

Supplemental Figure 1. Whole mouse genome meDIP-on-chip and genome tilling array screen for DMRs using PG- and AG-derived stem cells and sperm.

A. Known imprinted DMRs in PG- and AG-derived cells were characterized by the COBRA method. The bisulphite-treated DNA amplified by PCR was digested with restriction enzymes (as representative results IG-DMR: *TaqI* and *Lit1*: *HpyCH4IV*) that cut only when the site in the genomic sample is methylated. The sizes of digested fragments are indicated on right (IG-DMR: 337 bp and *Lit1*: 185 bp). TS; DNA of TS

cells, PG; DNA of PG-derived cells, AG; DNA of AG-derived cells, Sp; DNA of mature sperm.

B. Known imprinted DMRs and non-imprinted methylated regions estimated by meDIP quantitative real-time PCR method against DNA precipitated by the antibody against 5-methyl-cytosine. Black, gray and white bars represent cycle threshold (Ct) number subtracted Ct of meDIP DNA (meDIP) from that of whole genomic DNA (WG).

Paternal DMRs: *H19*, IG-DMR and *Rasgrf1*. Maternal DMRs: *Nespas*, *Peg10*, *Peg3*, *Lit1*, *U2af1-rs1* and *Igf2r* (DMR2). Non-DMRs: *Nanog*, *Rest*, *Aicda*, *Tdrd12*, *Gdf3*, *Slc2a3*, *Aicda*, *Tdrd12* and *Utf1*.

Black, gray and white bars indicate data for sperm, AG- and PG-derived cells, respectively, which are different number of real-time PCR cycles of meDIP and amplified DNA, using Whole Genome Amplification kit.

Supplemental Figure 2. Three paternally methylated DMRs in the *Gpr1-Zdbf2* imprinted domain.

A. Bisulphite-PCR sequencing results for DMR1 (region 7) on genomic DNA prepared from E13.5 B6/JF1 fetus and placenta, and adult brain, liver, lung, heart and spleen. Each row represents a unique methylation profile within the pool of 20 clones sequenced. Closed and open circles represent methylated and unmethylated CpGs, respectively.

B. Bisulphite-PCR sequencing results for 16 regions on genomic DNA prepared from B6 sperm and the kidney from B6/JF1 adult mouse.

Supplemental Figure 3. Tissue specific-imprinted expression of the mouse *Gpr1*.

A. Direction expression analysis of mouse *Gpr1* gene. The 1st cDNA strands syntheses were performed using either the sense (S) or the antisense (AS) primer of the mouse *Gpr1* gene. Arrow indicates the cDNA product of *Gpr1* gene amplified by RT-PCR on right.

B. Analysis of mouse *Gpr1* gene. cDNA and genomic PCR products were amplified and sequenced directly from E13.5 embryos, placenta and yolk sac and adult materials obtained from B6/JF1 and JF1/B6 mice. Expression was biallelic in all tissues examined.

