

Table 1 Suppl. Forward (Fw) and reverse (Rv) primers for each gene assessed by RT-qPCR.

Name	Sequence 5'-3'	Tm [°C]
ScCadmium-new-69-array-Fw	AGAAGGGCTGCATCTACGCA	64.29
ScCadmium-new-69-array-Rv	GCACTCACAGGTCTCGTAGCA	64.61
ScHarpin-new-90-array-Fw	CCTTCTTCCAGGGCCACCA	64.36
ScHarpin-new-90-array-Rv	AGGTTGGACTGGGTAACATCCC	64.25
ScABA-new-91-array-Fw	ATCATGATCCCCGCTGGCCA	64.6
ScABA-new-91-array-Rv	TCGACGGTGACGATGTGGA	63.68
ScMulti-new-111-array-Fw	TCAAGTTGCAACTGATGCTGTC	62.15
ScMulti-new-111-array-Rv	TCCCTGTTTCCTTAAAGCTTCAC	61.27
ScAqua-new-148-array-Fw	CTCTTCTACTGGGTCGCGCA	64.55
ScAqua-new-148-array-Rv	AACGTCATCACCGCTCCA	64.33
ScbHLH-new-85-array-Fw	GTGGTGAGCCAAGTGAAGGAA	62.50
ScbHLH-new-85-array-Rv	TTAGCCTCCGGAGGGATGG	63.27
ScGAPDH-Fw	GTGAGGCTGGTGCTGATTACG	61.56
ScGAPDH-Rv	TGGTGCAGCTAGCATTTGAGAC	61.28

Table 2 Suppl. Genes showing larger AI-dependent changes in expression of *3R-AL* than the other genotypes. For each gene the ProbeID, fold-change in expression, log Signal A, FDR (RankProd), probe ID, and a brief description of predicted function are shown.

Index	Fold change	LogSignal (A)	FDR (RankProd)	Probe ID	Description
341	-39.84	11.13	0	BJ279889	phosphoenolpyruvate carboxykinase [ATP]-like (<i>Brachypodium distachyon</i>)
10697	-14.12	10.34	0	TC278715	32 kDa protein (<i>Hordeum vulgare</i>)
40307	-6.12	8.17	0.00113636	CK217811	light-inducible protein CPRF2-like isoform 1 (<i>Triticum aestivum</i>)
20683	-4.25	10.42	0.00464789	TA102006_4565	targeting protein for Xklp2 containing protein
17220	3.98	9.20	0.00146067	TA50923_4565	<i>H. vulgare</i> putative protease inhibitor
37093	5.46	10.14	0.00338129	TA79831_4565	beta-ketoacyl-ACP synthase (<i>B. distachyon</i>)
14551	5.79	11.64	0.00203883	BQ168115	ethylene-responsive transcription factor 4-like (<i>B. distachyon</i>)
12741	7.68	11.81	0.0002381	TC328403	unknown protein
30844	7.70	9.23	0.00041667	TC335318	thaumatin-like protein (<i>T. aestivum</i>)
41097	7.74	9.85	0.00051948	TA93415_4565	pectinesterase/pectinesterase inhibitor 41 (<i>B. distachyon</i>)
2316	8.04	8.37	0.00030769	DR739825	<i>T. aestivum</i> mRNA for glycosyltransferase (<i>al</i> gene)
38328	8.14	11.87	0	TA101801_4565	aluminum-induced protein (al1) (<i>Zea mays</i>)
21675	8.43	9.00	0.00017544	TC366539	<i>B. distachyon</i> protein SRG1-like
11397	8.97	12.47	0.00023256	TC336347	oxalate oxidase (<i>T. aestivum</i>)
23590	9.67	13.4	0	DN949100	oxalate oxidase (<i>T. aestivum</i>)
19004	9.98	8.56	0	TA89135_4565	<i>Setaria italica</i> putative lipid-transfer protein DIR1
14092	10.40	8.40	0	TA57430_4565	<i>Prunus mume</i> methylenetetrahydrofolate reductase 2-like
33351	10.80	9.38	0	TA67617_4565	<i>B. distachyon</i> cell number regulator 2-like
3424	11.00	9.01	0	TA95904_4565	polygalacturonase inhibiting protein-like (<i>H. vulgare</i>)
40715	11.11	9.48	0	TA66702_4565	<i>B. distachyon</i> zinc finger CCCH domain-containing protein 44-like
5242	11.70	8.92	0	TA105821_4565	<i>B. distachyon</i> subtilisin-like protease SBT3.3
22771	16.25	9.80	0	DR741149	thaumatin-like protein (<i>T. aestivum</i>)
25335	16.87	9.38	0	TA59735_4565	thaumatin-like protein (<i>T. aestivum</i>)
13219	17.05	9.49	0	TA57429_4565	proline-rich protein (<i>T. aestivum</i>)
12171	18.20	9.99	0	DR740180	fatty acyl coA reductase (<i>T. aestivum</i>)

