

Supplementary Table 1

SYBR GREEN PRIMERS (Eurogentec, Seraing, Belgium)			TAQMAN PRIMERS & PROBES	
GENE ID	STRAND	Primer sequences 5'- 3'	GENE ID	Life Technologies cat. #
ACTA2	Forward	CATCCTCATCCTCCCTTGAG	HPRT1	Hs02800695-m1
	Reverse	ATGAAGGATGGCTGGAACAG	IGFBP5	Hs00181213-m1
ALDOB	Forward	GCATCTGTCAGCAGAATGGA	LEF1	Hs01547250-m1
	Reverse	TAGACAGCAGCCAGGACCTT	LGR5	Hs00173664-m1
CD44	Forward	GGCTTTCAATAGCACCTTGC		
	Reverse	CACGTGCCCTTCTATGAACC		
COL1A1	Forward	CCGGCTCCTGCTCCTCTTAGCG		
	Reverse	CGTTCTGTACGCAGGTGATTGGTGG		
COL4A1	Forward	CCTGGCTTGAAAAACAGCTC		
	Reverse	CCCTGCTGAGGTCTGTGAAC		
DKK1	Forward	CCGAGGAGAAATTGAGGAAAC		
	Reverse	TCTGGAATACCCATCCAAGG		
FZD1	Forward	GCCGAGAAAGTATGGCTGAG		
	Reverse	GGCACAAAGTTCCCAGCTC		
FZD7	Forward	GAGGTGCACCAGTTCTACCC		
	Reverse	GCGCATACATGGAGCATAAG		
GPC3	Forward	TGAAGATGAGTGCATTGGAGG		
	Reverse	TGCTTATCTCGTTGTCCTTCG		
HPRT1	Forward	TGACACTGGCAAAACAATGCA		
	Reverse	GGTCCTTTTACCAGCAAGCT		
LAMC1	Forward	AGATGGAAGCTGAGAATCTGG		
	Reverse	CGGTCTGCTGTTCACTCTTG		
RNA18S	Forward	CGCCGCTAGAGGTGAAATTC		
	Reverse	TTGGCAAATGCTTTCGCTC		
SOX9	Forward	TCTGGAGACTTCTGAACGAGAGCGA		
	Reverse	CGTTCTTCACCGACTTCTCCGC		
SFRP1	Forward	AGCGAGTTTGCACTGAGGA		
	Reverse	GACAATCTTCTTGTCGCCATT		
SFRP2	Forward	CGAGGAAGCTCCAAAGGTAT		
	Reverse	GCGTTTCCATTATGTCGTTG		
SFRP3	Forward	GAAACTGTAGAGGGGCAAGC		
	Reverse	TCCGGAATAGGTCTTCTGTG		
SFRP4	Forward	CCGGAGGATGTTAAGTGGAT		
	Reverse	GGGCTTAGGCGTTTACAGTC		
SFRP5	Forward	TGTGCTCCAGTGACTTTGTG		
	Reverse	CGGTCCCCATTCTCTATCTT		
TBP	Forward	GAGCTGTGATGTGAAGTTTCC		
	Reverse	TCTGGGTTTGATCATTCTGTAG		
WNT2	Forward	GGTGATGTGCGATAATGTGC		
	Reverse	CTAATGGCACGCATCACATC		
WNT3	Forward	AGCTGCCAGGAGTGATTCCG		
	Reverse	CACACACTTCACCCCTTCC		

Supplementary Table 2

PRIMARY ANTIBODIES		
GENE ID	CAT. #	Supplier
CD44	20282	ProMab
COL4A1	M0785	Dako
LAMC1	Z0097	Dako
ACTA2	M0851	Dako
EPCAM	14-9326-82	eBioscience
ALB	A80229A3	Bethyl Laboratories
GPC3	cmc26129021	Cell Marque
KRT19	M0888	Dako
LGR5	HPA012530	Sigma Aldrich
SOX9	AB5535	Millipore

