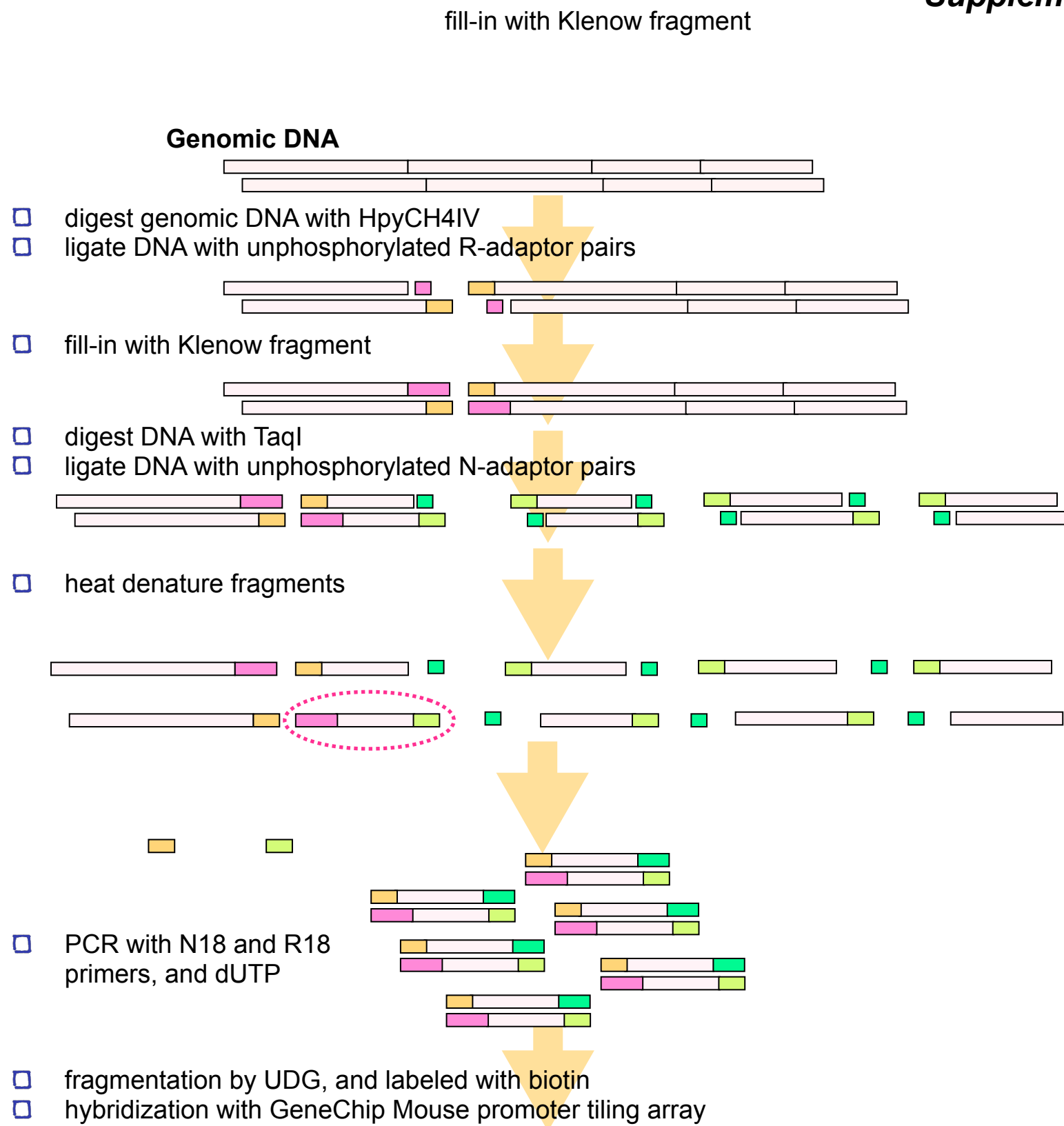
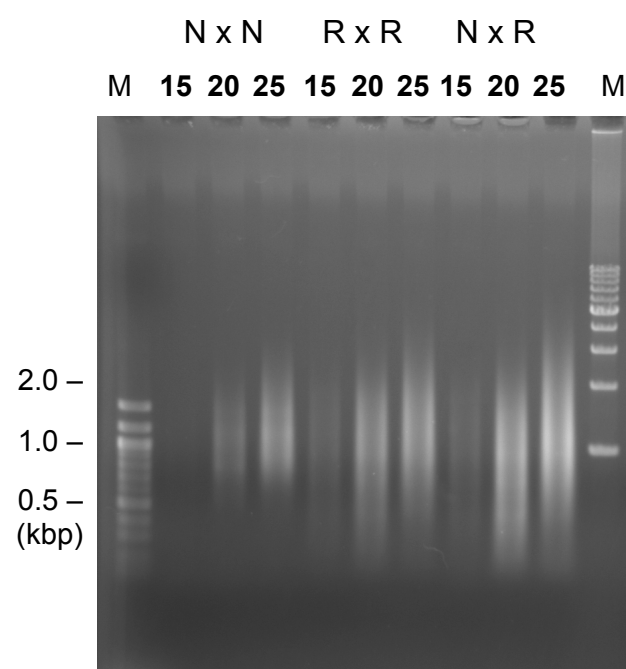


