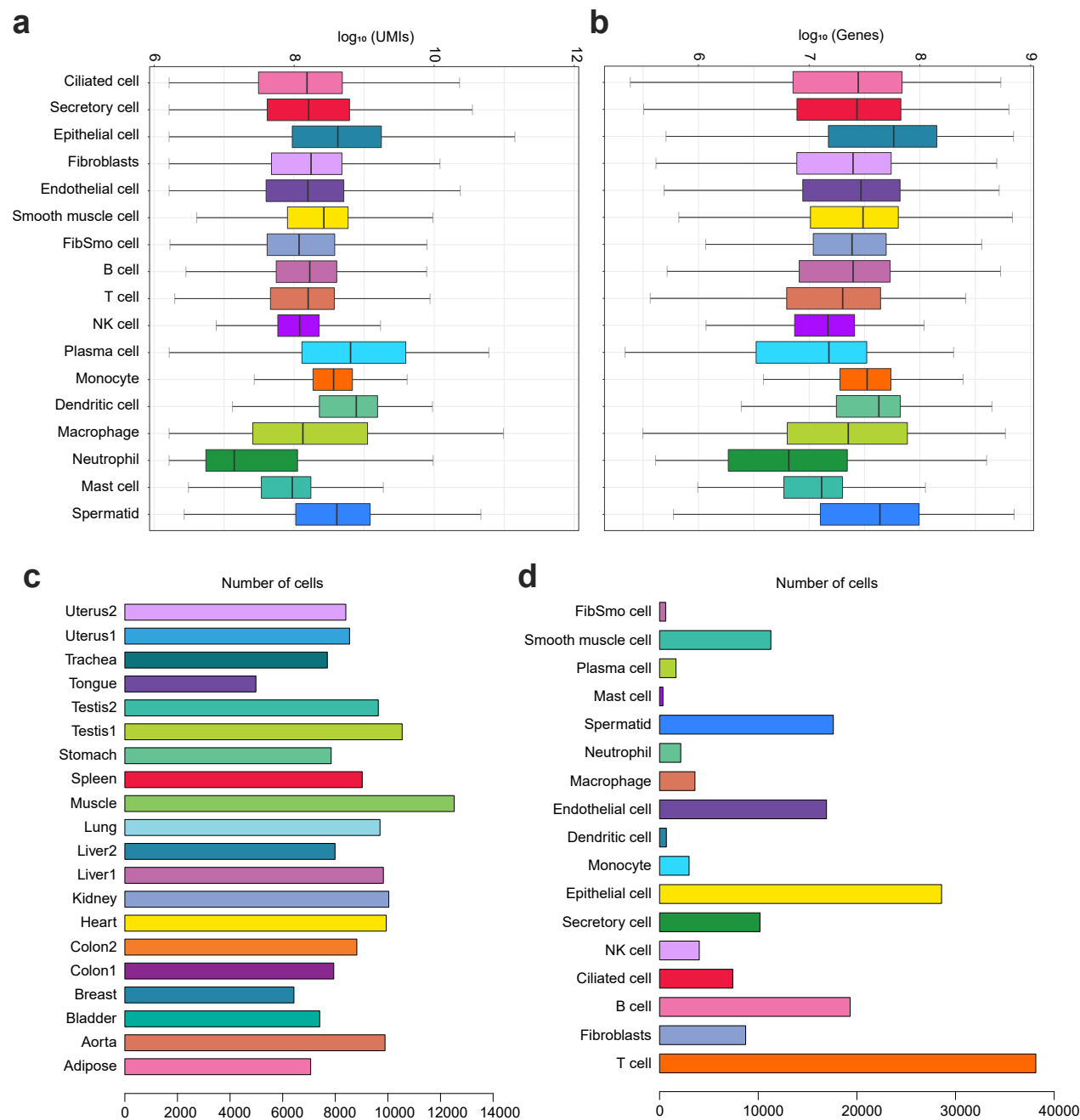
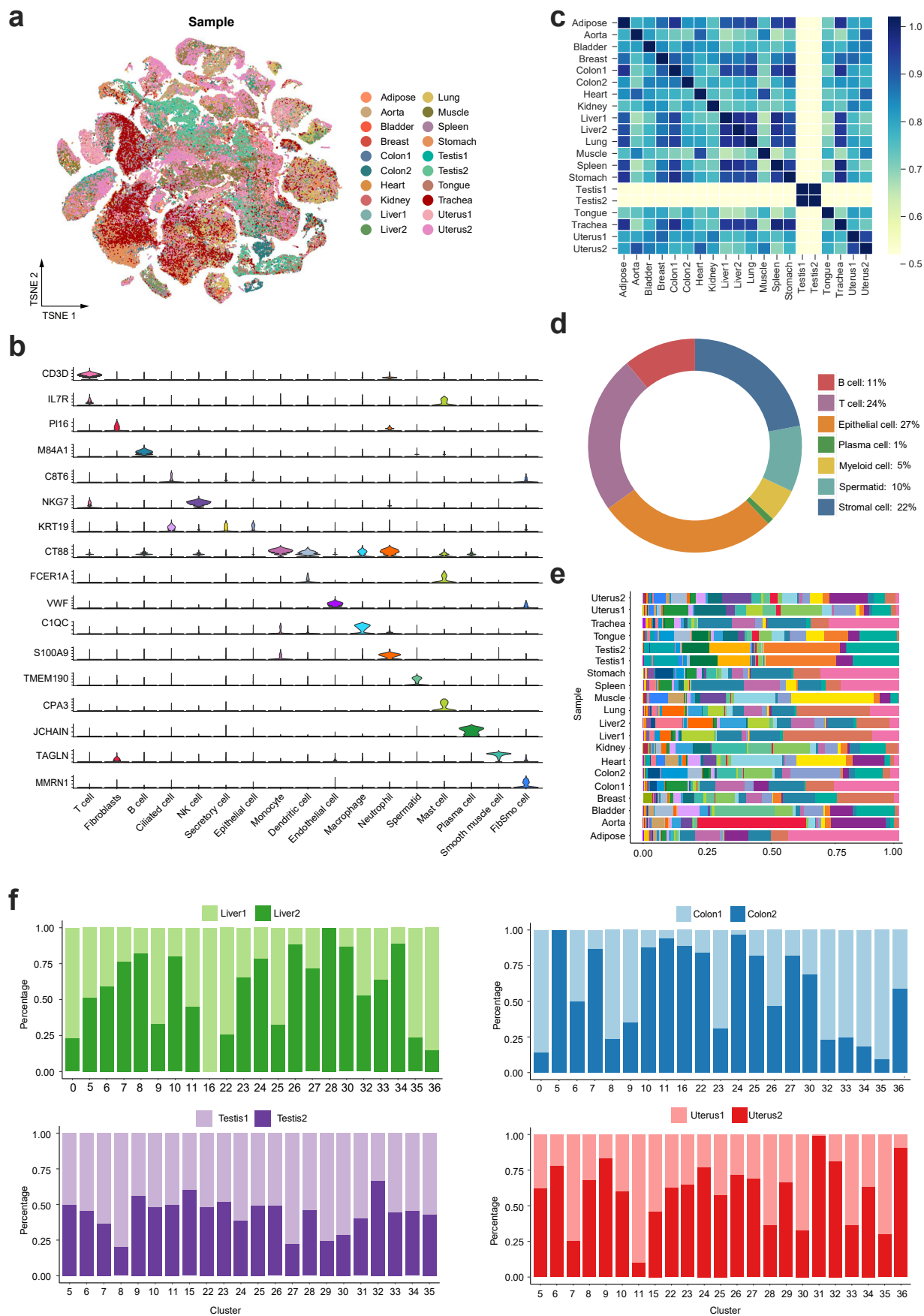


