

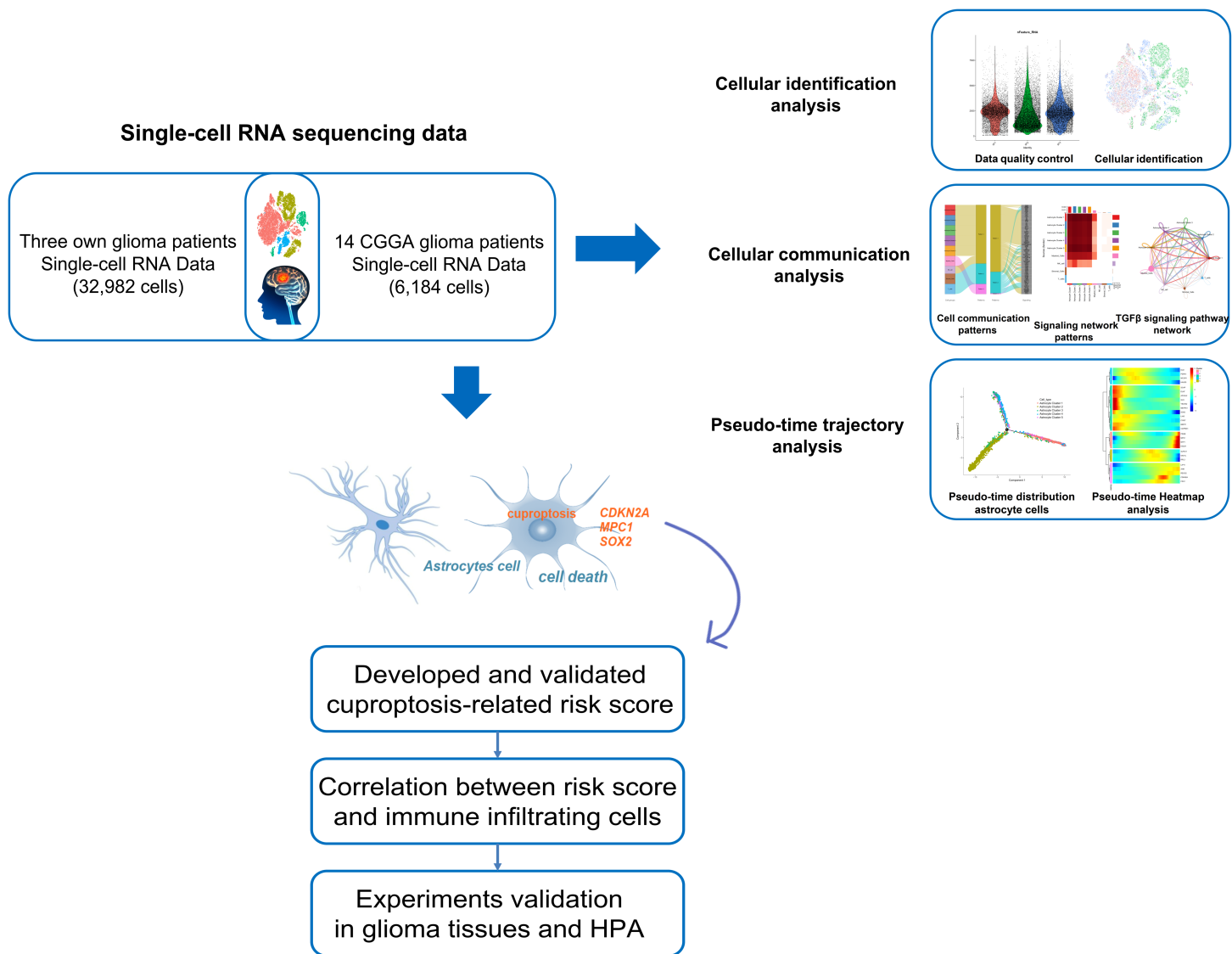


Figure S1. Flowchart of the research. CGGA, Chinese Glioma Genome Atlas; HPA, Human Protein Atlas.

