Supplementary table 1. Detailed number of CpGs on CGI and up to upstream 2 kb of TSS

Data types	Libraries	No. total CpGs	No. CpGs mapped to CGIs (%)	No. CpGs mapped to up2kb[a](%)
In silico simulations	Genome[b]	28,032,349	2,367,139 (100.00)	300,187 (100.00)
	*Msp*I[c]	3,617,307	1,295,120 (54.71)	250,631 (83.49)
Experiments	3D4/2	2,419,143	912,506 (38.55)	181,292 (60.39)
	Neocortex	2,536,176	942,083 (39.80)	186,794 (62.23)
	OE	2,384,526	900,171 (38.03)	176,372 (58.75)
	Spleen	2,535,855	940,582 (39.73)	186,776 (62.22)
	Liver	2,795,733	1,025,384 (43.32)	203,535 (67.80)
	Muscle	2,503,177	939,897 (39.71)	183,719 (61.20)

[a] up2kb, upstream 2 kb region of TSS; [b] library for whole genome; [c] RRBS libraries selected for 40–220 bp fragments after *Msp*I digestion. OE, olfactory epithelium.

Supplementary table 2. Coverage of >10× CpG sites (CpG10) inferred from the RRBS analysis of the pig genome among different tissues

Libraries	No. mapped CpG10 sites	Mean coverage of CpG10 sites (folds)
3D4/2	2,986,591	37.05
Neocortex	3,163,431	40.68
OE	2,514,630	44.53
Spleen	3,103,243	39.17
Liver	2,997,913	56.56
Muscle	2,644,434	51.47

OE, olfactory epithelium

Supplementary table 3. Distribution of methyl-CpG (mCpG) with different methylation levels

Libraries	Heavy (>95%)	Hyper (>90%)	Intermediate (20~80%)	Hypo (<10%)	Unmethylated (<5%)
3D4/2	25.60%	34.40%	20.30%	34.50%	26.40%
Neocortex	16.40%	26.60%	21.30%	36.40%	29.80%
OE	16.60%	27.30%	18.30%	40.20%	34.50%
Spleen	17%	28.50%	18.60%	36.60%	29.90%
Liver	11.60%	21.40%	23.80%	38.50%	32.90%
Muscle	11.70%	21.40%	23.30%	39.60%	34.20%

*OE: olfactory epithelium

Supplementary table 4. The positions of differentially methylated cytosine (DMCs) with CGI feature annotation – separated excel file, see the “supplementary tables.xlsx”

Supplementary table 5. Percentage CpG sites mapped to various gene-related regions from RRBS of different tissues

Libraries	exon	intron	up2kb [a]	up5kb [b]	up10kb [c]	total
3D4/2	8.18%	16.32%	4.04%	10.48%	20.92%	45.41%
Neocortex	7.88%	16.07%	3.94%	10.24%	20.48%	58.62%
OE	8.28%	15.81%	4.11%	10.62%	21.10%	59.92%
Spleen	7.88%	16.13%	3.93%	10.22%	20.47%	58.63%
Liver	7.99%	15.99%	4.00%	10.39%	20.74%	59.11%
Muscle	8.28%	15.82%	4.11%	10.63%	21.12%	59.96%
Average	8.08%	16.02%	4.02%	10.43%	20.81%	59.36%

[a, b, and c] 2, 5, and 10 kb upstream regions of transcription start sites (TSS), respectively. OE: olfactory epithelium

Supplementary table 6. Average methylation levels of eight imprinted genes and three non-imprinted genes

	Genebody[4]						UP2K[5]					
	NC[1]	OE[2]	liver	MS[3]	spleen	PAM	NC	OE	liver	MS	spleen	PAM
DIO3	5.0	3.0	14.0	6.0	11.0	59.0	74.8	76.4	78.8	73.0	70.6	60.0
DIRAS3	59.6	50.6	52.6	67.6	59.0	85.5	N/D	N/D	N/D	N/D	N/D	N/D
MEG3	29.5	30.8	31.7	41.9	40.0	80.3	33.8	76.8	65.3	75.3	69.8	84.5
MEST	N/D[8]	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D
NAP1L5	51.5	52.3	49.1	51.8	56.6	48.5	72.3	39.0	38.0	48.0	53.3	54.8
NECD	N/D	N/D	N/D	N/D	N/D	N/D	9.3	7.2	12.2	6.7	12.2	50.3
NNAT	45.5	42.5	48.9	46.6	52.5	84.7	65.3	71.1	52.8	71.8	78.0	75.6
PHLDA2	2.3	0.8	1.9	0.3	0.5	1.0	28.6	19.0	11.2	13.0	15.4	10.6
ACTA1	3.0	0.0	3.0	0.0	3.0	96.0	3.1	1.9	6.2	3.4	7.1	81.4
GAPDH	33.0	37.5	40.0	32.0	40.5	6.5	6.4	3.3	1.8	5.8	7.0	21.5
COX5B	0.0	8.7	0.0	0.0	0.0	0.0	N/D	N/D	N/D	N/D	N/D	N/D

