MicroRNA 196B regulates FAS-mediated apoptosis in colorectal cancer cells

Supplementary Material

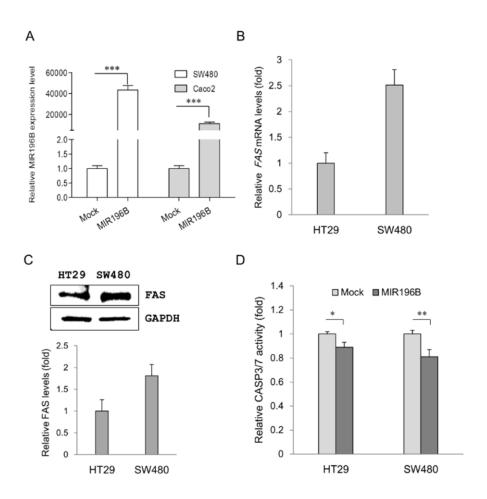


Figure S1: MIR196B transfection efficiency, FAS levels in colon cancer cell lines, and CASP3/7 levels by MIR196B

(A) SW480 or Caco2 cells were transfected with MIR196B. Cells were collected at 24 h to confirm the transfection efficiency. Data assessed from three independent experiments and the P values were calculated by t-test (*** P < 0.001). (B) qRT-PCR analysis and (C) western blot analysis in SW480 and HT29 cells. (D) MIR196B regulated caspase 3/7 activities in SW480 and HT29 cells. At 48 h after transfection of MIR196B, there were significantly decreased in caspase 3/7 activities compared to mock conditioned cells, respectively. The P values were calculated by t-test (* P < 0.05; ** P < 0.01).

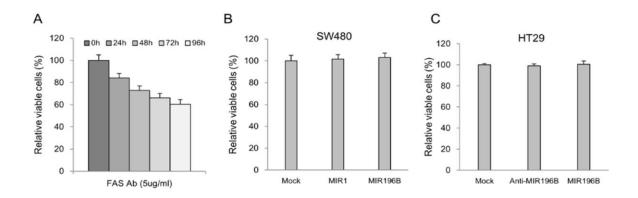


Figure S2: The effect of MIR196B on cell proliferation in human colon cancer cells

(A) SW480 cells (2×10^4 cells/ well) were cultured with FAS mAb (5 µg/ml) for 96 h. Cells were collected at 24 h intervals for the MTT assay. SW480 cells (B) or HT-29 cells (C) were transfected with 50 nM MIR196B, anti-MIR196B, or MIR1 in a 48-well plate and grown for 72 h. The relative proliferation of cells transfected with each miRNA precursor was compared with the proliferation of mock-transfected control cells.

Table S1: MIR196B candidate target genes identified by mRNA microarray analysis

Gene symbol	Accession	Gene name	Chromosome
			location
AIF1L	NM_031426.2	allograft inflammatory factor 1-like	9q34.13
ANKDD1A	NM_182703.3	ankyrin repeat and death domain containing 1A	15q22.31
ANXA1	NM_000700.1	annexin A1	9q21.13
APEX2	NM_014481.2	APEX nuclease 2	Xp11.21
ATP6V0B	NM_004047.3	ATPase, H+ transporting, lysosomal 21kDa, V0 subunit b	1p32.3
B3GALT6	NM_080605.3	UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 6	1p36.33
BTG3	NM_006806.3	BTG family, member 3	21q21.1
C14orf109	NM_015676.1	transmembrane protein 251	14q32.12
C7orf23	NM_024315.2	transmembrane protein 243, mitochondrial	7q21.12
C7orf55	NM_197964.3	chromosome 7 open reading frame 55	7q34
C7orf59	NM_001008395.2	late endosomal/lysosomal adaptor, MAPK and MTOR activator 4	7q22.1
CCDC72	NM_015933.3	translation machinery associated 7 homolog	3p21.31
CCND3	NM_001760.2	cyclin D3	6p21
CTSZ	NM_001336.2	cathepsin Z	20q13.32
DDX26B	NM_182540.3	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	Xq26.3
DIRAS2	NM_017594.3	DIRAS family, GTP-binding RAS-like 2	9q22.2
DLX1	NM_001038493.1	distal-less homeobox 1	2q32
EEF1A1	NM_001402.5	eukaryotic translation elongation factor 1 alpha 1	6q14.1
FAS	NM_152877.1	cell surface death receptor	10q24.1
GLRX	NM_002064.1	glutaredoxin (thioltransferase)	5q14
GLTP	NM_016433.3	glycolipid transfer protein	12q24.11
H3F3B	NM_005324.3	H3 histone, family 3B	17q25.1

