

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Gene expression (RPKM) of acutely purified, serum-free culture, and serum-selected culture of human astrocytes.

File Name: Supplementary Data 2

Description: GO terms associated with genes differentially expressed by serum-free cultured and acutely purified human astrocytes and hypoxia, poly I:C, and TNF α treatment-induced genes.

File Name: Supplementary Data 3

Description: GO terms associated with genes differentially expressed by human and mouse astrocytes.

File Name: Supplementary Data 4

Description: Top 20 hub genes in the protein-protein interaction networks of genes with higher expression in human or mouse astrocytes. Genes are ranked by the number of connections in the protein-protein interaction networks. Those with the highest number of connections are considered hub genes.

File Name: Supplementary Data 5

Description: Gene expression (RPKM) of grafted human astrocytes and host mouse astrocytes.

File Name: Supplementary Data 6

Description: Differentially expressed genes between xenografted host mouse and naïve mouse astrocytes. Genes with FDR < 0.05 and average RPKM > 0.1 are shown. Unpaired t-test followed by post hoc multiple comparison adjustment using the Benjamini and Hochberg FDR method.

File Name: Supplementary Data 7

Description: GO terms enriched in genes differentially expressed by xenografted host mouse and naïve mouse astrocytes.

File Name: Supplementary Data 8

Description: Age of patients and mice used in RNA-seq comparison of astrocyte gene expression across species.

File Name: Supplementary Data 9.

Description: WGCNA coexpression modules, member genes, and kMEs.

File Name: Supplementary Data 10

Description: Gene expression (RPKM) of hypoxia-, poly I:C-, and TNF α -treated astrocytes.

File Name: Supplementary Data 11

Description: Differentially expressed genes induced by hypoxia, poly I:C, and TNF α treatment. The DESeq2 package was used to calculate differential gene expression and statistical significance.

File Name: Supplementary Data 12

Description: Expression of cell death-associated genes by human and mouse astrocytes. The top 10 cell death-associated genes are based on Sharma et al. The RPKM of cell death-associated genes in all our experimental conditions (acutely purified, serum-selected culture, serum-free culture, xenograft, host, hypoxia, poly I:C, TNF α -treated, and untreated control astrocytes from both human and mouse) are listed.

File Name: Supplementary Data 13

Description: Differentially expressed genes in neurons treated with control and hypoxia-treated ACM. Genes with FDR < 0.05 are shown. The DESeq2 package was used to calculate differential gene expression and statistical significance.