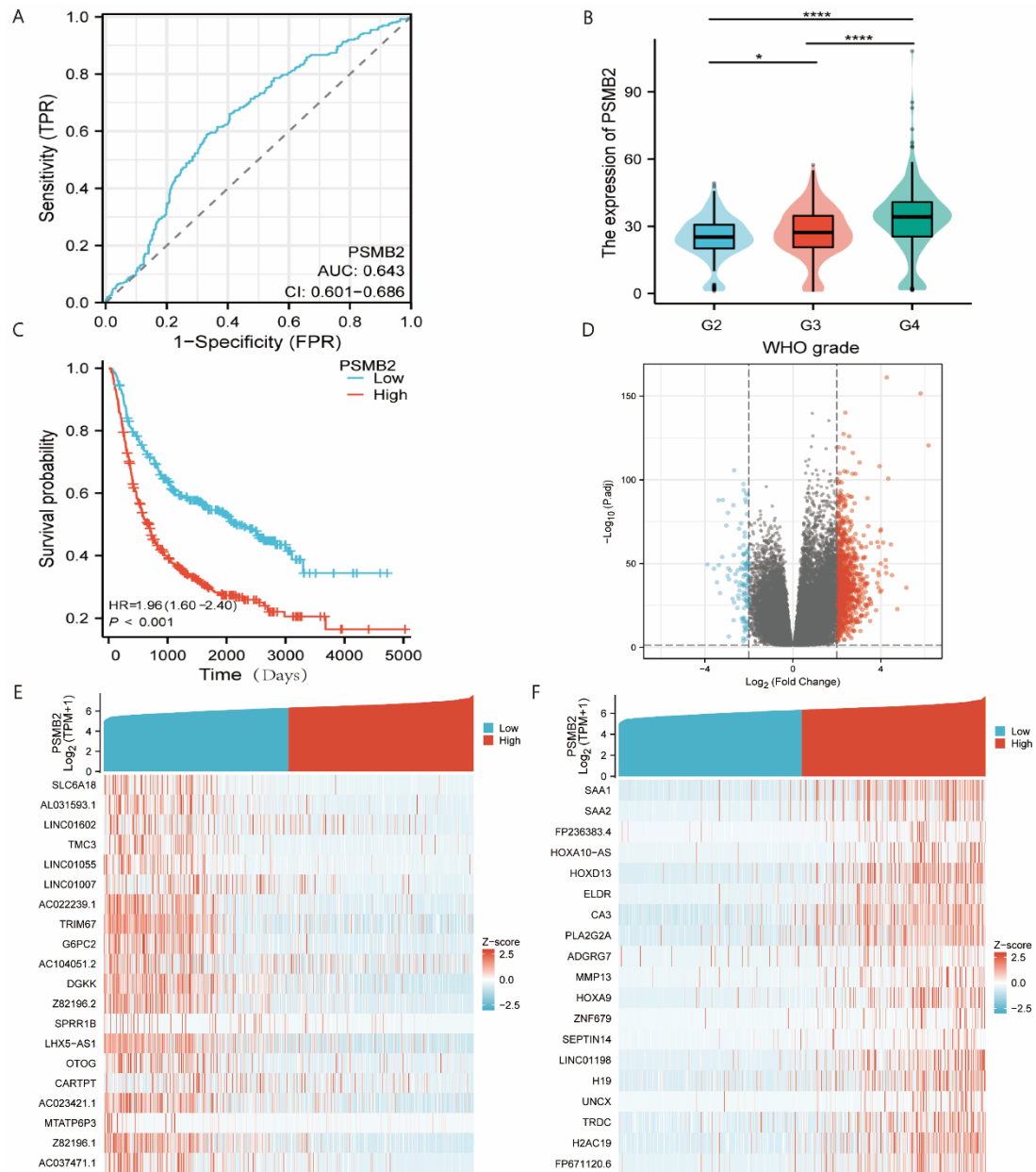




Supplementary Figure 1

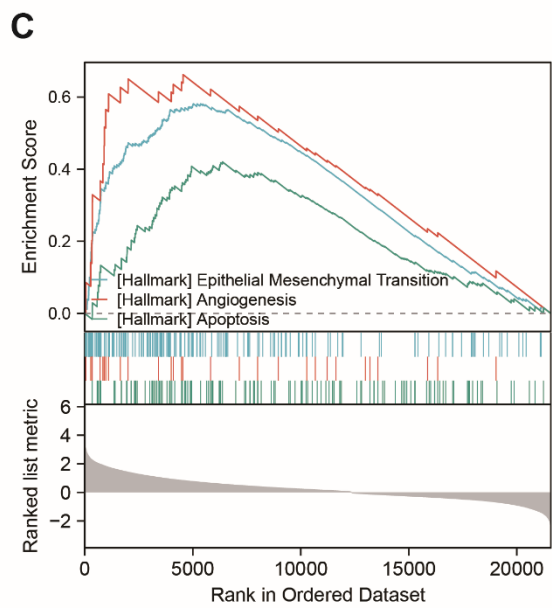
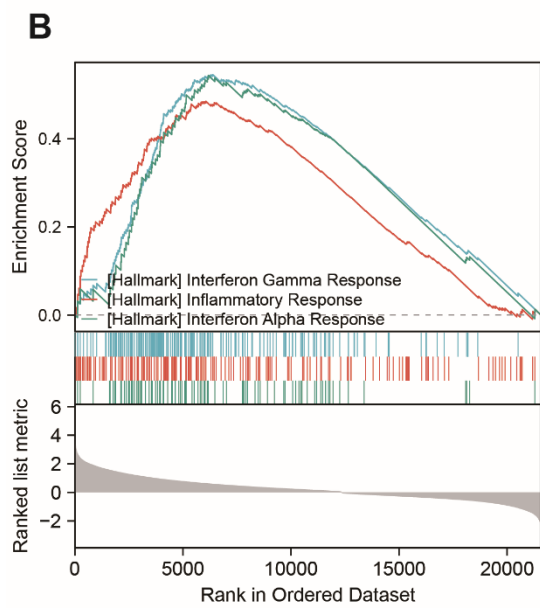
