

# Embryonic Development following Somatic Cell Nuclear Transfer Impeded by Persisting Histone Methylation

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<http://dx.doi.org/10.1016/j.cell.2014.09.055>

## SUMMARY

Mammalian oocytes can reprogram somatic cells into a totipotent state enabling animal cloning through somatic cell nuclear transfer (SCNT). However, the majority of SCNT embryos fail to develop to term due to undefined reprogramming defects. Here, we identify histone H3 lysine 9 trimethylation (H3K9me3) of donor cell genome as a major barrier for efficient reprogramming by SCNT. Comparative transcriptome analysis identified reprogramming resistant regions (RRRs) that are expressed normally at 2-cell mouse embryos generated by in vitro fertilization (IVF) but not SCNT. RRRs are enriched for H3K9me3 in donor somatic cells and its removal by ectopically expressed H3K9me3 demethylase *Kdm4d* not only reactivates the majority of RRRs, but also greatly improves SCNT efficiency. Furthermore, use of donor somatic nuclei depleted of H3K9 methyltransferases markedly improves SCNT efficiency. Our study thus identifies H3K9me3 as a critical epigenetic barrier in SCNT-mediated reprogramming and provides a promising approach for improving mammalian cloning efficiency.

## INTRODUCTION

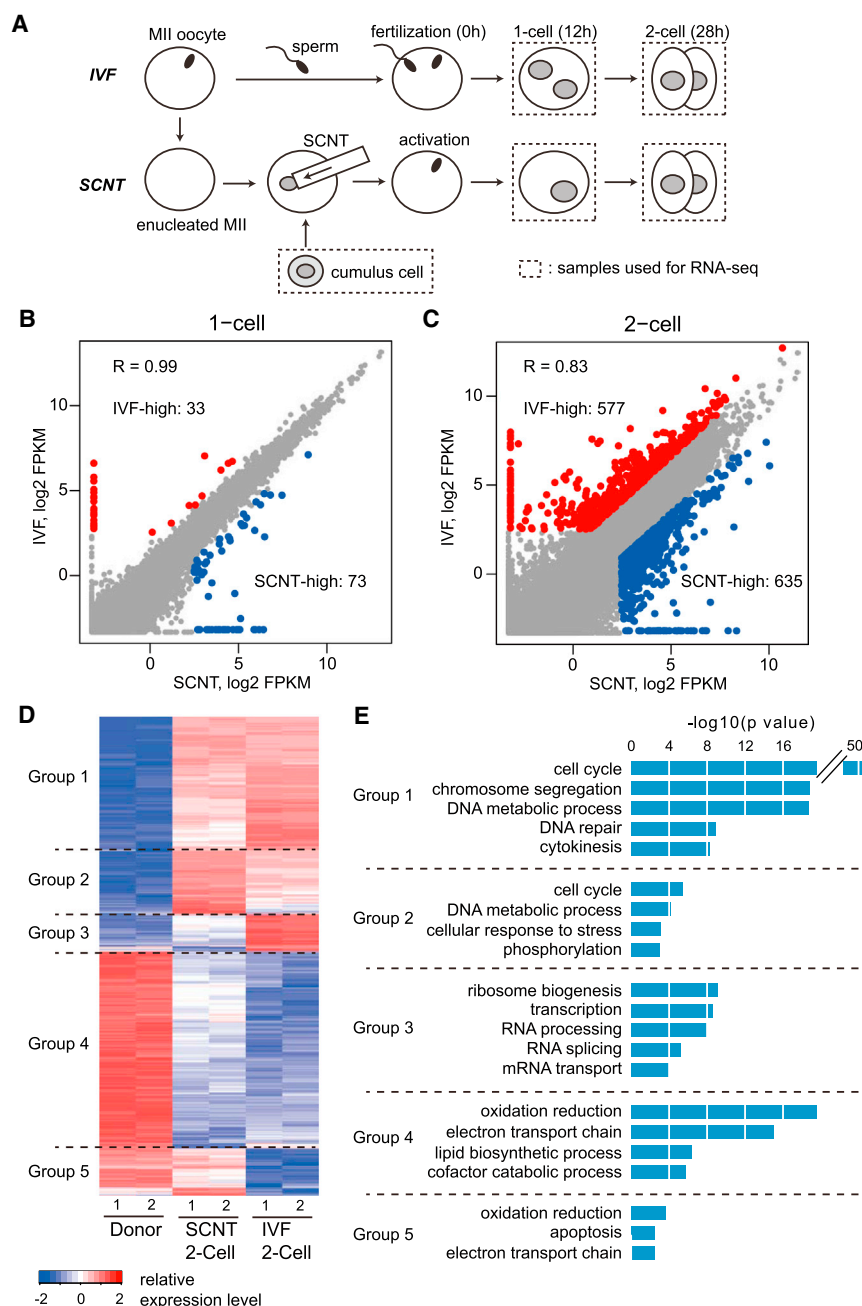
Terminally differentiated somatic cells can be reprogrammed to the totipotent state when transplanted into enucleated oocytes by means of somatic cell nuclear transfer (SCNT) (Gurdon, 1962). Because SCNT allows the generation of a whole organism from the nucleus of single differentiated somatic cell, this technique holds great potential for agriculture, biomedical industry, and endangered species conservation (Yang et al., 2007). Indeed, since the first successful mammalian cloning was performed in sheep (Wilmut et al., 1997), more than 20 mammalian species have been cloned through SCNT (Rodriguez-Orsorio

et al., 2012). Moreover, because pluripotent embryonic stem cells can be established from SCNT-generated blastocysts (Wakayama et al., 2001), SCNT is a promising technique for human therapeutics (Hochedlinger and Jaenisch, 2003). Following the recent successful derivation of the first human nuclear transfer embryonic stem cells (ntESCs) (Tachibana et al., 2013) and the generation of human ntESCs from aged adult or patient cells (Chung et al., 2014; Yamada et al., 2014), this promise is now closer to reality. ntESCs can serve as a valuable cell source for in vitro disease modeling and cell/tissue-replacement therapies.

Despite its tremendous potential, several technical limitations have prevented the practical use of SCNT. One such limitation is the extremely low efficiency in producing cloned animals. For example, approximately half of mouse SCNT embryos display developmental arrest prior to implantation, and only 1%–2% of embryos transferred to surrogate mothers can develop to term (Ogura et al., 2013). With the exception of bovine species, which have relatively higher rates of reproductive cloning efficiency (5% to 20%), the overall reproductive cloning efficiency in all other species is remarkably low (1% to 5%) (Rodriguez-Orsorio et al., 2012). Similarly, the success rate for human ntESC establishment is also low owing to poor preimplantation development (10% to 25% to the blastocyst stage) (Tachibana et al., 2013; Yamada et al., 2014).

Given that developmental defects of SCNT embryos first appear at the time of zygotic genome activation (ZGA), which occurs at the 2-cell stage in mouse and at the 4- to 8-cell stage in pig, bovine, and human (Schultz, 2002), it has been postulated that SCNT embryos have difficulties in ZGA due to undefined epigenetic barriers preexisting in the genome of donor cells. Although previous studies have identified a number of dysregulated genes in mouse 2-cell SCNT embryos (Inoue et al., 2006; Suzuki et al., 2006; Vassena et al., 2007), and in the late cleavage stage human SCNT embryos (Noggle et al., 2011), the nature of the presumed “preexisting epigenetic barriers” and their relationship with impaired ZGA in SCNT embryos remains unknown.

Here, through comparative analysis, we report the identification of genomic domains resistant to ZGA in SCNT embryos. These



**Figure 1. Abnormal Gene Expression of SCNT Embryos at the 1- and 2-Cell Stage**

(A) Schematic illustration of the experimental approach. Samples used for RNA-seq are marked by dashed rectangles.

(B and C) Scatter plots comparing gene expression levels between IVF and SCNT embryos at the 1-cell stage (B) and the 2-cell stage (C). Genes expressed higher in IVF embryos ( $FC > 3.0$ , IVF-high) and higher in SCNT embryos ( $FC > 3.0$ , SCNT-high) are colored with red and blue, respectively.