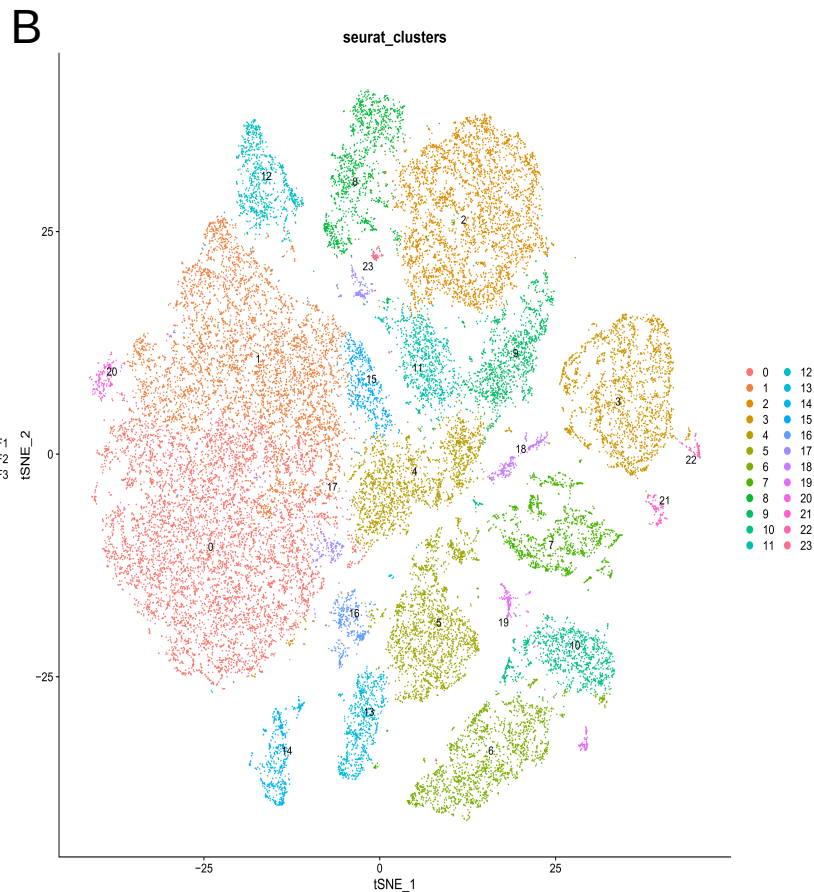
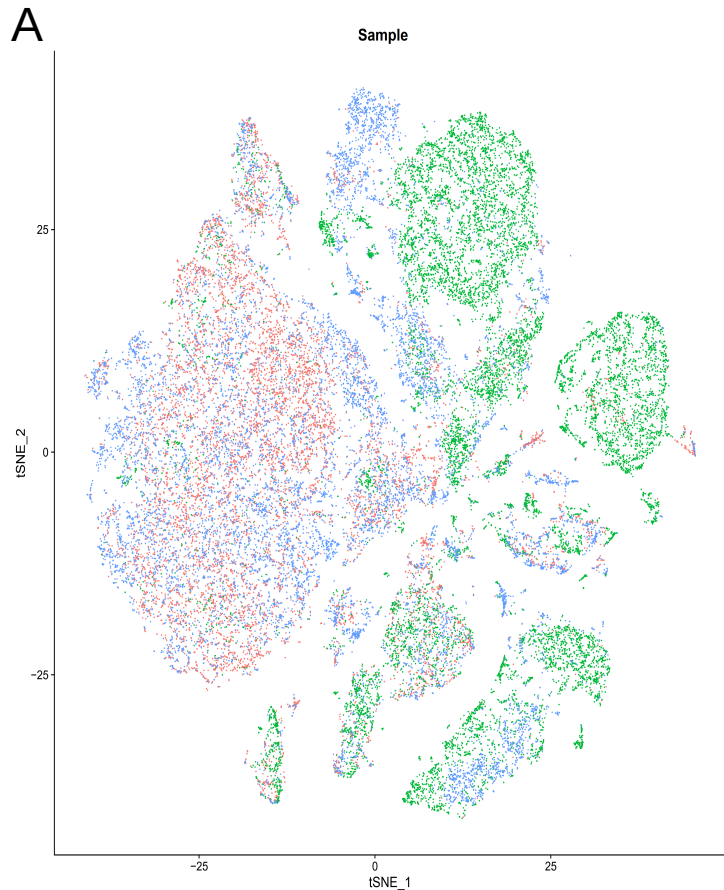


Figure S2. t-Distributed Stochastic Neighbor Embedding visualization of normalized glioma single-cell transcriptional profiles based on samples (A) and cell clusters (B) in our single-cell data.

