

Figure S1. Immune cell infiltration analysis. (A) Immune cell and immunofunction heat maps for the PD group and the healthy control group. (B, C) Correlation matrix of immune cells and immune function. Red indicates a positive correlation, blue indicates a negative correlation, and darker color indicates a stronger correlation. (D) Correlation analysis of the four characteristic NFRGs and immune cells and immune function.

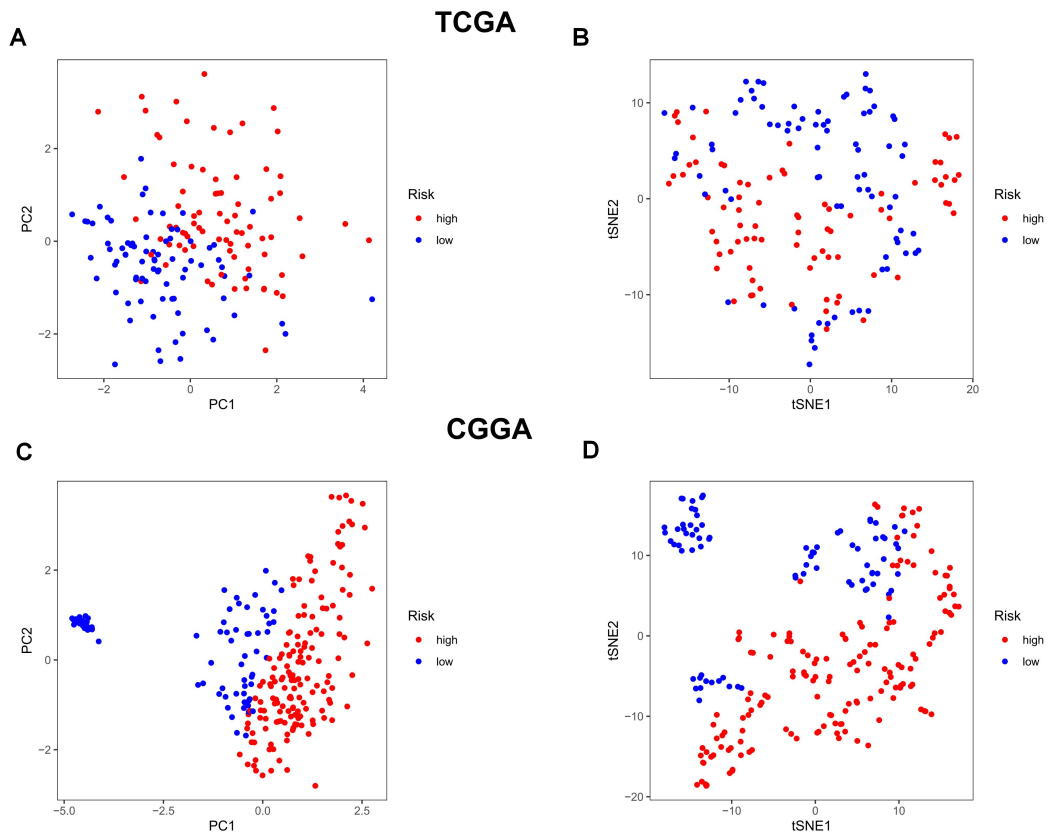


Figure S2. PCA plot and t-SNE analysis in both TCGA and CGGA cohorts. (A) PCA plot in TCGA cohort. **(B)** t-SNE analysis in TCGA cohort. **(C)** PCA plot in CGGA cohort. **(D)** t-SNE analysis in CGGA cohort.

