Integrated biochemical and mechanical signals regulate multifaceted human embryonic stem cell functions

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Human embryonic stem cells (ESCs [hESCs]) proliferate as colonies wherein individual cells are strongly adhered to one another. This architecture is linked to hESC self-renewal, pluripotency, and survival and depends on epithelial cadherin (E-cadherin), NMMIIA (nonmuscle myosin II A), and p120-catenin. E-cadherin and p120-catenin work within a positive feedback loop that promotes localized accumulation of E-cadherin at intercellular junctions. NMMIIA stabilizes p120-catenin protein and controls E-cadherin–mediated intercellular adhesion. Perturbations of this signaling network disrupt colony formation, destabilize the transcriptional regulatory circuitry for pluripotency, and impair long-term survival of hESCs. Furthermore, depletion of E-cadherin markedly reduces the efficiency of reprogramming of human somatic cells to an ESC-like state. The feedback regulation and mechanical–biochemical integration provide mechanistic insights for the regulation of intercellular adhesion and cellular architecture in hESCs during long-term self-renewal. Our findings also contribute to the understanding of microenvironmental regulation of hESC identity and somatic reprogramming.

Introduction

Human embryonic stem cells (ESCs [hESCs]), derived from the inner cell mass of blastocyst-stage human embryos, can self-renew in culture indefinitely and have the remarkable potential to develop into nearly all differentiated cell types (Thomson et al., 1998), allowing them to be used for biomedical research, drug discovery, and cell-based therapies (Daley and Scadden, 2008; Rossant, 2008). hESC long-term self-renewal requires cell proliferation and survival with continuous repression of differentiation. Recent studies have revealed some important molecular elements that support hESC long-term undifferentiated growth and survival. Extrinsic factors such as basic FGF (bFGF; Thomson et al., 1998; Levenstein et al., 2006), TGF-β (Xu et al., 2008), and insulin-like growth factor 1 (Bendall et al., 2007) are required for stability of a network of transcription factors including OCT-4, NANOG, and SOX2, which function in concert to positively regulate target genes necessary for pluripotency and repress a variety of lineage specification factors (Jaenisch and Young, 2008). Receptor tyrosine kinases, including ERBB2 and insulin-like growth factor 1 receptor (Wang et al., 2007), are necessary for hESC proliferation and survival. The signals from the extrinsic factors are integrated by intracellular molecules, such as mammalian target of rapamycin (mTOR; Zhou et al., 2009), to repress differentiation activities and/or...
promote proliferation and survival of hESCs. Despite the understanding of hESC regulation by soluble factors, little is known mechanistically about how other microenvironmental factors including cell–cell and cell–ECM interactions control hESC functions.

In this study, we investigate a distinctive feature of hESCs. Like ESCs established from other species, hESCs proliferate in culture as tight and compact colonies, wherein cells are associated strongly with one another (Thomson et al., 1998). The compact structure of hESCs appears integral to the normal functions of hESCs. Perturbations of hESC pluripotency as the result of the removal or inhibition of key extrinsic factors, intracellular signaling molecules, and transcription factors are associated with profound changes in cell and colony morphologies (Levenstein et al., 2006; Okita and Yamanaka, 2006; Zhou et al., 2009). One of the changes is loss of colony integrity and disruption of proper intercellular interactions. Therefore, maintenance of cellular association and colony integrity is a widely accepted indicator of the ESC state. Accordingly, in the recent derivation of induced pluripotent stem cells (iPSCs) from somatic cells, development of compact colonies with tight cellular association has been used as a simple and reliable readout for conversion of non-ESCs to an ESC-like state (Takahashi and Yamanaka, 2006; Takahashi et al., 2007; Yu et al., 2007; Park et al., 2008). Despite the evident role of cellular association in regulating hESC functions, the mechanisms and molecular connections to pluripotency remain largely undefined.

Cadherins (calcium-dependant adhesion molecules) are a class of type 1 transmembrane proteins that play important roles in intercellular cell adhesion (Takeichi, 1995). In particular, epithelial cadherin (E-cadherin) plays a pivotal role in tissue morphogenesis, development, tumorigenesis, and signal transduction (Gumbiner, 2005). E-cadherin is highly expressed in hESCs, and inhibition of E-cadherin function impairs cell survival (Li et al., 2010; Xu et al., 2010). β-Catenin and β-Catenin and p120-catenin bind the cytoplasmic domain of E-cadherin and are critical regulators of E-cadherin functions (Cowin and Burke, 1996; Davis et al., 2003; Xiao et al., 2003). α-Catenin, an actin-binding protein, regulates interaction of the E-cadherin—β-catenin complex with the actin cytoskeleton (Drees et al., 2005; Yamada et al., 2005). α-, β-, and p120-catenin have established roles in early development; ablation or depletion of these molecules caused embryonic lethality in mice and other animals (Haegel et al., 1995; Torres et al., 1997; Fang et al., 2004; unpublished data). The roles of α-, β-, and p120-catenin in regulating hESC adhesion and pluripotency have not been explored. This can be largely attributed to the difficulties associated with genetic manipulations of hESCs, including the use of RNAi-mediated knockdown of genes of interest.

In this study, we identified a highly integrated signaling network that controls intercellular adhesion in hESCs. This network contains NMIIA (nonmuscle myosin IIA), E-cadherin, and p120-catenin and is essential for colony formation, stability of the transcriptional regulatory circuitry for pluripotency, and long-term survival of hESCs.

Results

Inhibition of NMII causes profound defects in hESCs

To identify the regulatory components of pluripotency in hESCs, we screened a collection of pharmacological inhibitors against kinases and other signaling molecules. To eliminate indirect effects of feeders on hESCs, we used feeder-free culture conditions, under which untreated control cells grew as compact and tight colonies with well-defined edges (Fig. 1 A; Xu et al., 2001). Wepassaged hESCs as small cell clusters, a condition known to improve cell survival. This screening effort led us to identify mTOR as a central regulator of hESC pluripotency (Zhou et al., 2009). With this screen, we also found that treatment of cells with blebbistatin, a highly specific inhibitor of NMII (Straight et al., 2003), induced profound morphological changes in H9 hESCs. Blebbistatin-treated cells formed poorly developed colonies in which a significant fraction of cells were dissociated from one another and spread out as single cells (Fig. 1 A; several representative cell morphologies are shown in Fig. S1 A). The effect of blebbistatin on colony formation was dose dependent, with an inhibitory concentration for 50% inhibition (IC50; disruption of ~50% of colonies) of ~4 µM, which is close to the reported IC50 value for inhibiting ATPase activity of myosin II (~2 µM; Straight et al., 2003). Exposure of cells to 10 µM blebbistatin caused the poorly aggregated colonies to increase from 9 (for control cells) to 82% (Table S1). This dose was used for the rest of the experiments.

