Genetic Deletion of Hesx1 Promotes Exit from the Pluripotent State and Impairs Developmental Diapause

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SUMMARY

The role of the homeobox transcriptional repressor HESX1 in embryonic stem cells (ESCs) remains mostly unknown. Here, we show that Hesx1 is expressed in the preimplantation mouse embryo, where it is required during developmental diapause. Absence of Hesx1 leads to reduced expression of epiblast and primitive endoderm determinants and failure of diapaused embryos to resume embryonic development after implantation. Genetic deletion of Hesx1 impairs self-renewal and promotes differentiation toward epiblast by reducing the expression of pluripotency factors and decreasing the activity of LIF/STAT3 signaling. We reveal that Hesx1-deficient ESCs show elevated ERK pathway activation, resulting in accelerated differentiation toward primitive endoderm, which can be prevented by overexpression of Hesx1. Together, our data provide evidence for a novel role of Hesx1 in the control of self-renewal and maintenance of the undifferentiated state in ESCs and mouse embryos.

INTRODUCTION

HESX1 (Homeobox gene expressed in stem cells 1) is a homeobox transcriptional repressor that was initially isolated from murine embryonic stem cells (ESCs) over 25 years ago (Thomas and Rathjen, 1992; Webb et al., 1993). Hesx1 is crucial for proper forebrain and pituitary development in both mice (Andoniadou et al., 2007) and humans, and inactivating mutations in HESX1 underlie septo-optic dysplasia (Dattani et al., 1998). It has been proposed that HESX1 might be required for the maintenance of pluripotency in human ESCs (Richards et al., 2004), and more recently a beneficial role during somatic cell reprogramming has been demonstrated (Polo et al., 2012), suggesting a role for HESX1 in regulation of pluripotency. However, the consequences of the genetic deletion of Hesx1 in ESCs have not been yet investigated. Here, we reveal a critical function of Hesx1 in self-renewal and maintenance of the undifferentiated state in ESCs and mouse embryos.

RESULTS

Loss of Hesx1 Results in Failure to Resume Embryonic Development Following Diapause

Hesx1 expression in preimplantation embryos has not been reported (Thomas and Beddington, 1996). RT-PCR analysis revealed the presence of Hesx1 mRNA in wild-type (WT) embryos (C57BL/6J background) at 3.5 and 4.5 days post coitum (dpc) (Figure 1A). Analysis of published data from single-cell microarray gene expression (Ohnishi et al., 2014) confirmed the expression of Hesx1 from early (embryonic day 3.25 [E3.25]) to late blastocyst stages (E4.5) (Figure 1B). At later stages, Hesx1 expression was detected in the primitive endoderm (PrE) (n = 4, p < 0.01). Immunofluorescence staining against GFP, to detect YFP expression, revealed the presence of YFP+ blastomeres in one of nine 8-cell stage morulas, two of 18 3.5-dpc blastocysts and none of nine 4.5-dpc blastocysts derived from Hesx1Cre+/;R26YFP/+ X Hesx1−/− crosses (Figure 1C). YFP expression was restricted to cells in the inner cell mass (ICM), and no staining was observed in the trophoblast. The low proportion of embryos showing YFP expression is likely due to the loss of regulatory elements in the Hesx1 locus caused by the targeting approach (i.e., introns 1–3 and exons 1–4 were replaced by a Cre cDNA [Andoniadou et al., 2007]).

A preimplantation phenotype for Hesx1 mutants has not been previously described. However, the role of Hesx1 in diapause has not been investigated, despite the conservation of the core transcriptional circuitry operating in the preimplantation epiblast (Epi) (Boroviak et al., 2015). To test the ability of diapaused embryos to resume development, we transferred a total of 81 blastocysts diapaused for 8 days directly into the uterus of pseudo-pregnant females and dissected the embryos 8 days later. At this point, embryos were staged around 10.5 dpc, despite having been gestated for 18.5 days in total (Figure 1D). A total of 58 embryos were recovered, and genotyping
Figure 1. Lack of Hesx1 Expression in Embryos Disrupts Developmental Diapause

