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Supplemental Material to:

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Epigenetic and transcriptional features of the novel human imprinted lncRNA GPR1AS suggest it is a functional ortholog to mouse Zdbf2linc

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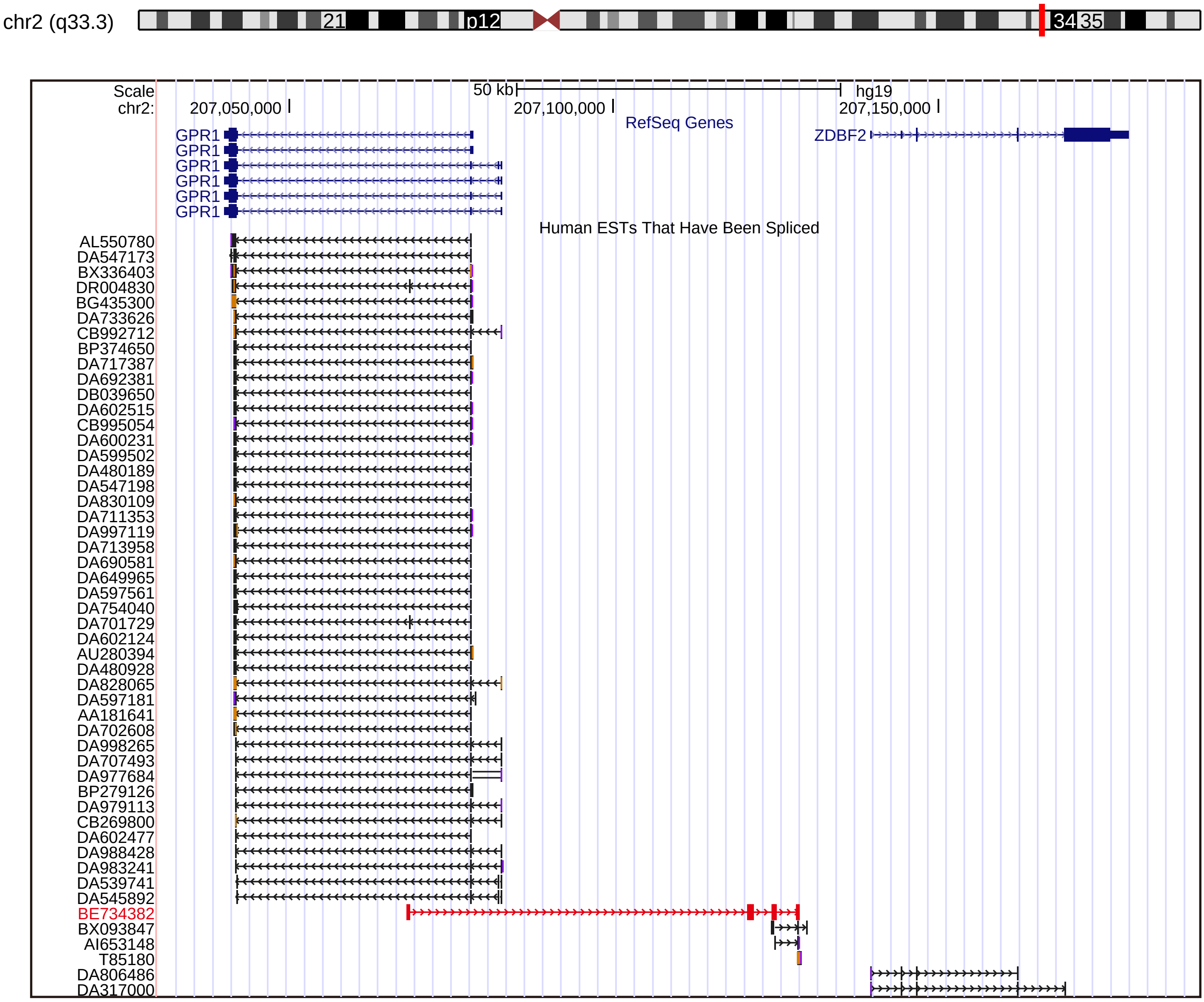
article/24887/

