

## Supplementary Materials

### **IL-32 as a prognostic biomarker and therapeutic target in glioma: implications for tumor progression and immune modulation**

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Fig. S1: TCGA glioma mutation summary; Fig. S2: Subtype identification in glioma; Fig. S3: Evaluation of the prognostic risk model for glioma; Fig. S4: Decision curve analysis of the prognostic risk model for glioma; Table S1: Functional enrichment analysis of IL-32 in glioma.

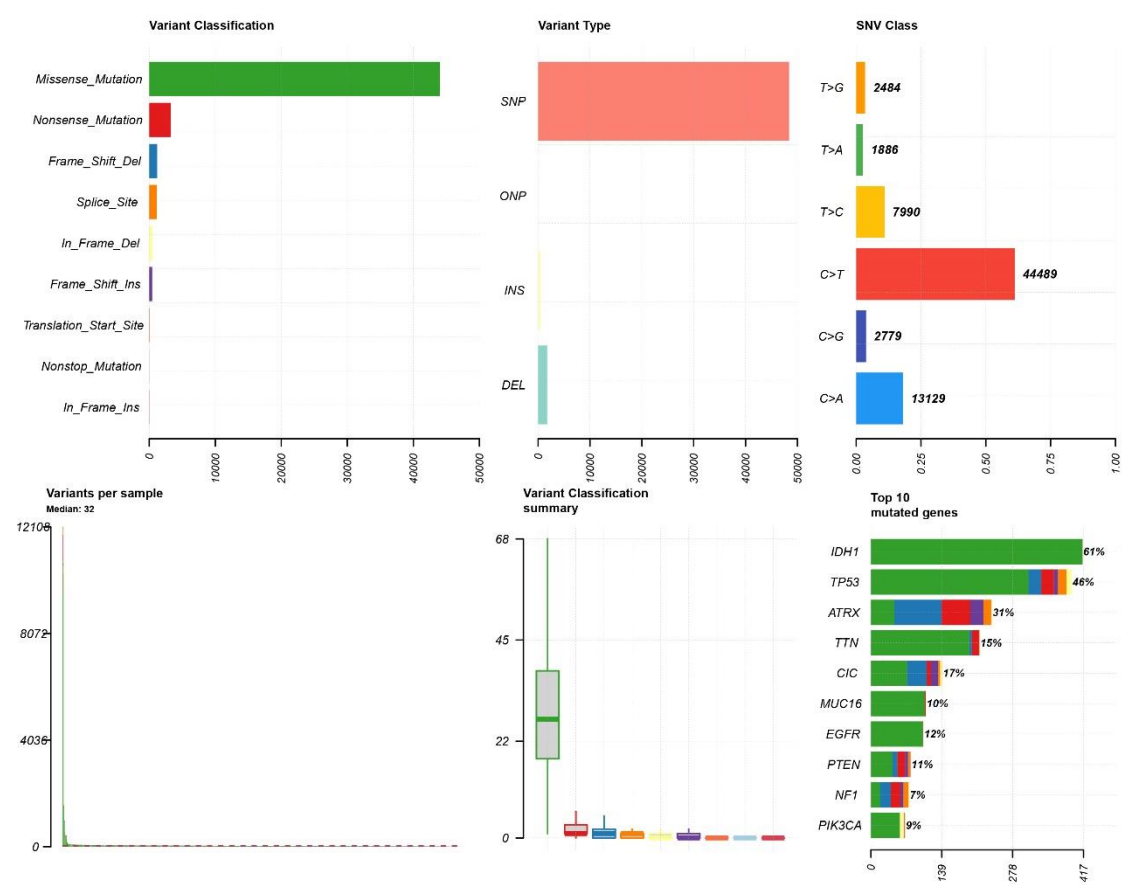


**Fig. S1.** TCGA glioma mutation summary. The panel displays the distribution of variant classifications and types across glioma samples, along with single nucleotide variant (SNV) spectra. The number of variants per sample (median: 32). The mutation frequency of the top 10 most frequently mutated genes, including IDH1, TP53, ATRX, TTN, CIC, MUC16, EGFR, PTEN, NF1, and PIK3CA.

