Sequence-based bioinformatic prediction and QUASEP identify genomic imprinting of the KCNK9 potassium channel gene in mouse and human

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Received June 12, 2007; Revised July 19, 2007; Accepted July 30, 2007

Genomic imprinting is the epigenetic marking of gene subsets resulting in monoallelic or predominant expression of one of the two parental alleles according to their parental origin. We describe the systematic experimental verification of a prioritized 16 candidate imprinted gene set predicted by sequence-based bioinformatic analyses. We used Quantification of Allele-Specific Expression by Pyrosequencing (QUASEP) and discovered maternal-specific imprinted expression of the Kcnk9 gene as well as strain-dependent preferential expression of the Rarres1 gene in E11.5 (C57BL/6 × Cast/Ei)F1 and informative (C57BL/6 × Cast/Ei) × C57BL/6 backcross mouse embryos. For the remaining 14 candidate imprinted genes, we observed biallelic expression. In adult mouse tissues, we found that Kcnk9 expression was restricted to the brain and also was maternal-specific. QUASEP analysis of informative human fetal brain samples further demonstrated maternal-specific imprinted expression of the human KCNK9 orthologue. The CpG islands associated with the mouse and human Kcnk9/KCNK9 genes were not differentially methylated, but strongly hypomethylated. Thus, we speculate that mouse Kcnk9 imprinting may be regulated by the maternal germline differentially methylated region in Peg13, an imprinted non-coding RNA gene in close proximity to Kcnk9 on distal mouse chromosome 15. Our data have major implications for the proposed role of Kcnk9 in neurodevelopment, apoptosis and tumorigenesis, as well as for the efficiency of sequence-based bioinformatic predictions of novel imprinted genes.

INTRODUCTION

Imprinted genes are exclusively or predominantly expressed from only one of their two parental alleles (1). The imprints are parent-specific epigenetic modifications of DNA and chromatin that are erased and established when the gene passes through the germline (2). Aberrant genomic imprinting can cause human diseases, including disorders affecting development and behaviour. Loss of imprinting (LOI) is often associated with human cancers. Increasing evidence also supports a role for imprinted genes in the pathogenesis of obesity, diabetes and malformations after assisted reproductive technology and mammalian embryo cloning (3). To date, more than 80 imprinted transcripts are known in mice and humans (4). Imprinted genes frequently cluster in domains with imprinting control centres that are shared by

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multiple neighbouring imprinted genes. However, several examples of imprinted genes occurring apparently isolated in
the mouse and human genomes have also been described (5,6).

Most approaches to identify novel imprinted genes have
determined differential expression of maternal and paternal
alleles by subtractive hybridization, differential mRNA display
or cDNA microarray screening (5,6). Recently, Luedi et al. (7)
described an innovative bioinformatics approach, in which
specific DNA sequence characteristics of known imprinted
genes were used to screen for novel potentially imprinted
genes. In a first step, they analysed 44 known imprinted genes
for the presence and position of specific sequence motifs such
as repetitive elements, transcription factor binding sites and
CpG islands. Subsequently, Luedi et al. used the collected
data to train a classifier for the prediction of either imprinted
or non-imprinted expression and the parental allele preferen-
tially expressed. Application of this classifier to a total of
23 788 mouse genes resulted in the prediction of 600 candi-
date imprinted genes, 64% of which were predicted to be matern-
ally expressed. These candidate imprinted genes provide
an excellent resource for the identification of causative genes
in multifactorial diseases associated with parent-of-origin
differences.

In an earlier study, we described the successful application
of Quantification of Allele-Specific Expression by Pyrose-
quencing (QUASEP) for experimental validation of candi-
date imprinted genes selected from an expression profiling
study of uniparental mouse embryos (8,9). We identified
three novel imprinted transcripts encoding putative non-
protein-coding RNAs on the basis of parent-of-origin-
specific monoallelic expression in E11.5 (C57BL/6 × Cast/
Ei)F1 and informative (C57BL/6 × Cast/Ei) × C57BL/6 backcross embryos. In addition, we found four transcripts
with preferential expression of a strain-specific allele.

