The mesenchymal signature of high-grade glioma

Unsupervised clustering of 76 high grade tumors by expression of 108 genes that are positively or negatively associated with survival reveals 3 tumors classes - Proneural (PN), Mesenchymal (Mes) and Proliferative (Prolif).

Malignant gliomas belonging to the mesenchymal sub-class express genes linked to the most aggressive properties of glioblastoma (migration, invasion and angiogenesis) and mark the worst clinical outcome.
The mesenchymal network of six major hubs of transcription factors in high-grade gliomas
STAT3 and C/EBPβ inhibit neuronal differentiation and induce mesenchymal transformation in neural stem cells.
Knockdown of Stat3 and C/EBPβ cooperates to inhibit tumor cell invasion and angiogenesis.
Loss of Stat3 and C/EBPβ in human glioma cells inhibits tumorigenesis in the mouse brain.
The combined expression of Stat3 and C/EBPβ correlates with the poorest outcome of glioma patients.

$p < 1 \times 10^{-3}$
Glioblastoma
From systems biology to prognosis to personalized therapy

Stat3 and C/EBPβ are Master Regulators
Stat3 and C/EBPβ are Transforming Oncogenes of Neural Stem Cells
Stat3 and C/EBPβ are Predictors of Negative Clinical Outcome

Mesenchymal Signature Of High Grade Glioma

ARACNe Regulatory Network