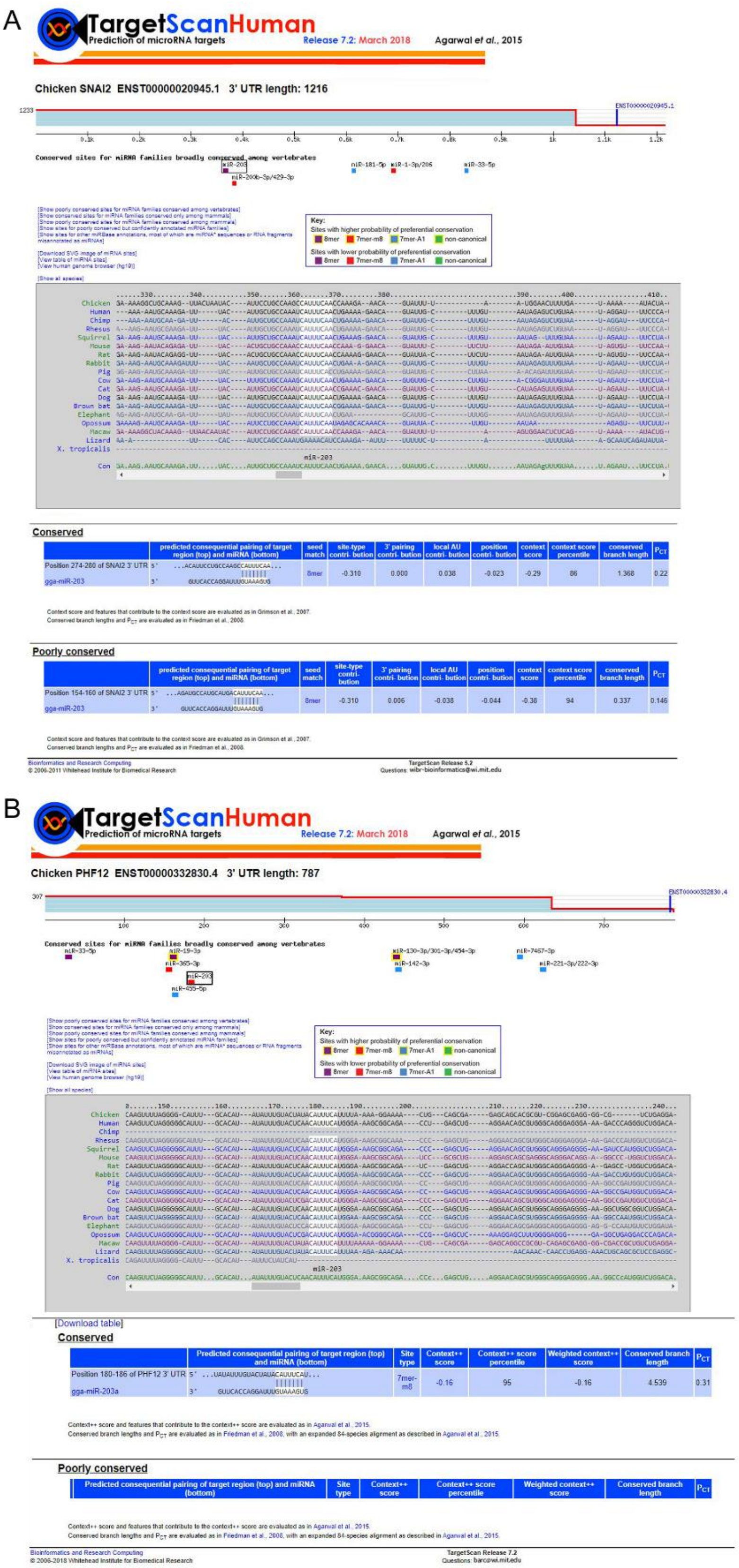


**Figure S1.** TargetScan results for miR-203 binding sites on (A) Snail2 and (B) Phf12 3'UTRs. We want to highlight that Snail2 3'UTR has 2 binding sites, one conserved and other poorly conserved, while Phf12 3'UTR have only one conserved site.

