

**Glycolysis-related gene expression profiling serves as a novel prognosis risk  
predictor for human hepatocellular carcinoma**

**Lingyu Zhang<sup>1,\*</sup>, Yu Li<sup>2,\*</sup>, Yibei Dai<sup>1</sup>, Xuchu Wang<sup>1</sup>, Ying Cao<sup>1</sup>, Weiwei Liu<sup>1</sup>, Zhihua Tao<sup>1</sup>**

<sup>1</sup>Department of Laboratory Medicine, The Second Affiliated Hospital of Zhejiang University  
School of Medicine, Hangzhou, 310009, China

<sup>2</sup>Department of Biochemistry and Molecular Biology, Bengbu Medical College, Anhui 233030,  
China

\*These authors contributed equally to the work.

*Correspondence to:* Zhihua Tao, Department of Laboratory Medicine, The Second Affiliated  
Hospital of Zhejiang University School of Medicine, 88 Jiefang Road, Hangzhou, Zhejiang  
310009, P.R. China, Email: zrtzh@zju.edu.cn; Weiwei Liu, Department of Laboratory Medicine,  
The Second Affiliated Hospital of Zhejiang University School of Medicine, 88 Jiefang Road,  
Hangzhou, Zhejiang 310009, P.R. China, Email: liuweiwei@zju.edu.cn.

**Table S1.** Core genes of 6 solid tumors.

Cancer Type	Sample numbers	Genes	Core Enrichment
BLCA	Normal 19 Tumor 414	<p>AAAS, ACSS2, ADPGK, AGRN, AKR1A1, ALDOA, ALDOC, ALG1, ANKZF1, ARTN, AURKA, B3GALT6, B3GAT3, B3GNT3, B4GALT2, B4GALT7, BPGM, BPNT1, CASP6, CDK1, CENPA, CHPF, CHPF2, CHST1, CHST12, CHST6, CLDN9, CLN6, COG2, COPB2, DDIT4, DEPD C1, DHTKD1, EFNA3, EIF6, ENO1, ENO2, ERO1A, EXT1, EXT2, FH, FKBP4, G6PC, GALE, GALK1, GALM, GAPDH, GAPDHS, GFPT1, GLCE, GMPPA, GMPPB, GPI, GUSB, GYS1, HAX1, HK1, HK2, HK3, HMMR, HS2ST1, HS6ST2, HSPA5, IDH2, IDH3B, IDH3G, IDUA, IGFBP3, IL13RA1, KDELR3, KIF20A, LDHA, LDHAL6A, LDHC, MDH2, MED24, MIF, MIOX, MIR210, NANP, NASP, NDC1, NDUFV3, NOL3, NSDHL, NUP107, NUP155, NUP160, NUP188, NUP205, NUP210, NUP35, NUP37, NUP42, NUP43, NUP50, NUP58, NUP62, NUP85, NUP93, OGT, P4HA1, PAXIP1, PC, PCK2, PDHA1, PDK3, PFKFB1, PFKFB2, PFKFB4, PFKL, PGK1, PGLS, PGM2, PGP, PHKA2, PKM, PLOD1, PMM2, POLR3K, POM121C, PPFIA4, PPIA, PPP2R1A, PPP2R1B, PPP2R5D, PRKAG1, PSMC4, PYGM, RAE1, RARS1, RBCK1, RPE, SDHB, SDHC, SEC13, SEH1L, SLC16A3, SLC25A10, SLC25A13, SLC37A4, SOD1, SOX9, SPAG4, SRD5A3, STC2, STMN1, TGFA, TGFB1, TP53, TPI1, TPR, TREH, TSTA3, VCAN, XYLT2</p>	YES
BRAC	Normal 113 Tumor 1103	<p>AAAS, ACSS2, ADH1A, ADH1B, ADH1C, ADH4, ADH5, ADH6, ADPGK, AGRN, AKR1A1, ALDH1A3, ALDH2, ALDH3A2, ALDH7A1, ALDOA, ALDOC, ALG1, ARTN, AURKA, B3GALT6, B3GAT3, B4GALT1, B4GALT2, B4GALT4, B4GALT7, BIK, BPGM, BPNT1, CACNA1H, CASP6, CBFA2T3, CDK1, CENPA, CHPF, CHPF2, CHST6, CLDN3, CLN6, COG2, COL5A1, COPB2, CXCR4, DEPDC1, DHTKD1, EFNA3, EGLN3, EIF6, ELF3, ENO1, ENO2, ERO1A, FAM162A, FBP1, FH, FKBP4, FUT8, GALE, GALK1, GAPDH, GMPPA, GMPPB, GNPDA1, GOT2, GPC1, GPC4, GPI, HAX1, HK1, HMMR, HSPA5, IDH2, IDH3G, IDUA, IER3, ISG20, JMJD8, KDELR3, KIF20A, LDHA, LDHB, MDH2, ME2, MED24, MIF, MIOX, MIR210, NASP, NDC1, NSDHL, NUP107, NUP133, NUP155, NUP188, NUP205, NUP210, NUP37, NUP43, NUP50, NUP58, NUP62, NUP85, NUP93, OGDHL, P4HA1, P4HA2, PAXIP1, PCK1, PCK2, PDK3, PFKFB1, PFKFB3, PFKFB4, PFKL, PFKP, PGAM1, PGK1, PGK2, PGLS, PGM1, PGM2, PGM2L1, PGP, PKM, PLOD1, PMM2, POLR3K, PPIA, PPP2CA, PPP2CB, PPP2R1A, PPP2R1B, PPP2R5D, PRKAG1, PRPS1, PSMC4, SOX1, RAE1, RARS1, RBCK1, RPE, SAP30, SDC1, SDHC, SEC13, SEH1L, SLC16A3, SLC25A10, SLC25A13, SLC35A3, SLC37A4, SOD1, SPAG4, SRD5A3,</p>	YES

		STMN1, TALDO1, TFF3, TIGAR, TP53, TPBG, TPI1, TPR, TSTA3, TXN, VCAN, VEGFA, XYLT2, ZBTB7A	
<b>HNSC</b>	<b>Normal 44 Tumor 502</b>	AAAS, ABCB6, AC016586.1, ACSS2, ACTN3, ADH1A, ADH1B, ADH4, ADH6, ADH7, ADPGK, AGRN, AKR1A1, ALDH1A3, ALDH2, ALDH3A1, ALDH3A2, ALDH3B1, ALDH3B2, ALDH7A1, ALDH9A1, ALDOA, ALDOC, ALG1, ANKZF1, ARPP19, ARTN, AURKA, B3GALT6, B3GAT3, B4GALT1, B4GALT2, B4GALT7, BPGM, CACNA1H, CASP6, CD44, CDK1, CENPA, CHPF, CHPF2, CHST1, CHST12, CHST2, CLN6, COL5A1, COPB2, CXCR4, DDIT4, DEPDC1, DLAT, DLGFR, EGLN3, ENO1, ENO2, ENO3, EXT1, EXT2, FBP2, FKBP4, G6PC2, G6PD, GALK2, GAPDH, GCK, GMPPA, GNPDA1, GPC1, GPI, GPR87, HIF1A, HK1, HK2, HK3, HKDC1, HMMR, HS2ST1, HSPA5, IGFBP3, INS, ISG20, KDELR3, KIF20A, LDHA, MET, MIF, MIOX, NANP, NASP, NDC1, NT5E, NUP107, NUP133, NUP153, NUP155, NUP160, NUP188, NUP205, NUP210, NUP214, NUP35, NUP37, NUP42, NUP43, NUP50, NUP54, NUP58, NUP62, NUP85, NUP93, OGT, P4HA1, P4HA2, PC, PDHA1, PDHB, PDK3, PFKFB1, PFKFB3, PFKFB4, PFKL, PFKM, PFKP, PGAM1, PGK1, PGM1, PGM2, PGP, PKLR, PKM, PLOD1, PLOD2, POLR3K, POM121, POM121C, PPIA, PPP2CA, PPP2CB, PPP2R1A, PPP2R5D, PRKACA, PRKACB, PRPS1, PRXL2C, PSMC4, PYGL, PYGM, RAE1, RBCK1, RPE, SAP30, SEH1L, SLC16A3, SLC25A12, SLC25A13, SPAG4, STC2, STMN1, TGFA, TGFB1, TIGAR, TPBG, TPI1, TPR, TPST1, TREH, VCAN, VEGFA, XYLT2	<b>YES</b>
<b>LIHC</b>	<b>Normal 50 Tumor 374</b>	AAAS, ABCB6, AC016586.1, ACO2, ADH1A, ADH1B, ADH1C, ADH4, ADH6, ADPGK, AGRN, ALDH1B1, ALDH2, ALDH9A1, ALDOA, ALDOB, ALG1, ANKZF1, ARNT, ARPP19, ARTN, AURKA, B3GALT6, B3GAT3, B3GNT3, B4GALT2, B4GALT4, B4GALT7, BIK, BPGM, BPNT1, CDK1, CENPA, CHPF2, CHST1, CHST12, CHST6, CLN6, COG2, COL5A1, COPB2, DDIT4, DEPDC1, DPYSL4, ECDEFNA3, EGLN3, EIF6, ENO1, ENO3, ERO1A, EXT2, FBP1, FKBP4, G6PC, G6PD, GAL3ST1, GALE, GALK1, GALK2, GAPDH, GFPT1, GLCE, GMPPA, GMPPB, GNPDA1, GNPDA2, GPC3, GPI, GYS1, HAX1, HDAC4, HDLBP, HK2, HK3, HKDC1, HMMR, HOMER1, HS2ST1, HSPA5, IDH3B, IDH3G, IDUA, KDELR3, KHK, KIF20A, KIF2A, MDH1, MDH2, ME1, ME2, MED24, MET, MIF, MIOX, MIR210, MLXIPL, MPL, NANP, NASP, NDC1, NDUFV3, NOL3, NSDHL, NUP107, NUP133, NUP153, NUP155, NUP160, NUP188, NUP205, NUP210, NUP214, NUP35, NUP37, NUP42, NUP43, NUP62, NUP85, NUP93, OGDH, OGT, P4HA2, PAM, PAXIP1, PCK1, PCK2, PFKFB2, PFKFB4, PFKL, PFKM, PGK1, PGLS, PGM1, PGP,	<b>YES</b>