SUPPLEMENTARY FIGURES

```
ZDBF2_V1    1:MQKRQGYCSYCRVQYNNLEQHLFSAQHRSLTRQSRRQICTSSLMERFLQDVLQHHPYHCQESSSTQDETHVNTGSSSEVVHLDDAFSEEEEEDEDKVEDE 100
ZDBF2_V2    1:--MIPDGSSEIQEVMKNSGKHLFSAQHRSLTRQSRRQICTSSLMERFLQDVLQHHPYHCQESSSTQDETHVNTGSSSEVVHLDDAFSEEEEEDEDKVEDE 98
                      *       *   ********************************************************************************

ZDBF2_V1  101:DATEERPSEVSEPIEELHSRPHKSQEGTQEVSVRPSVIQKLEKGQQQPLEFVHKIGASVRKCNLVDIGQATNNRSNLVRPPVICNAPASCLPESSNDRPV 200
ZDBF2_V2   99:DATEERPSEVSEPIEELHSRPHKSQEGTQEVSVRPSVIQKLEKGQQQPLEFVHKIGASVRKCNLVDIGQATNNRSNLVRPPVICNAPASCLPESSNDRPV 198
              ****************************************************************************************************

ZDBF2_V1  201:TANTTSLPPAAHLDSVSKCDPNKVEKYLEQPDGASRNPVPSSHVETTSFSYQKHKESNRKSLRMNSDKLVLWKDVKSQGKTLSAGLKFHERMGTKGSLRV 300
ZDBF2_V2  199:TANTTSLPPAAHLDSVSKCDPNKVEKYLEQPDGASRNPVPSSHVETTSFSYQKHKESNRKSLRMNSDKLVLWKDVKSQGKTLSAGLKFHERMGTKGSLRV 298
              ****************************************************************************************************

ZDBF2_V1  301:KSPSKLAVNPNKTDMPSNKGIFEDTIAKNHEEFFSNMDCTQEEKHLVFNKTAFWEQKCSVSSEMKFDCISLQSASDQPQETAQDLSLWKEEQIDQEDNYE 400
ZDBF2_V2  299:KSPSKLAVNPNKTDMPSNKGIFEDTIAKNHEEFFSNMDCTQEEKHLVFNKTAFWEQKCSVSSEMKFDCISLQSASDQPQETAQDLSLWKEEQIDQEDNYE 398
              ****************************************************************************************************

ZDBF2_V1  401:SRGSEMSFDCSSSFHSLTDQSKVSAKEVNLSKEVRTDVQYKNNKSYVSKISSDCDDILHLVTNQSQMIVKEISLQNARHISLVDQSYESSSSETNFDCDA 500
ZDBF2_V2  399:SRGSEMSFDCSSSFHSLTDQSKVSAKEVNLSKEVRTDVQYKNNKSYVSKISSDCDDILHLVTNQSQMIVKEISLQNARHISLVDQSYESSSSETNFDCDA 498
              ****************************************************************************************************

ZDBF2_V1  501:SPQSTSDYPQQSVTEVNLPKEVHIGLVDKNYGSSSSEVSADSVFPLQSVVDRPPVAVTETKLRKKAHTSLVDNYGSSCSETSFDCDVSLESVVDHPQLTV 600
ZDBF2_V2  499:SPQSTSDYPQQSVTEVNLPKEVHIGLVDKNYGSSSSEVSADSVFPLQSVVDRPPVAVTETKLRKKAHTSLVDNYGSSCSETSFDCDVSLESVVDHPQLTV 598
              ****************************************************************************************************

ZDBF2_V1  601:KGRNLKGRQVHLKHKKRKPSSAKAHLDCDVSLGTVADESQRAVEKINLLKEKNADLMDMNCESHGPEMGFQADAQLADQSQVAEIERQKVDVDLENKSVQ 700
ZDBF2_V2  599:KGRNLKGRQVHLKHKKRKPSSAKAHLDCDVSLGTVADESQRAVEKINLLKEKNADLMDMNCESHGPEMGFQADAQLADQSQVAEIERQKVDVDLENKSVQ 698
              ****************************************************************************************************

ZDBF2_V1  701:SSRSSLSSDSPASLYHSAHDEPQEALDEVNLKELNIDMEVRSYDCSSSELTFDSDPPLLSVTEQSHLDAEGKERHIDLEDESCESDSSEITFDSDIPLYS 800
ZDBF2_V2  699:SSRSSLSSDSPASLYHSAHDEPQEALDEVNLKELNIDMEVRSYDCSSSELTFDSDPPLLSVTEQSHLDAEGKERHIDLEDESCESDSSEITFDSDIPLYS 798
              ****************************************************************************************************

ZDBF2_V1  801:VIDQPEVAVYEEETVDLESKSNESCVSEITFDSDIPLHSGNDHPEVAVKEVIQKEEYIHLERKNDEPSGSEISSDSHAPLHSVTNSPEVAVKKLNPQKEE 900
ZDBF2_V2  799:VIDQPEVAVYEEETVDLESKSNESCVSEITFDSDIPLHSGNDHPEVAVKEVIQKEEYIHLERKNDEPSGSEISSDSHAPLHSVTNSPEVAVKKLNPQKEE 898
              ****************************************************************************************************

ZDBF2_V1  901:QVHLENKENEPIDSEVSLDYNIIFHSVTGRSEDPIKEISLHTKEHMYLENKSVFETSLDSDVPLQAATHKPEVIVKETWLQREKHAEFQGRSTEFSGSKT 1000
ZDBF2_V2  899:QVHLENKENEPIDSEVSLDYNIIFHSVTGRSEDPIKEISLHTKEHMYLENKSVFETSLDSDVPLQAATHKPEVIVKETWLQREKHAEFQGRSTEFSGSKT 998
              ****************************************************************************************************

ZDBF2_V1 1001:SLDSGVPHYSVTEPQVAVNKINRKKQYVLENKNDKCSGSEIILDSNVPPQSMTDQPQLAFLKEKHVNLKDKNSKSGDSKITFDSEQLQEAVKKIDQWKEE 1100
ZDBF2_V2  999:SLDSGVPHYSVTEPQVAVNKINRKKQYVLENKNDKCSGSEIILDSNVPPQSMTDQPQLAFLKEKHVNLKDKNSKSGDSKITFDSEQLQEAVKKIDQWKEE 1098
              ****************************************************************************************************

ZDBF2_V1 1101:VIGLKNKINEPSTYKLIHHPDVSVQSVADQPKVAIKHVNLGNENHMYLEVKNSQYSCSEMNLDSGFLGQSIVNRPQITILEQEHIELEGKHNQCCGSEVS 1200
ZDBF2_V2 1099:VIGLKNKINEPSTYKLIHHPDVSVQSVADQPKVAIKHVNLGNENHMYLEVKNSQYSCSEMNLDSGFLGQSIVNRPQITILEQEHIELEGKHNQCCGSEVS 1198
              ****************************************************************************************************

ZDBF2_V1 1201:FDSDDPLQSVADRLRETVKEISLWKDEEVDTEDRRNEAKGFEIMYDSDVLQPVAGQPEEVVKEVSLWKEHVDLENKIVKPTDSRINFDSHEPLQSVTNKI 1300
ZDBF2_V2 1199:FDSDDPLQSVADRLRETVKEISLWKDEEVDTEDRRNEAKGFEIMYDSDVLQPVAGQPEEVVKEVSLWKEHVDLENKIVKPTDSRINFDSHEPLQSVTNKI 1298
              ****************************************************************************************************

ZDBF2_V1 1301:PGANKEINLLREEHVCLDDKGYVPSDSEIIYVSNIPLQSVIKQPHILEEEHASLEDKSSNSYSPEESSDSNDSFQAAADELQKPVKEINLWKEDHIYLED 1400
ZDBF2_V2 1299:PGANKEINLLREEHVCLDDKGYVPSDSEIIYVSNIPLQSVIKQPHILEEEHASLEDKSSNSYSPEESSDSNDSFQAAADELQKPVKEINLWKEDHIYLED 1398
              ****************************************************************************************************

ZDBF2_V1 1401:KSYKLGDFDVSYASHIPVQFVTDQSSVPVKEINLQKKDHNDLENKNCEVCGSEIKCHSCVHLQSEVDQPQVSYKEADLQKEEHVVMEEKTDQPSDSEMMY 1500
ZDBF2_V2 1399:KSYKLGDFDVSYASHIPVQFVTDQSSVPVKEINLQKKDHNDLENKNCEVCGSEIKCHSCVHLQSEVDQPQVSYKEADLQKEEHVVMEEKTDQPSDSEMMY 1498
              ****************************************************************************************************

ZDBF2_V1 1501:DSDVPFQIVVNQFPGSVKETHLPKVVLVDLVPGDSDYEVISDDIPLQLVTDPPQLTVKDISCINTECIDIEDKSCDFFGSEVRCNCKASTPSMTNQCKET 1600
ZDBF2_V2 1499:DSDVPFQIVVNQFPGSVKETHLPKVVLVDLVPGDSDYEVISDDIPLQLVTDPPQLTVKDISCINTECIDIEDKSCDFFGSEVRCNCKASTPSMTNQCKET 1598
              ****************************************************************************************************

ZDBF2_V1 1601:FKIINRKKDYIILGEPSCQSCGSEMNFNVDASDQSMTYESQGPDEKMVKYIDSEDKSCGYNGSKGKFNLEDTSHRTTHRLQKAHKEASLRKDPRNAGLKG 1700
ZDBF2_V2 1599:FKIINRKKDYIILGEPSCQSCGSEMNFNVDASDQSMTYESQGPDEKMVKYIDSEDKSCGYNGSKGKFNLEDTSHRTTHRLQKAHKEASLRKDPRNAGLKG 1698
              ****************************************************************************************************

ZDBF2_V1 1701:KSCQSSASAVDFGASSKSALHRRADKKKRSKLKHRDLEVSCEPDGFEMNFQCAPPLPSDTDQPQETVKKRHPCKKVSSDLKEKNHDSQSSSVLKVDSVRN 1800
ZDBF2_V2 1699:KSCQSSASAVDFGASSKSALHRRADKKKRSKLKHRDLEVSCEPDGFEMNFQCAPPLPSDTDQPQETVKKRHPCKKVSSDLKEKNHDSQSSSVLKVDSVRN 1798
              ****************************************************************************************************

ZDBF2_V1 1801:LKKAKDVIEDNPDEPVLEALPHVPPSFVGKTWSQIMREDDIKINALVKEFREGRFHCYFDDDCETKKVSSKGKKKVTWADLQGKEDTAPTQAVSESDDIV 1900
ZDBF2_V2 1799:LKKAKDVIEDNPDEPVLEALPHVPPSFVGKTWSQIMREDDIKINALVKEFREGRFHCYFDDDCETKKVSSKGKKKVTWADLQGKEDTAPTQAVSESDDIV 1898
              ****************************************************************************************************

ZDBF2_V1 1901:CGISDIDDLSVALDKPCHRHPPAERPPKQKGRVASQCQTAKISHSTQTSCKNYPVMKRKIIRQEEDPPKSKCSRLQDDRKTKKKVKIGTVEFPASCTKVL 2000
ZDBF2_V2 1899:CGISDIDDLSVALDKPCHRHPPAERPPKQKGRVASQCQTAKISHSTQTSCKNYPVMKRKIIRQEEDPPKSKCSRLQDDRKTKKKVKIGTVEFPASCTKVL 1998
              ****************************************************************************************************

ZDBF2_V1 2001:KPMQPKALVCVLSSLNIKLKEGEGLPFPKMRHHSWDNDIRFICKYKRNIFDYYEPLIKQIVISPPLSVIVPEFERRNWVKIHFNRSNQNSSAGDNDADGQ 2100
ZDBF2_V2 1999:KPMQPKALVCVLSSLNIKLKEGEGLPFPKMRHHSWDNDIRFICKYKRNIFDYYEPLIKQIVISPPLSVIVPEFERRNWVKIHFNRSNQNSSAGDNDADGQ 2098
              ****************************************************************************************************

ZDBF2_V1 2101:GSASAPLMAVPARYGFNSHQGTSDSSLFLEESKVLHARELPKKRNFQLTFLNHDVVKISPKSVRNKLLESQSKKKIHGKRVTTSSNKLGFPKKVYKPIIL 2200
ZDBF2_V2 2099:GSASAPLMAVPARYGFNSHQGTSDSSLFLEESKVLHARELPKKRNFQLTFLNHDVVKISPKSVRNKLLESQSKKKIHGKRVTTSSNKLGFPKKVYKPIIL 2198
              ****************************************************************************************************

ZDBF2_V1 2201:QQKPRKASEKQSIWIRTKPSDIIRKYISKYSVFLRHRYQSRSAFLGRYLKKKKSVVSRLKKAKRTAKVLLNSSVPPAGAEELSSAMANPPPKRPVRASCR 2300
ZDBF2_V2 2199:QQKPRKASEKQSIWIRTKPSDIIRKYISKYSVFLRHRYQSRSAFLGRYLKKKKSVVSRLKKAKRTAKVLLNSSVPPAGAEELSSAMANPPPKRPVRASCR 2298
              ****************************************************************************************************

ZDBF2_V1 2301:VARRRKKTDESYHGRQKGPSTPVRAYDLRSSSCLQQRERMMTRLANKLRGNEVK                                               2354
ZDBF2_V2 2299:VARRRKKTDESYHGRQKGPSTPVRAYDLRSSSCLQQRERMMTRLANKLRGNEVK                                               2352
              ******************************************************
```

