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An epistatic mini-circuitry between the transcription factors Snail and HNF4α controls liver stem cell and hepatocyte features exhorting opposite regulation on stemness-inhibiting microRNAs

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Preservation of the epithelial state involves the stable repression of epithelial-to-mesenchymal transition program, whereas maintenance of the stem compartment requires the inhibition of differentiation processes. A simple and direct molecular mini-circuitry between master elements of these biological processes might provide the best device to keep balanced such complex phenomena. In this work, we show that in hepatic stem cell Snail, a transcriptional repressor of the hepatocyte differentiation master gene HNF4α, directly represses the expression of the epithelial microRNAs (miRs)-200c and -34a, which in turn target several stem cell genes. Notably, in differentiated hepatocytes HNF4α, previously identified as a transcriptional repressor of Snail, induces the miRs-34a and -200a, b, c that, when silenced, causes epithelial dedifferentiation and reacquisition of stem traits. Altogether these data unveiled Snail, HNF4α and miRs-200a, b, c and -34a as epistatic elements controlling hepatic stem cell maintenance/differentiation.

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Cellular differentiation implies an orchestrated sequence of events guiding stem cells/precursors toward specialized cell types based on the contemporary and strictly correlated phenomena of loss of stemness and acquisition of histotypic markers and functions. The homeostasis of the stem cell compartment requires mechanisms actively counteracting differentiation;1,2 similarly, the maintenance of the differentiated state involves a stable repression of elements capable to induce morphological transition and dedifferentiation.2 The observation that a number of stem cells are restricted to a particular cell types based on the contemporary and strictly correlated phenomena of loss of stemness and acquisition of histotypic markers and functions. The homeostasis of the stem cell compartment requires mechanisms actively counteracting differentiation;1,2 similarly, the maintenance of the differentiated state involves a stable repression of elements capable to induce morphological transition and dedifferentiation.2 The observation that a number of stem cells are restricted to a theoretical best device to trigger such complex phenomena.

We previously characterized a number of stable liver stem cell lines named RLSCs (from resident liver stem cells) that spontaneously acquire an epithelial morphology and differentiate into hepatocytes (named RLSCdH from RLSC-derived hepatocytes). Notably, RLSCs were also proved to recapitulate the hepatocyte post-differentiation patterning defined as ‘zonation’: their spontaneous differentiation, in fact, generates periporal hepatocytes that may be induced to switch into perivenular hepatocytes by means of the convergence of Wnt signaling on the HNF4α-driven transcription.2,5 Furthermore, we identified a simple cross-regulatory circuitry between HNF4α (master regulator of hepatocyte differentiation) and Snail (master regulator of the epithelial-to-mesenchymal transition, EMT), whose expression is mutually exclusive because of their direct reciprocal transcriptional repression.2,5 These findings, relevant for the comprehension of the EMT and of the reverse process mesenchymal-to-epithelial transition (MET), have been demonstrated pivotal also for the maintenance of a stable epithelial phenotype.2 Notably, EMT/MET dynamics are proposed to be relevant in the reacquisition of stem cell features from differentiated cells. In particular, a pioneering work of Mani et al.6 provided evidence that untransformed human mammary epithelial cells acquire stem cell-like characteristics through an EMT induced by ectopic expression of Twist or Snail transcription factors and that the EMT promotes the generation of cancer stem cells.

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2These authors contributed equally to this work.

Keywords: Snail; HNF4α; miRs-200; miR-34a; stemness; hepatocyte differentiation

Abbreviations: BMI1, BMI1 polycomb ring finger oncogene; ChIP, chromatin immunoprecipitation; CNN1, calponin 1; E-CAD, E-cadherin; EMT, epithelial to mesenchymal transition; FSP1, fibroblast-specific protein-1; FOXA1, forkhead box protein A1; HNF4α, hepatocyte nuclear factor 4 alpha; KL4, Krüppel-like-4; KO mouse, knock out mouse; MET, mesenchymal to epithelial transition; NES, nestin; RLSCs, resident liver stem cells; RLSCdH, resident liver stem cells-derived hepatocytes; RUNX2, runt-related transcription factor 2; SCA1, stem cell antigen 1; SOX2, Sex Determining Region Y-box 2; SIRT1, sirtuin 1; ZEB, zinc finger E-box-binding homebox

