

Table 1 Suppl. Primers used in this work. (F - forward, R - reverse).

Name	Sequence	Enzyme site	Note
H1-F	5' AAGCCGCAAGCGAGCAGAG 3'		clone
H1-R	5' GAAGCCTAAATCAGGGAGGATGAG3'		
H1-OF	5'GCTCTAGA ATGACTGCTTTGGCCAAGC3'	XbaI	overexpression
H1-OR	5'CGGGATCC TCAAGCCGCGGCGACCC3'	BamHI	
H2A-1-F	5'ATCCCCTCCAAGCACTGTAG3'		clone
H2A-1-R	5'CGAGCACCCACGACCA 3'		
H2A-1-OF	5'GCTCTAGA TTATGGAGCCAGGTTTGTCA 3'	XbaI	overexpression
H2A-1-OR	5' GCTCTAGACACCGAGGAGTCGTCATCTA 3'	XbaI	
H2A-2-F	5' GCAGTCTGGCTCTCTCCATCC 3'		clone
H2A-2-R	5' CTTCACCTCCGCTATTTCAGACGA 3'		
H2A-2-SF	5' CGGGATCCTCTCCATCCCAATCCC 3'	BamHI	subcellular localization
H2A-2-SR	5' CCCAAGCTTGGCCTTCTTCGGGGTGG3'	HindIII	
H2A-2-OF	5' GCTCTAGA TCTCTCCATCCCAATCCC 3'	XbaI	overexpression
H2A-2-OR	5'CGGGATCCGCACACAGACTAAACAACCTCAG 3'	BamHI	
H2A-3-F	5' CTCGCCGGAAGAAGTAGAAAGA 3'		clone
H2A-3-R	5' CTCGGCGAATCTAAGGACAG 3'		
H2A-3-SF	5' CGGGATCCGGAAGAAGTAGAAAGAAGATG 3'	BamHI	subcellular localization
H2A-3-SR	5'CCCAAGCTTCTCCTTGGCGGCGACC 3'	HindIII	
H2A-3-OS	5'GCTCTAGACGCCGGAAGAAGTAGAAAGAA 3'	XbaI	overexpression
H2A-3-OA	5' CGGGATCC AGAAATGGAACGAGGCAACA 3'	BamHI	
H2A-4-F	5' CGGAGAAGCAGCAAGCAAGA 3'		clone
H2A-4-R	5' AACACTGGCTAGGCTATGGGG 3'		
H2A-4-SF	5' CGGGATCCAAGCAGCAAGCAAGATGG 3'	BamHI	subcellular localization
H2A-4-SR	5'CCCAAGCTTCTCCTTGGTGGCGGCGAC 3'	HindIII	
H2A-4-OF	5'CGGGATCCCGAGAAGCAGCAAGCAAGATG 3'	BamHI	overexpression
H2A-4-OA	5'TCCCCCGGGGATAACACTGGCTAGGCTATGG3'	SmaI	
H2A.Z-1-F	5' TGCTGCAAAGGGAGATGGC 3'		clone
H2A.Z-1-R	5' CTACCCGTTATTGCATTTCATTC 3'		
H2A.Z-1-SF	5'CGGGATCCAGGGCGAATTGAAGCT3'	BamHI	subcellular localization
H2A.Z-1-SR	5'CCCAAGCTTCTCCTTGGAGGTCTTGTTGA 3'	HindIII	
H2A.Z-1-OF	5'GCTCTAGACGTGCTGCAAAGGGAGATGGC3'	XbaI	overexpression
H2A.Z-1-OR	5'CGGGATCCGCCTACCCGTTATTGCATTTCATTC3'	BamHI	
H3-1-F	5' CGAGTCCCTCCGATCCGATG 3'		clone
H3-1-R	5' ACGGCGGCAGAGAACAGAGAC 3'		
H3-1-SF	5' CGGGATCCGGTCTCCCTCGCTTCCA 3'	BamHI	subcellular localization
H3-1-SR	5' CCCAAGCTTGGCCCTCTCGCCCTGAT3'	HindIII	
H3-1-OF	5' CGCGGATCC GAGTCCCTCCGATCCGATG 3'	BamHI	overexpression