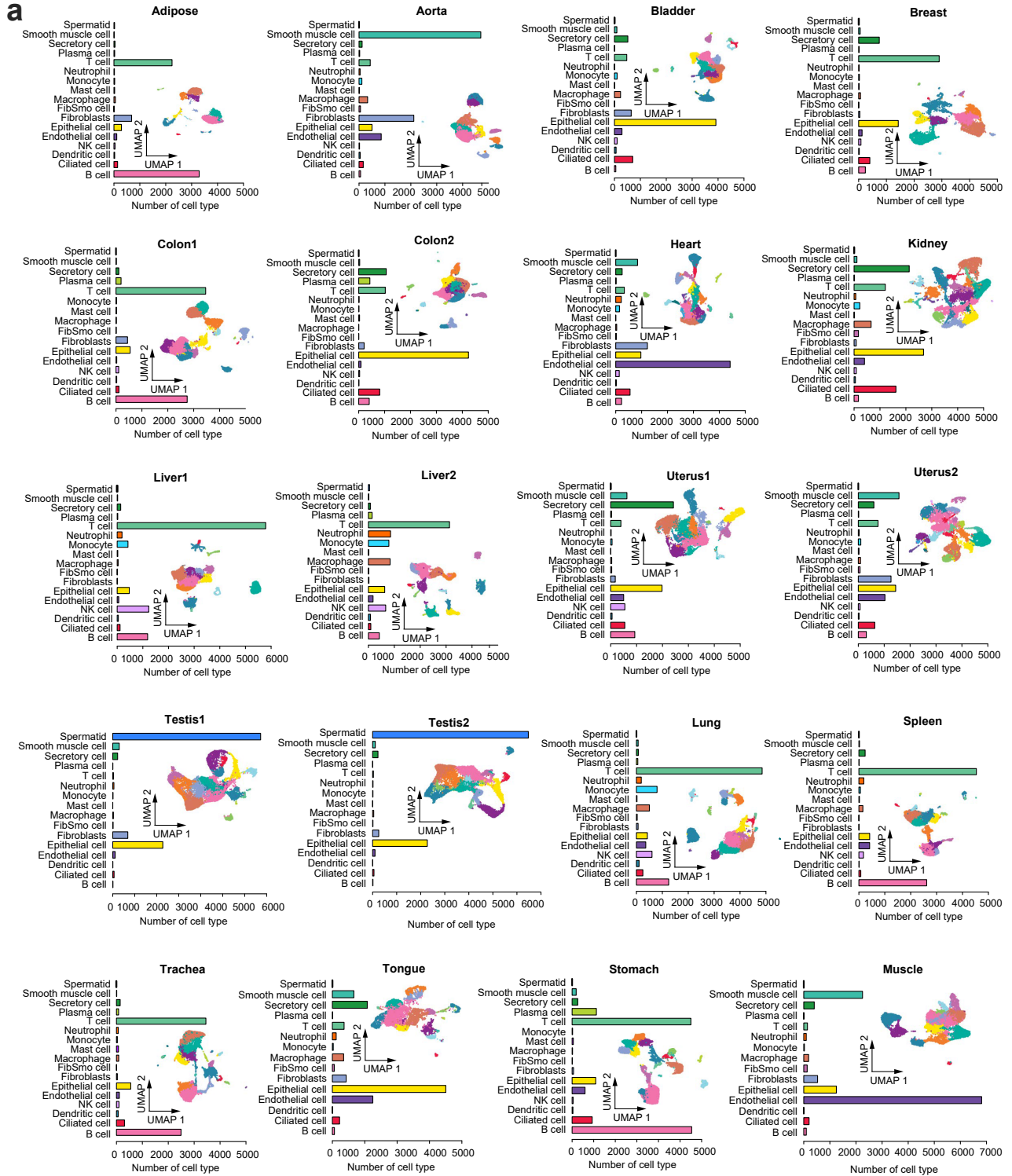
Supplementary Figures



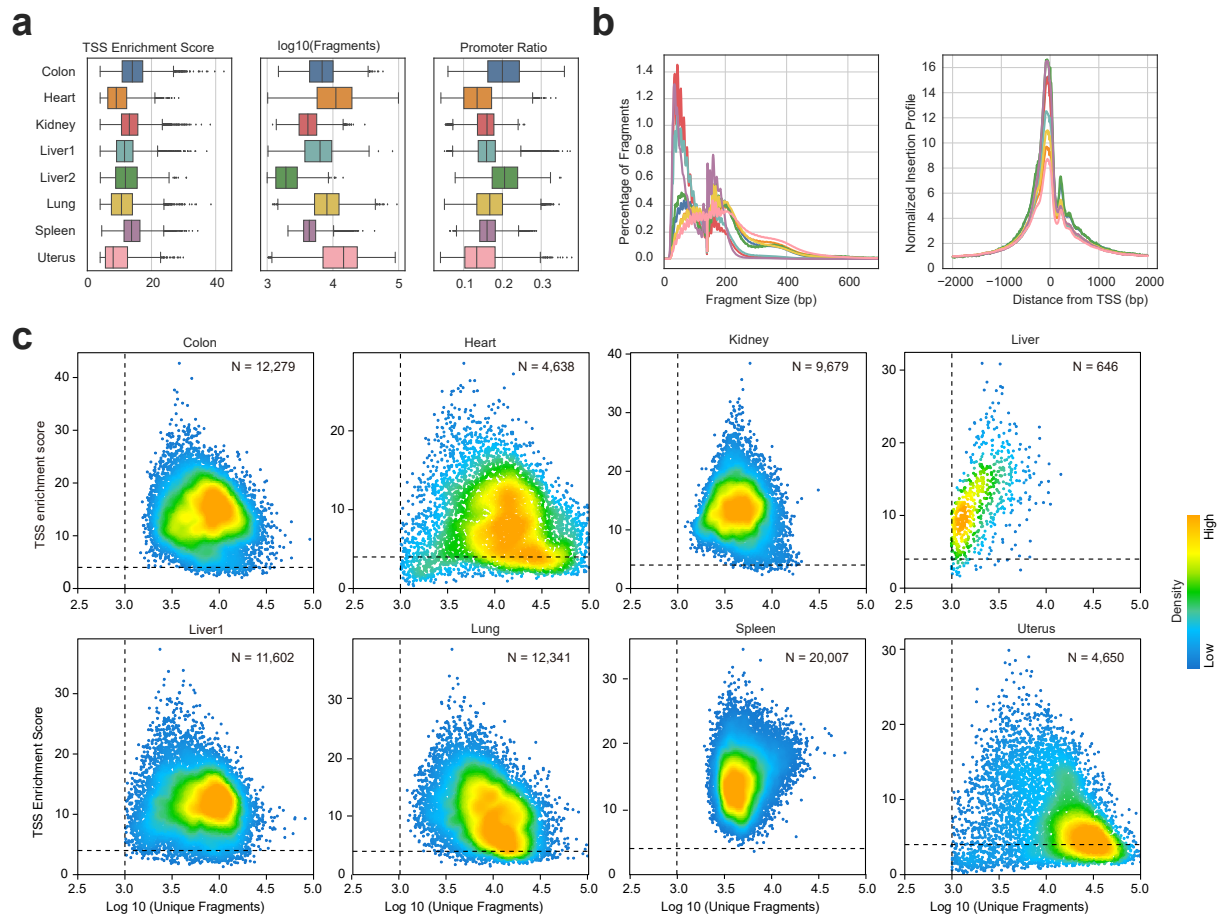
Supplementary Fig. 1: Data quality of scRNA. Related to figure 1. a-b Box plot showing the number of UMIs and genes in major cell types respectively. c-d Bar plot showing the number of cells in major cell types and in samples.



