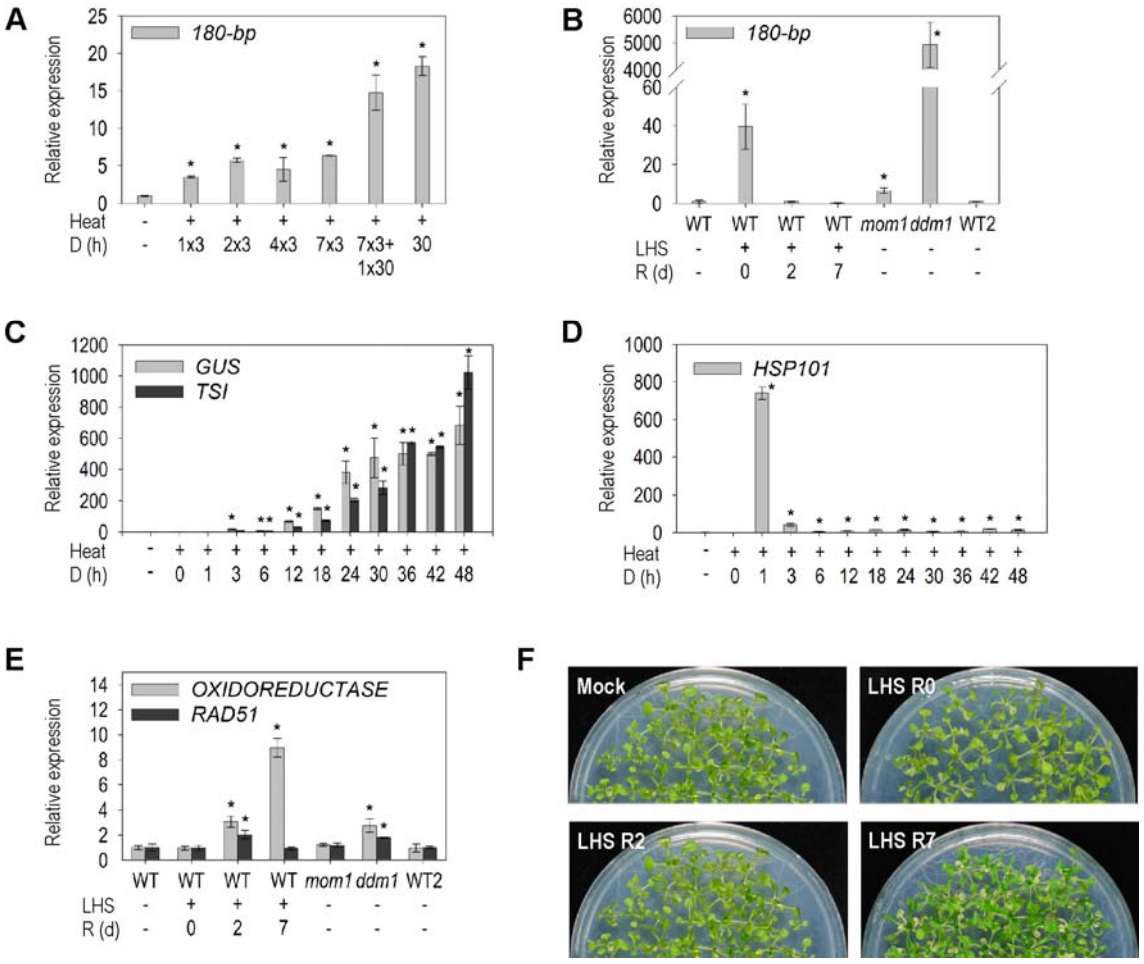
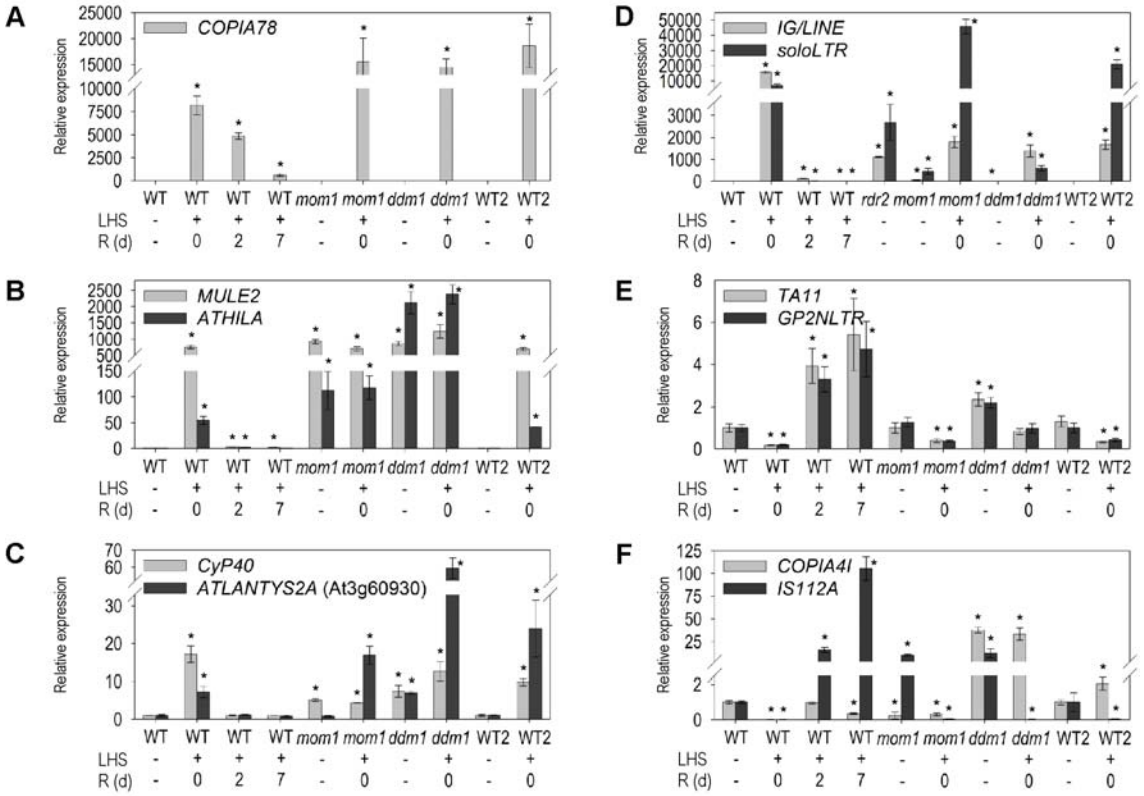
Supplemental data to Pecinka et al., "Epigenetic control of repetitive elements is attenuated by prolonged heat stress in *Arabidopsis"*