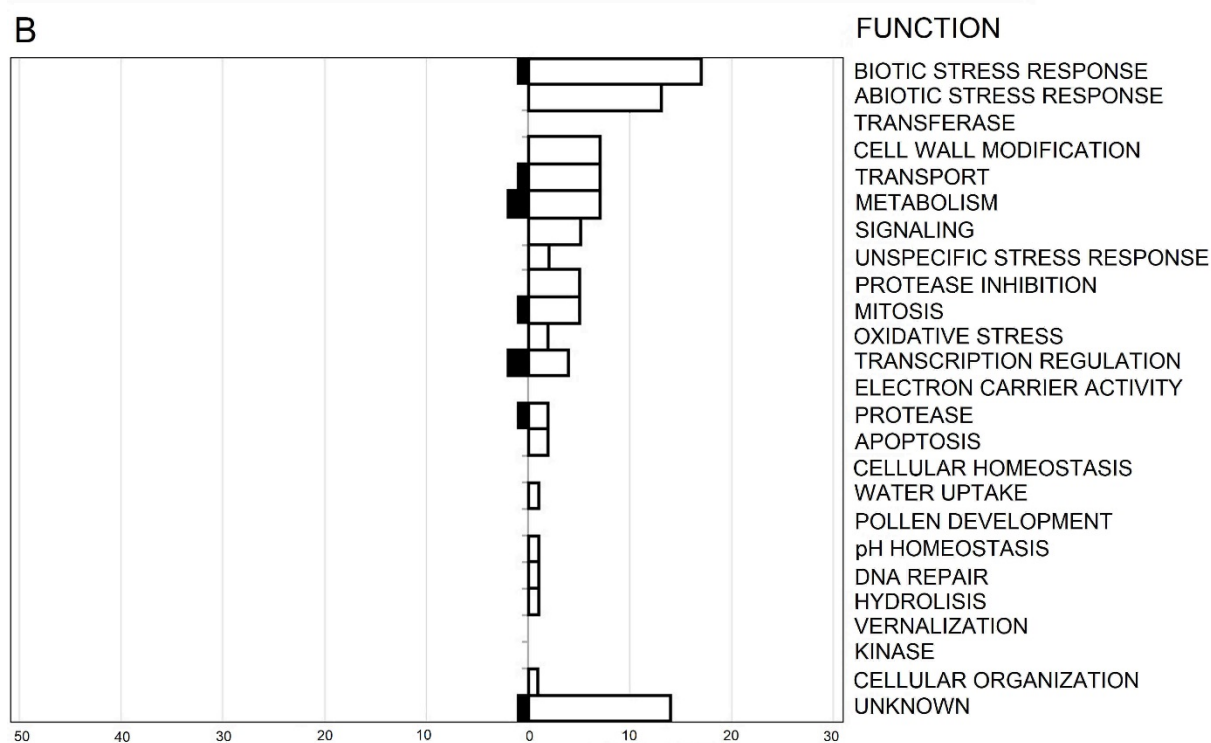
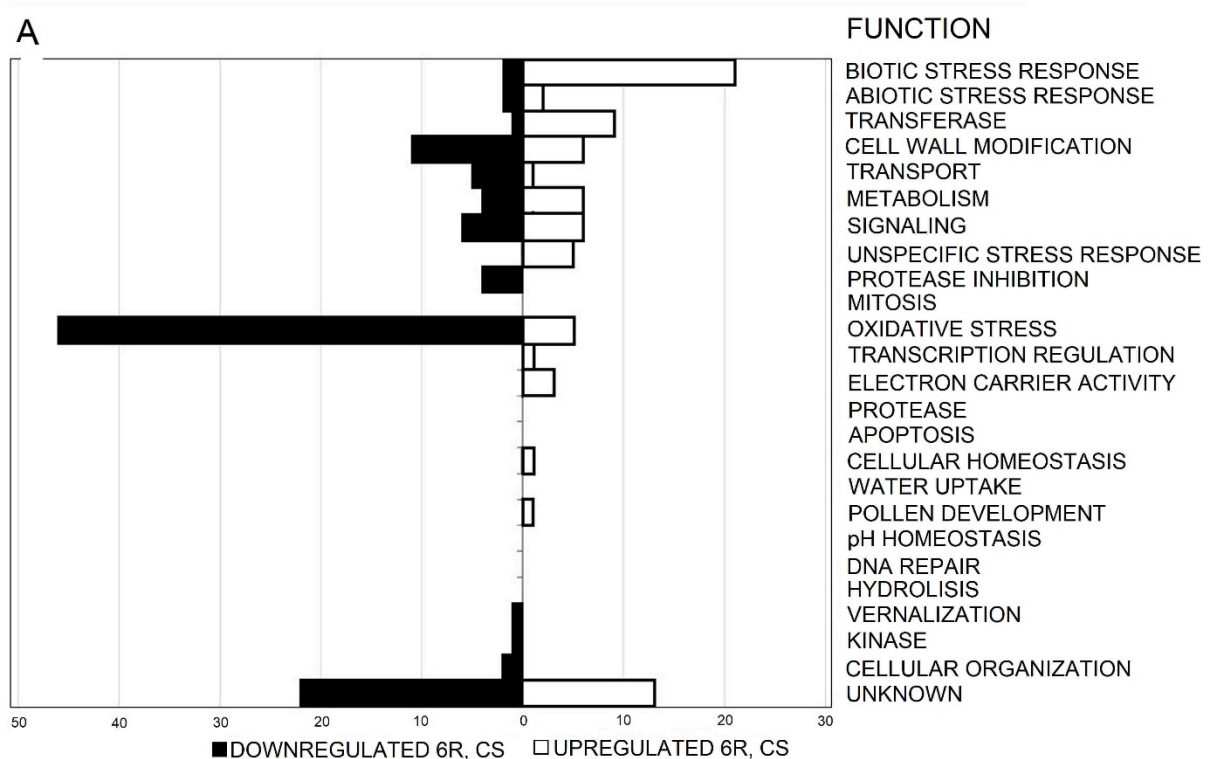