Disruption of colony integrity is often associated with altered expression of pluripotency markers. Indeed, blebbistatin treatment reduced the activity of AP (an ESC marker) and the levels of SOX2, NANOG, and OCT-4 proteins in H9 cells (Fig. 1, B and C; and Fig. S1 B; quantification of SOX2, NANOG, and OCT-4 levels is shown in Table S1). SOX2, NANOG, and OCT-4 are components of the core transcriptional regulatory circuitry for pluripotency (Jaenisch and Young, 2008) and have also been used to derive human and mouse iPSCs (Takahashi and Yamanaka, 2006; Takahashi et al., 2007; Yu et al., 2007; Park et al., 2008). Interestingly, the mRNA levels of POU5F1 (the gene encoding OCT-4), SOX2, and NANOG decreased only slightly after blebbistatin treatment (Fig. S1 C), indicating that the regulation largely occurred posttranscriptionally. Blebbistatin’s effect on the pluripotency factors was also observed in H1 hESCs (Thomson et al., 1998), a human iPSC (hiPSC) line MMW2 (Mali et al., 2010) and W4/129 mouse ESCs (mESCs; Fig. S1, D–F), implying a conserved function of NMII in pluripotent stem cells. Furthermore, although blebbistatin treatment for 5 d exerted little effect (blebbistatin-treated cells, 7 ± 4%; vs. control cells, 5 ± 3%), long-term treatment (>7 d) caused increased apoptosis in hESCs (17 ± 7%; vs. control cells on day 8, 6 ± 3%; P < 0.001). The increase in apoptosis was likely the result of the gradual loss of cellular association after prolonged treatment. It is well known that cellular association is required for survival of hESCs (Watanabe et al., 2007).

To ask whether NMII inhibition also impaired de novo colony formation in hESCs, we assessed the effects of blebbistatin on hESCs plated as single cells. Interestingly, blebbistatin
SOX2 proteins (Fig. S1 H). Thus, NMMII is necessary for stability of the OCT-4–SOX2–NANOG circuitry and colony formation in hESCs, regardless of whether they are plated as single cells or small clusters.

We next determined whether the changes induced by myosin II inhibition were reversible. To test this, we removed blebbistatin from cells after a 3-d treatment and allowed them to continue to grow for 3 d without blebbistatin. In a separate experiment, we incubated the cells with blebbistatin for 5 d, treatment increased the number of surviving single cells (from ~7 to 35%) 24 h after plating (Fig. S1 G), which is consistent with a previous report that inhibition of ROCK or other components of the Rho–ROCK–NMMII cascade improved survival of dissociated hESCs (Watanabe et al., 2007; Xu et al., 2010). Under this condition, prolonged blebbistatin treatment markedly impaired colony formation and increased the colonies with poor cellular association to 86% (Fig. S1 G and not depicted). The treatment also reduced the levels of OCT-4, NANOG, and SOX2 proteins (Fig. S1 H). Thus, NMMII is necessary for stability of the OCT-4–SOX2–NANOG circuitry and colony formation in hESCs, regardless of whether they are plated as single cells or small clusters.

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Figure 2. NMMIIA modulates E-cadherin adhesion and protein expression in hESCs. (A) Fluorescence and phase-contrast images of H9 cells stained with antibodies against NMMIIA and E-cadherin. (B) Immunofluorescence experiments of E-cadherin in H9 with NMMIIA depletion (for 4 d) or treated with 10 µM blebbistatin for 24 h or 4 d. Corresponding phase-contrast images of the cells are also shown. (A and B) Insets show fractions of fluorescence images at a higher magnification. Bars, 100 µm. (C) Relative cell adhesion to the E-cadherin substrate hE/Fc with or without 10 µM blebbistatin treatment (2 h). Values were normalized to the number (100%) of control cells. Results from five separate experiments are shown. Student’s t tests compared data between the two experimental groups. (D) Representative traction maps for hESCs plated on elastic polyacrylamide gels coated with hE/Fc with or without blebbistatin treatment. The pseudocolor bar represents tractions. Bar, 5 µm. (E) Mean tractions in control cells and cells with blebbistatin treatment. Cells were analyzed 1 h after being plated on elastic polyacrylamide gel coated with hE/Fc. A customized MATLAB program (MathWorks) was used to calculate the traction values. (F) Western blot analysis of E-cadherin, OCT-4, and SOX2 proteins in H9 cells treated or not with 10 µM blebbistatin for various times.
replaced the cells, and allowed them to grow for 5 d in the absence of blebbistatin. Under both conditions, cells with prior treatment were able to resume their original cellular morphology and rescue the levels of pluripotency proteins when cultured without blebbistatin (Fig. S1, I and J; and not depicted).

Disruption of the OCT-4–NANOG–SOX2 circuitry often causes differentiation activities in hESCs (Jaenisch and Young, 2008), leading us to examine the expression of lineage-specific differentiation markers in blebbistatin-treated cells. Blebbistatin treatment for 5 d enhanced expression of lamin A/C (Fig. S1 K), which was reportedly activated upon differentiation of mouse and hESCs (Constantinescu et al., 2006) but only induced slight up-regulation of NEUROD1 (ectoderm), MESP1, MIXL1 (mesoderm), GATA4, GATA6 (endoderm), CDX2, and CGB7 (trophoectoderm) (Fig. S1 L and not depicted).

Depletion of NMMIIA but not NMMIIB mimics blebbistatin treatment

NMMIIs are actin-binding proteins that regulate the contractile functions in cells. Of the three different NMMII isozymes identified, two (NMMIIA and NMMIIB) are almost ubiquitously found in higher organisms and are essential for development. Deletion of NMMIIA or NMMIIB in mice leads to embryonic lethality (Tullio et al., 1997; Conti et al., 2004). However, NMMIIA knockout leads to lethality in periimplantation stage embryos, whereas NMMIIB-null mice die late in gestation. hESCs, like mESCs (Conti et al., 2004), express both NMMIIA and NMMIIB (Fig. 1, D and E). To verify the specificity of blebbistatin and identify the NMMII isozymes required for hESC colony integrity and stability of the transcriptional circuitry for pluripotency, we exploited RNAi-induced knockdown to deplete NMMIIA and NMMIIB in hESCs. By infecting the cells with shRNA-containing lentivirus followed by puromycin selection, we achieved consistent knockdown of genes of interest in hESCs (see following paragraphs; Fig. 1 D; the effect of OCT-4 knockdown is shown in Fig. S2, A and B). To ensure specificity, we used at least two shRNAs to deplete the same target genes. Depletion of NMMIIA for 4 d sharply increased the proportion of colonies with poor cellular association (from 11% for control cells to 78%; Fig. 1 A) and markedly down-regulated OCT-4, NANOG, and SOX2 proteins (Fig. 1 D; and quantifications are shown in Table S1), which is highly reminiscent of blebbistatin treatment. In addition, although short-term depletion (4 d) of NMMIIA caused little effects (control, 6 ± 4%; vs. NMMIIA depletion, 7 ± 3%), long-term depletion (>7 d) led to marked apoptosis in hESCs (NMMIIA-depleted cells, 32 ± 5%; non-targeting shRNA control cells on day 8, 7 ± 3%; P < 0.001). The elevated apoptosis in NMMIIA-depleted cells was preceded by a robust reduction in the c-Myc protein (see Fig. 3 F; unpublished data). c-Myc is a transcription factor and acts as a key regulator of cell growth and survival. In contrast, depletion of NMMIIB had little effect on the pluripotency factors, colony formation, and long-term cell survival (Fig. 1, A and E; Table S1; and not depicted). The shRNA sequences targeting NMMIIA or NMMIIB effectively depleted their respective targets in h9 cells, demonstrating high specificity of shRNAs (Fig. 1 F). These results suggest that NMMIIA but not NMMIIB is necessary for colony formation, stability of the OCT-4–NANOG–SOX2 circuitry, and long-term survival of hESCs. The requirement of NMMIIA for supporting the ESC state might explain in part the early developmental defects observed in NMMIIA-null mice.