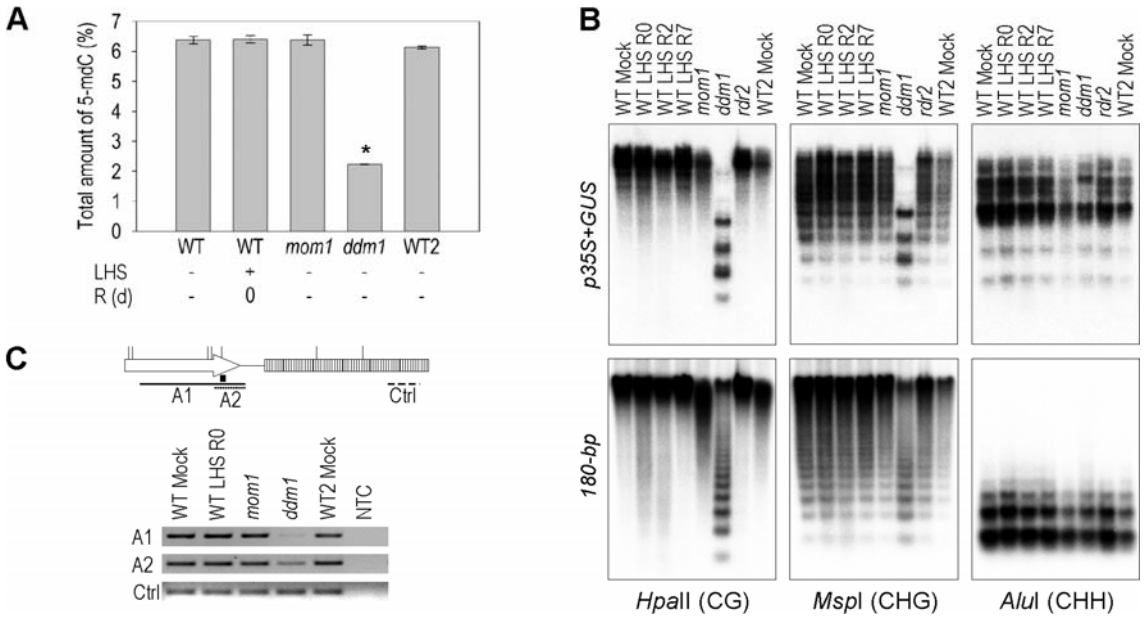
Supplemental Figure 1. LHS transiently abolishes TGS.

(A-C) Expression analysis of transcriptional gene silencing markers *180-bp*, *GUS* and *TSI* repeats, **(D)** heat stress marker *HSP101*, **(E)** senescence marker *OXIDOREDUCTASE* and DNA repair marker *RAD51* by qRT-PCR after short and long heat stress (SHS and LHS, respectively; D = duration in hours and R = recovery in days). Error bars indicate SD of triplicate measurement. Statistically significant differences to mock-treated wild type are indicated by asterisks (t-test, *P<0.05*). **(F)** Phenotype of L5 plants after mock-treatment or LHS-treatment without or with 2 or 7 days of recovery (R0, R2 and R7, respectively).



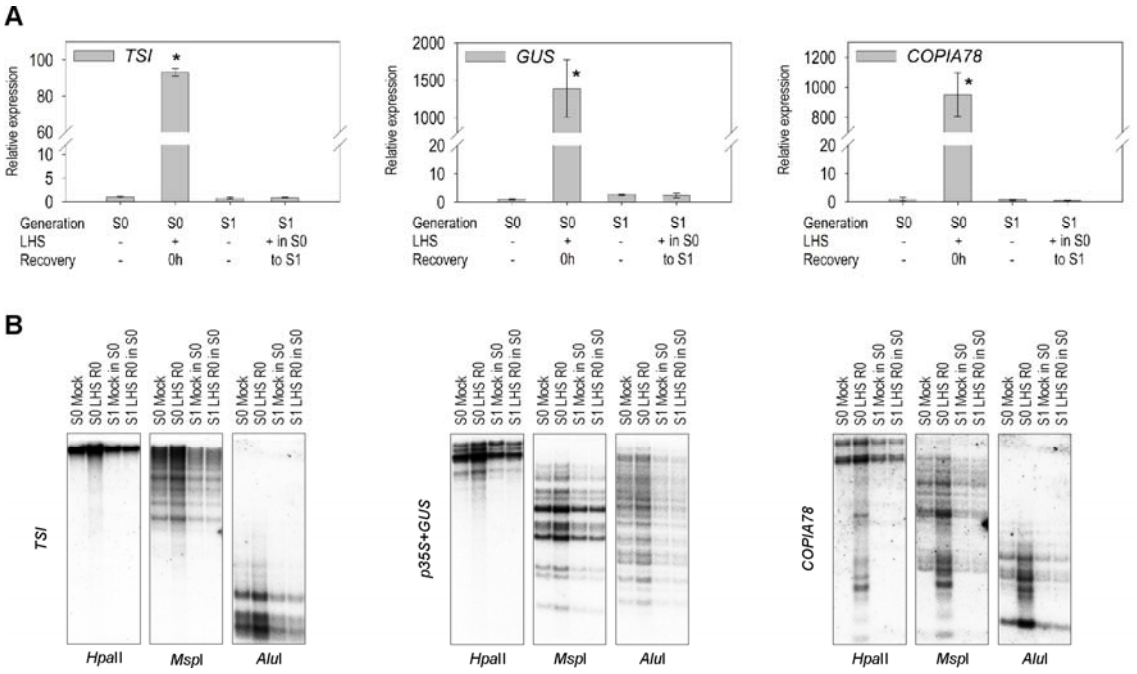
Supplemental Figure 2. Expression of endogenous TGS targets under LHS.

