

Figure S1. The proportion of mCGs, mCHGs, and mCHHs in plants.

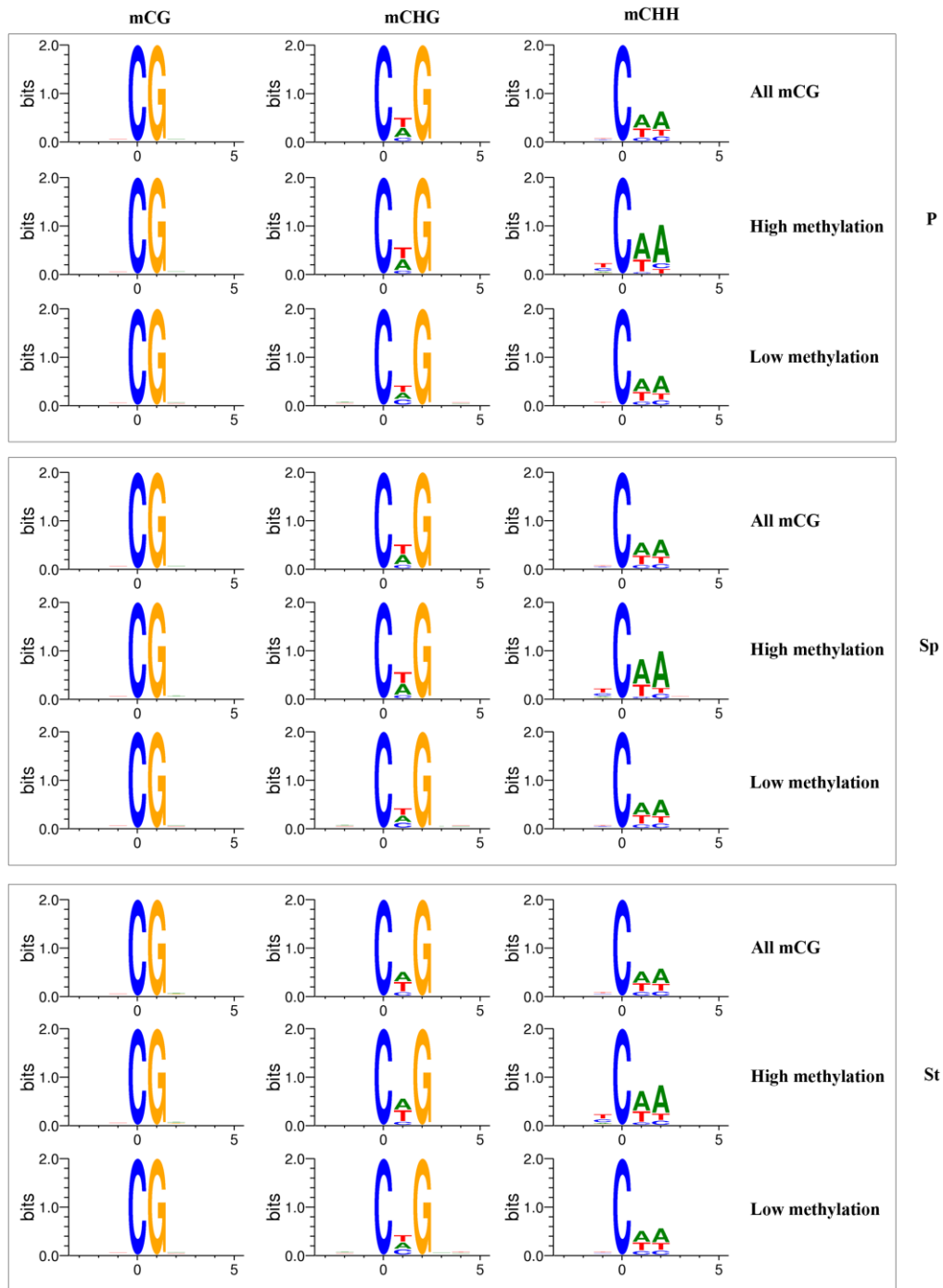


Figure S2. Sequence preferences for methylation in CG, CHG, and CHH contexts. The mC site methylation level was divided into three groups: All mC sites; High Methylation ($ML \geq 0.75$), Low Methylation ($ML < 0.75$). ML indicated methylation level.