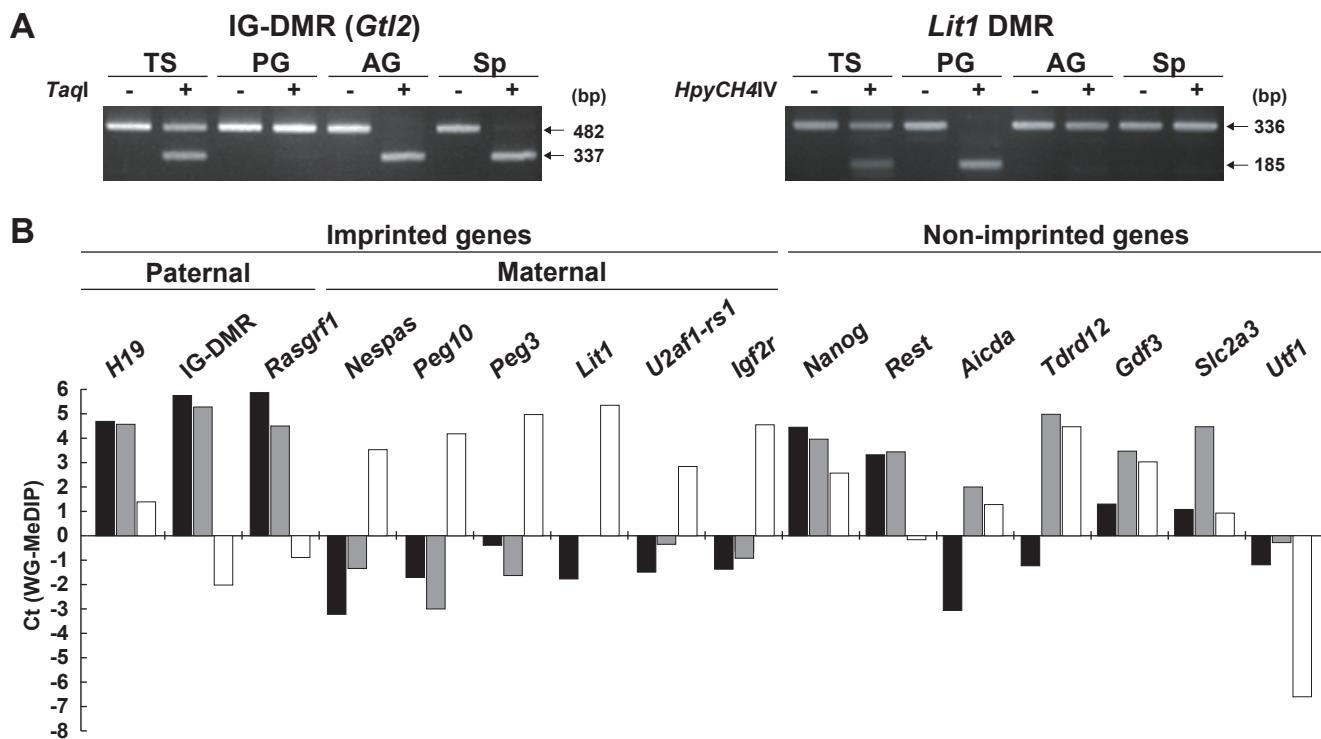
Supplemental Figure 4. Dot-plot comparison of the mouse DMR1 and human DMRh1.

Dots were placed at locations with identical