(D) Heatmap illustration showing differentially expressed genes (DEGs) ( $FC > 5.0$ , FPKM  $> 5$  in each replicates) obtained by a pairwise comparison between donor cumulus cells, IVF 2-cell and SCNT 2-cell embryos. A total of 3,775 DEGs are classified into five groups by unsupervised hierarchical clustering.

(E) Gene ontology analysis of the five groups classified in (D).

See also Figure S1.

## RESULTS

### Abnormal ZGA in 2-Cell SCNT Embryos

To identify the earliest transcriptional differences between mouse embryos derived through in vitro fertilization (IVF) and SCNT, we performed RNA sequencing (RNA-seq) experiments using pooled embryos (25–40 embryos/sample) at 1-cell (12 hr postactivation [hpa]) and late 2-cell (28 hpa) stages (Figure 1A). We obtained more than 30 million uniquely mapped reads for each sample, with the two biological replicates of each sample being highly reproducible (Figures S1A and S1B available online). Analysis of the 1-cell stage transcriptome revealed that SCNT and IVF embryos feature nearly identical transcriptomes ( $R = 0.99$ ; Figure 1B). Specifically, among the 5,517 genes detected (FPKM  $> 5$  in at least one sample), only 106 genes showed more than 3-fold difference between SCNT and IVF embryos (Figure 1B). This is consistent with the fact that ZGA largely begins after the first

cleavage in mouse embryos (Schultz, 2002) and that the majority of transcripts present in 1-cell stage embryos, regardless of IVF or SCNT, are maternally stored transcripts. We therefore focused our analyses on the late 2-cell stage where the major ZGA becomes apparent in mouse embryos. Transcriptome comparison between IVF and SCNT embryos at the 2-cell stage identified 1,212 genes that showed more than 3-fold expression difference (Figure 1C, FPKM  $> 5$  in at least one sample). Pairwise comparison of the transcriptome of donor cumulus cells, 2-cell IVF, and 2-cell SCNT embryos identified 3,775 differentially expressed genes (fold change

reprogramming resistant regions (RRRs) are enriched for the repressive histone modification, H3K9me3, in somatic cells and removal of this epigenetic mark either through ectopic expression of an H3K9me3-specific demethylase in oocytes or through knocking-down the H3K9 methyltransferases, *Suv39h1/2*, in donor cells not only attenuated the ZGA defect, but also greatly improved the reprogramming efficiency of SCNT. Our study therefore identifies *Suv39h1/2*-mediated H3K9me3 as one of the long sought-after “epigenetic barriers” of SCNT and provides a promising approach for improving mammalian cloning efficiency.

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[FC] > 5, FPKM > 5) that can be classified into five groups by unsupervised hierarchical cluster analysis (Figure 1D). Of these 3,775 differentially expressed genes, 1,549 were activated in both SCNT and IVF embryos (groups 1 and 2). Gene ontology (GO) analysis revealed that these genes were significantly enriched in cell-cycle-related biological processes (Figure 1E), suggesting that SCNT embryos are as transcriptionally prepared for proper cell-cycle progression as IVF embryos. Despite a portion of the highly expressed genes in donor cumulus cells still being expressed in 2-cell SCNT embryos (372 genes; group 5), the majority of these genes were silenced following SCNT, similar to those in IVF embryos (1,553 genes; group 4). Genes in Group 4 were significantly enriched in cell metabolism-related biological processes, such as oxidation/reduction and electron transport chain, suggesting that cumulus cell-specific metabolic processes are quickly terminated after SCNT. Interestingly, a group of 301 genes failed to be properly activated in SCNT embryos compared to IVF embryos (group 3). GO analysis revealed that these genes were enriched in transcription or mRNA processing, suggesting a possible defect in activation of developmentally important regulators in SCNT embryos (Figure 1E). Given that proper activation of zygotic genes in 2-cell embryos is believed to be important for embryonic development, we focused our analysis on this group of genes and related genomic loci.

### Identification of Reprogramming Resistant Regions in 2-Cell SCNT Embryos

In addition to protein coding genes, previous studies have revealed that nongenic repetitive elements, such as LTR class III retrotransposons and major satellite repeats, are highly expressed in mouse preimplantation embryos, especially at the 2-cell stage (Evsikov et al., 2004; Peaston et al., 2004; Probst et al., 2010). To comprehensively characterize the transcriptome difference between IVF and SCNT 2-cell stage embryos, we applied a sliding window strategy to identify all genomic regions associated with detectable transcripts. First, we identified 811 genomic regions, ranging from 100 to 800 kb, that were significantly activated (Fisher's exact test  $p$  value < 0.01) in 2-cell stage IVF embryos compared to 1-cell stage IVF embryos (Figure 2A, FC > 5, RPM [reads per millions of uniquely mapped reads] > 10 in IVF 2-cell embryos). Among the 811 genomic regions, 342 regions were activated in SCNT embryos at a similar level as those in IVF embryos (FC  $\leq$  2 comparing IVF with SCNT 2-cell embryos), and these regions were termed as fully reprogrammed regions (FRRs). We also identified 247 regions, termed "partially reprogrammed regions" (PRRs), that were partially activated (FC > 2 and FC  $\leq$  5) in SCNT embryos compared to IVF embryos (Figure 2A). Interestingly, the remaining 222 regions, termed "reprogramming resistant regions" (RRRs), failed to be activated in SCNT embryos (FC > 5, Figure 2A). Notably, transcripts generated within RRRs are largely unannotated as exemplified in a representative region on chromosome 13 (Figure S2A). Indeed, RRRs are relatively gene-poor regions when compared to FRR and PRR (Figure S2B). However, RRRs are enriched for specific repeat sequences, such as LINE and LTR, but are depleted of SINE (Figure S2C). Thus, comparative transcriptome analysis allowed us to identify 222 RRRs that are refractory

to transcriptional activation in 2-cell embryos generated by SCNT.

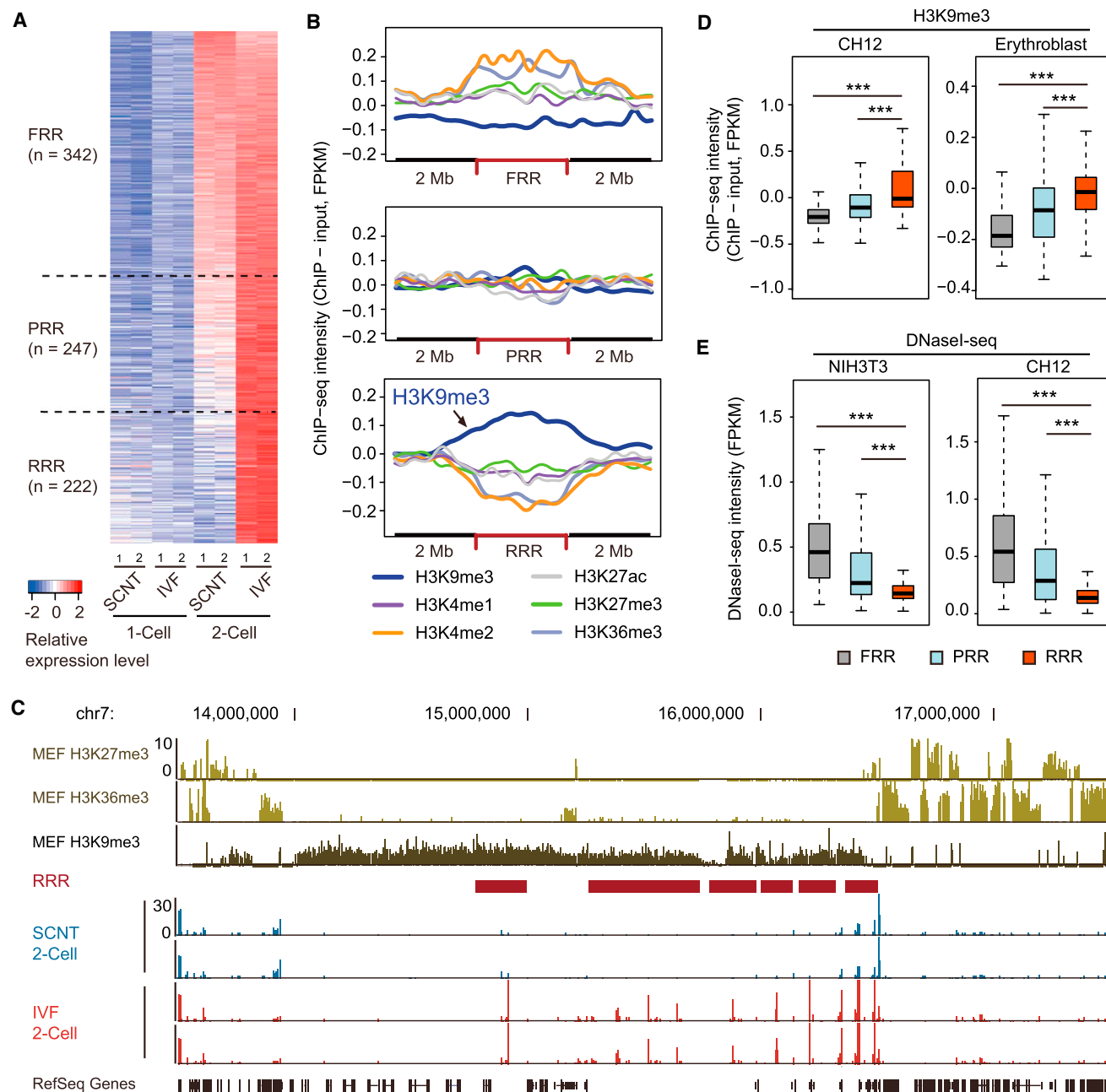
### RRRs Are Enriched for H3K9me3 in Somatic Cells

