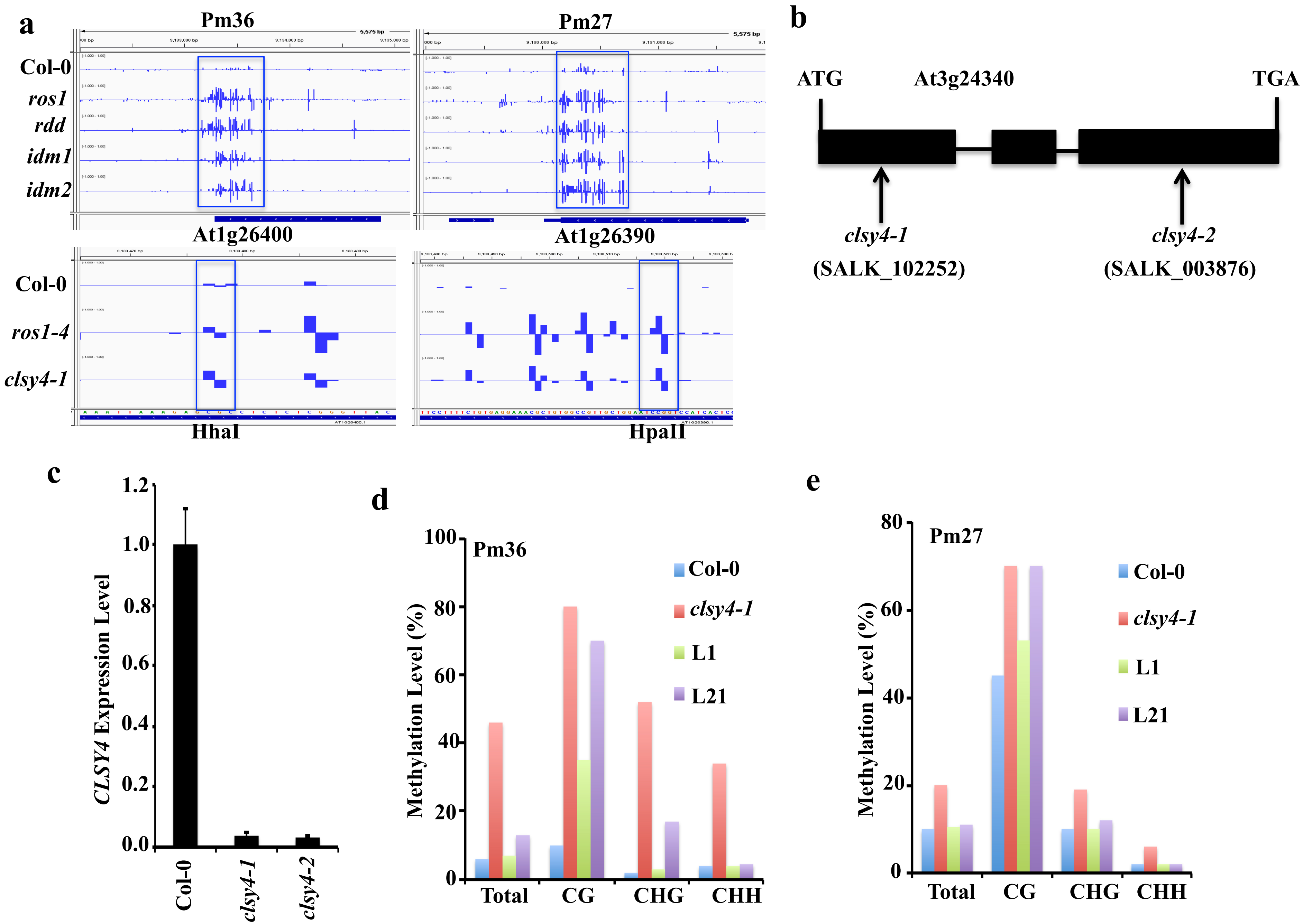
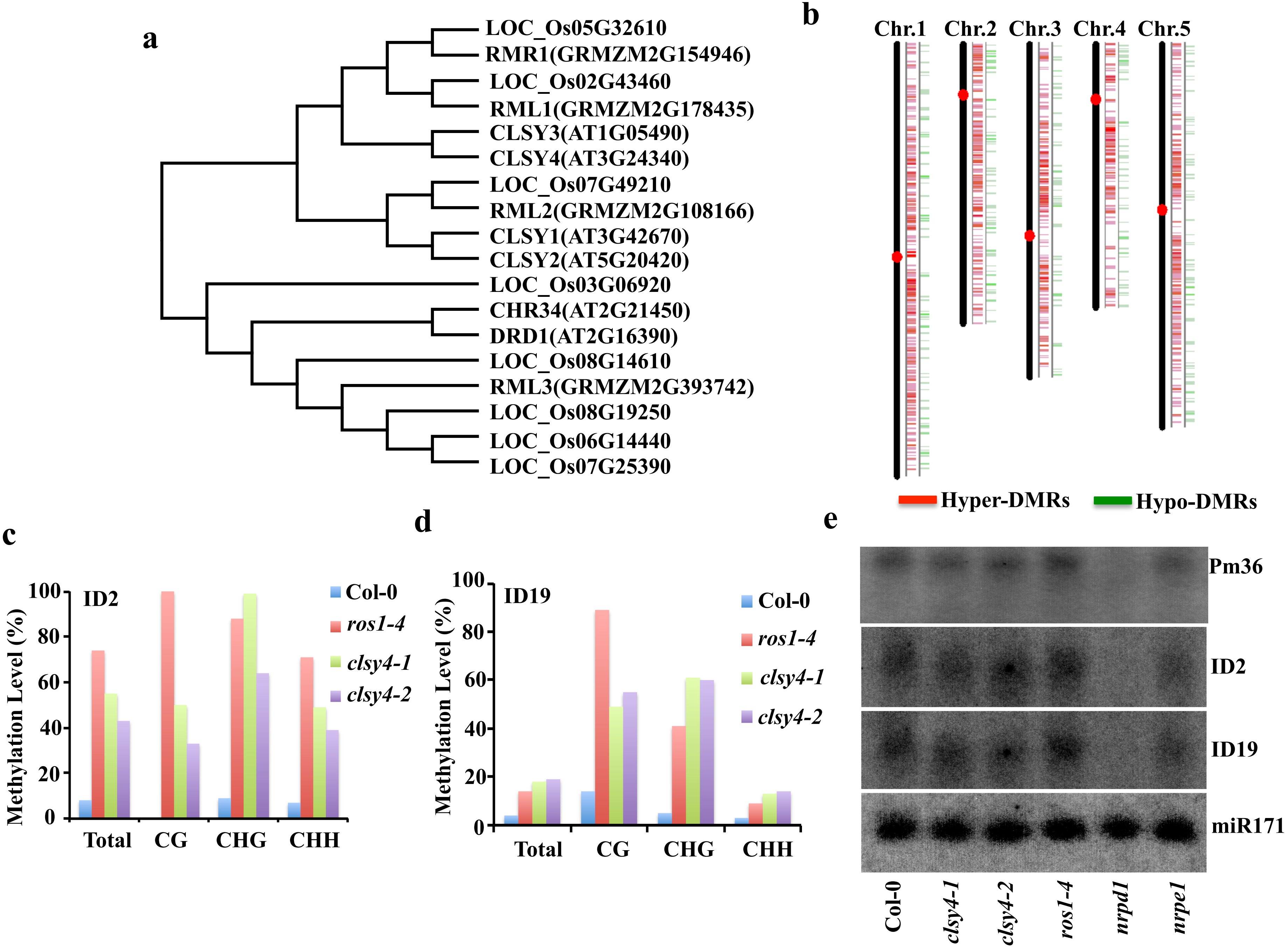
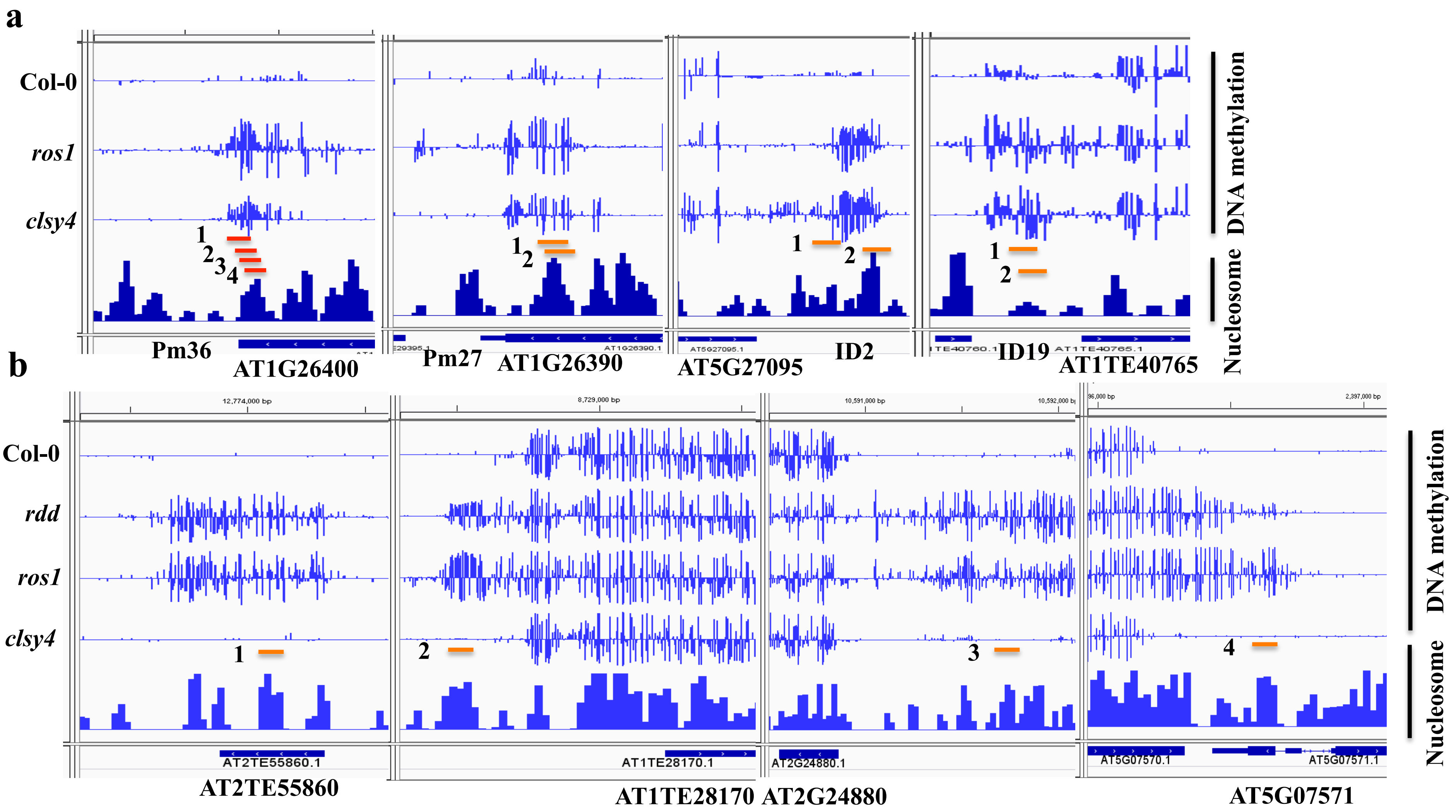
Supplementary Figure 1