In the present study, we also used QUASEP to experimentally
validate a prioritized set of 16 promising candidate imprinted
genes selected from the bioinformatics prediction of Luedi
et al. (7). We identified one novel imprinted gene, Kcnk9,
which is already known to play an important role in apoptosis
and tumourigenesis as well as neuronal development and
function.

RESULTS

Selection of promising candidate genes

We extracted 600 murine candidate imprinted genes and the
their prediction strength from the previous bioinformatics
study (7). On the basis of prediction strength, associated
biomedical interest as well as properties shared with known
imprinted genes (e.g. proximity to other candidate genes
and, thus, potential clustered organization), we subsequently
selected 18 promising candidate imprinted genes for experi-
mental validation (Table 1, Supplementary Material, Table S1).

Identification of tSNPs and QUASEP analysis

For imprinting analysis, we used the previously described
QUASEP method (9,10). This method, based on Pyrosequencing
technology, enables the discrimination of subtle differences in
allele-specific transcript ratios and uses heterozygous tran-
scribed single nucleotide polymorphisms (tSNPs) for distin-
guishing the parental origin of a transcribed allele. Thus,
we screened the selected 18 candidate imprinted genes for
tSNPs by sequencing genomic DNA samples derived from
C57BL/6, Cast/Ei and interspecific (C57BL/6 × Cast/Ei)F1
hybrid mice. Using the Pyrosequencing Assay Design soft-
ware, we identified tSNPs appropriate for QUASEP in 16 of
these genes (Supplementary Material, Table S2). Then, we
evaluated the imprinted expression of these 16 candidate
imprinted genes by QUASEP of RT–PCR products derived from
(C57BL/6 × Cast/Ei)F1, C57BL/6 and Cast/Ei E11.5
whole embryos.

We identified monoallelic expression of the maternal allele
of Kcnk9 predicted by Luedi et al. (7). Furthermore and in
contrast to the bioinformatics prediction, we observed prefer-
ential expression of the paternal allele of Rarres1. The remain-
ing 14 candidate imprinted genes showed biallelic expression
(Table 1). To confirm the putative imprinting expression of
Kcnk9 and Rarres1, we performed a QUASEP analysis of
informative embryos derived from reciprocal (C57BL/6 × Cast/
Ei) × C57BL/6 crosses. In these experiments, the
Kcnk9 gene again exhibited monoallelic expression of the pre-
dicted maternal allele, confirming imprinting (Fig. 1A, Sup-
plementary Material, Fig. S1A), whereas the preferential
expression of Rarres1 turned out to be strain-specific and
not imprinted (data not shown). We further confirmed
imprinted expression of Kcnk9 by conventional sequence
analysis of the tSNP in the corresponding RT–PCR product
(Supplementary Material, Fig. S2).

Maintenence of imprinted Kcnk9 expression
in the adult stage

To address whether imprinted expression of Kcnk9 is also
maintained in the adult, we performed RT–PCR to determine
Kcnk9 expression in skeletal muscle, kidney, liver, lung, heart,
brain, testis and spleen. Kcnk9 RT–PCR products were
detected only in adult brain, but not in the other tissues
(Fig. 2). QUASEP assays with RT–PCR products from adult
brain of (C57BL/6 × Cast/Ei)F1 as well as informative recip-
rocal backcross mice revealed complete maintenance of
monoallelic maternal Kcnk9 expression in adult brain
(Fig. 1B, Supplementary Material, Fig. S1B).

Imprinted expression of the human KCNK9 orthologue

Many genes that are imprinted in the mouse are also imprinted
in humans (1,4). Therefore, we analysed the allele-specific
expression of the human KCNK9 gene, which is predomi-
nantly expressed in brain (11,12). We tested 15 fetal brain
DNA samples by genomic PCR and conventional sequence
analysis and found that seven were heterozygous for the
known T/C-SNP in exon 2 of KCNK9 (NCBI dbSNP:
rs2615374). We further performed QUASEP assays with RT–
PCR products from the seven heterozygous samples (T/C) and
detected strict or predominant monoallelic expression from
either the T- or the C-allele (Fig. 1C, Supplementary Material,
Fig. S1C). As the maternal deciduas for two heterozygous
samples expressing the T-allele and C-allele, respectively,
were homozygous for the T (T/T) and C alleles (C/C), respectively (data not shown), we concluded that the expressed allele was of maternal origin.