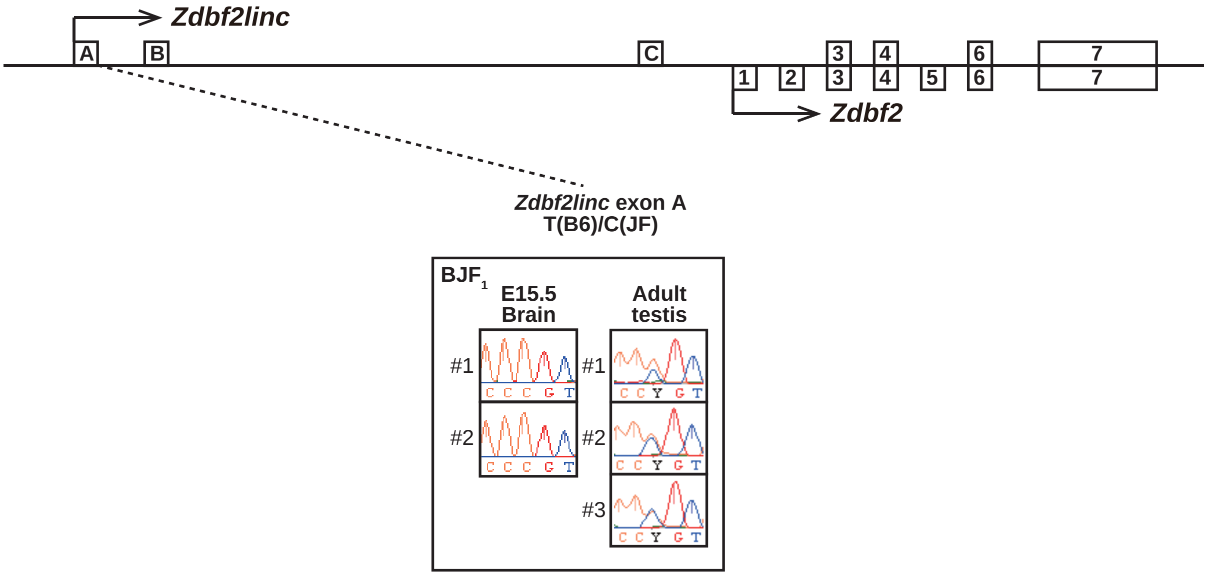
Supplementary Figure 1. Amino acid sequence alignment of the human ZDBF2 isoforms encoded by ZDBF2 splicing variants *ZDBF2_v1* and *ZDBF2_v2*. ZDBF2_V1 matches the original ZDBF2 protein sequence (accession number: NP_065974).