Supplementary Table 3

DESCRIPTION OF THE SAMPLE POPULATION (N= 70)		
Variables	N of Missing Values	Mean±SD or N(%)
Age (Years)	2	63.63 ± 9.31
Gender (Male)	2	64 (94.12%)
Etiology	8	
Alcohol		48 (68.57%)
Alcohol + Haemochromatosis		3 (4.29%)
Alcohol + HBV		2 (2.86%)
Alcohol + HCV		3 (4.29%)
Haemochromatosis		4 (5.71%)
HBV		1 (1.43%)
HCV		1 (1.43%)
Unknown		8 (11.43%)
Child-Pugh score	16	
A		43 (61.43%)
B		6 (8.57%)
C		5 (7.14%)
Unknown		16 (22.86%)
METAVIR Score (Fibrosis) *	0	
F0		3 (4.29%) [3 (4.29%)]
F1		2 (2.86%) [1 (1.43%)]
F2		1 (1.43%) [1 (1.43%)]
F3		1 (1.43%) [1 (1.43%)]
F4		63 (90%) [60 (91%)]
METAVIR Score (Activity)	5	
0		25 (35.71%)
1		27 (38.57%)
2		12 (17.14%)
3		1 (1.43%)
Not reported		5 (7.14%)
Edmondson-Steiner's grading	0	
1		4 (5.71%)
2		34 (48.57%)
3		32 (45.71%)
4		0 (0%)

*Data within brackets [] indicate matching non-tumor samples available for molecular analyses (66 non-tumor samples out of 70 HCC patients).

Supplementary Table 4.

	MsigDB SIGNATURE NAME	SIZE	NES	P value
EXTRACELLULAR MATRIX REMODELLING	ST_INTEGRIN_SIGNALING_PATHWAY	80	1.67	0.000
	ROZANOV_MMP14_TARGETS_SUBSET	33	1.61	0.000
	REACTOME_SIGNALING_BY_PDGF	118	1.58	0.000
	PID_INTEGRIN_CS_PATHWAY	25	1.57	0.000
	KEGG_FOCAL_ADHESION	197	1.55	0.000
	BIOCARTA_INTEGRIN_PATHWAY	37	1.54	0.045
	PID_INTEGRIN5_PATHWAY	17	1.52	0.000
	SUNG_METASTASIS_STROMA_UP	106	1.51	0.000
	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_UP	277	1.51	0.000
	ASTIER_INTEGRIN_SIGNALING	57	1.50	0.000
	PID_AVB3_INTEGRIN_PATHWAY	75	1.48	0.000
	REACTOME_COLLAGEN_FORMATION	58	1.48	0.000
	RODWELL_AGING_KIDNEY_UP	464	1.47	0.000
	CROONQUIST_STROMAL_STIMULATION_UP	59	1.46	0.000
	PID_A6B1_A6B4_INTEGRIN_PATHWAY	46	1.45	0.000
	DURAND_STROMA_S_UP	294	1.44	0.000
	KEGG_ECM_RECEPTOR_INTERACTION	83	1.41	0.000
WNT/β-CATENIN PATHWAY	ST_WNT_BETA_CATENIN_PATHWAY	34	1.69	0.000
	BIOCARTA_PITX2_PATHWAY	15	1.61	0.000
	BIOCARTA_WNT_PATHWAY	26	1.50	0.000
	KEGG_WNT_SIGNALING_PATHWAY	150	1.49	0.000
	ONDER_CDH1_SIGNALING_VIA_CTNNB1	83	1.49	0.000

	SANSOM_WNT_PATHWAY_REQUIRE_MYC	57	1.48	0.000
	PID_BETA_CATENIN_NUC_PATHWAY	80	1.46	0.000
	BIOCARTA_GSK3_PATHWAY	27	1.45	0.031
	WNT_SIGNALING	89	1.45	0.000
TGFB SIGNALING	VERRECCHIA_DELAYED_RESPONSE_TO_TGFB1	39	1.61	0.000
	REACTOME_TGF_BETA_RECEPTOR_SIGNALING_ACTIVATES_SMADS	24	1.56	0.000
	VERRECCHIA_RESPONSE_TO_TGFB1_C5	21	1.56	0.000
	KARAKAS_TGFB1_SIGNALING	18	1.55	0.000
	MCBRYAN_PUBERTAL_TGFB1_TARGETS_UP	168	1.53	0.000
	VERRECCHIA_EARLY_RESPONSE_TO_TGFB1	56	1.51	0.000
	LABBE_TARGETS_OF_TGFB1_AND_WNT3A_UP	108	1.45	0.018
	VERRECCHIA_RESPONSE_TO_TGFB1_C1	19	1.45	0.000
	PLASARI_TGFB1_TARGETS_10HR_DN	244	1.44	0.000
	VERRECCHIA_RESPONSE_TO_TGFB1_C2	24	1.44	0.000
	PLASARI_TGFB1_SIGNALING_VIA_NFIC_1HR_DN	105	1.42	0.000
	PID_SMAD2_3NUCLEAR_PATHWAY	82	1.41	0.000
STEM CELLS	SCHAEFFER_SOX9_TARGETS_IN_PROSTATE_DEVELOPMENT_DN	45	1.70	0.000
	CAIRO_LIVER_DEVELOPMENT_UP	165	1.61	0.000
	HADDAD_B_LYMPHOCYTE_PROGENITOR	284	1.53	0.000
	MATZUK_EMBRYONIC_GERM_CELL	19	1.52	0.000
	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_SCP2_QTL_TRANS	24	1.51	0.000
	LIM_MAMMARY_STEM_CELL_UP	481	1.50	0.000
	LEE_NEURAL_CREST_STEM_CELL_UP	145	1.49	0.000
	BENPORATH_OCT4_TARGETS	282	1.47	0.031
	REACTOME_DEVELOPMENTAL_BIOLOGY	381	1.46	0.000
	HOEBEKE_LYMPHOID_STEM_CELL_UP	94	1.45	0.000

