Genome-wide high resolution parental specific DNA and histone methylation maps uncover patterns of imprinting regulation in maize

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Running title: Allele specific chromatin maps for maize imprinting

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Supplementary Figures and Tables

Figure S1. Comparison of bulk DNA methylation levels in shoot, embryo and endosperm.

The *y* axis shows the bulk methylation of shoot, embryo, endosperm of 12DAP B73 inbred in CG, CHG and CHH contexts, which are calculated by the ratio of the Cs with all the Cs and Ts from all the analyzable CG, CHG or CHH sites (at least 5 reads per site in all three tissues).

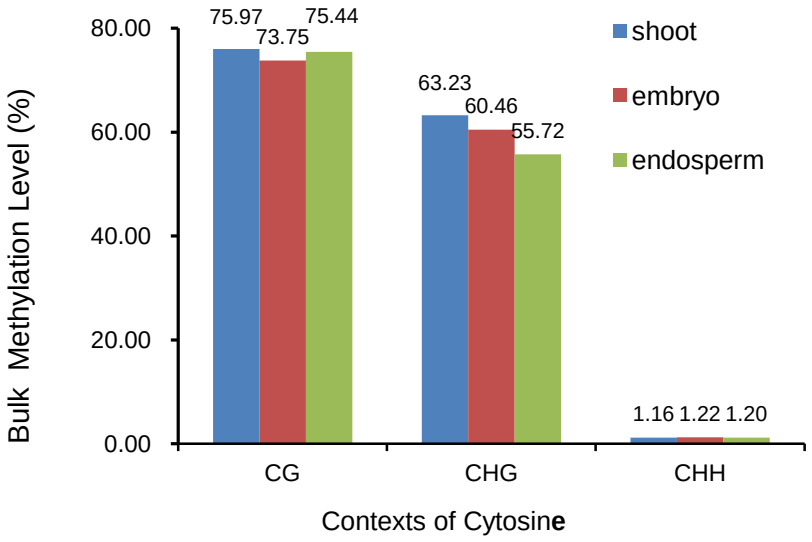

Figure S2. Comparison of bulk DNA methylation levels between two parental alleles of hybrid endosperm.

The analyzable sites shared by all four alleles for both BM and MB were used to calculate the bulk methylation of paternal and maternal alleles. The genotype-dependent differentially methylated sites (DMS) (FDR < 0.05) were excluded.

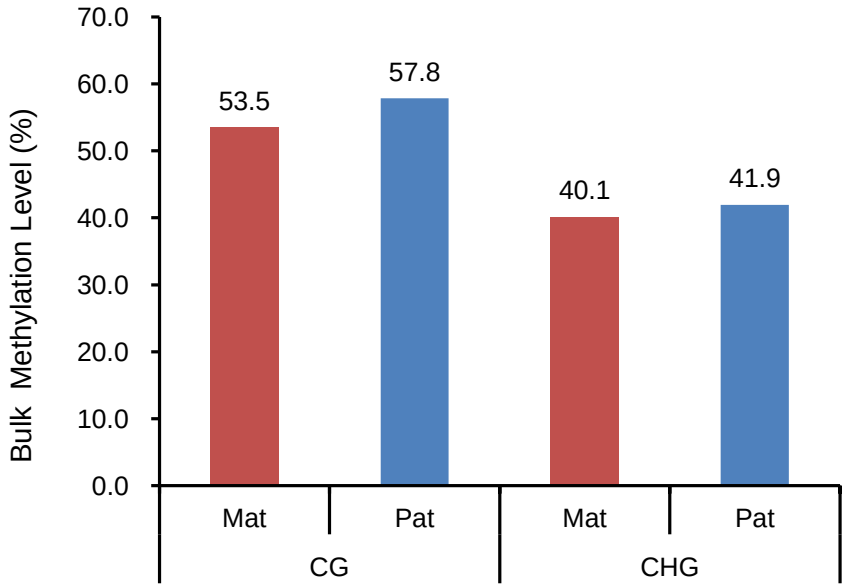

Figure S3. DNA methylation of *Fie1.*

The methylation profile of *Fie1* in shoot, embryo and endosperm of B73, and the allelic methylation from BM and MB are shown. Red lines indicate the paternal allele and blue lines indicate the maternal allele. The analyzable sites shared by four alleles for both BM and MB were represented by grey points. The dotted rectangle highlights the position of pDMR. The methylation of shoot, embryo and endosperm of *Fie1* are shown as purple, orange and green line. Black rectangle (exon), black line (intron).

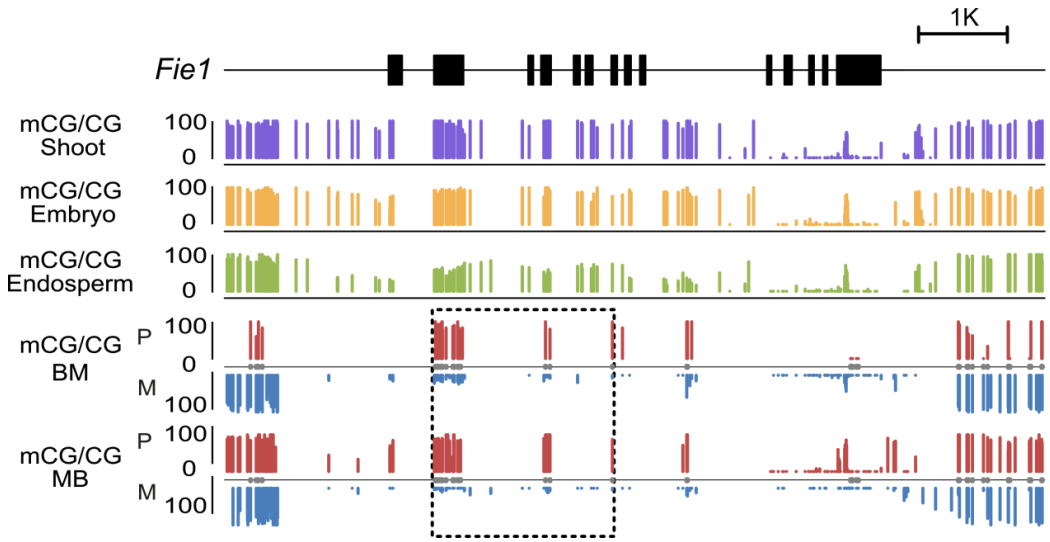

Figure S4. Comparison of CG content among all the identified CG_pDMRs, CHG_pDMRs, and all CG and CHG tested regions.

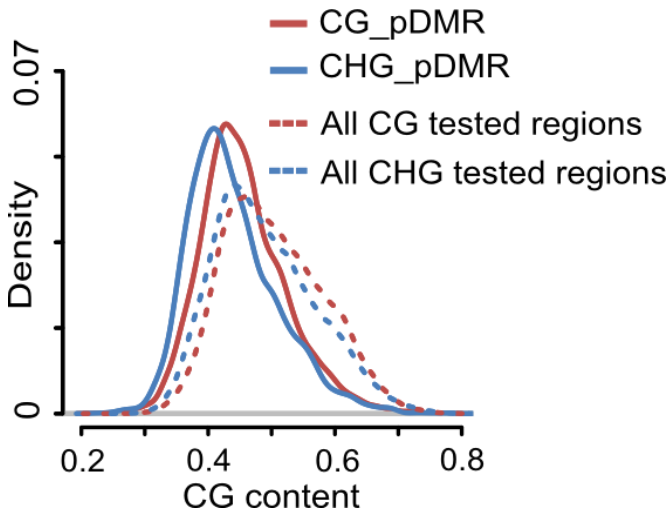

Figure S5. The genomic distributions of CG_pDMRs and CHG_pDMRs.

(A, B, C, D) The middle points of the identified 6,910 CG_pDMRs and 4,456 CHG_pDMRs were used to investigate the genomic distribution of pDMRs in CG and CHG contexts. All the analyzable regions in CG or CHG context were used as the control for the CG_pDMRs and CHG_pDMRs, respectively. The length of the extended upstream and downstream region is 2 kb.

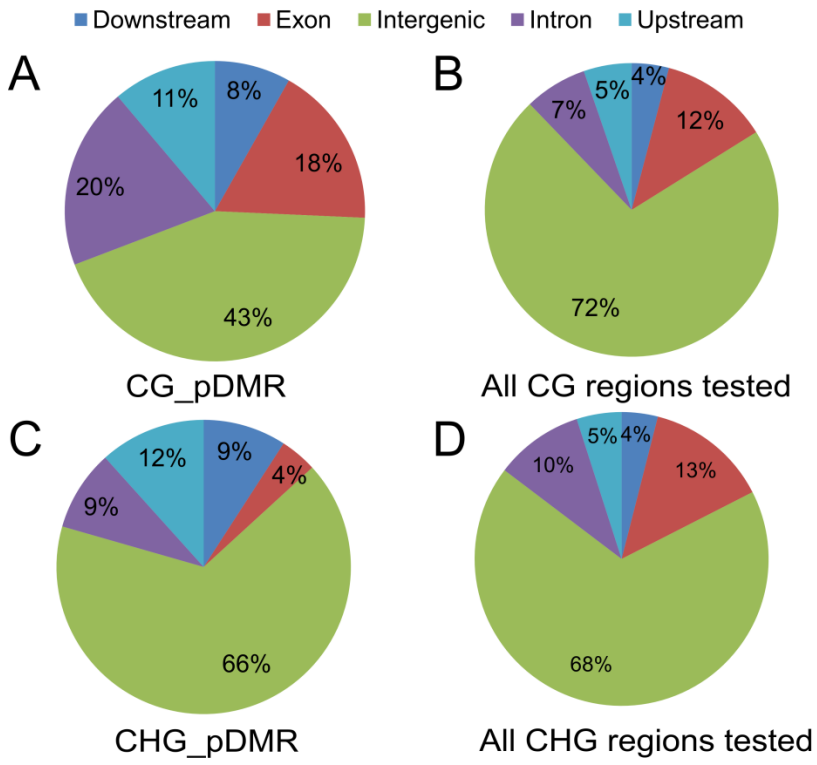

Figure S6. Differential DNA methylation for CG_pDMRs and CHG_pDMRs that corresponded to CHG and CG contexts, respectively. P-M represented the differential methylation level between paternal and maternal alleles.