nucleotides when more than 28 of 70 nucleotides were identical.

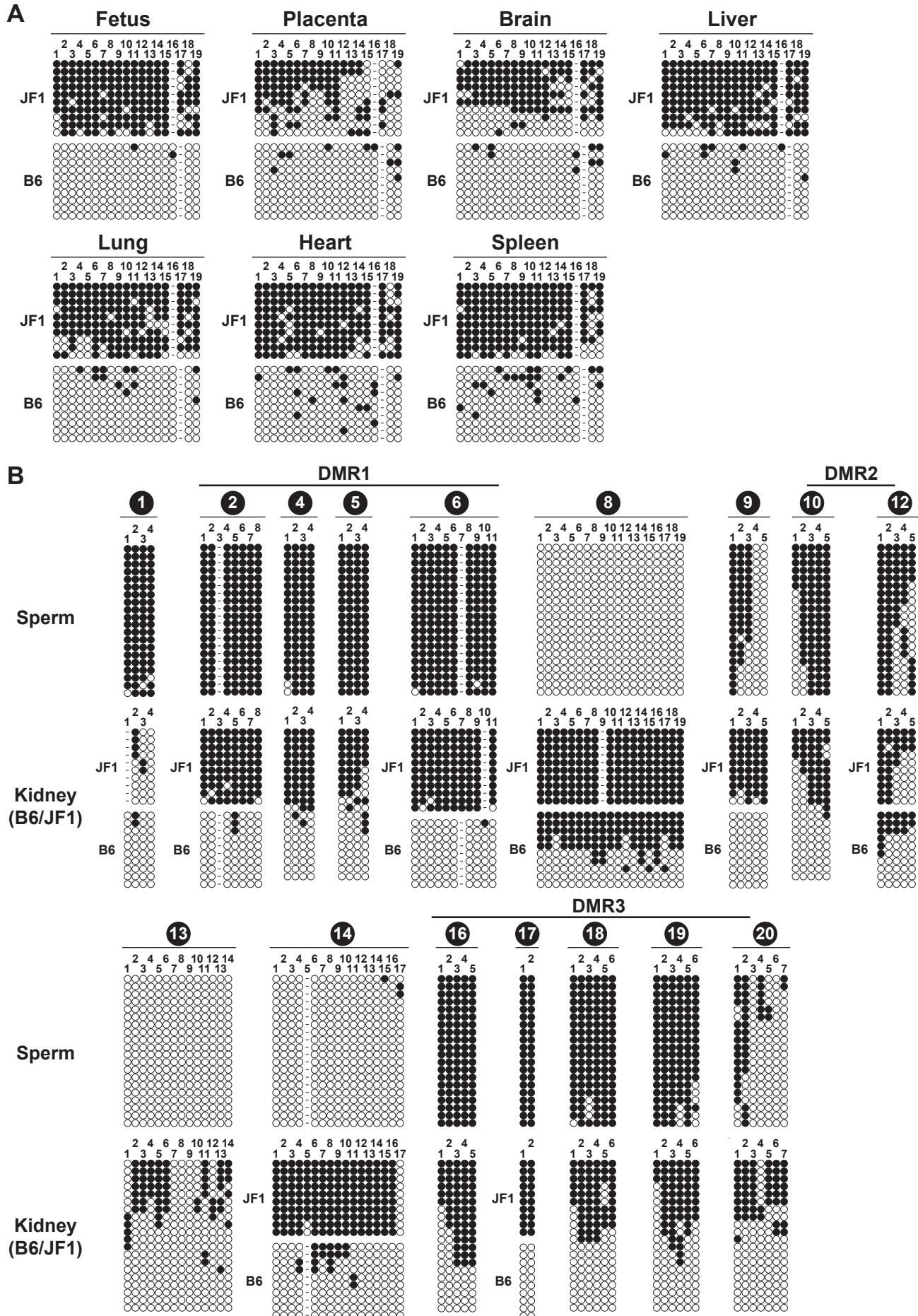
Supplemental Table S1. Primer sequences and PCR conditions.

