

Fig. S2. Imprinting Status of PEGs in TSCs.

(A-C) RFLP analysis of long (A) and short (B) isoforms of *Sfmbt2* as well as *Peg3* (C) in F1-TSCs amplified with *Sfmbt2*SNP4103 F/R, *Sfmbt2* short 3'end and *Peg3*-F1/R1 primers, respectively. Restriction enzymes used are as indicated. Note in (a) Hinf1 digests the *Mus castaneus* allele, and SnaBI digests the C57BL/6 allele (Kuzmin et al., 2008). (D-F) Sequence traces showing SNPs in gDNA and cDNA from F1-FTS cell line for *Ndn* (D), *Mcts2* (E) and *Igf2* (F). BC, C57BL/6 X *Mus castaneus*; gDNA, genomic DNA.

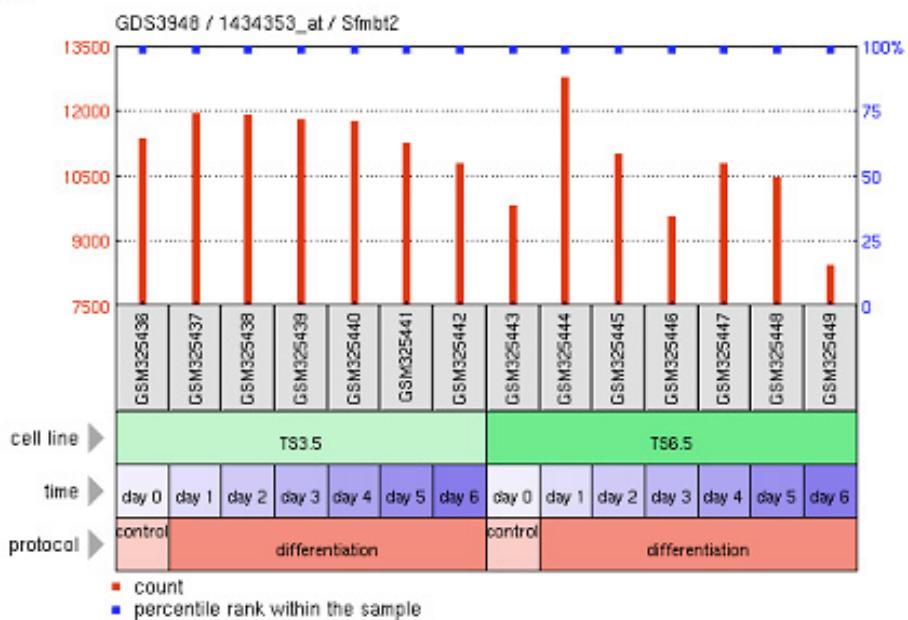
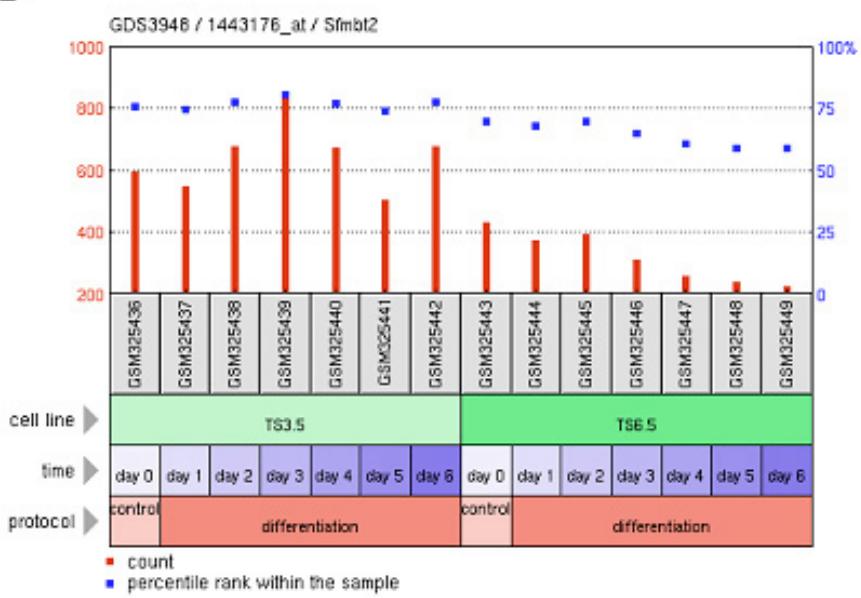
A**B**

Fig. S3. *Sfmbt2* transcript level decrease with TSC differentiation. (A,B) Transcript profile of the long (A) and short (B) isoforms of *Sfmbt2* in TSCs at various stages of differentiation (0 to 6 days); TSCs were derived from e3.5 blastocysts outgrowths (TS3.5) as well as e6.5 extraembryonic ectoderm (TS6.5). Graphs are from GEO series GSE12999, profile ID: 73697359 (A) and 73706182 (B) (Ralston et al., 2010).