	IVANOVA_HEMATOPOIESIS_STEM_CELL	243	1.44	0.000
	IZADPANAH_STEM_CELL_ADIPOSE_VS_BONE_DN	107	1.44	0.000
	KORKOLA_EMBRYONAL_CARCINOMA_UP	41	1.43	0.000
	BOQUEST_STEM_CELL_UP	257	1.42	0.000
BAD OUTCOME IN CANCER	POMEROY_MEDULLOBLASTOMA_PROGNOSIS_DN	43	1.73	0.000
	HOSHIDA_LIVER_CANCER_SUBCLASS_S1	235	1.60	0.000
	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP	344	1.55	0.000
	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP	168	1.53	0.000
	LINDGREN_BLADDER_CANCER_HIGH_RECURRENCE	48	1.53	0.000
	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_UP	31	1.53	0.000
	LANDIS_BREAST_CANCER_PROGRESSION_DN	70	1.53	0.000
	LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_DN	15	1.49	0.000
	RHODES_CANCER_META_SIGNATURE	64	1.48	0.000
	WOO_LIVER_CANCER_RECURRENCE_UP	105	1.43	0.000
	SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_DN	45	1.43	0.000
	HOSHIDA_LIVER_CANCER_SURVIVAL_UP	73	1.42	0.000
	BOYVAULT_LIVER_CANCER_SUBCLASS_G5_DN	27	1.41	0.018
DRUG RESISTANCE	GYORFFY_DOXORUBICIN_RESISTANCE	50	1.56	0.000
	KANG_CISPLATIN_RESISTANCE_UP	18	1.48	0.000
	KANG_FLUOROURACIL_RESISTANCE_UP	21	1.46	0.000

Supplementary Table 5A

NORMAL LIVER CONTROLS (n=23)										
	COL4A1	LAMC1	ACTA2	SFRP1	SFRP2	SFRP5	DKK1	FZD1	FZD7	WNT2
LAMC1	0.51 NS									
ACTA2	0.58 *	0.53 NS								
SFRP1	0.12 NS	0.35 NS	-0.03 NS							
SFRP2	0.6 *	0.21 NS	0.33 NS	0.1 NS						
SFRP5	0.2 NS	0.51 NS	0.04 NS	0.59 NS	0.08 NS					
DKK1	0.25 NS	0.32 NS	-0.06 NS	0.13 NS	0.27 NS	0.1 NS				
FZD1	0.27 NS	0.43 NS	0 NS	0.36 NS	0.24 NS	0.24 NS	0.84 ***			
FZD7	0.05 NS	0.4 NS	0.02 NS	0.41 NS	0.2 NS	0.11 NS	0.44 NS	0.56 *		
WNT2	0.16 NS	0.44 NS	0.01 NS	0.38 NS	0.06 NS	0.3 NS	0.59 *	0.77 ***	0.25 NS	
WNT3	0.3 NS	0.7 NS	0.4 NS	1 ***	0.1 NS	-0.5 NS	0.2 NS	0.6 NS	0.3 NS	0.6 NS

