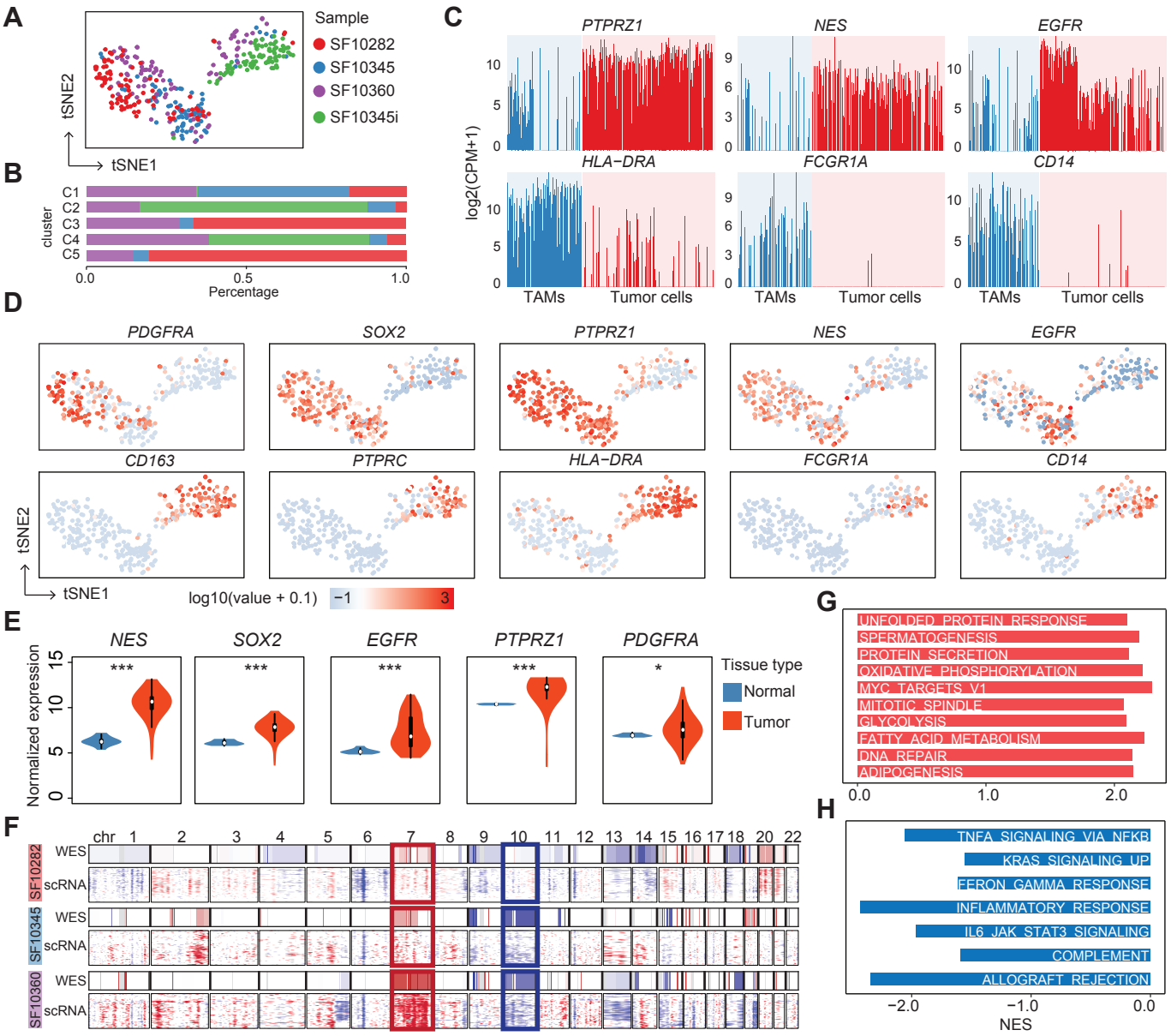
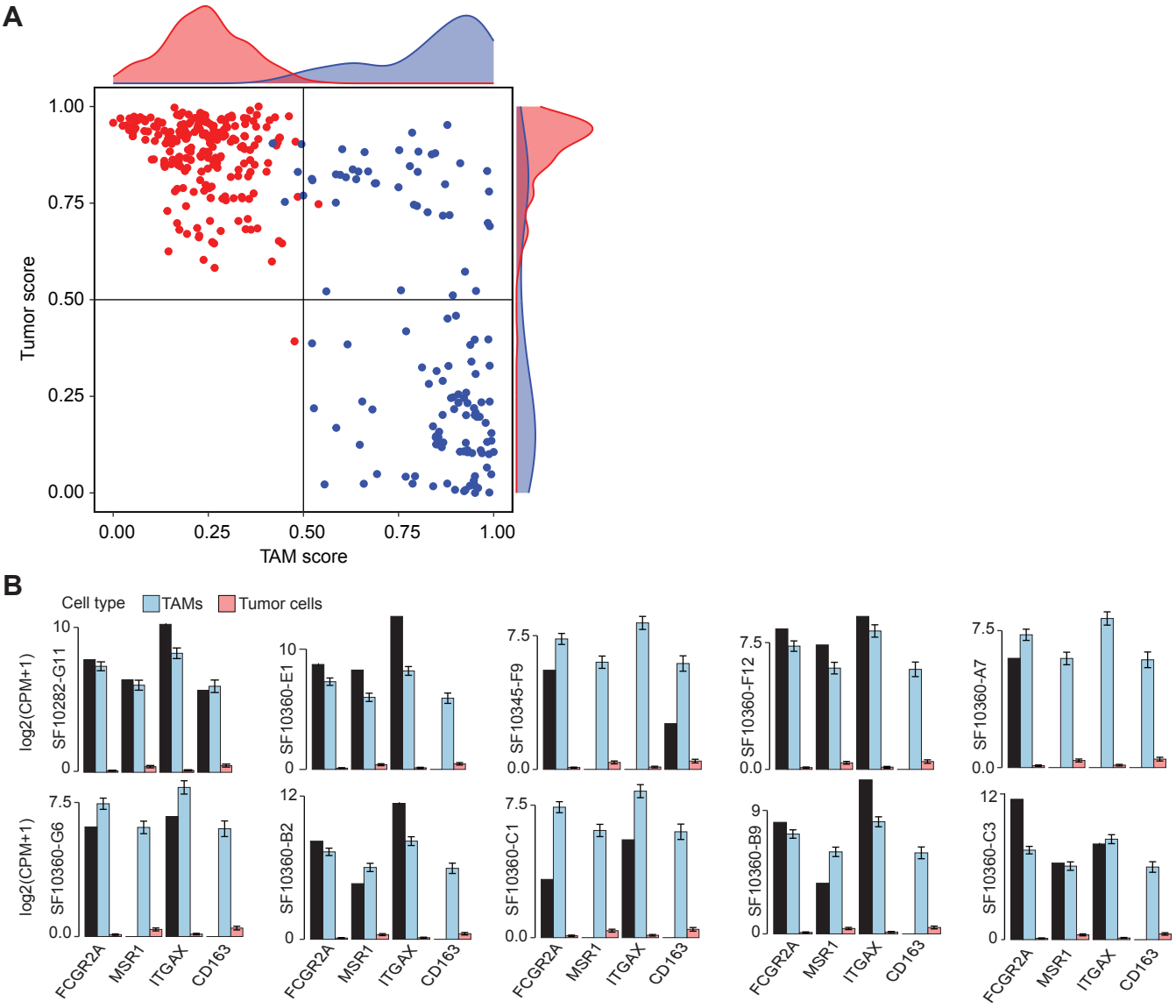