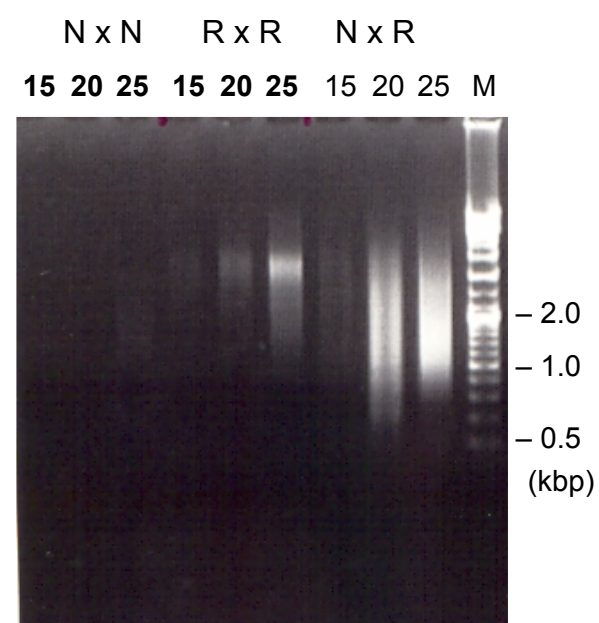
A



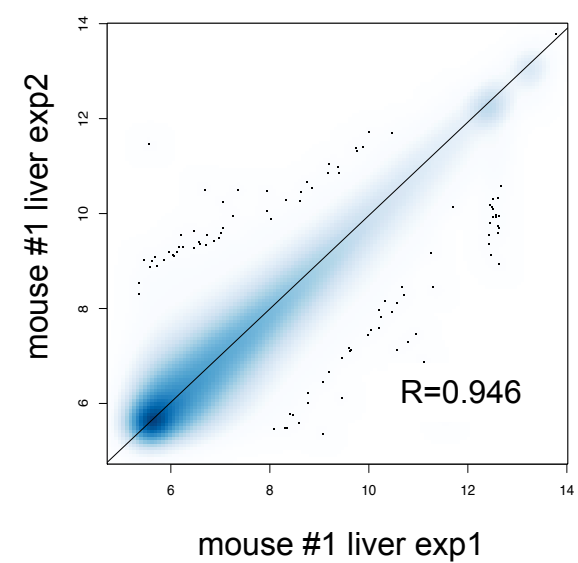
B



C

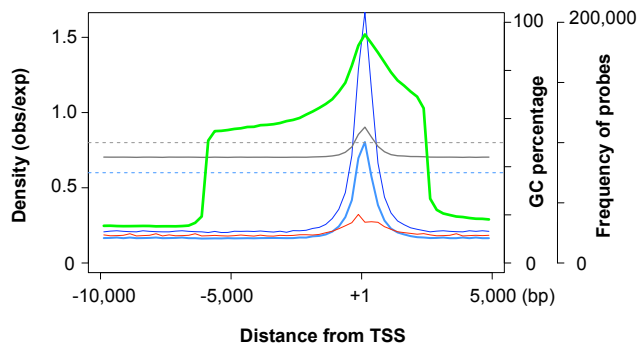


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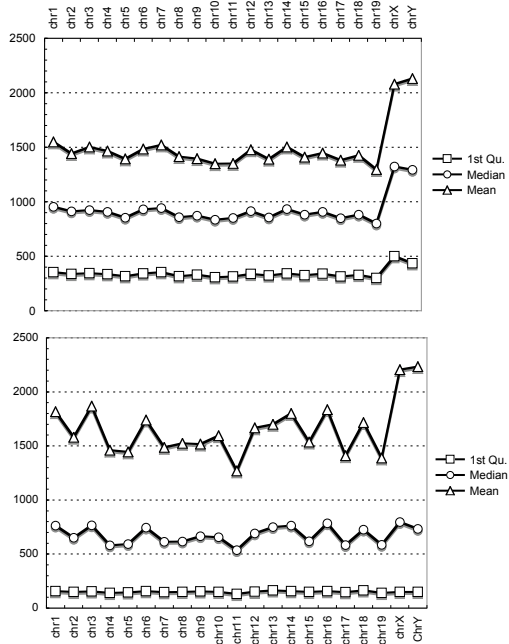


Supplementary Figure S2

A



B



A

CHIP-CHIP

Entrez ID	Symbol
HNF1A CGI	
14194	<i>Fh1</i>
56794	<i>Hacl1</i>
16432	<i>Itm2b</i>
HFN1A non-CGI	
16790	<i>Anpep</i>
55938	<i>Apom</i>
15112	<i>Hao1</i>
15378	<i>Hnf4a</i>
15486	<i>Hsd17b2</i>
16006	<i>Igfbp1</i>
17777	<i>Mttp</i>
100163	<i>Pafah2</i>
20704	<i>Serpina1e</i>
12401	<i>Serpina6</i>
27219	<i>Sgk2</i>
72094	<i>Ugt2a3</i>
CGI	
66540	<i>3110001A13Rik</i>
11637	<i>Ak2</i>
224727	<i>Bat3</i>
66205	<i>Cd302</i>
28126	<i>D13Wsu177e</i>
76843	<i>Dtl</i>
27395	<i>Mrpl15</i>
17750	<i>Mt2</i>
17966	<i>Nbr1</i>
18510	<i>Pax8</i>
215615	<i>Rnpep</i>
20019	<i>Rpo1-4</i>
269831	<i>Tspan12</i>
217109	<i>Utp18</i>
56490	<i>Zbtb20</i>
non-CGI	
11606	<i>Agt</i>
11699	<i>Ambp</i>
11818	<i>Apoh</i>
242557	<i>Atg4c</i>
12263	<i>C2</i>
110382	<i>C8b</i>
13809	<i>Enpep</i>
14373	<i>G0s2</i>
15458	<i>Hpx</i>
23957	<i>Nr0b2</i>
18534	<i>Pck1</i>
11905	<i>Serpinc1</i>
218103	<i>Slc17a2</i>