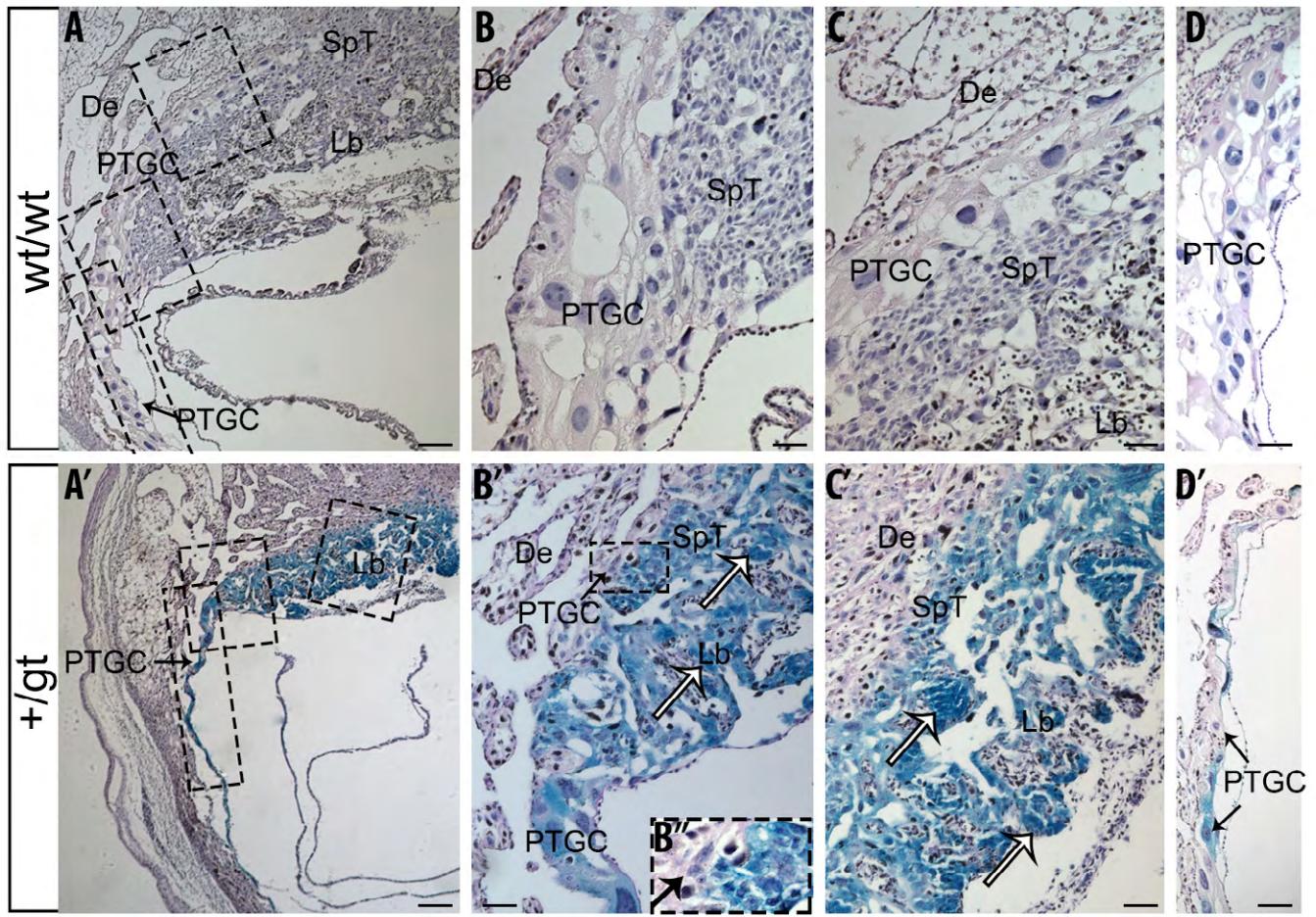


Fig. S4. Lac-Z staining confirms immunostaining against SFMBT2.