FOCAL NODULAR HYPERPLASIAS (n=11)										
	COL4A1	LAMC1	ACTA2	SFRP1	SFRP2	SFRP5	DKK1	FZD1	FZD7	WNT2
LAMC1	0.69 NS									
ACTA2	0.19 NS	0.6 NS								
SFRP1	0.3 NS	0.64 NS	0.69 NS							
SFRP2	0.19 NS	0.41 NS	0.12 NS	0.55 NS						
SFRP5	0.48 NS	0.85 *	0.61 NS	0.85 *	0.65 NS					
DKK1	0.75 *	0.87 *	0.53 NS	0.37 NS	0.3 NS	0.6 NS				
FZD1	0.64 NS	0.77 *	0.55 NS	0.83 *	0.66 NS	0.86 *	0.61 NS			
FZD7	0.45 NS	0.8 *	0.62 NS	0.63 NS	0.48 NS	0.78 *	0.67 NS	0.66 NS		
WNT2	0.46 NS	0.07 NS	-0.19 NS	-0.32 NS	0.2 NS	-0.15 NS	0.43 NS	0.15 NS	0 NS	
WNT3	0.03 NS	-0.18 NS	-0.14 NS	-0.41 NS	0.04 NS	-0.38 NS	0.15 NS	-0.09 NS	-0.06 NS	0.84 *

NON-TUMOR LIVER SAMPLES (n=66)										
	COL4A1	LAMC1	ACTA2	SFRP1	SFRP2	SFRP5	DKK1	FZD1	FZD7	WNT2
LAMC1	0.71 ***									
ACTA2	0.62 ***	0.74 ***								
SFRP1	0.62 ***	0.75 ***	0.77 ***							
SFRP2	0.44 ***	0.5 ***	0.56 ***	0.62 ***						
SFRP5	0.65 ***	0.69 ***	0.7 ***	0.76 ***	0.51 ***					
DKK1	0.32 *	0.35 **	0.45 ***	0.32 *	0.56 ***	0.36 **				
FZD1	0.39 **	0.35 **	0.45 ***	0.43 ***	0.46 ***	0.43 ***	0.69 ***			
FZD7	0.55 ***	0.57 ***	0.65 ***	0.64 ***	0.47 ***	0.61 ***	0.5 ***	0.68 ***		
WNT2	0.33 **	0.47 ***	0.51 ***	0.47 ***	0.66 ***	0.43 ***	0.71 ***	0.61 ***	0.48 ***	
WNT3	0.09 NS	0.09 NS	0.02 NS	-0.16 NS	0.11 NS	0.11 NS	0.16 NS	0.14 NS	0.15 NS	0.19 NS

HEPATOCELLULAR CARCINOMAS (n=82)										
	COL4A11	LAMC1	ACTA2	SFRP1	SFRP2	SFRP5	DKK1	FZD1	FZD7	WNT2
LAMC1	0.51 ***									
ACTA2	0.56 ***	0.61 ***								
SFRP1	0.35 **	0.32 **	0.43 ***							
SFRP2	0.36 **	0.28 *	0.44 ***	0.42 ***						
SFRP5	0.21 NS	0.2 NS	0.3 *	0.55 ***	0.26 *					
DKK1	0.23 NS	0.36 **	0.33 **	0.21 NS	0.61 ***	0.09 NS				
FZD1	0.17 NS	0.23 NS	0.07 NS	0.16 NS	0.51 ***	0.14 NS	0.6 ***			
FZD7	0.3 *	0.31 *	0.2 NS	0.3 *	0.43 ***	0.25 *	0.44 ***	0.55 ***		
WNT2	0.29 *	0.36 **	0.32 **	0.23 NS	0.43 ***	0 NS	0.53 ***	0.47 ***	0.39 **	
WNT3	-0.26 *	-0.12 NS	-0.2 NS	-0.01 NS	0.12 NS	0.08 NS	0.07 NS	0.12 NS	-0.02 NS	-0.06 NS

