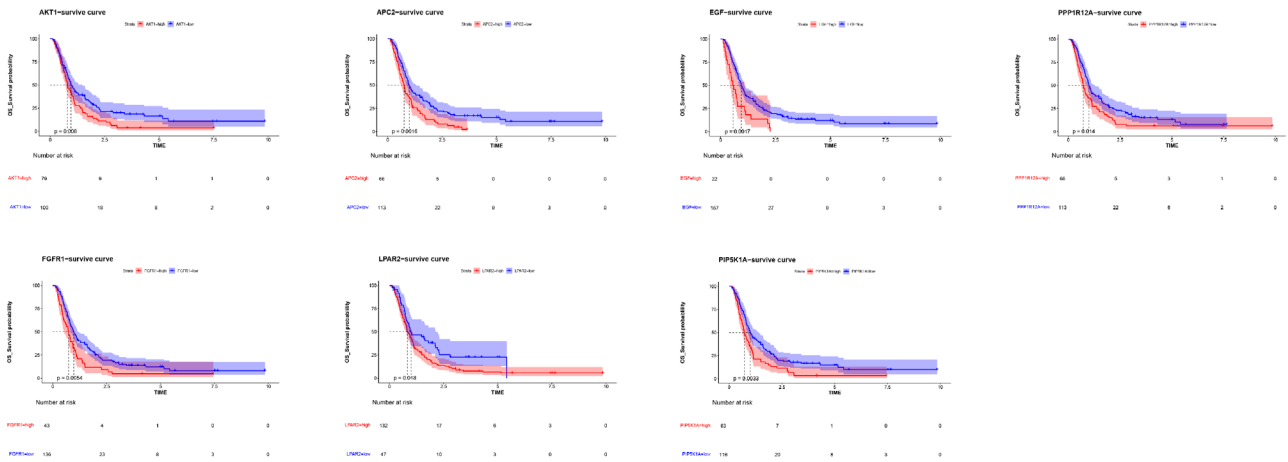
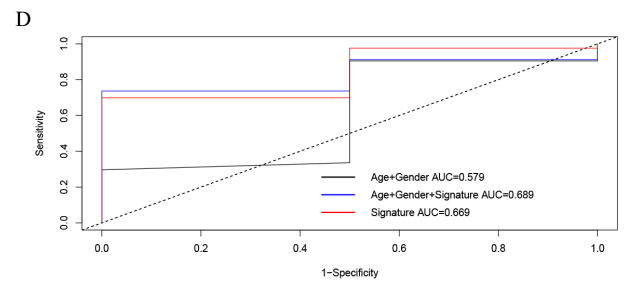
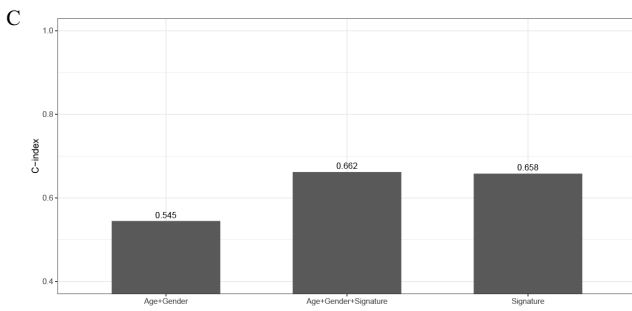
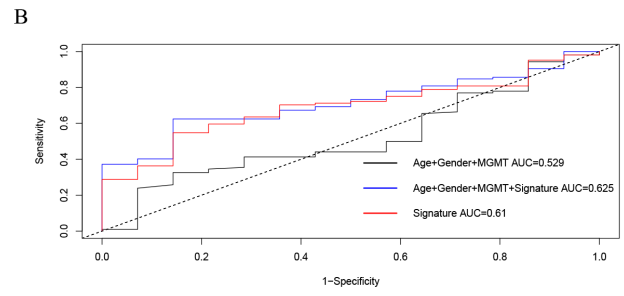
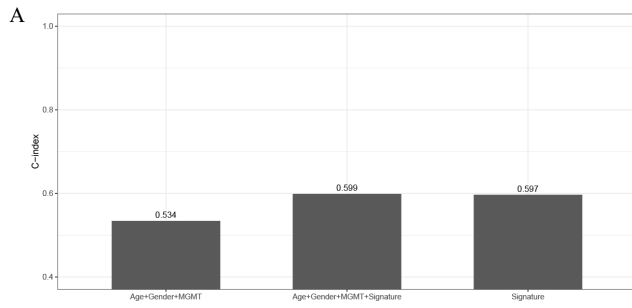


