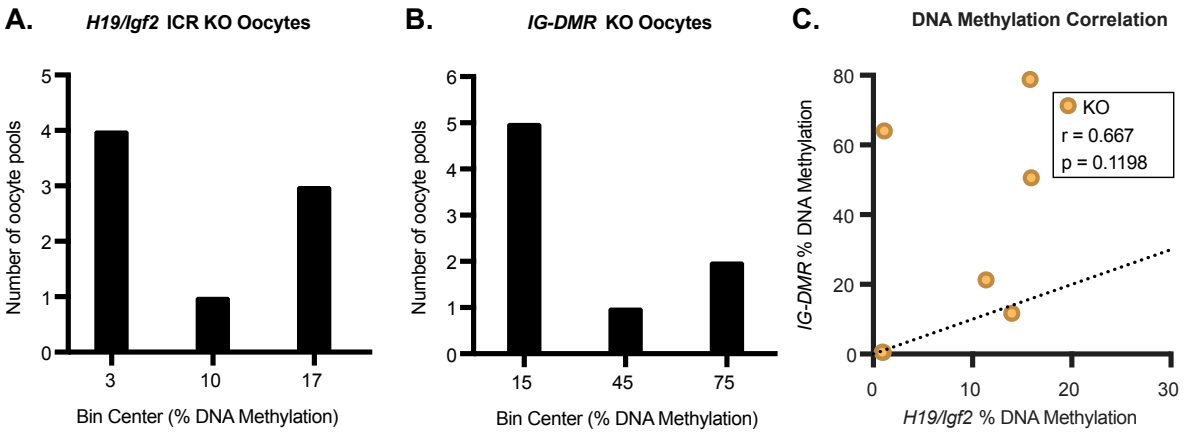
FIG. S1



Supplemental Figure 1. **Further characterization of oocyte DNA methylation.** The DNA methylation data from Figure 1 (A) KO oocytes at the *H19/Igf2* ICR and (B) KO oocytes at the *IG-DMR* are plotted as histograms. (C) Correlation plot between KO oocyte pools at the *H19/Igf2* ICR versus the *IG-DMR*. r = Spearman correlation coefficient. Dashed line represents a hypothetical perfect correlation.

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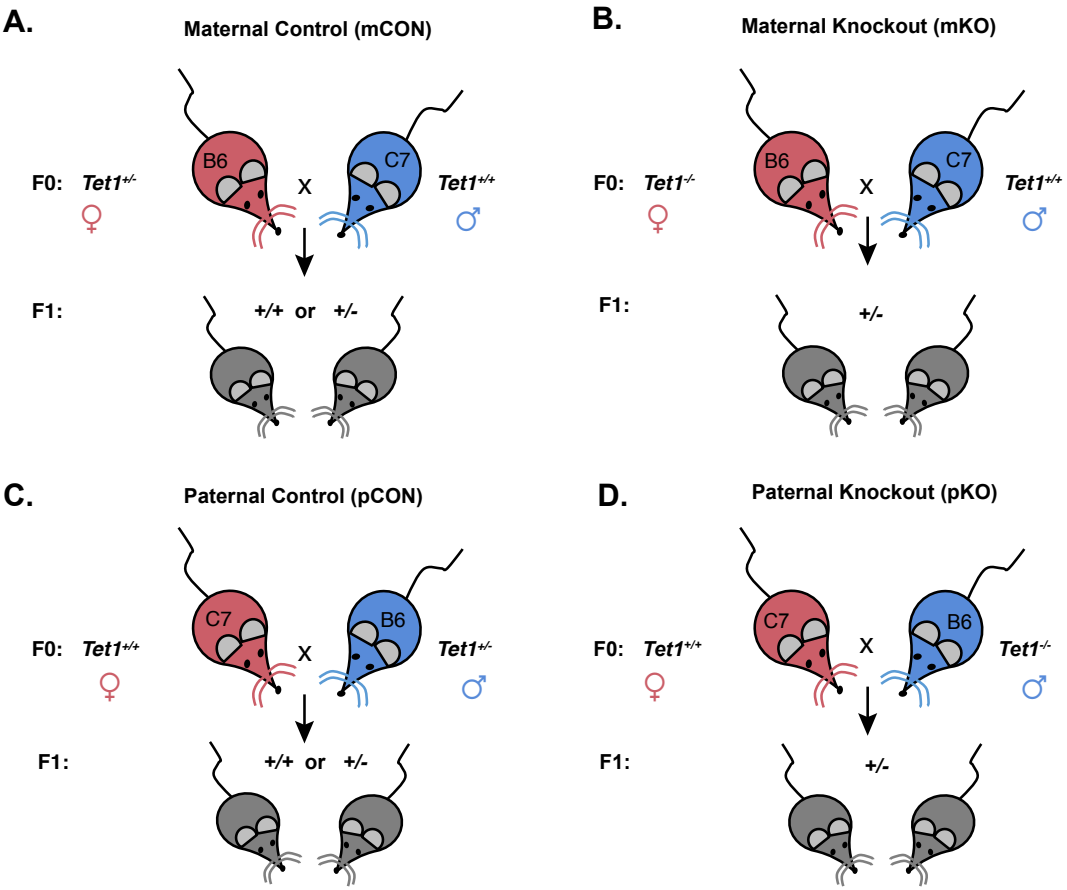
FIG. S2



Supplemental Figure 2. **F1 hybrid breeding schemes for analyzing allele-specific expression.** (A) *Tet1*$^{+/-}$ female mice on the B6 background were mated to *Tet1*$^{+/+}$ mice on the C7 background to generate maternal control offspring (mCON) for analysis. (B) *Tet1*$^{-/-}$ female mice on the B6 background were mated to *Tet1*$^{+/+}$ mice on the C7 background to generate maternal KO offspring (mKO) for analysis. (C) *Tet1*$^{+/+}$ females on the C7 background were crossed to *Tet*$^{+/-}$ males on the B6 background to generate paternal control offspring (pCON) for analysis. (D) *Tet1*$^{+/+}$ females on the C7 background were crossed to *Tet1*$^{-/-}$ males on the B6 background to generate paternal KO offspring (pKO) for analysis.

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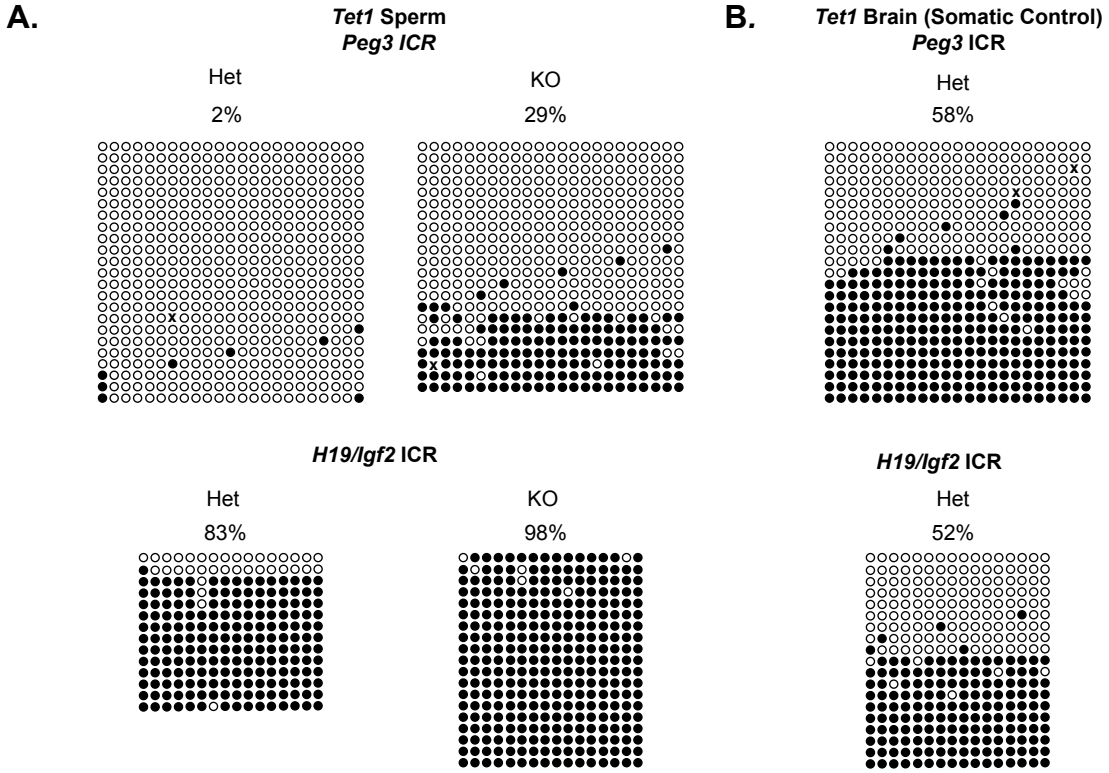
FIG. S3



Supplemental Figure 3. Bisulfite sequencing validation of Tet1 sperm DNA methylation. (A) Bisulfite sequencing of the *Peg3* ICR for both control heterozygous sperm and KO sperm. Bisulfite plots for the *H19/Igf2* ICR is shown as a control. (B) Bisulfite sequencing of a somatic control brain showing the expected methylation pattern at the *Peg3* ICR as a control. Each circle represents a CpG, white = unmethylated, black = methylated. Each row represents one cloned strand of DNA. Each bisulfite plot represents one animal and results from two technical PCR replicates.