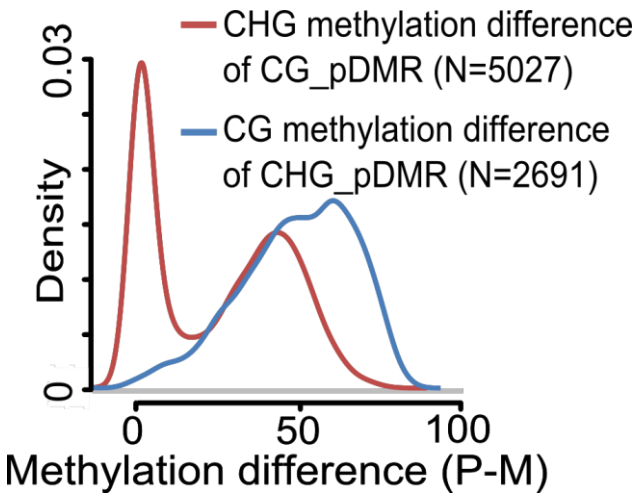

Figure S7. DNA Methylation patterns of CG_pDMRs (A) and CHG_pDMRs (B) and their up- and down-stream 20 kb regions.

The average methylation levels of shoot, embryo, endosperm, maternal (Mat) and paternal (Pat) alleles are shown. pDMR regions were separated into 20 bins and extended 20 kb up- and down-stream regions were separated into 200 bins. Average methylation levels for each bin were calculated and plotted. Shoot, embryo and endosperm come from B73, while Pat and Mat refer to the methylation levels of paternal and maternal genomes in endosperm from averaging hybrids of both reciprocal crosses. The average methylation level of shoot, embryo, endosperm, maternal and paternal alleles for each bin was calculated by the ratio of the methylated Cs and total number of Cs and Ts from all the shared analyzable sites among shoot, embryo, endosperm, and four alleles from BM and MB. The genotype-dependent differentially methylated sites (DMS) (FDR <0.05) were excluded.

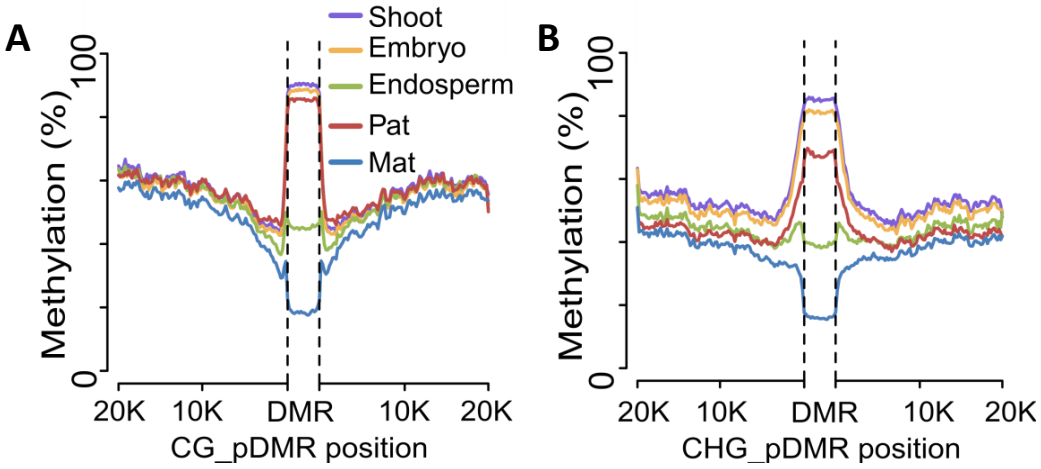

Figure S8. CG content for MEGs, PEGs and non-imprinted genes.

The CG content of the genome average (0.46) is shown as the control.

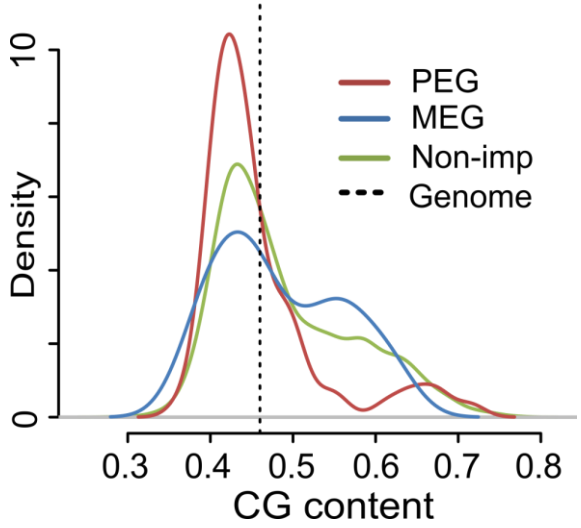

Figure S9. DNA methylation profiles of two PEGs in CG context.

(A, B) The PEGs GRMZMG028366 and GRMZM2G406553 are two confirmed imprinted genes in our previous study (Zhang et al. 2011). The methylation level of each analyzable CG site is shown.

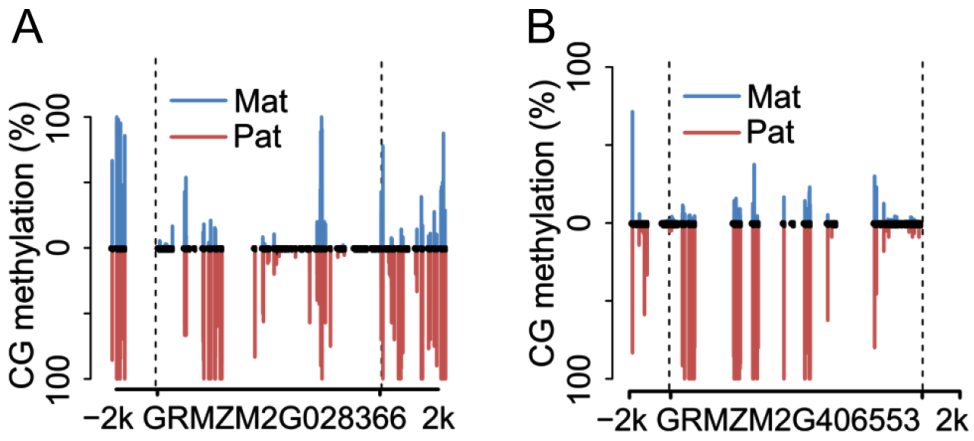

Figure S10. The distribution of CG_pDMRs in MEGs, PEGs and non-imprinted genes.

To investigate the distribution of CG_pDMRs in genes, gene body regions were separated into 60 bins and extended 2 kb of up- and down-stream regions were separated into 20 bins. Bins that contain more than 10 analyzable genes were investigated.

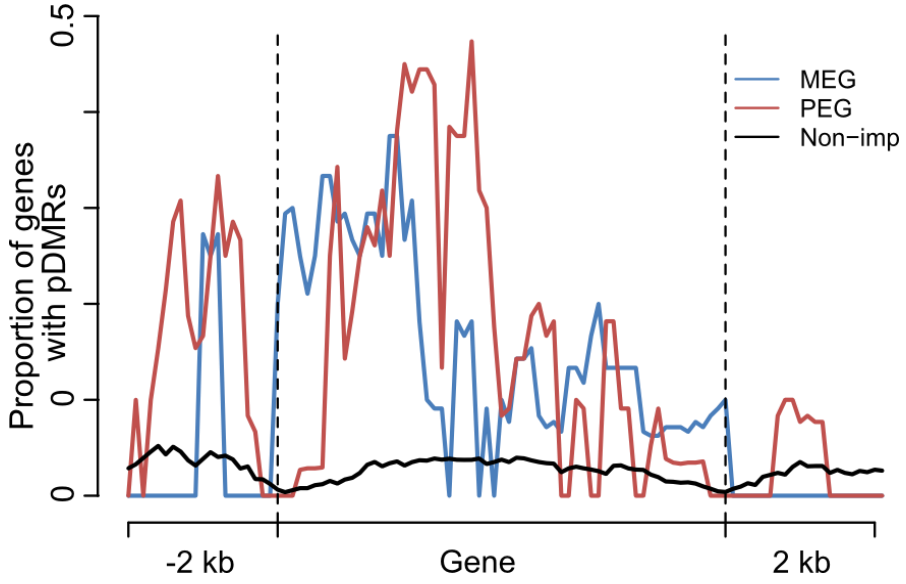

Figure S11. Verification of H3K27me3 peaks by qRT-PCR.

(A, B, C, D) The samples (pre_BM and pre_MB) are the controls used in BM and MB, respectively.

