Supplemental Figures

Figure S1. Reverse transcription polymerase chain reaction using wild-type blastocysts recovered from the uterus *in vivo*.

Abundant expression of the *Fthl17* gene in female embryos was confirmed using wild-type blastocysts recovered from the uterus (see the Materials and Methods for details).

Figure S2. Alignment of the *Fthl17* family of genes and position of specific PCR primers for each gene.

Dots indicate identical nucleotides among the seven sequences. The sequence of each primer is listed in Supplemental Table S1. The RT–PCR primers for *Fthl17-L2* and *Fthl17-L4* could not be designed to distinguish between these genes.

Figure S3. Southern genomic hybridization analysis of the *Fthl17* family of genes.

Southern hybridization was carried out using the full length *Fthl17* sequence as a probe.

Figure S4. Analysis of X inactivation status at the blastocyst stage.

Comparison of our microarray data (fold change in female/male gene expression) with *in situ* hybridization data (relative Xp expression level at the blastocyst stage) reported by Patrat et al. (Proc Natl Acad Sci U S A 106: 5198–5203). The gray box indicates our group 1 genes (see Results; fold change –1.2 to +1.2) considered to be inactivated at this stage. The results from the *in situ* hybridization experiments were consistent with our microarray data. Although some probes were redundant, the results from all probes are listed. The relative positions of X-linked genes are indicated.

Figure S5. Methylation analysis of the H19 locus at the blastocyst stage.

The differentially methylated region of the H19 locus was also analyzed by bisulfite sequencing as a control.

