

**Supplementary Table 1 The Clinical, operative and pathologic data of 120 enrolled early stage hepatocellular carcinoma patients in this study**

Clinical factors		Surgical and Pathologic factors	
Age (yr)	59.8 ± 13.2	Major resection	29 (24.2%)
Sex (M/F)	99 (82.5)/21 (18.5)	Minor resection	91(75.8%)
HBsAg (+)	73 (60.8%)	Bleeding	511.6 ± 481.4 mL
HCV-Ab (+)	30 (25.0%)	Operation time	293.2 ± 95.4 min
Alcoholism	26 (21.7%)	Margin involvement (%)	1 (0.8)
AST (U/L)	48.1 ±36.5	Tumor size (cm)	4.2 ± 2.7
ALT (U/L)	47.0 ± 35.9	Satellite lesions (%)	9 (7.5)
Albumin (g/ dL)	4.15 ± 0.43	Vascular invasion (%)	34 (28.3)
Bilirubin (mg/ dL)	0.69 ± 0.33	Grading I/ II/ III, IV (%)	19(16.7)/49(40.0)/52(43.3)
Alk-P (U/L)	109.0 ± 296.5	Encapsulation (%)	101 (84.2)
AFP (ng/ mL)	3456 ± 27653	Cirrhosis (%)	65 (54.2)
ICG R15 (%)	10.4 ± 12.0	Stage I/II (%)	72 (60)/48 (40)

**Supplementary Table 2** The tumor recurrence was analyzed by performing area under receiver operating characteristic comparisons for percent genome changed, AFP, and tumor size. The p-value, cut-off point, sensitivity and specificity of each factor are listed

	AUROC	<i>P</i> value	Cut-off point	Sensitivity	Specificity
% genome changes	0.657	0.002	30.3%	46.7%	80.0%
AFP (ng/mL)	0.598	0.073	5.2	78.7%	42.2%
Tumor Size (cm)	0.633	0.015	4.25	41.3%	82.2%

AUROC: Area under receiver operating characteristic curve.

**Supplementary Table 3 The CNAs of genes associated with disease-free survival in early stage of hepatocellular carcinoma patients**

Genes	Chromosome	Position		P value		
		Start	End	Amplification	Deletion	LOH
<i>MPL</i>	1	43761804	43861804	0.032*	0.997	0.805
<i>TAL1</i>	1	47638702	47738702	0.211	0.671	0.005*
<i>STIL</i>	1	47697814	47797814	0.211	0.671	0.005*
<i>GSTM1</i>	1	110183392	110283392	0.046*	0.849	0.459
<i>TRIM33</i>	1	114925398	115063781	0.046*	0.944	0.444
<i>NRAS</i>	1	115203299	115303299	0.046*	0.858	0.551
<i>PRCC</i>	1	156703941	156803941	0.030*	1.000	0.834
<i>NTRK1</i>	1	156768591	156868591	0.010*	1.000	0.987
<i>INSRR</i>	1	156769688	156869688	0.010*	1.000	0.987
<i>FCRL4</i>	1	157505704	157605704	0.009*	1.000	1.000
<i>SDHC</i>	1	161259350	161359350	0.011*	1.000	1.000
<i>FCGR2B</i>	1	161590674	161690674	0.020*	1.000	1.000
<i>PBX1</i>	1	164518596	164831060	0.032*	1.000	1.000
<i>PRRX1</i>	1	170620926	170720926	0.024*	1.000	1.000
<i>RNASEL</i>	1	182500581	182600581	0.045*	1.000	0.147
<i>TPR</i>	1	186262621	186362621	0.043*	1.000	0.473
<i>PTGS2</i>	1	186595251	186695251	0.043*	1.000	0.473
<i>CDC73</i>	1	193081087	193233942	0.027*	1.000	0.933
<i>BTG2</i>	1	203226696	203326696	0.031*	1.000	0.618
<i>ELK4</i>	1	205539535	205639535	0.027*	1.000	0.853
<i>SLC45A3</i>	1	205588305	205688305	0.027*	1.000	0.853

