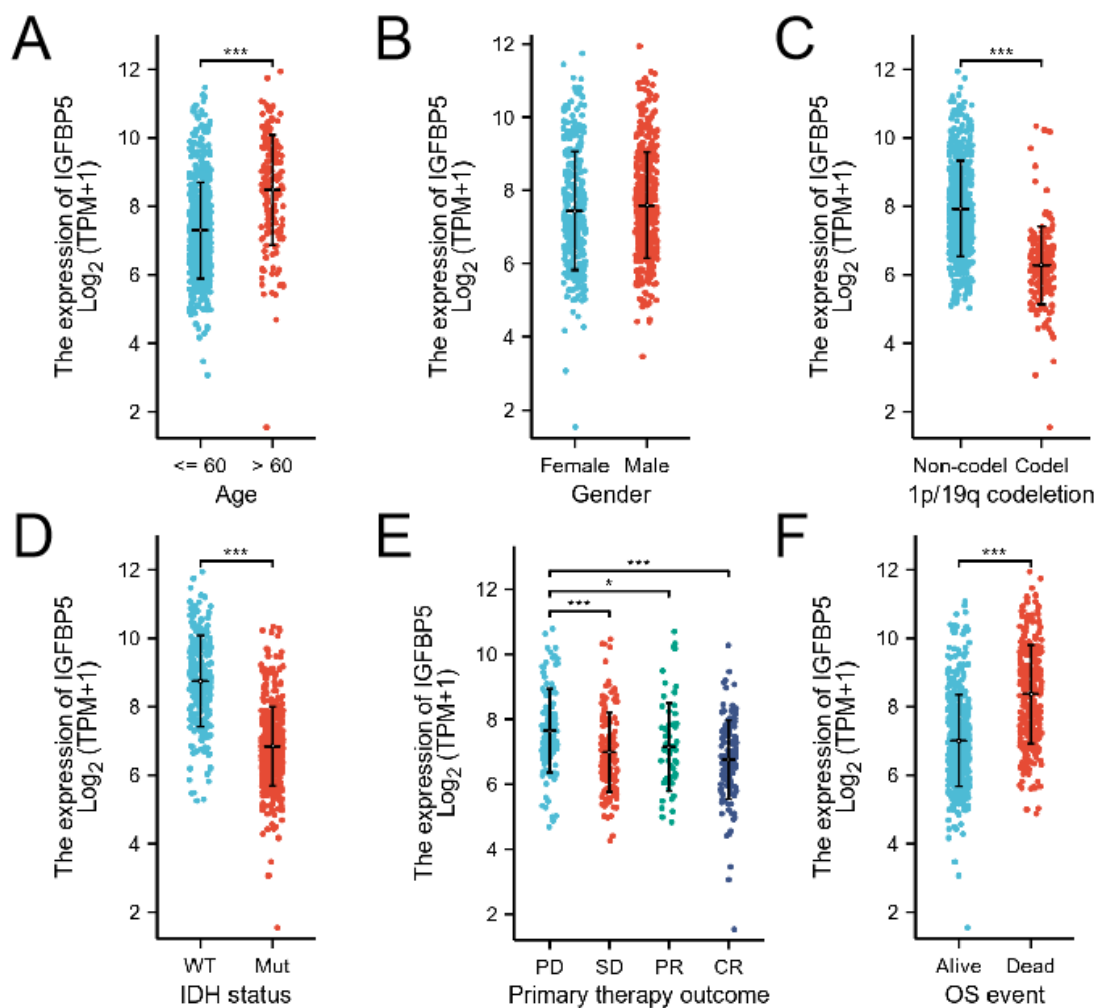
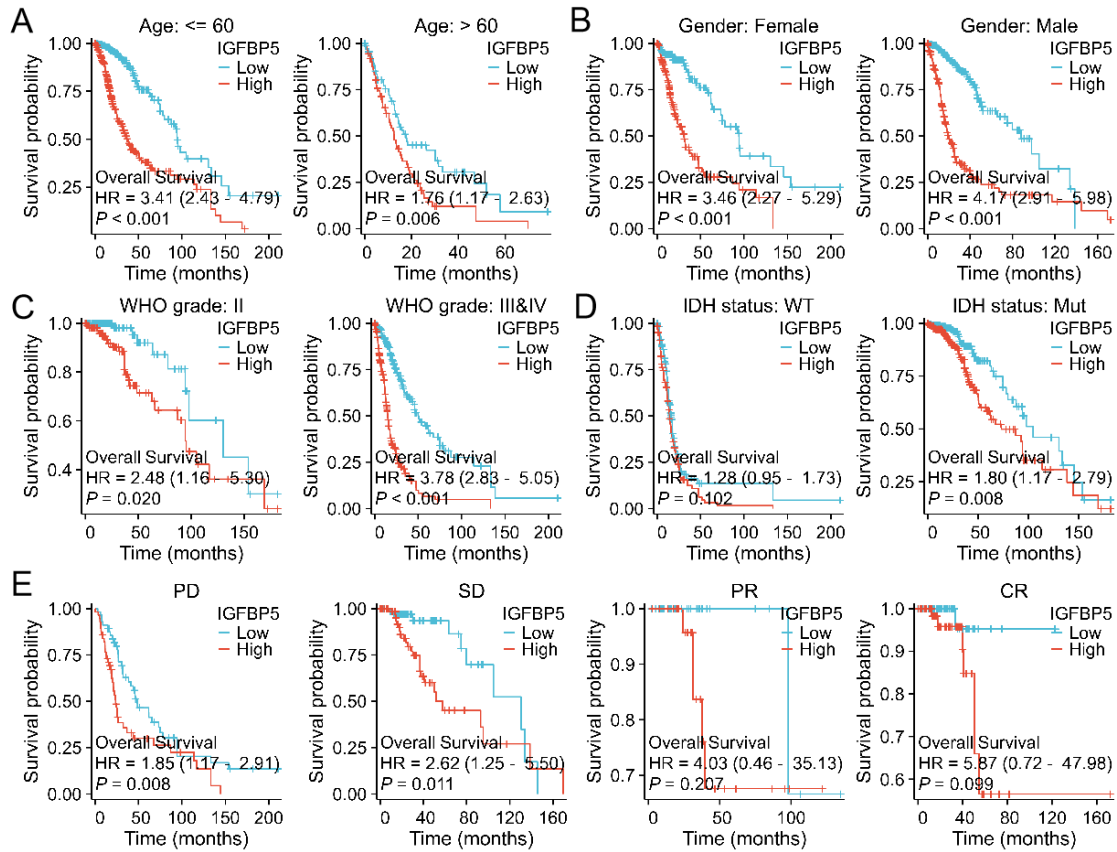


