

Supplementary Table 1. Primers used in the present study

Primer	Sequence (5'-3')
FIRRE	Forward: CTGTGACCTCGCTTCACTTCT
	Reverse: GTGGCAAAGAGCAGAAGATAGA
PFKFB4	Forward: GGAGTTCAATGTTGGCCAGT
	Reverse: TCAGGATCCACACAGATGGA
PKM2	Forward: CCGCCGCCTGGCGCCCATTA
	Reverse: CGGTCAGCACAATGACCACATC
β -actin	Forward: TTCCTTCCTGGGCATGGAGT
	Reverse: TACAGGTCTTTGCGGATGTC

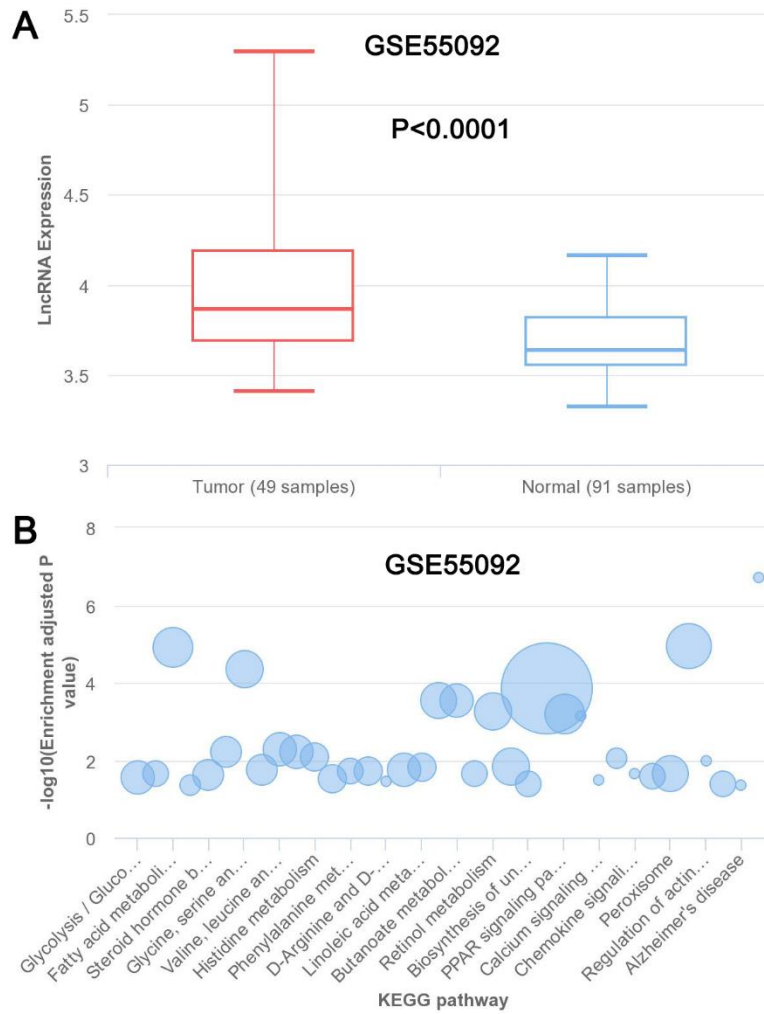
Supplementary Table 2. The correlation between PFKFB4 expression and clinicopathologic characteristics of hepatocellular carcinoma

Variable	n	PFKFB4 expression		P
		Low (n=40)	High (n=40)	
Age (year)	<50	35	13	0.809
	≥50	45	27	
Gender	Male	63	29	0.172
	Female	17	11	
HBV infection	Absent	28	17	0.160
	Present	52	23	
Serum AFP level (ng/mL)	<20	27	17	0.098
	≥20	53	23	
Tumor size (cm)	<5	26	16	0.152
	≥5	54	24	
No. of tumor nodules	1	65	31	0.390
	≥2	15	9	
Cirrhosis	Absent	35	19	0.499
	Present	45	21	
Venous infiltration	Absent	44	23	0.653
	Present	36	17	
Edmondson-Steiner grading	I+II	57	33	0.026*
	III+IV	23	7	
TNM stage	I+II	63	37	0.003*
	III+IV	17	3	