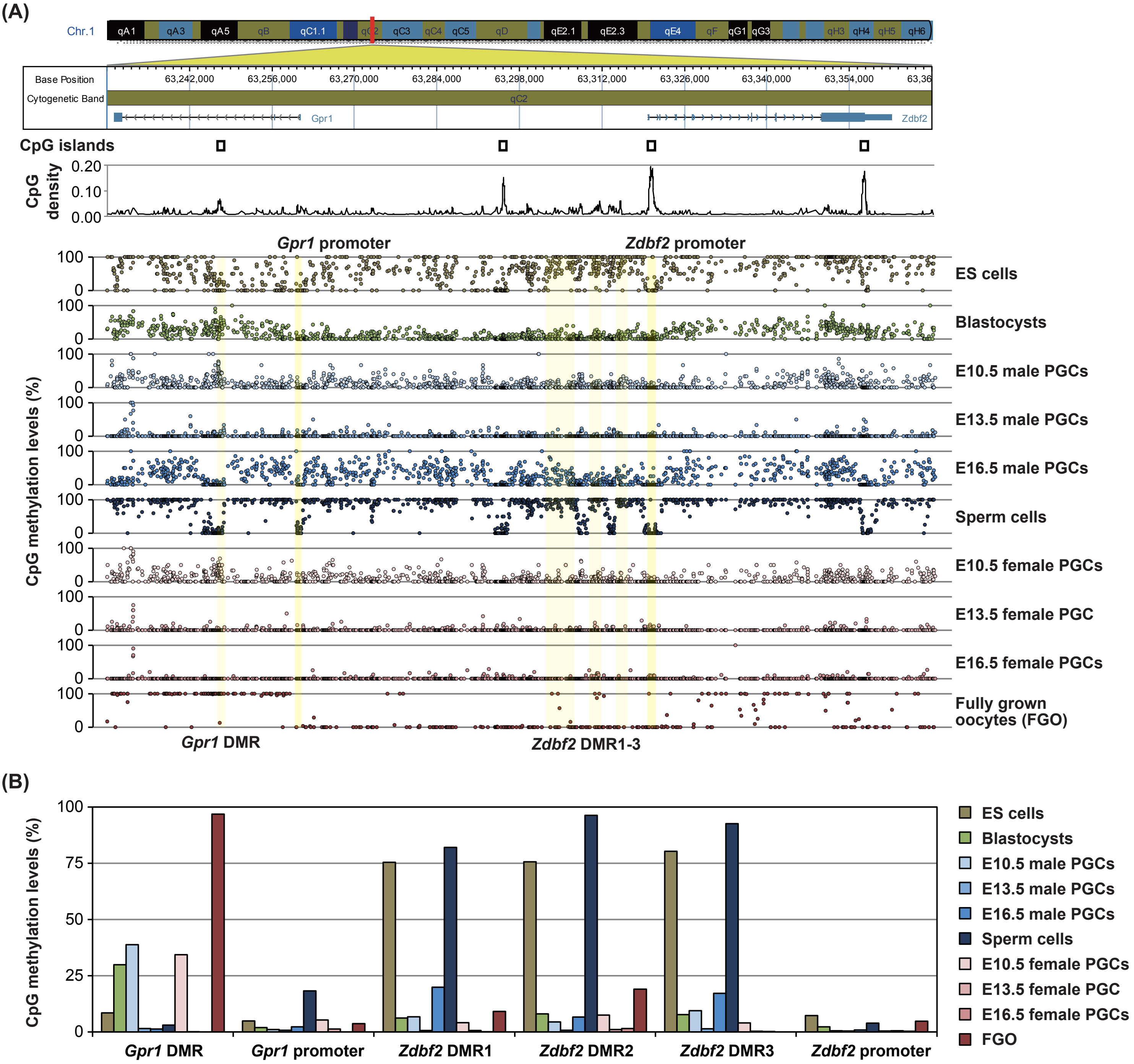
Supplementary Figure 2. Map of the *GPR1-ZDBF2* locus on human chromosome 2q33.3 (GRCh37/hg19, chr2: 207,030,001-207,190,000). Human RefSeq genes and ESTs were obtained from the UCSC Genome Browser (http://genome.ucsc.edu/). Exons and orientation of the BE734382 EST are highlighted in red.

```
        10         20         30         40         50         60         70         80         90        100
GCATTCATTA CAAATCGTGT CCACAGCCCG CTTCCCAGCT TCCAACTTCC ACCTCCAGGG GAGGACTGGG GGCTGGAGAT TGCATTAATT TCCAATGGCC
       110        120        130        140        150        160        170        180        190        200
AGTGGTTTAA TCAATCATGA CTAAGTAATG AGCCTCCGTA AAAACCAGAG CTTCCGGTCT GGTGAACACA CGGAGGTCCT GGAAATGGTG GCGCGCCCAG
       210        220        230        240        250        260        270        280        290        300
AGGGCATGGA AGCTCCGCGC CCCTTCCCAC AGACCTTGTC CCGTGCATCG CTTCCATCCG GCTCTTCCTG AGTTCtGGCC CTTGTAGTAA ACCTGCAGTC
       310        320        330        340        350        360        370        380        390        400
TTgatcaatt ttctctcagg aggctcttca ttgactcatg caaacagatt tctggcggga actgctccaa ggccttccag atgtgcacag gcatggatga
       410        420        430        440        450        460        470        480        490        500
atcagagcag aagtggacag atgtagctca aatggagggt tctgctatAA TCTCAATAAG TATCCAGGCT GGAGTGCAGT GGCGCGATCT CGGCTCACTG
       510        520        530        540        550        560        570        580        590        600
AAACCTCTGC CTCCCAGGTT CAAGCGATTC TCCTGCCTCA GCCTCTCGAA TAGCTGGGAT TACAGgcaac taccattttt ccccctctgt cttttgatgt
       610        620        630        640        650        660        670        680        690        700
tcacctgaca agctcctggt ggtagccggt agctctgaca gagagcaaaa gaaataagGG GCGGTTTTAG CTGATAACCT CACCAGTCTT CACTTCGGCT
       710        720        730        740        750        760        770        780        790        800
CTTCCTTCGC TGCCCCTTCA GCTGCGGGGA ACTTGCTCTA GGGCATCTTG GCAGGAGGGA GGGCGTCTGA GGGTACTGGT GCCTGCAGAC TTCAAGCACG
       810        820        830        840        850        860        870        880        890        900
GAGAGACTTC TTGAAGCGGT GCTGCCTGGC CACTTGGAAA AAGgtggatt aatttgggga tatccgagga gccccagagg gccattgtaa ttcaagatct
       910        920        930        940        950        960        970        980        990       1000
tcagtaaact tctgccgcgg agaaagaacc cggccagtat tgggaccatc gtggtgacgc aggattggag gaacaggggt ttcggttgac tgagaagttc
      1010       1020       1030       1040       1050       1060       1070       1080       1090       1100
ctgtgagaga aacaggctca aatagagaga atagaaagat gtcgtgagga gccaggaaac aaaattttcc aggggtcagg gaatgaattc taatcagaac
      1110       1120       1130       1140       1150       1160       1170       1180       1190       1200
aaggagccag caagaacttc cagcctagga ggtacttttc aaaagaagcc tgggactcta acccagcttc tgagagtata ctcagaattg ttaagaatca
      1210       1220       1230       1240       1250       1260       1270       1280       1290       1300
ggcagggcgc ggcggctcat gcctgtaatc ccagcacttt gggaggctga ggcgggtgga tcacttgagg tccggagtgt gagatcagcc tgactaacaa
      1310       1320       1330       1340       1350       1360       1370       1380       1390       1400
gatgaaaccc catctctact aaaaaaatac aaaattagct gggcgtcgta gcgcatgcct gtaatcccag ctacttggga ggctgaggca ggagaattgc
      1410       1420       1430       1440       1450       1460       1470       1480       1490       1500
ttgaacccag gaggtggagg ttgcagtgag ccaagatcgc gcccttgcac tccagcctgg gcaacaagag tgaaactctg cctcggaggg aaaaaaaaaa
      1510       1520       1530       1540       1550       1560       1570       1580       1590       1600
aaaaa
```

Supplementary Figure 3. The *GPR1AS* lncRNA sequence. Odd and even exons are showed by upper and lower cases, respectively. Allows indicated the positions of the primer sets used in the RACE (blue) and allelic expression (red) analyses. Red circles indicated positions of the SNPs.



Supplementary Figure 4. Allele-specific RT-PCR sequencing analysis of the *Zdbf2linc*-specific exon in fetal brain at E15.5 and the adult testis from BJF$_1$ hybrids.



