

Figure S1. High confidence protein-protein interactions identified using the STRING database. Based on an interaction score of ≥ 0.7 (maximum 1.0), 60/125 (48%) of the differentially abundant protein have previously documented evidence of a physical interaction, implying biological relatedness. Interaction scores range from 0 to 1.0, and are calculated from genome neighborhood & co-occurrence, gene fusions, co-expression, experimental/biochemical data, and association in curated databases including PubMed. The number of connections (edges) identified was 76, which is significantly higher than the number expected by chance (38; $p = 3.44E^{-08}$).

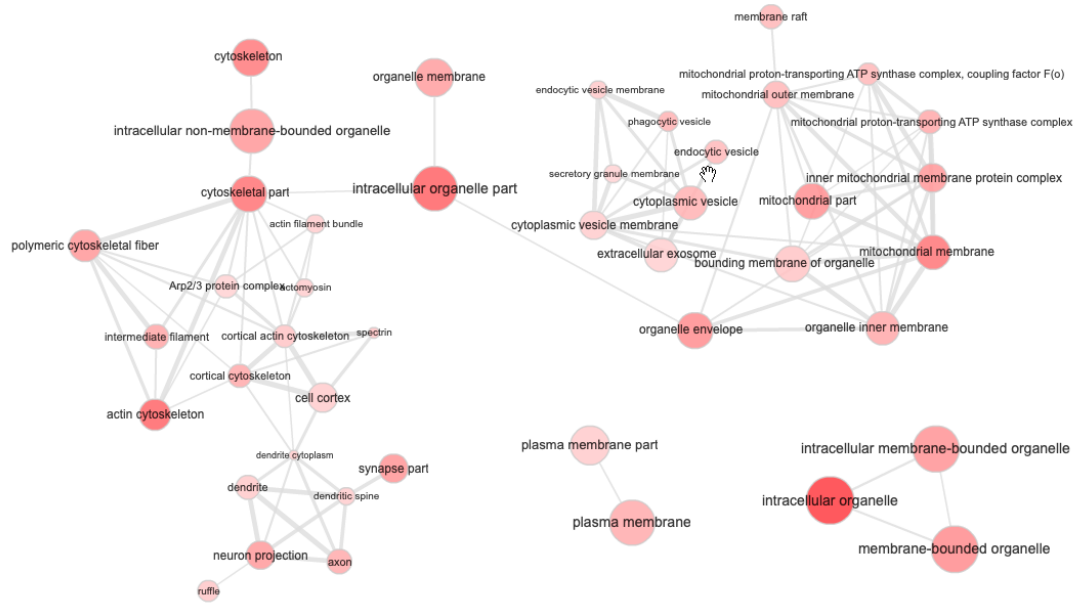


Figure 2. Cytoscape cellular component network constructed from 125 differentially abundant proteins identified in tumor-associated brain tissue. Two major component clusters make up the bulk of the network – cytoskeletal components of neural projections (left) and mitochondrial and vesicular components (right). Connections and distance are proportional to semantic similarity of GO titles and descriptions. Node size is inversely proportional to the false discovery rate.