B

HNF-1A motif

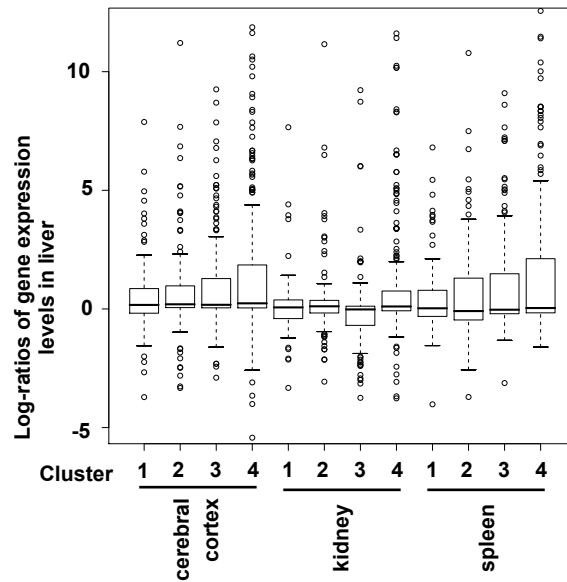
CGI genes

Entrez ID	Symbol
66665	<i>5730528L13Rik</i>
77803	<i>A930021C24Rik</i>
70317	<i>Arl16</i>
11899	<i>Astn1</i>
71132	<i>Cabyr</i>
234388	<i>Ccdc124</i>
27784	<i>Commd8</i>
352968	<i>D830050J10Rik</i>
13143	<i>Dapk2</i>
13178	<i>Dck</i>
13511	<i>Dsg2</i>
13518	<i>Dst</i>
192193	<i>Edem1</i>
13839	<i>Epha5</i>
13885	<i>Esd</i>
14048	<i>Eya1</i>
384009	<i>Glpr2</i>
216871	<i>Gltpd2</i>
14732	<i>Gpam</i>
14782	<i>Gsr</i>
15199	<i>Hebp1</i>
15473	<i>Hrsp12</i>
207683	<i>Igsf11</i>
16949	<i>Loxl1</i>
116748	<i>Lsm10</i>
212679	<i>Mars2</i>
108645	<i>Mat2b</i>
230125	<i>Mcart1</i>
17434	<i>Mocs2</i>
270685	<i>Mthfd1l</i>
23959	<i>Nt5e</i>
18242	<i>Oat</i>
231602	<i>P2rx2</i>
75552	<i>Paqr9</i>
18769	<i>Pkig</i>
263406	<i>Plekhg3</i>
22038	<i>Plscr1</i>
217734	<i>Pomt2</i>
212627	<i>Prpsap2</i>
14083	<i>Ptk2</i>
75212	<i>Rnf121</i>
54170	<i>Rragc</i>
110809	<i>Sfrs1</i>
20384	<i>Sfrs5</i>
20425	<i>Shmt1</i>
74011	<i>Slc25a27</i>
109108	<i>Slc30a9</i>
58246	<i>Slc35b4</i>
240726	<i>Slco5a1</i>
66616	<i>Snx9</i>
20660	<i>Sorl1</i>
234857	<i>Spire2</i>
52331	<i>Stbd1</i>
71954	<i>Suds3</i>
381085	<i>Tbc1d22b</i>
232078	<i>Thnsl2</i>
235300	<i>Tmem136</i>
56407	<i>Trpc4ap</i>
209584	<i>Tyw3</i>
56491	<i>Vapb</i>
52357	<i>Wwc2</i>