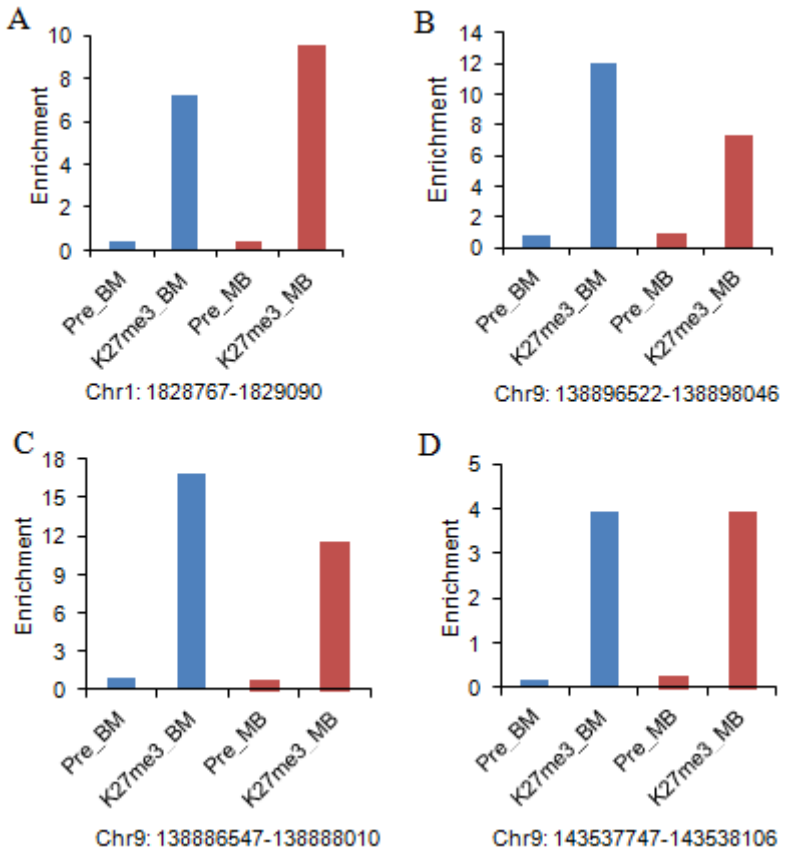

Figure S12. Verification of maternally preferred H3K27me3 peaks.

(A, B) Gel photos are restriction enzyme digested RT-PCR products of ChIP DNA with H3K27me3 antibody. The PCR products of B73 and Mo17 were digested as the control.

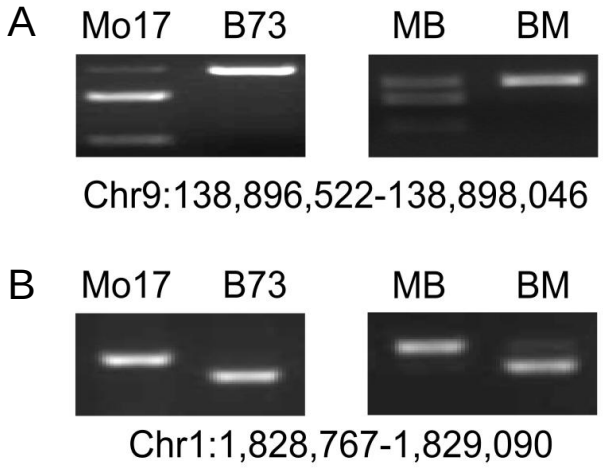

Figure S13. The CG content of H3K27me3 peaks.

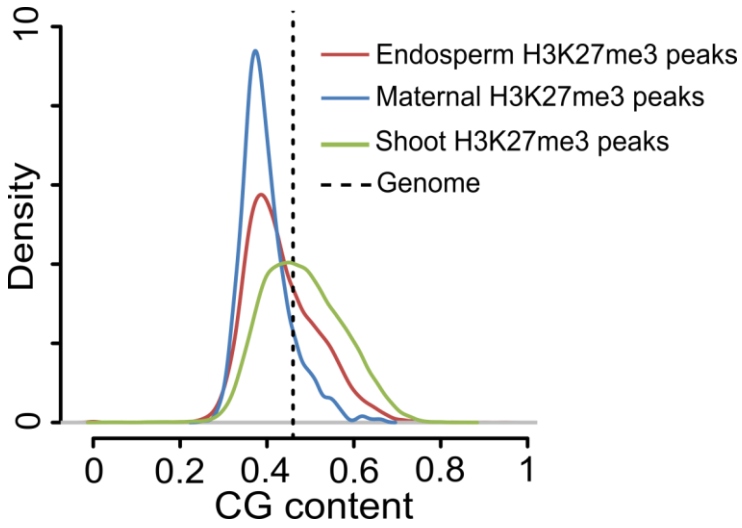

Figure S14. DNA methylation of H3K27me3 peaks in CHG contexts.

(A and B) CHG DNA methylation of maize endosperm H3K27me3 peaks (A), and maternal peaks (B). (C) CHG DNA methylation of two parental genomes for maternal peaks.

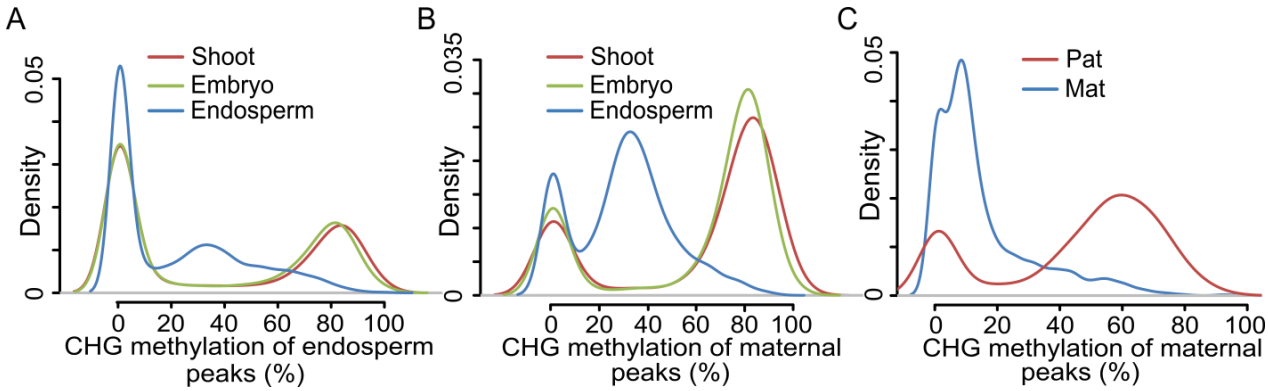

Figure S15. Expression profile of MEGs and PEGs over various maize tissues.

MEGs (A) and PEGs (B) were each divided into two subgroups based on their expression patterns over various tissues. MEG^{a} indicates MEGs that expressed in many tissues, while MEG^{b} indicates MEGs that expressed specifically in endosperm. Similarly, PEG^{a} indicates PEGs that expressed in many tissues, while PEG^{b} indicates PEGs that expressed specifically in endosperm. For each gene, the value is a relative expression normalized by the maximum RPKM value of the gene over all tissue samples.

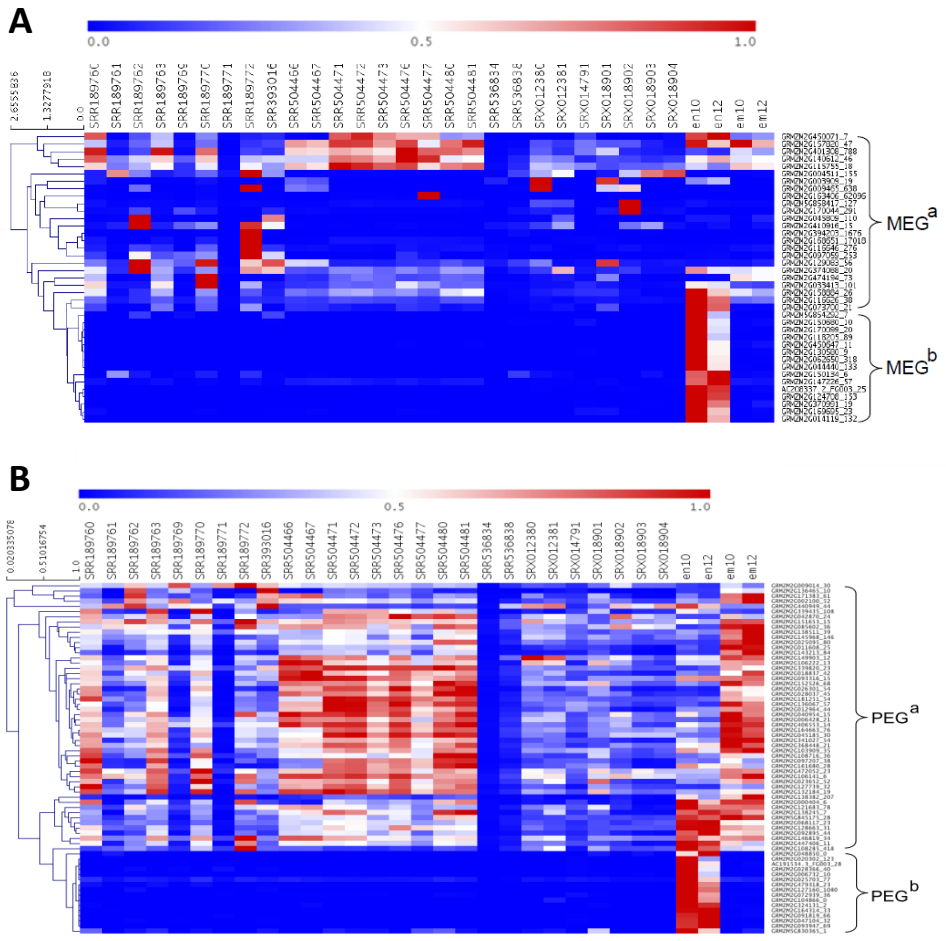

Figure S16. Differential DNA methylation between two subgroups of MEGs and PEGs.