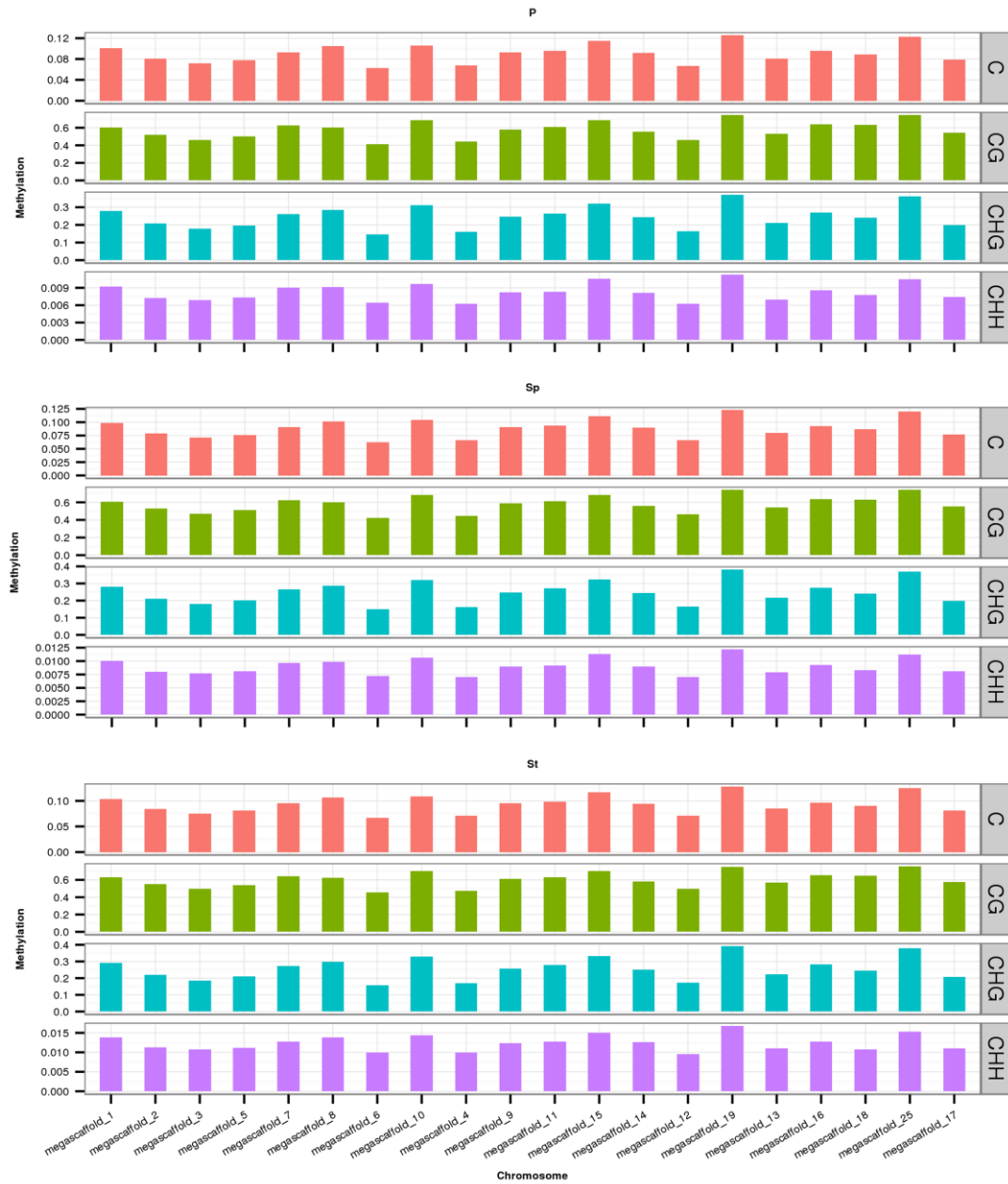


Figure S3. The distribution of methylated cytosine in all contexts in the main chromosome.

