

Table SI. List of websites used in the present study.

Website name	URL
GEPIA 2	http://gepia2.cancer-pku.cn/#index
TCGA-LIHC	https://portal.gdc.cancer.gov/
Draw Venn Diagram	http://bioinformatics.psb.ugent.be/webtools/Venn/
KEGG	https://www.genome.jp/kegg/
miRDB	http://www.mirdb.org/
TargetScan	http://www.targetscan.org/vert_72/
LncBase	http://carolina.imis.athena-innovation.gr/diana_tools/web/index.php?r=lncbasev2%2Findex
GEO	https://www.ncbi.nlm.nih.gov/geo/

KEGG, Kyoto Encyclopedia of Genes and Genomes; GEO, Gene Expression Omnibus; TCGA, The Cancer Genome Atlas.

Table SII. Thermocycling conditions used for quantitative PCR.

Gene	Initial denaturation	Denaturation	Annealing	Extension	Cycles, n	Extension
XRCC4	95°C, 10 min	95°C, 10 sec	55°C, 25 sec	72°C, 20 sec	35	65°C, 5 sec
BRCA1	95°C, 10 min	95°C, 10 sec	60°C, 25 sec	72°C, 20 sec	35	65°C, 5 sec
RAD51	95°C, 10 min	95°C, 10 sec	57°C, 25 sec	72°C, 20 sec	35	65°C, 5 sec
GAPDH	95°C, 10 min	95°C, 10 sec	57°C, 25 sec ^a	72°C, 20 sec	35	65°C, 5 sec
U6	95°C, 10 min	95°C, 10 sec	57°C, 25 sec	72°C, 20 sec	40	65°C, 5 sec
ZFPM2-AS1	95°C, 10 min	95°C, 10 sec	55°C, 25 sec	72°C, 20 sec	35	65°C, 5 sec
miR-3065-5p	95°C, 10 min	95°C, 10 sec	57°C, 25 sec	72°C, 20 sec	40	65°C, 5 sec

^aThe optimal thermocycling conditions for GAPDH were the same for target genes except that the annealing temperature was 57°C for GAPDH.

Table SIII. Primer, shRNA and miRNA sequences.

Name	Sequences (5'-3')
XRCC4	F, TGGAATGATGTTCAAGGACGAT; R, GGATCTCGGTCAGCAGTCA
BRCA1	F, TAAGGTTGTTGATGTGGAGGAG; R, GCAGAGGTTGAAGATGGTATGT
RAD51	F, TTCAACACAGACCACCAGACC; R, CGCAGAAGCATCCGCAGAA
GAPDH	F, GGTGAAGGTCGGAGTCAACG; R, TGGGTGGAATCATATTGGAACA
U6	F, CTCGCTTCGGCAGCACA; R, AACGCTTCACGAATTTGCGT
ZFPM2- AS1	F, CAATGGGACTAAGCCAGGCA; R, GGGCTCCACCAACAACCATA
miR-3065- 5p	RT, GTCGTATCGACTGCAGGGTCCGAGGTATTCGCAGTCGATACGACTCCAGC; F, GCGGCTCAACAAAATCACTGAT; R, ACTGCAGGGTCCGAGGTATT
sh-control	GCTTCGCGCCGTAGTCTTA
shRNA#1	ACCGGGCAGAGTTGCACAGAAGAAGTTCGAGTTCTTCTGTGCAACTCTGCTTTTTG
shRNA#2	ACCGGGAAGGAAGTGGATAAACAAGTTCGAGTTGTTTATCCACTTCCTTCTTTTTG
shRNA#3	ACCGGGGAAGTGGAGAAGACATACTCGAGTATGTCTTCTCCAAGTTCCTTTTTG
Mock	UUACUCGACACGUGUCAAGUTT
miR-3065- 5p mimic	UCAACAAAAUCACUGAUGCUGGA
miR-548x- 3p mimic	UAAAAACUGCAAUUACUUUC

miR-186-
5p mimic CAAAGAAUUCUCCUUUUGGGCU
miR-548j-
3p mimic CAAAAACUGCAUUACUUUUGC
miR-548aj-
3p mimic UAAAAACUGCAAUUACUUUUA
miR-3065-
5p inhibitor UCCAGCAUCAGUGAUUUUGUUGA

F, forward; R, reverse; RT, reverse transcription; miR, microRNA; shRNA, short hairpin RNA.

