https://doi.org/10.17305/bb.2022.8586

Biomolecules and Biomedicine
ISSN: 2831-0896 (Print) | ISSN: 2831-090X (Online)

Journal Impact Factor® (2021): 3.76
CiteScore® (2021): 5.2
www.biomolbiomed.com | blog.biomolbiomed.com

SUPPLEMENTAL DATA

Fc fragment of IgG binding protein is correlated with immune infiltration levels in hepatocellular carcinoma

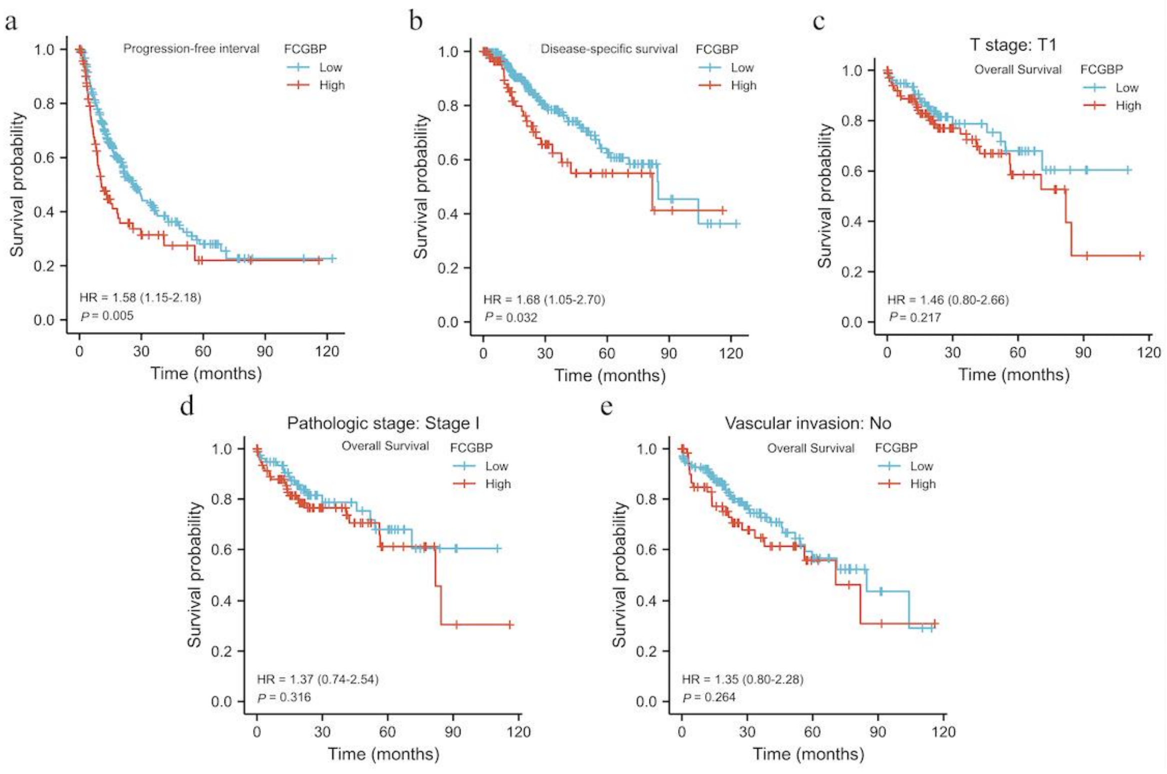


Figure S1. Prognostic value of *FCGBP* in HCC. (a and b) Relationships between *FCGBP* expression levels and progression-free interval and disease-specific survival in patients with HCC, respectively. (c-e) Overall survival in patients with HCC for *FCGBP* expression stratified by T1 stage, pathologic stage I, and non-vascular invasion. *FCGBP*, Fc fragment of IgG binding protein; HCC, hepatocellular carcinoma.

