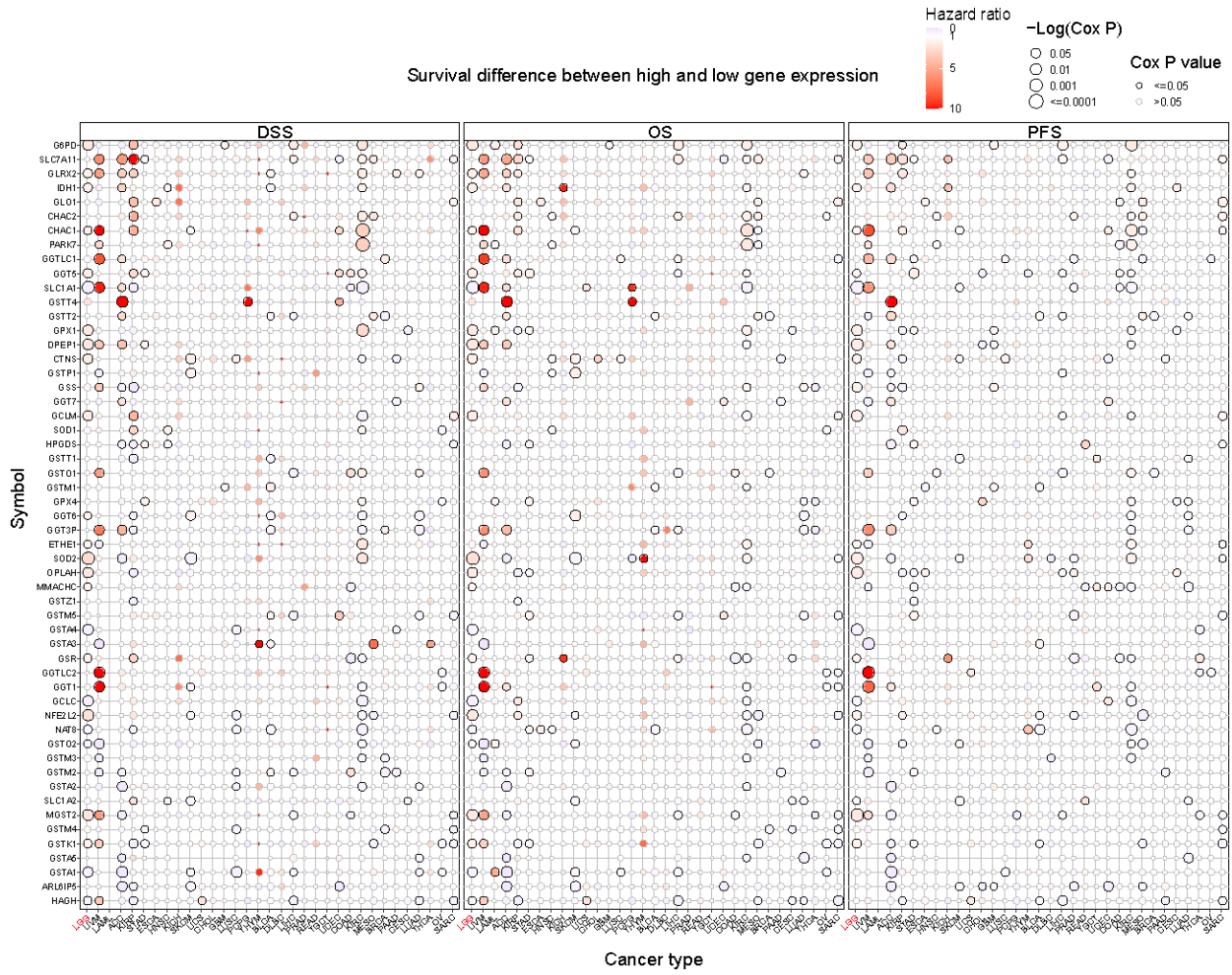
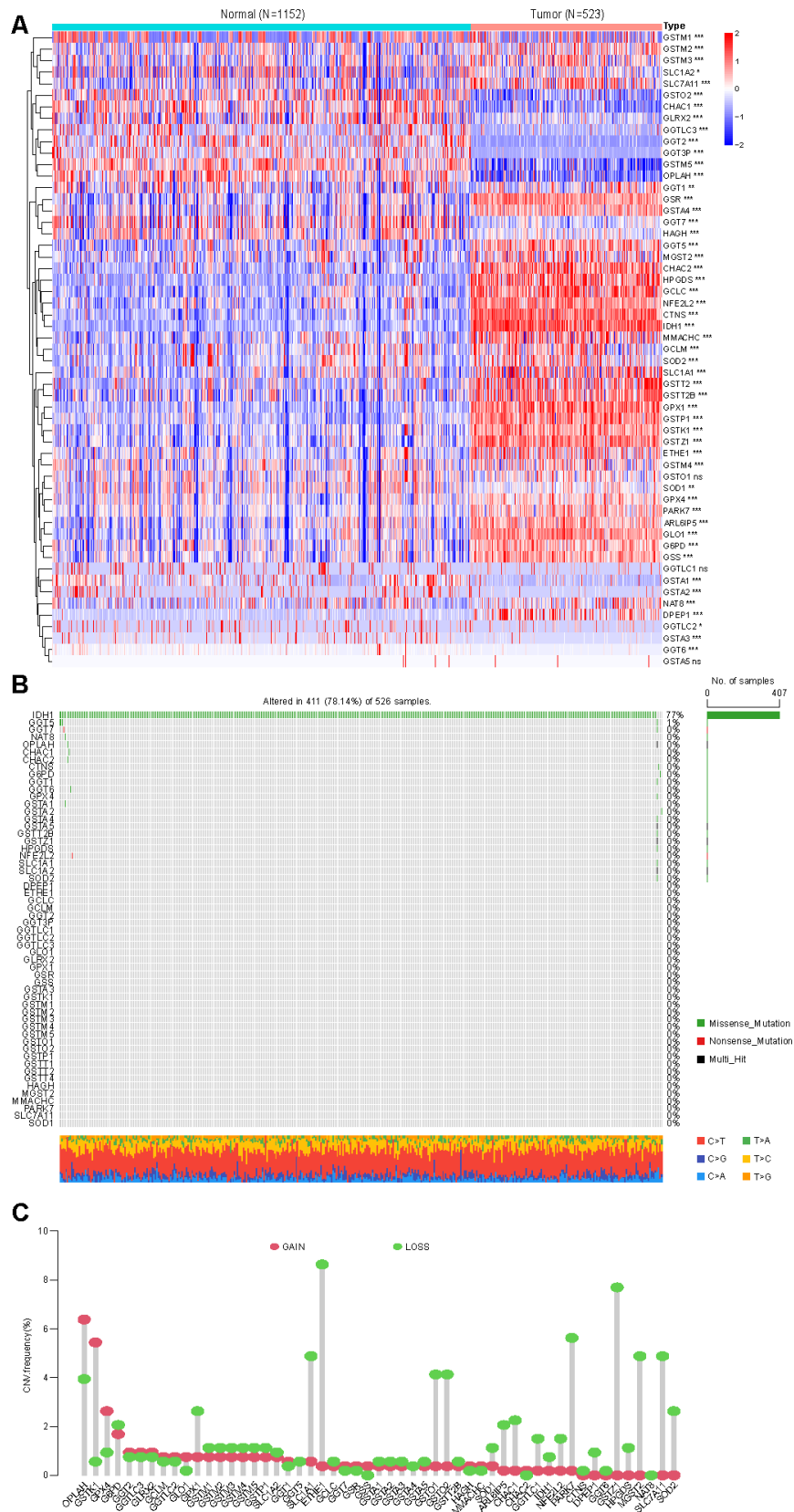


