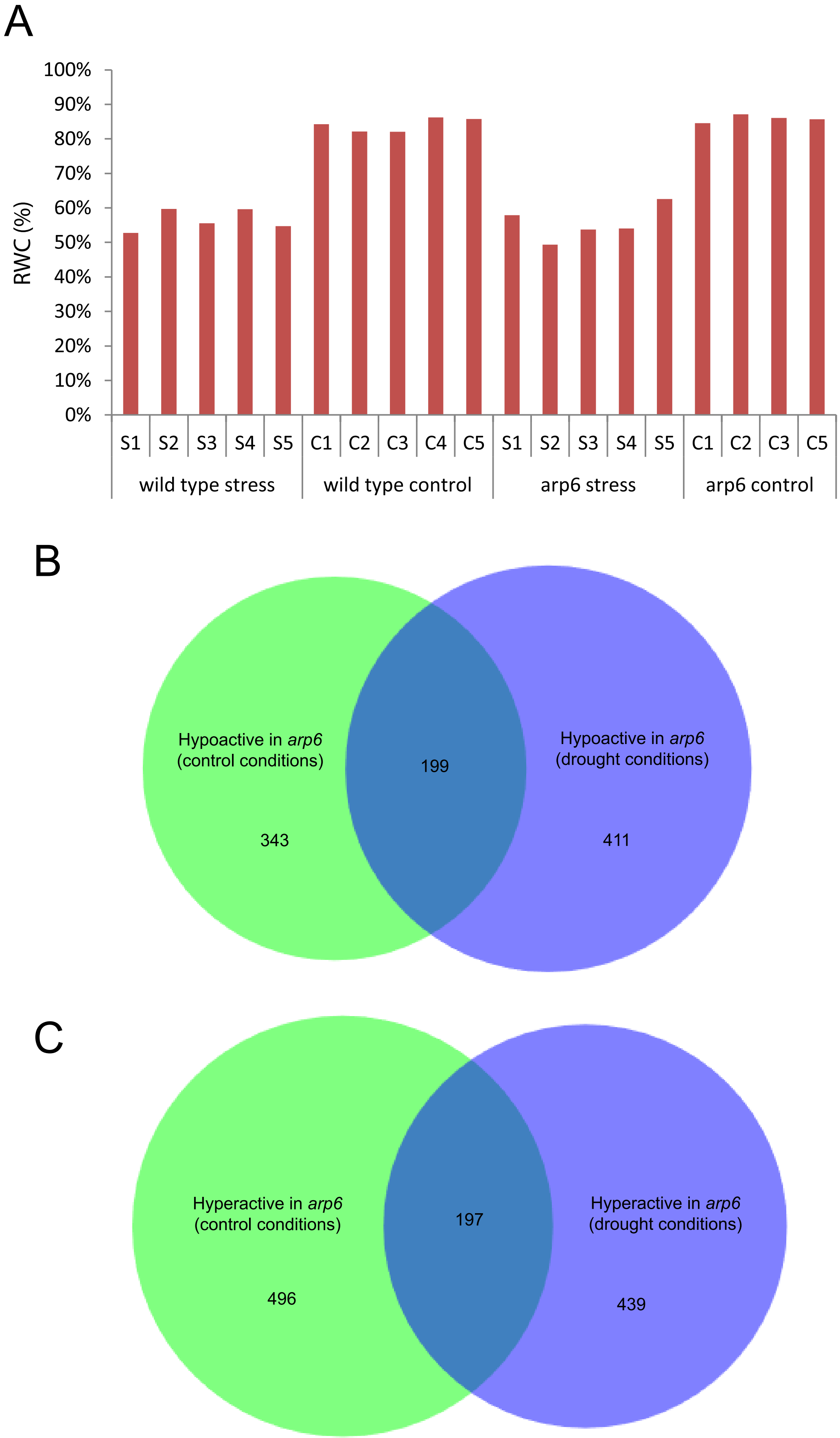
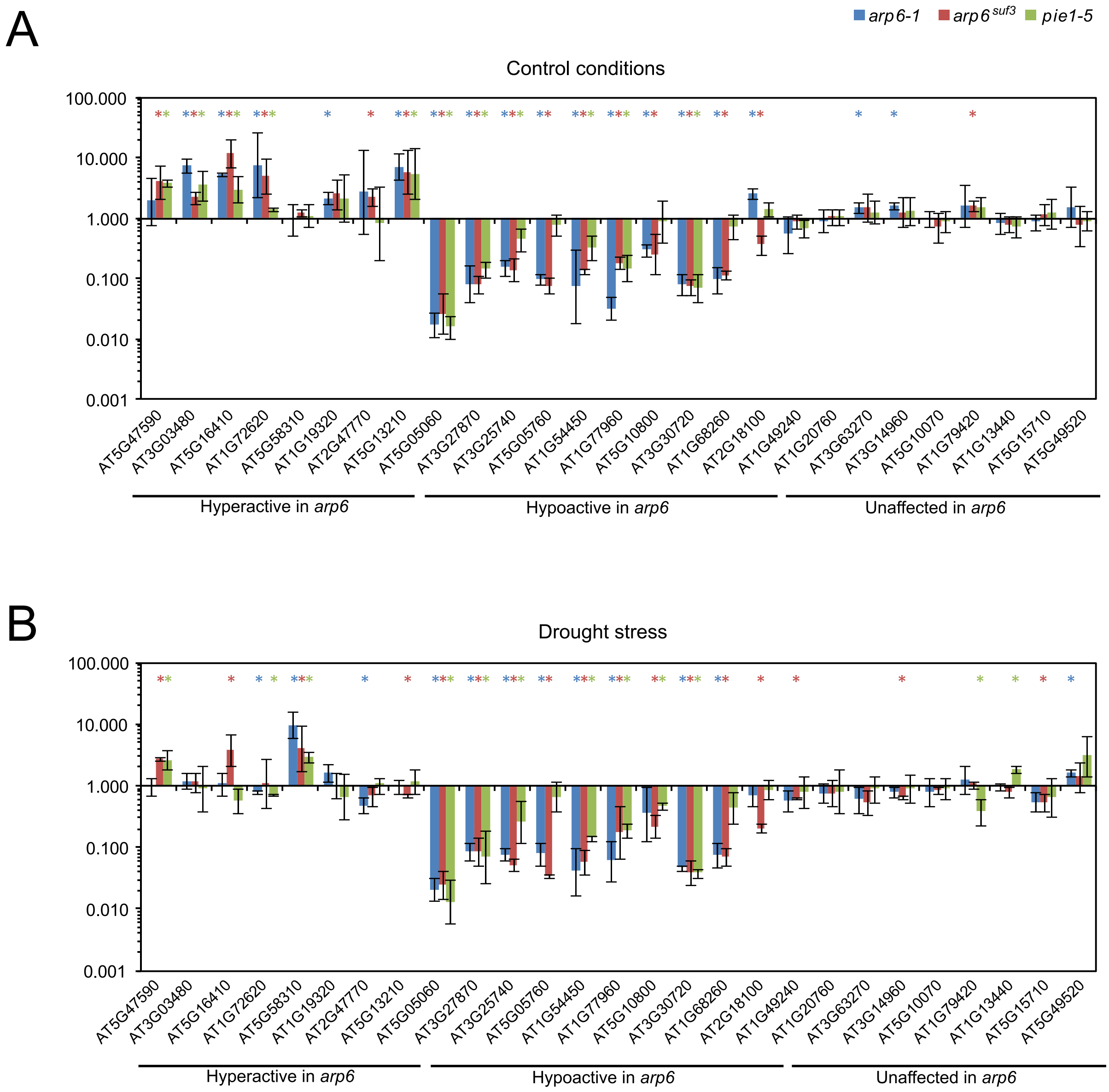
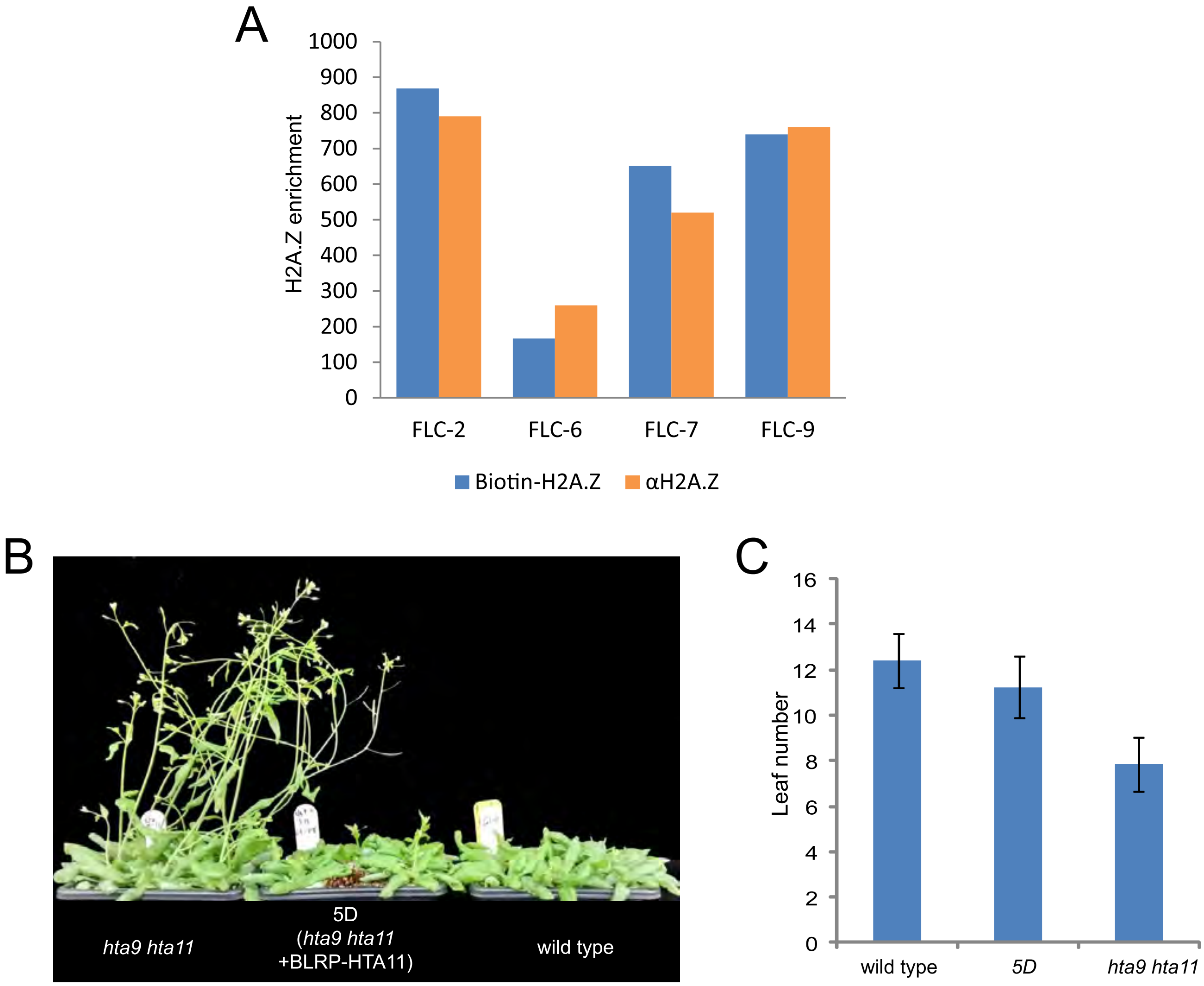