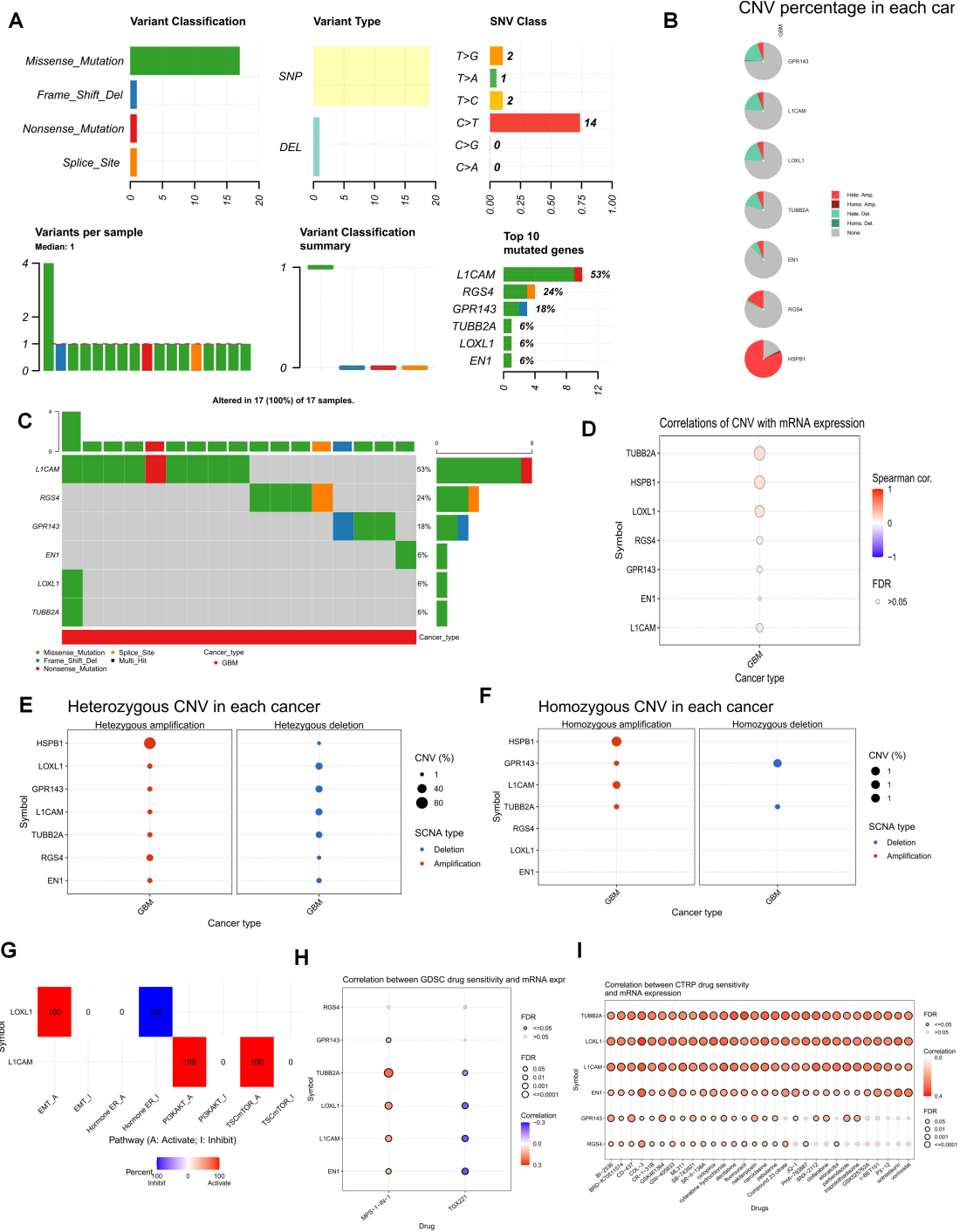


Figure S3. Multi-omics mutation characteristics of NFRGs. (A, B) Classification of mutations in NFRGs in GBM and their mutation incidence. (C) The proportion of different types of copy number variants in NFRGs. (D) Correlation analysis of copy number variants of NFRGs with expression. (E, F) Distribution of copy number variants amplification and deletion of NFRGs in Homozygous mutation and heterozygous mutations. (G) Analysis of the role of NFRGs' expression activity in the regulation of cancer-related pathways. (H, I) Correlation analysis of NFRGs' expression and sensitivity to chemotherapeutic drugs in CDRP and CDSC cohorts.