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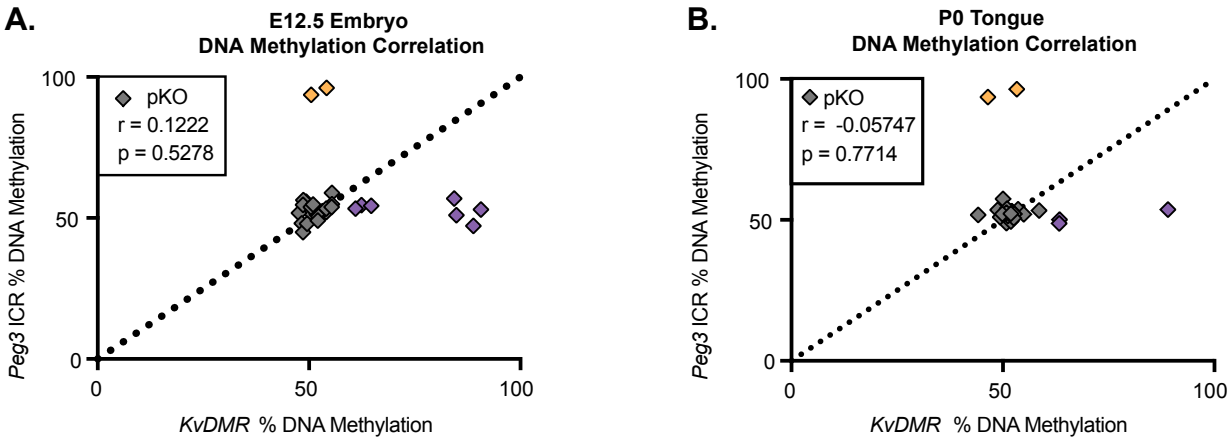
FIG. S4



Supplemental Figure 4. Hypermethylation at the *KvDMR* and *Peg3* ICRs is mutually exclusive in E12.5 pKO embryos and P0 newborns. (A) Correlation plot showing DNA methylation per E12.5 pKO embryo at the *KvDMR* and *Peg3* ICRs. (B) Correlation plot showing DNA methylation per P0 pup (tongue) at the *KvDMR* and *Peg3* ICRs. Gray diamonds show unaffected pKO pups. The orange diamonds highlight pups with *Peg3* hypermethylation. The purple diamonds highlight pups with *KvDMR* hypermethylation. r = Spearman correlation coefficient. Dotted line represents hypothetical perfect correlation.

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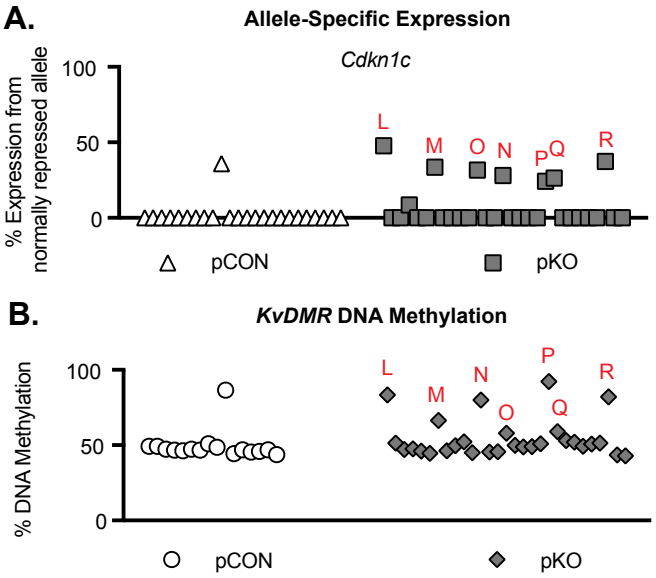
FIG. S5



Supplemental Figure 5. Abnormal biallelic expression and DNA hypermethylation are consistent in the E12.5 placental tissues. (A) Allele-specific expression of *Cdkn1c* in the E12.5 placenta (corresponding to the embryos from Figure 6 in the main text). *Cdkn1c* (n) pCON = 24 placentas from 3 litters; pKO = 29 placentas from 7 litters. (B) Percent DNA methylation at the *KvDMR*. (n) pCON = 16 placentas from 2 litters; pKO = 29 placentas from 7 litters. Abnormal placentas are indicated with red letters and this lettering is consistent between all graphs in Figures 6B and 6C and supplemental Figures 5A and 5B. All placentas are in the same order from left to right in A and B.

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Table S1: % DNA methylation at ICRs in Tet1 oocytes with inclusion data.

		ICR DNA Methylation (% Average)									
		Paternally Methylated		Maternally Methylated (Control)							
Mouse #	Genotype	*H19*	*IG-DMR*	*Peg3*	*Snrpn*	*Peg1*	*KvDMR*	*H19/Igf2* and/or *IG-DMR*?	Number of Control ICRS	TOP 2 avg >90%	Both Criteria Met?
5629A	WT	1.4	0.0	**97.2**		**97.4**		yes	2	97.3	yes
5826	WT		0.8	**93.7**	**98.2**	75.6		yes	3	95.9	yes
W956	WT	4.1	7.2	93.0	**97.9**	**96.0**		yes	3	96.9	yes
W1096	WT	3.1	15.1	84.9	**92.6**	**94.5**		yes	3	93.5	yes
W1542	WT	1.0	0.9	**97.9**		**92.7**		yes	2	95.3	yes
5442	Het	6.7	0.5	**98.7**	81.1	**95.6**		yes	3	97.1	yes
Het442	Het	2.0	0.8	**89.0**	**97.7**	81.9	64.9	yes	4	93.4	yes
H1095	Het	6.7	0.6	**86.7**	76.7	**95.7**		yes	3	91.2	yes
H1550	Het	0.7	5.5	**91.4**		**94.6**		yes	2	93.0	yes
LEP	KO	2.3		**95.0**		60.8	**96.8**	yes	3	95.9	yes
5619	KO	1.0	0.5	**99.1**	**85.3**	83.5		yes	3	92.2	yes
5828	KO	1.1	64.0	**95.0**	**98.1**	94.6		yes	3	96.5	yes
5834B	KO	0.9	0.5	**98.0**	**98.0**	94.7		yes	3	98.0	yes
Mut554A	KO	14.0	11.7	**89.9**	**97.5**	80.5	67.8	yes	4	97.8	yes
Mut445	KO	11.4	21.3	**95.0**	**97.8**	74.4		yes	3	96.4	yes
M1097	KO		0.8	**96.1**	**98.3**	91.9		yes	3	97.2	yes
M1027	KO	15.9	50.6	**99.3**	92.4	**100.0**		yes	3	99.6	yes
M1541	KO	15.8	78.8	**92.1**	89.5	**100.0**		yes	3	96.0	yes

Bold type indicates the top two most highly methylated maternally methylated ICRs

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Table S2: Litter (denoted with unique letters), sex (M= male, F = female), allele-specific expression, and DNA methylation data for all E10.5 mCON and mKO embryo and placentas.

