down-regulat	ted		
miRNAs	function [†]	cancer	roles [representative target]
miR-34a	TS	prostate cancer (1)	inhibits clonogenic expansion, tumor regeneration, and metastasis [CD44]
miR-210	TS	head & neck and pancreatic cancer (2)	regulates the hypoxic response of tumor cells and tumor growth
miR-326	TS	medullobalstoma (3)	induces differentiation, cell maturation and growth inhibition
miR-224	TS	ovarian cancer (4)	inhibits cell proliferation
miR-193a	TS	acute myeloid leukemia (5)	induces growth inhibition, apoptosis and differentiation [c-KIT]
miR-370	TS	cholangiocarcinoma (6)	down-regulated by IL-6 [MAP3K8]
miR-331	-	-	
miR-183	TS	pancreatic and colorectal cancer (7)	suppresses expression of stem cell factors in cancer cells
	OG	rhabdomyosarcoma, and colon cancer (8)	promotes tumor cell migration [EGR1]
miR-96	TS	pancreatic cancer (9)	inhibits Akt signaling and induces apoptosis [KRAS]
	OG	breast cancer (10)	[FOXO1]
miR-182	OG	breast cancer (10)	[FOXO1]
miR-141	TS	breast cancer (11)	suppresses EMT [ZEB1]
miR-200b	TS	breast cancer (11)	suppresses EMT [ZEB1]
miR-200c	TS	breast cancer (11)	suppresses EMT [ZEB1]
miR-200a	TS	breast cancer (11)	suppresses EMT [ZEB1]
miR-206	TS	rhabdomyosarcoma (12)	inhibits cell proliferation and migration [c-MET]
miR-148a	TS	gastric cancer (13)	suppresses tumor cell invasion and metastasis [ROCK1]
miR-605	-		
miR-126	TS	lung cancer (14)	inhibits proliferation by inducing G1 cell cycle arrest
miR-658	-		
miR-92b	-		
miR-467a	-		
miR-297	-		
miR-466	-		
miR-203	TS	pancreatic and colorectal cancer (7)	suppresses expression of stem cell factors in cancer cells
miR-429	TS	breast cancer (11)	suppresses EMT [ZEB1]
miR-516-5p	-		
miR-555	-		
up-regulated			
miRNAs	function	cancer	roles [representative target]
miR-470	-		
miR-581	-		
miR-542-3p	TS	colon cancer (15)	inhibits cell proliferation by inducing cell cycle arrest [BIRC5]
miR-351	-	· · · · · · · · ·	
miR-503	TS	hepatocellular carcinoma (16)	inhibits proliferation, migration and invasion
miR-324-5p	TS	medullobalstoma (3)	induces differentiation, cell maturation and growth inhibition
miR-181a*	-		
miR-140*	-		
miR-142-5p	TS	lung cancer (17)	represses lung cancer cell growth
miR-181b	OG	hepatocellular carcinoma (18)	induced by TGFβ, enhances MMP2/9 activity and promoted growth, clonogenic survival, migration and invasion [TIMP3]
	TS	glioma (19)	induces growth inhibition and apoptosis, and inhibits invasion
miR-99a	TS	prostate cancer (20)	induces growth inhibition
miR-181a	TS	glioma (19)	induces growth inhibition and apoptosis, and inhibits invasion
miR-614	-		

Supplemental Table 1. MicroRNAs regulated by ZEB1.

miR-181d	OG	hepatocellular carcinoma (18)	induced by TGFβ, enhances MMP2/9 activity and promoted growth, clonogenic survival, migration and invasion [TIMP3]
miR-298	-		
miR-10a	OG	pancreatic cancer (21)	promotes metastasis [HOXB1/B3]
miR-344	-	-	
miR-185	TS	ovarian cancer (22)	inhibits cell migration and tumor growth in vivo [SIX1]
miR-181c	-		