HADH	NM 005327.2	hydroxyacyl-CoA dehydrogenase	4q22-q26
HAND1	NM 004821.1	heart and neural crest derivatives expressed 1	5q33
HBXIP	NM 006402.2	late endosomal adaptor, MAPK and MTOR activator 5	1p13.3
HNRPDL	NR 003249.1	heterogeneous nuclear ribonucleoprotein D-like	4q21.22
HOXA5	NM 019102.2	homeobox A5	7p15.2
HOXA9	NM 152739.3	homeobox A9	7p15.2
HOXB6	NM 018952.4	homeobox B6	17q21.3
HOXB7	NM 004502.3	homeobox B7	17q21.3
HOXC8	NM 022658.3	homeobox C8	12q13.3
HSD17B10	NM_004493.2	hydroxysteroid (17-beta) dehydrogenase 10	Xp11.2
IFI6	NM 022873.2	interferon, alpha-inducible protein 6	1p35
KCNIP3	NM_013434.4	Kv channel interacting protein 3, calsenilin	2q21.1
LAGE3	NM_006014.3	L antigen family, member 3	Xq28
LOC100132805	XM 001719188.1	Homo sapiens similar to predicted protein	chr. 3
LOC400455	XR 018793.1	Homo sapiens hypothetical LOC400455	chr. 15
LOC645058	XM_930423.1	similar to hepatitis B virus x-interacting protein (LOC645058)	Chr. 1
LRRC49	NM 017691.2	leucine rich repeat containing 49	15q23
MED10	NM 032286.2	mediator complex subunit 10	5p15.31
MRPL39	NM_017446.3	mitochondrial ribosomal protein L39	21q21.3
MYBBP1A	NM 014520.2	MYB binding protein (P160) 1a	17p13.3
NHP2	NM 001034833.1	NHP2 ribonucleoprotein	5q35.3
NOTCH1	NM 017617.3	notch 1	9q34.3
NUDT22	NM 032344.1	nudix (nucleoside diphosphate linked moiety X)-type motif 22	11q13.1
OSBPL8	NM_001003712.1	oxysterol binding protein-like 8	12q14
PABPC4	NM 003819.2	poly(A) binding protein, cytoplasmic 4	1p34.2
PDE6D	NM 002601.2	phosphodiesterase 6D, cGMP-specific, rod, delta	2q35-q36
PHLDA2	NM 003311.3	pleckstrin homology-like domain, family A, member 2	11p15.4
PPP1CB	NM 206876.1	protein phosphatase 1, catalytic subunit, beta isozyme	2p23
PRKAG2	NM 024429.1	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	7q36.1
RASL11B	NM_023940.2	RAS-like, family 11, member B	4q12
RBP1	NM 002899.2	retinol binding protein 1, cellular	3q23
RNASEH2A	NM 006397.2	ribonuclease H2, subunit A	19p13.2
S100A3	NM_002960.1	S100 calcium binding protein A3	1q21
S100A4	NM 019554.2	S100 calcium binding protein A4	1q21
SCNN1A	NM 001038.4	sodium channel, non-voltage-gated 1 alpha subunit	12p13
SERBP1	NM 001018069.1	SERPINE1 mRNA binding protein 1	1p31
SPRED1	NM 152594.1	sprouty-related, EVH1 domain containing 1	15q14
TGFB1I1	NM 015927.3	transforming growth factor beta 1 induced transcript 1	16p11.2
TMEM2	NM 013390.1	transmembrane protein 2	9q21.13
TNNC1	NM 003280.1	troponin C type 1	3p21.1
TPD52	NM_005079.2	tumor protein D52	8q21.13
TSPO	NM 000714.4	translocator protein (18kDa)	22q13.31
UFSP1	NM 001015072.3	UFM1-specific peptidase 1	7q22.1
VSNL1	NM 003385.4	visinin-like 1	2p24.3
, D. 1D.	1.171_005505.7	zinc finger protein 512	2p23

Table S2: Primer sequences used for qRT-PCR analysis and luciferase assays in this study

Applications	Primers	Primer sequence $(5' \rightarrow 3')$
qRT-PCR	FAS-QF1	ATGGCCAATTCTGCCATAAG
	FAS-QR1	GACAAAGCCACCCCAAGTTA
Luciferase	FAS-LF1	CAGCTCGAGCTACCTCAAAGACCTTTGCAC
assay	FAS-LR1	CAGCTCGAGTATTTCCATGTTTGGGGGTGC
	FAS-LF2	CTGAGAAAGAAGTGAGCCAGTAAAA
	FAS-LR2	TTTTACTGGCTCACTTCTTTCTCAG