					Allele-Specific Expression- % Expression from normally repressed allele				ICR DNA Methylation - (% Average)							
Cross	Original ID	Paper ID	Sex	Litter	*H19* Embryo	*H19* Placenta	*Igf2* Embryo	*Igf2* Placenta	*H19/Igf2* Embryo	*H19/Igf2* Placenta	*IG-DMR* Embryo	*IG-DMR* Placenta	*Peg3* Embryo	*Peg3* Placenta	*KvDMR* Embryo	*KvDMR* Placenta
mCON	1		F	A	0.0	0.0	0.0	0.0	56.1	58.2	44.3	54.3			52.3	46.8
mCON	2		M	A	0.0	0.0	0.0	0.0	55.2	55.1	42.1	63.0			52.5	48.1
mCON	3		F	A	0.0	0.0	0.0	0.0	56.6	53.7	46.2	42.3			53.4	49.4
mCON	4		F	A	0.0	0.0	0.0	0.0	57.0	57.6	41.6	62.7			51.5	50.3
mCON	5		M	A	0.0	0.0	0.0	0.0	56.4	56.8	46.6	42.7			49.7	47.6
mCON	6		M	A		0.0			57.4		46.2				51.0	
mCON	7		M	A	0.0	0.0	0.0	0.0	58.5	55.3	45.3	51.0			51.9	47.4
mCON	8		F	A	0.0	0.0	0.0	0.0	57.6	58.0	42.2	53.3			51.9	48.0
mCON	9		F	B	0.0	0.0	0.0	0.0	55.7	60.5	51.3	60.0			48.8	52.2
mCON	10		M	B	0.0	0.0	0.0	0.0	57.5	57.2	50.7	69.4			49.2	54.6
mCON	11		M	B	0.0	0.0	0.0	0.0	55.1	55.4	47.6	60.9			50.5	56.0
mCON	12		M	B	0.0	0.0	0.0	0.0	56.6	60.3	49.7	43.4			50.1	55.1
mCON	13		M	B	0.0	0.0	0.0	0.0	57.9	62.1	45.3	59.5			53.8	53.5
mCON	14		F	B	0.0	0.0	0.0	0.0	53.2	57.0	46.4	48.4		51.2	50.6	53.8
mCON	15		M	B		0.0			57.2		52.1				49.8	
mCON	16		M	B	0.0	0.0	0.0	0.0	56.2	61.6	48.7	62.5		50.0	52.6	52.4
mCON	17		M	B	0.0	0.0	0.0	0.0		56.0		47.3				53.4
mCON	24		F	C	0.0	0.0	0.0	0.0	55.2		43.5		49.0		50.6	
mCON	25		F	C	0.0	0.0	0.0	0.0	57.2	58.7	44.3	52.2	48.5	55.9	50.2	51.5
mCON	26		M	C	0.0	0.0	0.0	0.0	55.3	59.1	43.8	46.5	48.8	49.6	51.1	48.5
mCON	27		M	C	0.0	0.0	0.0	0.0	54.7	57.9	43.7	46.8	49.8	50.7	51.3	53.9
mCON	28		F	C	0.0	0.0	0.0	0.0	56.2	61.2	44.1	48.9	50.8	49.9	51.7	52.7
mCON	29		M	C	0.0	0.0	0.0	0.0	59.0	59.6	45.0	51.4	50.3	51.1	50.1	53.2
mCON	30		M	C	0.0	0.0	0.0	0.0	55.4	59.0	41.5	48.1	48.9	47.8	50.3	51.4
mCON	31		M	C	0.0	0.0	0.0	0.0	55.8	57.4	43.7	56.4	50.2	50.6	50.7	51.6
mCON	32		F	D	0.0	0.0	0.0	0.0	55.3		47.0		46.2		48.6	
mCON	33		M	D	0.0	0.0	0.0	0.0	54.6		45.7		46.2		49.9	
mCON	34		F	D	0.0	0.0	0.0	0.0	55.3		45.4		49.8		50.9	
mCON	35		F	D	0.0	0.0	0.0	0.0	53.4		41.7		48.0		48.0	
mCON	36		F	D	0.0	0.0	0.0	0.0	53.2		46.6		50.6		52.3	
mCON	37		F	D	0.0	0.0	0.0	0.0	58.8		42.4		45.5		49.9	
mCON	38		M	D	0.0	0.0	0.0	0.0	55.1		46.1		51.3		53.4	
mCON	39		F	D	0.0	0.0	0.0	0.0	51.7		43.9		47.4		50.2	
mCON	40		F	D	0.0	0.0	0.0	0.0	55.0		95.0		51.9		50.2	
mCON	49		M	E												
mCON	50		F	E												
mCON	51		M	E												
mCON	52		F	E												
mCON	53		M	E												
mCON	54		M	E												
mCON	55		F	E												
mCON	56		F	E												
mCON	57		M	E												
mKO	1		M	F	0.0	0.0	0.0	0.0	56.6	55.6	45.3	40.9			52.7	47.9
mKO	2		M	F	0.0	0.0	0.0	0.0	59.5	58.0	46.0	55.5			50.6	50.1
mKO	3		F	F	0.0	0.0	0.0	0.0	56.7	59.4	43.2	50.1			50.5	49.7
mKO	4		M	F	0.0	0.0	0.0	0.0	62.9	57.9	41.9	58.9			53.2	49.8
mKO	5		F	F	0.0	0.0	0.0	0.0	52.5	52.5	49.9	46.4			51.0	47.2
mKO	6	D	F	F	0.0	0.0	0.0	0.0	58.2	61.3	96.0	80.7			50.7	49.1
mKO	8		F	F	0.0	0.0	0.0	0.0	59.9	58.1	41.9	47.0			50.6	46.9
mKO	9	E	M	G	0.0	0.0	0.0	0.0	53.3	57.0	96.7	86.5			51.2	56.7
mKO	10		M	G	0.0		0.0	0.0	54.6	50.7	49.4	69.4			49.4	51.5
mKO	11		F	G	0.0		0.0	0.0	60.0	62.3	48.7	47.6			49.9	48.2
mKO	12	A	F	G	0.0	0.0	51.5	52.4	95.5	93.2	95.7	84.5			49.9	53.0
mKO	13	F	F	G	0.0	0.0	0.0	0.0	57.9	65.1	95.7	82.2			51.1	52.1
mKO	14	G	F	G	0.0	0.0	0.0	0.0	57.4	59.0	95.7	86.2			52.3	49.5
mKO	15	H	F	G	0.0	0.0	0.0	0.0	54.6		96.0				49.1	
mKO	16		F	G	0.0	0.0	0.0	0.0	55.0	58.3	51.6	55.9			50.7	49.9
mKO	18		F	H	0.0	0.0	0.0	0.0	55.3	56.1	41.7	51.4	50.6	46.9	53.3	47.6
mKO	19		M	H	0.0	0.0	0.0	0.0	59.3	59.7	43.4	56.2	50.8	51.4	53.0	53.2
mKO	20		M	H	0.0	0.0	0.0	0.0	55.7	58.4	45.7	61.9	50.8	51.6	52.0	53.2
mKO	21	I	F	H	0.0	0.0	0.0	0.0	55.1	57.0	95.7	83.0	51.0	52.1	50.9	51.6
mKO	22		F	H	0.0	0.0	0.0	0.0	60.3	57.2	44.8	52.7	49.1	49.9	50.4	51.5
mKO	23		M	I	0.0	0.0	0.0	0.0	55.0		43.4		52.9		50.5	
mKO	25		M	I	0.0	0.0	0.0	0.0	54.5		45.5		50.9		51.3	
mKO	26		M	J	0.0	0.0	0.0	0.0	54.5		44.9		53.1		48.2	
mKO	27	B	F	J	0.0	0.0	53.3	55.5	90.0		45.0		50.0		51.3	
mKO	28	J	F	J	0.0	0.0	0.0	0.0	54.0		95.4		50.2		51.2	
mKO	29		M	J	0.0	0.0	0.0	0.0	55.1		43.5		49.8		50.1	
mKO	30		M	J	0.0	0.0	0.0	0.0	53.2		44.3		50.3		50.1	
mKO	31		F	J	0.0	0.0	0.0	0.0	54.4		43.8		48.3		50.3	
mKO	33		M	J	0.0	0.0	0.0	0.0	57.4		41.1		49.7		51.4	
mKO	34	K	M	K	0.0	0.0	0.0	0.0	55.8	49.3	96.4	87.1	50.3	36.0	53.5	47.8
mKO	35	L	F	K	0.0	0.0	0.0	0.0	61.9	54.3	94.5	84.7	55.1	44.7	52.9	46.9
mKO	36		M	L	0.0	0.0	0.0	0.0	55.2	54.8	43.9	46.6	51.1	48.5	56.8	49.1
mKO	37		M	L	0.0	0.0	0.0	0.0	56.4	53.3	43.1	53.8	50.3	45.8	52.2	47.5
mKO	39	C	M	L	0.0	0.0	60.1	60.0	81.1	78.5	42.7	65.6	51.7	39.6	53.7	43.5
mKO	40		F	L	0.0	0.0	0.0	0.0	54.5	53.1	46.0	53.0	52.8	46.4	49.6	51.5
mKO	41		M	L	0.0	0.0	0.0	0.0	61.8	57.0	43.3	46.1	51.5	50.6	50.2	47.9

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Table S3: Sex ratio information for both maternal and paternal Tet1 offspring.

Maternal E10.5	**mCON**		
	Observed	Expected	TOTAL
Male	21	17	38
Female	13	17	30
TOTAL	34	34	68
Two-tailed Chi-Square: p = 0.170			
Sex ratio is not significantly different			

Maternal E10.5	**mKO**		
	Observed	Expected	TOTAL
Male	18	18	36
Female	18	18	36
TOTAL	36	36	72
Two-tailed Chi-Square: 1.000			
Sex ratio is not significantly different			

Maternal E10.5	**mKO**	
	Affected	Unaffected
Male	3	16
Female	9	8
The two-tailed P value = 0.033		
The association between rows and columns is significant.		

Maternal P0	**mCON**		
	Observed	Expected	TOTAL
Male	8	8	16
Female	8	8	16
TOTAL	16	16	32
Two-tailed Chi-Square: p = 1.000			
Sex ratio is not significantly different			

Maternal P0	**mKO**		
	Observed	Expected	TOTAL
Male	14	15	29
Female	16	15	31
TOTAL	30	30	60
Two-tailed Chi-Square: p = 0.715			
Sex ratio is not significantly different			

Maternal P0	**mKO**		
	Affected	Unaffected	
Male	0	16	
Female	3	13	Affected = J, K, and # (see Table S6)
Two-tailed Fisher's Exact Test: p = 0.226			
The association between rows and columns is not significant.			

