Supplemental Figure 1

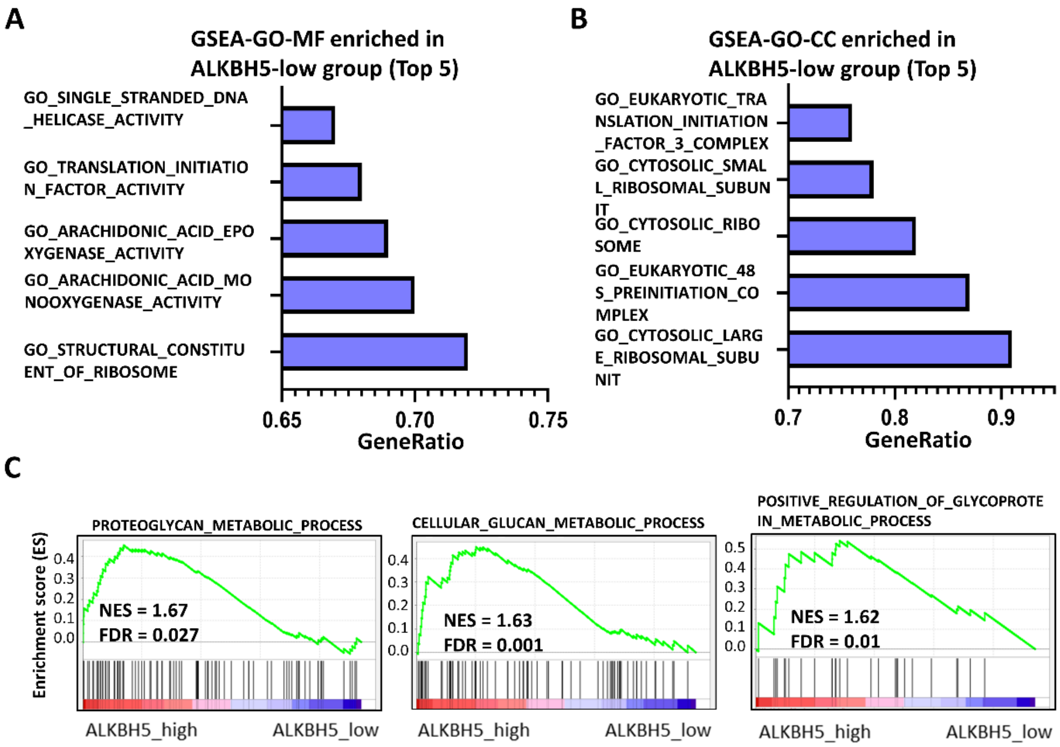


Figure S1

Identification and Landscape of ALKBH5

(**A, B**) Top 5 GO-MF (A) and CC (B) gene sets enriched in the ALKBH5-low group obtained by GSEA. (**C**) Three additional representative glucometabolic gene sets enriched in the ALKBH5-high group. NES: normalized enrichment score. FDR: false discovery rate.