HEPATOCELLULAR CARCINOMAS, HIGH TF _i (n=34)										
	COL4A1	LAMC1	ACTA2	SFRP1	SFRP2	SFRP5	DKK1	FZD1	FZD7	WNT2
LAMC1	0.52 *									
ACTA2	0.49 NS	0.52 *								
SFRP1	0.56 *	0.38 NS	0.68 **							
SFRP2	0.46 NS	0.29 NS	0.55 *	0.68 **						
SFRP5	0.29 NS	0.25 NS	0.44 NS	0.4 NS	0.35 NS					
DKK1	0.37 NS	0.38 NS	0.44 NS	0.43 NS	0.6 *	0.32 NS				
FZD1	0.52 *	0.41 NS	0.3 NS	0.36 NS	0.56 *	0.34 NS	0.51 *			
FZD7	0.31 NS	0.4 NS	0.2 NS	0.32 NS	0.3 NS	0.21 NS	0.3 NS	0.53 *		
WNT2	0.4 NS	0.48 NS	0.31 NS	0.29 NS	0.42 NS	-0.08 NS	0.4 NS	0.51 *	0.39 NS	
WNT3	-0.23 NS	0.02 NS	-0.1 NS	-0.16 NS	0.15 NS	-0.17 NS	-0.01 NS	-0.02 NS	-0.25 NS	-0.17 NS

HEPATOCELLULAR CARCINOMAS, LOW TF _i (n=43)										
	COL4A1	LAMC1	ACTA2	SFRP1	SFRP2	SFRP5	DKK1	FZD1	FZD7	WNT2
LAMC1	0.52 **									
ACTA2	0.66 ***	0.66 ***								
SFRP1	0.21 NS	0.23 NS	0.21 NS							
SFRP2	0.26 NS	0.24 NS	0.28 NS	0.2 NS						
SFRP5	0.2 NS	0.18 NS	0.2 NS	0.69 ***	0.14 NS					
DKK1	0.07 NS	0.32 NS	0.2 NS	0.03 NS	0.65 ***	0 NS				
FZD1	-0.16 NS	0.05 NS	-0.17 NS	0.05 NS	0.46 **	0.08 NS	0.64 ***			
FZD7	0.26 NS	0.2 NS	0.16 NS	0.31 NS	0.59 ***	0.42 *	0.55 ***	0.55 ***		
WNT2	0.22 NS	0.24 NS	0.35 NS	0.21 NS	0.5 **	0.09 NS	0.64 ***	0.49 **	0.41 *	
WNT3	-0.27 NS	-0.16 NS	-0.27 NS	0.07 NS	0.16 NS	0.23 NS	0.14 NS	0.25 NS	0.13 NS	0.02 NS

Supplementary Table 5B

HEPATOCELLULAR CARCINOMAS				
Variable #1	Variable #2	n=	R=	<i>P</i>
COL4A1	LAMC1	54	0.71	<0.001
COL1A1	LAMC1	53	0.52	<0.001
COL1A1	COL4A1	53	0.79	<0.001
MMP14	LAMC1	53	0.43	<0.01
LAMC1	active MMP2	47	0.38	<0.01
MMP2	active MMP2	47	0.54	<0.001
MMP14	active MMP2	47	0.64	<0.001

Supplementary Table 6

DESCRIPTION OF THE SAMPLE POPULATION	
First author	Roessler S.
Annotated patients in cohort (N)	247
Available HCC samples (N)	247
Included HCC samples (N)	247
Samples excluded after quality analysis (N)	0
Samples excluded because of unavailable mutational status	/
Inclusion criteria	HCCs after surgical resection
Country of origin	China
Gender (Male)	214 (87%)
Age	
Mean, SD	50.8 ± 10.8
Median, range	NA
>55 years	NA
>60 years	NA
HCV positive	5 (2%)
HBV positive	241 (99%)
HBV active viral replication	62 (26%)
Alcohol	NA
Hemochromatosis	NA
Cirrhosis	224 (91%)
Intact capsule	129 (53%)
Satellite nodule	NA
CTNNB1 mutation	NA
TP53 mutation	NA
Tumor size	
cm, mean, SD	NA
cm, median, range	NA
Tumour volume (cm ³) (mean, SD)	NA
Less than 2.0 cm	NA
Between 2.0 cm and 3.0 cm	NA
Between 2.0 cm and 5.0 cm	NA
Greater than 3.0 cm	NA
Greater than 5.0 cm	89 (36%)
Number of tumor nodules	
Mean, SD	NA
Single	193 (78%)
Multiple	52 (21%)
Vascular invasion	
None	90 (46%)
Microscopic	107 (54%)