<i>ATF3</i>	1	212716397	212816397	0.026*	1.000	0.807
<i>TGFB2</i>	1	218508675	218627961	0.047*	1.000	0.807
<i>REL</i>	2	61079464	61179464	0.347	0.188	0.048*
<i>SRGAP3</i>	3	9012277	9301311	0.262	0.261	0.049*
<i>FANCD2</i>	3	10054728	10154728	0.670	0.212	0.019*
<i>VHL</i>	3	10139336	10239336	0.669	0.212	0.019*
<i>PPARG</i>	3	12319348	12485855	0.442	0.261	0.043*
<i>RAF1</i>	3	12615099	12715700	0.743	0.261	0.043*
<i>XPC</i>	3	14153409	14253409	0.521	0.072	0.046*
<i>ATR</i>	3	142158076	142307668	0.615	0.021*	0.677
<i>MECOM</i>	3	168782689	168882689	0.901	0.024*	0.776
<i>GAK</i>	4	833064	936174	0.043*	0.003*	0.884
<i>FGFR3</i>	4	1752818	1852818	0.029*	0.008*	0.907
<i>WHSC1</i>	4	1863122	1993934	0.029*	0.008*	0.907
<i>DHX15</i>	4	24507635	24607635	0.059	0.004*	0.018
<i>RHOH</i>	4	40172403	40272403	0.175	0.027*	0.171
<i>PHOX2B</i>	4	41698542	41798542	0.051	0.027*	0.244
<i>KCTD8</i>	4	44165919	44460824	0.073	0.012*	0.108
<i>GABRA2</i>	4	46241580	46401396	0.073	0.027*	0.042
<i>PDGFRA</i>	4	55079837	55179837	0.299	0.035*	0.245
<i>KIT</i>	4	55514094	55616881	0.087	0.049*	0.185
<i>KDR</i>	4	55918093	56018093	0.264	0.020*	0.368
<i>AIM1</i>	6	106939031	107039031	0.032*	0.663	0.316
<i>SGK1</i>	6	134443208	134543208	0.023*	0.911	0.217
<i>PARK2</i>	6	161758589	163158834	0.032*	0.185	0.101

<i>FGFR1OP</i>	6	167383440	167483440	0.048*	0.234	0.094
<i>LMTK2</i>	7	97726196	97848944	0.047*	1.000	1.000
<i>PILRB</i>	7	99899570	99999570	0.047*	1.000	0.780
<i>EPHB6</i>	7	142510819	142610819	0.767	0.303	0.002*
<i>CASP2</i>	7	142945048	143045048	0.767	0.303	0.004*
<i>WRN</i>	8	30880777	31041277	0.943	0.012*	0.153
<i>KAT6A</i>	8	41776996	41919505	0.048*	0.921	0.600
<i>IKBKB</i>	8	42109495	42209495	0.011*	0.634	0.437
<i>HOOK3</i>	8	42742032	42895682	0.026*	0.925	0.350
<i>PREX2</i>	8	68854602	69027654	0.005*	1.000	0.778
<i>SLCO5A1</i>	8	70574567	70755404	0.005*	1.000	0.236
<i>NCOA2</i>	8	71014266	71326020	0.009*	1.000	0.038
<i>JPH1</i>	8	75136938	75243562	0.024*	1.000	1.000
<i>ZFHX4</i>	8	77583514	77789521	0.013*	1.000	0.351
<i>PKIA</i>	8	79418335	79527502	0.015*	1.000	0.520
<i>E2F5</i>	8	86058185	86158185	0.018*	1.000	0.904
<i>NBN</i>	8	90921231	91021231	0.009*	1.000	0.993
<i>RUNX1T1</i>	8	92948551	93048551	0.018*	1.000	0.966
<i>SDC2</i>	8	97495881	97634037	0.021*	1.000	1.000
<i>COX6C</i>	8	100848232	100948232	0.019*	1.000	0.486
<i>NCALD</i>	8	102688769	102813439	0.025*	1.000	1.000
<i>RRM2B</i>	8	103183893	103283893	0.025*	1.000	1.000
<i>ATP6V1C1</i>	8	104009266	104109266	0.025*	1.000	0.326
<i>TRPS1</i>	8	116410723	116691228	0.043*	1.000	0.965
<i>EIF3H</i>	8	117647054	117778062	0.043*	1.000	1.000