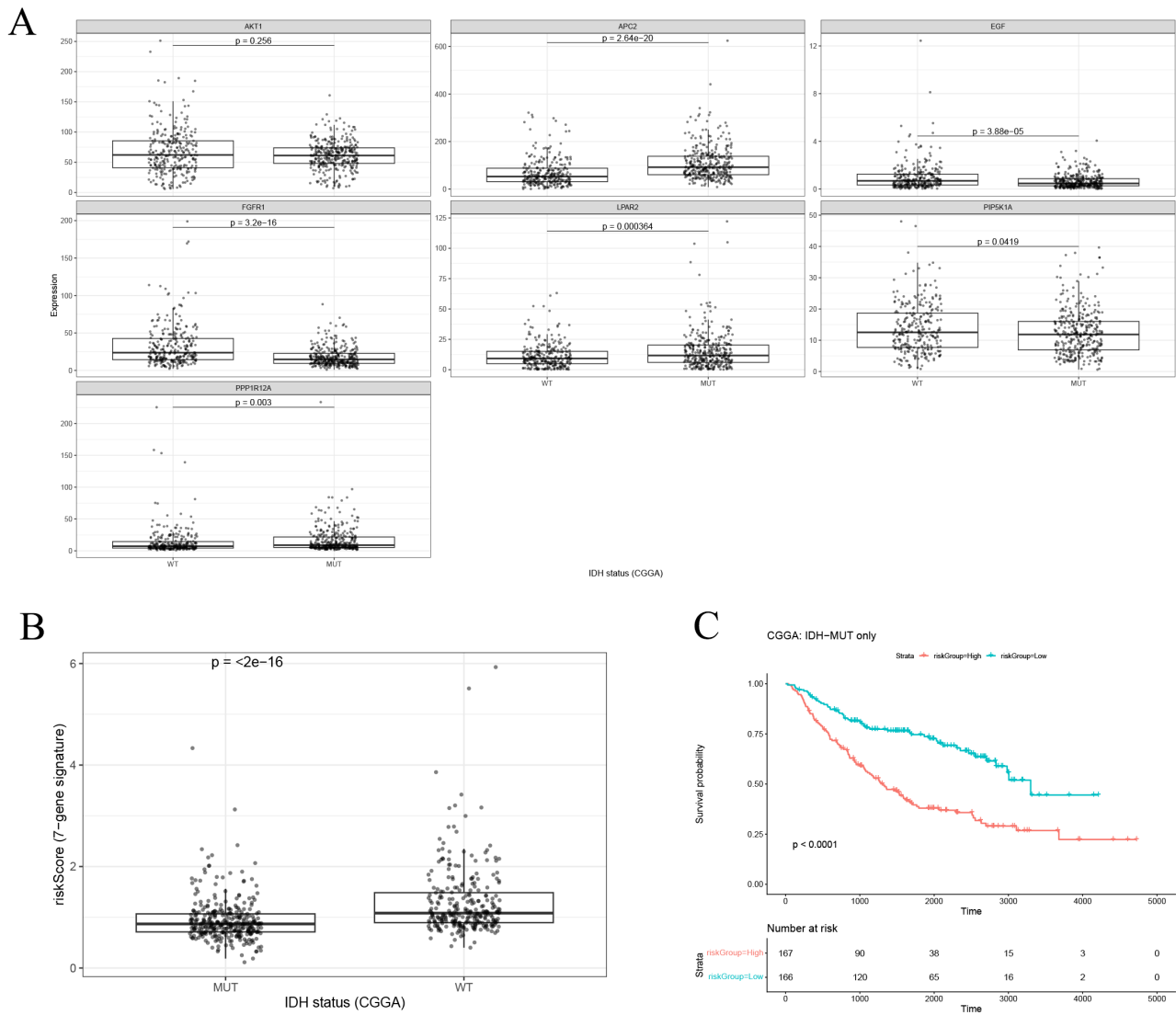
**Figure S1** Expression distribution of the seven signature genes in the CGGA cohort. CGGA, Chinese Glioma Genome Atlas; OS, overall survival.