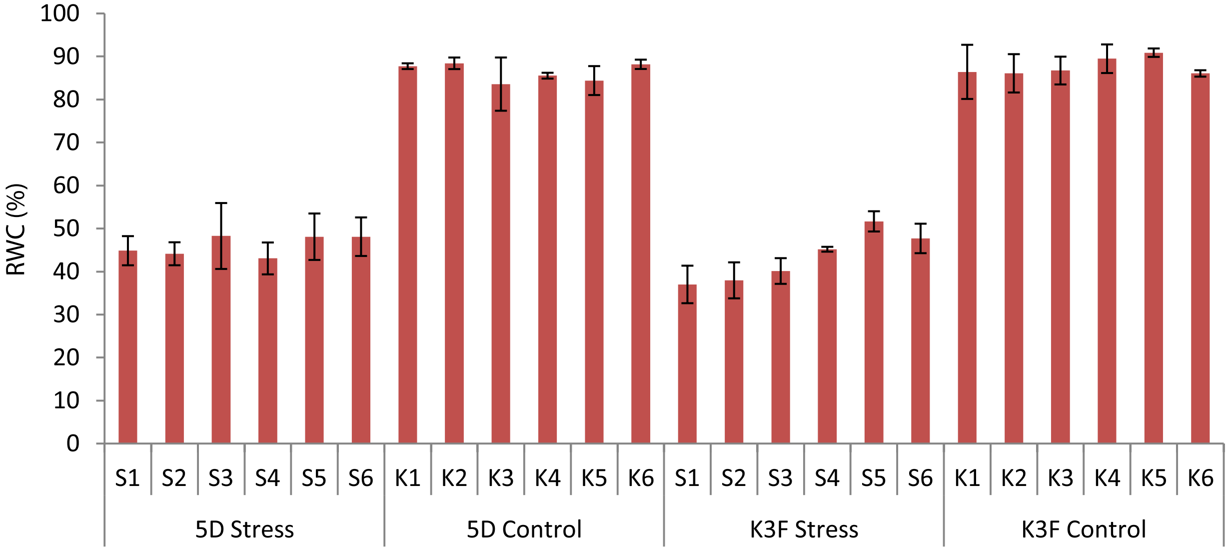
Supplemental Fig. 1. A) Comparison of the RWC for control plants and plants subjected to drought stress in wild-type and *arp6* plants used for RNA-seq and ChIP-seq analysis. **B)** Venn diagram showing genes hypoactive in *arp6* mutant in control and drought stress conditions. **C)** The same as in (B), but for genes hyperactive in *arp6* mutant.



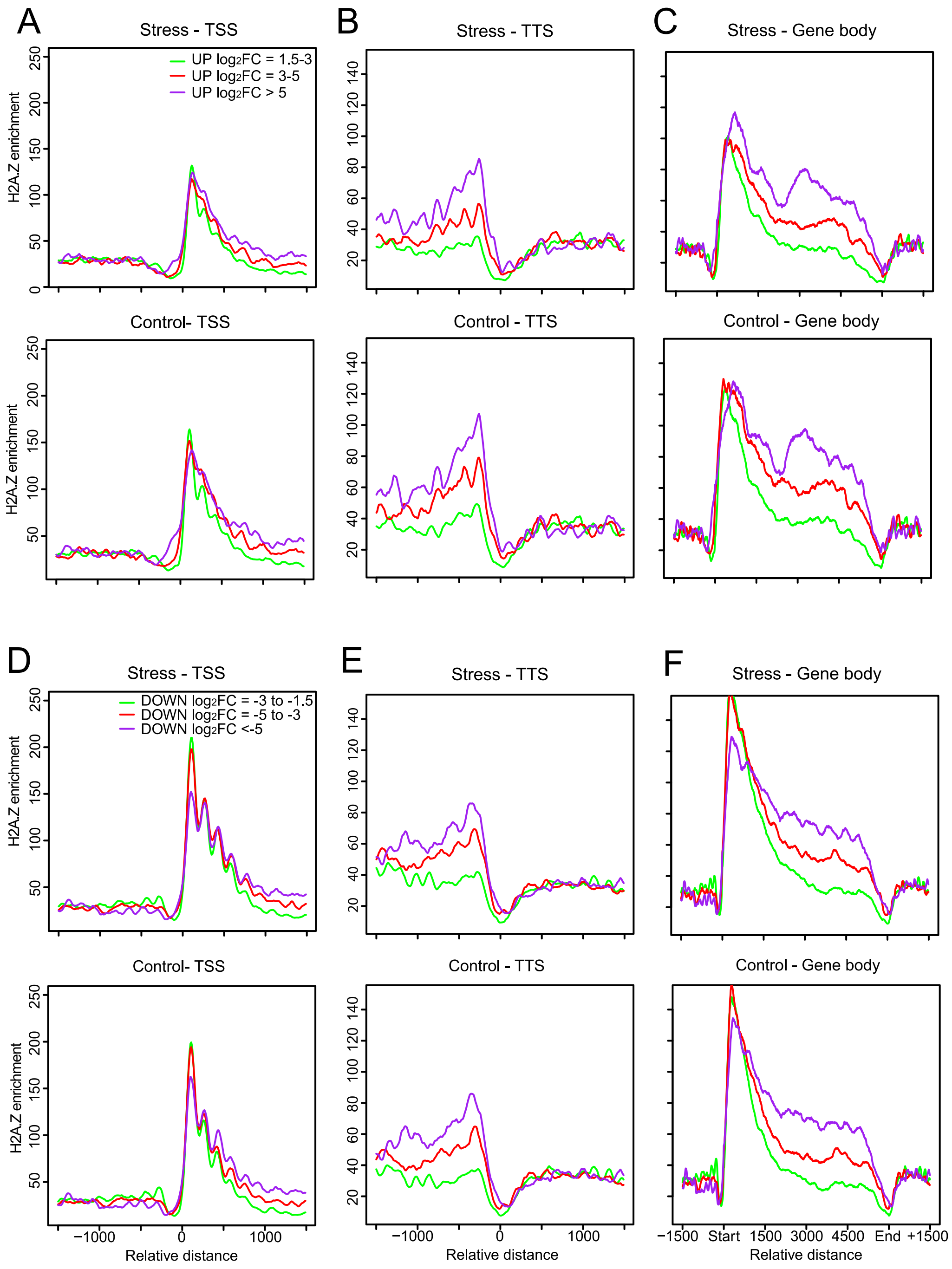
Supplemental Fig. 2. Different SWR1C mutants exhibit similar changes in transcription when compared to wild-type plants. **(A-B)** Expression level of selected genes which were hyperactive, hypoactive or unaffected in *arp6* according to RNA-seq results, measured by RT-qPCR in *arp6-1*, *arp6*^{suf3}, and *pie-1* mutant background as fold change relative to wt. Analysis was performed in control conditions **(A)** and drought stress **(B)**. Significantly different expression relative to wt is indicated as a star above each data point (color of stars correspond to color of the data series). Error bars represent SD of independent biological repeats.