(A-F) Transcripts identified in the ATH1 data set as differentially expressed by LHS or controlled by RdDM (*IG/LINE* and *soloLTR*) were quantified by qRT-PCR after LHS with or without recovery (R) for 2 or 7 days. Their levels were compared to those in TGS mutants with or without LHS. Error bars indicate SD of triplicate measurement. Statistically significant differences to mock-treated wild type are indicated by asterisks (t-test, $P<0.05$).



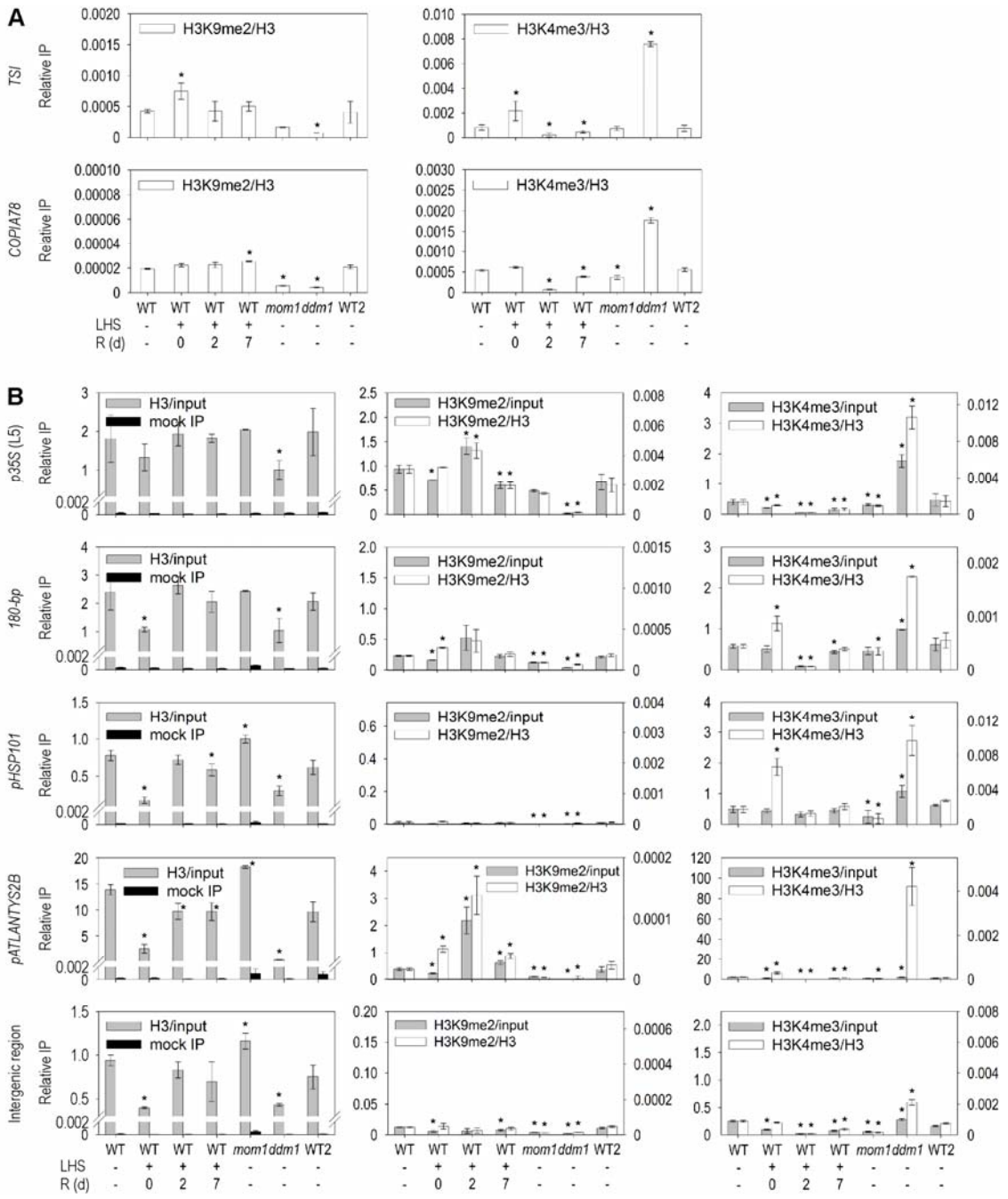
Supplemental Figure 3. DNA methylation analysis after LHS.

(A) HPLC measurements of global DNA methylation are expressed as percentages of 5-methyl deoxycytidine (5-mdC) in relation to the total amount of cytosine. Statistically significant difference to mock-treated wild type is indicated by an asterisk (t-test, *P<0.05*). **(B)** Methylation analysis for *p35S+GUS* and *180-bp* by Southern blotting of LHS samples without (R0) and with recovery for 2 or 7 days (R2 and R7). **(C)** Methylation analysis of a specific CG-containing transcription factor binding site (black box) in the CaMV35S promoter (arrow) upstream of the GUS coding region (dashed box) of the L5 transgene. The PCR amplicons A1 (full horizontal line), A2 (dotted horizontal line) and Ctrl (dashed horizontal line) overlap with three, one and no *Tai*I restriction sites (vertical bars), respectively. The results of PCR for A1, A2 and Ctrl in mock- or LHS-treated samples, transcriptional gene silencing mutants *mom1* and *ddm1*, and template-free controls (NTC) are shown below.