Macroscopic	0 (0%)
TNM staging	
I	97 (43%)
I-II	NA
II-III	130 (57%)
III-IV	NA
IV	0 (0%)
CLIP Staging	
0	99 (44%)
1-5	128 (56%)
Tumor differentiation	
Well differentiated	NA
Moderately differentiated	NA
Poorly differentiated	NA
Edmondson grade	
I	NA
I-II	NA
II	NA
III	NA
III-IV	NA
IV	NA
Child-Pugh class	
A	NA
B	NA
C	NA
AJCC stage	
I	NA
II	NA
III	NA
IV	NA
Fibrosis score	
F0	NA
F1	NA
F2	NA
F3	NA
F4	NA
Barcelona Clinic Liver Cancer stage	
0	0 (0%)
0-A	174 (77%)
A	NA
B	NA
B-C	53 (23%)
C	NA
D	0 (0%)
Serum AFP levels (ng/ml)	
Mean, SD	NA

Less than 10	NA
Between 10 and 100	NA
Less than 100	NA
Between 100 and 1000	NA
Greater than 100	NA
Greater than 300	111 (46%)
Greater than 400	NA
Greater than 1000	NA
Albumin (g/dl)	
Mean, SD	NA
Median, range	NA
Less than 3,5	NA
Platelets (x1000/ml)	
Mean, SD	NA
Median, range	NA
Less than 100	NA
Greater than 150	NA
Bilirubin	
mg/dl, mean, SD	NA
mg/dl, median, range	NA
Greater than 1 mg/dl	NA
ALT (U/L)	
Mean, SD	NA
Greater than 50	101 (41%)
ASAT (U/L), mean, SD	NA

Supplementary Table 7

VARIABLE	NA	RI > 62; N (%)	RI < 62; N (%)	p value
Metastasis Signature (high)	0	44 (72.13%)	77 (42.54%)	5.00E-04
Age (Mean ± SD)	0	47.3 ± 11.59	52.04 ± 10.4	9.30E-03
AFP (>300ng/ml)	4	35 (58.33%)	75 (42.13%)	3.70E-02
TNM staging (II-III vs I)	17	39 (69.64%)	90 (53.25%)	4.22E-02
BCLC staging (B-C vs A-0)	17	19 (33.93%)	34 (20.12%)	4.52E-02
CGH_survival_group (G2 vs G1)*	0	16 (26.23%)	28 (15.47%)	1.34E-01
Multinodular (yes vs no)	0	17 (27.87%)	35 (19.34%)	2.09E-01
CLIP staging (1-5 vs 0)	17	21 (37.5%)	77 (45.56%)	3.51E-01
ALT (>50 U.L.)	0	27 (44.26%)	73 (40.33%)	6.60E-01
Main tumor size (>5 cm)	1	21 (34.43%)	67 (37.22%)	7.54E-01
Gender (Male)	0	54 (88.52%)	157 (86.74%)	8.31E-01
HBV status (AVR-CC vs CC)*	18	14 (25%)	44 (26.19%)	9.56E-01
Cirrhosis (yes vs no)	0	56 (91.8%)	167 (92.27%)	1.00E+00

Supplementary Table 8

GENE SYMBOL	VARIABLE	N (%) ≥ 0.5 centile	N (%) < 0.5 centile	p value
FZD7	Metastasis Signature (high)	81 (66.94%)	40 (33.06%)	8.86E-03
COL4A1	Age (Mean ± SD)	48.18 ± 11.14	53.5 ± 9.98	8.86E-03
LAMC1	Metastasis Signature (high)	83 (68.6%)	38 (31.4%)	8.86E-03
	AFP (>300ng/ml)	70 (58.82%)	40 (33.61%)	1.62E-02
DKK1	Metastasis Signature (high)	84 (70%)	37 (30.33%)	8.86E-03
	CLIP staging (1-5 vs 0)	83 (74.77%)	44 (38.6%)	1.06E-05
	AFP (>300ng/ml)	78 (65.55%)	32 (26.89%)	8.86E-03
SOX9	Metastasis Signature (high)	80 (66.12%)	41 (33.88%)	8.86E-03
	CLIP staging (1-5 vs 0)	77 (68.14%)	50 (44.64%)	8.86E-03
	AFP (>300ng/ml)	75 (62.5%)	35 (29.66%)	8.86E-03
GPC3	Main tumor size (>5 cm)	32 (26.45%)	56 (46.67%)	2.78E-02
	AFP (>300ng/ml)	72 (59.02%)	38 (32.76%)	8.86E-03
LEF1	Metastasis Signature (high)	79 (65.29%)	42 (34.71%)	8.86E-03
	AFP (>300ng/ml)	68 (56.2%)	42 (35.9%)	2.78E-02