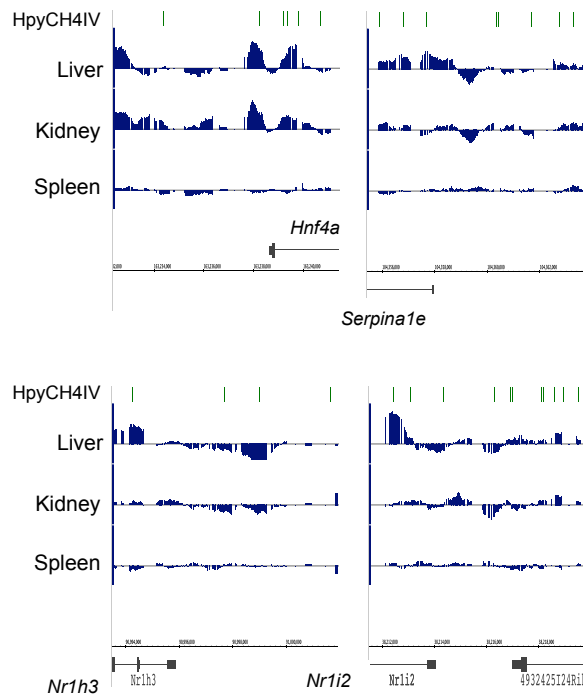
non-CGI genes

Entrez ID	Symbol	Entrez ID	Symbol
67432	<i>0610010D20Rik</i>	83379	<i>Klb</i>
71775	<i>1300017J02Rik</i>	259301	<i>Leap2</i>
67119	<i>2510048L02Rik</i>	64898	<i>Lpin2</i>
109280	<i>9330176C04Rik</i>	17288	<i>Mep1b</i>
210373	<i>A530095I07Rik</i>	69826	<i>Ms4a10</i>
93732	<i>Acox2</i>	17700	<i>Mstn</i>
11431	<i>Acp1</i>	17882	<i>Myh2</i>
233799	<i>Acsm2</i>	338370	<i>Nalcn</i>
280662	<i>Afm</i>	18105	<i>Nqo2</i>
11576	<i>Afp</i>	22259	<i>Nr1h3</i>
98870	<i>AI182371</i>	18171	<i>Nr1i2</i>
11727	<i>Ang</i>	67528	<i>Nudt7</i>
72074	<i>Anks4b</i>	258623	<i>Olfr123</i>
69787	<i>Anxa13</i>	259162	<i>Olfr427</i>
11807	<i>Apoa2</i>	18346	<i>Olfr47</i>
231287	<i>Atp10d</i>	258731	<i>Olfr491</i>
26877	<i>B3galt1</i>	258307	<i>Olfr493</i>
545366	<i>BC026782</i>	259126	<i>Olfr623</i>
170752	<i>Bcdo2</i>	258934	<i>Olfr802</i>
228662	<i>Btbd3</i>	258812	<i>Olfr923</i>
230558	<i>C8a</i>	628813	<i>OTTMUSG00000000997</i>
12352	<i>Car5a</i>	13180	<i>Pcbd1</i>
30952	<i>Cngb3</i>	110385	<i>Pde4c</i>
239447	<i>Colec10</i>	18815	<i>Plg</i>
71791	<i>Cpa4</i>	67000	<i>Prl3a1</i>
70062	<i>Ctag2</i>	56189	<i>Prodh2</i>
107869	<i>Cth</i>	30053	<i>Reg3d</i>
15945	<i>Cxcl10</i>	192658	<i>Rfpl4</i>
107141	<i>Cyp2c50</i>	19733	<i>Rgn</i>
433247	<i>Cyp2c68</i>	12309	<i>S100g</i>
226105	<i>Cyp2c70</i>	20209	<i>Saa2</i>
13909	<i>EG13909</i>	20700	<i>Serpina1a</i>
240327	<i>EG240327</i>	20701	<i>Serpina1b</i>
14060	<i>F13b</i>	20702	<i>Serpina1c</i>
544763	<i>F830116E18Rik</i>	20703	<i>Serpina1d</i>
14080	<i>Fabp1</i>	20388	<i>Sftpb</i>
14161	<i>Fga</i>	20495	<i>Slc12a1</i>
110135	<i>Fgb</i>	319848	<i>Slc17a4</i>
240894	<i>Fmo9</i>	320718	<i>Slc26a9</i>
14317	<i>Ftcd</i>	28253	<i>Slco1b2</i>
14538	<i>Gcnt2</i>	20730	<i>Spink3</i>
14618	<i>Gjb1</i>	100689	<i>Spon2</i>
66283	<i>Gkn1</i>	84112	<i>Sucnr1</i>
217674	<i>Gphb5</i>	69083	<i>Sult1c2</i>
107022	<i>Gramd3</i>	72003	<i>Synpr</i>
14823	<i>Grm8</i>	21391	<i>Tbxas1</i>
226243	<i>Habp2</i>	21789	<i>Tfpi2</i>
56185	<i>Hao3</i>	66261	<i>Tm4sf20</i>
54426	<i>Hgfac</i>	217203	<i>Tmem106a</i>
387510	<i>Ifnk</i>	22139	<i>Tr</i>
16171	<i>Il17a</i>	76654	<i>Upp2</i>
16552	<i>Kif12</i>	360216	<i>Zranb1</i>