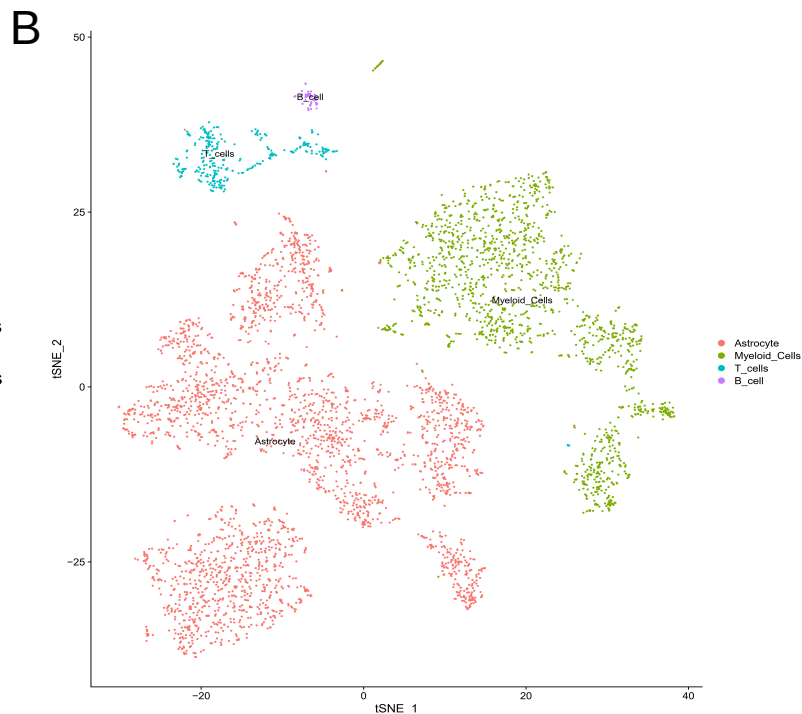
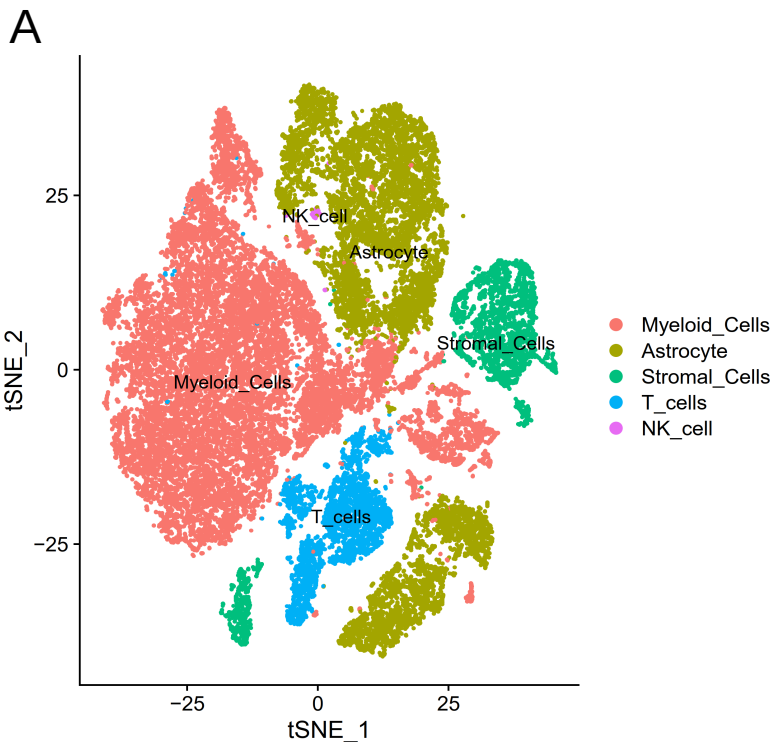
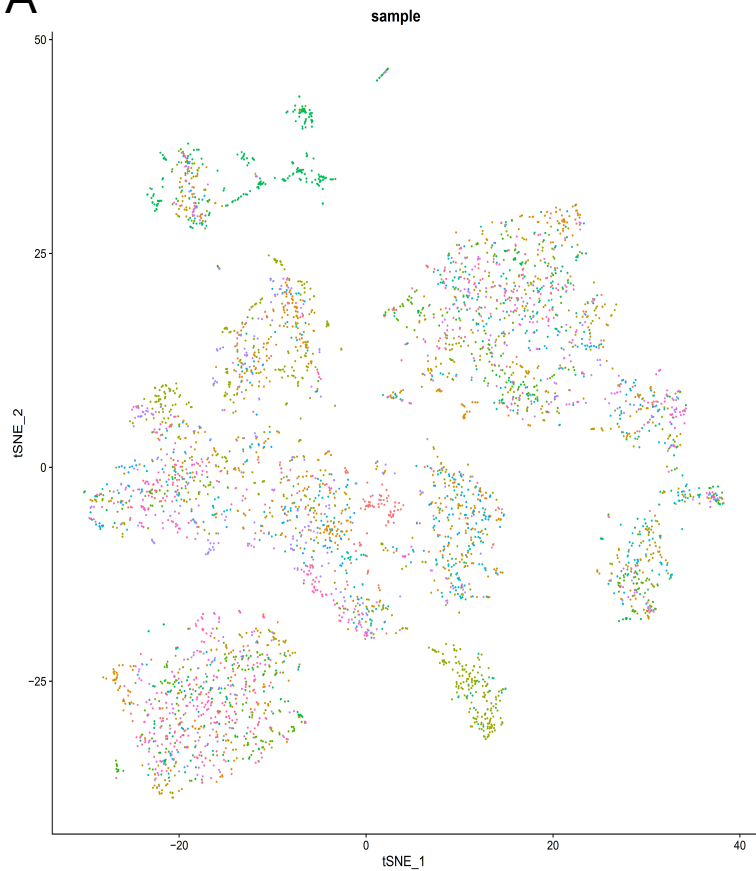


Figure S3. t-Distributed Stochastic Neighbor Embedding visualization of glioma single-cell transcriptional profiles based on cell subpopulations in our (A) and CGGA single-cell data (B). CGGA, Chinese Glioma Genome Atlas.