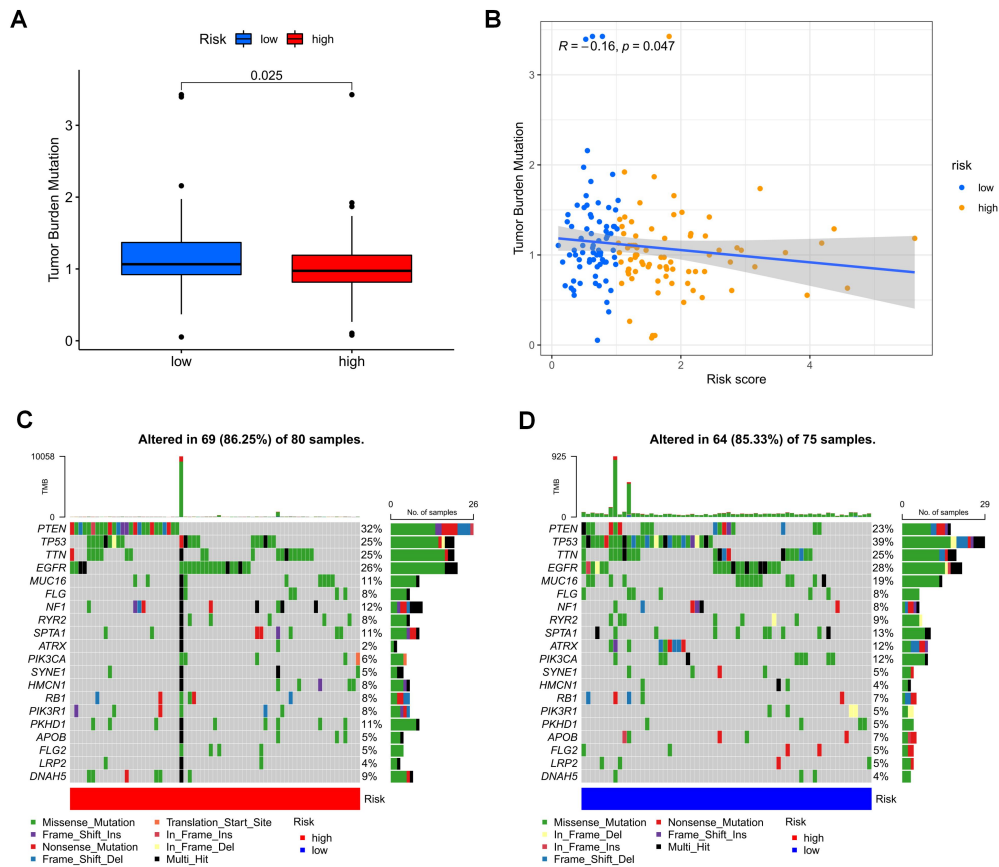


Figure S4. Mutation landscapes based on risk score models. (A) Tumor mutation loads differ between groups with high and low risk scores. (B) Correlation of risk score and TMB. (C, D) summarizing the mutations in high- and low-risk patients using waterfall plots.