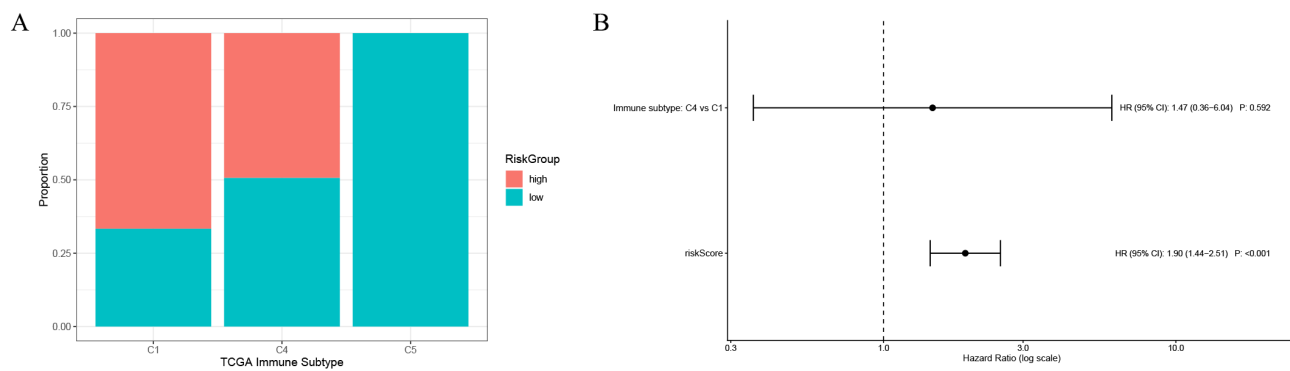
**Figure S2** Survival analysis of seven key genes.



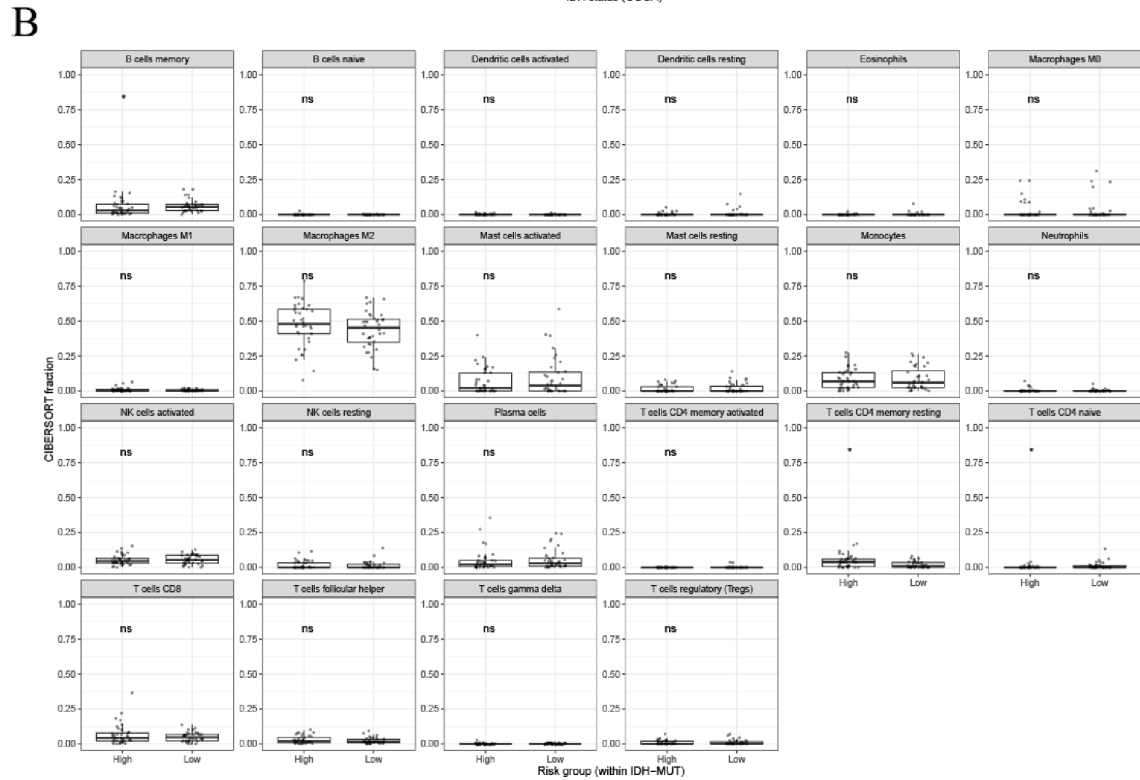