NMMIIA modulates E-cadherin adhesion and protein expression in hESCs

We next assessed NMMIIA’s subcellular localization in hESCs. Immunofluorescence of NMMIIA was mainly distributed at cell–cell junctions, colocalizing with the adhesion molecule E-cadherin (Fig. 2 A). This raises the possibility that NMMIIA might regulate intercellular junctions in hESCs. Consistent with this idea, NMMIIA depletion for 4 d markedly impaired the accumulation of E-cadherin at the junctional sites and caused it to distribute diffusely or in punctuate structures in the cytoplasm (Fig. 2 B). Interestingly, although NMMIIB was also localized to cell–cell junctions (Fig. S2 C), its depletion failed to alter E-cadherin localization (not depicted). Similar to NMMIIA depletion, blebbistatin treatment caused redistribution of E-cadherin immunofluorescence to the cytoplasm (Fig. 2 B). The effect of blebbistatin was rapid, altering E-cadherin localization within 24 h of treatment (Fig. 2 B).

To further dissect how NMMIIA regulates E-cadherin, we asked whether NMMIIA was necessary for E-cadherin–dependent intercellular adhesion in hESCs. We used an established adhesion assay (Verma et al., 2004) to assess the ability of cells to attach to the immobilized E-cadherin/Fc proteins (hE/Fc). In this assay, short-term blebbistatin treatment (2 h) robustly reduced the number of cells adhered to the E-cadherin substrate (Fig. 2 C), suggesting that NMMII activity is required for E-cadherin–mediated intercellular contact formation and adhesion.

NMMII-dependent cytoskeletal contractility has been implicated as a key regulator of mechanical signals in a variety of cell types including stem cells (McBeath et al., 2004; Engler et al., 2006; Chowdhury et al., 2010). In this study, we also showed that NMMII was necessary for E-cadherin–mediated mechanical tension in hESCs. We applied traction force microscopy, which assesses the mechanical interactions between cells and the substrate, to determine the traction stress in cells adhered to hE/Fc-coated substrates with an elastic modulus of 8.5 kPa. This stiffness is in the range of normal tissues (1–10 kPa), as documented previously (Janmey and McCulloch, 2007). Single H9 cells were found to exert a mean traction stress of ~650 Pa on the substrates (Fig. 2, D and E), whereas blebbistatin treatment...
markedly reduced the level of tractions (by 57%; to ~280 Pa; Fig. 2, D and E).

Prolonged inhibition of NMMII in hESCs reduced the levels of E-cadherin protein. Blebbistatin treatment for 72 h caused both H9 and H1 cells to markedly down-regulate E-cadherin expression, which continued to decrease with longer treatments (Fig. 2, F and G; and Fig. S1 D). The reduced E-cadherin expression was also observed in MMW2 hiPSCs (Fig. S1 E), indicating conserved modulation in human pluripotent stem cells. Interestingly, down-regulation of E-cadherin was either concomitant with or preceded the down-regulation of the pluripotency proteins (Fig. 2, F and G; and Fig. S1 D). In keeping with the effect of blebbistatin, depletion of NMMIIA but not NMMIIB reduced E-cadherin levels (Fig. 2 H and not depicted). Thus, NMMIIA is required for E-cadherin-dependent intercellular adhesion and mechanical tension and modulates the levels of E-cadherin protein in hESCs.

E-cadherin serves as a bona fide target of NMMIIA in hESCs

The effect of blebbistatin and NMMIIA depletion on E-cadherin-mediated adhesion and E-cadherin expression led us to ask whether decreased E-cadherin activity and levels might be responsible for the impaired cellular compaction and stability of the OCT-4–NANOG–SOX2 circuitry.

First, we assessed the effect of DECMA-1, a function-blocking antibody that is thought to prevent homophilic binding between the E-cadherin extracellular domains (Hordijk et al., 1997). Addition of 12 μg/ml DECMA-1 (sufficient to prevent E-cadherin functions in other cell types; Hordijk et al., 1997) to H9 cell clusters failed to affect cell morphology or alter expression of pluripotency markers (unpublished data). We reasoned that the lack of inhibition might be attributed to reduced accessibility of antibodies to cells that already establish junctions, as demonstrated previously (Peignon et al., 2006). To test this, we seeded H9 cells as single cells and cultivated them in the presence of the DECMA-1 antibody, which, after a 4-d incubation with the cells, markedly reduced the number (to 36%, relative to the nonspecific IgG-treated cells) and size of cell colonies (Fig. 3, A and B; and not depicted). Furthermore, in contrast to the control cells, which grew as compact colonies with well-defined smooth edges, colonies in the presence of DECMA-1 exhibited small projections around the periphery (Fig. 3 A). Concomitant to the morphological changes, the levels of OCT-4, NANOG, SOX2, and c-Myc proteins were markedly reduced (Fig. 3 C and not depicted). Moreover, long-term treatment of cells with DECMA-1 (≥6 d) caused significant cell death (33 ± 8% vs. control cells on day 6, 5 ± 3%; P < 0.001), most likely because of the lack of proper intercellular adhesion.

Depletion of E-cadherin in hESCs led to similar results. Two specific shRNAs effectively depleted E-cadherin in H9 cells, produced colonies with poor cellular association, reduced the levels of OCT-4, NANOG, SOX2, and c-Myc proteins (Fig. 3, D and E; and Table S1), and induced apoptosis after prolonged depletion (E-cadherin–depleted cells, 30 ± 8%; and nontargeting shRNA control cells on day 8, 7 ± 3%; P < 0.001). The mRNA levels of POU5F1, SOX2, NANOG, and c-Myc were only slightly decreased (Fig. S2 D). Therefore, inhibiting E-cadherin activity or reducing E-cadherin expression in hESCs impaired cellular association, colony formation, and stability of the transcription factors. Furthermore, E-cadherin depletion mildly up-regulated markers for the three germ layers and trophectoderm (Fig. S2 D and not depicted). The defects were highly reminiscent of those caused by NMMII inhibition or NMMIIA depletion.

Finally, overexpression of E-cadherin in hESCs nearly completely rescued the defects induced by NMMIIA depletion. Ectopic expression of E-cadherin caused H9 cells to maintain a high level of E-cadherin protein even with NMMIIA depleted. Sustained E-cadherin expression in NMMIIA-depleted cells prevented colony disruption and the down-regulation of OCT-4, NANOG, SOX2, and c-Myc (Fig. 3 F, Fig. S2 E, and not depicted). Thus, E-cadherin was capable of supporting colony formation and stability of the circuitry for pluripotency, although NMMIIA expression was largely absent. Together, our results confirm and extend previous evidence (Conti et al., 2004; Shewan et al., 2005; Smuny et al., 2010), suggesting that E-cadherin serves as a bona fide target of NMMIIA in hESCs to control intercellular adhesion and the pluripotency circuitry.

NMMIIA controls E-cadherin expression via p120-catenin

p120-catenin is the prototypic member of a subfamily of Armadillo domain proteins. It binds to the juxtamembrane region of cadherin intracellular domains (Thoreson et al., 2000). p120-catenin ablation in mice and other vertebrates led to embryonic lethality (for review see McCrea and Park, 2007), demonstrating a critical role in early development. Earlier studies showed that p120-catenin regulates E-cadherin expression levels at the cell surface and modulates its signaling behavior (Davis et al., 2003; Xiao et al., 2003; Wildenberg et al., 2006). Thus, we tested the possibility that p120-catenin might be involved in the regulation of E-cadherin expression by NMMIIA.