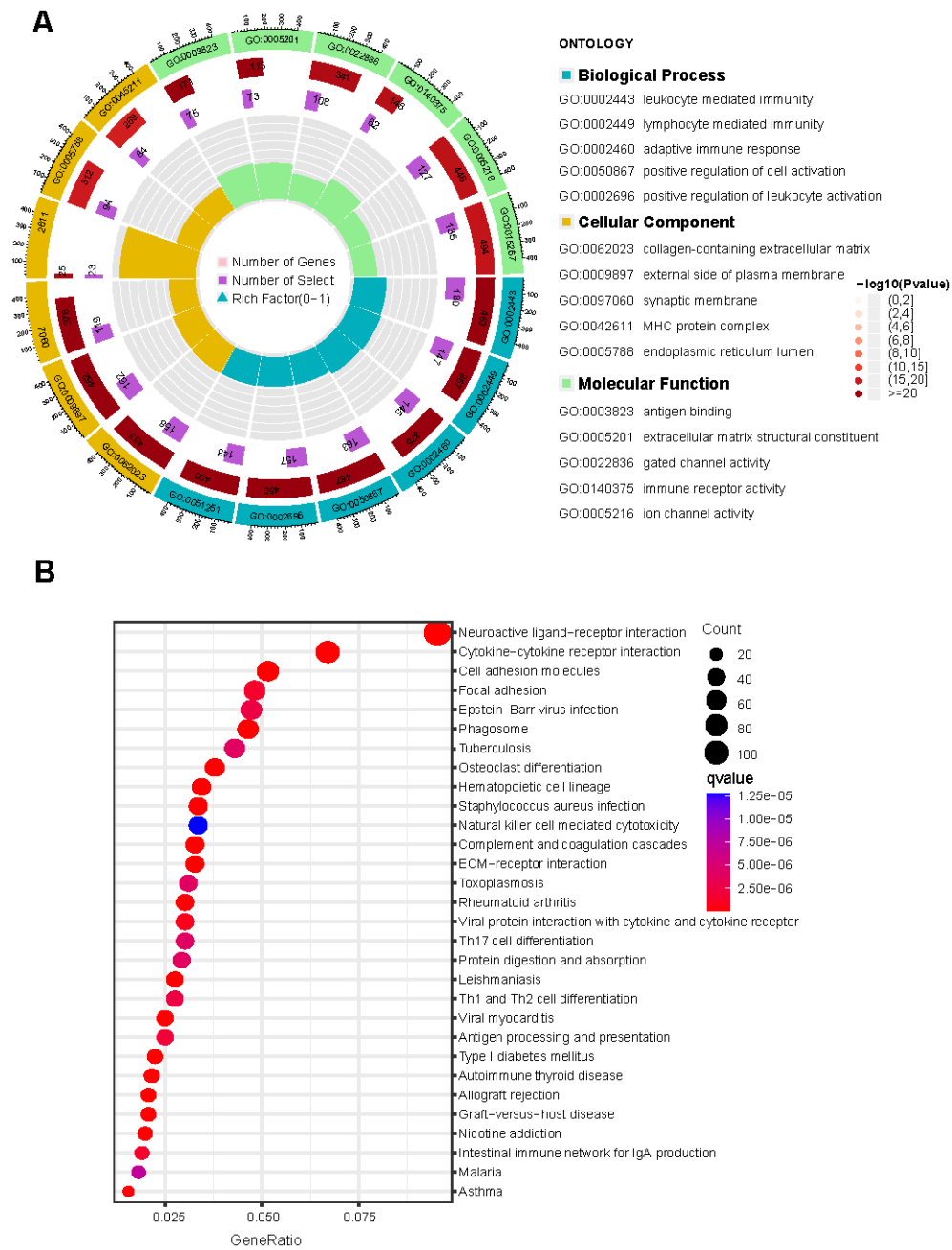
SUPPLEMENTARY FIGURES