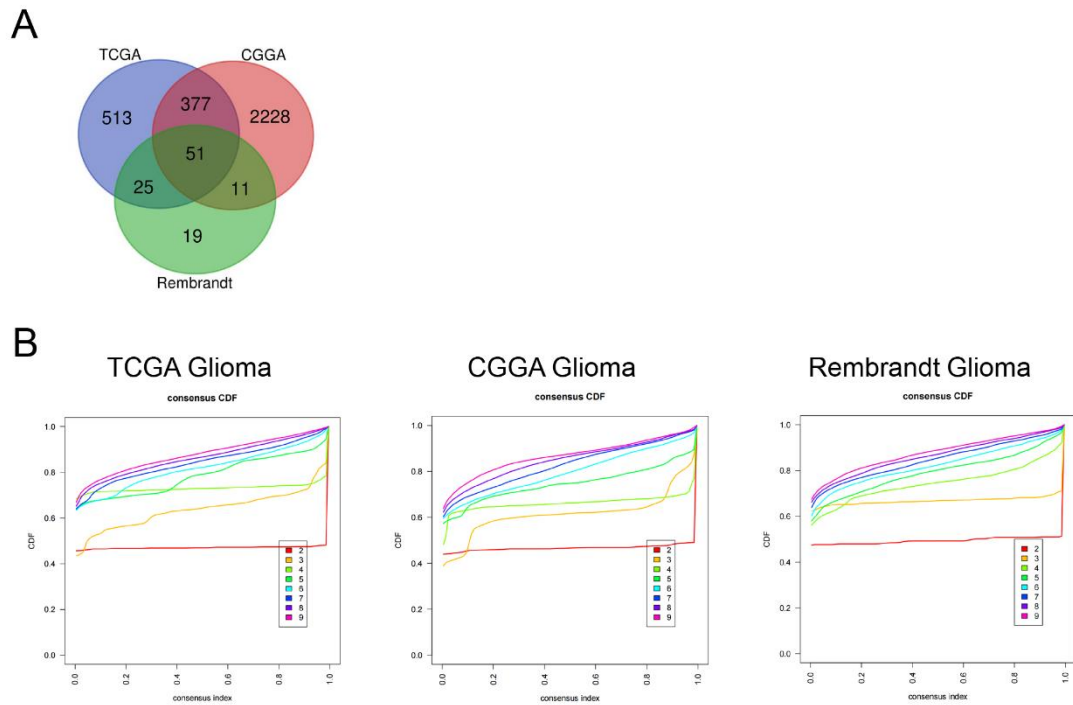


**Fig. S2.** Subtype identification in glioma. A. Venn diagram showing shared and unique upregulated DEGs in group 2 compared to group 1 across the TCGA, CGGA, and Rembrandt glioma cohorts. B. Consensus cumulative distribution function (CDF) plots used to determine the optimal clustering number. The curves display the consensus index distribution for k values ranging from 2 to 9 in each of the three glioma cohorts.