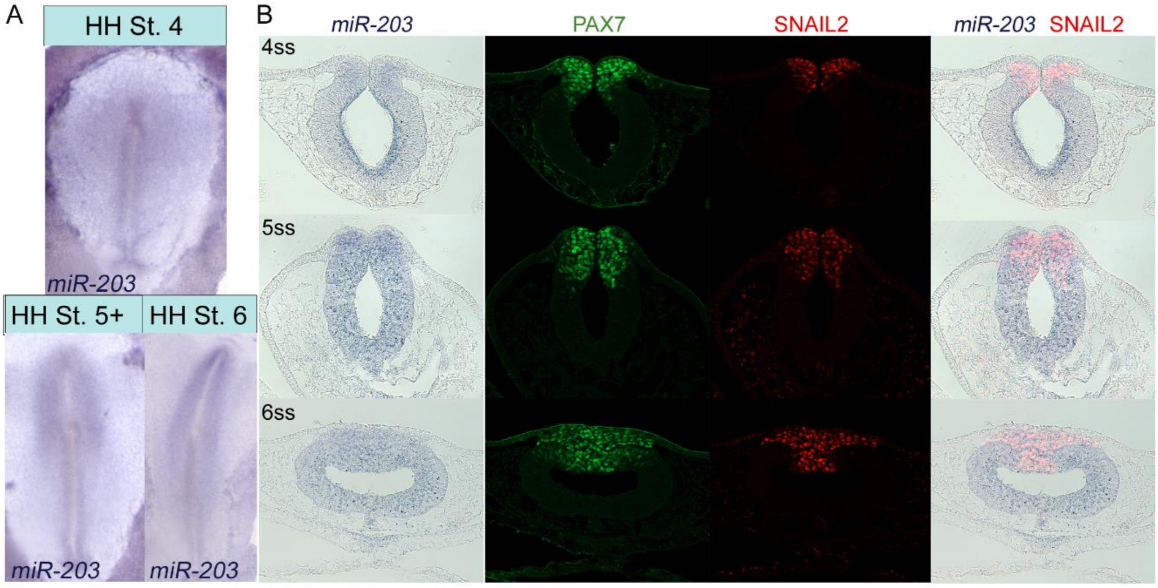


**Figure S2.** (A) Whole-mount *in situ* hybridization using DIG-labeled LNA probes (Exiqon) against miR-203 at early chick developmental stages. (B) miR-203 is present in the pre-migratory neural crest from 4ss (somites stage) until 6ss. miR-203 expression overlaps with well-known neural crest markers: Pax7 (green) and Snail2 (red).

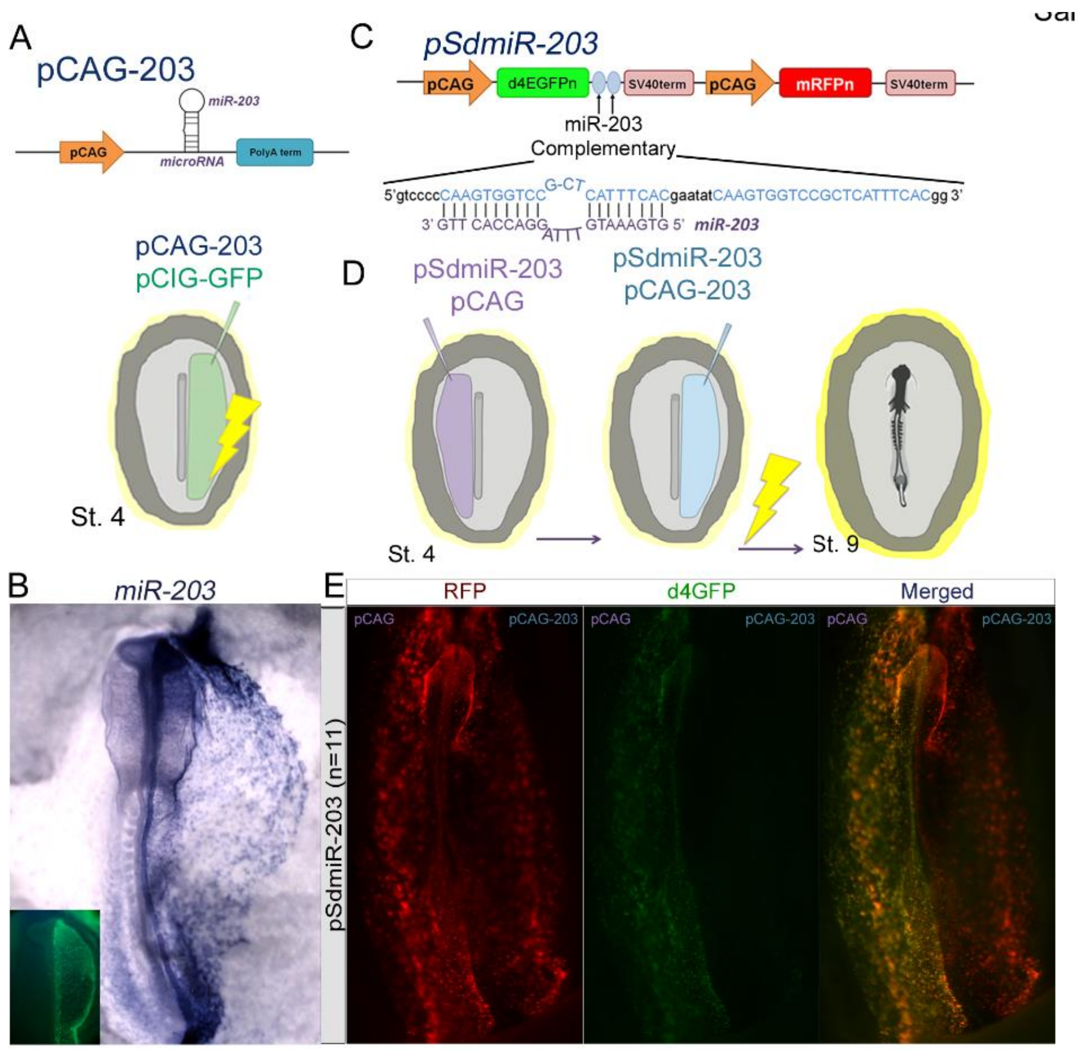


**Figure S3.** (A) Scheme of pCAG-203 vector to overexpress miR-203. Diagram of electroporation assay for gain-of-function experiments. pCAG-miR-203 does not have a fluorescent marker, for this reason, was co-electroporated with a fluorescent vector that express GFP downstream the CAG promoter. We injected the vectors in the right side of the embryos at stage 4. Following injection, embryos were electroporated and cultured until stage 9. (B) Electroporation of pCAG-203 vector (right side) successfully overexpress a mature miR-203 evidenced by *in situ* hybridization using LNA probes. (C) Schematic drawing of the miRNA dual-sensor vector (pSdmiR-203) containing two copies of complementary sequences to the mature miR-203. (D) Illustration of bilateral electroporation assay to evaluate if pCAG-203 express a functional miR-203. (E) Co-electroporation pSdmiR-203 and the empty pCAG vector (left side) caused that most of the cells are yellow because of the expression of both green and red reporters. Whereas, co-electroporation pSdmiR-203 and pCAG-203 vector (right side) caused that most of the cells are only red, because of the strong repression of the green reporter. pCAG, Chick β-actin promoter; $d4EGFP_N$ nuclear-localized destabilized EGFP with a half-life of 4 h; $mRFP_N$, nuclear-localized monomeric red fluorescent protein.