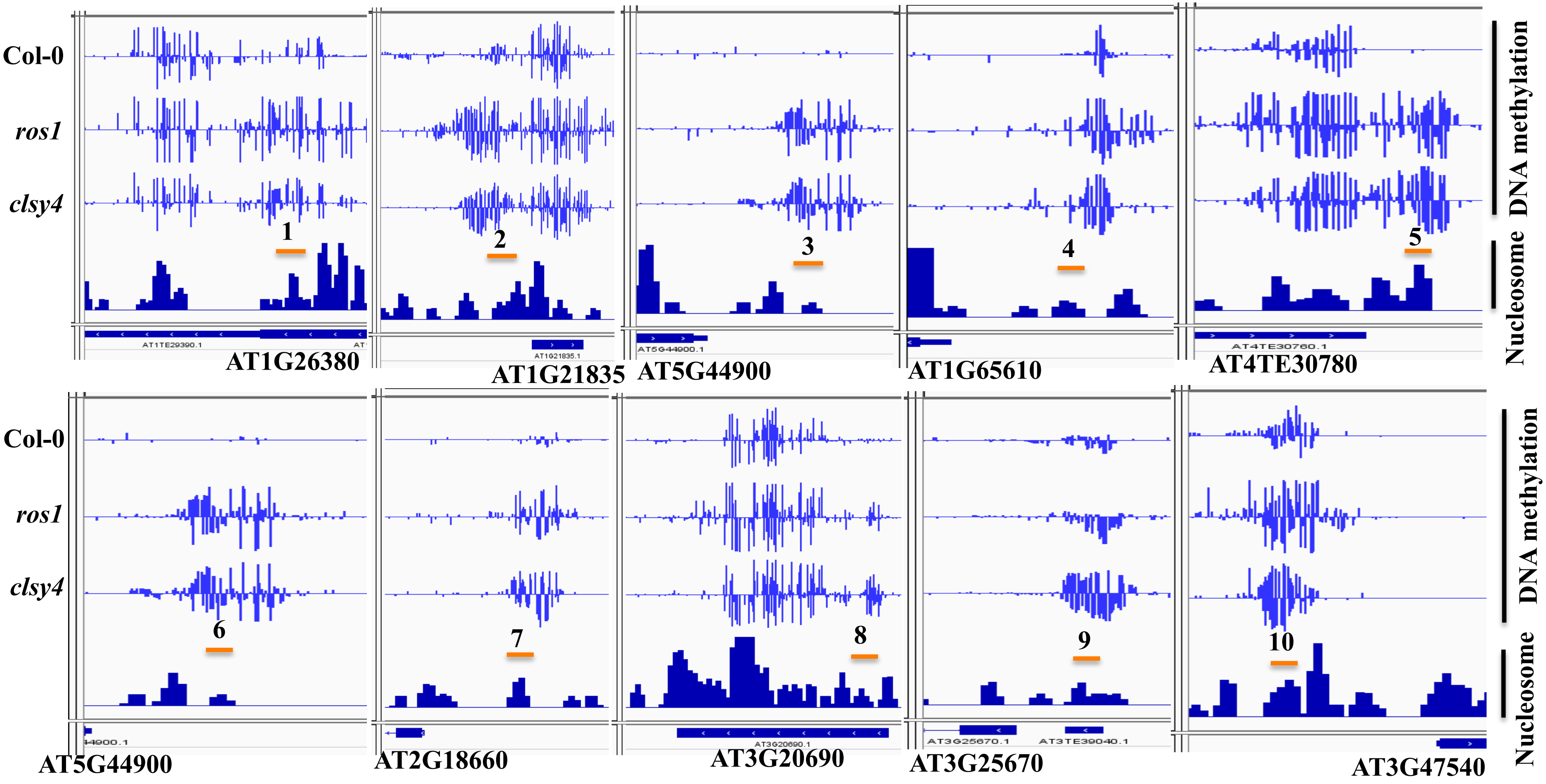
Supplementary Figure 2



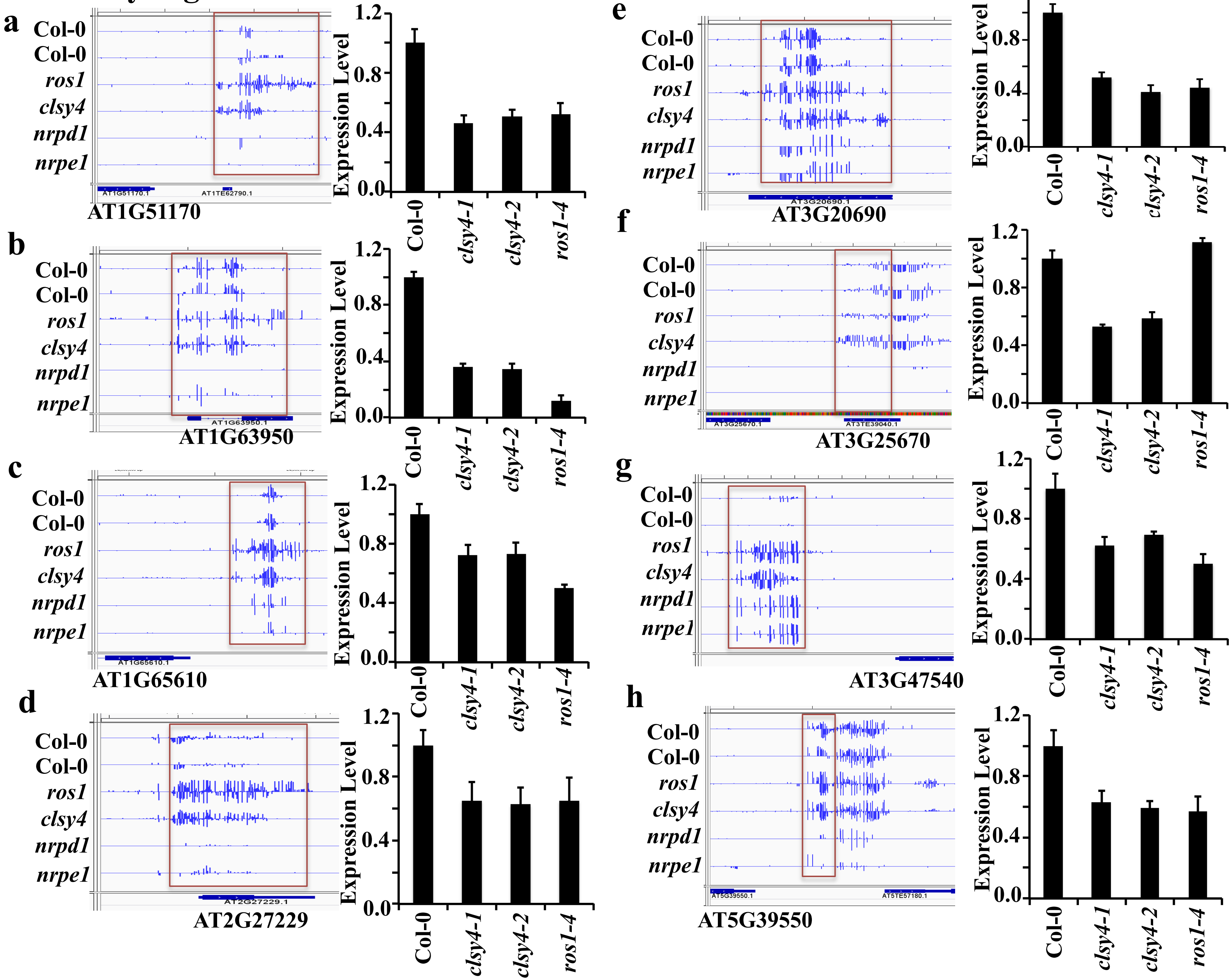
Supplementary Figure 3



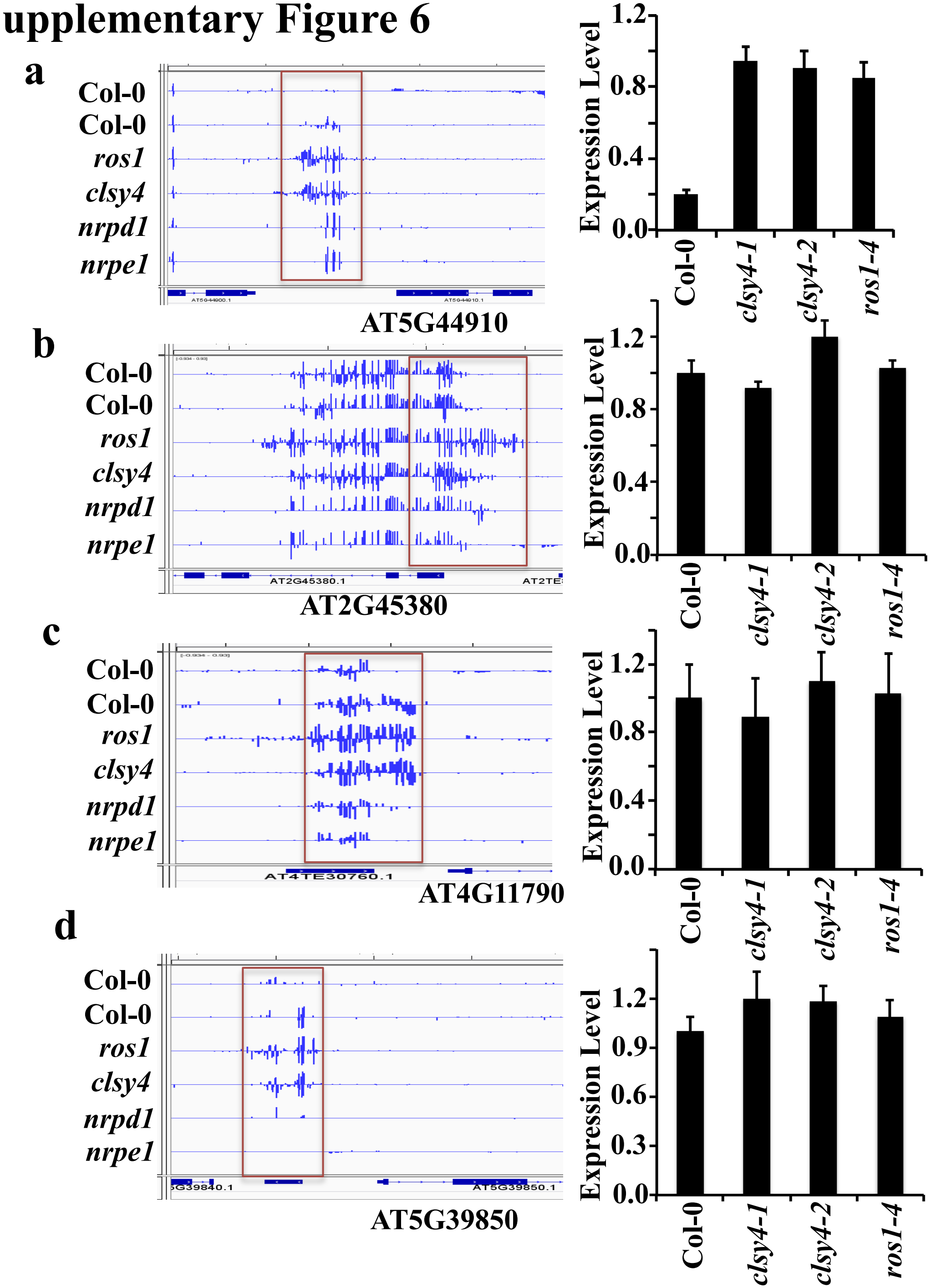
Supplementary Figure 4