[†]TS: tumor suppressive, OG: oncogenic microRNAs

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Supplemental table 2. Q-PCR primers

murine gene	forward $(5' \rightarrow 3')$	reverse (5'→3')
Acbd3	AAACGTCCCAGCGTTGCCCTG	ACAGACAGCAATGCGCCCTCC
Acsl4	GTGAAGGCTCTGCTGGGAGGGA	GCGCCGCCAGACAGCATCAT
Adam10	GCGGTTAACCCGTGAGGAGGC	GTCGGCAACACCATCTTCCCCG
Adam17	AGAAGGTTTCCCAGAGAGGTGGTGG	GGAGACGCCGCCTCATGTTCC
Bmp7	CCGTAGTATCCGGTCCACGGGG	GGAGCGATTCTGGCTGCGCT
Cdc42	CGGAGAAGCTGAGGACAAGATCT	CACCATCACCAACAACAACAACACT
Cdh1	TACGGCGGTGGTGAGGACGA	GCCACACGGGGGGGAGACTTGC
Chd2	CCTCCAGAGTTTACTGCCATGAC	CCACCACTGATTCTGTATGCCG
Clcn3	TTCAGCGGGTCAGGGCTGGT	CTGGCGAGGTGACAGCCGAG
Crb3	CGGACCCTTTCACAAATAGCA	CGTTGGACTCATCACCTGGG
Ctnnb1	GCCATCTTAAGCCCTCGCTCGG	CACAGGACACGAGCTGACGCG
DNn63	TTGTACCTGGAAAACAATG	GCATCGTTTCACAACCTCG
E2f5	CGTTGCTGCAGGAGGCGCA	GCAGCCGCTTTGAGATCCAGGAC
E2f8	GGGGGTCAAGATCCCAAAGCCCT	CTAAGCGCACGACCGGGCAT
Galant7	GGAGCATGGGACTGGAGTATGCTCT	CGAGAGGTCAGAGGCACCCGT
Gmfh	AAGGGGCCCAAGAGATCGCACG	TCCTTCCGGTCGTCAGCGGC
Hifla	ACAAGCCGGGGGGGGGGGGGGGGGGG	AGCACCTTCCACGTTGCTGACT
Hsnhl	CACGCAGTCAGCGGAGATCACC	GGCGCGGGCCTCGAAAGTAA
Itoav	CACCTGGGGCATTCAGCCGG	GATCACCCACACAGGCACAGGC
Lenr	TCCCAGCAGCTATGGTCTCCCTT	TGCTTTCAGGGTCTGGTGTGGTC
Marcks	GTGGCCTCGTCGCCTTCCAAA	TTACGTGGCCATTCTCCTGCCCA
Plk4	CCTCCTGTGGACCCAAGCTGC	TGCTTGCTGACGCCTGCTCT
Prn	GGACGAGCTCATGGCGTCACT	ТСССТБСССАТСААСТТСААА
$Rn^{1}32(I32)$	GGAGAAGGTTCAAGGGCCAG	TGCTCCCATAACCGATGTTTG
Scrib	CCCAGGAAGGCCGTGGCAAG	GCCTCAGCCAGCCGTTCCAA
Smad3	AGAGGGAACCGGCACTGCTCA	GTGTGCCTCCAGAAGCCGCC
Smail	CCCAAGGCCGTAGAGCTGA	GCTTTTGCCACTGTCCTCATC
Snai?	ATCCTCACCTCGGGGGGGGGATA	TGCCGACGATGTCCATACAG
T	ATCCACCCAGACTCGCCCAATT	CTCTCACGATGTGAATCCGAGG
T T2	TCCACCTCCCTTGCTAACATGG	CTCTTGGTGGAACATCTGCCTG
TAn63	TGTATCCGCATGCAAGACTC	CCGGGTAATCTGTGTTGGAG
Tofhr1	GCTGCCCCTGGCTCAGAGAC	AGGCTGGAGGTGGGGTCAGGA
Tshzl	AGGTCACCAATGGCTGCGGC	CCGCCGAGTGGTCCGTGATG
Twistl	TCGACTTCCTGTACCAGGTCCT	CCATCTTGGAGTCCAGCTCG
Vcl	GCCTCAGATGCTGGTCGCTGG	CGGTTGGCCCGACGAGCAAT
Vim	GCGTGCGGCTGCTTCAAGAC	ATGGCGTCGGCCAGCGAGAA
Wifl	CGGAACCTGCCACGAACCCA	CGTGCCAGCCCTCTCGACAC
Zehl	GCTCAGCCAGGAACCCGCAG	TGGGCACCCTCTGCCACACA
Zeb?	AGGCGCGAGAGAGAAAGGGCAC	CCCGGTTCATCAGCAGCTCGG
human gene	forward $(5' \rightarrow 3')$	reverse $(5' \rightarrow 3')$
ARHGAP1	CACCACCGAGGGCATCTTCCG	CCGGACCACTTGGGTGTTGGC
CDH1	GACACACCCCCTGTTGGTGT	CAGCCATCCTGTTTCTCTTTCAA
CDH2	ATCTCGGGTCAGCTGTCGG	GGCTATCTGCTCGCGATCC
RPL32 (L32)	CCTTGTGAAGCCCAAGATCG	TGCCGGATGAACTTCTTGGT
SNAI2	TGTGTGGACTACCGCTGCTC	GAGAGGCCATTGGGTAGCTG
VIM	GGAACAGCATGTCCAAATCGA	GCCGTGAGGTCAGGCTTG
ZEB1	CACTGGTGGTGGCCCATTAC	TGCACCATGCCCTGAGG