Table SIV. Primary and secondary antibodies.

Antigens	Manufacturer	Catalog number	Application
XRCC4	Proteintech	15817-1-AP	1:400 for IHC 1:1,000 for WB
BRCA1	Proteintech	22362-1-AP	1:1,000 for WB
RAD51	Proteintech	27071-1-AP	1:1,000 for WB
GAPDH	Proteintech	60004-1-Ig	1:10,000 for WB
Cyclin E1	Proteintech	11554-1-AP	1:1,000 for WB
Cyclin B1	Proteintech	55004-1-AP	1:2,000 for WB
CDK2	Proteintech	22060-1-AP	1:1,000 for WB
CDK4	Proteintech	11026-1-AP	1:1,000 for WB
CDK6	Proteintech	14052-1-AP	1:1,000 for WB
P21	Proteintech	10355-1-AP	1:2,000 for WB
Caspase 3	Proteintech	19677-1-AP	1:1,000 for WB
Cleaved caspase-3	Cell Signaling Technology, Inc.	9661T	1:1,000 for WB
Ki67	Proteintech	27309-1-AP	1:2,000 for IHC
HRP-conjugated Affinipure goat anti- rabbit IgG (H+L)	Proteintech	SA00001-2	1:5,000 for WB
HRP-conjugated Affinipure goat anti- mouse IgG (H+L)	Proteintech	SA00001-1	1:5,000 for WB
HRP-conjugated goat anti-rabbit IgG	Aspen	AS1107	1: 200 for IHC

CDK, cyclin-dependent kinase; IHC, immunohistochemistry; WB, western blot.

Table SV. Clinical characteristics of the three groups of patients with hepatocellular carcinoma.

Parameter	Training group (n=172)	Testing group (n=171)	TCGA group (n=343)	P-value
Age, years				0.888
≥65	87 (50.6)	91 (52.3)	178 (51.9)	
<65	85 (49.4)	80 (46.8)	165 (48.1)	
Gender				0.883
Female	53 (30.8)	57 (33.3)	110 (32.1)	
Male	119 (69.2)	114 (66.7)	233 (67.9)	
T stage				0.939
T1	79 (45.9)	89 (52.0)	168 (49.0)	
T2	47 (27.3)	37 (21.6)	84 (24.5)	
T3	36 (20.9)	39 (22.8)	75 (21.9)	
T4	8 (4.7)	5 (2.9)	13 (3.8)	
Unknown	2 (1.2)	1 (0.6)	3 (0.9)	
N stage				0.909
N0	117 (68.0)	122 (71.3)	239 (69.7)	
N1	1 (0.6)	2 (1.2)	3 (0.9)	
Unknown	54 (31.4)	47 (27.5)	101 (29.4)	
Pathological stage				0.158
I	74 (43.0)	87 (50.9)	161 (46.9)	
II	43 (25.0)	34 (19.9)	77 (22.4)	
III	38 (22.1)	42 (24.6)	80 (23.3)	
IV	0 (0.0)	3 (1.8)	3 (0.9)	
Unknown	17 (9.9)	5 (2.9)	22 (6.4)	
Vital status				0.251
Alive	67 (39.0)	52 (30.4)	119 (34.7)	

Dead	105 (61.0)	119 (69.6)	224 (65.3)
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Values are expressed as n (%). TCGA, The Cancer Genome Atlas.

Table SVI. Detailed parameters of the GIlncsig.

Gene symbol	Coefficient	HR	95% CI	P-value
ZFPM2-AS1	0.631	1.880	1.380-2.561	<0.001
LUCAT1	0.371	1.449	1.029-2.041	0.034
MIR210HG	0.339	1.403	1.036-1.901	0.029
AC004862.1	-0.252	0.777	0.569-1.062	0.114
KCNMB2-AS1	-0.401	0.670	0.438-1.024	0.064
AC010205.1	-0.717	0.488	0.228-1.046	0.065

HR, hazard ratio; ZFPM2-AS1, zinc finger protein, FOG family member 2 antisense 1; MIR210HG, MIR210 host gene; LUCAT1, lung cancer-associated transcript 1; KCNMB2-AS1, potassium calcium-activated channel subfamily M regulatory β subunit 2 antisense 1.