	UP5K[6]						UP10K[7]					
	NC	OE	liver	MS	spleen	PAM	NC	OE	liver	MS	spleen	PAM
DIO3	70.0	72.3	69.0	65.0	69.8	24.3	69.2	78.7	74.0	72.7	76.7	48.3
DIRAS3	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D
MEG3	59.3	50.3	50.3	55.3	57.5	48.0	66.0	75.5	64.8	78.0	78.5	54.3
MEST	33.3	27.9	37.7	51.8	44.6	36.0	54.3	29.2	18.7	58.8	24.7	78.2
NAP1L5	N/D	N/D	N/D	N/D	N/D	N/D	78.4	79.0	76.4	77.8	81.2	81.8
NECD	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D
NNAT	55.8	64.3	53.0	65.5	93.3	99.0	N/D	N/D	N/D	N/D	N/D	N/D
PHLDA2	22.7	22.7	20.2	18.9	22.6	8.8	70.9	70.4	58.7	67.6	72.8	45.3
ACTA1	N/D	N/D	N/D	N/D	N/D	N/D	85.0	79.0	82.0	75.7	82.0	81.5
GAPDH	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D
COX5B	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D

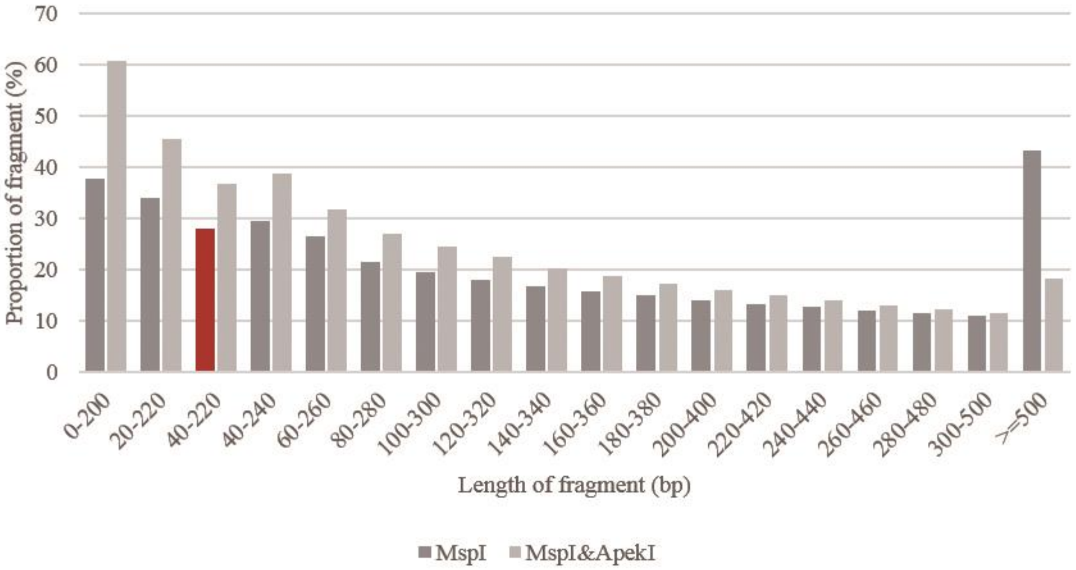
[1]neocortex, [2]olfactory epithelium, [3]muscle, [4]exon and intron region, [5,6,7] upstream 2 kb, 5 kb and 10 kb region from TSS, [8]not detected

Supplementary table 7. The list of chromosomal positions for individual differentially methylated cytosine (DMCs) of five tissues and a cell line. – separated excel file, see the “supplementary tables.xlsx”

