

Supplementary Material

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Table S1 Clinical characteristics of glioma patients included in this study

Characteristics	TCGA	CGGA	GTEX
Number of cases	711	1018	1152
Normal/Glioma			
Normal	5	0	1152
Glioma	706	1018	-
Age			
<60	546	901	-
≥60	158	116	-
Gender			
Male	403	601	792
Female	301	417	360
Pathological stage			
LGG	538	291	-
WHO Stage III	0	334	-
GBM	168	388	-
IDH mutation status			
Wildtype	-	435	-
Mutant	-	531	-
1p19q codeletion status			
Codel	-	212	-
Non-codel	-	728	-

Table S2 38 pyroptosis-related genes analyzed in this study

Genes	Full-names
AIM2	Absent in melanoma 2
BAX	BCL2 associated X
CASP1	cysteine-aspartic acid protease-1
CASP3	cysteine-aspartic acid protease-3
CASP4	cysteine-aspartic acid protease-4
CASP5	cysteine-aspartic acid protease-5
CASP6	cysteine-aspartic acid protease-6
CASP8	cysteine-aspartic acid protease-8
CASP9	cysteine-aspartic acid protease-9
ELANE	elastase, neutrophil expressed
GPX4	glutathione peroxidase 4
GSDMA	gasdermin A
GSDMB	gasdermin B
GSDMC	gasdermin C
GSDMD	gasdermin D
GSDME	gasdermin E
GZMA	granzyme A
HMGB1	high mobility group box 1
IL18	interleukin 18
IL1B	interleukin 1 beta
IL6	interleukin 6
IRF1	interferon regulatory factor 1
IRF6	interferon regulatory factor 6
NLRC4	NLR family CARD domain containing 4
NLRP1	NLR family pyrin domain containing 1
NLRP2	NLR family pyrin domain containing 2
NLRP3	NLR family pyrin domain containing 3
NLRP6	NLR family pyrin domain containing 6
NLRP7	NLR family pyrin domain containing 7
NOD1	nucleotide binding oligomerization domain containing 1
NOD2	nucleotide binding oligomerization domain containing 2
PJVK	pejvakín/deafness, autosomal recessive 59
PLCG1	phospholipase C gamma 1
PRKACA	protein kinase cAMP-activated catalytic subunit alpha
PYCARD	PYD and CARD domain containing
SCAF11	SR-related CTD associated factor 11
TIRAP	TIR domain containing adaptor protein
TNF	tumor necrosis factor

Figure S1 Construction of risk score model and validation

(A-B) The optimum selection of parameter selection in 11-gene risk-score model with TCGA data. (C) Patients' distribution between the high- and low-risk subgroups using the model with CGGA data. Analysis of (D) PCA, (E) t-SNE plot, and distribution of survival status (F) between high- or low-risk groups in CGGA database.

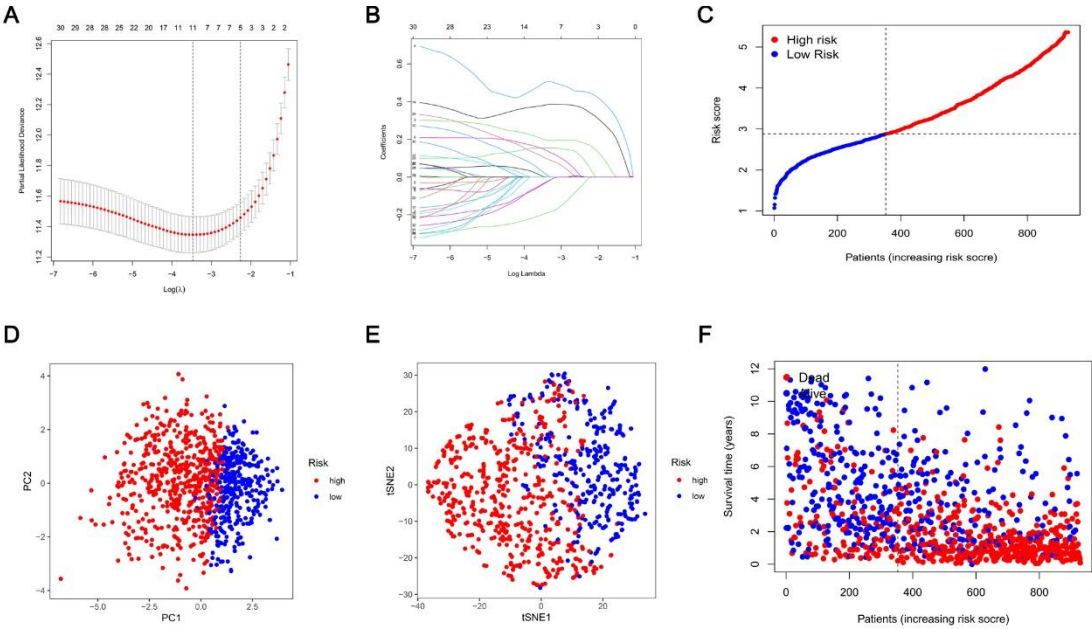


Figure S2 Prognostic cox regression analyses of risk scores

Multivariate (A) and univariate (B) Cox regression analysis in CGGA database. Heatmap of clinical features and 11-gene signature panel based on risk model in TCGA (C) and CGGA (D) databases.

