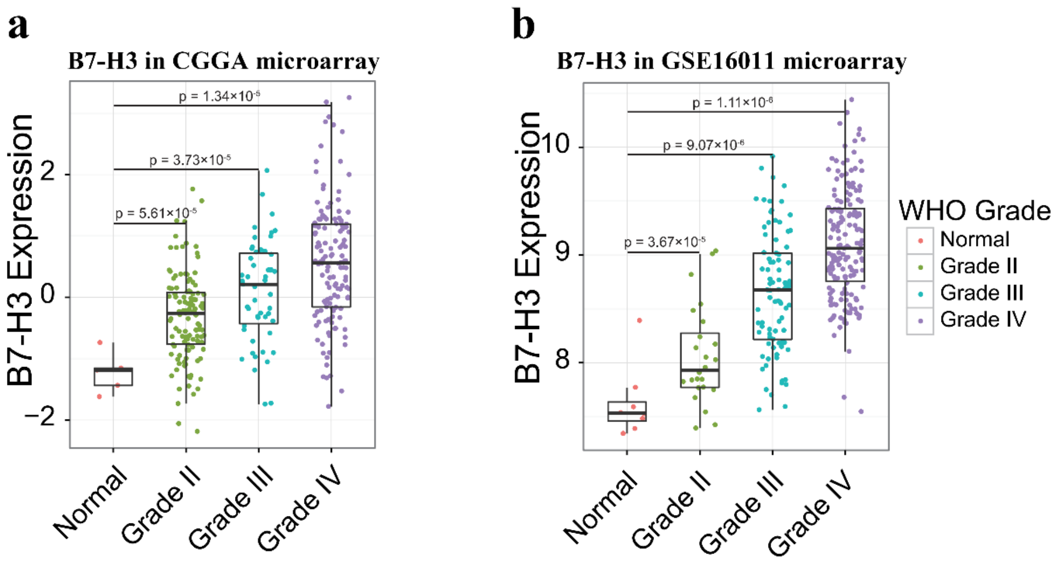


Fig S1. Comparison of B7-H3 expression between tumor-naive brain tissue and glioma in CGGA microarray dataset (a) and GSE16011 microarray dataset (b).

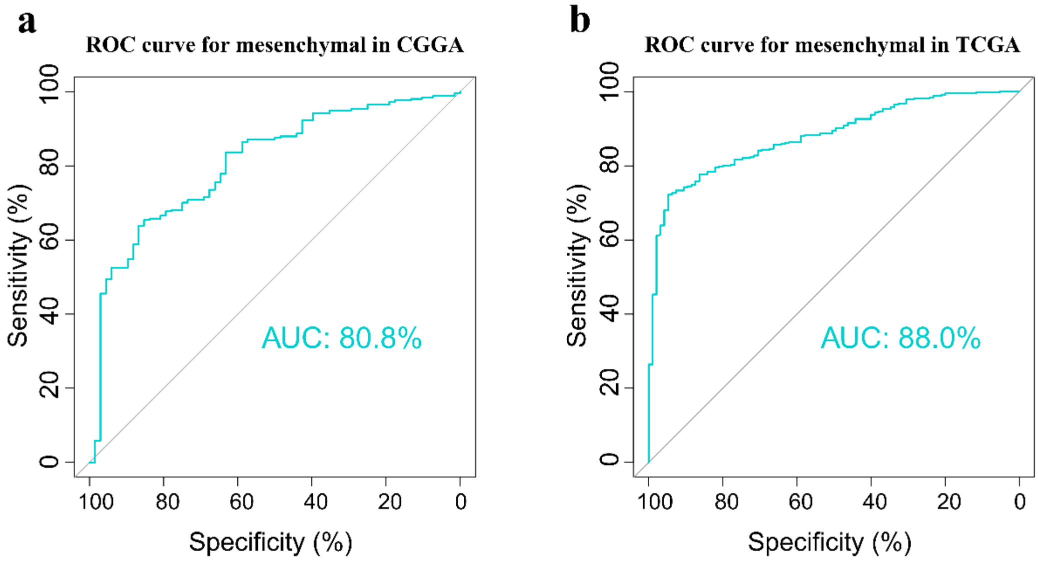


Fig S2. ROC curves for predicting mesenchymal subtype in CGGA (a) and TCGA (b) dataset.