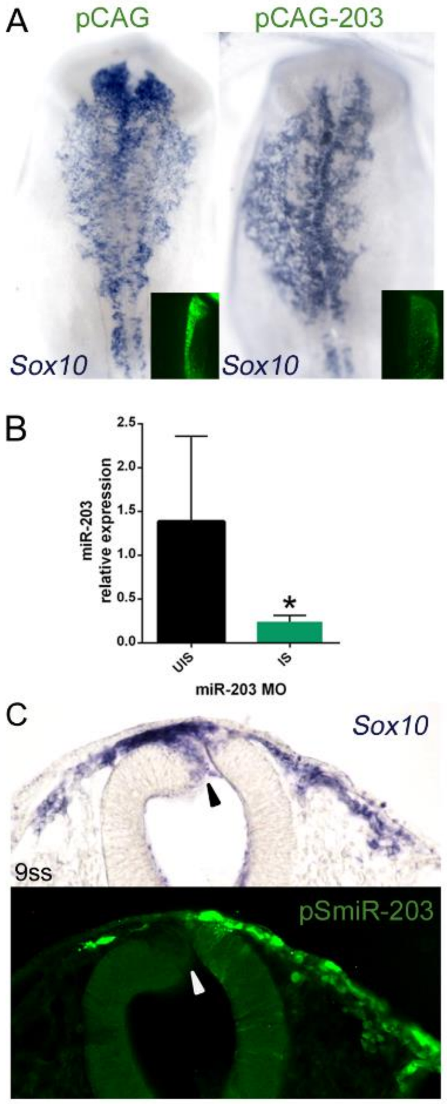


**Figure S4.** (A) miR-203 overexpression causes inhibition of neural crest migration. *In situ* hybridization for *Sox10* confirms that inhibition of NCC migration is caused by pCAG-203. (B) Real time qPCR confirm morpholino-mediated loss of miR-203 (miR-203 MO) on the IS compared with the UIS of the same group of embryos (n=6). Asterisk (*) indicate significant differences (P<0.05) by Student's t-test. (C) Neural crest cells from the sponge IS complete their delamination in advance compare with the UIS where many Sox10 expressing cells are still on the neural tube (see black arrowhead).