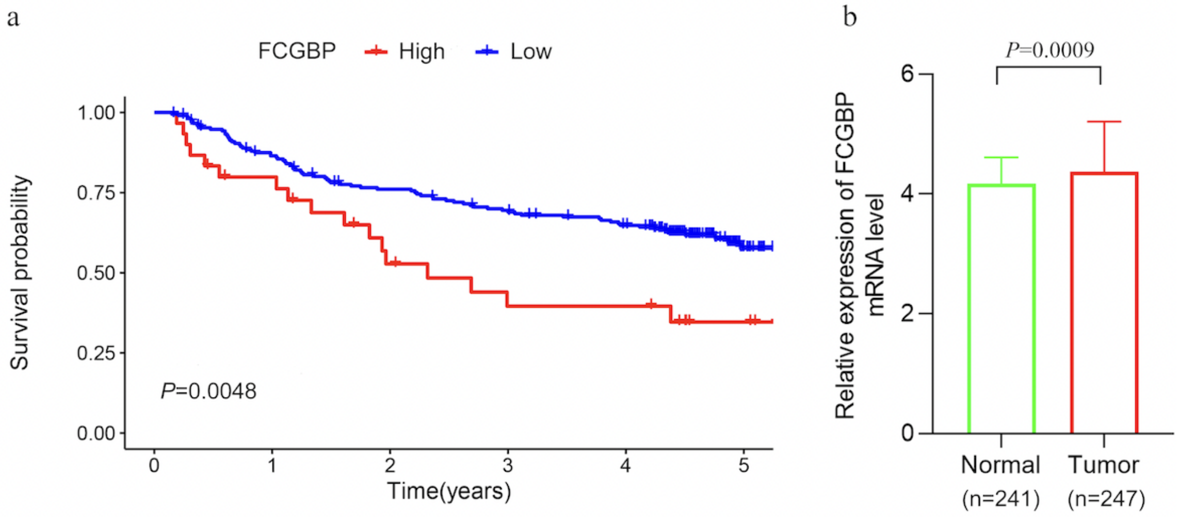
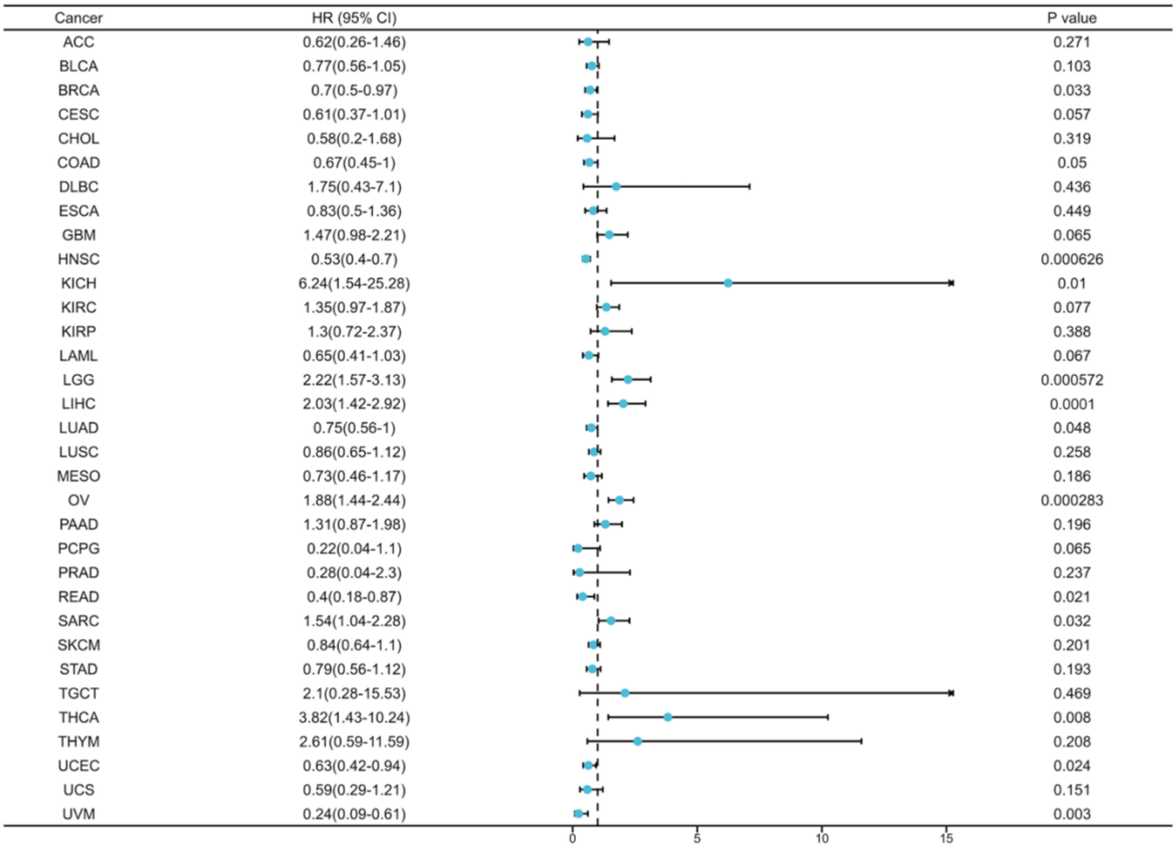