		PHKA2,PKM,PLOD1, POLR3K, POM121,POM121C,PPFIA4, PPIA, PPP2CA, PPP2R1A, PPP2R5D, PRKAA2, PRKAG1, PRPS1, PSMC4, PYGB, RAE1, RARS1, RBCK1, RPE, RRAGD, SAP30, SDC2, SDHC, SEC13, SLC16A3, SLC25A10, SLC25A12, SOX9,SPAG4, SRD5A3, STC1, STC2, STMN1, TALDO1, TGFBI, TIGAR, TP53, TPI1, TPR, TREH, TSTA3, TXN, VCAN,VEGFA,XYLT2, ZBTB7A, ZNF292	
<b>LUAD</b>	<b>Normal 59 Tumor 533</b>	AAAS, ABCB6,ADORA2B,AGL,AGRN,AK4, AKR1A1,ALDH1B1, ALDH3B2, ALDH7A1, ALDOA, ALDOC,ALG1, ANKZF1,ARTN, AURKA, B3GALT6, B3GAT1,B3GAT3, B3GNT3, B4GALT1, B4GALT2, B4GALT4,B4GALT7,BIK,BPGM,BPNT1, CAPN5, CASP6, CDK1,CENPA, CHPF, CHPF2,CLDN3, CLDN9, COG2,COL5A1,COPB2, CTH,DDIT4,DEPDC1,DHTKD1, DLAT,DLDDSC2,ECD, EFNA3,EGLN3,EIF6, ELF3, ENO1,ENO2, ENO3, ENTPD5, ERO1A,FAM162A, FH, FKBP4,FUT8,G6PD, GAL3ST1, GALE, GALK1, GALM,GAPDH, GAPDHS, GCKR,GCLC, GFPT1, GLCE,GMPPA, GMPPB,GNPDA1,GOT1, GOT2,GPC1, GPI,GPR87, GUSB, GYS1, HAX1,HDLBP, HIF1A,HKDC1,HMMR,HS2ST1, HS6ST2, HSPA5, IDH1, IDH2, IDH3B, IDH3G, IDUA, IER3, IGFBP3, ISG20, KDEL3, KHK,KIF20A, KIF2A, LCT, LDHA, LDHB, LHPP, MDH1,MDH2, ME1, ME2, MET, MIF, MIOX, MIR210,MPI, NANP, NASP, NDC1, NDUFV3,NOL3, NSDHL,NT5E, NUP107, NUP133, NUP153, NUP155, NUP160,NUP188, NUP205, NUP210, NUP35, NUP37, NUP42, NUP43,NUP50, NUP54, NUP62, NUP85, NUP88, NUP93,OGTP4HA1, PAM, PAXIP1, PC, PDHA1, PDHB, PDK3,PFKFB1, PFKFB4, PFKL, PFKP, PGAM1, PGAM4, PGK1,PGK2, PGLS, PGM2, PGM2L1, PGP, PHKA2, PKM,PKP2,PLOD1,PLOD2, PMM2, POLR3K, POM121, POM121C,PPARA,PPFIA4,PPIA,PPP2R1A,PPP2R1B,PPP2R5D,PRKAA1, PRKAA2, PRKAG1, PRPS1, PSMC4, PYGB, PYGL,QSOX1, RAE1,RRS1, RBCK1, RPE, SAP30, SDC1,SDHA, SDHB, SDHC,SEC13, SEH1L, SLC16A3,SLC25A10, SLC25A12, SLC25A13, SLC35A3,SLC37A4,SOD1, SOX9, SPAG4, SRD5A3, STMN1, SUCLG1,TALDO1,TGFA, TIGAR, TP53, TPBG, TPI1, TPR,TPST1, TSTA3, TXN,UGP2, VCAN, VEGFA, XYLT2,ZNF292	<b>YES</b>
<b>LUSC</b>	<b>Normal 49 Tumor 502</b>	AAAS, ABCB6,ADH7,ADORA2B, AK4,ALDH3A1, ALDH3B2, ALDOA, ALDOC, ANKZF1, ARTN, AURKA, B3GAT3, B3GNT3, B4GALT2, B4GALT4, B4GALT7, BIK, CASP6, CDK1, CENPA, CHPF, CHPF2, CHST2, COL5A1, COPB2, DDIT4, DEPDC1, DHTKD1, DLD, DPYSL4, DSC2, EFNA3, EGFR, EGLN3, EIF6, ENO1, ENO2, ERO1A, EXT1,FAM162A, FH, FKBP4, FUT8,	<b>YES</b>

		G6PD, GAPDH, GCLC, GMPPA, GNPDA1, GOT1, GOT2, GPC1, GPI, GPR87, GYS1, HAX1, HIF1A, HK2, HMMR, HS6ST2, HSPA5, IDH1, IDH2, IGFBP3, KDELR3, KIF20A, KIF2A, LDHA, LDHB, LDHC, MDH1, MDH2, ME1, MIF, MIOX, MIR210, MPI, NANP, NASP, NDC1, NOL3, NSDHL, NUP107, NUP155, NUP205, NUP210, NUP35, NUP37, NUP42, NUP43, NUP50, NUP62, NUP85, NUP88, NUP93, OGDHL, P4HA1, PAXIP1, PC, PDK3, PFKFB1, PFKFB2, PFKFB3, PFKFB4, PFKP, PGAM1, PGAM4, PGK1, PGK2, PGM1, PGM2, PGM2L1, PKM, PKP2, PLOD1, PLOD2, PMM2, POLR3K, PPFIA4, PPIA, PPP2CA, PPP2CB, PRKACA, PRKACB, PRKACG, PSMC4, PYGL, PYGM, RAE1, RARS1, RPE, SAP30, SDC1, SDHA, SDHC, SEH1L, SLC16A3, SLC25A10, SLC25A12, SLC25A13, SLC37A4, SOD1, SOX9, SPAG4, SRD5A3, STC2, STMN1, TALDO1, TGFA, TP53, TPBG, TPI1, TPST1, TREH, TSTA3, TXN, VCAN, XYLT2	
--	--	---	--

**Table S2.** Multivariable Cox regression analysis of predictors of survival outcomes in the TCGA discovery cohort for 6 solid tumors.