Supplemental Figure 4. LHS-activated TGS targets are transcriptionally silenced and DNA is methylated in the next generation.

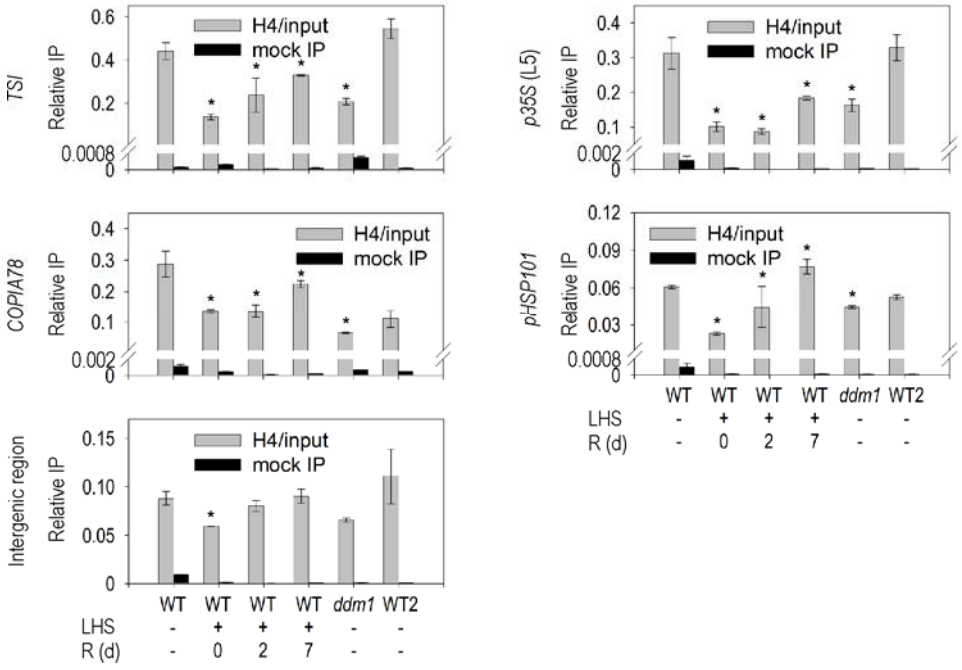
(A) qRT-PCR expression analysis and **(B)** DNA blot methylation analysis of TGS markers *TSI*, *GUS* and *COPIA78* in mock,and LHS-treated plants (S0), and in their non-stressed progeny (S1). **(A-B)** All tested targets showed complete transcriptional silencing and full DNA methylation in the S1 generation. Error bars indicate SD of triplicate measurement. **(A)** Statistically significant differences to mock-treated wild type in corresponding generations are indicated by asterisks (t-test, $P<0.05$).



Supplemental Figure 5. Analysis of histone H3 modification and occupancy after LHS.

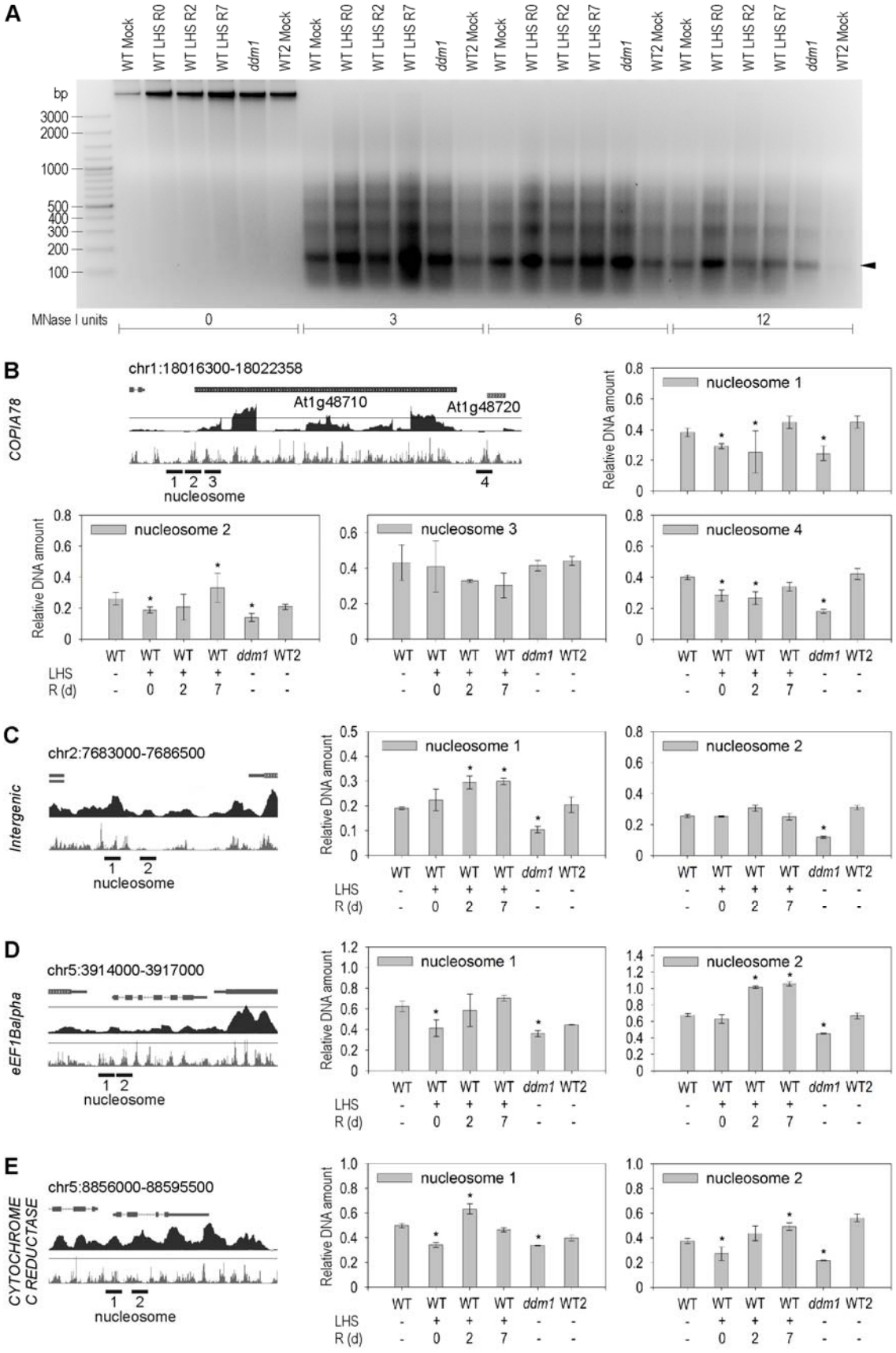
(A) Histone H3 modifications (H3K9me2, H3K4me3) at *TSI* and *COPIA78* were assessed by ChIP and qPCR relative to H3. For data relative to input see Figure 2B. **(B)** Histone H3 occupancy (left panels) and histone modifications (middle and right panels) relative to input (left y-axis) or H3 (right y-axis) are shown for additional target regions. With the exception of the *180-bp* repeats