Figure S2: Effect of *FCGBP* expression on the prognosis of patients with HCC and *FCGBP* expression levels in HCC obtained from the GEO database. (a) Relationship between *FCGBP* expression levels and OS in patients with HCC. (b) *FCGBP* mRNA expression levels in unpaired HCC/normal samples. *FCGBP*, Fc fragment of IgG binding protein; HCC, hepatocellular carcinoma; OS, overall survival; GEO, the Gene Expression Omnibus.



Cancer	HR (95% CI)	P value
ACC	0.62(0.26-1.46)	0.271
BLCA	0.77(0.56-1.05)	0.103
BRCA	0.7(0.5-0.97)	0.033
CESC	0.61(0.37-1.01)	0.057
CHOL	0.58(0.2-1.68)	0.319
COAD	0.67(0.45-1)	0.05
DLBC	1.75(0.43-7.1)	0.436
ESCA	0.83(0.5-1.36)	0.449
GBM	1.47(0.98-2.21)	0.065
HNSC	0.53(0.4-0.7)	0.000626
KICH	6.24(1.54-25.28)	0.01
KIRC	1.35(0.97-1.87)	0.077
KIRP	1.3(0.72-2.37)	0.388
LAML	0.65(0.41-1.03)	0.067
LGG	2.22(1.57-3.13)	0.000572
LIHC	2.03(1.42-2.92)	0.0001
LUAD	0.75(0.56-1)	0.048
LUSC	0.86(0.65-1.12)	0.258
MESO	0.73(0.46-1.17)	0.186
OV	1.88(1.44-2.44)	0.000283
PAAD	1.31(0.87-1.98)	0.196
PCPG	0.22(0.04-1.1)	0.065
PRAD	0.28(0.04-2.3)	0.237
READ	0.4(0.18-0.87)	0.021
SARC	1.54(1.04-2.28)	0.032
SKCM	0.84(0.64-1.1)	0.201
STAD	0.79(0.56-1.12)	0.193
TGCT	2.1(0.28-15.53)	0.469
THCA	3.82(1.43-10.24)	0.008
THYM	2.61(0.59-11.59)	0.208
UCEC	0.63(0.42-0.94)	0.024
UCS	0.59(0.29-1.21)	0.151
UVM	0.24(0.09-0.61)	0.003

Figure S3: Forest plot of the relationships between *FCGBP* expression and OS of patients among the 33 tumors. *FCGBP*, Fc fragment of IgG binding protein; OS, overall survival.