Two subgroups of MEGs and PEGs are designated as: MEG^a for MEGs expressed also in other tissues, MEG^b for MEGs expressed specifically in endosperm, PEG^a for PEGs expressed also in other tissues, PEG^b for PEGs expressed specifically in endosperm. Gene body regions were separated into 60 bins and extended 2 kb up- and down-stream regions were separated into 20 bins. The average DNA methylation levels were calculated with the same method as Supplemental Fig. S7.

(A-D) Average methylation levels for shoot, embryo and endosperm in CG context throughout the gene body and their 2 kb up- and down-stream regions. (E-H) Comparison of average methylation levels between two parental genomes in CG context throughout gene body and their 2 kb up- and down-stream regions. (I-L) Average methylation levels for shoot, embryo and endosperm in CHG context throughout the gene body and their 2 kb up- and down-stream regions. (M-P) Comparison of average methylation levels between two parental genomes in CHG context throughout gene body and their 2 kb up- and down-stream regions.

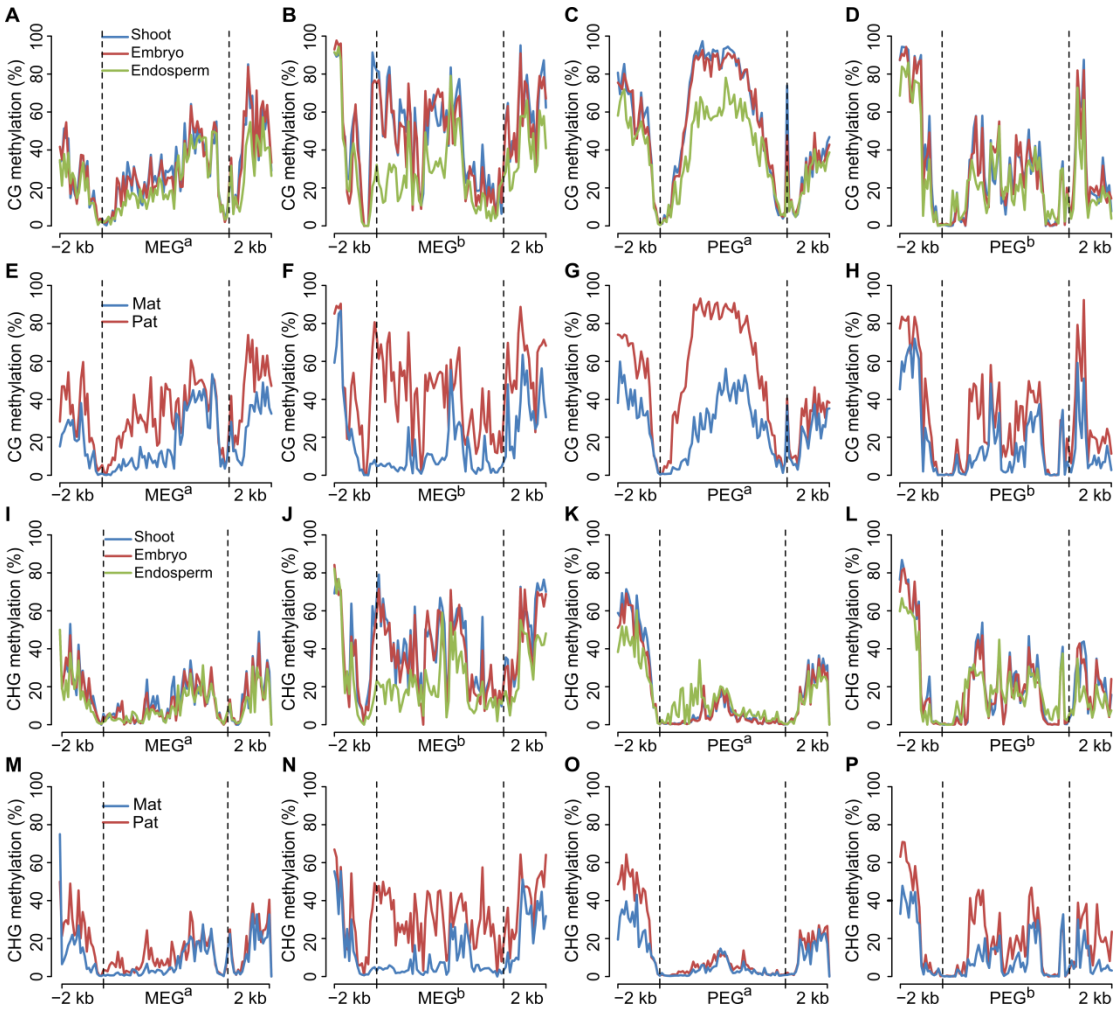
A
B
C
D
E
F
G
H
I
J
K
L
M
N
O
P
Shoot
Embryo
Endosperm
Mat
Pat
CG methylation (%)
CHG methylation (%)
0
20
40
60
80
100
−2 kb
2 kb
MEG^a
MEG^b
PEG^a
PEG^b

Table S1. Summary of the sequenced data used in this study.

Sequencing Type	Sample	Read length (bp)	Reads	Yields (Gb)
RNA-seq (Paired end)	12 DAP Endosperm (BM)	100	36,999,038	3.70
	12 DAP Endosperm (MB)	100	39,971,664	4.00
	10 DAP Endosperm (BM)	100	87,491,772	8.75
	10 DAP Endosperm (MB)	100	106,760,366	10.68

Sequencing Type	Sample 12 DAP	Run type	Read length (bp)	Yields (Gb)	Coverage
MethylC-seq	Endosperm (BB)	Single end Paired end	100	60.04	12
	Endosperm (BM)	Single end Paired end	100	112.01	25
	Endosperm (MB)	Paired end	100	153.02	34
	Embryo (B73)	Single end Paired end	100	47.65	8
	Shoot (B73)	Single end Paired end	100	56.61	8

Sequencing Type	Sample 12 DAP	Read length (bp)	No. of Reads	Yields (Gb)
ChIP-seq H3K27me3	BM12DAPpre-1	36	181,528,368	6.54
	BM12DAPkang-1	36	156,071,401	5.62
	MB12DAPpre-1	36	242,898,214	8.74
	MB12DAPkang-1	36	168,535,941	6.07

Table S2. List of imprinted non-coding RNAs identified in this study.

Candidate non-coding RNA	Genomic Locus	Imprinting Status of NC	Gene ID	Imprinting Status of Genes
chr3:23,435,556-23,435,814	intronic	PNC	GRMZM2G121683	PEG
chr3:202,365,040-202,365,295	intronic	PNC	GRMZM2G121683	PEG
chr5:161,398,888-161,399,250	intronic	PNC	GRMZM2G164314	PEG
chr5:202931813-202932195	intergenic	PNC	NA	NA
chr6:70,572,246-70,572,414	intronic	PNC	GRMZM2G014705	PEG
chr6:123,433,586-123,433,847	intronic	PNC	GRMZM2G127160	PEG
chr6:123,434,581-123,435,277	intronic	PNC	GRMZM2G127160	PEG
chr7:50,117,940-50,118,194	intronic	PNC	GRMZM2G061702	2:1 PEG
chr1:171,767,164-171,768,131	intronic	MNC	GRMZM2G072939	PEG
chr4:29614080-29614413	intergenic	MNC	NA	NA
chr5:864,078-864,444	intronic	MNC	GRMZM2G072894	2:1 PEG
chr7:10,791,732-10,792,078	intronic	MNC	AC208337.2_FG003	2:1 PEG
chr7:28354008-28354373	intergenic	MNC	NA	NA
chr9:119808372-119811022	intergenic	MNC	NA	NA
chr1:51,041,960-51,042,290	intergenic	MNC	NA	NA
chr1:171,769,764-171,770,232	intronic	MNC	GRMZM2G072939	PEG
chr1:226,179,078-226,179,369	intergenic	MNC	NA	NA
chr10:63482727-63482984	intergenic	MNC	NA	NA
chr10:66,310,013-66,311,970	intronic	MNC	GRMZM2G140612	MEG
chr10:148,301,712-148,302,096	intronic	MNC	GRMZM2G406553	PEG
chr2:134,841,066-134,841,626	intronic	MNC	GRMZM2G471115	2:1 PEG
chr3:63,370,905-63,371,395	intergenic	MNC	NA	NA
chr4:22,614,270-22,617,097	intronic	MNC	GRMZM2G127598	PEG
chr4:61400244-61401451	intergenic	MNC	NA	NA
chr5:3,088,382-3,089,537	intronic	MNC	GRMZM5G854045	PEG
chr5:18696087-18696869	intergenic	MNC	NA	NA
chr6:112004140-112,004,683	intronic	MNC	GRMZM2G073700	MEG
chr6:155,653,271-155,653,798	intronic	MNC	GRMZM2G140817	PEG
chr7:8,059,058-8,059,810	intronic	MNC	GRMZM2G074479	2:1 PEG
chr7:27659680-27660785	intronic	MNC	GRMZM5G897856/AC191534.3_FG003	PEG
chr7:133252473-133252923	intergenic	MNC	NA	NA
chr7:146,765,331-146,766,038	intronic	MNC	GRMZM2G107987	2:1 MEG
chr7:153,430,636-153,431,193	intronic	MNC	GRMZM2G480480	2:1 MEG
chr8:13,780,012-13,780,252	intronic	MNC (MNC-18)	GRMZM2G477503	PEG
chr9:114,818,715-114,819,137	intronic	MNC	GRMZM2G093880	NO
chr9:124,152,336-124,153,065	intronic	MNC	GRMZM2G075104	2:1 PEG

Table S3. List of high quality imprinted transcripts. They exhibited imprinted expression in 12 DAP, 10 DAP and 14 DAP endosperm of reciprocal crosses of B73 and Mo17.

