Supplementary

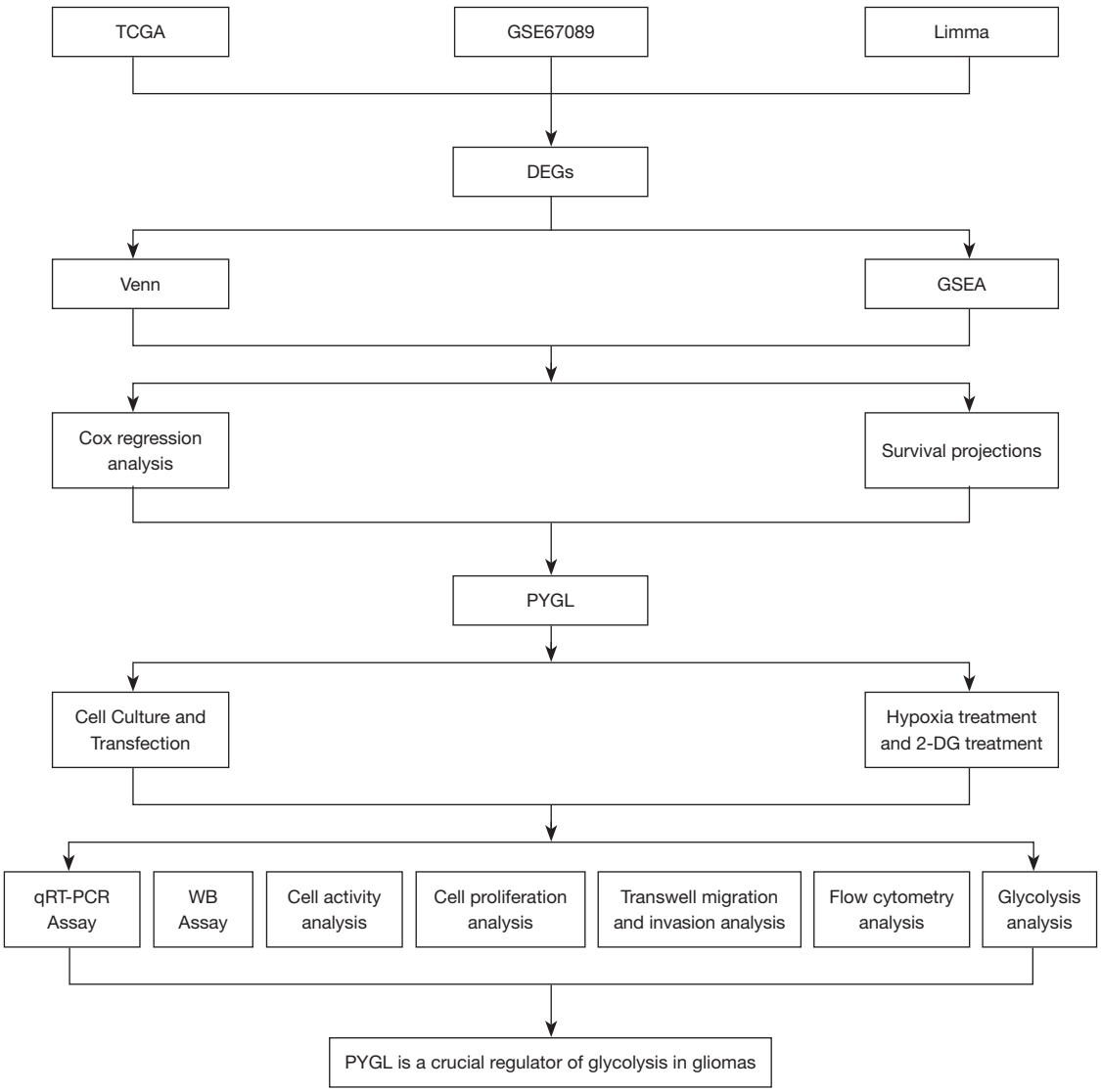

Figure S1 By examining the gene expression data of glioma samples and corresponding normal tissue samples in the TCGA and GEO databases, we identified DEGs associated with gliomas using the 'Limma' package in R software. Common DEGs between the two datasets were subsequently identified using the Venn diagram tool, and glycolysis-related genes from the GSEA database were integrated to further dissect the interactions between these genes and the glycolytic pathway. Key genes associated with glioma prognosis were identified by Cox regression analysis, which led to the construction of nomograms predicting the probability of patient survival. HBMECs and glioma cell lines were cultured in the experimental phase, and the cells were subjected to hypoxic conditions and 2-DG treatment to investigate the effects of these stressors on *PYGL* expression and cellular metabolism. Using qRT-PCR and Western blotting, PYGL expression levels in cells were monitored and various cellular functions including viability, proliferation, clonogenicity, migration, invasion and apoptosis were assessed. The results suggest that PYGL is a key regulator of glycolysis in gliomas, and targeting PYGL and its associated metabolic pathways may provide novel therapeutic strategies for glioma treatment. DEGs, differentially expressed genes; HBMECs, human brain microvascular endothelial cells; 2-DG, 2-deoxy-D-glucose; PYGL, glycogen phosphorylase L; qRT-PCR, quantitative reverse transcription polymerase chain reaction.

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