(A-D) Histological sections of e10.5 +/+ (Lac-Z negative) and (A'-D') +/gt (Lac-Z positive) extaembryonic tissues stained with H&E and X-gal. (B-D,B'-C') PTGCs and SpT cells of the +/gt (B'-D') embryos showing a drastic reduction in their numbers when compared to wild type counterparts (B-D). (B',B'',D') X-gal staining of PTGCs showing only a subset is positive for Lac-z expression. White arrows (B',C') indicate pockets of cells with higher intensity of staining, consistent with immunostaining in Fig. 3. De, decidua; Lb, labyrinth; SpT, spongiotrophoblast; PTGC, Parietal trophoblast giant cells; Al, allantois; Ch, chorion; PrE, parietal endoderm.

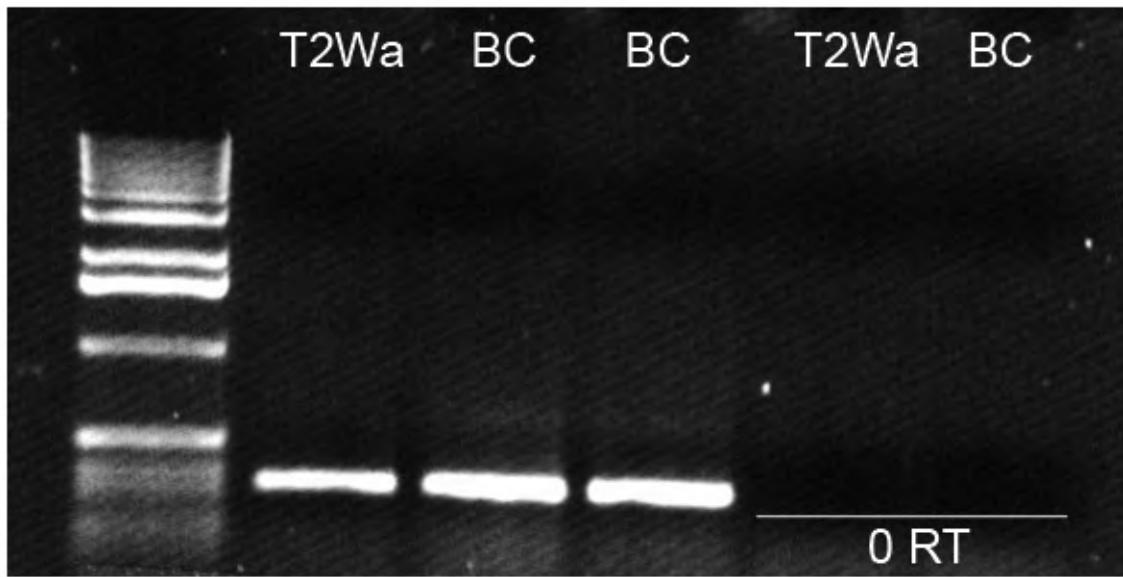


Fig. S5. MatDup Placenta Expresses Reactivated *Sfmbt2*

RNA from a MatDup placenta at e18.5 from the T(2;8)Wa line was extracted and used for RT-PCR analysis of *Sfmbt2* using primers from the 3' UTR. RT-PCR product from C57BL6 X *Mus castaneus* placenta is shown in BC lanes.

