

SUPPLEMENTARY TABLES

Supplementary Table 1. The sequence of small interfering RNA (shRNA) targeting human FEN1.

shRNA	Target sequence
Sh-control	TTCTCCGAACGTGTCACGT
Sh1-FEN1	GCCCGTGTATGTCTTTGAT
Sh2-FEN1	CCTCATGGGCATCCCTTAT
Sh3-FEN1	GCTCACTCTCTTCAGCTAA

Supplementary Table 2. Primer sequences for FEN1 overexpressing vector.

Gene	Primer sequences
FEN1	CMV-F CGCAAATGGGCGGTAGGCGTG WPRE-R CATAGCGTAAAAGGAGCAACA

Supplementary Table 3. Primer sequences for quantitative RT-PCR.

Gene	Primer sequences
FEN1	Forward (5'-3') : CTGTGGACCTCATCCAGAAGCA Reverse (5'-3') : CCAGCACCTCAGGTTCCAAGA
GAPDH	Forward (5'-3') : GGTGGTCTCCTCTGACTTCAACA Reverse (5'-3') : GTTGCTGTAGCCAAATTCGTTGT
hsa-miR-140-5p	Forward (5'-3') : CGCGCGCAGTGGTTTTACCCTA Reverse (5'-3') : ATCCAGTGCAGGGTCCGAGG RT Primer: GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCTACCA
U6	Forward (5'-3') : AGAGAAGATTAGCATGGCCCTG RT Primer: GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACAAAATA

Supplementary Table 4. FEN1 expression and clinicopathological features in 34 paired HCC patients.

Clinicopathological features	Cases (n=34)	FEN1 expression		P value
		High (%)	Low (%)	
All case (n=34)	34	25	9	
Gender				1.000
Male	29	21(61.8%)	8(23.5%)	
Female	5	4(11.8%)	1(2.9%)	
Age(y)				0.403
<45	8	7(20.6%)	1(2.9%)	
≥45	26	18(52.9%)	8(23.5%)	
Tumor size				0.047
<5cm	19	11(32.4%)	8(23.5%)	
≥5cm	15	14(41.2%)	1(2.9%)	
Tumor stage				1.000
I ~ II	23	17(50.0%)	6(17.6%)	
III ~ IV	11	8(23.5%)	3(8.8%)	
Differentiation				1.000

Well/moderate	27	20(58.8%)	7(20.6%)	
Poor	7	5(14.7%)	2(5.9%)	
Metastasis				0.013
With	12	12(35.3%)	0(0.0%)	
Without	22	13(38.2%)	9(26.5%)	
HBsAg				1.000
Positive	30	22(64.7%)	8(23.5%)	
Negative	4	3(8.8%)	1(2.9%)	
Liver cirrhosis				0.687
With	12	8(23.5%)	4(11.8%)	
Without	22	17(50.0%)	5(14.7%)	

Note: *P* value is calculated with χ^2 test.