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from more differentiated neoplastic cells. More recently, MET was shown as an essential step for the nuclear reprogramming of mouse fibroblasts in induced pluripotent stem cells via exogenous transcription factors.\(^7,\)\(^8\)

In this work, starting from the finding that Snail is expressed in RLSCs, we demonstrate its positive role in stemness markers expression. This observation, unexpected considering that the transcriptional repression is the only function so far attributed to Snail, prompted us to investigate on other factors integrating/mediating Snail activity. Mirror observations made in RLSCs and RLSCdH allowed us to conclude that (1) in RLSC Snail inhibits the hepato-specific program through direct repression of $\text{HNF4}_\alpha$ gene and of the epithelial microRNAs (miR)-200c and -34a, (2) in RLSCdH HNF4$_\alpha$, together with a direct repression of Snail gene, directly upregulates miR-200 family members (200a, b and c) and miR-34a transcription, thus further stabilizing the hepatic phenotype. Altogether these data unveiled Snail, HNF4$_\alpha$ and miRs-200a, b, c and -34a as epistatic elements controlling hepatic stem cell maintenance/differentiation.

**Results**

The transcriptional repressor Snail positively controls the expression of stemness markers. Our analysis evidenced as RLSCs differentiation, underscored by morphological modifications and changes in Snail/HNF4$_\alpha$ expression (Figures 1a and b), is accompanied by a negative regulation of several stemness markers (i.e. the endoderm fork head DNA-binding protein FOXA1, RUNX2, the thin filament-associated protein calponin1 ($\text{CNN}_1$), the intermediate filament protein nestin ($\text{NES}_1$), the stem cell antigen 1 ($\text{SCA}_1$), the polycomb ring fingers member $\text{BMI}_1$ and the transcription factor Sex Determining Region Y-box 2 (SOX2)) (Figures 1b–d).

Although a role in the reacquisition of stemness features by differentiated epithelial cells has been recently attributed to Snail,\(^6\) the influence of this factor on the stable maintenance of stem cell properties is yet unknown. We knocked down endogenous Snail expression in RLSC and overexpressed it in RLSCdH. As shown in Figure 2a, Snail silencing in RLSC

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**Figure 1** RLSC differentiation in RLSCdH is underlined by the negative regulation of Snail and stemness markers. (a) Phase-contrast micrographs magnification $\times 20$, nuclei (TOPRO3) and immunofluorescence staining for Snail and HNF4$_\alpha$ in RLSC and RLSCdH, examined with a Leica TCS2 confocal microscope (Leica Microsystems, Mannheim, Germany) magnification $\times 64$. (b) RT-qPCR analysis on RLSC and RLSCdH cells for the indicated markers. Values are expressed as fold change in gene expression with means $\pm$ S.D. for triplicate samples ($\Delta\Delta_C^t$ method). (c) FACS analysis for SCA1-positive cells on RLSC and RLSCdH. (d) Western blot analysis of BMI1, SOX2 and, as control, CDK4 in RLSC and RLSCdH cells.
resulted in the negative regulation of stem cell factors such as SOX2, the deacetylase Sirtrin 1 (SIRT1), RUNX2, Krüppel-like-4 (KLF4), CNN1, BMI1, FOXA1, NES and SCA1. Consistently, in a mirror experiment, the stable overexpression of Snail in RLScdH determined a significant positive regulation of SOX2, SIRT1, KLF4, BMI1, FOXA1, NES and SCA1 transcription (Figure 2b), the appearance of a large SCA+ cell population (Figure 2c) and the increase of BMI1 and SOX2 protein expression (Figure 2d).

Altogether these data indicate that Snail has a significant and yet unveiled role in the maintenance of stemness traits in RLSc, whereas in differentiated hepatocytes it causes the upregulation of a broad repertoire of stem markers.

