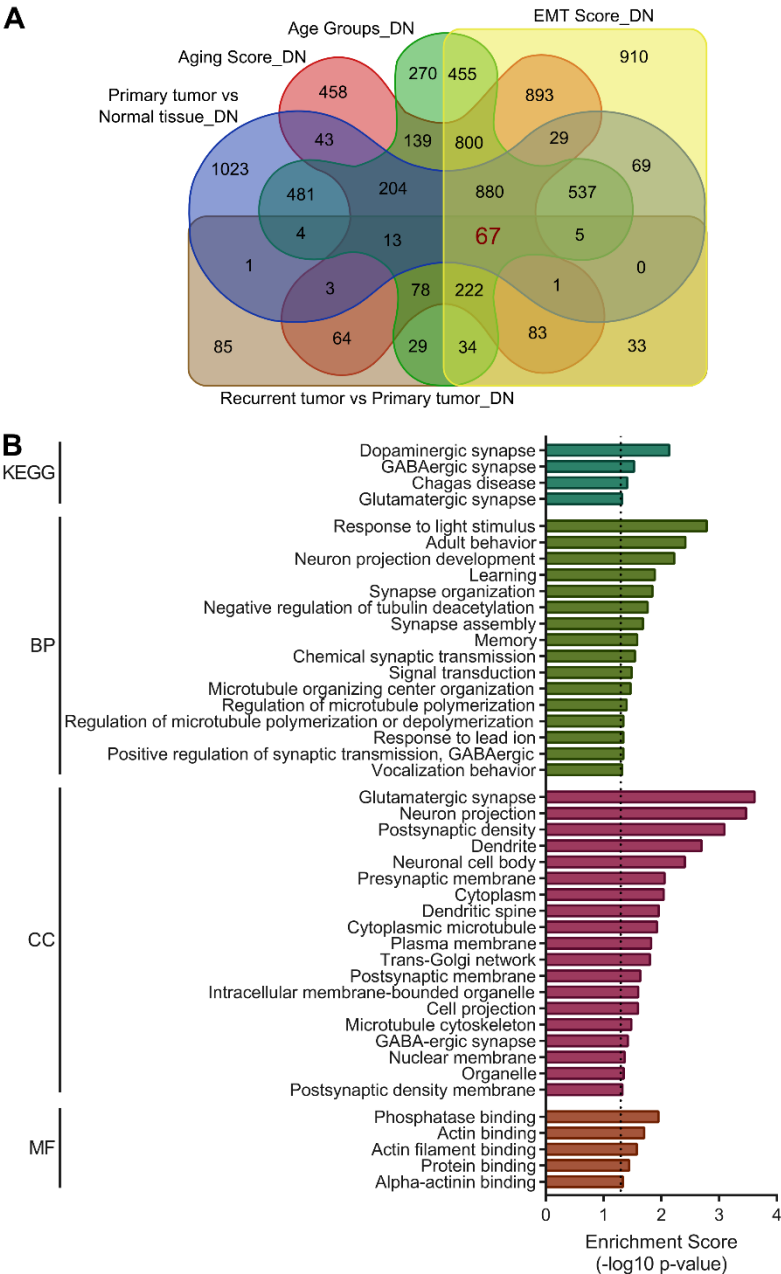


ER stress-driven unfolded protein response fuels aging-related tumor aggressiveness in gliomas

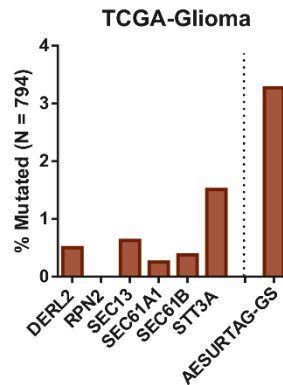
Supplementary Figures

Figure S1



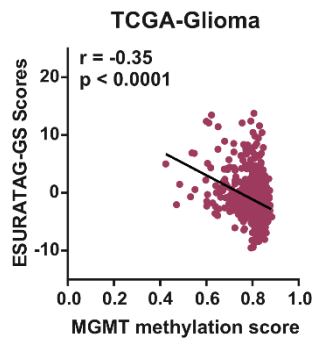
Supplementary Figure S1: Aging-related tumor aggressiveness-targeted expression analysis identifies brain function-related mechanisms as tumor suppressor pathways in glioma patients. (A) Venn diagram showing number of aging-related tumor aggressiveness-associated tumor suppressor hubs through pipeline in Figure 1A. (B) Bar-graph showing enrichment score of KEGG pathways, biological processes, cellular compartments and molecular functions in which tumor suppressor hubs, identified in (A), are enriched.

Figure S2



Supplementary Figure S2. Genes comprising ESURTAG-GS are not mutated in glioma patients. Bar-graph showing number of glioma patients from TCGA dataset having mutations in genes comprising ESURTAG-GS.

Figure S3



Supplementary Figure S3. ESURTAG-GS is inversely correlated with MGMT methylation in gliomas. Scatter-plot showing Pearson correlation of ESURTAG-GS scores with MGMT methylation scores in glioma patients from TCGA dataset.