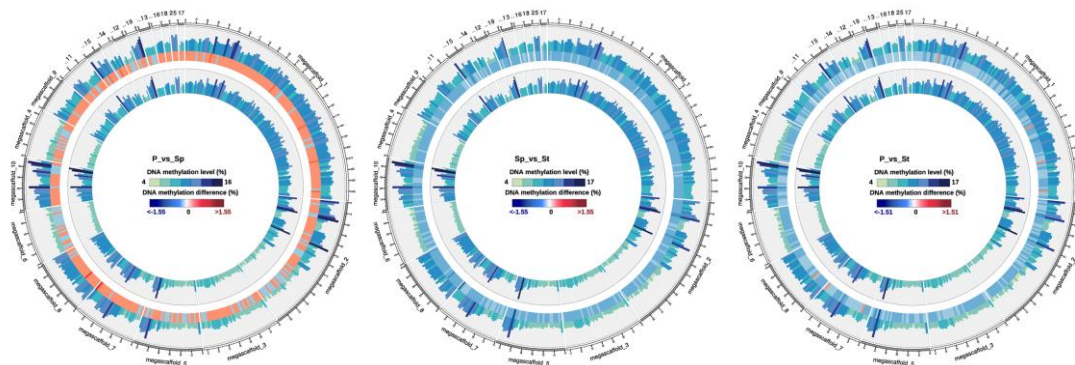


Figure S4. A circos plot of DNA methylation in P vs Sp, Sp vs St, and P vs St.