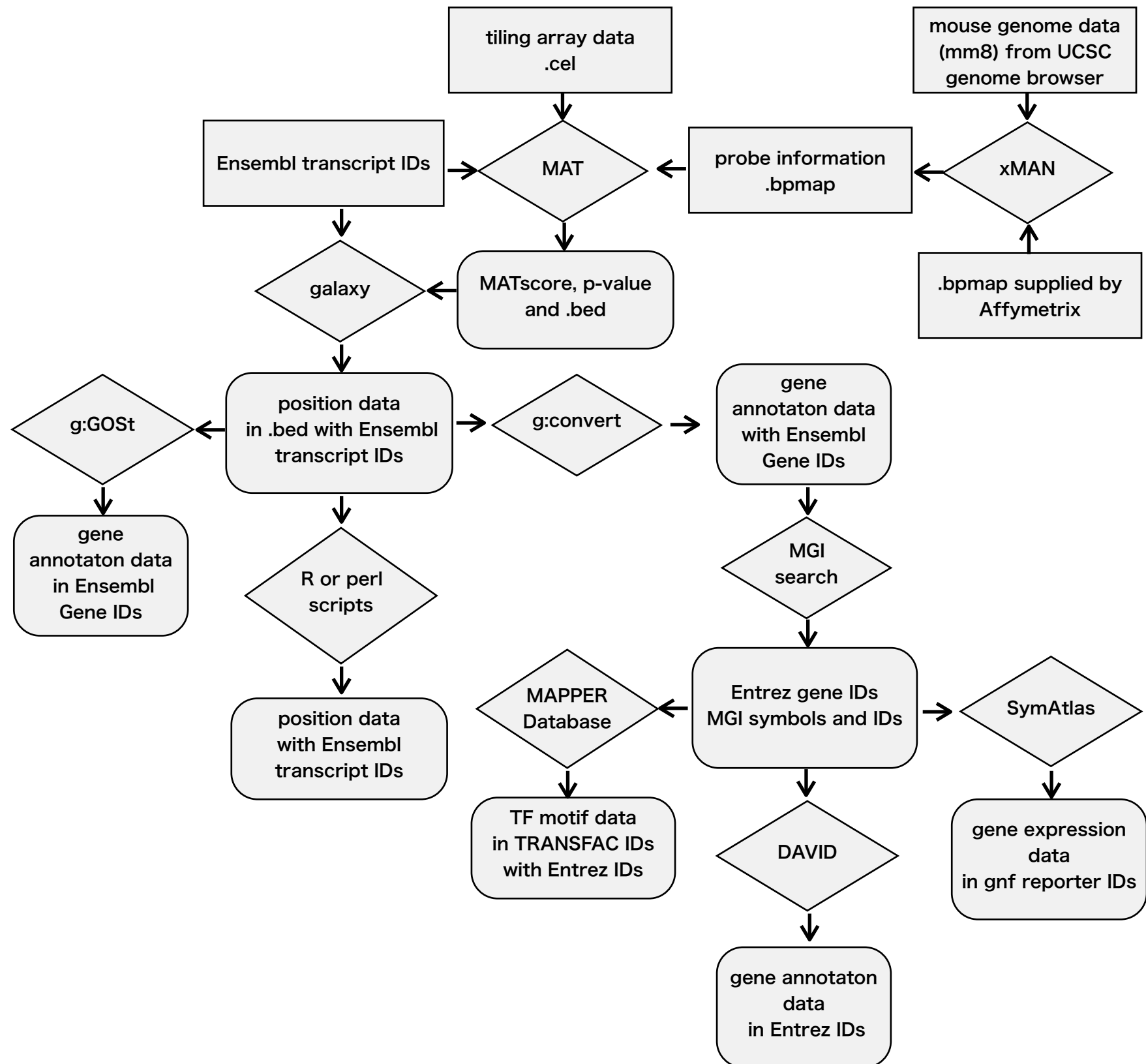
A



B



Supplementary Figure S6



Supplementary Table S1.

Distribution of probes and ENSEMBL transcripts along mouse chromosomes

	probes		ENSEMBL transcript Ids	
	number	%	number	%
chr1	264,858	6.06	1,738	5.77
chr2	359,931	8.23	2,481	8.24
chr3	210,691	4.82	1,430	4.75
chr4	279,996	6.4	1,861	6.18
chr5	248,152	5.67	1,761	5.85
chr6	240,327	5.5	1,586	5.27
chr7	352,011	8.05	2,572	8.54
chr8	199,046	4.55	1,440	4.78
chr9	229,342	5.24	1,608	5.34
chr10	200,262	4.58	1,368	4.54
chr11	311,061	7.11	2,458	8.16
chr12	153,099	3.5	1,047	3.48
chr13	171,579	3.92	1,161	3.85
chr14	170,459	3.9	1,167	3.87
chr15	168,974	3.86	1,104	3.67
chr16	137,301	3.14	930	3.09
chr17	194,934	4.46	1,444	4.79
chr18	116,740	2.67	737	2.45
chr19	140,689	3.22	969	3.22
chrX	218,003	4.98	1,228	4.08
chrY	6,098	0	30	0.1
total	4,373,553		30,120	

Probes were remapped to the mm8 mouse genome assembly by xMAN.

The tiling probes were originally designed to cover 33,559 ENSEMBL genes located on the mouse genome assembly of mm5.