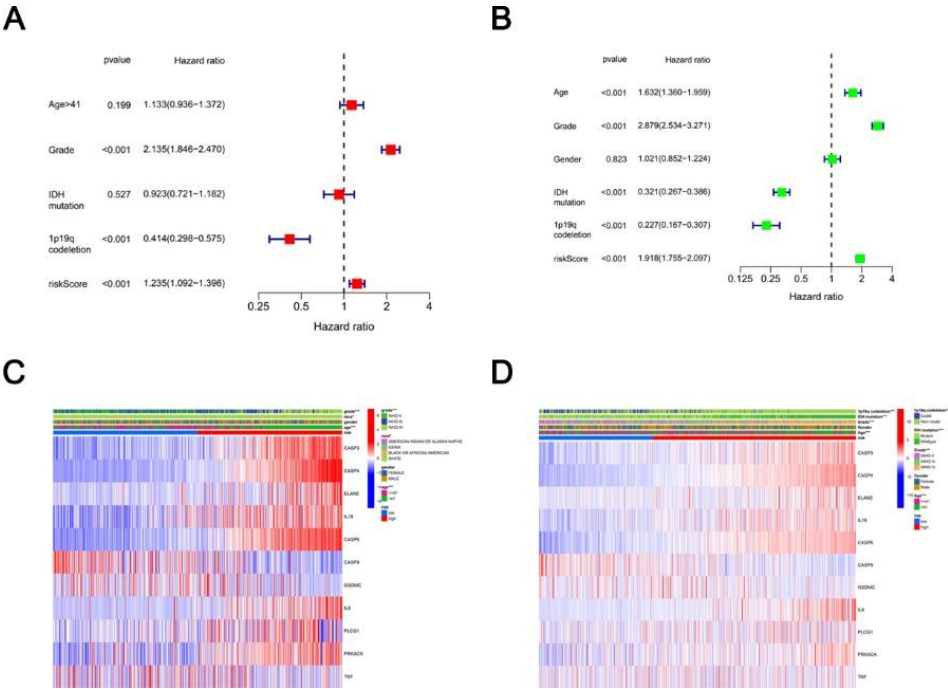


Figure S3 Analysis of immune cells and activity based on risk-score model with CGGA data
Immune infiltration scores of immune cells (A) and immune-related pathways (B) analyzed by ssGESA method. * indicates $P < 0.05$; ** indicates $P < 0.01$; *** indicates $P < 0.001$.

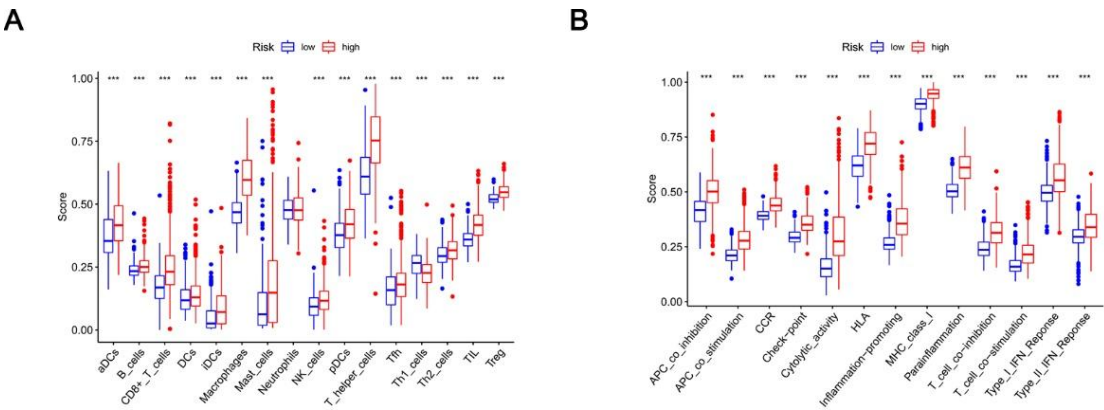


Figure S4 Calculation and investigation of PRKACA activity
(A) The activities of PRKACA in normal and tumour tissues in 33 cancer types
(B) The average activity (from high to low) of PRKACA (* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$).