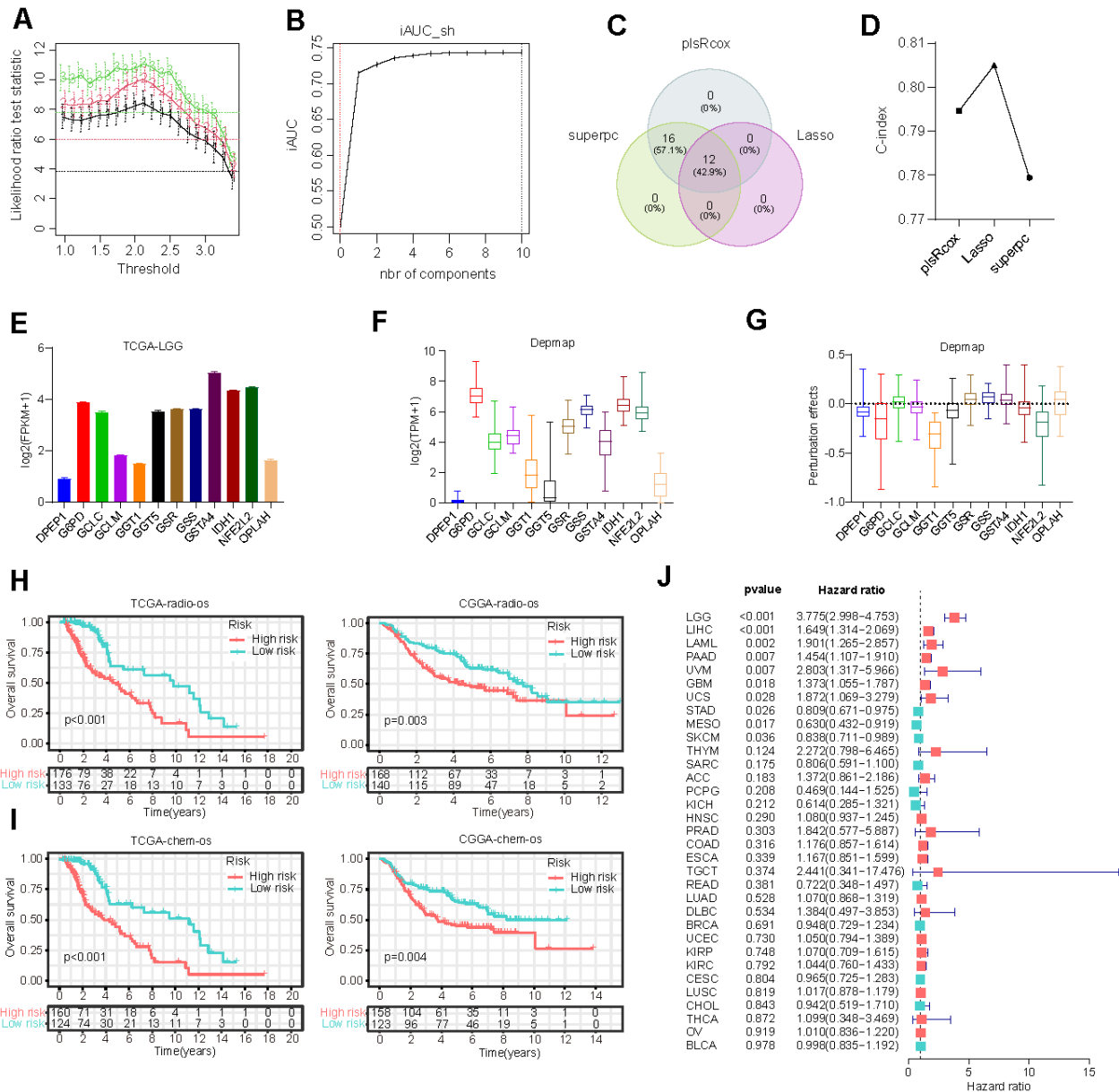
Supplementary Figure 1. Survival analysis of glutathione metabolism genes across 33 cancer types using the GSCA website.