Supplementary Table S2. Annotation analysis of genes with liver T-DMRtags

p-values of g:GOST analysis	Num- ber of genes	Percen- tage of no-CGI	χ square test* (p-values)	Ontology Type**	Term	DAVID [#]
3.06×10^{-9}	94	62.80%	7.3×10^{-2}	GO:BP	lipid metabolic process	NC
4.06×10^{-9}	82	63.40%	7.3×10^{-2}		cellular lipid metabolic process	NC
1.89×10^{-6}	106	59.40%	2.2×10^{-1}		response to stress	
1.41×10^{-6}	80	60.00%	2.4×10^{-1}		generation of precursor metabolites and energy	NC
1.40×10^{-9}	81	53.10%	9.7×10^{-1}		organic acid metabolic process	NC
2.91×10^{-9}	80	53.80%	9.4×10^{-1}		carboxylic acid metabolic process	NC
4.98×10^{-6}	38	68.40%	6.5×10^{-2}		monocarboxylic acid metabolic process	
1.02×10^{-6}	19	52.60%	9.5×10^{-1}	GO:MF	vitamin binding	NC
1.59×10^{-6}	31	48.40%	5.9×10^{-1}		cofactor binding	NC
4.47×10^{-6}	16	68.80%	2.2×10^{-1}		FAD binding	NC
5.97×10^{-8}	28	71.40%	5.6×10^{-2}	TF	M00790_1 (HNF-1)	n.d.
biased to no CGI genes						
4.85×10^{-6}	69	81.20%	<u>5.2×10^{-6}</u>	GO:BP	defense response	
1.96×10^{-10}	64	84.40%	<u>9.4×10^{-7}</u>		response to wounding	NC
1.18×10^{-8}	48	83.30%	<u>3.8×10^{-5}</u>		inflammatory response	
1.38×10^{-8}	23	95.70%	<u>5.2×10^{-5}</u>		acute inflammatory response	
9.46×10^{-9}	253	66.00%	<u>1.4×10^{-4}</u>	GO:CC	extracellular region	NC
2.39×10^{-8}	234	65.80%	<u>3.0×10^{-4}</u>		extracellular region part	
2.08×10^{-8}	224	66.50%	<u>1.8×10^{-4}</u>		extracellular space	NC
1.53×10^{-7}	23	91.30%	<u>2.8×10^{-4}</u>	KEGG	Complement and coagulation cascades	NC
2.61×10^{-6}	83	69.90%	<u>3.1×10^{-3}</u>	TF	M00790_2 (HNF-1)	n.d.
1.68×10^{-8}	33	72.70%	<u>2.7×10^{-2}</u>	TF	M00132_3 (HNF-1)	n.d.
8.18×10^{-12}	32	75.00%	<u>1.5×10^{-2}</u>	TF	M01011_1 (HNF1)	n.d.
biased to CGI genes						
2.06×10^{-6}	401	37.20%	<u>4.7×10^{-9}</u>	GO:CC	cytoplasm	NC
8.65×10^{-8}	313	38.30%	<u>9.8×10^{-8}</u>		cytoplasmic part	NC
1.55×10^{-6}	108	32.40%	<u>2.4×10^{-5}</u>		mitochondrion	NC,CGI
5.03×10^{-6}	58	32.80%	<u>2.0×10^{-3}</u>		mitochondrial part	
7.34×10^{-10}	526	46.80%	<u>8.1×10^{-3}</u>	GO:MF	catalytic activity	NC

* χ -square tests were applied to examine the difference in the proportions of CGI-containing and CGI-lacking genes for each criterion among all the genes containing T-DMRtags. Percentage of no CGI genes among 1817 genes carrying T-DMRtags is 53.6%. Statistically significant (less than 5%) are designated by underlined boldface.

**Ontology types of GO:BP, GO:CC, and GO:MF indicate biological process, cellular component, and molecular function in Gene Ontology criteria, respectively. KEGG and TF represent KEGG pathway database, and TRANSFAC database, respectively.

[#]The DAVID column indicates the over-representation of the terms in DAVID analysis among all genes classified into the same criterion according to the position of CGIs. NC: non CGI genes, CGI: CGI genes, n.d.: not determin