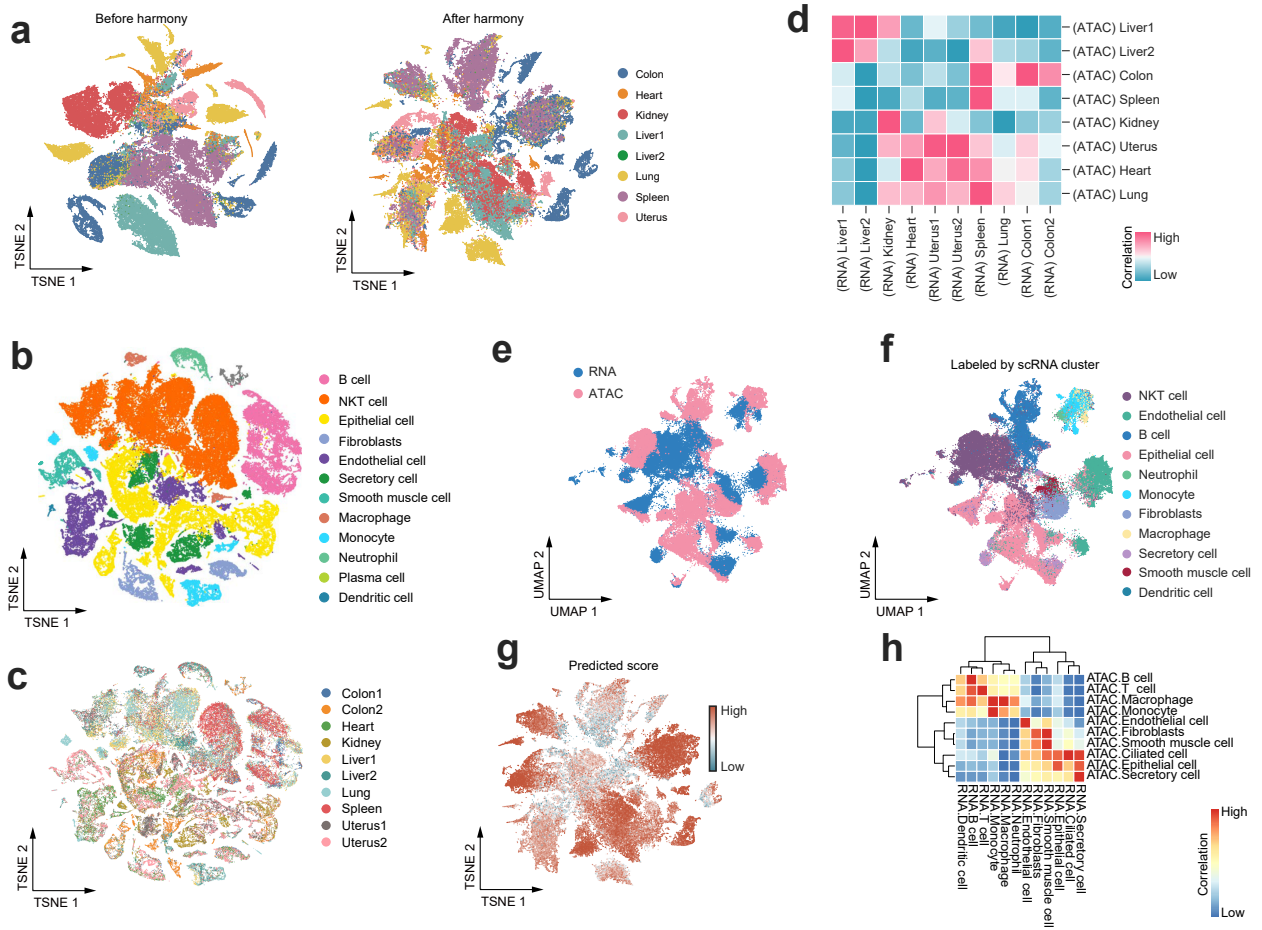
Supplementary Fig. 2: Data quality of scRNA. Related to figure 1. a Distribution of 20 samples of cells on the tSNE. b Violin diagram showing the expression of marker genes in major cell types. c Heatmap showing correlation of highly expressed genes in 20 samples. d Circle diagram showing the cell proportions of seven cell types. e Bar plot showing the percentage of cells in each sample. f Bar Plot showing the proportion of cells in different clusters from repeated samples of liver, colon, testis and uterus.



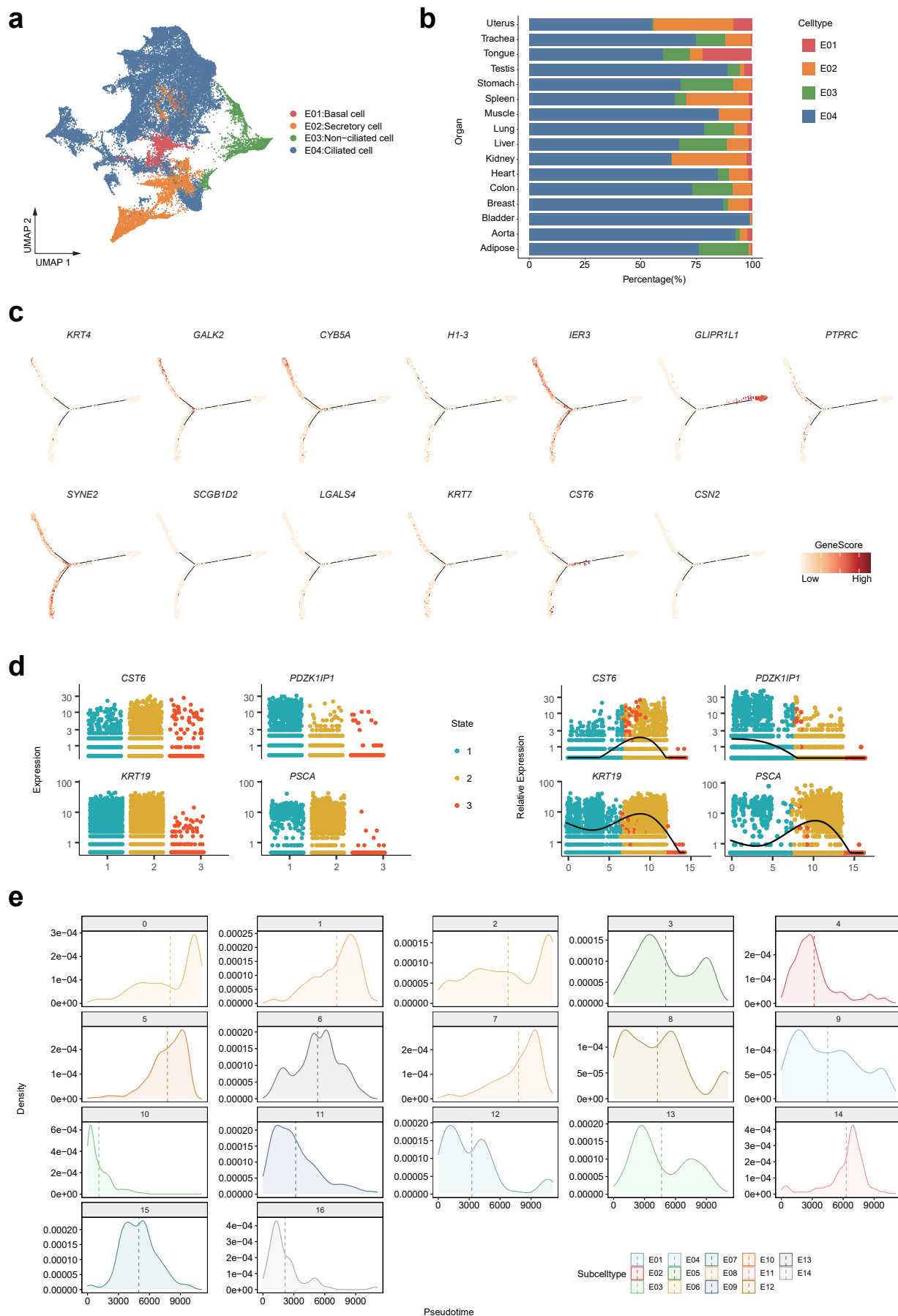
Supplementary Fig. 3: The UMAPs of all organs and bar plots of the proportion of different cell types (scRNA). Related to figure 1. a Distribution of different clusters on the UMAP in 20 samples, and bar plot shows the cell proportion of 20 samples of major cell types.



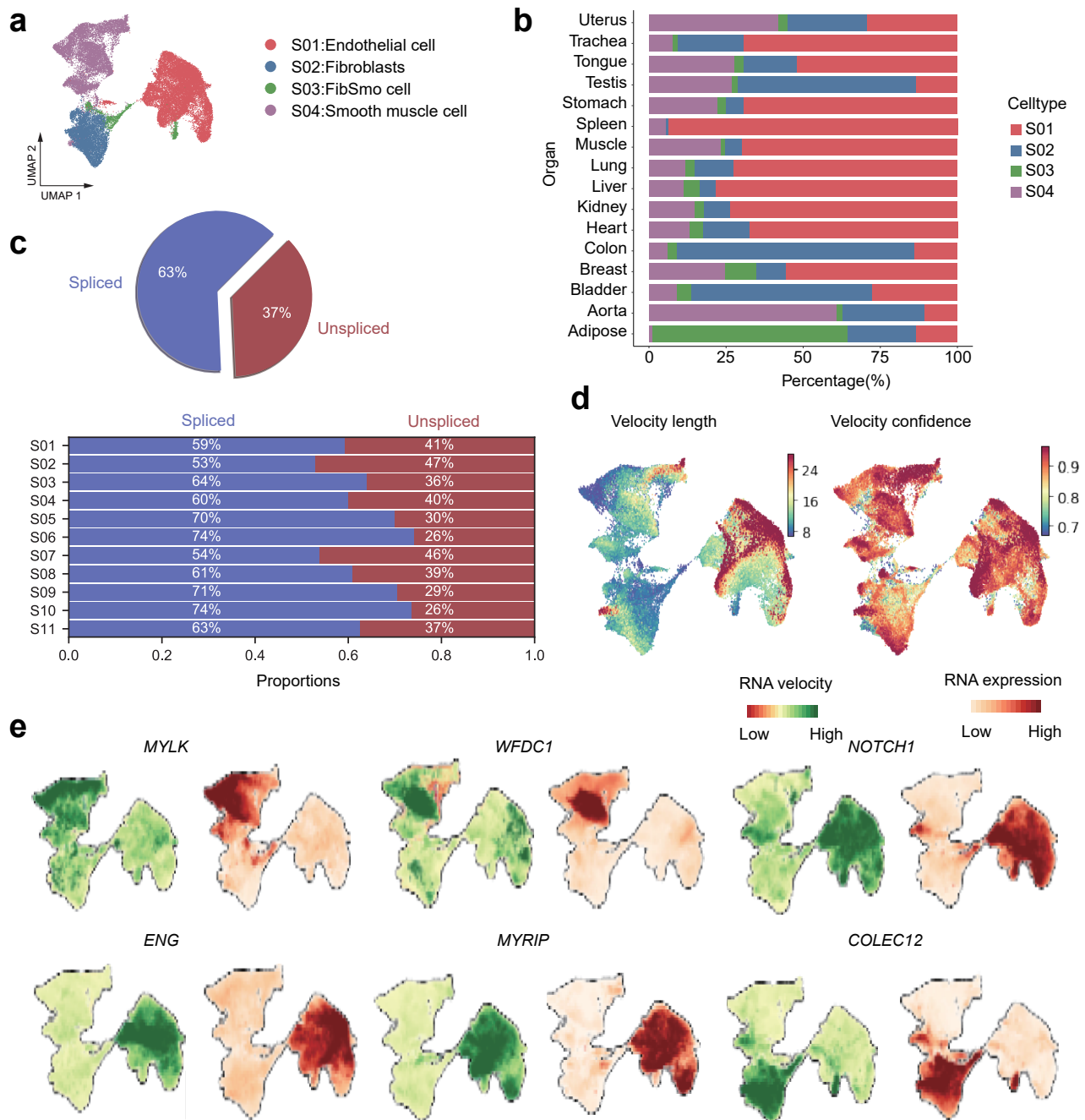
Supplementary Fig. 4: Data quality of scATAC. Related to figure 1. a Box plot showing the distribution of TSS enrichment score, number of fragments and promoter ratio across eight samples. Each dot represents a cell. b Fragment size distributions of eight samples (left). Aggregate TSS insertion profiles centred at all TSS regions. The showing cells are passing ArchR QC thresholds for each sample (right). The line colour matches the one in a. c Scatter plot showing the TSS enrichment score vs unique nuclear fragments per cell. The colour of the dots represents the density of each point in the plot.