H3-1-OR	5' CGAGCTC CGTTCATCAGGCCCTCTCG 3'	SacI	
H3-2-F	5' CAACCGAAGCCAAGTTTC 3'		clone
H3-2-R	5' GGAGGCTAATCAACTACTAGTACA 3'		
H3-2-SF	5' CGGGATCCGCCGAGGAGCAGTAGACG3'	BamHI	subcellular localization
H3-2-SR	5' CCCAAGCTTGGCGCGCTCCCCG3'	HindIII	
H3-2-OF	5' CGCGGATCC CCGAGGAGCAGTAGACGC 3'	BamHI	overexpression
H3-2-OR	5' CGAGCTC ATTGGCCTCGCTCGCTTAG 3'	SacI	
H4-1-F	5' CGTCGCCAGCCATGTCGG 3'		clone
H4-1-R	5' AGAACGACGACCCGCCTAACC 3'		
H4-1-OF	5' GCTCTAGA AATCCACCTTCGGAGCAG 3'	XbaI	overexpression
H4-1-OR	5' CGGGATCC CGACCCGCCTAACCACAT 3'	BamHI	
H2A-2-QF	5' ACAACAAGAAGAGCCGCATC 3'		RT qPCR
H2A-2-QR	5' GGTGATCTTGGGGATGACG 3'		
H2A-3-QF	5' CAACAAGAAGACCCGCATCATC 3'		RT qPCR
H2A-3-QR	5' GCAGCACGGAGTTGATGTTG 3'		
H2A-4-QF	5' AACAAGAAGACCCGGATCATCC 3'		RT qPCR
H2A-4-QR	5' ACGGAGTTGATGTTGGGGATC 3'		
H3-2-QF	5' ATCCGCAAGTACCAGAAGAGC 3'		RT qPCR
H3-2-QR	5' TTGAAGTCCTGCGCGATCTC 3'		
H2A.Z-1-QR	5' AGGACAAGGACAAGAAGAAGGC 3'		RT qPCR
H2A.Z-1-QF	5' TTGAGCTGCCTGTGTATACGG 3'		
H1-GF	5' AAGGGCAAGCTCGTCAAGGTCAA 3'		genomic and RT-sqPCR
H1-GR	5' TTCGCGGCCACCGTCTTCTT 3'		
H2A-1-GF	5' TCTGGAGTTGGCCGGAACG 3'		genomic and RT-sqPCR
H2A-1-GR	5' ACCACCGCTGGCGATTGTGA 3'		
H2A-2-GF	5' GTGAAGGCGGGGCTCCAGTTC 3'		genomic and RT-sqPCR
H2A-2-GR	5' GGGGATGATGCGGCTCTTCTTG 3'		
H2A-3-GF	5' CGCATCGGGCGCTACCTCAA 3'		genomic and RT-sqPCR
H2A-3-GR	5' TGGGCAGCAGCACGGAGTTGA 3'		
H2A-4-GF	5' AAGGAAGGGAGGCGACAGGAAGA 3'		genomic and RT-sqPCR
H2A-4-GR	5' TTTGGGAGCAGCACGGAGTTGA 3'		
H2A.Z-1-GF	5' AAGCAGAGGGTCTCGGCTAATG 3'		genomic and RT-sqPCR
H2A.Z-1-GR	5' GGACTTGTGGATGTGAGGGATGA 3'		
H3-1-GF	5' GCGAGATCCGCAAGTACCAGAAGAG 3'		genomic and RT-sqPCR
H3-1-GR	5' GATGGCGCAGAGGTTGGTGTC 3'		
H3-2-GF	5' ACCACGGGCGGAGTGAAGAAGC 3'		genomic and RT-sqPCR
H3-2-GR	5' GCGCACAGGTTGGTGTCTCGA 3'		
H4-1-GF	5' CGAAGCGGCACAGGAAGGTG 3'		genomic and RT-sqPCR
H4-1-GR	5' GTGACGGCGTCGCGGATGA 3'		
TaACTIN-F	5' CGAAACCTTCAGTTGCCAGCAAT 3'		reference wheat <i>actin</i> gene
TaACTIN-R	5' ACCATCACCAGAGTCGAGCACAAT 3'		
AtTUBULIN-F	5' CTCAAGAGGTTCTCAGCAGTA 3'		reference <i>Arabidopsis</i>