Supplemental Figure 2

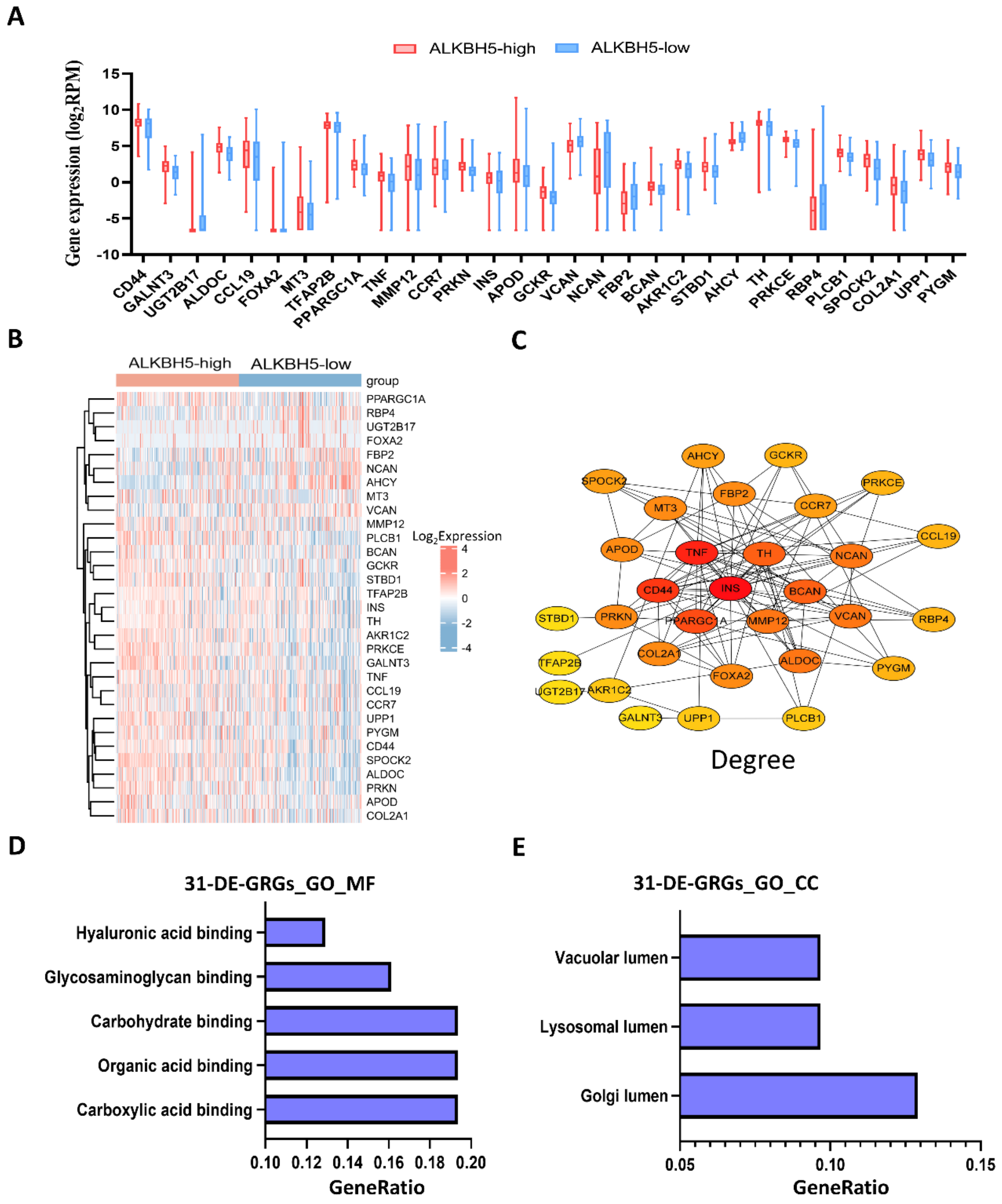


Figure S2

Identification and Functional Enrichment Analyses of DE-GRGs

(**A, B**) Gene expression profile of 31 DE-GRGs in the boxplot (A) and heatmap (B). All difference reaches statistical significance. (**C**) Thirty-one DE-GRGs in the PPI network calculated by Degree. (**D, E**) Top 5 and 3 gene sets functionally enriched by GO-MF (D) and CC (E) annotations.