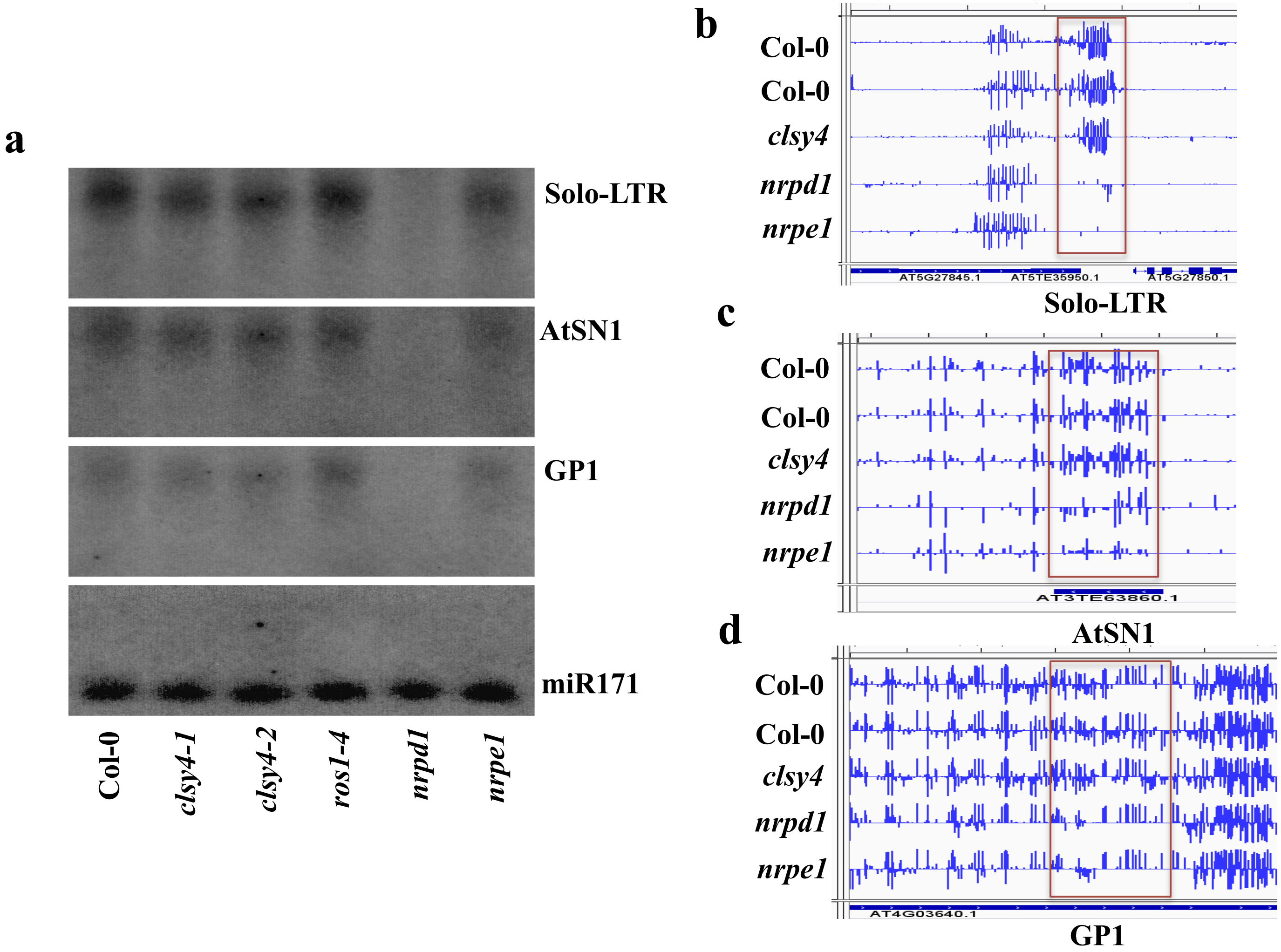
Supplementary Figure 5



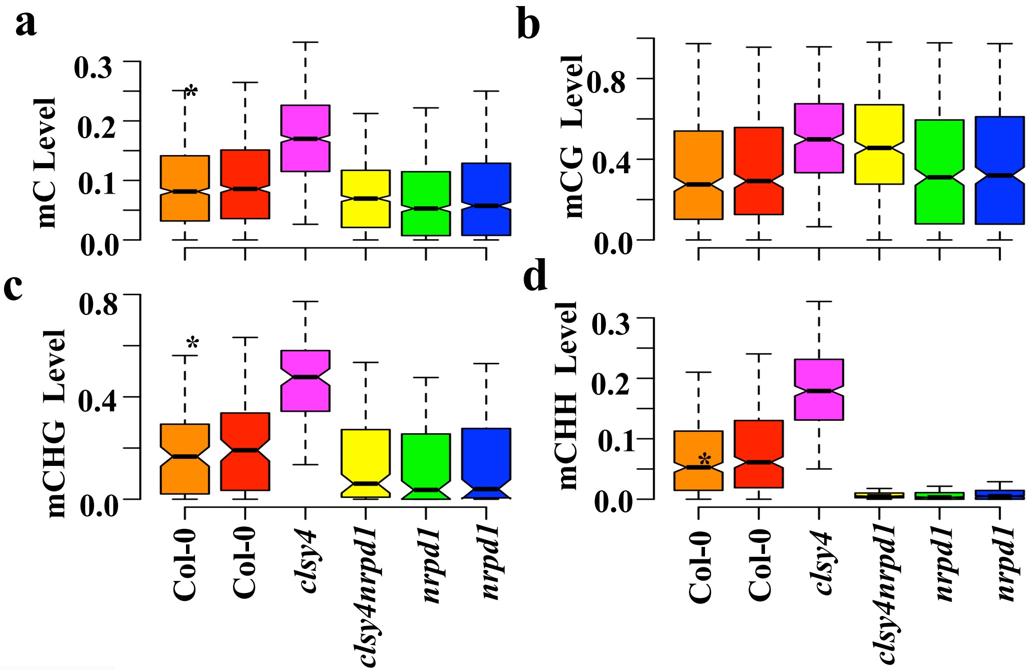
Supplementary Figure 6

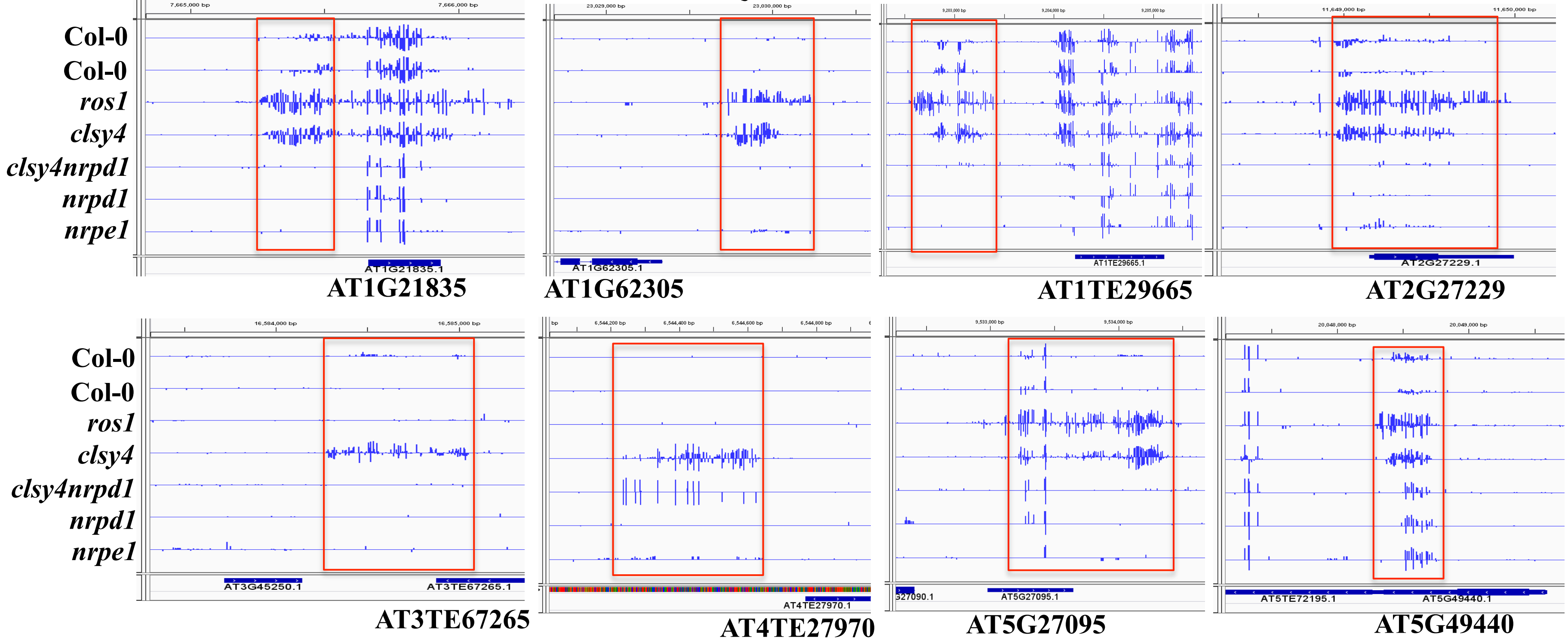


Supplementary Figure 7

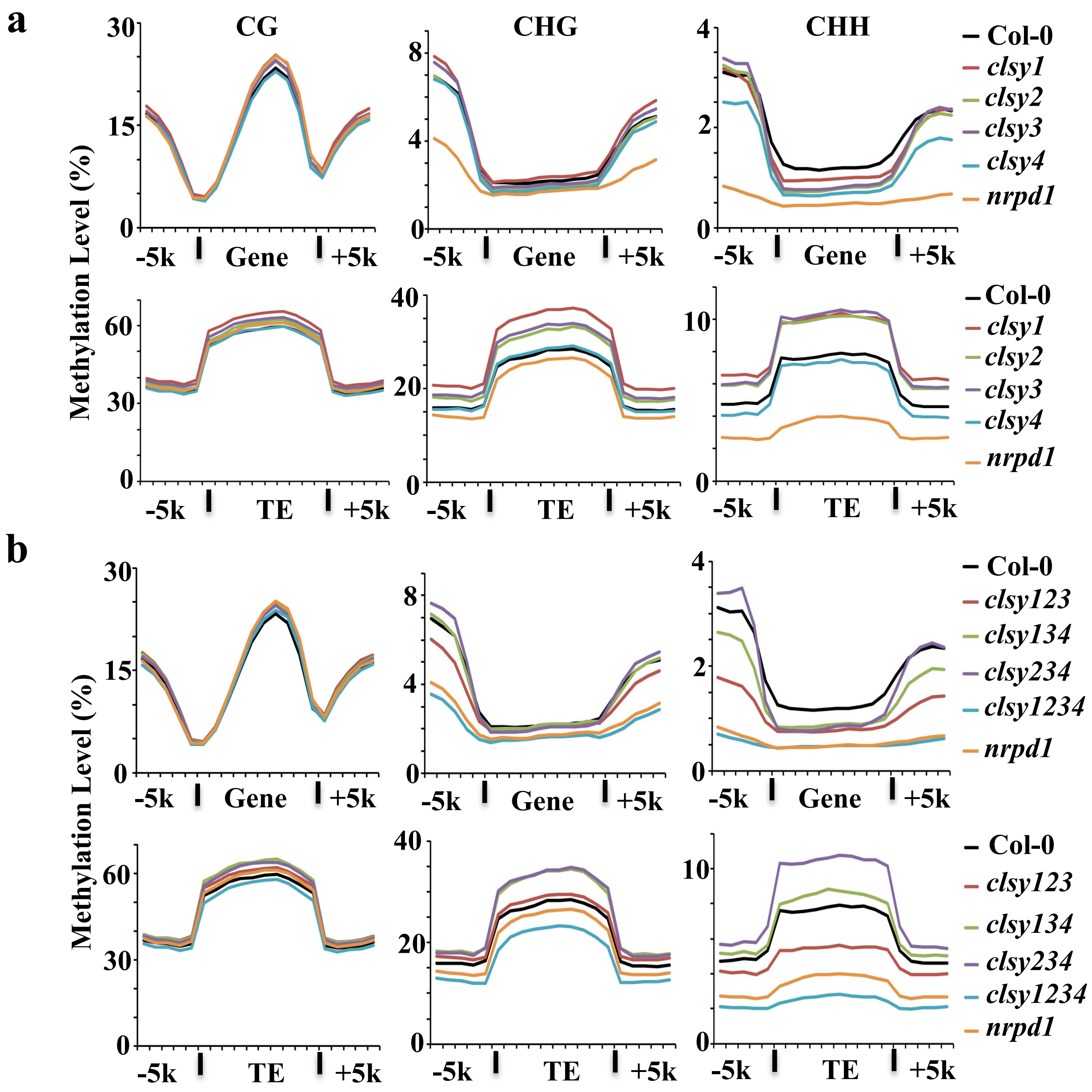


