(C)The TCGA GBM and LGG expression data were downloaded from UCSC Xena. And samples from GBM and LGG were combined, as well as the clinical data. Each of the 41 genes was scaled to a z-score across all samples. Then we calculated the average values of the gene z-scores for each sample defined as the gene signature score of the sample. The samples were sorted based on the gene signature scores, and classified into two groups by median value: High group and Low group. Lastly, we conducted the survival analysis using the clinical data based on the classified groups.

(D) For each of the 41 genes, the combined samples from TCGA GBM and LGG were sorted and classified into two groups by the median value of the gene expression data. Then the survival analysis was conducted using the clinical data based on the classified groups for each gene respectively. The Hazard Ratio values, lower and upper boundaries of 95% CI were recorded and plotted.