A



B

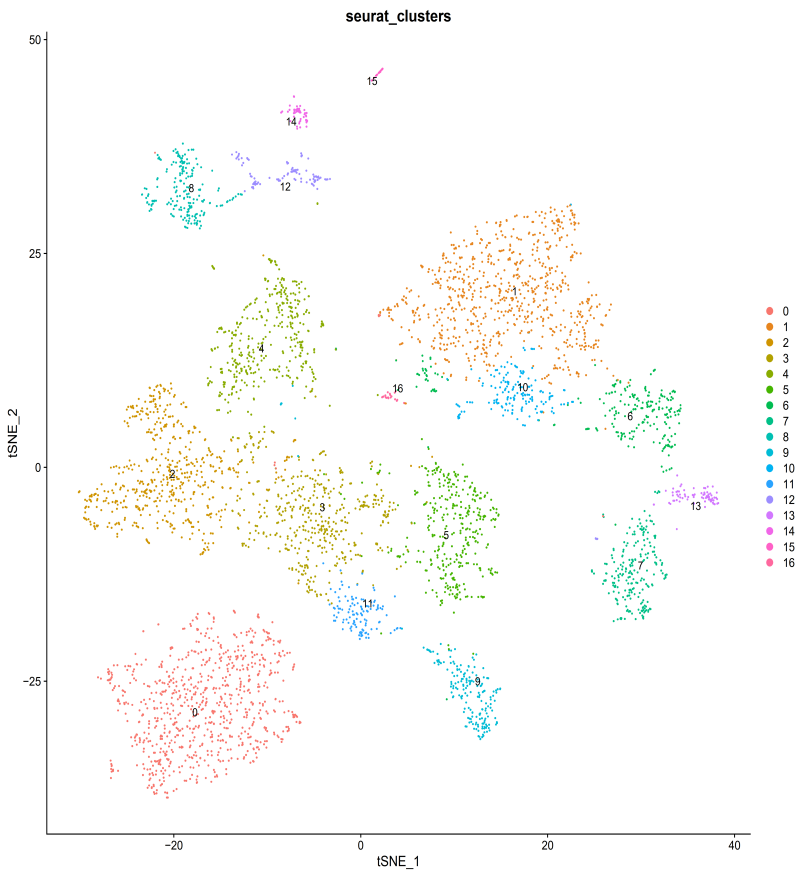
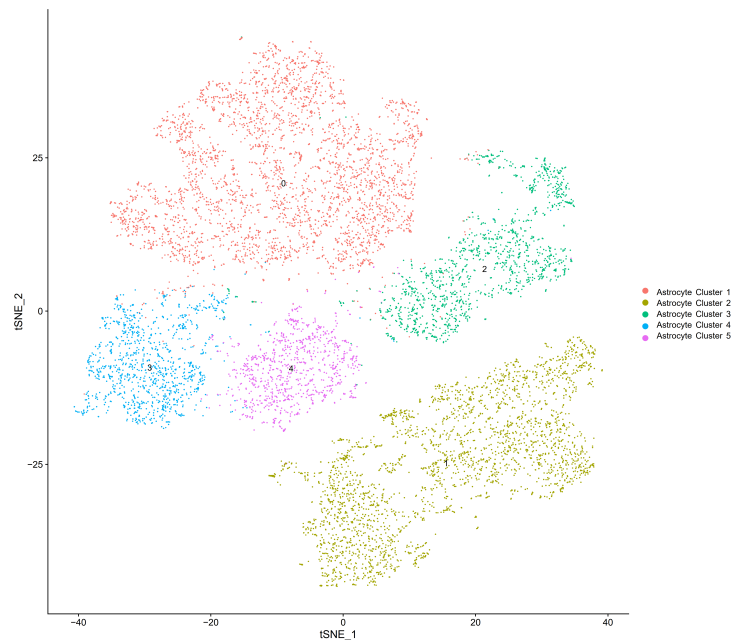


Figure S4. t-Distributed Stochastic Neighbor Embedding visualization of normalized glioma single-cell transcriptional profiles based on samples (A) and cell clusters (B) in CGGA single-cell data. CGGA, Chinese Glioma Genome Atlas.

A



B

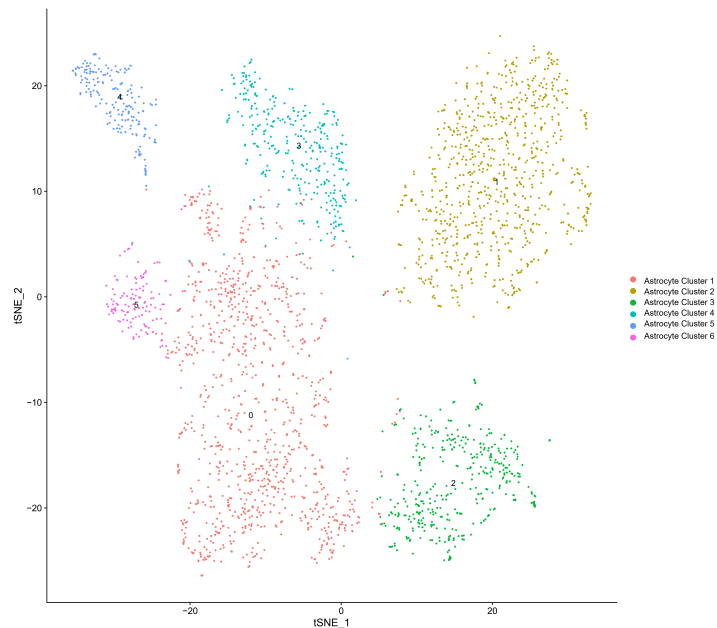


Figure S5. t-Distributed Stochastic Neighbor Embedding visualization of glioma single-cell transcriptional profiles based on astrocyte cell subpopulations in our data (A) and CGGA data (B). CGGA, Chinese Glioma Genome Atlas.

