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Supplemental Information

Tsix RNA and the Germline Factor, PRDM14, Link X Reactivation and Stem Cell Reprogramming

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SUPPLEMENTAL FIGURES



Figure S1, related to Figure 1. Ectopic XCI in *Tsix*-mutant E5.5 diapause embryos

(A) Male *Tsix*^{-/Y} embryo displaying H3K27me3(green)-positive spots (arrows) suggesting ectopic XCI in some NANOG(red)-negative cells. The boxed ICM region is shown in a close-up in the middle and right panel. Projection of z-series (full embryo). Scale bars = $20 \ \mu m$

(B) Female $Tsix^{-/-}$ embryo with two H3K27me3-spots in several extraembryonic cells (stars, PE and/or TE cells). Projection of 20 μ m thick z-stack (partial embryo).





Figure S2, related to Figure 7. Pluripotency factor binding across the *Rnf12* locus and the *Jpx/Xist/Tsix* region

(A) ChIP-seq data (also shown in Figure 7B) for binding of NANOG, OCT4, SOX2 (Marson et al., 2008) and PRDM14 (Ma et al., 2010) along the *Xic*, retrieved via the NCBI epigenomics database. Arrows indicate binding sites assayed in (B).

(B) ChIP-qPCR for pluripotency factor binding 5' of *Rnf12* (a, b, c) and at *Xist* intron 1 (d) in undifferentiated *Prdm14*^{+/+} (black) and *Prdm14*^{-/-} (red) ESCs. Error bars = SD. Goat IgG = negative control for α OCT4 and α SOX2. Rat IgG = negative control for α NANOG.

				Xic loci		
		Rnf12	Xist promoter	Xist intron 1	DXPas34/ Tsix	Xite
ctors	OCT4		-			
	SOX2	\bigcirc	-		-	\bigcirc
y fa	KLF4	\triangle	_	_	\triangle	\triangle
anc	NANOG	0	-	0	-	-
pote	C-MYC	-	-	-		-
uri	REX1	-	igodol	-	igodol	-
Б	PRDM14	\bigcirc	-	\bigcirc	-	-

Α



RNF12 ---> REX1:ub

Jpx RNA

Јрх

Rnf12

⊢ Tsix F

Xite

intron 1

Figure S3, related to Figure 7. Extended model for molecular mechanisms of XCR

(A, B) XCR and XCI are controlled by multiple mechanisms. The master regulator *Xist* is the target of opposing factors. Several pluripotency factors bind to regulatory regions of *Rnf12*, *Xist* and *Tsix*, where they act either as activators or repressors. One of those factors is PRDM14, which acts repressively by binding to *Xist* intron1 and by recruiting PRC2 to *Rnf12*, which PRC2 silences through establishing H3K27 tri-methylation. *Tsix*, which is activated by pluripotency factors, in turn represses *Xist*, at least in part by recruiting PRDM14 to *Xist* intron 1. In addition to these repressive forces, the lack of the expression of *Xist*-activators RNF12 and Jpx contribute to the *Xist* "off" state during XCR. The question mark indicates that nothing is known about the regulation of *Jpx*.

(C) In the absence of *Tsix*, PRDM14 dissociates from *Xist* intron 1. During XCR in blastocysts, *Xist*-repression is thereby delayed. However, in *Tsix^{-/-}* mutant pluripotent stem cells, *Xist* is not upregulated due to the lack of RNF12 and Jpx and by repression through other pluripotency factors.

(D) In *Prdm14*-mutant cells/embryos, *Rnf12* gets de-repressed and its protein ubiquitinates REX1, another *Xist* and *Tsix* regulator, resulting in REX1 degradation. Due to other repressive pluripotency factors this is not sufficient to lead to upregulation of *Xist* in *Prdm14^{-/-}* ESCs. However, in *Prdm14^{-/-}* blastocysts and during iPSC reprogramming this leads to a reduced XCR-efficiency.