Gene ID	Gene ID	Gene ID
GRMZM2G474194	GRMZM2G033413	GRMZM2G138511
GRMZM2G450071	GRMZM2G115755	GRMZM2G108716
GRMZM2G394203	GRMZM2G014119	GRMZM2G138245
GRMZM2G003909	GRMZM2G009014	GRMZM2G097207
GRMZM2G009465	GRMZM2G040954	GRMZM2G028366
GRMZM5G858417	GRMZM2G149903	GRMZM2G164314
GRMZM2G004511	GRMZM2G152526	GRMZM2G136465
GRMZM2G140612	GRMZM2G072939	GRMZM2G012964
GRMZM2G150680	GRMZM2G479318	GRMZM2G002100
GRMZM2G116626	GRMZM2G146819	GRMZM2G161680
GRMZM2G168651	GRMZM2G128663	GRMZM2G092895
GRMZM2G045809	GRMZM2G068117	GRMZM2G341027
GRMZM2G158884	GRMZM2G138382	GRMZM2G127160
GRMZM2G410916	GRMZM2G048850	GRMZM2G440949
GRMZM2G062650	GRMZM2G324131	GRMZM2G368448
GRMZM2G170099	GRMZM2G181251	GRMZM2G106222
GRMZM2G116646	GRMZM2G091819	GRMZM2G472052
GRMZM2G118205	GRMZM2G103909	AC191534.3_FG003
GRMZM2G374088	GRMZM2G339820	GRMZM2G106141
GRMZM2G129083	GRMZM5G845175	GRMZM2G000404
GRMZM2G130580	GRMZM2G164663	GRMZM2G006732
GRMZM2G370991	GRMZM2G171383	GRMZM2G447406
GRMZM2G163406	GRMZM2G006428	GRMZM2G085602
GRMZM5G854292	GRMZM2G406553	GRMZM2G339435
GRMZM2G157820	GRMZM2G145968	GRMZM2G047104
GRMZM2G073700	GRMZM2G045185	GRMZM2G042870
AC208337.2_FG003	GRMZM2G026301	GRMZM2G104866
GRMZM2G401308	GRMZM2G025095	GRMZM2G143213
GRMZM2G170044	GRMZM2G121683	GRMZM2G127739
GRMZM2G124708	GRMZM2G151653	GRMZM2G023652
GRMZM2G097059	GRMZM2G028037	GRMZM2G025703
GRMZM2G450647	GRMZM2G011608	GRMZM2G093947
GRMZM2G044440	GRMZM2G020302	GRMZM2G132184
GRMZM2G150134	GRMZM2G136067	GRMZM2G108285
GRMZM2G147226	GRMZM2G093316	GRMZM5G830365
GRMZM2G169695	GRMZM2G018837	

Table S4. The number of imprinted genes associated with pDMRs.

Gene Type	CG_ or CHG_pDMR	CG_ and CHG_pDMR	CG_pDMR only	CHG_pDMR only
PEG (68)	41 (60.3%)	6 (8.8%)	34 (50.0%)	1 (1.5%)
MEG (39)	21 (53.8%)	14 (35.9%)	6 (15.4%)	1 (2.7%)
Non-imp (3937)	633 (16.1%)	110 (2.8%)	478 (12.1%)	45 (1.1%)

Non-imp indicates non-imprinted genes, as the control for imprinted genes.

Table S5. List of imprinted genes that are associated with pDMRs.

Gene ID	Type	DMR_position in Chr			DMR_position in Gene	Location in gene	pDMR type
AC209208.3_FG001	PEG	chr5	193313246	193313521	4795	body	CG
AC209208.3_FG001	PEG	chr5	193318361	193318611	-320	upstream	CG
AC226373.2_FG010	PEG	chr6	156417736	156417886	1645	body	CG
GRMZM2G009014	PEG	chr1	8513301	8513601	-1228	upstream	CG
GRMZM2G009014	PEG	chr1	8515871	8516296	1467	body	CG
GRMZM2G009808	PEG	chr9	151768871	151769120	3130	body	CG
GRMZM2G010422	PEG	chr8	14094721	14095521	1651	body	CG
GRMZM2G011608	PEG	chr3	230658811	230658886	567	body	CG
GRMZM2G012964	PEG	chr6	39078501	39078880	1609	body	CG
GRMZM2G018837	PEG	chr4	235267911	235268036	992	body	CG
GRMZM2G020302	PEG	chr4	34925541	34925866	4741	body	CG
GRMZM2G020302	PEG	chr4	34927086	34927461	6336	body	CG
GRMZM2G020302	PEG	chr4	34926426	34926726	5601	body	CHG
GRMZM2G020302	PEG	chr4	34927381	34927706	6581	body	CHG
GRMZM2G020302	PEG	chr4	34927961	34928376	7251	body	CHG
GRMZM2G022359	PEG	chr10	73128751	73129601	1620	body	CG
GRMZM2G023652	PEG	chr2	226202876	226203076	1352	body	CG
GRMZM2G026301	PEG	chr2	158612131	158612380	2330	body	CG
GRMZM2G026301	PEG	chr2	158613301	158613851	1160	body	CG
GRMZM2G031893	PEG	chr1	224256311	224256511	3393	body	CG
GRMZM2G031893	PEG	chr1	224256846	224256946	3828	body	CG
GRMZM2G040954	PEG	chr1	63351621	63352696	-591	upstream	CG
GRMZM2G040954	PEG	chr1	63352276	63352776	-511	upstream	CHG
GRMZM2G041050	PEG	chr1	162584001	162584251	-1387	upstream	CG
GRMZM2G041050	PEG	chr1	162590286	162590386	4748	body	CG
GRMZM2G041312	PEG	chr2	62100586	62101080	1926	body	CG
GRMZM2G041312	PEG	chr2	62103001	62103376	4222	body	CG
GRMZM2G042870	PEG	chr9	91043401	91043726	2334	body	CG
GRMZM2G044531	PEG	chr8	89089051	89089426	4532	body	CG
GRMZM2G044531	PEG	chr8	89091611	89091920	1972	body	CG
GRMZM2G044531	PEG	chr8	89094896	89095271	-1313	upstream	CG
GRMZM2G044531	PEG	chr8	89094921	89095140	-1338	upstream	CHG
GRMZM2G045503	PEG	chr1	196639161	196639680	1251	body	CG
GRMZM2G047104	PEG	chr9	48744541	48744916	6117	body	CG
GRMZM2G049322	PEG	chr9	138888761	138889036	4348	body	CG
GRMZM2G053500	PEG	chr5	60030426	60030501	5057	body	CG
GRMZM2G053500	PEG	chr5	60033081	60033306	2402	body	CG
GRMZM2G053500	PEG	chr5	60034301	60034551	1182	body	CG

GRMZM2G053500	PEG	chr5	60036606	60036806	-1123	upstream	CG
GRMZM2G069886	PEG	chr3	114445701	114445976	-939	upstream	CG
GRMZM2G069886	PEG	chr3	114445616	114445766	-854	upstream	CHG
GRMZM2G070343	PEG	chr4	147221086	147221261	1398	body	CG
GRMZM2G072939	PEG	chr1	171766546	171766821	26211	body	CG
GRMZM2G072939	PEG	chr1	171769066	171769716	29106	body	CG
GRMZM2G072939	PEG	chr1	171772231	171772306	31696	body	CG
GRMZM2G072939	PEG	chr1	171778136	171778486	37876	body	CG
GRMZM2G072939	PEG	chr1	171778276	171778526	37916	body	CHG
GRMZM2G080519	PEG	chr4	200827226	200827501	1506	body	CG
GRMZM2G082809	PEG	chr2	232991181	232991620	1805	body	CG
GRMZM2G085602	PEG	chr8	172346221	172346296	774	body	CG
GRMZM2G085602	PEG	chr8	172346691	172346891	1369	body	CG
GRMZM2G085602	PEG	chr8	172348141	172348366	2844	body	CG
GRMZM2G087482	PEG	chr5	7453861	7453961	5562	body	CG
GRMZM2G087482	PEG	chr5	7457946	7458046	1477	body	CG
GRMZM2G087482	PEG	chr5	7458841	7458941	582	body	CG
GRMZM2G092101	PEG	chr4	6530746	6530896	-580	upstream	CG
GRMZM2G092101	PEG	chr4	6532271	6532546	1070	body	CG
GRMZM2G092895	PEG	chr6	99882861	99883240	-1257	upstream	CHG
GRMZM2G093316	PEG	chr4	153637356	153637481	3772	body	CG
GRMZM2G093316	PEG	chr4	153639986	153640186	1142	body	CG
GRMZM2G093316	PEG	chr4	153641841	153642041	-713	upstream	CG
GRMZM2G093947	PEG	chr7	86198981	86199031	2913	body	CG
GRMZM2G093947	PEG	chr7	86206106	86206281	10163	downstream	CHG
GRMZM2G097207	PEG	chr5	77920481	77920956	3975	body	CG
GRMZM2G102745	PEG	chr8	93797741	93797960	-2355	body	CG
GRMZM2G102745	PEG	chr8	93799766	93800091	-224	body	CG
GRMZM2G103909	PEG	chr10	22123911	22124500	8577	downstream	CG
GRMZM2G103909	PEG	chr10	22129381	22129760	3107	body	CG
GRMZM2G103909	PEG	chr10	22131606	22131706	882	body	CG
GRMZM2G103909	PEG	chr10	22123851	22124076	8637	downstream	CHG
GRMZM2G104294	PEG	chr10	146055486	146055736	1097	body	CG
GRMZM2G106141	PEG	chr7	28764031	28764620	1498	body	CG
GRMZM2G106222	PEG	chr7	6297996	6298540	1320	body	CG
GRMZM2G107867	PEG	chr1	44368861	44369280	1915	body	CG
GRMZM2G107867	PEG	chr1	44374116	44374191	6826	downstream	CG
GRMZM2G107867	PEG	chr1	44369051	44369151	1786	body	CHG
GRMZM2G107867	PEG	chr1	44374161	44374511	7146	downstream	CHG
GRMZM2G108716	PEG	chr5	2793641	2794416	2183	body	CG
GRMZM2G115518	PEG	chr5	60802641	60802741	987	body	CG
GRMZM2G117153	PEG	chr9	140590861	140591280	1738	body	CG
GRMZM2G117153	PEG	chr9	140594026	140594360	-1427	upstream	CG
GRMZM2G117153	PEG	chr9	140594321	140594621	-1722	upstream	CHG