Supplementary Figures and Tables



Supplementary Figure 1. The correlation between IGFBP5 expression and different Clinical Parameters. (A-F) The correlation between IGFBP5 expression and different clinical features, including the age (A), gender (B), 1p/19q codeletion (C), IDH mutation status (D), primary therapy outcome (E) and Overall Survival (F). Primary therapy outcome: including PD, progressive disease; SD, stable disease. PR, partial response; CR, complete response.



Supplementary Figure 2. Analysis of the prognostic value of IGFBP5 in different glioma subgroups. Analysis of the prognostic value of IGFBP5 in different subgroups, including (A) age, (B) gender, (C) WHO grade, (D) IDH mutation status, and (E) Primary therapy outcome. PD: progressive disease; SD: stable disease; PR: partial response; CR: Complete response.

Supplementary Table 1 Four Datasets used in this study

Dataset	Data type	WHO grade II	WHO grade III	WHO grade IV
TCGA	RNA-seq	224	245	168
CGGA	RNA-seq	291	334	388
Rembrandt	Microarray	98	85	130
Gravendeel	Microarray	24	85	159

Supplementary Table 2 The primers and siRNAs of IGFBP5

Primers	IGFBP5	5'-ACAAGAGAAAGCAGTGCAAACC-3'
		5'-CGTCAACGTACTCCATGCCT-3'
Primers	GAPDH	5'-GCGTGACATTAAGGAGAAGC-3'
		5'-CCACGTCACACTTCATGATGG-3'
si-RNAs	si-NC	5'-UUC UCC GAA CGU GUC ACG UTT-3'
		5'-ACG UGA CAC GUU CGG AGA ATT-3'
	si-IGFBP5 (# 1)	5'-GCU GAC CCA GUC CAA GUU UTT-3'
		5'-AAA CUU GGA CUG GGU CAG CTT-3'
	si-IGFBP5 (# 2)	5'-UCA UCU CUG CAC CUG AGA UTT-3'
		5'-AUC UCA GGU GCA GAG AUG ATT-3'
si-IGFBP5 (# 3)	5'-GUG ACC GCA AAG GAU UCU ATT-3'	
	5'-UAG AAU CCU UUG CGG UCA CTT -3'	

Supplementary Table 3 The correlation of IGFBP5 expression with immune markers of glioma

Description	Gene marker	CGGA		TCGA	
		Cor	p	Cor	p
CD8+ T cell	CD8A	0.37	***	0.36	***
	CD8B	0.25	***	0.38	***
T cell (general)	CD3D	0.15	***	0.37	***
	CD3E	0.35	***	0.38	***
	CD2	0.35	***	0.41	***
B cell	CD19	-0.02	ns	0.17	***
	CD79A	0.08	**	0.21	***
	CD27	0.05	ns	0.20	***
Monocyte	CD14	0.35	***	0.39	***
	CSF1R	0.37	***	0.24	***
TAM	CCL2	0.52	***	0.45	***
	CD68	0.51	***	0.43	***
	IL10	0.42	***	0.37	***
M1 Macrophage	NOS2	0.30	***	0.35	***
	IRF5	0.34	***	0.31	***
	IL6	0.45	***	0.36	***
M2 Macrophage	CD163	0.55	***	0.55	***
	VSIG4	0.47	***	0.44	***
	MS4A4A	0.48	***	0.42	***
Dendritic cell	ITGAX	0.33	***	0.25	***
	CD1C	0.27	***	0.49	***
	NRP1	0.66	***	0.50	***
	THBD	0.60	***	0.48	***
Neutrophils	CCR7	0.35	***	0.33	***
	ITGAM	0.41	***	0.38	***
Natural killer cell	KIR2DL1	/	/	0.13	***
	KIR2DL3	/	/	0.13	***
	KIR3DL1	/	/	0.13	***
	KIR3DL3	/	/	0.04	ns
Th1	STAT4	-0.02	ns	-0.09	*
	TBX21	0.12	***	0.23	***
	CD4	0.55	***	0.39	***
Th2	GATA3	0.32	***	0.39	***
	CCR4	0.24	***	0.36	***
	CCR8	/	/	0.22	***
Treg	FOXP3	0.11	**	0.07	ns
	STAT5B	0.45	**	-0.09	*
	TGFB1	0.35	***	0.48	***
T cell exhaustion	CD274	0.58	***	0.53	***
	CTLA4	0.21	***	0.26	***
	HAVCR2	0.48	***	0.39	***

TAM, tumor-associated macrophage; Th, T helper cell; Tfh, Follicular helper T cell; Treg, regulatory T cell; Cor, R value of Pearson's correlation; ns, no significant difference. *P < 0.05; **P < 0.01; ***P < 0.001.