(E) In cells before or after XCR, the lack of pluripotency factor-driven repressive mechanisms and the expression of the *Xist* activators RNF12 and Jpx lead to full upregulation of *Xist*.

SUPPLEMENTAL EXPERIMENTAL PROCEDURES

Expression analysis by qPCR

ESC and iPSC RNA was isolated and DNase I-treated using RNeasy Mini kit (Qiagen). RNA was then reverse transcribed with Oligo(dT)₁₅ primers (Promega) and Superscript III reverse transcriptase (Invitrogen). QPCR on cDNA of at least three biological replicates each for *Prdm14*^{+/+} and *Prdm14*^{-/-} ESCs was performed on an Bio-Rad iCycler using iQ SYBR Green Supermix (Bio-Rad). Ct values were normalized to Gapdh in order to calculate expression changes (Pfaffl, 2001).

Stable transfection of ESCs

2x10⁷ EL 16.7 and *Tsix*-^{*StopTST*} (Ogawa et al., 2008) mouse ESCs were electroporated with 30 mg of linearized pCAGGS plasmid vector containing recombinant PRDM14 fused to C-terminal Flag and Hemagglutinin tags (PRDM14-FH) (Yamaji et al., 2013), in PBS using GenePulser II (Bio-Rad) as described (Anguera et al., 2011). Cells were selected using media supplemented with 1µg/ml Puromycin (Gibco). PRDM14-FH expression was confirmed by Western Blot using anti-HA tag antibody (Sigma, H-6908).

Chromatin immunoprecipitation

EL 16.7, *Tsix*-Stop, *Prdm14*^{+/+} or *Prdm14*^{-/-} mouse ESCs were trypsinized and crosslinked with 1.1% formaldehyde. $5x10^6$ cells were subjected to chromatin immunoprecipitation as described previously (Jeon and Lee, 2011) using specific antibodies (see below). Enrichment was quantified using a Bio-Rad iCycler.

List of antibodies used for immunostainings

Antibody	Dilution
Alexa Fluor 488/555/647 secondary antibodies (Invitrogen)	1:500
goat anti-GATA4 (Santa Cruz, sc-1237))	1:50
mouse anti-H3K27me3 (Abcam, ab6002)	1:100
rabbit anti-NANOG (Novus Biologicals, NB100-588)	1:750
rat anti-NANOG (eBioscience, 14-5761)	1:200
mouse anti-SSEA1 (Developmental Studies Hybridoma	1:200
Bank, University of Iowa, MC-480)	

Primer list for quantitative RT-PCR

Target	Primers	Primer Sequence
Dnmt3b ¹	Dnmt3bBP1F	CTC GCA AGG TGT GGG CTT TTG TAA C
	Dnmt3bBP1R	CTG GGC ATC TGT CAT CTT TGC ACC
Dnmt3l ¹	Dnmt3IBP1F	CCA GGG CAG ATT TCT TCC TAA GGT C
	Dnmt3IBP1R	TGA GCT GCA CAG AGG CAT CC
Gapdh ¹	GapdhBP1F	ATG AAT ACG GCT ACA GCA ACA GG
	GapdhBP1R	CTC TTG CTC AGT GTC CTT GCT G
Gata6 ¹	Gata6BP1F	CAC AGT CCC CGT TCT TTT ACT G
	Gata6BP1R	GTG GTA CAG GCG TCA AGA GTG
Jpx ²	Jpx76+	TTA GCC AGG CAG CTA GAG GA
	Jpx255-	AGC CGT ATT CCT CCA TGG TT
Nanog ¹	NanogBP1F	CTT TCA CCT ATT AAG GTG CTT GC
	NanogBP1R	TGG CAT CGG TTC ATC ATG GTA C
Oct4 ¹	Oct4BP1F	GAT GCT GTG AGC CAA GGC AAG
	Oct4BP1R	GGC TCC TGA TCA ACA GCA TCA C
Rnf12 ³	Rnf12 ex4-5 for	GGT CCA CCA CAG AGC
	Rnf12 ex4-5 rev	TGA CCA CTT CTT GTT GTA TTT CC
Sox2 ¹	Sox2BP1F	CAT GAG AGC AAG TAC TGG CAA G
	Sox2BP1R	CCA ACG ATA TCA ACC TGC ATG G
Tsix ⁴	TsixBP6F	TGG GTC ATT GGC ATC TTA GTC
	TsixBP6R	CCC AGG GTG TCT GAT CTC TT
Xist ⁵	XistBP2F	CCC GCT GCT GAG TGT TTG ATA TG
	XistBP2R	CAG AGT AGC GAG GAC TTG AAG AG