Supplemental Figure 1. Ectopic *Zeb1* levels in 393P_ZEB1 cells relative to that of endogenous *ZEB1* levels in human lung cancer cells.

Q-PCR analysis of *Zeb1* mRNA levels. Results normalized on the basis of snoRNA-135. Mean±SD, n=3.



Supplemental Figure 2. ZEB1 down-regulates the expression of miR-34a but not miR-34b or miR-34c.

Q-PCR analysis of miR-34a, -34b, and -34c expression in KP cells with high ZEB1 (344SQ and 393P_ZEB1) or low ZEB1 (393P and 393P_vec). Mean±SD, n=3. P-value, two-tailed Student's t-test.



Supplemental Figure 3. ZEB1 down-regulates $\triangle Np63$ but not *TAp63* promoter activity. Luciferase activity in 393P cells co-transfected with ZEB1 (+ ZEB1) or empty (+ vec) expression vectors and pGL2 reporter plasmids subcloned with promoters from *TAp63* or $\triangle Np63$ genes or nothing (pGL2). Results expressed relative to pGL2 transfectants, which was set at 1.0. Mean±SD, n=3. P-value, two-tailed Student's t-test.



Supplemental Figure 4. $\Delta Np63\beta$ up-regulates the expression of miR-34a but not miR-34b or miR-34c.

Q-PCR analysis of miR-34a, -34b, and -34c levels. Results normalized on the basis of snoRNA-135. Mean±SD, n=3. P-value, two-tailed Student's t-test.



Supplemental Figure 5. 344SQ cells express primarily Δ Np63 isoforms, which bind to the miR-34a promoter.

(A) Q-PCR analysis of $\triangle Np63$ and TAp63 isoforms in 344SQ cells using primers that recognize all alternatively spliced variants (α , β , and γ) of $\triangle Np63$ and TAp63 gene transcripts. Values were normalized on the basis of *L32* levels. Mean±SD, n=3. (**B**) Binding of endogenous p63 to the miR-34a promoter in 393P cells (left bar graph) and mouse primary keratinocytes isolated from E18.5 day embryos (right bar graph). Graph denotes DNA amount at specific (p53/p63) and non-specific (NS) sites of the miR-34a promoter precipitated by anti-p63 antibody corrected for non-specific binding activity by IgG precipitation and expressed as % p63 bound. Mean±SD, n=3. P-values are indicated (two-tailed Student's t-test).



Supplemental Figure 6. Ectopic miR-34a expression induces apoptosis of 344SQ cells in anchorage-independent but not anchorage-dependent conditions.

(A) Western blot analysis of PARP and cleaved Caspase-3 in adherent $344SQ_vec$ and $344SQ_miR-34a$ cells cultured in the presence or absence of doxycycline (Dox). UV-irradiated (250 J/m², 24 h-incubation) $344SQ_vec$ cells were used as a positive control. Cleaved PARP band (arrow). ACTIN used as loading control. (**B** and **C**) $344SQ_vec$ and $344SQ_miR-34a$ cells were cultured in suspension on low-adhesion plates and counted (**B**) or subjected to western blot analysis of PARP (**C**) at day 2. Mean \pm SD, n=4. Cleaved PARP band (arrow). ACTIN used as loading control.



Supplemental Figure 7. miR-34a hairpin inhibitor enhances the migration and invasion of 393P cells.

(A) Q-PCR quantification of miR-34a in 393P cells transiently transfected with 100 nM of miRIDIAN[®] negative control (con) or miR-34a hairpin inhibitor (anti-34a). Migrating (**B**) and invading (**C**) cells in Boyden chambers were photographed (images) and counted (bar graphs). Scale bars=100 μ m. Mean±SD, n=3. P-values, two-tailed Student's t-test.



Supplemental Figure 8. miR-34a inhibits the migration and invasion of H1299 human lung cancer cells.