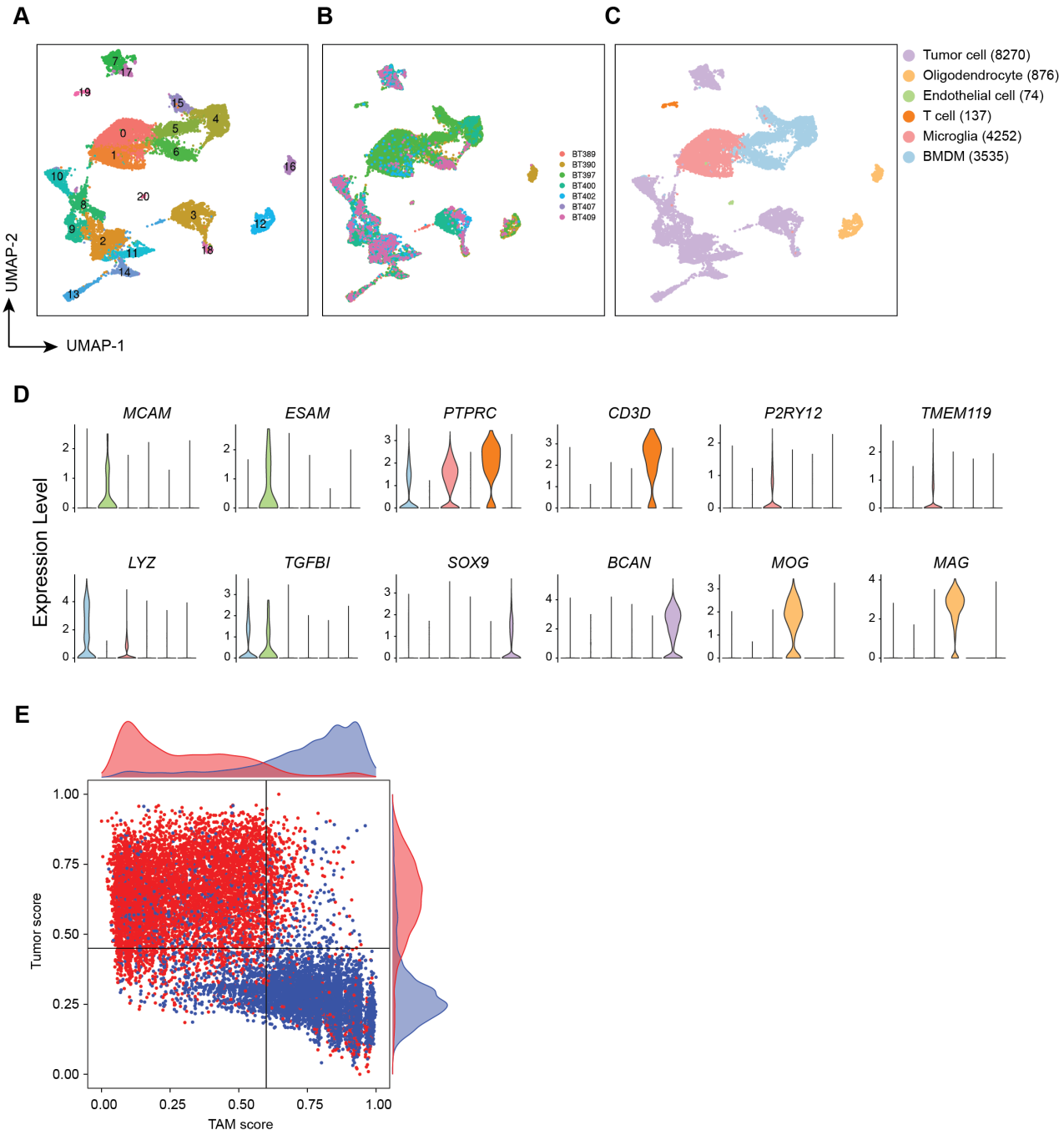