GRMZM2G121570	PEG	chr1	252319686	252319786	-337	upstream	CG
GRMZM2G121570	PEG	chr1	252318571	252318646	-1477	upstream	CHG
GRMZM2G121683	PEG	chr3	23432606	23432931	2106	body	CG
GRMZM2G127598	PEG	chr4	22615716	22615991	2263	body	CG
GRMZM2G127598	PEG	chr4	22616631	22616856	3128	body	CG
GRMZM2G127598	PEG	chr4	22621291	22621816	8088	body	CG
GRMZM2G127598	PEG	chr4	22616536	22616861	3133	body	CHG
GRMZM2G127598	PEG	chr4	22621406	22621660	7932	body	CHG
GRMZM2G127739	PEG	chr1	165412706	165412906	-1440	upstream	CG
GRMZM2G128663	PEG	chr1	291927806	291928080	2012	body	CG
GRMZM2G128663	PEG	chr1	291928801	291929026	1017	body	CG
GRMZM2G131165	PEG	chr1	211438816	211439100	1273	body	CG
GRMZM2G132184	PEG	chr7	97337721	97337946	1595	body	CG
GRMZM2G136067	PEG	chr4	65960236	65960361	2451	body	CG
GRMZM2G136465	PEG	chr5	202419161	202419560	1607	body	CG
GRMZM2G137479	PEG	chr6	102200371	102200896	3244	body	CG
GRMZM2G137479	PEG	chr6	102196171	102196546	-1106	upstream	CHG
GRMZM2G138245	PEG	chr5	22800181	22800456	-357	upstream	CG
GRMZM2G138511	PEG	chr5	1836906	1837140	1745	body	CG
GRMZM2G138511	PEG	chr5	1840256	1840380	-1605	upstream	CG
GRMZM2G141273	PEG	chr1	43751586	43752061	1679	body	CG
GRMZM2G143213	PEG	chr9	154092001	154092506	1428	body	CG
GRMZM2G145968	PEG	chr2	17356551	17356826	-552	upstream	CG
GRMZM2G145968	PEG	chr2	17356541	17356766	-542	upstream	CHG
GRMZM2G146819	PEG	chr1	246658076	246658251	9643	body	CG
GRMZM2G146819	PEG	chr1	246660161	246660411	7558	body	CG
GRMZM2G146819	PEG	chr1	246666001	246666220	1718	body	CG
GRMZM2G152526	PEG	chr1	143623681	143624156	1861	body	CG
GRMZM2G158595	PEG	chr9	44482986	44483111	3786	body	CG
GRMZM2G161680	PEG	chr6	93499521	93499720	2485	body	CG
GRMZM2G161680	PEG	chr6	93500826	93500926	1180	body	CG
GRMZM2G167999	PEG	chr10	8705286	8705361	776	body	CG
GRMZM2G171383	PEG	chr10	123292601	123293101	4345	body	CG
GRMZM2G171383	PEG	chr10	123295401	123295651	1545	body	CG
GRMZM2G181251	PEG	chr10	16203921	16204171	-1228	upstream	CG
GRMZM2G302160	PEG	chr4	37012596	37012771	3611	body	CG
GRMZM2G302160	PEG	chr4	37015421	37015746	786	body	CG
GRMZM2G339820	PEG	chr10	89498741	89499066	-144	body	CG
GRMZM2G365731	PEG	chr1	236150361	236150461	36102	body	CG
GRMZM2G365731	PEG	chr1	236151501	236151826	34962	body	CG
GRMZM2G365731	PEG	chr1	236182221	236182420	4242	body	CG
GRMZM2G365731	PEG	chr1	236151441	236151660	35022	body	CHG
GRMZM2G365888	PEG	chr10	27267341	27267466	6521	body	CG
GRMZM2G365888	PEG	chr10	27269841	27269916	4021	body	CG

GRMZM2G365888	PEG	chr10	27272166	27272616	1696	body	CG
GRMZM2G368448	PEG	chr6	157755751	157756001	3597	body	CG
GRMZM2G368448	PEG	chr6	157757546	157757796	1802	body	CG
GRMZM2G368448	PEG	chr6	157758341	157758816	1007	body	CG
GRMZM2G368448	PEG	chr6	157759886	157759986	-538	upstream	CG
GRMZM2G393471	PEG	chr9	154392576	154393151	1387	body	CG
GRMZM2G406553	PEG	chr10	148301721	148302021	3075	body	CG
GRMZM2G419806	PEG	chr10	9223596	9223721	1783	body	CG
GRMZM2G447406	PEG	chr8	160602311	160602540	-1994	upstream	CG
GRMZM2G447406	PEG	chr8	160603401	160603726	-808	upstream	CG
GRMZM2G447406	PEG	chr8	160609361	160609511	4977	body	CG
GRMZM2G472052	PEG	chr7	21141636	21141900	1287	body	CG
GRMZM2G477503	PEG	chr8	13779956	13780331	1860	body	CG
GRMZM2G477503	PEG	chr8	13782941	13783160	4689	body	CG
GRMZM5G845175	PEG	chr10	112400721	112401196	1399	body	CG
GRMZM5G854045	PEG	chr5	3087841	3088841	1997	body	CG
GRMZM5G868647	PEG	chr10	23391096	23391396	1006	body	CG
AC208337.2_FG003	MEG	chr7	10791781	10791931	616	body	CG
AC208337.2_FG003	MEG	chr7	10784611	10784686	7786	downstream	CHG
GRMZM2G007736	MEG	chr4	61407111	61407711	-3520	upstream	CG
GRMZM2G007736	MEG	chr4	61407281	61407606	-3625	upstream	CHG
GRMZM2G008913	MEG	chr4	29933866	29934506	723	body	CHG
GRMZM2G009465	MEG	chr1	120193651	120193776	858	body	CHG
GRMZM2G014119	MEG	chr6	95840826	95840926	2619	downstream	CG
GRMZM2G014119	MEG	chr6	95842746	95843521	699	body	CG
GRMZM2G014119	MEG	chr6	95842746	95843521	699	upstream	CG
GRMZM2G014119	MEG	chr6	95841101	95842066	2344	downstream	CHG
GRMZM2G014119	MEG	chr6	95841101	95842066	2344	body	CHG
GRMZM2G014119	MEG	chr6	95843066	95843491	379	body	CHG
GRMZM2G014119	MEG	chr6	95843066	95843491	379	upstream	CHG
GRMZM2G022987	MEG	chr4	231338341	231338491	2773	body	CG
GRMZM2G044440	MEG	chr8	104901921	104902171	-758	upstream	CG
GRMZM2G044440	MEG	chr8	104902921	104903446	517	upstream	CG
GRMZM2G044440	MEG	chr8	104902921	104903446	517	body	CG
GRMZM2G044440	MEG	chr8	104905256	104905606	2677	downstream	CG
GRMZM2G044440	MEG	chr8	104902981	104903420	491	body	CHG
GRMZM2G044440	MEG	chr8	104904021	104904680	1751	body	CHG
GRMZM2G044440	MEG	chr8	104905496	104905580	2651	downstream	CHG
GRMZM2G049373	MEG	chr3	173009151	173009476	-1534	upstream	CG
GRMZM2G049373	MEG	chr3	173009231	173009406	-1614	upstream	CHG
GRMZM2G063498	MEG	chr1	64541226	64541580	809	body	CG
GRMZM2G063498	MEG	chr1	64541256	64541581	810	body	CHG
GRMZM2G073700	MEG	chr6	112008261	112008860	-434	upstream	CG
GRMZM2G073700	MEG	chr6	112009681	112009906	-1854	upstream	CG