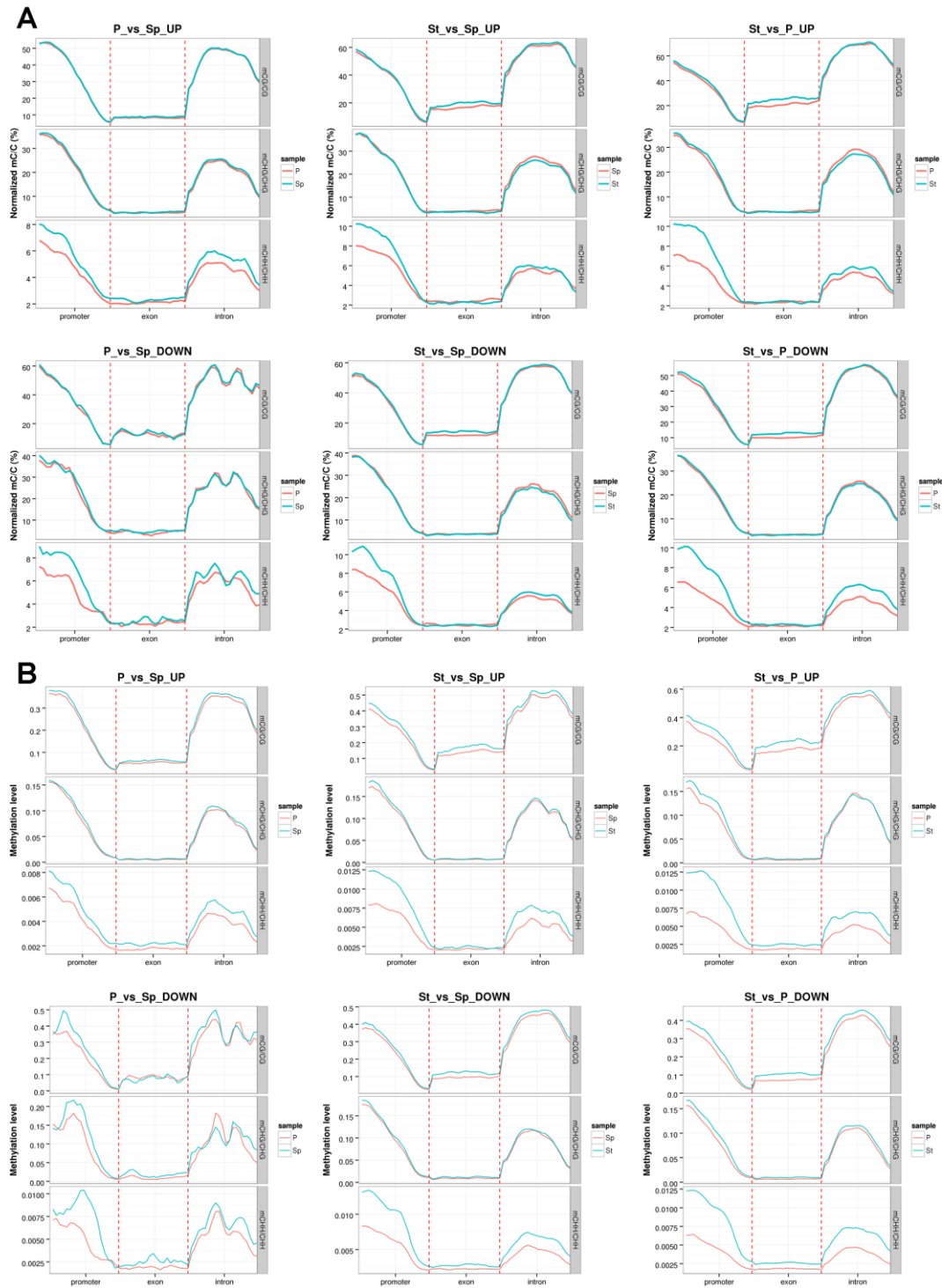


Figure S5. The DNA methylation patterns in gene regions in DEGs. (A) The DNA Methylation density of DEGs (P vs Sp, St vs Sp, and St vs P) throughout the gene regions in different floral organs. **(B)** The DNA Methylation level of DEGs (P vs Sp, St vs Sp, and St vs P) throughout the gene regions in different floral organs.

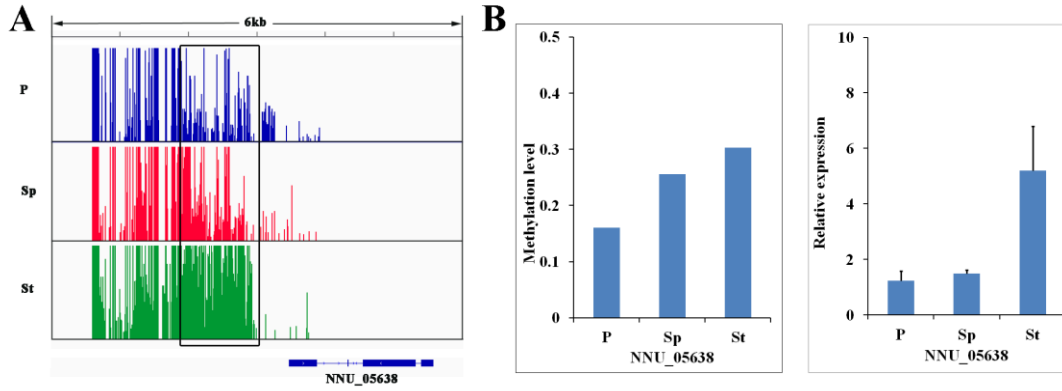


Figure S6. IGV software depicts the demethylation of NNU_05638 promoter region promoting stamen to petaloid (A) and the methylation difference and expression analysis of NNU_05638 in P, Sp, and St (B).

Table S1. Summary of sequencing and reads.

Sample name	Raw Reads	Raw Bases (G)	Clean Reads	Clean Bases (G)	Clean ratio (%)	Q20 (%)	GC Content (%)	BS Conversion Rate (%)	Mapped reads	Mapping rate (%)	Duplication rate (%)	Genome coverage mean	Cytosines coverage mean
P	122171421	36.65	116929861	32.55	88.81	96.1	22.23	99.835	88738071	75.89	8.89	21.26	12.7
Sp	119687017	35.91	115231027	32.24	89.78	96.34	21.54	99.809	86089100	74.71	9.00	20.68	12.3
St	117771103	35.33	113981900	31.84	90.12	96.45	21.37	99.778	86797216	76.15	9.33	20.74	11.9

Table S2. Summary of methylcytosines in each sequence context.

Sample	P		Sp		St		Mean
	proportion of mCs	reads	proportion of mCs	reads	proportion of mCs	reads	proportion of mCs
mCG	33.14%	15307291	31.66%	14635358	30.04%	13602715	31.61%
mCHG	35.83%	16554080	34.94%	16150150	32.42%	14681366	34.40%
mCHH	31.03%	14334879	33.39%	15434846	37.54%	16999686	33.99%

Table S3. List of hypomethylated DMR-associated genes in all organs.

Hypomethylated DMR-associated up-regulated genes in P vs Sp

Gene ID	Annotation
NNU_14779	uncharacterized protein LOC104603194 [Nelumbo nucifera]

Hypomethylated DMR-associated down-regulated genes in P vs Sp

Gene ID	Annotation
NNU_03683	PK1: Putative receptor protein kinase ZmPK1 (Zea mays)
NNU_25355	ARA12: Subtilisin-like protease (Arabidopsis thaliana)

Hypomethylated DMR-associated up-regulated genes in Sp vs St

Gene ID	Annotation
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NNU_05638 PUB33: U-box domain-containing protein 33 (Arabidopsis thaliana)