Fig. S1

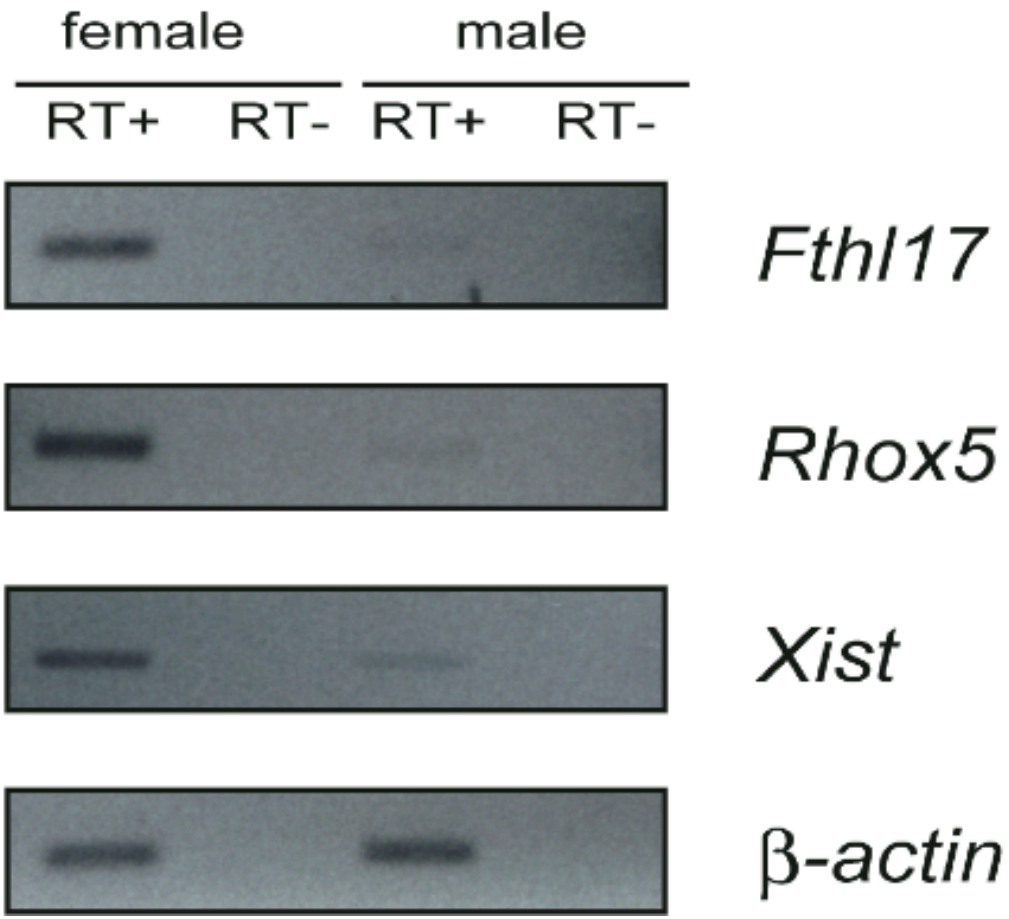

Fig.S2

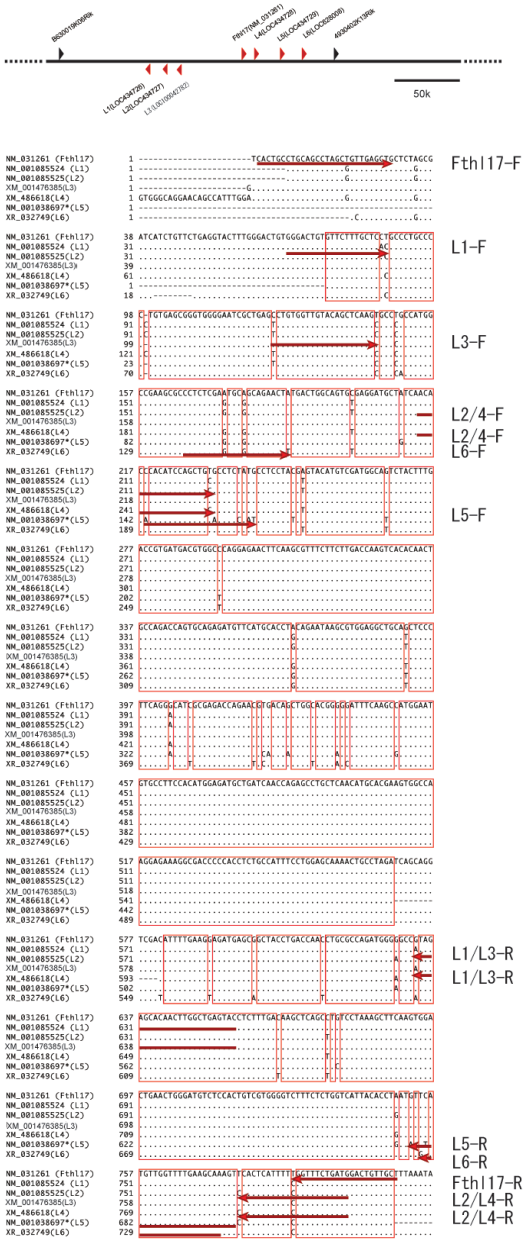
50k
Fthl17-F
L1-F
L3-F
L2/4-F
L2/4-F
L6-F
L5-F
L1/L3-R
L1/L3-R
L5-R
L6-R
Fthl17-R
L2/L4-R
L2/L4-R

Fig. S3

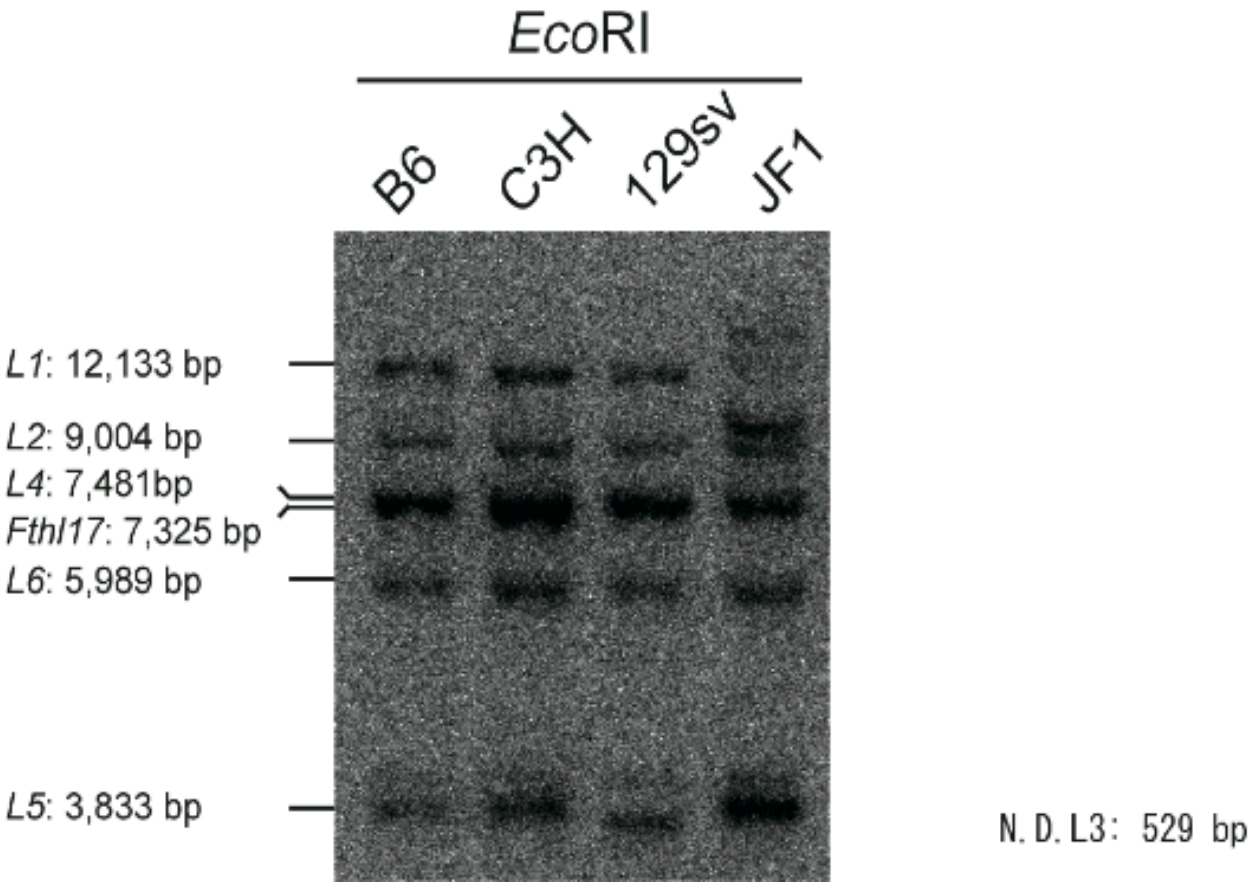
EcoRI
B6
C3H
129sv
JF1
L1: 12,133 bp
L2: 9,004 bp
L4: 7,481bp
Fthl17: 7,325 bp
L6: 5,989 bp
L5: 3,833 bp
N.D.L3: 529 bp

