**Supplementary Table 1. Expression of 24 imprinted genes relative to 2 control genes (control = *AU042671* and *Cry2*: these genes were chosen to represent the average gene expression of all nonimprinted genes in mouse) in 14.5-dpc female mouse conceptuses, based on quantitative real-time PCR results.**

| | | Tissue | | | | | |
|---|---|---|---|---|---|---|---|
| Gene | Expressed Allele | Brain | Gonads | Heart | Liver | Troph-ectoderm | Umbilical Cord |
| *Asb4* | Maternal | -0.318 | -0.480 | 0.870 | 0.298 | -1.234 | 3.496 |
| *Cd81* | Maternal | -3.527 | -3.402 | -2.415 | -4.925 | -4.003 | -2.699 |
| *Cdkn1c* | Maternal | 2.435 | 5.095 | 6.402 | 2.892 | 5.477 | 4.947 |
| *Dcn* | Maternal | -0.767 | 0.278 | 0.062 | -1.027 | 4.608 | 4.262 |
| *Gtl2* | Maternal | 1.052 | 0.643 | -0.830 | 2.356 | 2.022 | 4.893 |
| *H19* | Maternal | -5.961 | -1.902 | -3.683 | -3.818 | -3.681 | -0.035 |
| *Igf2r* | Maternal | -0.060 | 3.430 | 5.098 | 0.644 | 2.720 | 3.692 |
| *Mash2* | Maternal | -4.985 | 0.382 | -4.172 | -3.745 | 2.403 | -2.832 |
| *Osbpl5* | Maternal | -0.060 | 1.530 | 0.355 | -2.473 | 1.781 | 1.340 |
| *Ppp1r9a* | Maternal | -4.547 | -3.538 | NA | -7.424 | -4.722 | -4.172 |
| *Tssc3* | Maternal | -6.330 | 0.301 | NA | -1.600 | 1.597 | -5.685 |
| *Zim1* | Maternal | -0.912 | 0.215 | 1.733 | 0.127 | 2.777 | 3.858 |
| *Air* | Paternal | -2.412 | -0.022 | -0.058 | -0.942 | -0.470 | 1.338 |
| *Dio3* | Paternal | -4.620 | -3.925 | -5.592 | -8.987 | -0.177 | -4.437 |
| *Igf2* | Paternal | 2.642 | 3.982 | 5.877 | 3.953 | 4.687 | 7.282 |
| *Impact* | Paternal | -4.623 | 0.000 | NA | -6.707 | -3.842 | -1.886 |
| *Nap1l5* | Paternal | -2.244 | -3.272 | NA | -4.142 | -5.076 | -5.128 |
| *Ndn* | Paternal | 3.202 | 1.746 | 2.026 | -4.030 | -0.512 | 3.322 |
| *Nnat* | Paternal | 3.483 | -2.320 | -4.379 | -4.673 | -3.712 | -1.228 |
| *Peg1* | Paternal | 5.122 | 5.528 | 7.038 | 4.801 | 6.722 | 7.102 |
| *Peg10* | Paternal | -0.059 | 0.450 | -1.822 | -0.471 | 6.525 | 0.593 |
| *Peg3* | Paternal | 2.922 | 8.140 | 5.772 | 2.642 | 5.922 | 7.177 |
| *Slc38a4* | Paternal | -0.763 | 2.392 | 3.699 | 2.832 | 6.948 | 3.643 |
| *Zac1* | Paternal | 1.906 | 1.490 | 1.652 | 1.352 | 3.393 | 5.553 |

NA, not available

Supplementary table 2 Primer sequences used for 24 imprinted genes, two control genes and housekeeping gene, *Gapdh,* used in this study.

| Primer Name | Sequence 5'----3' |
|---|---|
| Peg3_F | TGGAGACAACTGGCAAGAGG |
| Peg3_R | AGGGCTTGAGCGTTTCAGG |
| Mash2_F | CTCTCGGACCCTCTCTCAG |
| Mash2_R | CCAGTCAAGGTGTGCTTCC |
| Peg10_F | GTCTCTACTGTGGCAATGG |
| Peg10_R | GGGACCTTATTCGTTCTGG |
| Asb4_F | GAGCTGGTTGCCTTCTACG |
| Asb4_R | GCAGATGAGGTGGTGTTCC |
| Cdkn1c_F | CAGGACGAGAATCAAGAGC |
| Cdkn1c_R | AGAAGTCGTTCGCATTGG |
| Gtl2_F | GCAGCAGTGGACATGAACC |
| Gtl2_R | CTGGAGTGGCGAGGAAGG |
| Igf2r_F | AGACACCAGAACCAGACACTCC |
| Igf2r_F | GCTCTCCTCTCCCATCCTTACC |
| Dcn-F* | CATACTCAAATAAGGCTTCACCAA |
| Dcn-R* | AAAGTTGTCTGTAGTTGTGAACTGA |
| Tssc3-F* | TGGAGAAGCGAAGCGACAGC |
| Tssc3-R* | GGTGGGTTGGAAGCAGGTAA |
| Impact-F* | GGACTGTGAAGATGATGGAG |
| Impact-R* | ACACGTCTTCCCTGCCTAAC |
| Zac1-F* | GATCCCATGCCTCCTTTCCA |
| Zac1-R* | CCTTGCCATCTGCTTTGACG |
| Air-F** | GTGGATTCAGGTTTCATG |
| Air-R** | GGCCCAGATATAGAATGT |
| Peg1-F** | TCTCCAAAAGCTCCTCAAAG |
| Peg1-R** | ATGAATGGGGATGGACACAG |
| Nnat-F** | AAGCCCTACATCTCGGTGCAGAAG |
| Nnat-R** | TCCCTGTCTCCAGGAGCTTACAATC |
| Ndn-F** | AGGACTAAAAAGGTCCAGGGGCAC |
| Ndn-R** | CAGTCCATTCCACATGGATGCTTCC |
| Zim1-F | ATGCTGGAGAACTACGAGAACC |
| Zim1-R | GACTCCTGCCTCACCTTGC |
| Cd81_F | GTGATGATGTTTGTAGGCTTCC |
| Cd81_R | GCGATCTGGTCTTTGTTTACG |
| Dio3_F | AGTGAAGGCGAGGAGATGC |
| Dio3_R | TGGGCTTGCTTGAAGAAATCC |
| Ppp1r9a_F | ACCAGGACAAGTGAGTGAGG |

| | |
|---|---|
| Ppp1r9a_R | TCATCGTCGTCAGCATCATAC |
| H19_F | GCGAGGATGACAGGTGTGG |
| H19_R | GGTGGTTGAGCGGACTAGC |
| Nap1l5_F | GATGAAGATGACGAGGAAGAGG |
| Nap1l5_R | TTGCTGTGCTCACTTCTTGG |
| Osbpl5-F | GCACAGAAGGAGAACTATCG |
| Osbpl5-R | TTCGTCCAGCTCTTCAGG |
| Slc38a4-F | CATGGGCAGTGGGATCTTAGG |
| Slc38a4-R | CCTCCTTCCTTGGCTGTCTTC |
| *Gaph-F* | GTCGTGGAGTCTACTGGTGTC |
| *Gapdh-R* | GAGCCCTTCCACAATGCCAAA |
| AU042671_F | AGGAAGGTTGCTGAGTATGG |
| AU042671_R | AAGGAGAAGGTGACTGTATCG |
| Cry2_F | AGCACTTGGAACGGAAGG |
| Cry2_R | CAGGCGGTAGTAGAAGAGG |

*: Ogawa et al., 2003
**: Ogawa et al., 2006