The fact that RRRs are refractory to transcriptional activation in 2-cell SCNT embryos suggests that RRRs may possess certain epigenetic modifications that serve as a barrier for SCNT-mediated reprogramming. Given that developmental failure of SCNT embryos has been observed in different donor somatic cell types, including mouse embryonic fibroblast (MEF) cells (Ono et al., 2001), we hypothesized that such epigenetic barrier for SCNT-mediated reprogramming may be common to different somatic cell types. Because MEF cells are one of the few somatic cell types with comprehensive histone modification data sets (Bernstein et al., 2012; Chang et al., 2014; Pedersen et al., 2014), we asked whether any of the six major histone modifications are specifically enriched in the RRRs. We found that H3K9me3, but not any other modifications analyzed, was specifically enriched at RRRs, while no obvious enrichment of any histone modifications was observed in FRRs or PRRs (Figure 2B). Indeed, a careful examination of a representative region on chromosome 7 indicated that RRRs failed to activate in 2-cell SCNT embryos were clearly enriched for the H3K9me3 mark, and regions outside of H3K9me3-enriched regions were properly activated in 2-cell SCNT embryos (Figure 2C). This observation is not unique to MEF cells as similar enrichment of H3K9me3 in the RRRs was also observed in four other somatic cell- or tissue-types (CH12, Erythroblast, Megakaryocyte and whole brain) following analysis (Figures 2D and S2D) of the H3K9me3 chromatin immunoprecipitation sequencing (ChIP-seq) data sets from the ENCODE project (Bernstein et al., 2012). Therefore, we conclude that RRRs in somatic cells are enriched for H3K9me3.

Previous studies have also shown that H3K9me3 is generally enriched in tightly-packaged large domains of "heterochromatin regions" (Lachner et al., 2001). One possible explanation for the failure of RRRs to be activated in 2-cell SCNT embryos is its chromatin inaccessibility. To test this possibility, we analyzed the DNaseI hypersensitivity of six different somatic cell types using the data derived from the ENCODE project. Remarkably, we found that RRRs were significantly less sensitive to DNaseI compared to FRR and PRR in all somatic cell- or tissue-types analyzed (Figures 2E and S2E). Collectively, these results suggest that RRRs possess features of heterochromatin that generally exist in somatic cell types.

### Removal of H3K9me3 by *Kdm4d* Restores Transcriptional Reprogramming in SCNT Embryos

Having established a correlation between RRRs and H3K9me3 enrichment, we next attempted to address whether removal of H3K9me3 could facilitate transcriptional reprogramming of RRRs in SCNT embryos. To this end, we synthesized mRNAs encoding an H3K9me3-specific histone demethylase, *Kdm4d* (Krishnan and Trievel, 2013) and injected the mRNAs into SCNT embryos at 5 hpa (Figure 3A). Immunostaining revealed that injection of wild-type, but not a catalytic defective mutant, *Kdm4d* mRNAs greatly reduced H3K9me3 levels in SCNT embryos (Figure 3B).



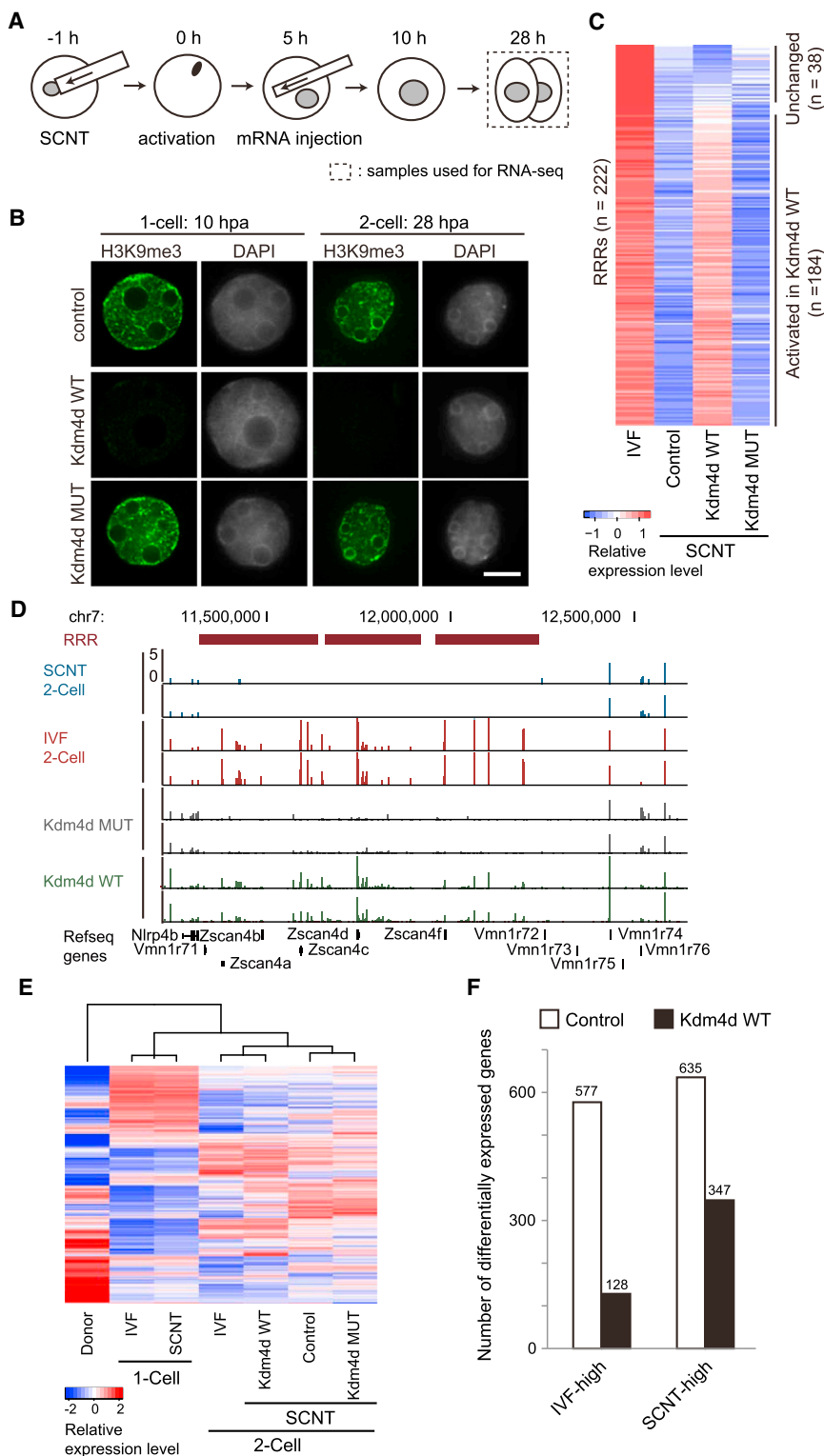
**Figure 2. Reprogramming Resistant Regions Are Enriched for H3K9me3 in Somatic Cells**

