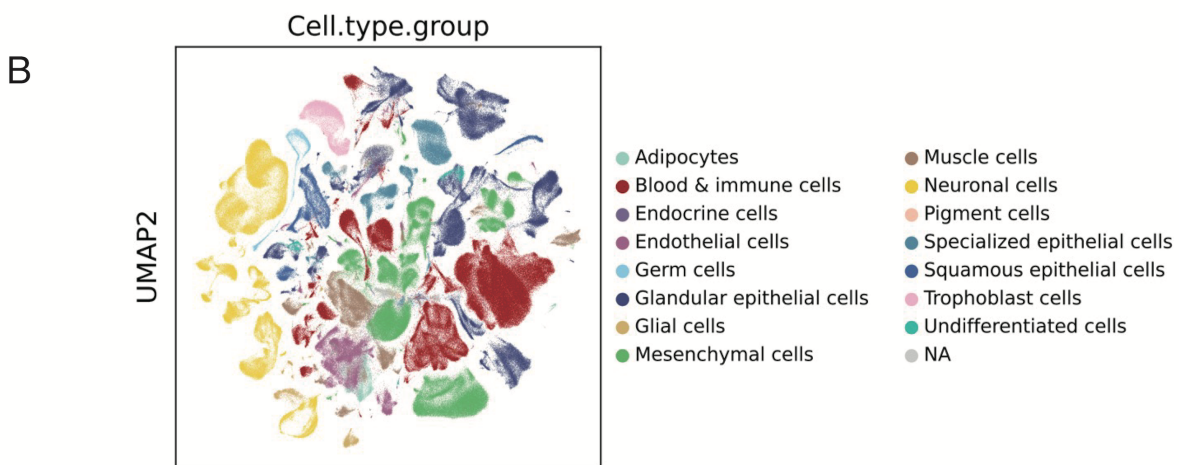
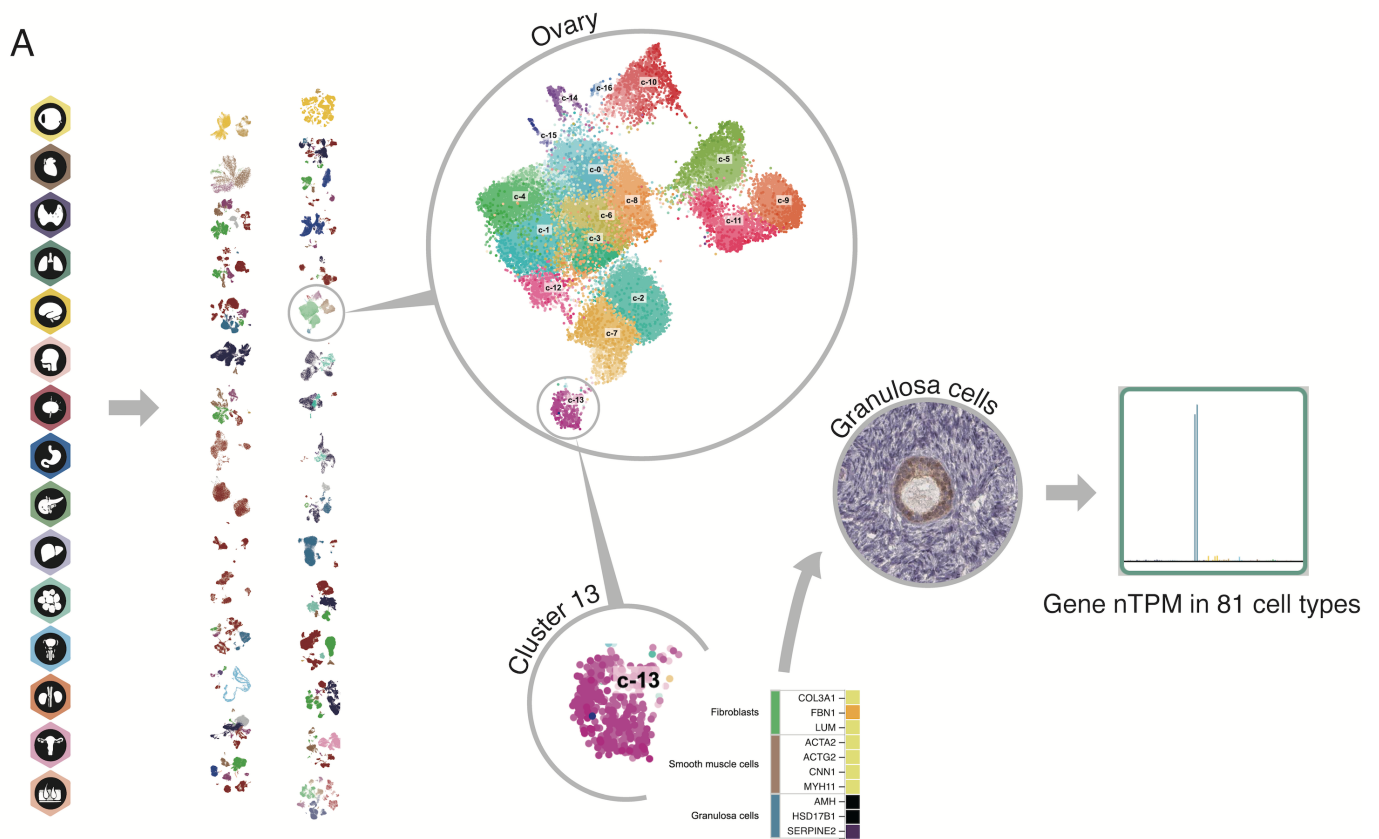