Supplementary Figure 8

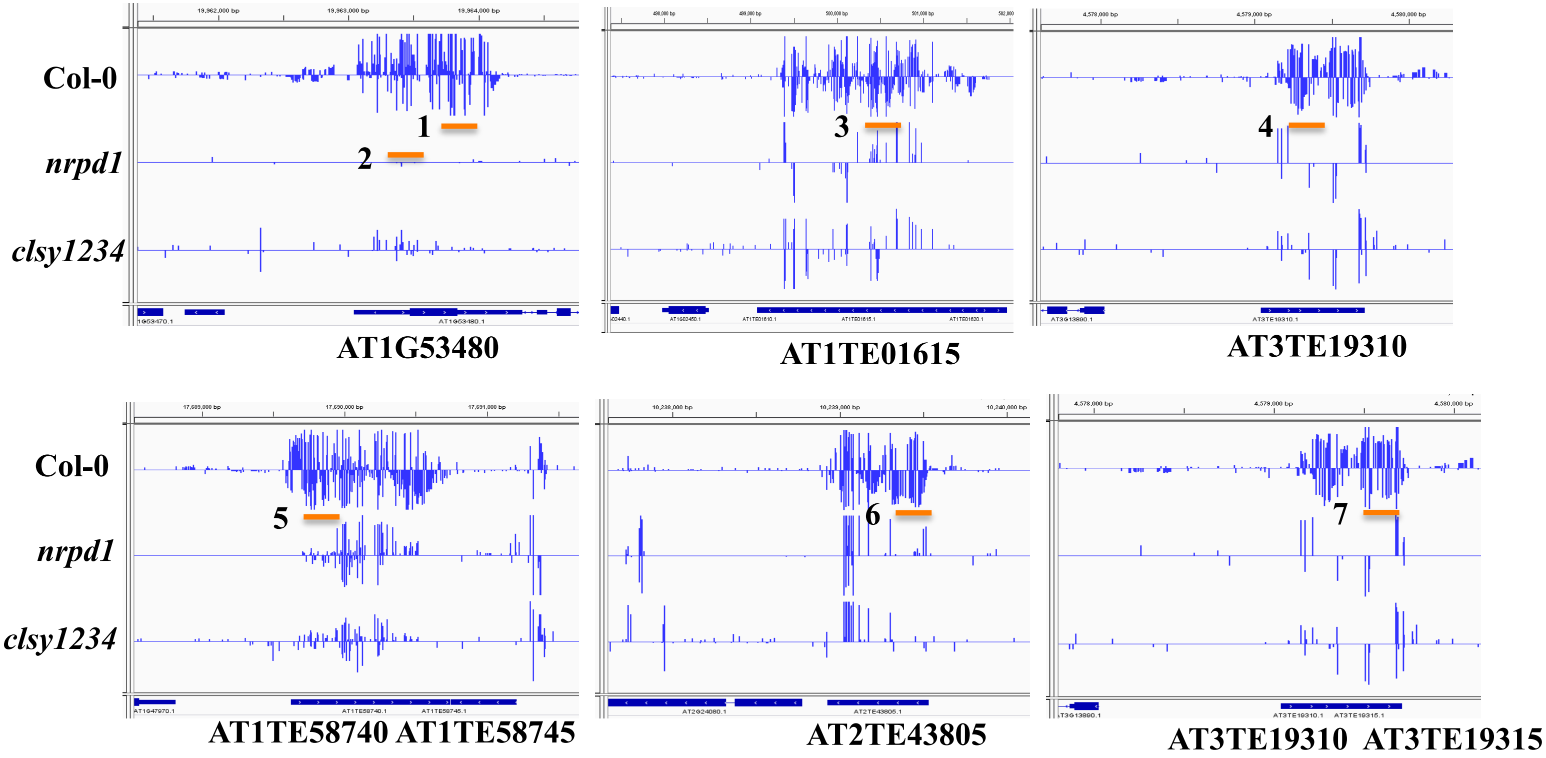




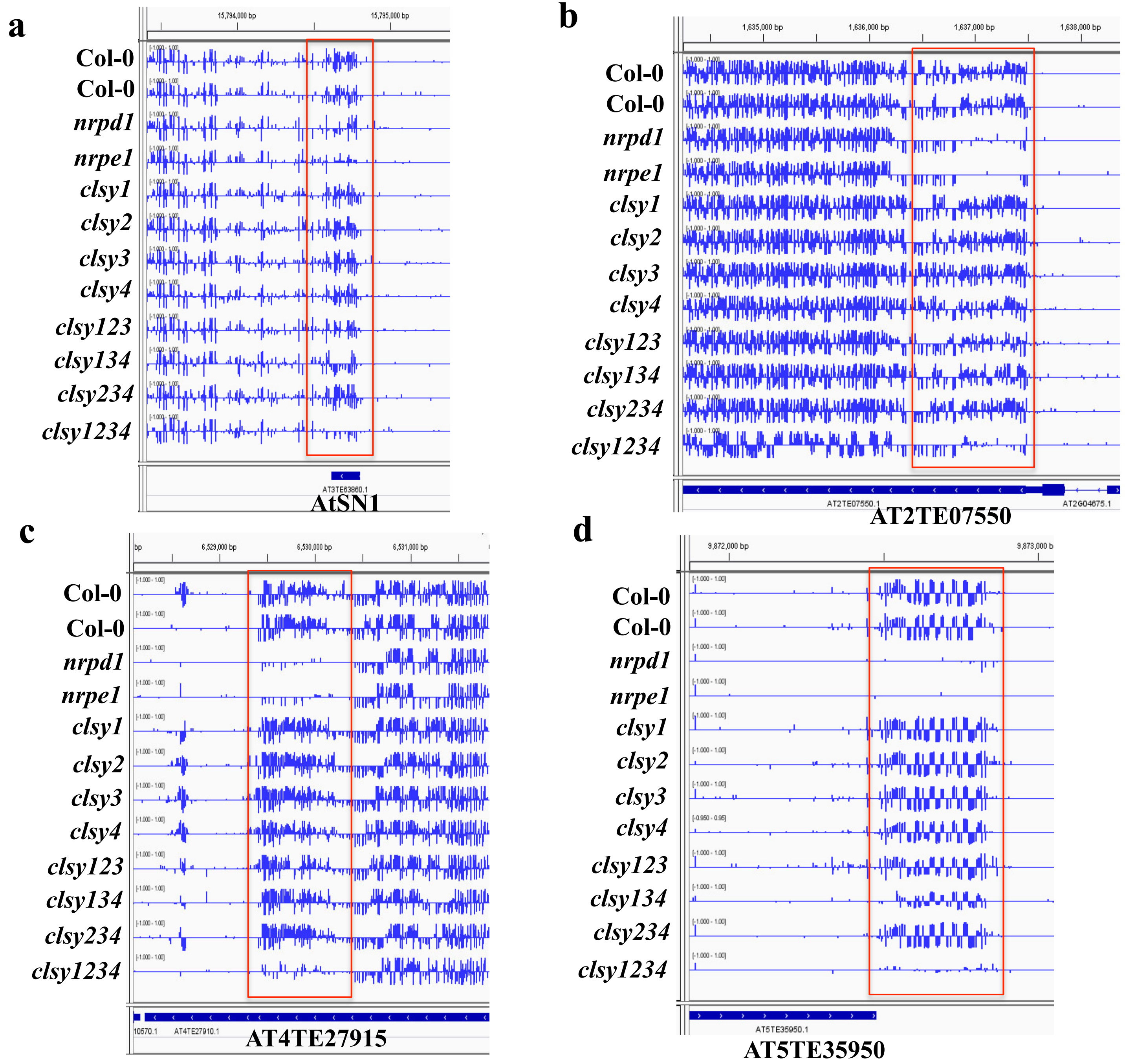
Supplementary Figure 9



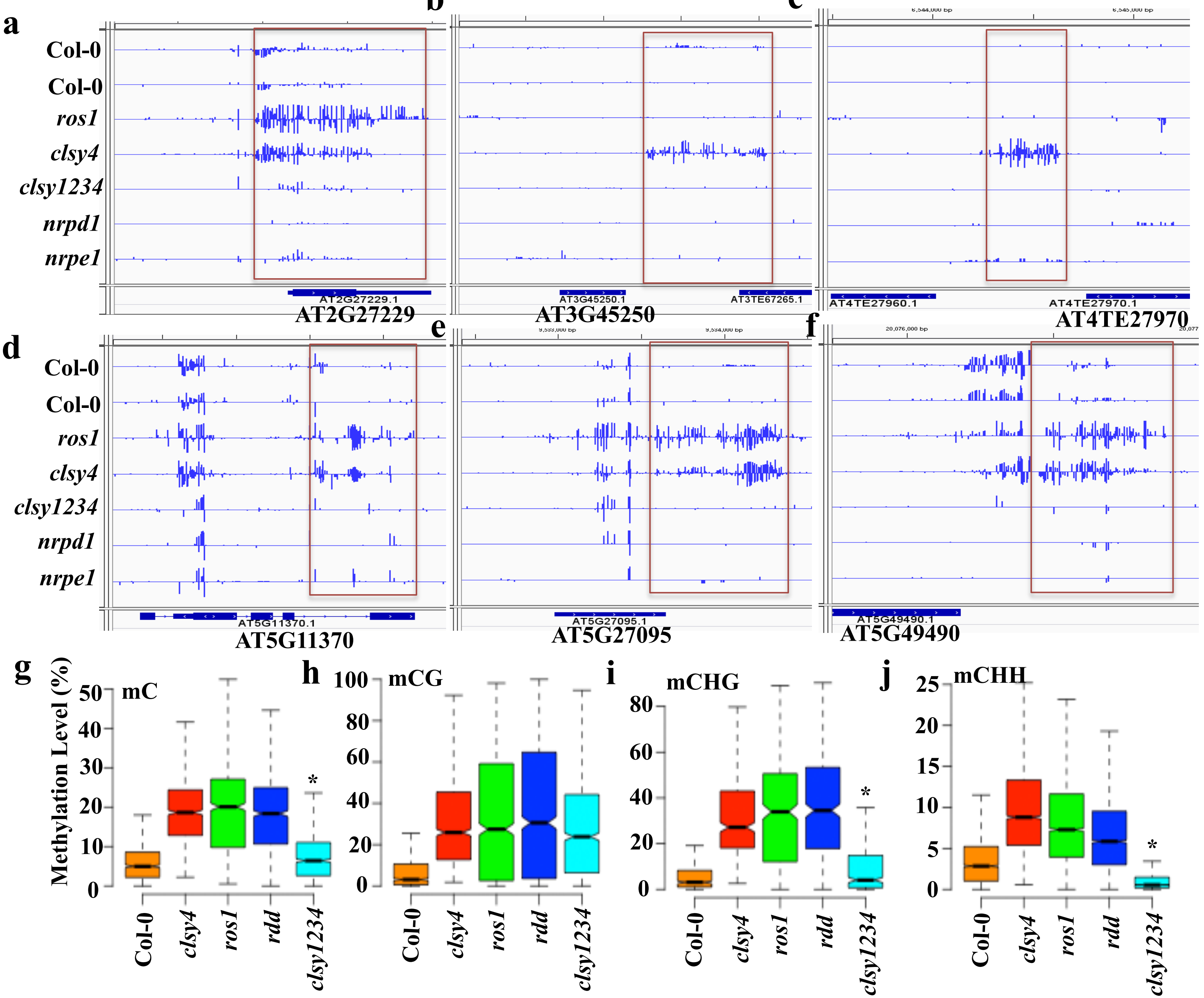
Supplementary Figure 10