(A) Heatmap illustration of the transcripts of IVF and SCNT embryos. Each tile represents an average of peaks within the region obtained by sliding-window analysis. Shown are the 811 regions that are activated from the 1-cell (12 hr) to the 2-cell (28 hr) stage in IVF embryos. These regions were compared to cumulus derived SCNT embryos and classified into three groups based on the fold-change (FC) in transcription levels between SCNT- and IVF 2-cell embryos. FRRs, PRRs, and RRRs indicate fully reprogrammed regions ( $FC \leq 2$ ), partially reprogrammed regions ( $2 < FC \leq 5$ ) and reprogramming resistant regions ( $FC > 5$ ), respectively. (B) The average ChIP-seq intensity of six histone modifications in MEF cells are shown within FRR, PRR, and RRR compared with 2 MB flanking regions. Reads counts are normalized by input, total mapped reads and region length. (C) Representative genome browser view of RRRs on chromosome 7.

(D and E) Box plots comparing the average intensity of H3K9me3-ChIP-seq (D) or DNase-seq (E) within FRR, PRR and RRR in different somatic cell types. ChIP-seq and DNase-seq data sets shown in (B–E) were obtained from ENCODE projects (Bernstein et al., 2012; ENCODE Project Consortium, 2011). Middle line in the colored space indicates the median, the edges indicate the 25<sup>th</sup>/75<sup>th</sup> percentiles, and the whiskers indicate the 2.5<sup>th</sup>/97.5<sup>th</sup> percentiles. \*\*\* $p < 0.001$ .

See also Figure S2.





**Figure 3. Injection of *Kdm4d* mRNA Removes H3K9me3 of Transferred Somatic Cells and Derepresses Silenced Genes in 2-Cell SCNT Embryos**

(A) Schematic illustration of the experimental procedure. SCNT embryos derived from cumulus cells were injected with wild-type or a catalytic defective *Kdm4d* mRNA at 5 hr postactivation (hpa). Samples used for RNA-seq are marked by dashed rectangles.

(B) Representative nuclear images of 1-cell and 2-cell stage SCNT embryos stained with anti-H3K9me3 and DAPI. Shown in each panel is a nucleus of a single blastomere. Scale bar represents 10  $\mu$ m.

(C) Heatmap comparing transcription levels of the 222 RRRs at the 2-cell stage. The expression level of 184 out of the 222 RRRs are significantly (FC > 2) increased in response to wild-type, but not the catalytic mutant, *Kdm4d* injection.

(D) A genome browser view of an example of RRRs on chromosome 7.

(E) Hierarchical clustering of all samples used in this study. Note that 2-cell SCNT embryos injected with wild-type *Kdm4d* were clustered together with 2-cell IVF embryos based on their transcriptome analysis.

(F) Bar graph illustrates reduced number of differentially expressed genes (FC > 3) between IVF and SCNT 2-cell embryos after *Kdm4d* injection. See also Figure S3.

83% (184/222) of RRRs were activated by the injection of wild-type, but not a catalytic defective mutant, *Kdm4d* (Figure 3C, FC > 2). This result indicates that erasure of H3K9me3 facilitates transcriptional activation within RRRs. As exemplified in Figure 3D, an RRR on chromosome 7 containing the *Zscan4* gene cluster was markedly activated by injection of wild-type *Kdm4d*, but not a catalytic defective mutant. Notably, not only protein coding genes, but also the majority of nonannotated transcripts from RRRs, were also activated upon *Kdm4d* mRNA injection (Figures S3A and S3B). Interestingly, hierarchical clustering transcriptome analysis revealed that the transcriptome of SCNT embryos injected with wild-type *Kdm4d* was more similar to that of IVF embryos than that of control SCNT embryos, or of mutant *Kdm4d*-injected embryos (Figure 3E). Indeed, the total number of differentially expressed genes (FC > 3) between SCNT and IVF 2-cell embryos decreased

To examine the effects of *Kdm4d*-mediated H3K9me3 removal on the transcriptional outcome of 2-cell SCNT embryos, we performed RNA-seq analysis focusing on the 222 RRRs that failed to be activated in SCNT. Compared to control SCNT embryos,

from 1,212 to 475 by *Kdm4d* injection (Figures 3F and S3C), suggesting that removal of H3K9me3 from transferred somatic nuclei not only restores transcriptional activation of RRRs but also restores the global transcriptome of SCNT embryos.

### Injection of *Kdm4d* mRNA Greatly Improves Development of SCNT Embryos

To examine the biological consequence of transcriptional restoration of SCNT embryos following *Kdm4d* injection, we first analyzed the developmental potential of SCNT embryos with *Kdm4d* mRNA injection using cumulus cells as donor cells. In control SCNT embryos, the developmental rate began to decline after the first cleavage with only 26.0% of cleaved embryos successfully developing to the blastocyst stage after 96 hr of culturing (Figures 4A and 4B; Table S1), a finding consistent with previous studies (Kishigami et al., 2006). Strikingly, SCNT embryos injected with wild-type *Kdm4d* mRNA rarely arrested during 2- to 4-cell and 4-cell to morula stage transition and developed to the blastocyst stage with high efficiency (88.6%; Figures 4A and 4B; Table S1). In contrast, injection of a catalytic defective mutant *Kdm4d* mRNAs had no significant impact on the developmental rate of the SCNT embryos, indicating the improvement of *Kdm4d* injection on SCNT embryo development depends on its enzymatic activity. Given that H3K9me3 enrichment in RRRs appears to be a general phenomenon in different somatic cell types, we anticipated that the positive effect of *Kdm4d* on SCNT embryo development should be able to be extended to other somatic donor cell types. Indeed, *Kdm4d* mRNA injection also significantly improved the developmental efficiency of SCNT embryos when Sertoli cells or C57BL/6 background MEF cells were used as donor cells (Figures 4A and 4B; Table S1). Together, these results demonstrate that H3K9me3 removal by *Kdm4d* mRNA injection can significantly improve preimplantation development of SCNT embryos, regardless of the somatic donor cell type.

Previous studies have demonstrated that temporal treatment with histone deacetylase (HDAC) inhibitors can also significantly improve developmental efficiency of SCNT embryos (Kishigami et al., 2006; Van Thuan et al., 2009). To explore a possible relationship between HDAC inhibitors and *Kdm4d*, we performed a combinatorial treatment of SCNT embryos with the HDAC inhibitor, TSA and *Kdm4d*. Treatment of TSA alone improved the blastocyst rate from 26.0% to 53.8% (Figure 4C; Table S1), similar to previous report (Kishigami et al., 2006). *Kdm4d* mRNA injection combined with TSA further increased the blastocyst rate to 87.5%, which is statistically similar to *Kdm4d* injection alone (88.6%; Figure 4C; Table S1). This result indicates that TSA treatment and *Kdm4d* mRNA injection does not have synergistic effect on SCNT reprogramming, at least in the preimplantation stage, and TSA treatment may exert its effects through a similar pathway as that of *Kdm4d*.