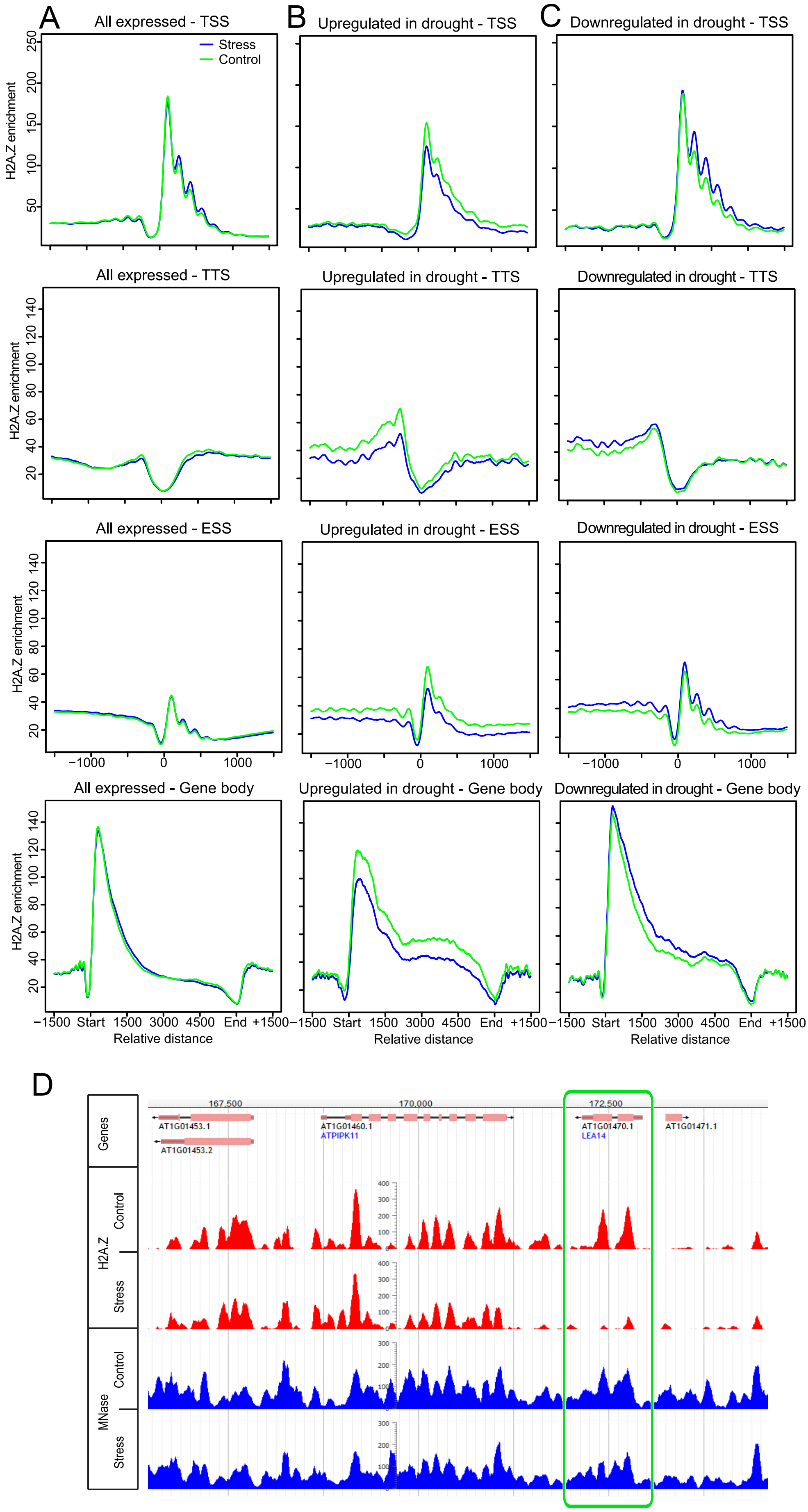
Supplemental Fig. 3. H2A.Z-tagged lines exhibit similar nucleosomal H2A.Z levels on the *FLC* gene and complement *hta9 hta11* mutations. **A)** Comparison of H2A.Z enrichment on the *FLC* gene for H2A.Z-tagged line 5D with endogenous H2A.Z at the locus (ChIP using αH2A.Z) based on the results described in Deal et al. (2007). The graph show average enrichment as measured by ChIP and quantitative PCR (delta delta Ct method). As the two datasets had different scales, the arbitrary units were used to simplify comparison. The line 5D was further used for the genome-wide ChAP-seq study. **B)** Early-flowering phenotype of *hta9 hta11* double mutant line is abolished by expression of HTA11-tagged construct used in the ChAP study. **C)** Rosette leaf number at the bolting time in wild type (*n*=27), *hta9 hta11* mutant (*n*=29), and the complemented mutant line 5D (*n*=30) as measured in LD conditions. Error bars show SD.



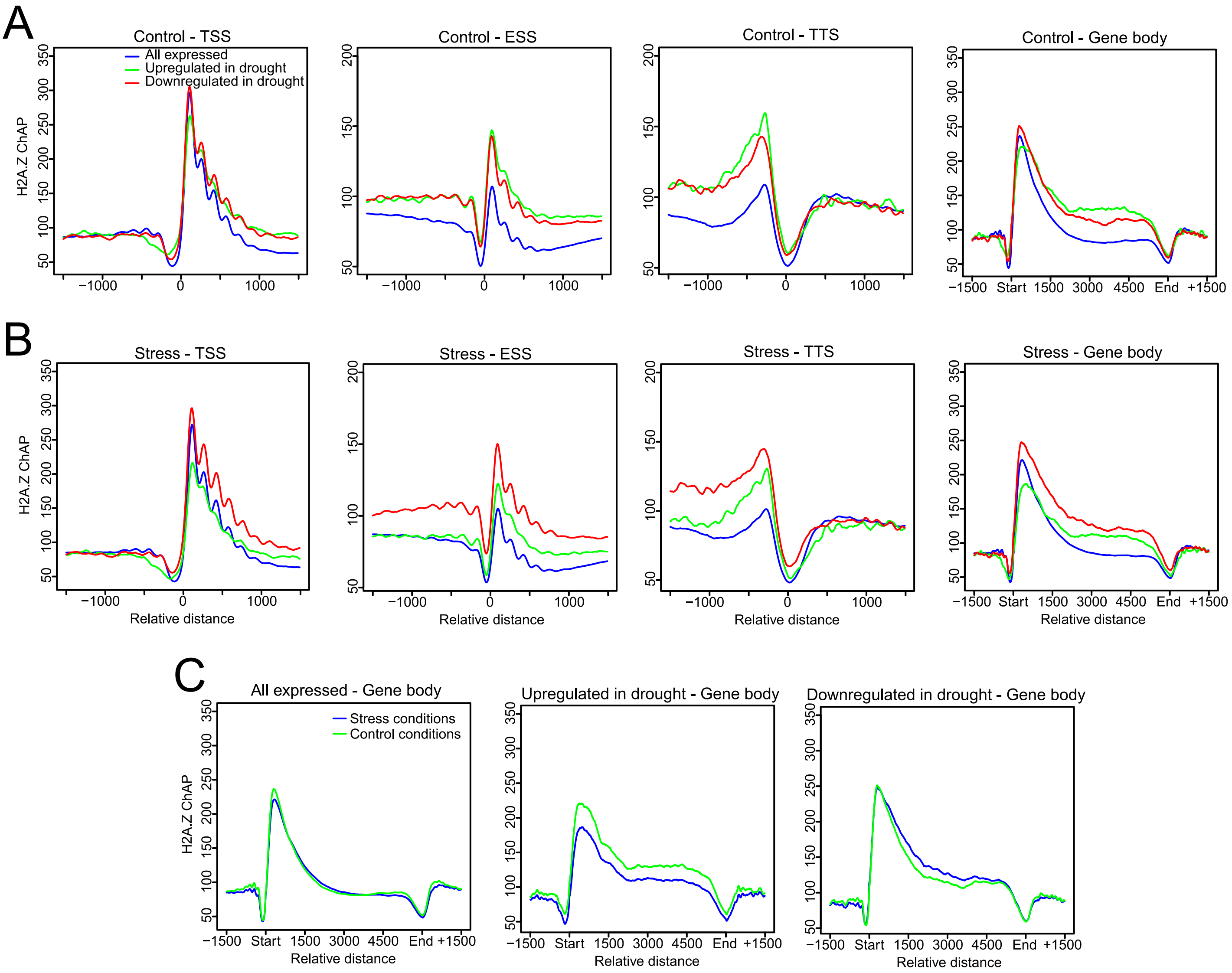
Supplemental Fig. 4. Comparison of the RWC for H2A.Z-tagged line 5D and lined K3F transformed with an empty vector in control and drought stress conditions. Error bars represent standard deviations from three technical replicates.