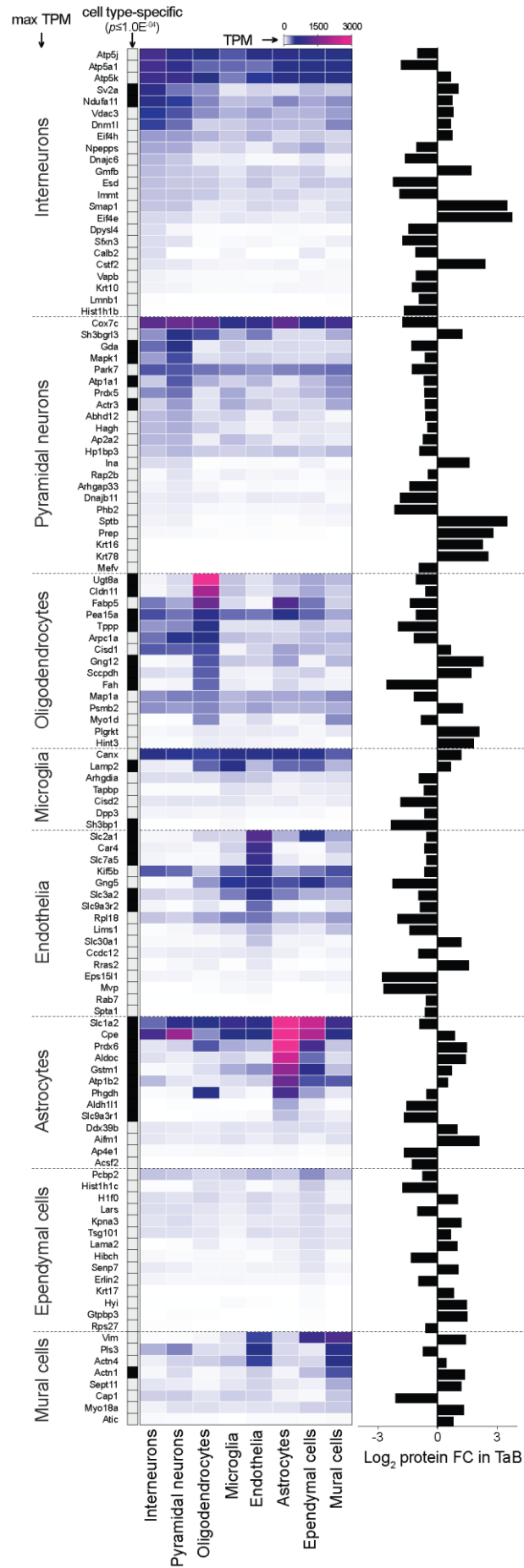


Figure S3. Heatmap showing average expression of differentially abundant proteins at the RNA level in cell types of the mouse brain (meta-analysis of [15]). Transcripts are grouped according to the cell type exhibiting maximal expression, and ranked in descending order for each category. TPM = transcripts per million. Cell type specificity was determined using an ANOVA test; transcripts significantly associated with one particular cell type are indicated with black tiles. Bar chart shows protein fold change (FC) in tumor-associated brain (TaB) tissue.

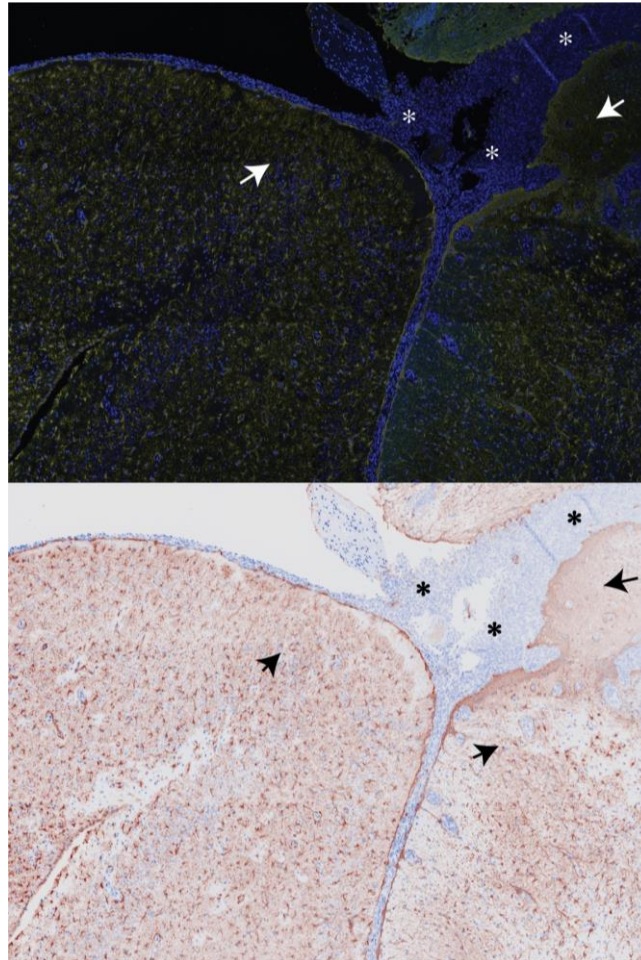


Figure 4. Example of GFAP expression in tumor-associated brain tissue. GFAP (yellow; upper panel) was multiplexed with investigational antibodies to guide tissue segmentation in xenograft images prior to fluorescence analysis. Lower panel: simulated diaminobenzidine tetrahydrochloride (DAB) detection of the same section, incorporating bright-field exposure so that morphological features can also be considered during tissue segmentation. *Arrows: brain tissue; asterisks, tumor.*