Table SI. Highly connected genes screened according to the protein-protein interaction network (connectivity >4).

Ensembl ID	Connectivity	TFs	Gene	Gene description
ENSG00000137337	16	Yes	MDC1	Mediator of DNA damage checkpoint 1
ENSG00000005339	15	Yes	CREBBP	CREB binding protein
ENSG00000132424	11	No	PNISR	PNN interacting serine and arginine rich protein
ENSG00000108848	10	No	LUC7L3	LUC7 like 3 pre-mRNA splicing factor
ENSG00000198707	9	No	CEP290	Centrosomal protein 290
ENSG00000183495	9	Yes	EP400	E1A binding protein p400
ENSG00000131051	9	Yes	RBM39	RNA binding motif protein 39
ENSG00000085840	8	No	ORC1	Origin recognition complex subunit 1
ENSG00000135336	8	No	ORC3	Origin recognition complex subunit 3
ENSG00000002016	8	No	RAD52	RAD52 homolog, DNA repair protein
ENSG00000163029	8	No	SMC6	Structural maintenance of chromosomes 6
ENSG00000138346	7	No	DNA2	DNA replication helicase/nuclease 2
ENSG00000147162	7	Yes	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase
ENSG00000115942	7	No	ORC2	Origin recognition complex subunit 2
ENSG00000164815	7	No	ORC5	Origin recognition complex subunit 5
ENSG00000164548	7	No	TRA2A	Transformer 2 alpha homolog
ENSG00000101191	6	No	DIDO1	Death inducer-obliterator 1
ENSG00000198690	6	No	FAN1	FANCD2 and FANCI associated nuclease 1
ENSG00000160299	6	No	PCNT	Pericentrin
ENSG00000068885	5	Yes	IFT80	Intraflagellar transport 80
ENSG00000113971	5	Yes	NPHP3	Nephrocystin 3
ENSG00000116001	5	Yes	TIA1	TIA1 cytotoxic granule associated RNA binding protein
ENSG00000186812	5	Yes	ZNF397	Zinc finger protein 397
ENSG00000132485	5	No	ZRANB2	Zinc finger RANBP2-type containing 2

TFs, transcription factors.

Table SII. Expression levels of transcription factors and their effects on the survival of patients with hepatocellular carcinoma.

A, Highly connected transcription factors screened based on the eigengene-based connectivity

	Differential expression between tumor and adjacent tissue			Overall survival	Disease free survival	Relapse free survival	
Ensembl ID	Log2 fold change	P-value	Adjusted P-value	P-value	P-value	P-value	Symbol
ENSG00000116001	0.28	0.04	0.08	0.09	0.04	0.01	TIA1
ENSG00000179912	0.33	0.02	0.04	0.69	0.91	0.06	R3HDM2
ENSG00000163666	0.29	0.15	0.24	0.72	0.29	0.49	HESX1
ENSG00000124459	0.46	0.01	0.02	0.11	0.56	0.09	ZNF45
ENSG00000185670	0.28	0.04	0.07	0.43	0.20	0.26	ZBTB3
ENSG00000148200	0.14	0.40	0.51	0.01	0.01	<0.01	NR6A1
ENSG00000167081	0.39	0.04	0.09	0.88	0.06	0.12	PBX3
ENSG00000162086	0.12	0.43	0.54	0.23	0.14	0.03	ZNF75A
ENSG00000089335	0.44	0.01	0.02	0.76	0.20	0.09	ZNF302
ENSG00000177463	0.33	0.04	0.08	0.14	0.21	0.30	NR2C2
ENSG00000133111	0.55	<0.01	<0.01	0.08	<0.01	<0.01	RFXAP
ENSG00000100307	0.34	0.07	0.13	0.73	0.20	0.02	CBX7
ENSG00000254004	0.62	<0.01	<0.01	0.01	0.01	0.04	ZNF260
ENSG00000173153	0.16	0.21	0.32	0.22	0.58	0.14	ESRRA
ENSG00000137337	0.65	<0.01	<0.01	0.02	0.07	0.04	MDC1
ENSG00000068885	0.75	<0.01	<0.01	0.03	0.45	0.20	IFT80
ENSG00000166432	0.08	0.76	0.83	0.38	0.46	0.11	ZMAT1

