

Table 1 Suppl. Primers used in PCR and RT-qPCR experiments and plant survival results.

Gene	Forward (5'-3')	Reverse (5'-3')
Identification of transgenic NHX plants by PCR	ATGGTTTTTGAAATCAGTTCTGTTGTTT	GCCACAAACGATGAACAGTG
<i>GmNHX3</i> (for RT-sqPCR and RT-qPCR in transgenic lines)	GCATCACGATAATCACAGATCC	GCCACAAACGATGAACAGTG
<i>GmNHX1</i> (for RT-sqPCR and RT-qPCR in transgenic lines)	GTGGCAAAAGCTCGCATATT	TGCCAATAGCACCAAACAAC
<i>EF1c</i> (At1G18070)	AGCACGCTCTTCTTGCTTTC	GGGTTGTATCCGACCTTCTTC
<i>RD22</i> (At5G25610)	ACCCTTTCGTGTATAACTATGC	TTGCCTCCGTAACCATCC
<i>RD29A</i> (At5G52310)	GATGACGAGCTAGAACCCTGAAG	CCTTTGTCCCTGGTGGAATAA
<i>RAB18</i> (At5G66400)	GGCGTCTTACCAGAACCGTC	TCATACTGCTGCTGGATCGG
<i>P5CS</i> (At2G39800)	GAGGGGGTATGACTGCAAAA	AACAGGAACGCCACCATAAG
<i>COR15A</i> (At2G42540)	CTCACTGGTATGGCTTCTTCTT	GGCGTAGATCAACGACTTCTT

Table 2 Suppl. Plant survival rate of wild type and *GmNHXs* transgenic lines after a withholding water for 12 d and 2 d of rewatering. Data was collected from four independent experiments with three biological replicates each ($n = 12$). Numbers in () represent total number of plants collected after each treatment for each genotype.

Plants	Survival rate [%]
Wild type	25.0 (3)
<i>GmNHX3</i> L1	83.3 (6)
<i>GmNHX3</i> L2	50.0 (6)
<i>GmNHX1</i> L1	75.0 (9)
<i>GmNHX1</i> L2	41.6 (5)

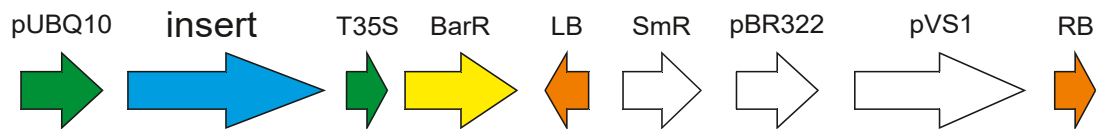


Fig. 1. Suppl. Details of the binary vector, pUB-DEST, used for genetic transformation of *A. thaliana*. Captions: pUBQ10: promoter of the *A. thaliana* ubiquitin-10 gene; Blue arrow: Insertion site for the *GmNHXs* genes; T35S: terminator; BarR: BASTA herbicide tolerance gene; LB: left border for transfer of *A. tumefaciens* T-DNA to plant cell; SmR: streptomycin resistance gene for selection in bacteria; pBR322: origin of replication in *E. coli*; pVS1: replication sequence for *A. tumefaciens*; RB: right border for transfer of *A. tumefaciens* T-DNA to the plant cell.

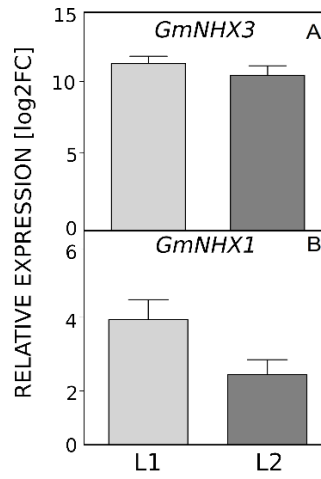


Fig. 2 Suppl. Relative expression levels of *GmNHX3* and *GmNHX1* (lines L1 and L2) genes determined by RT-qPCR. Four-week-old leaves of wild-type (WT) and transgenic lines were used to collect plant material. The relative expression levels of *GmNHX3* (A) and *GmNHX1* (B) are shown. Gene expression values are relative to the *EF1c* housekeeping gene. Transgene levels were not detectable in WT plants. Values are averages $\pm$ SDs from samples (biological replicates) per line. Asterisks indicate statistically significant differences (* p values < 0.05).