The stemness inhibiting miR-200c and miR-34a are transcriptional targets of Snail. The described results designate for Snail, so far characterized only as a
transcriptional repressor, a positive role on the transcription of several genes belonging to the ‘stemness’ functional category. Bioinformatics search by MatInspector (http://www.genomatix.de) failed to find putative binding sites for Snail on the promoter regions of SOX2, RUNX2, KLF4, SIRT1, BMI1, FOXA1, CNN1, NES and SCA1, suggesting that the influence of Snail on the transcription of these genes is more likely an indirect one. Thus, we hypothesized that the observed Snail-induced positive regulation of stem markers expression might be mediated by stemness inhibitors miR-200 family members and miR-34a. MicroRNAs-200 are in fact known to suppress the expression of BMI1, SOX2, KLF4 and SIRT1, whereas miR-34a tends to target SIRT1. Moreover, our bioinformatics research by TargetScan (http://www.targetscan.org/) indicated the other stem cell markers BMI1, SIRT1, KLF4, FOXA1, and SCA1 are direct targets of Snail repression in RLSC and in hepatocytes induced to EMT by TGF-β.

HNF4α is required for the expression of miR-200a, b, c and -34a. Given both the positive regulation of miR-200 family members and miR-34a during hepatocyte differentiation and our recent findings that unveiled a circuitry of reciprocal repression between Snail and HNF4α,2 we next asked whether these miRNAs are regulated by HNF4α. Notably, our bioinformatics analysis revealed putative consensus for HNF4α on all these miRNA promoters.

Indeed, silencing of HNF4α in RlSCdh significantly decreased miR-200a, b, c and -34a expression (Figure 4a). Moreover, it resulted in the (1) positive regulation of the miR-200a, b and -34a promoters but not on the promoter shared by miR-200a and miR-200b, we first verified the involvement of the first two miRs, overexpressing them in RLSC. As shown in Figure 3b, transient transfection of hepatic stem cells with a miR-34a precursor correlated with the negative regulation of expression of the stemness markers FOXA1, SCA1, SIRT1, KLF4, BMI1 and of the mesenchymal/stemness genes Desmin and Vimentin. Notably, the repertoire of stem cell markers we empirically found downregulated by miRNA-34a overexpression was broader than what predicted by Targetscan.

The overexpression of the miR-200c precursor correlated with the negative regulation of the stemness markers SIRT1, KLF4, BMI1 and Vimentin expression. Co-expression of the two miRs enhances the downregulation of all the targets analyzed, with the exception of BMI1 and SCA1 (this last, in particular, appearing to be regulated only by miR-34a).

To validate the hypothesis that Snail positively controls the stemness markers through repression of these stemness inhibiting miRs, we therefore monitored miR-200c and -34a expression in RLSCdh overexpressing Snail. As shown in Figure 3c, Snail overexpression caused a significant down-regulation of endogenous miR-200c and -34a. Notably, TGF-β treatment, that triggers EMT and Snail expression in hepatocytes, caused a transcriptional downregulation of these miRs in RLSCdh (Figure 3c).

The causal correlation between Snail expression and inhibition of miRs transfection has been explored by chromatin immunoprecipitation (ChIP). Figure 3d shows the direct recruitment of endogenous Snail on the miR-200c and -34a axes both in RLSCs and in TGF-β-treated RLSCdh.

Overall, (1) the ectopic expression of miR-200c and -34a in RLSC recapitulated features of Snail silencing, and (2) miR-200c and -34a are direct targets of Snail repression in RLSC and in hepatocytes induced to EMT by TGF-β.

miR-200 family maintains the hepatocytic epithelial phenotype. Finally, the effects of the inhibition of endogenous miR-34a or miRs-200 in RLSCdh have been analyzed at the morphological, transcriptional and immunophenotypical levels. Although reiterated rounds of miR-34a inhibitor transfection up to 2 weeks did not alter the hepatocyte-differentiated phenotype (data not shown), a combination of miR-200a, b and c inhibitors led RlSCdh cells to adopt a mesenchymal-like morphology with delocalization of E-CAD and acquisition of mesenchymal markers FOXA1, KLF4, SMA, RUNX2, N-CAD and SMA. Murine miR-200c promoter expression (Figure 4b) and from KLF4, miR-200c, and miR-34a was observed (Figure 4c). Notably, ChIP analysis showed the recruitment of endogenous HNF4α on all promoters of these miRNAs in WT murine livers (Figure 4h).