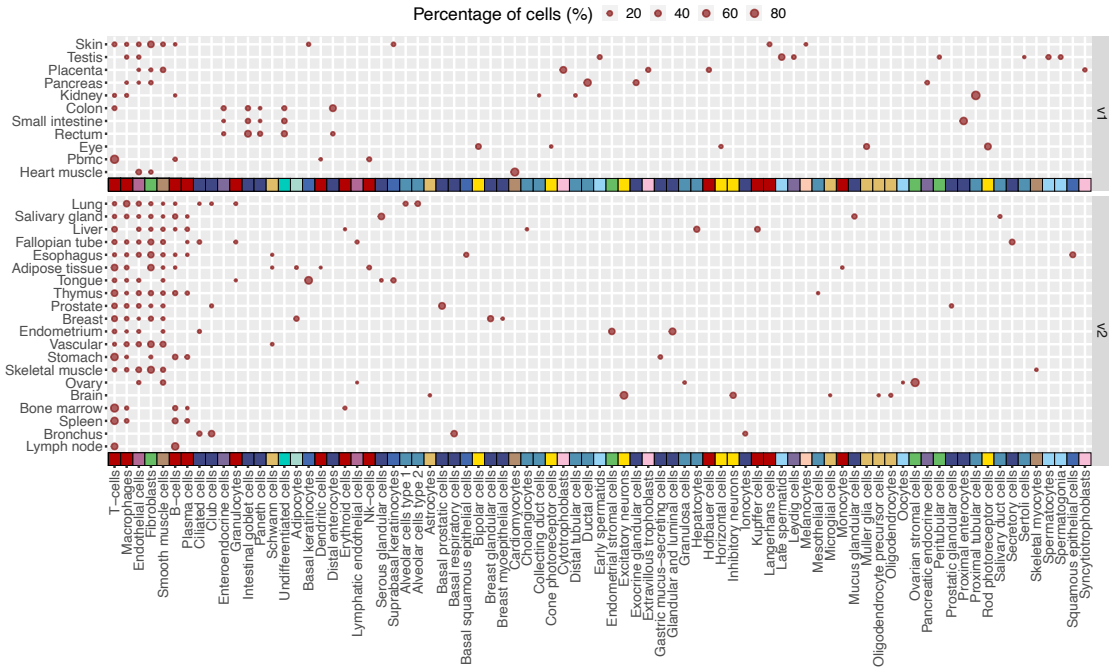


