Table S9: Validation of differential gene expression by quantitative real-time PCR. Individual lesions from each liver tumorigenesis stage (hyperplastic liver, HL; hepatocellular carcinoma, HCC) were examined for the expression level of the selected genes. The $\log_2$ fold change obtained from microarray data and RT-PCR for the genes validated are as shown in the table.

No.	Gene symbol		Gene name	Log_2 fold change							
				Microarray		Quantitative real-time PCR					
	Zebrafish	Human		HL	HCC	HL1	HL2	HL3	HCC1	HCC2	HCC3
1	akt2l	AKT2	V-akt murine thymoma viral oncogene homolog 2, like	1.06	2.91	3.54	2.95	2.78	6.75	5.46	6.03
2	angpt1	ANGPT1	Angiopoietin 1	0.12	2.54	0.26	0.73	0.23	1.58	2.34	1.87
3	ccnb1	CCNB1	Cyclin B1	5.48	7.85	5.11	4.12	4.09	9.67	9.46	8.23
4	mapk1	MAPK1	Mitogen-activated protein kinase 1	2.13	2.18	3.28	2.54	4.45	5.79	6.78	6.92
5	mapk3	MAPK3	Mitogen-activated protein kinase 3	2.31	2.64	2.73	1.12	3.67	3.92	4.65	3.75
6	mapk8	MAPK8	Mitogen-activated protein kinase 8	2.09	3.91	2.58	2.56	2.91	4.71	3.56	4.42
7	mdm2	MDM2	Transformed 3T3 cell double minute 2 homolog	5.66	3.07	2.91	3.40	3.66	3.64	4.07	4.54
8	nfya	NFYA	Nuclear transcription factor Y, alpha	6.56	1.74	4.83	5.13	5.76	0.47	0.56	0.91
9	nlk1	NLK	Nemo like kinase b	2.16	2.35	1.02	2.34	2.61	1.64	1.07	1.13
10	rpl19	RPL19	Ribosomal protein 19	1.20	2.81	2.98	1.45	2.76	4.78	4.75	4.12
11	stat3	STAT3	Signal transduction and activation of transcription 3	-1.06	2.53	-0.67	-1.05	0.12	3.76	3.21	2.65
12	stmn1a	STMN1	Stathmin 1a	-1.30	3.93	-0.59	-0.33	-0.67	4.76	4.12	5.23
13	tgfb1	TGFB1	Transforming growth factor, beta 1	0.41	1.88	0.79	0.04	-0.32	3.40	2.11	2.18
14	tp53	TP53	Tumor protein p53	2.47	-3.54	3.55	2.76	4.29	-0.18	-1.12	-1.56
15	zgc:194152	NBN	Nibrin	2.15	2.05	1.54	2.25	2.71	3.76	1.10	1.75