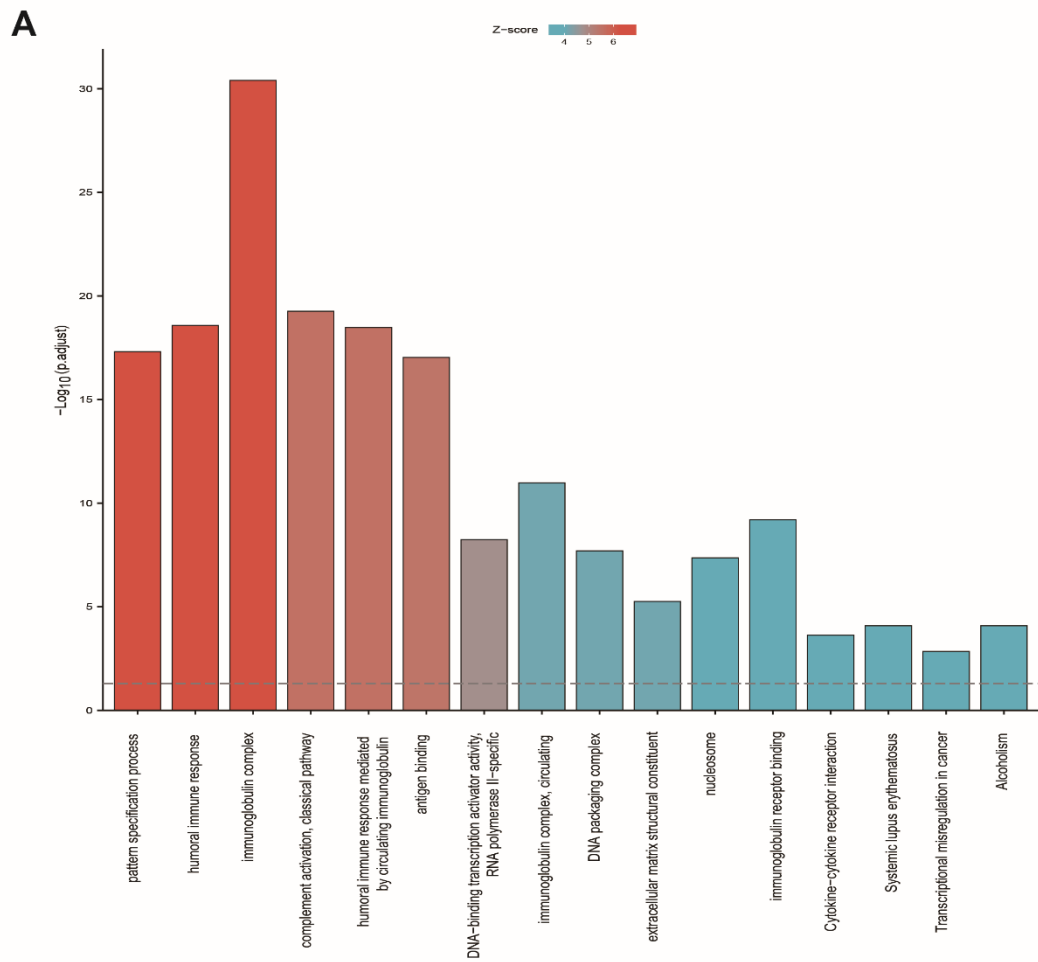
(A)Receiver operating characteristic analysis (ROC) of PSMB2 in glioma from CGGA database.