Complete NHX3 cDNA sequence from *Glycine max* cv. Munasqa (1 657 bp)

ATGGTTTTGAAAATCAGTTCGTGTTTCCACAATTTGCAACGTGTATCCACCTCAGACCATGCCTCCGTGGTCTCCATG
AACTATTTGTGGCACTTCTTTGTGGTTGTATTGTCCTTGGCCATCTTCTTGAGGAGAATCGATGGATGAACGAGTCTA
TCACTGCCCTTTTGATTGGTGTATGCACTGGCGTAGTCATTTTGTCTGTTTAGTGGTGGCAAAAAGCTCACATATCTTGT
TTCAGTGAAGATCTTTTCTTATATATCTTCTACCACCTATAATATTCAATGCCGGGTTTCAGGTGAAAAAGAAGCAGT
TTTTTGTTAACTTCATGACCATCATGTTGTTTGGTGCTATTGGTACATTAATATCATGTACCATCATAACTTTGGGTGCC
ACACAAATTTTAAAGAGGTTGGATGTTGGTCTCTGGAATTAGGGGATTTCCCTAGCAATTGGTGCAATATTTGCTGCAA
CGGATTCTGTTTGCACATTGCAGGTGCTAAATCAGGATGAGACACCTTTGCTGTACAGTCTTGTATTTGGGGAGGGTGT
TGTGAATGATGCTACATCAGTGGTGTCTTTCAATGCAATCCAAAGCTTTGACCTCAACCAAATTGACTCTTCAATTGCT
GTACACTTTTTGGGAAATTTCTTGTATCTATTTATCGCAAGCACAAATGCTTGGAGTTTGGACAGGTCTACTTAGTGCTTA
CATTATTA AAAAGCTGTACATTGGCAGGCACTCTACAGATCGTGAGGTTGCTCTTATGATGTTAATGGCATACTGTCC
TACATGCTTGCTGAATTATGTTATCTGAGTGGCATTCTCACTGTATTCTTTTGTGGTATTGTTATGCTCATTATACCTG
GCATAACGTGACCGAGAGTTCAAGAACTCACTACCAAGCATTCTTTTGCAACCTTGTCATTTGTTGCTGAGATCTTTATC
TTCCTTTATGTTGGTATGGATGCCTTGGACATTGAAAAATGGAAATTCGTCAGTGATAGCCCTGGAACATCTGTAGCA
ACTAGTGGAGTATTGTTGGGTCTAATTCTTCTTGGAAAGAGCAGCTTTTGTTTTCCCCTTATCCTTCATATCCAACTGGC
TAAAAAATCACCAAATGAGAAAATCAGCTTCAGACAGCAAGTTATCATTGTTGGGCTGGCCCTTATGAAAAGGTGC
TGTTTCCATCGCCACTTGCCATATAAATCAGTTTCACCATGGTCGGGGGCACACTTCCCTGGCGAAACAATGGCAATCC
TGAATCCCAAGCCCCATCCACGGTTGTGGCTTTTACCACAAGGGGTGTTTGGGCCCGTTAACCAAGCCACTCATA
AGGCTTTTACTGCCCCATACTCCACATCATAAAGAATCAAGCATCACGATAATCACAGATCCATCTACTCCAAGTCCA
AAATCAGTCACTATCCCACTTCTTGGGAGTGCCCAAGAATCTGAAGTTGATATTGATGGCCATGATATCCATCGTCCA
AGCAGTATTCGTGCCTTGCTTACGACTCCAACACACACTGTTTCATCGTTTGTGGCGTAAGTTGATGATGCATTTCATGC
GTCCCTGTTTTTGGTGGCAGGGGTTTTGTCTTTAGAACCTGTCCCCTACATTTACCCCGCCCATCAATGGCGTTGA

Complete NHX1 cDNA sequence from *Glycine max* cv. Munasqa (1 661 bp)