Supplementary Figure S1. Distinguish TAMs from tumor cells, related to Figure 1. **(A)** t-SNE map showing the clustering of 346 cells. Each dot represents a single cell colored by the patient source. **(B)** Stacked bar plot showing the patient composition in each cluster. Colors are consistent with (A). **(C)** Bar plots displaying the mRNA expression levels of the indicated markers, measured by log2-transformed CPM. Each bar represents a single cell colored by cell type. **(D)** t-SNE map showing the mRNA expression level of the indicated markers, colored by expression level. Tumor markers: *PDGFRA*, *SOX2*, *PTPRZ1*, *NES*, and *EGFR*; TAMs markers: *CD163*, *PTPRC*, *HLA-DRA*, *FCGR1A*, and *CD14*. **(E)** Violin plots showing the mRNA expression levels of indicated markers in normal (n = 10) and tumor tissues (n = 529) from the TCGA-GBM cohort. p-values are calculated by two-sided Wilcoxon rank sum test. **(F)** Chromosomal landscape of inferred CNVs in tumor cells, colored by CNV levels (amplification in red and deletion in blue). For each patient, the inferred CNV pattern (bottom) is consistent with the results of WES (top). Regarding the inferred CNV from scRNA-seq, rows represent chromosomal locations and columns represent cells. **(G-H)** Bar plots displaying the enriched HALLMARK pathways in tumor cells (G) and TAMs (H).