Human cells express multiple isoforms of p120-catenin (Keirsebilck et al., 1998). Isoforms 1–4 differ from each other by the start codon used, whereas additional combinations are based on the alternative use of exons A–C. Western blot analysis of protein lysates from hESCs with two monoclonal antibodies, one against isoforms 1 and 2 (6H11; Wu et al., 1998) and the other against all isoforms (15D2; Wu et al., 1998), recognized one and two major bands, respectively (Fig. 4 A, top). A side-by-side analysis of lysates from IMR-90, a human fibroblast cell line, indicated that the band of higher molecular mass might be isoform 1 (Fig. 4 A, bottom). Mesenchymal cells such as fibroblasts express p120-catenin isoform 1 (Mo and Reynolds, 1996; Keirsebilck et al., 1998). RT-PCR analysis of alternative splicing events at the 5′ region confirmed that hESCs expressed mRNA of isoforms 1, 3, and (at a much lower level) 4 (Fig. S3 A). Based on the results from Western blot and RT-PCR analyses, we inferred that hESCs mainly express isoforms 1 and 3. In addition, RT-PCR analysis of alternative splicing at the 3′ region suggested that hESCs expressed transcripts of isoforms A and C in high abundance and, to a much lesser degree, isoform B (Fig. S3 B).
Treatment of H9 cells with blebbistatin caused marked reduction of all detectable p120-catenin protein isoforms (Fig. 4, B and C). The reduction occurred 24 h after the treatment and preceded that of E-cadherin protein (Fig. 2, F and G). Interestingly, in contrast to the reduced protein levels, the amount of p120-catenin transcripts only decreased moderately after NMMII inhibition (Fig. S3 C), indicating that the regulation occurred posttranscriptionally. In addition, short-term blebbistatin treatment (24 h) caused p120-catenin redistribution from cell–cell junctions to the cytoplasm (Fig. 4 D). In keeping with these results, NMMIIA depletion also led to substantial reduction of total p120-catenin protein (unpublished data).

In addition, p120-catenin was required for colony formation and the pluripotency maintenance circuitry of hESCs. Depletion of p120-catenin by shRNAs sharply reduced the number of hESC colonies (to 35%), induced a significant down-regulation of OCT-4, NANOG, and SOX2 (Fig. 4, E and F; and Table S1), and caused marked apoptosis after longer treatment (not depicted).
Figure 4. NMMIIA modulates E-cadherin expression via p120-catenin. (A) Western blot analysis of p120-catenin proteins in H9 cells. (top) Two blots showing bands recognized by 6H11 (left) or 15D2 (right) in H9 cells. (bottom) Western blot analysis of H9 and IMR-90 cell lysates with 6H11. (B) Western blot analysis of p120-catenin protein in H9 cells with or without 10 µM blebbistatin treatment for various time points. (C) Quantification of the experiment described in B. The y axis represents relative intensities (measured with ImageJ) with values normalized to the signal (100%) at 0 h. Results from four separate experiments are shown as mean ± SEM. (D) Immunofluorescence experiments of p120-catenin in H9 cells with or without blebbistatin treatment. Fluorescent images of p120-catenin staining and phase-contrast image of cells are shown. Insets show fractions of fluorescent images at a higher magnification. Cells were treated with 10 µM blebbistatin for 24 h. The monoclonal antibody 15D2 was used. (E) Phase-contrast images of H9 cells treated with nontargeting shRNA (NT shRNA) or p120-catenin–targeting shRNAs. Cells were analyzed 4 d after lentiviral infection. (D and E) Bars, 100 µm. (F) Western blot analysis of p120-catenin (with 15D2), OCT-4, NANOG, and SOX2 proteins in H9 cells with or without p120-catenin depletion for 4 d. Qualification of the results is.
p120-catenin depletion slightly decreased *POUSF1*, *SOX2*, and *NANOG* mRNA levels and moderately up-regulated markers for the three germ layers and trophoectoderm (Fig. S3 D). These responses were highly reminiscent of those caused by E-cadherin depletion. The shRNAs used in these experiments targeted all p120 isoforms. Consistent with earlier findings (Davis et al., 2003; Xiao et al., 2003), p120-catenin depletion markedly reduced the level of E-cadherin protein in hESCs (Fig. 4 G).

Together, these data suggest that p120-catenin acts as a downstream effector of NMMIIA to regulate E-cadherin expression levels in hESCs. This inference was confirmed by the effect of ectopic expression of p120-catenin, which nearly completely rescued the decrease in E-cadherin protein levels in hESCs caused by blebbistatin treatment. In addition, p120-catenin overexpression largely rescued the defects in colony formation and the reduction in OCT-4, Sox2, and NANOG protein levels (Fig. 4 H, Fig. S3 E, and not depicted). Isoform 1A of p120-catenin, which was highly expressed in hESCs, was used for overexpression (Fig. 4 A; and Fig. S3, A and B).

**p120-catenin and E-cadherin are coupled reciprocally to stabilize E-cadherin adhesion**

The modulation of p120-catenin and E-cadherin appeared to be bidirectional in hESCs. Fig. 4 I shows that inhibition of E-cadherin with the DECA-mAb antibody drastically reduced the level of p120-catenin protein, which was associated with reduced E-cadherin protein levels. Similarly, depletion of E-cadherin in hESCs by shRNAs also led to reduction of p120-catenin protein levels (Fig. 4 J). Interestingly, the reciprocal modulation appears lacking in epithelial cells: the absence of E-cadherin fails to reduce the levels of p120-catenin, which becomes stranded in the cytoplasm (Thoreson et al., 2000).

It appears that the major role of p120-catenin is to support E-cadherin expression and E-cadherin–mediated intercellular adhesion, as suggested by experiments with ectopic expression of E-cadherin in hESCs with p120-catenin depletion (Fig. 4 K). We overexpressed E-cadherin in H9 cells followed by treatment with p120-catenin–targeting shRNAs. Although p120-catenin protein was nearly completely depleted, ectopic expression of E-cadherin was capable of supporting colony formation and preventing the down-regulation of OCT-4, Sox2, NANOG, and c-Myc proteins in p120-catenin–depleted cells (Fig. 4 K, Fig. S3 F, and not depicted).

**Depletion of E-cadherin impairs directed somatic reprogramming**

Murine and human somatic cells can be reprogrammed directly to pluripotency by ectopic expression of a subset of transcription factors (Takahashi and Yamanaka, 2006; Takahashi et al., 2007; Yu et al., 2007; Park et al., 2008). We found that E-cadherin depletion markedly reduced the efficiency of reprogramming of human primary fibroblasts and keratinocytes (Fig. S4).

**The effects of depleting α- or β-catenin in hESCs**

In addition to p120-catenin, the cytoplasmic domain of E-cadherin can bind directly to β-catenin, and the resulting E-cadherin–β-catenin complex binds to α-catenin. α-Catenin dynamically remodels and polymerizes the associated actin cytoskeleton at the site of cadherin-mediated cell–cell adhesion (Ozawa and Kemler, 1992; Drees et al., 2005; Yamada et al., 2005). Coupling between E-cadherin and the actin cytoskeleton is thought to be necessary for the adhesion activity of E-cadherin (Nagafuchi and Takeichi, 1988).