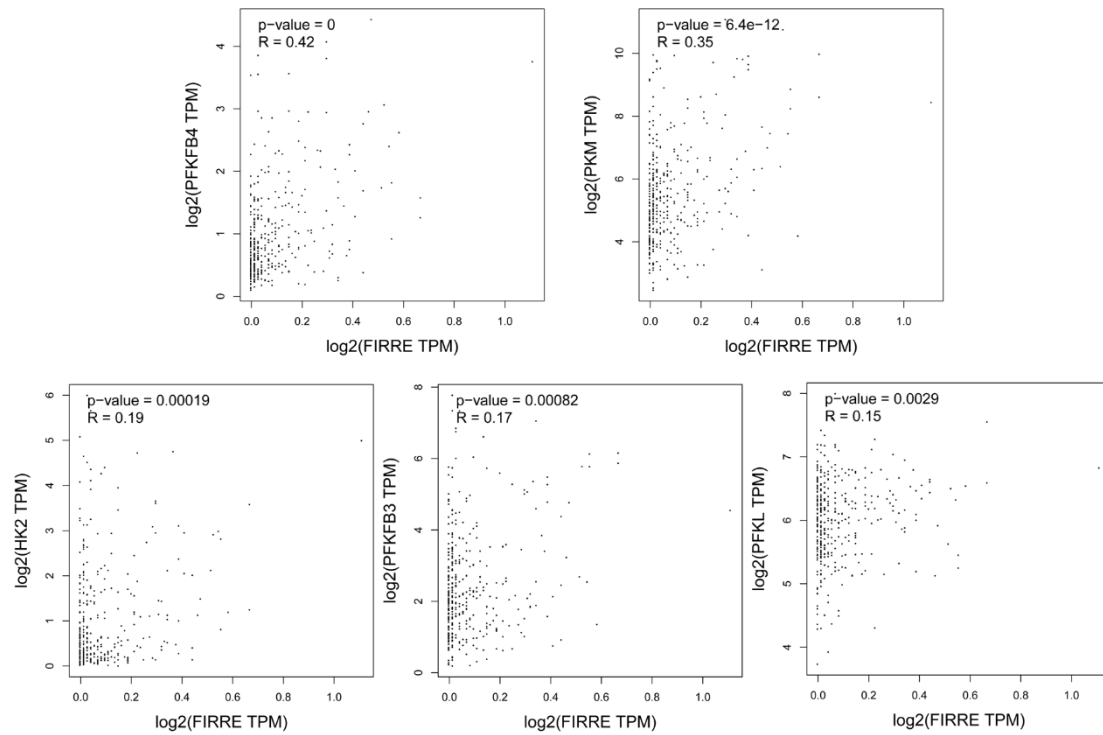
HBV, hepatitis B virus; AFP, alpha-fetoprotein; TNM, tumor-node-metastasis.

The “low” or “high” expression of PFKFB4 level was defined according to the cut-off value, which was defined as the median value of the cohort of patients tested.

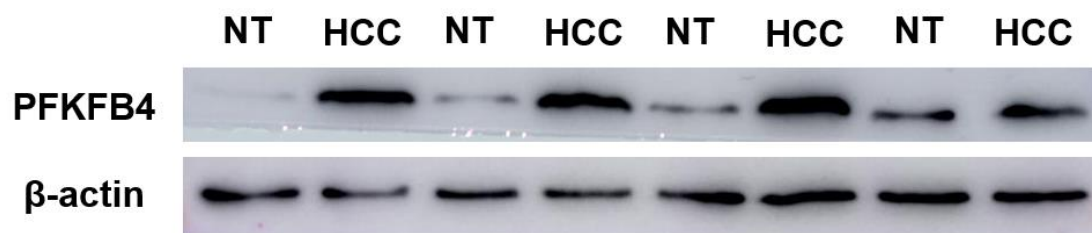
*Statistically significant.



Supplementary Figure 1 The expression and KEGG pathway analysis of FIRRE in HCC using GEO data from InCAR website. (A) The expression of FIRRE between HCC and normal liver tissues. (B) KEGG pathway analysis of FIRRE based on GSE55092 dataset.



Supplementary Figure 2 The correlations between FIIRE and glycolic enzymes in TGCA-LICH from the GEPIA website.



Supplementary Figure 3 The expression of PFKFB4 protein in four pairs of HCC and adjacent nontumor tissues.