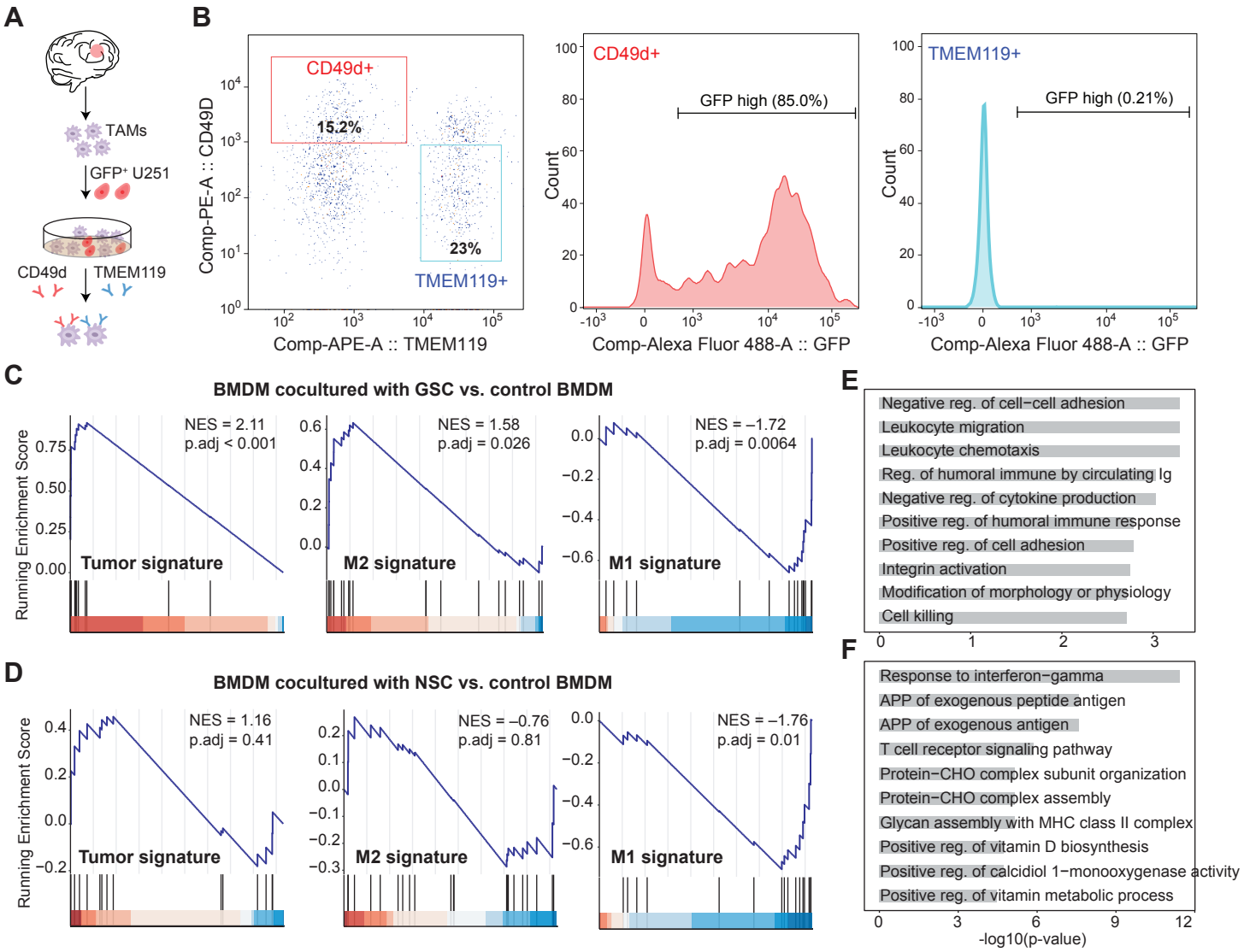


Supplementary Figure S2. Definition of double-positive TAMs and expression levels of TAMs markers, related to Figure 2.

