

Figure S1. Coding potential of small nucleolar RNA host gene 22 was calculated using the protein-coding potential assessment tools, CPAT and LNCipedia.

## LNCipedia

Result for species name : hg19 with job ID :1588424160							
Data ID	Sequence Name	RNA Size	ORF Size	Ficket Score	Hexamer Score	Coding Probability	Coding Label
0	NC_000018.10:49839867-49840526	660	87	0.8177	-0.14747491465	0.0036810312526446	no

## CPAT

Structure:

### Protein coding potential

Metric	Raw result	Interpretation
PRIDE reprocessing 2.0	0	non-coding ?
Lee translation initiation sites		non-coding ?
PhyloCSF score	-40.8741	non-coding ?
CPAT coding probability	0.69%	non-coding ?
Bazzini small ORFs	0	non-coding ?

Figure S2. Analysis of cell cycle progression in CRC cells overexpressing SNHG22. (A) Reverse transcription-quantitative PCR analysis post-transfection with SNHG22 or control vectors in CRC cells. (B) Flow cytometric analysis of cell cycle progression in CRC cells post-transfection with SNHG22 or control vectors. \*\*\* $P < 0.001$  vs. vector. CRC, colorectal cancer; SNHG22, small nucleolar RNA host gene 22.

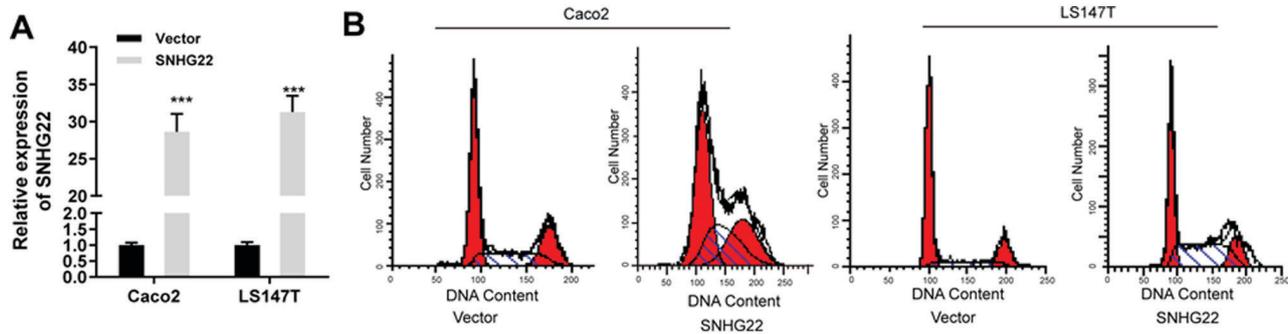


Figure S3. Analysis of cell cycle progression in CRC cells with SNHG22 knockdown. (A) Reverse transcription-quantitative PCR analysis confirmed the knockdown efficiency of both siRNAs targeting SNHG22 in LoVo cells. (B) Flow cytometric analysis of cell cycle progression in LoVo cells transfected with both siRNAs. \*\*\* $P < 0.001$  vs. siNC. NC, negative control; siRNA, small interfering RNA; SNHG22, small nucleolar RNA host gene 22.