Supplemental Figure 3

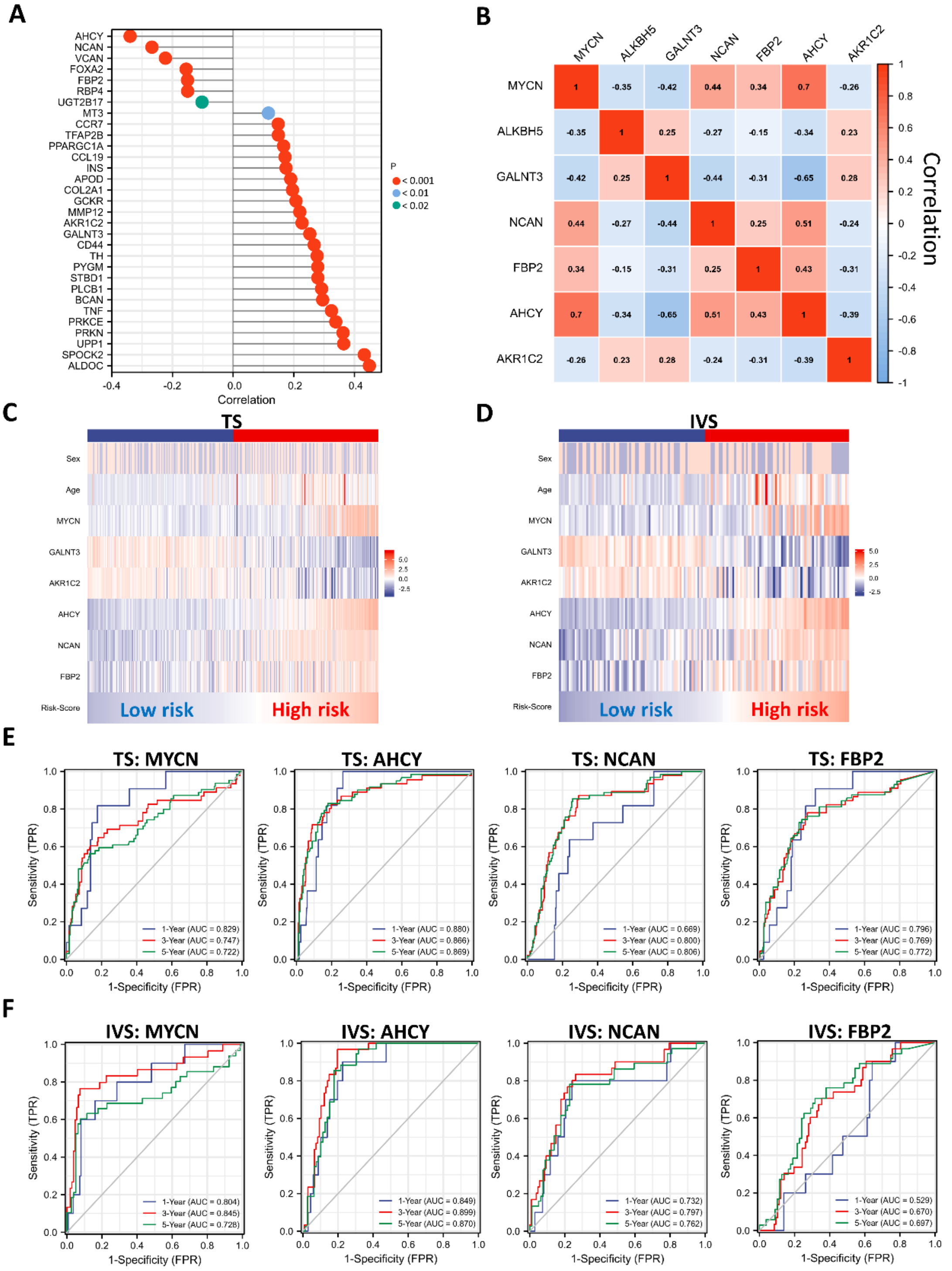
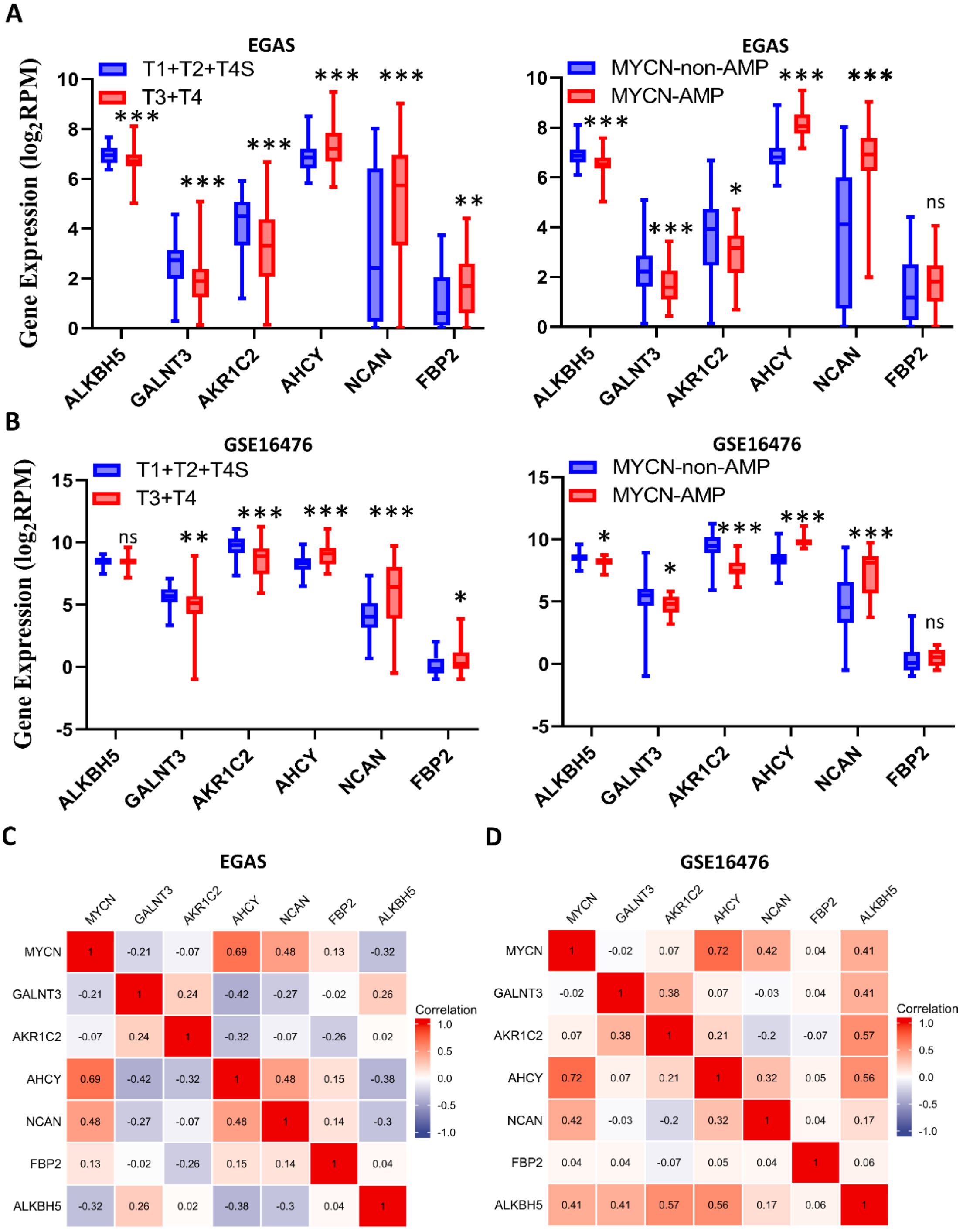


