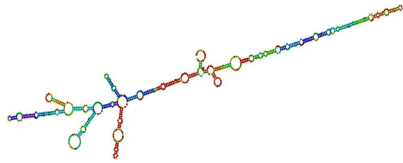


SUPPLEMENTARY FIGURES AND TABLE

A



B

^ EVIDENCE FEATURES SUMMARY

HOMOLOGY FEATURES	HIT NUM	2	
	HIT SCORE	39.0228787452803	
	FRAME SCORE	507.595021856284	
ORF_FRAMEFINDER	COVERAGE	84.42 %	
	LOG-ODDS SCORE	63.54	
	TYPE	Partial	

legend: non-coding coding

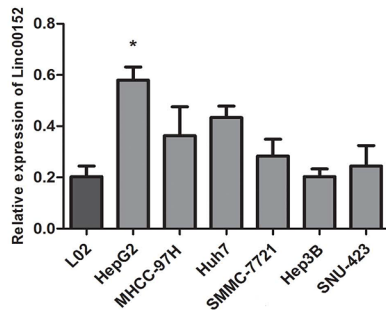
C

Protein coding potential

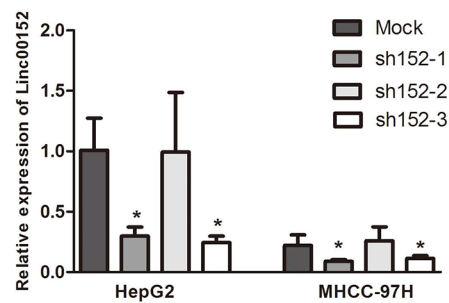
	Metric	Raw result	Interpretation
	PRIDE reprocessing 2.0	0	non-coding ?
	Lee translation initiation sites	0	non-coding ?
+	PhyloSCF score	-75.9943	non-coding ?
	Bazzini small ORFs	0	non-coding ?

In stringent set: yes

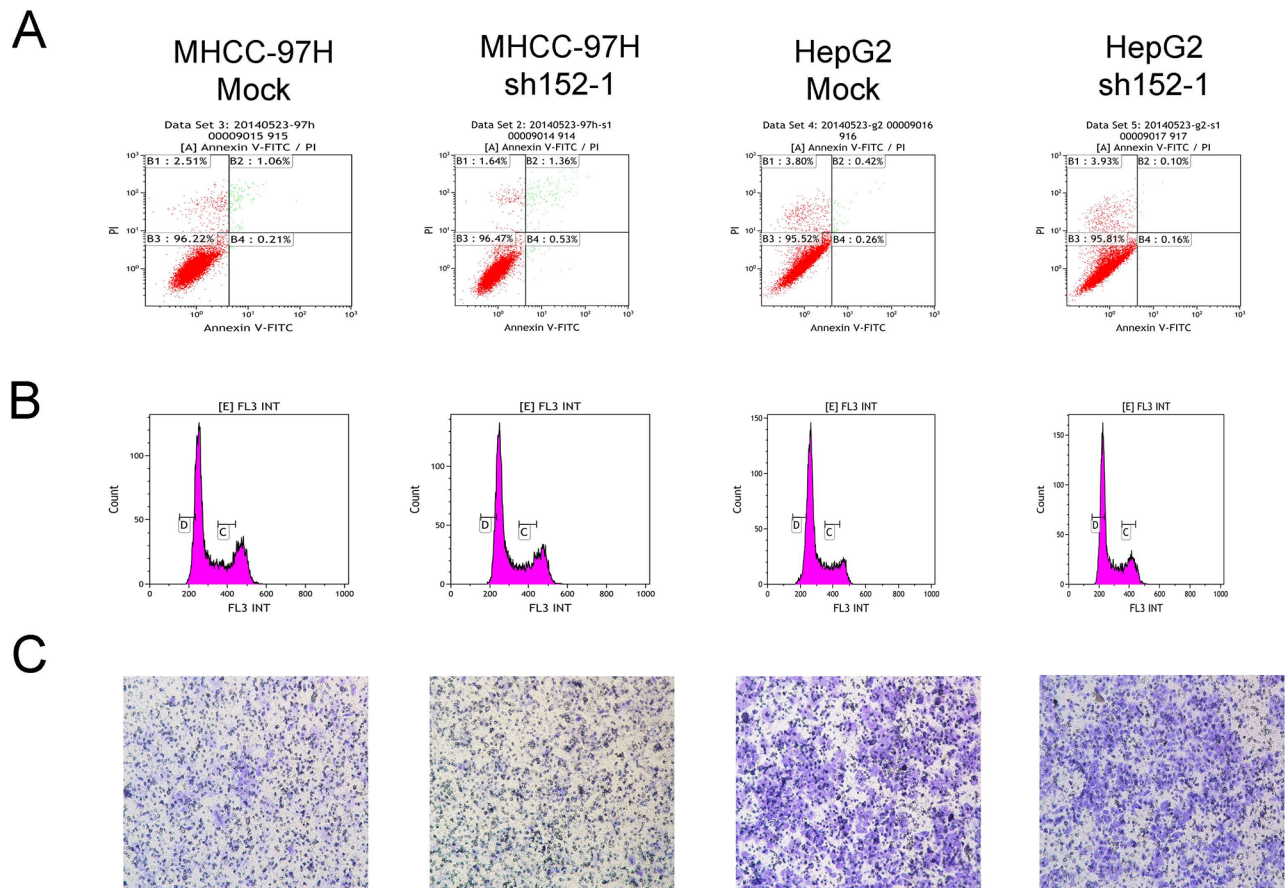
D



E



Supplementary Figure S1: Non-coding RNA validation and the expression of LINC00152 in cell lines. A. The second structure of LINC00152. B, C. Non-coding RNA validation by bioinformatics prediction. D. Different expression level of LINC00152 in HCC cells. E. Expression of LINC00152 in cells treated with shRNA-1, shRNA-2, shRNA-3 and the empty plasmid. Data were presented as the mean ± SEM. * indicates a significant difference compared with controls ($P < 0.05$).



Supplementary Figure S2: No significant of LINC00152 on cell apoptosis, cell cycle or invasion. Cells were treated with shRNA of LINC00152 and empty plasmid in MHCC-97H and HepG2. **A, B.** Apoptosis and cell cycle detection by Flow Cytometry assay. **C.** Invasion was detected by Transwell assay with matrigel.

Supplementary Table S1: Detailed sequence information of primers and shRNAs

	Forward primer (5'-3')	Reverse primer (5'-3')
Linc00152	CTCCAGCACCTCTACCTGTTG	GGACAAGGGATTAAGACACACA
EpCAM	GGCTCTTTAAGCCAAGCAG	CACTCGCTCAGAGCAGGTTAT
GAPDH	GCACCGTCAAGGCTGAGAAC	GGATCTCGCTCCTGGAAGATG
5S RNA	GGAGAGGGAGCCTGAGAAACG	TTACAGGGCCTCGAAAGAGTCC
sh152-1	TCTATGTGTCTTAATCCCTTGTCCT	
sh152-3	TGTGGACTCTGAGGCCTCTGCATT	