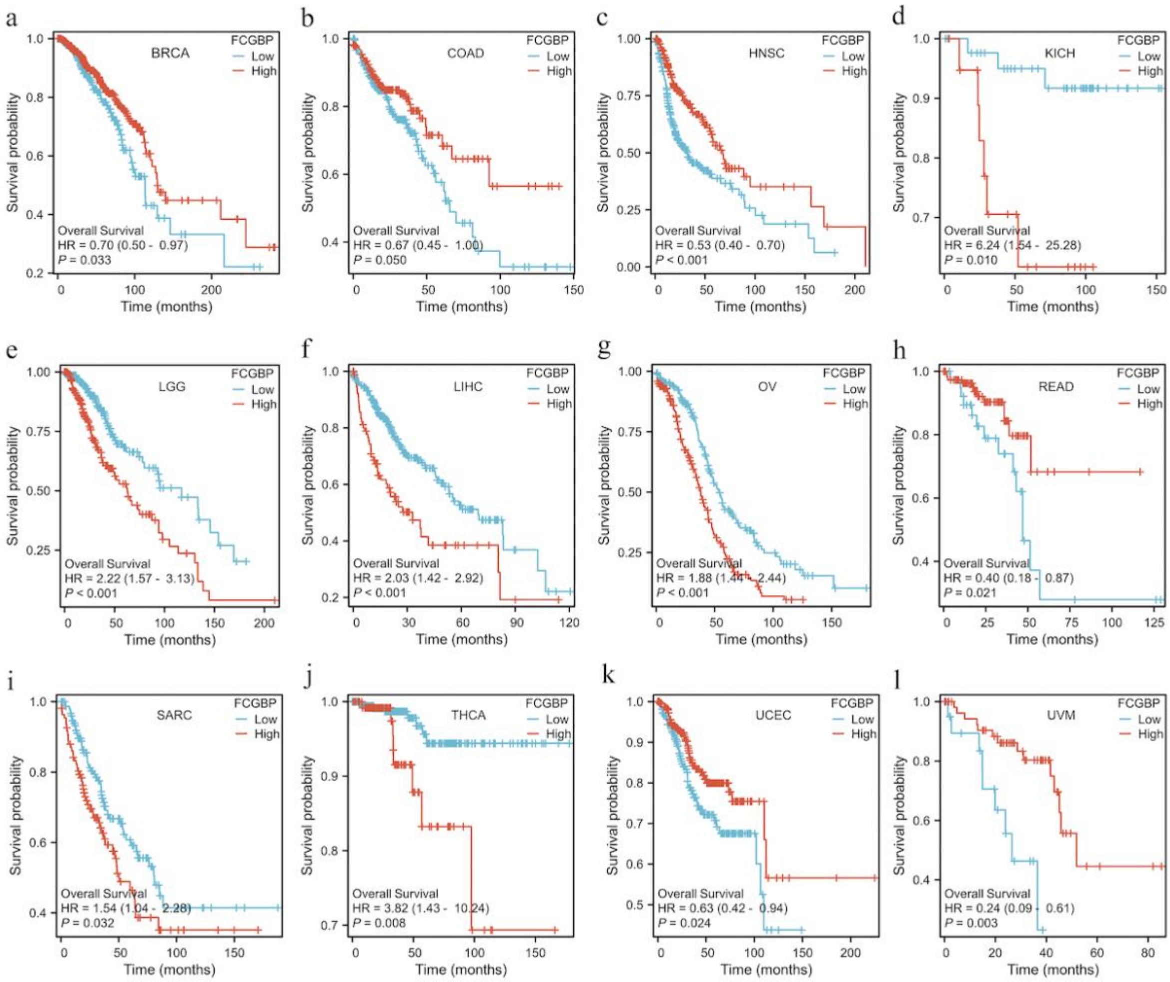


Figure S4: Kaplan-Meier OS curves of *FCGBP* expression in the 12 most significantly associated tumors across 33 tumors. (a) BRCA. (b) COAD. (c) HNSC. (d) KICH. (e) LGG. (f) LIHC. (g) OV. (h) READ. (i) SARC. (j) THCA. (k) UCEC. (l) UVM. *FCGBP*, Fc fragment of IgG binding protein.