Supplementary Figure 5. High-resolution DNA methylome map of mouse chromosome 1 imprinting cluster. (A) Illumina GenomeStudio viewer displays the locations of genes in the *Gpr1-Zdbf2* locus (NCBI37/mm9, chr1: 63,228,001-63,368,000). Open boxes represent the location of CpG islands. Black line plots depict the distribution of CpG densities (number of CpG per 200 nucleotides) of individual CpGs. Dot plots represent the methylation levels at individual CpGs in ES cells (khaki), blastocysts (green), male PGCs at E10.5 (pale blue), E13.5 (light blue), and E16.5 (blue), sperm cells (dark blue), female PGCs at E10.5 (pale red), E13.5 (light red), and E16.5 (red), and fully grown oocytes (dark red). Yellow-shaded areas show the extent of the *Gpr1* DMR (63,246,657-63,247,300), *Gpr1* promoter (63,260,283-68,261,282), *Zdbf2* DMR1 (63,302,559-63,307,835), *Zdbf2* DMR2 (63,309,532-63,312,061), *Zdbf2* DMR3 (63,313,912-63,316,206), and *Zdbf2* promoter (63,319,260-63,320,704). (B) Bar graphs show the average methylation levels of *Gpr1* DMR, *Gpr1* promoter, *Zdbf2* DMRs, and *Zdbf2* promoter.

```
==================================================
file name: GPR1
sequences:            1
total length:      2326 bp
GC level:         41.06 %
bases masked:       340 bp ( 14.62 %)
==================================================
               number of      length   percentage
               elements*    occupied  of sequence
--------------------------------------------------
SINEs:                1          326 bp   14.02 %
      ALUs            1          326 bp   14.02 %
      MIRs            0            0 bp    0.00 %

LINEs:                0            0 bp    0.00 %
      LINE1           0            0 bp    0.00 %
      LINE2           0            0 bp    0.00 %
      L3/CR1          0            0 bp    0.00 %

LTR elements:         0            0 bp    0.00 %
      ERVL            0            0 bp    0.00 %
      ERVL-MaLRs      0            0 bp    0.00 %
      ERV_classI      0            0 bp    0.00 %
      ERV_classII     0            0 bp    0.00 %

DNA elements:         0            0 bp    0.00 %
     hAT-Charlie      0            0 bp    0.00 %
     TcMar-Tigger     0            0 bp    0.00 %

Unclassified:         0            0 bp    0.00 %

Total interspersed repeats:      326 bp   14.02 %


Small RNA:            0            0 bp    0.00 %

Satellites:           0            0 bp    0.00 %
Simple repeats:       0            0 bp    0.00 %
Low complexity:       1           14 bp    0.60 %
==================================================
```

```
==================================================
file name: GPR1AS
sequences:            1
total length:      1505 bp
GC level:         51.76 %
bases masked:      1079 bp ( 71.69 %)
==================================================
               number of      length   percentage
               elements*    occupied  of sequence
--------------------------------------------------
SINEs:                2          409 bp   27.18 %
      ALUs            2          409 bp   27.18 %
      MIRs            0            0 bp    0.00 %

LINEs:                0            0 bp    0.00 %
      LINE1           0            0 bp    0.00 %
      LINE2           0            0 bp    0.00 %
      L3/CR1          0            0 bp    0.00 %

LTR elements:         3          670 bp   44.52 %
      ERVL            1          258 bp   17.14 %
      ERVL-MaLRs      0            0 bp    0.00 %
      ERV_classI      1          311 bp   20.66 %
      ERV_classII     0            0 bp    0.00 %

DNA elements:         0            0 bp    0.00 %
     hAT-Charlie      0            0 bp    0.00 %
     TcMar-Tigger     0            0 bp    0.00 %

Unclassified:         0            0 bp    0.00 %

Total interspersed repeats:     1079 bp   71.69 %


Small RNA:            0            0 bp    0.00 %

Satellites:           0            0 bp    0.00 %
Simple repeats:       0            0 bp    0.00 %
Low complexity:       0            0 bp    0.00 %
==================================================
```

```
==================================================
file name: ZDBF2_v1
sequences:            1
total length:     10304 bp
GC level:         38.21 %
bases masked:       459 bp ( 4.45 %)
==================================================
               number of      length   percentage
               elements*    occupied  of sequence
--------------------------------------------------
SINEs:                1          287 bp    2.79 %
      ALUs            1          287 bp    2.79 %
      MIRs            0            0 bp    0.00 %

LINEs:                1           80 bp    0.78 %
      LINE1           0            0 bp    0.00 %
      LINE2           0            0 bp    0.00 %
      L3/CR1          1           80 bp    0.78 %

LTR elements:         0            0 bp    0.00 %
      ERVL            0            0 bp    0.00 %
      ERVL-MaLRs      0            0 bp    0.00 %
      ERV_classI      0            0 bp    0.00 %
      ERV_classII     0            0 bp    0.00 %

DNA elements:         0            0 bp    0.00 %
     hAT-Charlie      0            0 bp    0.00 %
     TcMar-Tigger     0            0 bp    0.00 %

Unclassified:         0            0 bp    0.00 %

Total interspersed repeats:      367 bp    3.56 %


Small RNA:            0            0 bp    0.00 %

Satellites:           0            0 bp    0.00 %
Simple repeats:       3           92 bp    0.89 %
Low complexity:       0            0 bp    0.00 %
==================================================
```

```
==================================================
file name: ZDBF2_v2
sequences:            1
total length:     10198 bp
GC level:         37.43 %
bases masked:       567 bp ( 5.56 %)
==================================================
               number of      length   percentage
               elements*    occupied  of sequence
--------------------------------------------------
SINEs:                1          287 bp    2.81 %
      ALUs            1          287 bp    2.81 %
      MIRs            0            0 bp    0.00 %

LINEs:                2          188 bp    1.84 %
      LINE1           1          108 bp    1.06 %
      LINE2           0            0 bp    0.00 %
      L3/CR1          1           80 bp    0.78 %

LTR elements:         0            0 bp    0.00 %
      ERVL            0            0 bp    0.00 %
      ERVL-MaLRs      0            0 bp    0.00 %
      ERV_classI      0            0 bp    0.00 %
      ERV_classII     0            0 bp    0.00 %

DNA elements:         0            0 bp    0.00 %
     hAT-Charlie      0            0 bp    0.00 %
     TcMar-Tigger     0            0 bp    0.00 %

Unclassified:         0            0 bp    0.00 %

Total interspersed repeats:      475 bp    4.66 %


Small RNA:            0            0 bp    0.00 %

Satellites:           0            0 bp    0.00 %
Simple repeats:       3           92 bp    0.90 %
Low complexity:       0            0 bp    0.00 %
==================================================
```

Supplementary Figure 6. Identification of repetitive elements in nucleotide (cDNA) sequences of human *GPR1*, *GPR1AS*, and *ZDBF2*. The repeat files were generated by RepeatMasker (http://www.repeatmasker.org/).

Query sequence: Human GPR1 protein
Target sequence: Mouse GPR1 protein

```
Query Range: 1 - 355
Sbjct Range: 1 - 353
355 bp, INT.Score: 936, OPT.Score: 1690
Identity: 284 / 355 (80%)
Similarity: 336 / 355 (94%)

Query  1    MEDLEETLFEEFENYSYDLDYYSLESDLEEKVQLGVVHWVSLVLYCLAFVLGIPGNAIVIWFTGFKWKKTVTTLWFLNLAIADFIFLLFLPLYISYVAMN  100
            ||  .| ||||..||||.||||| ||| |||| ||.|||.|| || |||||||||||||||. |||||||||||||||||||||||.|||||||||||..
Sbjct  1    MEVSKEMLFEELDNYSYALDYYSQESDPEEKVYLGLVHWISLFLYALAFVLGIPGNAIVIWLMGFKWKKTVTTLWFLNLAIADFIFVLFLPLYISYVALS  100

Query  101  FHWPFGIWLCKANSFTAQLNMFASVFFLTVISLDHYIHLIHPVLSHRHRTLKNSLIVIIFIWLLASLIGGPALYFRDTVEFNNHTLCYNNFQKHDPDLTL  200
            ||||||.||||.|||.||||||.|||||||||||.||||.|| |||||||||.||.|.|..||||||.|||.||||||.| |||..||||||.|  .|||
Sbjct  101  FHWPFGLWLCKVNSFIAQLNMFSSVFFLTVISLDRYIHLLHPGLSHRHRTLKSSLVVVILVWLLASLLGGPTLYFRDTMEVNNHIICYNNFQEH--ELTL  198

Query  201  IRHHVLTWVKFIIGYLFPLLTMSICYLCLIFKVKKRSILISSRHFWTILVVVVAFVVCWTPYHLFSIWELTIHHNSYSHHVMQAGIPLSTGLAFLNSCLN  300
            .||||||||||..|||||||||| ||||||||.|||.||||..|.| || ||.||.||||||||||||||.|||||  ..|.|.||||||||||||||||
Sbjct  199  MRHHVLTWVKFLFGYLFPLLTMSSCYLCLIFKMKKRNILISRKHLWMILSVVIAFLVCWTPYHLFSIWELSIHHNSSFQNVLQGGIPLSTGLAFLNSCLN  298

Query  301  PILYVLISKKFQARFRSSVAEILKYTLWEVSCSGTVSEQLRNSETKNLCLLETAQ  355
            |||||||||.||||||.||||.|| .|||.|||||||||||..|||.|.||||||
Sbjct  299  PILYVLISKTFQARFRASVAEVLKRSLWEASCSGTVSEQLRSAETKSLSLLETAQ  353
```