Supplemental Table S2. DNA polymorphisms between B6 and JF1 strain and position of GenBank accession number AL669947.

Supplemental Figure S1

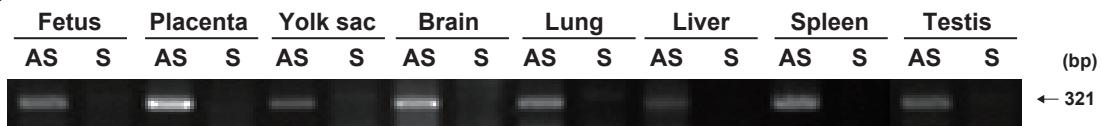


Supplemental Figure S2

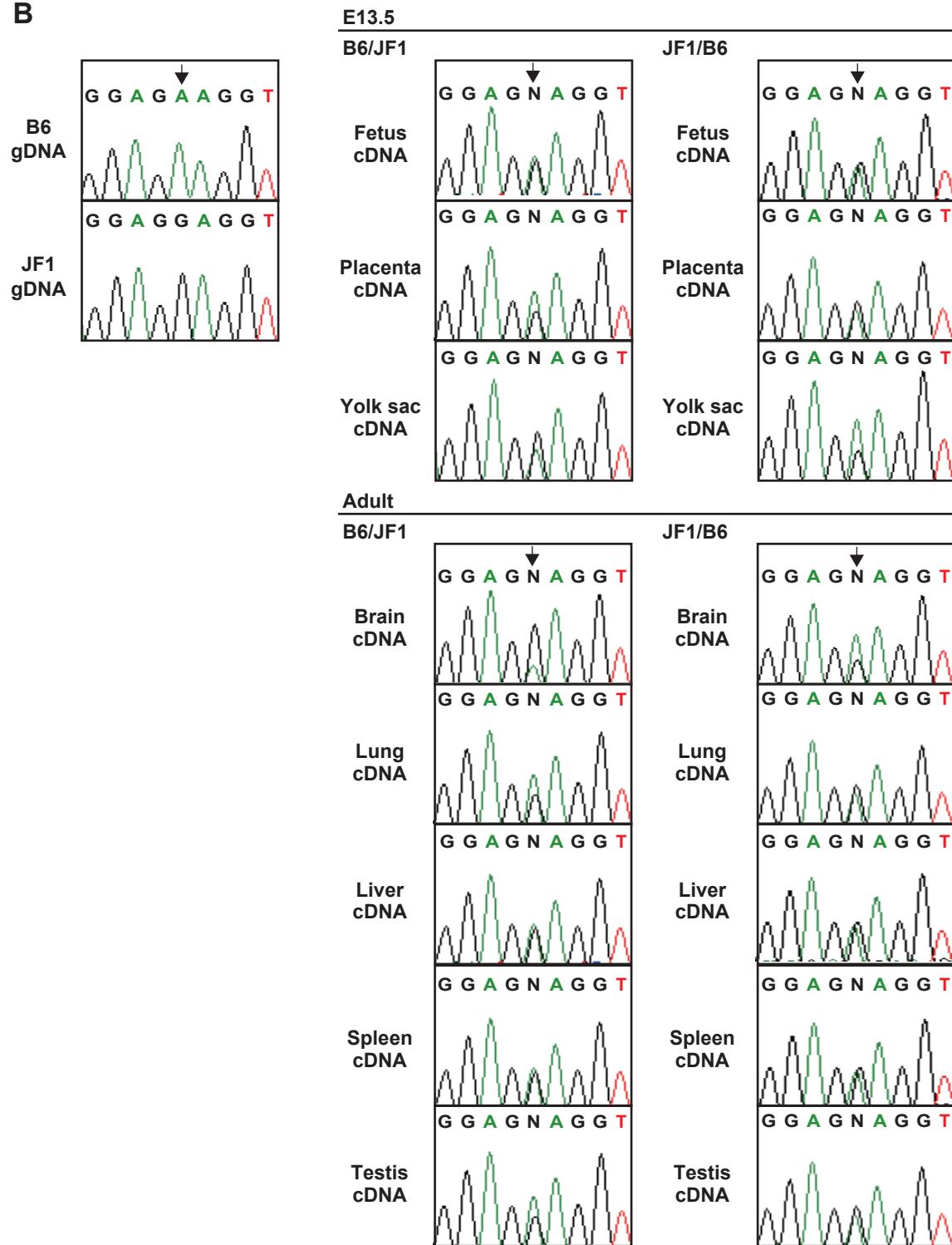


Supplemental Figure S3

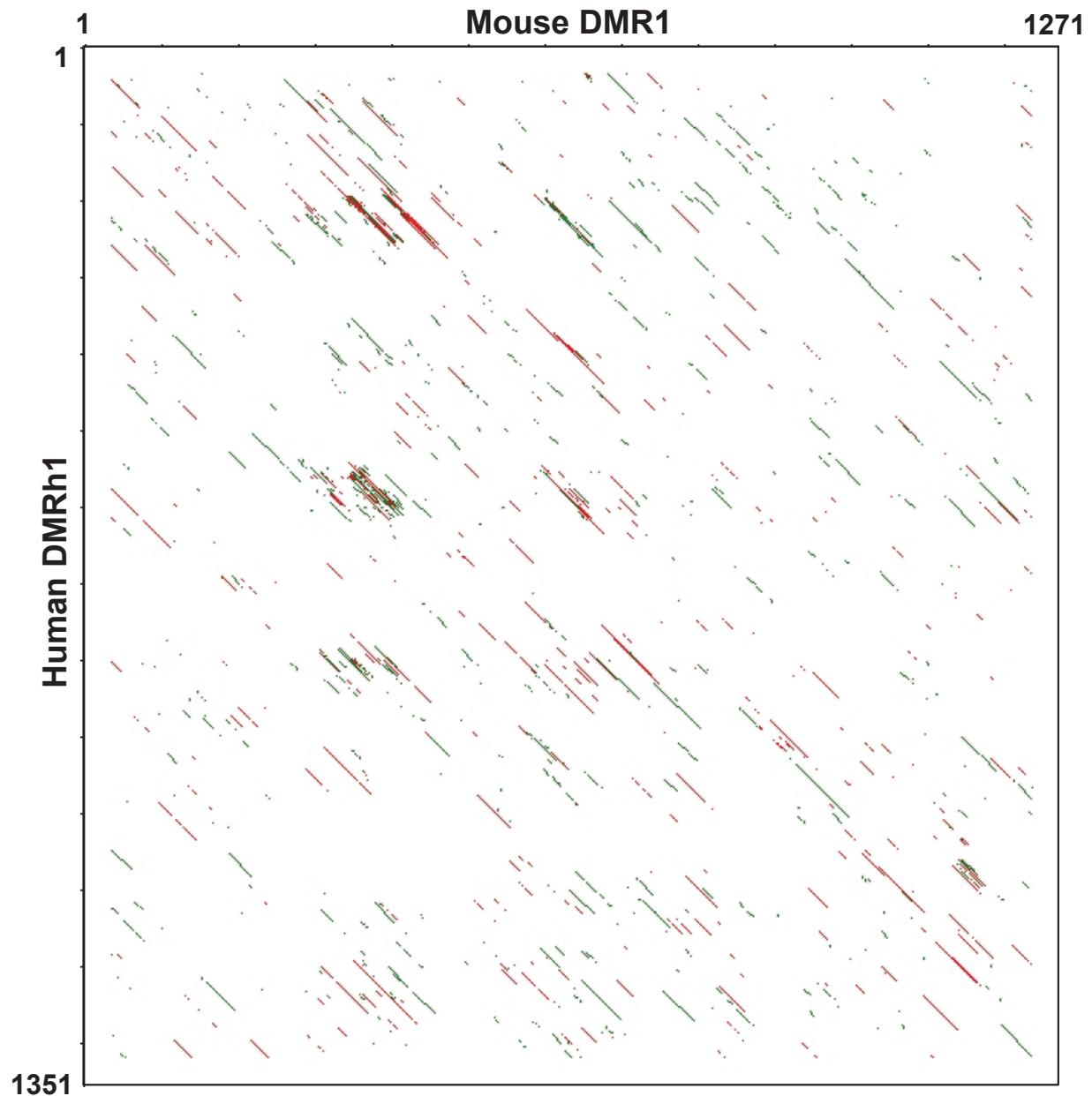
A



B



Supplemental Figure S4



Supplementary Table S1. Primer sequences and PCR conditions.

