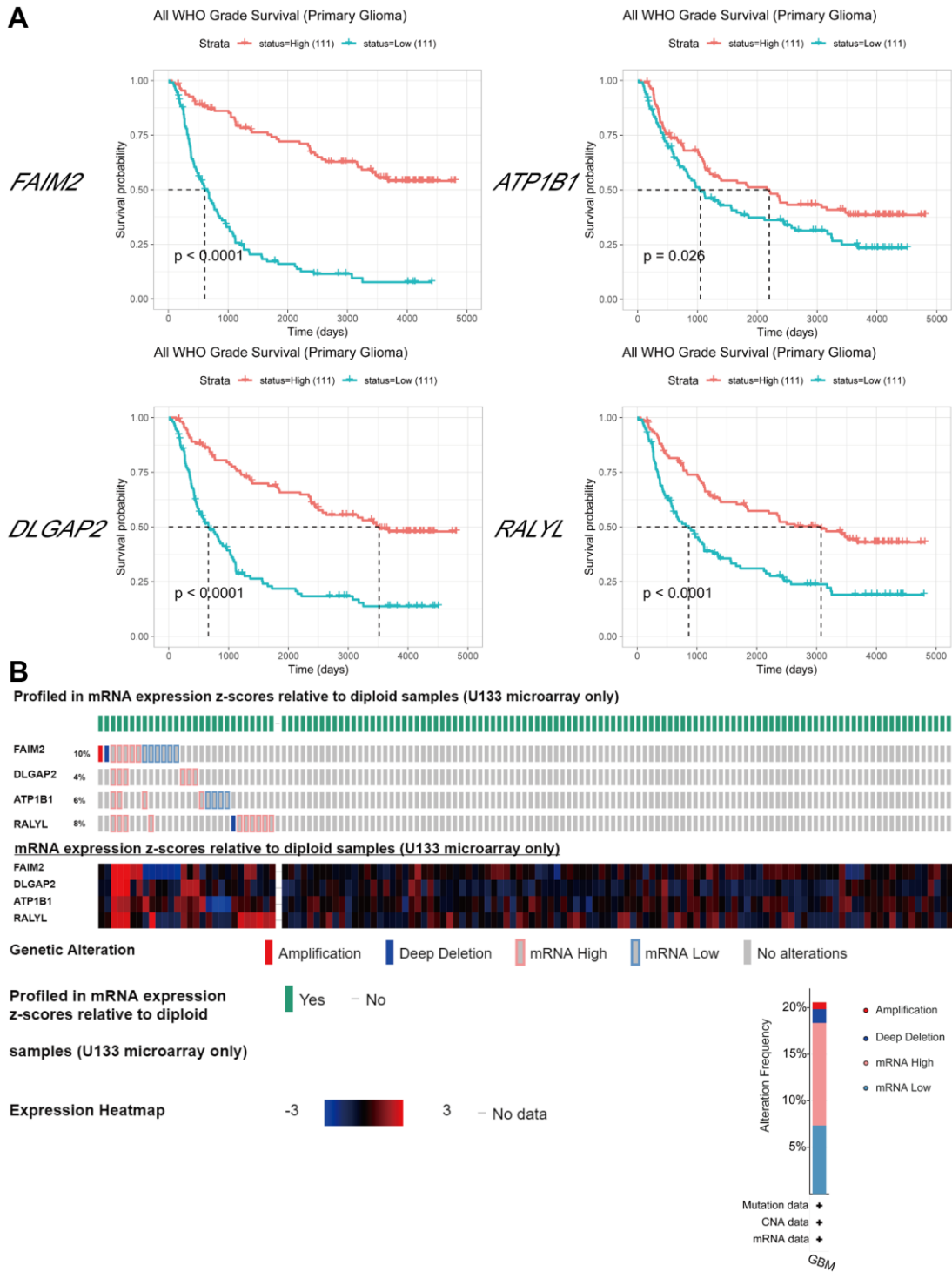
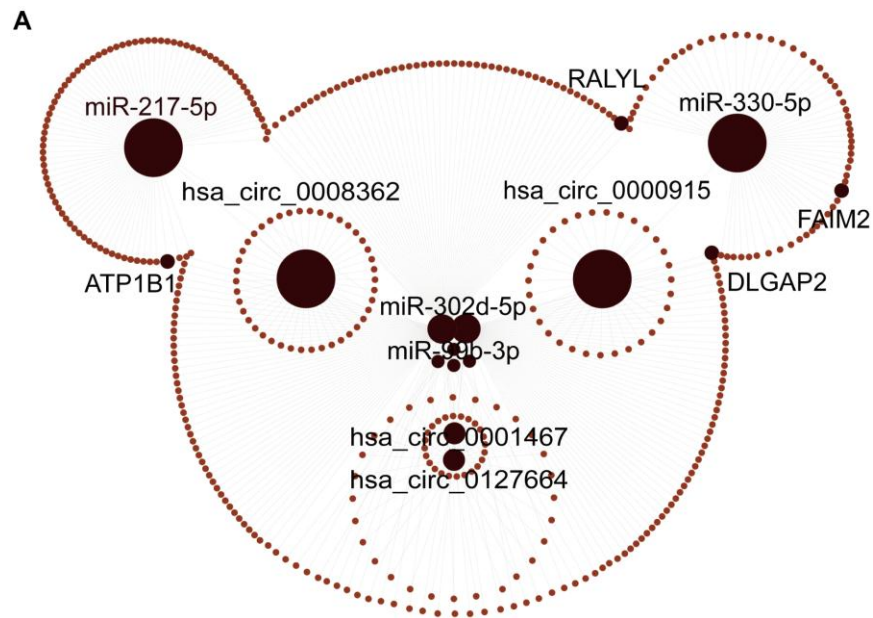