GRMZM2G073700	MEG	chr6	112008296	112008720	-469	upstream	CHG
GRMZM2G084296	MEG	chr4	234210181	234210331	1457	downstream	CG
GRMZM2G084296	MEG	chr4	234209746	234210246	1892	downstream	CHG
GRMZM2G087150	MEG	chr3	214007861	214008336	5018	downstream	CG
GRMZM2G087150	MEG	chr3	214007626	214007976	4658	downstream	CHG
GRMZM2G087150	MEG	chr3	214008191	214008366	5048	downstream	CHG
GRMZM2G093119	MEG	chr3	167369421	167369680	6761	body	CG
GRMZM2G093119	MEG	chr3	167370811	167370911	7992	body	CG
GRMZM2G094867	MEG	chr7	18229601	18229776	1215	body	CG
GRMZM2G100246	MEG	chr5	15728191	15728400	2519	body	CHG
GRMZM2G112925	MEG	chr1	40510781	40510981	-658	upstream	CG
GRMZM2G112925	MEG	chr1	40510881	40511006	-633	upstream	CHG
GRMZM2G115721	MEG	chr9	55509386	55509486	3923	body	CHG
GRMZM2G115755	MEG	chr5	181835406	181835631	3957	downstream	CG
GRMZM2G116626	MEG	chr10	91718261	91718561	-3126	body	CG
GRMZM2G118205	MEG	chr4	35762276	35762651	910	body	CG
GRMZM2G118205	MEG	chr4	35762346	35762621	840	body	CHG
GRMZM2G127598	MEG	chr4	22615716	22615991	2263	body	CG
GRMZM2G127598	MEG	chr4	22616631	22616856	3128	body	CG
GRMZM2G127598	MEG	chr4	22621291	22621816	8088	body	CG
GRMZM2G127598	MEG	chr4	22616536	22616861	3133	body	CHG
GRMZM2G127598	MEG	chr4	22621406	22621660	7932	body	CHG
GRMZM2G128663	MEG	chr1	291927806	291928080	2012	body	CG
GRMZM2G128663	MEG	chr1	291928801	291929026	1017	body	CG
GRMZM2G129781	MEG	chr10	115842061	115842440	-1141	upstream	CG
GRMZM2G129781	MEG	chr10	115842116	115842731	-1196	upstream	CHG
GRMZM2G130580	MEG	chr5	31696541	31696916	386	body	CG
GRMZM2G130580	MEG	chr5	31697941	31698066	-1014	upstream	CG
GRMZM2G130580	MEG	chr5	31696536	31696861	391	body	CHG
GRMZM2G140612	MEG	chr10	66308101	66308320	1459	body	CG
GRMZM2G140612	MEG	chr10	66310706	66311156	4295	body	CG
GRMZM2G140612	MEG	chr10	66311496	66312720	5859	body	CG
GRMZM2G140612	MEG	chr10	66313821	66314021	7160	body	CG
GRMZM2G140612	MEG	chr10	66317671	66317940	11079	downstream	CG
GRMZM2G140612	MEG	chr10	66305001	66305301	-1560	upstream	CHG
GRMZM2G140612	MEG	chr10	66310301	66310580	3719	body	CHG
GRMZM2G140612	MEG	chr10	66312351	66312476	5615	body	CHG
GRMZM2G141382	MEG	chr3	183561626	183561751	-3511	upstream	CG
GRMZM2G141382	MEG	chr3	183561671	183561720	-3556	upstream	CHG
GRMZM2G147226	MEG	chr8	160597896	160599576	4401	body	CG
GRMZM2G147226	MEG	chr8	160597896	160599576	4401	downstream	CG
GRMZM2G147226	MEG	chr8	160599986	160601426	6251	downstream	CG
GRMZM2G147226	MEG	chr8	160598426	160599176	4001	body	CHG
GRMZM2G147226	MEG	chr8	160600001	160600200	5025	downstream	CHG

GRMZM2G147226	MEG	chr8	160600476	160600760	5585	downstream	CHG
GRMZM2G147226	MEG	chr8	160601041	160601466	6291	downstream	CHG
GRMZM2G150134	MEG	chr8	110689401	110689526	2731	downstream	CG
GRMZM2G150680	MEG	chr10	74609711	74609936	955	body	CG
GRMZM2G150680	MEG	chr10	74610216	74610391	450	body	CHG
GRMZM2G152764	MEG	chr5	18695886	18697996	-739	upstream	CG
GRMZM2G152764	MEG	chr5	18697226	18697726	-1009	upstream	CHG
GRMZM2G158884	MEG	chr2	190933771	190934196	-3648	upstream	CG
GRMZM2G158884	MEG	chr2	190934031	190934206	-3638	upstream	CHG
GRMZM2G160687	MEG	chr3	137226701	137226801	7244	downstream	CHG
GRMZM2G169695	MEG	chr8	170002141	170002366	150	body	CG
GRMZM2G169695	MEG	chr8	170002141	170002366	150	upstream	CG
GRMZM2G170099	MEG	chr3	50603686	50603986	1315	body	CG
GRMZM2G170099	MEG	chr3	50603761	50603986	1315	body	CHG
GRMZM2G174572	MEG	chr5	130947806	130947856	-729	upstream	CG
GRMZM2G370991	MEG	chr5	186864156	186864306	430	body	CG
GRMZM2G370991	MEG	chr5	186864921	186865246	1370	body	CG
GRMZM2G370991	MEG	chr5	186864916	186865116	1240	body	CHG
GRMZM2G370991	MEG	chr5	186868481	186868706	4830	body	CHG
GRMZM2G374088	MEG	chr4	239432561	239432800	2886	body	CG
GRMZM2G374088	MEG	chr4	239433536	239433861	1911	body	CG
GRMZM2G374088	MEG	chr4	239434701	239435020	746	body	CG
GRMZM2G374088	MEG	chr4	239435286	239435511	161	body	CG
GRMZM2G401308	MEG	chr7	11444901	11445300	-2369	body	CG
GRMZM2G401308	MEG	chr7	11444971	11445171	-2439	body	CHG
GRMZM2G424205	MEG	chr7	174340126	174340251	1853	body	CG
GRMZM2G424205	MEG	chr7	174343181	174343231	-1202	upstream	CHG
GRMZM2G450071	MEG	chr1	9046581	9046860	860	body	CG
GRMZM2G476175	MEG	chr3	135129206	135129381	-1679	upstream	CHG
GRMZM5G832908	MEG	chr1	158475016	158475191	1268	body	CG
GRMZM5G858417	MEG	chr1	263004986	263005286	-1977	upstream	CG
GRMZM5G858417	MEG	chr1	263004996	263005271	-1987	upstream	CHG

Table S6. Maternal specific H3K27me3 peaks those are overlapped with PEGs.

Chr	Gene.ID	peak_position		snp	reads				maternal allele%		chisq.test	
		start	end		BM_B	BM_M	MB_B	MB_M	BM	MB	BM	MB
chr9	GRMZM2G104866	97036663	97037650	7	79	1	10	63	98.75	86.30	1.15E-09	3.73E-04
chr1	GRMZM2G152526	143623605	143624602	7	95	4	14	109	95.96	88.62	6.30E-10	2.41E-07
chr1	GRMZM2G152526	143625422	143626189	2	31	4	3	47	88.57	94.00	5.98E-03	4.13E-05
chr10	GRMZM2G048850	9468644	9473127	16	227	10	40	358	95.78	89.95	2.20E-16	2.20E-16
chr4	GRMZM2G020302	34923093	34931916	30	452	41	39	734	91.68	94.95	2.20E-16	2.20E-16
chr1	GRMZM2G138382	295000549	295001335	4	24	1	3	111	96.00	97.37	1.86E-03	3.56E-12
chr1	GRMZM2G138382	295001878	295003340	16	187	11	16	252	94.44	94.03	2.20E-16	2.20E-16
chr9	GRMZM2G047104	48739874	48742308	42	705	53	100	1006	93.01	90.96	2.20E-16	2.20E-16
chr9	GRMZM2G047104	48742686	48742949	7	130	9	11	191	93.53	94.55	1.85E-11	2.20E-16
chr9	GRMZM2G047104	48743118	48743972	19	238	15	30	342	94.07	91.94	2.20E-16	2.20E-16
chr9	GRMZM2G047104	48744272	48744682	10	292	18	13	460	94.19	97.25	2.20E-16	2.20E-16
chr9	GRMZM2G047104	48744823	48747599	42	549	56	99	1354	90.74	93.19	2.20E-16	2.20E-16
chr9	GRMZM2G047104	48742372	48742537	7	98	3	9	140	97.03	93.96	9.60E-11	1.58E-12
chr1	GRMZM2G040954	63353715	63355540	25	333	17	14	584	95.14	97.66	2.20E-16	2.20E-16
chr1	GRMZM2G040954	63355617	63356122	10	101	0	20	250	100.00	92.59	1.19E-12	2.20E-16
chr1	GRMZM2G040954	63357376	63357518	5	41	3	2	133	93.18	98.52	1.91E-04	4.14E-15
chr1	GRMZM2G040954	63358100	63359639	16	122	17	15	413	87.77	96.50	1.31E-07	2.20E-16
chr1	GRMZM2G040954	63356594	63357303	11	79	2	6	289	97.53	97.97	3.80E-09	2.20E-16
chr4	GRMZM2G093316	153636806	153640774	27	251	14	28	599	94.72	95.53	2.20E-16	2.20E-16