### Table 1. Allelic expression analysis of the studied candidate imprinted genes

<table>
<thead>
<tr>
<th>Gene</th>
<th>Ensembl-ID (Mus musculus)</th>
<th>Expression predicted</th>
<th>Chromosome including cytogenetic band and coordinate (in base pairs)</th>
<th>Allelic expression ratio (C57BL/6J: Cast/Ei)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kcnk9</td>
<td>ENSMUSG00000036760</td>
<td>Maternal</td>
<td>15e3 (72591862–72626022)</td>
<td>Monoallelic maternal (99%: 1%; SD 1.6)</td>
</tr>
<tr>
<td>Hes5</td>
<td>ENSMUSG000000048001</td>
<td>Paternal</td>
<td>4e2 (153950465–153951913)</td>
<td>No expressed SNP available</td>
</tr>
<tr>
<td>Nkx6-2</td>
<td>ENSMUSG00000041309</td>
<td>Paternal</td>
<td>7e5 (135993086–135996580)</td>
<td>Biallelic (43%: 57%; SD 2.2)</td>
</tr>
<tr>
<td>Ntn2</td>
<td>ENSMUSG00000035513</td>
<td>Maternal</td>
<td>2a3 (29202132–29255351)</td>
<td>Biallelic (51%: 49%; SD 3.2)</td>
</tr>
<tr>
<td>Camk2b</td>
<td>ENSMUSG00000020466</td>
<td>Paternal</td>
<td>11a1 (5921675–6017751)</td>
<td>Biallelic (51%: 49%; SD 3.9)</td>
</tr>
<tr>
<td>Irx4</td>
<td>ENSMUSG00000021604</td>
<td>Maternal</td>
<td>13c1 (70192290–70201087)</td>
<td>Biallelic (50%: 50%; SD 1.6)</td>
</tr>
<tr>
<td>Rarr1s</td>
<td>ENSMUSG00000049404</td>
<td>Maternal</td>
<td>3e2 (67579972–67616169)</td>
<td>Preferential strain-specific Cast/Ei (33%: 67%; SD 9.3)</td>
</tr>
<tr>
<td>Foxg1</td>
<td>ENSMUSG00000020950</td>
<td>Paternal</td>
<td>12c1 (47396718–47400567)</td>
<td>Biallelic (49%: 51%; SD 0.6)</td>
</tr>
<tr>
<td>Dok1</td>
<td>ENSMUSG00000006964</td>
<td>Paternal</td>
<td>6d1 (83056368–83058999)</td>
<td>Biallelic (54%: 46%; SD 1.8)</td>
</tr>
<tr>
<td>Wnt7b</td>
<td>ENSMUSG00000022382</td>
<td>Maternal</td>
<td>15e3 (85617762–85663903)</td>
<td>Biallelic (53%: 47%; SD 3.4)</td>
</tr>
<tr>
<td>Disc1</td>
<td>ENSMUSG00000043051</td>
<td>Paternal</td>
<td>8e2 (123641593–123849582)</td>
<td>No expressed SNP available</td>
</tr>
<tr>
<td>Ly6d</td>
<td>ENSMUSG00000034634</td>
<td>Maternal</td>
<td>15e1 (7482606–74844117)</td>
<td>Biallelic (59%: 41%; SD 4.2)</td>
</tr>
<tr>
<td>Gad2</td>
<td>ENSMUSG00000022144</td>
<td>Maternal</td>
<td>15a2 (7637824–76624388)</td>
<td>Biallelic (47%: 53%; SD 2.4)</td>
</tr>
<tr>
<td>Gad6</td>
<td>ENSMUSG00000033820</td>
<td>Maternal</td>
<td>5a1 (3350318–3528231)</td>
<td>Biallelic (47%: 53%; SD 1.4)</td>
</tr>
<tr>
<td>Nppc</td>
<td>ENSMUSG00000026241</td>
<td>Maternal</td>
<td>3c1 (86566967–86571248)</td>
<td>Biallelic (50%: 50%; SD 1.5)</td>
</tr>
<tr>
<td>Prdm16</td>
<td>ENSMUSG00000039410</td>
<td>Paternal</td>
<td>4e2 (153309834–153626302)</td>
<td>Biallelic (55%: 45%; SD 2.8)</td>
</tr>
<tr>
<td>Stk32c</td>
<td>ENSMUSG00000015981</td>
<td>Paternal</td>
<td>7f5 (13552391–135602224)</td>
<td>Biallelic (52%: 48%; SD 0.9)</td>
</tr>
</tbody>
</table>