Fig. S4

no	gene name	primary sequence name	fold change	relative Xp expression (%)
1	Atp6ap2	TF11785	1.79	70-99
2	Utx	TB5892	1.27	50-69
2	Utx	1D121-5 A02	1.25	50-69
3	Slc25a5	TB759	1.40	14-29
4	**Lamp2**	**TB3265**	**1.16**	**14-29**
5	Fmr1	TB2174	1.29	14-29
5	Fmr1	1L014 E01	1.22	14-29
6	**Mecp2**	**TB3649**	**1.10**	**50-69**
6	**Mecp2**	**TF32714**	**1.06**	**50-69**
7	**G6pdx**	**TB2240**	**1.12**	**30-49**
8	**Kif4**	**TB3151**	**-1.02**	**14-29**
9	Rps4x	TB4924	1.56	14-29
10	**Chic1**	**Y11896.1**	**1.02**	**<15**
11	**Rnf12**	**TB6737**	**1.12**	**<15**
11	**Rnf12**	**1D118-5 F05**	**1.05**	**<15**
11	**Rnf12**	**TB4862**	**1.02**	**<15**
12	**Atrx**	**TB6003**	**1.11**	**<15**
13	**Atp7a**	**TB919**	**1.20**	**<15**
13	**Atp7a**	**1K012 B12**	**1.03**	**<15**
13	**Atp7a**	**TF23690**	**-1.05**	**<15**
13	**Atp7a**	**TF27254**	**-1.09**	**<15**
14	**Gla**	**TB650**	**-1.20**	**30-49**
15	**Fgd1**	**TB2102**	**1.04**	**<15**
16	Huwe1	TF31367	1.30	100
16	Huwe1	TB7858	1.26	100
17	**Jarid1c**	**TB5217**	**1.03**	**<15**