AtTUBULIN-R	5' TCACCTTCTTCATCCGCAGTT 3'	<i>tubulin</i> gene
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Table 2 Suppl. The characteristics and comparison of histone variant genes.

Histone variant	cDNA length [bp]	Genomic DNA length [bp]	Intron number
<i>TaH1-1</i>	525	504	1 (79bp)
<i>TaH1-2</i>	546	625	1 (79bp)
<i>TaH1-3</i>	456	535	1 (79bp)
<i>TaH1-4</i>	537	586	1 (50bp)
<i>TaH2A-1</i>	405	405	0
<i>TaH2A-2</i>	480	480	0
<i>TaH2A-3</i>	441	441	0
<i>TaH2A-4</i>	444	538	1 (94 bp)
<i>TaH2A.Z-1</i>	420	420	0
<i>TaH3-1</i>	411	411	0
<i>TaH3-2</i>	411	508	1 (97 bp)
<i>TaH4-1</i>	312	312	0

Table 3 Suppl. The chemical properties and secondary structure prediction of histone variants (NLS - nuclear localization signal).

Histone variant	Animo acid components				Mr	pI	α -helix	β -sheet	NLS
	number	arginine [%]	lysine[%]	alanine[%]					
TaH1-1	174	2.9	24.1	26.4	18.0	10.65	5	1	1
TaH1-2	181	2.8	25.4	26.0	18.7	10.75	5	1	1
TaH1-3	151	3.3	22.5	25.2	15.7	10.68	3	1	1
TaH1-4	178	2.8	23.6	28.1	18.3	10.65	5	1	1
TaH2A-1	134	7.5	8.2	17.9	13.9	10.23	4	1	1
TaH2A-2	159	6.3	16.4	15.7	16.7	10.66	3	1	1
TaH2A-3	146	7.5	14.4	14.4	15.6	10.66	4	1	1
TaH2A-4	147	7.5	14.3	15.0	15.7	10.66	4	0	1
TaH2A.Z-1	139	6.5	12.2	14.4	14.6	10.32	4	0	1
TaH3-1	136	12.5	10.3	14.0	15.3	11.29	5	0	1
TaH3-2	136	12.5	10.3	13.2	15.4	11.15	5	0	1
TaH4-1	103	14.6	9.7	6.8	11.4	11.48	3	0	1

Table 4 Suppl. The detection of *Arabidopsis thaliana* transgenic lines with wheat histone variants. Genomic PCR - detection whether wheat histone variant genes were integrated into the genome of *Arabidopsis*. RT-PCR - detection whether wheat histone variant genes were expressed in transgenic lines.

Histone variant	Number of one-copy transgenic lines	Genomic PCR	RT-PCR
<i>aH1-1</i>	3	positive	positive
<i>TaH1-2</i>	5	positive	negative
<i>TaH1-3</i>	5	positive	negative
<i>TaH1-4</i>	5	positive	negative
<i>TaH2A-1</i>	4	positive	negative
<i>TaH2A-2</i>	4	positive	positive
<i>TaH2A-3</i>	4	positive	positive
<i>TaH2A-4</i>	4	positive	negative
<i>TaH2A.Z-1</i>	4	positive	negative
<i>TaH3-1</i>	3	positive	positive
<i>TaH3-2</i>	4	positive	negative
<i>TaH4-1</i>	4	positive	negative

Table 5 Suppl. The characteristics of *Arabidopsis* overexpressing wheat histone variants. Means $\pm$ SDs, $n = 15$ for root length and lateral root density; $n = 10$ for leaf area, height, rosette-leaf branch, cauline-leaf branch, and flowering time; $n = 4$ for seed mass and seed yield. According to one-way *ANOVA* test, differences are not significant at $P > 0.05$. The experiment was repeated three times; sd - short day (8 h light/16 h dark); ld - long day (16 h light/16 h dark). Col-0- *Arabidopsis* wild type; VC - a vector control transgenic line; OE1, OE2 - overexpression lines.