Supplementary Table S3. List of adaptors and primers

Name	Sequence	Genomic location of PCR *	Description
R24	AGCACTCTCCAGCCTCTCACCGCT		R-Adaptor pairs
R10	CGAGCGGTGA		R-Adaptor (NotI)
R12	GGCCAGCGGTGA		R-Adaptor (NotI)
N24	AGGCAACTGTGCTATCCGAGGGAA		N-Adaptor pairs
Ncg10	CGTTCCTCG		N-Adaptor pairs
N18	GGCAACTGTGCTATCCGA		LM-PCR
R182	GCACTCTCCAGCCTCTCA		LM-PCR
Gnmt_F1	ACTACAACCCCAACCTTACTAAAA	chr17:46196405-46196775	Fig. 2D Gnmt-1
Gnmt_R1	TGGTTGTTAGGATTTGAATTTAGGA		
Gnmt_F2	AGGTAGTAAGTTTGGTTTTGGGTTT	chr17:46192018-46192480	Fig. 2D Gnmt-2
Gnmt_R2	TCCCATAACCCATACTACCTAATAA		
Gnmt_F3	AATTGGGGTAAAGTTTGTGTTTGTAG	chr17:46189976-46190462	Fig. 2D Gnmt-3
Gnmt_R3	TCCCAAAAACACATAAAAACTCATT		
Hnf1a_F	GGGAGTTAGAGGTAGGAAAATTAGG	chr5:115232432-115232905	Fig. 4A Hnf1a
Hnf1a_R	AAAATAAATCACTACACCTCAATCC		
Hnf4a_F1	GTTTGTGATAGGGTTTGGGAATTAT	chr2:163230407-163230741	Fig. 4B Hnf4a-1
Hnf4a_R1	CTTTCATTTAAACAACACATTCCA		
Hnf4a_F2	GGTTTTTGGTGGTTTTTGTAGAGATTT	chr2:163231804-163232291	Fig. 4B Hnf4a-2
Hnf4a_R2	AAAACCATTAACCTCTCCACACATA		
Hnf4a_F3	GGGAGGGGTATGTATTGTGTAAGTA	chr2:163237981-163238371	Fig. 4B Hnf4a-3
Hnf4a_R3	ACAAACACCCCAACAACAACTAACATT		
Hnf4a_F4	AAAAATCAATCTATCCAACATAACC	chr2:163239167-163239466	Fig. 4B Hnf4a-4
Hnf4a_R4	TGAAGTTGGGATATAAATTTAAAAAGG		
Hnf4a_F5	TTTGTGTTGGTGGTTTTGTATGGTA	chr2:163239647-163240004	Fig. 4B Hnf4a-5
Hnf4a_R5	AACCAACTCAAAAACACATATACCC		
Nr1h3_F	TTAGGAAGAGATGTTTTGTGGTTG	chr2:90994114-90994508	Fig. 4C Nr1h3
Nr1h3_R	CCACTACCCAACATAACATCAAAA		
Nr1i2_F	AGATTGGTTTTGTAGGTGGTTATTG	chr16:38212169-38212611	Fig. 4D Nr1i2
Nr1i2_R	AAAAACCTAACTCCTTCCCTAAAA		
Rxra_F1	TTGGATAGGTTTGGTATTGTTTGT	chr2:27525521-27525845	Fig. 4E Rxra-1
Rxra_R1	CACAAATCACTCTTTAAAAACACCA		
Rxra_F2	AAGTGTAGGATTGGAGGGAAAGTATT	chr2:27527859-27528199	Fig. 4E Rxra-2
Rxra_R2	ATCTCCAAAATCACACATCCTTAAA		
C1r_F1	GGGAAGGTTTGTGTTTTATGAAGATT	chr6:124475717-124476066	Fig. S3A C1r-1
C1r_R1	ACCTTAAACTTATAATCCTTCTACCTCAAC		
C1r_F2	AAGGTTATTGTTAAGGGGAGATTGT	chr6:124477322-124477721	Fig. S3A C1r-2
C1r_R2	CATCTTTTCCCTAAACATATAATCAACTC		
Proc_F1	ATTGTAAGATTGTGAAGGATTGTGG	chr18:32280721-32281125	Fig. S3A Proc-1
Proc_R1	CTAATATCCCCCAAAACCAATAAAAC		
F2_F1	GATGGATTTTGTGAATTGTGTGTGA	chr2:91439647-91440086	Fig. S3A F2-1
F2_R1	AACACCATCCAACCTCTAACTTACA		
F2_F2	TGTTAGGGGTGGATATTTGTTTTTA	chr2:91436998-91437368	Fig. S3A F2-2
F2_R2	ACCTACACCACACACATAACTCCTT		
Fga_F1	TGTATTAGTTGGGGAATATAGGAGGT	chr3:83108768-83109144	Fig. S3A Fga-1
Fga_R1	CAACCAAAAATTCACACATTTAACA		
Fga_F2	GGAGGAATAAGGGGTTATATTTATTTT	chr3:83110480-83110781	Fig. S3A Fga-2
Fga_R2	CCAAATCTAAATCTCAAAACAAACAA		
Fga_F3	TGAATTTTTATTAGAAGGAGGAGGA	chr3:83114472-83114909	Fig. S3A Fga-3
Fga_R3	TTCCAAATAAATCCAAACTCAAAAA		
Fgb_F1	TTTGTGTTGGGGTTATTAGATAATTT	chr3:83137743-83138091	Fig. S3A Fgb-1
Fgb_R1	ACCAAATTAACAAATCCAACCTCA		
Fgb_F2	TGGTTTATGAGAAGTGATAAAAGAAAA	chr3:83136383-83136693	Fig. S3A Fgb-2
Fgb_R2	CCCAAAATCTCAATTTCTACCCTA		
Fgb_F3	GAGTTTGGTAAGAAAGGTGTAAGG	chr3:83134219-83134562	Fig. S3A Fgb-3
Fgb_R3	TTCATATTAACCAATAATCTTCATCAA		
F9_F1	GTAAGTTTTATTAGTTTGTATTTGGAA	chrX:56346175-56346555	Fig. S3A F9-1
F9_R1	ATAAAAATACACCACAAACCCCTAT		
Serpina1e_F1	TTTTTGGGAGTAGGGGTAATATAGG	chr12:104357440-104357836	Fig. S3A Serpina1e-1
Serpina1e_R1	ACACAAATCTCCAAACCACTATAC		
Serpina1e_F2	TAGGTGTTTTTGGGAGTTTTGAATA	chr12:104356571-104356882	Fig. S3A Serpina1e-2
Serpina1e_R2	CCAAACAACTAAATCACATTCTCA		
Serpind1_F1	TGATTTTATGTAAGTTGGGTGAGTG	chr16:17247783-17248189	Fig. S3A Serpind1-1
Serpind1_R1	AAATCCAAATTTCTACCCAATAACT		
Cpt2_F1	TTTGATAAGGATAGGTTTGTAAATGTT	chr4:107421333-107421793	Fig. S3C Cpt2-1
Cpt2_R1	ACTAAAACCTCCAAAACAAAC		
Cpt2_F2	GGTTGTGAGTTTAAAGTTTGTGTTTAT	chr4:107419415-107419712	Fig. S3C Cpt2-2
Cpt2_R2	CCTCAAAATTAACCACTCCTTACCAAAT		
Gstz1_F1	GGAGGGAGGTTATTAGTTTAAATTTT	chr12:88036830-88037318	Fig. S3C Gstz1-1
Gstz1_R1	CATCTTTCCCTTACCTTTAATAC		
Gstz1_F2	TTTAAGTTATTGTTGGAATGGAGTTG	chr12:88037537-88037932	Fig. S3C Gstz1-2
Gstz1_R2	AAACACTAACAAACAAACCACTAAC		
Pygl_F1	GAGGTAATGGTTTTATTGGGAATTT	chr12:71146232-71146507	Fig. S3C Pygl-1
Pygl_R1	ACTAACCTCCTCCCTTCTTACTTA		
Pygl_F2	GTTGTATGATGGTTTTGTGGAAT	chr12:71144064-71144491	Fig. S3C Pygl-2
Pygl_R2	CAACAAACCTATAAACCTCTCAAC		
Ahcy_F1	TATATGTGTTTGGGTGTTTTGTTT	chr2:154763215-154763572	Fig. S3C Ahcy-1
Ahcy_R1	ACCCACTCCTATCTACCAACTATT		

