Supplementary tables

Genotype	Treatment	Leaf area (mm^2)	Leaf number	Plant height (mm)	Fresh weight - FW (mg)	Dry weight - DW (mg)	RWC (%)	Water content (g g(DW)$^{-1}$)	A (mM CO$_2$ plant^{-1} h^{-1})	Fv/Fm	fPSII	qP	NPQ	SPAD
WT	Control	403 a	7.0 a	15.38 a	103.9 a	10.7 a	82.0 a	8.69 a	16.25 a	0.807 ab	0.446 a	0.951 ab	1.561 a	29.0 a
h1.3		365 a	6.5 a	5.38 b	89.5 a	9.3 a	77.4 b	8.45 a	14.06 a	0.817 ac	0.456 a	0.968 a	1.590 a	27.7 a
WT	Low light/ drought	62 b	5.4 b	6.50 b	8.5 b	0.8 b	84.3 a	9.69 ab	1.98 b	0.789 b	0.484 a	0.882 c	1.027 b	19.6 b
h1.3		142 c	6.3 ab	7.38 b	18.8 c	1.5 c	78.0 b	11.69 b	4.49 c	0.836 c	0.588 b	0.915 bc	0.931 c	20.6 b

Table S1. Growth analysis and physiological parameters of wild-type (WT) and *h1.3* plants in the early-growth phase experiment. Homogeneity groups are marked with letters ($p<0.05$, Tukey's HSD test).

Genotype	**Treatment**	**Leaf area (cm^2)**		**Leaf number**		**Plant height (cm)**		**Fresh weight - FW (mg)**		**Dry weight DW (mg)**		**RWC (%)**		**Water content (g g(DW)$^{-1}$)**		**Pn (mM CO$_2$ plant^{-1} h^{-1})**		**Fv/Fm**		**fPSII**		**qP**		**NPQ**		**SPAD**	
WT	Control	25	a	25.9	a	19.9	a	1797	a	190	a	84.9	a	8.52	abc	98.35	a	0.845	a	0.670	abc	0.949	ab	0.731	a	39.9	a
h1.3		24	a	30.1	a	20.3	a	1648	a	209	a	83.2	a	8.02	bc	63.48	b	0.841	abc	0.684	a	0.960	ac	0.664	a	37.5	ab
h1.3 /H1.3		26	a	29.3	a	16.6	b	1697	a	188	a	86.0	a	9.74	ab	99.48	a	0.834	c	0.687	a	0.976	c	0.673	a	38.1	ab
WT	Drought/low light	5	b	14.4	b	10.7	c	219	b	22	b	72.3	b	7.72	c	6.75	c	0.846	abc	0.648	bcd	0.923	d	0.842	b	33.5	b
h1.3		8	c	18.9	c	7.0	d	470	c	34	c	70.2	c	7.73	c	8.52	d	0.846	abc	0.642	cd	0.911	d	0.708	a	40.6	a
h1.3 /H1.3		5	b	14.0	b	8.8	cd	184	b	22	b	72.9	b	8.40	bc	5.79	c	0.839	abc	0.627	d	0.928	bd	0.850	b	33.2	b

Table S2. Growth analysis and physiological parameters of wild-type (WT) and *h1.3* plants, and the *h1.3* mutant complemented with H1.3-GFP (*h1.3*/H1.3) in the late-growth phase experiment. Homogeneity groups are indicated by letters ($p<0.05$, Tukey’s HSD test).

Observation	***H1 subtype***	***p-value***
H1 **enrichment on transposons** compared to the whole genome	Main variants	$p<10^{-167}$
	H1.3 LL	10^{-27}
H1 **depletion on introns** compared to the whole genome	Main variants	$p<10^{-166}$
	H1.3 LL	10^{-87}
H1 **depletion on 5'ends** compared to whole genes	Main variants	$p<10^{-230}$
	H1.3 LL	
H1 **enrichment on exons** compared to whole genes	Main variants	$p<10^{-4}$
	H1.3 LL	0.009

Table S3. Statistics for H1 enrichment and depletion at genic features. Supplementary to Figure 5A and Figure S15.