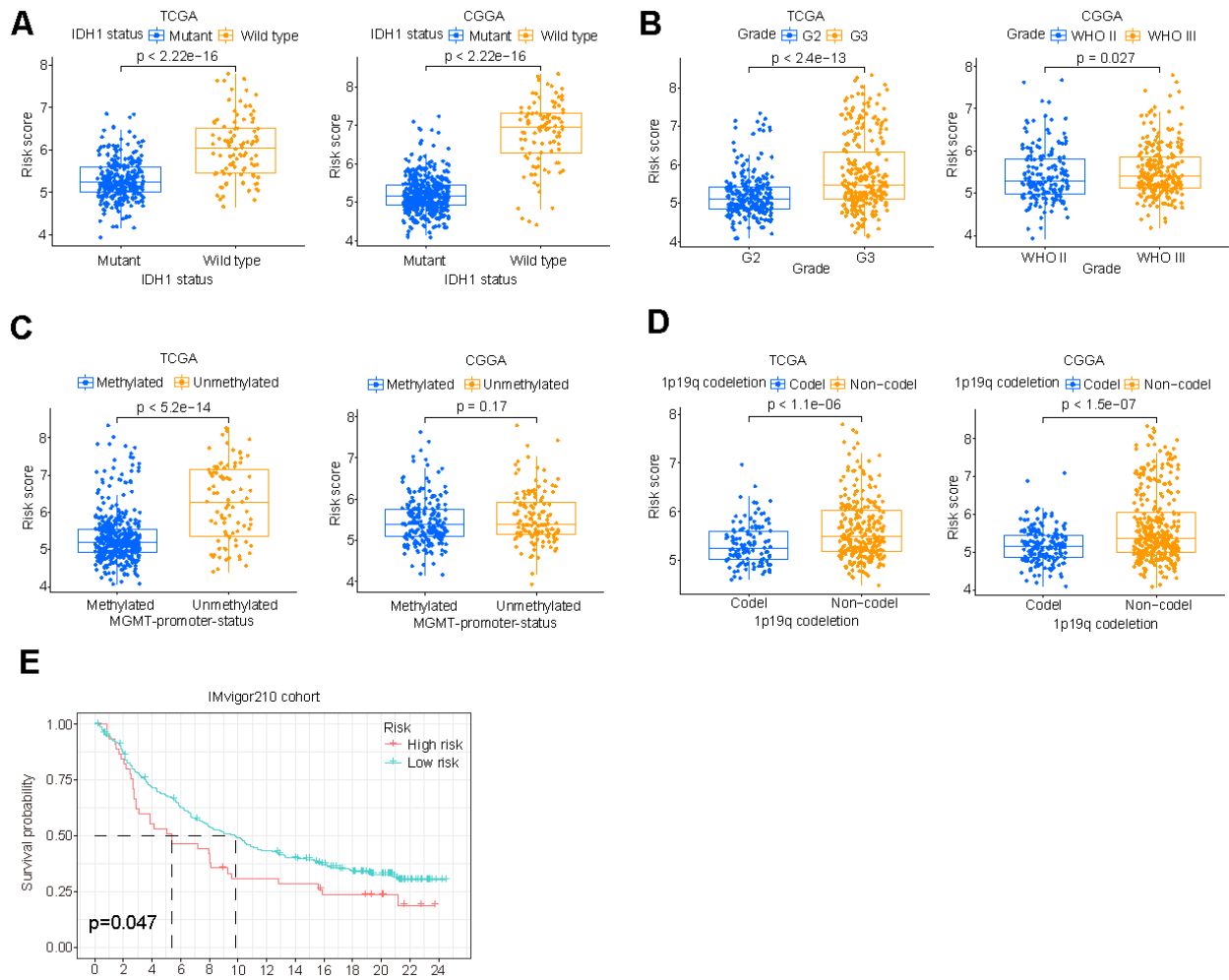
Supplementary Figure 2. Expression levels and genetic variation landscape of GMRGs. (A) Comparative expression levels of 56 GMRGs between LGG cancer and normal brain tissues. (B) Mutation frequency of GMRGs in patients from the TCGA-LGG dataset. (C) Copy number variation (CNV) frequency of GMRGs in the TCGA-LGG dataset.