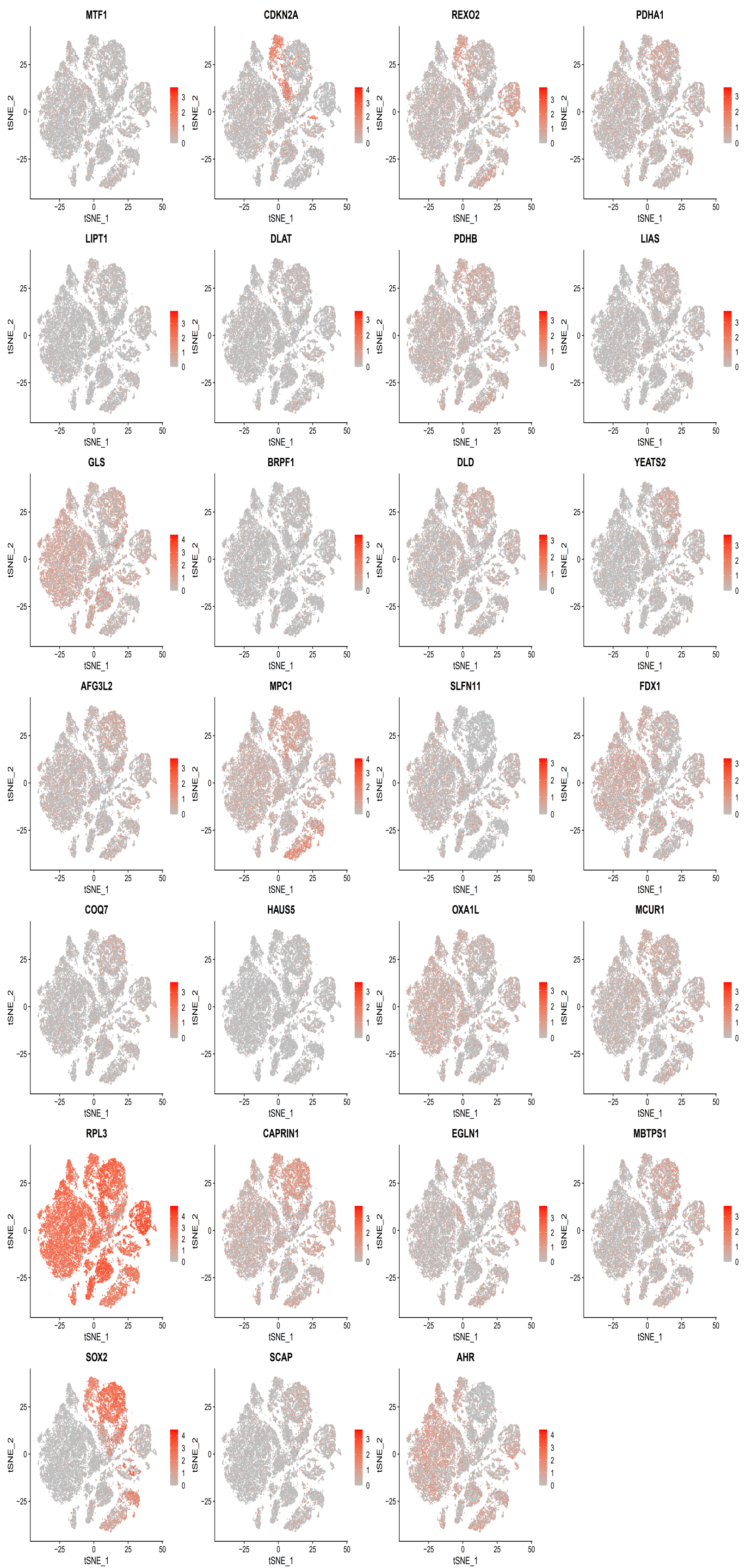


Figure S6. Scatter plot displaying the distribution of cell types in 27 cuproptosis-related genes.

