Figure S8. Resemblance of the A2B5 Signature to Glioma and Neural Precursor Cells Compendium Studies, Related to Figure 5

Heat-map representation of enrichment patterns of the A2B5 signatures across previously established gene expression profiles related to human gliomas, glioma stem cells (A-C), embryonic stem cells (ESCs) and neural precursor cells (NPCs) (D-F) using parametric gene set enrichment (PGSEA) analysis.

(A and D) PGSEA analysis was performed and PAGE Z scores were calculated following normalization of the gene expression data to the median of non-tumor unsorted cells extracted from adult human white matter and cortex. The color scale ranges from red to blue indicating positive and negative z scores respectively (in A range of 16.1 to ?16.1 scores, D, ± 15).

(B and E) PGSEA analysis and Z scores following normalization to non-tumor A2B5+GPCs extracted from adult human white matter and cortex (range: B, ± 19.3, E, ± 15).

(C and F) PGSEA analysis was performed on expression ratios of individually normalized A2B5$^+$glioma cells compared to their matched A2B5$^-$ sorted cells control (range: C, ± 24.3, F, ± 20.2).

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.