	DNA methylation context		
	CG	**CHG**	**CHH**
Mutant - WT			
h1.1h1.2h1.3	[0.131, 0.151] [a] 2.009e-26 [b] [-0.005, 0.05] [c] 2.154e-84 [d]	[0.111, 0.181][a] 5.407e-256[b] [-0.021, 0.12] [c] 0.0 [d]	[0.068, 0.097] [a] 1.570e-101 [b] [-0.016, 0.012] [c] 4.966e-70 [d]
h1.3 (control)	[0.073, 0.091] [a] 2.483e-66 [b] [-0.001, -0.005] [c] 0.005 [d]	[0.061, 0.102] [a] 9.906e-164 [b] [-0.001, -0.013] [c] 1.041e-10 [d]	[0.039, 0.067] [a] 1.14e-121 [b] [0.001, -0.002] [c] 0.003 [d]
h1.3 (stress)	[0.063, 0.081] [a] 2.75e-75 [b] [-0.004, -0.001] [c] 0.072 [d]	[0.056, 0.092] [a] 1.318e-172 [b] [-0.007, -0.005] [c] 0.161 [d]	[0.042, 0.067] [a] 1.252e-127 [b] [-0.008, -0.008] [c] 0.808 [d]
Response to stress (Stress - control)			
WT	[0.052, 0.077] [a] 1.555e-134 [b] [0.007, 0.012] [c] 4.853e-05 [d]	[0.054, 0.09] [a] 1.027e-170 [b] [0.012, 0.020] [c] 3.929e-07 [d]	[0.040, 0.067] [a] 4.516e-121 [b] [0.013, 0.028] [c] 1.281e-43 [d]
h1.3	[0.059, 0.083] [a] 1.216e-102 [b] [0.004, 0.017] [c] 1.731e-17 [d]	[0.061, 0.101] [a] 2.563e-164 [b] [0.007, 0.028] [c] 4.918e-33 [d]	[0.041, 0.069] [a] 4.188e-146 [b] [0.004, 0.022] [c] 4.895e-58 [d]

Table S4. Statistics for changes in methylation of euchromatic and heterochromatic transposable elements (TEs). Euchromatic TEs – 6499 TEs with the lowest H3K9me2 level; heterochromatic TEs – 5188 TEs with the highest H3K9me2 level. Letters indicate the following: a – standard deviations, b – Levene (Brown-Forsythe) test p-value, c – mean values, d – T-test. The first value in brackets is for euchromatic TEs and the second is for heterochromatic TEs.

	DNA methylation context		
	CG	**CHG**	**CHH**
Mutant - WT			
h1.1h1.2h1.3	[0.059, 0.138] [a] 1.799e-159 [b] [0.0014, 0.0053] [c] 0.092 [d]	[0.047, 0.135] [a] 0.0 [b] [0.0016, 0.0400] [c] 2.683e-81 [d]	[0.032, 0.075] [a] 5.226e-165 [b] [0.0010, -0.0040] [c] 6.924e-05 [d]
h1.3 (control)	[0.032, 0.076] [a] 9.687e-155 [b] [-0.0004, -0.0049] [c] 0.0008 [d]	[0.027, 0.072] [a] 1.118e-217 [b] [0.0000, -0.0028] [c] 0.016 [d]	[0.018, 0.049] [a] 4.204e-187 [b] [-0.0002, 0.0018] [c] 0.008 [d]
h1.3 (stress)	[0.028, 0.069] [a] 7.868e-152 [b] [-0.0028, -0.0021] [c] 0.566 [d]	[0.025, 0.067] [a] 6.684e-247 [b] [-0.0032, -0.0038] [c] 0.581 [d]	[0.019, 0.051] [a] 2.576e-174 [b] [-0.0031, -0.0067] [c] 3.154e-06 [d]
Response to stress (Stress - control)			
WT	[0.023, 0.053] [a] 1.387e-177 [b] [0.0041, 0.0063] [c] 0.018 [d]	[0.023, 0.063] [a] 2.373e-214 [b] [0.005, 0.01] [c] 1.716e-07 [d]	[0.019, 0.036] [a] 2.036e-58 [b] [0.0047, 0.0092] [c] 6.661e-16 [d]
h1.3	[0.026, 0.065] [a] 1.292e-228 [b] [0.0019, 0.0089] [c] 3.938e-11 [d]	[0.025, 0.071] [a] 1.088e-237 [b] [0.002, 0.009] [c] 5.322e-12 [d]	[0.019, 0.047] [a] 7.899e-182 [b] [0.0016, 0.0083] [c] 1.988e-18 [d]

Table S5. Statistics for changes in methylation of euchromatic and heterochromatic genes. Euchromatic genes – 17,026 genes with the lowest H3K9me2 level; heterochromatic genes – 1308 genes with the highest H3K9me2 level. Letters indicate the following: a – standard deviations, b – Levene (Brown-Forsythe) test p-value, c – mean values, d – T-test. The first value in brackets is for euchromatic genes and the second is for heterochromatic genes.