Cancer type	Gene	Hazard Ratio	$\beta$ (Cox)	P value
BLCA	NUP188	1.598825	0.058158	0.002597
	CHPF	1.551001	0.549488	0.002997
	AK3	0.969007	-0.314831	0.002906
BRAC	PGK1	1.266736	0.665145	0.001651
	SDC1	1.162645	0.162513	9.40E-05
	CHPF	1.490339	0.048914	0.000140
	NUP43	1.469928	0.059221	4.43E-05
HNSC	ALDH1B1	1.229825	0.227224	0.004188
	STC2	1.303147	0.298643	9.03E-06
	ALDH2	0.985525	-0.145801	0.005879
	PGK1	1.247946	0.247639	4.03E-05
	PYGL	1.463654	0.462582	0.013119
	GPR87	1.585657	0.583949	0.004114
	KIF20A	1.128769	0.242487	1.37E-09
	AURKA	1.019880	0.012238	0.000375
LIHC	HMMR	1.121071	0.114007	1.01E-05
	STMN1	1.021461	0.091125	1.46E-05
	DEPDC1	1.229999	0.132254	8.40E-06
	PFKFB4	1.252219	0.156219	1.69E-05
	CENPA	1.176523	0.092026	1.40E-07
	CDK1	1.052063	0.053426	1.25E-06
	PPP2R1A	1.116637	0.115962	4.26E-11
	RBCK1	1.104909	0.104363	0.010349
	SLC16A3	1.103470	0.102935	8.73E-05

<b>LUAD</b>	FKBP4	1.814383	0.281108	4.50E-08
	ERO1A	1.547494	0.546001	1.67E-06
	PPIA	1.476700	0.475567	0.021940
	B4GALT1	1.353855	0.353231	0.013259
	LDHA	1.295509	0.295073	9.01E-07
<b>LUSC</b>	PFKM	1.333626	0.133353	0.007008
	HMMR	1.431428	0.314246	0.018149
	TPST1	1.14307	0.143068	0.000486

**Table S3.** Clinicopathological characteristics of the HCC patients enrolled in the TCGA cohort.

Clinicopathological Characteristics	Risk Score (OS)		$\chi^2$	P value	Risk Score (RFS)		$\chi^2$	P value
	High Risk n (%)	Low Risk n (%)			High Risk n (%)	Low Risk n (%)		
<b>Gender</b>			0.08769	0.7671			0.0215	0.8832
Male	126(50.40%)	124(49.60%)			124(49.60%)	126(50.40%)		
Female	59(48.76%)	62(51.24%)			61(50.41%)	60(49.59%)		
<b>Age</b>			2.818	0.0932			1.560	0.2116
≤65	124(53.22%)	109(46.78%)			122(52.36%)	111(47.64%)		
>65	61(44.20%)	77(55.80%)			63(45.65%)	75(54.35%)		
<b>T</b>			13.77	0.0032			11.46	0.0095
T1	76(42.70%)	102(57.30%)			76(41.30%)	108(58.70%)		
T2	48(48.00%)	52(52.00%)			55(58.51%)	39(41.49%)		
T3	51(63.75%)	29(36.25)			45(56.25%)	35(43.75%)		
T4	10(76.92%)	3(23.08%)			9(69.23%)	4(30.77%)		
<b>Stage</b>			42.73	<0.001			13.74	0.0033
I	66(37.93%)	108(62.07%)			78(41.71%)	109(58.29%)		
II	42(42.86%)	56(57.14%)			48(55.17%)	39(44.83%)		
III	68(78.16%)	19(21.84%)			51(57.96%)	37(42.05%)		
IV	9(75.00%)	3(25.00%)			8(88.89%)	1(11.11%)		
<b>Grade</b>			10.12	0.0175			2.965	0.0851
G1	16(35.56%)	29(64.44%)			40(56.34%)	31(43.66%)		
G2	77(47.83%)	84(52.17%)			43(31.85%)	92(68.15%)		
G3	80(53.33%)	70(46.67%)			91(64.54%)	50(35.46%)		
G4	12(80.00%)	3(20.00%)			11(45.83%)	13(54.17%)		
<b>Family Cancer History</b>			0.00129	0.0359			0.1665	0.6832
NO	125(49.80%)	126(50.20%)			127(50.60%)	124(49.40%)		
YES	60(50.00%)	60(50.00%)			58(48.33%)	62(51.67%)		
<b>Hepatitis Virus Infection</b>			2.481	0.4787			2.104	0.5511
None Risk	91(46.67%)	104(53.33%)			103(52.82%)	92(47.18%)		
HBV	32(52.46%)	29(47.54%)			31(50.82%)	30(49.18%)		
HCV	8(44.44%)	10(55.56%)			8(44.44%)	10(55.56%)		
HCV&HBV	54(55.67%)	43(44.33%)			43(44.33%)	54(55.67%)		

<b>Child Pugh Score</b>			5.206	0.0741			3.480	0.1755
A	88(44.44%)	110(55.56%)			90(45.46%)	108(54.54%)		
B	54(54.55%)	45(45.45%)			53(53.54%)	46(46.46%)		
C	43(58.11%)	31(41.89%)			42(56.76%)	32(43.24%)		
<b>BMI</b>			1.683	0.1946				
<=24	93(53.45%)	81(46.55%)			93(53.45%)	81(46.55%)		
>24	92(46.70%)	105(53.30%)			92(46.70%)	105(53.30%)		
<b>AFP</b>			5.952	0.0147			1.424	0.2328
<=200	83(43.68%)	107(56.32%)			89(46.84%)	101(53.18%)		
>200	102(56.35%)	79(43.65%)			96(53.04%)	85(46.96%)		
<b>Cancer Status</b>			16.64	<0.001				
Tumor Free	98(41.88%)	136(58.12%)						
With Tumor	72(65.45%)	38(34.55%)						
<b>Recurrence Event</b>			76.91	<0.001				
NO	82(42.93%)	109(57.07%)						
YES	103(57.22%)	77(42.78%)						
<b>Status</b>								
Alive	90(37.34%)	151(62.66%)	43.13	<0.001				
Dead	95(73.08)	35(26.92)						

**Table S4.** Clinicopathological characteristics of the HCC patients enrolled in the GEO cohort.

Clinicopathological Characteristics	Risk Score (OS)		$\chi^2$	P value
	High Risk n (%)	Low Risk n (%)		
<b>Gender</b>			2.553	0.1101
Male	91(47.64%)	100(52.36%)		
Female	19(63.33%)	11(36.67%)		
<b>Age</b>			0.0430	0.8355
≤65	100(50.00%)	100(50.00%)		
>65	10(47.62%)	11(52.38%)		
<b>Stage</b>			39.37	<0.001
I	26(27.96%)	67(72.04%)		
II	43(55.13%)	35(44.87%)		
III	41(82.00%)	9(18.00%)		
<b>BCLC Staging</b>			28.23	<0.001
Zero	9(42.86%)	12(57.14%)		
A	59(39.60%)	90(60.40%)		
B	18(81.82%)	4(18.18%)		
C	24(82.76%)	5(17.24%)		
<b>Child Pugh Score</b>			26.43	<0.001
A	32(32.99%)	65(67.01%)		
B	40(53.33%)	35(46.67%)		
C	38(77.55%)	11(22.45%)		
<b>Cirrhosis</b>			3.792	0.0515