ATGGTTTTGAAAATCAGTTCGTGTTTCCCTATTGCAATCGTGTATCCACCTGAGACCATGCCTCCGTGGTCTCCATGA
ACTTATTGTGGCACTTCTTTGTGGTTGTATTGTCCTTGGCCATCTTCTTGAGGAGAATCGGTGGATGAACGAGTCTAT
CACTGCTCTTTTGATTGGTGTATGCACTGGCATAGTCATTTTGTCTGTTTAGTGGTGGCAAAAAGCTCGCATATCTTGT
TCAGTGAAGATCTTTTCTTATATACCTTCTGCCGCCATAATATTTAATGCCGGGTTTCAGGTGAAAAAGAAGCAGTT
TTTTGTAACTTCATGACCATCATGTTGTTTGGTGCTATTGGCACATTAATATCTTGTACCATCATAACTTTGGGTGCCA
CACAAATTTTAAAGAGGTTGGATGTTGGTCCACTGGAATTAGGGGATTTCCCTAGCAATTGGTGCAATATTTGCTGCAAC
GGATTCTGTTTGCACATTGCAGGTGCTAAATCAGGATGAGACACCTTTGCTGTACAGTCTTGTATTTGGGGAGGGTGT
GTGAATGATGCTACATCAGTGGTGTCTTTCAATGCAATCCAAAGCTTTGACCTCAACCAAATCGACCCCTCAATTGCTG
GGCATTTTTTGGGAAATTTCTTGTATCTATTTATTGCAAGCACAAATGCTTGGAGTGTGACAGGTCTACTTAGTGCTTA
CATTATTA AAAAGCTGTACATTGGCAGGCACTCTACAGATCGCGAGGTTGCTCTTATGATGTTAATGGCATACTCTCC
TACATGCTTGCTGAATTGTCCTATCTGAGTGGCATTCTCACTGTATTCTTTTGTGGGATTGTCATGTCTCATTATACCTG
GCATAATGTGACTGAGAGTTCAAGAACTCACTACCAAGCATTCTTTTGCAACCTTGCTTTTTGTTGCTGAGATCTTTATC
TTCCTTTATGTTGGTATGGATGCCTTGGACATTGAAAAATGGAAATTTGTCAGTGATAGCCCTGAAACATCTGTAGC
AACTAGTTCAGTATTGTTGGGGTCTAATTCTTCTTGGAAAAAGCAGCTTTTGTTTTCCCCTTATCCTTTCTATCCAA
CTTGGGCTAAAAAATCACCAAATGAAGAAAATCAGCTTTCAGAACAGCAAGTTAATCATTGTTGGTGGGGCTGGTTC
TTATGAGAAGGTGCTGTTTTCAATCCGCACTTTGCATATAAATCAATTTACCATGGTCGGGGGCAACCTTTCCCTTAA
GAAGCCAGGCAATCATGATCACAAGCACCATCACTGTTGTGCTTTTCAGCACAGTGGTGTGTTGGTCTGTTGACTAAGC
CACTAATAAGGCTTTTACTGCCCCATACTCCACATCATAAAGAATCAAGCATCACGATAACCACAGATCCATCTACTC
CAAGTCCAAAATCAGTCACTGTCCCACTTCTTGGGAGTGCCCAAGAATCTGAAGTCGATATTGATGGCCATGATATTC
ATTGTCCAAGCAGCATCCGTGCTTTACTTTCCACTCCAACACACACTGTTTCATCGTTTGTGGCGTAAGTTGATGATGC
ATTCATGCGTCCTGTTTTTGGTGGCAGGGGTGAGTCCTTAGAAACCGATCACAAAAAATGTCGCCATCAATGGCGTT

Fig. 3A Suppl. Complete cDNA sequences for *GmNHX3* and *GmNHX1* from soybean cultivar, MUNASQA, used to transform *A. thaliana*. Nucleotides highlighted in green represents forward and reverse primers used for amplifying the cDNA sequences.