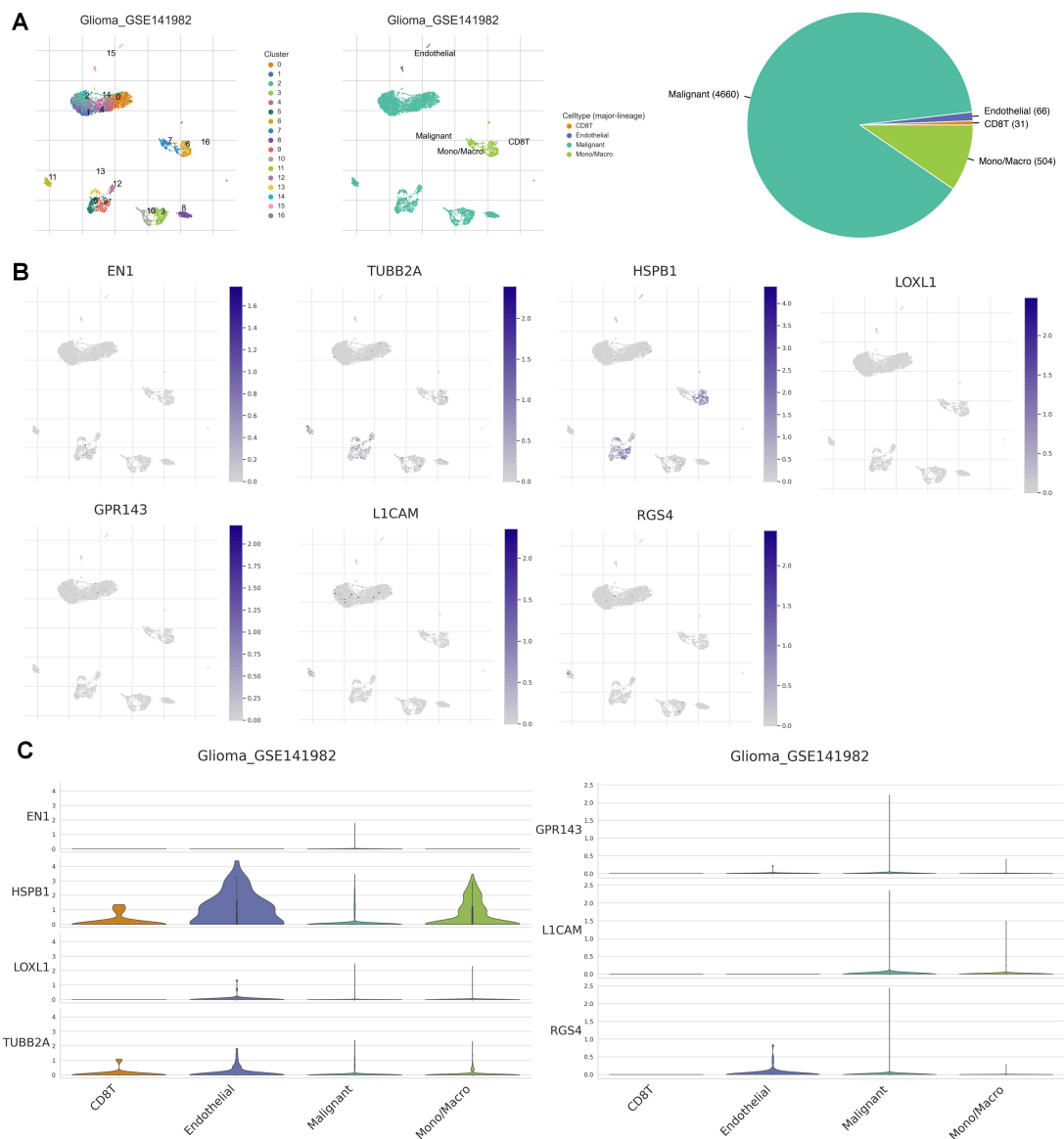


Figure S5. 7-NFRGs in single-cell RNA sequencing. (A) Annotation of all cell types in GSE141982 and the percentage of each cell type. (B, C) Expression of EN1, HSPB1, LOXL1, TUBB2A, GPR143, L1CAM, and RGS4 in each cell type.

Table S1. Results of univariate and multivariate Cox analysis in the CGGA cohort

unixoc	id	HR	HR. 95L	HR. 95H	pvalue
	Gender	1.073123 671	0.84396116 1	1.36451114 8	0.56474527 5
	Age	1.007471 216	0.99861214 8	1.01640887 7	0.09858098 7
	IDH_status	1.368698 278	1.03066199 2	1.81760362 9	0.03010984 4
	MGMTp_methylatio n	1.101797 197	0.87069364 4	1.39424132 9	0.41959290 1
	riskScore	1.247845 234	1.07712550 8	1.44562329 7	0.00318047 1
multiCox	id	HR	HR. 95L	HR. 95H	pvalue
	Gender	1.055861 087	0.82668865 1	1.34856409 6	0.66326699 1
	Age	1.005585 86	0.99662993 5	1.01462226 5	0.22232036 2
	IDH_status	1.155415 696	0.84505101 2	1.57976904 5	0.36540433 8
	MGMTp_methylatio n	1.048644 241	0.82282351 9	1.33644058 3	0.70106969 3
	riskScore	1.199107 921	1.02214312 8	1.40671082 8	0.02582744 3