and the intergenic region, the 3' regions of corresponding promoters were analyzed. *ATLANTYS2B* was not transcriptionally activated by LHS (see footnote 13 in Table S1). The intergenic region is located between genes At2g01670 and At2g01680. The expression of neither sequence is affected by LHS. Error bars indicate SD of triplicate measurement. Statistically significant differences to mock-treated wild type are indicated by asterisks (t-test, $P<0.05$).



Supplemental Figure 6. Analysis of histone H4 occupancy after LHS.

Histone H4 amounts relative to input were assessed by ChIP and qPCR. With the exception of the intergenic region, the 3' regions of the corresponding promoters were analyzed. The intergenic region is located between genes At2g01670 and At2g01680. The expression of this sequence is not affected by LHS. Error bars indicate SD of triplicate measurements. Statistically significant differences to mock-treated wild type are indicated by asterisks (t-test, *P<0.05*).


A
WT Mock
WT LHS R0
WT LHS R2
WT LHS R7
ddm1
WT2 Mock
bp
3000
2000
1000
500
400
300
200
100
MNase I units
0
3
6
12
B
COPIA78
chr1:18016300-18022358
At1g48710
At1g48720
1 2 3
nucleosome
4
nucleosome 1
nucleosome 2
nucleosome 3
nucleosome 4
Relative DNA amount
WT WT WT WT ddm1 WT2
LHS - + + + - -
R (d) - 0 2 7 - -
C
Intergenic
chr2:7683000-7686500
1 2
nucleosome
D
eEF1Balpha
chr5:3914000-3917000
E
CYTOCHROME C REDUCTASE
chr5:8856000-88595500

Supplemental Figure 7. Analysis of nucleosome occupancy after LHS.

(A) Ethidium bromide-stained agarose gel of mock-treated or heat-stressed samples after digestion with 0, 3, 6 and 12 units of MNase I. The arrowhead indicates the position of the mononucleosome fraction. **(B-E)** Nucleosome occupancy was analyzed by qPCR for samples treated with 12 units of MNase I and normalized to untreated samples. Primers were positioned within regions associated with individual nucleosomes according to the genome-wide nucleosome map of Arabidopsis (Chodavarapu et al., 2010) (smooth peaks, upper row) or according to bioinformatic prediction of nucleosome loading (Segal et al., 2006) (unrefined peaks, lower row). **(B)** For *COPIA78*, 5' regions of two neighboring elements (At1g48710 and At1g48720) were analyzed. Error bars indicate SD of triplicate measurement. Statistically significant differences to mock-treated wild type are indicated by asterisks (t-test, $P<0.05$). **(C)** The intergenic region is the same as for the ChIP analysis. **(D-E)** These target genes were found to be significantly up-regulated by LHS according to the microarray data.

Supplemental Table 1. Repeats with significantly altered expression after SHS and LHS without (R0) and after 2 days (R2) of recovery.

ATH1 ID	ORF	Repeat Annotation[1]	Expression (Log fold-change)[2]			Verified by
			SHS R0	LHS R0	LHS R2	qRT-PCR
256136_s_at	multiple	*COPIA78*[3)11)]	-	6.996	5.325	+
255246_at	AT4G05640	*ATHILA6A*[4)12)]	-	5.507	-	+
265483_at	AT2G15790	*MULE2; CyP40 (SQN)*[5)]	4.012	5.279	-	+
255987_s_at	multiple	*ARNOLD1*[6)]	-	3.828	-	
264451_s_at	multiple	*COPIA78*[3)11)]	2.684	3.147	-	+
261389_s_at	multiple	*ROMANIAT5*[7)]	-	2.751	-	
246178_s_at	multiple	*ATLANTYS2A*[4)13)]	4.759	2.609	-	+
254985_x_at	multiple	*GP1I*[4)]	-	2.605	-	
262578_at	AT1G15300	*TAG2*[7)]	-	2.473	-	
260622_at	AT1G07980	*REP2*[8)]	-	2.281	-	
262699_at	AT1G75980	*REP10*[8)]	2.267	-	-	
267576_at	AT2G30640	*ARNOLD2*[6)]	-	2.137	-	
250279_at	AT5G13200	*COPIA78LTR*[3)]	-	2.008	-	
258952_at	AT3G01410	*ATLANTYS1*[4)]	-2.201	-	-	
248510_at	AT5G50315	*MULE13*[5)]	-2.216	-	-	
253049_at	AT4G37300	*LINE1*[10)]	-	-2.378	-	
255365_at	AT4G04040	*REPX1*[8)]	-	-2.435	-	
262382_at	AT1G72920	*TA11*[4)]	-	-2.579	-	+
252170_at	AT3G50480	*META1*[4)]	-	-2.670	-	
257057_at	AT3G15310	*IS112A*[9)]	-2.746	-	-	
249727_at	AT5G35490	*IS112A*[9)]	-	-3.184	-	+
265893_at	AT2G15040	*GP2NLTR*[4)]	-	-3.204	-	+
259560_at	AT1G21270	*COPIA22I*[3)]	-	-3.502	-	
245448_at	AT4G16860	*COPIA4LTR*[3)]	-	-3.611	-	
262010_at	AT1G35612	*VANDAL12*[5)]	-	-3.962	-	
245449_at	AT4G16870	*COPIA4I*[3)]	-3.590	-5.385	-	+