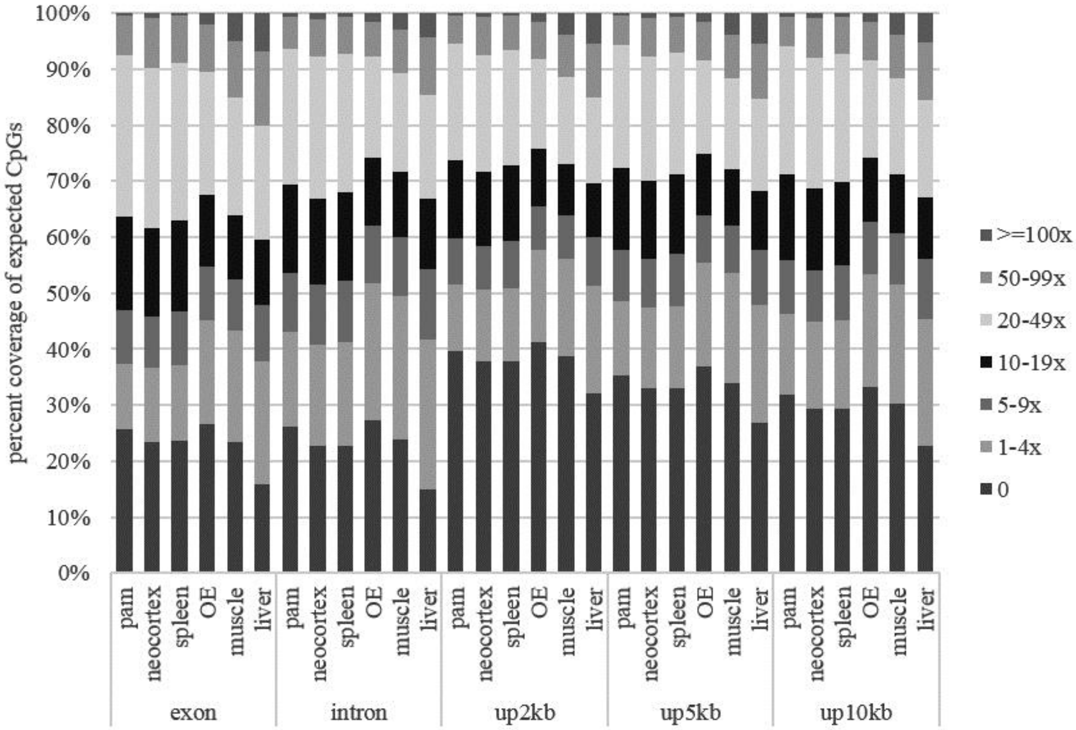
Supplementary table 8. The list of chromosomal positions for individual tissue specific differentially methylated cytosine (tDMCs) of five tissues and a cell line. – separated excel file, see the “supplementary tables.xlsx”

Supplementary table 9. The result of hypergeometric test of five tissues and a cell line with multiple testing correction. – separated excel file, see the “supplementary tables.xlsx”

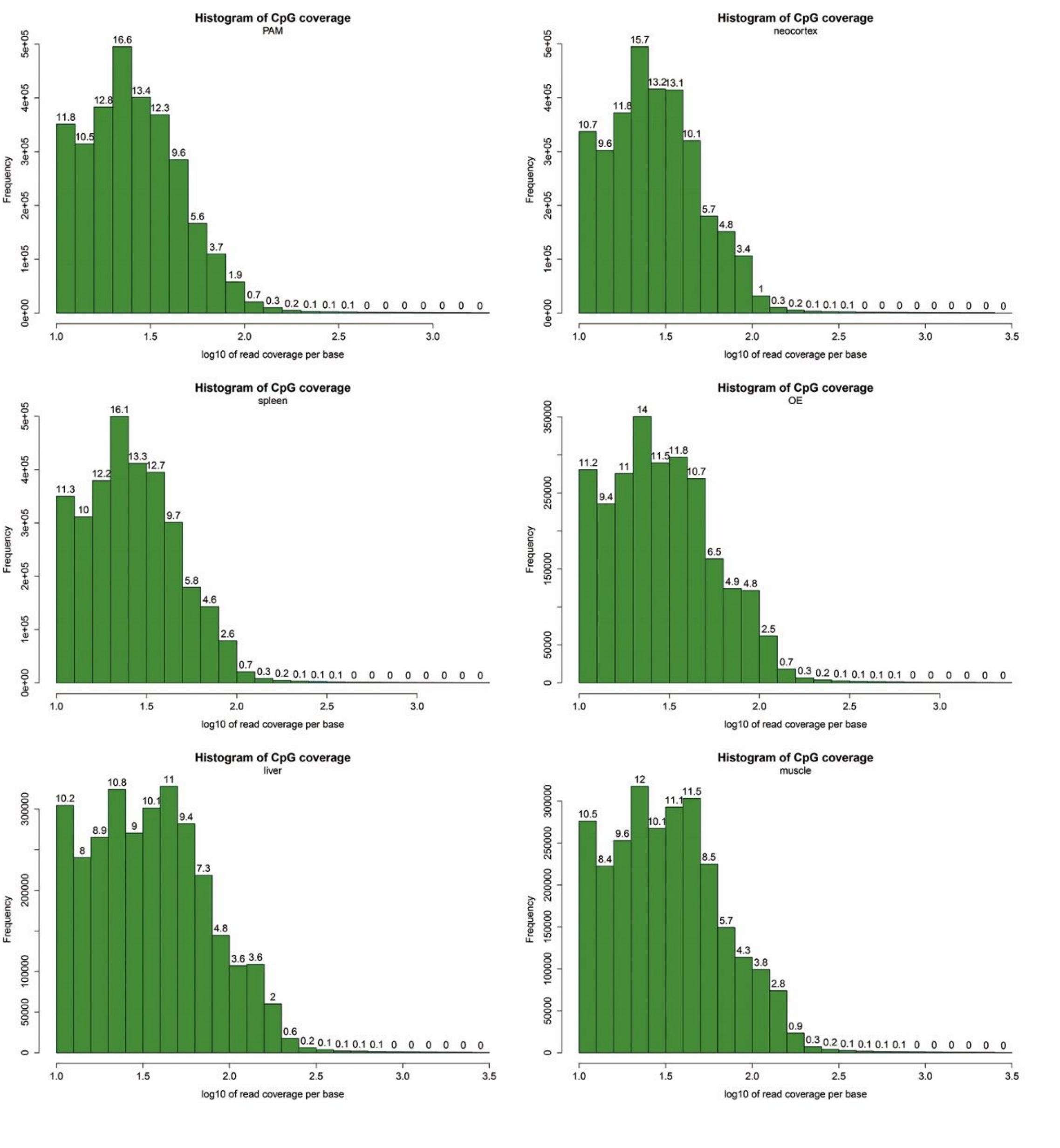
Supplementary table 10. The list of genes associated with tissue specific differentially methylated cytosine (tDMCs) of five tissues and a cell line. – separated excel file, see the “supplementary tables.xlsx”