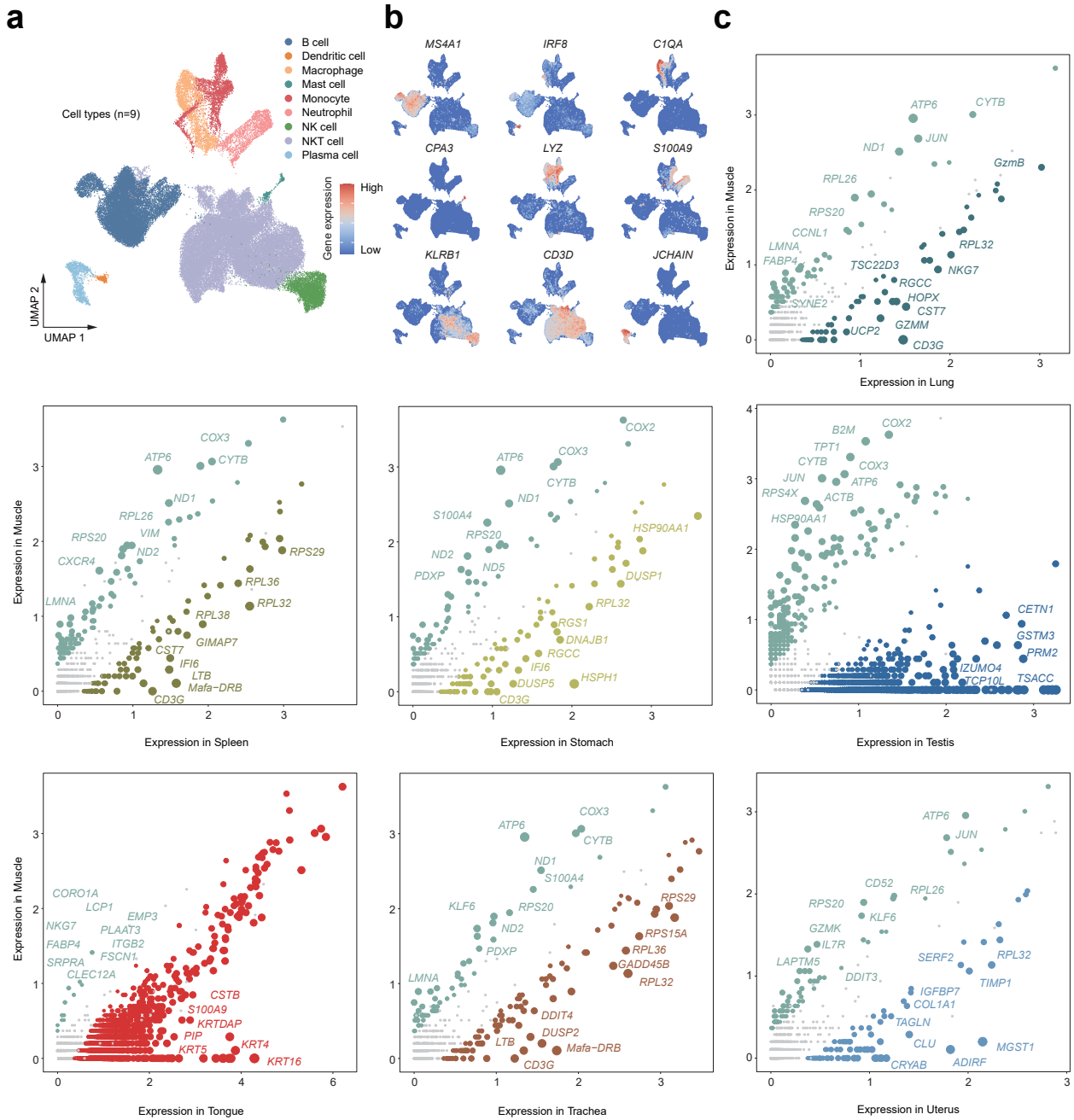
Supplementary Fig. 5: Data quality of scATAC. Related to figure 1. a (left) TSNE of ArchR iterative LSI and (right) ArchR iterative LSI with Harmony-based batch correction for all samples. b TSNE embedding showing the subset of seven organs from scRNA-seq. Colored by cell type in Fig.1b. c TSNE embedding showing the subset of seven organs from scRNA-seq. Colored by organ. d Heatmap showing the spearman correlations between scATAC-seq and scRNA-seq samples. Correlations are calculated from the top 5,000 expressed genes for each sample. e UMAP co-embedding of scATAC-seq and scRNA-seq cell. 40,000 cells with scATAC-seq and scRNA-seq were sampled according to the percentage of cell types. f Co-embedded cells colored by scRNA-seq cell-type annotations. g Scatter plot showing the predicted score distribution for scATAC-seq and scRNA-seq integration. h Heatmap showing the spearman correlations between scATAC-seq and scRNA-seq cell types. Correlations are calculated from the top 3,000 expressed genes for each cell type.