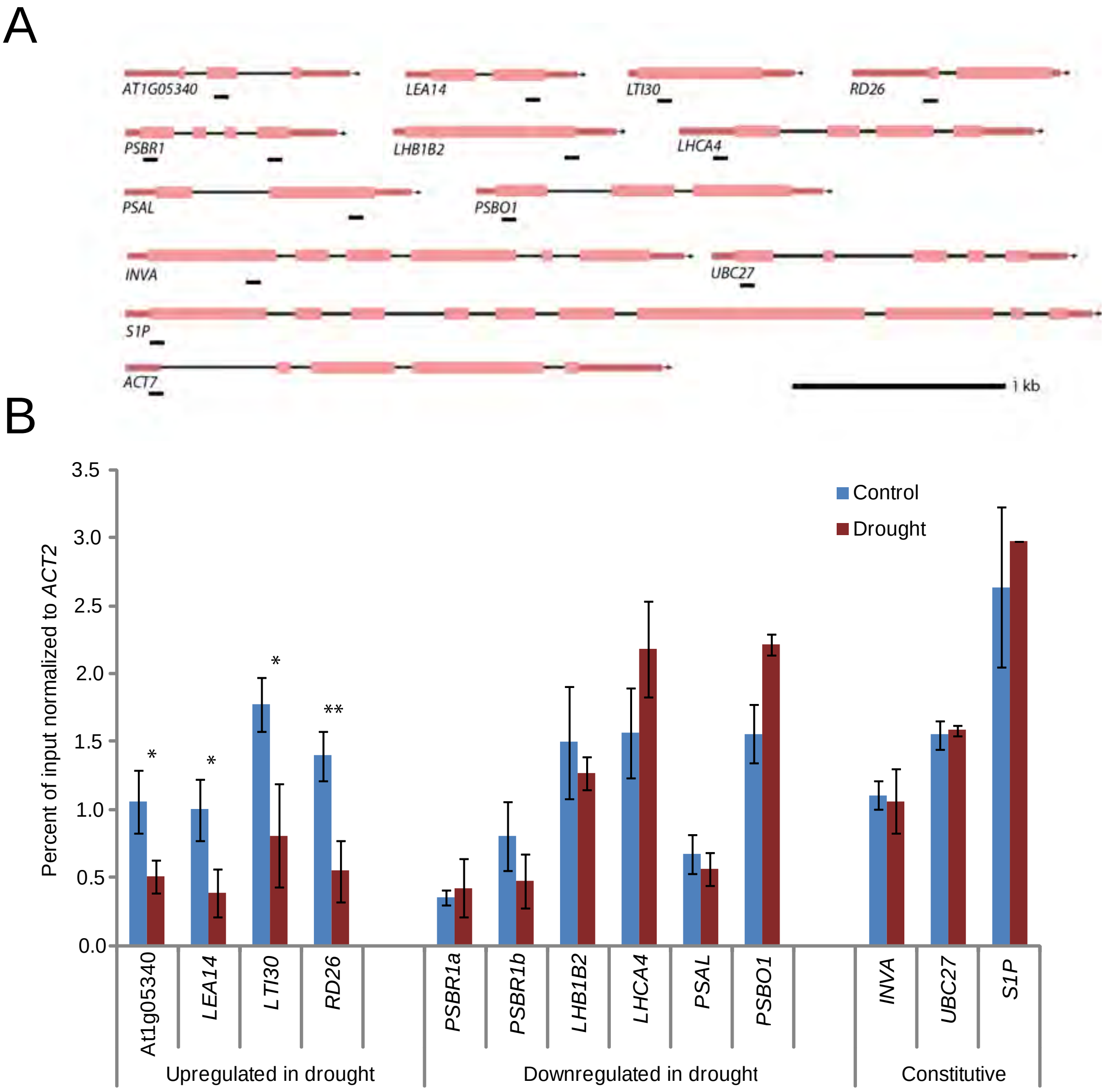
Supplemental Fig. 5. H2A.Z levels in gene-bodies correlates with gene responsiveness. (Supports Figure 2.) H2A.Z profiles for three gene classes divided according to the change of transcription level (for upregulated genes $\log_2$ fold-change from 1.5 to 3 (*n*=644), from 3 to 5 (*n*=358), and >5 (*n*=291), and for downregulated genes <-5 (*n*=463), from -5 to -3 (*n*=722), and from -3 to -1.5 (*n*=896)) are shown for genes induced **(A-C)** and repressed **(D-F)** in stress.



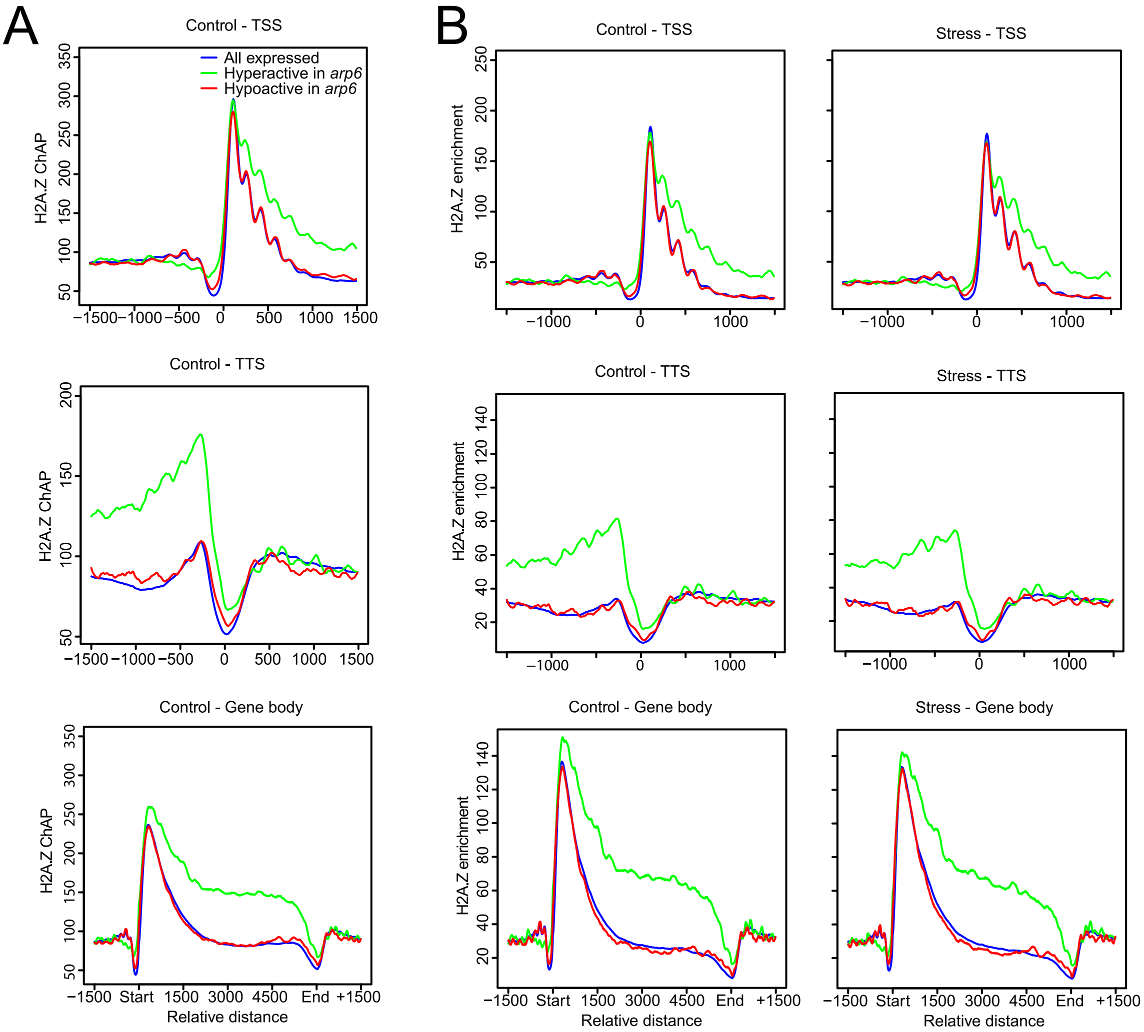
Supplemental Fig. 6. H2A.Z levels in control and stress conditions. (Supports Figure 3.) Changes in H2A.Z level (normalized H2A.Z-ChAP reads minus normalized MNase-seq [input]) between control (blue) and stress (green) conditions as analyzed for all expressed **(A)**, stress-induced **(B)**, and stress-repressed **(C)** genes. Plots are shown for TSS, TTS, ESS, and across gene bodies. **(D)** An example of changes in H2A.Z occupancy in a drought induced (color frame) gene upon transcriptional activation, created using JBrowse software (Skinner et al., 2009).