(A) Hesx1 expression in 3.5- and 4.5-dpc C57BL/6J WT blastocysts.
(B) Hesx1 expression at different time points of preimplantation development measured by single-cell microarray. Hesx1 is expressed at higher levels in the Epi lineage at 3.5 dpc (n = 10, ^p < 0.01), but its expression becomes associated with PrE at 4.5 dpc (n = 4, **p < 0.005).
(C) Bright-field and immunofluorescence images of 2.5- and 3.5-dpc Hesx1^{Cre+}/;R26^{YFP+} embryos. Only 1 of 9 and 2 of 18 embryos showed YFP expression. Scale bars, 50 μm.
(D) 18.5-dpc diapaused embryos (8 days in diapause, then transferred to recipient females for further 10 days). Scale bar, 1 mm.
(E) 10.5-dpc Hesx1^{+/+} and Hesx1^{−/−} embryos derived from conventional matings. Scale bar, 1 mm.
(F) Immunofluorescence against NANOG and GATA6 in embryos after 6 days of diapause. Scale bar, 50 μm.
(G) Scatterplot of NANOG and GATA6 mean fluorescence intensity in Hesx1^{+/+} (n = 6) and Hesx1^{−/−} (n = 3) embryos subjected to 6 days of diapause.
analysis revealed 23 Hesx1+/−, 29 Hesx1+/−, and only 6 Hesx1−/−, therefore demonstrating a significant loss of Hesx1−/− mutants and a strong deviation from the expected Mendelian ratios (Table S1; p = 0.0069). In addition to the expected forebrain defects (Andoniadou et al., 2007), diapaused mutant embryos displayed severe developmental delay and small size (Figure 1D). These defects have not been previously observed in Hesx1-deficient mutants derived from conventional matings (Figure 1E) (Andoniadou et al., 2007), suggesting an involvement of Hesx1 in the maintenance of the expanded Epi when the preimplantation period is prolonged during diapause.

To further investigate failure in resuming development, we induced and maintained 2.5-dpc embryos from Hesx1+/− intercrosses in a diapause state for 6 days. Diapaused blastocysts were then stained with antibodies against NANOG (Epi) and GATA6 (PrE), and the maximum fluorescence intensity (MFI) of the two markers was quantified. This analysis revealed a trend toward a reduction in the expression of both markers in Hesx1−/− blastocysts (Figures 1F and 1G). Taken together, our results suggest that Hesx1 is expressed at preimplantation stages, when it is required to maintain normal expression of NANOG and GATA6 and to resume embryonic development after implantation.

Hesx1 Expression Is Controlled by Intrinsic and Extrinsic Signals Associated with Maintenance of the Naive Pluripotent State

The discovery of an early role for Hesx1 in diapause prompted us to investigate whether Hesx1 might regulate maintenance of the ESC state. Analysis of published chromatin immunoprecipitation sequencing (ChIP-seq) data (Marson et al., 2008) (Figure S1A) revealed the potential co-occupancy of different core pluripotency factors (CPF) on the Hesx1 promoter region. ChIP-qPCR on WT ESCs cultured in serum/leukemia inhibitory factor (LIF) revealed a significant enrichment in the amount of chromatin bound to SOX2 and NANOG and a non-significant increase in OCT3/4-bound chromatin (Figure 2A). To assess possible functional consequences, we carried out luciferase assays in HEK-293T cells. Co-transfection of a plasmid expressing SOX2 with a reporter containing a 600-bp region upstream of the ATG of the Hesx1 locus, which includes the CPF binding sites, revealed a significant upregulation of luciferase activity relative to the controls (Figure 2B). Simultaneous co-transfection of plasmids expressing SOX2, NANOG, and OCT3/4 resulted in a further elevation of the luciferase activity compared with cells transfected only with SOX2 (Figure 2B). SOX2 binding sites are found in the Hesx1 promoter (Eroshkin et al., 2002), but the elements bound to OCT4 and NANOG have not been described. The reasons underlying the lack of consensus sequences for OCT4 and NANOG are not known, despite it having been shown that both these factors are bound to the Hesx1 promoter by ChIP-seq.

Naive pluripotency can be stimulated by cultivating ESCs in defined conditions known as 2iLIF. This comprises inhibitors of mitogen-activated protein kinase (PD03) and glycogen synthase kinase 3 (CHIR), in addition to the cytokine LIF. These conditions stimulate the expression of factors involved in the maintenance of the naive state (Ying et al., 2008). Culture of WT ESCs in 2iLIF for 48 h followed by qRT-PCR analysis revealed a 9-fold increase Hesx1 mRNA levels compared with serum/LIF conditions (Figure 2C). Conversely, Hesx1 expression was downregulated 9-fold 24 h after removal of PD03 and CHIR (Figure 2D). The up- and downregulation in Hesx1 expression was similar to that observed for Nanog and Rex1 (Figures 2C and 2D).