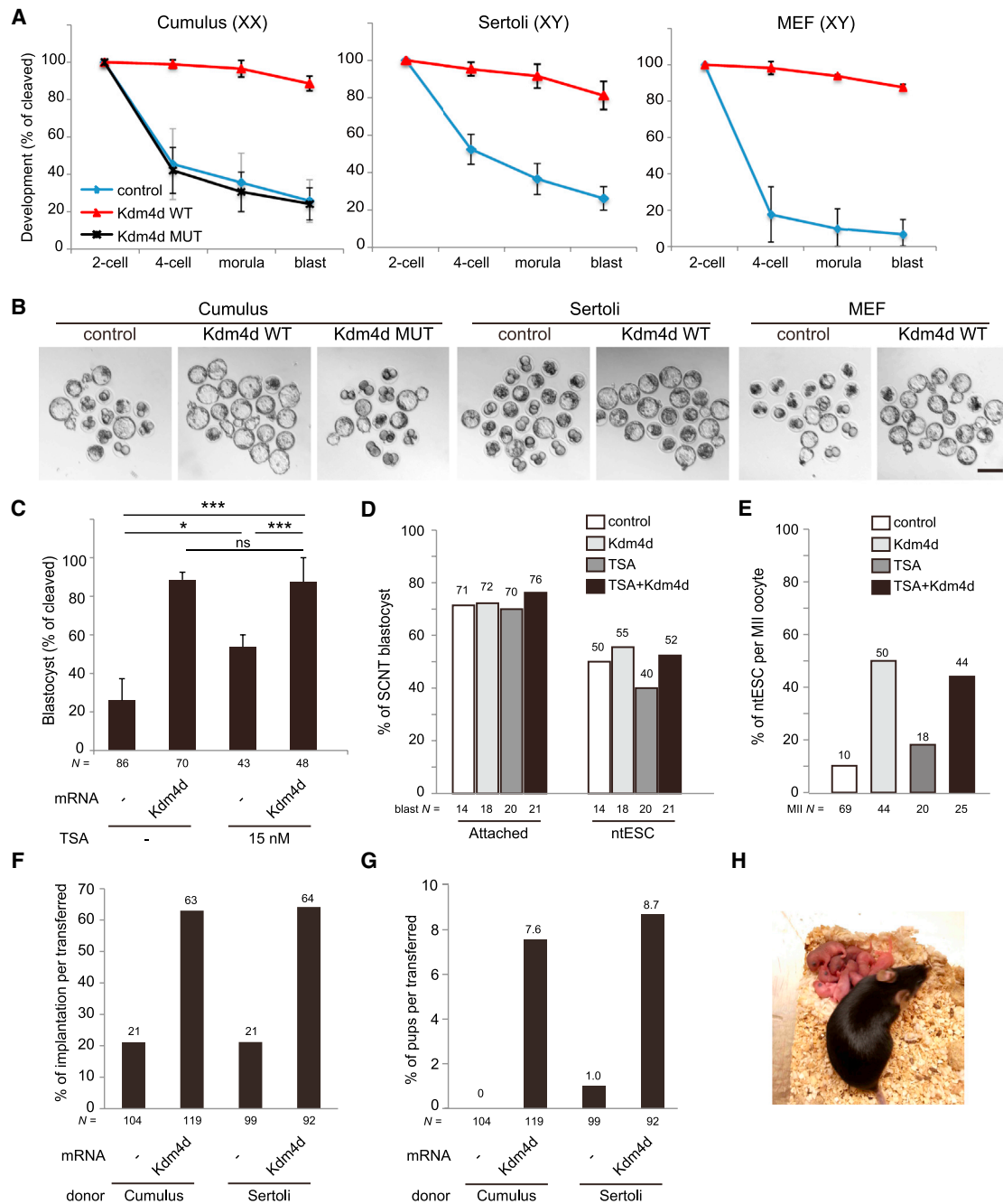
We also examined the efficiency of ntESC derivation from the blastocysts. When control SCNT blastocysts were cultured on feeder MEF cells with ES cell derivation medium, 71% of the blastocysts attached to the feeder cells and 50% of the blastocysts eventually gave rise to the established ntESC lines (Figure 4D; Table S2). Blastocysts generated through *Kdm4d* mRNA injection, TSA treatment, or a *Kdm4d*/TSA combination did not show any significant difference in efficiency of attachment or ntESC derivation when compared to control (Figure 4D; Table S2). Importantly, efficiency was greatly improved by *Kdm4d* injection when calculations were based on the total number of MII oocytes used for SCNT (Figure 4E; Table S2).

To examine whether the positive effect of *Kdm4d* on preimplantation development could be maintained through postimplantation development, we transferred 2-cell stage SCNT embryos generated from cumulus cells into the oviducts of pseudopregnant female mice. Caesarian section at E19.5 (the day of term) revealed that the rate of implantation, evidenced by implantation sites, was 3-fold higher in *Kdm4d*-injected SCNT embryos (63.0%) than in control SCNT embryos (21.2%, Figure 4F). Importantly, 7.6% (9/119) of transferred *Kdm4d*-injected 2-cell SCNT embryos developed to term, while none of the 104 transferred control embryos developed to term under the same conditions (Figure 4G; Table S3). Similar experiments using Sertoli cell-derived SCNT embryos also demonstrated the positive effect of *Kdm4d* on the implantation rate (21% versus 64%) and the development to term rate (1% versus 8.7%) (Figures 4F and 4G; Table S3). Furthermore, SCNT pups generated through *Kdm4d* injection grew normally to adulthood and generated offspring by natural mating (Figure 4H). These results demonstrate that H3K9me3 in somatic cells is a barrier for oocyte-mediated genomic reprogramming and removal of H3K9me3 by *Kdm4d* injection at very early stages of SCNT embryo development can significantly improve the overall efficiency of mouse reproductive cloning.

### Candidate Genes Responsible for the Poor Developmental Phenotype of SCNT Embryos

We next asked which of the genes repressed by H3K9me3 could be responsible for the poor developmental phenotype of SCNT embryos. Given that *Kdm4d* overexpression greatly increases the rate of SCNT embryos reaching the blastocyst stage, the responsible genes must be derepressed in the wild-type *Kdm4d*-injected SCNT embryos. Analysis of the genes that failed to be activated in the 2-cell SCNT embryos (Group 3 genes in Figure 1D), and the genes derepressed in wild-type *Kdm4d*-injected, but not the mutant *Kdm4d*-injected 2-cell SCNT embryos, allowed us to identify 49 common genes (Figures 5A and 5B, FC > 5). GO analysis indicated that this group of genes are enriched for genes involved in transcription and RNA metabolic processes (Figure 5A). While the function of most of the 49 genes in preimplantation development is unknown, the 2-cell-specific *Zscan4* family member, *Zscan4d*, has been shown to be important for preimplantation development (Falco et al., 2007). Therefore, we examined whether supplement of exogenous *Zscan4d* mRNA could enhance the developmental efficiency of SCNT embryos.

We microinjected mRNA encoding full-length *Zscan4d* into SCNT embryos at the early 2-cell stage (20 hpa; Figure 5C) following the expression pattern of endogenous *Zscan4d*. However, injection of *Zscan4d* mRNA failed to rescue the poor developmental phenotype of SCNT embryos, regardless of concentration (Figure 5D; Table S4). Therefore, a defect in *Zscan4d* activation in 2-cell SCNT embryos is unlikely to be solely responsible for the poor preimplantation development of SCNT embryos. Rather, complicated gene networks including transcripts derived from nongenic repetitive elements (Figure S4) may underlie the defects of SCNT embryonic development.



**Figure 4. Injection of *Kdm4d* mRNA Improves Developmental Potential of SCNT Embryos**

(A) *Kdm4d* mRNA injection greatly improves preimplantation development of SCNT embryos derived from cumulus cells, Sertoli cells and MEF cells. Shown is the percentage of embryos that reaches the indicated stages. XX and XY indicate the sex of donor mice. Error bars represent SD.

(B) Representative images of SCNT embryos after 120 hr of culturing in vitro. Scale bar represents 100  $\mu$ m.

(C) *Kdm4d* mRNA injection has additional effect over the treatment with Trichostatin A (TSA; 15 nM). Shown is the percentage of embryos that reached the blastocyst stage at 96 hpa. Error bars represent SD. \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ . ns, not significant.

