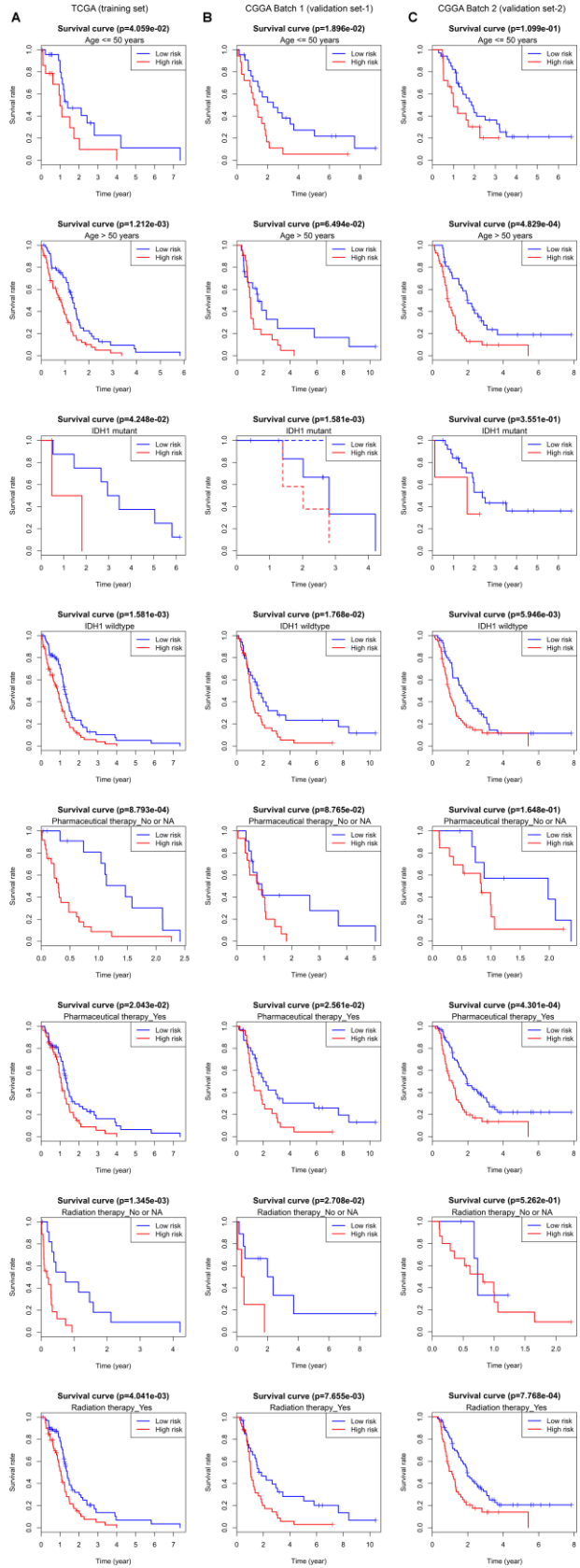
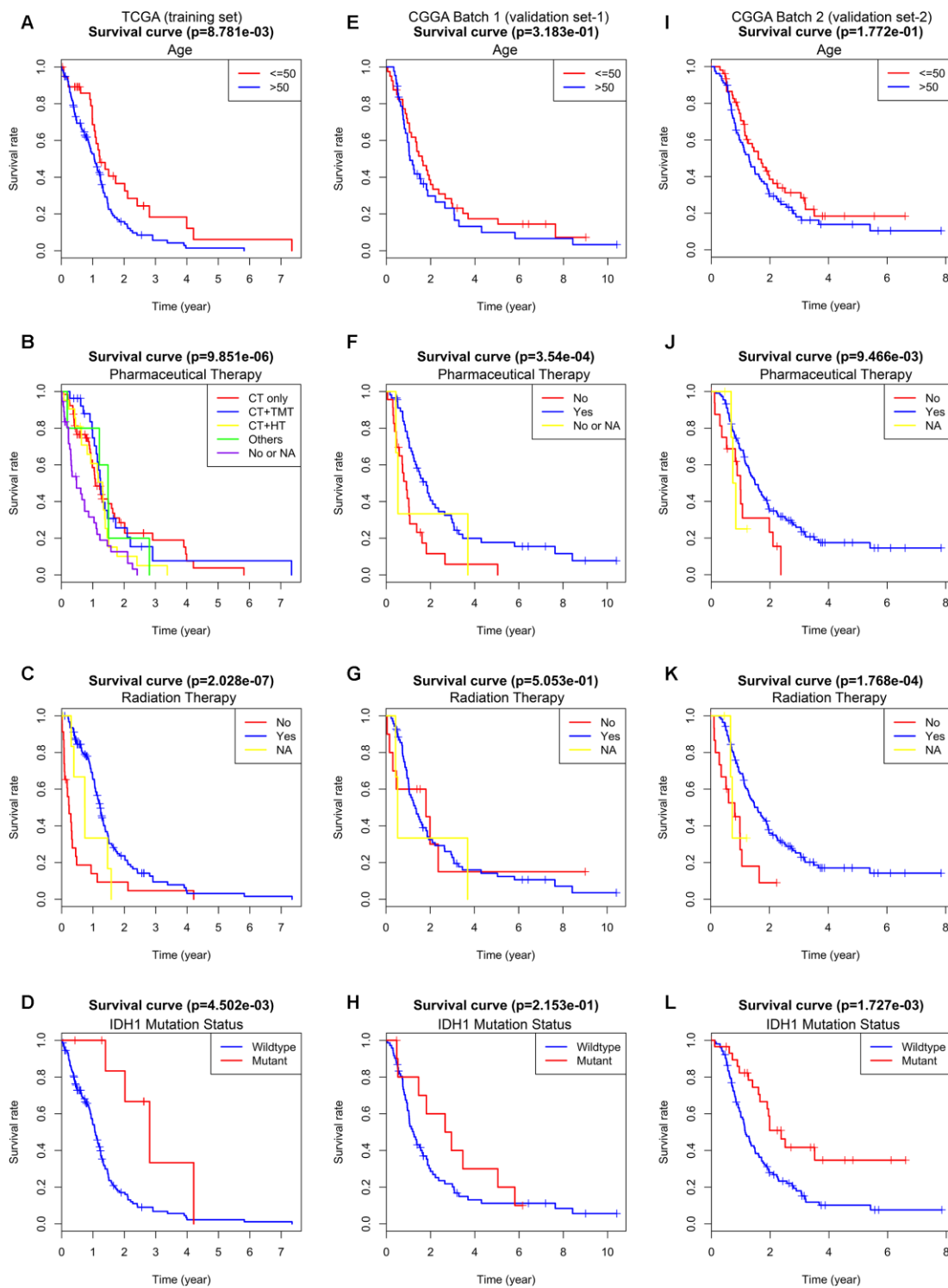


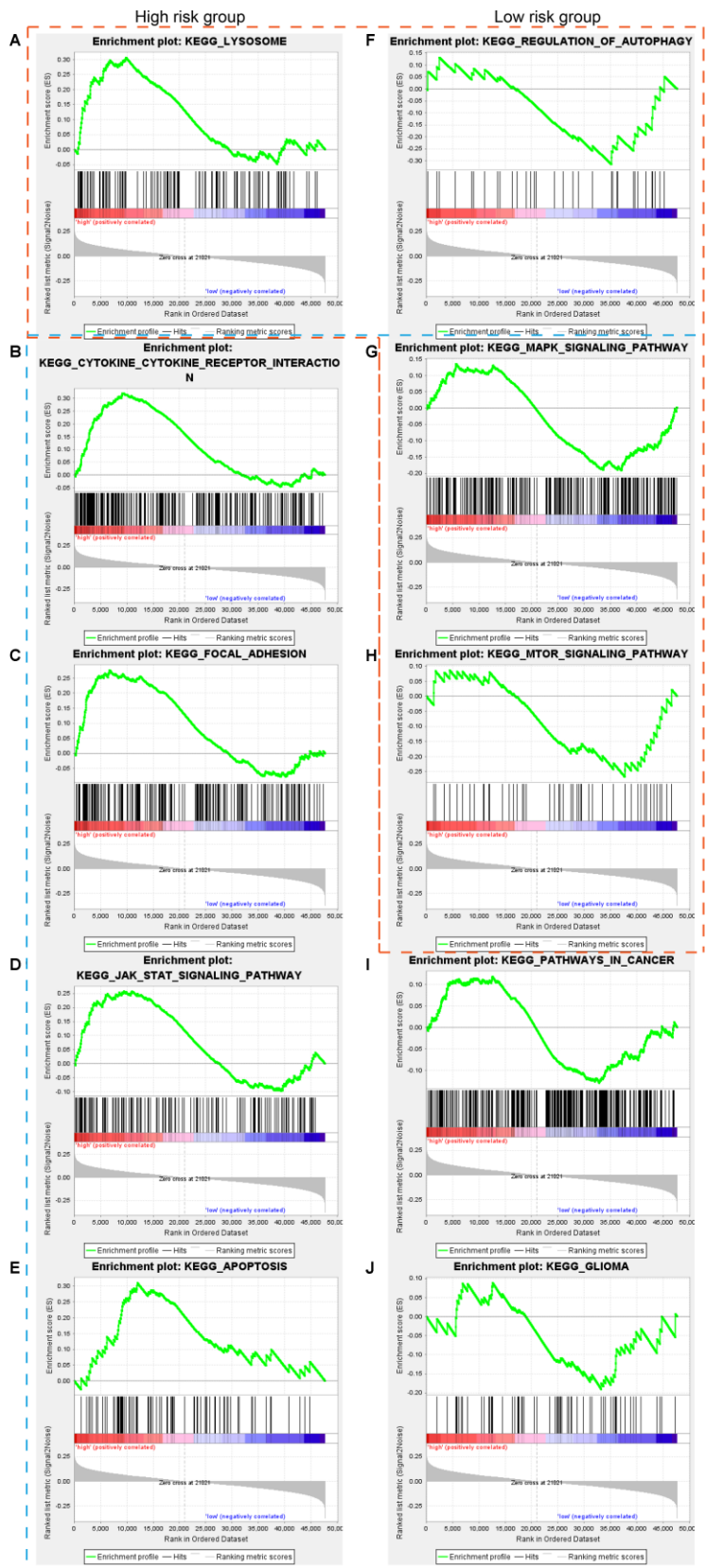
# SUPPLEMENTARY FIGURES