Hesx1 Expression in ESCs Restricts Exit toward an Epi Fate by Reinforcing LIF Signaling

To assess whether the lack of Hesx1 in ESCs may have molecular consequences, we generated Hesx1-deficient clones by direct derivation of ESC lines from Hesx1-deficient (Hesx1−/−) and Hesx1+/− control blastocysts. qRT-PCR detected the downregulation of pluripotency markers (i.e., Nanog, Rex1, Klf4) and upregulation of lineage commitment markers (i.e., Fgf5, FoxA2, Otx2) in Hesx1−/− relative to Hesx1+/− ESCs (Figure 3A). Immunostaining revealed a significant reduction in number of NANOG+ nuclei in Hesx1−/− ESCs (Figure 3B). The ability to self-renew was evaluated by clonal assay followed by alkaline phosphatase (AP) staining. Hesx1−/− ESCs showed a marked reduction in numbers of AP+ colonies after 6 days in culture compared with control cells (Figure 3C), suggesting that Hesx1 is important for suppressing ESC differentiation.

Hesx1 has been proposed to be a direct transcriptional target of LIF/STAT3 signaling (Martello et al., 2013), and analysis of STAT3 ChIP-seq data suggests a direct binding on the Hesx1 promoter (Figure S1). In agreement with this notion, when Hesx1+/− ESCs were cultured in serum/LIF and subsequently deprived of LIF signaling through removal of LIF in the medium, Hesx1 as well as Nanog

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and Rex1 expression were significantly reduced (Hesx1, 70%; Nanog, 40%; Rex1, 40%) (Figure 3D). We next sought to evaluate whether the ability to respond to LIF signaling may be impaired in Hesx1-deficient cells. To this end, Hesx1+/− and Hesx1−/− ESCs were cultured in serum-free medium for 12 h and subsequently subjected to LIF stimulation (Figures 3E and 3F). Western blot analyses revealed that while the amount of total STAT3 did not differ between genotypes (Figures 3E and 3F), levels of phospho-STAT3 were significantly reduced in Hesx1−/− relative to Hesx1+/− ESCs (Figures 3E and 3F). Next, we evaluated the response of Hesx1-deficient and WT ESCs to LIF stimulation in 2i conditions. STAT3 targets such as Socs3, Klf4, and Stat3 were rapidly upregulated in Hesx1+/− ESCs in response to LIF supplementation (Figure 3G). However, the transcriptional activation of these target genes was reduced in Hesx1−/− relative to Hesx1+/− ESCs (Figure 3G). Response to LIF was further evaluated in a LIF-withdrawal assay to assess the ability of ESCs to resist differentiation. In this assay, Hesx1−/− ESCs showed reduced retention of AP activity when compared with Hesx1+/− ESCs, as evidenced by the lower number of AP colonies. Conversely, numbers

Figure 2. Hesx1 Expression in ESCs Is Regulated by Naive Pluripotency-Promoting Signals
(A) ChIP-PCR showing the binding of SOX2, NANOG, and OCT3/4 to the Hesx1 promoter (n = 3 experiments). Diagram depicting part of the Hesx1 locus, where POS is the region reported to be occupied by core pluripotency factors (CPF) and NEG represents a region in which binding was not reported.
(B) Schematic diagram of the firefly luciferase reporter used in the co-transfection experiments in HEK-293T cells. Synergistic activation of Hesx1 transcription by SOX2, NANOG, and OCT3/4 (n = 3 experiments).
(C) qRT-PCR for Hesx1, Nanog, and Rex1 expression in 2iLIF relative to serum/LIF (n = 3 experiments).
(D) qRT-PCR for Hesx1, Nanog, and Rex1 expression upon removal of the PD03 and CHIR (2i). Point 0H represents cells in 2i prior to inhibitor withdrawal (n = 3 experiments).
(E) qRT-PCR showing that Hesx1 expression is rapidly upregulated in WT ESCs upon LIF stimulation and MEK inhibition. Point 0H represents cells after a starvation period of 12 h in serum-free medium (n = 3 experiments).
Figure 3. Loss of *Hesx1* in ESCs Leads to Reduced Response to LIF and Premature Epiblast Differentiation

(A) qRT-PCR evaluating the levels of expression of both pluripotency and commitment-related factors (n = 3 experiments).