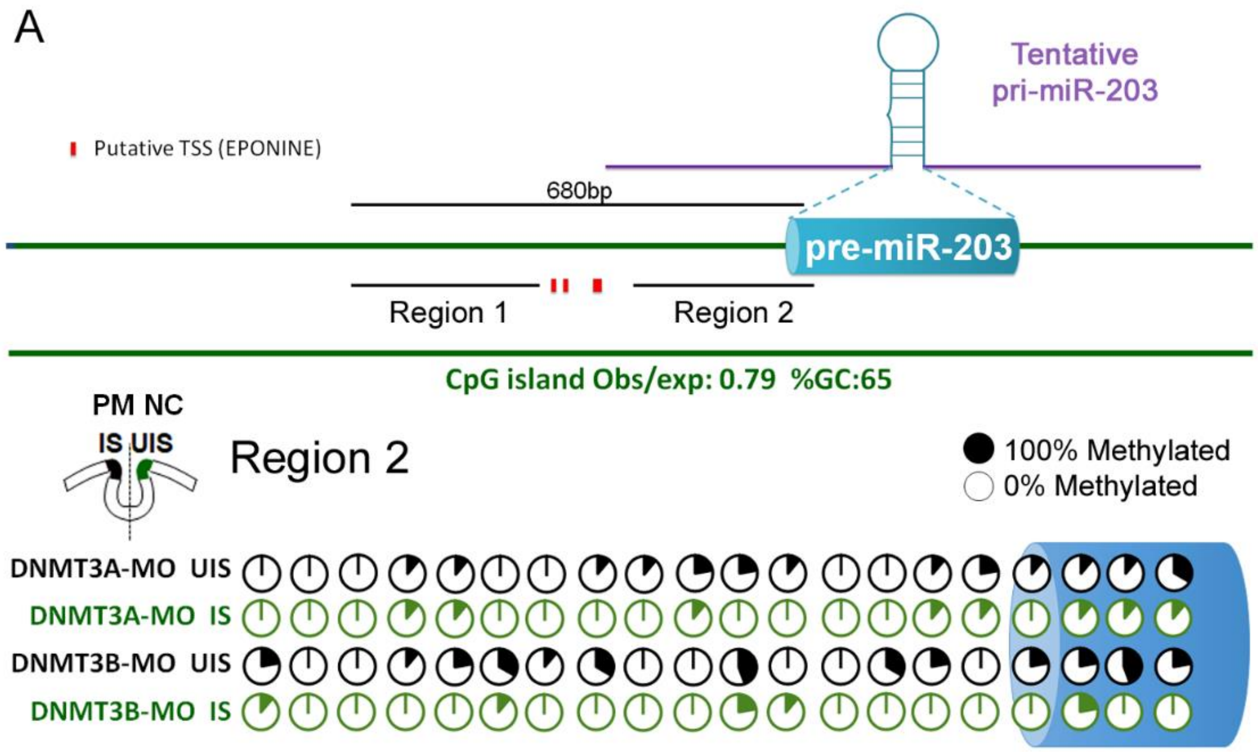


**Figure S5.** Bisulfite sequencing profiles of CpGs methylation on the region 2 on the injected side (IS) compared with the uninjected side (UIS) of the same group of embryos (n=6) electroporated with morpholinos against DNMT3A (DNMT3A-MO) and DNMT3B (DNMT3B-MO). Independent clones (n=10) were sequenced for each sample. Percentage of each methylated CpG sites are shown with filled (100% methylated) and open (0% methylated) circles. Total percentage of methylation in each condition is normalized with the UIS to make graphs in figure 5 F.

**Table S1.** *In silico* analyzes of conserved and poorly conserved microRNA-binding sites on Snail2 and Phf12 3'UTRs (TargetScan), their known functions, demonstrated targets, and chick expression (GEISHA).

**GEISHA microRNAs expression in chick development**
http://geisha.arizona.edu/geisha/quick_search.jsp?table=mir

**miR-1** (Heidersbach et al. 2013; Wystub et al. 2013; Wei et al. 2014)

**miR-19** (Olive et al. 2009; Mavrakis et al. 2010; Liu et al. 2011)

**miR32-5p/92-3p/367** (Zhu et al. 2013; Zhu et al. 2015; Sharifi and Salehi 2016)

**miR-33-5p** (Mi et al. 2016; Wang et al. 2016)

**miR130-3p/301-3p/454-3p** (Leone et al. 2015; Xia et al. 2015; Egawa et al. 2016; Lv et al. 2016)

**miR-142** (Lu et al. 2013; Sonda et al. 2013; Borges et al. 2016; Dickman et al. 2017)

**miR-155** (Gracias et al. 2013; Robertson et al. 2014; Forzati et al. 2017)

**miR-181-5p** (Korhan et al. 2014; Li et al. 2015; Ma et al. 2015)

**miR-200b-3p/429-3p** (Ye et al. 2014; Wu et al. 2016; Gui et al. 2017)

**miR-203**(Yi et al. 2008; Wei et al. 2010; Zhang et al. 2011; Benaich et al. 2014; Shi et al. 2015)

**miR-221-3p/222-3p** (Takigawa et al. 2016; Yan et al. 2016; Wu et al. 2017)

**miR-365-3p** (Wang et al. 2013; Gastaldi et al. 2014)

**miR-455-5p** (Chai et al. 2015; Li et al. 2016; Liu et al. 2016)

| | | Conserved sites | | | Poorly conserved sites | | | | | Known function | Known Target Gene | Reference | Expression (GEISHA) Stages 3-25 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | 8mer | 7mer-m8 | 7mer-1A | 8mer | 7mer-m8 | 7mer-1A | 6mers | Pct | | | | |
| Phf12 | miR-19-3p | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0,85 | Oncogene | Pten,Bim,TNF-α | Olive et al. 2009; Mavrakis et al. 2010; Liu et al. 2011 | Broadly expressed but at much reduced levels in the heart |
| | miR-130-3p /301-3p /454-3p | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0,77 | Oncogene | Coiled-coil domain-containing protein 6 (CCDC6), Smad4, Pten | Leone et al. 2015; Xia et al. 2015; Egawa et al. 2016; Lv et al. 2016 | Hindbrain, spinal cord, widespread expression after stage 21 except in heart |
| | miR-365-3p | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0,41 | Tumor suppressor | KRAS, MAX, PAX6 | Wang et al. 2013; Gastaldi et al. 2014 | No expression detected until stage 14, extraembryonic, notochord, surface ectoderm, widespread expression after stage 19 |
| | miR-142-3p | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0,4 | Tumor suppressor, hematopoietic development | Interferon regulatory factor 7 ( Irf7 ), interleukin 6 signal transducer (IL6st), transforming growth factor beta receptor 1(TGFBR1) | Lu et al. 2013; Sonda et al. 2013; Borges et al. 2016; Dickman et al. 2017 | No expression detected until stage 20, atria, sinus venosus |
| | miR-455-5p | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0,38 | Tumor suppressor | RAB18, ZEB1, RA F proto-oncogene serine/threonine-protein kinase (RAF1) | Chai et al. 2015; Li et al. 2016; Liu et al. 2016 | Unknown |
| | miR-221-3p /222-3p | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0,36 | Osteoblasts/ osteocytes develop | RUNX2, Smad5, tartrate-resistant acid phosphatase (TRAP), ADP-ribosylation factor 4(ARF4) | Takigawa et al. 2016; Yan et al. 2016; Wu et al. 2017 | No expression detected until stage 14, low level ubiquitous from stage 16-25 |
| | miR-33-5p | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0,32 | | | | |
| | miR-203 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0,31 | | | | |
| | miR-7467-3p | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0,24 | Unknown | Unknown | Unknown | Unknown |
| Snail2 | miR-1-3p/206 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0,72 | Cardiovascular development | ERβ1, myocardin, telokin | Heidersbach et al. 2013; Wystub et al. 2013; Wei et al. 2014 | Atria, heart, myocardium, myotome, somites, ventricles |
| | miR-181-5p | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0,47 | Tumor suppressor | KRAS,matrix metalloproteinase MMP-14, c-Met | Korhan et al. 2014; Li et al. 2015; Ma et al. 2015 | Ubiquitous |
| | miR-200b-3p /429-3p | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0,43 | Tumor suppressor | Zeb1, multiple members of RAB family, extracellular-regulated protein kina se 5 (ERK5) | Ye et al. 2014; Wu et al. 2016; Gui et al. 2017 | Surface ectoderm from stage 13-18, diverse expression before stage 20 |
| | miR-203 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0,38 | Skin development, tumor suppressor | p63, Snail2, LIM and SH3 domain protein 1 (LASP1) | Yi et al. 2008; Wei et al. 2010; Zhang et al. 2011; Benaich et al. 2014; Shi et al. 2015 | Ubiquitous after stage 15, no expression detected at stage 5 |
| | miR-33-5p | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0,31 | Osteoblasts/ osteocytes develop | Special AT-rich sequence-binding protein 2 (SATB2), high-mobility group AT-hook 2(HMGA2) | Mi et al. 2016; Wang et al. 2016 | No expression detected until stage 21, amnion, atria, extraembryonic |
| | miR-155 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0,23 | Oncogene | ELK3 (ETS Transcription Factor), several mRNAs | Gracias et al. 2013; Robertson et al. 2014; Forzati et al. 2017 | No expression detected stage 3-24 |
| | miR-32-5p /92-3p/367 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0,22 | Oncogene | Pten, Smad7, estrogen-related receptor β (ERβ1) | Zhu et al. 2013; Zhu et al. 2015; Sharifi and Salehi 2016 | Neural Plate/Tube, spinal cord, widespread expressión |