Fig. 1 Suppl.: Visual comparison of the number of genes up- and down-regulated in functional categories for wheat (cv. Chinese Spring) and the addition lines. Two comparisons are displayed: *A* - number and functional categories of genes up-regulated (*white*) and down-regulated (*black*) by AI treatment by ten-fold or more in the wheat and 6R-AL; *B* - number and functional categories of all genes up-regulated (*white*) and down-regulated (*black*) by AI in 3R-AL only (not just the 10-fold threshold). For (3A) the total number of genes up-regulated was 98 and down-regulated was 101. For (3B) the total number of genes up-regulated was 79 and down-regulated 9.

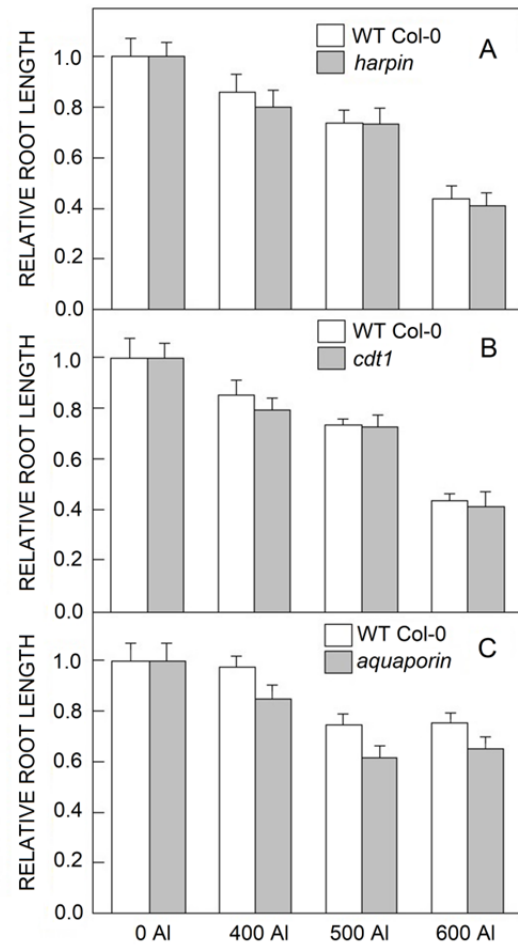


Fig. 2 Suppl. Relative root length of *Arabidopsis* lines grown under different concentrations of Al. Germplasm includes wild type Col-0, mutant lines with knockouts in the harpin induced gene (*harpin*), in the gene coding the cadmium tolerance protein CDT1 (*cdt1*), in the tonoplast intrinsic protein aquaporin gene (*aquaporin*), and in the AtALMT1 gene (*ataltmt1*). Plants were grown for 8 d on agar plates with different Al concentrations as described by Ryan *et al.* (2007). Means $\pm$ Ses, $n = 18$, ** - significantly different ($P < 0.01$) according to Student *t*-test.