(B) Immunofluorescence staining against NANOG showing a reduction in NANOG+ cells in *Hesx1<sup>−/−</sup>* ESCs (n = 3 independent ESC clones).

Scale bar, 50 μm.

(C) AP staining after 6 days of culture at clonal density (n = 4 experiments using three ESC clones).

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of AP− colonies were increased in the absence of Hesx1 (Figure 3H). Together, these data suggest that loss of Hesx1 in ESCs results in reduced LIF signaling.

The transition from naïve pluripotency to differentiated primed Epi state is associated with a loss in STAT3 responsiveness, which seems to be partly regulated by a reduction in pSTAT3 levels (Yang et al., 2010). We sought to explore whether Hesx1−/− ESCs may be prompted to transit from naïve to Epi state. Hesx1+/− and Hesx1−/− ESCs were cultured in either serum/LIF or in the presence of activin and fibroblast growth factor 2 (FGF2) to induce Epi stem cell (EpiSC) differentiation (Tesar et al., 2007). Growth analysis showed no apparent differences in total cell numbers between Hesx1-deficient and control cells when cultured in the presence of serum/LIF. In contrast, numbers of Hesx1−/− cells were significantly increased in the presence of activin and FGF2 relative to the Hesx1+/− control cells (Figure 3J). In accordance, numbers of EpiSC colonies were increased in the Hesx1−/− relative to the Hesx1+/− cell cultures, while both genotypes generated comparable ESC colony numbers in serum/LIF conditions (Figure 3I). Together, these analyses demonstrate that loss of Hesx1 leads to decreased LIF/STAT3 signaling and elevated morphology when switched from serum/LIF to 2iLIF medium (Figure 4C). As signaling downstream of pERK initiates epithelial-to-mesenchymal transition, these morphological defects are consistent with the elevated ERK activity observed in Hesx1−/− ESCs.

To assess molecularly the ability of Hesx1−/− ESCs to exit the naïve state and differentiate, we performed RNA sequencing on Hesx1+/− and Hesx1−/− ESCs 24 h after 2iLIF removal from ground-state culture conditions (Figure 4D). Whole-transcriptome analysis revealed lower expression of pluripotency markers in Hesx1−/− ESCs compared with wildtype controls (i.e., Lin28a, Pou5f1, Sox2, Piiwil2). In addition, Hesx1−/− ESCs showed higher expression of Epi markers (Gsc, Wnt3a) and PrE (Sox7, Sox17, Foxa2, Gata4) markers relative to control Hesx1+/− ESCs (Figure 4D). Gene ontology term analysis of the top 500 up- and downregulated genes in Hesx1−/− ESCs (log2 fold change >1 and <−1, respectively, with adjusted p value <0.05) revealed a significant enrichment of early developmental terms (i.e., Theiler stage 2–5), whereas genes upregulated in Hesx1−/− ESCs belonged mostly to terms related to extraembryonic tissues and visceral organs (Figures S2A and S2B). GREAT (Genomic Regions Enrichment of Annotation Tool [McLean et al., 2010]) analysis of genes common between ERK targets (Hamilton and Brickman, 2014) and genes downregulated in Hesx1−/− ESCs (Figure S3A) revealed a significant enrichment toward a negative regulation of both MAPK cascade activation and ERK protein phosphorylation (Figure S2C, see starred terms). For instance, negative regulators of this pathway such as Dusp6, Dusp1, Sry1, and Spry4, among others, were downregulated in Hesx1−/− relative to Hesx1+/− ESCs, suggesting that HESX1 might act as a negative regulator of MAPK signaling (Tables S2A and S2B).

The activation/phosphorylation of ERK has been shown to derepress PrE gene expression to promote functional priming toward this cell lineage (Hamilton and Brickman, 2014). As Hesx1−/− ESCs showed increased pERK protein levels and upregulation of endodermal transcripts following exit from the naïve state, we tested the ability of these mutant cells to undergo PrE differentiation.