[1)] According to (Slotkin et al., 2009).

[2)] Based on Affymetrix ATH1 array data, only significantly up or downregulated repeats are listed.

[3)] Retrotransposon.LTR.Copia, [4)] Retrotransposon.LTR.Gypsy, [5-6)] Transposon.MuDR. TIR[5)] or nonTIR[6)], [7-9)] Transposon.nonMuDR. HAT[7)] Helitron[8)] or IS112[9)], [10)]Retrotransposon.nonLTR.

[11)] qRT-PCR primers used in this study can amplify from series of *COPIA78* elements covering ATH1 probesets 256136_s_at and 264451_s_at.

[12)] ATH1 probeset 255246_at, annotated as *ATHILA6A,* can crosshybridize with other *ATHILA* elements. qRT-PCR primers were based on the *ATHILA6A* sequence but may amplify from multiple *ATHILA* copies.

[13)] Probeset 246178_s_at hybridizes with two elements. *ATLANTYS2A* (AT3G60930) is activated by LHS (Table 1 and Supplementary Fig. 2c) while *ATLANTYS2B* (AT5G28430) remains silent (data not shown).

Supplemental Table 2. Activation of genes in a nuclear cluster of mitochondrial origin under SHS and LHS without (R0) and after 2 days (R2) of recovery.

DNA origin	ATH1 ID[1]	ATH1 expression (Log fold-change)			ORF		Identification of origin[2]		
		SHS R0	LHS R0	LHS R2	nuclear	mitochondrial	SNPs	LHS R0 clones	Expressed copy
nuclear	265548_s_at	-0.27	0.00	0.00	AT2G07620 AT3G31980	-			
	265551_at	0.15	0.00	0.00	AT2G07630	-			
	263058_at	0.28	0.00	0.00	AT2G07650	-			
	263059_at	0.03	0.00	0.00	AT2G07660	-			
mitochondrial insert	257318_at[3]	3.72	7.60	0.27	AT2G07777	ORF262[3]			
	263502_s_at	4.33	7.12	2.09	AT2G07675	ATMG00980			
	263504_s_at	4.16	5.95	0.00	AT2G07677	ATMG00940	1	13	100% nuclear
	263505_s_at	4.22	4.50	0.07	AT2G07678	ATMG00920			
	263510_s_at	5.24	4.31	0.14	AT2G07681 AT2G07771	ATMG00900			
	244914_at[3]	1.19	5.51	0.00	AT2G07682	multiple[3][4]			
	263508_s_at	0.18	0.16	0.00	AT2G07685	ATMG00760			
	244910_s_at	2.05	3.48	0.00	AT2G07686	ATMG00750			
	263509_s_at	3.97	8.94	2.23	AT2G07687	ATMG00730			
	265241_at[3]	1.38	1.68	0.00	AT2G07693	ORF111C[3]			
	265227_s_at	2.27	6.53	0.14	AT2G07695	ATMG01280	2	13	100% mitochondrial
	265238_s_at	2.33	5.07	0.41	AT2G07696	ATMG01270			
	257326_s_at	0.12	3.87	0.00	AT2G07697	ATMG01230			
	265228_s_at	2.48	7.18	1.48	AT2G07698	ATMG01190			
	266012_s_at	3.30	8.07	2.65	AT2G07699 AT2G07741	ATMG00410 ATMG01170			
	265229_s_at	5.32	7.12	0.00	AT2G07701	ATMG00430 ATMG01150			
	265242_at[3]	3.96	4.99	0.00	AT2G07705	unannotated[3]			
	265237_s_at	1.75	2.27	0.00	AT2G07706	ATMG00470			
	265230_s_at	2.78	6.07	0.68	AT2G07707	ATMG00480			
	257338_s_at	4.26	7.54	1.90	AT2G07711	ATMG00513	3	10	100% nuclear
	265236_s_at	0.28	0.00	0.00	AT2G07714	ATMG00550			
	244928_s_at	1.74	4.79	0.06	AT2G07716	ATMG00570			
	265233_s_at	1.72	2.75	0.58	AT2G07718	ATMG00590			
	265235_s_at	3.70	4.29	0.31	AT2G07719	ATMG00610			
	265234_at[3]	2.10	3.80	0.00	AT2G07721	unannotated[3]			
	266043_at[3]	0.34	0.70	0.08	AT2G07724	ORF107B[3]			
	266044_s_at	4.37	6.02	0.80	AT2G07725	ATMG00210			
	266046_at[3]	2.58	3.07	0.00	AT2G07728	unannotated[3]			
	244953_s_at	5.93	7.99	2.09	AT2G07731	ATMG00270			
	244954_s_at	3.31	5.59	0.07	AT2G07732	ATMG00280			
	266042_s_at	3.20	4.60	1.35	AT2G07734	ATMG00290			
	244956_s_at	1.33	1.89	0.08	AT2G07737	ATMG00310			
nuclear	266040_at	0.66	2.04	0.01	AT2G07738	?			
	266038_at	-2.33	-0.74	-0.14	AT2G07680	-			
	266959_at	-0.85	5.11	-0.14	AT2G07690	-			
	266961_at	0.21	-0.01	0.00	AT2G07720	-			
	266931_at	0.20	0.00	0.00	AT2G07730	-			
	257361_at	0.18	-0.09	0.00	AT2G07740	-			

[1] Ordered as on chromosome 2

[2] Based on polymorphisms between nuclear and mitochondrial copies

[3] No mitochondrial ORF specified for this ATH1 ID. Corresponding ORF was found by blast search with nuclear copy cDNA sequence

[4] ORFs: 107E, 121B, 158, 184, 187.

