Table S1. Characteristics of patients

Case	Age (years)	Gender	Virus infection[#]	Degree of diferentiation	Background liver pathology*	mtRNA[$] (T/N)	HMGA2 expression[¥]	IGFBP1 mRNA (T/N)[@]
1	69	F	C	Mod-Poor	C (incomplete)	>1	(-)	ND
2	79	F	C	Mod-Poor	C	<1	(-)	0.68
3	83	M	(-)	Mod-Poor	F	>1	(-)	0.08
4	73	M	C	-	-	<1	+	10.27
5	67	M	B	Mod	C (probable)	>1	(-)	0.29
6	74	M	(-)	-	-	<1	+	2.43
7	69	M	C	-	-	<1	(-)	1.31
8	69	F	C	Mod	C (probable)	<1	+	0.1
9	69	M	C	Poor	C	<1	(-)	1.42
10	68	M	C	Mod	F2	>1	(-)	0.26
11	84	M	(-)	-	-	<1	+	0.56
12	55	F	(-)	-	-	<1	+	0.02
13	55	M	(-)	Poor	C	<1	+	0.02
14	61	M	unknown	-	-	<1	+	0.03
15	69	M	C	Well	F1~2	>1	(-)	0.71
16	69	M	B,C	Poor	F1	<1	+	0.03
17	71	M	C	Poor	F2	>1	(-)	4.99
18	58	M	C	Well	C (incomplete)	ND	+	ND
19	77	M	C	Mod	F2	<1	(-)	0.28
20	79	M	(-)	Well-Mod	F2	ND	(-)	ND
21	69	M	B,C	Mod	C	>1	(-)	1.66
22	65	M	(-)	Well	F2	<1	+	5.58
23	69	M	(-)	Mod	F2	<1	+	0.02
24	79	M	(-)	Well-Mod	F2	<1	+	0.14
25	77	M	(-)	Mod	-	<1	(-)	2.16
26	84	F	C	Poor	C	>1	+	3.9
27	75	F	C	Poor	C	>1	+	0.5
28	65	F	B	Poor	F4	<1	+	0.04
29	62	F	B	Poor	F3~4	>1	+	5.37
30	65	F	C	Poor	F4	ND	+	ND
31	54	M	C	Mod	C	ND	(-)	ND
32	72	F	(-)	Mod-Poor	F0	>1	+	0.08
33	85	F	(-)	Mod	F0	ND	(-)	ND
34	50	M	C	Well-Mod	F3	ND	+	ND

#Virus infection: B; HBV, C; HCV, (-); negative

*Background of liver pathology: F0~3; staging of fibrosis (F), F4; cirrhosis (C), (-); unknown

[$]mtRNA: mitochondrial transcripts (MT-CYB, MT-ND1, MT-ND6, MT-CO1, MT-ATP6, and MT-ATP8) were quantified, averaged, and normalized with the average of nuclear transcripts (ACTB, B2M, GAPDH, GUSB, HPRT1, RNA18SN2, and TBP) in each sample of a pair of HCC (T) and normal (N) tissues. ND: not determined.

[¥]HMGA2 expression in tumor samples: +/(-); detectable/undetectable signal amplified by qPCR with HMGA2-specific primers

[@]IGFBP1 mRNA expression in tumor samples relative to non-tumorous peritumor samples was analyzed by qPCR.