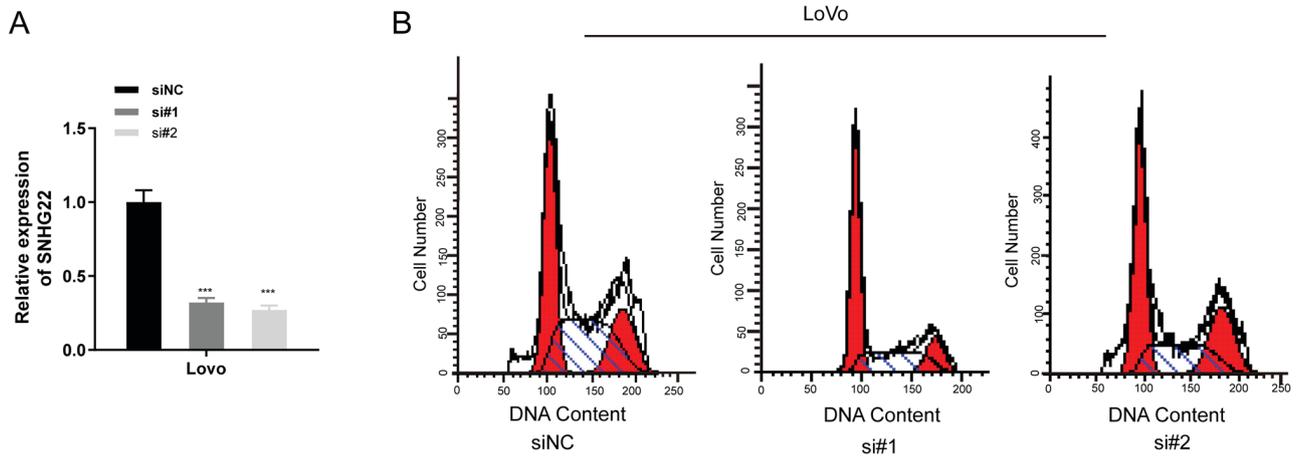


Figure S4. Results from the IncLocator indicated that SNHG22 was preferentially localized to the cell cytoplasm. SNHG22, small nucleolar RNA host gene 22.

<b>SNHG22 IncLocator Prediction Result</b>	
Subcellular locations	score
Cytoplasm	0.837455931993
Nucleus	0.0372657324011
Ribosome	0.0165690597846
Cytosol	0.106034775911
Exosome	0.00267449991073
<b>Predicted location</b>	<b>Cytoplasm</b>

Figure S5. Analysis of clinical significance of E2F3 expression in The Cancer Genome Atlas-colorectal adenocarcinoma dataset. E2F3 expression was significantly associated with (A) tumor stage and (B) overall survival in patients with colorectal cancer. Reverse transcription-quantitative PCR analysis of the transfection efficiencies of miR-128-3p (C) mimics and (D) inhibitor in colorectal cancer cells. \*\*\* $P < 0.001$  vs. NC mimics or NC inhibitor. E2F3, E2F transcription factor 3; miR, microRNA; NC, negative control.

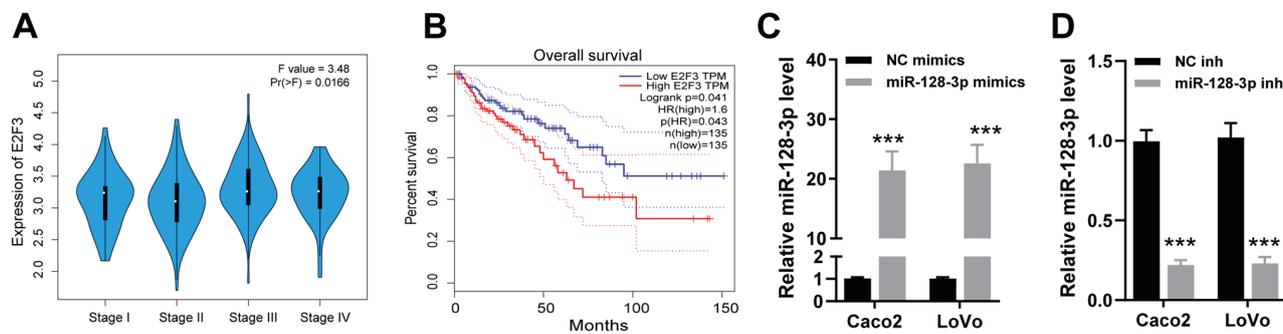


Figure S6. SNHG22 exerts its function by inhibiting the miR-128-3p/E2F3 axis in CRC cells. Reverse transcription-quantitative PCR analysis of the transfection efficiencies of (A) E2F3 overexpression and (B) knockdown in colorectal cancer cells. Flow cytometric analysis of the early apoptotic rates of (C) Caco2 and (D) LoVo cells after transfection with the indicated vectors and sequences. \*\*\* $P < 0.001$  vs. pcDNA3.1, siNC or as indicated. E2F3, E2F transcription factor 3; EV, empty vector; NC, negative control; si, small interfering.

