



LncRNA *SNHG16* promotes colorectal cancer proliferation by regulating ABCB1 expression through sponging miR-214-3p

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Supplementary Table 1 The target sequences of siRNAs and shRNAs

siRNAs	Target sequences (5'-3')
si-SNHG16#1	CCTTCCAGGAACAGATCTT
si-SNHG16#2	TGTTGACTCACCAAGGCAA
si-SNHG16#3	GGAACAGATCTTTGCATAG
si-ABCB1	CGAUACAUGGUUUUCCGAU
shRNAs	
sh-SNHG16#1	GGAACAGATCTTTGCATAG

Supplementary Table 2 The clinic-pathological factors of colorectal cancer patients in TCGA cohort

Characteristics	No. of cases	SNHG16 expression		P-value ^a
		Low (n=206)	High (n=206)	
Gender				
Female	196	98	98	1.000
Male	216	108	108	
Tumor invasion depth				
T1-2	81	52	29	0.004
T3-4	331	154	177	
Lymph node metastasis				
N0	248	134	114	0.044
N1+N2	164	72	92	
Distant metastasis				
M0	346	176	170	0.420
M1+M2	66	30	36	
TNM stage				
I + II	239	127	112	0.134
III + III	173	79	94	
Bold fonts indicate P-values <0.05				

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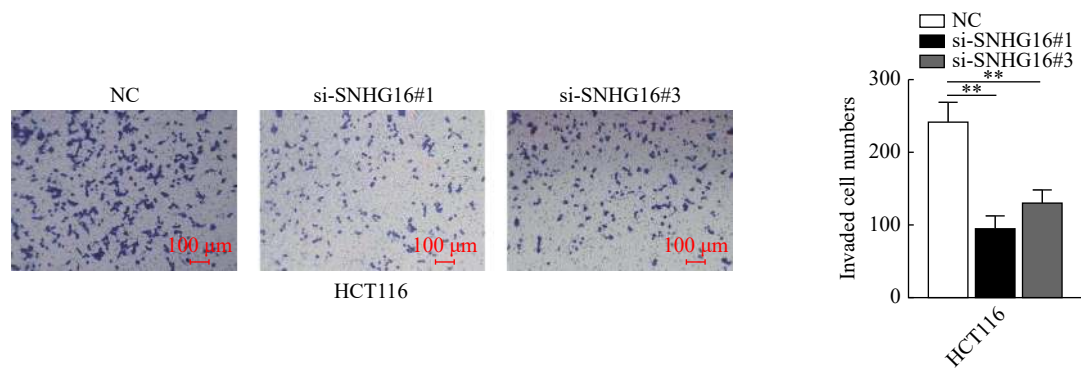
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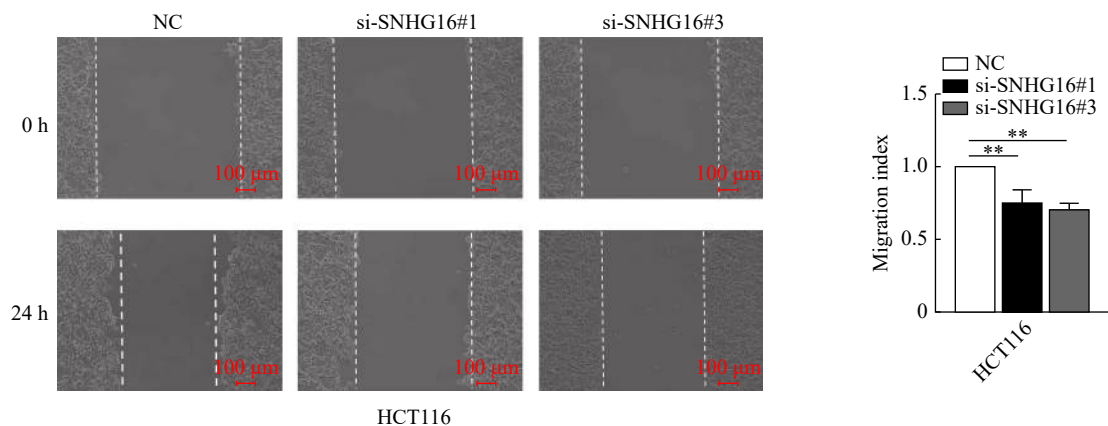
The authors reported no conflict of interests.

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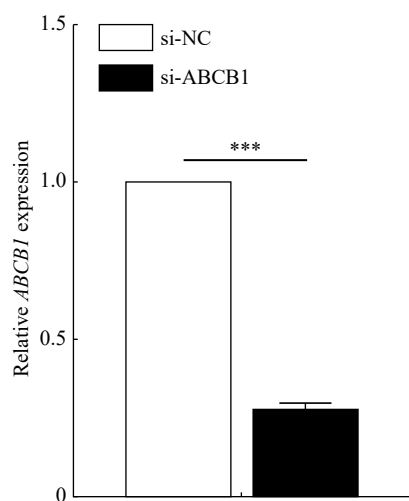
A



B



Supplementary Fig. 1 *SNHG16* promoted CRC cell invasion and migration *in vitro*. A: Transwell assays were used to determine the invasion and migration abilities of *SNHG16* siRNAs transfected cells. B: Representative images of wound healing assays performed using HCT116 cells after *SNHG16* silenced. Cells of the NC group were transfected with si-NC. Values are presented as mean±SD. Student's *t*-test was performed to indicate significance. Scale bar: 100 μ m. * P <0.05, ** P <0.01, and *** P <0.001.



Supplementary Fig. 2 The relative efficiency of knocking down *ABCB1* expression in HCT116 cells. *ABCB1* was quantified by quantitative reverse transcription PCR after transfection of *ABCB1* siRNAs in HCT116 cells. Cells of the NC group were transfected with si-NC. Values are presented as mean±SD. Student's *t*-test was performed to indicate significance. * P <0.05, ** P <0.01, and *** P <0.001.