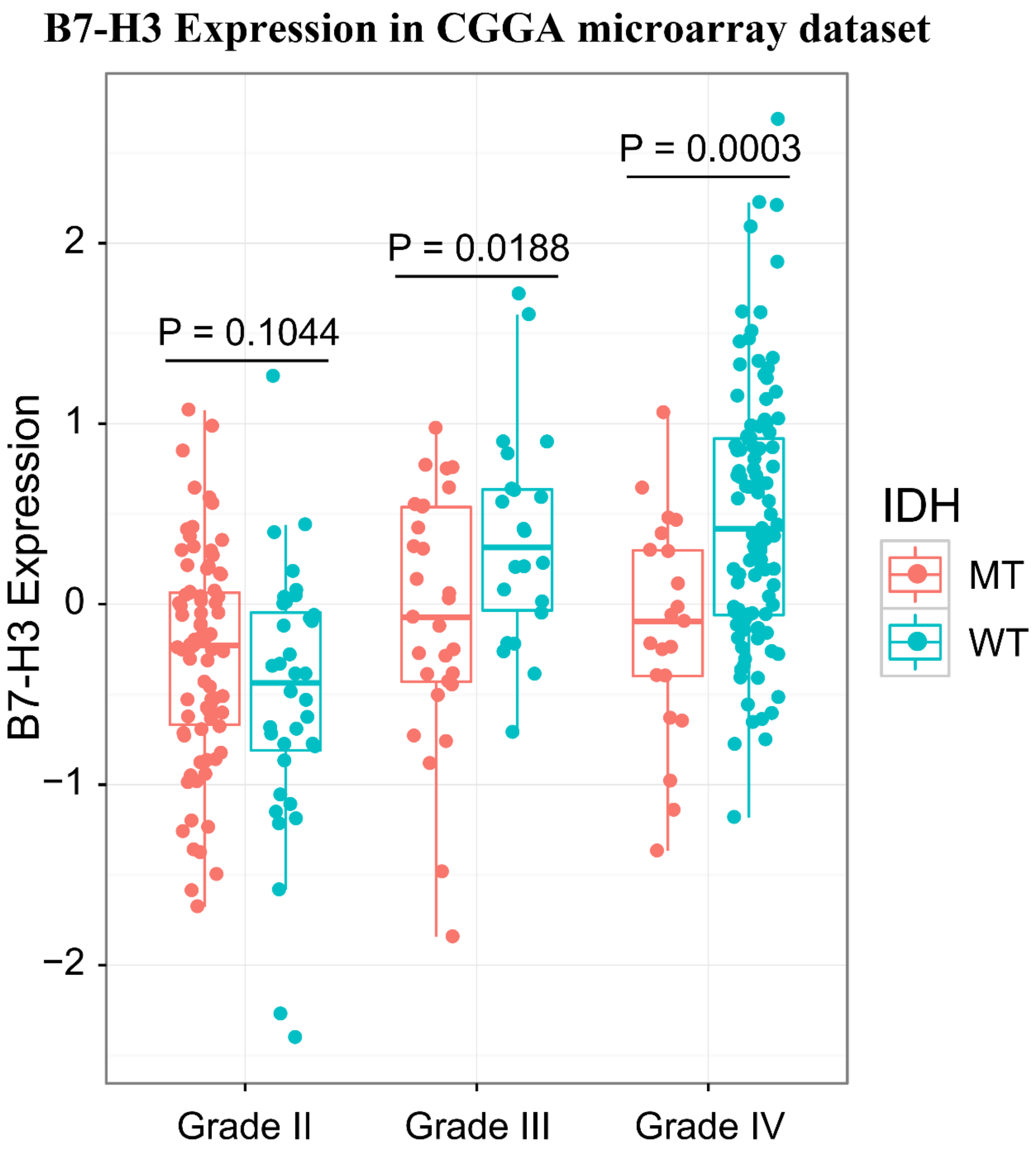