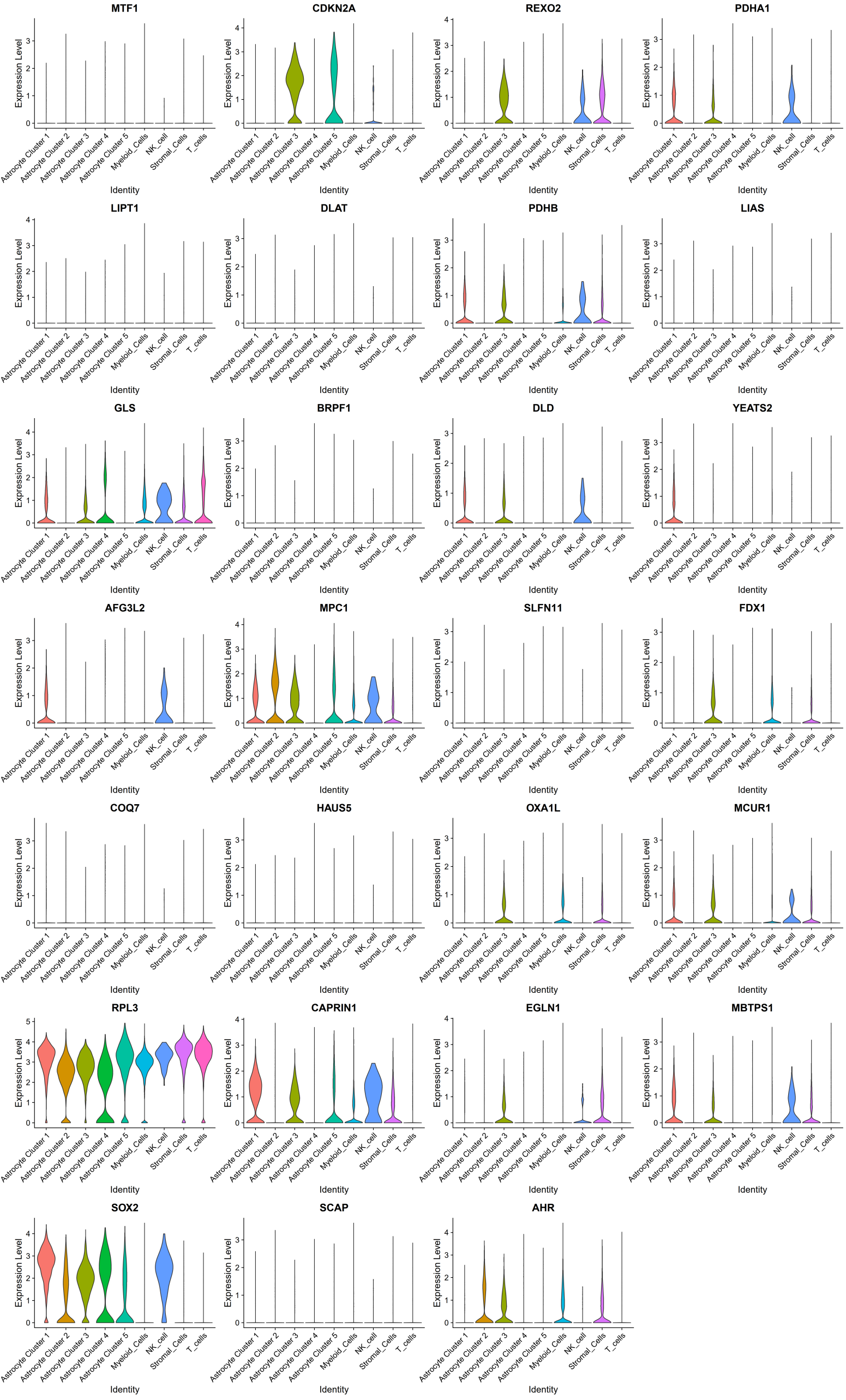
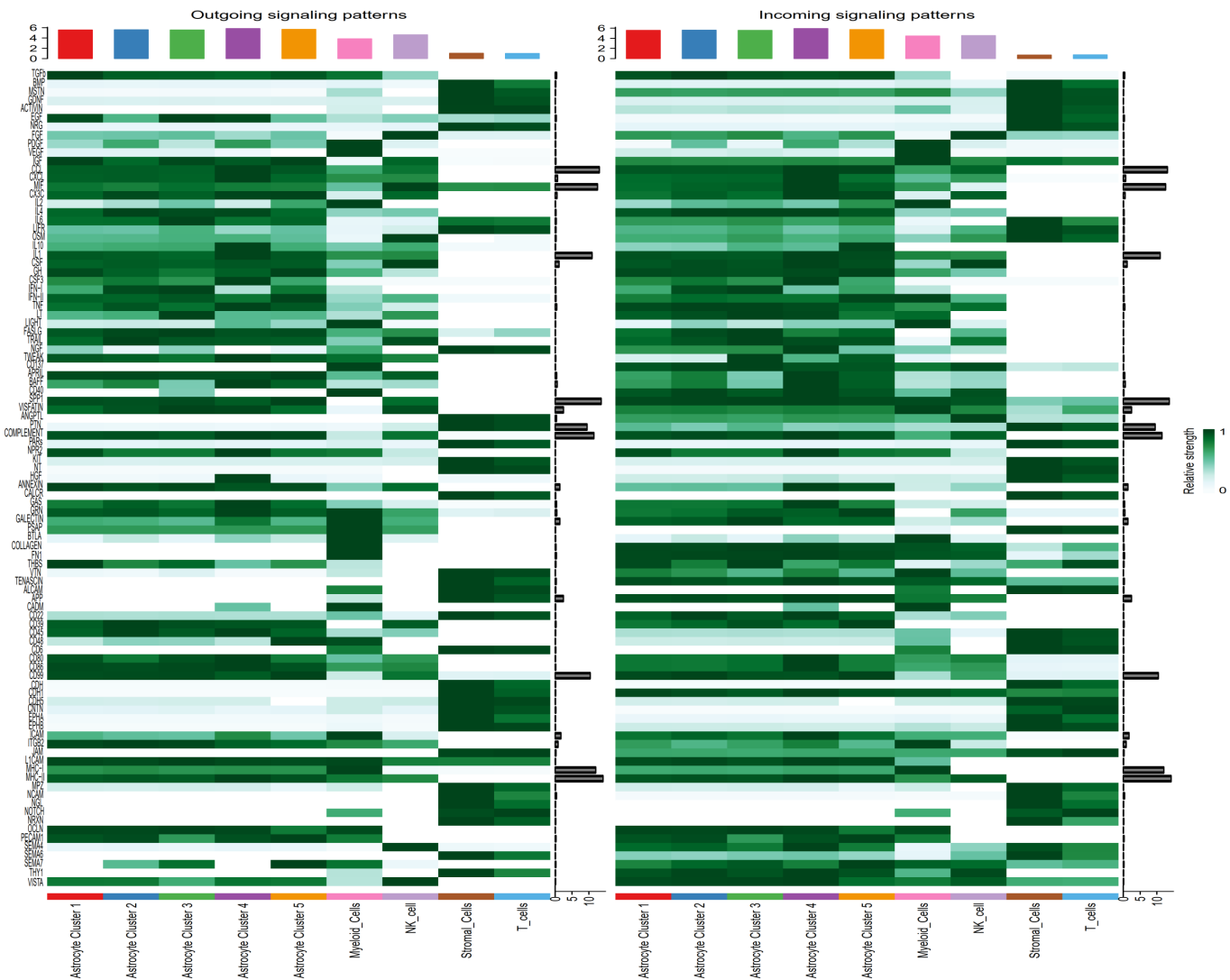