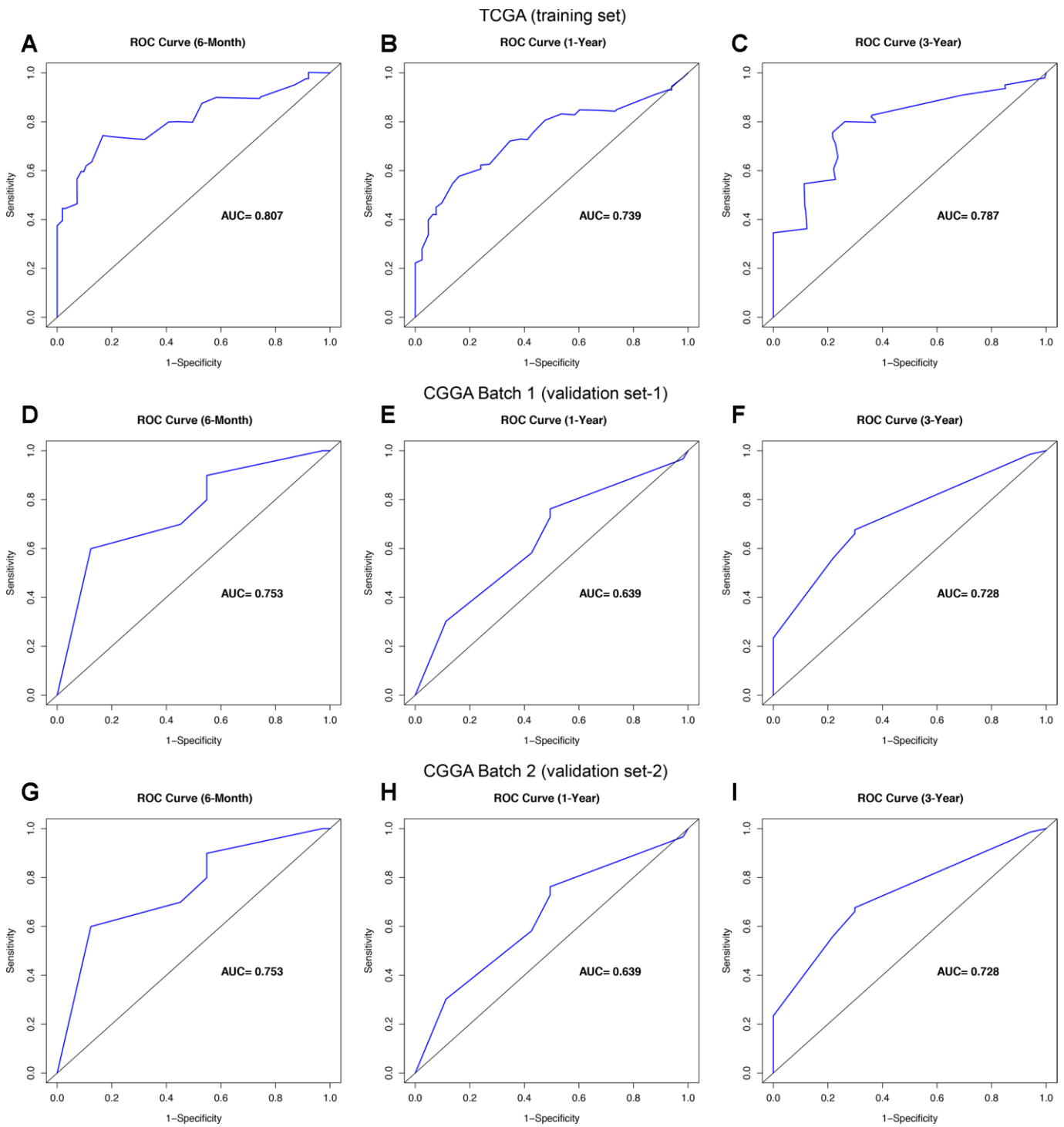
**Supplementary Figure 1.** Kaplan-Meier survival curves of OS according to low or high risk scores stratified by age, IDH mutation status, pharmaceutical therapy, and radiation therapy in the TCGA training cohort (A), CGGA Batch-1 validation cohort (B), and CGGA Batch-2 validation cohort (C).