(A) Scatter plot showing the TAM score and tumor score of cells. Each dot represents a single cell, colored by cell types (red for tumor cells and blue for TAMs). Top and right margins show the density plots of the TAM score and tumor score, respectively. **(B)** Bar plots showing the mRNA expression levels of the indicated markers in TAMs harboring tumor-derived mutations, colored by cell types (red for tumor cells, blue for TAMs, and black for the indicated single cell). Data are presented as the mean ± SEM.

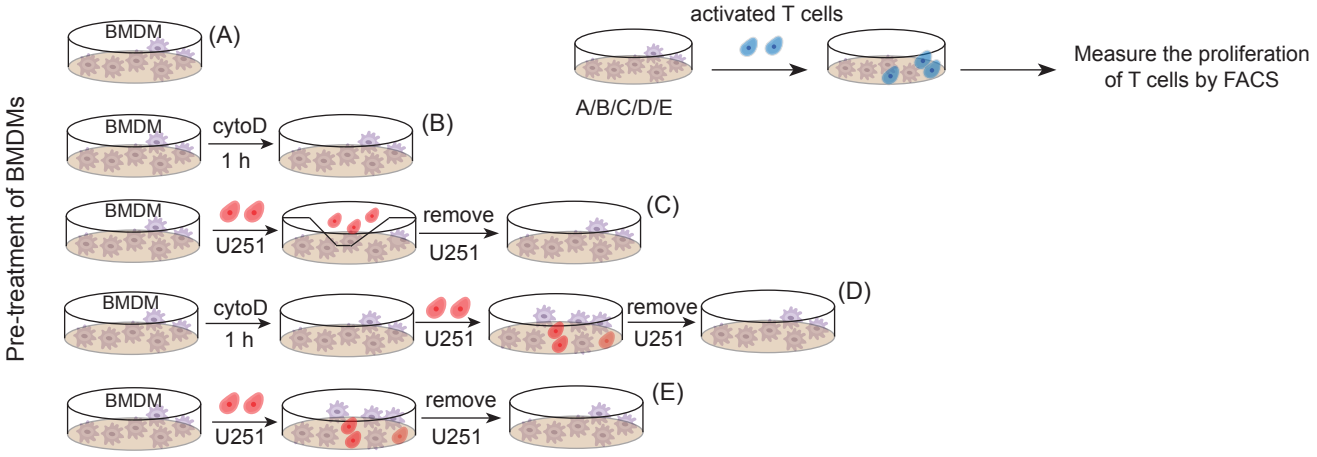


Supplementary Figure S3. Cell type annotation based on scRNA-seq data, related to Figure 3. **(A)** UMAP plot, colored by clusters. **(B)** UMAP plot, colored by patients. **(C)** UMAP plot, colored by cell types. **(D)** Violin plots, colored by cell types, showing the expression levels of cell type-specific markers. **(E)** Scatter plot showing the TAMs score and tumor score of cells. Each dot represents a single cell, colored by cell type (red for tumor cells and blue for TAMs). Top and right margins show the density plots of the TAMs score and tumor score, respectively.