Expression values:

- ≥2
- 1 to 2
- -1 to 1
- ≤-1

Supplemental Table 3. Primers used in this study.

Target	ORF	Primer name	DNA sequence (5' to 3')	Application
180-bp	multiple	180bpF siRNA	ACCATCAAAGCTTTGAGAAGCAAGAAGAAGCTT	qRT-PCR, qChIP-PCR, FISH and Southern blot probe amplification
		180bpR siRNA	CCATATGAGTCTTTGTCTTTGTATCTTCT	
263504_s_at	AT2G07677	PrA2-F	GACTTTGTGGTGAAGGCAGAA	Detection of transcript origin (nuclear versus mitochondrial)
	ATMG00940	PrA2-R	GGGAATAGTGAAGGGGATCTT	
265227_s_at	AT2G07695	PrB-F	CAATTTCTCCTTGTGATGCAG	Detection of transcript origin (nuclear versus mitochondrial)
	ATMG01280	PrB-R	CTGCCCTTTCTCTTTTCCAA	
257338_s_at	AT2G07711	PrD2-F	TGCTTGCGGCATCTCTAACT	Detection of transcript origin (nuclear versus mitochondrial)
	ATMG00513	PrD2-R	CCG AGA GCC AGA AGT ATT GA	
5S rDNA and rRNA	multiple	5SrRNAqF	GATCATACCAGCACTAATGCACCGGATCC	qRT-PCR, FISH probe amplification
		5SrRNAqR	GAGGACTTCCCGGGAGGTCACCCAT	
ATLANTYS2	AT3G60930	AT3G60930qF	GATGCTGAGGTAAATCTTAATCGCT	qRT-PCR (LHS activated)
		AT3G60930qR	TTCGGATGGTCGATTATCCTTGGCA	
	AT5G28430	AT5G28430qF	GAGAAAATATGCCGAGGCGGA	qRT-PCR, qChIP-PCR (LHS not activated)
		AT5G28430qR	ATAGCCGAATCATACGAATGTACCA	
ATHILA6A	(At4g05640)	ATHILA6AqF	CAGGTCGAGTAACCTCAGGTCA	qRT-PCR
	mutiple	ATHILA6AqR	GAGTAACTTGGTAGAGTGAATGGTC	
CaMV p35S	-	qP35-Tail-F	CTTCAAAGCAAGTGGATTGATGTGATATC	methylation sensitive PCR, qChIP-PCR (2nd and 3rd)
		qP35-Tail-2F	GTGGATTGATGTGATATCTCCACTGA	
		qP35-Tail-R	CTGGTGATTTCAGCGTGTCCTCTCCAAAT	
		P35SPr2	CACAAACCAAGGCAAGTAATAGAG	Southern blot probe amplification
		GU3	GAATGCCCACAGGCCGTCGAG	
COPIA4I	At4g16870	AtCOPIA4qF	ACCTTACTCACTCAAGCTTCGGTTCC	qRT-PCR
		AtCOPIA4qR	GTTGTTGTTGGTGAAGGACCGTACA	
COPIA78	multiple	COPIA78qF2	CGGTGCTCACAAAGAGCAACTATG	qRT-PCR, qChIP-PCR
		COPIA78qR3	ATCCTTGATAGATTAGACAGAGAGCT	
		COPIA78mSB-F	TCTAGAATCATCTTCCACCTCCTTA	methylation sensitive Southern blot probe
		COPIA78qR3	ATCCTTGATAGATTAGACAGAGAGCT	
		COPIA78-710nu0qF	CACTTAAACACTTTCTCCATTACCTCT	MNase I sensitivity, nucleosome 1 in this paper
		COPIA78-710nu0qR	CGTAGACTCCAATTATCATAGTTGCTC	
		COPIA78-710nu-1qF	CTTATGTAAGAACTCTCTAGACTTAGGA	MNase I sensitivity, nucleosome 2 in this paper
		COPIA78-710nu-1qR	CTTGAATACAACTTCACAACATTGCAACA	
		COPIA78qFnu1	CTTGAGAAGTAATCGGAGACAAGTTCA	MNase I sensitivity, nucleosome 3 in this paper
		COPIA78qRnu1	TGGGAGAAGCTTCGAACCTCTTACA	
		COPIA78-720qFnu0	GCAATGTTGTGAAGTTGTATTCAAGT	MNase I sensitivity, nucleosome 4 in this paper
		COPIA78-720qRnu0	CAAGCTCTGATACCACTTTGTTAGAGT	
CyP40 (SQN)	At2g15790	CyP40qF	TCTGAATGAAAGCCCAGCTGAGTTATCT	qRT-PCR
		CyP40qR	TTACGCAAGGCAGTACTCGTCTCTTCA	
CYTOCHROME C REDUCTASE	At5g25450	CYTOCqFnu0	GACGCCATTATCTTCTTCGGAGT	MNase I sensitivity, nucleosome 1 in this paper
		CYTOCqRnu0	TCATACGACGGCGTTTAAACAGATGT	
		CYTOCqFnu1	TGCGTGCAATGGATCTTTCTATGA	MNase I sensitivity, nucleosome 2 in this paper
		CYTOCqRnu1	CTTGCAAGCTCTATCTACAAACTCCA	
eEF1Balpha1	AT5G12110	eEFIBqFnu0	GAGCTCGTCTTCTCTCCACAGAAACT	MNase I sensitivity, nucleosome 1 in this paper
		eEFIBqRnu0	TATGCGTGTTTACCCGGAGATGTA	
		eEFIBqFnu1	ACTTACATCTTGGAACTCGGTTTTGT	MNase I sensitivity, nucleosome 2 in this paper
		eEFIBqRnu1	GAGAAGCAACAGAATCGTACCACT	
GP2NLTR	AT2G15040	AtGP2NLTRqF	TTGCTCTTCTTTCGAGGAGAATGCA	qRT-PCR
		AtGP2NLTRqR	GTATGAATCCAATTGTAGCTGCTATCC	

Supplemental Table 3. Primers used in this study (continued).