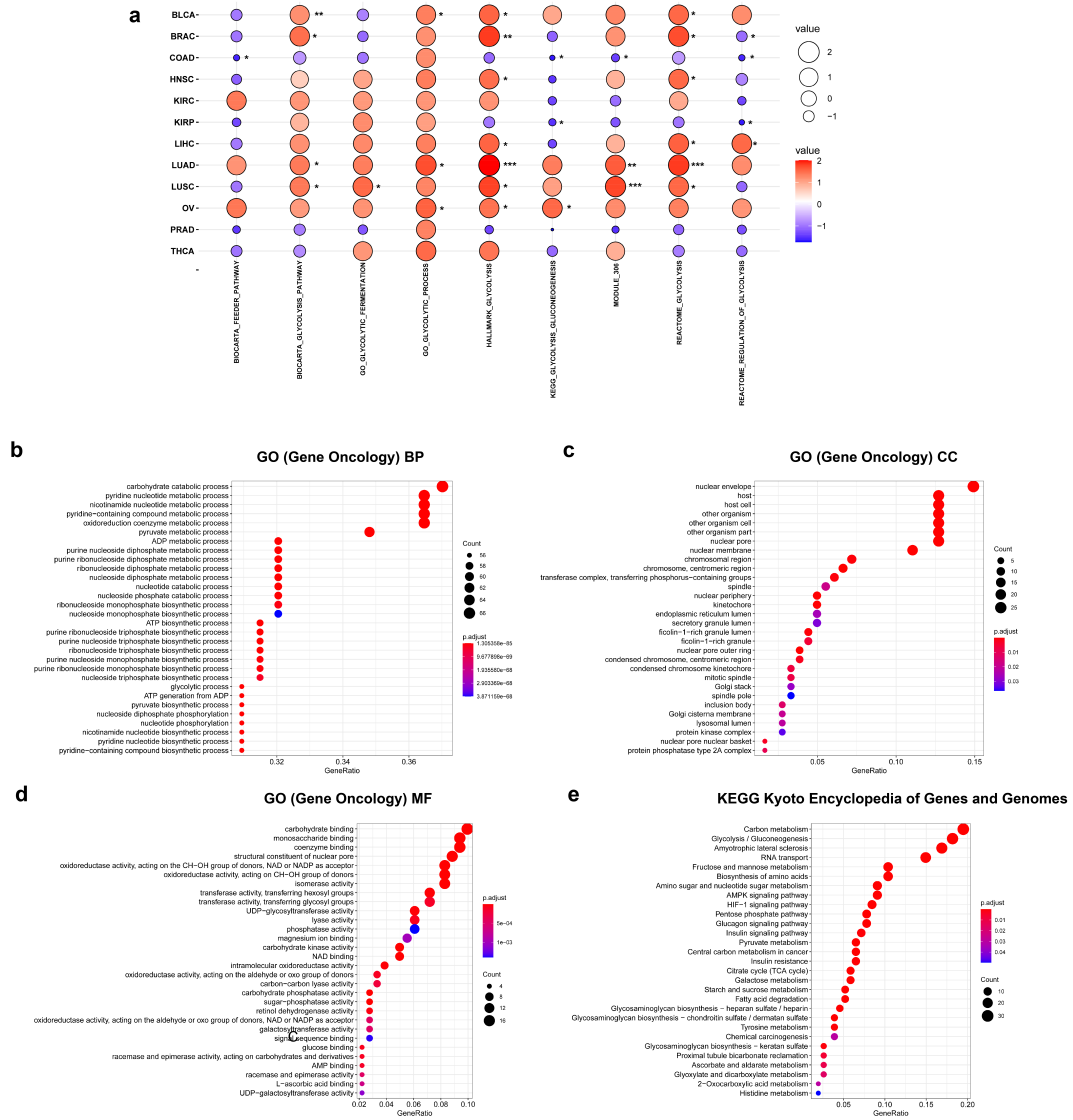
NO	5(27.78%)	13(72.22%)		
YES	105(51.72%)	98(48.28%)		
<b>Multi Nodular</b>			8.259	0.0041
NO	79(44.89%)	97(55.11%)		
YES	31(68.89%)	14(31.11%)		
<b>Tumor Size</b>			12.54	<0.001
<=5	57(40.71%)	83(59.29%)		
>5	53(65.43%)	28(34.57%)		
<b>AFP</b>			14.79	<0.001
<=300	46(38.02%)	75(61.98%)		
>300	64(64.00%)	36(36.00%)		
<b>ALT</b>			1.655	0.1983
<=50	60(46.15%)	70(53.85%)		
>50	50(54.95%)	41(45.05%)		
<b>Recurrence Event</b>			23.08	<0.001
NO	32(32.00%)	68(68.00%)		
YES	78(64.46%)	43(35.54%)		
<b>Status</b>			54.48	<0.001
Alive	41(30.15%)	95(69.85%)		
Dead	69(81.18%)	16(18.82%)		

**Table S5.** Clinicopathological characteristics of the HCC patients enrolled in the ICGC cohort.

Clinicopathological Characteristics	Risk Score (OS)		$\chi^2$	P value
	High Risk n (%)	Low Risk n (%)		
<b>Gender</b>			2.691	0.1009
Male	80(46.78%)	91(53.22%)		
Female	36(59.02%)	25(40.98%)		
<b>Age</b>			2.074	0.1498
≤65	35(42.17%)	48(57.83%)		
>65	74(52.11%)	68(47.89%)		
<b>Stage</b>			10.98	0.0118
I	17(47.22%)	19(52.78%)		
II	46(43.40%)	60(56.60%)		
III	37(52.11%)	34(47.89%)		
IV	16(84.21%)	3(15.79%)		
<b>Grade</b>			28.20	<0.001
G1	6(27.27%)	16(72.78%)		
G2	56(41.55%)	83(58.45%)		
G3	42(71.19%)	17(28.81%)		
G4	9(100.00%)	0(0.00%)		
<b>Family Cancer History</b>			0.6868	0.4072
NO	79(51.97%)	73(48.03%)		



YES	37(46.25%)	43(53.75%)		
<b>Prior Malignancy</b>			0.6125	0.4338
NO	99(49.01%)	103(50.99%)		
YES	17(56.67%)	13(43.33%)		
<b>Status</b>			27.43	<0.001
Alive	79(41.80%)	110(58.20%)		
Dead	37(86.05%)	6(13.95%)		



**Figure S1. a** Distribution of NES value and FDR q value in GSEA analysis results. **(b-e)** Gene Ontology (GO) enrichment analysis and KEGG pathways enriched core genes form GSEA results.

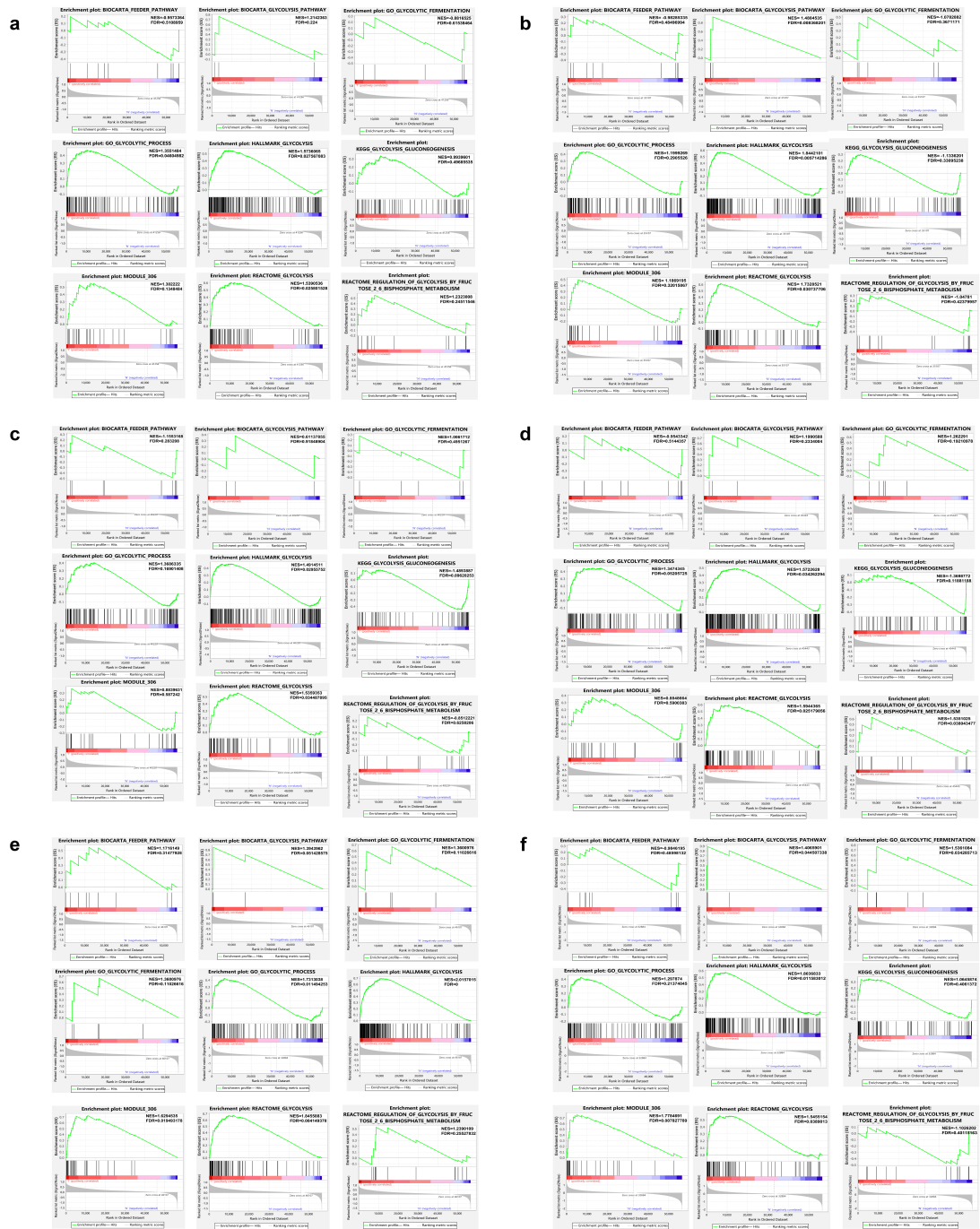
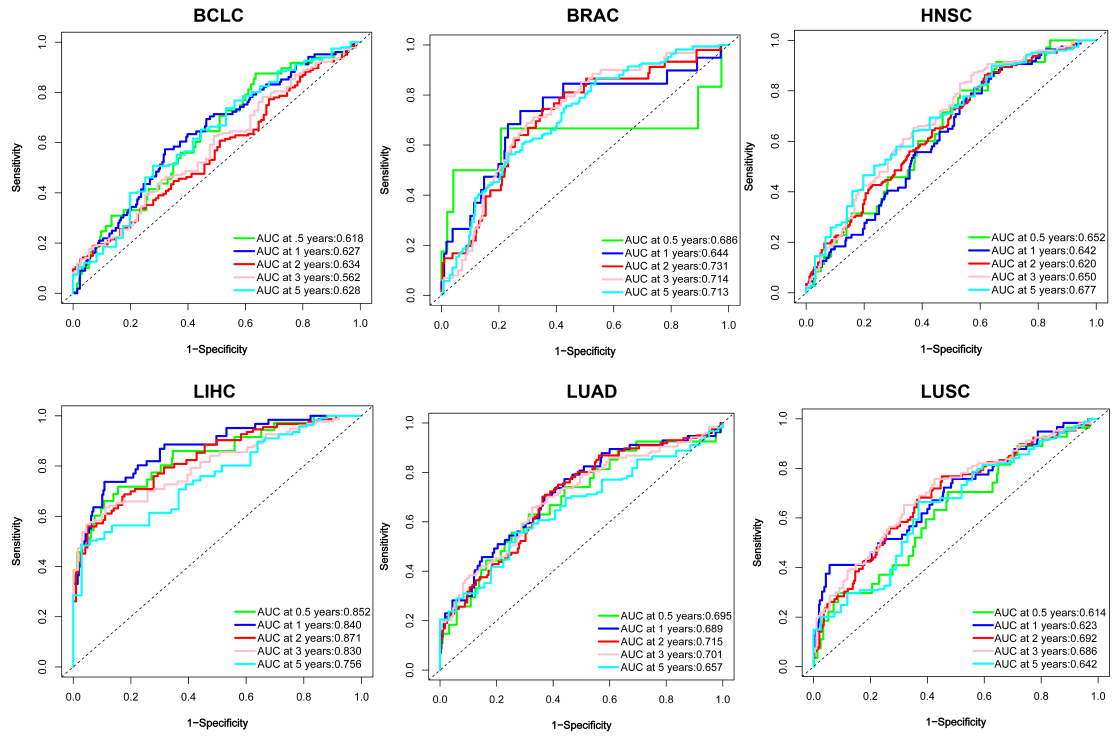