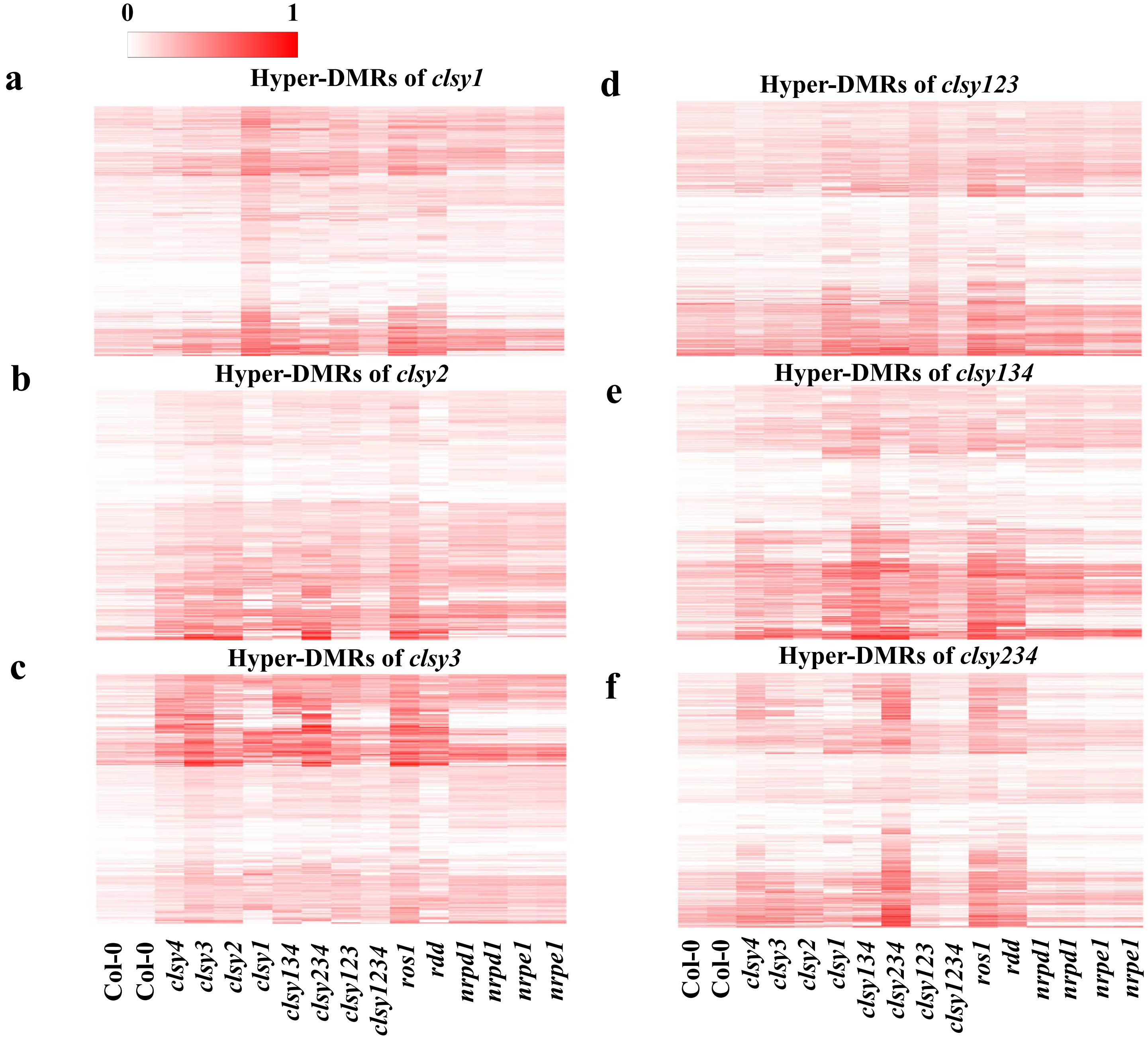
Supplementary Figure 11



Supplementary Figure 12



Supplementary Figure 13



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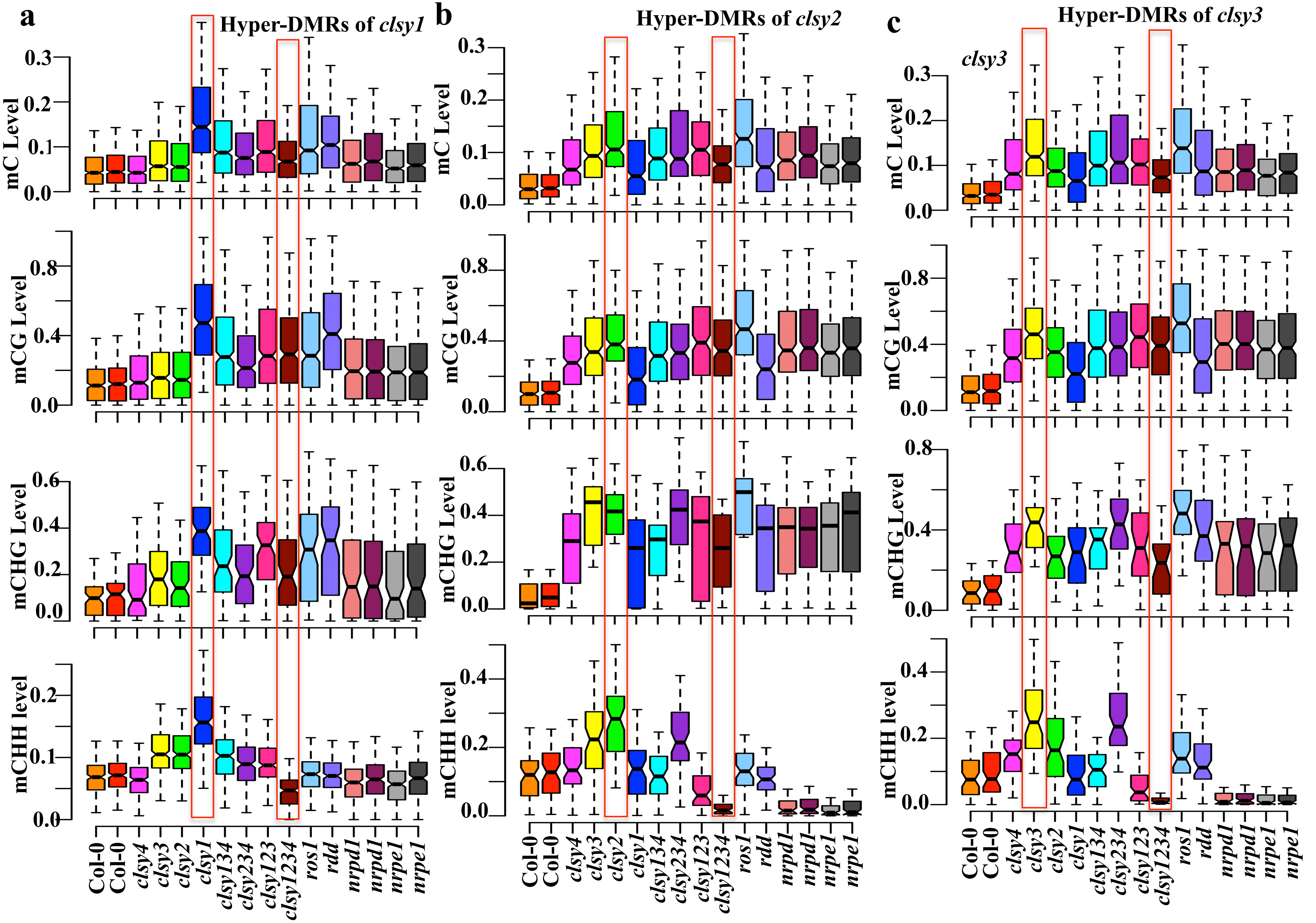