Figure S3

Five-gene Prognostic Signature Based on 31 DE-GRGs

(**A**) Correlation analysis between ALKBH5 and 31 DE-GRGs in GSE62564. (**B**) Correlation analysis between MYCN/ALKBH5 and genes in the model in GSE62564. (**C, D**) Heatmap showing the profile of clinical characteristics and the 5-gene model in TS (C) and IVS (D). (**E, F**) Time-dependent ROC curve in TS (E) and IVS (F) for independent risk factors including MYCN, AHCY, NCAN and FBP2. TS: training set. IVS: internal validation set. AUC: area under curve.

Supplemental Figure 4



C EGAS

	MYCN	GALNT3	AKR1C2	AHCY	NCAN	FBP2	ALKBH5
MYCN	1	-0.21	-0.07	0.69	0.48	0.13	-0.32
GALNT3	-0.21	1	0.24	-0.42	-0.27	-0.02	0.26
AKR1C2	-0.07	0.24	1	-0.32	-0.07	-0.26	0.02
AHCY	0.69	-0.42	-0.32	1	0.48	0.15	-0.38
NCAN	0.48	-0.27	-0.07	0.48	1	0.14	-0.3
FBP2	0.13	-0.02	-0.26	0.15	0.14	1	0.04
ALKBH5	-0.32	0.26	0.02	-0.38	-0.3	0.04	1

D GSE16476

	MYCN	GALNT3	AKR1C2	AHCY	NCAN	FBP2	ALKBH5
MYCN	1	-0.02	0.07	0.72	0.42	0.04	0.41
GALNT3	-0.02	1	0.38	0.07	-0.03	0.04	0.41
AKR1C2	0.07	0.38	1	0.21	-0.2	-0.07	0.57
AHCY	0.72	0.07	0.21	1	0.32	0.05	0.56
NCAN	0.42	-0.03	-0.2	0.32	1	0.04	0.17
FBP2	0.04	0.04	-0.07	0.05	0.04	1	0.06
ALKBH5	0.41	0.41	0.57	0.56	0.17	0.06	1

Figure S4

External Validation of the Gene Signature with Public Datasets

(**A, B**) Gene expression profile of ALKBH5 and 5 genes in the model based on INSS and MYCN amplification status from EGAS (A) and GSE16476 (B). (**C, D**) Matrix showing gene-gene correlation value among MYCN, ALKBH5 and other 5 genes in the model in EGAS (C) and GSE16476 (D). NS: not significant. P<0.05 was shown as *, P<0.01 as ** and P<0.001 as ***.