Paternal E12.5	**pCON**		
	Observed	Expected	TOTAL
Male	11	11.5	22.5
Female	12	11.5	23.5
TOTAL	23	23	46
Two-tailed Chi-Square: p = 0.835			
Sex ratio is not significantly different			

Paternal E12.5	**pKO**		
	Observed	Expected	TOTAL
Male	10	14.5	24.5
Female	19	14.5	33.5
TOTAL	29	29	58
Two-tailed Chi-Square: p = 0.095			
Sex ratio is not significantly different			

Paternal E12.5	**pKO**	
	Affected	Unaffected
Male	3	7
Female	4	15
Two-tailed Fisher's Exact Test: p = 0.665		
The association between rows and columns is not significant.		

Paternal P0	**pCON**		
	Observed	Expected	TOTAL
Male	13	11.5	24.5
Female	10	11.5	21.5
TOTAL	23	23	46
Two-tailed Chi-Square: p = 0.532			
Sex ratio is not significantly different			

Paternal P0	**pKO**		
	Observed	Expected	TOTAL
Male	17	14	31
Female	11	14	25
TOTAL	28	28	56
Two-tailed Chi-Square: p = 0.257			
Sex ratio is not significantly different			

Paternal P0	**pKO**	
	Affected	Unaffected
Male	0	17
Female	3	8
Two-tailed Fisher's Exact Test: p = 0.050		
The association between rows and columns is not significant.		

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Table S4: Litter (denoted with unique letters), sex (M= male, F = female), allele-specific expression, and DNA methylation data for all P0 mCON and mKO brain, liver, and tongue.

					Allele-Specific Expression- % Expression from normally repressed allele						ICR DNA Methylation- (% Average)											
					H19			*Igf2*			*H19/Igf2*			*IG-DMR*			*Peg3*			*KvDMR*		
Cross	Original ID	Paper ID	Sex	Litter	Brain	Liver	Tongue	Brain	Liver	Tongue	Brain	Liver	Tongue	Brain	Liver	Tongue	Brain	Liver	Tongue	Brain	Liver	Tongue
mCON	5313-1		F	A		0.0	0.0		0.0	0.0			63.3			51.9			53.1			57.1
mCON	5313-2		M	A		0.0	0.0		0.0	0.0			57.1			49.9			50.8			51.8
mCON	5313-3		M	A		0.0	0.0		0.0	0.0			58.9			48.3			52.8			52.2
mCON	5313-4		F	A		0.0	0.0		0.0	0.0			57.5			45.8			51.2			52.1
mCON	5313-5		M	A		0.0	0.0		0.0	0.0			57.7			45.6			51.5			51.1
mCON	5313-6		F	A		0.0	0.0		0.0	0.0			55.4			48.4			51.5			51.8
mCON	5314-1		F	B		0.0	0.0		0.0	0.0			57.6			49.5			51.5			51.4
mCON	5314-2		M	B		0.0	0.0		0.0	0.0			58.4			49.8			53.0			52.0
mCON	5314-3		M	B		0.0	0.0		0.0	0.0			61.6			48.6			52.4			52.7
mCON	1330-1		F	C		0.0	0.0		0.0	0.0			59.8			48.1			51.6			54.6
mCON	1330-2		F	C		0.0	0.0		0.0	0.0			57.0			46.6						55.1
mCON	1330-3		F	C		0.0	0.0		0.0	0.0			55.9			44.2			54.0			49.7
mCON	1330-4		M	C		0.0	0.0		0.0	0.0			59.4			46.2			51.9			50.7
mCON	1330-5		M	C		0.0	0.0		0.0	0.0			55.6			48.1			52.6			51.0
mCON	1330-6		F	C		0.0	0.0		0.0	0.0			55.6			47.4			51.0			53.3
mCON	1330-7		M	C		0.0	0.0		0.0	0.0			57.7			45.9			52.7			53.0
mKO	5106-1		M	D		0.0	0.0		0.0	0.0			58.3			48.9			53.2			52.7
mKO	5106-2		F	D		0.0	0.0		0.0	0.0			57.5			52.6			53.4			52.6
mKO	5106-3		M	D		0.0	0.0		0.0	0.0			58.6			48.3			50.7			52.7
mKO	5106-4		F	D		0.0	0.0		0.0	0.0			58.4			46.8			50.3			51.3
mKO	5106-5		M	D		0.0	0.0		0.0	0.0			50.6			49.3			50.0			53.4
mKO	5106-6		F	D		0.0	0.0		0.0	0.0			60.0			51.9			52.6			51.6
mKO	5108-1		F	E		0.0	0.0		0.0	0.0			55.1			46.4			51.5			51.2
mKO	5108-2		M	E		0.0	0.0		0.0	0.0			55.7			45.1			51.1			50.6
mKO	5108-3		M	E		0.0	0.0		0.0	0.0			58.4			46.1			53.2			49.8
mKO	5108-4		F	E		0.0	0.0		0.0	0.0			58.7			45.4			52.9			53.7
mKO	5108-5	J	F	E		0.0	0.0		39.4	52.1			86.0			43.5			52.1			48.7
mKO	5108-6		F	E		0.0	0.0		0.0	0.0			55.7			47.2			52.9			52.3
mKO	5106-7		F	F		0.0	0.0		0.0	0.0			62.6			48.0			43.8			52.4
mKO	5106-8		M	F		0.0	0.0		0.0	0.0			53.5			44.0			53.2			51.3
mKO	5106-9		M	F		0.0	0.0		0.0	0.0			58.8			45.3			56.1			53.2
mKO	5106-10			F		0.0	0.0		0.0	0.0			49.1			42.0			40.6			64.6
mKO	5106-11		M	F		0.0	0.0		0.0	0.0			57.5			41.6			51.0			52.1
mKO	5106-12		F	F		0.0	0.0		0.0	0.0			56.4			47.3			52.5			51.5
mKO	5106-13		M	F		0.0	0.0		0.0	0.0			62.7			47.1			53.3			47.6
mKO	mKO-8		F	G		0.0	0.0		0.0	0.0			60.4			46.6			51.9			51.2
mKO	mKO-9		F	G		0.0	0.0		0.0	0.0			57.0			51.1			51.8			51.3
mKO	mKO-10		F	G		0.0	0.0		0.0	0.0			57.1			49.4			52.4			54.6
mKO	912-1	# (See IG-DMR & Table S5)	F	H		0.0			0.0				57.6			94.2			52.6			54.1
mKO	912-2		F	H		0.0	0.0		0.0	0.0			57.2			50.4			52.0			52.8
mKO	912-3		M	H		0.0	0.0		0.0	0.0			58.9			50.4			50.8			55.3
mKO	912-4		M	H		0.0	0.0		0.0	0.0			59.1			53.2			51.7			56.1
mKO	912-5		F	H		0.0	0.0		0.0	0.0			59.1			49.4			51.7			52.3
mKO	912-6		M	I		0.0	0.0		0.0	0.0			57.8			49.0			50.5			52.1
mKO	912-7		M	I		0.0	0.0		0.0	0.0			57.2			48.8			51.5			51.8
mKO	976-2	K	F	J		0.0	0.0		6.7	11.7			60.2			50.2			50.8			52.5
mKO	976-3		M	J		0.0	0.0		0.0	0.0			58.9			52.4			51.7			53.7

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Table S5: % DNA methylation at ICRs in Tet1 Sperm