Query sequence: Human ZDBF2 protein
Target sequence: Mouse ZDBF2 protein

```
Query Range: 20 - 2294
Sbjct Range: 15 - 2257
2362 bp, INT.Score: 340, OPT.Score: 3257
Identity: 996 / 2362 (42%)
Similarity: 1815 / 2362 (76%)

Query  20   QHLFSAQHRSLTRQSRRQICT-SSLMERFLQDVLQHHPYHCQESSSTQDETHVNTGSSSEVVHLDDAFSEEEEEDEDKVED-EDATEERPSEVSEPIEEL  117
            |||||.|||||||||||.. | ..||||||||||.||||..|...|...|...........  . .  .   .....| .| .|...|| || |...||.
Sbjct  15   QHLFSSQHRSLTRQSRRRTATNNTLMERFLQDVLRHHPYNYQDNRSAPNEPEAAAAAAAAADPGSPEVVVVLDDSDEKEDDTADSGAERNSEDSGSVEEI  114

Query  118  HSRPHKSQEGTQEVSVRPSVIQKLEKGQQQPLEFVHKIGASVRKCNLVDIGQATNNRSNLVRPPVICNAPASCLPESSNDRPVTANTTS-LPPAAHLDSV  216
             . || .|||  .||.||||||||||.||||.||..||....|.| | |.. |||.. ..||||||||||||.||..| .|||.||... |  |.  ||
Sbjct  115  DYRPGTSQE-HAEVAVRPSVIQKLERGQQQSLELAHKVESGVKKVNSVGVVQATTSGKKLVRPPVICNAPASSLPSGSFERPVAANSVPRLVLAVASDSF  213

Query  217  SKCDPNKVEKYLEQPDGASRNPVPSSHVETTSFSYQKHKESNRKSLRMNSDKLVLWKDVKSQGKTLSAGLKFHERMGTK-GSLRVKSP---SKLAVNPNK  312
             . ||....|.|.. || ...|  |||.        .| |....| |..| |||.  ......| ..|. .. .|  |..  |.|..|.    .  | ||..
Sbjct  214  PACDTENLETYFDSPDQGPSN--PSSQ--------PKTKDPKKK-LSINLDKLLAQRNLRAKGASFSPVVRVRELTGSELCSVRAESSELEAGTAGNPRE  302

Query  313  TDMPSNKGIFEDTIAKNHEEFFSNMDCTQEEKHLVFNKTAFWEQKCSVSSEMKFDCISLQSASDQPQETAQDLSLW-----------------------  388
            ||  ....  |..|.|..|.  ||   .|||..||.||... .|| ||||| .|.| | |......|....||||
Sbjct  303  TDTLPEQAR-EGAIPKRREASRSNTVRPQEETRLVLNKPTLLKQKRSVSSEERFSCGSRQAVPGPSQAAVRDLSLLEEEVEEEKQEEEEEEEQEEEEEHE  401

Query  389  -KEEQIDQED-NYESRGSEMSFDCSSSFHSLTDQSKVSAKEVNLSKEVRTDVQYKNNKSYVSKISSDCDDILHLVTNQSQMIVKEISLQNARHISLVDQS  486
             .|| .|||| .||||||.|||||.|| .||.. |...|.|.|.|.|   . .|.. .. ....|.. .|      .. .|.|...| |     |||||.|
Sbjct  402  EEEEGVDQEDASYESRGSDMSFDCGSSCQSLSALSELTAREINVSEE---THAYSQPRNETPTVSGATSD---NGSSSRQVITQNIQL-----ISLVDES  490

Query  487  YESSSSETNFDCDASPQSTSDYPQQSVTEVNLPKEVHIGLVDKNYGSSSSEVSADSVFPLQSVVDRPPVAVTETKLRKKAHTSLVDNYGSSCSETSFDCD  586
            ||||.||.||| |.| .|||. |.|.| || .|     . ||||.|||.||| ..||      | .| .|.|  . .  ...|..|||.   .....||..|
Sbjct  491  YESSGSEVNFDGDDSLPSTSHRPPQPV-EVVVP----LRLVDKSYGSGSSEPCEDS----GSSADETPAASRQQNPVRNTHANLVDE---NYGSSSFSSD  578

Query  587  VSLESVVDHPQLTVKGRNLKGRQVHLKHKKRKPSSAKAHLDCDVSLGTVADESQRAVEKINLLKEKNADLMDMNCESHGPEMGFQADAQLADQSQVAEIE  686
              ....||||..|..  . .||.|  . .. .||||.|| . | ||.|||.| ||. ..||| ..||..| ||||||||||.||.|||||  ... . ..
Sbjct  579  --SDAALDHPQVPVQEGSPRGRAVG-QGNEEQPSSAEAHPERDGSLETVAHELQRESQEINLPNQKNTSLGDMNCESHGPEVGFHADAQL--EADQSPVN  673

Query  687  RQKVDVDLENKSVQSSRSSLSSDSPASLYHSAHDEPQEALDEVNLKELNIDMEVRSYDCSSSELTFDSDPPLLSVTEQSHLDAEG-KERHIDLEDESCES  785
            ...||.||||.||.|. |.|| || || |.||.|.||.| .||||.|||.||||.| .|||||||||||.|||||||.| || || .| ...||||.| |
Sbjct  674  PEEVDLDLENQSVHSGISNLSFDSNAS-YQSANDQPQGAWGEVNLDELNVDMEVKSNGCSSSELTFDSDSPLLSVTERSLLDFEGLNEDDFNLEDENCVS  772

Query  786  DSSEITFDSDIPLYSVIDQPEVAVYEEETVDLESKSNESCVSEITFDSDIPLHSGNDHPEVAVKEVIQKE-EYIHLERKNDEPSGSEISSDSHAPLHSVT  884
            .||.||||||||  || |||.|||||||.|.||.||||||||.|||||||||||||||||||||||||| || | .||| |||.||||||. ||..||||||
Sbjct  773  SSSDITFDSDIPDDSVADQPQVAVYEEEPVGLENKSNESCVSGITFDSDIPLHSGNDHPEVAVKEVIIKEDENVHLEGKNDNPSGSEICLDSNVPLHSVT  872

Query  885  NSPEVAVKKLNPQKEEQVH---LENKENEPIDSE------------------------VSLDYNIIFHSVTGRSEDPIKEISLHTKEHMYLENKSVFET  956
            || .|||||.||.||.||.   .|.|||||.|||                        ..|| .. |.||. ..|  .|...|....|  |..||. |.
Sbjct  873  NS-DVAVKKINPPKEDQVQIEQIEQKENEPTDSELNLDCNSVNSKPGCSEDPIILRVSETRLDSHVPFQSVIRKCEVVVKNVCLQKEKHAELTSKST-ES  970

Query  957  SLDSDVPLQAATHKPEVIVKETWLQREKHAEFQGRSTEFSGSKTSLDSGV-PHYSVTEPQVAVNKINRKKQYVLENKNDKCSGSEIILDSNVPPQSMTDQ  1055
              . .  . |. . .|  |  ..  ...|| |  ....|..||..... .| |.   ...|| |. | .. ..     ..| .. .| ..  ....   .|. .|
Sbjct  971  HSEVSSASTASHPVTEPYVGKKAKRKTKHLEEVNSDDEYGGSQPTFKFDVFPRTMTEKPQPAALKEGHADP---KDKITELRGMAVNVNTADCLDSVLSQ  1067

Query  1056 PQLAFLKEKHVNLKDKNSKSGDSK------ITFDSEQLQE--AVKKIDQWKEEVIGLKNKINEPSTYKLIHHPDVSVQSVADQPKVAIKHVNLGNENHMY  1147
            ||||  .|. |.|||...|..|||        |.| . ||  .|.|...||.|.  |..||..     |.||...|| .|. || ..|.|...|||....