Hesx1 Expression in ESCs Limits Exit toward a PrE Fate by Inhibiting ERK Signaling

FGF/ERK signaling is required to instruct the exit of ESCs from the self-renewal to initiate differentiation program (Kunath et al., 2007). Three Hesx1+/− and three Hesx1−/− ESC clones were cultured under self-renewing and ground-state conditions, and whole-cell lysates were collected to evaluate the levels of phosphorylation of ERK1/2 (Figure 4A). Hesx1−/− ESCs showed increased levels of pERK1/2 compared with Hesx1+/− controls (Figure 4A), both in serum/LIF and 2iLIF culture conditions (Figure 4B). Although ESCs from both genotypes formed tightly packed colonies in ground-state conditions, Hesx1−/− ESCs showed a marked delay in acquiring this typical cellular morphology when switched from serum/LIF to 2iLIF medium (Figure 4C). As signaling downstream of pERK initiates epithelial-to-mesenchymal transition, these morphological defects are consistent with the elevated ERK activity observed in Hesx1−/− ESCs.
Figure 4. Loss of Hesx1 in ESCs Results in Increased ERK Signaling and Promotion of the PrE Fate

(A and B) Western blot for pERK1/2 and ERK1/2 on WT and Hesx1-/- ESCs cultured in serum/LIF (A) and 2iLIF (B) conditions (n = 3 ESC clones in three independent experiments).

(C) Bright-field images of Hesx1+/+ and Hesx1-/- ESCs cultured in serum/LIF or 2iLIF. Scale bars, 200 μm.

(D) Heatmap of the differentially expressed genes showing the lower expression of pluripotency-associated (green) and higher expression of differentiation (blue and red) markers in Hesx1-/- relative to WT ESCs. Data represent the differentially expressed genes 24 h after 2i removal.

(E) Flow-cytometry density plots of Hesx1+/+, Hesx1-/-, and Hesx1over ESCs cultured in 2iLIF or after 3 days of PrE differentiation. Cells are stained with PECAM-1 (y axis) and PDGFRα (x axis).

(F) Immunofluorescence staining for NANOG (red) and GATA6 (purple) on Hesx1+/+, Hesx1-/-, and Hesx1over cells following 7 days of PrE differentiation. DNA is counterstained with DAPI. Scale bar, 100 μm.

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in vitro (Anderson et al., 2017). We introduced Hesx1
toxESCs, which were generated by cloning a doxycycline-
inducible HA-tagged-HEX1 cDNA into ESCs, thus
providing a Hesx1 overexpression system (Figures S3A–
S3C). During PrE differentiation (day 3), numbers of
platelet-derived growth factor receptor α (PDGFRα; an
dermaternal marker) positive cells were approximately
27% in Hesx1−/− ESCs (26.67 ± 5.61%) but around 5%
in Hesx1+/− ESCs (5.14 ± 0.59%) (Figure 4E). Hesx1 overex-
pressing cells maintained an undifferentiated phenotype
comparable with cells cultured in 2iLIF (Figure 4E), which
resulted in a complete lack of PrE differentiation. In
contrast, Hesx1−/− ESC cells acquired a complete PrE
phenotype, as demonstrated by GATA6 expression and
loss of NANOG staining (Figure 4F). qRT-PCR analysis at
day 7 of PrE differentiation revealed a downregulation of
pluripotency-associated markers (Nanog, Oct4) and upregu-
ation of endodermal transcripts (Gata6, Pdgfra) in
Hesx1−/− ESCs relative to Hesx1+/− control cells. In contrast,
Hesx1loxESCs showed a complete lack of PrE markers
expression at day 7 (Figure 4G). These results suggest that
Hesx1 expression in naive ESCs prevents their differentia-
tion into PrE by negatively regulating the activation of
ERK signaling.

Collectively, this study demonstrates that Hesx1 is a
novel factor involved in the regulation of ESC fate (Fig-
ure 4H). We show that Hesx1 expression responds to both
intrinsic and extrinsic pluripotency-stimulating signals to
promote self-renewal and inhibit differentiation toward
both the Epi and PrE cell fates. Consistent with the
in vitro data, we reveal that Hesx1 is expressed in the ICM
of the preimplantation mouse embryo, where it is required
to resume development following diapause.

**EXPERIMENTAL PROCEDURES**

**Cell Culture**

ESCs were cultured as described in Supplemental Experimental
Procedures. Differentiation of ESC to EpiSC or PrE followed stan-
dard procedures (Tesar et al., 2007; Anderson et al., 2017; Supple-
mental Experimental Procedures).

**ESC Derivation**

Hesx1lox, Hesx1−/−, Hesx1+/− ESCs were derived from breeding of mice previously
mentioned. Hesx1−/− and Hesx1+/− ESCs were derived from
Hesx1+/− intercrosses (129/Sv background [Dattani et al., 1998]),
Hesx1+lox, R26YFP/+, Hesx1−lox, R26YFP/+, and Hesx1−lox, R26YFP/+ ESCs
from differential crosses between Hesx1−/− (see above), Hesx1lox/+ (C57BL/6 background [Andoniadou et al., 2007]), and Hesx1+/−;
R26YFP/YFP mice (C57BL/6 background). For ESC isolation, 3.5-dpc
embryos were cultured on a layer of mitotically inactive mouse em-
bryonic fibroblasts in N2B27 supplemented with 2iLIF.