		ICR DNA Methylation (% Average)					
		Paternally Methylated		Maternally Methylated			
Sample ID	**Genotype**	***H19/Igf2***	***IG-DMR***	***KvDMR***	***Peg3***	***Peg1***	***Snrpn***
W5062	WT	94.6		8.5	7.3		5.1
W5068	WT	95.7		2.5	1.6		2.3
WT1	WT	96.0	95.0	11.0	8.0	5.0	7.0
WT2	WT	96.0	95.0	12.0	4.0	5.0	3.0
WT3	WT	94.0	92.0	7.0	5.0	8.0	6.0
WT5183	WT	97.6	97.6	3.8	3.3	4.8	3.2
H4852	Het	95.4	96.9	4.0	3.4	5.8	4.2
H5059	Het	93.7	97.4	4.4	2.9	5.4	4.5
H5069	Het	97.7		9.6	5.3		13.8
H5103	Het	95.9	95.4	4.5	3.6	6.4	6.8
H5104	Het	94.0	97.3	4.8	6.0	6.9	4.6
H5105	Het	95.0	96.3	3.8	3.3	5.5	5.9
H5184	Het	94.1	97.0	4.4	6.0	6.1	2.3
Hep3	Het	93.9		6.7	5.0		5.3
Het5787	Het	97.4	96.9	5.3	5.3	8.2	5.0
Het5791	Het	97.1	97.2	4.4	3.4	6.6	3.9
M4848	KO	95.2		29.8	3.0		5.6
M4851	KO	93.7		33.6			18.5
M4859	KO	95.0		30.9	4.6		14.2
M5060	KO	94.8	95.1	33.9	10.6	20.4	5.1
M5064	KO	96.8	95.9	32.7	10.3	21.5	5.9
M5109	KO	91.6		39.0	9.8		28.8
M5311	KO	92.6	96.1	33.8	10.8	18.9	6.1
Mutep3	KO	93.0	96.4	34.3	11.6	23.5	7.0
Mutep4	KO	96.9	95.6	31.3	10.7	21.2	3.1
Mut5339	KO	91.7	88.4	36.5	19.9	26.0	10.1
Mut5781	KO	96.8	96.2	34.4	11.7	19.8	5.4
Mut5318	KO	95.2	89.4	37.9	11.9	21.4	5.5
Mut5333	KO	96.2	95.5	34.2	10.4	18.4	5.2
Mut5058	KO	96.5	95.1	35.8	11.2	21.4	5.2
Mut5728	KO	96.8	97.2	35.5	9.8	17.3	3.1
DKO 1	DKO	94.0	93.0	23.0	6.0	10.0	7.0
DKO 2	DKO	96.0	96.0	30.0	5.0	20.0	8.0
DKO 3	DKO	96.0	93.0	37.0	9.0	22.0	11.0
		H19/Igf2	***IG-DMR***	***KvDMR***	***Peg3***	***Peg1***	***Snrpn***
KO vs DKO, Mann-Whitney (p-value)		0.985	0.440	0.360	0.065	0.660	0.203

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Table S6: Litter (denoted with unique letters), sex (M= male, F = female), allele-specific expression, and DNA methylation data for all E12.5 pCON and pKO embryo and placentas.

					Allele-Specific Expression- % Expression from normally repressed allele										ICR DNA Methylation - (% Average)									
Cross	Original ID	Paper ID	Sex	Litter	*Cdkn1c* Embryo	*Cdkn1c* Placenta	*Kcnq1ot1* Embryo	*Kcnq1ot1* Placenta	*H19* Embryo	*H19* Placenta	*Igf2* Embryo	*Igf2* Placenta	*Peg3* Embryo	*Peg3* Placenta	*H19/Igf2* Embryo	*H19/Igf2* Placenta	*IG-DMR* Embryo	*IG-DMR* Placenta	*Peg3* Embryo	*Peg3* Placenta	*KvDMR* Embryo	*KvDMR* Placenta	*Peg1* Embryo	*Peg1* Placenta	*Snrpn* Embryo	*Snrpn* Placenta
pCON	CE2		F	A	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			50.6	45.4	41.6	42.8	47.7	45.1	51.3	49.2	49.3	41.0	44.1	39.1
pCON	CE3		F	A	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	49.2	49.4	38.7	39.0	47.8	46.2	52.8	49.3	49.8	41.2	43.9	38.8
pCON	CE4		F	A	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	51.4	48.8	40.7	39.3	48.9	46.5	52.0	47.4	50.2	42.8	43.4	39.9
pCON	CE5		F	A	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			50.9	50.4	38.9	36.5	48.9	45.1	52.3	46.7	49.7	42.2	42.5	41.6
pCON	CE6		M	A	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			53.3	48.1	42.4	39.6	46.7	46.7	50.3	46.2	50.5	42.1	43.0	39.5
pCON	CE7		M	A	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			50.1	52.4	42.0	41.4	51.0	46.9	52.1	47.3	50.9	44.2	44.7	39.5
pCON	CE8		F	A	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			48.6	51.4	42.5	40.0	48.5	47.3	49.5	46.6	49.0	42.3	44.9	41.5
pCON	CE18		M	B	0.0	0.0			0.0	0.0	0.0	0.0			50.8	50.9	44.0	54.2	47.5	49.5	51.4	51.0	49.4	47.6	43.9	42.6
pCON	CE19		M	B	0.0	0.0			0.0	0.0	0.0	0.0	0.0	0.0	49.9	46.9	47.7	48.1	52.5	49.1	52.6	48.7	51.6	42.7	45.8	42.0
pCON	CE20		M	B	37.7	35.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	48.5	59.3	48.4	52.7	50.4	53.4	92.2	86.5	50.4	45.3	37.2	41.3
pCON	CE21		M	B	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	52.2	52.7	54.7	52.0	52.7	48.2	49.4	44.5	49.8	46.5	45.9	40.9
pCON	CE22			B		0.0		0.0		5.1		0.0	0.0	0.0		51.6		46.8		48.4		47.0		42.7		39.5
pCON	CE23		M	B	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	52.7	54.0	50.5	53.2	51.3	49.4	48.0	45.5	51.4	45.0	44.9	41.7
pCON	CE24		F	B	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	54.5	53.2		49.3	50.4	45.9	49.3	45.9	50.7	43.6	48.6	40.2
pCON	CE25		M	B	0.0	0.0	0.0	0.0					0.0	0.0	52.1	51.5	47.1	46.7	50.7	48.4	47.1	46.8	49.8	39.1	42.9	39.2
pCON	CE26		F	B	0.0	0.0	0.0	0.0							53.4	47.2	43.1	51.7	50.5	45.3	46.6	43.9	49.8	42.6	48.0	40.8
pCON	CE27		M	C	0.0	0.0									55.4		53.6		54.5		55.4				49.5	
pCON	CE28		F	C	0.0	0.0									56.0		50.7		54.2		53.7				48.5	
pCON	CE29		F	C	0.0	0.0									55.1		49.4		53.4		54.8				49.5	
pCON	CE30		F	C	0.0	0.0									55.1				52.2		54.4				49.6	
pCON	CE31		M	C	0.0	0.0																				
pCON	CE32		F	C	0.0	0.0																				
pCON	CE33		F	C	0.0	0.0																				
pCON	CE34		M	C	0.0	0.0																				
pKO	ME1	L	F	D	47.5	47.7	0.0	0.0	0.0	0.0	0.0	0.0			51.5	53.7	45.5	52.9	53.1	50.8	90.7	83.3	49.3	44.6	40.1	40.1
pKO	ME2		M	D	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			47.5	46.5	42.4	44.1	52.2	48.3	50.2	51.3	58.0	43.6	46.4	40.8
pKO	ME3		F	D	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			49.4	56.5	42.9	47.1	52.1	49.5	54.1	47.2	57.9	45.7	45.1	37.9
pKO	ME4		F	D	6.1	8.5	0.0	0.0	0.0	0.0	0.0	0.0			51.5	53.7	38.5	39.8	52.4	50.4	53.2	47.6	51.5	42.0	42.8	37.5
pKO	ME6		F	D	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			52.8	57.4	44.4	52.8	55.9	51.9	49.3	46.2	51.7	43.5	43.9	43.2
pKO	ME7		F	D	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			52.7	47.1	45.6	58.0	54.2	49.2	51.0	44.5	51.3	44.8	47.6	36.0
pKO	ME8	M	M	D	12.6	33.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0		53.1	52.1	43.9	50.2	54.5	54.3	62.4	66.3	53.5	44.7	45.1	43.4
pKO	ME24		F	E	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	50.8	47.5	50.3	44.5	56.4		48.7	46.3	52.1	42.6	43.6	39.6
pKO	ME25		F	F	0.0	0.0		0.0	0.0	0.0	0.0	0.0		0.0	51.7	48.9	43.5	50.2	96.2	77.5	54.2	49.7	52.9	45.7	45.1	40.7
pKO	ME26		F	F	0.0	0.0		0.0	0.0	0.0	0.0	0.0		0.0	53.1	54.0	46.5	51.6	51.2	48.7	51.9	52.3	53.6	44.2	45.7	42.9
pKO	ME28		F	F	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	57.5	47.0	66.3	38.2	59.0	46.8	55.4	45.0	54.9	41.3	45.6	38.7
pKO	ME29	N	M	F	34.6	31.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	47.0	45.3	43.5		56.9	48.3	84.4	80.0	54.8	41.5	52.6	39.1
pKO	ME30		M	F	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	51.6	43.8	46.5	44.6	51.8	47.1	47.6	45.5	49.3	42.4	48.5	39.5
pKO	ME32		M	F	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	53.1	55.7	46.3	40.2	54.7	48.0	48.6	45.6	52.8	42.8	47.2	41.3
pKO	ME34	O	M	G	19.6	28.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	53.2	50.4	50.7	46.0	53.4	49.4	61.0	58.1	53.2	45.7	48.5	42.8
pKO	ME35		F	G	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	53.5	48.7	50.0	47.9	53.6	52.2	50.7	49.8	53.2	51.4	47.3	43.9
pKO	ME38		F	G	0.0	0.0	0.0	0.0		0.0		0.0	0.0	0.0	55.3	52.1	47.8	53.9	53.9	52.8	50.5	48.7	53.3	45.7	46.6	43.8
pKO	ME41		F	G	0.0	0.0	0.0	0.0		0.0		0.0	0.0	0.0	53.9	50.7	49.9	55.0	54.8	53.2	50.9	49.1	55.9	46.7	46.1	42.7
pKO	ME43		M	H	0.0	0.0				0.0					54.9	54.7	52.1	50.9	54.9	52.1	55.4	50.9	59.8	51.4	50.4	47.0
pKO	ME44	P	F	H	36.0	24.2				0.0					55.7	57.3	48.2	55.9	51.0	53.0	84.9	92.3	56.9	60.3	46.4	48.9
pKO	ME46	Q	F	H	21.8	26.4									57.1	56.9	50.1	52.3	54.4	52.4	64.7	59.1	64.0	54.4	47.4	46.2
pKO	ME48		M	H	0.0	0.0									57.7	55.6	52.7	55.1	53.3	54.9	54.1	53.0	58.1	53.5	47.2	44.4
pKO	ME50		F	H	0.0	0.0									53.5	52.5	50.8	59.8	53.9	52.5	55.4	52.0	61.6	52.6	50.1	
pKO	ME52		F	I	0.0	0.0									49.5	49.8	45.7	48.7	93.7	90.3	50.5	49.3	47.9	42.5	46.3	42.5
pKO	ME54		M	I	0.0	0.0									47.8	55.0	42.8	52.7	48.1	48.9	48.3	50.7	47.7	42.7	42.4	37.7
pKO	ME55		F	I	0.0	0.0									46.6	50.7	39.2	42.8	45.0	50.0	48.6	51.4	40.1	48.2	38.0	41.2
pKO	ME56	R	F	I	39.0	37.5									49.1	52.0	42.3	51.1	47.2	46.2	88.9	82.2	51.7	41.2	42.3	36.4
pKO	ME57		M	I	0.0	0.0									49.4	50.1	41.8	39.6	48.0	47.2	49.5	43.6	49.1	46.5	42.4	41.2
pKO	ME63		F	J	0.0	0.0									51.3	49.8	46.9	42.5	49.1	46.5	52.1	42.9	51.9	37.8	48.8	39.2