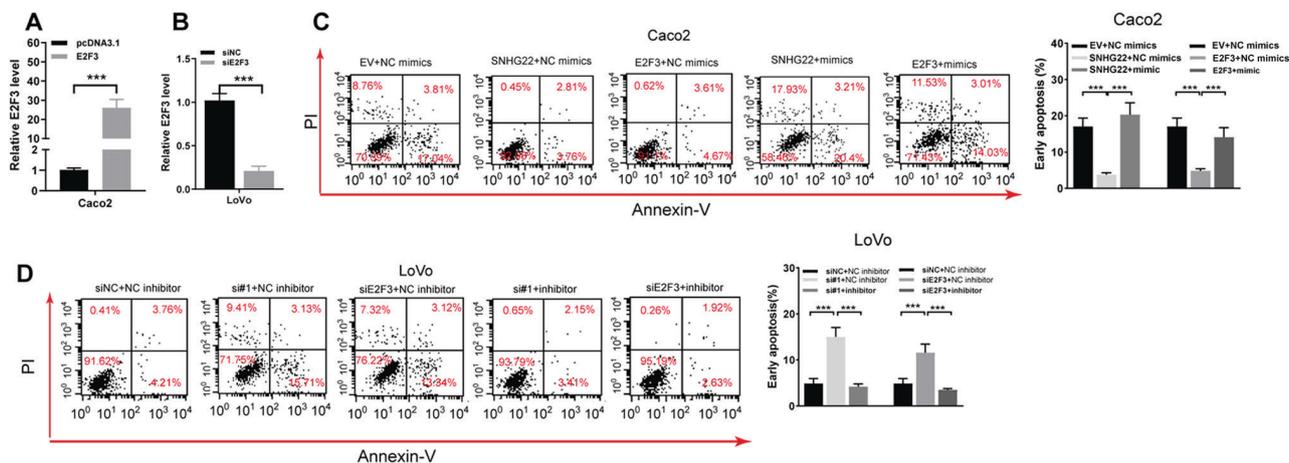


Table SI. Selected demographic and clinicopathologic characteristics of patients with colorectal cancer and adenoma.

Parameter	Value	%
Adenoma <sup>a</sup>		
Age, years		
<60	21	63.6
≥60	12	36.4
Sex		
Male	19	57.6
Female	14	42.4
Colorectal cancer <sup>b</sup>		
Age, years		
<60	41	44.1
≥60	52	55.9
Sex		
Male	53	57.0
Female	40	43.0
Tumor site		
Colon	55	59.1
Rectum	38	40.9
T stage		
T1-T2	27	29.0
T3-T4	66	71.0
N stage		
N0	51	54.8
N1-N2	42	45.2
M stage		
M0	71	76.3
M1-2	22	23.7
Tumor grade		
Poor	15	16.1
Moderate-well	78	83.9
CEA, ng/ml		
<5	35	37.6
≥5	58	62.4

<sup>a</sup>n=33; <sup>b</sup>n=93. CEA, carcinoembryonic antigen.

Table SII. Sequences of primers used for RT-qPCR and siRNAs.

Sequence	Forward (5'-3')	Reverse (5'-3')
RT-qPCR primers		
$\beta$ -actin	GATCATTGCTCCTCCTGAGC	ACTCCTGCTTGCTGATCCAC
SNHG22	GACTCAAGCCCTGAGCATGT	CTGGTCACCTCCAAGTCAA
miR-128-3p	GCCGGCGCCCGAGCTCTGGCTC	TCACAGTGAACCGGTCTCTTT
E2F3	AGAAAGCGGTCATCAGTACCT	TGGACTTCGTAGTGCAGCTCT
U6	GTGCTCGCTTCGGCAGCACAT	TACCTTGCGAAGTGCTTAAAC
siRNA sequences		
SNHG22 siRNA-1	GTGGGCAAGTGAGATTATC	
SNHG22 siRNA-2	GGTCTCCTGTGAACCCTGA	
E2F3 siRNA	GCGATCTCTTCGAGCTTA	
NC siRNA	CUAGAGCAAAACGGTCTCGG	
miR-128-3p mimics	UCACAGAGAACCGGUCUCUUU	
miR-128-3p inhibitor	AAAGAGACCGGUUCACUGUGA	
NC mimic	UCACAGCCUCCUAGAAAGAGUAGA	
NC inhibitor	UACUCUUUCUAGGAGGUUGUAUU	

E2F3, E2F transcription factor 3; miR-128-3p, microRNA-128-3p; RT-qPCR, reverse transcription-quantitative PCR; siRNA, small interfering RNA; SNHG22, small nucleolar RNA host gene 22.