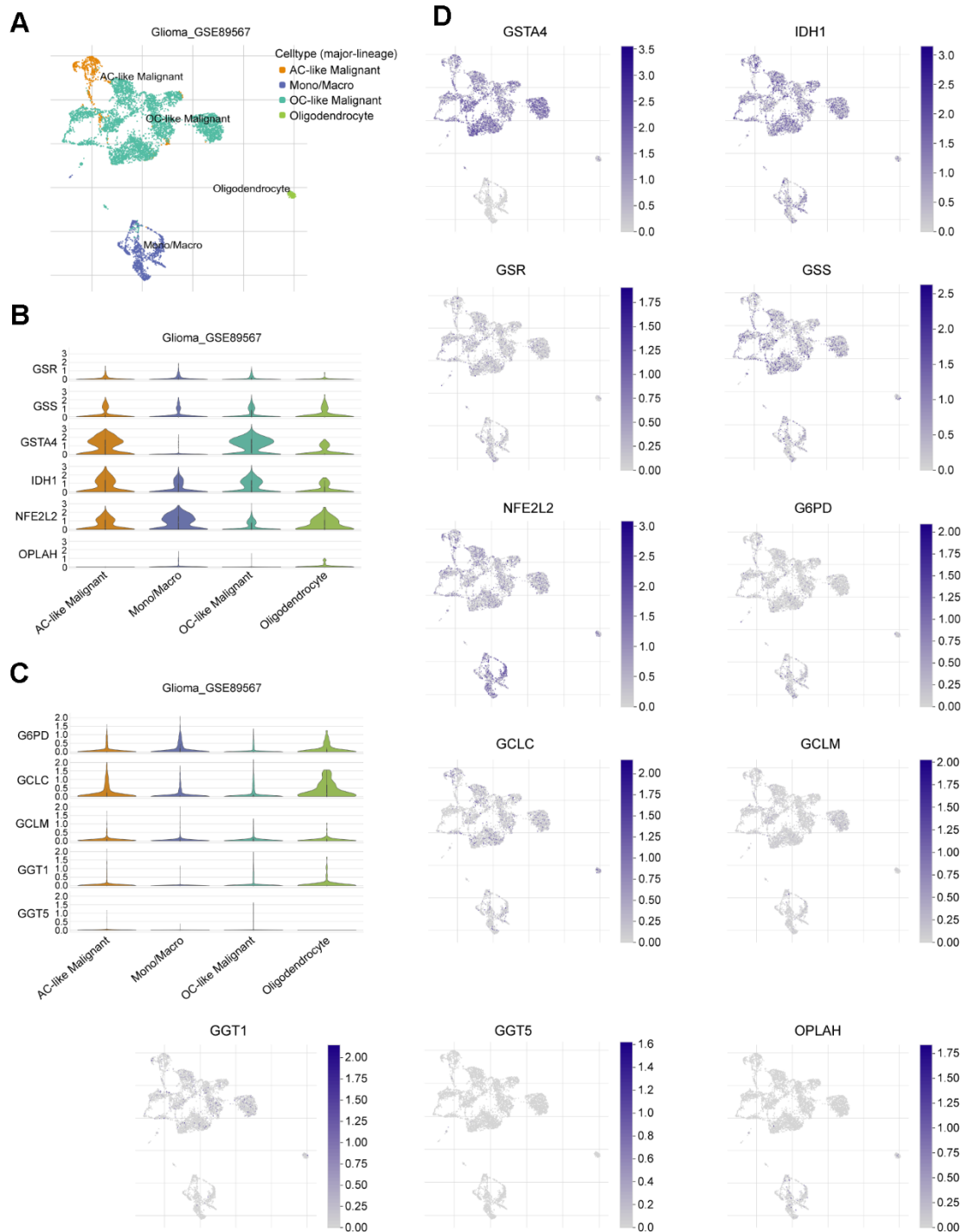
Supplementary Figure 3. Functional enrichment analysis of GMRGs-related clusters. (A) Gene Ontology (GO) enrichment analysis based on the Differentially Expressed Genes (DEGs). (B) Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analysis based on the DEGs.



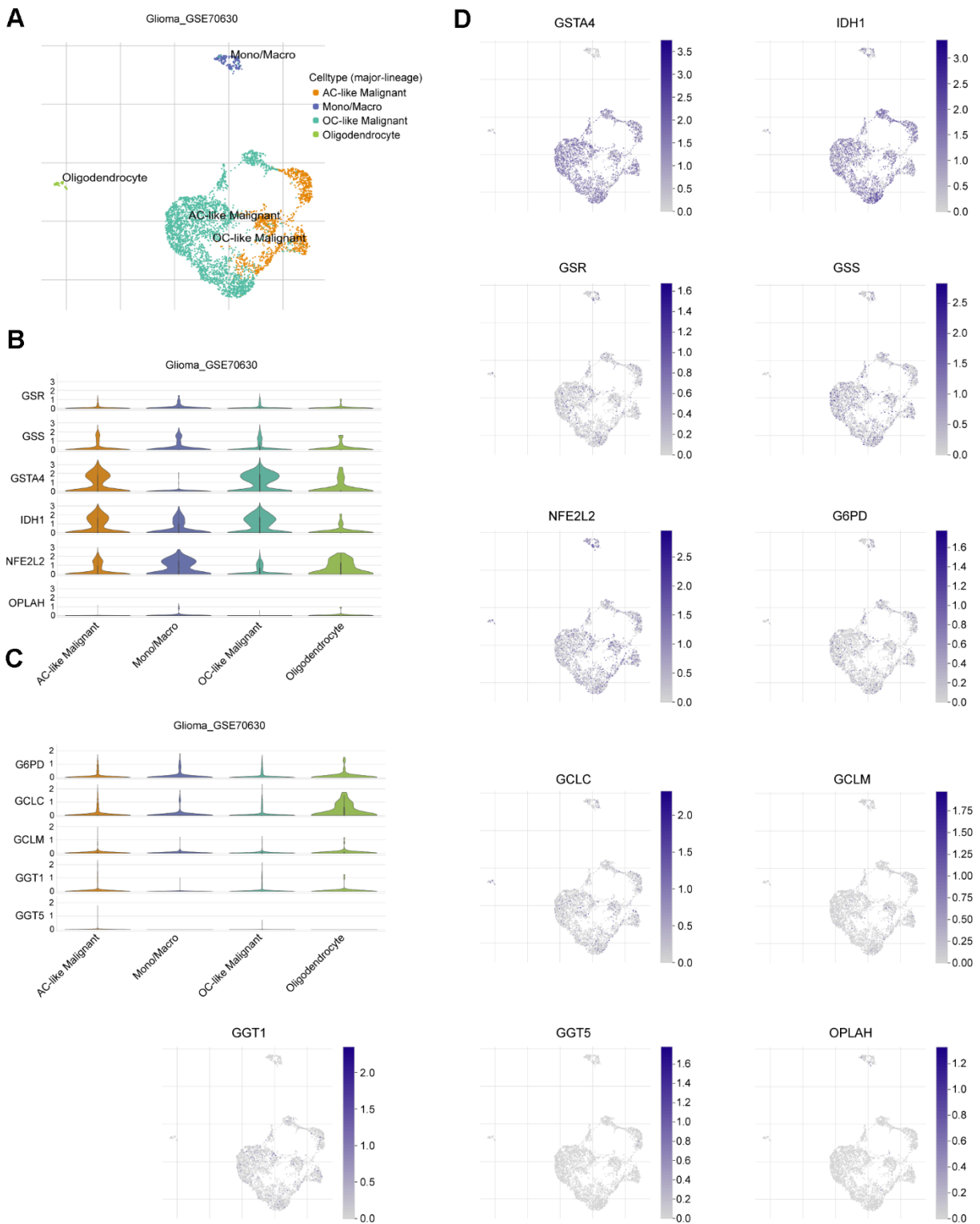
Supplementary Figure 4. Construction and confirmation of GMRGs-based risk score. (A) Cross-validation based on the SuperPC model. (B) Cross-validation based on the plsRcox model. (C) The Venn diagram displays the intersection of model genes from the three machine learning algorithms. (D) The C-index of the three machine learning algorithms. (E) Expression levels of model genes in TCGA-LGG dataset (F) Expression levels of model genes in the CNS/brain cell lines in the CCLE database. (G) Gene perturbation effects of model genes in the CNS/brain cell lines in the CCLE database. (H, I) OS curves for patients in high-risk and low-risk groups receiving radiation therapy or chemotherapy in TCGA-LGG or CGGA-LGG datasets. (J) Univariate Cox regression analysis based on the risk score across 33 kinds of cancer types.