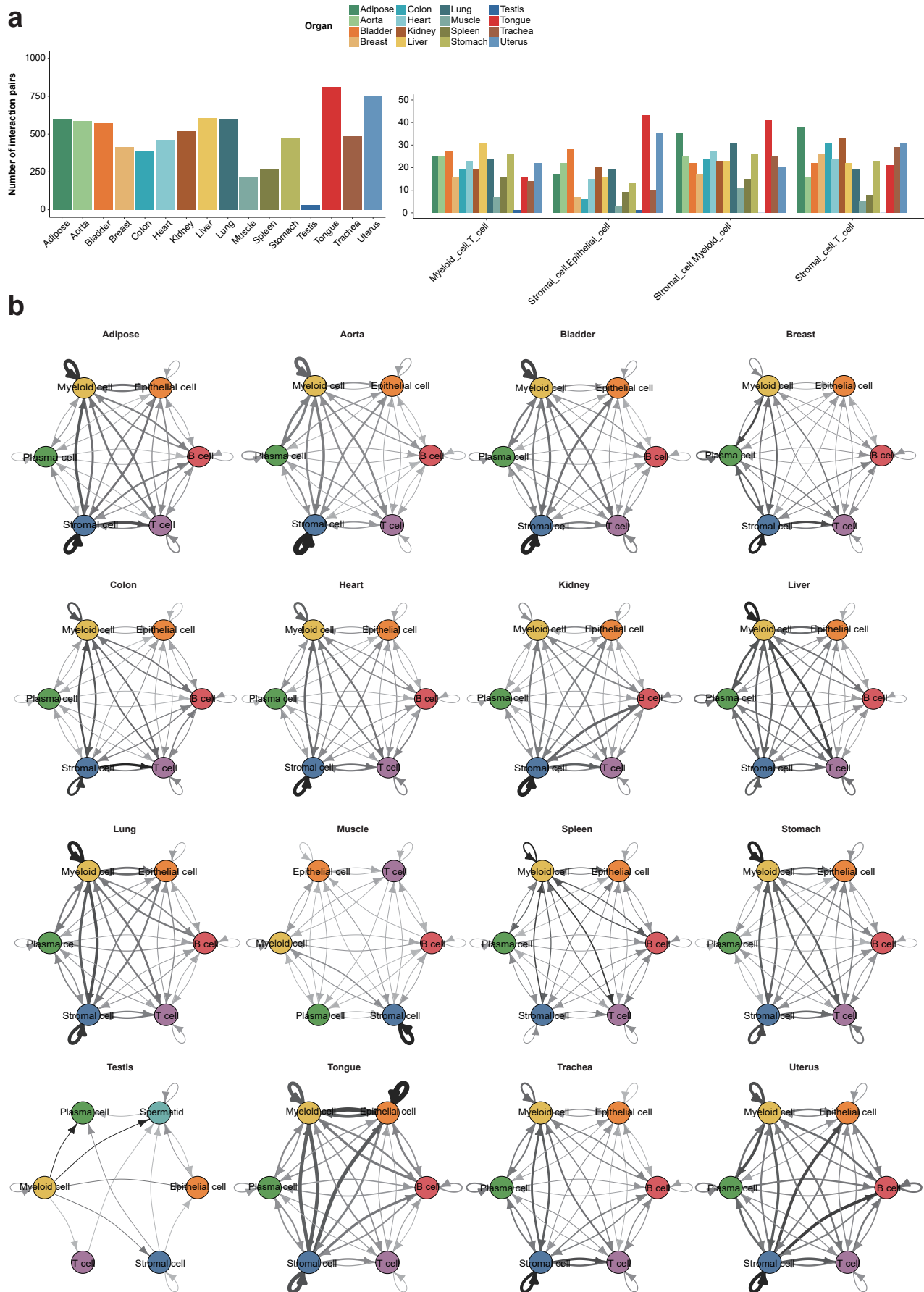
Supplementary Fig. 6: Pseudotime trajectory analysis by monocle2. Related to figure 2. a Distribution of 4 epithelial cell subtypes on the UMAP. b Bar plot showing the percentage of cell subtypes in each organ. c Distribution of marker genes on branches during pseudotime differentiation trajectory. The shade of the color represents high or low gene scores. d Fitting curve showing the dynamic expression levels of CST6, PDZK1IP1, KRT19, PSCA in cell states. The dots represent the distribution of cells along pseudotime. e Diagrams showing the density distribution of 14 cell subtypes (16 clusters) during pseudotime differentiation trajectory.



Supplementary Fig. 7: Pseudotime trajectory analysis by RNA velocity. Related to figure 3. a Distribution of 4 stromal cell subtypes on the UMAP. b Bar plot showing the percentage of cell subtypes in each organ. c Pie chart showing the proportion of stromal cells that are spliced versus un-spliced. Bar plot showing the proportion of stromal cell subtypes that are spliced versus un-spliced. d UMAPs diagram showing the velocity length and velocity confidence of stromal cells by RNA Velocity analysis. e Distribution of marker genes on the UMAPs by running RNA Velocity.

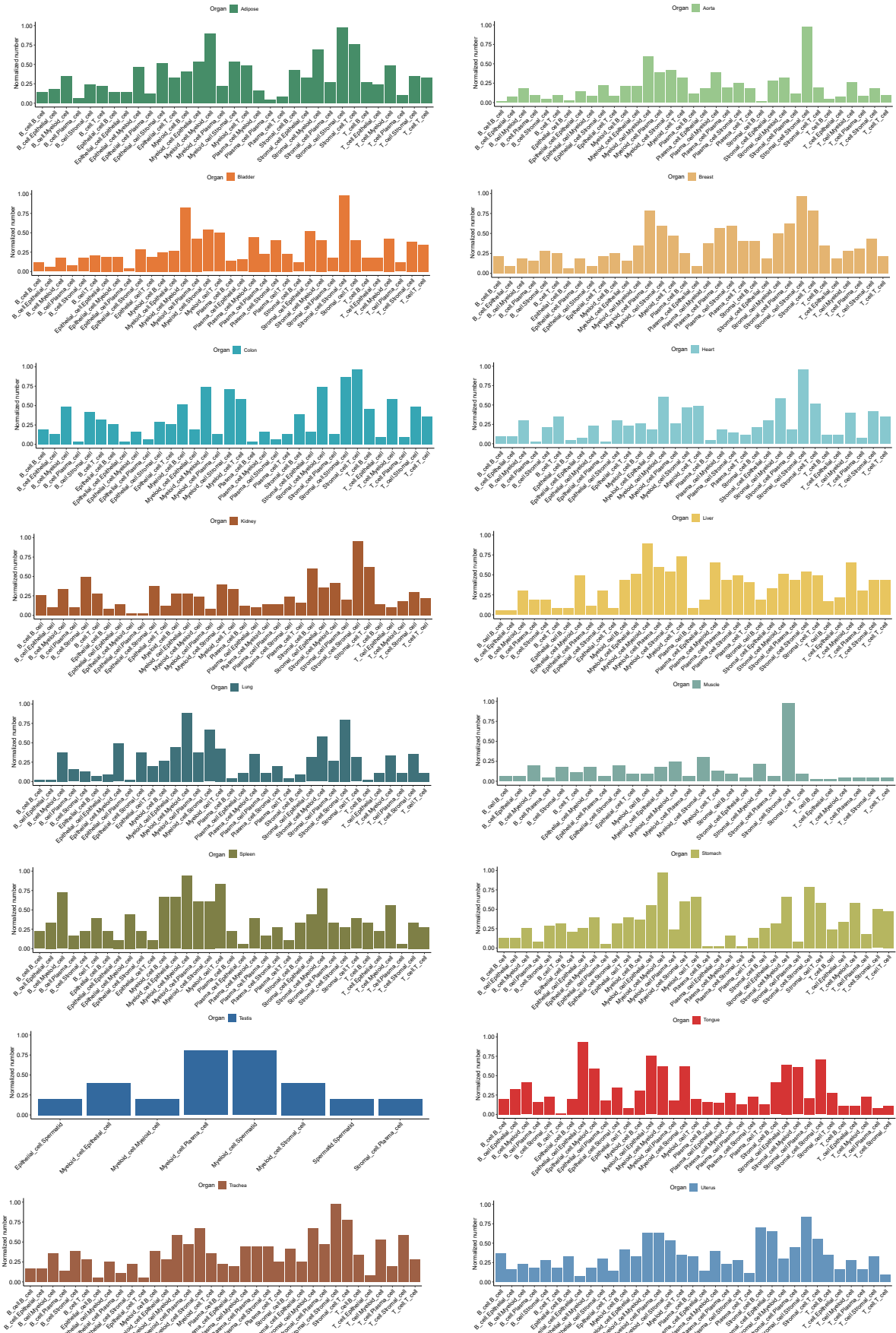


Supplementary Fig. 8: DEGs analysis of immune cell subsets. Related to figure 4. a Distribution of 9 immune cell subtypes on the UMAP. b Feature Plot showing the expression of marker genes. c Scatter plots shows pairings of gene expression between muscle and other organs. Each point represents a DEG, and its size is proportionate to the fold change.