**ChIP-PCR**

Chromatin immunoprecipitation was adapted from the Young
lab (Marson et al., 2008). Primers used to screen chromatin
enrichment are listed in Table S3. Enrichment values were
calculated using the percent input method (100 × 2 (adjusted
input – Ct(IP))).

**Dual-Luciferase Assay**

Cells were lysed and analyzed for luciferase activity at 48 h post
transfection. Total amount of transfected DNA was normalized
by addition of an empty vector (pBluescript). Cells were harvested
and assayed for luciferase activity using the Dual Luciferase Reporter
Assay System (Promega) and luminescence was measured using
a BMG FLUOstar Optima multiplate reader (BMG Labtech).
More details can be found in Supplemental Experimental
Procedures.

**Immunofluorescence Staining, Western Blot, and Flow
Cytometry**

See Supplemental Experimental Procedures for details. Quantifica-
tion of NANOG and GATA6 levels was carried out by manually
drawing a line through the nucleus of each cell (either NANOG/GATA6
or NANOG/GATA6) and measuring the MFI of NANOG
or GATA6 across the line. For flow cytometry, cells were dissociated
to a single-cell suspension and resuspended in FACS buffer (PBS +
10% fetal calf serum). Cells were then stained with DAPI to eli-
minate dead cells and gated using SSC-H against SSC-W to exclude
doublets. Samples were processed on a BD Fortessa (BD Bioscience)
and data analyzed using FCS Express. A list of antibodies used can be
found in Table S4.

**qRT-PCR**

Total RNA from cells or embryos was extracted using RNeasy micro
or mini kits (Qiagen). Reverse transcription was performed using
the iScript cDNA synthesis kit. Real-time PCR was performed using
an iTaq Universal SYBR Green Supermix (Bio-Rad). Gene expres-
sion was calculated relative to Gapdh via the ΔΔCt method. A list of
primers used can be found in Table S3.

**Diapause Induction**

For induction of diapause (MacLean Hunter and Evans, 1998),
2.5-dpc Hesx1+/− pregnant females from Hesx1+/− intercrosses
were injected intraperitoneally with 10 μg of tamoxifen (Sigma)
and 3 mg of Depo-Provera (Pfizer). Diapausd blastocysts were surg-
cally transferred into the uterus of 2.5-dpc pseudo-pregnant CD1
mice (C57BL/6 background [Andoniadou et al., 2007]), and Hesx1+/−;
R26YFP/YFP mice (C57BL/6 background). For ESC isolation, 3.5-dpc
embryos were cultured on a layer of mitotically inactive mouse em-
bryonic fibroblasts in N2B27 supplemented with 2iLIF.

(G) qRT-PCR after 7 days of PrE differentiation (n = 3 ESC clones in three independent experiments).
(H) Schematic depicting the summary of the findings. HESX1 promotes the undifferentiated state in ESCs by negatively regulating ERK
activation and by reinforcing LIF/STAT3 signaling. Loss of Hesx1 results in increased ERK and concomitant decreased in pSTAT3 signaling
with a consequent premature differentiation toward endoderm and epiblast lineages, respectively.
recipient females and embryos collected at the specific developmental stages. All mouse experiments were performed under the umbrella of a UK Home Office Project Licence and by trained Personal Licence holders.

**Statistical Analysis**

Unless stated, all experiments were carried out on biological and experimental triplicates. All data represent mean ± SEM. Statistical significance was calculated with Student’s t test.

**ACCESSION NUMBERS**

The accession number for the RNA-sequencing data is ArrayExpress: E-MTAB-5816.

**SUPPLEMENTAL INFORMATION**

Supplemental Information can be found online at https://doi.org/10.1016/j.stemcr.2019.10.014.

**AUTHOR CONTRIBUTIONS**

S.P. and J.P.M.-B. conceived and designed the study, S.P. carried out the majority of the experiments. S.B. performed experiments. J.A. performed the bioinformatics analysis. T.A.R. and J.M.B. helped with experimental design and data interpretation. S.P. and J.P.M.-B. wrote the manuscript.

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