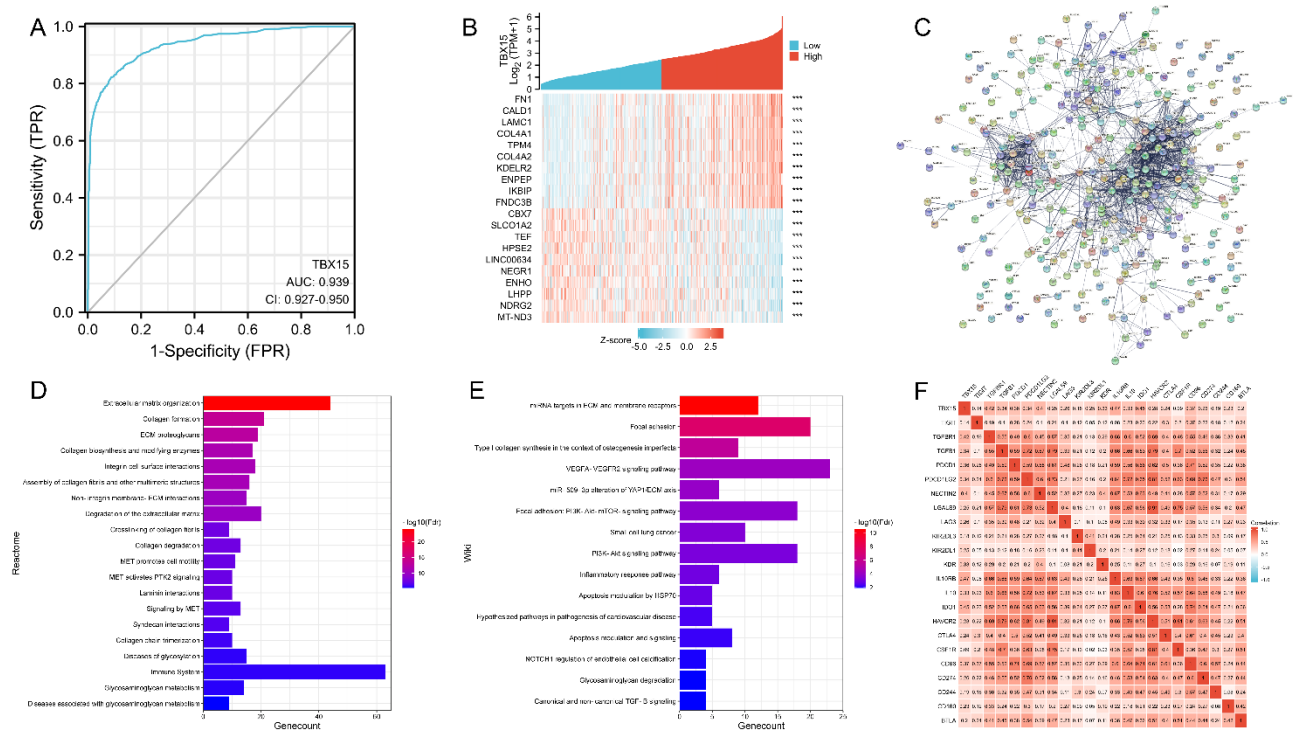


Supplementary Material

1.1 Supplementary Figures



Supplementary Figure1. (A) TBX15 exhibited high accuracy in predicting normal tissue and glioma outcomes. (B) Top 10 genes most positively and negatively associated with FCGBP are shown in a heatmap. (C) TBX15 and its top 300 co-expression genes formed a network. (D) Significant Reactome pathways of the top 300 genes most positively associated with TBX15. (E) Significant Wiki pathways of the top 300 genes most positively associated with TBX15. (F) TBX15 was positively correlated with most immunosuppressive genes.

1.2 Supplementary Tables

Supplementary Table 1: Clinicopathological characteristics and TBX15 expression of 696 samples from glioma patients in TCGA database

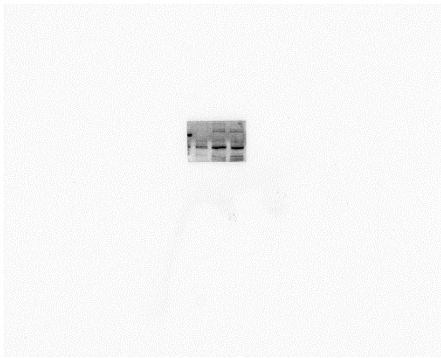
Characteristic	Low expression of TBX15	High expression of TBX15	P
n	348	348	
WHO grade, n (%)			< 0.001
G2	152 (23.9%)	72 (11.3%)	
G3	113 (17.8%)	130 (20.5%)	
G4	41 (6.5%)	127 (20%)	

Characteristic	Low expression of TBX15	High expression of TBX15	p
IDH status, n (%)			< 0.001
WT	76 (11.1%)	170 (24.8%)	
Mut	266 (38.8%)	174 (25.4%)	
1p/19q codeletion, n (%)			0.321
code1	92 (13.4%)	79 (11.5%)	
non-code1	254 (36.9%)	264 (38.3%)	
Age, median (IQR)	40 (31, 52.25)	52 (38, 62)	< 0.001

Supplementary Table 2: Cox-regression analysis of prognostic variables in glioma patients by both univariate and multivariate analyses

Characteristics	Total(N)	Univariate analysis		Multivariate analysis	
		Hazard ratio (95% CI)	P value	Hazard ratio (95% CI)	P value
WHO grade	634				
G2	223				
G3	243	2.999 (2.007-4.480)	<0.001	2.023 (1.279-3.202)	0.003
G4	168	18.615 (12.460-27.812)	<0.001	9.240 (3.002-28.440)	<0.001
1p/19q codeletion	688				
code1	170				
non-code1	518	4.428 (2.885-6.799)	<0.001	1.470 (0.855-2.527)	0.163
IDH status	685				
WT	246				
Mut	439	0.117 (0.090-0.152)	<0.001	0.462 (0.282-0.759)	0.002

TBX15



β -Actin

