A screenshot of a graph

AI-generated content may be incorrect.

**Figure S1. Principal component analysis (PCA) before and after batch correction.** PCA was performed on log2-transformed expression data from TCGA GBM (n=192), and GTex-brain cortex (n=270) samples.

(a) Before batch correction: PCA revealed a clear separation of the samples primarily driven by batch effects. The first two principal components (PC1 and PC2) explained 93.4% and 3.4% of the total variance, respectively.

(b) After ComBat-seq batch correction: PCA of the same samples after ComBat-seq adjustment showed reduced inter-batch separation, with clustering reflecting biological differences rather than batch origin. PC1 and PC2 explained 96.2% and 0.3% of the total variance, respectively.

A diagram of a funnel

AI-generated content may be incorrect.

**Figure S2. Stratification of TCGA-GBM samples based on BORIS mRNA expression levels.** Distribution of BORIS mRNA expression across TCGA-GBM samples. Dashed lines indicate the quartile-based thresholds used to define low (Q1) and high (Q4) *CTCFL* expression groups for subsequent differential expression analysis.