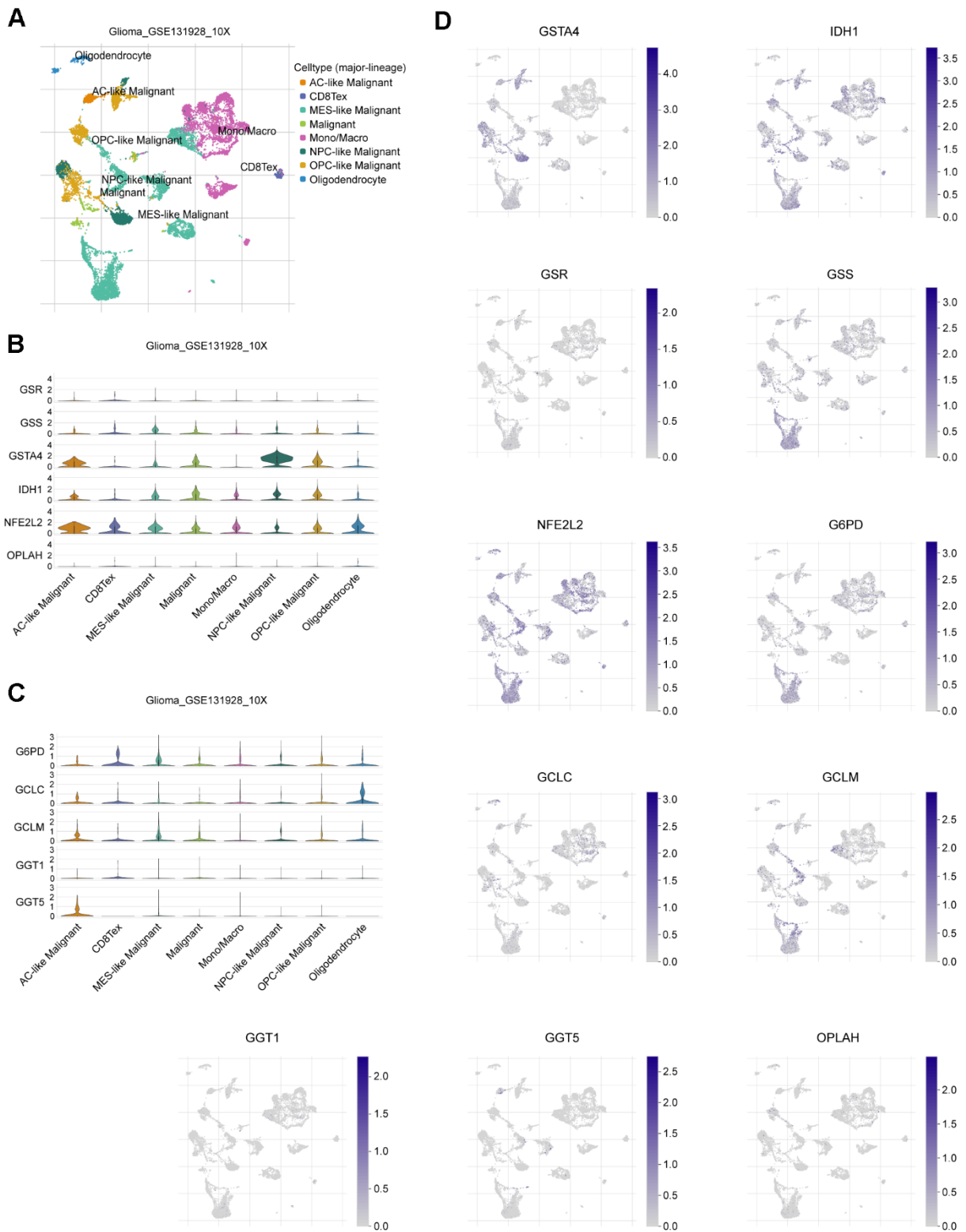
Supplementary Figure 5. Association of GS with clinical characteristics of LGG. (A–D) The risk scores are associated with clinical characteristics of IDH1 status (A), Grade (B), MGMT promoter status (C), and 1p19q co-deletion (D) in TCGA-LGG and CGGA-LGG datasets. (E) Survival analysis of the high-risk and low-risk groups in the immunotherapy IMvigor210 cohort.



Supplementary Figure 6. Model gene expression patterns at the single-cell level. (A) Identification of major cell subtypes in the LGG single-cell dataset Glioma GSE89567. (B, C) Expression patterns of model genes across different cell populations. (D) Expression patterns of model genes in different cell populations.



Supplementary Figure 7. Model gene expression patterns at the single-cell level. (A) Identification of major cell subtypes in the LGG single-cell dataset Glioma_GSE70630. (B, C) Expression patterns of model genes across different cell populations. (D) Expression patterns of model genes in different cell populations.



Supplementary Figure 8. Model gene expression patterns at the single-cell level. (A) Identification of major cell subtypes in the Glioma_GSE131928_10X single-cell dataset. (B, C) Expression patterns of model genes across different cell populations. (D) Expression patterns of model genes in different cell populations.