B, Highly connected transcription factors screened according to the protein-protein interaction network

	Differential expression between tumor and adjacent tissue			Overall survival	Disease free survival	Relapse free survival	
Ensembl ID	Log2 fold change	P-value	padj	P-value	P-value	P-value	Symbol
ENSG00000137337	0.65	<0.01	<0.01	0.02	0.07	0.04	MDC1
ENSG00000005339	0.26	0.07	0.12	0.05	0.46	0.10	CREBBP
ENSG00000183495	0.41	<0.01	0.01	<0.01	0.02	<0.01	EP400
ENSG00000131051	0.38	0.01	0.02	<0.01	0.03	0.22	RBM39
ENSG00000147162	0.37	<0.01	0.01	0.04	0.59	0.07	OGT
ENSG00000068885	0.75	<0.01	<0.01	0.03	0.45	0.20	IFT80
ENSG00000113971	0.13	0.44	0.55	0.01	0.54	0.28	NPHP3
ENSG00000116001	0.28	0.04	0.08	0.09	0.04	0.01	TIA1
ENSG00000186812	0.30	0.02	0.06	0.11	0.47	0.04	ZNF397

C, Differentially connected transcription factors between the relapsed and non-relapsed subnetworks

	Differential expression between tumor and adjacent tissue			Overall survival	Disease free survival	Relapse free survival	
Ensembl ID	Log2 fold change	P-value	Adjusted P-value	P-value	P-value	P-value	Symbol
ENSG00000117569	0.60	<0.01	<0.01	<0.01	0.04	<0.01	PTBP2
ENSG00000267680	0.47	0.01	0.02	0.65	0.65	0.35	ZNF224
ENSG00000076108	0.39	<0.01	0.01	0.01	0.16	0.03	BAZ2A
ENSG00000183495	0.41	<0.01	0.01	<0.01	0.02	<0.01	EP400
ENSG00000185946	0.49	0.01	0.02	0.36	0.52	0.29	RNPC3
ENSG00000186908	0.13	0.24	0.35	0.26	0.37	0.17	ZDHHC17
ENSG00000116001	0.28	0.04	0.08	0.09	0.04	0.01	TIA1
ENSG00000177463	0.33	0.04	0.08	0.14	0.21	0.30	NR2C2

Table SII. Continued.

D, Transcription factors regulated by ZNF143 and correlated to ZNF143 in the expression levels

	Differential expression between tumor and adjacent tissue			Overall survival	Disease free survival	Relapse free survival	
Ensembl ID	Log2 fold change	P-value	Adjusted P-value	P-value	P-value	P-value	Symbol
ENSG00000089335	0.44	0.01	0.02	0.76	0.20	0.09	ZNF302
ENSG00000109118	0.12	0.24	0.34	0.07	0.18	<0.01	PHF12
ENSG00000124459	0.46	0.01	0.02	0.11	0.56	0.09	ZNF45
ENSG00000131115	0.34	0.02	0.04	0.35	0.74	0.34	ZNF227
ENSG00000137337	0.65	<0.01	<0.01	0.02	0.07	0.04	MDC1
ENSG00000175787	0.70	<0.01	<0.01	0.11	0.04	0.04	ZNF169
ENSG00000254004	0.62	<0.01	<0.01	0.01	0.01	0.04	ZNF260

E, Transcription factors regulating ZNF143 and correlated to ZNF143 in the expression levels