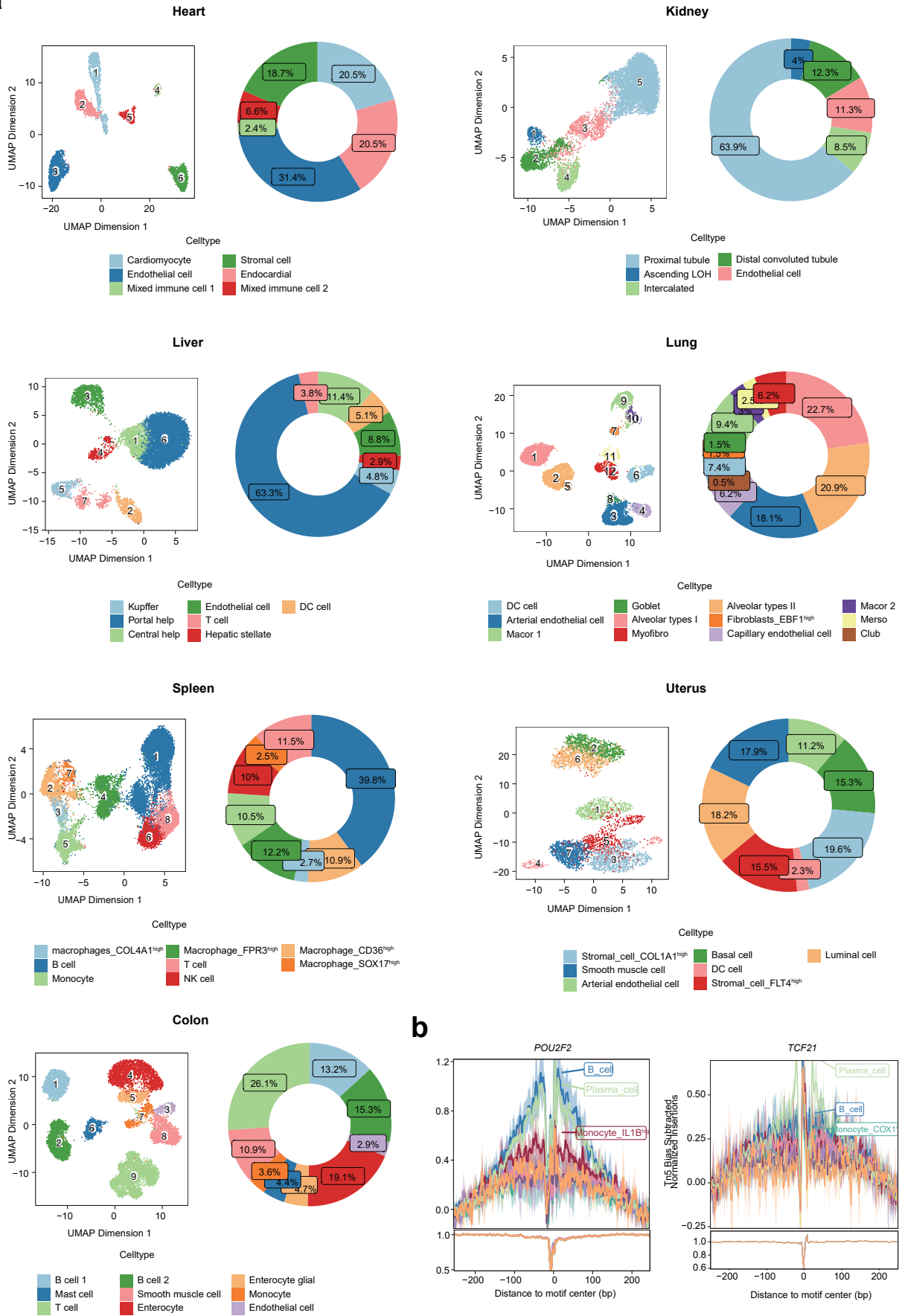


Supplementary Fig. 9: Cell-cell interactions and network diagram. Related to figure 5. a Bar chart showing the number of interaction pairs in 16 organs (left). Bar chart showing the number of interaction pairs among four cell interaction types (Fig 6d) in 16 organs (right). b Network diagram showing cell-cell interactions among major cell types in 16 organs. Line thickness represents the strength of cell-cell interaction.

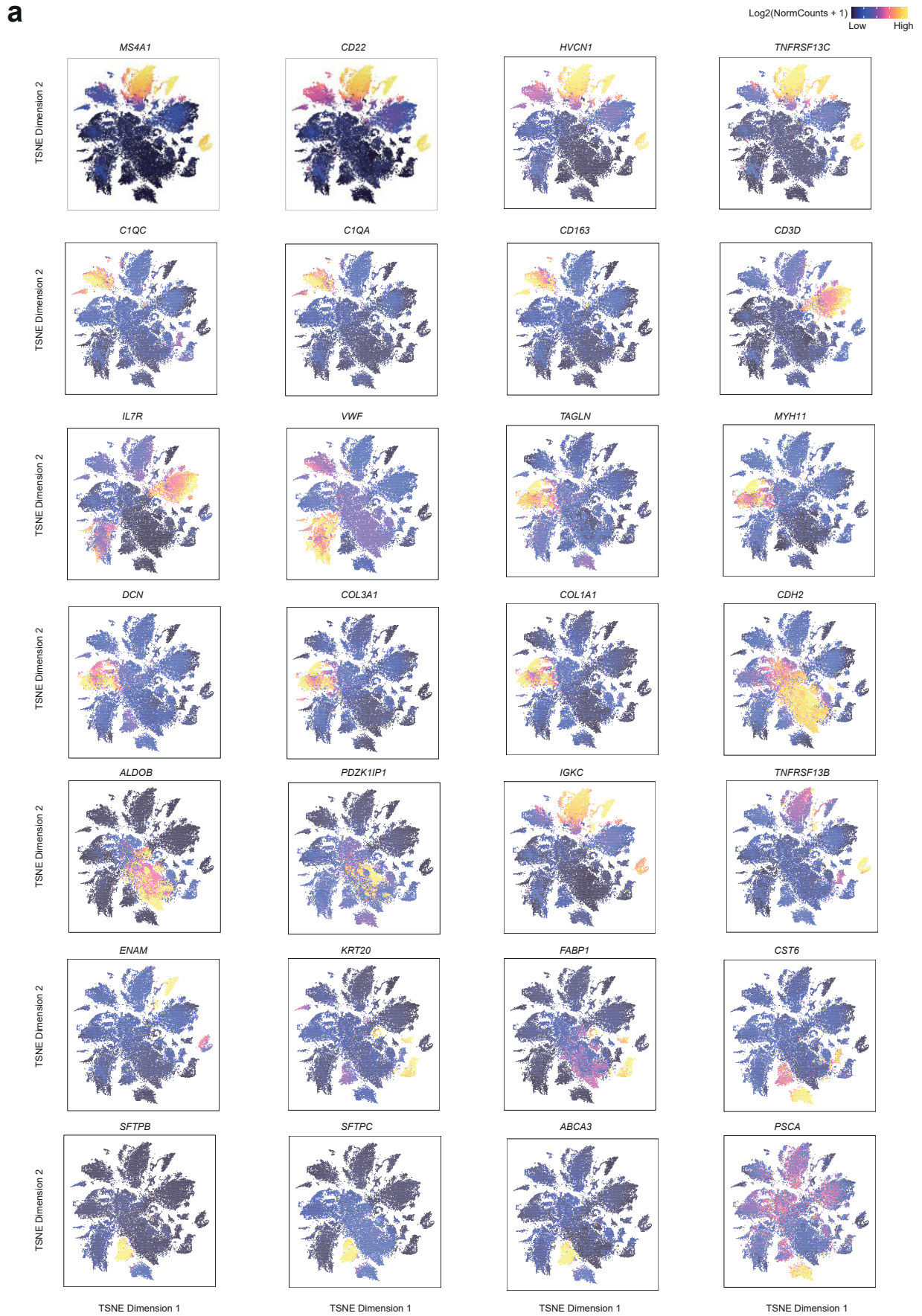
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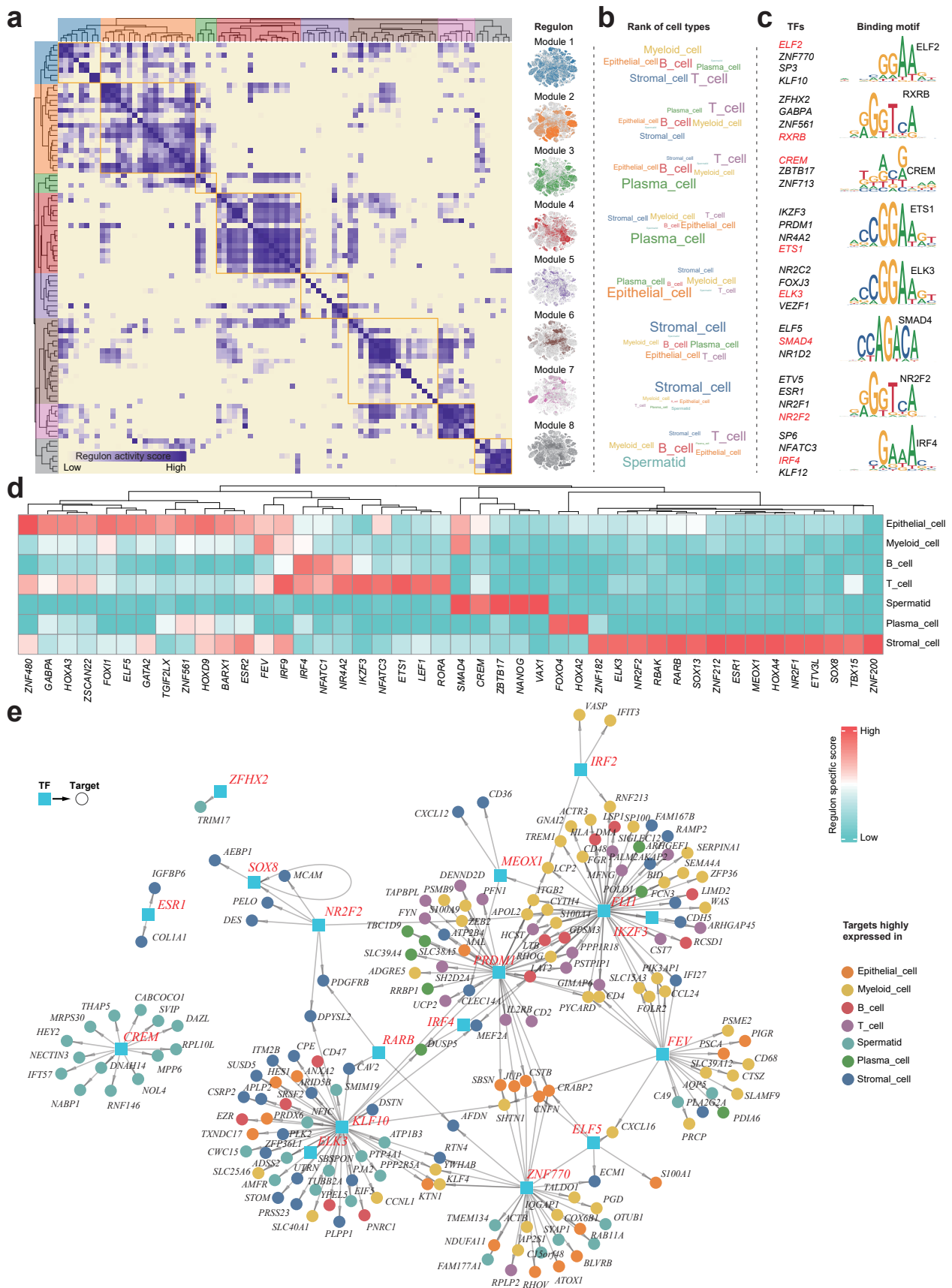
Supplementary Fig. 10: Cell-cell interactions. Related to figure 5. a Bar chart showing the normalized number of interaction pairs of different cell-cell interaction types in 16 organs.