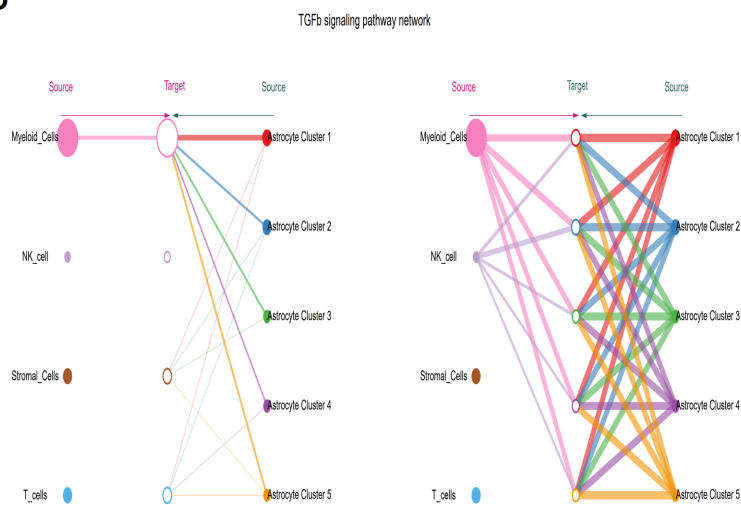