SD, standard deviation (calculated from at least four samples); genes are sorted by descending prediction strengths.

Identification and methylation analysis of CpG islands

Many imprinted genes are associated with CpG islands, showing differential methylation of maternal and paternal alleles [termed differentially methylated regions (DMRs)] (1,6,13). Consequently, the proximity of CpG islands was an important feature for the genome-wide prediction of novel imprinted genes by Luedi et al. (7). To identify CpG islands associated with the murine Kcnk9 gene and its human orthologue, we used the EMBOSS CpGPlot tool. The program identified putative CpG islands within the promoter regions of both orthologues, reaching from −1326 to +153 bp in the mouse (denoted mCpG1 in Fig. 3A) and from −1498 to +640 bp in the human (denoted hCpG1 in Fig. 3B), each with respect to the translational start codon. In addition, we detected multiple putative binding sites (mouse: n = 2 and human: n = 6) of the methylation-sensitive CTCF insulator protein within these CpG-rich regions (14). Thus, we performed bisulphite sequencing of mouse adult brain and spleen genomic DNA samples, as well as human fetal brain and blood DNA samples, to investigate both CpG islands for the presence of differential methylation. This analysis revealed that both mCpG1 and hCpG1 are not differentially methylated, but instead strongly hypomethylated (Fig. 4A and B). Consequently, a mechanism other than DNA methylation of their promoter regions is presumably involved in regulating the imprinted expression of the mouse and human Kcnk9/KCNK9 genes.

In the mouse, Kcnk9 is located on chromosome 15 ~260 kb downstream of the imprinted Peg13 gene, a non-protein-coding RNA gene of unknown function (Fig. 3A). Similar to Kcnk9, Peg13 is expressed predominantly in brain, but, in contrast, the maternal allele is silenced and marked by DNA methylation in somatic tissues (15). We therefore hypothesized that imprinting of the murine Kcnk9 gene is controlled by the Peg13-DMR (located from +195 to +833 bp relative to the 5′ end of the Peg13 transcript and denoted mCpG2 in Fig. 3A). To lend support to this hypothesis, we performed bisulphite sequence analysis of the Peg13-DMR in male and female germ cells. We found full methylation of the Peg13-DMR in mature oocytes and near complete absence of methylation in sperm DNA (Fig. 4C).

Although there was no direct human orthologue of Peg13 identified, conceivably, the Peg13-DMR is at least positionally conserved and differentially methylated in both species and, consequently, also acts as a regulatory region for human KCNK9 imprinting. The mouse Peg13-DMR is located in intron 16 of the gene 1810044A24Rik (also known as Nibp or KIAA1882, Fig. 3A) which was already described to be not imprinted (15). Taking into account an additional exon belonging to the 5′ untranslated region of human NIBP, the Peg13-DMR orthologous region in humans is located in intron 17 of NIBP on chromosome 8q24.3. In this region, the EMBOSS CpGPlot tool identified a 730 bp CpG island (located from −75 316 to −74 586 bp relative to the 5′ end of exon 18 of the human NIBP gene and denoted hCpG2 in Fig. 3B), with putative CTCF binding sites (n = 2). However, bisulphite sequencing of human fetal brain and blood DNA samples showed that hCpG2 is not differentially methylated but strongly hypermethylated (Fig. 4D).
We used QUASEP of E11.5 (C57BL/6/C2 Cast/Ei)F1 hybrid embryos to systematically analyse and verify imprinted expression of 16 promising candidate imprinted genes predicted by a recent bioinformatics study. Our analysis identified one novel imprinted gene, Kcnk9, and one gene with strain-specific preferential expression, Rarres1. The other analysed 14 candidate genes were biallelically expressed. We cannot, however, rule out the possibility that some of the remaining candidates have highly selective, tissue-specific imprinting, which would not have been detected in our analysis.