Legends for Supplementary Figures

Figure S1

Selective amplification of DNA fragments by D-REAM. **(A)** Genomic DNA was digested with HpyCH4IV and subsequently ligated with the unphosphorylated R-adaptor pairs. The complementary strand of the ligated R24 were filled-in by using Klenow fragments of DNA polymerase I. The DNA fragments were then digested with TaqI and ligated with the unphosphorylated N-adaptor pairs (**Supplementary Table S2**). By complete fragment denaturation and hot-start Taq DNA polymerase, only strands obtained from fragments digested with HpyCH4IV can be used as templates for PCR with the N18 and R18 primers (indicated by the red dotted oval). **(B)** Monitoring selective amplification of HpyCH4IV digested fragments. The PCR mixture with different primer sets was sampled at different cycles of the thermal cycles (15, 20 and 25) and was subjected to agarose gel electrophoresis. **(C)** Selective amplification of NotI digested fragments. Genome DNA, which was digested by NotI instead of HpyCH4IV, was performed by D-REAM. The positions of the DNA molecular markers (M) of 0.5, 1, and 2 kbp are indicated along the sides of the figure. **(D)** The correlation of intensities of the probes between an experimental duplicated liver DNA samples of a mouse.

Figure S2

in silico analysis of mouse genome. **(A)** Steep peaks of HpaII (narrow blue), CpG dinucleotides (blue) and the GC percentage (gray) at TSS indicated that HpaII mainly localized in the CGI on promoter array, and agree the large quantity of tiny fragments. The frequencies of probes (green), HpyCH4IV (red) of the genomic regions, which were covered by the mouse promoter tiling array, are plotted. Dotted horizontal lines at CpG (obs/exp) 0.6 and GC percentage 50% represent the cutoff values for defining CpG islands. **(B)** The mouse genome (mm8, UCSC genome browser) was digested *in silico* with HpyCH4IV (upper panel) or HpaII (lower panel) by using the EMBOSS software package. The distribution of the length of fragments was plotted. The median and average sizes of HpyCH4IV and HpaII fragments were 907, 1468, 658 and 1620 bp, respectively. These plots

indicated that the range of distribution of HpyCH4IV fragments size is narrower than that of HpaII. The first quantile of sizes of HpaII fragments indicate the presence of large quantities of tiny fragment. On the other hands, the average sizes of them are larger than those of HpyCH4IV, indicating that HpyCH4IV is distributed throughout genome in more uniform manner than HpaII.

Figure S3

COBRA confirmed the methylation status of T-DMRtags. **(A)** The methylation status of T-DMRtags of the non-CGI genes involved in the coagulation and complement cascades are shown as plots displayed by the integrated genome browser (IGB) indicating T-DMRtags as arrowheads, and the chromosomal locations are indicated at the top of the panels. The regions indicated as yellow boxes were analyzed by restriction mapping. **(B)** The numbers at the top of the gel images correspond to those on the plots. L and C indicate liver and cerebral DNA, respectively. + and – indicate digestion with HpyCH4IV and no digestion, respectively. **(C)** The methylation status of T-DMRtags and CGIs in CGI genes. **(D)** Agarose electrophoresis gel images are displayed.

Figure S4

The list of candidate genes under the control of HNF1 and DNA methylation. **(A)** Forty-three of mouse orthologs of human genes that had been identified by ChIP-chip experiment of hepatocytes with anti-HNF1 antibody have T-DMRs. **(B)** Genes displayed in shadowed rectangle are classified to have HNF-1A motifs in 1-kb upstream regions of TSSs by MAPPER database. Those in list A are omitted from list B.

Figure S5

Tissue specificity of genes clustered by K-means clustering according to the methylation status of T-DMRs. **(A)** The expression levels of the genes in each cluster of **Figure 5E** are expressed in box-plot of the log-ratios (base = 2) of expression levels in tissues compared to those in the liver. The expression data were downloaded from SymAtlas web site. **(B)** The methylation status of T-

DMRs of the genes are shown as plots displayed in MATscores, which were obtained by MAT using cerebrum as control samples, by the integrated genome browser (IGB)..

Figure S6

Data flow of bioinformatics analysis in this study. Rectangles with right corners stand for public domain or raw data. Rhombuses and rectangles in round corners represent software and treated data, respectively.