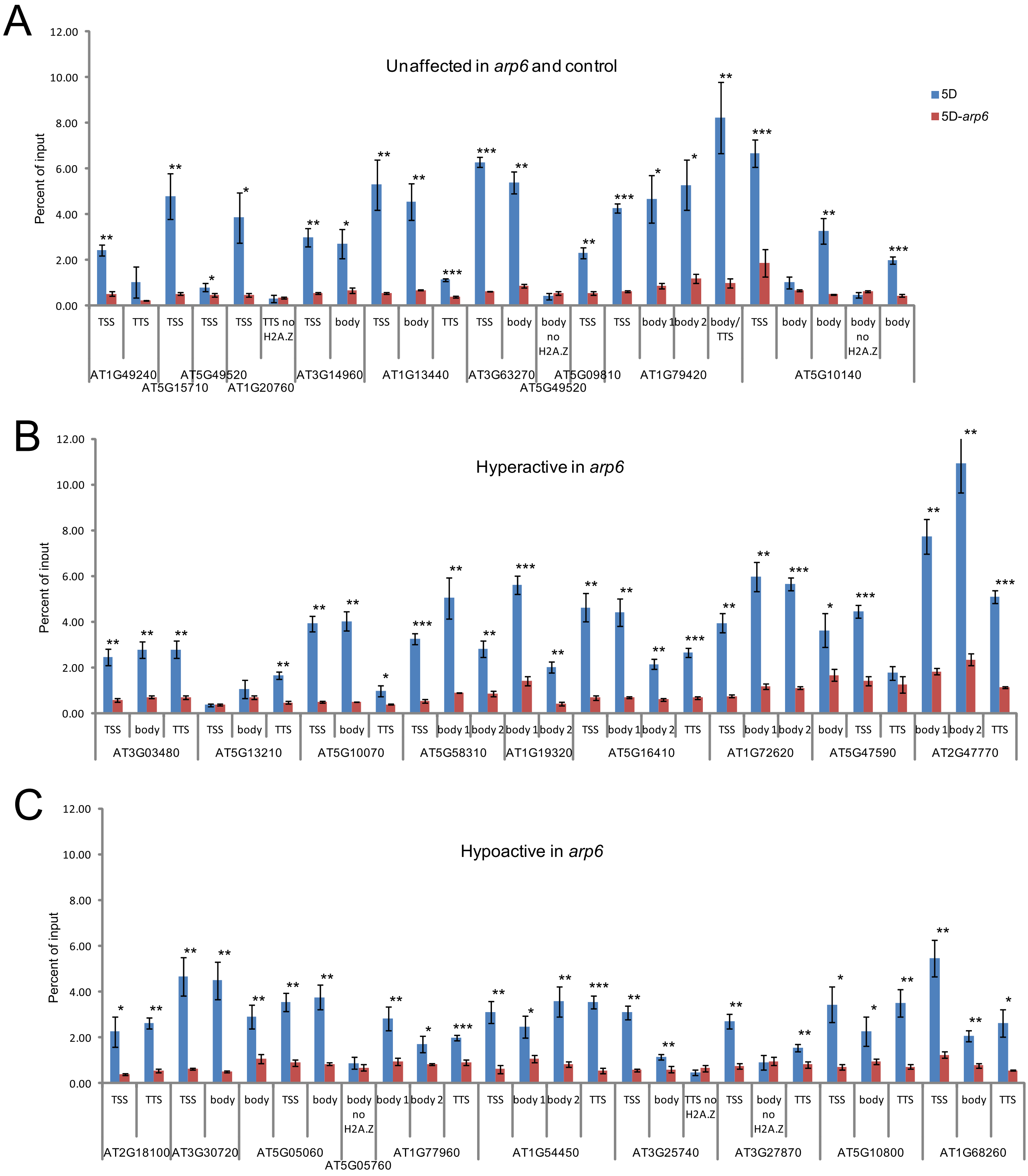
Supplemental Fig. 7. H2A.Z-ChAP signal in control conditions relative to TSS, ESS, TTS, and across gene body is shown for genes upregulated (green), and downregulated (red) in drought stress in comparison with 'All expressed genes' (blue). (Supports Figure 3.) The plots show the same data as in Fig. 3, but with reads data normalized only to library size. **(B)** As for (A) but in stress conditions. **(C)** Comparison of changes in H2A.Z-ChAP signals (the same normalization as for A and B) between control (blue) and stress (green) conditions shown for all expressed, stress-induced and stress-repressed genes.



Supplemental Fig. 8. ChAP-qPCR validation of changes in H2A.Z occupancy in drought stress at selected genes. (Supports Figure 3.) Four-weeks-old plants were subjected to water deficit for 8 days and compared to untreated plants using an MNase assay followed by ChAP-qPCR. **(A)** Schematic representation of regions analyzed by qPCR (short black bars). **(B)** The percent of input for H2A.Z ChAP-qPCR at selected drought-responsive and constitutive genes normalized to *ACT7* ChAP-qPCR. Error bars represent SD of independent experiments. * $P<0.05$, ** $P<0.01$.



Supplemental Fig. 9. Genes hyperactive in *arp6* have significantly higher levels of H2A.Z across their bodies. (Supports Figure 4.) **(A)** H2A.Z ChAP (ChAP reads normalized to library size) for TSS, TTS and Gene body in control conditions. **(B)** H2A.Z enrichment (H2A.Z-ChAP reads normalized to library size minus by MNase-seq [input] reads normalized to library size) relative to TSS in control and stress conditions, relative to TTS in control and stress conditions, and across gene body in control and stress conditions is shown for genes *arp6*-upregulated (green), and *arp6*-downregulated (red) in comparison with 'All expressed' genes (blue).



Supplemental Fig. 10. ARP6-dependent pathway is a major determinant of H2A.Z enrichment within Arabidopsis genes. (Supports Figure 6.) Comparison of H2A.Z enrichment (calculated as percent of input) for 5D plants (blue) and 5D-*arp6* plants (red) show significant reduction in H2A.Z levels in the absence of the ARP6 protein in genes unaffected in *arp6* **(A)**, hyperactive in *arp6* **(B)** and hypoactive in *arp6* **(C)**. Error bars represent SD of independent experiments. * *P*<0.05, ** *P*<0.01, *** *P*<0.001.

Supplemental Table 1. Germination assay in *wt* (Col), *arp6*, *hta9 hta11* and *pie1-5* plants in osmotic stress. *P*-values were calculated using Student's *t*-test.

Control conditions		**Col**		***arp6***		***hta9 hta11***		***pie1-5***	
		Radicle	**Cotyledons**	**Radicle**	**Cotyledons**	**Radicle**	**Cotyledons**	**Radicle**	**Cotyledons**
21 h	Mean	75.00	0.00	63.89	0.00	57.78	0.56	19.30	0.62
	SD	10.56	0.00	8.78	0.00	13.66	1.76	10.76	1.85
	P-value			*0.020*		*0.006*		*9.9E-10*	
24 h	Mean	87.78	34.44	83.89	7.22	75.56	17.78	26.49	0.62
	SD	7.31	15.67	7.61	5.27	9.87	7.77	12.13	1.85
	P-value			*0.259*	*2.9E-04*	*0.006*	*0.010*	*2.3E-11*	*8.1E-05*
48 h	Mean	97.22	97.22	99.44	97.22	91.67	90.56	76.61	55.13
	SD	3.93	3.93	1.76	2.93	7.05	8.30	7.86	9.28
	P-value			*0.128*	*1.000*	*0.047*	*0.039*	*2.0E-05*	*6.9E-08*
72 h	Mean	98.89	98.89	99.44	99.44	93.33	92.78	88.30	79.04
	SD	2.34	2.34	1.76	1.76	5.74	6.44	7.08	10.73
	P-value			*0.556*	*0.556*	*0.015*	*0.017*	*0.002*	*4.2E-04*
96 h	Mean	98.89	98.89	100.00	99.44	94.44	94.44	90.77	88.92
	SD	2.34	2.34	0.00	1.76	5.86	5.86	6.23	6.24
	P-value			*0.168*	*0.556*	*0.046*	*0.046*	*0.004*	*0.001*
120 h	Mean	99.44	99.44	100.00	100.00	96.11	95.00	90.77	90.16
	SD	1.76	1.76	0.00	0.00	4.57	6.11	6.23	6.10
	P-value			*0.343*	*0.343*	*0.053*	*0.052*	*0.003*	*0.002*
144 h	Mean	99.44	99.44	100.00	100.00	96.11	96.11	92.59	92.01
	SD	1.76	1.76	0.00	0.00	4.57	4.57	6.21	4.92
	P-value							*0.011*	*0.002*
168 h	Mean	99.44	99.44	100.00	100.00	96.11	96.11	92.59	93.21
	SD	1.76	1.76	0.00	0.00	4.57	4.57	6.21	5.40
	P-value							*0.011*	*0.008*
192 h	Mean	99.44	99.44	100.00	100.00	96.11	96.11	93.83	93.21
	SD	1.76	1.76	0.00	0.00	4.57	4.57	4.34	5.40
	P-value							*0.005*	*0.008*
216 h	Mean	99.44	99.44	100.00	100.00	96.11	96.11	94.44	93.83
	SD	1.76	1.76	0.00	0.00	4.57	4.57	3.93	4.34
	P-value							*0.005*	*0.005*
240 h	Mean	99.44	99.44	100.00	100.00	96.11	96.11	95.06	93.83
	SD	1.76	1.76	0.00	0.00	4.57	4.57	4.34	4.34
	P-value							*0.018*	*0.005*