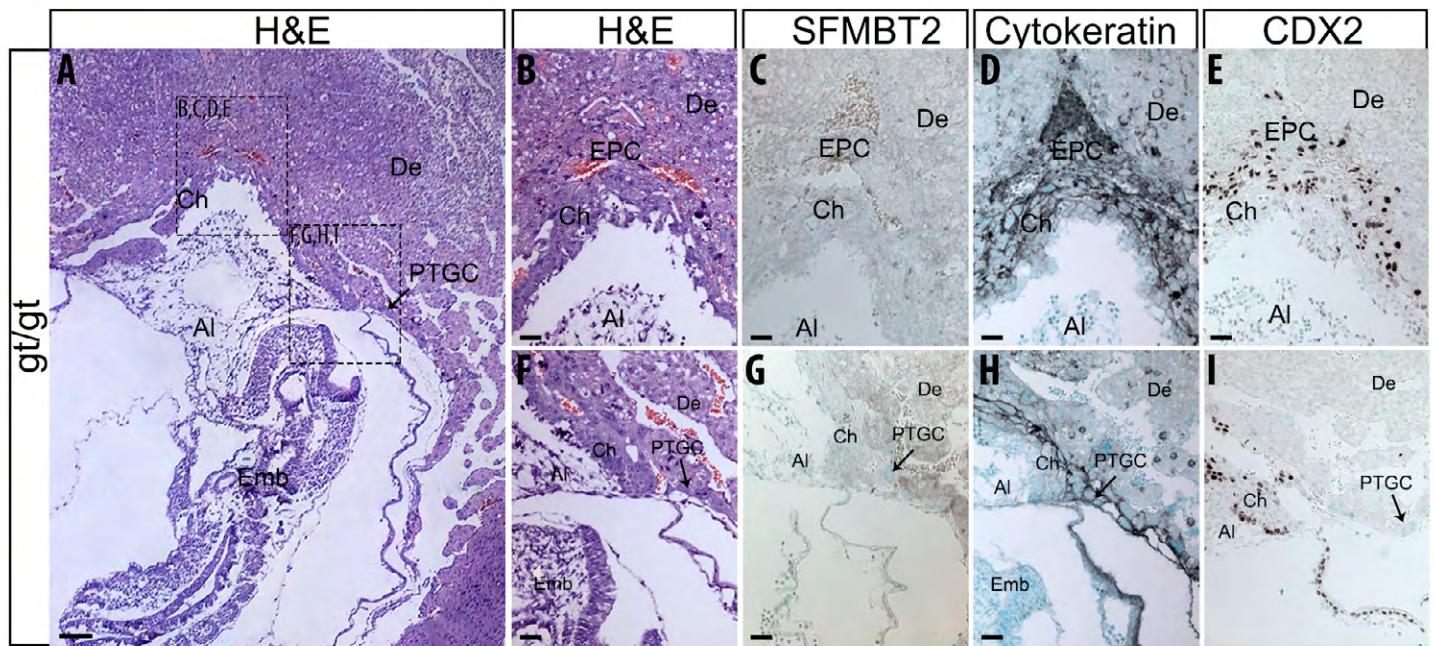


Fig. S6. Phenotype of SFMBT2 null embryos at e9.25.

(A-I) Histology of e9.25 *Sfmbt2* null (gt/gt) embryos. (A,B,F) H&E staining showing structural features of mutant embryos and extraembryonic tissues. (C,G) Immunohistochemistry against SFMBT2 showing no staining. (D,H) Immunohistochemistry against pan-cytokeratin showing the outline of the extraembryonic tissues with the highest level of expression in the PTGCs. (E,I) Immunohistochemistry against CDX2. De, decidua; PTGC, Parietal trophoblast giant cells; Al; allantois; Ch, chorion; EPC, ectoplacental cone; Emb, embryo. Scale bars: (A: 200µm); (B-I: 100µm).