**Table S2.** Results obtained with the Jaspar 2018 (http://jaspar.genereg.net/) for SNAIL2 binding site in the tentative promoter of miR-203. High binding sites (>9) are mapped in figure 2A. We also show the sequence analyzed in Jaspar 2018.

| Matrix ID | Name | Score | Relative score | Sequence ID | Start | End | Strand | Predicted sequence |
|---|---|---|---|---|---|---|---|---|
| MA0745.1 | SNAI2 | 12,6931 | 0.999707221414 | miR_203_tentative_promoter | -1162 | -1153 | + | AACAGGTGC |
| MA0745.1 | SNAI2 | 9,71729 | 0.94034684341 | miR_203_tentative_promoter | -1552 | -1543 | + | GGCAGGTAC |
| MA0745.1 | SNAI2 | 8,48966 | 0.915858769456 | miR_203_tentative_promoter | -1089 | -1080 | - | CACAGGTTG |
| MA0745.1 | SNAI2 | 7,98092 | 0.905710714071 | miR_203_tentative_promoter | -1273 | -1264 | - | ATCAGGTTG |
| MA0745.1 | SNAI2 | 4,63965 | 0.839061031445 | miR_203_tentative_promoter | -1599 | -1590 | - | TGCATGTTT |
| MA0745.1 | SNAI2 | 3,94346 | 0.825173896668 | miR_203_tentative_promoter | -1527 | -1518 | + | TCAAGGTGT |
| MA0745.1 | SNAI2 | 3,5435 | 0.817195747557 | miR_203_tentative_promoter | -1199 | -1190 | - | TGGAGGTTG |
| MA0745.1 | SNAI2 | 3,51455 | 0.816618237138 | miR_203_tentative_promoter | -1293 | -1284 | + | AGAAAGTGA |
| MA0745.1 | SNAI2 | 3,24005 | 0.811142584031 | miR_203_tentative_promoter | -1082 | -1071 | + | TGCCAGTGC |

>miR_203_tentative_promoter Chr 5:50767590-50768212
AGGACTGGCTTGAGTTGCCTATATATTTATAAAGAGCCAAAGATCATAGGATCTGGAGTGCCAGAATTCATACACAGCACATATACAGCTCTTTAAACATGCAAAACACTCTATTAACATGA
GTGAAGCCTCATAAGATGAGGCAGGTACGCATTATCTCTCCTCCTCAAGGTGTGGCGAAGTGACTTGGTGAAGGCCTGAGGCTGAGTCGCTGGCAGAGCAGGGCCGACTATCCACAACTT
TCCTACACCACACAGGCTGCCCCGTCCCAGCATGGCAAAGCGTGAAGGCCTTCCCGTCCACCCCAGCAGCAGGGCTCCGAAAGCCCAGTGGGTTGTGTTTCATTCTTCTCCTATAGACAAAG
AGGGTGAAATATTAATGGAAGAAAGTCAAAATTCAGAGAAAGTGACTCCCGGCAAGCAACCTGATTTCTGGAAGTTCATGAAATCATACAATTGTTTGAGTTGGAAGGGACCCCTAAAGG
CCATCCAGTCCAACCTCCATGCAATAAGTAGGGACTCCCACGGCTCCAACAGGTGCTCAGAGCCCCGTCCAGCCTGACCTTGGCTGTCTCTAAGGACAGGGCACCCACCACATCTCTGGGCA
ACCTGTGCCAGTGCCTC