https://doi.org/10.17305/bb.2022.8586

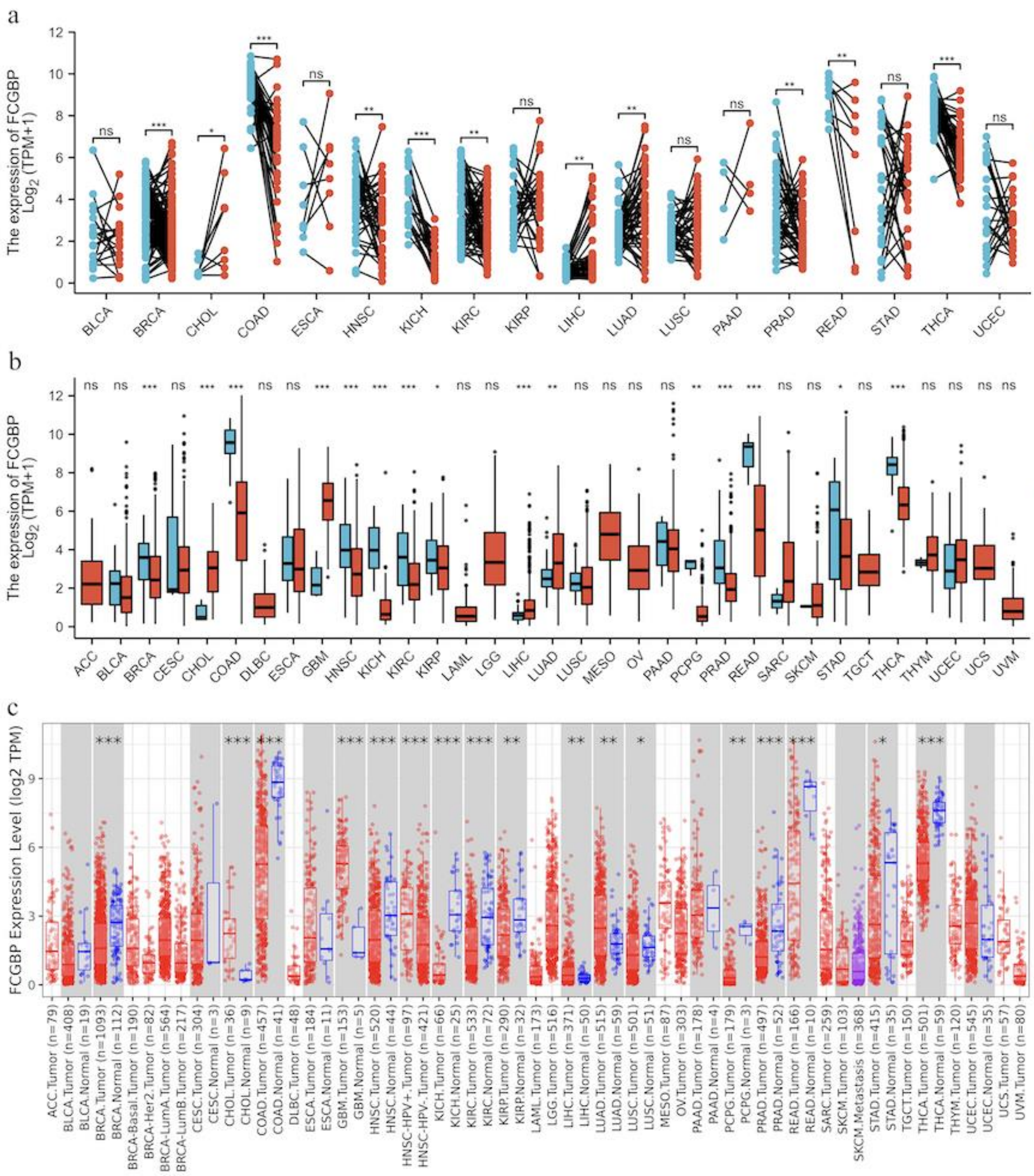


Figure S5: *FCGBP* expression levels in pan-cancer. (a and b) *FCGBP* expression in paired and unpaired tumor/normal samples in pan-cancer from TCGA database, respectively. (c) *FCGBP* expression in unpaired tumor/normal samples in pan-cancer from TIMER database. *FCGBP*, Fc fragment of IgG binding protein; TCGA, The Cancer Genome Atlas; TIMER, Tumor Immune Estimation Resource. ns, no significant difference; *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$.