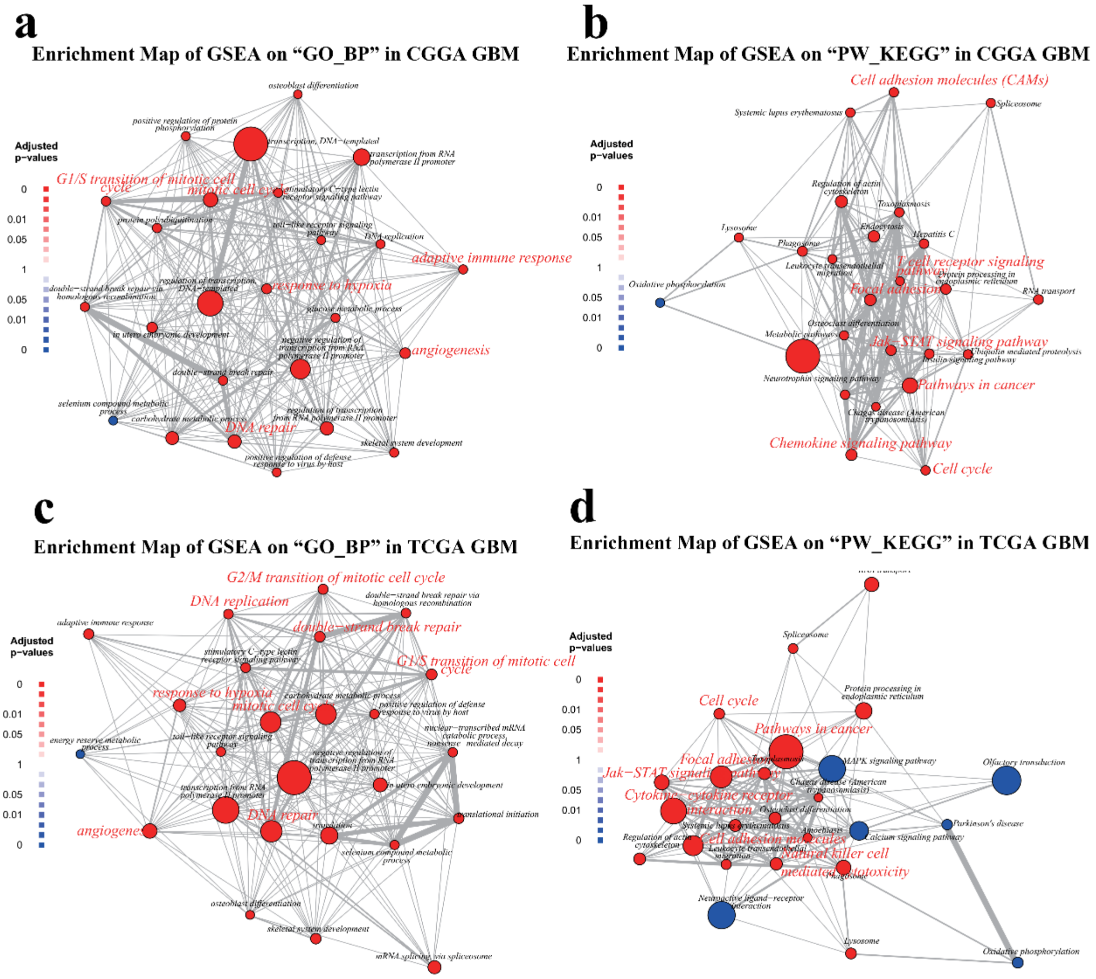