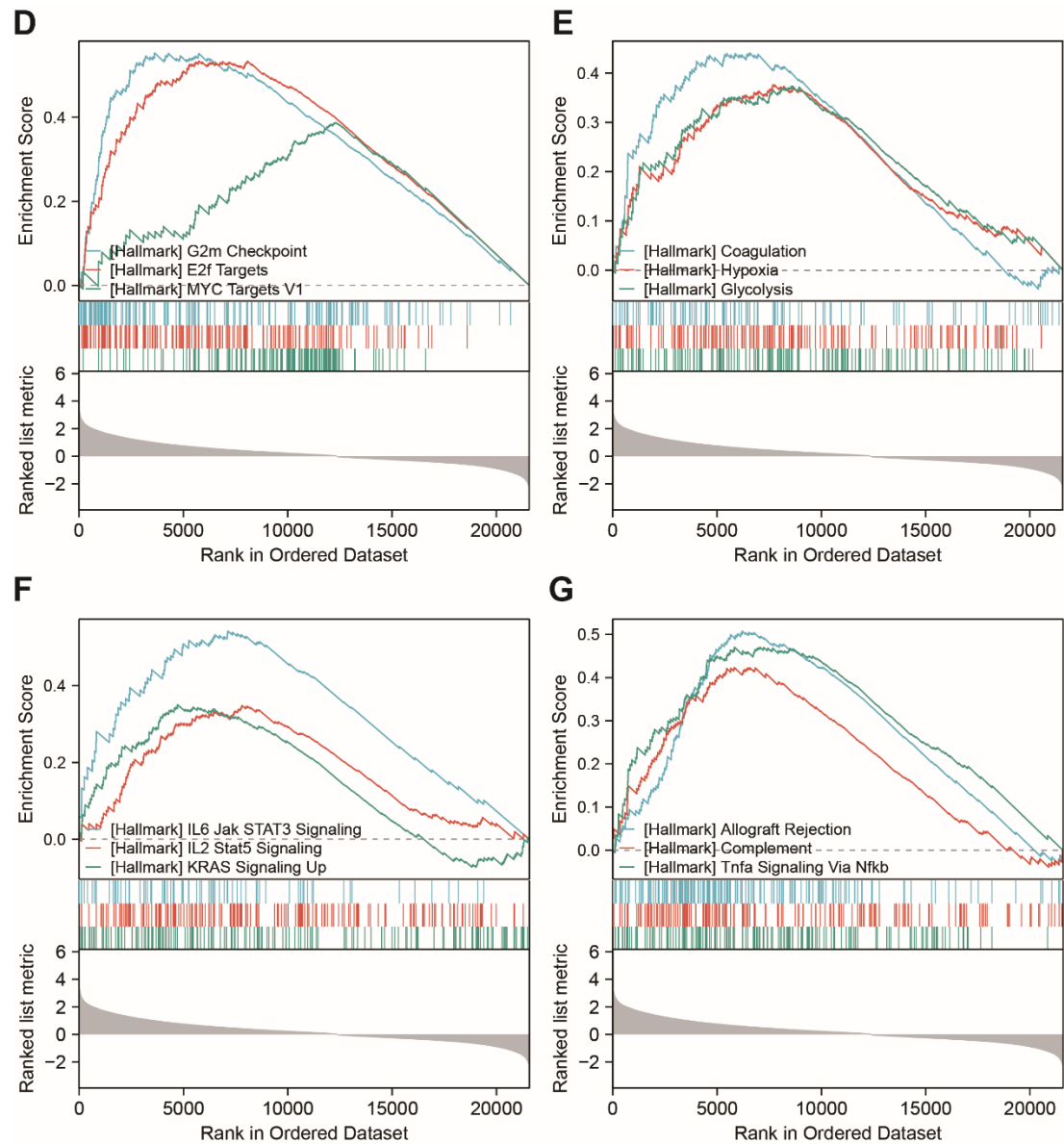
(B)The association of PSMB2 expression and clinical Grade in glioma from CGGA database.