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Supplementary Fig. 11: The UMAPs of all organs and Donut charts of the proportion of different cell types (scATAC). Related to figure 6. a Distribution of different clusters on the UMAP in 7 organs (scATAC-seq), and donut chart shows the cell proportion of 7 organs of cell types. b Tn5 bias-adjusted TF footprint analysis of the POU2F2 and TCF21 transcription factors.

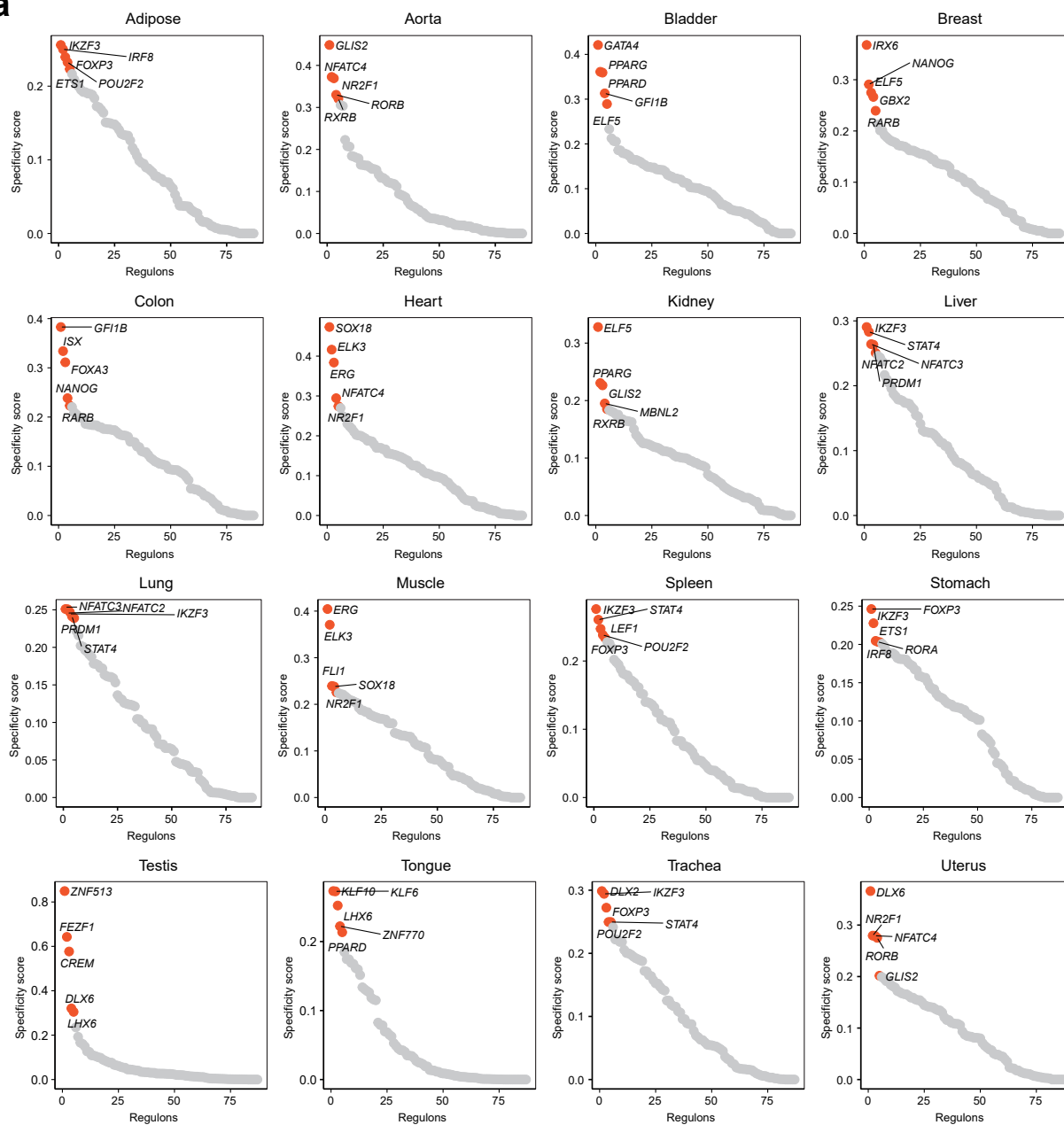


Supplementary Fig. 12: The TSNEs of marker genes expression (scATAC). Related to figure 6. a Distribution of marker genes in cell types such as B cells (MS4A1, CD22, HVCN1, TNFRSF13C, IGKC, TNFRSF13B, ENAM), macrophages (C1QC, C1QA, CD163), T cells (CD3D, IL7R), endothelial cells (VWF), fibroblasts (TAGLN, MYH11, DCN, COL3A1, COL1A1), secretory cells (CDH2, ALDOB, PDZK1IP1), epithelial cells (KRT20, FABP1) and ciliated cells (CST6, SFTPB, SFTPC, ABCA3, PSCA) on the TSNEs.