**Figure 3** The stemness inhibiting miR-200c and -34a targets of Snail. (a) RT-qPCR analysis on RLSC and RLSCdh cells for the indicated miRs. Values are expressed as fold change in gene expression with means ± S.D. for replicate samples (ΔΔCt method). (b) RT-qPCR analysis for the indicated markers on RLSC expressing a miR precursor as negative control, RLSC overexpressing pre-miR 34a, RLSC overexpressing pre-miR 200c and RLSC overexpressing both pre-miR 34a and pre-miR 200c. Values are expressed as fold change in gene expression with means ± S.D. for replicate samples (ΔΔCt method). (c) RT-qPCR analysis for the indicated miRs on RLSCdh-pWZL as control, RLScpWZL and RLSCdh treated for 24 h with TGF-β. Values are expressed as fold change in gene expression with means ± S.D. for replicate samples (ΔΔCt method). (d) PCR analysis of an anti-Snail ChIP assays on RLSC, RLSCdh and RLSCdh treated for 24 h with TGF-β. Murine miR-200c promoter consensus sites for Snail (from −459 to −454 and from −341 to −336 with respect to the transcriptional start +1), (left panel) and murine miR-34a promoter consensus site for Snail (from −149 to −125 with respect to the transcriptional start +1; right panel), are schematically depicted as black boxes; the regions amplified are depicted as arrows. As controls, ChIPs were also performed without antibody (no Ab) or with unrelated IgG (IgG). A 1:10 dilution of starting chromatin DNA was used as PCR template for input normalization.
Molecular circuitry driving liver stem cell fate

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[Diagrams and graphs showing expression levels of miR-200a, miR-200b, miR-200c, and miR-34a in different conditions.]

b

DESMIN, VIM

Fold change in gene expression

b

FOXa1, SCA1, SIRT1, KLF4, BMI1

Fold change in gene expression

[Bar graphs showing expression levels of FOXa1, SCA1, SIRT1, KLF4, and BMI1 in different conditions.]

c

miR-200c, miR-34a

[Bar graphs showing expression levels of miR-200c and miR-34a in different conditions.]
Overall, we unveiled an epistatic mini-circuitry between the transcription factors Snail and HNF4α that, exerting opposite regulation on stemness-inhibiting miRs, controls liver stem cell and hepatocyte features (Figure 6).

**Discussion**

In our work we highlighted a network involving regulatory elements previously, otherwise extensively, characterized for their biological properties: (1) Snail, a transcription factor...
known to repress the epithelial program in EMT,\(^5\) (2) HNF4\(\alpha\), an orphan nuclear receptor key factor in hepatocyte differentiation that both activates epithelial program and represses the mesenchymal one;\(^14,15\) (3) stemness and proliferation inhibiting miRs-200 and -34a that reinforce epitheliality.\(^16\) The major contribution of this work has been to ascribe to these elements a role in the control of hepatic stem properties and to place them in new epistatic relationships.

The transcriptional repressor Snail, such us other members of the Snail family, has long been associated to EMT and cancer metastasis mainly for its E-cadherin-suppressive activity. Moreover, beyond this function, recent findings demonstrate that Snail functions in opposition to miRs-200 to regulate EMT and germ-layer fate restriction in differentiating ES cells.\(^17\) The transcription factor HNF4\(\alpha\) orchestrates the expression of several epithelial markers in

**Figure 5** The miRs-200 family maintains the hepatocytic epithelial phenotype. (a) Phase-contrast micrographs, nuclei (DAPI) and immunofluorescence staining for FSP1 and E-Cadherin in RLSCdH transfected with the pool of inhibitors against miR-200 family members (200a, b and c) or the control negative inhibitor, examined with a Leica TCS2 confocal microscope magnification \(\times\) 64. (d) RT-qPCR analysis on RLSCdH transfected with the pool of inhibitors against miR-200 family members (200a, b and c) or the control negative inhibitor for the indicated markers. Values are expressed as fold of change in gene expression with means \(\pm\) S.D. for triplicate samples (\(\Delta\Delta Ct\) method). (e) FACS analysis for SCA1-positive cells in RLSCdH transfected with the pool of inhibitor against miR-200 family members (200a, b and c) or the control negative inhibitor...