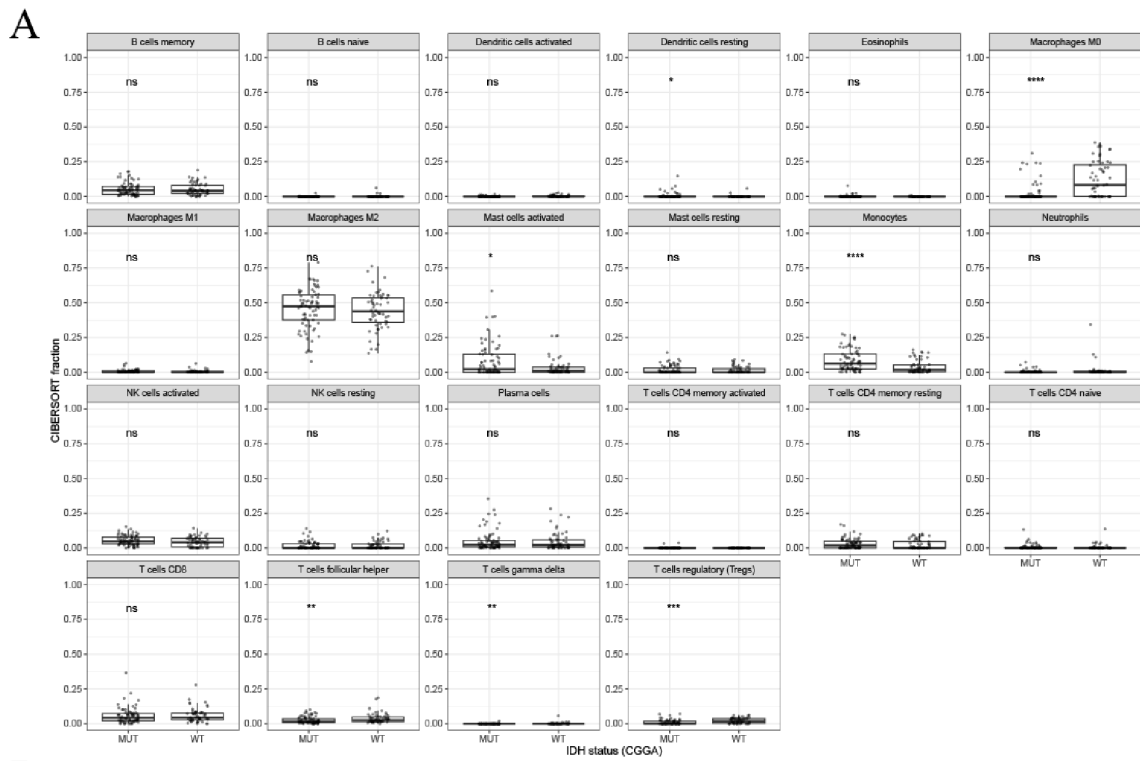
**Figure S3** Incremental prognostic value of the actin cytoskeleton-related gene signature compared with clinical variables.