CG	***h1.3***	**WT stress**	***h1.3* stress**
WT	0.0008	3.2593e-33	
h1.3			1.6916e-17
WT stress			8.9125e-12

CHG	***h1.3***	**WT stress**	***h1.3* stress**
WT	9.4357e-18	1.5502e-197	
h1.3			1.9566e-122
WT stress			1.0462e-49

CHH	***h1.3***	**WT stress**	***h1.3* stress**
WT	0.3106	<10e-256	
h1.3			<10e-256
WT stress			<10e-256

Table S6. Statistics (T-test) for differences in the average global methylation level between genotypes and conditions in three different DNA methylation contexts. Supplementary to Figure 8A.

Name	**Sequence 5'→ 3'**	**Aim**
156AW_L	GAAAACCACCACTCATCCTCCATACTTTCA	*h1.3* genotyping
157AW_R	CCTTCTTCACTTTCCTCTTCTTTTCTTGTTTGTTC	
Ds5-4_R	TACGATAACGGTCGGTACGG	
164AW_ins-L	TTCTTTTGATTTATAAGGGATTTTGCCGATTT	*h1.1* genotyping
165AW_gen_R	CAGTCTTAGGTTTAACGGCGATTGTTTTCTT	
166AW_gen_L	AAACGAATTTCATCGAGTATATCACGAGTTATGG	
167AW_gen_L	CGTTACAATCGCATCTTTAATCATCTGCATC	*h1.2* genotyping
168AW_ins_R	CATCATACTCATTGCTGATCCATGTAGATTTCC	
169AW_gen_R	GCACACCAATACAATACACAAAAGCACCTATC	
13MP_H1.3_SalI_L	GTCGACAAGTCATGCAGAACTCCATTG	Cloning the promoter and coding region (without stop codon) of H1.3
14MP_H1.3_BamHI_R	GGATCCAGCAGCGGAAGCTTTCATG	
19MP_H1.3utr_EcoRI_L	GAATTCTGATCACTGAGGAGGAGGAG	Cloning the 3'UTR of H1.3
10MP_H1.3utr_NcoI_R	CCATGGACGAGACTTTGGGAGCAAGA	
H1.1qPCR3-R	CCCTAAGGCGGCAGCGGAGA	qPCR, expression of H1.1
H1.1qPCR3-L	GCAGTGGCACGAGGAACGGG	
H1.2_qPCR_L	GTCTGTTGCTGCTGTTTCCA	qPCR, expression of H1.2
H1.2_qPCR_R	CCGGAGCCTTCTTAGTCACA	
H1.3_qPCR_L	CGGATCAAGCCCTTATGCTA	qPCR, expression of H1.3
H1.3_qPCR_R	CCTGCTGCCTCGTTATCATC	
ml83_SPCH_F	TAAGCCCAAGAAAACCGCCT	qPCR, expression of SPCH
ml84_SPCH_R	ATGAGTGGTAGTTGCGGTGG	
ml85_MKK7/MKK9_F	ATTTTCCTTTGCTTCCGCCG	qPCR, expression of MKK7/MKK9
ml86_MKK7/MKK9_R	GCGGTTCTCCAAAACACACC	
ml91_TMM_F	TAAGCCCAAGAAAACCGCCT	qPCR, expression of TMM
ml92_TMM_R	ATGAGTGGTAGTTGCGGTGG	
ml99_JAZ1_F	TTCGTCGGTAGCCGGAGATT	qPCR, expression
ml100_JAZ1_R	CGTGAGTTGCCTAAAGTTCCA	

