

Supplementary Table S2. The statistical information of DNA methylation change between mutants and WT.

Region	Gmdrm vs WT	Gmcmt vs WT	Ctype
euchromatin	19.00%	31.00%	CHG
heterochromatin	3.00%	29.00%	CHG
euchromatin	20.00%	62.00%	CHH
heterochromatin	2.00%	82.00%	CHH
euchromatin	13.00%	3.00%	CG
heterochromatin	4.00%	0.00%	CG

Compound	class	CMT	DRM
ABA	ABA	132340.828	120861.5719
5OHIAA	Auxin	163314.279	822754.1412
acy-ser	Auxin	584622.493	42408.25436
IAA-ASP	Auxin	43804.5247	9504.939711
IAA-Glu	Auxin	89773.969	9969.439153
OxIAA	Auxin	119045.04	891608.1201
OxIAAsp	Auxin	237362.268	154691.6842
Adenine	CK	1481247933	1298716435
Adenosine	CK	216303414	180959384.5
cZ	CK	77868.39	66186.58835
tZ9G	CK	313876.313	762993.4205
ZR-2	CK	428117.253	173536.8108
ACC	ETH	1858634.13	1477634.901
GA1	GA	4818.91596	7725.708587
GA12	GA	25030771.2	66090894.83
GA24	GA	26919.4116	10388.62526
GA6	GA	9516.2327	25334.57578
GA8-1	GA	85416.4249	124339.9286
JA	JA	47450.4646	14266.3022
JA-ILE	JA	87685.2978	183652.3027
SA	SA	28041126.5	29173573.63

W82

72061.2598	1.09497854	1.67720593
880810.782	0.19849706	0.93408727
389060.54	13.7855826	0.10900168
51338.8468	4.60860626	0.18514128
148721.602	9.00491669	0.06703424
834655.531	0.13351722	1.06823484
257528.581	1.53442164	0.60067773
209224368	1.14054762	6.20729051
51361451.2	1.19531471	3.52325295
19392.6286	1.17649802	3.41297664
312030.472	0.41137486	2.44525291
120004.431	2.46701118	1.4460867
1356381.25	1.25784396	1.08939496
9917.43823	0.62375068	0.77900244
21321059.1	0.37873252	3.09979418
7110.83233	2.59123907	1.4609577
8088.95871	0.37562234	3.1319947
100446.706	0.68695893	1.23786965
64933.1166	3.32605211	0.21970765
332655.657	0.47745275	0.5520793
14902441.7	0.96118243	1.95763716