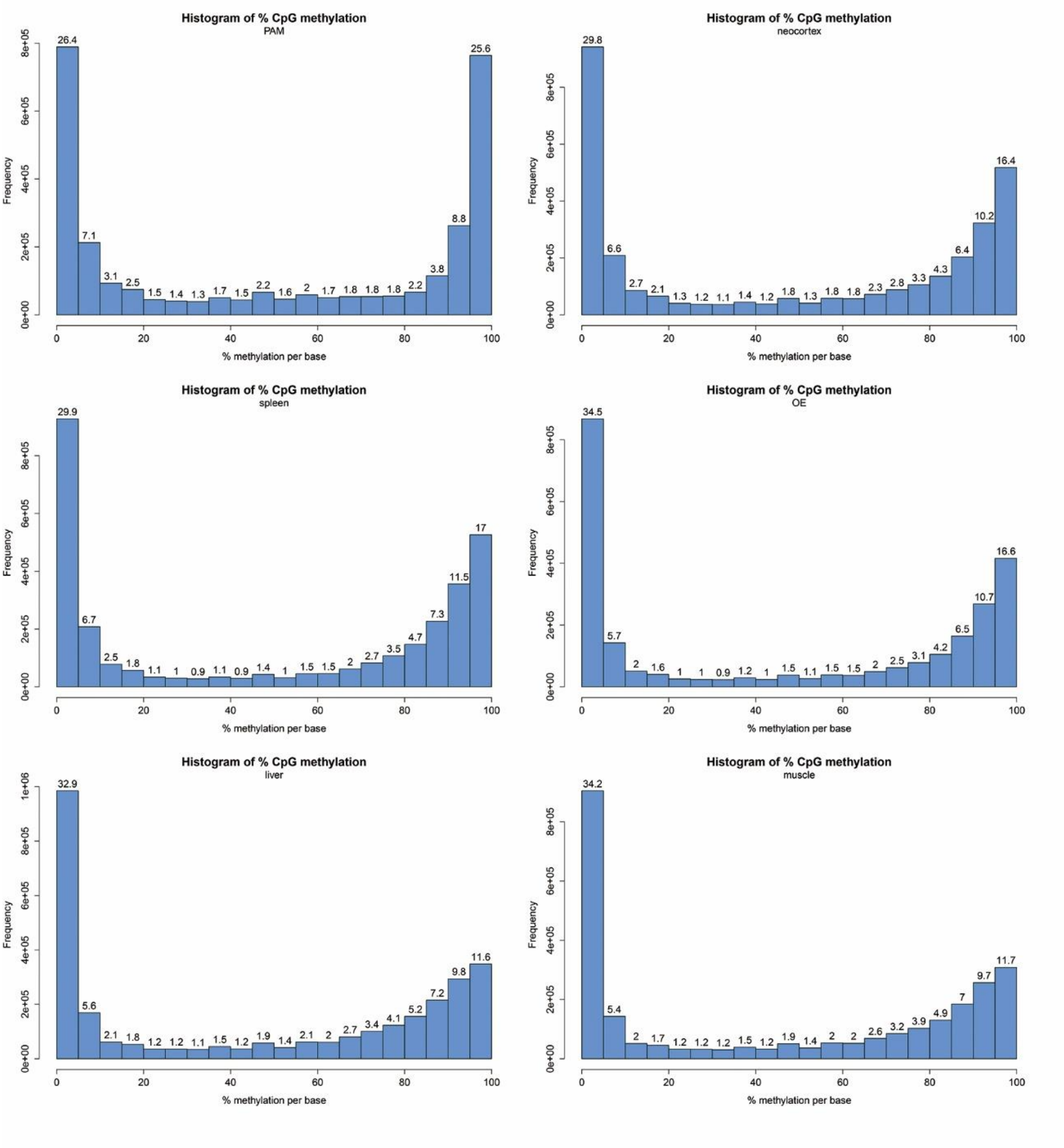
Supplementary figure 1. Comparison of the distribution of DNA fragments in different selection windows of the pig genome. The size of the fragment selection window was 200 bp except for the 40–220 bp (180 bp) in red, which was used for this study. The simulation was performed for both *Msp*I alone and *Msp*I and *ApeK*I double digestion.