Item	Col-0	VC	<i>TaH1-1</i>		<i>TaH2A-2</i>		<i>TaH2A-3</i>		<i>TaH3-1</i>	
			OE1	OE2	OE1	OE2	OE1	OE2	OE1	OE2
Root length 7 d [cm]	1.85 $\pm$ 0.04	1.87 $\pm$ 0.06	1.86 $\pm$ 0.05	1.86 $\pm$ 0.04	1.89 $\pm$ 0.03	1.87 $\pm$ 0.06	1.82 $\pm$ 0.03	1.80 $\pm$ 0.03	1.86 $\pm$ 0.02	1.86 $\pm$ 0.03
Root length 13 d [cm]	8.83 $\pm$ 0.10	8.94 $\pm$ 0.07	8.85 $\pm$ 0.11	8.96 $\pm$ 0.05	9.00 $\pm$ 0.08	9.03 $\pm$ 0.08	8.92 $\pm$ 0.08	8.94 $\pm$ 0.07	8.98 $\pm$ 0.05	9.08 $\pm$ 0.06
Lateral root density [cm ⁻¹]	1.91 $\pm$ 0.06	1.87 $\pm$ 0.03	1.99 $\pm$ 0.04	1.93 $\pm$ 0.05	1.92 $\pm$ 0.06	1.99 $\pm$ 0.07	1.95 $\pm$ 0.05	1.97 $\pm$ 0.08	1.93 $\pm$ 0.04	1.92 $\pm$ 0.04
Leaf 6 area 21 d [mm ²]	233.71 $\pm$ 3.4	231.86 $\pm$ 6.2	226.43 $\pm$ 5.1	237.86 $\pm$ 9.2	227.00 $\pm$ 5.9	231.43 $\pm$ 4.9	231.00 $\pm$ 6.6	235.71 $\pm$ 6.4	229.14 $\pm$ 6.8	238.71 $\pm$ 4.7
Height [cm])	36.86 $\pm$ 0.91	36.71 $\pm$ 0.94	37.09 $\pm$ 0.82	36.04 $\pm$ 0.83	36.56 $\pm$ 0.90	37.25 $\pm$ 0.63	36.93 $\pm$ 0.71	37.84 $\pm$ 0.94	37.26 $\pm$ 0.74	37.79 $\pm$ 0.77
Rosette-leaf branch	2.43 $\pm$ 0.20	2.29 $\pm$ 0.18	2.43 $\pm$ 0.20	2.57 $\pm$ 0.20	2.29 $\pm$ 0.18	2.57 $\pm$ 0.30	2.57 $\pm$ 0.20	2.43 $\pm$ 0.30	2.29 $\pm$ 0.18	2.57 $\pm$ 0.20
Cauline-leaf branch	3.43 $\pm$ 0.20	3.57 $\pm$ 0.20	3.14 $\pm$ 0.26	3.57 $\pm$ 0.20	3.14 $\pm$ 0.26	3.57 $\pm$ 0.43	3.29 $\pm$ 0.29	3.43 $\pm$ 0.37	3.43 $\pm$ 0.20	3.57 $\pm$ 0.20
Flowering time [ld]	11.29 $\pm$ 0.61	11.43 $\pm$ 0.65	11.86 $\pm$ 0.67	11.14 $\pm$ 0.46	11.86 $\pm$ 0.67	12.00 $\pm$ 0.53	11.29 $\pm$ 0.52	11.86 $\pm$ 0.63	11.57 $\pm$ 0.37	11.86 $\pm$ 0.51
Flowering time [sd]	36.29 $\pm$ 1.08	35.57 $\pm$ 0.95	35.71 $\pm$ 1.23	36.86 $\pm$ 0.77	36.00 $\pm$ 1.25	35.43 $\pm$ 0.97	36.57 $\pm$ 0.92	37.00 $\pm$ 1.15	36.29 $\pm$ 0.97	36.14 $\pm$ 1.18
1000-seed mass [g]	99.00 $\pm$ 1.53	98.67 $\pm$ 1.76	101.67 $\pm$ 2.0	99.67 $\pm$ 1.45	97.00 $\pm$ 1.15	99.33 $\pm$ 0.88	101.00 $\pm$ 0.6	99.33 $\pm$ 1.86	98.33 $\pm$ 1.86	100.67 $\pm$ 2.0
Seed yield [g plant ⁻¹]	1.32 $\pm$ 0.01	1.31 $\pm$ 0.02	1.32 $\pm$ 0.02	1.33 $\pm$ 0.01	1.32 $\pm$ 0.01	1.32 $\pm$ 0.01	1.32 $\pm$ 0.01	1.31 $\pm$ 0.01	1.31 $\pm$ 0.01	1.31 $\pm$ 0.01