We asked whether α- and β-catenin play a role in the regulation of cellular association and pluripotency in hESCs. Immunofluorescence of α- and β-catenin was predominantly located at intercellular junctions of hESC colonies (Fig. 5, A and B), implying a role in the regulation of intercellular adhesion. Depletion of α- or β-catenin for 4 d mildly reduced colony formation of hESCs (to 66% and 64%, respectively) and moderately reduced the level of OCT-4, Nanog, and Sox2 proteins (Fig. 5, C–F). The effects of α- and β-catenin depletion were similar (Fig. 5 and Table S1). Notably, although >60% of the catenin-depleted colonies exhibited largely normal compact morphology, their periphery appeared to be more spread out than the control colonies (Fig. 6, C and E). These moderate defects of α- and β-catenin depletion indicate that these catenins were partially involved in the regulation of intercellular adhesion and the pluripotency circuitry in hESCs.

It was previously shown that E-cadherin homophilic binding triggers the Rac signaling pathway (Kovacs et al., 2002). Thus, we tested the possibility that Rac might mediate E-cadherin’s effects on pluripotency in hESCs. Two specific shRNAs effectively depleted Rac1 in hESCs (Fig. S5 A). However, they failed to affect hESC colony formation or the expression of pluripotency markers (Fig. S5 B). These results suggest that Rac1 is not responsible for the effects of E-cadherin in hESCs.

**Discussion**

In conclusion, we identified critical components and signaling mechanisms that control intercellular adhesion and cellular structure, maintain stability of the transcriptional pluripotency circuitry and c-Myc expression, and support long-term survival in hESCs. A highly integrated signaling network containing NMMIIA, E-cadherin, and p120-catenin is uncovered (Fig. 6). In this network, NMMIIA regulates E-cadherin–mediated adhesion activity and the cellular levels of E-cadherin. The latter...
plays an active role in generating or transmitting signals that control the functions of hESCs. We present evidence that NMMIIA is necessary not only for E-cadherin-mediated intercellular adhesion and mechanical tension, but also for stability of p120-catenin. Inhibition of NMMII causes the level of p120-catenin protein to decrease within 24 h, which in turn reduces E-cadherin expression levels in hESCs. Our results add to emerging evidence that cellular mechanics and myosin II-dependent cytoskeletal contractility are key regulators of fate determination in stem cells. In an earlier study, human mesenchymal stem cells (hMSCs) are shown to specify lineage and commit to phenotypes with extreme sensitivity to tissue level elasticity (Engler et al., 2006). Inhibition of NMMII blocks all elasticity directed lineage specification, implicating mechanical factors in the regulation of the directed differentiation. In a separate study, McBeath et al. (2004) showed that cell shape regulates commitment of hMSCs to adipocyte or osteoblast fate, which requires actin-myosin-generated tension. The critical role of mechanical and physical factors has also been revealed in pluripotent

**Figure 5.** The effects of depleting α- and β-catenin on colony formation and pluripotency. (A and B) Immunofluorescence experiments of β-catenin (A) and α-catenin (B) in H9 cells. The corresponding phase-contrast images are also shown. The insets show fractions of fluorescence images at a higher magnification. (C) Phase-contrast images of H9 cells treated with nontargeting shRNA (NT shRNA) or shRNAs targeting β-catenin. (D) Western blot analysis of β-catenin, OCT-4, NANO, and SOX2 proteins in H9 cells with or without 4-d depletion of β-catenin. (E) Phase-contrast images of H9 cells treated with nontargeting shRNA or shRNAs targeting α-catenin. (F) Western blot analysis of α-catenin, OCT-4, NANO, and SOX2 proteins in H9 cells with or without 4-d depletion of α-catenin. (D and F) Quantification of the results is shown in Table S1. Bars, 100 µm.

response is mediated by p120-catenin, which requires NMMIIA to stabilize and in turn controls E-cadherin levels. Furthermore, we have revealed a bidirectional cross-modulation between E-cadherin and p120-catenin that promotes localized accumulation of E-cadherin at intercellular junctions. The effects of E-cadherin on hESC structures and functions might be mediated partially by α- and β-catenin or other E-cadherin-dependent mechanical and biochemical signals (Fig. 6, dashed lines). Our results unveil a mechanobiochemical mechanism central to multifaceted functions of hESCs and provide mechanistic insights into microenvironmental regulation of hESC identity.

**Integration of mechanical and biochemical signals**

The model in Fig. 6 suggests closely integrated mechanical and biochemical signals that cooperate to regulate intercellular adhesion and colony structures during undifferentiated growth of hESCs. In this scenario, NMMIIA-based contractility does not serve simply as a read-out of intracellular signals but, instead, plays an active role in generating or transmitting signals that control the functions of hESCs. We present evidence that NMMIIA is necessary not only for E-cadherin-mediated intercellular adhesion and mechanical tension, but also for stability of p120-catenin. Inhibition of NMMII causes the level of p120-catenin protein to decrease within 24 h, which in turn reduces E-cadherin expression levels in hESCs. Our results add to emerging evidence that cellular mechanics and myosin II-dependent cytoskeletal contractility are key regulators of fate determination in stem cells. In an earlier study, human mesenchymal stem cells (hMSCs) are shown to specify lineage and commit to phenotypes with extreme sensitivity to tissue level elasticity (Engler et al., 2006). Inhibition of NMMII blocks all elasticity directed lineage specification, implicating mechanical factors in the regulation of the directed differentiation. In a separate study, McBeath et al. (2004) showed that cell shape regulates commitment of hMSCs to adipocyte or osteoblast fate, which requires actin-myosin-generated tension. The critical role of mechanical and physical factors has also been revealed in pluripotent
stem cells. Application of local stress induces cell spreading and down-regulation of OCT-4 in mESCs, and the spreading and down-regulation depend upon NMMII activity (Chowdhury et al., 2010). Our results provide an additional example of mechanical regulation of fate decisions in stem cells. In addition, our data begin to reveal some molecular details underlying the integration of mechanical and biochemical signals.

Our findings suggest a potential positive feedback loop that controls localized accumulation of E-cadherin at the intercellular adhesion sites of hESCs. The components of the feedback loop include E-cadherin and p120-catenin. First, inhibition (or depletion) of one protein markedly decreases the level of the other, demonstrating bidirectional regulation between them. Furthermore, phenotypes of hESCs with E-cadherin or p120-catenin depletion are remarkably similar. One arc of the feedback loop, in which p120-catenin regulates the cellular levels of E-cadherin, is in keeping with the previously reported role of p120-catenin in stabilizing cadherin junctions in cell types including epithelial and endothelial cells (Davis et al., 2003; Xiao et al., 2003). Interestingly, the reciprocal arc, in which E-cadherin modulates the accumulation of p120-catenin, has not been documented. In epithelial cells, the absence of E-cadherin fails to reduce the levels of p120-catenin, which instead becomes stranded in the cytoplasm (Thoreson et al., 2000). Thus, the potential feedback loop might be a feature uniquely related to the identity of ESCs. We envision that the positive feedback regulation could lead to rapid and robust accumulation of E-cadherin protein at the intercellular junctions, thus allowing hESCs to quickly establish, consolidate, and strengthen their cellular association and colony structures during undifferentiated growth. Interestingly, the stability of the putative feedback loop depends on the input from NMMIIA, which controls E-cadherin levels via p120-catenin. We also envision that integration of mechanical regulation with the biochemical signals may provide greater robustness to the feedback loop and create additional levels of regulation for E-cadherin–mediated intercellular adhesion, which might be essential for the diverse fate decisions hESCs (or other pluripotent stem cells) are poised to make in response to various extrinsic and intrinsic cues. More complete understanding of the detailed mechanisms underlying the feedback regulation and mechanical–biochemical integration awaits future experimentation.