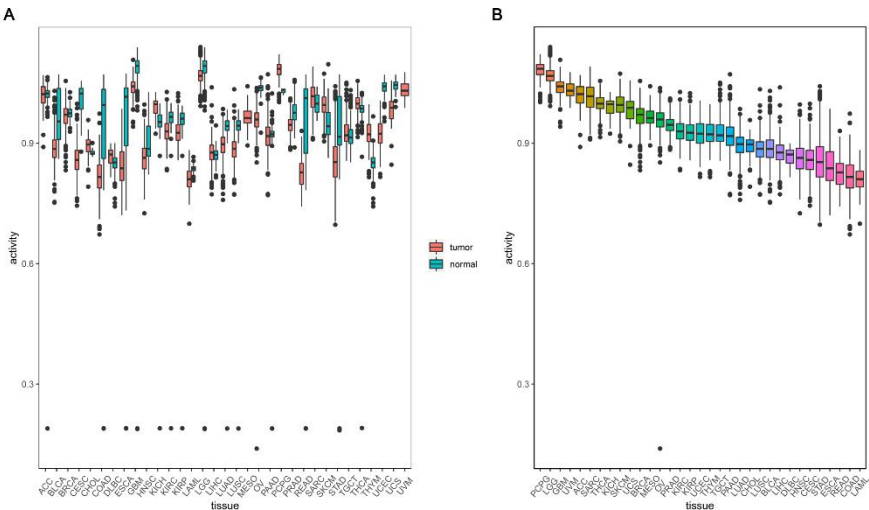


Figure S5 Relationship between PRKACA expression and patients' disease-specific survival (DSS) using (A) Forest map and (B–D) Kaplan-Meier analysis. (B)UVM, (C)LGG, (D)KIRC. Relationship between PRKACA expression and patients' progression-free interval (PFI) using (E) Forest map and (F–G) Kaplan-Meier analysis. (F)LGG, (G)KIRC. Correlation of PRKACA expression with TMB (H) and MSI (I). The blue and green number represent Spearman's correlation coefficient for TMB and MSI, respectively (* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$).

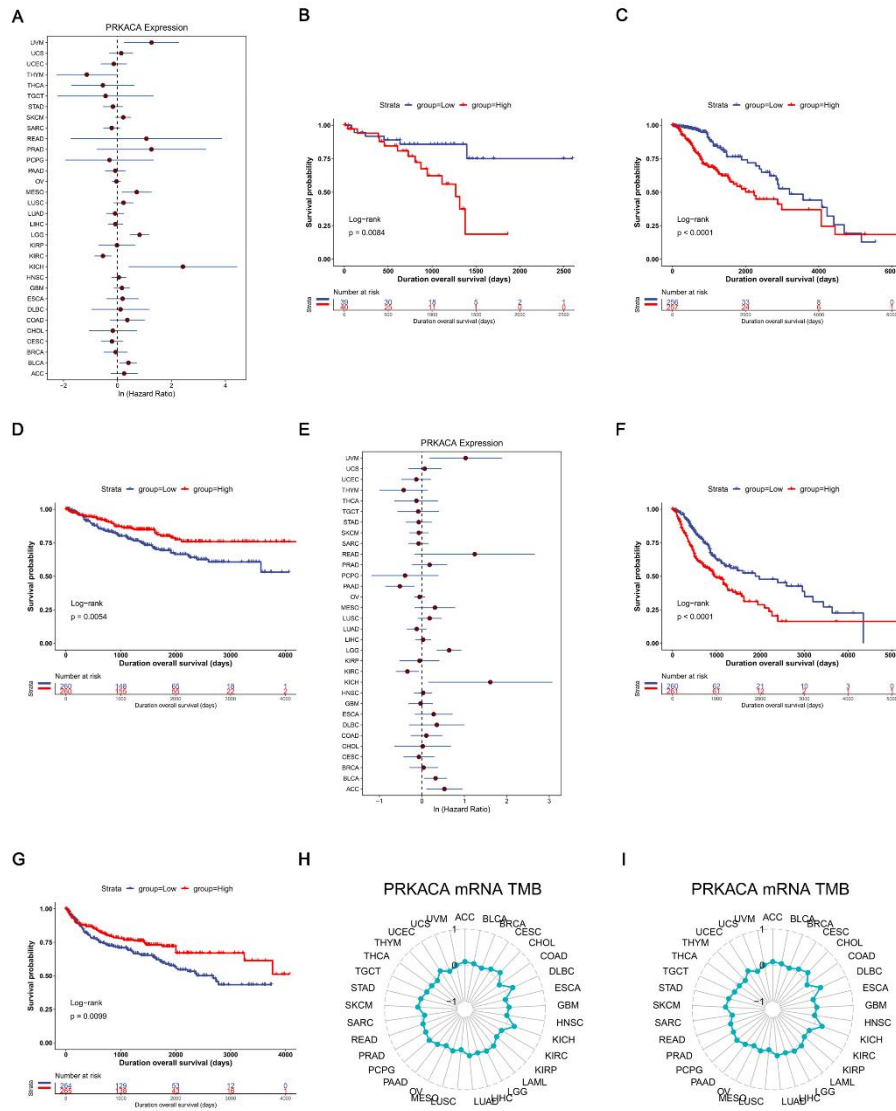


Figure S6 Correlation analysis between PRKACA expression and immune cell infiltration using CIBERSORT algorithm.