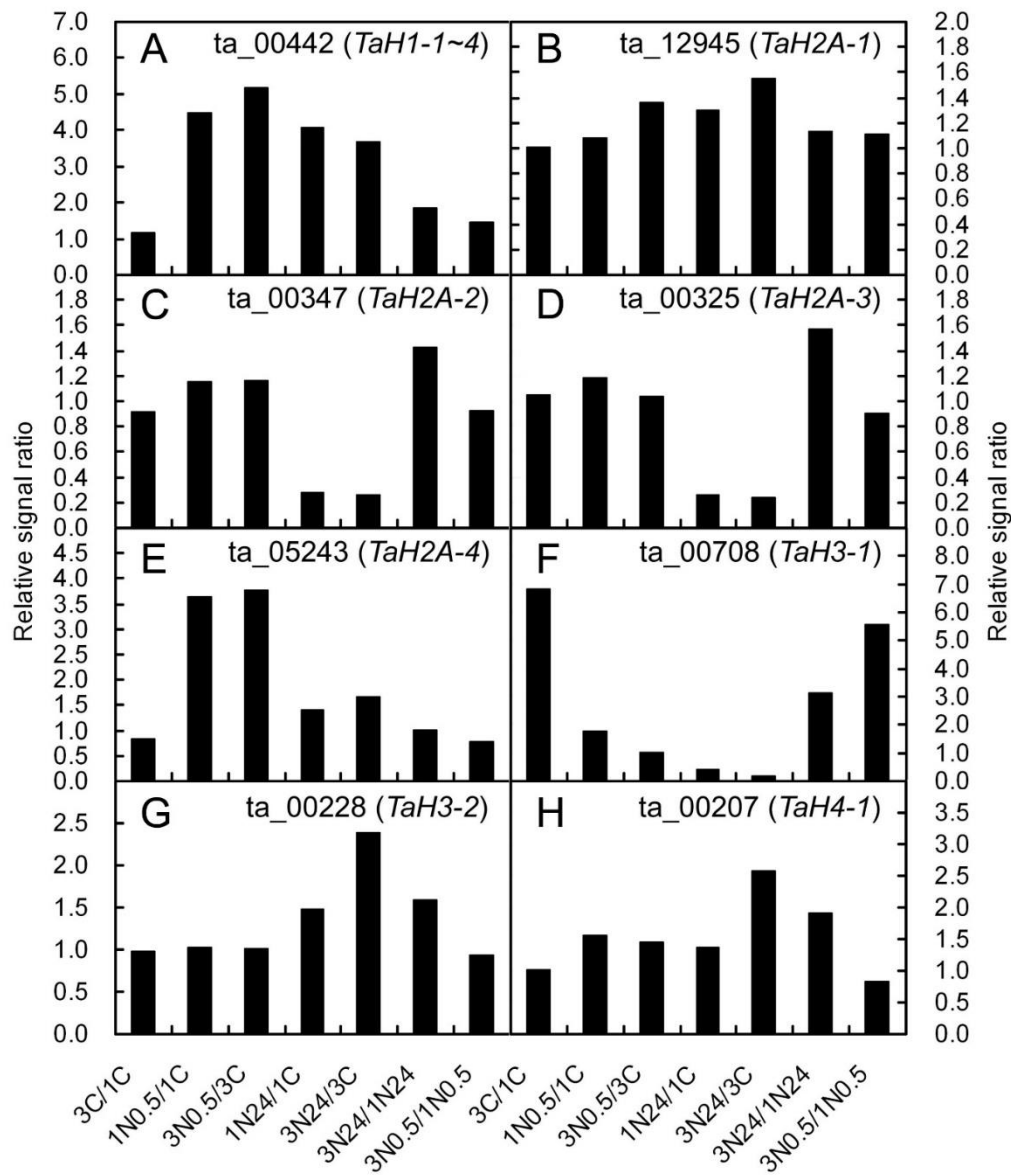


Fig. 1 Suppl. Salinity responsive histone-like genes identified by Liu *et al.* (2012). 3 - SR3, 1 - JN177, C - non-stressing growth conditions, N - growth under 340 mM NaCl; 0.5, 24 indicate the exposure for 0.5 and 24 h, respectively.

A	TaH1-2_ORF	CTTCG.....	85
	TaH1-2_DNA	CTTCGAGGTGAGCGTCCGAGCCTCTCATGTGTCCCCCTCT	120
	TaH1-2_ORF		85
	TaH1-2_DNA	GATTGAATGGTTTTGATTGCGATTGGGCTGATTGGATCTT	160
	TaH1-2_ORF	AGATGATCAAGGAGGCGATCGCGGCTCTCAAGGACA	121
	TaH1-2_DNA	GCGCAGATGATCAAGGAGGCGATCGCGGCTCTCAAGGACA	200
B	TaH2A-4_ORF	AGTACCTCGCCGCTG.....	175
	TaH2A-4_DNA	AGTACCTCGCCGCTGAGGTACGCACCTATCTTTCCCGTCC	200
	TaH2A-4_ORF		175
	TaH2A-4_DNA	TTCATTGTTCTTCTTCCATGTTCTTCTCGTGCCTCGACGGG	240