**Table S3.** Complete list of utilized primers, LNA probe, and morpholinos

| Gene/Direction | Sequence |
|---|---|
| **LNA Probe** | |
| dre-miR-203a(gga-miR-203) | CAAGTGGTCCTAAACATTTCAC |
| **RT-qPCR Primer Sequences** | |
| stem-loop-gga-miR-203 | GTCTCCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGGAGACCAAGTG |
| stem-loop-gga-miR-16 | GTCTCCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGGAGACCAAGTG |
| qPCR-gga-miR-203 Fwd | CCGGCGTGAAATGTTTAGG |
| qPCR-gga-miR-16 Fwd | CGCCGCTAGCAGCACGTAAA |
| qPCR-gga-miR-universal Rev | GAGGTATTCGCACCAGAGGA |
| qPCR-Snail2 Fwd | GCCAAACTACAGCGAACTGG |
| qPCR-Snail2 Rev | CGGAGAGAGGTCATTGGGTA |
| qPCR-Phf12-Fwd | CTGAGGAACCCTTGCAGAAG |
| qPCR-Phf12-Rev | AGAGTCCCAAAGCGAAGTCA |
| qPCR-HPRT1-Fwd | TGGTGAAAGTGGCCAGTTTG |
| qPCR-HPRT1-Rev | TCATTGTAGTCGAGGGCGTATC |
| **Bisulfite Primer Sequences** | |
| Proximal region | |
| P-miR-203 Fwd | AGGTAGTTTGGAAAAATTGGTTT |
| P-miR_203 Rev | CTCCTTTAAAAACATTACAACCC |
| PN-miR-203 Fwd | AAGTTTTGTTGTTGTTGTTATTTT |
| PN-miR-203 Rev | TAAACTATTAAAAACCACTACACCA |
| Distal region | |
| D-miR-203 Fwd | TTTATATTTGTTGAGGGGAAGG |

Development • Supplementary information

| | |
|---|---|
| D-miR-203 Rev | TTTCCAAACTACCTTCTCCCTA |
| DN-miR-203 Fwd | TTGTGTGAGGTTGGTAGTTAGG |
| DN-miR-203 Rev | ATCATCATCATCTAAAACAACCC |
| pCAG-miR-203 cloning | |
| XhoI-gga-miR-203 Fwd | AAACTCGAGCTCCGAGCTGAGAAGAATGG |
| EcoRV-gga-miR-203 Rev | AAAGATATCCGCGCACTACAAGCCTATTT |
| Sponge cloning | |
| miR-203 sponge Fwd | gtcccCAAGTGGTCCGCTCATTTCACgaatatCAAGTGGTCCGCTCATTTCACgg |
| miR-203 sponge Rev | gacccGTGAAATGAGCGGACCACTTGatattcGTGAAATGAGCGGACCACTTGgg |
| Scramble sponge Fwd | gtcccATCTAGCTGATCTAATCGAACaatatATCTAGCTGATCTAATCGAACgg |
| Scramble sponge Rev | gacccGTTCGATTAGATCAGCTAGATatattGTTCGATTAGATCAGCTAGATgg |
| pUTRs cloning | |
| Snail2-3'UTR Fwd | ACGCGTGTCATGCAGTCAATGTTTAC |
| Snail2-3'UTR Rev | GCTAGCTTTCACTTCACGCTTTCTTC |
| mutSnail2-3'UTR SITIO A Fwd | ATGCATGAGACCCGCAGTAGATCTAAACG |
| mutSnail2-3'UTR SITIO A Rev | GCGGGTCTCATGCATGGCATCTTTCCCC |
| mutSnail2-3'UTR SITIO B Fwd | CAAGCGACCCGCACCAAAGAAACAGTATTTTAATGG |
| mutSnail2-3'UTR SITIO B Rev | GGTGCGGGTCGCTTGGCAGGAATGTATTAGTAAC |
| Phf12-3'UTR SanDI Fwd | AAAGGGTCCCGAATTTGGAGGAAGGGAGCT |
| Phf12-3'UTR Rev | GCTAGCTACAGTGGAGCTAGCTGGCC |
| mutPhf12-3'UTR Rev | AAAACGCGTGCTGCTCTCGCTGCAGTTTTCCTTTTAAAAGCGGGTCTATAG |
| | |
| Morpholinos Sequences | |
| DNMT3A MO | TGGGTGTGTCACTGCTTTCCACCAT |
| DNMT3B MO | CGAGGCTCGTTACCATGCTCATCGC |
| SNAIL2 MO | TCTTGACCAG GAAGGAGC |
| miR-203 MO | GGTCAAGTGGTCCTAAACATTTCAC |

Benaich N, Woodhouse S, Goldie SJ, Mishra A, Quist SR, Watt FM. 2014. Rewiring of an epithelial differentiation factor, miR-203, to inhibit human squamous cell carcinoma metastasis. *Cell reports* **9**: 104-117.

Borges E, Jr., Setti AS, Braga DP, Geraldo MV, Figueira RC, Iaconelli A, Jr. 2016. miR-142-3p as a biomarker of blastocyst implantation failure - A pilot study. *JBRA assisted reproduction* **20**: 200-205.

Chai J, Wang S, Han D, Dong W, Xie C, Guo H. 2015. MicroRNA-455 inhibits proliferation and invasion of colorectal cancer by targeting RAF proto-oncogene serine/threonine-protein kinase. *Tumour biology : the journal of the International Society for Oncodevelopmental Biology and Medicine* **36**: 1313-1321.