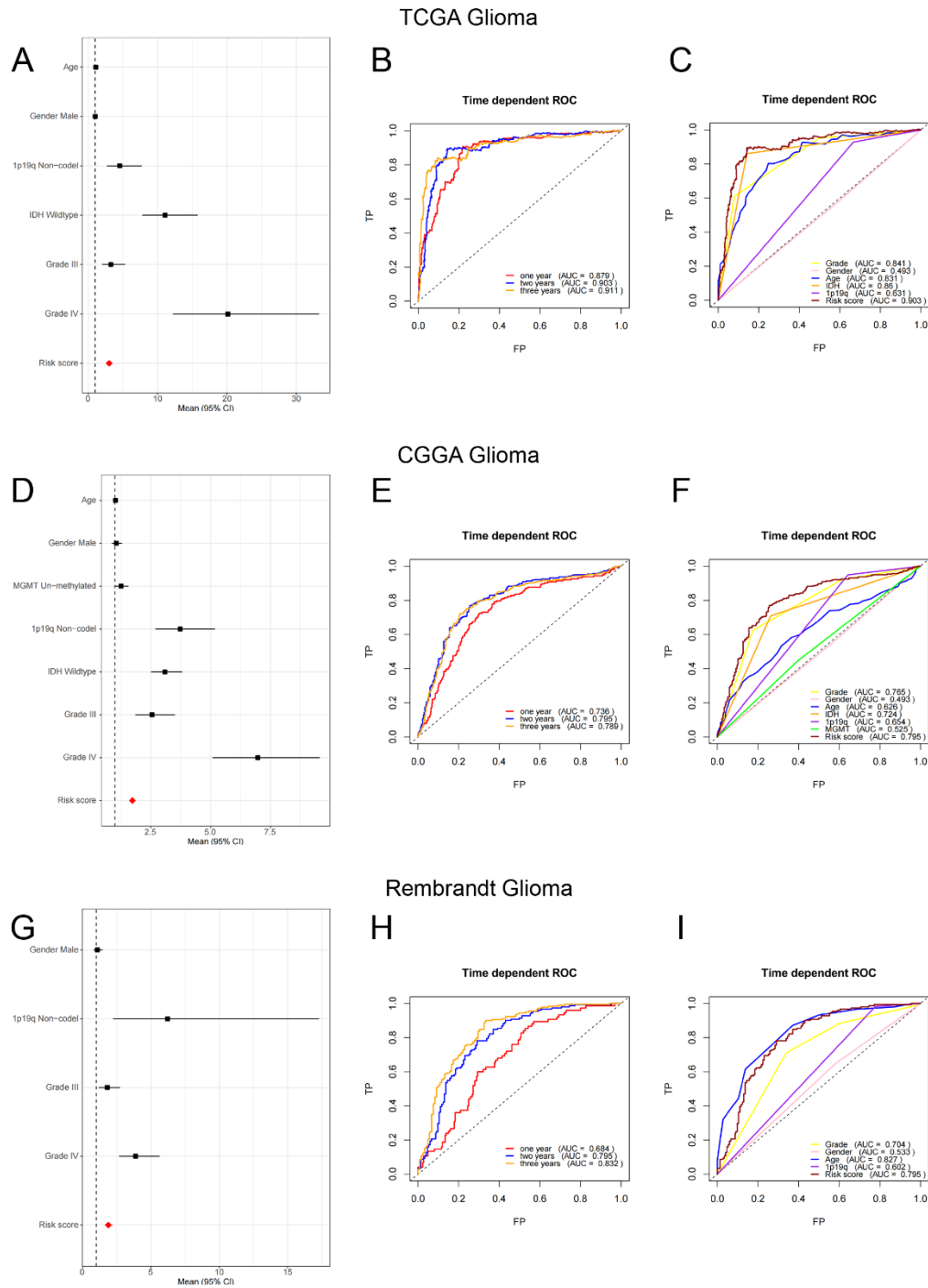


**Fig. S3.** Evaluation of the prognostic risk model for glioma. Evaluation of the association between clinical parameters, risk score, and survival outcomes via univariate Cox regression forest plots in three independent cohorts (A, TCGA glioma; D, CGGA glioma; G, Rembrandt glioma). Time-dependent ROC curves showing the predictive accuracy of the risk model at 1, 2, and 3 years (B, E, H). Comparison of AUC values between the risk score and conventional clinical parameters including grade, age, IDH status, and 1p19q codeletion status (C, F, I).

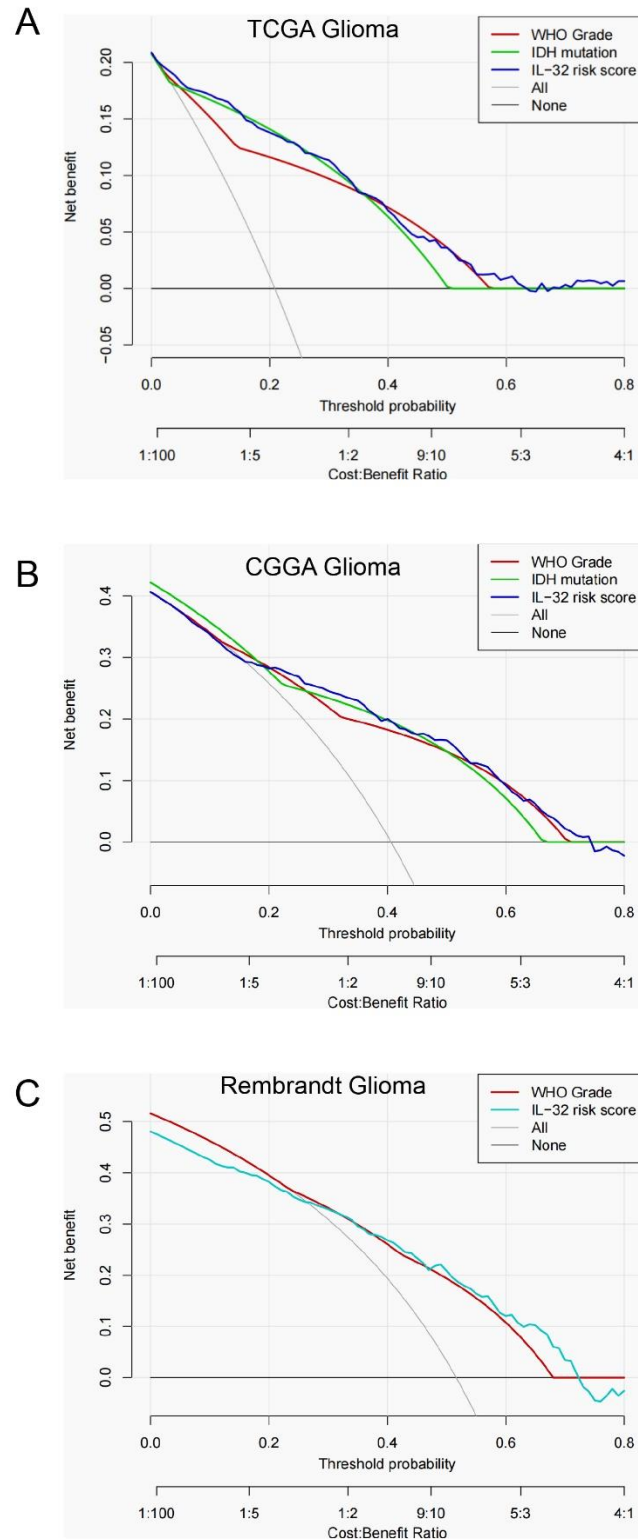


**Fig. S4.** Decision curve analysis of the prognostic risk model for glioma. The IL-32-related model provided greater net clinical benefit than WHO grade and IDH status across a wide range of clinically relevant threshold probabilities (A, TCGA glioma; B, CGGA glioma; C, Rembrandt glioma).