Figure S2. Detailed GSEA analyses in 6 solid tumors.



**Figure S3.** Performance of ROC curves in BLCA, BRCA, HNSC, LIHC, LUAD, and LUSC.

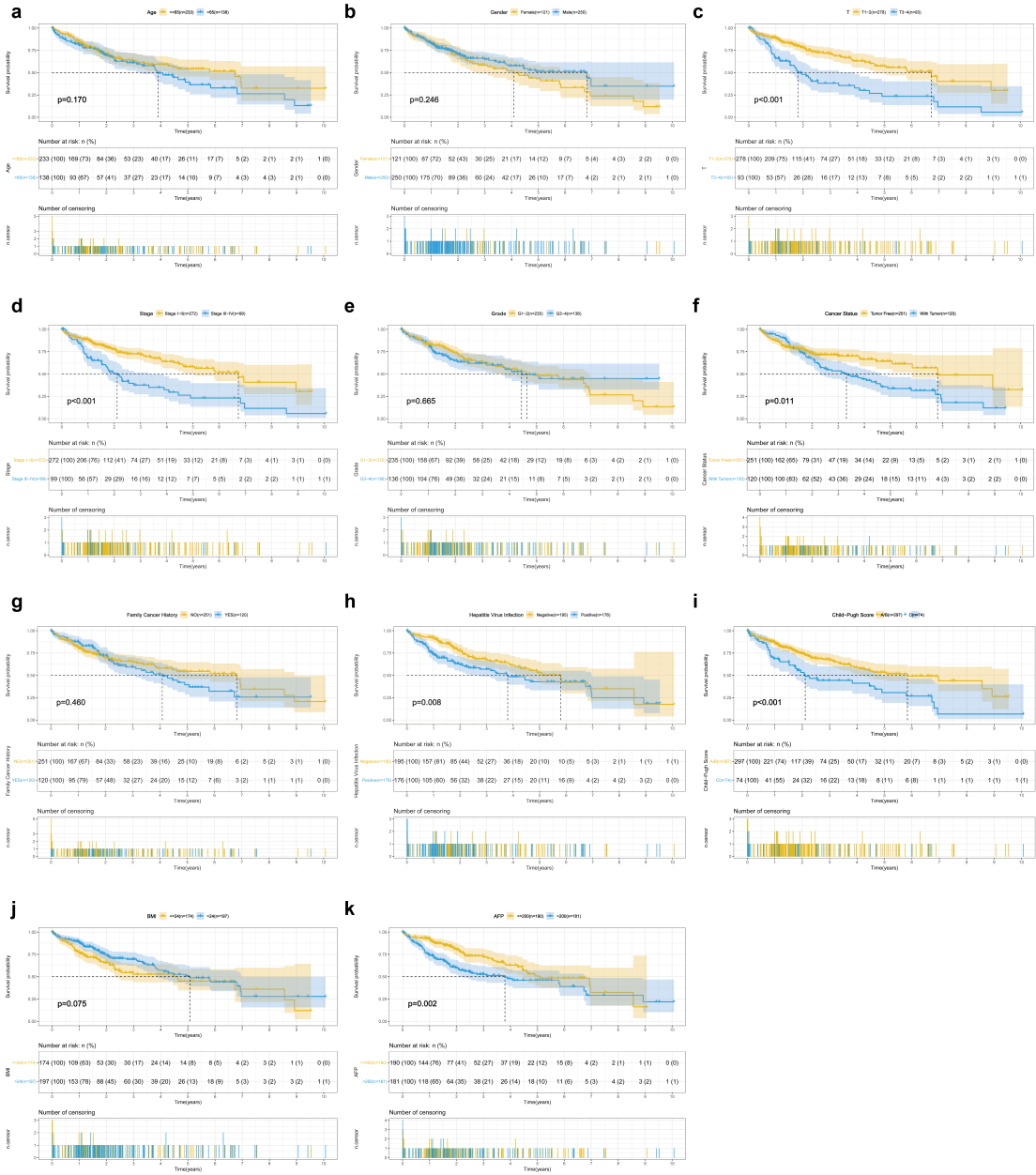
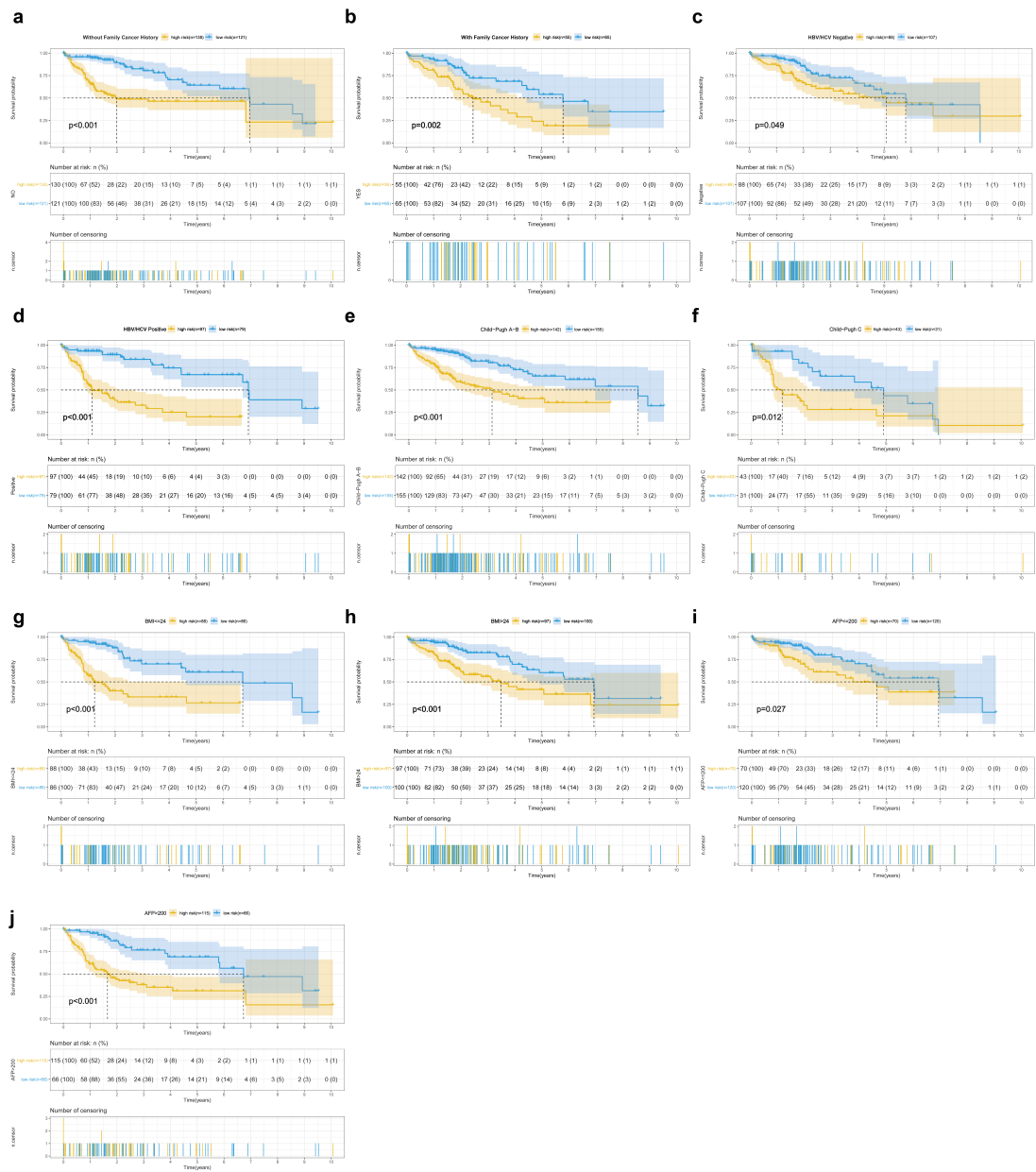