Figure S7. The expression levels of 27 cuproptosis-related genes in various cell subpopulations.

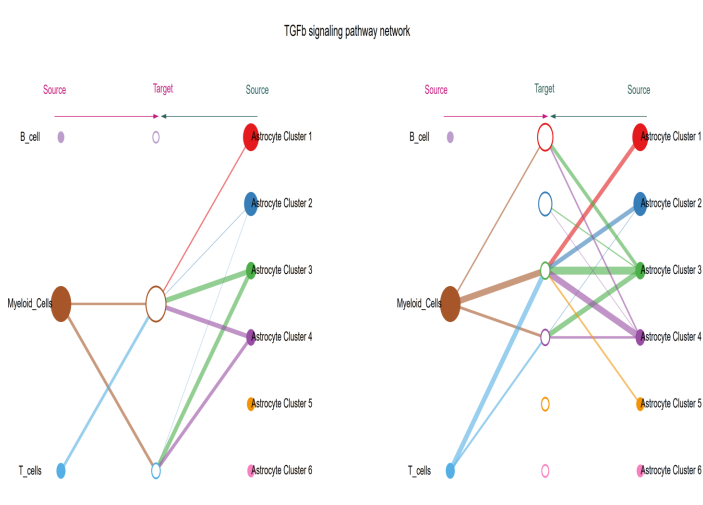
A



B



C



D

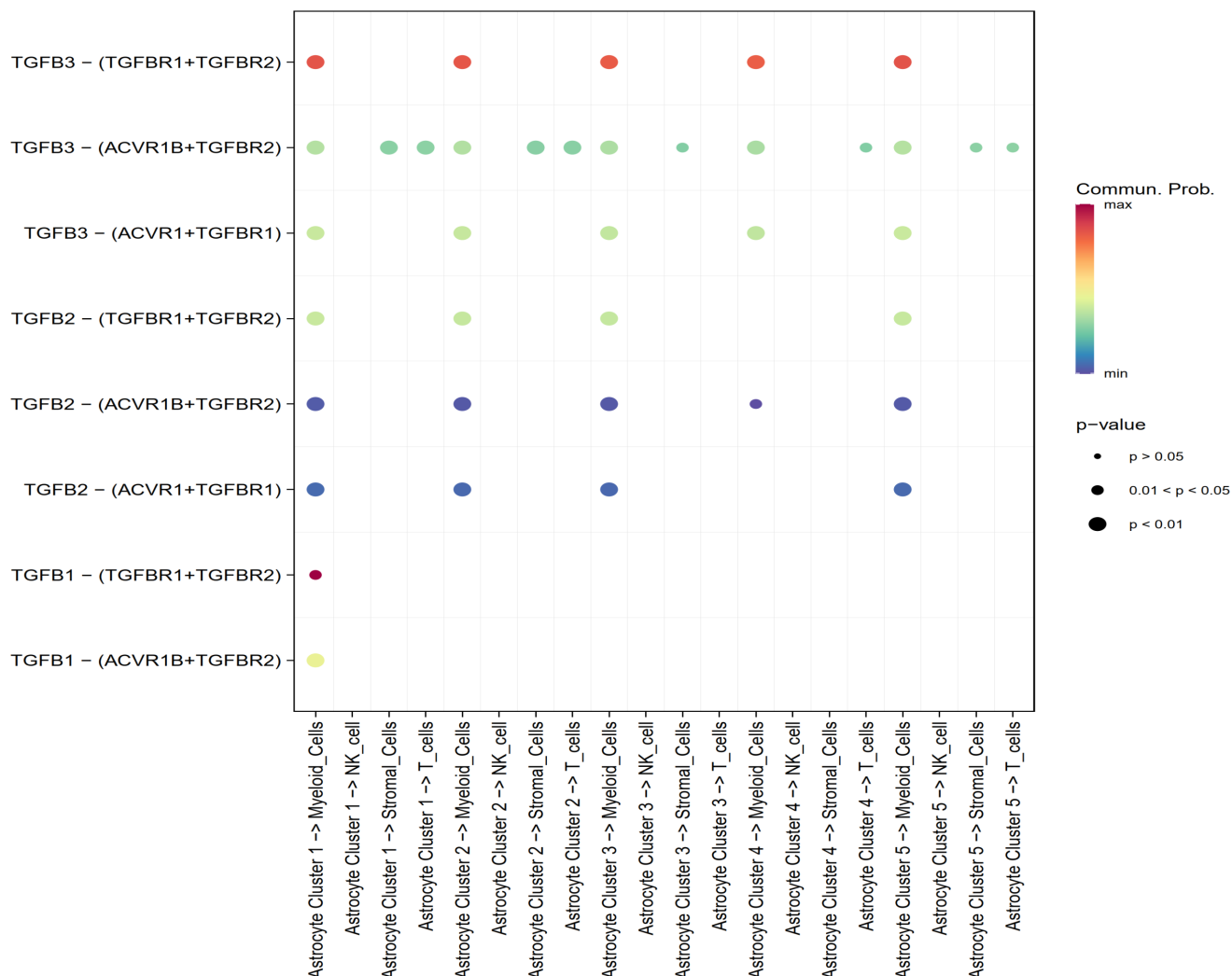


Figure S8. Identification of signaling pathways in glioma. A) Heatmap analysis of outgoing (Left) and incoming (Right) signaling patterns. **B)** Hierarchical analysis of the cell-cell communication network of TGFβ signaling in our glioma scRNA-seq dataset. **C)** Hierarchical analysis of the cell-cell communication network of TGFβ signaling in CGGA scRNA-seq dataset. **D)** Probability of communication between ligands and receptors of astrocyte cell subpopulation to other cell types in the TGFβ signaling pathway. The increased signal indicates higher communication strength for those signals. CGGA, Chinese Glioma Genome Atlas.

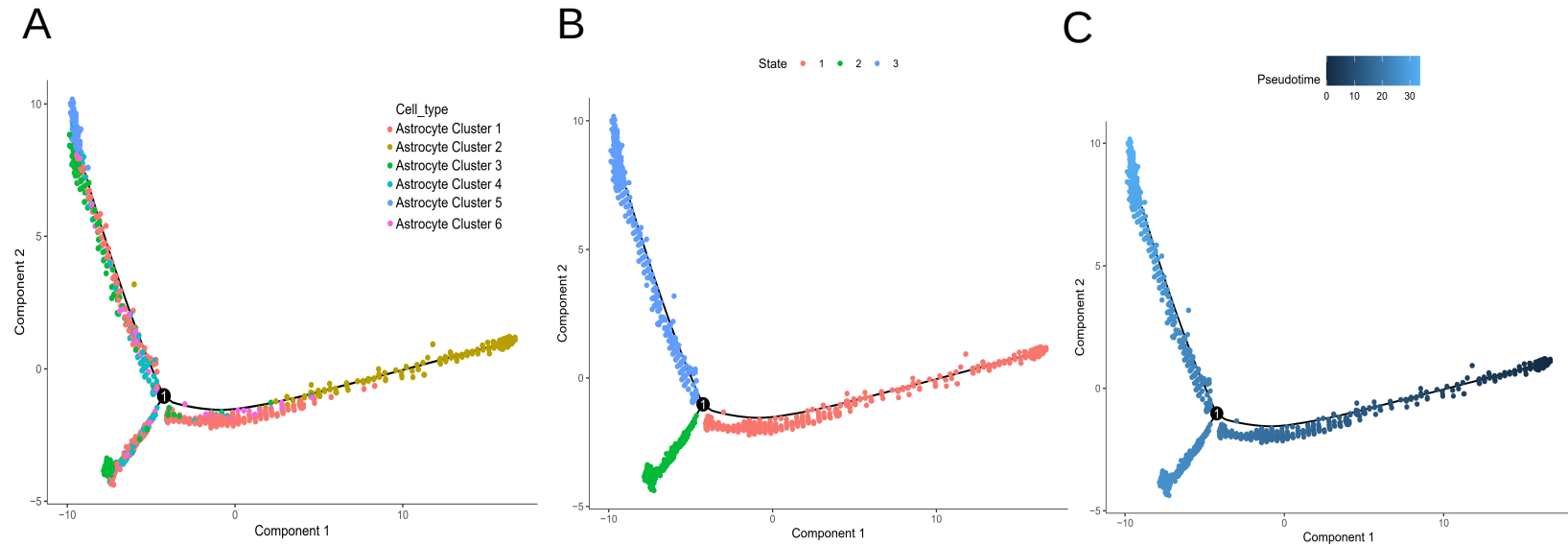


Figure S9. Distribution of astrocyte cells along the pseudo-time trajectory based on astrocyte cell subpopulations (A), state (B), and pseudo-time (C) in the CGGA dataset. CGGA, Chinese Glioma Genome Atlas.