The primer sequences have been previously described in 1 (Kurimoto et al., 2006), 2 (Sun et al., 2013), 3 (Barakat et al., 2011), 4 (Sugimoto et al., 2007) and 5 (Shibata and Lee, 2003).

List of antibodies used for ChIP experiments

Antibody	Isotype Control	Amount per
		Reaction (mg)
Anti-Histone H3K27me3 rabbit	Rabbit IgG (Abcam, ab46540)	5
polyclonal (Active Motif, cat# 19155)		
Anti-Sox2 (Y-17) goat polyclonal	Normal goat IgG (Santa Cruz, sc-	5
antibody (Santa Cruz, sc-17320)	2028)	
Anti-Oct3/4 (N-19) goat polyclonal	Normal goat IgG (Santa Cruz, sc-	5
antibody (Santa Cruz, sc-8628)	2028)	
Anti-Mouse Nanog clone eBioMLC-	Rat IgG2A (Abcam, ab18450)	2.5
51 rat monoclonal antibody		
(eBioscience, cat# 14-5761)		

Primer list for genomic loci tested on ChIP experiments

Amplicon	Primers	Primer Sequence	
β -actin promoter ¹	b_actin_prom_F	CCG TTC CGA AAG TTG CCT T	
	b_actin_prom_R	CGC CGC CGG GTT TTA TA	
5' Rnf12	RNF12_P14_3F	AGC GCC AGC TCG GAG ACG TA	
	RNF12_P14_3R	GGC CTG TGA AGC TGG GAG CG	
4kb upstream to Rnf12 ¹	RNF12_4kb_F	CAG CCT CTG GCT CTA CCA GT	
	RNF12_4kb_R	GTG ACC TGC TGG GGA GAA TA	
5kb upstream to Rnf12 ¹	RNF12_5kb_F	GCC TGT CAA ACG TCC TGT TTA	
	RNF12_5kb_R	GGA GGT TGT GGG AGA AAC AA	
H3K27me3 upstream to			
Rnf12	RNF12_K27_F	CTC CCA AAT GAC CCT TCC CC	
	RNF12_K27_R	TGA GAG GAC TGC AAG AAG GC	
Xist Intron 1 ²	XIn1_F	AAC CCT TTT AAG TCC ACT GTA AAT TCC	
	Xln1_R	TAG AGA GCC AGA CAA TGC TAA GCC	
Xist Intron 1 (Mus-specific)	Xin1_ASP_F	CTA GAG AGC CAG ACA ATG CT	
	Xin1_ASP_R2 (Mus)	TTT TGC ATT TGC CTT TTG AA	
Xist Intron 1 (Cas-specific)	Xin1_ASP_F3	AAA TGT TTC CTT TTG AAG CA	
	Xin1_ASP_R1 (Cas)	TTT TGC ATT TGC CTT TTG AT	

¹ Primer sequences for regions 4 kb and 5 kb upstream to *Rnf12* transcription start site as well as control non-binding β -actin promoter region were adopted from (Navarro et al., 2011).

² Xist intron 1 primer pair was described in (Navarro et al., 2008).

SUPPLEMENTAL REFERENCES

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