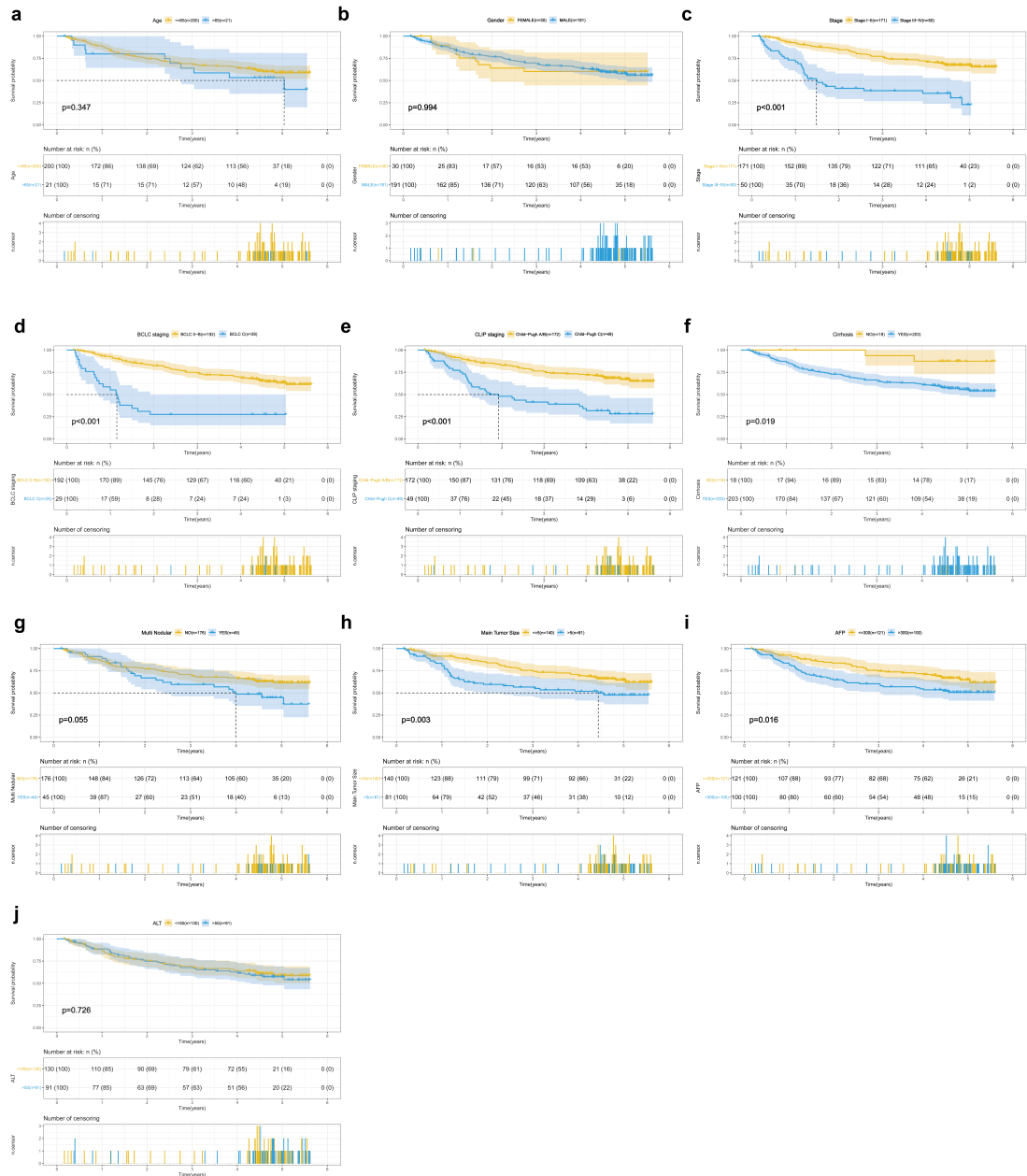
Figure S4. K-M survival analysis in different clinicopathological subgroups in the TCGA cohort.



**Figure S5.** K-M analysis of patients stratified by age (**a, b**), gender (**c, d**), T classification (**e, f**), stage (**g, h**), grade (**i, j**), and tumor status (**k, l**) in TCGA cohort. Patients in the high-risk group achieved shorter overall survival.



**Figure S6.** K-M analysis of patients stratified by family cancer history (**a, b**), hepatitis virus infection (**c, d**), Child-Pugh score (**e, f**), BMI (**g, h**), and AFP level (**i, j**) in TCGA cohort. Patients in the high-risk group achieved shorter overall survival.