How might E-cadherin regulate the transcriptional circuitry for pluripotency? Our data confirm and extend previous evidence, suggesting that the OCT-4–SOX2–NANOG circuitry is intimately linked to intercellular adhesion and colony integrity of hESCs during undifferentiated growth. Disruption of cellular association and compact structures of hESCs in each case causes concomitant down-regulation of the transcription factors. Our results have also assigned an essential role for E-cadherin in the maintenance of the hESC circuitry: depletion or inhibition of E-cadherin induces down-regulation of OCT-4, SOX2, and NANOG within 4 d. Although inhibition (or depletion) of NMMIIA and p120-catenin leads to similar defects, our findings suggest that the effects of NMMIIA and p120-catenin are mediated by E-cadherin. Ectopic expression of E-cadherin in hESCs supports stability of the pluripotency circuitry, although NMMIIA and p120-catenin are largely absent.

How might E-cadherin–mediated cell–cell adhesion regulate the transcriptional circuitry for pluripotency? Our results imply two possible mechanisms. First, α- or β-catenin depletion produces defects that partially recapitulate those caused by E-cadherin depletion/inhibition. Recent studies demonstrated that cadherin clusters at the plasma membranes cause the release of α-catenin dimers, which in turn induces actin bundling by reportedly competing with Arp2/3-binding sites on actin (Drees et al., 2005; Yamada et al., 2005). Thus, these results indicate that dynamic actin assembly mediated by the interactions between E-cadherin and α- and β-catenin might be partially involved in the signal transduction from intercellular adhesion sites to the nuclear pluripotency circuitry (Fig. 6). Second, we show that E-cadherin–mediated adhesion induces mechanical tension, which could transduce information to influence the pluripotency network (Fig. 6, dashed lines). Other speculative mechanisms alone or in combination could also contribute to the cross-modulation between cellular compaction and pluripotency. Unidentified molecular components downstream of E-cadherin adhesion in hESCs could transmit signals to stabilize the core transcriptional circuitry. In addition, it might be that E-cadherin–dependent intercellular adhesion is a prerequisite for the activation of pluripotency-promoting signaling pathways such as those mediated by bFGF, TGF-β, and mTOR.

Materials and methods

Cell culture
hESC lines H9 and H1 (WiCell Research Institute, Madison, WI) were routinely maintained under feeder conditions as previously described (Thomson et al., 1998). In brief, primary mouse embryonic fibroblasts (MEFs) prepared...
from embryos of pregnant CF-1 mice (day 13.5 of gestation; Charles River) were cultured in Dulbecco’s minimum essential medium (DMEM) containing 10% FBS (HyClone) and 1 mM nonessential amino acid and penicillin/streptomycin and mitotically inactivated by γ-irradiation. H1 and H9 cells were cultured on irradiated MEFs in medium containing DMEM/F12, 20% knockout serum replacement, 4 ng/ml bFGF (Invitrogen), 1% nonessential amino acid, 1 mM glutamine, and 0.1 mM β-mercaptoethanol. For feeder-free cultures, cells were cultured on Matrigel (BD)-coated plates in MEF-conditioned medium as previously described (Xu et al., 2001). MMW2 hiPSCs (Maia et al., 2010) were cultured under the same conditions as hESCs. W4/129 mESCs (Tacoiic) were cultured on 0.1% gelatin-coated 6-well plates in medium containing DMEM (high glucose; Invitrogen), 15% FBS, 1,000 U/ml LIF (Millipore), 0.1 mM nonessential amino acids, 2 mM glutamine, 1 mM sodium pyruvate, 10−8 M 2-mercaptoethanol, and 100 U/ml penicillin/streptomycin. Medium changes were administered every other day. HEK293T, HT29, and IMR90 cells were purchased from American Type Culture Collection (ATCC) and cultured following ATCC recommendations.

**Inhibitor and antibodies**

Blebbistatin was purchased from EMD. Rat monoclonal antibody against E-cadherin (DECaMA-1) was obtained from Abcam. Antibodies against p120-catenin (15D2 and 6H11) were described previously (Wu et al., 1998). The polyclonal antibody against α-catenin was provided by B. Gumbiner (University of Virginia, Charlottesville, VA; Funayama et al., 1998). The polyclonal antibody against E-cadherin (DECMA-1) was obtained from Abcam. Antibodies against β-catenin was provided by J. Massague (Columbia University, New York, NY; Massague et al., 1986). The pattern of p120-catenin expression in hESCs was analyzed as described previously (Zhou et al., 2009). Positively clones containing the α-catenin promoter and human E-cadherin cDNA were confirmed by sequencing.

**DNA constructs**

Full-length E-cadherin cDNA was amplified from pCDNA3 containing human E-cadherin-YFP (provided by A. Yap, The University of Queensland, Brisbane, Queensland, Australia) by PCR using forward primer hE-cad-wt-F (Table S4) and reverse primer hE-cad-wt-R (Table S4). The PCR product was cloned into PGEX/GW/TOPO entry vector (Invitrogen). The final overexpression construct was attained by recombination of the resulting entry clone with the pENTR TOPO vector containing the EF1-α promoter and the 2k7neo lentiviral vector as previously described [Zhou et al., 2009]. Positive clones containing the EF1-α promoter and human E-cadherin cDNA were confirmed by sequencing.

**Lentivirus production and hESC infection**

For shRNA-mediated gene knockdown, plKO vectors containing different shRNA sequences (Sigma-Aldrich; Table S3) were used to package virus with Viralpower Lentivirus Packaging System (Invitrogen) as previously described (Zhou et al., 2009). For lentiviral infection, hESCs cultured on MEFs were dissociated as clusters and plated onto Matrigel-coated plates. Lentivirus (MOI, 10–200) was directly added into MEF-conditioned medium containing 6 µg/ml polybrene (Sigma-Aldrich) and incubated for ~20 h before medium change. Selection commenced 48 h after infection with 2 µg/ml puromycin. Cells were analyzed 4–5 d after selection.

For ectopic expression of human E-cadherin and p120-catenin in hESCs, lentiviral-mediated delivery and selection (400 µg/ml G418 or 2 µg/ml puromycin, respectively) were performed after the aforementioned procedure.

**Induction of directed reprogramming**

The lentiviral constructs containing overexpression cassettes for OCT-4, SOX2, NANOG, Lin28, KLF4, and c-Myc were obtained from Addgene. Lentivirus for the six factors was mixed at equal amounts in medium containing 6 µg/ml polybrene (Invitrogen) and administered to IMR90 passages 1–5; ATCC) or human naive embryonic stem cells (JCRB) were transfected with lentivirus containing non-targeting shRNA or E-cadherin-targeting shRNA. 48 h after infection, cells (102 cells) were dissociated into single cells by trypsin and plated onto culture dishes coated with γ-irradiated MEFs. Cells colony types typically emerged within 4–6 (keratinocytes) or 8–9 d (IMR90). The number of ESC-like colonies was counted 2 wk after the initial plating. ESC-like colonies were scored based on morphology and AP activity. Reprogramming efficiency was calculated as the number of ESC-like colonies divided by the total number of cells plated on MEFs after infection.

**Western blotting**

Cells were lysed directly with Laemmli 2x sample buffer (Bio-Rad Laboratories). lysates were separated by SDS-PAGE and analyzed by Western blotting. Dilutions used for various antibodies are described in Table S2. The blots were developed using SuperSignal West Pico Chemiluminescent Substrate (Thermo Fisher Scientific).