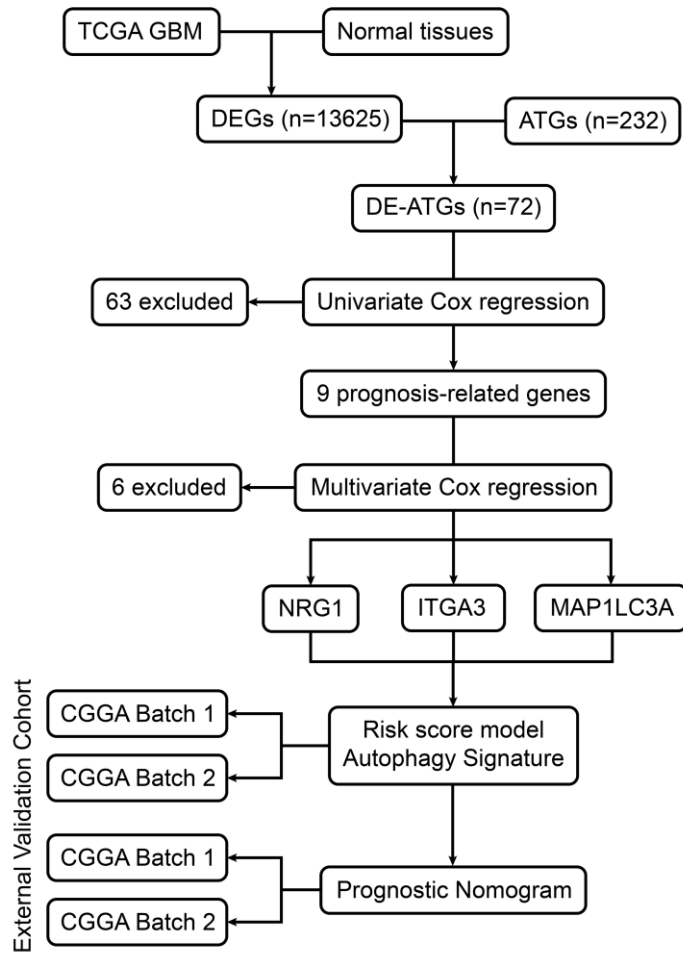
**Supplementary Figure 2.** Kaplan-Meier survival curves of age, pharmaceutical therapy, radiation therapy, and IDH mutation status for the OS of patients in the TCGA training cohort, CGGA Batch-1 validation cohort, and CGGA Batch-2 validation cohort.



**Supplementary Figure 3. Gene set enrichment analysis (GSEA) was performed between the ATG-based high-risk and low-risk groups based on the TCGA GBM cohort. Red box: regulation of autophagy and autophagy-related KEGG pathways. Blue box: pathways in cancer and their related KEGG pathways, including glioma.**



**Supplementary Figure 4.** The prognostic performance of the nomogram demonstrated by the ROC curve for predicting the 0.5-, 1-, and 3-year OS rate in the TCGA training cohort (A–C), CGGA Batch-1 validation cohort (D–F), and CGGA Batch-2 validation cohort (G–I).



Supplementary Figure 5. The schematic diagram for constructing the prognostic prediction model based on autophagy signature.