150 mM NaCl		**Col**		***arp6***		***hta9 hta11***		***pie1-5***	
		Radicle	**Cotyledons**	**Radicle**	**Cotyledons**	**Radicle**	**Cotyledons**	**Radicle**	**Cotyledons**
21 h	Mean	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	SD	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	P-value								
24 h	Mean	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	SD	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	P-value								
48 h	Mean	2.78	0.00	0.56	0.00	4.44	0.56	0.00	0.00
	SD	2.93	0.00	1.76	0.00	3.51	1.76	0.00	0.00
	P-value			*0.057*		*0.265*	*0.343*	*0.015*	
72 h	Mean	63.33	10.00	28.10	1.11	68.33	28.89	0.00	0.00
	SD	12.34	7.77	12.09	2.34	8.30	10.41	0.00	0.00
	P-value			*4.5E-06*	*0.005*	*0.304*	*2.6E-04*	*5.7E-08*	*0.003*
96 h	Mean	85.56	61.67	66.32	23.71	80.00	73.89	6.08	0.00
	SD	5.97	13.97	7.93	8.51	8.76	7.43	6.62	0.00
	P-value			*1.1E-05*	*2.5E-06*	*0.117*	*0.028*	*2.4E-16*	*2.1E-07*
120 h	Mean	95.56	88.89	82.87	64.09	86.67	80.56	15.00	0.00
	SD	5.11	5.24	7.63	12.86	9.15	8.78	6.59	0.00
	P-value			*4.7E-04*	*1.1E-04*	*0.018*	*0.021*	*2.7E-16*	*1.4E-12*
144 h	Mean	97.22	97.22	90.06	83.98	90.00	87.22	20.00	3.58
	SD	3.93	3.93	5.73	8.05	7.31	9.09	7.17	3.15
	P-value			*4.9E-03*	*4.3E-04*	*0.016*	*0.008*	*4.4E-14*	*4.3E-21*
168 h	Mean	97.22	97.22	94.47	89.50	91.11	91.11	31.08	7.47
	SD	3.93	3.93	5.24	7.15	6.52	6.52	10.07	6.41
	P-value			*0.202*	*0.010*	*0.023*	*0.023*	*2.1E-10*	*2.7E-16*
192 h	Mean	97.22	97.22	95.58	94.47	92.22	91.67	42.23	14.60
	SD	3.93	3.93	5.73	5.24	6.52	7.05	9.57	8.43
	P-value			*0.467*	*0.202*	*0.055*	*0.047*	*1.0E-09*	*5.0E-13*
216 h	Mean	97.22	97.22	95.58	95.58	92.22	92.22	46.12	21.82
	SD	3.93	3.93	5.73	5.73	6.52	6.52	10.54	8.39
	P-value			*0.467*	*0.467*	*0.055*	*0.055*	*1.8E-08*	*1.5E-12*
240 h	Mean	97.22	97.22	96.67	95.58	93.33	92.78	51.15	26.82
	SD	3.93	3.93	5.97	5.73	5.74	5.89	9.23	9.57
	P-value			*0.809*	*0.467*	*0.096*	*0.064*	*5.6E-09*	*5.9E-11*

300 mM Sorbitol		**Col**		***arp6***		***hta9 hta11***		***pie1-5***	
		Radicle	**Cotyledons**	**Radicle**	**Cotyledons**	**Radicle**	**Cotyledons**	**Radicle**	**Cotyledons**
21 h	Mean	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	SD	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	P-value								
24 h	Mean	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	SD	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	P-value								
48 h	Mean	17.22	5.00	3.33	0.56	11.67	3.89	1.11	0.00
	SD	13.72	6.11	3.88	1.76	9.60	4.57	2.34	0.00
	P-value			*0.012*	*0.052*	*0.310*	*0.651*	*0.004*	*0.029*
72 h	Mean	89.44	68.89	52.22	10.00	76.11	59.44	15.85	2.22
	SD	8.05	13.66	12.34	6.31	11.13	11.43	7.91	3.88
	P-value			*8.8E-07*	*1.4E-08*	*0.007*	*0.112*	*5.7E-14*	*3.9E-08*
96 h	Mean	96.11	92.78	72.22	37.78	82.78	80.00	38.50	9.92
	SD	4.57	4.57	5.24	15.23	9.60	11.17	12.00	7.33
	P-value			*2.5E-09*	*3.0E-07*	*0.002*	*0.006*	*7.3E-09*	*7.0E-15*
120 h	Mean	96.67	96.11	83.89	72.78	87.78	84.44	57.93	19.24
	SD	3.88	4.57	4.10	11.25	8.61	9.37	15.78	12.35
	P-value			*1.2E-06*	*5.5E-05*	*0.011*	*0.004*	*2.0E-05*	*1.3E-09*
144 h	Mean	96.67	96.67	87.78	82.22	88.33	87.78	65.51	43.47
	SD	3.88	3.88	5.11	4.38	8.86	8.61	13.27	11.97
	P-value			*4.1E-04*	*3.5E-07*	*0.018*	*0.011*	*1.9E-05*	*3.8E-08*
168 h	Mean	97.78	96.67	91.11	86.67	90.56	88.33	70.02	52.22
	SD	3.88	3.88	4.68	3.88	6.95	8.86	14.02	11.13
	P-value			*0.003*	*1.9E-05*	*0.012*	*0.018*	*1.3E-04*	*1.2E-07*
192 h	Mean	98.33	97.78	93.33	91.67	90.56	90.56	77.04	57.69
	SD	3.75	3.88	5.11	4.72	6.95	6.95	10.11	11.02
	P-value			*0.023*	*0.006*	*0.008*	*0.012*	*6.3E-05*	*3.2E-07*
216 h	Mean	98.33	98.33	95.56	93.33	91.67	90.56	79.20	63.22
	SD	3.75	3.75	3.51	5.11	7.97	6.95	9.09	10.40
	P-value			*0.105*	*0.023*	*0.032*	*0.008*	*4.9E-05*	*7.1E-07*
240 h	Mean	98.33	98.33	97.22	94.44	91.67	91.11	81.43	66.53
	SD	3.75	3.75	3.93	3.70	7.97	7.50	10.22	11.22
	P-value			*0.526*	*0.031*	*0.032*	*0.017*	*4.6E-04*	*3.6E-06*

Supplemental Table 2. ChAP-qPCR analysis of H2A.Z enrichment (calculated as percent of input) for 5D and 5D-*arp6* plants in 78 amplicons corresponding to different genic regions and gene groups (unaffected in *arp6*, hyperactive in *arp6* and hypoactive in *arp6*).

Amplicon name	**Gene**	**Genic region**	**5D***	***arp6*-5D***	**5D SD**	***arp6*-5D SD**	**Difference 5D - *arp6*-5D**	**Expression in *arp6***	***P* value****	**Significance****
PZ113	AT2G18100	TSS	2.27	0.40	0.66	0.03	1.87	Hypoactive	0.0194	*
PZ115		TTS	2.64	0.55	0.23	0.06	2.09	Hypoactive	0.0011	**
PZ103	AT3G30720	TSS	4.68	0.65	0.84	0.05	4.03	Hypoactive	0.0070	**
PZ105		body	4.49	0.53	0.81	0.04	3.95	Hypoactive	0.0068	**
PZ025	AT5G05060	body	2.91	1.08	0.54	0.21	1.84	Hypoactive	0.0085	**
PZ077		TSS	3.54	0.90	0.40	0.13	2.64	Hypoactive	0.0020	**
PZ079		body	3.77	0.84	0.53	0.06	2.92	Hypoactive	0.0049	**
PZ081	AT5G05760	body no H2A.Z	0.88	0.69	0.26	0.13	0.19	Hypoactive	0.1684	
PZ093	AT1G77960	body 1	2.84	0.95	0.52	0.17	1.89	Hypoactive	0.0082	**
PZ095		body 2	1.73	0.83	0.36	0.04	0.90	Hypoactive	0.0238	*
PZ091		TTS	2.01	0.91	0.13	0.11	1.10	Hypoactive	0.0002	***
PZ083	AT1G54450	TSS	3.10	0.62	0.49	0.17	2.48	Hypoactive	0.0036	**
PZ085		body 1	2.47	1.08	0.47	0.16	1.39	Hypoactive	0.0129	*
PZ087		body 2	3.57	0.82	0.68	0.12	2.75	Hypoactive	0.0085	**
PZ089		TTS	3.54	0.55	0.29	0.13	2.99	Hypoactive	0.0004	***
PZ071	AT3G25740	TSS	3.09	0.58	0.29	0.06	2.51	Hypoactive	0.0017	**
PZ073		body	1.16	0.61	0.13	0.14	0.54	Hypoactive	0.0039	**
PZ075		TTS no H2A.Z	0.48	0.66	0.12	0.12	-0.17	Hypoactive	0.0765	
PZ065	AT3G27870	TSS	2.72	0.75	0.33	0.11	1.96	Hypoactive	0.0026	**
PZ069		body no H2A.Z	0.91	0.97	0.32	0.18	-0.07	Hypoactive	0.3874	
PZ067		TTS	1.56	0.82	0.18	0.14	0.74	Hypoactive	0.0029	**
PZ097	AT5G10800	TSS	3.45	0.72	0.78	0.13	2.73	Hypoactive	0.0119	*
PZ099		body	2.28	0.95	0.64	0.14	1.32	Hypoactive	0.0317	*
PZ101		TTS	3.51	0.73	0.61	0.11	2.78	Hypoactive	0.0069	**
PZ107	AT1G68260	TSS	5.47	1.25	0.78	0.13	4.22	Hypoactive	0.0049	**
PZ109		body	2.08	0.78	0.25	0.10	1.30	Hypoactive	0.0027	**
PZ111		TTS	2.62	0.57	0.60	0.02	2.05	Hypoactive	0.0137	*
PZ117	AT1G49240	TSS	2.42	0.52	0.25	0.09	1.90	Unaffected	0.0013	**
PZ119		TTS	1.02	0.22	0.67	0.01	0.80	Unaffected	0.0868	
PZ155	AT5G15710	TSS	4.79	0.52	0.99	0.07	4.26	Unaffected	0.0085	**
PZ157	AT5G49520	TSS	0.80	0.47	0.17	0.07	0.33	Unaffected	0.0341	*
PZ121	AT1G20760	TSS	3.85	0.48	1.10	0.08	3.37	Unaffected	0.0167	*
PZ123		TTS no H2A.Z	0.32	0.34	0.16	0.03	-0.01	Unaffected	0.4459	
PZ129	AT3G14960	TSS	3.00	0.54	0.40	0.05	2.46	Unaffected	0.0039	**