Fig S2. Overview of the study, related to Figure 1.

(A) The workflow of HPA single cell section. Whole cell UMAP plot visualization on cell type groups (B) and tissues (C).

A



B

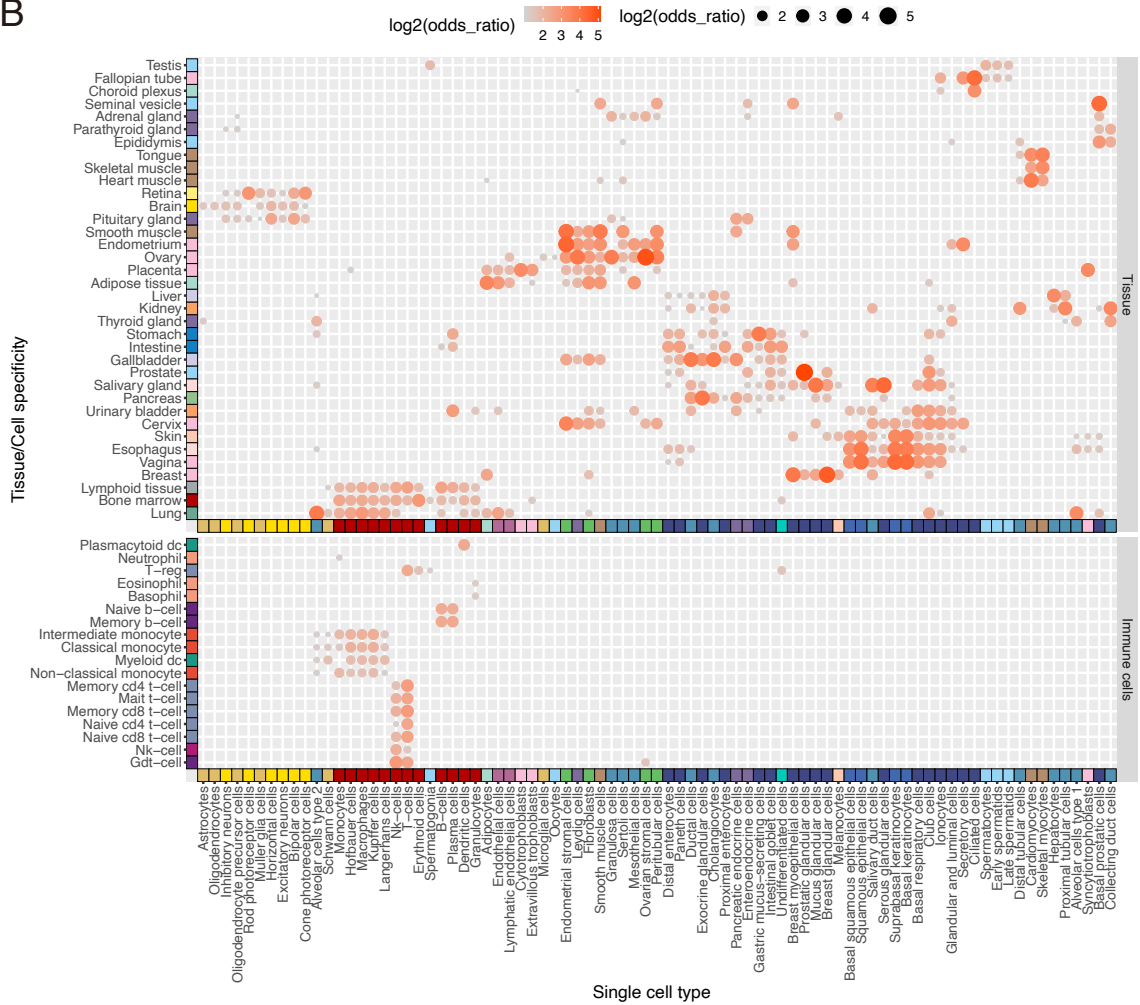


Fig S3. Overview of the 81 cell types, related to Figure 1 and Figure 4.

(A) The bubble plot shows the percentage of cells of 31 tissues in 81 cell types. (B) The bubble heatmap shows the enrichment of enriched genes of cell types in bulk and immune cell transcriptomics.