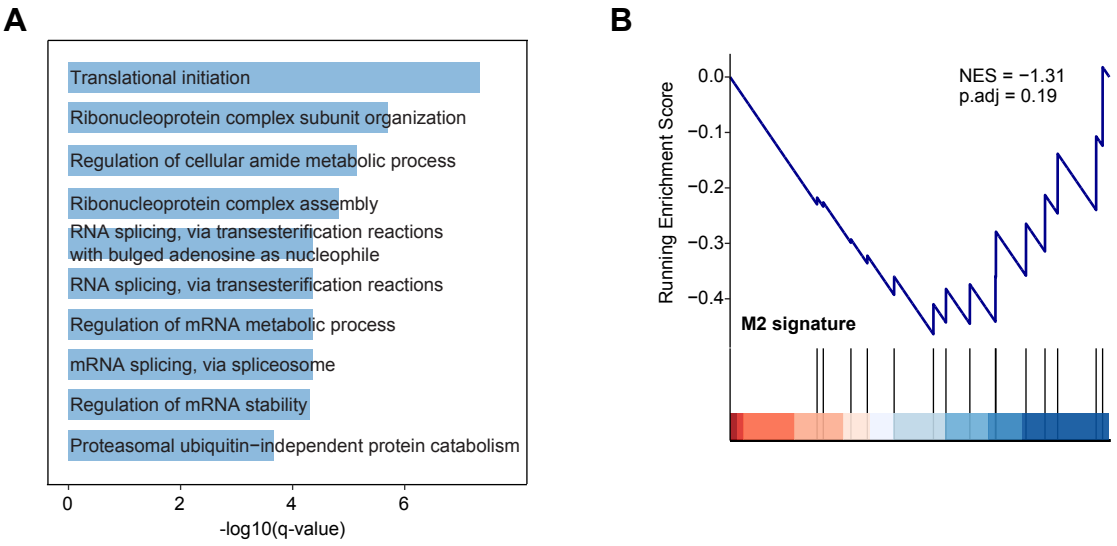


Supplementary Figure S4. Comparison of expression profiles in BMDMs under different culture conditions, related to Figure 4.

(A) Schematic workflow for determining the double-positive TAMs. CD11b$^+$ cells isolated from tumor tissues are co-cultured with GFP-labelled U251 for 24 h to induce phagocytosis. Phagocytosis of U251 is determined by the GFP signal within BMDMs and MG. **(B)** Representative flow cytometry plots depicting the phagocytosis of GFP$^+$ U251 cells by BMDMs and MG. **(C-D)** GSEA plots of BMDMs co-cultured with GSCs (C) or NSCs (D) compared with the control BMDMs. GSEA is performed by R package clusterProfiler. **(E-F)** GO terms enriched by upregulated (E) or downregulated (F) genes in BMDMs co-cultured with GSCs, as compared with BMDMs co-cultured with NSCs and control BMDMs. APP: antigen processing and presentation, CHO: carbohydrate. Over-representation analysis (ORA) is performed, and q values are calculated via R package clusterProfiler.