(C)Survival curves of OS from CGGA database.

(D)Volcano maps of differentially expressed gene.

(E-F) Heat maps of differentially expressed genes.



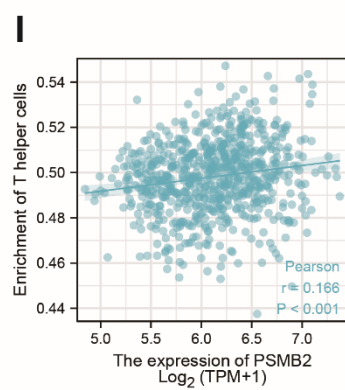
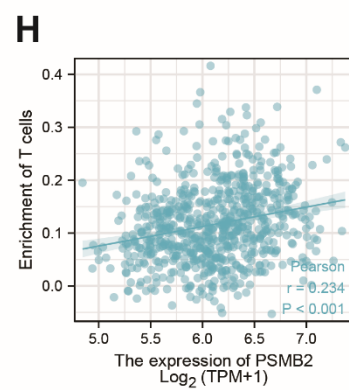
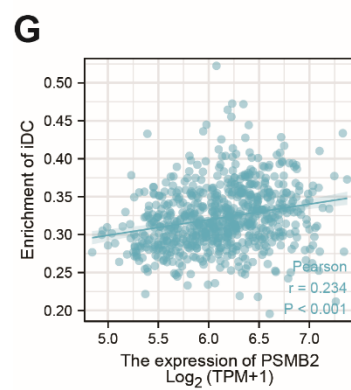
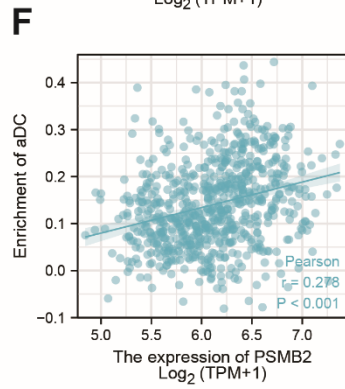
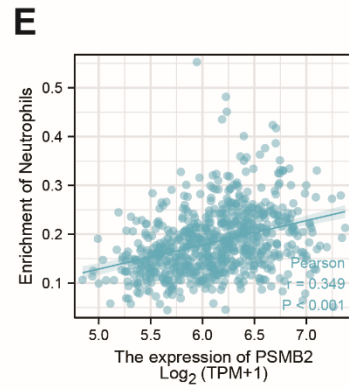
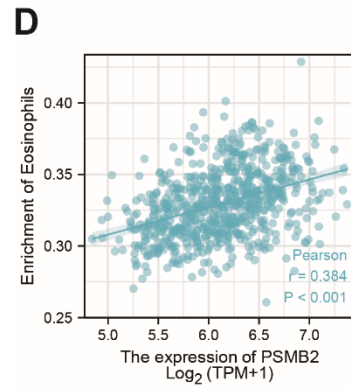
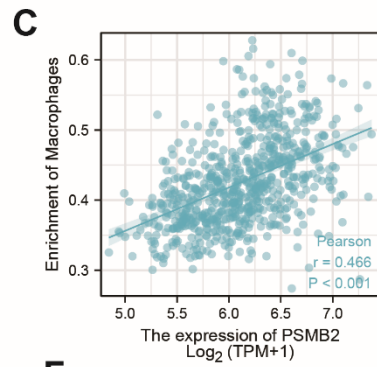
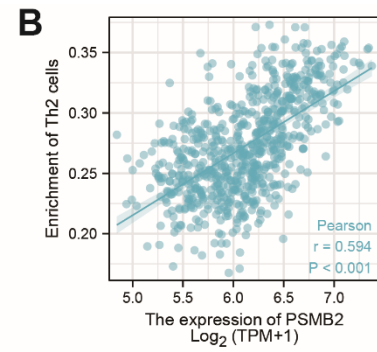
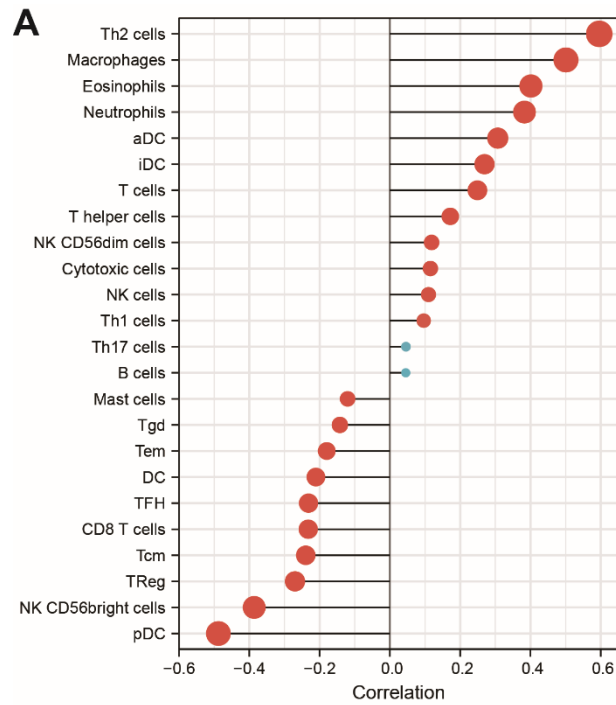