(A) Q-PCR quantification of miR-34a levels in H1299 cells transiently transfected with 40 nM of Pre-miRTM negative control (con) or Pre-miR-34a (miR-34a). Mean±SD, n=3. Migrating (**B**) and invading (**C**) cells in Boyden chambers were photographed (images) and counted (bar graphs) (Scale bars=100 μ m. Mean±SD, n=3. P-values, two-tailed Student's t-test. (**D** and **E**) To exclude the possibility that the reduced migration and invasion was a consequence of apoptosis or reduced proliferation, H1299 cells and MDA-MB-231 cells were transiently transfected with 40 nM of Pre-miRTM negative control (con) or Pre-miR-34a (miR-34a), seeded in equal numbers onto 24-well plates, and subjected to western blot analysis of PARP (**D**) or counted (**E**) after 24 hrs. UV-irradiated (250 J/m², 24 h-incubation) H1299 cells were used as a positive control for PARP cleavage (arrow). ACTIN used as loading control. Mean±SD, n=4.



Supplemental Figure 9. Global mRNA profiling of tumors.

Heat map depiction of 805 mRNAs up- or down-regulated in 344SQ_miR-34a (miR-34a) tumors, using 344SQ_vector tumors (vec) as the reference. Scale bar at bottom.

Symbol	Gene Title	fold [†]	P-value
Wifl	Wnt inhibitory factor 1	15.1446	0.00471
Hspb1	Heat shock protein 1	10.1599	0.03498
Lepr	Leptin receptor	7.2687	0.00152
Marcks	Myristoylated alanine rich protein kinase C substrate*	0.6462	0.00152
Clcn3	Chloride channel 3*	0.6321	0.00123
Galnt7	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N- acetylgalactosaminyltransferase 7*	0.6273	0.00320
Tshzl	Teashirt zinc finger family member 1*	0.6257	0.00689
Hifla	Hypoxia inducible factor 1, alpha subunit	0.6018	0.00080
Cdc42	Cell division cycle 42 homolog	0.5862	0.00056
Smad3	MAD homolog 3	0.5855	0.00171
Adam17	A disintegrin and metallopeptidase domain 17	0.5770	0.00131
E2f5	E2F transcription factor 5*	0.5487	0.00086
Vcl	Vinculin*	0.5350	0.00155
Adam10	A disintegrin and metallopeptidase domain 10	0.5348	0.00196
Acsl4	Acyl-CoA synthetase long-chain family member 4*	0.5142	0.00097
Pxn	Paxillin	0.4999	0.00364
Ctnnb1	Catenin (cadherin associated protein), beta 1	0.4805	0.00163
Plk4	Polo-like kinase 4	0.4745	0.00063
Acbd3	Acyl-Coenzyme A binding domain containing 3*	0.4724	0.00081
E2f8	E2F transcription factor 8	0.4452	0.00185
Itgav	Integrin alpha V	0.4448	0.00306
Bmp7	Bone morphogenetic protein 7	0.4377	0.00173
Tgfbr1	Transforming growth factor, beta receptor I	0.4322	0.00059
Gmfb	Glia maturation factor, beta*	0.3683	0.00288

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Supplemental Figure 10. Q-PCR confirmation of mRNAs up- or down-regulated in microarrays. (A) List of genes tested by Q-PCR analysis. [†]fold = miR-34a/vector; P-values, two-tailed Student's t-test; *putative miR-34a targets from TargetScan. (B) Q-PCR analysis of mRNAs in 344SQ_vector (vec) and 344SQ_miR-34a (miR-34a) tumor samples. Mean±SD, n=3 RNA samples. Results expressed relative to that of 344SQ_vector, which was set at 1.0. *p<0.01, **p<0.05 (two-tailed Student's t-test).

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Supplemental Figure 11. miR-34a down-regulates ARHGAP1 expression.

(A) Western blot analysis of ARHGAP1 and ACTIN in 393P cells transiently transfected with 100 nM of miRIDIAN[®] negative control (con) or miR-34a hairpin inhibitor (anti-34a). Densitometric analysis of ARHGAP1 protein levels normalized to those of ACTIN and expressed relative to control transfectants, which was set at 1.0. (B) Q-PCR analysis of *ARHGAP1* mRNA levels in H1299 human lung cancer cells 72 hrs after transient transfection with Pre-miRTM negative control (con) or Pre-miR-34a (miR-34a). Results normalized on the basis of mRNA for ribosomal protein *L32*. Mean±SD, n=3. P-value, two-tailed Student's t-test.

Full uncut blots-1













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Full uncut blots-2







Full uncut blots-3