Fig. S5

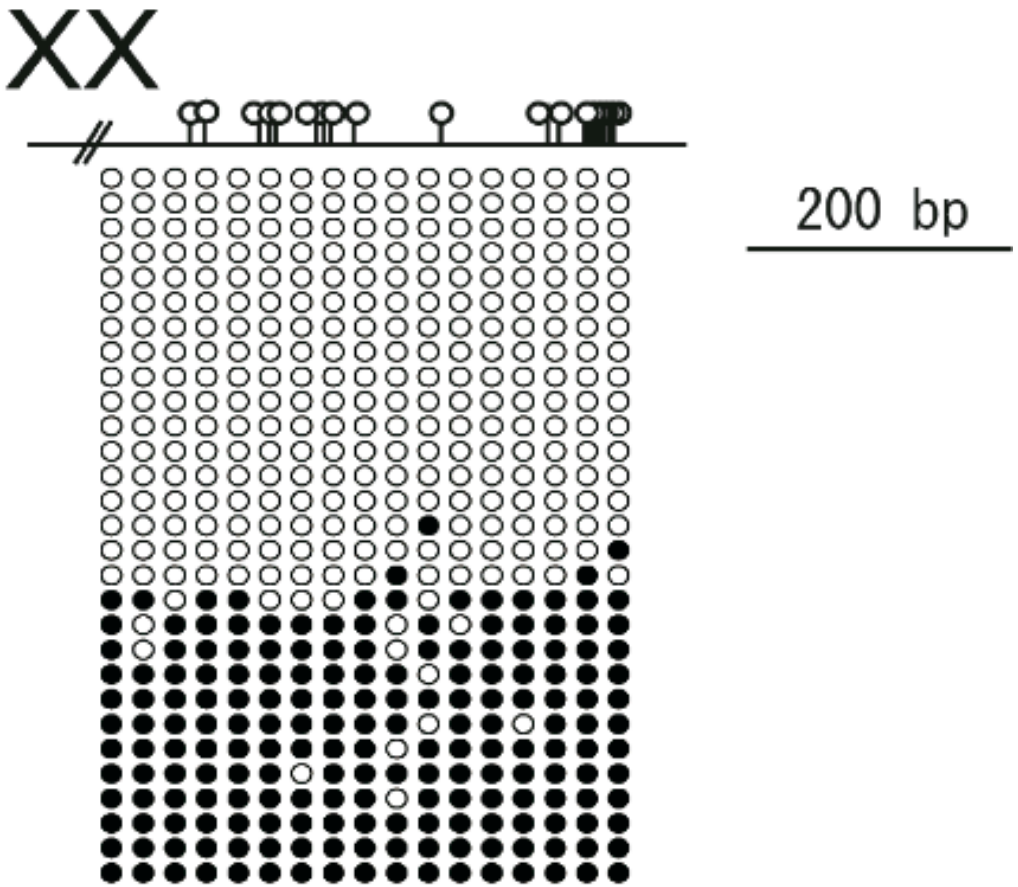

Table S1 Specific PCR primers used for amplifying the *Fthl17* gene family members.

Gene name	Official symbol	Protein	mRNA	PCR primer: forward	PCR primer: reverse
Fthl17	*Fthl17*	NP_112551	NM_031261	cactgcctgcagcctagct	gcaacagtccatcagaaacca
Fthl17-L1	*EG434726*	NP_001078993	NM_001085524	gggactgtgttctttgctca	gtactcagccaagttgtgctctat
Fthl17-L2	*EG434727/ OTTMUSG00000016933*	NP_001078994	NM_001085525	aacacccacatccagctgc	tcagaaaccgaaaatgagtgg
Fthl17-L3	*OTTMUSG00000016694*	XP_001476435	XM_001476385	cctgtggttgtacagctcaagt	gtactcagccaagttgtgctctat
Fthl17-L4	*EG434728/ OTTMUSG00000016862*	XP_486618	XM_486618.4	aacacccacatccagctgc	tcagaaaccgaaaatgagtgg
Fthl17-L5	*EG434729*	NP_001033786	NM_001038697.1**	acatccagctgtacctccaat	actttgcttcaaaaccaacataaat
Fthl17-L6	*EG628008*	pseudo	XR_031510/XR_032749	tctcgagtgcggcagaactt	ttgcttcaaaaccaacatgc

**Differences found between NM_001038697 and the mouse C57BL/6J genome (NT_039700) are described in 'misc_difference features of BC104362'.

Table S2 PCR primers used for searching DMR of *Fthl17* loci

primer name	sequence	mer	amplified fragment size(bp)	amplified loci
Fthl17 CpG1-F	actcaactttctccaaacttctaaacc	27	776	CpG1
Fthl17 CpG1-R	ggtagtttttggaatagttgta	22		
Fthl17 CpG2-9-F	gaggtattttgggattgtgggat	23	314	CpG2,3,4,6,7,8,9*
Fthl17 CpG2-9-R	aaacatctctacactaatctaacaattatataacttaatc	40		
Fthl17 CpG5-F	tgaaggtgaaggtttaaaataggatt	26	635	CpG5
Fthl17 CpG5-R	ataccaaaaaacaaaaaattaaaaccc	27		

*This primer set amplified all seven *Fthl17* family loci（Fthl17, L1, L2, L3, L4, L5, L6）, and each locus was distinguished with its SNPs inside *Fthl17* genes.