PZ131		body	2.70	0.68	0.63	0.11	2.02	Unaffected	0.0140	*
PZ147	AT1G13440	TSS	5.30	0.54	1.10	0.03	4.76	Unaffected	0.0086	**
PZ149		body	4.56	0.68	0.81	0.03	3.88	Unaffected	0.0071	**
PZ151		TTS	1.14	0.39	0.05	0.04	0.75	Unaffected	0.0000	***
PZ125	AT3G63270	TSS	6.28	0.62	0.22	0.01	5.66	Unaffected	0.0002	***
PZ127		body	5.38	0.87	0.49	0.09	4.52	Unaffected	0.0015	**
PZ159	AT5G49520	body no H2A.Z	0.41	0.54	0.13	0.07	-0.13	Unaffected	0.1156	
CHIP_Act7	AT5G09810	TSS	2.31	0.55	0.25	0.09	1.76	Unaffected	0.0017	**
PZ139	AT1G79420	TSS	4.26	0.63	0.20	0.04	3.62	Unaffected	0.0003	***
PZ141		body 1	4.68	0.88	1.03	0.12	3.79	Unaffected	0.0113	*
PZ143		body 2	5.28	1.18	1.10	0.19	4.10	Unaffected	0.0104	*
PZ145		body/TTS	8.23	0.99	1.57	0.19	7.24	Unaffected	0.0072	**
FLC-2	AT5G10140	TSS	6.67	1.88	0.61	0.59	4.79	Control	0.0003	***
FLC-7		body	1.01	0.66	0.24	0.05	0.35	Control	0.0621	
FLC-9		body	3.27	0.49	0.54	0.02	2.78	Control	0.0061	**
FLC-6		body no H2A.Z	0.47	0.62	0.12	0.04	-0.15	Control	0.0789	
FLC-1		body no H2A.Z	1.98	0.45	0.15	0.07	1.53	Control	0.0004	***
PZ019	AT3G03480	TSS	2.45	0.57	0.36	0.07	1.88	Hyperactive	0.0050	**
PZ021		body	2.76	0.71	0.36	0.06	2.06	Hyperactive	0.0043	**
PZ023		TTS	2.79	0.70	0.38	0.07	2.09	Hyperactive	0.0046	**
PZ059	AT5G13210	TSS	0.37	0.38	0.05	0.04	-0.01	Hyperactive	0.3860	
PZ061		body	1.05	0.70	0.41	0.08	0.35	Hyperactive	0.1357	
PZ063		TTS	1.64	0.48	0.16	0.04	1.16	Hyperactive	0.0020	**
PZ133	AT5G10070	TSS	3.93	0.49	0.34	0.03	3.44	Hyperactive	0.0015	**
PZ135		body	4.03	0.50	0.41	0.01	3.53	Hyperactive	0.0022	**
PZ137		TTS	0.96	0.40	0.24	0.02	0.57	Hyperactive	0.0276	*
PZ041	AT5G58310	TSS	3.26	0.54	0.23	0.07	2.72	Hyperactive	0.0006	***
PZ045		body 1	5.04	0.90	0.90	0.02	4.14	Hyperactive	0.0077	**
PZ043		body 2	2.83	0.85	0.36	0.12	1.98	Hyperactive	0.0032	**
PZ049	AT1G19320	body 1	5.62	1.41	0.41	0.20	4.21	Hyperactive	0.0003	***
PZ051		body 2	2.02	0.43	0.25	0.08	1.59	Hyperactive	0.0022	**
PZ027	AT5G16410	TSS	4.63	0.68	0.62	0.11	3.95	Hyperactive	0.0033	**
PZ029		body 1	4.43	0.71	0.60	0.04	3.72	Hyperactive	0.0041	**
PZ031		body 2	2.14	0.60	0.22	0.06	1.54	Hyperactive	0.0023	**
PZ033		TTS	2.65	0.69	0.20	0.06	1.96	Hyperactive	0.0008	***
PZ035	AT1G72620	TSS	3.94	0.76	0.42	0.07	3.18	Hyperactive	0.0025	**
PZ039		body 1	5.97	1.19	0.62	0.13	4.78	Hyperactive	0.0021	**
PZ037		body 2	5.66	1.11	0.28	0.06	4.55	Hyperactive	0.0004	***
PZ015	AT5G47590	body	3.63	1.67	0.74	0.26	1.96	Hyperactive	0.0163	*
PZ013		TSS	4.46	1.41	0.29	0.20	3.05	Hyperactive	0.0001	***

PZ017		TTS	1.76	1.26	0.30	0.37	0.50	Hyperactive	0.0723	
PZ053	AT2G47770	body 1	7.74	1.83	0.76	0.14	5.91	Hyperactive	0.0022	**
PZ055		body 2	10.93	2.35	1.30	0.28	8.57	Hyperactive	0.0029	**
PZ057		TTS	5.09	1.14	0.29	0.05	3.95	Hyperactive	0.0007	***

* BLRP-H2A.Z enrichment calculated as percent of input; average values from three biological replicates;
** *P*-value for the difference between H2A.Z enrichment in 5D and arp6-5D lines calculated as one-tailed t-test assuming unequal variances.