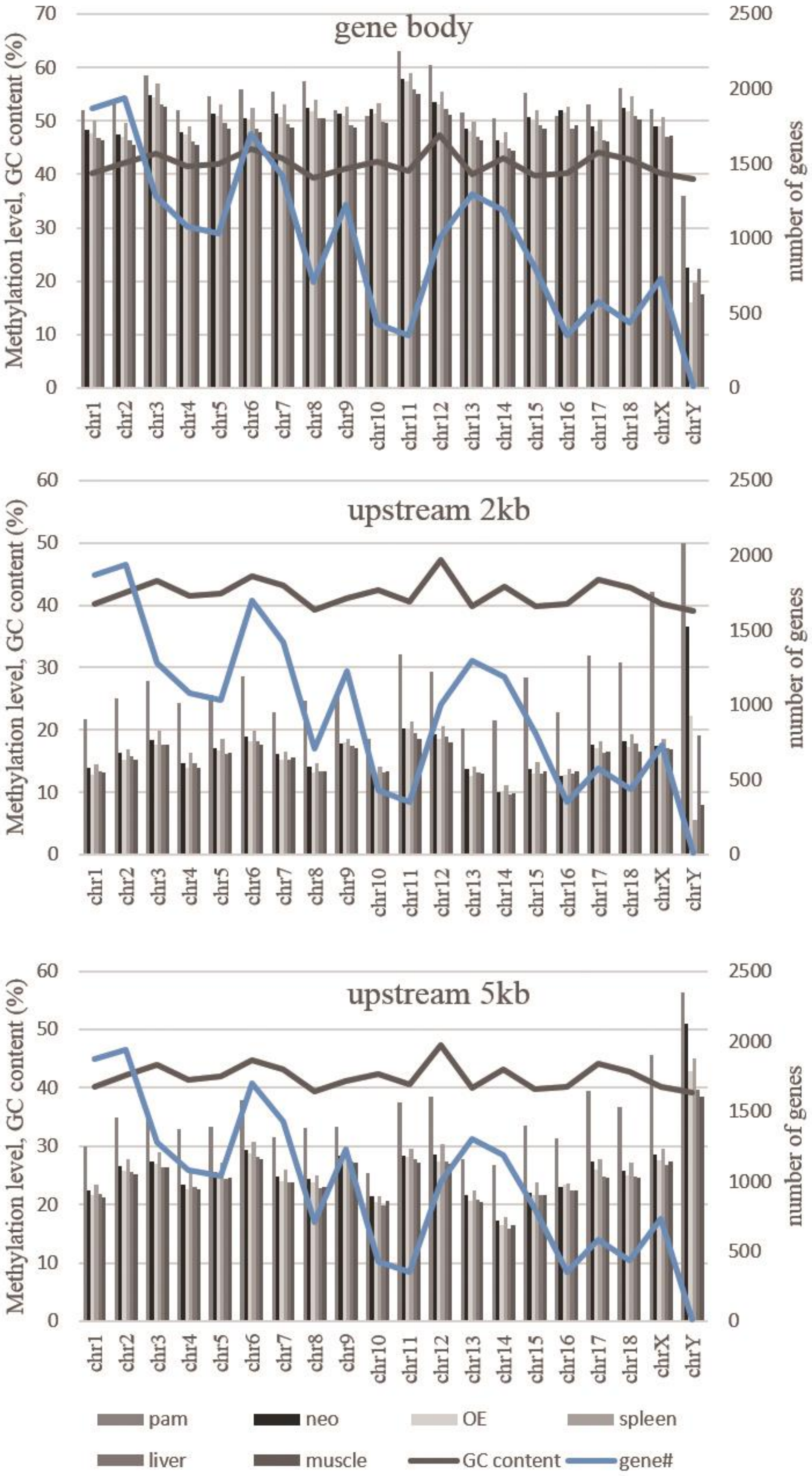
Supplementary figure 2. Distribution of CpG sites in gene related regions (exon, intron, upstream 2 kb, 5 kb, and 10 kb regions of TSS) and their coverage in different libraries. OE, olfactory epithelium.



