

Figure S7 (related to Figure 5): Enrichment of the proneural and the mesenchymal signature in, respectively, low-grade and high-grade derived A2B5⁺ glioma cells

(A) Heat map representation of Gene set enrichment analysis (GSEA), performed using the 233-gene 'proneural' gene set of Phillips and colleagues (Phillips et al., 2006), showed a significant enrichment of proneural genes enriched in A2B5⁺ cells isolated from low-grade glioma. (B) Heat map representation of Gene set enrichment analysis (GSEA), performed using the 132-gene 'Epithelial-Mesenchymal transition' (EMT) gene set of Phillips and colleagues (Phillips et al., 2006), identified a significant number of EMT genes enriched in HG-derived A2B5⁺ cells relative to their LG counterparts.

LG: Low-grade; HG: High-grade; MG: microglia; UNS CTX: unsorted cortical cells; UNS WM: unsorted white matter cells; CTX: A2B5⁺ cells from normal cortex; WM: A2B5⁺ cells from normal white matter; AST: Astrocytoma; AAST: anaplastic astrocytoma; OLG: Oligodendroglioma; OLG-AST: Oligo-astrocytoma; GBM: Glioblastoma; GBM sc: small cell GBM; GSC, gliosarcoma;