**Immunofluorescence**

hESCs cultured under feeder-free conditions were washed twice with cold PBS, fixed with 3.7% paraformaldehyde for 20 min at room temperature, permeabilized with 0.1% Triton-X100 in PBS, and blocked with PBS containing 2% normal donkey serum. Samples were incubated overnight at 4°C with primary antibody (Table S2) followed by two washes with PBS and a 1-h room temperature incubation with Alexa Fluor 488 (or 594)–conjugated secondary antibody. Nuclei were counterstained with DAPI (Sigma-Aldrich) for 5 min. Phase-contrast and fluorescent images were collected with a 10X 0.3 NA EC Plan Neofluor Ph1 objective [Carl Zeiss, Inc.] on a microscope (Axiovert 200M; Carl Zeiss, Inc.). All images were collected with a cooled charge-coupled device camera (AxioCam MR3; Carl Zeiss, Inc.) at room temperature and processed using Photoshop (Adobe).

**AP staining**

An AP detection kit (Millipore) was used following the manufacturer’s instructions. In brief, cells were fixed with 4% paraformaldehyde for 2 min and washed and stained with the staining solution for 15 min at room temperature. After three washes, cells were visualized using light microscopy.

**RNA preparation and real-time PCR**

For real-time PCR, total RNA was isolated from cells with Trizol reagent (Invitrogen) and purified with RNasy mini kit (QIAGEN) following the manufacturer’s instructions. cDNA was synthesized from the purified RNA using a reverse transcription system (Promega) with random primers. Real-time PCR was performed using SYBR green PCR kit (Quantitech; QIAGEN). Reactions were performed in 25 µl containing 2X 12.5 µl SYBR green mix, 10X primer solution (2.5 µl mixture of forward and reverse primers), 2 µl cDNA, and nuclelease-free water. The PCR program following QIAGEN protocols was used as described previously [Zhou et al., 2009]. 95°C for 15 min followed by 40 cycles of 94°C for 15 s, 56°C for 15 s, and 72°C for 34 s. All gene-specific primers were generated based on sequences at PrimerBank or purchased from QIAGEN (Table S4). β-Actin was used to normalize gene expression levels.

**RT-PCR analysis of p120-catenin isoforms**

The pattern of p120-catenin expression in hESCs was analyzed as described previously [Keisebirk et al., 1998]. In brief, total RNA was prepared from hESCs, and cDNA was synthesized from the purified RNA using a reverse transcription system (Promega) with oligo(dT) primers. The synthesized cDNA was amplified by PCR in reactions containing cDNA template, p120-catenin isoform-specific primers (Table S4), 0.25 U Taq DNA polymerase, and deoxyribonucleoside 5′-triphosphates. The following program was used: 94°C for 5 min, 80°C for 1 min followed by 35 cycles of 94°C for 45 s, 55°C for 45 s, and 72°C for 45 s. All gene-specific primers were generated based on sequences at PrimerBank or purchased from QIAGEN (Table S4). β-Actin was used to normalize gene expression levels.

**E-cadherin adhesion assay**

Adhesion of hESCs to hE/Fc-coated substrata was measured by the resistance to detachment as previously described (Verma et al., 2004). In brief, nitrocellulose-coated 96-well plates were incubated with 0.1% hE/Fc (in HBSS containing 5 mM CaCl2) overnight at 4°C. The plate was blocked with 10 µg/ml bovine serum albumin for 2 h at 4°C. H9 cells were pre-treated with Y-27632 for 2 h and digested with accutase (Invitrogen) for 7 min. Freshly isolated cells were allowed to attach to substrata for 2 h at 37°C in a CO2 incubator with or without 10 µM blebbistatin and subjected to detachment by shear stress created by systematic pipetting. Cells remaining adherent to the wells were incubated with calcine-AM for 30 min, washed, and measured with a fluorescence plate reader (iX8, 485 nm; and λEM, 535 nm; CytoFluor 2300; Millipore).

**Apoptosis assay**

To determine the rate of apoptosis in hESCs, H9 cells with or without various treatments were dissociated into single cells using 0.25% trypsin-EDTA.