Locus	PCR	Primer sequence (5'-3')		Annealing temp	Cycles	Amplicon (bp)
Methylation assay						
Mouse						
IG-DMR (<i>Gli2</i>)	1st	IG-DMR cBSF1 IG-DMR cBSR1	TTAAGGTATTTTATTGATAAAAATAATGTAGT CCTACTCTATAATACCCCTATATAATTATACCA	55°C	30	
	2nd	IG-DMR cBSF2 IG-DMR cBSR2	TTAGGAGTTAAGGAAAAGAAAGAAGAAATAGTAT/ TATACACAAAATAATCTATATAACACCATA	55°C	30	482
H19 DMR		H19 BisOF1 H19 BisOR2	TTGTGAGTGAAAGATTAAATTGTTG ATCTTACCCCTATAAATCCCT	57°C	40	423
Rasgrf1 DMR	1st	Rasgrf-1 BSF1 Rasgrf-1 BSR1	ATGTGGTTTGTAGTTGA CAAAAACACAAATAAATCACT	55°C	30	
	2nd	Rasgrf-1 BSF1 Rasgrf-1 BSR2	ATGTGGTTTGTAGTTGA CAATAAAAAACAAAAACAC	55°C	30	467
Nespas DMR		Nespas BSF Nespas BSR	AGGGATGGTTATGGGGTTTTGATT AACCAACTAAATCTAACCTAAC	57°C	40	337
Gnas1A DMR		Gnas1A-C_F Gnas1A-C_R	GGTATTATGTTGAAGATGGTTAGAAGTTAA AACATCATCTTCATCAATATCACTATCC	60°C	40	519
Peg10 DMR		Peg10-E_F Peg10-E_R	GTATTTAATTGGAAAGTTGAGGAG CTCCCAACCAACATCCCT	60°C	40	603
Peg1 DMR	1st	Peg1/Mest BSF1 Peg1/Mest BSR1	GATTTGGGATAAAAAGCTTAATGAG TCATTTAAAACACAAACCTCTTAC	55°C	30	
	2nd	Peg1/Mest BSF2 Peg1/Mest BSR2	TTTTAGATTTGGAGGGTTAGGTG AATCCCTAAATCATCTTACAC	55°C	30	563
Peg3 DMR	1st	KH63 Peg3 F1 KH64 Peg3 R1	TTTTAGATTGTTGGGGTTTATA AATCCCTATCACCTAAACATCCCTACA	57°C	30	
	2nd	KH65 Peg3 F2 KH66 Peg3 R2	TTGATAATAGTTGATTGGTAGGTG ATCTACAACTTATCAATTACCTTAAAAA	57°C	30	451
Snrpn DMR	1st	KH99 Snrpn F1 KH100 Snrpn R1	AAATTTGTGATGTTGTAATTATTGGG AAAATCCACAAAACCAACTAACCTTCC	57°C	30	
	2nd	KH101 Snrpn F2 KH102 Snrpn R2	AATTATTTATTATTTAGATGAGTGT TTTACAAATCACTCCTCAAACCAA	57°C	30	294
Lit1 DMR	1st	Lit-BS4 Lit-BS2	TAAGGTGAGTGGTTAGGAT AATCCCCACACCTTAAATT	57°C	30	
	2nd	Lit-BS4 Lit-BS21	TAAGGTGAGTGGTTAGGAT CCACTATAAACCCACACATA	57°C	30	336
Zac1 DMR	1st	Zac1 BSF1 Zac1 BSR1	GGGTAGGTAAGTAGTGTAA CCTAAACACCAAAATAACA	54°C	30	
	2nd	Zac1 BSF2 Zac1 BSR2	ATTGGGTCTTTAGTGT TACAAAACCCAAAACCTTAC	54°C	30	383
U2af1-rs1 DMR	1st	U2af1-rs1 BSF1 U2af1-rs1 BSR1	GGTTGAGTATTATTTGTA TACATAAACCTACCCATACA	55°C	30	
	2nd	U2af1-rs1 BSF3 U2af1-rs1 BSR1	ATTGTAGATTTGGATGAT TACATAAACCTACCCATACA	55°C	30	502
Igf2r DMR2	1st	Igf2r 13B-4 Igf2r 13B-2	TAGAGGATTAGTATAATTAA CACTTTAAACTTACCTCTTAC	55°C	30	
	2nd	Igf2r 13B-5 Igf2r 13B-2	GAGGTTAAGGGTAAAAGTTGAT CACTTTAAACTTACCTCTTAC	57°C	30	490
Impact DMR		Impact-C_F Impact-C_R	TGTTTGAAAGGATGAGTGGAGGTTT CCCTACTAAACCTTACCTACCTCAAC	60°C	40	405
DMR region 1		R0-6467 BSF1 R0-6467 BSR1	TTTTAAATTGTTGTTGTTT AAAACAACTAACAAATAATCTAATT	55°C	40	291
DMR region 2		R1-0208 BSF1 R1-0208 BSR1	GTTCAGTTGTTGGTTGGTTT CCAAACAAAACAACAAACCAACT	58°C	40	505
DMR region 3		1700039101Rik BSF 1700039101Rik BSF	TTTGTGTTGGTATGTTGAGGTTT ACAAATCATACTATCTACAAAAAAAC	55°C	40	451
DMR region 4		R1-2831 BSF1 R1-2831 BSR1	GGAGTAGTATTTAGTTGTTT AAAATAAAAAAACACTAATAAT	57°C	40	241
DMR region 5		R1-3235 BSF1 R1-3235 BSR1	TAGGATTTGGAGTTGGAGTT TTAACATCTAACAAATCATACCA	57°C	40	380
DMR region 6		R1-3948 BSF1 R1-3948 BSR1	TGTGTATAGTTGTTGTTGTT ATAATCAACTACYAAAAAACCTAA	55°C	40	365
DMR region 7		1P1 BSF2 1P1b BSR1	GATTAGATTAGTTGGTTAGTTTAT CAAACCTAACACAAATACCTTATTAC	57°C	40	840
DMR region 8		R2-1331 BSF1 R2-1331 BSR1	TTATATTAGTTGGGGAGAGTT AAAACAACTAACTAAAAAAATCTTAA	55°C	40	406
DMR region 9		R2-3337 BSF1 R2-3337 BSR1	AAAGGGATATGATTTTTATGTAA ACTTTATTTCCAACAAATCCTAAAC	55°C	40	414
DMR region 10		R2-3842 BSF1 R2-3842 BSR1	TATATATTGTTAGATTTGAAGTT AACAAAAAAATCAAATAAAACAT	55°C	40	503
DMR region 11		1P1down BSF1 1P1down BSR1	TAAATAATATAAGGGTTGGTAGTT AAATCAAACCTACAAACTCCAAACT	55°C	40	334
DMR region 12		R3-0105 BSF1 R3-0105 BSR1	GGTAGGAAGAGTAAATAAGGT CTCCAAAATAACAAATACTACAAATA	57°C	40	387
DMR region 13		R3-0619 BSF1 R3-0619 BSR1	TTATTGAGATGGAGTTAGTGAAT TACTAAACAACTTAAATCAATATAA	55°C	40	386