Table S1. Primer sequences used for various experiments

| Paternally expressed genes and cell-type makers: | | |
|---|---------------------------|---------------------------|
| Primer name | Forward | Reverse |
| Cdx2 | TCAAGAAGAACGAGCAGCAG | GCAAGGAGGTACAGGACTC |
| Dlk | TCAGGCAACTTCTGTGAGATCG | CGCACTTGTGAGAAAGACGATGG |
| Fgfr2 | CAAATCTCCAACCAGAAGC | CTCCCCATAAGCACTGTCC |
| Igf2-F2/R2 | TCCTCTTGAGCAGGGACAGT | TTGGGTTGTTAGAGCCAATC |
| Ins2 | AACATGCCCTGTGGATG | TTGTGGGTCTCCACTTCAC |
| Mash2 | TGAATGCAAGCTTGATGGAC | CCAAGTTTACCAAGCTTACGC |
| Mets2 | TGCCATCCTCCTGTAGACC | CCACAGCCCCTCATTTAGATA |
| Megal2 | TCAACCGTGCCAACACTAAG | AGGCTCAAGACCACCATCAG |
| Mit1 | TCTCCCTCTTGGTGGAAAG | TGAACCCATTGAAAATCCAG |
| Mkrn3 | TCCTCTGGCTTGTATTCC | TGGTCTGGAGGCTGATCTC |
| Ndn-F1/R2 | AGGCGCAGTGCTCAGTAAAG | AATTCTGCTGGACGAACCTCC |
| Nnat | AGATCGAACAGCCCACAC | AGCAAGGCAGGAATATGTGTG |
| 10/04/12 | ACCAGGCTCAGAGGTATTGG | CCCTCTGAGTTGCTTCCAC |
| Peg1-F3/R3 | AAAGCCCTGGGTTCAGTTC | TCAGCACCAATTGCTCTTAGG |
| Peg10 | GTGGAGTTGCTTGCACAGAG | CTTCAAGGCAGTCATCATCG |
| Peg13 | TCCTTACCCAGCGAACATG | GCTGCAATCCAAAGAGGAAG |
| Peg3-F1/R1 | CCGGACTTCACATCAAAGACT | CCAGGATTCAAAGACACACG |
| Plagl1 | TTTGGGAAAGTCACCCGTG | GTTATCCTATGGGGCAGTGG |
| Rasgrf1 | GTGCGTAGCAGTCTCTCAGG | GTTTGCCATTGGGGTTGTC |
| Sfmbt2SNP4103 | CACATGGAAAGCAAGCACAA | CTGATTAGTCTACAAATGACTTAGC |
| Sfmbt2 short 3'end | TTCCTGTTATTAACTGAATTCCATA | TGCTGCTTAACCTGGGCATT |
| Sgce | AACAAAGCAAGTGTCCACCTATC | CGGCAGCACATGATATAAGC |
| Slc38a4 | CTCCACCCCCAGATTAACAG | GATCCTCACAGGGACAGCTC |
| snrpn | ATTGCTCGTGTGCCTCTTG | GGCCTCCAACCTCTGAC |
| Insertion site mapping | | |
| DCOF17 | TGGGGTTCTTGGAACTTTG | |
| DCOF2885 | GACTTGGGTGTGGTGTGTTG | |
| DCOF1448 (amplification) | AAAACTCGCACTTGCACCTCC | |
| DCOF1475 (sequencing) | GCATGCATATGCTGTTCA | |
| GtintronR4 (amplification) | | CGTCACCGCATGTTAGAAGA |
| GtintronR5 (sequencing) | | GCTTGAGGTTGCAGATACTGG |
| GtflankF (Amplification) | TTCGATGTAACCCACTCGTG | |
| GtflankR338 (Amplification) | | AGAAACATGGCAGCTGTGTG |
| GtflankR122 (sequencing) | | ACGGGTCAGTGAAGTGCTTT |
| Other: | | |
| Primer name | Forward | Reverse |
| DCOSNP | CATACAGCTCTGTGCCACA | CAACCCCCAAGAAAGTAAA |