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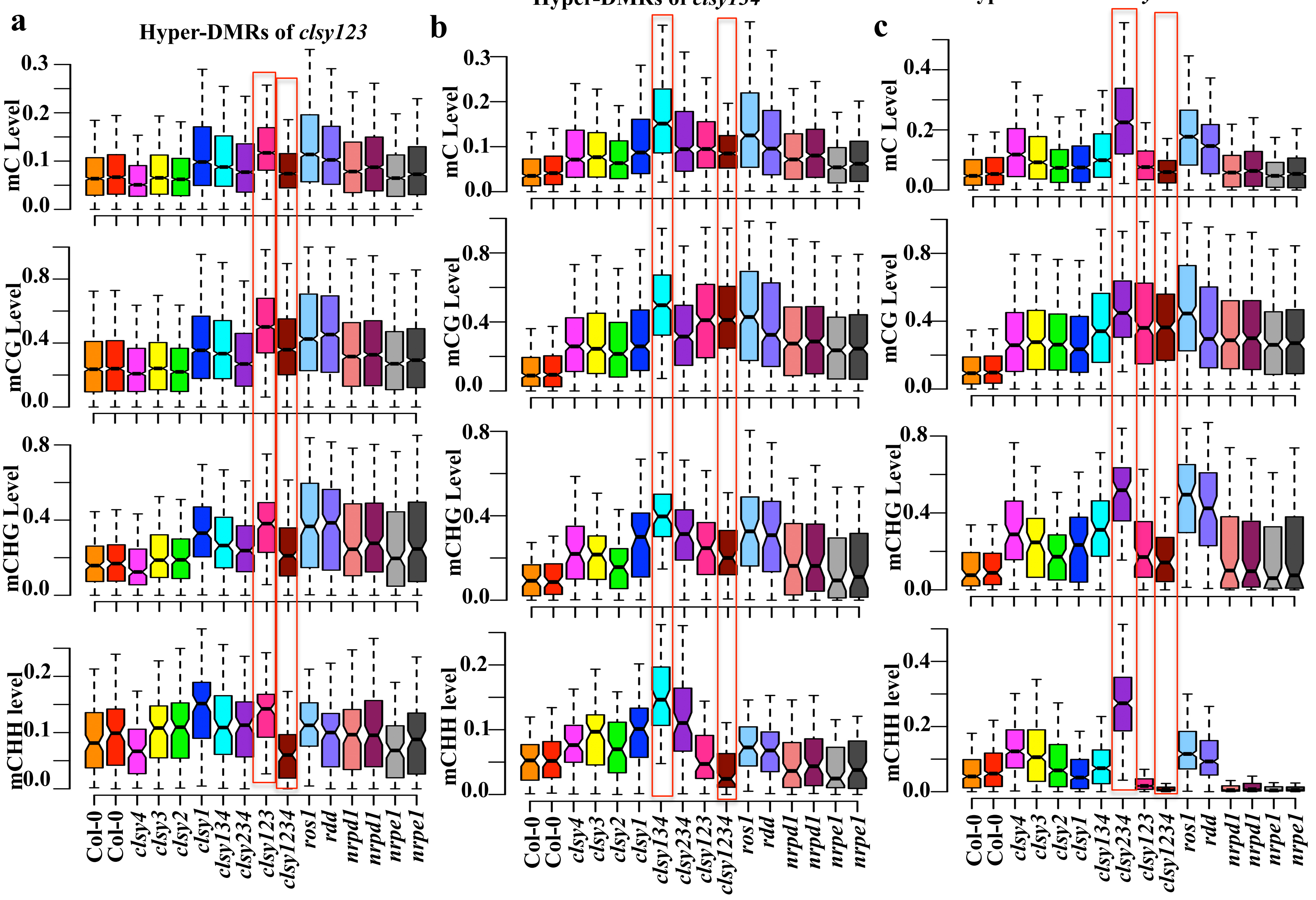

Supplementary Figure 1. The mutation in *CLSY4* was responsible for DNA hypermethylation.

(a) Integrated Genome Viewer display of the genomic location and DNA methylation level of the chop-PCR markers Pm36 and Pm27 in the indicated genotypes. The cytosine methylation levels at enzyme cutting sites are indicated by the IGV screenshots. (b) Schematic diagram showing the positions of two T-DNA insertions. (c) The *CLSY4* transcript levels in *clsy4* mutants as indicated by real-time PCR assay. (d) DNA methylation analysis of Pm36 in *clsy4* and complementation lines. (e) DNA methylation analysis of Pm27 in *clsy4* and complementation lines.

Supplementary Figure 2. There was no increase in siRNA at *clsy4* hyper-DMRs.

(a) The phylogenetic tree of plant-specific SNF2 proteins from Arabidopsis, rice, and maize generated by MEGA 5.2.2. (b) The distribution of DMRs of *clsy4* in the genome, with the red circle representing the centromere. (c) Individual locus bisulfite sequencing at a *clsy4* hyper-DMR, ID2. (d) Individual locus bisulfite sequencing at a *clsy4* hyper-DMR, ID19. (e) siRNA abundance at Pm36, ID2, and ID19 in *clsy4* and RdDM mutants measured by northern blotting.

Supplementary Figure 3. DNA methylation levels and nucleosome positions of the regions tested in ChIP assays for nucleosome positioning.

(a) Integrated Genome Viewer (IGV) display of the DNA methylation level in Col-0, *ros1-4*, and *clsy4-1*, and nucleosome position in Col-0[37]. The regions for ChIP-PCR are indicated by the orange lines. The identities of the common DMRs of *clsy4* and *rdd* are shown below each IGV snapshot. (b) Integrated Genome Viewer (IGV) display of the DNA methylation levels in Col-0, *rdd*, *ros1-4*, and *clsy4-1*, and nucleosome positioning in Col-0 at four *rdd*-specific hyper-DMRs.

Supplementary Figure 4. DNA methylation levels and nucleosome positioning of 10 hyper-DMRs of *clsy4*.

Integrated Genome Viewer (IGV) display of the DNA methylation levels in Col-0, *ros1-4*, and *clsy4-1*, and nucleosome positioning in Col-0[37]. The regions for ChIP-PCR are indicated by the orange lines.

Supplementary Figure 5. Hyper-DMRs in the *clsy4* mutant repress nearby gene expression.

(a-h) The IGV images on the left show the DNA methylation levels at hyper-DMRs in various genotypes, and IGV images on the right show the relative expression levels of nearby genes in the wild type *clsy4*, and *ros1*. Bars indicate the standard errors of three biological replicates.

Supplementary Figure 6. Effect of hyper-DMRs on nearby gene expression.

(a) A hyper-DMR in the *clsy4* mutant increases nearby gene expression. (b-d) Hyper-DMRs in the *clsy4* mutant have no substantial effect on nearby gene expression. Bars indicate the standard errors of three biological replicates.

Supplementary Figure 7. The *clsy4* mutation does not affect siRNA abundance or DNA methylation level of several known RdDM loci.

(a) Northern blotting showing the abundance of 24-nt siRNA at Solo-LTR, AtSN1, and GP1 (three RdDM target loci in the indicated genotypes). miR171 served as a loading control. (b-d) Snapshots showing the DNA methylation levels of Solo-LTR, AtSN1, and GP1 in *clsy4, nrpd1*, and *nrpe1* mutants.

Supplementary Figure 8. DNA hypermethylation in *clsy4* depends on RdDM.

(a-d) DNA methylation levels of C, CG, CHG, and CHH at *clsy4* hyper-DMRs in the indicated genotypes. * indicates significant difference between *clsy4* and *clsy4nrpd1* (P <0.01, Wilcoxon sum test). (e) Snapshots showing the DNA methylation of eight hyper-DMRs of *clsy4* in various genotypes.

Supplementary Figure 9. Role of the CLSYs in regulating DNA methylation at genes and transposons.

Methylation levels of CG, CHG, and CHH at genes and transposons and their flanking regions in (a) the *clsy* single mutant and in (b) the *clsy* triple and quadruple mutants. The wild type and *nrpd1* served as controls.

Supplementary Figure 10. DNA methylation levels of hypo-DMRs of *clsy1234*.

Integrated Genome Viewer (IGV) display of the DNA methylation levels in Col-0, *nrpd1*, and *clsy1234*. The regions for ChIP-PCR are indicated by the orange line.

Supplementary Figure 11. The four CLSYs redundantly regulate DNA methylation at transposons.

Snapshots showing the DNA methylation levels at RdDM-targeted transposons AtSN1 (a), AT2TE07550 (b), AT4TE27915 (c), and AT2TE07550 (d) in various *clsy* mutants.

Supplementary Figure 12. DNA hypermethylation in *clsy4* depends on the other three CLSYs.

(a-f) Snapshots showing the DNA methylation level of *clsy4* hyper-DMRs in the indicated genotypes. (g-j) Boxplots showing the DNA methylation of C, CG, CHG, and CHH at *clsy4* hyper-DMRs in the indicated genotypes. * indicates significant difference between *clsy4* and *clsy1234* ($P < 0.01$, Wilcoxon sum test).

Supplementary Figure 13. The four CLSYs antagonistically regulate DNA methylation and demethylation at the hyper-DMRs in individual *clsy* mutants.

Total C methylation levels of various mutants at (a) *clsy1* hyper-DMRs, (b) *clsy2* hyper-DMRs, (c) *clsy3* hyper-DMRs, (d) *clsy123* hyper-DMRs, (e) *clsy134* hyper-DMRs, and (f) *clsy234* hyper-DMRs.

Supplementary Figure 14. DNA hypermethylation of *clsy* single mutants depends on CLSYs.

Boxplot showing the DNA methylation level of C, CG, CHG, and CHH at hyper-DMRs of (a) *clsy1*, (b) *clsy2*, and (c) *clsy3* in the indicated genotypes.

Supplemental Figure 15. DNA hypermethylation of *clsy* triple mutants depends on CLSYs.

Boxplot showing the DNA methylation level of C, CG, CHG, and CHH at hyper-DMRs of (a) *clsy123*, (b) *clsy134*, and (c) *clsy234* in the indicated genotypes.