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hepatocytes, re-estabishes a differentiated phenotype to invasive hepatocellular carcinoma, and, as recently we demonstrated, controls the hepatic epithelial phenotype by direct repression of master EMT regulators including Snail. MiRs-200 induce epithelial differentiation of cancer stem cells by direct targeting the transcriptional repressors of E-cadherin ZEB1 and ZEB2, and other stemness genes. MiR-34a, first identified as direct transcriptional target of p53, has been found to regulate apoptosis, expression of metasta-

Figure 6 Schematic representation of the epistatic relationship among elements controlling stemness and differentiation of liver cells. Snail and HNF4ζ, regulating in opposite manner stemness-inhibiting miRs expression, control liver stem cell and hepatocyte features. Arrows and end-blocked lines indicate positive and negative regulation, respectively.

Regarding miRs, we highlighted as the inhibition of the 200a, b, c members of miR-200 family (and not of miR-34a) is sufficient to induce the mesenchymal phenotype in hepatocytes. Our data are in line with previous evidences indicating these miRs as central factors of the regulation of epithelial phenotype.

Our results suggest the epistatic relationship depicted in Figure 6 in which transcriptional and post-transcriptional regulators are involved. The proposed mechanism implies that the execution of a stemness program requires the active repression of a differentiation program, whereas the main-

Materials and Methods

Cell cultures and transfections. RLSCs were grown in DMEM with 10% FBS (Cambrex BioSciences, Verviers, Belgium), 2 mM L-glutamine (Sigma-Aldrich, St. Louis, MO, USA) and antibiotics. RLSCâ€™s hepatocytes were grown in RPMI 1640 with 10% FBS ( Gibco, Grand Island, NY, USA), 50 ng/ml EGF, 30 ng/ml IGF II (PeproTech Inc., Rocky Hill, NJ, USA), 10 ng/ml insulin (Roche, Mannheim, Germany) and antibiotics, on collagen I (Upstate Biotechnology, Waltham, MA, USA)-coated dishes. When indicated, cells were treated with 2 ng/ml TGF-Î² (PeproTech Inc.), pWZL RLSCâ€™s and pWZL-Snail RLSCâ€™s cells were generated by stable transfection by Lipofectamine 2000 (Invitrogen, San Diego, CA, USA), respectively, with empty or Snail carrying pWZL-bas vectors, as described previously. Cells were selected in 5 Î¼g/ml blasticidin for a week.

For RNA interference, RLSCâ€™s cells were transfected with siRNA oligos against mouse HNF4ζ, or LaminA/C (5'-GGUGUGACGAUCCUGCUUUTT-3') using ON-TARGET plus SMARTpool siRNA (Dharmacon, Lafayette, CO, USA), by Lipofectamine 2000 (Invitrogen, San Diego, CA, USA). RLSCâ€™s cells were transfected with siRNA oligos against mouse Snail (sense 5'-GCCUCUUCGU CCUUUCUCU-3'; antisense: 5'-AGGAGAGAGGCAAGGCG-3'; Sigma-Aldrich), or LaminA/C by Lipofectamine 2000 (Invitrogen).

RNA extraction, reverse transcription, PCR and real-time quantitative PCR (RT-qPCR). Total RNA was extracted by TRizol (Invitrogen, Carlsbad, CA, USA) or NucleoSpin RNA II kit (Macherey-Nagel, Düren, Germany) and reverse transcribed with MMLV-reverse transcriptase (Promega, Milan, Italy). For miRs retrotranscription, single-stranded cDNA was obtained by reverse transcription of 200 ng of total RNA using Superscript kit reaction (Invitrogen, Carlsbad, CA, USA). RT-qPCR was performed using Bio-Rad Miniconcept with KAPA SYBR Green FAST qPCR mix (Kapa Biosystems, Woburn, MA, USA). Relative amounts were obtained with 2-ΔΔCT method and normalized to β-actin. Primers are listed in Table 1.