Fig S3. Relationship between B7-H3 expression and IDH mutation in CGGA Agilent microarray dataset. Red dots and cyan dots indicate IDH mutant and wild-type samples, respectively. Student's t-test was used to check the statistical difference between binary samples.



Enrichment Map of GSEA on "GO_BP" in CGGA GBM

Enrichment Map of GSEA on "PW_KEGG" in CGGA GBM

Enrichment Map of GSEA on "GO_BP" in TCGA GBM

Enrichment Map of GSEA on "PW_KEGG" in TCGA GBM

Fig S4. B7-H3 related biological processes (a, c) and pathways (b, d) in GBM. In the enrichment map for GSEA, nodes are colored by the sign of the enrichment scores (red: +, blue: -). The sizes of nodes are in proportion to the sizes of gene sets, while the width of edges is proportionate to Jaccard coefficients.

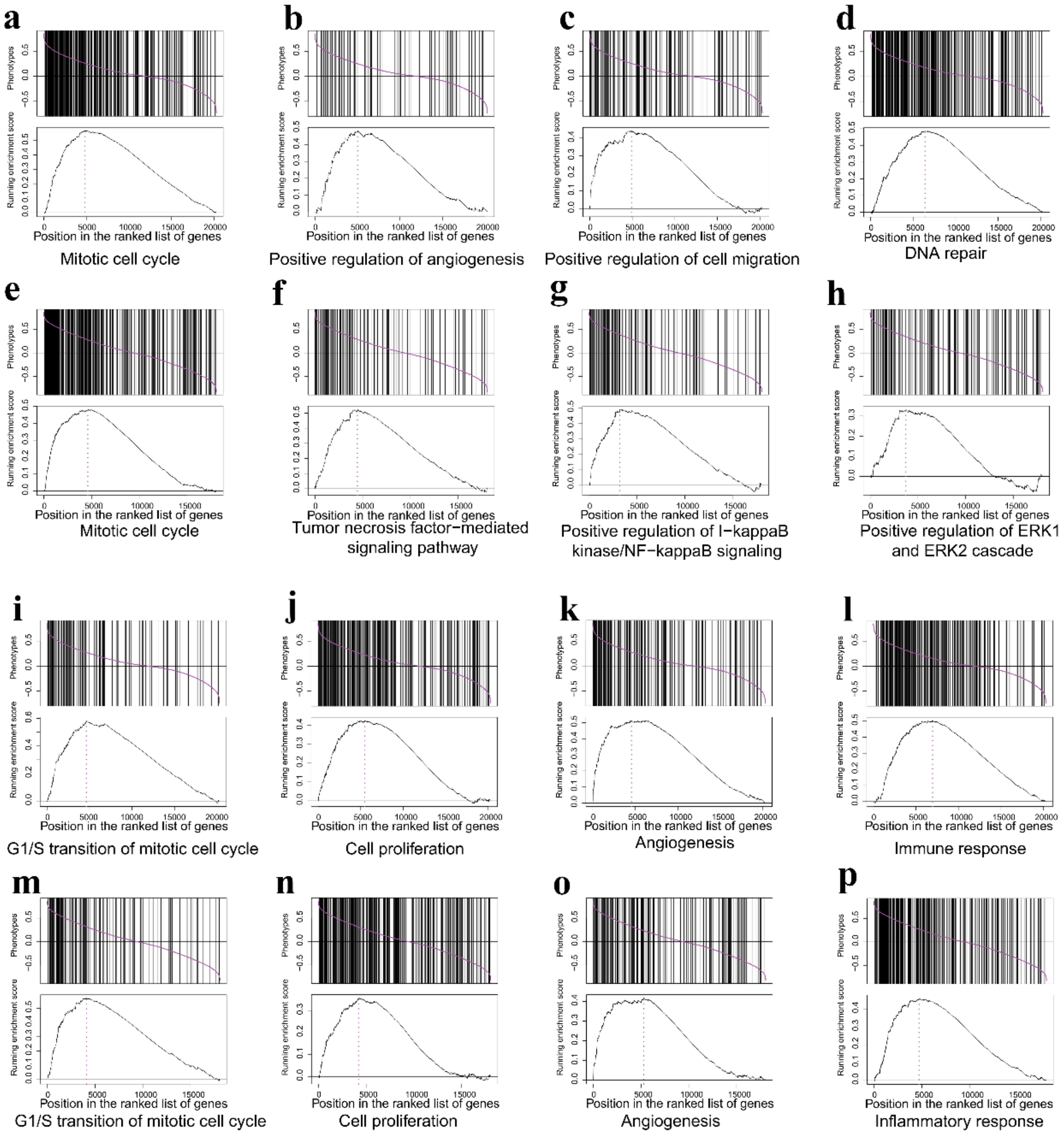


Fig S5. Concerted B7-H3 related biological processes and pathways in whole grade glioma of CGGA (a-d) and TCGA dataset (e-h).

Top 25 B7-H3 most related biological processes and pathways in GBM of CGGA (i-l) and TCGA dataset (m-p).