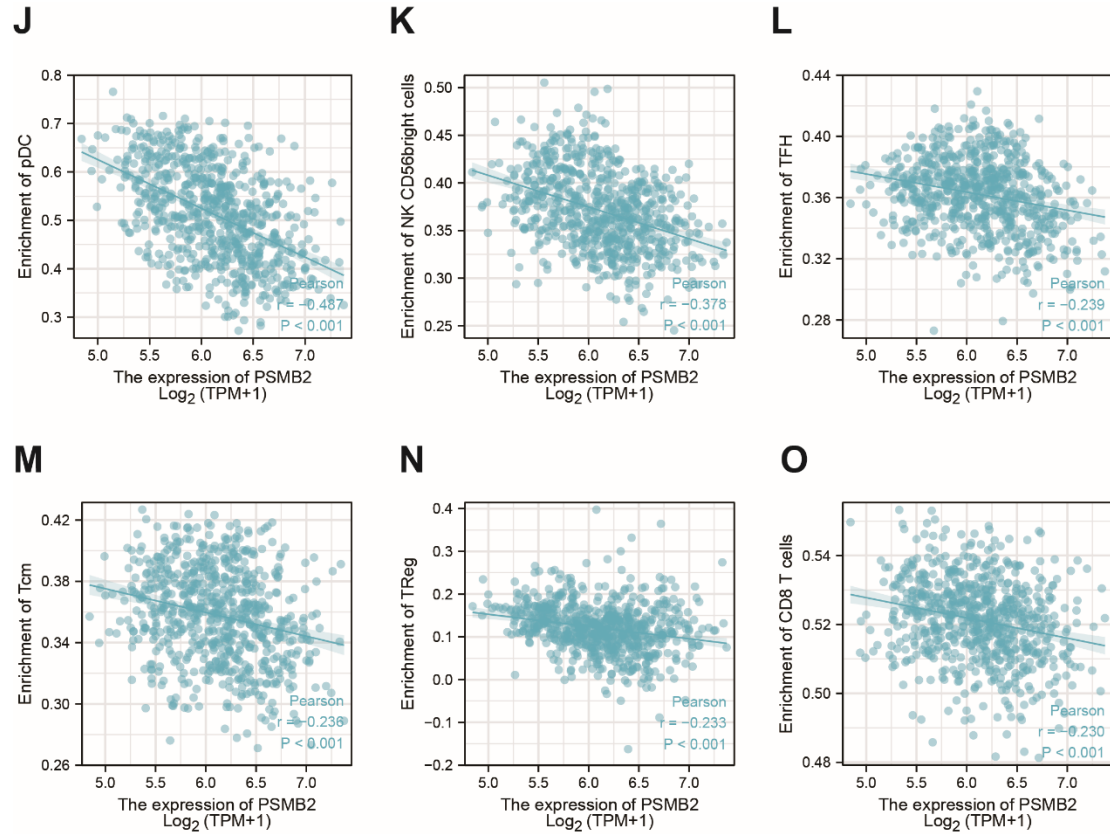
Supplementary Figure 2

Functional enrichment of PSMB2 in glioma.

(A) GO and KEGG enrichment analysis