Hypomethylated DMR-associated up-regulated genes in P vs St

Gene ID	Annotation
NNU_00424	Protein of unknown function
NNU_00560	gluP: Rhomboid protease gluP (Bacillus subtilis)
NNU_01525	Protein of unknown function
NNU_01772	CYP71A1: Cytochrome P450 71A1 (Persea americana)
NNU_03180	V-type proton ATPase catalytic subunit A (Daucus carota)
NNU_03373	GSVIVT00027310001: UPF0497 membrane protein 16 (Vitis vinifera)
NNU_05638	PUB33: U-box domain-containing protein 33 (Arabidopsis thaliana)
NNU_09335	AGD5: Probable ADP-ribosylation factor GTPase-activating protein AGD5 (Arabidopsis thaliana)
NNU_11143	LAL5: MATE efflux family protein LAL5 (Arabidopsis thaliana)
NNU_14184	AGD11: Probable ADP-ribosylation factor GTPase-activating protein AGD11 (Arabidopsis thaliana)
NNU_14834	Putative clathrin assembly protein At1g25240 (Arabidopsis thaliana)
NNU_15184	Protein of unknown function
NNU_16725	ADH: Alcohol dehydrogenase (Fragaria ananassa)
NNU_19124	DREB1E: Dehydration-responsive element-binding protein 1E (Arabidopsis thaliana)
NNU_21147	ELI3: Probable mannitol dehydrogenase (Mesembryanthemum crystallinum)
NNU_22678	ZNF828: Zinc finger protein 828 (Homo sapiens)
NNU_23350	PXL2: Leucine-rich repeat receptor-like protein kinase PXL2 (Arabidopsis thaliana)
NNU_24014	SRPK1: Serine/threonine-protein kinase SRPK1 (Homo sapiens)

Hypomethylated DMR-associated down-regulated genes in P vs St

Gene ID	Annotation
NNU_08735	SEC22: 25.3 kDa vesicle transport protein (Arabidopsis thaliana)
NNU_20806	Protein of unknown function
NNU_19557	Probable peptide/nitrate transporter At1g72125
NNU_13621	Uncharacterized protein At4g06744 (Arabidopsis thaliana)
NNU_01487	4-coumarate--CoA ligase 2 (Glycine max)
NNU_08358	SCPL35: Serine carboxypeptidase-like 35 (Arabidopsis thaliana)
NNU_03683	PK1: Putative receptor protein kinase ZmPK1 (Zea mays)
NNU_07659	PSRP3: 30S ribosomal protein 3%2C chloroplastic (Spinacia oleracea)
NNU_00792	bysl: Bystin (Nematostella vectensis)
NNU_15841	GGR: Geranylgeranyl pyrophosphate synthase-related protein%2C chloroplastic (Arabidopsis thaliana)
NNU_08534	UBC4: Ubiquitin-conjugating enzyme E2 4 (Arabidopsis thaliana)

Table S4. The primers for qRT-PCR.

Gene name	Forward primer (5'-3')	Reverse primer (5'-3')
NUU_01774	GATGGTGCTGAGGGTGAGTG	ATCAACAGCCCACCTCGTAA
NUU_11434	TGATGTTGTGACGGTAGCCC	CGGTAAACCCTCCAGAAGAC
NUU_17480	CTATGGTCGCTTGTTCCTG	TCTGAGGCACTTGCCTAATAG
NUU_17715	GATTATCCCACCGCTCACTC	AAAGCCTCGCACCAGTCG
NUU_21025	ATGCTATGAGGATGGGACA	ATTCATTGCTGTTTGCCAC
NUU_24864	ATACGCCAGTGGTAGAACAAC	CAGCAAGGTCCAACCGAAG
NUU_05638	TGAAAGGATGGCTGGAGGG	AACGAAGAGCGTGATTAGGGA

Table S5. Three primers designed for bisulphate sequencing PCR on the promoter of NUU_05638.

Primer site (bp)	Forward primer (5'-3')	Reverse primer (5'-3')
-1648 to -1396	GGGATTAAATTTGGATTGAAGTTTA	AACCACCCACCTTTTTAAAAATAAA
-777 to -333	TTATTTTGGTTATTGGTGTAATGT	CTACTAAACCCATTAAATCCAATTT
-348 to -61	TTAATGGGTTTAGTAGTGGAGG	ATTCRATAACAAAATCTATAAACAAA