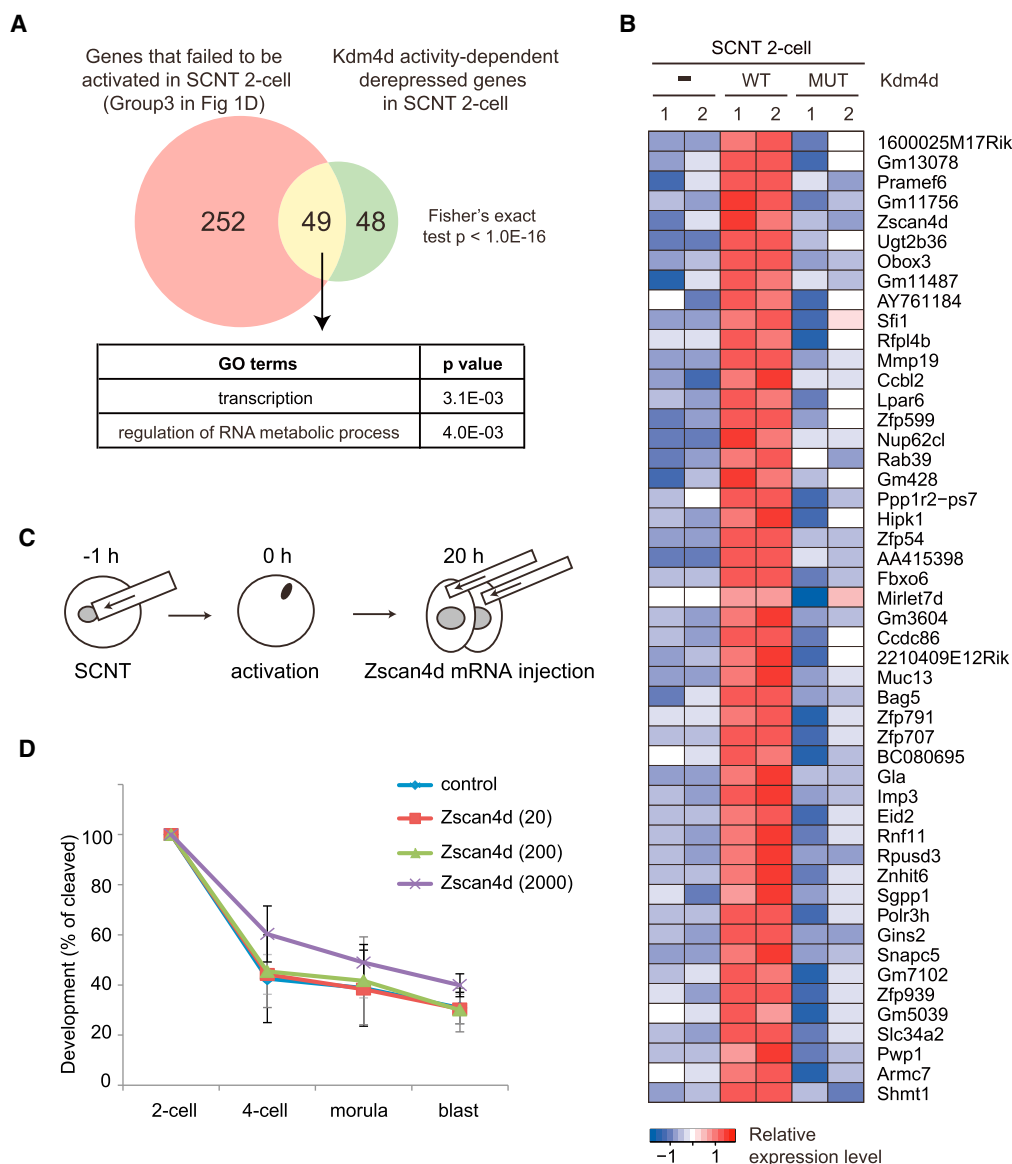
(D) Bar graph showing the efficiency of attachment to the feeder cells and ntESC derivation of SCNT blastocysts.

(E) Bar graph showing the efficiency of ntESC derivation. The efficiency was calculated based on the total number of MII oocytes used for the generation of SCNT embryos.

(F and G) Implantation rate (F) and birth rate (G) of SCNT embryos examined by caesarian section on E19.5.

(H) An image of an adult female mouse derived by SCNT of a cumulus cell with *Kdm4d* mRNA injection and its pups generated through natural mating with a wild-type male.

See also Tables S1, S2, and S3.



**Figure 5. Candidate Genes Responsible for the Poor Developmental Phenotype of SCNT Embryos**

(A) Venn diagram showing the overlap between the genes that failed to be activated in SCNT 2-cell embryos (group 3 in Figure 1D) and *Kdm4d* enzyme activity-dependent derepressed genes in SCNT 2-cell embryos. GO enrichment analysis was performed on the 49 overlap genes.

(B) Heatmap showing the expression pattern of 49 overlap genes in (A).

(C) Schematic illustration of the experimental procedure. *Zscan4d* mRNA was injected into both of 2-cell blastomeres of SCNT embryos at 20 hpa (early 2-cell stage).

(D) Preimplantation development rate of SCNT embryos injected with *Zscan4d* mRNA at 0, 20, 200, or 2,000 ng/μl. Error bars represent SD of three biological replicates.

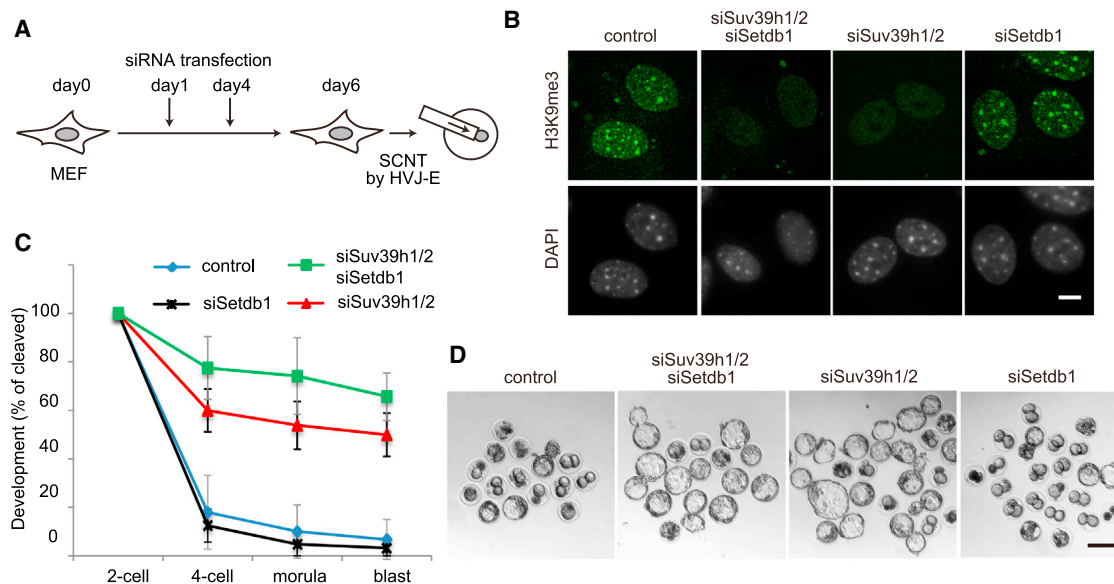
See also Figure S4 and Table S4.

### ***Suv39h1* and *Suv39h2* Establish the H3K9me3 Barrier in Somatic Cells**

Having demonstrated that H3K9me3 is an epigenetic barrier of SCNT-mediated reprogramming, we next attempted to identify the histone methyltransferase(s) responsible for the deposition of H3K9me3 within RRRs in somatic genomes. Previous studies have revealed that at least three histone lysine methyltransferases, *Suv39h1*, *Suv39h2*, and *Setdb1*, can catalyze the gener-

ation of H3K9me3 in mammalian cells (Matsui et al., 2010; Peters et al., 2001). First, we depleted the three H3K9me3 methyltransferases in MEF cells by transfecting a mixture of short interfering RNAs (siRNAs) targeting *Suv39h1*, *Suv39h2*, and *Setdb1* (Figure 6A). RT-qPCR analysis confirmed a knockdown (KD) efficiency of 80%–60% was achieved 48 hr after transfection (Figure S5). Immunostaining showed that transfection of these siRNAs (twice within 6 days of cell culture) could greatly reduce





**Figure 6. *Suv39h1/2* Is Responsible for the Establishment of the H3K9me3 Barrier**

(A) Schematic illustration of SCNT using siRNA transfected MEF cells (see [Extended Experimental Procedures](#) for details).