Immunofluorescence and FACS analysis. For indirect immunofluorescence analysis, cells were grown on collagen I-coated dishes, fixed and treated as described previously. The antibodies were used at the following dilutions: anti-Snail rabbit polyclonal (ab85931 Abcam, Cambridge, UK) 1:500, goat polyclonal anti-HNF4ζ (C-19 sc-6556, Santa Cruz Biotechnology, Santa Cruz, CA, USA) 1:50, rabbit polyclonal anti-FSP1 (S100A4 Abcam, Cambridge, UK) 1:50; mouse monoclonal anti-E-cadherin (Transduction Laboratories, BD Biosciences Pharmingen, Palo Alto, CA, USA) 1:50. Secondary antibodies (anti-goat Alexa-Fluor 488, anti-mouse Alexa-Fluor 594, anti-rabbit Alexa-Fluor 594 diluted 1:1000) were from Molecular Probes (Eugene, OR, USA). Preparations were examined with a Zeiss Axioskop microscope (Carl Zeiss Microscopy, Thornwood, NY, USA). Flow cytometry was undertaken using a FACS Calibur
Table 1 Murine oligonucleotides used for quantitative real-time RT-PCR

<table>
<thead>
<tr>
<th>Gene (Mus musculus)</th>
<th>Accession number</th>
<th>RT-qPCR primers</th>
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<tbody>
<tr>
<td>Bmi1</td>
<td>NM_007552</td>
<td>For 5'-CACAGTTCCCTCACATTCCC-3'</td>
</tr>
<tr>
<td>CNN1</td>
<td>NM_009922</td>
<td>Rev 5'-AGATGAATGGTGATGACC-3'</td>
</tr>
<tr>
<td>Foxa1</td>
<td>NM_008259</td>
<td>For 5'-AAACAGAGGGGGAGTTTGGAG-3'</td>
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<tr>
<td>HNF4f</td>
<td>NM_008261</td>
<td>Rev 5'-CCCATCAGGGTAAAACCAAAGA-3'</td>
</tr>
<tr>
<td>Klf4</td>
<td>NM_010637</td>
<td>Rev 5'-ATCTCTTGTATCACAGATGCC-3'</td>
</tr>
<tr>
<td>Mmu-miR-200a</td>
<td>NR_029723</td>
<td>Rev 5'-GGGCGAAGGGTGCTGCTG-3'</td>
</tr>
<tr>
<td>Mmu-miR-200c</td>
<td>NR_029792</td>
<td>Rev 5'-TGTTGATGTAATCCTCAGGC-3'</td>
</tr>
<tr>
<td>Mmu-miR-34a</td>
<td>NR_029751</td>
<td>Rev 5'-CCACACTTGTGACATCGC-3'</td>
</tr>
<tr>
<td>Nestin</td>
<td>NM_016701</td>
<td>Rev 5'-GGGAAGGTCGCTGTTG-3'</td>
</tr>
<tr>
<td>Runx2</td>
<td>NM_001145920</td>
<td>Rev 5'-GTTGGAAGGTCGCTGTTG-3'</td>
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<td>Sca1</td>
<td>NM_009124</td>
<td>Rev 5'-CCAGATAATTCTGACATGCC-3'</td>
</tr>
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<td>Snail (Snail1)</td>
<td>NM_011427</td>
<td>Rev 5'-CCAGAAACATTCTCATAGACGC-3'</td>
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<td>Sox2</td>
<td>NM_011443</td>
<td>Rev 5'-GCAAACATTCTCATAGACGC-3'</td>
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<td>U6</td>
<td>NM_026309</td>
<td>Rev 5'-GGGAAGGTCGCTGTTG-3'</td>
</tr>
<tr>
<td>β-actin</td>
<td>NM_007393</td>
<td>Rev 5'-GGGAAGGTCGCTGTTG-3'</td>
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(Becton Dickinson, Franklin Lakes, NJ, USA) using a monoclonal FITC-conjugated anti-Sca1 purchased from BD Pharmingen (Erembodegem, Belgium).