Supplementary Table 1. T-DNA mutants for genetic screen

No.	Gene ID	T-DNA Number
1	AT5G04290	SALK_001254
2	AT4G32700	SALK_001669
3	AT5G44750	SALK_005721
4	AT1G14790	SALK_007638
5	AT5G45720	SALK_007734
6	AT3G18090	SALK_008535
7	AT2G34710	SALK_008924
8	AT4G19550	SALK_008553
9	AT2G25170	SALK_010693
10	AT2G01280	SALK_011937
11	AT4G24660	SALK_017963
12	AT4G29090	SALK_023866
13	AT5G13240	SALK_026637
14	AT1G08540	SALK_045706
15	AT2G02090	SALK_054130
16	AT4G17460	SALK_059835
17	AT5G20420	SALK_061962
18	AT2G04630	SALK_064868
19	AT1G10520	SALK_075391
20	AT5G13730	SALK_078760
21	AT1G03280	SALK_081307
22	AT3G28920	SALK_085482
23	AT2G19920	SALK_088175
24	AT1G60620	SALK_088247
25	AT4G24790	SALK_092209
26	AT5G42780	SALK_092897
27	AT3G24340	SALK_102252
28	AT5G09380	SALK_113934
29	AT4G31900	SALK_115303
30	AT4G25180	SALK_125873
31	AT4G08350	SALK_126891
32	AT5G18620	SALK_128524
33	AT1G08060	SALK_131757
34	AT1G63160	SALK_127244
35	AT5G22010	SALK_140231
36	AT1G13870	SALK_140551
37	AT3G54490	SALK_148046
38	AT3G19670	SALK_151254
39	AT4G32040	SALK_000339
40	AT5G63950	SALK_007071

41	AT5G65410	SALK_014023
42	AT3G60390	SALK_014055
43	AT4G31900	SALK_014672
44	AT4G21710	SALK_015933
45	AT2G46020	SALK_030046
46	AT1G79840	SALK_039825
47	AT1G67120	SALK_057010
48	AT5G65310	SALK_058055
49	AT2G21450	SALK_059100
50	AT2G34320	SALK_059700
51	AT1G67630	SALK_064094
52	AT1G63210	SALK_086163
53	AT5G44800	SALK_089483
54	AT1G14790	SALK_112300
55	AT1G63020	SALK_143437
56	AT5G04290	SALK_001254
57	AT3G18520	SALK_004027
58	AT1G79350	SALK_004087
59	AT5G44750	SALK_005721
60	AT5G25060	SALK_011832
61	AT3G06290	SALK_013326
62	AT1G63490	SALK_014109
63	AT4G21710	SALK_015933
64	AT5G26610	SALK_018458
65	AT2G13370	SALK_020296
66	AT5G45190	SALK_021004
67	AT5G24740	SALK_021356
68	AT1G34360	SALK_022422
69	AT3G45830	SALK_024862
70	AT4G31880	SALK_024683
71	AT4G39450	SALK_026025
72	AT2G17410	SALK_026835
73	AT1G02080	SALK_030822
74	AT5G12400	SALK_031040
75	AT4G32620	SALK_039205
76	AT3G01460	SALK_039302
77	AT1G09730	SALK_040576
78	AT1G79090	SALK_040660
79	AT4G29790	SALK_042026
80	AT2G44900	SALK_043325
81	AT1G55040	SALK_043472
82	AT5G46190	SALK_051182

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85	AT1G51520	SALK_053222
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274	AT3G20020	SALK_024873
275	AT5G53770	SALK_090264
276	AT1G48560	SALK_008422

Supplementary Table 2. Bs-sequencing basic information

Sample Name	Read length(bp)	Clean Reads	Clean bases	Q20(%)	GC(%)	Depth(x)	Mapped Reads	Mapped ratio
Col-0	90	97,347,534	8,761,278,060	99.47;99.72	25.64	58	89,350,773	91.79%
clsy4-1	90	99,441,528	8,949,737,520	99.52;99.62	26.32	60	92,260,137	92.78%
clsy4-1/nrpd1-3	90	96,645,602	8,698,104,180	99.47;99.73	25.77	58	88,949,959	92.04%
clsy1-3	90	94,908,790	8,541,791,100	99.50;99.63	27.04	57	86,233,177	90.86%
clsy2-1	90	96,278,326	8,665,049,340	99.54;99.59	26.28	58	81,265,311	84.41%
clsy3-1	90	97,817,498	8,803,574,820	99.49;99.72	25.89	59	89,516,627	91.51%
clsy1-3/clsy2-1/clsy3-1	90	96,637,408	8,697,366,720	99.54;99.69	24.74	58	88,689,955	91.78%
clsy1-3/clsy3-1/clsy4-1	90	98,649,196	8,878,427,640	99.53;99.64	26.22	59	89,188,094	90.41%
clsy2-1/clsy3-1/clsy4-1	90	96,425,168	8,678,265,120	99.43;99.51	26.89	58	87,716,664	90.97%
clsy1-3/clsy2-1/clsy3-1/clsy4-1	90	97,113,818	8,740,243,620	99.54;99.65	26.61	58	90,014,686	92.69%

Supplementary Table 3. Mutants used in this study

Mutant name	T-DNA
clsy1-3	
clsy2-1	SALK_106745
clsy3-1	SALK_040366
clsy4-1	SALK_102252
clsy4-2	SALK_003876
ros1-4	SALK_045303
nrpd1-3	SALK_128428
nrpe1-11	SALK_029919
dtf1-2	SALK_074540
clsy4nrpd1	*clsy4-1*/*nrpd1-3* (SALK_102252/SALK_128428)
clsy4nrpe1	*clsy4-1*/*nrpe1-11* (SALK_102252/SALK_029919)
clsy4ros1	*clsy4-1*/*ros1-4* (SALK_102252/SALK_029919)
ros1nrpd1	*ros1-4*/*nrpe1-11* (SALK_045303/SALK_128428)
ros1nrpe1	*ros1-4*/*nrpe1-11* (SALK_045303/SALK_029919)
clsy12	*clsy1-3/clsy2-1* (*clsy1-3*/SALK_106745)
clsy34	*clsy3-1/clsy4-1* (SALK_040366/SALK_102252)
clsy123	*clsy1-3/clsy2-1/clsy3-1*(*clsy1-3*/SALK_106745/SALK_040366)
clsy134	*clsy1-3/clsy3-1/clsy4-1*(*clsy1-3*/SALK_040366/SALK_102252)
clsy234	*clsy2-1/clsy3-1/clsy4-1*(SALK_106745/SALK_040366/SALK_102252)
clsy1234	*clsy1-3/clsy2-1/clsy3-1/clsy4-1*(*clsy1-3*/SALK_106745/SALK_040366/SALK_102252)

Supplementary Table 4. Oligos used in this study

Oligos Name	**Oligos Sequence**	**Experiments**
*clsy1-3*F	GACCTATTGGGAATGTGGTTCAT	genotyping
*clsy1-3*R	CCGATTTCTTCATTCAATTCATAG	genotyping
*clsy2-1*F	TAGCCATGTATTTCCGGTGAG	genotyping
*clsy2-1*R	AGTGTTGTTGACCAGTGGGAG	genotyping
*clsy3-1*F	CTTCTTGCAGTGGCATTCTTC	genotyping
*clsy3-1*R	ATTAGGCGAAGAGGATGAAGC	genotyping
*clsy4-1*F	CTATGGAAACTCCTCCGTTCC	genotyping
*clsy4-1*R	TGATGCTTGTTCACCTTCTCC	genotyping
*clsy4-2*F	ACGACTTTGTCCTGGATGATG	genotyping
clsy4-2R	TTCGGATATGCGATGTTTCTC	genotyping
*nrpd1-3*F	GATCTGTTCAGCTTGCTCGTC	genotyping
*nrpd1-3*R	TTAATGTTCTTCATGCGGGAC	genotyping
*nrpe1-11*F	TTTTCCTCCAAGTTGTGATCG	genotyping
*nrpe1-11*R	AACAAGACCCAACGACTGTTG	genotyping
*ros1-4*F	CCAGTTAAGGACAGAACACCG	genotyping
*ros1-4*R	TCGTCTTTCGATCAAATCCAC	genotyping
LB1.3	ATTTTGCCGATTTCGGAAC	genotyping
AT5TE25535-RealF	GTCGTTGTTCCTTGAGTGTTTG	real-time PCR
AT5TE25535-RealR	CGGTTTCTCTCATACATCTCCTTT	real-time PCR
AtSN1-RealF	CCAGAAATTCATCTTCTTTGGAAAAG	real-time PCR
AtSN1-RealR	GCCCAGTGGTAAATCTCTCAGATAGA	real-time PCR
AT2TE07550-RealF	GTCCCTCGAGCAACAATACTAA	real-time PCR
AT2TE07550-RealR	ATGATGGATGGTAAGGCATAGAG	real-time PCR
AT4TE27915-RealF	GTCACGCACTCACCTTAACA	real-time PCR
AT4TE27915-RealR	GGACTTGTTGTAGGACGTTTCT	real-time PCR
AT5TE35950-RealF	CTAACGTCATTACATACACATCTTG	real-time PCR
AT5TE35950-RealR	TTGTTGATGTGAACTTTCATCC	real-time PCR
CLSY4-RealF	TGGGCCAGCAACATTAGGAACTCT	real-time PCR
CLSY4-RealR	TCCACTGATGCGGATGAAGTCGAT	real-time PCR
ROS1-RealF	AAGGACCAACTTGTTGCGAC	real-time PCR
ROS1-RealR	AGGACTCTATTAGCACTGAGC	real-time PCR
IGN5-RealF	AAGCCCAAACCATACACTAATAATCTAAT	real-time PCR
IGN5-RealR	CCGAATAACAGCAAGTCCTTTTAATA	real-time PCR
IGN6-RealF	TTTCGCCGTCACTAACATGTAATG	real-time PCR
IGN6-RealR	GAAGTAGCTTTTTCGGTCCAGTTC	real-time PCR
IGN20-RealF	AAGAACCGGACCAATACGG	real-time PCR
IGN20-RealR	CCACCGCCTCTATTGAAATG	real-time PCR
IGN22-RealF	TGGTCCATAGGTTCGGAATTT	real-time PCR
IGN22-RealR	GGCATGGTTTGATATCAGGAG	real-time PCR
IGN25-RealF	AAACCCACCTCTTTAGGTCCA	real-time PCR
IGN25-RealR	GGCTTGGAGAGTCCAACAAT	real-time PCR
IGN27-RealF	CGTTGTTCCGCCTAATTCTG	real-time PCR
IGN27-RealR	GCCAGGAAACCCTAACTTCC	real-time PCR
IGN29-RealF	CGTTTGTTTATGTAGGGCGAAAG	real-time PCR
IGN29-RealR	TAAAACTTTTCCCGCCAACCA	real-time PCR
IGN31-RealF	CAATCTGGCACACACGAAAC	real-time PCR
IGN31-RealR	CAGGTTGGATCTGTTGACGA	real-time PCR

