



Supplementary Figure S1. Elevated oxidative stress challenge in the microglia of glioma, related to Figure 1

(A) Expression of signature genes selected from the immune marker panel to identify cell types of clusters (Table S4).

(B) t-SNE plots display and graph-based re-clustering of microglia from normal brain (left) and tumor tissue (right).

(C) Heatmap showing DEGs and different functions in each cluster of microglia from tumor tissue compared with normal brain.

(D) Violin plot comparing oxidative stress-related genes expression in different immune cell clusters. The mean expression level was calculated for a specific oxidative stress gene signature (GO term: 0006979, Response to oxidative stress).

(E) Heat map of DEGs from GO term 'Response to oxidative stress' per single cell cluster of microglia (GSE162631). Seven clusters from microglia in tumor peripheral tissue and tumor core respectively for visualization.

(F) Violin plot comparing oxidative stress-related genes expression in microglia. The mean expression level was calculated for a specific oxidative stress gene signature (GO term: 0006979, Response to oxidative stress).

(G) A schematic model to describe the mRNA sequencing analysis of microglia isolated from surrounding healthy parenchyma and tumor of GL261 glioma-bearing mice by flow cytometry sorting.

(H) Normalized expression for comparing oxidative stress-related genes expression in surrounding healthy parenchyma and tumor of glioma bearing C57BL/6J mice.

(I) Quantification of cell proliferation (GL261) treated by conditional medium of primary microglia from adult mice brain in respective group.

(J) Quantification of cell proliferation of GL261-GFP cocultured with microglia isolated from normal brain and GL261 glioma-bearing brain by cell count.

(K) Primary neutrophils isolated from bone marrow were treated with H₂O₂ (500 μM) in the absence or presence of NAC (5 mM) for 12 hours. Conditional medium from treated primary neutrophils was used to incubate with glioma cells (GL261) for 24 hours. Cell proliferation of glioma cells were assessed by cell count.

Data are shown as mean \pm SEM. In (I) and (K), P value was calculated using one-way ANOVA analysis. In (D), (F), (H) and (J), P value was calculated using the two-tailed Student's *t* test. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.