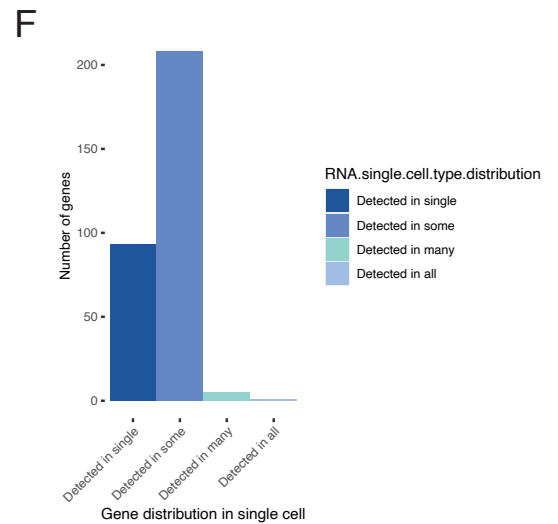
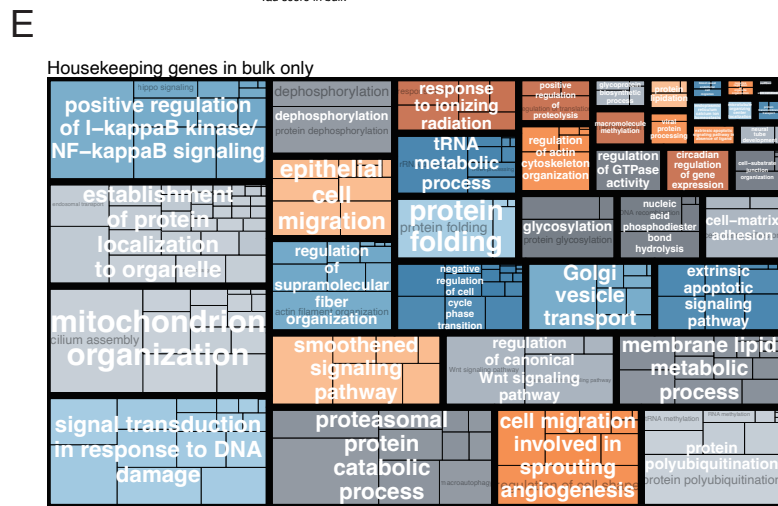
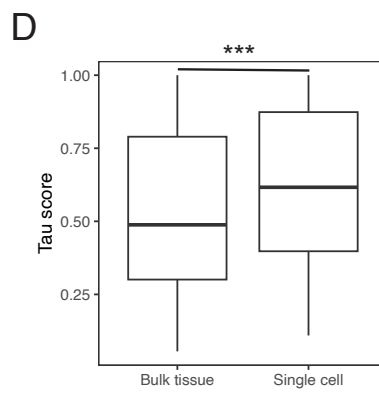
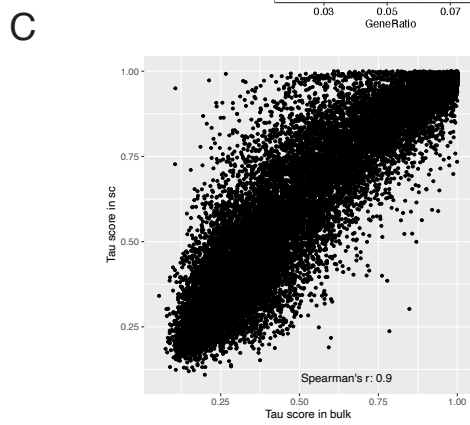
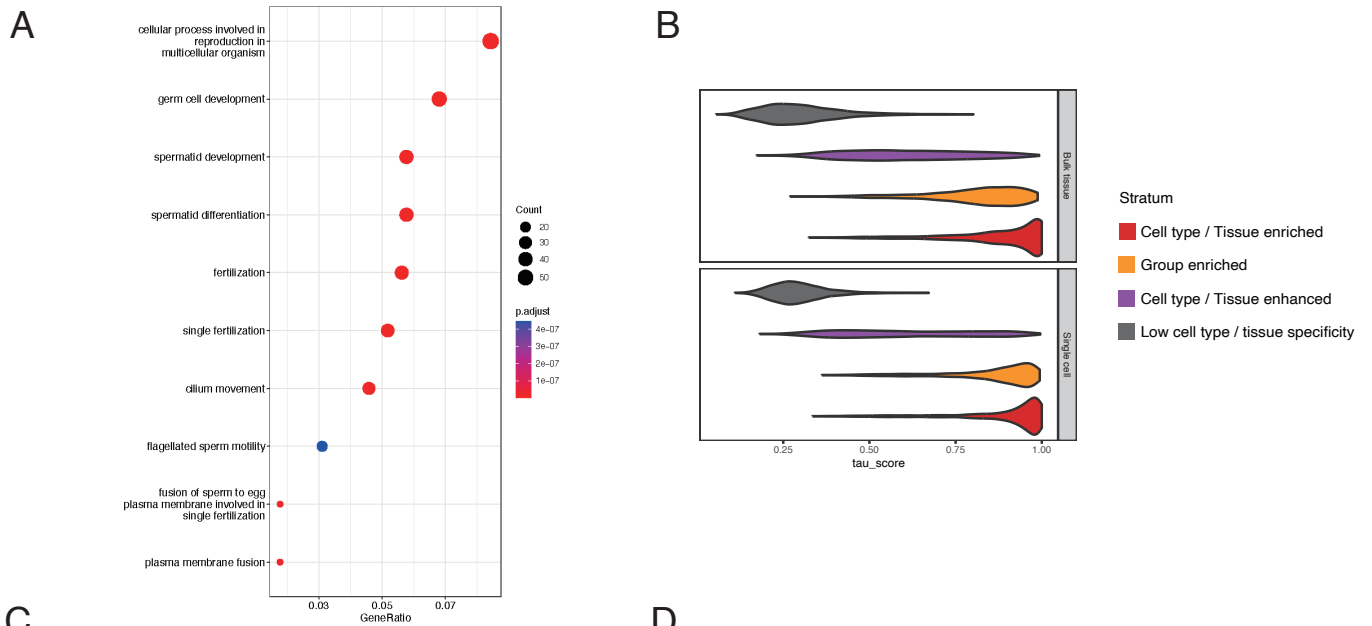


Fig S4. Gene classifications, related to Figure 2 and Figure 3.

(A) The bubble heatmap shows the enriched GO BP terms of spermatid enriched genes. (B) The violin plot shows the gene classification of genes and their corresponding tau score in single cell transcriptomics. The scatter plot (C) and the box plot (D) shows the similarity and differences of tau scores of consensus genes between single cell and bulk transcriptomics, respectively. (E) The tree map shows the enriched parent GO BP terms of bulk-only low specificity genes. (F) The bar plot shows the distribution of genes that only detected in single cell transcriptomics.