Supplemental Figure 5

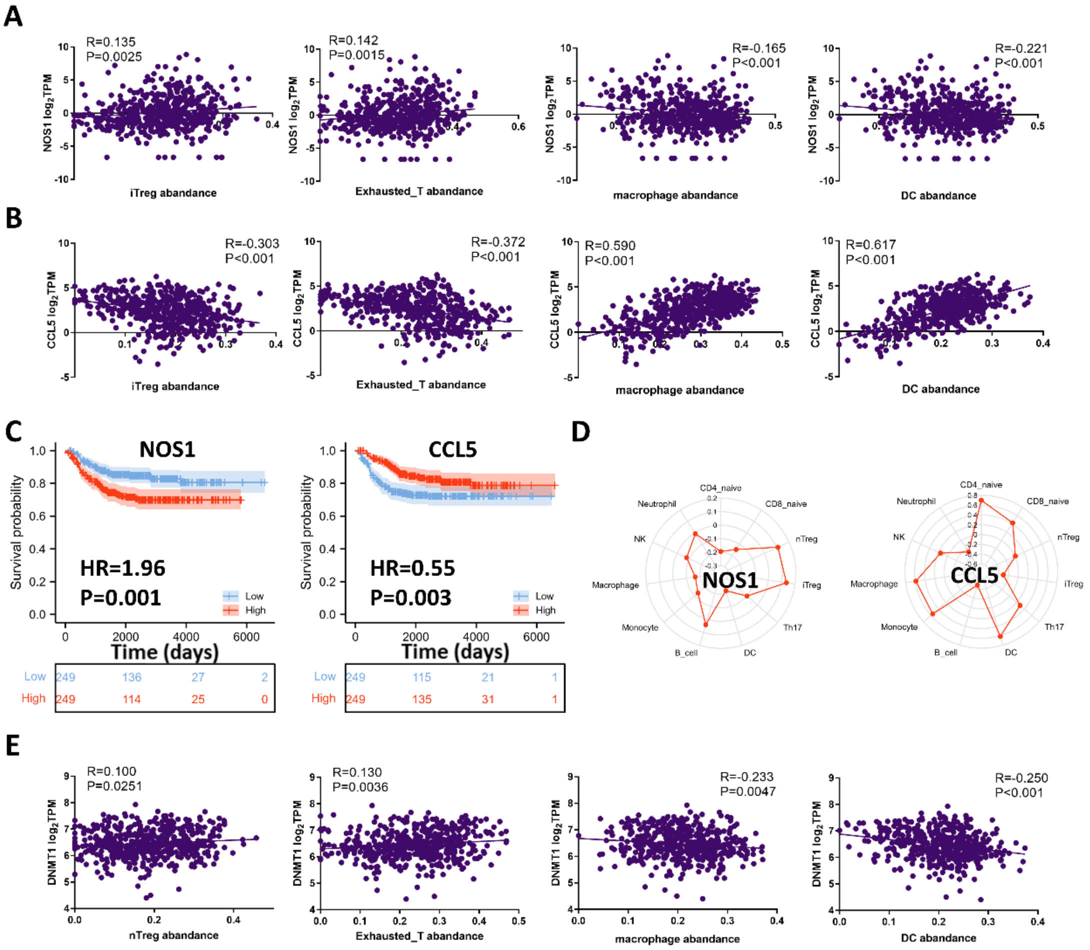


Figure S5

Immune Landscape of Neuroblastoma Patients and Potential Targets

(**A, B**) Pearson correlation analysis between NOS1 (A)/CCL5 (B) and iTregs/Exhausted T cells/macrophages/DCs. (**C**) Kaplan-Meier curve of GSE62564 between the NOS1-high and NOS1-low groups (left panel), the CCL5-high and CCL5-low groups (right panel). (**D**) Radar map showing relationship between immune cells and NOS1 (left panel)/CCL5 (right panel). (**E**) Pearson correlation analysis between DNMT1 and nTregs/Exhausted T cells/macrophages/DCs. nTregs: natural T regulatory cells. iTregs: inducible T regulatory cells. DCs: dendritic cells.