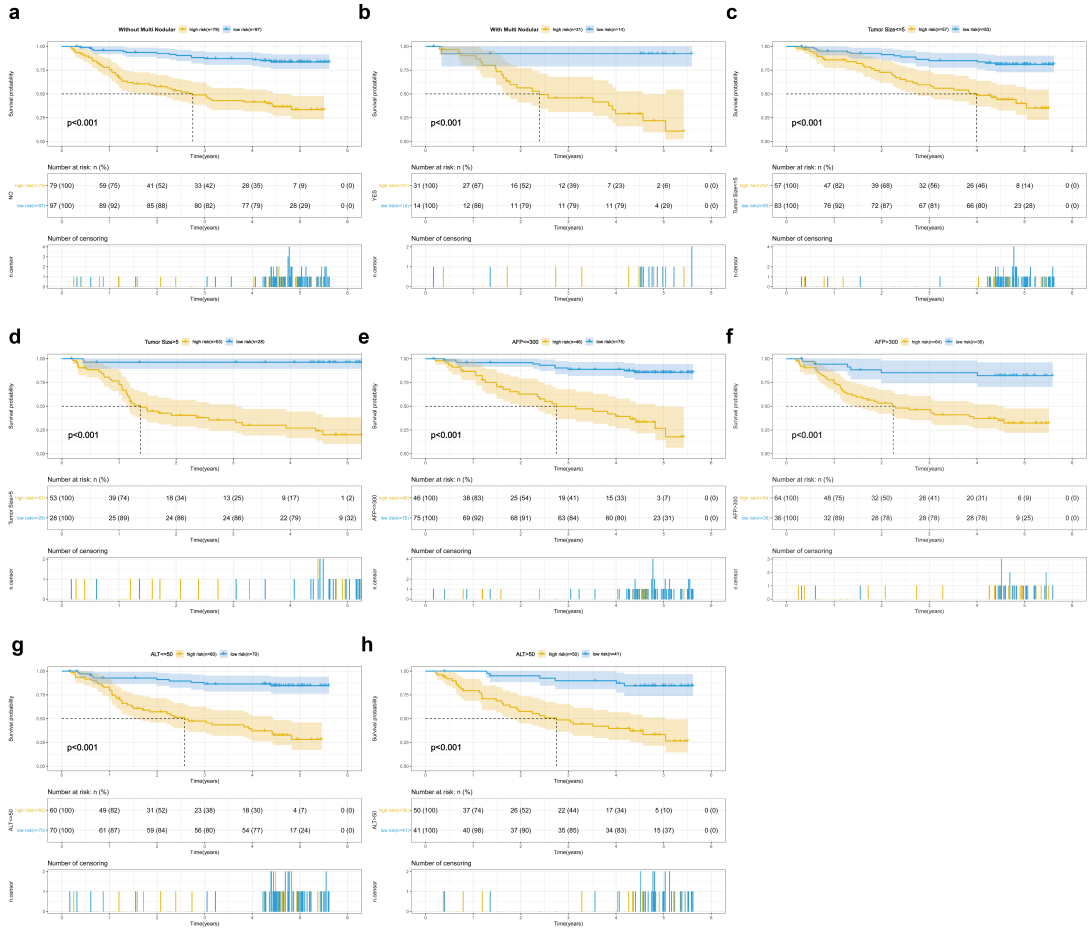


**Figure S7.** K-M survival analysis in different clinicopathological subgroups in the GEO cohort.

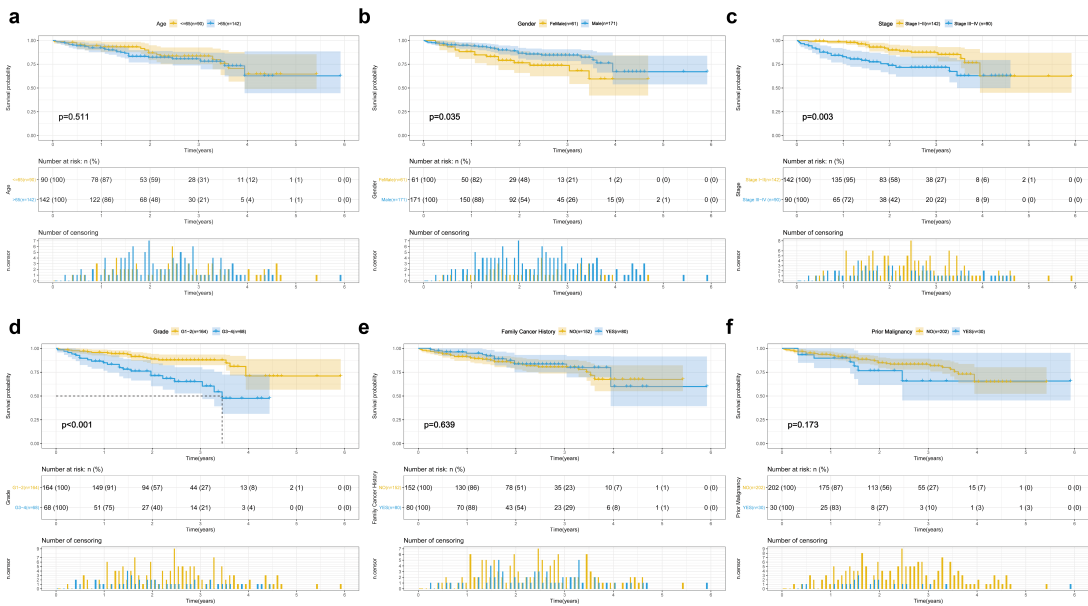


**Figure S8.** K-M analysis of patients stratified by Age (**a, b**), Gender (**c, d**), Stage (**e, f**), BCLC Staging (**g, h**), Child-Pugh Score (**i, j**), and Cirrhosis status (**k, l**) in GEO cohort. Patients in the high-risk group achieved shorter overall survival.