https://doi.org/10.17305/bb.2022.8586

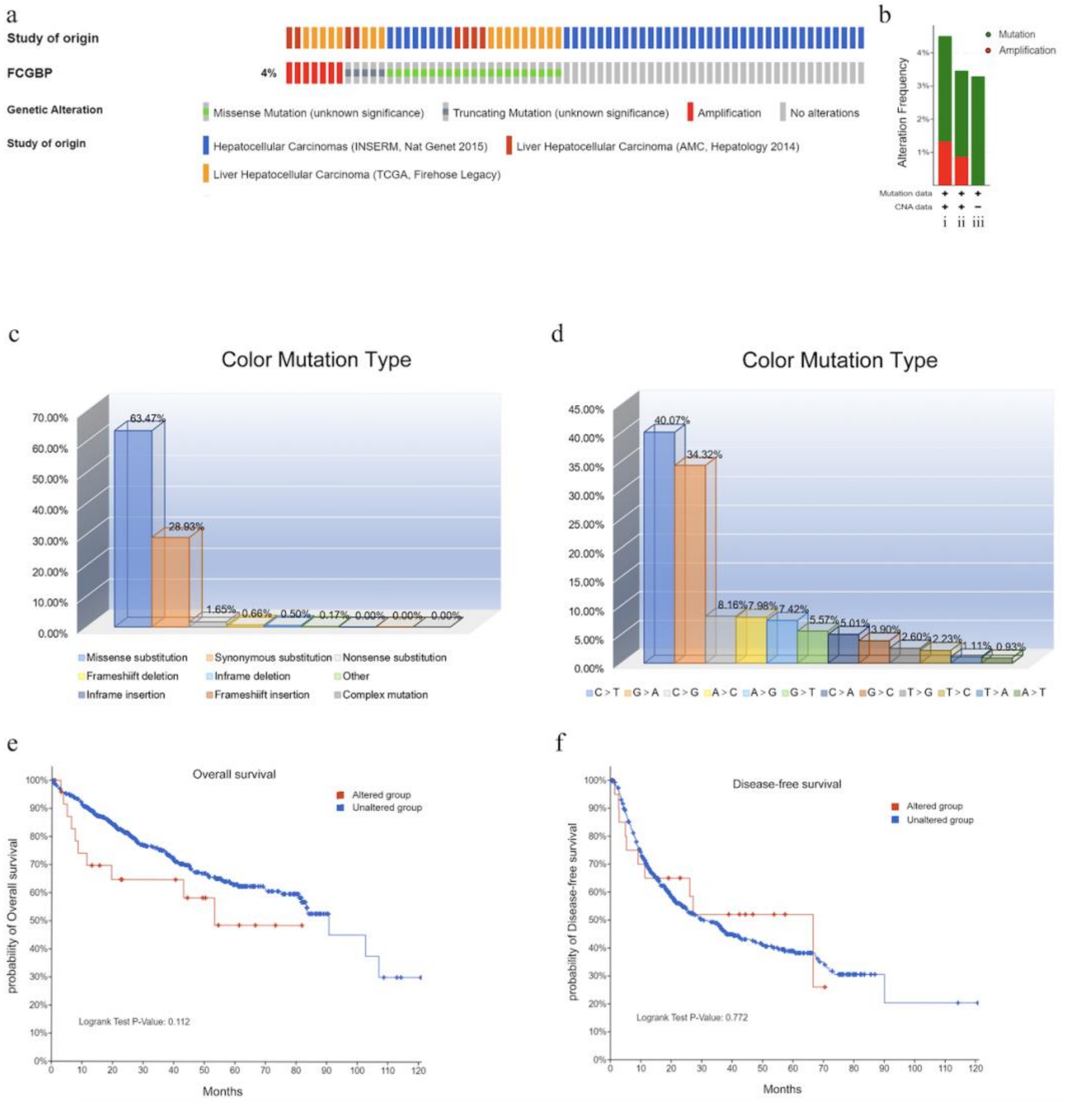


Figure S6: Genetic alterations of *FCGBP* in HCC. (a) Summary of *FCGBP* genetic alterations in HCC. (b) Alteration frequency of *FCGBP* in HCC from TCGA, Firehose Legacy (i); AMC Hepatology 2014 (ii); and INSERM, Nat genet 2015 (iii). (c and d) Mutation types of *FCGBP* in HCC. (e and f) Relationship between *FCGBP* genetic alteration and the prognosis of patients with HCC. *FCGBP*, Fc fragment of IgG binding protein; HCC, hepatocellular carcinoma.