chr4	GRMZM2G093316	153631597	153636686	28	312	29	33	571	91.50	94.54	2.20E-16	2.20E-16
chr7	GRMZM2G006732	173038862	173041755	16	207	28	40	468	88.09	92.13	3.28E-12	2.20E-16
chr7	GRMZM2G006732	173041925	173042952	2	14	0	0	26	100.00	100.00	8.15E-03	3.12E-04
chr8	GRMZM2G085602	172346261	172346901	3	27	0	2	24	100.00	92.31	2.39E-04	5.55E-03
chr6	GRMZM2G127160	123431983	123436193	21	320	7	21	563	97.86	96.40	2.20E-16	2.20E-16
chr7	AC191534.3_FG003	27668959	27669767	3	65	4	5	33	94.20	86.84	1.22E-06	8.33E-03
chr7	GRMZM2G000404	127724493	127725895	2	32	4	3	81	88.89	96.43	4.68E-03	7.19E-09
chr7	GRMZM2G000404	127726030	127726433	2	26	4	3	39	86.67	92.86	2.01E-02	3.18E-04
chr7	GRMZM2G472052	21141043	21141116	2	13	0	1	16	100.00	94.12	1.08E-02	1.64E-02
chr7	GRMZM2G472052	21141562	21142741	13	131	2	16	182	98.50	91.92	6.87E-15	4.78E-14
chr7	GRMZM2G132184	97337042	97341831	30	440	17	35	1022	96.28	96.69	2.20E-16	2.20E-16
chr7	GRMZM2G106222	6297470	6299839	31	268	20	26	677	93.06	96.30	2.20E-16	2.20E-16
chr7	GRMZM2G106222	6300103	6300846	4	23	1	1	83	95.83	98.81	2.44E-03	4.12E-10
chr7	GRMZM2G106222	6301154	6301677	3	27	3	7	115	90.00	94.26	6.71E-03	1.01E-10
chr7	GRMZM2G106222	6301891	6302226	5	39	1	4	81	97.50	95.29	3.52E-05	2.16E-08
chr10	GRMZM2G324131	9532592	9533299	5	68	2	9	100	97.14	91.74	6.34E-08	2.80E-08
chr7	GRMZM2G093947	86197817	86197954	4	47	6	2	91	88.68	97.85	6.75E-04	1.78E-10
chr7	GRMZM2G093947	86198023	86198415	7	84	10	13	185	89.36	93.43	3.05E-06	1.35E-15
chr7	GRMZM2G093947	86198520	86199219	20	166	16	34	389	91.21	91.96	2.16E-12	2.20E-16
chr7	GRMZM2G093947	86199298	86199798	9	122	16	17	204	88.41	92.31	6.05E-08	6.16E-16
chr7	GRMZM2G093947	86200797	86204834	68	976	78	148	1679	92.60	91.90	2.20E-16	2.20E-16
chr7	GRMZM2G093947	86195616	86197549	11	140	18	42	256	88.61	85.91	4.90E-09	1.85E-12
chr7	GRMZM2G106141	28763412	28765379	18	201	12	12	385	94.37	96.98	2.20E-16	2.20E-16
chr7	GRMZM2G106141	28766243	28767107	14	130	9	8	312	93.53	97.50	1.85E-11	2.20E-16
chr10	GRMZM2G164663	114491763	114494040	9	86	6	9	133	93.48	93.66	4.89E-08	8.85E-12
chr10	GRMZM2G164663	114487884	114491689	9	82	4	4	165	95.35	97.63	1.68E-08	2.20E-16

chr10	GRMZM5G845175	112396042	112398421	12	134	1	9	348	99.26	97.48	9.49E-16	2.20E-16
chr10	GRMZM5G845175	112399903	112401921	18	147	12	26	282	92.45	91.56	5.29E-12	2.20E-16
chr10	GRMZM5G845175	112401975	112402196	2	25	0	1	23	100.00	95.83	4.07E-04	2.44E-03
chr1	GRMZM2G068117	293623636	293624425	7	102	7	15	217	93.58	93.53	2.52E-09	2.20E-16
chr1	GRMZM2G068117	293624690	293626525	17	203	17	20	503	92.27	96.18	7.83E-16	2.20E-16
chr1	GRMZM2G068117	293626732	293627687	7	88	5	19	198	94.62	91.24	1.07E-08	1.59E-14
chr6	GRMZM2G440949	155661628	155662211	6	67	3	9	69	95.71	88.46	2.53E-07	4.44E-05
chr6	GRMZM2G440949	155666157	155667685	9	105	8	15	129	92.92	89.58	3.22E-09	5.42E-09
chr6	GRMZM2G440949	155662324	155666099	60	766	36	93	1305	95.51	93.35	2.20E-16	2.20E-16
chr10	GRMZM2G103909	22125247	22126188	11	130	8	10	245	94.20	96.08	6.79E-12	2.20E-16
chr10	GRMZM2G103909	22126400	22128037	13	112	13	13	239	89.60	94.84	5.36E-08	2.20E-16
chr10	GRMZM2G103909	22128268	22129314	6	47	1	1	122	97.92	99.19	4.37E-06	2.00E-14
chr10	GRMZM2G103909	22130293	22131963	14	156	9	6	408	94.55	98.55	3.04E-14	2.20E-16
chr10	GRMZM2G103909	22132023	22132689	2	16	0	3	44	100.00	93.62	4.68E-03	8.88E-05
chr1	GRMZM2G127739	165407628	165408974	9	82	9	8	148	90.11	94.87	2.10E-06	7.84E-14
chr1	GRMZM2G127739	165409505	165410488	13	101	9	10	205	91.82	95.35	2.20E-08	2.20E-16
chr2	GRMZM2G026301	158609493	158609717	4	26	2	4	57	92.86	93.44	3.28E-03	9.15E-06
chr2	GRMZM2G026301	158610252	158611696	12	116	13	16	256	89.92	94.12	2.11E-08	2.20E-16
chr2	GRMZM2G026301	158611803	158614141	21	270	13	7	426	95.41	98.38	2.20E-16	2.20E-16
chr10	GRMZM2G339820	89495761	89500115	13	216	3	20	468	98.63	95.90	2.20E-16	2.20E-16
chr3	GRMZM2G028037	221434915	221439651	15	188	13	20	432	93.53	95.58	6.49E-16	2.20E-16
chr1	GRMZM2G149903	110080030	110083172	12	111	8	7	218	93.28	96.89	7.37E-10	2.20E-16
chr1	GRMZM2G149903	110085053	110086598	7	76	2	7	129	97.44	94.85	8.19E-09	3.11E-12
chr1	GRMZM2G149903	110083432	110084902	7	69	5	8	144	93.24	94.74	1.24E-06	2.12E-13
chr3	GRMZM2G121683	23432596	23434645	17	161	11	41	401	93.60	90.72	6.66E-14	2.20E-16
chr3	GRMZM2G121683	23434750	23436459	13	187	4	19	341	97.91	94.72	2.20E-16	2.20E-16

chr6	GRMZM2G002100	74598593	74599641	6	64	11	5	79	85.33	94.05	6.05E-04	1.02E-07
chr6	GRMZM2G002100	74601234	74603461	6	35	5	3	90	87.50	96.77	5.19E-03	7.31E-10
chr10	GRMZM2G006428	127341359	127344115	4	35	5	5	116	87.50	95.87	5.19E-03	9.50E-12
chr5	GRMZM2G028366	155030272	155031142	4	30	2	8	62	93.75	88.57	1.15E-03	1.01E-04
chr5	GRMZM2G028366	155031229	155031401	3	37	0	3	34	100.00	91.89	1.70E-05	1.13E-03
chr5	GRMZM2G028366	155032454	155033078	7	74	1	7	111	98.67	94.07	4.13E-09	2.72E-10
chr5	GRMZM2G028366	155033494	155034209	5	43	4	7	52	91.49	88.14	3.06E-04	4.68E-04
chr5	GRMZM2G028366	155035285	155036815	6	61	1	6	154	98.39	96.25	1.17E-07	2.05E-15
chr5	GRMZM2G028366	155037266	155038341	4	41	0	3	37	100.00	92.50	5.96E-06	5.28E-04

Table S7 RNA-seq data used for the analysis of expression profile of MEGs and PEGs.

Tissue Samples	Description	Reference
SRR189760	B73 pre-emergence cob	Davidson et al.,2011
SRR189761	B73 20DAP leaf	Davidson et al.,2011
SRR189762	B73 pre-pollination tassel	Davidson et al.,2011
SRR189763	B73 post-emergence cob	Davidson et al.,2011
SRR189769	B73 whole anthers	Davidson et al.,2011
SRR189770	B73 ovule	Davidson et al.,2011
SRR189771	B73 pollen	Davidson et al.,2011
SRR189772	B73 silk	Davidson et al.,2011
SRR393016	B73 post-pollination tassel	Davidson et al.,2011
SRR504466	B73 leaf rep1	Bolduc et al., 2012
SRR504467	B73 leaf rep2	Bolduc et al., 2012
SRR504471	B73 tassel rep1	Bolduc et al., 2012
SRR504472	B73 tassel rep2	Bolduc et al., 2012
SRR504473	B73 tassel rep3	Bolduc et al., 2012
SRR504476	B73 ear rep1	Bolduc et al., 2012
SRR504477	B73 ear rep2	Bolduc et al., 2012
SRR504480	B73 SAM rep1	Bolduc et al., 2012
SRR504481	B73 SAM rep2	Bolduc et al., 2012
SRX012380	B73 shoots	Wang et al., 2009
SRX012381	B73 roots	Wang et al., 2009
SRX014791	B73 SAM	Jia et al., 2009
SRX018901	B73 leaf base	Li et al., 2010
SRX018902	B73 leaf -1cm	Li et al., 2010
SRX018903	B73 leaf 4cm	Li et al., 2010
SRX018904	B73 leaf tip	Li et al., 2010
SRR536834	B73 ovaries	Kakumanu et al.,2012
SSR536838	B73 basal leaf meristem	Kakumanu et al.,2012

Table S8. Primers used in this study.

H3K27me3 peak ID	SNP position	Allelic enzyme	Primers sequence (5'→3')	Usage
chr9:143537747_143538106	-	-	GGTGACATCACATATGACCCCAC GACATTGTGCGGTCTTGCGTA	Quantitative real-time PCR
chr1:1828767_1829090	-	-	ACCTCGTCACCATCAACAACC GCAACGAACCTATATAATCCCCAG	Quantitative real-time PCR
chr9:138896522_138898046	-	-	AGCACCTGTGTGACTGTGTTCTGT GGACTGGTCATATTGTCTTGAGGTG	Quantitative real-time PCR
chr9:138886547_138888010	-	-	TTTAGTTGCCCCCAGAAAGTCA CCCTGCTGTTGAGCGTAGAGTG	Quantitative real-time PCR
chr9:138896522_138898046	570	AluI	ATAAGCATGTCAAACCAAGGAGAAT ATTTATGACGACTTGATATCCCGAA	RT- PCR
chr1:1828767_1829090	218	MseI	ACCTCGTCACCATCAACAACC GCAACGAACCTATATAATCCCCAG	RT- PCR