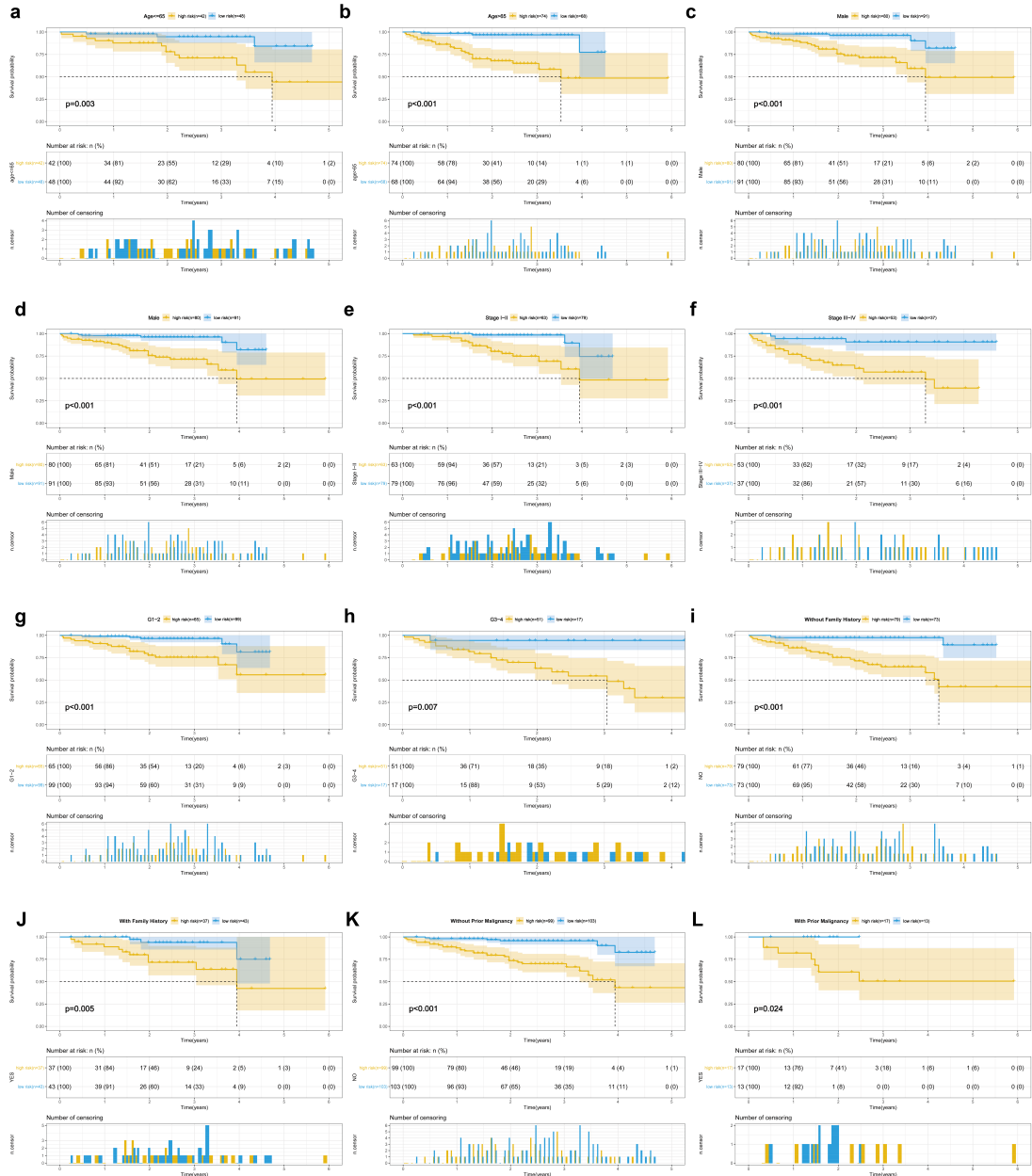




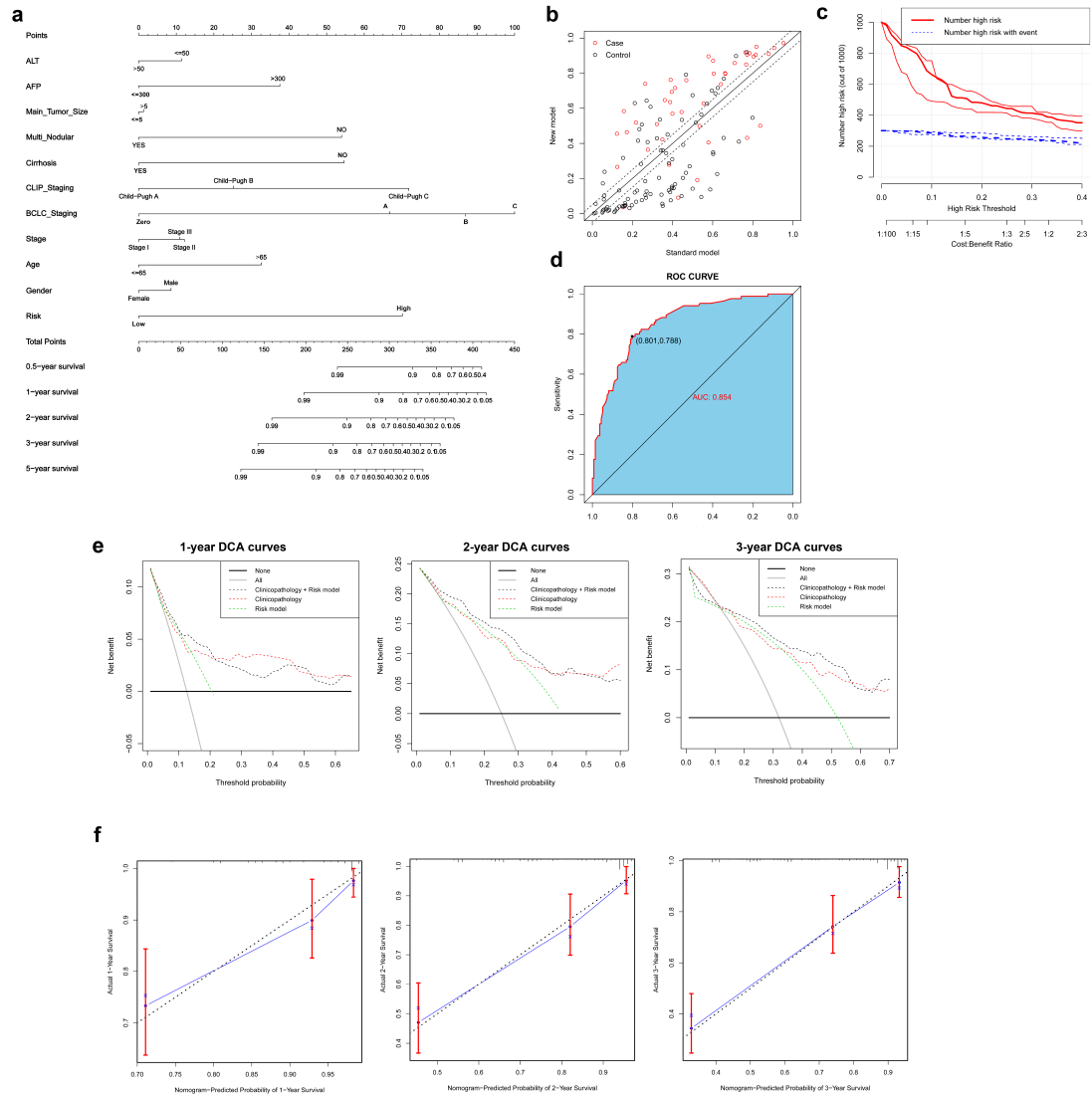
**Figure S9.** K-M analysis of patients stratified by Muti Nodular status (**a, b**), Tumor Size (**c, d**), AFP level (**e, f**), and ALT level (**g, h**) in GEO cohort. Patients in the high-risk group achieved shorter overall survival.



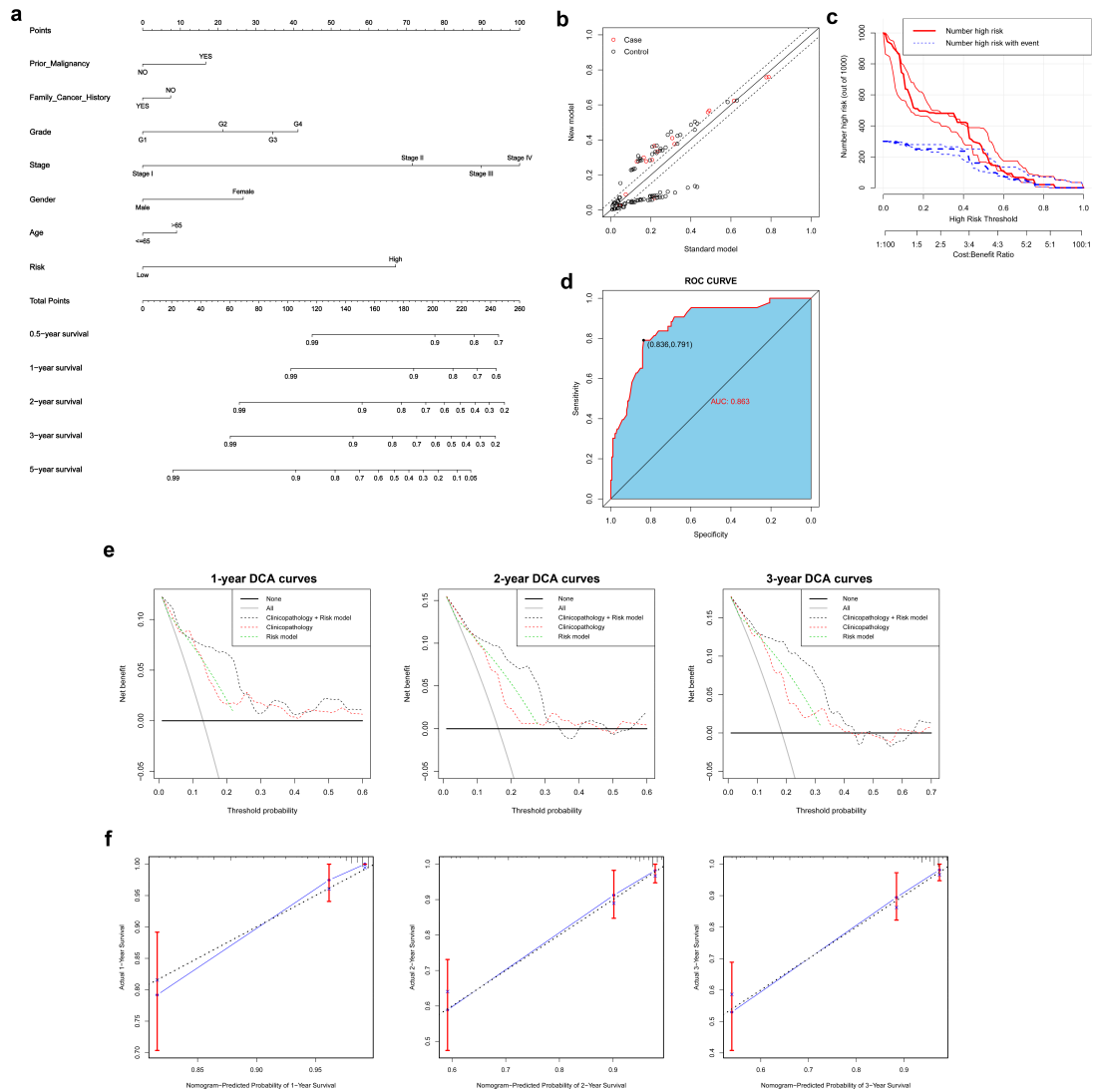
**Figure S10.** K-M survival analysis in different clinicopathological subgroups in the ICGC cohort.



**Figure S11.** K-M analysis of patients stratified by Age (**a, b**), Gender (**c, d**), Stage (**e, f**), Grade (**g, h**), Family Cancer History (**i, j**), and Prior Malignancy (**k, l**) in GEO cohort. Patients in the high-risk group achieved shorter overall survival.



**Figure S12.** Performance of a nomogram integrated the GRGPI model and clinicopathological characteristics in the GEO cohort. A Nomograph for predicting overall survival probability of HCC patients. **(b-c)** The Nomogram model improves the identification of high-risk patients, and 221 HCC patients are reclassified between the standard model and the Nomogram model. **d** ROC curve for Nomogram model. **(e, f)** Decision curve and calibration curves analyses of Nomogram for 1-, 2-, and 3-year.



**Figure S13.** Performance of a nomogram integrated the GRGPI model and clinicopathological characteristics in the ICGC cohort. A Nomograph for predicting overall survival probability of HCC patients. **(b-c)** The Nomogram model improves the identification of high-risk patients, and 221 HCC patients are reclassified between the standard model and the Nomogram model. **d** ROC curve for Nomogram model. **(e, f)** Decision curve and calibration curves analyses of Nomogram for 1-, 2-, and 3-year.