Dickman CT, Lawson J, Jabalee J, MacLellan SA, LePard NE, Bennewith KL, Garnis C. 2017. Selective extracellular vesicle exclusion of miR-142-3p by oral cancer cells promotes both internal and extracellular malignant phenotypes. *Oncotarget*.

Egawa H, Jingushi K, Hirono T, Ueda Y, Kitae K, Nakata W, Fujita K, Uemura M, Nonomura N, Tsujikawa K. 2016. The miR-130 family promotes cell migration and invasion in bladder cancer through FAK and Akt phosphorylation by regulating PTEN. *Scientific reports* **6**: 20574.

Forzati F, De Martino M, Esposito F, Sepe R, Pellecchia S, Malapelle U, Pellino G, Arra C, Fusco A. 2017. miR-155 is positively regulated by CBX7 in mouse embryonic fibroblasts and colon carcinomas, and targets the KRAS oncogene. *BMC cancer* **17**: 170.

Gardiner-Garden M, Frommer M. 1987. CpG islands in vertebrate genomes. *Journal of molecular biology* **196**: 261-282.

Gastaldi C, Bertero T, Xu N, Bourget-Ponzio I, Lebrigand K, Fourre S, Popa A, Cardot-Leccia N, Meneguzzi G, Sonkoly E et al. 2014. miR-193b/365a cluster controls progression of epidermal squamous cell carcinoma. *Carcinogenesis* **35**: 1110-1120.

Gracias DT, Stelekati E, Hope JL, Boesteanu AC, Doering TA, Norton J, Mueller YM, Fraietta JA, Wherry EJ, Turner M et al. 2013. The microRNA miR-155 controls CD8(+) T cell responses by regulating interferon signaling. *Nature immunology* **14**: 593-602.

Gui Z, Luo F, Yang Y, Shen C, Li S, Xu J. 2017. Oridonin inhibition and miR200b3p/ZEB1 axis in human pancreatic cancer. *International journal of oncology* **50**: 111-120.

Heidersbach A, Saxby C, Carver-Moore K, Huang Y, Ang YS, de Jong PJ, Ivey KN, Srivastava D. 2013. microRNA-1 regulates sarcomere formation and suppresses smooth muscle gene expression in the mammalian heart. *eLife* **2**: e01323.

Korhan P, Erdal E, Atabey N. 2014. MiR-181a-5p is downregulated in hepatocellular carcinoma and suppresses motility, invasion and branching-morphogenesis by directly targeting c-Met. *Biochemical and biophysical research communications* **450**: 1304-1312.

Leone V, Langella C, Esposito F, De Martino M, Decaussin-Petrucci M, Chiappetta G, Bianco A, Fusco A. 2015. miR-130b-3p Upregulation Contributes to the Development of Thyroid Adenomas Targeting CCDC6 Gene. *European thyroid journal* **4**: 213-221.

Li Y, Kuscu C, Banach A, Zhang Q, Pulkoski-Gross A, Kim D, Liu J, Roth E, Li E, Shroyer KR et al. 2015. miR-181a-5p Inhibits Cancer Cell Migration and Angiogenesis via Downregulation of Matrix Metalloproteinase-14. *Cancer research* **75**: 2674-2685.

Li YJ, Ping C, Tang J, Zhang W. 2016. MicroRNA-455 suppresses non-small cell lung cancer through targeting ZEB1. *Cell biology international* **40**: 621-628.

Liu J, Zhang J, Li Y, Wang L, Sui B, Dai D. 2016. MiR-455-5p acts as a novel tumor suppressor in gastric cancer by down-regulating RAB18. *Gene* **592**: 308-315.

Liu M, Wang Z, Yang S, Zhang W, He S, Hu C, Zhu H, Quan L, Bai J, Xu N. 2011. TNF-alpha is a novel target of miR-19a. *International journal of oncology* **38**: 1013-1022.

Lu X, Li X, He Q, Gao J, Gao Y, Liu B, Liu F. 2013. miR-142-3p regulates the formation and differentiation of hematopoietic stem cells in vertebrates. *Cell research* **23**: 1356-1368.

Lv M, Zhong Z, Chi H, Huang M, Jiang R, Chen J. 2016. Genome-Wide Screen of miRNAs and Targeting mRNAs Reveals the Negatively Regulatory Effect of miR-130b-3p on PTEN by PI3K and Integrin beta1 Signaling Pathways in Bladder Carcinoma. *International journal of molecular sciences* **18**.

Ma Z, Qiu X, Wang D, Li Y, Zhang B, Yuan T, Wei J, Zhao B, Zhao X, Lou J et al. 2015. MiR-181a-5p inhibits cell proliferation and migration by targeting Kras in non-small cell lung cancer A549 cells. *Acta biochimica et biophysica Sinica* **47**: 630-638.

Mavrakis KJ, Wolfe AL, Oricchio E, Palomero T, de Keersmaecker K, McJunkin K, Zuber J, James T, Khan AA, Leslie CS et al. 2010. Genome-wide RNA-mediated interference screen identifies miR-19 targets in Notch-induced T-cell acute lymphoblastic leukaemia. *Nature cell biology* **12**: 372-379.

Mi W, Shi Q, Chen X, Wu T, Huang H. 2016. miR-33a-5p modulates TNF-alpha-inhibited osteogenic differentiation by targeting SATB2 expression in hBMSCs. *FEBS letters* **590**: 396-407.