(B) Representative images of MEF cells stained with anti-H3K9me3 antibody and DAPI at day 6 of transfection. Scale bar represents 10  $\mu$ m.

(C) Preimplantation development rate of SCNT embryos derived from different knockdown MEF cells. Error bars represent SD of three biological replicates.

(D) Representative images of SCNT embryos after 120 hr of culturing in vitro. Scale bar represents 100  $\mu$ m.

See also [Figure S5](#) and [Table S1](#).

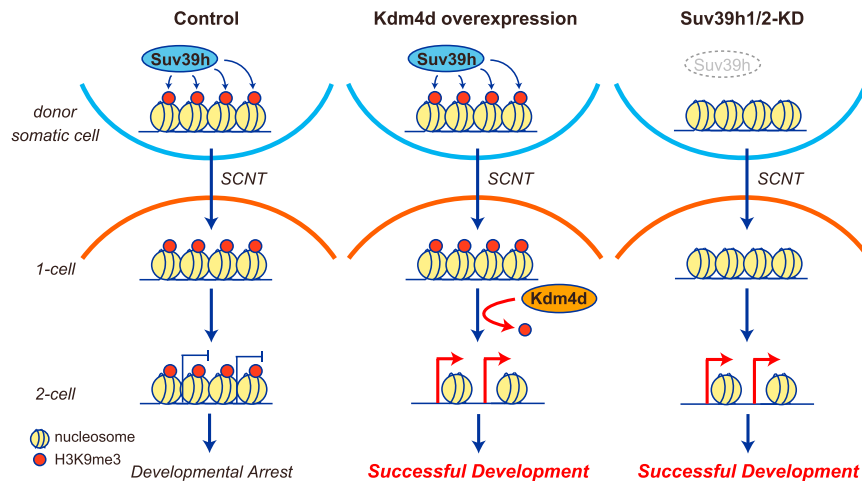
H3K9me3 levels in MEF cells ([Figures 6A and 6B](#)), demonstrating the three H3K9me3 methyltransferases, and not other unidentified enzymes, as the responsible factors for the H3K9me3 deposition in the somatic cells. Using triple KD MEF cells as donors, we generated SCNT embryos and examined their preimplantation development. We found that while only 6.7% of control SCNT embryos developed to the blastocyst stage after 96 hr culture ([Figures 6C and 6D; Table S1](#)), 65.6% of the triple KD MEF-derived embryos developed to blastocyst stage ([Figures 6C and 6D; Table S1](#)). This result not only confirms that somatic H3K9me3 is an epigenetic barrier of SCNT-mediated reprogramming, but also demonstrates that these three enzymes are responsible for generating this epigenetic barrier.

We next examined which of the three histone methyltransferases could be responsible for establishing the H3K9me3 reprogramming barrier by individually depleting them in MEF cells. Because *Suv39h1* and *Suv39h2* have redundant functions in H3K9 trimethylation ([Peters et al., 2001](#)), we knocked down both genes at the same time. Immunostaining at day 6 of KD demonstrated that *Suv39h* KD reduced global H3K9me3 levels, especially at pericentric regions, while *Setdb1* KD did not cause a global change in H3K9me3 levels ([Figure 6B](#)), a finding consistent with a previous report ([Matsui et al., 2010](#)). When these KD MEF cells were used as donors for SCNT analysis, the developmental rate to the blastocyst stage was greatly improved from 6.7% in control to 49.9% in the *Suv39h* KD MEF group, very close to that of the triple KD MEF group ([Figures 6C and 6D; Table S1](#)). In contrast, KD of *Setdb1* did not significantly alter the developmental rate ([Figures 6C and 6D; Table S1](#)). Collectively, these results suggest that *Suv39h1/2* are primarily responsible

for establishing H3K9me3 in somatic cells, which functions as a barrier in genomic reprogramming of SCNT embryos.

## DISCUSSION

More than 50 years have passed since the first demonstration of animal cloning through somatic cell nuclear transfer in *Xenopus* eggs ([Gurdon, 1962](#)). Despite tremendous efforts, cloning efficiency has remained quite low in most of the species, and the mechanism underlying epigenetic reprogramming following SCNT has remained poorly understood. In this study, through comparative transcriptome and integrated epigenomic analysis, we have identified that *Suv39h1/2*-deposited H3K9me3 in donor somatic cells functions as an epigenetic barrier for somatic cell nuclear reprogramming in mouse oocytes. By comparing to the transcriptome of IVF embryos, we identified 222 genomic regions, termed as RRRs (reprogramming resistant regions), resistant to transcriptional reprogramming in SCNT embryos. RRRs are characterized by significant enrichment of *Suv39h1/2*-deposited H3K9me3 and low DNase I accessibility, both of which are general features of heterochromatin, in several somatic cell types analyzed. Efficient activation of transcripts within RRRs appears to be instrumental for the development of SCNT embryos, as removal of H3K9me3 either by *Suv39h1/2* knockdown or by expression of exogenous *Kdm4d* results in activation of RRRs and significant improvement in the development of SCNT embryos. Thus, our data support a model where *Suv39h1/2*-deposited H3K9me3 in somatic cells serves as a barrier for the activation of developmentally important genes in oocytes, leading to developmental arrest of SCNT embryos



**Figure 7. A Model Illustrating How the H3K9me3 Reprogramming Barrier Can Be Overcome**

*Suv39h*-deposited H3K9me3 in somatic cells serves as a transcriptional barrier for SCNT-mediated reprogramming which affects normal embryonic development (left). Removal of this barrier either by the expression of exogenous *Kdm4d* (middle) or by prevention of H3K9me3 establishment by *Suv39h* knockdown (right) can lead to activation of developmental regulators in SCNT embryos, resulting in successful embryonic development.

(Figure 7). Removal of this epigenetic barrier either by exogenous *Kdm4d* following SCNT, or by depletion of *Suv39h1/2* in donor cells allows the expression of developmental genes and thus improves the development of SCNT embryos (Figure 7).

How does H3K9me3 impede reprogramming? Previous studies have demonstrated that H3K9me3 can be recognized and bound by the heterochromatin protein, HP1 (Bannister et al., 2001; Lachner et al., 2001), which can nucleate the formation of heterochromatin (Canzio et al., 2013). Interaction between heterochromatin and nuclear lamina can tether heterochromatin to the nuclear periphery leading to epigenetic silencing (Poleshko and Katz, 2014). Therefore, H3K9me3-initiated heterochromatin assembly can prevent access to reprogramming and transcriptional factors and thereby prevent the activation of developmentally important genes in RRRs. In addition to preventing access to reprogramming and transcription factors, H3K9me3 may inhibit subsequent deposition of activation marks, such as H3K9 acetylation and H3K4 methylation, as we have demonstrated previously (Wang et al., 2001).

It is likely that H3K9me3-mediated heterochromatin formation may function as a general reprogramming barrier, which is supported by the recent demonstration that both H3K9me3 (Chen et al., 2013; Soufi et al., 2012) and HP1 (Sridharan et al., 2013) in MEF cells inhibit iPS cell generation. Nonetheless, several differences exist regarding the barrier between SCNT and iPS reprogramming. First, the H3K9me3-barrier in mouse iPS reprogramming is established primarily by *Setdb1* (Chen et al., 2013; Sridharan et al., 2013). In contrast, our results clearly point to *Suv39h1/2*, but not *Setdb1*, as critical enzymes that establish the H3K9me3 barrier for SCNT reprogramming. Second, the downstream gene networks necessary for successful reprogramming, repressed by the H3K9me3 barrier, are likely different. In iPS reprogramming, the key downstream factors within the H3K9me3 barrier are the core pluripotency network genes, such as *Nanog* and *Sox2*, which operate during relatively late stages of reprogramming (Chen et al., 2013; Sridharan et al., 2013). In contrast, in SCNT reprogramming, transcripts that play a critical function at the 2-cell stage are the key factors repressed by H3K9me3 (discussed below). This distinction

most likely stems from the differences in the set of transcription factors required for successful reprogramming in each context. Indeed, Oct4/Pou5f1, a core transcription factor of iPS reprogramming, has recently been demonstrated to be dispensable in SCNT reprogramming (Wu et al., 2013). Therefore, although H3K9me3 is a common reprogramming barrier, its deposition and how it affects the reprogramming process are likely different between iPS and SCNT.