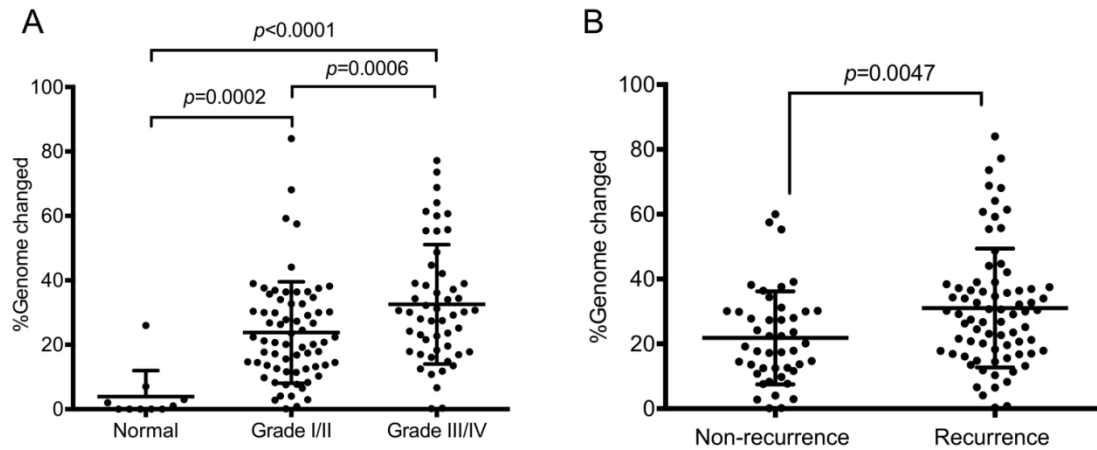
<i>ZHX2</i>	8	123783900	123996755	0.046*	1.000	1.000
<i>MYC</i>	8	128700997	128800997	0.040*	1.000	1.000
<i>ADCY8</i>	8	131782546	132062835	0.032*	1.000	1.000
<i>PTK2</i>	8	141658480	142021412	0.034*	1.000	1.000
<i>BAI1</i>	8	143535376	143636368	0.027*	1.000	1.000
<i>RECQL4</i>	8	145689938	145789938	0.041*	1.000	1.000
<i>NFIB</i>	9	14071841	14324045	0.037*	0.427	0.392
<i>PAX5</i>	9	36828530	37044476	0.024*	0.182	0.037*
<i>GNAQ</i>	9	80325190	80656219	0.028*	0.595	0.611
<i>SYK</i>	9	93554011	93670842	0.003*	0.581	0.882
<i>XPA</i>	9	100398440	100498440	0.005*	0.581	0.818
<i>GATA3</i>	10	8056915	8156915	0.031*	1.000	1.000
<i>ABI1</i>	10	27025524	27160016	0.046*	1.000	1.000
<i>NRG3</i>	10	83625069	84756935	0.028*	0.844	0.808
<i>BMPR1A</i>	10	88506395	88694945	0.028*	0.874	0.867
<i>TLX1</i>	10	102844303	102944303	0.028*	0.490	0.941
<i>SUFU</i>	10	104253718	104389220	0.028*	0.490	0.932
<i>CYP17A1</i>	10	104543788	104643788	0.047*	0.381	0.921
<i>ILK</i>	11	6578531	6678531	0.036*	0.279	0.046*
<i>LMO1</i>	11	8215631	8315631	0.068*	0.386	0.046*
<i>SESN3</i>	11	94885189	94985189	0.038*	0.791	0.532
<i>MAML2</i>	11	95701439	96086344	0.038*	0.667	0.912
<i>KRAS</i>	12	25331016	25431016	0.004*	0.546	0.318
<i>WNT1</i>	12	49324315	49424315	0.032*	0.501	0.156
<i>HMGA2</i>	12	66208239	66319307	0.043*	1.000	0.183

<i>CCT2</i>	12	69937282	70037282	0.039*	1.000	0.033*
<i>NAV3</i>	12	78215068	78616790	0.383	0.916	0.010*
<i>BTG1</i>	12	92486863	92586863	0.478	0.387	0.031*
<i>APAF1</i>	12	99029077	99139211	0.654	0.902	0.031*
<i>IGF1</i>	12	102779644	102882429	0.745	0.423	0.008*
<i>CCNB1IP1</i>	14	20738530	20838530	0.041*	0.488	0.607
<i>HIF1A</i>	14	62138547	62238547	0.945	0.217	0.018*
<i>RAB15</i>	14	65375703	65475703	0.712	0.347	0.049*
<i>MLH3</i>	14	75449350	75549350	0.715	0.397	0.015*
<i>FUS</i>	16	31148811	31248811	0.015*	0.719	0.947
<i>ELAC2</i>	17	12858154	12958154	0.002*	0.728	0.964
<i>FLCN</i>	17	17078014	17178014	0.043*	0.479	0.649
<i>HNF1B</i>	17	36025764	36125764	0.078	0.131	0.026*
<i>MED1</i>	17	37534032	37634032	0.148	0.752	0.001*
<i>CDK12</i>	17	37604269	37704269	0.153	0.752	0.001*
<i>ERBB2</i>	17	37814653	37914653	0.198	0.845	0.000*
<i>THRA</i>	17	38184282	38284282	0.106	0.672	0.036*
<i>RARA</i>	17	38439658	38539658	0.045*	0.755	0.118
<i>TOP2A</i>	17	38509487	38609487	0.045*	0.755	0.118
<i>IGFBP4</i>	17	38556828	38656828	0.045*	0.671	0.118
<i>BRCA1</i>	17	41186221	41286221	0.060	0.749	0.037*
<i>ETV4</i>	17	41564257	41664257	0.463	0.200	0.037*
<i>CLTC</i>	17	57685683	57785683	0.594	1.000	0.015*
<i>GDF15</i>	19	18448476	18548476	0.577	0.859	0.032*
<i>ELL</i>	19	18543204	18643204	0.434	0.859	0.032*

<i>NF2</i>	22	29989544	30089904	0.030*	0.134	0.939
<i>PATZ1</i>	22	31682019	31782019	0.004*	0.313	0.578

\* $P < 0.05$ .





**Supplementary Figure 1 Percent genome change in early stage hepatocellular carcinoma specimens and tumor recurrence.** A: Percent genome change in normal, grade I/II, and grade III/IV patients with HCC. The statistical significance between normal versus grade I/II and normal versus grade III/IV, as indicated by the *P* value. B: A significant difference ( $P = 0.0047$ ) in the percent genome change between recurrence and non-recurrence in patients with HCC is shown.