Olive V, Bennett MJ, Walker JC, Ma C, Jiang I, Cordon-Cardo C, Li QJ, Lowe SW, Hannon GJ, He L. 2009. miR-19 is a key oncogenic component of mir-17-92. *Genes & development* **23**: 2839-2849.

Robertson ED, Wasylyk C, Ye T, Jung AC, Wasylyk B. 2014. The oncogenic MicroRNA Hsa-miR-155-5p targets the transcription factor ELK3 and links it to the hypoxia response. *PloS one* **9**: e113050.

Sharifi M, Salehi R. 2016. Blockage of miR-92a-3p with locked nucleic acid induces apoptosis and prevents cell proliferation in human acute megakaryoblastic leukemia. *Cancer gene therapy* **23**: 29-35.

Shi Y, Tan YJ, Zeng DZ, Qian F, Yu PW. 2015. miR-203 suppression in gastric carcinoma promotes Slug-mediated cancer metastasis. *Tumour biology : the journal of the International Society for Oncodevelopmental Biology and Medicine*.

Sonda N, Simonato F, Peranzoni E, Cali B, Bortoluzzi S, Bisognin A, Wang E, Marincola FM, Naldini L, Gentner B et al. 2013. miR-142-3p prevents macrophage differentiation during cancer-induced myelopoiesis. *Immunity* **38**: 1236-1249.

Takigawa S, Chen A, Wan Q, Na S, Sudo A, Yokota H, Hamamura K. 2016. Role of miR-222-3p in c-Src-Mediated Regulation of Osteoclastogenesis. *International journal of molecular sciences* **17**: 240.

Wang H, Sun Z, Wang Y, Hu Z, Zhou H, Zhang L, Hong B, Zhang S, Cao X. 2016. miR-33-5p, a novel mechano-sensitive microRNA promotes osteoblast differentiation by targeting Hmga2. *Scientific reports* **6**: 23170.

Wang J, Wang X, Wu G, Hou D, Hu Q. 2013. MiR-365b-3p, down-regulated in retinoblastoma, regulates cell cycle progression and apoptosis of human retinoblastoma cells by targeting PAX6. *FEBS letters* **587**: 1779-1786.

Wei T, Orfanidis K, Xu N, Janson P, Stahle M, Pivarcsi A, Sonkoly E. 2010. The expression of microRNA-203 during human skin morphogenesis. *Experimental dermatology* **19**: 854-856.

Wei Y, Peng S, Wu M, Sachidanandam R, Tu Z, Zhang S, Falce C, Sobie EA, Lebeche D, Zhao Y. 2014. Multifaceted roles of miR-1s in repressing the fetal gene program in the heart. *Cell research* **24**: 278-292.

Wu J, Cui H, Zhu Z, Wang L. 2016. MicroRNA-200b-3p suppresses epithelial-mesenchymal transition and inhibits tumor growth of glioma through down-regulation of ERK5. *Biochemical and biophysical research communications* **478**: 1158-1164.

Wu Q, Ren X, Zhang Y, Fu X, Li Y, Peng Y, Xiao Q, Li T, Ouyang C, Hu Y et al. 2017. MiR-221-3p targets ARF4 and inhibits the proliferation and migration of epithelial ovarian cancer cells. *Biochemical and biophysical research communications*.

Wystub K, Besser J, Bachmann A, Boettger T, Braun T. 2013. miR-1/133a clusters cooperatively specify the cardiomyogenic lineage by adjustment of myocardin levels during embryonic heart development. *PLoS genetics* **9**: e1003793.

Xia X, Zhang K, Cen G, Jiang T, Cao J, Huang K, Huang C, Zhao Q, Qiu Z. 2015. MicroRNA-301a-3p promotes pancreatic cancer progression via negative regulation of SMAD4. *Oncotarget* **6**: 21046-21063.

Yan J, Guo D, Yang S, Sun H, Wu B, Zhou D. 2016. Inhibition of miR-222-3p activity promoted osteogenic differentiation of hBMSCs by regulating Smad5-RUNX2 signal axis. *Biochemical and biophysical research communications* **470**: 498-503.

Ye F, Tang H, Liu Q, Xie X, Wu M, Liu X, Chen B, Xie X. 2014. miR-200b as a prognostic factor in breast cancer targets multiple members of RAB family. *Journal of translational medicine* **12**: 17.

Yi R, Poy MN, Stoffel M, Fuchs E. 2008. A skin microRNA promotes differentiation by repressing 'stemness'. *Nature* **452**: 225-229.

Zhang Z, Zhang B, Li W, Fu L, Fu L, Zhu Z, Dong JT. 2011. Epigenetic Silencing of miR-203 Upregulates SNAI2 and Contributes to the Invasiveness of Malignant Breast Cancer Cells. *Genes & cancer* **2**: 782-791.

Zhu G, Chai J, Ma L, Duan H, Zhang H. 2013. Downregulated microRNA-32 expression induced by high glucose inhibits cell cycle progression via PTEN upregulation and Akt inactivation in bone marrow-derived mesenchymal stem cells. *Biochemical and biophysical research communications* **433**: 526-531.

Zhu Z, Xu Y, Zhao J, Liu Q, Feng W, Fan J, Wang P. 2015. miR-367 promotes epithelial-to-mesenchymal transition and invasion of pancreatic ductal adenocarcinoma cells by targeting the Smad7-TGF-beta signalling pathway. *British journal of cancer* **112**: 1367-1375.