	TaH2A-4_ORF	AGGTTCTGGAG	186
	TaH2A-4_DNA	TAAC TGACAGATTTGGTTTCTGAATATGCAGGTTCTGGAG	280
C	TaH3-2_ORF	GCAAGGCGCCCCGCAAGCAGCTCGCCACCA.....	70
	TaH3-2_DNA	GCAAGGCGCCCCGCAAGCAGCTCGCCACCAAGGTCCGTCC	80
	TaH3-2_ORF		70
	TaH3-2_DNA	CCTCCCGTCTTCTGAATTCGATCTGTTTCATCCTTGTGT	120
	TaH3-2_ORF		70
	TaH3-2_DNA	TCGAGATTTGTTGGCTGACGTTTTGGATTTGAATCGTTGT	160
	TaH3-2_ORF	AGGCGGCCAGGAAGTCGGCGCCGACCACCGGC	102
	TaH3-2_DNA	GTGTTTGCAGGCGGCCAGGAAGTCGGCGCCGACCACCGGC	200

Fig. 2 Suppl. The presence of introns in *H1-2* (A), in *H2A-4* (B), and in *H3-2* (C) as shown by the alignment of their open reading frames and associated genomic DNA sequences (*light blue colour* indicates introns, *dark blue colour* indicates exons).