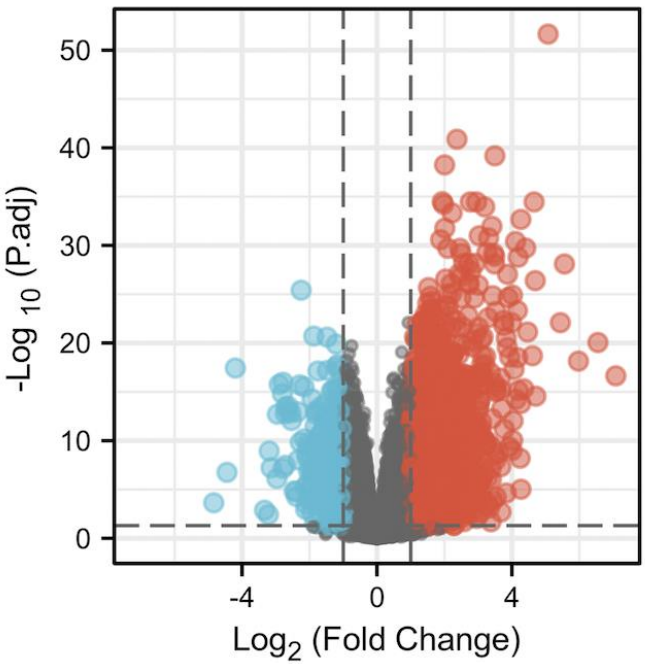


Figure S7: Volcano plot of differentially expressed genes between the high and low *FCGBP* expression samples in HCC. *FCGBP*, Fc fragment of IgG binding protein.

Table S1: List of clinical information of 25 patients with HCC.

Patients	Gender	Age	Organ	Diagnosis
Patient 1	Man	66	Liver	HCC
Patient 2	Man	40	Liver	HCC
Patient 3	Man	51	Liver	HCC
Patient 4	Woman	83	Liver	HCC
Patient 5	Man	46	Liver	HCC
Patient 6	Man	66	Liver	HCC
Patient 7	Woman	48	Liver	HCC
Patient 8	Man	74	Liver	HCC
Patient 9	Man	56	Liver	HCC
Patient 10	Man	72	Liver	HCC
Patient 11	Man	55	Liver	HCC
Patient 12	Man	78	Liver	HCC

Patient 13	Man	63	Liver	HCC
Patient 14	Man	64	Liver	HCC
Patient 15	Woman	65	Liver	HCC
Patient 16	Man	79	Liver	HCC
Patient 17	Man	40	Liver	HCC
Patient 18	Man	46	Liver	HCC
Patient 19	Man	50	Liver	HCC
Patient 20	Man	50	Liver	HCC
Patient 21	Man	64	Liver	HCC
Patient 22	Woman	24	Liver	HCC
Patient 23	Man	38	Liver	HCC
Patient 24	Man	30	Liver	HCC
Patient 25	Man	48	Liver	HCC

HCC, hepatocellular carcinoma

Table S2: Association between *FCGBP* expression levels and clinicopathologic characteristics in HCC.

Characteristic	Low expression of *FCGBP*	High expression of *FCGBP*	*p*
n	187	187	
T stage, n (%)			0.167
T1	102 (27.5%)	81 (21.8%)	
T2	41 (11.1%)	54 (14.6%)	
T3	36 (9.7%)	44 (11.9%)	
T4	6 (1.6%)	7 (1.9%)	
N stage, n (%)			1.000
N0	127 (49.2%)	127 (49.2%)	
N1	2 (0.8%)	2 (0.8%)	