Actin2-RealF	GAGAGATTCAGATGCCCAGAAGTC	real-time PCR
Actin2-RealR	TGGATTCCAGCAGCTTCCA	real-time PCR
At1g51170-RealF	TCGTCTCCTTCCTTCTCATCT	real-time PCR
At1g51170-RealR	ACTTTGAGTCTGTCGAGGTTAAG	real-time PCR
At1g63950-RealF	GATTGTGTGGATGGGTGTTTATG	real-time PCR
At1g63950-RealR	AGATGAGTGAATTCCGGGTAAG	real-time PCR
At1g65610-RealF	TAGCTGCTCTCGTTTCCTTAAC	real-time PCR
At1g65610-RealR	TCAAGGCTTCCAGGCTTTAG	real-time PCR
At2g27229-RealF	CATCTTCTAAATCGCCACTCCT	real-time PCR
At2g27229-RealR	TCCCTCACAATGATCTCTCTCT	real-time PCR
AT3g20690-RealF	TCTCTCTAGGCTTCCGTTGATA	real-time PCR
AT3g20690-RealR	TACATTGCCGATGTGCTTATTTG	real-time PCR
AT3g25670RealF	GGAGAAGGCAGAGGATAGTTTG	real-time PCR
AT3g25670RealR	CTAGTAACCATCACACCCATTGA	real-time PCR
At3g47540RealF	TGCCTCGTAGGTCCTTGTATAG	real-time PCR
At3g47540RealR	CCATTACCGGCTTGGTTGATAA	real-time PCR
At5g39550RealF	TCCAAGACCGTTGCCTAATG	real-time PCR
At5g39550RealR	GACCCTCAGCTTCATCGAAAT	real-time PCR
AT5g44910RealF	CGAGGAACTGAGGGAGAAATAC	real-time PCR
AT5g44910RealR	TGCCCTCACAAGACCTAAAC	real-time PCR
At2g45380RealF	CAACTCAAGTGGTGGTGTAGAG	real-time PCR
At2g45380RealR	GAATTGCCTTTCCATGCTTCTT	real-time PCR
At4g11790RealF	ACGGCCATCCAAGAATACG	real-time PCR
At4g11790RealR	AGAGAGAGGACGACTCGATAAG	real-time PCR
AT5g39850RealF	AAGCCACGTCGTCCTTATG	real-time PCR
AT5g39850RealR	TTGAACTCTCCAAAGCTCTCTC	real-time PCR
PM36-ChIP-1F	CACATAACCGGTGGAGGATTT	ChIP assay
PM36-ChIP-1R	GTAGCTCGATCCAAGAGCTTTC	ChIP assay
PM36-ChIP-2F	GTGTCAAGTAACCCGAGAGAG	ChIP assay
PM36-ChIP-2R	GATCTTAGCTTCATCCACGTTTG	ChIP assay
PM36-ChIP-3F	ACCACTCGGATTGATTCCAATA	ChIP assay
PM36-ChIP-3R	GACGCAAAGGAAACAGAGAATAAG	ChIP assay
PM36-ChIP-4F	GTAAGGTCCCGCAACTTCATAA	ChIP assay
PM36-ChIP-4R	CCGGAAAGGAAACTTGTTCAATC	ChIP assay
PM27-ChIP-1F	ATTACACGAACCGGAGGAATG	ChIP assay
PM27-ChIP-1R	GGGAATTTGAAGAGATTGATGGATG	ChIP assay
PM27-ChIP-2F	TTTACACGAACCGGAGGAATAC	ChIP assay
PM27-ChIP-2R	GGTGAGACAAACGTGGATGA	ChIP assay
ID2-ChIP-1F	AGGCATGTTTCCATGTTTGATG	ChIP assay
ID2-ChIP-1R	TCCAGTGATGACAGGATCTTATTG	ChIP assay
ID2-ChIP-2F	GCTGCGAGGAACTGAAATTG	ChIP assay
ID2-ChIP-2R	TGCTCTGGTTGGTATGTGTATAA	ChIP assay
ID19-ChIP-1F	CTATCGGCTGATATGGTCAGTTT	ChIP assay
ID19-ChIP-1R	TGACCTCCTGACAAACATTCC	ChIP assay
ID19-ChIP-2F	TCTCTAAAGGGCCACCATACT	ChIP assay
ID19-ChIP-2R	ACTTGGACCAAAGGCTCAAC	ChIP assay
clsy4-hyperDMR-1F	CCAAACGCCACAGAGAGTAA	ChIP assay
clsy4-hyperDMR-1R	CGCTTGGATTGCTTCCAATATC	ChIP assay
clsy4-hyperDMR-2F	ACTAAACTCTACAGAATTTGTTGGC	ChIP assay

clsy4-hyperDMR-2R	GGTAATATTGGGTTAGTCTAGGTGAT	ChIP assay
clsy4-hyperDMR-3F	TCTCCGCTTCTCTATTCCAAAC	ChIP assay
clsy4-hyperDMR-3R	AGGGACACTCAACAACTTCAT	ChIP assay
clsy4-hyperDMR-4F	GGGCTACTTGTTGTATACCTTGA	ChIP assay
clsy4-hyperDMR-4R	TCAGACAATCAGAACCCGAAATA	ChIP assay
clsy4-hyperDMR-5F	CATCGGACATACAAACCTGAAAC	ChIP assay
clsy4-hyperDMR-5R	CTGGAGAAGCTGAAACACTTTG	ChIP assay
clsy4-hyperDMR-6F	ACACATAGTCTCTTCGCTTGAC	ChIP assay
clsy4-hyperDMR-6R	CCGAGCTGCTTGATGACTT	ChIP assay
clsy4-hyperDMR-7F	CCTTCTGATGAGTGTTAGGTTCT	ChIP assay
clsy4-hyperDMR-7R	TCAATTGGTAATAGGTGGAGTGA	ChIP assay
clsy4-hyperDMR-8F	AAAGCTCCGATGTTTGGATAGA	ChIP assay
clsy4-hyperDMR-8R	CACATGATTTGGTGGAGGAGA	ChIP assay
clsy4-hyperDMR-9F	TAGAGCAACTCCAACCTTGTATC	ChIP assay
clsy4-hyperDMR-9R	GCTAAGGCTTGTTGGTTTCATT	ChIP assay
clsy4-hyperDMR-10F	CAGTCAAGCTTCCTTGTTCATTAC	ChIP assay
clsy4-hyperDMR-10R	ATGCATGGTTGCCCATCT	ChIP assay
Tublin8-RealF	ATAACCGTTTCAAATTCTCTCTCTC	ChIP assay
Tublin8-RealR	TGCAAATCGTTCTCTCCTTG	ChIP assay
ros1-hyperDMR-1F	CCAAGAAGCCAAGCAGGAAA	ChIP assay
ros1-hyperDMR-1R	TGCTTGAATCGGTGTCTTCG	ChIP assay
ros1-hyperDMR-2F	ACAGTGTTCGTAAAGATGTAGCC	ChIP assay
ros1-hyperDMR-2R	AGCACATCACAATGAACGTA	ChIP assay
ros1-hyperDMR-3F	AACTCAGGCAACGGTATGGT	ChIP assay
ros1-hyperDMR-3R	CCGCGTCGAGGAAATAAGTC	ChIP assay
ros1-hyperDMR-4F	TGGTCCAAATTATTTCTCCAAAGACA	ChIP assay
ros1-hyperDMR-4R	TATATCAGGCGGGAGCGTAG	ChIP assay
DTF1-ChIP-1F	GATCTACCAACGAACCTCCATC	ChIP assay
DTF1-ChIP-1R	TCCTCCTTCTTTGTGGCTTAAT	ChIP assay
DTF1-ChIP-2F	CGCCTACCTCTGTACCTTCTTA	ChIP assay
DTF1-ChIP-2R	CTGGTGGATTTCTTCGTCAGTC	ChIP assay
DTF1-ChIP-3F	TAGCTAATAACATAAGAGTGCACCA	ChIP assay
DTF1-ChIP-3R	AAACCGACTATCGTTTCTTATCTCT	ChIP assay
DTF1-ChIP-4F	CCCATATTGAAACGGTGGATTA	ChIP assay
DTF1-ChIP-4R	TGGTGCACTCTTATGTTATTAGC	ChIP assay
DTF1-ChIP-5F	CACGTGGAATTCAGTGGATGA	ChIP assay
DTF1-ChIP-5R	CGTCCTGTATCATCACATCAGC	ChIP assay
DTF1-ChIP-6F	TGTTATTAAGTAACGTCATTCCAAACCC	ChIP assay
DTF1-ChIP-6R	ATTAGCGGTGTACTGCGGTT	ChIP assay
DTF1-ChIP-7F	GGCTTATTGTACATTATCTCGATCTC	ChIP assay
DTF1-ChIP-7R	TGTTACCGACAATACCCTAACC	ChIP assay
IGN5-ChopF	TCCCGAGAAGAGTAGAACAAATGCTAAAA	Chop-PCR
IGN5-ChopR	CTGAGGTATTCCATAGCCCCTGATCC	Chop-PCR
Solo-LTR-ChopF	ATTAACCACACGCTGCATCTAAT	Chop-PCR
Solo-LTR-ChopR	GAGAGACGATCGTGCTGATAAC	Chop-PCR
AtSN1-ChopF	ACTTAATTAGCACTCAAATTAAACAAAATAAGT	Chop-PCR
AtSN1-ChopR	TTTAAACATAAGAAGAAGTTCCTTTTTCATCTAC	Chop-PCR

PM36-ChopF	TGACCTGCATAGGCTATAACACA	Chop-PCR
PM36-ChopR	ATTGGAATCAATCCGAGTGG	Chop-PCR
PM27-ChopF	ATAGATCCTAATAGAGGCGTAA	Chop-PCR
PM27-ChopR	AGAATAACAAATGGCACAGA	Chop-PCR
Pm36-Bis-F	GTAGTTTGAGATGATTAATGATAGAGTT	Bisulphite sequencing
Pm36-Bis-R	AAACTTATTCAATCTTCAATACTCTAC	Bisulphite sequencing
Pm27-Bis-F	GATTATTTAGTYGGTATTTYGAYGAGT	Bisulphite sequencing
Pm27-Bis-R	CCAAAAAATACTTAAATCCATAAATCTTAA	Bisulphite sequencing
ID2-Bis-F	AGGGGTAAAAATGAGAGGATTAATTTA	Bisulphite sequencing
ID2-Bis-R	CTCTTACCTCTAAATTATATAACATT	Bisulphite sequencing
ID19-Bis-F	GATAGAAATGTATGAATTTTTTTAGAG	Bisulphite sequencing
ID19-Bis-R	TCACAAAATAACTACAAAAATATATAT	Bisulphite sequencing
ID30-Bis-F	GTATGTTTTTTTATATATAAAAGAGAGT	Bisulphite sequencing
ID30-Bis-R	ATCTTATCCTCATTAATCACACATAACA	Bisulphite sequencing
CLSY4-F	ATGAATTCGAAGCTAAAATCAAGCAAAAAACG	Gene cloning
CLSY4-R	TATCTAGAGAAGAAGCTGGTATTCATGTCAG	Gene cloning
Pm36-probeF	TGACCTGCATAGGCTATAACACA	Northern blotting
Pm36-probeR	ATTGGAATCAATCCGAGTGG	Northern blotting
ID2-probeF	AAGATCCTGTCATCACTGGAAAA	Northern blotting
ID2-probeR	TGGTGACAGTGCTTGTGGTT	Northern blotting
ID19-probeF	TTCTCTCTAAAGGGCCACCA	Northern blotting
ID19-probeR	TCTATCCGAACATTGGCACA	Northern blotting
miR171-probe	GATATTGGCGCGGCTCAATCA	Northern blotting
DD1-probeF	CGGGATCGATAGGATCTTCA	Northern blotting
DD1-probeR	GTTTTGCCTCTTTGGTGGTC	Northern blotting
DD2-probeF	CCTTTCTCTTGTTCGCCCTA	Northern blotting
DD2-probeR	CAAGGTTCGGGAAAAGATCA	Northern blotting
DD3-probeF	CTCTCCACATGTTTTGGGTTA	Northern blotting
DD3-probeR	TTCCAAGATGAGAACTGCACA	Northern blotting
DD12-probeF	CGGTGATGCAAACGGATAG	Northern blotting
DD12-probeR	TGGCAAAACTAACGCACAAA	Northern blotting
miR167-probe	TAGATCATGCTGGCAGCTTCA	Northern blotting