of differentially expressed gene.

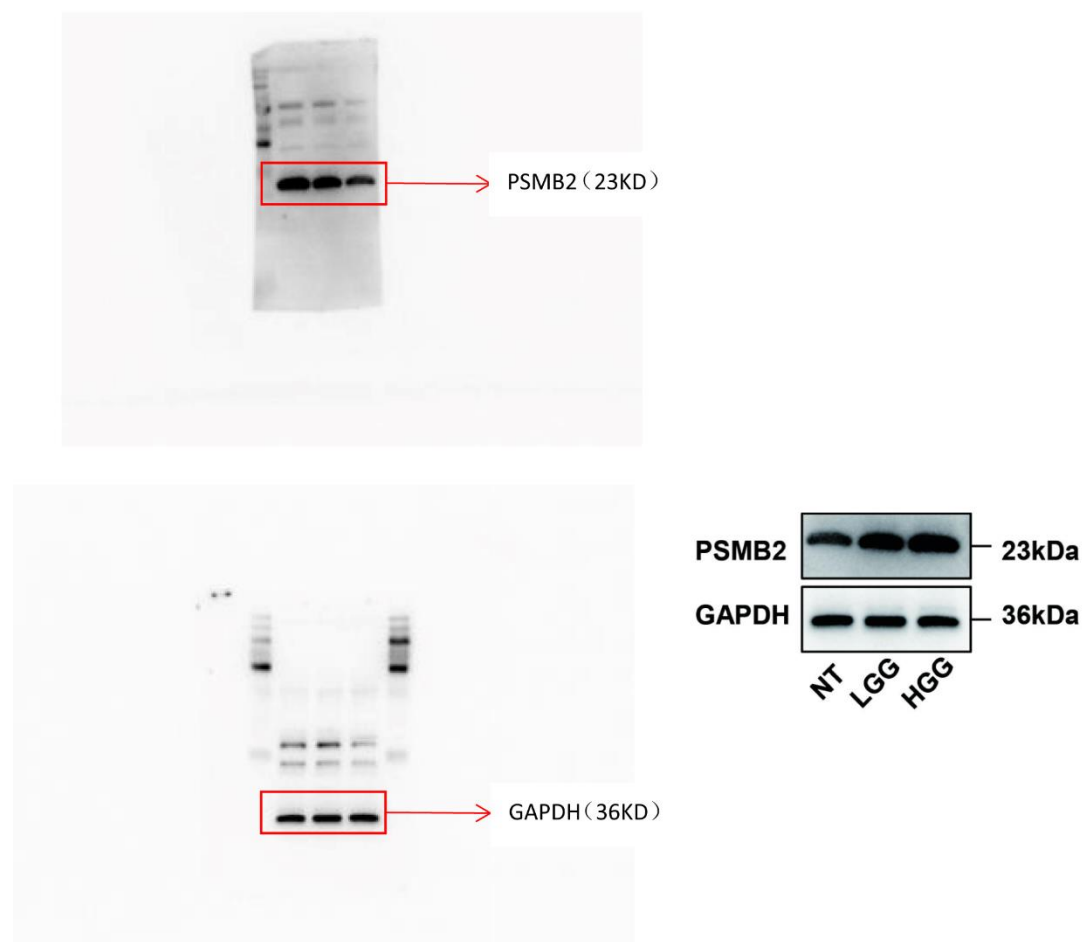
(B-G) The most significant enrichment pathways by GSEA.