Table S7: Litter (denoted with unique letters), sex (M= male, F = female), allele-specific expression and DNA methylation data for all P0 pCON and pKO brain, liver, and tongue.

					Allele-Specific Expression- % Expression from normally repressed allele															ICR DNA Methylation - (% Average)													
					Cdkn1c	*Cdkn1c*	*Cdkn1c*	*Kcnq1ot*	*Kcnq1ot1*	*Kcnq1ot1*	*H19*	*H19*	*H19*	*Igf2*	*Igf2*	*Igf2*	*Peg3*	*Peg3*	*Peg3*	*H19/Igf2*	*H19/Igf2*	*H19/Igf2*	*IG-DMR*	*IG-DMR*	*IG-DMR*	*Peg3*	*Peg3*	*Peg3*	*KvDMR*	*KvDMR*	*KvDMR*	*Peg1*	*Peg1*	*Peg1*	*Snrpn*	*Snrpn*	*Snrpn*
Cross	Original ID	Paper ID	Sex	Litter	Brain	Liver	Tongue	1 Brain	Liver	Tongue	Brain	Liver	Tongue	Brain	Liver	Tongue	Brain	Liver	Tongue	Brain	Liver	Tongue	Brain	Liver	Tongue	Brain	Liver	Tongue	Brain	Liver	Tongue	Brain	Liver	Tongue
pCON	5186-1		M	A	0.0	0.0	0.0													56.2	52.0	56.1	46.0	43.6	46.0	53.9	50.5	51.6	52.5	48.6	48.7	55.0	49.2	50.4	48.1	45.7	46.7
pCON	5186-2		M	A	0.0	0.0	0.0													55.6	47.7	51.5	47.7	43.5	47.5	53.3	49.2	52.8	50.5	46.1	48.8	54.9	49.2	52.3	46.5	43.9	47.6
pCON	5186-10		M	B	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			0.0				48.7	46.9	44.2		42.1	43.3	46.9	46.9	48.0	49.0	46.7	46.7		51.2	52.1	42.4	41.4	43.0
pCON	5186-11		F	B	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			0.0				48.9	47.2	49.5		43.4	46.7	47.8	47.7	47.7	48.1	46.3	45.2		56.6	63.0	44.3	40.4	40.1
pCON	5186-12		F	B	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			0.0				50.9	48.9	51.4		36.8	50.8	46.1	46.3	47.4	46.5	49.0	48.0		43.6	55.9	43.7	43.8	42.2
pCON	5186-13		F	B	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			0.0				53.0	49.4	51.0		41.2	40.2	45.8	42.8	50.3	51.4	46.8	50.8		52.4		41.0	42.2	42.3
pCON	5186-14		M	B	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			0.0				52.2	46.8	53.1		38.5	46.8	50.3	48.7	46.3	45.9	46.5	46.9		50.9	49.8	44.7	42.6	43.5
pCON	5186-15		F	B	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			0.0				53.0	46.4	52.0		41.0	47.3	46.2	45.7	50.4	44.9	45.1	50.2		47.6	53.7	42.6	42.6	41.8
pCON	5186-16		M	B	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			0.0				52.3	47.0	49.7		43.1		45.4	47.2	51.4	46.3	46.9	50.1		47.0	45.9	44.3	42.5	44.6
pCON	5186-17		M	B	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			0.0				53.0	49.5	53.6		41.4		48.5	46.9	48.9	50.4	46.9	52.3		45.6	51.4	47.5	40.5	43.0
pCON	5186-18		M	B	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			0.0				52.2	49.2	50.3		45.5	45.0	50.5	45.5	45.4	48.9	46.4	47.0		48.7	57.6	44.0	41.7	44.4
pCON	5186-19		M	B	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.0			0.0				53.4	51.3	49.7		55.8	59.9	47.8	47.7	50.9	50.0	48.5	50.0		46.9	50.9	45.2	42.2	43.8
pCON	5185-4		M	C	0.0	0.0	0.0	0.0			0.0						0.0			52.4	49.4	51.6		16.8	18.5	52.4	49.3	51.3	46.5	47.9	48.9	47.8	46.5	53.4	43.4	43.5	48.2
pCON	5185-5		M	C	0.0	0.0	0.0	0.0			0.0						0.0			51.4	51.1	52.4		33.5	35.3	53.7	50.6	53.4	47.7	46.7	49.6	49.6	49.9	52.2	44.3	45.8	45.4
pCON	5185-6		F	C	0.0	0.0	0.0	0.0			0.0						0.0			47.2	48.3	52.7		43.7	49.5	53.1	48.8	51.2	47.7	46.5	51.5	50.6	47.4	51.3	41.6	43.3	46.7
pCON	5185-7		M	C	0.0	0.0	0.0	0.0			0.0						0.0			53.6	51.4	53.3		43.3	47.4	53.8	50.9	51.1	49.4	48.4	49.4	52.4	48.8	52.3	43.9	45.9	47.4
pCON	5186-21		F	D	0.0	0.0	0.0													59.6		54.6				54.1	49.0	51.4	52.0	43.3	53.2	50.3		55.5	43.3		50.7
pCON	5186-22		F	D	0.0	0.0	0.0													57.5		56.8				51.2	49.9	52.0	47.7	43.3	53.4	49.3		57.6	44.6		51.0
pCON	5186-23		M	D	0.0	0.0	0.0													55.7		53.9				53.9	51.4	49.1	49.6	43.1	51.4	48.8		52.2	41.7		49.0
pCON	5186-24		M	D	0.0	0.0	0.0													55.4		55.1				52.7	51.9	52.3	52.8	46.0	53.3	49.2		51.9	47.0		51.9
pCON	5186-25		F	D	0.0	0.0	0.0													52.0		56.2				51.2	49.0	51.1	48.8	45.3	52.7	47.4		51.7	40.7		52.1
pCON	5186-26		F	D	0.0	0.0	0.0													55.1		60.0				51.2	50.5	50.0	49.4	44.7	50.6	48.8		55.4	45.7		48.9