Supplemental Table 3. List of primers used for ChAP-qPCR and RT-qPCR analyses

Amplicon Name	Gene	Left Primer Sequence	Right Primer Sequence	Used for RT-qPCR?
PZ013	AT5G47590.1	TCGAACTTTAGGAATTCTTGACATGT	AGAGAGAGATGGGTGAGACAA	
PZ015	AT5G47590.1	ATGTCCACTGCAAAGTGAGC	TCGCAAGGGAGCACTAATTG	yes
PZ017	AT5G47590.1	TCACTTGATTCGATAGCAAACACA	TGAGACATTGTGTGTGTGAGAGA	
PZ019	AT3G03480.1	GAGAGGCTTGAGCTCTCGTG	AAGGTGCATCGCCAGCAG	
PZ021	AT3G03480.1	TCCCTGATGCCACAAACATAGG	ACTACGTCCGTTCAGTGACC	yes
PZ023	AT3G03480.1	TCTGCTACGAACGTCTCCATC	AGGTGAGACAGGTACAGTTGTG	
PZ025	AT5G05060.1	CGTGATGTAGAGTGTGATTGCAG	GAACTTGTCAAGGTTTTGAGAGC	yes
PZ027	AT5G16410.1	AACCCTGTTTTCCGGCAAAG	CACGAGGAAGGAGGTCGTTG	
PZ029	AT5G16410.1	TCGGAGTTCCACGTCAGCAG	ACGAGATTCTCTGCAGTAACGG	
PZ031	AT5G16410.1	GTCGTGGCTTTAAGAGGGATC	CTCGATCCGATATACCGATTTCG	yes
PZ033	AT5G16410.1	GGAGCCACCGTTTTCCAC	ACCCGGGAGCAGAGCTG	
PZ035	AT1G72620.1	TTCAGATCATCACCACTGTAATGG	ATCGACGGAGAATATGAACGAAGC	
PZ037	AT1G72620.1	AAACACGGCGGAGATGTATC	CAACCGTAGATCTCTCGGATTAC	yes
PZ039	AT1G72620.1	TTCTGCGATCTCCGTCCAATC	TGGCCGGAGATCCAGAAATG	
PZ041	AT5G58310.1	AGCTTGTACCAACACCATCCTC	TGAGCATCATTTTGTGTTTGTGC	
PZ043	AT5G58310.1	AGAGTTGGTAATAAAGGACACACC	ACCTGAGTATGTTCGGGACAAG	
PZ045	AT5G58310.1	TTGATCGTTGGGAAGTTGGG	CTTCTTTGGATGACTACGACGAG	yes
PZ049	AT1G19320.1	CCGGTACAACCTTCACCTTAAC	GTTTGCGGTGAGGATTCCAG	
PZ051	AT1G19320.1	AAGCCGGAGTATTGTTGCAC	TAATTCGTGGGCGGACAAGTC	yes
PZ053	AT2G47770.1	TGTTCCTTCGATTCTGTTTTGGAC	CCGCGGTATCTGATGTCCTG	
PZ055	AT2G47770.1	CACCTCTGTGGCTCCTACAC	GCAGCCAAACCCATCAGAC	yes
PZ057	AT2G47770.1	ACCATAAAAGATGTCTTTGCGATCC	GTTCATGTCTATTACTCCACAATGAC	
PZ059	AT5G13210.1	CCTTATTAGTTTGTGACAACTTTCGG	ATGTGAAATAAGCCGACTACCTTAGC	
PZ061	AT5G13210.1	AGTGGCCGTACAAGAGAAGC	CACTGAACACAAACACCCTCTTG	yes
PZ063	AT5G13210.1	CAATCGATGCTCTCTCTACACG	AGTGATTGTTTCCGGCGAAC	
PZ065	AT3G27870.1	TCTCAGATTGGTTCAAGAGGTT	AGCTTCAGGATTATCAGGATCATT	
PZ067	AT3G27870.1	TGAACAGAGGAGAACAGAACGG	AACTCAACTTGCACCGGAAG	yes
PZ069	AT3G27870.1	CACGCTGTTTTGGTATGAAGC	AGCACGACATGTACCAATCG	
PZ071	AT3G25740.1	CACCAGGGAAAAATGTTGCAG	AGCTCCGGCGAGGTATATTAAC	
PZ073	AT3G25740.1	AGCAAAGTTCCAGAGATATCAAGTG	GCTCACACGCTTTCTTCATTTTC	yes
PZ075	AT3G25740.1	ACATGGCCTGACAAATGGAC	AAGAATTGTATGCTCAAACTGTGC	
PZ077	AT5G05760.1	CCACCGTCCGATCTCTGAAC	GCCGGTGACTTTAGTTCAATTCC	
PZ079	AT5G05760.1	AGCCTCGTGATCTTCTGTGAC	AATAAGAAGGCTTCCCGGATCG	yes
PZ081	AT5G05760.1	GCTTAGTAGCTCCCATAAGTCTG	CCAAGTTGGTCATTACACTGCTG	
PZ083	AT1G54450.1	TTGATTAGATTTCATCGACATTGGC	ACGTTAGATATAGAGCTGTTGCAG	
PZ085	AT1G54450.1	AGAAAGAGGAGGCCCATTGC	GCACGAATTCAGGGTCGAATAG	
PZ087	AT1G54450.1	GCGCCATGCATTCCATTCTATG	ATGGAGTTTTGACGCGGAAC	yes
PZ089	AT1G54450.1	AGCATCTTCGACATCTTCTTCC	GTGGGATCGTTTTGCTCATAGAG	

PZ091	AT1G77960.1	TAACCTGTAAAACAAGGTGTCCAC	TCTTATGGTACCTGTGATTTCTCG	
PZ093	AT1G77960.1	TGGGGGTATGATTGCGTTTG	CCATTGAGGTTTAGGTTACCCAAC	
PZ095	AT1G77960.1	TGGGAGGTTCATTTTGCCTACG	TGGCATGTATCCACAGCAAC	yes
PZ097	AT5G10800.1	GGGTGATCGAGAAAGAACTCATC	TTGGTGCCGTGCTATTATCG	
PZ099	AT5G10800.1	GCCTCCAGTTCTACTAGATGAAGC	AGCTCAAGCCTGATTCTCAAGG	
PZ101	AT5G10800.1	CTCGCTCTCTGCTTCTATCATG	GGACCGAAAACGAAGAGCAAAG	yes
PZ103	AT3G30720.1	AACCTCCTTTCGATCTGTCAGC	TCAATGGCTGACCGTGTGAG	yes
PZ105	AT3G30720.1	CCAGGTTATAGAAGATCTGGGTTG	AGGATGAAAAGAATATTACCTGTGGAG	
PZ107	AT1G68260.1	TGCCTCCTTTGAGATCGAAG	TTCCTCTCCGGAGCGTAAAAAC	
PZ109	AT1G68260.1	GTCAACTCTGAAATTGCTAAGGC	TCGGTATCAACTGCGACGAAG	yes
PZ111	AT1G68260.1	AGGACGGTACTTGTTGTCGAG	CCTATATTGGAGGCAAAAGGAATAGC	
PZ113	AT2G18100.1	TACCGGAGAGCCAATCAGCAG	ACCCAGAGATCCGCCTCATC	
PZ115	AT2G18100.1	ATCCTGGAAAGACTCGAACTCG	TGGGTTTAGTTAGAGAGTGTTTCG	yes
PZ117	AT1G49240.1	TTCATCGGCCGTTGCATTTC	ACGATGAAGATCTGGCTCACTC	yes
PZ119	AT1G49240.1	CGAGTTTTAGAACAAATCAGTAAGC	AACTTGGTGCACCGATGTAC	
PZ121	AT1G20760.1	CGAATCGGGCAATTTTCGTC	ACTGAGATTAGAGCTTAGAAATCG	
PZ123	AT1G20760.1	AGGATTTCAGTGGTAGCCATGG	AAGGGACCTGTGGAACCAAAC	yes
PZ125	AT3G63270.1	ATGGCACTGCGTTGACTCTC	CTGGATAAGGCGAAGAAGTTGG	
PZ127	AT3G63270.1	TGACGAGCGAGCAAATGTAG	GACGAAGACTATGCGTTCAAGC	yes
PZ129	AT3G14960.1	GACGATCAAAGGCGTCGATC	TTCTCCCAAGCTGTTTCACG	yes
PZ131	AT3G14960.1	CGGTTGAGAGAAGGTTGAATCAG	CTCAGGAACACATGGATGCC	
PZ133	AT5G10070.2	GCAAGATTATCAGTCCGACCAC	CGGGAAGCATAATCGATCTAAAGG	
PZ135	AT5G10070.2	GCAGATCACATAACCACCACAC	CGCTTCCTCTTGATCAAGGTAC	
PZ137	AT5G10070.2	ATCAAATAGGATTTCTCCAATGGC	ATTAGAAGACAGTGAGGAGGAAG	yes
PZ139	AT1G79420.1	GAGCAACTCAAAGTCATACTGGAG	TAACGGTGTTAGGGCTTGTGG	
PZ141	AT1G79420.1	GGTCCAACCACTTTGCAACAG	CAAGAGCCTCAAGTCTTGTCC	
PZ143	AT1G79420.1	GAGCTTGTTCTCGGTGGAAC	TGGCGCCAAACTGTTTTACC	yes
PZ145	AT1G79420.1	GAGGCGGTTTACTGGGAGAC	CGTCAACGTCACGGTAATCTC	
PZ147	AT1G13440.1	CGATCAGATTCAAAAAGTATCAACG	TCTCGCTCTTGTTGATCTGC	
PZ149	AT1G13440.1	CGAAGAGAAGAAGAAACGAACC	CGTCGCTGTTAACGATCCTTTC	
PZ151	AT1G13440.1	TTAAGAGAAAGCAAAAAGACAAAAGC	TCACTGATTCCATGCGCAGTC	yes
PZ155	AT5G15710.1	AAAAGGACGAAGCTTGTTGC	GAGTTGGAGCAAAGATTCGAAC	yes
PZ157	AT5G49520.1	CGAGCAAGAACAAGAACAAGAAC	TGACGTAACTAGATTCGCCATG	
PZ159	AT5G49520.1	AGCTAGGTTTGCGTTTCTGAC	TCCACCTATAACCGTCGTCAAG	yes
FLC2	AT5G10140.1	AGAAATCAAGCGAATTGAGAACAA	CGTTGCGACGTTTGGAGAA	yes
FLC6	AT5G10140.1	AAGCCAGCGCTATCACTAAACTTT	TCGGCAGATTGAAAATGACATT	
FLC1	AT5G10140.1	ATTTAGCAACGAAAGTGAAAACTAAGG	GCCACGTGTACCGCATGAC	
FLC7	AT5G10140.1	CATCTCTCCAGCCTGGTCAAG	GGCTTTAAGATCATCAGCATGCT	
FLC9	AT5G10140.1	CATCATGTGGGAGCAGAAGCT	CGGAAGATTGTCGGAGATTTG	