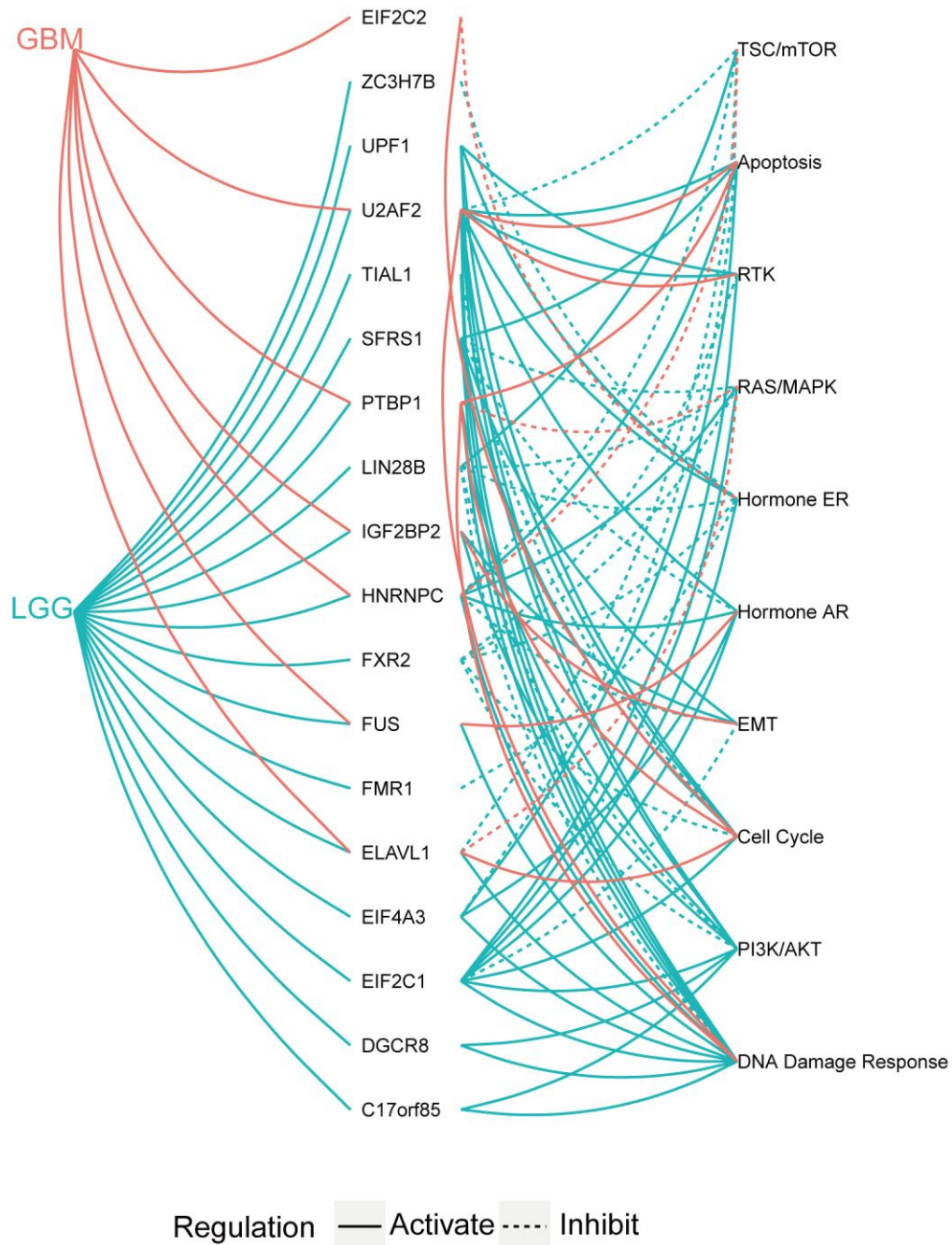
SUPPLEMENTARY FIGURES



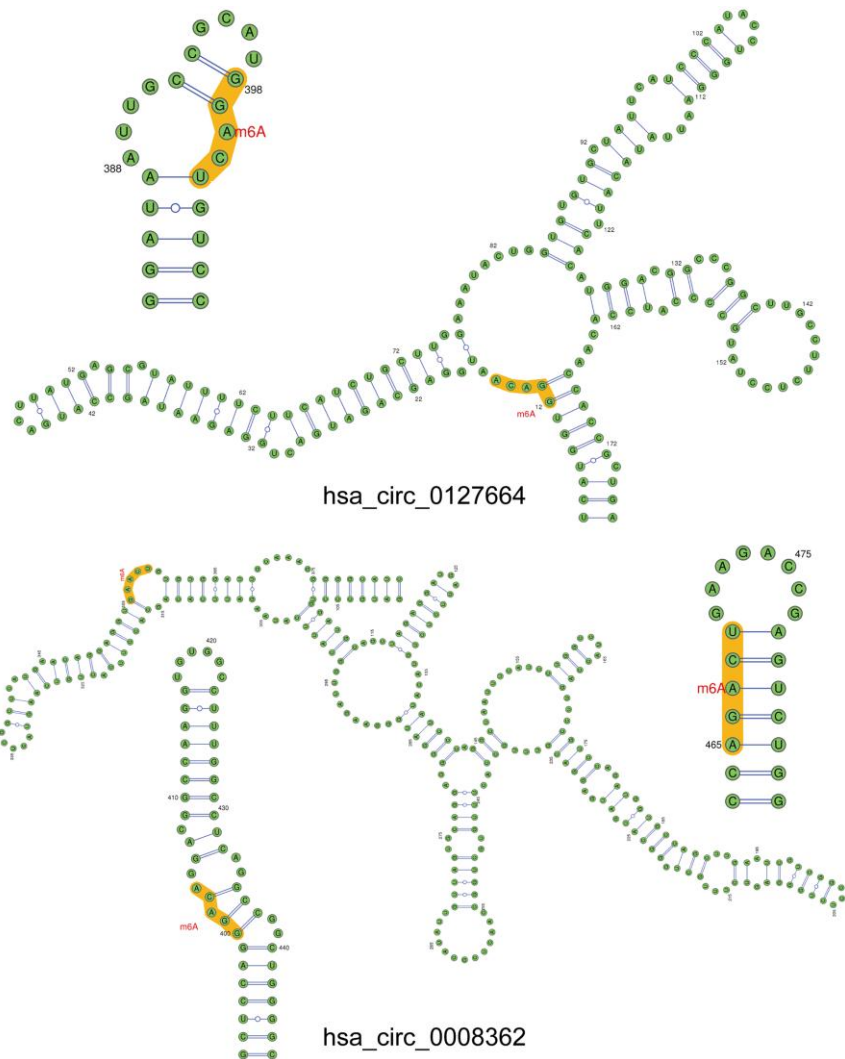
Supplementary Figure 1. Survival analysis and genomic alterations of 4 target mRNAs. (A) Survival analysis of 4 target mRNAs by CGGA. (B) Summarizes genomic alterations in the 4 queried genes, *FAIM2*, *DLGAP2*, *ATP1B1*, and *RALYL*, across a set of GBM samples by cBioPortal. Each row represents a gene, and each column represents a tumor sample. Red bars represent gene amplifications, and blue bars represent deep deletions.



Supplementary Figure 2. CircRNA-miRNA-mRNA network map. (A) network predicting target miRNAs of hsa_circ_0000915, hsa_circ_0127664, hsa_circ_0008362, and hsa_circ_0001467 and their top target genes. CircRNAs, target miRNAs and genes are represented by brown nodes. Gray lines indicate a regulatory relationship.



Supplementary Figure 3. Interaction map of RBP genes and activation and inhibition of cancer pathways.



Supplementary Figure 4. Visualization of the local m⁶A site structure of circRNAs.