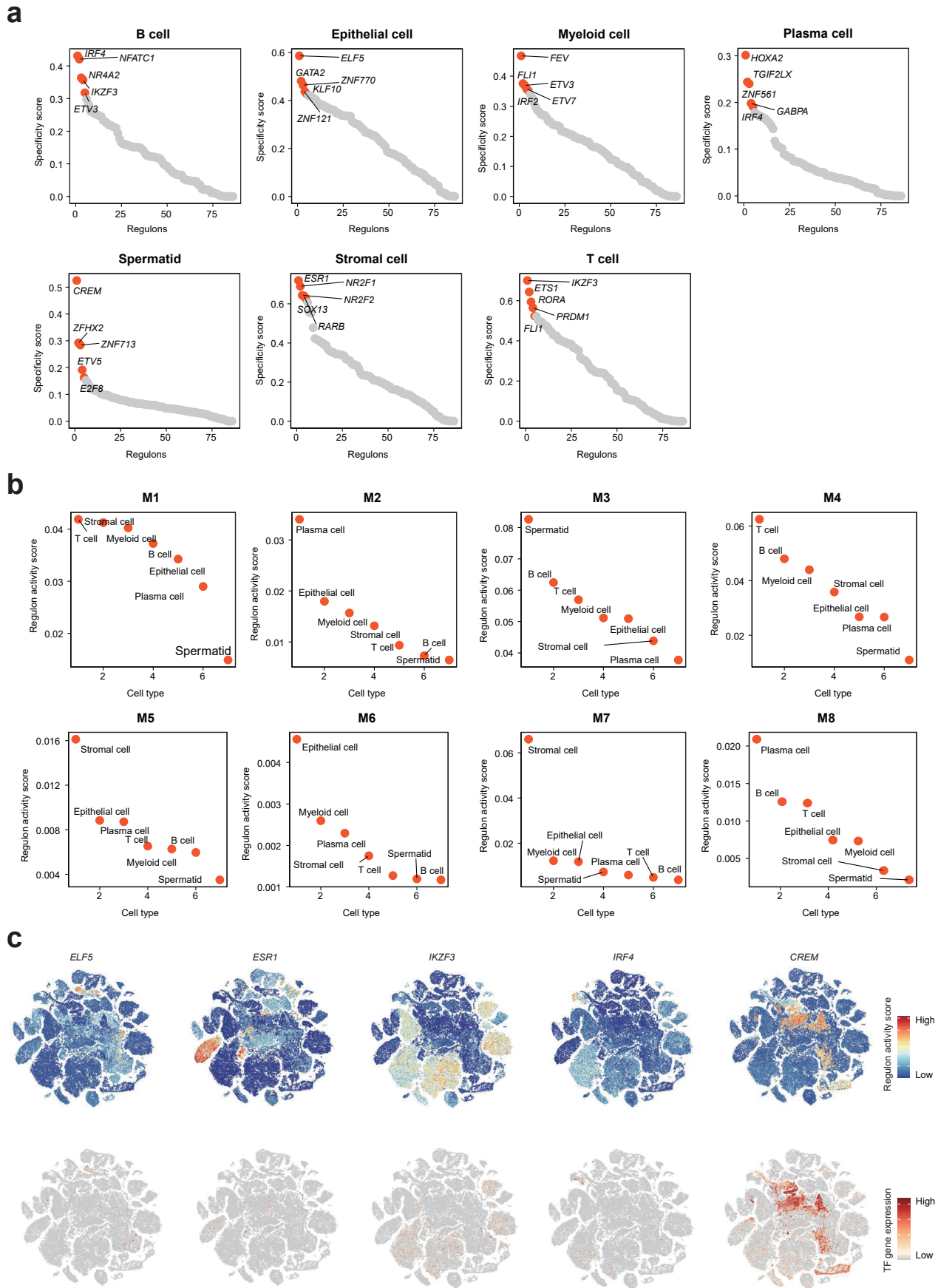


Supplementary Fig. 13: Transcriptional regulatory network of cells from cynomolgus monkey. Related to figure 7. a Identification of regulon modules using SCENIC. Heatmap (left) shows the similarity of different regulons ($n=86$) based on the AUCell score. Eight regulon modules were identified based on regulon similarity. UMAPs (right) illustrate the average AUCell score distribution for different regulon modules (in different colors). b Wordcloud plots shows enrichment of cell types in different regulon modules. c Representative transcription factors and corresponding binding motifs in different regulon modules. d Heatmap showing transcription factors enriched in different cell types. Color depth represents the level of regulon-specific score. e Integrated gene-regulatory networks of the regulons from (a). Regulon-associated TFs are highlighted in blue rectangles and target genes in circles. Target genes (in circles) are colored according to their highly expressed cell types.

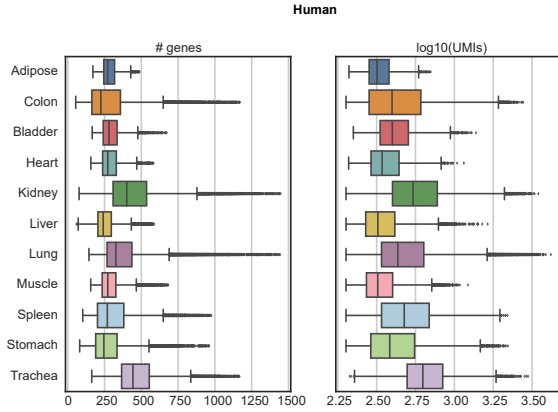
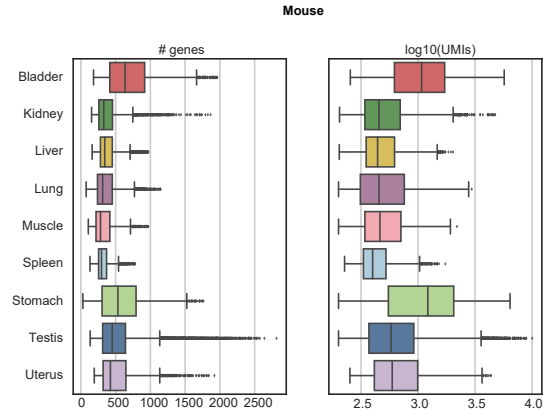
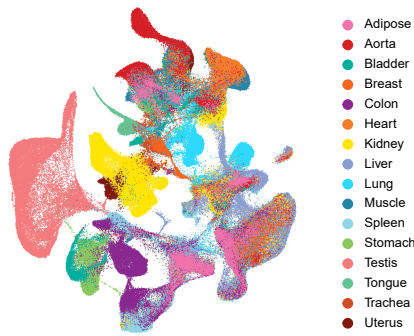
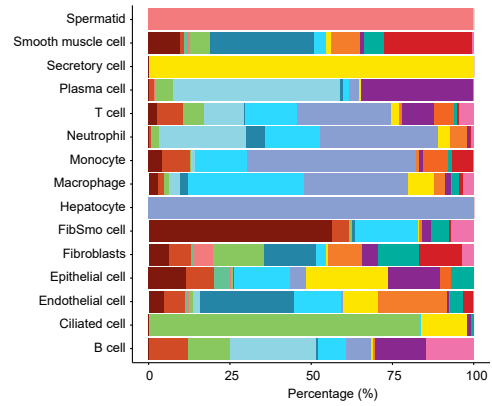
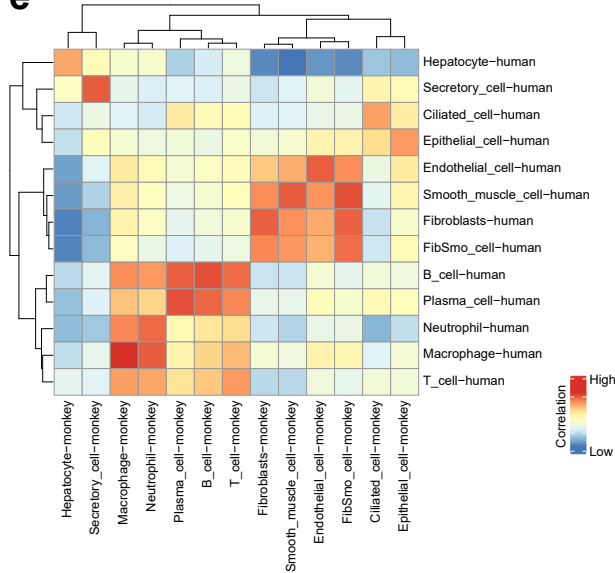
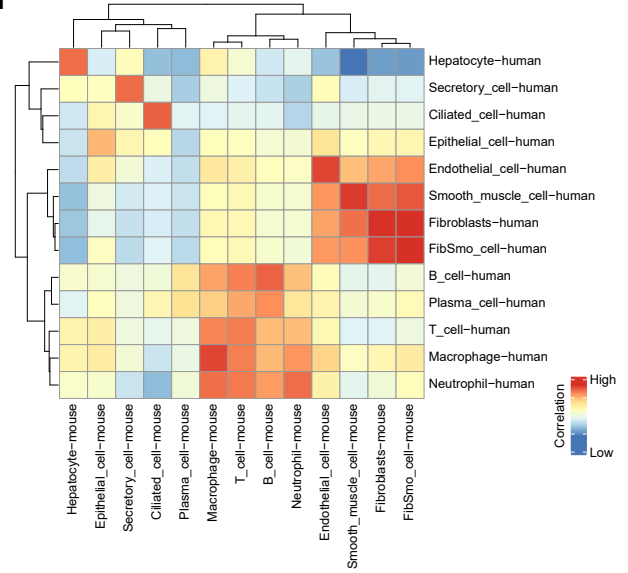
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Supplementary Fig. 14: Regulons and modules. Related to figure 7. a Scatter plot showing top regulons of 16 organs ordered by regulon specific score and red dots represent the highest activity.



Supplementary Fig. 15: Regulons and modules. Related to figure 7. a Scatter plot showing top regulons of 7 major cell types ordered by regulon specific score and red dots represent the highest activity. b Scatter plot showing major cell types of 8 regulon modules ordered by regulon activity score. c TSNEs displaying the AUCell score distribution for the selected regulons (above) and gene expression patterns for the corresponding TFs (below).

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Supplementary Fig. 16: Data quality across species. Related to figure 8. a Box plot showing the number of genes and UMIs in human organs. b Box plot showing the number of genes and UMIs in mouse organs. c Distribution of cynomolgus monkey, human and mouse cells by organs on the UMAP. d Bar plot showing the percentage of cell types in each organ. e Heatmap showing correlation of top gene expression in cell types in mouse and human (Spearman method). f Heatmap showing correlation of top genes expression in cell types cynomolgus monkey, and human (Spearman method).