Kcnk9 belongs to the family of two-pore domain potassium channel genes (K2P) and encodes the TASK-3 protein (16). The K2P channels regulate the resting membrane potential and also influence action potential duration and firing frequency of neurons (16). In humans, TASK-3 is expressed in the brain with particularly high levels in the cerebellum (11). Recent studies indicate a role of TASK-3 in development and maturation of cerebellar neurons (17). In this context, overexpression of TASK-3 has been linked to apoptosis of cerebellar granule neurons (18). The recent description of a Kcnk9 mutation in a rat model of absence epilepsy further suggests a prominent role of this gene in the central nervous system. 

***DISCUSSION***

We used QUASEP of E11.5 (C57BL/6 × Cast/Ei)F1 hybrid embryos to systematically analyse and verify imprinted expression of 16 promising candidate imprinted genes predicted by a recent bioinformatics study. Our analysis identified one novel imprinted gene, Kcnk9, and one gene with strain-specific preferential expression, Rarres1. The other analysed 14 candidate genes were biallelically expressed. We cannot, however, rule out the possibility that some of the remaining candidates have highly selective, tissue-specific imprinting, which would not have been detected in our analysis.
Interestingly, aberrant expression of TASK-3 has been repeatedly implicated in tumourigenesis. Mu et al. (20) reported that KCNK9 is amplified from 3- to 10-fold in 10% of breast tumours and overexpressed from 5- to over 100-fold in 44% of breast tumours. Moreover, KCNK9 was also overexpressed in lung, colon and prostate cancers (20,21). Overexpression of KCNK9 in cell lines promotes tumour formation and induces resistance to both hypoxia and serum deprivation (20). Furthermore, wild-type KCNK9 confers a growth advantage to cells, whereas the inactivating mutant has no effect on cell growth, suggesting that KCNK9 is directly involved in cell proliferation and has oncogenic properties (22).

In this context, the discovery of Kcnk9 imprinting has important implications. Numerous imprinted genes including IGF2, ARH1, PEG1/MEST, DLK-GTL2 and others have been described to be aberrantly expressed and/or aberrantly methylated in several types of cancers (23). A frequent finding in cancers is LOI, which refers to activation of the normally silenced allele, or silencing of the normally active allele, of an imprinted gene. The best-known example is the LOI of IGF2, which is found in both the neighbouring normal cells and the tumour cells in colon, breast and prostate cancers (23). Thus, it is tempting to speculate that the role of KCNK9 in tumourigenesis and its putative oncogenic properties are not only associated with its overexpression, but also with an LOI.

Both mouse and human Kcnk9/KCNK9 imprinting do not seem to be regulated by short-range cis-acting differential methylation at their CpG-island promoter. In this context, it
can be conjectured that the nearby murine Peg13-DMR acts as a long-range acting imprinting control element also capable of controlling the imprinting of the distal murine Kcnk9 gene, particularly as we have now been able to demonstrate that it is a maternal germline DMR. Intriguingly, however, the Peg13-DMR does not appear to confer imprinting on the Nibp gene, in an intron of which it resides (15). Several examples of long-range acting imprinting control elements including the H19-DMR, the Lit1-DMR/KvDMR1, the IG-DMR of Dlk1-Gtl2 and others have already been described in mouse and human (13,24,25). Parent-specific deletion of the Peg13-DMR in the mouse followed by parental allele-specific Kcnk9 expression analysis may reveal a function of the Peg13-DMR in murine Kcnk9 imprinting control. Furthermore, a more detailed analysis of the known expressed sequence tags and associated regulatory regions located in the equivalent intron of human NIBP to that which contains Peg13 in the mouse may lead to the identification of a functional equivalent of Peg13 and its DMR in humans (15).