		of JAZ1
ml101_EXPA11_F	GCCGCTCTTTTTATTGCGGT	qPCR, expression of EXPA11
ml102_EXPA11_R	GCTCCACCCATTGTTCCAGA	
ml105_CSLA03_F	AGTTGTGGCAGAGAAGAAAGC	qPCR, expression of CSLA03
ml106_CSLA03_R	CCACAGGACTTGAAACCAACC	
ml107_AGP21_F	CCAAGCCCAACTTCTGATGC	qPCR, expression of AGP21
ml108_AGP21_R	ACCAGATGCCAAAGCAACAA	
ml109_WAKL10_F	GACATCCCGTACCCGTTTGG	qPCR, expression of WAKL10
ml110_WAKL10_R	CCTACGTTAAAGAACCGGCGA	
ml113_EXPA6_F	GGCAATGTTGGGCTTGGTTT	qPCR, expression of EXPA6
ml114_EXPA6_R	ACCGTAGAAAGTGGCGTGAG	
ml115_FAD3_F	CATCAAACCCTTTCTTCACCAC	qPCR, expression of FAD3
ml116_FAD3_R	GTTCACATTGGTGCGTTGGT	
ml117_ERF38_F	AGACGACGGAGAGAAGAGTG	qPCR, expression of ERF38
ml118_ERF38_R	TGGAGAAAGTACCGAGCCAG	
ml119_ANNAT4_F	ATACTGCGGTGGTGATGTGG	qPCR, expression of ANNAT4
ml120_ANNAT4_R	TGTGCATGAGACCTCAACGA	
ml121_CA1_F	CCTGCTCCTATCATTGCCCC	qPCR, expression of CA1
ml122_CA1_R	GCTGTGATCTGCTCCACCTT	
ml125_FAD5_F	CAGCGACGGAGGGAGATTAC	qPCR, expression of FAD5
ml126_FAD5_R	GCCCAAAAGCAACCGAAACA	
ml129_CWLP_F	TTGCGACTGTACCCCTCCTA	qPCR, expression of CWLP
ml130_CWLP_R	AGGCGGTTTGACTGGATGTT	
ml131_CSLG2_F	AAAAACCAGTTGCCTTCCGT	qPCR, expression of CSLG2
ml132_CSLG2_R	CTGTATGGAATGGTTCGCCG	
ml133_FAD6_F	ACTCTCGCCTTCCTACCACT	qPCR, expression of FAD6
ml134_FAD6_R	TCAAACTCCTCTGGCGGAAC	
ml135_HCF136_F	TCAATGGCGTCTCTGCAACT	qPCR, expression of HCF136
ml136_HCF136_R	ATTGGTACAGAAGCTCCCGC	
ml137_G6PD1_F	AGGGCGTGGAGGTTACTTTG	qPCR, expression of G6PD1
ml138_G6PD1_R	CCACATCTTCAAGCCGCAAC	
ml139_RBCS3B_F	CGAGTTAGAGCACGGAAACACT	qPCR, expression of RBCS3B
ml140_RBCS3B_R	ATTGGACTTGACGGGTGTTGT	
ml141_RBCS1B_F	GACAACACCCGTCAAGTCCA	qPCR,

ml142_RBCS1B_R	TGGGTTCCGGATAGTCAACATT	expression of RBCS1B
ml143_GAMT2_F	TACAACGGCGATACACTGCC	qPCR, expression of GAMT2
ml144_GAMT2_R	CTCTGGGAAAAAGCCGGTCA	
ml145_ABI2_F	TCGCTGTTCCATTCAGACCA	qPCR, expression of ABI2
ml146_ABI2_R	CGCCAGAACAAGAACTTTCCG	
ml147_AGP1_F	TCTTCCGCAGTGGCTCAATC	qPCR, expression of AGP1
ml148_AGP1_R	GAGCCGGTGAGATCCGTCTA	
ml149_ANNAT2_F	GTGCGTCTGCTTCGTCTCA	qPCR, expression of ANNAT2
ml150_ANNAT2_R	TGAGAGACGCCATTGTTGGG	
ml151_XTH6_F	GTTCATTCGGGTTTCCGCTC	qPCR, expression of XTH6
ml152_XTH6_R	ATGTGAGATTCCGACCAGGC	
ml155_COR27_F	GGTAACGGATGAGCCCGAAA	qPCR, expression of COR27
ml156_COR27_R	CAACGCTGATTTGGTCGTGG	
ml157_COR15B_F	GCCAATGAAACTGCGACTGA	qPCR, expression of COR15B
ml158_COR15B_R	TGAATCAGGACTTTGTGGCA	
ml161_AT4G30650_F	GGCGAGCAACATGGAAGTTTT	qPCR, expression of AT4G30650
ml162_AT4G30650_R	TGCAACAGCCACGTTTGAGA	
ml163_MUTE_L	CGAAAGACCCTAAACCGACCA	qPCR, expression of MUTE
ml164_MUTE_R	GGTAGTGGCGGCTCCTAAAC	
ml165_CYCA2,3_L	CCCCAAAGAGCGGATTCAGG	qPCR, expression of CYCA2,3
ml166_CYCA2,3_R	TGGCCGAGACACAGCATTTT	
183KR_FAMA_qPCR_L	AGACTGCGGAGAACAAGTCG	qPCR, expression of FAMA
184KR_FAMA_qPCR_R	TCTTAATCAGCTGTCCCGGC	
207KR_ERECTA_qPCR_L	CGTGGAACGTAACCGGAGAA	qPCR, expression of ERECTA
208KR_ERECTA_qPCR_R	ATGATCGATGCTTGGTCCCC	
ml1_UBC_F	CTGCGACTCAGGGAATCTTCTAA	qPCR, expression of UBC
ml2_UBC_R	TTGTGCCATTGAATTGAACCC	

Table S7. Sequences of oligonucleotide primers used in this study. Restriction enzyme sites are underlined.