DMR region 14	R3-2035 BSF1	TATTTTGTGTTGGGTTTGAGGATT	58°C	40	492
	R3-2035 BSR1	ACATACTTAATAAAATCCCATAAATATA			
DMR region 15	CpG3com BSF1	AATTAAGATATTAGATTATGGATAGATTTT	57°C	40	339
	CpG3com BSR1	ATAAACTCTCCAAAACCAAAAAAAA			
DMR region 16	R3-7276 BSF1	TATAATGTGAGTGGATTGTTAATT	52°C	40	333
	R3-7276 BSR1	AATACCAAATAATAAACACAAATAC			
DMR region 17	R3-7980 BSF1	TGAGTTTTGTGTTGTGTATATTITA	55°C	40	185
	R3-7980 BSR1	CATCCTAACCAACAATTAAAAAAC			
DMR region 18	R4-0106 BSF1	TGTGATTATGTTTGAGTTAGTTG	55°C	40	383
	R4-0106 BSR1	ACTCTACTTAATAACAAAATACC			
DMR region 19	R4-0712 BSF1	TATGGTATTGGTAGTGGGGTT	55°C	40	411
	R4-0712 BSR1	CAACTATTTAACACTTACTTCAAAC			
DMR region 20	R4-1319 BSF1	GTGTTTAGTGAATAATAGTTATGTTAG	55°C	40	301
	R4-1319 BSR1	CCCTCTAACAAACTTAAACAAAC			
Human					
<i>H19</i> DMR	H19 F2	TATATGGGTATTTGGAGGTTTT	57°C	40	220
	H19 R1	ATAAAATATCCTATTCCAAATAACCCC			
<i>DMRh1</i>	h2Pc4 BSF1	GTTTGTAGTTAGATTGGAAAATA	55°C	40	210
	h2Pc4 BSR1	AAAATAATAATTACCTAAACAAAAAAAC			
<i>DMRh2</i>	h2Pc1 BSF1	TTTTATTTGGTTGTGGAAATA	55°C	40	394
	h2Pc1 BSR1	ACCTCTAACAAACTAAACATATAATCATA			
SNP analysis					
Human					
<i>GPR1</i>	GPR1 s3F2	ATCTTCACGTTCTTATCATTCACTG	60°C	35	324
	GPR1 s3R0	GGTGACTGTCTCTCCACTGAC			
Gene expression					
Mouse					
<i>Gpr1</i>	Gpr1 exF	CGGGGTGTCATTCAAAAGT	59°C	35	321
	Gpr1 exR	AGGGCATATAAGAACAGGGAGA			
<i>Gapdh</i>	Gapdh exF	GTCGTGGAGTCACTGGTGTGTC	60°C	30	241
	Gapdh exR	GAGCCCTTCCACATGCCAA			
Human					
<i>GPR1</i>	GPR1 exF2	GAAGGTACACCCAGGCATGACA	57°C	40	236
	GPR1 exR	TCCCCAGAACAAAGCCAACAA			
<i>GAPDH</i>	GAPDH exF	GTCGTGGAGTCCACTGGCGTC	60°C	30	244
	GAPDH exR	GAGTCCTTCCACAAATACCAA			
In situ hybridization probe					
Mouse					
<i>Zdbf2</i>	Zdbf2 H-F	CGGCAGCAGCAGCAGATCCT	60°C	40	593
	Zdbf2 H-R	AAAAGACGACCCCTTAGCCTAA			
<i>Gpr1</i>	Gpr1 exF2	CATTCAGTCTGGAGTTGGAAAG	60°C	35	453
	Gpr1 exR2	TGGGCAATGAAGGAATTAAAC			
Methylated-DNA immunoprecipitation					
Mouse					
<i>H19</i> DMR	ChIP-H19m3F1	AGGTTGGAACACTTGTGTTCTGGAG	65°C	40	159
	ChIP-H19m3R1	TGGGCCACGATATAGGAGTATGCT			