pCON	5186-27		F	D	0.0	0.0	0.0													56.0		50.5				50.1	50.4	51.1	47.9	45.8	52.8	47.9		58.9	43.4		49.2
pKO	ep4-26	S	F	E	17.2	20.1	21.6	0.0	0.0	0.0	0.0	0.0	0.0			0.0				51.1	46.6	52.9		41.7	50.5	50.3	48.1	50.1	62.6	55.8	63.4		49.3	57.1	41.7	42.3	44.6
pKO	ep4-27		M	E	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			0.0				50.5	49.2	50.6		44.3	39.4	49.6	46.7	50.2	48.3	45.3			44.7	50.7	43.0	44.9	42.8
pKO	ep4-28		M	E	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			0.0				50.4	46.6	54.0		42.7	51.8	47.8	48.0	51.8	48.2	47.4	44.2		42.7	57.5	46.5	42.8	45.3
pKO	ep4-29		F	E	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			0.0				52.6	49.2	54.2		40.8	47.0	49.7	45.5	53.5	48.4	45.9	48.8		44.8	58.0	42.2	42.0	42.3
pKO	ep4-30		F	E	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			0.0				51.7	46.7	51.2		41.6	44.7	48.9	46.5	48.9	46.8	44.4	50.8		43.6	53.0	44.5	40.4	44.4
pKO	ep4-31		M	E	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			0.0				52.4	46.9	52.8		38.3	44.4	94.2	86.8	93.6	51.5	45.1	46.5		46.6	60.1	41.8	41.8	45.8
pKO	ep4-32			E	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			0.0				51.8	47.6	50.0		39.2	48.1	48.6	48.4	51.0	47.2	47.5	49.4		47.7	55.7	42.8		42.5
pKO	ep4-33	T	F	E	40.3	28.6	28.9	0.0	0.0	0.0	0.0	0.0	0.0			0.0				52.1	48.0	48.1		45.8	45.4	50.1	48.4	48.8	72.0	67.0	63.3			52.9	44.6	42.7	41.9
pKO	REP-1		F	F	0.0	0.0	0.0													54.3		58.9				51.3	48.9	51.4	49.8	46.3	51.9	46.6		57.7	44.5		52.8
pKO	REP-2		M	F	0.0	0.0	0.0													54.7		58.0				49.5	51.1	53.8	49.4	45.9	53.6	48.6		55.2	43.1		52.0
pKO	REP-3		M	F	0.0	0.0	0.0													55.9		53.5				50.1	48.7	53.1	47.9	45.5	52.1	46.8		50.1	43.8		49.5
pKO	REP4		M	F	0.0	0.0	0.0													52.8		56.1				49.7	52.3	52.1	48.6	46.0	54.9	46.8		51.2	44.6		49.4
pKO	REP-5		M	F	0.0	0.0	0.0													54.5		52.0				50.9	52.8	49.4	49.1	46.3	51.9	49.4		57.1	40.5		48.0
pKO	ep4-20		M	G	0.0	0.0														53.8	46.8	56.2	49.4	41.7	46.0	55.1	46.1	53.0	54.7	47.9	51.8	52.2	47.7	52.7	48.4	44.4	47.4
pKO	ep4-21		M	G	0.0	0.0	0.0													53.0	48.1	56.5	45.6	39.9	46.0	52.3	47.5	53.3	50.8	46.9	58.6	53.0	44.4	51.0	46.8	41.7	48.0
pKO	ep4-22		M	G	0.0	0.0	0.0													55.0	49.1	50.8	46.0	42.4	44.1	53.4	48.5	52.7	52.0	50.0	51.0	53.5	48.6	51.6	46.6	42.4	47.3
pKO	ep4-23		M	G	0.0	0.0	0.0													51.4	49.5	54.4	44.4	41.7	47.1	55.8	90.1	52.9	52.1	46.1	52.1	53.1	46.0	51.2	45.7	42.3	46.0
pKO	ep4-24		F	G	0.0	0.0	0.0													57.7	46.1	54.7	48.5	40.2	48.2	54.8	50.7	57.5	54.1	47.5	50.1	54.1	49.1	54.0	46.5	42.1	46.8
pKO	ep4-25		M	G	0.0	0.0	0.0													54.6	49.8	54.8	44.5	46.8	44.4	97.3	46.7	96.4	52.0	50.8	53.3	51.9	48.2	52.2	48.7	43.2	47.8
pKO	ep3-1		F	H	0.0	0.0	0.0													52.7	47.1	54.7	49.1	43.1	45.9	52.2	47.0	52.7	52.4	49.2	52.2	53.5	45.0	53.0	46.9	43.3	47.6
pKO	ep3-2	U	F	H	36.8	35.8	39.2													55.7	49.5	52.7	45.8	42.1	45.3	54.9	46.8	53.6	89.3	86.9	89.1	51.1	44.6	51.8	45.4	42.9	43.6
pKO	ep3-3		M	H	0.0	0.0	0.0													55.9	49.0	56.1	46.5	41.9	43.5	51.7	47.3	51.5	52.0	49.4	51.2	52.9	46.7	50.5	47.9	42.4	46.2
pKO	ep3-4		M	H	0.0	0.0	0.0													56.7	47.2	55.6	49.7	44.1	45.7	58.3	48.7	54.0	49.5	49.6	51.0	51.9	47.1	52.3	49.1	42.0	45.5
pKO	ep3-5		M	H	0.0	0.0	0.0													57.1	48.0	53.9	54.6	38.9	45.2	57.2	45.9	52.1	48.8	48.6	52.0	53.7	45.7	50.9	47.6	42.2	46.0
pKO	5058-1		F	I	0.0	0.0	0.0													52.3	46.5	52.7	47.8	41.1	47.3	56.2	46.8	52.1	49.8	50.7	52.7	48.3	46.9	50.5	46.4	43.5	47.9
pKO	5058-2		M	I	0.0	0.0	0.0													55.1	46.0	53.5	47.9	41.3	48.6	53.8	47.0	52.6	50.7	47.6	50.9	51.4	45.9	52.3	49.2	40.5	47.4
pKO	5058-3		F	I	0.0	0.0	0.0													54.0	47.7	53.9	49.7	41.6	43.8	55.8	47.9	50.7	50.8	50.6	52.6	51.7	49.0	50.6	50.9	43.1	46.6
pKO	5058-4		F	I	0.0	0.0	0.0													51.4	49.1	51.2	45.3	42.1	45.5	52.2	47.5	52.2	52.3	48.7	49.9	57.2	45.0	51.6	46.4	41.9	47.1
pKO	5058-5		M	I	0.0	0.0	0.0													55.2	49.0	53.3	44.8	40.3	46.3	53.6	47.1	52.2	51.9	47.8	51.9	53.6	46.7	51.1	47.1	42.2	46.5