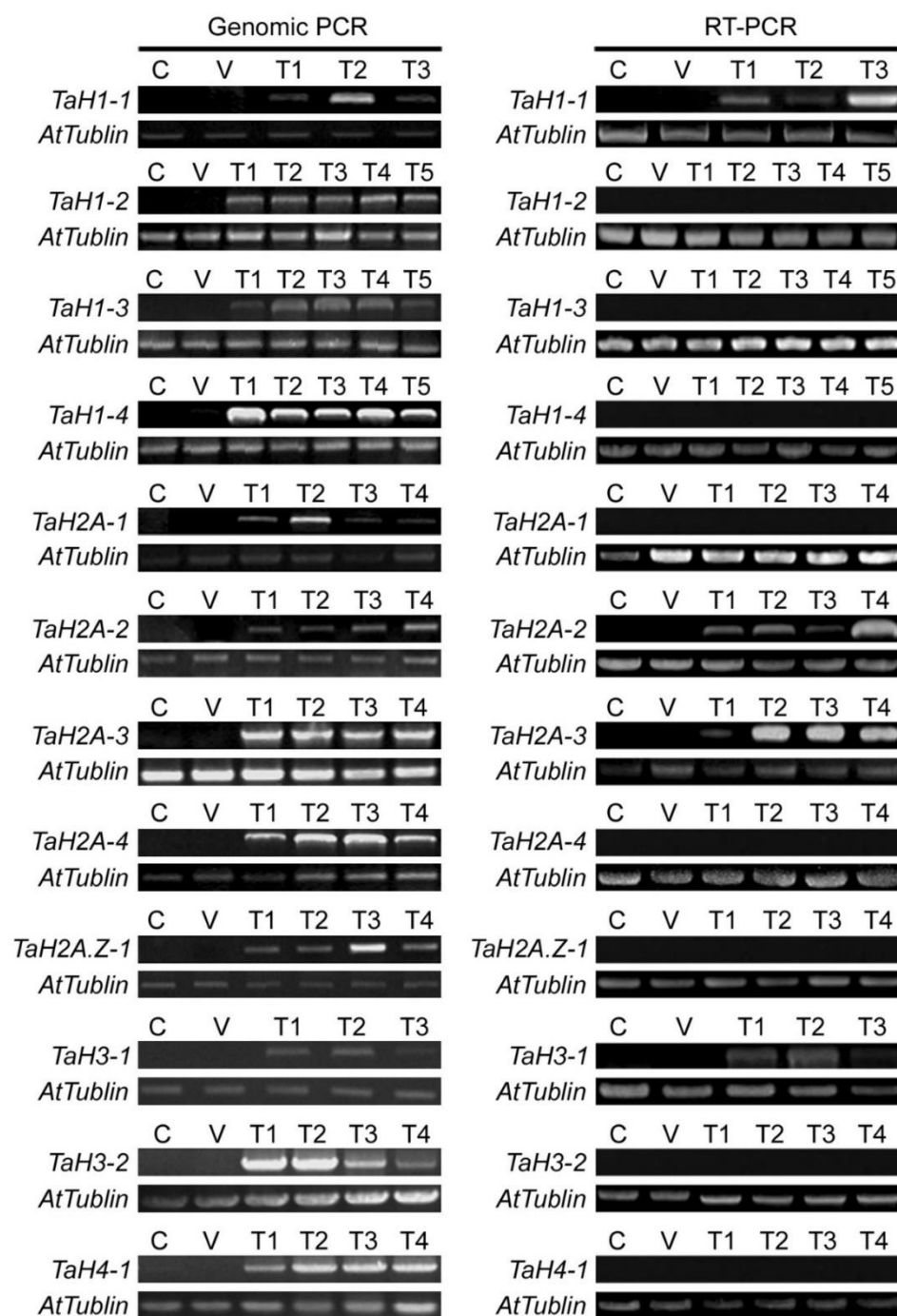


Fig. 3 Suppl. Eight of the 12 wheat histone variant transgenes were silenced in *Arabidopsis thaliana*. C - *A. thaliana* Col-0; V - *A. thaliana* Col-0 transformed with an empty pSTART vector; T1 to T4 - independent transgenic *A. thaliana* lines carrying a wheat histone transgene.