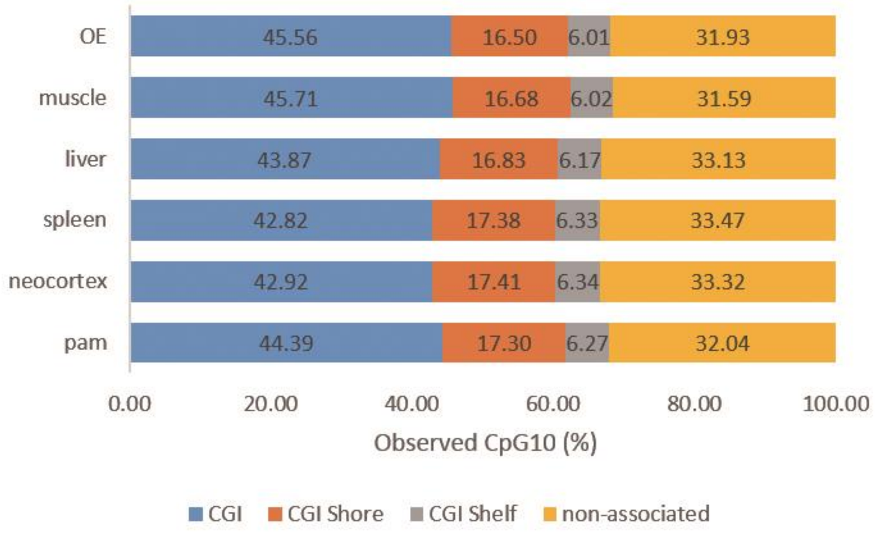
Supplementary figure 3. **Distribution of the read coverage per base and frequency from RRBS of different tissues**. The x-axis shows $\log_{10}$ values corresponding to the number of reads per CpG. Numbers above the bars denote the percentage of CpG sites contained in the respective bins.



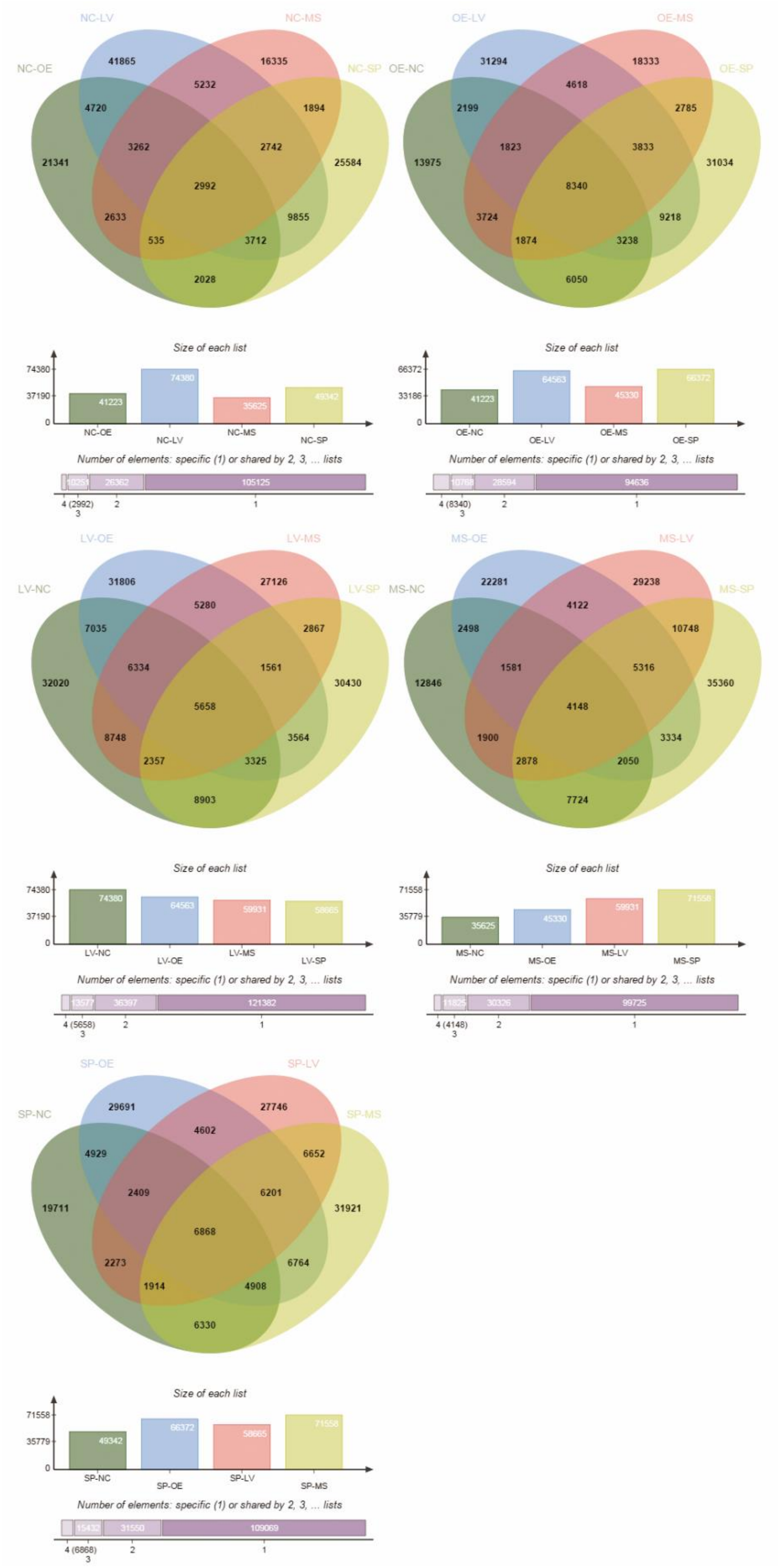
Supplementary figure 4. Distribution of the percentage methylation per base from RRBS of different tissues. The x-axis represents percentage methylation for each CpG. Numbers above the bars denote the percentage of CpGs contained in the respective bins.