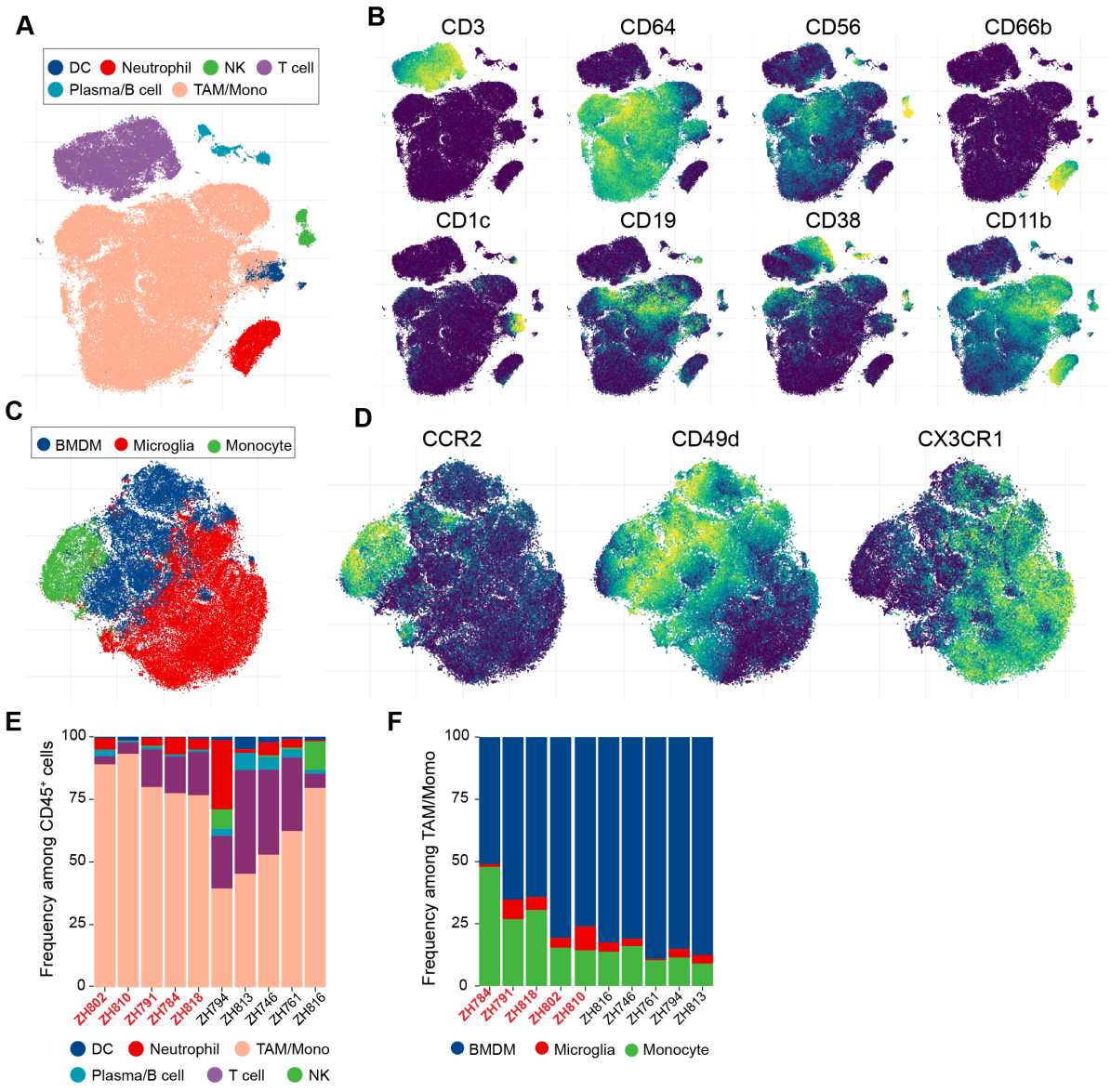


Supplementary Figure S5. Schematic workflow for measuring the immunosuppressive activity of BMDMs against activated T cells, related to Figure 5.
There are five BMDMs groups: 1) Group A for the control BMDMs; 2) group B for BMDMs treated with cytoD; 3) group C for BMDMs co-cultured with U251 for 24 h by transwell with 0.4 μm pore; 4) group D for BMDMs treated with cytoD and then co-cultured with U251 for 24 h; 5) group E for BMDMs directly co-cultured with U251 for 24 h. Then, BMDMs were co-cultured with activated T cells for three days, and their immunosuppressive activity was determined based on the number of proliferative T cells relative to the total number of T cells.



Supplementary Figure S6. Immune suppressive ability of the double-positive TAMs, related to Figure 6.

(A) Pathways that upregulated in GFP^{+}F4/80^{+} BMDMs, as compared with GFP^{-}F4/80^{+} BMDMs. **(B)** GSEA plots of GFP^{+}F4/80^{+} BMDMs compared with GFP^{-}F4/80^{+} BMDMs. GSEA is performed by the R package clusterProfiler.



Supplementary Figure S7. Infiltrated immune cells in GBM patients, related to Figure 7. **(A)** t-SNE map showing the immune cells infiltrated into the GBM tissues. Cells are colored by cell types. **(B)** t-SNE map showing the expression levels of CD3, CD64, CD56, CD66b, CD1c, CD19, CD38, and CD11b. Cells are colored by expression levels. **(C)** t-SNE map showing the BMDM, macroglia, and monocytes in GBM tissues. Cells are colored by cell types. **(D)** t-SNE map showing the expression levels of CCR2, CD49d, and CX3CR1. Cells are colored by expression levels. **(E)** Stacked bar plots showing the frequency of different immune cells in GBM patients. Bars are colored by cell types. Red text on the x-axis labels indicating MERTK-high GBM patients. **(F)** Stacked bar plots showing the frequency of BMBM, monocytes, and microglia in GBM patients. Bars are colored by cell types. Red text on the x-axis labels indicating MERTK-high GBM patients.