Sbjct  1068 PQLA-SNENCVELKDTDGKPSDSKASADSTGHFHSLPKQEFDVVSKMNEWKKEAKVLEQKISDLIYSKIIHDSNVSFRSAMDQLELALKQISLGNNDQVS  1166

Query  1148 LEVKNSQYSCSEMNLDSGFLGQSIVNRP--QITILEQEHIELEGKHNQCCGSEVSFDSDDPLQSVADRLRETVKEISLWKDEEVDTEDRRNEAKGFEIMY  1245
            || .||| .||| ||||||  |..|..|  ..|.||.||.| ||..|  |.|||| |.....|  |.. .|. .. |  .... |||..|..|.||.| .
Sbjct  1167 LE-DNSQDTCSETNLDSGFSVQAVVEPPEPEVTVLEPEHVEQEGRNNVPCDSEVSVDANGSVQLEAGQHSESGENRS--QKDTDDTEGKRDDAQGFGITC  1263

Query  1246 DSDVLQPVAGQPEEVVKEVSLWKEHVDLENKIVKPTDSRINFDSHEPLQSVTNKIPGANKEINLLREEHVCLDDKGYVPSDSEIIYVSNIPLQSVIKQPH  1345
            ||.| ||.||.  |||.... ||.|||||.|. ....|..||.|.||||.||| .... .|||| | .... ...|. | .|.|. |.|. . |||..|.
Sbjct  1264 DSNVPQPLAGH-IEVVQDIDHWKDHVDLEDKLGESKNSKVNFHSDEPLQAVTNATQEPVEEINLPR-GRASPNGNGCEPYGSTIVPVTNVIFCSVIQKPQ  1361

Query  1346 ILEEEHASLEDKSSN---------SYSPEESSDSNDSFQAAADELQKPVKEINLWKEDHIYLEDKSYKLGDFDVSYASHIPVQFVTDQS--SVPVKEINL  1434
             |... .||...|||           . .|| | ||||. |..|..|||| ||.|| ||||||||||||| ||. .|.|. ||||||  .|  .|..||.||
Sbjct  1362 RLQKKCTSLKENSSNPCPEVNVDSCDGPEVSVDSNDPCQSVAGHLQKPDKEMNL-KEDHIYLEDKSYKLVDFEPTYDSDDPVQFVTVPSVEAVSIKEVNL  1460

Query  1435 QKKDHNDLENKNCEVCGSEIKCHSCVHLQSEVDQPQVSYKEADLQKEEHVVMEEKTDQPSDSEMMYDSDVPFQIVVNQFPGSVKETHLPKVVLVDLVPGD  1534
            ||....||||.|  . | ||. |.| ||||||.|.|||..|||||.|.. . .|.|.. .. .|..|||||.|||||||  ..|  ||. |.||.||.|..|
Sbjct  1461 QKENPDDLENENFQPCCSEVACNSAVHLQSEADPPQVACKEADLDKKA-LDIEDKGSVTCVPEVVYDSDVSFQIVVNQVQTSDGETDSPQVVFVDVVSSD  1559

Query  1535 SDYE-VISDDIPLQLVTDPPQLTVKDISCINTECIDIEDKSCDFFGSEVRCNCKASTPSMTNQCKETFKIINRKKDYIILGEPSCQSCGSEMNFNVDASD  1633
            ||..  . .|  ..|  .|||.|||..| |||.... .... ... .   |...|| .|.|||.||.|||||||.||||||...|.||| |.|||||.||
Sbjct  1560 SDCDREVISDSNIPLQLEPPQMTVKETSDINTDSLGSAANE-KYYCKFCGCDYEAS-QSVTNQSKESFKIINRKNDYIILGDSTCPSCGHELNFNVDPSD  1657

Query  1634 QSMTYESQGPDEKMVKYIDSEDKSCGYNGSKGKFNLEDTSHRTTHRLQKAHKEASLRKDPRNAGLKGKSCQSSASAVDFGASSKSALHRRADKKKRSKLK  1733
            |. |.. | ||    ..||.|||. | . .| |.| |||.|..||.|||. ...|||||..|    .... .||. | | .| . |..           .
Sbjct  1658 QPTTCQLQQPD---RNFIDPEDKNFGSKCPKRKLNWEDTAHPVTHQLQKTGEATSLRKDQKNRFKRDRGWESSSFAGDHAAYAVSVI-----------R  1742

Query  1734 HRDLEVSCEPDGFEMNFQCAPPLPSDTDQPQETVKKRHPCKKVSSDLKEKNHDSQSSSVLKVDSVRNLKKAKDVIEDNPDEPVLEALPHVPPSFVGKTWS  1833
             . .|. ||   | |.||| ..  .||.|.||   ||. . |||. ||. .... .....   ..  . .. |.|.    .|.  ..  ..|||.|||| .
Sbjct  1743 QTALN-SC---GSELNFQDDTFYHSDIDPPQ--PKKKGQGKKVTFDLRVTKYEYPPNPMYGEGEEVAEDDLKEVV---VHEASPQG--QAPPSIVGKT-C  1830

Query  1834 QIMREDDIKINALVKEFREGRFHCYFDDDCETKKVSSKGKKKVTWADLQGKEDTAPTQAVSESDDIVCGISDIDDLSVALDKPCHRHPPAERPPKQKGRV  1933
             .  ||||.|.|.   .   .| |..|.|...||||.   ...|....||          .|.... ...   ..|..|.||.|.|  .. . ||  ..|.|.|
Sbjct  1831 PQGREDDVKTNT---QACQGYFYSYYDGGSETKKILLGEEEKTIRSDL--------NQNTTSIQHVKGKVGDTGDFSVDLGK--QSCSLAEGLHQQHGQV  1917

Query  1934 ASQCQTAKISHSTQTSCKNYPVMKRKIIRQEEDPPKSKCSRLQDDRKTKKKVKIGTVEFPASCTKVLKPMQPKALVCVLSSLNIKLKEGEGLPFPKMRHH  2033
             .|| . .... ..|.|     . .||||. ||||.||.||  ...|...|||.. |..|.|.. ||||.|.||..||...|||.  .||...|  || ..
Sbjct  1918 TSQ-NQVEVRCGIQAS----SGKKRKITEQEEDSPKRKC--FHHDSQKKKKAQAGITELPEPQTKVLEPVQPDSLVYIFSSLS--MKEDQSLNPPKTKPG  2008

Query  2034 SWDNDIRFICKYKRNIFDYYEPLIKQIVISPPLSVIVPEFERRNWVKIHFNRSNQNSSAGDNDADGQGSASAPLMAVPARYGFNSHQGTSDSSLFLEESK  2133
            | |.|.. |.... ..     .|  |..||.|| ...|||           |..|| .....|||..|. |. .|...||.| .  .. .. |..|| ||..|.
Sbjct  2009 S-DSDLPHIYSCREHT--SSGPRRKRTVINPPQNLMVPEV------GIDLNRHDPKPNAGDDSAKRQNLVSTSFMAMPKKSVLKFQR-TNQSS-FLKKSE  2097

Query  2134 VLHARELPKKRNFQLTFLNHDVVKISPKSVRNKLLESQSKKKIHGKRVTTSSNKLGFPKKVYKPIILQQKPRKASEKQSIWIRTKPSDIIRKYISKYSVF  2233
             . | ..||. ||| |..|.| .|  ||||... ||||...|.  |.. ...||| . |..||...|..|.. |||| .|||. |..||||||.|..  .
Sbjct  2098 DVGATQVPKD-NFQQTLVNRDGAKKFPKSVKKEDLESQNQRKFWKKKM-VAANKLCLIKNAYKTMVLRKKSKLASEKLAIWIQLKATDIIRKYVSRCHGL  2195

Query  2234 LRHRYQSRSAFLGRYLKKKKSVVSRLKKAKRTAKVL-LNSSVPPAGAEELSSAMANPPPKRP  2294
            ...|. |.....  .  |.||| |....|.|||.|..| |. | |.   .  .  ....|  ||. |
Sbjct  2196 MPRRHLSKTVLIRMQLRKKKIVARKIKEAKRAAEALALKLSRPSCPPRAPCPPRALCPPRAP  2257
```