Supplementary Figure 3 ssGSEA analyses of PSMB2 and the correlation of PSMB2 expression with immune infiltration level in glioma.

(A) The correlation between the infiltration of immune cells and the expression of PSMB2.
 (B-I) PSMB2 expression significantly positively correlates with infiltrating levels of Th2 cells, Macrophages, Eosinophils, Neutrophils, aDC, iDC, T cells, T helper cells.
 (J-O) PSMB2 expression significantly negatively correlates with infiltrating levels of pDC, NK CD56bright cells, TFH, Tcm, TReg, CD8 T cells.



Supplementary Figure 4 WB full film

Supplementary Table 1

The univariate and multivariate analysis of overall survival according to PSMB2 expression in TCGA dataset (n=695)

Characteristics	Total(N)	Univariate analysis		Multivariate analysis	
		Hazard ratio (95% CI)	P value	Hazard ratio (95% CI)	P value
WHO grade	634				
G2	223	Reference			
G3	243	2.999 (2.007-4.480)	<0.001	1.920 (1.253-2.945)	0.003
G4	168	18.615 (12.460-27.812)	<0.001	4.587 (2.707-7.772)	<0.001
IDH status	685				

Characteristics	Total(N)	Univariate analysis		Multivariate analysis	
		Hazard ratio (95% CI)	P value	Hazard ratio (95% CI)	P value
WT	246	Reference			
Mut	439	0.117 (0.090-0.152)	<0.001	0.296 (0.198-0.442)	<0.001
Gender	695				
Female	297	Reference			
Male	398	1.262 (0.988-1.610)	0.062	1.210 (0.921-1.589)	0.171
Age	695				
<=60	552	Reference			
>60	143	4.668 (3.598-6.056)	<0.001	1.528 (1.122-2.081)	0.007
1p/19q codeletion	688				
code1	170	Reference			
non-code1	518	4.428 (2.885-6.799)	<0.001	1.315 (0.762-2.268)	0.326
Race	682				
Asian&Black or African American	46	Reference			
White	636	0.821 (0.502-1.344)	0.433		
PSMB2	695				
Low	347	Reference			
High	348	5.950 (4.493-7.879)	<0.001	2.807 (1.484-5.310)	0.002

Supplementary Table 2

The univariate analysis of overall survival according to PSMB2 expression in CGGA dataset (n=656)

Characteristics	Total(N)	Univariate analysis	
		Hazard ratio (95% CI)	P value
Age	656		

<= 60	588	Reference	
> 60	68	0.671 (0.583 - 0.771)	< 0.001
Gender	656		
Female	283	Reference	
Male	373	0.969 (0.876 - 1.071)	0.537
IDH status	608		
Mut	333	Reference	
WT	275	0.733 (0.605 - 0.888)	0.001
1p/19q codeletion	590		
Codel	137	Reference	
Non-codel	453	0.442 (0.351 - 0.557)	< 0.001
WHO grade	656		
G2	172	Reference	
G3	247	0.383 (0.314 - 0.467)	< 0.001
G4	237	0.980 (0.843 - 1.138)	0.787
PSMB2	656		
Low	328	Reference	
High	328	2.032 (1.660 - 2.488)	< 0.001

Supplementary Table 3

Hallmark pathways enriched in high-risk groups and low-risk groups by using GSEA.