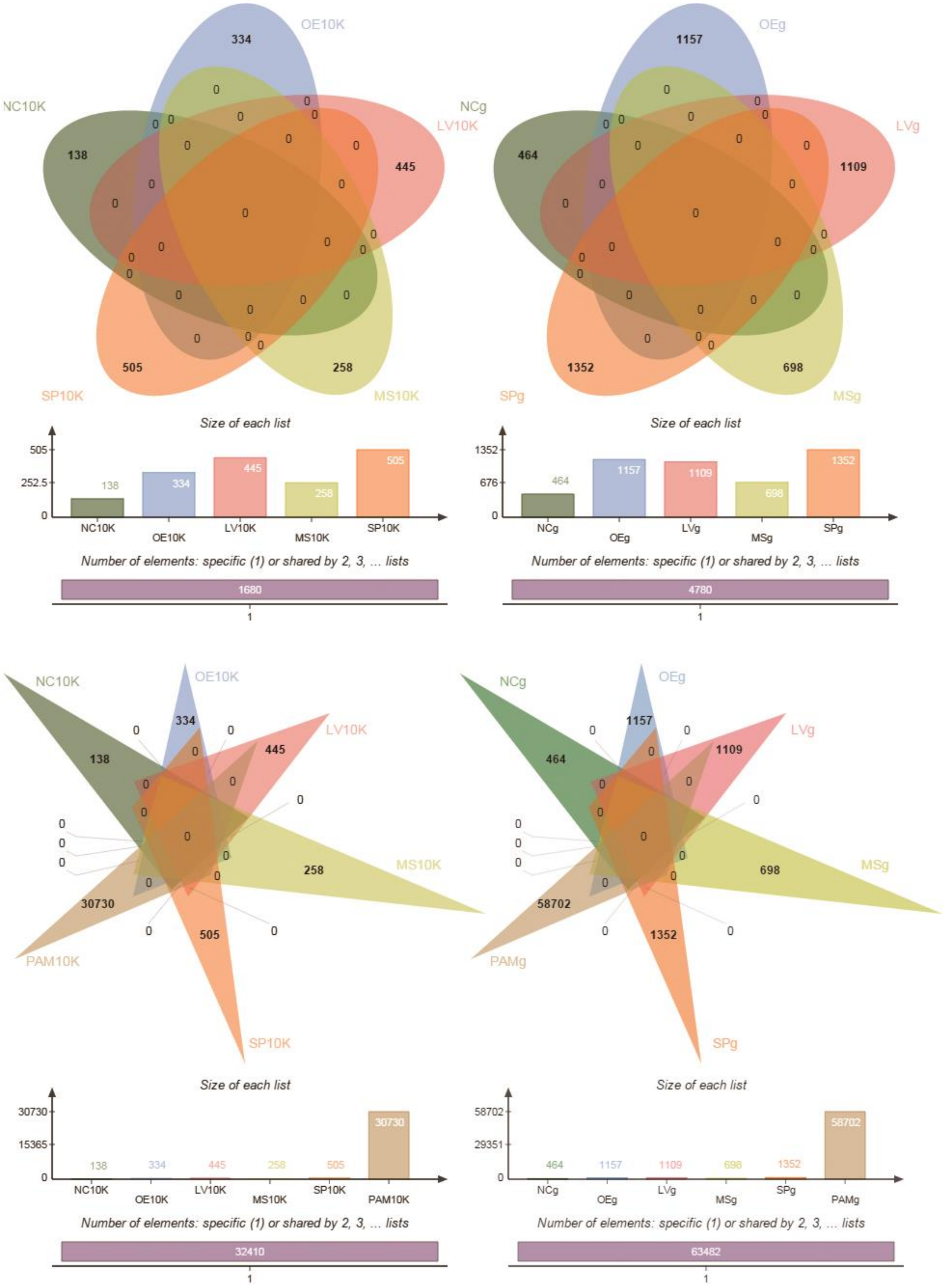
Supplementary figure 5. Comparison of the percentage methylation levels on gene-related regions in relation to the number of genes and the GC content for individual chromosomes in different tissues. Gene body, exon and intron; up2kb and up5kb, upstream 2 kb and 5 kb regions of TSS, respectively.