In our study, we also identified one gene, Rarres1, with a strain-dependent allele-specific transcript bias. Rarres1 is a retinoid-regulated gene and resides on mouse chromosome 3. Expression of its human orthologue, RARRES1, is frequently downregulated through DNA hypermethylation in

Figure 4. Methylation profiles of CpG islands associated with the murine and human Kcnk9/KCNK9 genes. The locations of the CpG islands analysed are indicated in Figure 3. Methylation profiles shown derive from sequences of PCR products cloned after amplification of bisulphite-treated DNAs. Unfilled circles represent unmethylated CpGs and filled circles represent methylated CpGs. The shaded circles indicate CpGs whose methylation status could not be determined unequivocally. (A) Parental allele-specific methylation profiles of mCpG1 (subregion 1, located from −1365 to −1006 bp relative to the translational start codon of the murine Kcnk9 gene), maternal and paternal alleles are hypomethylated. The half-filled circles in the paternal alleles indicate a SNP in which a CpG dinucleotide present in B6 (maternal alleles) is modified to a CpA dinucleotide in M. spretus (Spr, paternal alleles). (B) hCpG1 (located from −668 to −282 bp relative to the translational start codon of the human KCNK9 gene) methylation profiles demonstrate hypomethylation in human fetal brain and adult blood. (C) Methylation profiles of mCpG2 (subregion 1, located from +166 to +463 bp relative to the 5’ end of the murine Peg13 gene) in B6 oocytes, sperm and brain indicate that this region is a maternal germline DMR. (D) Methylation profiles of hCpG2 (located from −74 855 to −74 557 bp relative to the 5’ end of exon 18 of the human NIBP gene) in human fetal brain and adult blood illustrate hypermethylation of both parental alleles.
several types of cancers (26). Strain-dependent allele-specific transcript biases in the mouse have already been described for several genes (9,27). For four genes, Cowles et al. also identified promoter-associated SNPs in the strains analysed, which may act as cis-acting regulatory factors and, thus, cause the allele-specific transcript bias. Sequencing of the Rarres1 promoter in C57BL/6 and Cast/Ei strains may also reveal such candidate regulatory SNPs. With regard to the role of RARRES1 during tumourigenesis, it will be of interest to determine whether an allele-specific transcript bias of this gene is also found in humans.

Our findings must also be discussed with regard to the efficiency of sequence-based bioinformatics prediction of candidate imprinted genes. In several studies, specific sequence characteristics of imprinted genes have been reported and suggested to be appropriate for distinguishing between mono-allelically and biallelically expressed genes in a genome-wide screen to identify candidate imprinted genes (28–31). Luedi et al. (7) performed the first large-scale prediction of imprinted genes on the basis of the DNA sequence characteristics alone. From 600 murine genes predicted to be potentially imprinted, we prioritized 18 promising candidates using different parameters including prediction strength, associated biomedical interest as well as properties shared with known imprinted genes (Table 1, Supplementary Material, Table S1). We could experimentally analyse 16 of 18 genes by QUASEP and identified one gene (6%), Kcnk9, to be indeed imprinted. Interestingly, Kcnk9 was also the most promising candidate of the 18 prioritized genes, as it displayed the highest scores with regard to prediction strength and, thus, the highest priority (Table 1). This finding underscores the strength of the underlying bioinformatics prediction. If one considers that estimates of the total number of imprinted genes in the human and/or mouse genome range from 100 to 200 (3), one would assume an a priori likelihood of imprinting of a gene randomly chosen from the genome of <1%. Thus, the 6% rate of detection of an imprinted gene in our study is at least a six times improvement over chance and evidence for efficiency of the bioinformatics prediction. It is likely that new informatics analyses, for example, the identification of sequence properties correlated with the propensity of CpG islands to be methylated, (32), may further help refine sequence-based imprinted gene predictions.