Table SVII. Univariate and multivariate Cox regression analyses of the GILncsig.

A, Training group (n=172)						
Variable	Univariate model			Multivariate model		
	HR	95%CI	P-value	HR	95%CI	P-value
Age (≥ 65 vs. < 65 years)	1.016	0.989-1.043	0.241			
Gender (male vs. female)	0.699	0.349-1.397	0.310			
Grade (G3/G4 vs. G1/G2)	1.167	0.595-2.289	0.653			
Stage (III/IV vs. I/II)	2.216	1.067-4.603	0.033	1.977	0.837-4.670	0.120
AFP (high vs. low)	1.187	0.604-2.333	0.620			
GILncSig (≥ 0.911 vs. < 0.911)	1.310	1.188-1.445	< 0.001	1.278	1.144-1.428	< 0.001
B, Testing group (n=171)						
Variable	Univariate model			Multivariate model		
	HR	95%CI	P-value	HR	95%CI	P-value
Age (≥ 65 vs. < 65 years)	1.024	0.993-1.056	0.125			
Gender (male vs. female)	0.566	0.278-1.155	0.118			
Grade (G3/G4 vs. G1/G2)	1.860	0.892-3.880	0.098			
Pathological stage (III/IV vs. I/II)	2.348	1.151-4.789	0.019	1.554	0.729-3.315	0.254

AFP (high vs. low)	2.835	1.256-6.402	0.012	2.000	0.847-4.726	0.114
GILncSig (≥ 0.911 vs. < 0.911)	1.174	1.086-1.268	< 0.001	1.135	1.030-1.250	0.011

C, TCGA group (n=343)

Variable	Univariate model			Multivariate model		
	HR	95%CI	P-value	HR	95%CI	P-value
Age (≥ 65 vs. < 65 years)	1.021	1.001-1.042	0.041	1.013	0.992-1.035	0.230
Gender (male vs. female)	0.645	0.394-1.055	0.081			
Grade (G3/G4 vs. G1/G2)	1.450	0.890-2.363	0.135			
Stage (III/IV vs. I/II)	2.194	1.323-3.639	0.002	1.827	1.076-3.103	0.026
AFP (high vs. low)	1.659	1.007-2.732	0.047	1.179	0.690-2.015	0.547
GILncSig (≥ 0.911 vs. < 0.911)	1.187	1.123-1.256	< 0.001	1.161	1.086-1.241	< 0.001

TCGA, The Cancer Genome Atlas; AFP, α -fetoprotein; HR, hazard ratio; GILncSig, genomic instability-related lncRNA signature.

Table SVIII. Univariate and multivariate analyses of ZFPM2-AS1 expression in patients with hepatocellular carcinoma.

Variable	Univariate model			Multivariate model		
	HR	95%CI	P-value	HR	95%CI	P-value
Age (≥ 65 vs. < 65 years)	1.101	0.605-2.003	0.753			
Gender (male vs. female)	1.054	0.574-1.938	0.864			
Tumor diameter (≥ 5 vs. < 5 cm)	1.967	1.080-3.584	0.027	1.292	0.615-2.711	0.499
TNM (III/IV vs. I/II)	2.853	1.496-5.441	0.001	2.486	1.261-4.898	0.009
AFP (high vs. low)	1.655	0.904-3.031	0.103			
HBV (yes vs. no)	1.504	0.805-2.808	0.200			
PVTT (yes vs. no)	1.015	0.554-1.862	0.961			
Lymphatic invasion (yes vs. no)	2.089	1.106-3.945	0.023	1.589	0.781-3.230	0.201
ZFPM2-AS1 (high vs. low)	1.353	1.086-1.685	0.007	1.358	1.014-1.817	0.040

AFP, α -fetoprotein; HBV, hepatitis B virus; PVTT, portal vein tumour thrombus; HR, hazard ratio; ZFPM2-AS1, zinc finger protein, FOG family member 2 antisense 1.