M stage, n (%)			0.622
M0	135 (49.6%)	133 (48.9%)	
M1	1 (0.4%)	3 (1.1%)	
Pathologic stage, n (%)			0.089
Stage I	99 (28.3%)	74 (21.1%)	
Stage II	40 (11.4%)	47 (13.4%)	
Stage III	36 (10.3%)	49 (14%)	
Stage IV	2 (0.6%)	3 (0.9%)	
Tumor status, n (%)			0.226
Tumor free	108 (30.4%)	94 (26.5%)	
With tumor	71 (20%)	82 (23.1%)	
Gender, n (%)			0.122
Female	53 (14.2%)	68 (18.2%)	
Male	134 (35.8%)	119 (31.8%)	
Race, n (%)			0.202
Asian	78 (21.5%)	82 (22.7%)	
Race, n (%)			0.202
Black or African American	5 (1.4%)	12 (3.3%)	
White	96 (26.5%)	89 (24.6%)	
Histologic grade, n (%)			0.238
G1	32 (8.7%)	23 (6.2%)	
G2	93 (25.2%)	85 (23%)	
G3	54 (14.6%)	70 (19%)	
G4	5 (1.4%)	7 (1.9%)	
Adjacent hepatic tissue inflammation, n (%)			0.171
None	67 (28.3%)	51 (21.5%)	
Mild	50 (21.1%)	51 (21.5%)	
Severe	13 (5.5%)	5 (2.1%)	

Child-Pugh grade, n (%)			0.895
A	125 (51.9%)	94 (39%)	
B	13 (5.4%)	8 (3.3%)	
C	1 (0.4%)	0 (0%)	
Fibrosis ishak score, n (%)			0.492
0	43 (20%)	32 (14.9%)	
1/2	14 (6.5%)	17 (7.9%)	
3/4	18 (8.4%)	10 (4.7%)	
5/6	47 (21.9%)	34 (15.8%)	
Vascular invasion, n (%)			0.060
No	119 (37.4%)	89 (28%)	
Yes	50 (15.7%)	60 (18.9%)	
OS event, n (%)			0.232
Alive	128 (34.2%)	116 (31%)	
Dead	59 (15.8%)	71 (19%)	
DSS event, n (%)			1.000
Alive	145 (39.6%)	142 (38.8%)	
Dead	40 (10.9%)	39 (10.7%)	
PFI event, n (%)			1.000
Alive	95 (25.4%)	96 (25.7%)	
Dead	92 (24.6%)	91 (24.3%)	
Age, meidan (IQR)	61 (51, 69)	61.5 (52, 68.75)	0.496
Height, meidan (IQR)	168 (162, 175)	166 (160, 173)	0.044
Weight, meidan (IQR)	71 (61, 85)	69 (58, 79)	0.042
BMI, meidan (IQR)	24.88 (22.05, 29.1)	24.22 (21.03, 28.38)	0.153
AFP (ng/ml), meidan (IQR)	10 (4, 93.25)	24 (5, 481.5)	0.023
Albumin(g/dl), meidan (IQR)	4 (3.35, 4.3)	4.1 (3.6, 4.3)	0.269
Prothrombin time, meidan (IQR)	1.1 (1, 9.3)	1.1 (1, 8.8)	0.032

https://doi.org/10.17305/bb.2022.8586

FCGBP, Fc fragment of IgG binding protein; HCC, hepatocellular carcinoma; OS, overall survival; DSS, disease-specific survival; PFI, progression-free interval; IQR, interquartile range; BMI, Body Mass Index; AFP, alpha fetoprotein.

Table S3: GO term and KEGG pathway enrichment analysis of *FCGBP* expression in HCC.

Ontology	ID	Description	*p*-value	adjusted *p*-value	q-value
BP	GO:0070371	ERK1 and ERK2 cascade	5.42e-05	0.002	0.001
BP	GO:1904894	positive regulation of STAT cascade	0.003	0.025	0.020
BP	GO:0048863	stem cell differentiation	0.004	0.032	0.025
BP	GO:0046425	regulation of JAK-STAT cascade	0.004	0.032	0.025
BP	GO:0010574	regulation of vascular endothelial growth factor production	0.007	0.048	0.038
CC	GO:0005911	cell-cell junction	0.002	0.022	0.019
MF	GO:0017147	Wnt-protein binding	3.16e-04	0.005	0.004
KEGG	hsa04151	PI3K-Akt signaling pathway	1.54e-04	0.002	0.002
KEGG	hsa04015	Rap1 signaling pathway	0.002	0.017	0.013
KEGG	hsa05202	Transcriptional misregulation in cancer	0.003	0.020	0.015

GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; *FCGBP*, Fc fragment of IgG binding protein; HCC, hepatocellular carcinoma; BP, biological process; CC, cellular component; MF, molecular function.