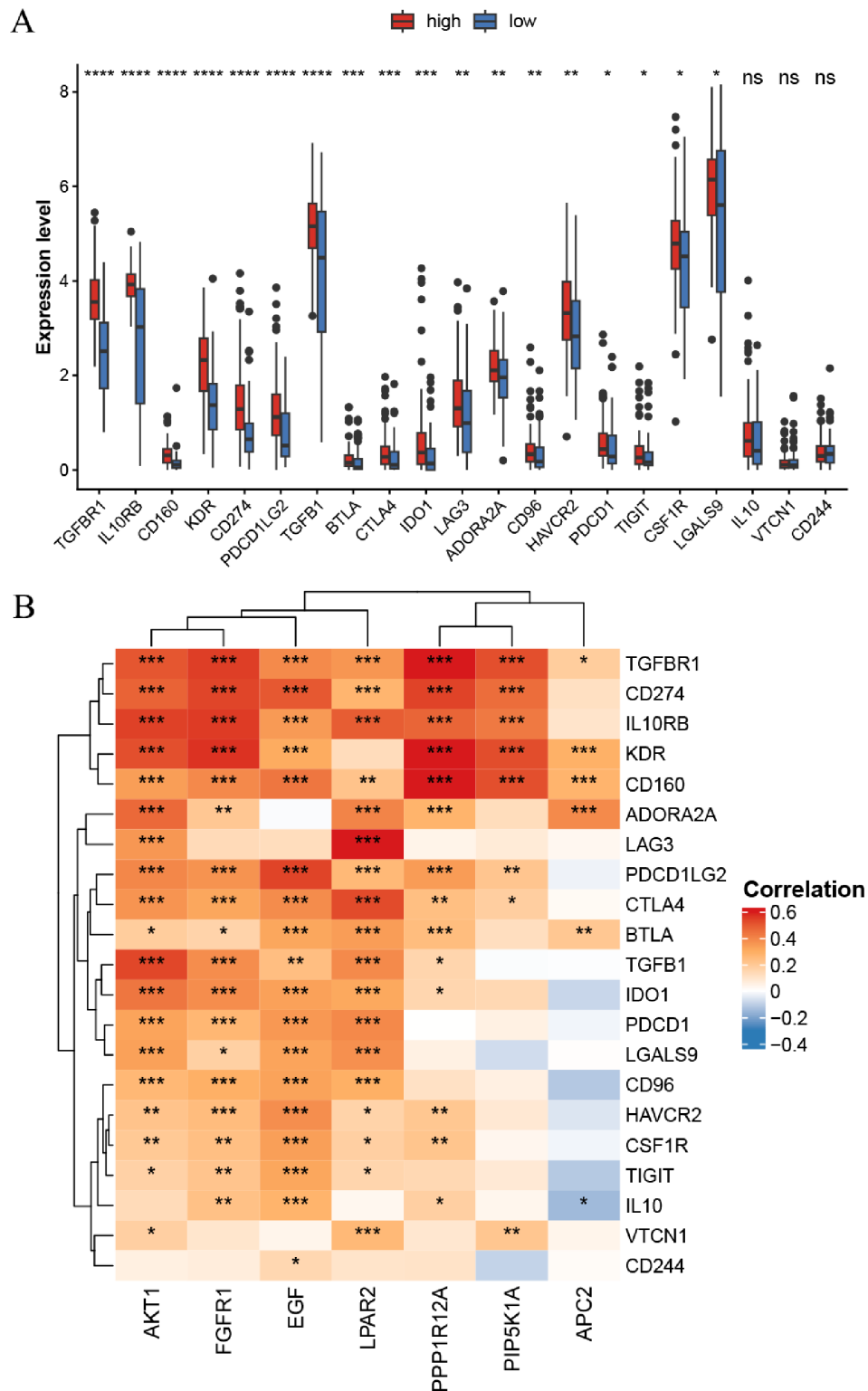
**Figure S4** Comparative analysis of the actin cytoskeleton-related gene signature between IDH wild-type and IDH-mutant gliomas in the CGGA cohort.



**Figure S5** Association between the riskScore and TCGA immune subtypes. TCGA, The Cancer Genome Atlas.



**Figure S6** Immune infiltration patterns associated with IDH status and riskScore in the CGGA cohort. Statistical significance is indicated as follows: \*, P<0.05; \*\*, P<0.01; \*\*\*, P<0.001; \*\*\*\*, P<0.0001. CGGA, Chinese Glioma Genome Atlas; ns, not significant.



**Figure S7** Association between the actin cytoskeleton-related gene signature and immune checkpoint molecules in the CGGA cohort. Statistical significance is indicated as follows: \*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$ ; \*\*\*\*,  $P < 0.0001$ . CGGA, Chinese Glioma Genome Atlas; ns, not significant.