We have listed 49 candidate genes that are potentially responsible for the poor developmental phenotype of SCNT embryos. Overexpression of one of the candidate genes, *Zscan4d*, did not improve the blastocyst rate. It is thus likely that other factors activated at 2-cell stage IVF embryos are necessary for SCNT embryos to successfully develop to the blastocyst stage. In addition to the protein coding genes we listed, the deregulated RRRs also harbor many unannotated transcripts and repeat sequences whose repression in 2-cell SCNT embryos exhibits H3K9me3 dependency. For example, expression of the major satellite repeats were greatly suppressed in 2-cell SCNT embryos, and this repression was completely restored by the wild-type, but not the catalytic mutant, *Kdm4d* injection (Figure S4). Similarly, *Kdm4d* injection also partially relieved SCNT-induced repression of class III retrotransposon elements, such as *MERVL*, in 2-cell SCNT embryos (Figure S4). Given that activation of both repeat sequences is important for preimplantation development (Kigami et al., 2003; Probst et al., 2010), transcriptional deregulation of these repeat sequences in 2-cell SCNT embryos may also contribute to the developmental defects observed in these embryos. Therefore, it is likely that defective activation of protein coding genes and repeat sequences that harbor the H3K9me3 mark inherited from somatic cells is collectively responsible for the developmental failure of SCNT embryos.

In addition to better understanding the detailed mechanism of how H3K9me3 removal contributes to increased SCNT efficiency, whether or not our observation can be generally applied to other animal species warrants future investigation. Similar to mice, developmental defects of SCNT embryos appear concurrently with ZGA in other mammalian species such as rabbit (Li et al., 2006), pig (Zhao et al., 2009), bovine (Akagi et al., 2011), and human (Noggle et al., 2011), with abnormal heterochromatin or H3K9me3 status observed in SCNT embryos of these species (Pichugin et al., 2010; Santos et al., 2003; Yang et al., 2009).

Therefore, the H3K9me3 reprogramming barrier might be conserved among different species. If so, *Kdm4d* mRNA injection has the potential to enhance cloning efficiency in a broad range of mammalian species, including humans. Importantly, injection of *Kdm4d* mRNA greatly enhanced ntESC derivation efficiency in mice. If this intervention can be successfully translated to human ntESC derivation, our method could hold great promise for human therapeutic cloning (Hochedlinger and Jaenisch, 2003; Yang et al., 2007). The simplicity of *Kdm4d* mRNA injection during SCNT makes the testing of our approach worthwhile. Furthermore, when a Suv39h-specific inhibitor becomes available, a simple incubation of the donor cells with such inhibitor prior to transferring to enucleated oocytes could drastically improve cloning efficiency.

## EXPERIMENTAL PROCEDURES

### SCNT and mRNA Injection

Somatic cell nuclear transfer was carried out as described previously (Matoba et al., 2011). Briefly, recipient MII oocytes were collected from superovulated adult BDF1 females by a brief treatment with 300 U/ml bovine testicular hyaluronidase (Calbiochem). Isolated MII oocytes were enucleated in HEPES-buffered KSOM medium containing 7.5  $\mu$ g/ml of cytochalasin B (Calbiochem 250233). The nuclei of donor cumulus cells or Sertoli cells were injected into the enucleated oocytes using a Piezo-driven micromanipulator (Primetech PMM-150FU). MEF cells were fused with enucleated oocytes by inactivated Sendai virus envelope (HVJ-E; Ishihara Sangyo). After 1 hr incubation in KSOM, reconstructed SCNT oocytes were activated by incubation in Ca-free KSOM containing 5  $\mu$ g/ml cytochalasin B for 1 hr and further cultured in KSOM with cytochalasin B for 4 hr. Activated SCNT embryos were washed 5 hr after the onset of SrCl<sub>2</sub> treatment (hours post activation, hpa) and cultured in KSOM in a humidified atmosphere of 5% CO<sub>2</sub> at 37.8°C. In some experiments, SCNT embryos were injected with  $\sim$ 10 pl of water (control), 1,800 ng/ $\mu$ l wild-type or mutant (H189A) *Kdm4d* mRNA at 5–6 hpa by using a Piezo-driven micromanipulator (Primetech). Microinjection of *Zscan4d* mRNA was performed at 20 hpa to correspond to the early 2-cell stage. In some experiments, trichostatin A (TSA) was added to the culture medium at 15 nM from the beginning of the activation for a total of 8 hr. Preimplantation developmental rates were statistically analyzed by Student's *t* test. Further details on donor cell preparation, embryo transfer, mRNA preparation and other procedures are included in the [Extended Experimental Procedures](#).

### RNA-Sequencing Analysis

The embryos were directly lysed and used for cDNA synthesis using the SMARTer Ultra Low Input RNA cDNA preparation kit (Clontech 634936). After amplification, the cDNA samples were fragmented using Covaris sonicator (Covaris M220). Sequencing libraries were made with the fragmented DNA using NEBNext Ultra DNA Library Prep Kit for Illumina according to manufacturer's instruction (New England Biolabs E7370). Single end 50 bp sequencing was performed on a HiSeq 2500 sequencer (Illumina). Sequencing reads were mapped to the mouse genome (mm9) with Novoa-lignV3.02.00. All programs were performed with default settings (unless otherwise specified). Uniquely mapped reads ( $\sim$ 70% of total reads) were subsequently assembled into transcripts guided by the reference annotation (UCSC gene models) with Cufflinks v2.0.2. Expression level of each gene was quantified with normalized FPKM (fragments per kilobase of exon per million mapped fragments). Functional annotation of significantly different transcripts and enrichment analysis was performed with DAVID. Statistical analyses were implemented with R (<http://www.r-project.org/>). Independent 2 group Wilcoxon rank sum test were used to compare distributions using the *wilcox.test* function in R. Pearson's *r* coefficient was calculated using the *cor* function with default parameters. The hierarchical clustering analysis of the global gene expression pattern in different samples was carried out using *heatmap.2* function (gplots package) in R.

### Identification of Reprogramming Resistant Regions

A sliding window (size 100 kb, step size 20 kb) was used to assess the genome-wide expression level of 1-cell and 2-cell embryos. For each window, the expression level was quantified with normalized RPM (reads per millions of uniquely mapped reads). The significantly activated regions in 2-cell relative to 1-cell IVF embryos were identified with stringent criteria (FC > 5, Fisher's exact test *p* value < 0.01, RPM > 10 in 2-cell IVF embryos), and the overlapping regions were merged. These activated regions were classed into three groups based on their expression differences in SCNT and IVF 2-cell embryos.

### ACCESSION NUMBERS

The Gene Expression Omnibus (GEO) accession number for the RNA-seq data sets reported in this paper is GSE59073.

### SUPPLEMENTAL INFORMATION

Supplemental Information includes Extended Experimental Procedures, five figures, and four tables and can be found with this article online at <http://dx.doi.org/10.1016/j.cell.2014.09.055>.

### AUTHOR CONTRIBUTIONS

S.M. and Y.Z. conceived the project and designed the experiments. S.M. performed most of the experiments. Y.L. analyzed RNA-seq and ChIP-seq data sets. F.L. prepared RNA-seq libraries. L.S. performed RNA-seq. K.A.I. prepared donor MEF cells. A.I. assisted in some of the experiments. S.M. and Y.Z. wrote the manuscript.

### ACKNOWLEDGMENTS

We thank Drs. Shinpei Yamaguchi, Luis M. Tuesta, and Hao Wu for critical reading of the manuscript. This project is supported by NIH U01DK089565 (to Y.Z.). S.M. and K.A.I. are supported by postdoctoral fellowship from the Japan Society for the Promotion of Science (JSPS). Y.Z. is an investigator of the Howard Hughes Medical Institute.

Received: July 1, 2014

Revised: September 1, 2014

Accepted: September 19, 2014

Published: October 30, 2014

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