In summary, our data have major implications for current and future studies analysing the role of Kcnk9 in neurodevelopment, neurobehaviour, apoptosis and tumorigenesis. In addition, our findings will also strongly influence current and future bioinformatic screens aimed at the identification of novel imprinted genes.

**MATERIALS AND METHODS**

**Mouse and human material**

We purchased C57BL/6 (B6) and *Mus musculus castaneus* (Cast/Ei) mice from Charles River Laboratories (Wilmington, MA, USA). We used these mice and their F1 hybrids and reciprocal backcross mice as sources of genomic DNA and total RNA. We performed natural matings to generate timed embryos with the day after conception considered as day 0.5. Note that for F1 hybrid and BC1 progeny, the maternal parent is designated first. For bisulphite sequence analysis of the mouse Kcnk9 CpG island, DNA was prepared from F1(C57BL/6 × CBA/Ca) × *M. spretus* adult brains; sperm and oocytes DNAs for analysis of the Peg13-DMR were obtained from C57BL/6, as described previously (33). For parental allele-specific expression analysis in human, we obtained fetal brain samples from aborted fetuses and matched paraffin-embedded maternal deciduas that underwent pathological examination and cytogenetic analysis in the Department of Paediatric Pathology at Mainz University School of Medicine as sources of genomic DNA and total RNA. The local Ethics Committee (Ärztekammer Rheinland-Pfalz, decision no. 837.103.04 (4261)) approved the use of anonymous ‘excess’ tissue material for scientific analyses. We selected only fetuses without detectable abnormal development and with normal karyotype. We dissected fetal tissues within 24 h after abortion and stored them at −80°C until further analysis.

**Isolation of nucleic acids and cDNA synthesis**

We prepared genomic DNA using standard salting out procedures or a specialized protocol (for paraffin-embedded deciduas) of the QIAamp DNA Mini Kit (Qiagen, Hilden, Germany). For the preparation of total RNA, we used Trizol reagent (Invitrogen GmbH, Karlsruhe, Germany). Afterwards, all isolated RNA samples were treated with the DNA-free kit (Ambion Ltd, Huntington, UK) to exclude or minimize contamination with genomic DNA. The cDNA samples were subsequently synthesized from 5 μg of each total RNA using an oligo(dT)18 primer and the RevertAid First Strand cDNA Synthesis kit (Fermentas GmbH, St. Leon-Rot, Germany). We prepared each sample with (+RT) and without (−RT) MuLV reverse transcriptase in parallel. This step was intended to detect contamination with genomic DNA later on.

**SNP discovery**

In order to identify SNPs in the transcribed regions of the candidate imprinted genes, genomic DNA from C57BL/6, Cast/Ei and F1 hybrid mice was subjected to PCR amplification (primer sequences and PCR conditions are available on request). By direct sequencing of the PCR products, we identified heterozygous tSNPs using an ABI 3730 DNA Analyzer and the BigDye Terminator v1.1 Cycle Sequencing kit (Applied Biosystems, Foster City, CA, USA).

**Allelic expression analysis by QUASEP**

The cDNA samples were amplified by PCR using one biotinylated primer per pair (primer sequences and PCR conditions are available on request). We next used the QUASEP approach for allelic expression analysis, as described previously (9). Owing to occasional background signals, depending on the particular assay, the peak heights must be normalized. Therefore, we repeated the QUASEP experiments at least four times for the homozygous B6 and Cast/Ei samples and 10 times for the heterozygous F1 hybrid and backcross samples and thereby calculated arithmetic mean and standard
deviation. With the results of the B6 and Cast/Ei samples, we drew calibration curves. We created these curves, representing the expected versus the measured relative amounts of a certain allele, for each QUASEP assay by linear regression analysis. Afterwards, we calculated the real allele ratio in F1 hybrid and backcross mice by interpolating the measured ratios by means of the calibration curve. For analysing the human KCNK9 gene, we used genomic DNAs of different homozygous and heterozygous samples for comparing and normalizing the data obtained from RT–PCR products, as described earlier.