Bioinformatics analysis. Regulatory sequences (up to 1 kb upstream of transcription start site) of murine miR-200a-b (ENSEMUSG00000065400), miR-200c (ENSEMUST00000083528) and miR-34a (ENSEMUST00000083599), were obtained from ENSEMBL (http://www.ensembl.org) and submitted to MatInspector Professional (release 8.0, Genomatix, Munchen, Germany), using the vertebrate matrix library and optimized thresholds, to identify putative Snail and HNF4 binding sites (see Figures 3 and 4). Bioinformatics search of putative miR-200 family and miR-34a targets has been performed by TargetScan (http://www.targetscan.org/).

Chromatin immunoprecipitation assay. ChIP analysis were performed according to the Upstate protocol with slight modifications, as described previously.2 For in vivo ChIP analysis, livers from seven mouse embryos were obtained at 17 d.p.c., cut with a razor blade and mechanically disaggregated with 15 strokes of a glass Potter–Elvehjem in ice-cold PBS/protease inhibitors before fixation in 1% formaldehyde. Cross-linked cells were disassociated in release nuclei. Immunoprecipitations were performed with anti-HNF4α (sc-8987), anti-SNAI1 H130, (sc 8987), anti-SNAI1 H130, (sc 8987), anti-Foxa1 (sc-8987), anti-Sox2 NM_011443 and anti-Sca1 NM_011427 purchased from BD Pharmingen (Erembodegem, Belgium). For 5′-ACTACGCGTTACCACTAGTA-3′, Rev 5′-AACCTGCGTGTGATTCTG-3′. Western blots. Cells were lysed in RIPA buffer containing protease inhibitors (Roche, Monza, Italy). Protein concentrations were determined by use of the Bio-Rad assay reagent (Bio-Rad Laboratories, Hercules, CA, USA). Equal amounts of protein were separated by SDS-PAGE and transferred to PVDF membranes (Millipore, Billerica, MA, USA). Blots were incubated in 5% non-fat milk prepared in TBST and incubated overnight with the primary antibody. The antibodies were used in the following dilutions: anti-BMI (Millipore) 1:1000; anti-SOX2 (R&D Systems, Minneapolis, MN, USA) 1:2500. Blots were incubated with HRP-conjugated species-specific secondary antibodies (Bio-Rad), followed by enhanced chemiluminescence reaction (Pierce Chemical, Rockford, IL, USA).

Transfection of miR precursors and inhibitors treatments. For miR overexpression, RLSC cells were transiently transfected with synthetic oligonucleotides for mmu-miR-200c precursor (PM12741 Ambion/Applied Biosystems, Austin, TX, USA) and mmu-miR-200a precursor (PM11030 Ambion/Applied Biosystems) at a final concentration of 60 pmol or with a cocktail of 60 nM of each of both precursors using Lipofectamine 2000 (Invitrogen, San Diego, CA, USA). A miRNA precursor negative control (Ambion/Applied Biosystems) was used at the same concentrations. RNAs were collected for assay 2 days post transfection and miR-200c and -34a expressions were confirmed by qPCR. For miR interference, RLSCdH cells were transfected by Lipofectamine 2000 (Invitrogen, San Diego, CA, USA) with a mixture of 200 nM miR-200c inhibitor (AM12741, Ambion/Applied Biosystems, Austin USA), 200 nM miR-200b inhibitor or 600 nM of an Anti-miR miRNA Inhibitor Negative Control (AM17010Ambion/Applied Biosystems). After 3 days of transfection, cells were split and re-transfected with the same miR inhibitors. This process has been repeated every 3–4 days for up to a total of 19 days before analysis.
Conflict of Interest
The authors declare no conflict of interest.

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