Description	NES	pvalue	p.adjust
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	2.243842	0.001015	0.004514
	84	23	27
	2.064329	0.001016	0.004514
HALLMARK_E2F_TARGETS	84	26	27
	2.136409	0.001016	0.004514
HALLMARK_G2M_CHECKPOINT	63	26	27
	2.118580	0.001016	0.004514
HALLMARK_INTERFERON_GAMMA_RESPONSE	47	26	27
	1.966085	0.001017	0.004514
HALLMARK_ALLOGRAFT_REJECTION	31	29	27

	1.635308	0.001017	0.004514
HALLMARK_COMPLEMENT	36	29	27
	1.878430	0.001017	0.004514
HALLMARK_INFLAMMATORY_RESPONSE	62	29	27
	1.815474	0.001017	0.004514
HALLMARK_TNFA_SIGNALING_VIA_NFKB	29	29	27
	1.593936	0.001030	0.004514
HALLMARK_APOPTOSIS	17	93	27
	1.642056	0.001050	0.004514
HALLMARK_COAGULATION	19	42	27
	1.991396	0.001062	0.004514
HALLMARK_INTERFERON_ALPHA_RESPONSE	37	7	27
	1.942932	0.001083	0.004514
HALLMARK_IL6_JAK_STAT3_SIGNALING	31	42	27
	2.065880	0.001209	0.004650
HALLMARK_ANGIOGENESIS	71	19	73
	1.483351	0.003064	0.010944
HALLMARK_MYC_TARGETS_V1	92	35	11
	1.454644	0.005086	0.016954
HALLMARK_HYPOXIA	96	47	9
	1.435635	0.008146	0.025458
HALLMARK_GLYCOLYSIS	75	64	25
	1.360327	0.019308	0.056791
HALLMARK_KRAS_SIGNALING_UP	33	94	01
	1.353965	0.022357	0.062104
HALLMARK_IL2_STAT5_SIGNALING	92	72	79
	1.716386	0.043478	0.114416
HALLMARK_KRAS_SIGNALING_DN	08	26	48
	1.301287	0.046795	0.116988
HALLMARK_MITOTIC_SPINDLE	7	52	81
	1.471011	0.053254	0.126796
HALLMARK_PANCREAS_BETA_CELLS	35	44	28

Supplementary Table 4

Relationship between PSMB2 mRNA expression and immune cell infiltration level

PSM		Correlation	P-value	Correlation	P-value
B2	Cells	(Pearson)	(Pearson)	(Spearman)	(Spearman)
	aDC	0.278	<0.001	0.307	<0.001
	CD8 T cells	-0.230	<0.001	-0.232	<0.001
	DC	-0.150	<0.001	-0.211	<0.001
	Eosinophils	0.384	<0.001	0.401	<0.001
	iDC	0.234	<0.001	0.269	<0.001
	Macrophages	0.466	<0.001	0.501	<0.001
	Neutrophils	0.349	<0.001	0.383	<0.001
	NK				
	CD56bright				
	cells	-0.378	<0.001	-0.386	<0.001
	pDC	-0.487	<0.001	-0.488	<0.001
	T cells	0.234	<0.001	0.249	<0.001
	T helper cells	0.166	<0.001	0.172	<0.001
	Tcm	-0.236	<0.001	-0.239	<0.001
	Tem	-0.166	<0.001	-0.180	<0.001
	TFH	-0.239	<0.001	-0.232	<0.001
	Tgd	-0.142	<0.001	-0.142	<0.001
	Th2 cells	0.594	<0.001	0.596	<0.001
	TReg	-0.233	<0.001	-0.270	<0.001
	Mast cells	-0.120	0.002	-0.120	0.001
	Cytotoxic				
	cells	0.102	0.007	0.115	0.002
	NK CD56dim				
	cells	0.123	0.001	0.119	0.002
	NK cells	0.105	0.005	0.110	0.004
	Th1 cells	0.097	0.010	0.096	0.011
	Th17 cells	0.032	0.395	0.046	0.228
	B cells	0.035	0.362	0.045	0.233