Figure S1. Effects of blebbistatin in hESCs and other pluripotent stem cells. (A) Phase-contrast images of H9 cell colonies. A normal colony (I) and three representative colonies from H9 cells treated with blebbistatin are shown. (II) The periphery of the colony was spread out, whereas the center remained largely intact, and the colony in III exhibited more peripheral spreading. In contrast, most cells within the entire colony in IV became disassociated. (B) AP staining of H9 cells with or without 10 µM blebbistatin treatment (5 d). [A and B] Bars, 100 µm. (C) mRNA levels of SOX2, POU5F1, and NANOG in H9 cells with or without 10 µM blebbistatin treatment (5 d) assessed by real-time PCR. Values were normalized to the level (1) of mRNA in the cells without blebbistatin. Student's t tests compared data between experimental groups. ACTB (β-actin gene) was used as an internal control. (D) Western blot analysis of E-cadherin, OCT4, and SOX2 proteins in H1 cells with or without 10 µM blebbistatin treatment for various times. A representative experiment from four separate experiments is shown. NANOG protein exhibited a similar pattern (not depicted). (E) Western blot analysis of E-cadherin, OCT4, and SOX2, and NANOG proteins in MMW2 hPSCs with or without 10 µM blebbistatin (5 d). (F) Western blot analysis of OCT-4 and SOX2 proteins in mESCs (W4/129) treated with or without 10 µM blebbistatin (5 d). (G) Phase-contrast images of H9 cells plated as single cells and allowed to grow for 24 and 48 h with or without 10 µM blebbistatin. (H) Western blot analysis of OCT-4, SOX2, and NANOG proteins in H9 cells treated with or without 10 µM blebbistatin (5 d) under conditions described in G. A typical blot (left) and quantification of blots from four separate experiments (right) are shown. All values were normalized to the signal (100%) detected without blebbistatin. (I) Phase-contrast images of H9 cells treated with 10 µM blebbistatin (5 d) and subsequently subcultured in the absence of blebbistatin for 5 d. Cells resumed normal morphology in the absence of blebbistatin. (J) Western blot analysis of OCT-4, SOX2, and NANOG proteins in H9 cells without 10 µM blebbistatin (control), with 10 µM blebbistatin treatment (5 d), or with blebbistatin treatment for 5 d followed by subculture in the absence of blebbistatin for 5 d (withdrawal) as described in I. A typical experiment from four separate experiments is shown. (K) Western blot analysis of lamin A/C in H9 cells with or without 10 µM blebbistatin treatment (5 d). A typical experiment from five separate experiments is shown. (L) Relative mRNA levels of various differentiation markers in H9 cells untreated or treated with 10 µM blebbistatin (5 d) assessed by real-time PCR. The markers include NEUROD1, SOX1 (ectoderm), MESP1, MIXL1 (mesoderm), GATA4, GATA6 (endoderm), CDX2, and CGB7 (trophoectoderm). Data for MIXL1 and CDX2 are not shown. Results from four separate experiments are shown as means ± SEM. Error bars represent the means ± SEM. Asterisks indicate that the values for blebbistatin differ statistically from untreated cells (*, P < 0.05; **, P < 0.001). Bars: (A and B) 100 µm; (G and I) 50 µm.
Figure S2. Additional results from E-cadherin depletion and overexpression. (A) Western blot analysis of OCT-4 and SOX2 proteins in H9 cells with or without OCT-4 deletion for 5 d. Four shRNAs targeting OCT-4 were used. α-Tubulin was used as a loading control. (B) Phase-contrast images of H9 cells treated with nontargeting shRNA (NT shRNA) or OCT-4–targeting shRNAs for 5 d. (A and B) shRNA1 and shRNA3 effectively depleted OCT-4 in H9 cells and induced differentiation morphology and SOX2 down-regulation. (C) Immunofluorescence experiments of NMMIIIB in H9 cells. Fluorescent images for NMMIIIB (green) and E-cadherin (red), the merged image of NMMIIIB and E-cadherin, and the corresponding phase-contrast image are shown. The insets show fractions of fluorescence images at a higher magnification. (D) Relative mRNA levels of various pluripotency and differentiation markers in H9 cells with or without E-cadherin depletion (E-cad KD) assessed by real-time PCR. Results from four separate experiments are shown. All values were normalized to the level (1) of mRNA in control cells on day 5. Asterisks indicate that the values differ statistically from control cells (*, P < 0.05). β-Actin was used as an internal control. (E) Relative protein levels of E-cadherin (E-cad), NMMIIIA, OCT-4, SOX2, NANOG, and c-Myc in H9 cells with or without E-cadherin overexpression (E-cad OE) and NMMIIIA depletion (NMMIIIA KD). Quantification of blots from four separate experiments is shown. A typical blot is shown in Fig. 3 F. Error bars represent the mean ± SEM. Bars, 100 µm.
Figure S3. Additional results for p120-catenin expression profile, depletion, and overexpression. [A and B] RT-PCR analysis of p120-catenin isoforms in H9 cells. HT29 cells (HT) were used as a control. Five primer pairs were selected as previously described (Keirsebilck et al., 1998), which include EX1F3/EX8R1, EX1F6/EX5R1, EX18F1/EX21R3, EX15F1/EX20R1, and EX8F1/EX11R1. HT29 cells, which expressed isoforms 2, 3, 4, A, B, and C, were used as a control. M indicates molecular weight. [A, I] The EX1F3/EX8R1 pair identified a band (785 bp) corresponding to isoform 4 in HT29 cells. This band was also present for H9 cells, albeit at a lower level. This primer pair also identified isoform 3 (1,500 bp) for both HT29 and H9 cells. [A, II] The second primer pair, EX1F6/EX5R1, recognized isoform 3 (297 bp) in both HT29 and H9 cells and isoform 1 (705 bp) in H9 cells. [B, III] The third primer pair, EX18F1/EX21R3, recognized a 557-bp band, indicating that HT29 cells expressed both isoforms A and B, whereas the same pair identified a 470-bp band, suggesting that H9 cells expressed isoform A, not isoform B. [B, IV] Experiments with the fourth primer pair, EX15F1/EX20R1, confirmed that H9 cells expressed very little isoform B. [B, V] The fifth primer pair, EX8F1/EX11R1, recognized a 379-bp band, indicating that isoform C was highly expressed in H9 cells. [C] Relative mRNA levels of p120-catenin in H9 cells untreated or treated with 10 µM blebbistatin at various times assessed by real-time PCR. All values were normalized to the level (100%) of mRNA in control cells at 0 h. [D] Relative mRNA levels of various pluripotency and differentiation markers in H9 cells with or without p120-catenin depletion (p120 KD) assessed by real-time PCR. All values were normalized to the level (1) of mRNA in control cells on day 3. Asterisks indicate that the values differ statistically from control cells (*, P < 0.05). [C and D] Results from four separate experiments are shown. β-Actin was used as an internal control. [E] Relative protein levels of p120-catenin in H9 cells with or without p120-catenin overexpression (p120 OE) and 10 µM blebbistatin. Quantification of blots from four separate experiments is shown. A typical blot is shown in Fig. 4 H. [F] Relative protein levels of E-cadherin, p120-catenin, OCT-4, SOX2, NANOG, and c-Myc in H9 cells with or without E-cadherin overexpression and p120-catenin depletion. Quantification of blots from four separate experiments is shown. A typical blot is shown in Fig. 4 K. Error bars represent the mean ± SEM.
**Figure S4.** E-cadherin depletion impairs directed reprogramming of human somatic cells. (A) Cellular morphology and immunofluorescence fluorescence of OCT-4, NANOG, and SOX2 proteins (red) in ESC-like colonies derived from primary human fetal fibroblasts (IMR-90). Introduction of the reprogramming factors including OCT-4, NANOG, SOX2, C-Myc, LIN28, and KLF-4 to IMR-90 gave rise to ESC-like colonies, which expressed OCT-4, SOX2, and NANOG proteins. Nuclei were stained with DAPI (blue). Bar, 50 µm. (B) Relative reprogramming efficiency of IMR-90 cells infected with nontargeting shRNA (NT shRNA) or E-cadherin–targeting shRNA (E-cad shRNA). Addition of E-cadherin–targeting shRNAs reduced the number of ESC-like colonies by >10-fold, suggesting that reactivation of E-cadherin expression in IMR-90 cells, which lack expression of endogenous E-cadherin, is necessary for their reprogramming to the ESC-like state. Reprogramming efficiency was calculated as the number of ESC-like colonies divided by total number of cells plated on MEFs and was normalized to the number of cells infected with nontargeting shRNA (100%). (C) Western blot analysis of E-cadherin in human neonatal keratinocytes infected with nontargeting or E-cadherin–targeting shRNA. The level of E-cadherin protein was reduced by >80% in cells containing E-cadherin shRNA. α-Tubulin was a loading control. (D) Relative reprogramming efficiency of human neonatal keratinocytes infected with nontargeting or E-cadherin–targeting shRNA. A similar reduction of colony formation was also observed after E-cadherin depletion. Human keratinocytes express E-cadherin endogenously and can be reprogrammed with the same factors [Aasen et al., 2008]. Reprogramming efficiency was determined as described in Materials and methods. It is well known that during the induction of reprogramming, only a small fraction of the donor somatic cells can be successfully driven to pluripotency. Recent studies showed that inhibition of p53–p21 pathway promotes iPSC generation, likely by increasing the cell division rate [Hanna et al., 2009; Hong et al., 2009]. In addition, chromatin-remodeling factors such as Chd1 are also necessary for efficient induction of reprogramming, likely because of its role in opening the chromatin and enabling transcription factor–mediated reprogramming to occur [Gaspar-Maia et al., 2009]. While this study was in review, it was reported in mouse somatic cells that inhibition (or depletion) of E-cadherin reduced the efficiency of reprogramming and that a mesenchymal to epithelial transition might be required for the initiation of the reprogramming process [Chen et al., 2010; Li et al., 2010; Samavarchi-Tehrani et al., 2010]. Our findings suggest that E-cadherin could also play an essential role in the reprogramming of human somatic cells. (B and D) Results from four separate experiments are shown as mean ± SEM.
Figure S5. **Rac1 depletion in hESCs.** (A) Phase-contrast images of H9 cells treated with nontargeting shRNA (NT shRNA) or Rac1-targeting shRNA for 5 d. Bar, 100 µm. (B) Western blot analysis of Rac, OCT-4, and SOX2 proteins in H9 cells with or without Rac1 deletion for 5 d. α-Tubulin was used as a loading control. A representative experiment from four separate experiments is shown.

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<th>SOX2 (%)</th>
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Numbers in parentheses indicate SEM. SOX2, OCT-4, and NANOG values shown are relative to control. *P < 0.05.
Table S2. **Sources and dilutions of antibodies used in this study**

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I, immunofluorescence; W, Western blotting.

Table S3. **shRNA sequences and targets used in this study**

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References


