

MIR133A regulate SOX9 in colorectal cancer

Table S1. Primer sequences used for MIR133A knock-in, qRT-PCR, luciferase assay and Taq-Man analysis in this study

Applications	Primers*	Primer sequence (5'→3')
Knock-In	MIR133A1-F	CACGGATCCCTAGCAGCACTACAATGC
	MIR133A1-R	CCGAAGCTTGTCCCCTAGTAATCAATGCATA
	MIR133A2-F	TATGGATCCTCCGACGTCGCTGTTC
	MIR133A2-R	TATAAGCTTCACGGCTGCGGGACCT
qRT-PCR	SOX9-QF1	CGAACAGATGGCCGAGATGATCC
	SOX9-QR1	GGATAGGTCATGTTGTGTCTGG
	GAPDH-F	CAATGACCCCTTCATTGACC
	GAPDH-R	GACAAAGCTTCCCCTTCAG
Luciferase assay	SOX9-WF	CGACGAGCTCCTCACCTACATGAACC
	SOX9-WR	GCTGCTCAGGTTGCCTTAGCTTAAATGTC
	SOX9-MF	CCGAAGAAAAGAGACCAGAATTCCCTTG
	SOX9-MR	CCAAAGGGAATTCTGGTCTTTCTCGG
Taq-Man analysis	Hsa-mir-133A	ID: PM10413 (Applied Biosystems)
	RNU48	GATGACCCAGGTAACTCTGAGTGTGTCGC TGATGCCATACCGCAGCGCTCTGACC

*QF: quantitative forward primer; QR: quantitative reverse primer; WF: forward primer for wild-type constructs; WR: reverse primer for wild-type constructs; MF: forward primer for mutant-type constructs; MR: reverse primer for mutant-type constructs.

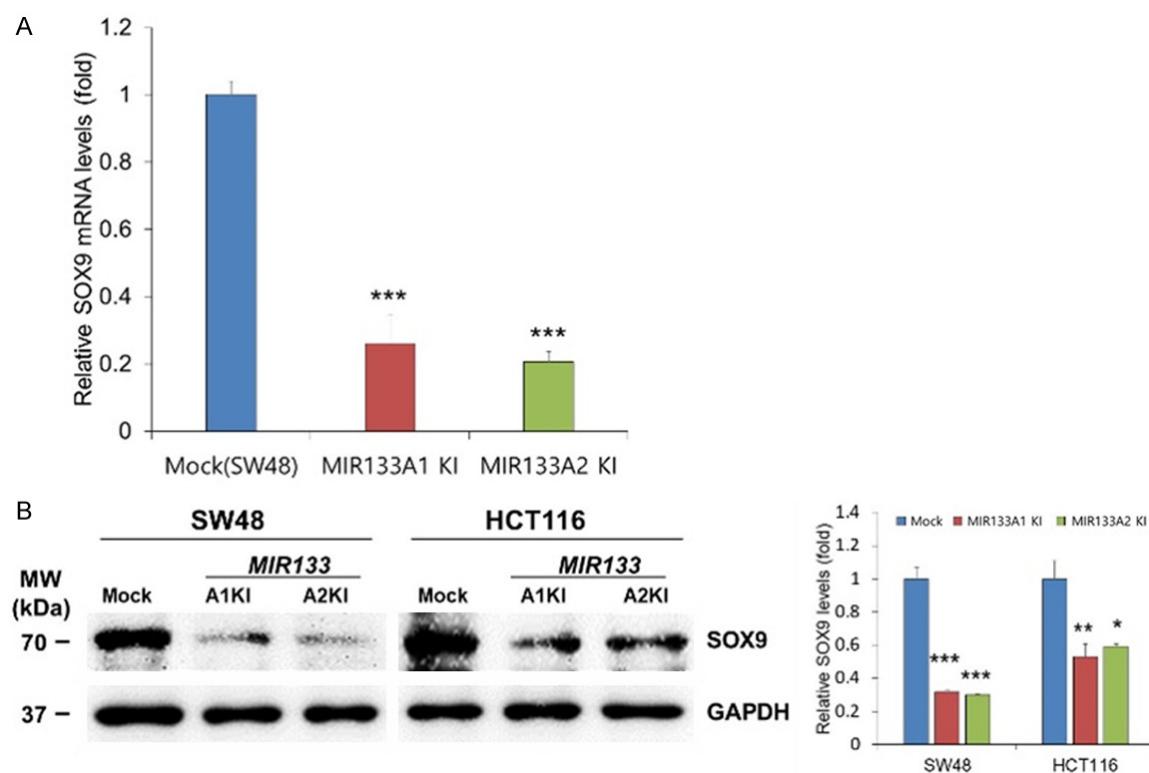


Figure S1. SOX9 mRNA and protein levels and MIR133A1 and A2 KI cell lines. A. qRT-PCR analysis of SOX9 mRNA expression in MIR133A1 and A2 KI SW48 cells relative to mock cells. B. Western blot analysis of SOX9 in MIR133A1 and A2 KI SW48 and HCT116 cells. Differences were considered statistically significant *P<0.05, **P<0.01, ***P<0.001 compared with control.

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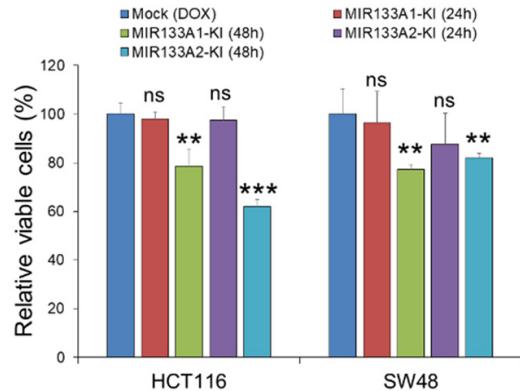


Figure S2. Cell proliferation in MIR133A1 and A2 KI cell lines. MTT assays of mock and MIR133A1 and A2. Representative data from at least three independent experiments are shown. Each bar represents mean fold alternation above or below control (\pm SD). Differences were considered statistically significant ** $P<0.01$, *** $P<0.001$ compared with control (ns = not significant).