	Differential expression between tumor and adjacent tissue			Overall survival	Disease free survival	Relapse free survival	
Ensembl ID	Log2 fold change	P-value	Adjusted P-value	P-value	P-value	P-value	Symbol
ENSG00000078399	2.23	<0.01	<0.01	0.30	0.90	0.11	HOXA9
ENSG00000100811	0.21	0.03	0.07	0.01	0.57	0.08	YY1
ENSG00000105866	1.20	<0.01	<0.01	0.02	0.22	0.06	SP4
ENSG00000106689	-1.53	<0.01	<0.01	0.93	0.23	0.01	LHX2
ENSG00000147133	0.51	<0.01	<0.01	0.75	0.76	0.04	TAF1
ENSG00000164002	0.42	0.01	0.02	NA	0.07	NA	EXO5
ENSG00000167182	0.78	<0.01	<0.01	0.02	0.11	0.28	SP2
ENSG00000168066	-0.46	<0.01	<0.01	<0.01	0.79	0.02	SF1
ENSG00000172845	0.45	<0.01	<0.01	0.20	0.40	0.20	SP3
ENSG00000177374	-0.48	<0.01	0.01	0.63	0.96	0.09	HIC1
ENSG00000185630	-1.03	<0.01	<0.01	0.84	0.77	0.06	PBX1

F, Transcription factors regulated by YY1 and correlated to YY1 in the expression levels

	Differential expression between tumor and adjacent tissue			Overall survival	Disease free survival	Relapse free survival	
Ensembl ID	Log2 fold change	P-value	Adjusted P-value	P-value	P-value	P-value	Symbol
ENSG00000005339	0.26	0.07	0.12	0.05	0.46	0.10	CREBBP
ENSG00000076108	0.39	<0.01	0.01	0.01	0.16	0.03	BAZ2A
ENSG00000089335	0.44	0.01	0.02	0.76	0.20	0.09	ZNF302
ENSG00000106261	0.37	0.08	0.14	0.66	0.67	0.16	ZKSCAN1
ENSG00000117569	0.60	<0.01	<0.01	<0.01	0.04	<0.01	PTBP2
ENSG00000124177	0.45	<0.01	0.01	0.01	0.19	0.07	CHD6
ENSG00000131051	0.38	0.01	0.02	<0.01	0.03	0.22	RBM39
ENSG00000131115	0.34	0.02	0.04	0.35	0.74	0.34	ZNF227
ENSG00000137337	0.65	<0.01	<0.01	0.02	0.07	0.04	MDC1
ENSG00000173575	0.03	0.82	0.88	0.63	0.07	0.39	CHD2
ENSG00000254004	0.62	<0.01	<0.01	0.01	0.01	0.04	ZNF260
ENSG00000166478	0.48	<0.01	<0.01	<0.01	0.21	0.27	ZNF143

Table SII. Continued.

G, Transcription factors regulating YY1 and correlated to YY1 in the expression levels

	Differential expression between tumor and adjacent tissue			Overall survival	Disease free survival	Relapse free survival	
Ensembl ID	Log2 fold change	P-value	Adjusted P-value	P-value	P-value	P-value	Symbol
ENSG00000100811	0.21	0.03	0.07	0.01	0.57	0.08	YY1
ENSG00000105866	1.20	<0.01	<0.01	0.02	0.22	0.06	SP4
ENSG00000112592	0.14	0.18	0.28	<0.01	0.33	0.16	TBP
ENSG00000147133	0.51	<0.01	<0.01	0.75	0.76	0.04	TAF1
ENSG00000167182	0.78	<0.01	<0.01	0.02	0.11	0.28	SP2
ENSG00000172845	0.45	<0.01	<0.01	0.20	0.40	0.20	SP3
ENSG00000177374	-0.48	<0.01	0.01	0.63	0.96	0.09	HIC1

Differential expressions were analyzed using R package DESeq2 (version 1.20.0). Overall survival results were obtained from 365 patients with hepatocellular carcinoma from the UALCAN database. Disease free survival results were obtained from 362 samples from the GEPIA database. Relapse free survival results were obtained from 323 samples from the KMplot database. YY1, Yin Yang 1; ZNF143, zinc finger protein 143.