<i>IG-DMR (Gtl2)</i>	MeDIP IG-DMR F1	CGCTATGAACTACCGCTACG	65°C	40	136
	MeDIP IG-DMR R1	CGGCATTAGTACACGGCGAACCTCC			
<i>Rasgrf1</i> DMR	MeDIP Rasgrf1 F1	CAGAGAGTATGAAAGGCCAGAGC	65°C	40	188
	MeDIP Rasgrf1 R1	CGCAATACTGGTAGGCCACGGATG			
<i>Nespas</i> DMR	MeDIP Nespas F	GCGTACCCCCAGGCCAATAGC	65°C	40	149
	MeDIP Nespas R	GCCAACACTACCTCCCCACATA			
<i>Peg10</i> DMR	MeDIP Peg10 F2	TGAGCTCCCAAATACCG	65°C	40	74
	MeDIP Peg10 R2	GCAGTGCACATCCGTTCTGTA			
<i>Peg3</i> DMR	ChIP Peg3 F1	ATGGGGTCTGGATTGGTTAG	65°C	40	136
	ChIP Peg3 R1	TCTCCGCTTCTCTCGATGCT			
<i>Lit1</i> DMR	ChIP Lit1 F2	TCGGTCGAGTCCAAAGGTGAGT	65°C	40	184
	ChIP Lit1 R2	ACAGCTACCAACATAACACAGC			
<i>U2af1-rs1</i> DMR	MeDIP U2af1-rs1 F	AGGGCTGAGCATCTACTG	65°C	40	151
	MeDIP U2af1-rs1 R	ATCCCGAGTATGCTGATCTG			
<i>Igf2r</i> DMR2	ChIP-Igf2r DMR2F	GAGTTTCTGTAGCCCAGAACATCTCA	65°C	40	127
	ChIP-Igf2r DMR2R	TACCGGAGGTGAGGGTTCACTGAT			
<i>Nanog</i>	Nanog-F5	TCAAGGCAACAGAGAAAAACCT	60°C	40	147
	Nanog-R5	GGGAAACCTGGGGAAATCT			
<i>Rest</i>	REST-F	GCCGTGCTTTATTGTC	60°C	40	91
	REST-R	ACGAAGTGAAGAGACCCAGTC			
<i>Aicda</i>	Aicda-F	AGTCACGCTGGAGACCGATA	60°C	40	133
	Aicda-R	GGCAAGCAGACGAGGAAAT			
<i>Tdrd12</i>	ECAT8-F	GGTGCCTGAAGGTGAGGGAGTG	60°C	40	109
	ECAT8-R	TAATCGGAACGCAAGCCTAC			
<i>Gdf3</i>	Gdf3-F	CGAGGCACAGGTTGAA	60°C	40	91
	Gdf3-R	GCCAGACATCCGAGTTCA			
<i>Slc2a3</i>	Slc2a3-F	AGGACCCAAACAAAGCAAAT	60°C	40	142
	Slc2a3-R	TCTGTAGGACCCGAGGAACA			
<i>Utf1</i>	UTF1-F1	AGAATAAGCAAGGCACAGG	60°C	40	127
	UTF1-R1	CCACACACGCTTAAGGAC			

Supplemental Table S2. DNA polymorphisms between B6 and JF1 strain and position of GenBank accession number AL669947.

Region	Nucleotide No. (AL669947)	C57BL/6	JF1
1	13907	G	A
2	14425	A	G
	14688–14689	–	TAATGTGTA
	14821	G	T
6	18187–18188	–	CGG
	18310–18346	GTTTGATCCAAACGGAAGATTTCAGGGCCTTCCCTTG	37 bp deletion
7	19155	G	A
	19243	G	C
8	19943	G	A
9	20780	G	A
11	23192	C	A
	23217–23218	GC	--
	23239–23240	–	TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
12	24484	A	G
	24540	A	G
14	25259	A	G
15	26681	C	T
	26819	C	T
17	29060	G	A