Table S8: List of primers used for each assay in this study.

Gene/Region	Primer	Primer Sequence	Assay	References
Tet1	13037	TCAGGGAGCTCATGGAGACTA	Tet1 Genotyping	The Jackson Laboratory (https://www2.jax.org/protocolsdb/f?p=116:5:0::NO:5:P5_MASTER_PROTOCOL_ID,P5_JRS_CODE:25442,017358)
Tet1	13038	TTAAAGCATGGGTGGGAGTC	Tet1 Genotyping	
Tet1	13039	AACTGATTCCCTTCGTGCAG	Tet1 Genotyping	
Kdm5c/Kdm5d	Smc1	TGAAGCTTTTGGCTTTGAG	Sex Genotyping	(Jay and Ciaudo, 2013)
Kdm5c/Kdm5d	Smc2	CCACTGCCAAATTCTTTGG	Sex Genotyping	
H19	*H19* F	GTCTCGAAGAGCTCGGACTG	qPCR	(Thorvaldsen et al., 2006)
H19	*H19 R*	ACTGGCAGGCACATCCAC	qPCR	
Igf2	*Igf2* F	CGCTTCAGTTTGTCTGTTCG	qPCR	(Lin et al., 2011)
Igf2	*Igf2 R*	GCAGCACTCTTCCACGATG	qPCR	
Meg3/Gtl2	*Meg3* F	TTGCTGTTGTGCTCAGGTTC	qPCR	
Meg3/Gtl2	*Meg3 R*	ATCCTGGGGTCCTCAGTCTT	qPCR	
Dlk1	*Dlk1 F*	CGGGAAATTCTGCGAAATAG	qPCR	
Dlk1	*Dlk1 R*	TGTGCAGGAGCATTCGTACT	qPCR	
Rplp0	*Arrpo F*	TCCCACTTACTGAAAAGGTCAAG	qPCR	
Rplp0	*Arrpo R*	TCCGACTCTTCCTTTGCTTC	qPCR	
Rpl13a	*Rpl13a F*	ATCCCTCCACCCTATGACAA	qPCR	(Bougault et al., 2008)
Rpl13a	Rpl13a R	GCCCCAGGTAAGCAAACTT	qPCR	
Nono	*Nono F*	GCTCGTGAGAAGCTGGAGAT	qPCR	(Plasschaert and Bartolomei, 2015)
Nono	*Nono R*	TTCTTGACGTCTCATCAAATCC	qPCR	
H19	HE2 (F)	TGATGGAGAGGACAGAAGGG	Allele-Specific Expression	(Thorvaldsen et al., 2006)
H19	HE4 (R)	TTGATTCAGAACGAGACGGAC	Allele-Specific Expression	
Igf2	*Igf2*-18	ATCTGTGACCTCCTCTTGAGCAGG	Allele-Specific Expression	(Fortier et al., 2008)
Igf2	*Igf2*-20	GGGTTGTTTAGAGCCAATCAA	Allele-Specific Expression	
Cdkn1c	p57-L	GCCAATGCGAACGGTGCG	Allele-Specific Expression	(Weaver et al., 2010)
Cdkn1c	p57-4	TACACCTTGGGACCAGCGTACTCC	Allele-Specific Expression	
Peg3	PG4	ATGCCCACTCCGTCAGCG	Allele-Specific Expression	(Bhatnagar et al., 2014)
Peg3	PG7	GCTCATCCTTGTGAACTTTG	Allele-Specific Expression	
Kcnq1ot1	Lit1 F	ATTGGGAACTTGGGGTGGAGGC	Allele-Specific Expression	(Rivera et al., 2008)
Kcnq1ot1	Lit1 R	GGCACACGGTATGAGAAAAGATTG	Allele-Specific Expression	
Snrpn	Sn1 (F)	CTCCACCAGGAATTAGAGGC	Allele-Specific Expression (Light Cycler)	(Szabo and Mann, 1995)
Snrpn	Sn3 (R)	GCAGTAAGAGGGGTCAAAAGC	Allele-Specific Expression (Light Cycler)	
Snrpn	SnMut (Snrpn sensor probe)	GAAGCATTGTAGGGGAAGAGAA-fluorescein	Allele-Specific Expression (Light Cycler Probe)	
Snrpn	SnAnc (Snrpn anchor probe)	LC-Red640-GGCTGAGATTTATCAACTGTATCTTAGGGTC-P	Allele-Specific Expression (Light Cycler Probe)	
H19/Igf2 ICR	H19/Igf2 ICR F	GGGTAGGATATATGTATTTTTTAGGTTG	Pyrosequencing PCR	(de Waal et al., 2014)
H19/Igf2 ICR	H19/Igf2 ICR R-biotinylated	CTCATAAAACCCATAACTATAAAATCAT	Pyrosequencing PCR	
H19/Igf2 ICR	H19/Igf2 ICR Sequencing	TGTAAAGATTAGGGTTGT	Pyrosequencing Sequencing Primer	
IG-DMR	IG-DMR F	GTGGTTTGTTATGGGTAAGTTT	Pyrosequencing PCR	
IG-DMR	IG-DMR R-biotinylated	CCCTTCCCTCACTCCAAAAATTAA	Pyrosequencing PCR	
IG-DMR	IG-DMR sequencing	GTTATGGATTGGTGTTAAG	Pyrosequencing Sequencing Primer	
Snrpn ICR	Snrpn F	GGTAGTTGTTTTTTGGTAGGATAT	Pyrosequencing PCR	
Snrpn ICR	Snrpn R- biotinylated	ACTAAAATCCACAAACCCAACTAACCT	Pyrosequencing PCR	
Snrpn ICR	Snrpn Sequencing	GTGTAGTTATTGTTTGGGA	Pyrosequencing Sequencing Primer	
Peg3 ICR	Peg3 F	GGTTTTTAAGGGTAATTGATAAGG	Pyrosequencing PCR	
Peg3 ICR	Peg3 R- biotinylated	CCCTATCACCTAAATAACATCCC	Pyrosequencing PCR	
Peg3 ICR	Peg3 Sequencing	AATTGATAAGGTTGTAGATT	Pyrosequencing Sequencing Primer	
KvDMR	*KvDMR* F	TTTTGTGTGATTTTATTTGGAGAGT	Pyrosequencing PCR	
KvDMR	*KvDMR* R-biotinylated	CCTCAAAACCACCCCTACT	Pyrosequencing PCR	
KvDMR	KvDMR Sequencing	GTAAGTATTTAAGGTTAGAAGTAGA	Pyrosequencing Sequencing Primer	
Peg1/Mest ICR	*Peg1/Mest* ICR F	GGAGGTTTTATATAAGTATTTGTTTTT	Pyrosequencing PCR	
Peg1/Mest ICR	*Peg1/Mest* ICR R-biotinylated	ACCACCCAACTAACACTAAA	Pyrosequencing PCR	
Peg1/Mest ICR	Peg1/Mest Sequencing	GGTTTTATATAAGTATTTGTTTTTT	Pyrosequencing Sequencing Primer	
Peg3 ICR	Peg3A-BL (1st round)	TTTTGATAAGGAGGTGTTT	Bisulfite Sequencing PCR	(Mann et al., 2004)
Peg3 ICR	Peg3D-BL (1st round)	ACTCTAATATCCACTATAATAA	Bisulfite Sequencing PCR	
Peg3 ICR	Peg3B-BL (2nd round)	AGTGTGGGTGTATTAGATT	Bisulfite Sequencing PCR	(Market-Velker et al., 2010)
Peg3 ICR	Peg3C-BL (2nd round)	TAACAAAACTTCTACATCATC	Bisulfite Sequencing PCR	
H19/Igf2 ICR	BMsp2t1 (H19 A) (1st round)	GAGTATTTAGGAGGTATAAGAATT	Bisulfite Sequencing PCR	(Tremblay et al., 1997)
H19/Igf2 ICR	BHha1t3 (H19 D) (1st round)	ATCAAAAACTAACATAAACCCCT	Bisulfite Sequencing PCR	
H19/Igf2 ICR	Bmsp2t2c (H19 B) (2nd round)	GTAAGGAGATTATGTTTTATTTTTGG	Bisulfite Sequencing PCR	(Ideraabdullah et al., 2014)
H19/Igf2 ICR	BHha1t4ct (H19 C) (second round)	CTAACCTCATAAAACCCATAACTAT	Bisulfite Sequencing PCR	

Development • Supplementary information

Table S9: List of PCR cycling conditions for each PCR used in this study.

Assay	Thermal Cycler	PCR conditions	Annealing Temperature (TA), °C	No. of cycles
Tet1	Thermo Electron Hybaid PCR Express Thermal Cycler	2 min denaturation at 94°C; number of cycles of [15 s at 94°C, 15 s at TA, and 40 s at 72°C]	60	35
Smc	BioRad C1000 Touch Thermal Cycler	5 min denaturation at 95°C; number of cycles of [15 s at 95°C, 1 min at TA, and 1 min at 72°C]; 7 min extension at 72°C	55	40
qPCR: All genes	7900HT Fast Real-Time PCR System	2 min hold at 50°C; 10 min hold at 95°C; number of cycles of [15 s at 95°C, 1 min at 60°C]; Melting Curve: 95°C for 15 s, 60°C for 15 s, 95°C for 15 s.	-	40
Allele-Specific *H19*	BioRad C1000 Touch Thermal Cycler	2 min denaturation at 95°C; number of cycles of [15 s at 95°C, 20 s at TA, and 20 s at 72°C]; 5 min extension at 72°C	58	21-31
Allele-Specific *Igf2*	BioRad C1000 Touch Thermal Cycler	2 min denaturation at 94°C; number of cycles of [20 s at 94°C, 20 s at TA, and 20 s at 72°C]; 5 min extension at 72°C	60	24-32
Allele-Specific *Cdkn1c*	BioRad C1000 Touch Thermal Cycler	2 min denaturation at 95°C; number of cycles of [15 s at 95°C, 20 s at TA, and 20 s at 72°C]; 5 min extension at 72°C	60	25-30
Allele-Specific *Peg3*	BioRad C1000 Touch Thermal Cycler	2 min denaturation at 94°C; number of cycles of [20 s at 95°C, 20 s at TA, and 20 s at 72°C]; 5 min extension at 72°C	60	29-34
Allele-Specific *Lit1/Kcnq1ot1*	BioRad C1000 Touch Thermal Cycler	2 min denaturation at 95°C; number of cycles of [20 s at 95°C, 20 s at TA, and 50 s at 72°C]; 5 min extension at 72°C	64	32-34
Allele-Specific *Snrpn*	Roche LightCycler 1.5	Amplification: 95°C 1 s (20°C/s), 50°C, 15 s (20°C/s), 72°C, 6 s (20°C/s); Melt: 95°C, 4 min (20°C/s), 35°C, 3 min (20°C/s), 40°C, 1 min (20°C/s), 45°C, 1 min (20°C/s), 85°C, 0 s, (0.5°C/s); Cooling: 40°C 30 s, (20°C/s)	-	Amplification: 45; Melt: 3; Cooling: 1
Pyrosequencing	BioRad C1000 Touch Thermal Cycler	(Hur et al., 2016)		
Peg3 Bisulfite	BioRad C1000 Touch Thermal Cycler	First Round: 5 min denaturation at 94°C; number of cycles of [94°C for 30 s, TA for 30 s, 72°C for 1 min]; 10 min extension at 72°C Second Round: 5 min denaturation at 94°C; number of cycles of [94°C for 30 s, TA for 30 s, 72°C for 1 min]; 10 min extension at 72°C	50 53	25 35
H19 Bisulfite	BioRad C1000 Touch Thermal Cycler	First Round: 5 min denaturation at 94°C; number of cycles of [94°C for 30 s, TA for 30 s, 72°C for 1 min]; 10 min extension at 72°C Second Round: 5 min denaturation at 94°C; number of cycles of [94°C for 30 s, TA for 30 s, 72°C for 1 min]; 10 min extension at 72°C	50 58	25 35

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