Programs used for sequence analysis
We used EMBOSS CpGPlot in order to identify putative CpG islands (http://www.ebi.ac.uk/emboss/cpgplot/). The following parameters were used: GC content of ≥ 50%, observed/expected ratio of ≥ 0.6 and window of 100 bp with a length of ≥ 500 bp. For the identification of putative CTCF binding sites, we employed the CTCF finder tool that comprises all known CTCF sequence motifs (http://www.essex.ac.uk/bs/molone/spa.html).

Bisulphite sequencing
We performed bisulphite treatment using the EpiTect Bisulfite Kit (Qiagen) and PCR-amplified the converted DNA with primers specific for mCpG1, mCpG2, hCpG1 and hCpG2. In the case of mouse oocytes, treatments were performed on aliquots of approximately 150 oocytes and PCR amplifications were carried out on approximately 30 oocyte equivalents. We amplified two subregions from mCpG1 associated with the mouse Kcnk9 promoter with the following primers: forward 5'-GTGAGTTTAGATTTT-3' and reverse 5'-CTCATAATACATAACTTT-3' (subregion 1, T
\text{ann} = 48.6°C, product size: 360 bp, with two SNPs between B6 and M. spretus) and forward 5'-GTTTGTAGTTTGGTGTTA3'-3' and reverse 5'-CCACCTAAAACACTAAAAAATC-3' (subregion 2, T
\text{ann} = 53.9°C, product size: 493 bp, with two SNPs between B6 and M. spretus). For mCpG2 in the Peg13-DMR, two subregions were amplified with the following primer sets: forward 5'-TTTTGATTAAATGTGGGTT-3' and reverse 5'-AAATAAAGAAACCAACC-3' (subregion 1, T
\text{ann} = 53.5°C, product size: 298 bp) and forward 5'-AGTTTTTGTTGTGATA3'-3' and reverse 5'-CTATCCACAAATAATAAC-3' (subregion 2, T
\text{ann} = 53.5°C, product size: 366 bp). For hCpG1 associated with the human KCNK9 promoter, we carried out PCR at 50°C with the following primers: forward 5'-TAGGG GATTTAGAGATTT-3' and reverse 5'-ACCAAAACAACA AACTACT-3' (product size: 387 bp). For hCpG2 associated with the positionally conserved Peg13-DMR orthologous region in humans, we performed PCR at 57°C with the following primers: forward 5'-TTGAGTTTATTTTGGGTGTT TT-3' and reverse 5'-TCTCAATACAATCCTTCAACACC-3' (product size: 299 bp). We cloned the PCR products using the pGEM-T Vector Systems (Promega, Mannheim, Germany) and sequenced positive clones using the CEQ™ DTCS Quick Start Kit (Beckman Coulter, Krefeld, Germany) and a Beckman CEQ 8000 Genetic Analysis System. For bisulphite analysis performed at the Babraham Institute, pGEM-Teasy clones were sequenced commercially (Cogenics Lark UK, Takeley, Essex). Sequences were analysed using the BiQ Analyzer program (34). Sequences that could not be distinguished on the basis of identical patterns of non-converted cytosines were discarded as possible clonal in origin.

SUPPLEMENTARY MATERIAL
Supplementary Material is available at HMG Online.

ACKNOWLEDGEMENTS
We are thankful to Cornelia Wetzig for excellent technical assistance as well as Wendy Dean for assistance with mouse oocyte collection. Moreover, we thank Tim Tralau, Larissa Seidmann and Annette Müller for providing human tissue samples.

Conflict of Interest statement. None declared.

FUNDING
German Academic Exchange Service (DAAD) fellowship to N.R.; German Research Foundation (DFG) (HA 1374/8-1 and ZE 442/3-1 to T.H. and U.Z.); DFG to S.B. and F.C.L.; Biotechnology and Biological Sciences Research Council (BBSRC) to G.K.

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