Supplementary Figure 7. Amino acid sequence alignment of imprinted gene products. Alignments of the human and mouse GPR1-ZDBF2 sequences are shown; >40% identity and >70% similarity were observed.

Table S1. Exon locations of human *GPR1AS-ZDBF2* isoforms and mouse *Zdbf2linc*

Gene/Transcript name	Exon number	Position (GRCh37/hg19)
GPR1AS	exon 1	chr2: 207,068,100 - 207,068,401
	exon 2	chr2: 207,105,167 - 207,105,312
	exon 3	chr2: 207,120,590 - 207,120,706
	exon 4	chr2: 207,121,153 - 207,121,245
	exon 5	chr2: 207,124,555 - 207,124,739
	exon 6	chr2: 207,128,103 - 207,128,764
ZDBF2_v1	exon 1a	chr2: 207,139,365 - 207,139,670
	exon 2	chr2: 207,144,264 - 207,144,316
	exon 4	chr2: 207,146,525 - 207,146,633
	exon 6	chr2: 207,161,970 - 207,162,097
	exon 7	chr2: 207,169,441 - 207,179,148
ZDBF2_v2	exon 1b	chr2: 207,139,752 - 207,139,803
	exon 2	chr2: 207,144,264 - 207,144,316
	exon 3	chr2: 207,145,273 - 207,145,317
	exon 4	chr2: 207,146,525 - 207,146,633
	exon 5	chr2: 207,156,738 - 207,156,840
	exon 6	chr2: 207,161,970 - 207,162,097
	exon 7	chr2: 207,169,441 - 207,179,148

Transcript name	Exon number	Position (NCBI37/mm9)
Zdbf2linc	exon A	chr1: 63,246,932 - 63,247,248
	exon B	chr1: 63,254,089 - 63,254,188
	exon C	chr1: 63,310,073 - 63,310,129
	exon 3	chr1: 63,324,505 - 63,324,557
	exon 4	chr1: 63,327,341 - 63,327,451
	exon 6	chr1: 63,341,490 - 63,341,620
	exon 7	chr1: 63,349,214 - 63,361,149

Table S2. PCR primer information

Primers name	Target region	Target SNP	Amplified region (hg19)	Primer sequence (forward and reverse)	Product size (bp)	PCR	PCR program					
							Pre-denature	Denature	Annealing	Elongation	Final elongation	Cycles
GPR1AS_Ex2SNP_F9 GPR1AS_Ex3SNP_R14	*GPR1AS* exon 2	ID: rs1024809 chr2: 207,105,300	chr2: 207,105,183 - 207,120,618	5'-GGAGGCTCTTCATTGACTCATGC-3' 5'-GCACTCCAGCCTGGATACTTATTG-3'	159	RT-PCR, Real-time RT-PCR	94°C, 1 min	94°C, 30 s	60°C, 30 s	72°C, 30 s	72°C, 5 min	40
GPR1AS_Ex6SNP_F6 GPR1AS_Ex7SNP_R7	*GPR1AS* exon 6	ID: rs34523400 chr2: 207,128,132	chr2: 207,124,691 - 207,128,270	5'-AGCACGGAGAGACTTCTTGAAG-3' 5'-TTCTCTCACAGGAACTTCTCAGTC-3'	217	RT-PCR	94°C, 1 min	94°C, 30 s	60°C, 30 s	72°C, 30 s	72°C, 5 min	40
GPR1AS_Ex5SNP_F13 GPR1AS_Ex7SNP_R15	*GPR1AS* exon 6	ID: rs10206513 chr2: 207,128,291	chr2: 207,124,719 - 207,128,340	5'-TGCCTGGCCACTTGGAAAAAG-3' 5'-CCCTGACCCCTGGAAAATTTTG-3'	259	RT-PCR	94°C, 1 min	94°C, 30 s	60°C, 30 s	72°C, 30 s	72°C, 5 min	40
GPRAS_BS_GA_F6 GPRAS_BSR3	*GPR1* DMR	ID: rs16838074 chr2: 207,067,553	chr2: 207,067,497 - 207,068,152	5'-AAAAAAAAACTCTACTCCTCTCAATATCTC-3' 5'-GGTGGAAGTTGGAAGTTGGGAA-3'	656	Bisulfite	98°C, 30 s	98°C, 10 s	60°C, 30 s	72°C, 30 s	72°C, 5 min	35
ZDBF2_DMR_BSF2 ZDBF2_DMR_BSR1	*ZDBF2* DMR	ID: rs10206513 chr2: 207,128,291	chr2: 207,128,034 - 207,128,504	5'-CTTCCTTAAATAAACAAACCATCATACATC-3' 5'-TTTTTAAAGTGTTGGGATTATAGGTATGAG-3'	471	Bisulfite	98°C, 30 s	98°C, 10 s	57°C, 30 s	72°C, 30 s	72°C, 5 min	40
ZDBF2_ex1a1b_BSF2 ZDBF2_ex1a1b_BSR2	*ZDBF2* promoter		chr2: 207,139,168 - 207,139,407	5'-GTTTATGAGTTTAGTTATTTTTGTTGG-3' 5'-TTACAACCCTAATAAAAATTTAACRTC-3'	240	Bisulfite	98°C, 30 s	98°C, 10 s	53°C, 30 s	72°C, 30 s	72°C, 5 min	40
ACTB_RT_F ACTB_RT_R	ACTB exon 3 & 4		chr7: 5,568,325 - 5,568,884	5'-TACAATGAGCTGCGTGTGG-3' 5'-GGGGTGTTGAAGGTCTCAAA-3'	119	Real-time RT-PCR	94°C, 1 min	94°C, 30 s	60°C, 30 s	72°C, 30 s	72°C, 5 min	40
Primers name	Target region	Target SNP	Amplified region (mm9)	Primer sequence (forward and reverse)	Product size (bp)	PCR	PCR program					
							Pre-denature	Denature	Annealing	Elongation	Final elongation	Cycles
Zdbf2linc_F6 Zdbf2linc_R6	*Zdbf2linc* exon A & B	B6: T, JF: C chr1: 63,247,248	chr1: 63,247,050 - 63,254,157	5'-TACGTCAGCAAGAGCATCATGG-3' 5'-TTAACTGAGTCCATCGGCTCTTC-3'	267	RT-PCR Real-time RT-PCR	94°C, 1 min 95°C, 30 s	94°C, 30 s 95°C, 5 s	62°C, 30 s 62°C, 30 s	72°C, 30 s 72°C, 30 s	72°C, 5 min	35 40
Zdbf2_RT_ex7F Zdbf2_RT_ex7R	*Zdbf2linc* exon 7	B6: A, JF: G chr1: 63,361,079	chr1: 63,360,906 - 63,361,130	5'-TACGTCAGCAAGAGCATCATGG-3' 5'-TTAACTGAGTCCATCGGCTCTTC-3'	225	RT-PCR	94°C, 1 min	94°C, 30 s	60°C, 30 s	72°C, 30 s	72°C, 5 min	35
Gpr1_DMR_BSF1 Gpr1_DMR_BSR2	*Gpr1* DMR	see **Fig. 6**	chr1: 63,246,988 – 63,247,117	5'-AGATTAGGTTAGTTTGGAATT-3' 5'-AACACTAATCACCAAATAATTC-3'	130	BS	98°C, 30 s	98°C, 10 s	57°C, 30 s	72°C, 30 s	72°C, 5 min	35
Actb_RT_F Actb_RT_R	*Actb* exon 1		chr5: 143,664,856 - 143,665,043	5'-AGGTGACAGCATTGCTTCTG-3' 5'-GCTGCCTCAACACCTCAAC-3'	188	Real-time RT-PCR	95°C, 30 s	95°C, 5 s	62°C, 30 s	72°C, 30 s		40