| | | |
|-------------------------------------|---------------------------|--------------------------|
| DCOSNPi | TAAGCAAAGCCTGGGACATT | TGGACGGTTACATTCTGTGG |
| DCOFi1 | AGCTGTATCCGCTTAGAATGG | |
| DCOFi2 | ACACAGATGGTCGCTGCAA | |
| Gene trap | GACGTCTCGTTGCTGCATAA | ACCACCGCACGATAGAGATT |
| DCO Internal SNP | GGACTCCCAGAACATCCCTTC | TACTGGCAAAATCCCCAAAG |
| DCO Internal SNP seq | ATGTCGGTGGAAAGATTACGC | AGCATCGTGGGTTATCAGC |
| H2A template | CGTCTTGCTTCAGCTTGGT | TCCAGTTCAGAACGCCAGAGG |
| H2A qRT-PCR | CATTGTTCCCTCGGTGTCA | CCGGCTTGTGCTGGTATCTA |
| Sfmbt2 template | AGCTGTATCCGCTTAGAATGG | CAACCCCCAAGAAAGTAAA |
| Sfmbt2 qRT-PCR | ACACAGATGGTCGCTGCAA | TGGACGGTTACATTCTGTGG |
| q-Cdx2Fo/Ro (template) | TAGCCCACGGTCTCAATGGT | CTGCGGTTCTGAAACCAAAT |
| q-Cdx2F/R (qRT-PCR) | CAGTC CCTAGGAAGCCAAGTGAAA | AAGTAAA ACTCCTCTCCAGCTCC |
| q-Tpbpa-Fo/Ro (template) | ATAGTCCCTGAAGCGCAGTT | TTGCCCCAGTTAGATCTTC |
| q-Tpbpa-Fi/Ri (qRT-PCR) | GAAGGCTCCAACATAGAAATGAGT | CTTCAAACATTGGGTGAAAACAG |
| q-GemI-Fo/Ro (template) | CATCTACAGCTGGACGACA | AACTCCCTGACTCGGGATT |
| q-GemI-Fi/Ri (qRT-PCR) | CTTCATTTTCCAGTCAAAG | CACTTCTTATGGCTCTTCTTG |
| q-PLI-Fo/Ro (template) | CGAGAGGAAGTCCACGAAAC | AACTGAGGAGGGGAAAGCAT |
| q-PLI-Fi/Ri (qRT-PCR) | GTCTTCAGAACGAATGTTGAGTG | AAGCATTACAAGTCTGGTCAACA |
| q-Sfmbt2-S-Fo/Ro (template) | GCAATCTCCATAAAACAAGAGG | CGTCTTTAACCCAGTGGTCA |
| q-Sfmbt2-S-Fi/Ri (qRT-PCR) | AACTCTGCCTAACGGTACACTGG | ATCTGTATCTTATCCGAAACAACA |
| q-Sfmbt2-L-Fo /Ro (template) | TCAGGACCTCTGAGTTCCCTC | GTCCTCCTGACCAAGTCACAGT |
| q-Sfmbt2-L-Fi/Ri (qRT-PCR) | AGAATACCTGTCCATTTGCTACC | ACTCTAAATCACAAATTGCTGCAC |
| q-Runx1-Fo /Ro (template) | CCTCTCTGCAGAACCTTCAGT | GTTGGTGGCGAGTTGCTAT |
| q-Runx1-Fi/Ri (qRT-PCR) | CTCTCGTACCCACACCTACCTG | AGGCGCCGTAGTATAGATGGTAG |
| q-TBP-Fo/Ro (template) | ATCTACCGTGAATCTGGCTGT | GGAGAACAAATTCTGGTTGA |
| q-TBP-Fi/Ri (qRT-PCR) | GAATAAGAGAGGCCACGGACAAC | TTCTTGCTGCTAGTCTGGATTG |

Table S2. ABI identifiers for primer sets used for real-time PCR analysis of uniparental blastocyst cDNA

| Gene symbol | Gene ID | Assay ID |
|-------------|---------|---------------|
| Dio3 | 107585 | Mm00548953_s1 |
| Igf2 | 16002 | Mm01163433_m1 |
| Impact | 16210 | Mm00492649_m1 |
| Mcts2 | 66405 | Mm00481540_s1 |
| Mest | 17294 | Mm00484993_m1 |
| Mkrn3 | 22652 | Mm00844003_s1 |
| Nap1l5 | 58243 | Mm02526917_s1 |
| Nnat | 18111 | Mm00440480_m1 |
| Peg10 | 170676 | Mm01167724_m1 |
| Peg3 | 18616 | Mm01337374_m1 |
| Peg6 (Ndn) | 17984 | Mm02524479_s1 |
| Plagl1 | 22634 | Mm00494250_m1 |
| Rtl1 | 353326 | Mm02392620_s1 |
| Sgce | 20392 | Mm00448714_m1 |
| Sfmbt2 | 352282 | Mm00616784_m1 |
| Snrpn | 20646 | Mm01310473_g1 |
| U2af1 | 108121 | Mn00495837_s1 |
| Zfp264 | 116812 | Mm01325530_m1 |
| A19 | | Mm01239081_m1 |
| Rasgrf1 | 19417 | Mm00441097_m1 |
| Peg9/Dlk1 | 13386 | Mm00494477_m1 |
| Slc38a4 | 69354 | Mm00459056_m1 |
| Ins2 | 16334 | Mm00731595_gH |
| Ddc-exon1a | 13195 | Mm01192098_m1 |
| Magel2 | 27385 | Mm00844026_s1 |
| Peg12/Fraf3 | 27412 | Mm00844053_s1 |

Table S3.[Download Table S3](#)**Table S4.**[Download Table S4](#)