Target	ORF	Primer name	DNA sequence (5' to 3')	Application
GUS	-	qPCR-GUS-F	TTAACTATGCCGGAATCCATCGC	qRT-PCR
		qPCR-GUS-R	CACCACCTGCCAGTCAACAGACGC	
		qPCR-GUS-F	TTAACTATGCCGGAATCCATCGC	Southern blot probe amplification
		GUS-R short	CCCGGCTAACGTATCCACGCCGTA	
HPT	-	HPTqF	GGGTAAATAGCTGCGCCGATGGTT	qRT-PCR, qChIP-PCR
		HPTqR	CACGGCGGGAGATGCAATAGGTC	
HSFA2	At2g26150	HSFA2qF	TCCAAGCTTGGGGACTATGGAGGA	qRT-PCR
		HSFA2qR	CTCCTTAGTAGGCATCGAATTATTCG	
		HSFA2qFnu0	GTAACGAAGTTTCTGGAACATTGTCT	MNase I sensitivity, nucleosome 1 in this paper
		HSFA2qR2nu0	ATGAAATTATAAGGGGAGAGAAGAGA	
		HSFA2qFnu1	CCACCACCGTTTCTGACTAAGACT	MNase I sensitivity, nucleosome 2 in this paper
		HSFA2qRnu1	AGGAGAGTTGTTGAGAACTTATGAGAA	
HSP101	At1g74310	HSP101qF	TGAGCTAGCTGTGAATGCAGGACATGCTC	qRT-PCR
		HSP101qR	ATCACTCTTTCAGCAGATTGAGCTGCGTT	
		pHSP101qF	TCTCTGGTAGCTTCTAGTTCTATGCA	qChIP-PCR
		pHSP101qR	TTCTTCAATGAGCCAGAGGACTTCT	
Intergenic between At2g17670 and 80	-	IG-2g17670-80qF	GGCTACTGTCTAGTTCATATCTTAGA	qChIP-PCR
		IG-2g17670-80qR	TAGGTTGGCATCCGATCCAGAGT	
		IG-2g17670qFnu2	TCTTGCATATCTATGACTATGTACTCT	MNase I sensitivity, nucleosome 1 in this paper
		IG-2g17670qRnu2	AATTATCTCTCTGTGACCACGAACA	
		IG-2qF-nu3	ACTCAAACTATATATCACGCCACAAT	MNase I sensitivity, nucleosome 2 in this paper
		IG-2qR-nu3	CGTAGTTATTTAAGATGTGTGTATAATAACC	
IG/LINE	At5g27845	soloLINEqF	GTGACATCAAAGAAGAATGGGGGACTTG	qRT-PCR
		soloLINEqR	TCCCTGAAGTATCTTGCTTTTGACATTCG	
IS112A	AT5G35490	AtIS112AqF	GAAGCTATTGCTTATTACGATCTATGGA	qRT-PCR
		AtIS112AqR	ATTGTAGAACTCGAAAGACTCGCTCA	
MULE2	At2g15800	MULE_2g15800qF	TACAAGCTTCCAGAAGAGGAAATCTAT	qRT-PCR
		MULE_2g15800qR	TGCAGGCTCCTCGTCTATGATATCTTC	
OXIDOREDUCTASE	At4g10500	At4g10500qF	GAGCGGTTATCGATTCCGACTTTCT	qRT-PCR
		At4g10500qR	TTTGAAGGCGTCTAGACAGCTCGCA	
RAD51	AT5G20850	AtRAD51fwd	CTCCGAGGAAGGATCTCTTGCAG	qRT-PCR
		AtRAD51rev	GCTCGCACTAGTGAACCCCAGAGG	
solo-LTR	-	LTR_625-F	AACTAACGTCATTACATACACATCTTG	qRT-PCR
		LTR_625-R	AATTAGGATCTTGTTTGCCAGCTA	
TA11	AT1G72920	Ta11qF	TCATGAGAAAGTAGCTTCGTGGAGA	qRT-PCR
		Ta11qR	AACCTTCAACCAACCAACCTTCAAC	
TSI	-	TSIqF	CTCTACCCTTTGCATTCATGAATCCTT	qRT-PCR, qChIP-PCR
		TSIqR	GATGGGCAAAAGCCCTCGGTTTTAAAATG	
		TSI probe F	GCTGACCTCCTTATTAGAGCAG	Southern blot probe amplification
		TSI probe R A2	CAGCTTGTCTGGTTGAGTGCGGA	
		TSIqFnu1	TCAAGCCATGTATCACTTGTGAGTGT	MNase I sensitivity, nucleosome 1 in this paper
		TSIqRnu1	CTAGTCTGAAAAATGTGAACTAGAACT	
		TSIqFnu2	ATTCATGAATGCAAAGGGTAGAGTTAG	MNase I sensitivity, nucleosome 2 in this paper
		TSIqRnu2	GCTTTAGTAGAATGCTAAAGGTAAGT	
UBC28	At1g64230	UBC28qF	TCCAGAAGGATCCTCCAACTTCCTGCAGT	qRT-PCR
		UBC28qR	ATGGTTACGAGAAAGACACCGCCTGAATA	