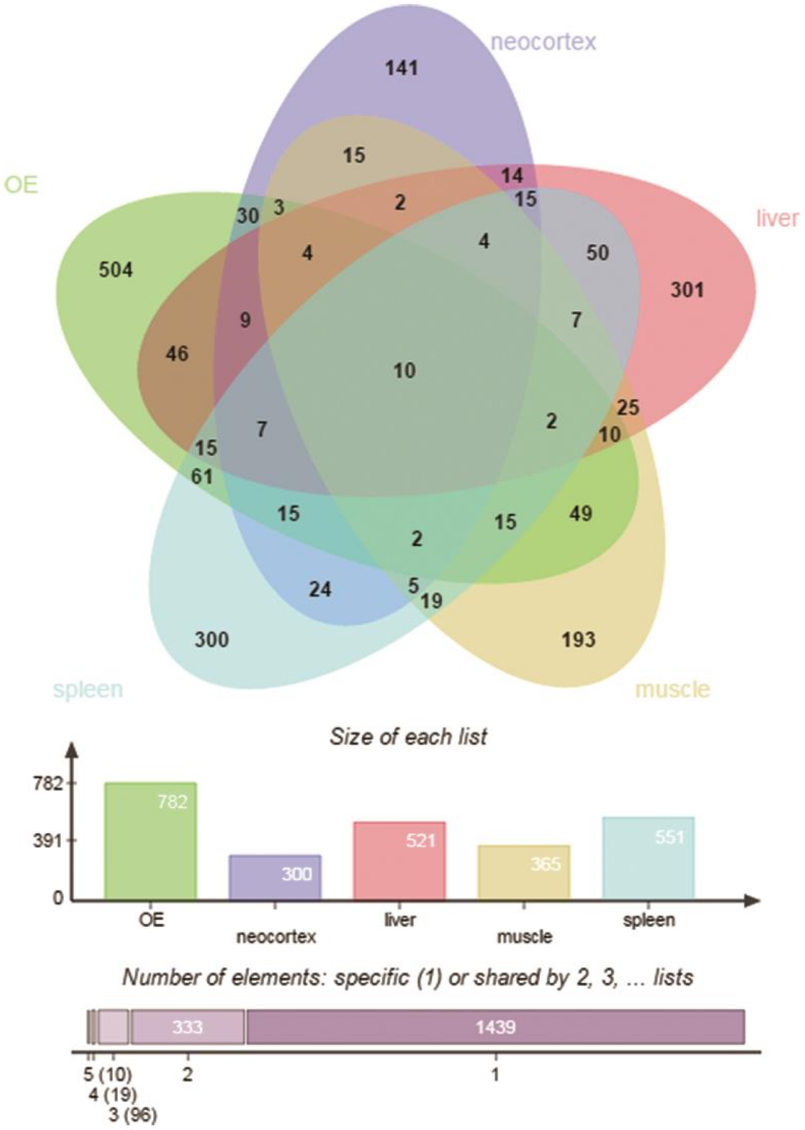
Supplementary figure 6. Percentage of CpG10 sites mapped to CGI features. CpG10, CpG sites with > 10× coverage.



Supplementary figure 7. Comparisons for positions of differentially methylated cytosine (DMCs) among pairwise tissue comparisons. Overlapped regions indicate the position of DMCs which were detected in multiple tissues NC;neocortex, OE;olfactory epithelium, LV;liver, MS; muscle and SP;spleen



Supplementary figure 8. The number of tDMCs in gene bodies and upstream 10 kb region from TSS among five or six tissues. The number of tDMCs was visualized by Venn diagrams. NC;neocortex, OE;olfactory epithelium, LV;liver, MS; muscle, SP;spleen and PAM;3D4/2 cell. g and 10K represent gene bodies and upstream 10 kb region from TSS, respectively.



Supplementary figure 9. The number of DMC associated genes from five tissues. The number of genes were visualized by Venn diagrams. OE;olfactory epithelium,