

Supplementary Legends

Supplementary Figure 1 | Cell Type Annotation.

- (A) Composition ratio of copy number variation subclones in individual GBM.
- (B) Heatmap of top10 marker genes in different cell types.

Supplementary Figure 2 | Correlations between GBM Cellular States and TCGA Subtypes.

- (A) Expression of *SOX2* in the six cellular states and stromal cells.
 - (B) Composition ratio of the six cellular states with stem-like and un-annotated tumor cells in individual GBM.
 - (C) Violin plot of the TCGA GBM subtypes ssGSEA scores.
- Grey dash line, average ssGSEA score; *****, $p < 0.0001$.

Supplementary Figure 3 | Developmental Trajectory of GBM Tumor Cells.

Inferred developmental trajectory of the six GBM tumor cell cellular states with un-annotated tumor cells by RNA velocity.

Supplementary Figure 4 | Survival Analysis of GBM Cellular State Signatures.

Survival analysis of the GBM cellular state signatures in the TCGA GBM database and the CGGA GBM database respectively.

Supplementary Figure 5 | Heterogeneity of TAMs.

- (A) Projection of TAMs based on PCA of microglial and macrophage marker genes.
 - Enrichment score of microglial (B) and macrophage (C) marker genes in TAMs.
 - (D) Correlation of enrichment score between microglial and macrophage marker genes in TAMs.
 - (E) Heatmap of top10 marker genes in different TAM clusters.
 - (F) Top 20 function analysis results of TAM-0, TAM-2 and TAM-3 cluster respectively.
 - (G) Correlation between the number of MES-like and TAM-1 cells.
 - (H) Violin plot of the Tumorigenesis, Cell Migration and Extracellular Matrix Organization gene set scores in TAMs.
- Survival analysis of the TAM-0 (I), TAM-2 (J) and TAM-3 (K) cluster signatures in the TCGA GBM and CGGA GBM databases respectively.
- Grey dash line, average ssGSEA score; *****, $p < 0.0001$.

Supplementary Figure 6 | Immunofluorescence Staining for TAM-1 Cluster (*CD14+ERO1A+*) in GBM.

Representative TAM-1 cluster cells were highlighted by white arrows; scale, 10 μm .

Supplementary Figure 7 | Cell-cell Communications in GBM.

Heatmap visualization of source cells (A) and target cells (B) related pathways in

cell-cell communication.

(C) Cluster of GBM cell types according to target cell functions in cell-cell communication.

(D) Cell-cell communication related pathways in different ingoing cell patterns.

Supplementary Figure 8 | TAMs M2-type Polarization.

Expression levels of M1-TAM (A) and M2-TAM (B) marker genes in TAMs.

(C) Heatmap of ligands secreted by GBM cellular states, which could target TAMs M2 marker genes. Ligands were ordered by Pearson correlation coefficient from high to low.

Supplementary Table 1 | Patient Information.

Supplementary Table 2 | Evaluation of scRNA-seq Data Quality.

Supplementary Table 3 | GBM Cellular States and Cell Type Constitutions.

Supplementary Table 4 | Top20 Regulons in Cellular States.

Supplementary Table 5 | Top20 Regulons in TAMs.

Supplementary Table 6 | DEG signatures of TAMs.

Supplementary Table 7 | Antibodies used in this study.