NHX3Mq	ATGGTTTTTGAATCAGTTCTGTTGTTTCCACAATTTGCAACGTGTATCCACCTCAGACC	60
NHX1Mq	ATGGTTTTTGAATCAGTTCTGTTGTT - TCCCTATTGCAATCGTGTATCCACCTGAGACC	59
	***** * * * *	
NHX3Mq	ATGCCTCCGTGGTCTCCATGAACCTATTTGTGGCACTTCTTTGTGGTTGTATTGTCCTTG	120
NHX1Mq	ATGCCTCCGTGGTCTCCATGAACCTATTTGTGGCACTTCTTTGTGGTTGTATTGTCCTTG	119

NHX3Mq	GCCATCTTCTTGAGGAGAATCGATGGATGAACGAGTCTATCACTGCCCTTTTGATTGGTG	180
NHX1Mq	GCCATCTTCTTGAGGAGAATCGGTGGATGAACGAGTCTATCACTGCTCTTTTGATTGGTG	179

NHX3Mq	TATGCACTGGCGTAGTCATTTTGCTGTTTAGTGGTGGCAAAAGCTCACATATTCTTGTTT	240
NHX1Mq	TATGCACTGGCATAGTCATTTTGCTGTTTAGTGGTGGCAAAAGCTCGCATATTCTTGTTT	239

NHX3Mq	TCAGTGAAGATCTTTTCTTTATATATCTTCTACCACCTATAATATTCAATGCCGGGTTTC	300
NHX1Mq	TCAGTGAAGATCTTTTCTTTATATACCTTCTGCCGCTATAATATTTAATGCCGGGTTTC	299

NHX3Mq	AGGTGAAAAAGAAGCAGTTTTTTTGTTAACTTCATGACCATCATGTTGTTGGTGCTATTG	360
NHX1Mq	AGGTGAAAAAGAAGCAGTTTTTTTGTTAACTTCATGACCATCATGTTGTTGGTGCTATTG	359

NHX3Mq	GTACATTAATATCATGTACCATCATAACTTTGGGTGCCACACAAATTTTAAGAGGTTGG	420
NHX1Mq	GCACATTAATATCTTGTACCATCATAACTTTGGGTGCCACACAAATTTTAAGAGGTTGG	419
	* * * * *	
NHX3Mq	ATGTTGGTCCTCTGGAATTAGGGGATTTCTAGCAATTGGTGCAATATTGCTGCAACGG	480
NHX1Mq	ATGTTGGTCCACTGGAATTAGGGGATTTCTAGCAATTGGTGCAATATTGCTGCAACGG	479

NHX3Mq	ATTCTGTTTGACATTGCAGGTGCTAAATCAGGATGAGACACCTTTGCTGTACAGTCTTG	540
NHX1Mq	ATTCTGTTTGACATTGCAGGTGCTAAATCAGGATGAGACACCTTTGCTGTACAGTCTTG	539

NHX3Mq	TATTTGGGGAGGGTGTGTGAATGATGCTACATCAGTGGTGCTTTTCAATGCAATCCAAA	600
NHX1Mq	TATTTGGGGAGGGTGTGTGAATGATGCTACATCAGTGGTGCTTTTCAATGCAATCCAAA	599

NHX3Mq	GCTTTGACCTCAACCAAAATGACTCTTCAATTGCTGTACACTTTTTGGGAAATTTCTTG	660
NHX1Mq	GCTTTGACCTCAACCAAAATCGACCCTTCAATTGCTGGGCACTTTTTGGGAAATTTCTTG	659

NHX3Mq	ATCTATTTATCGCAAGCACAATGCTTGGAGTTTTGACAGGTCTACTTAGTGCTTACATTA	720
NHX1Mq	ATCTATTTATTGCAAGCACAATGCTTGGAGTGTGACAGGTCTACTTAGTGCTTACATTA	719

NHX3Mq	TTAAAAAGCTGTACATTGGCAGGCACTCTACAGATCGTGAGGTTGCTCTTATGATGTTAA	780
NHX1Mq	TTAAAAAGCTGTACATTGGCAGGCACTCTACAGATCGCGAGGTTGCTCTTATGATGTTAA	779

NHX3Mq	TGGCATACTGTCTACATGCTTGTGAATTATGTTATCTGAGTGGCATTCTCACTGTAT	840
NHX1Mq	TGGCATACTGTCTACATGCTTGTGAATTGTCTATCTGAGTGGCATTCTCACTGTAT	839

NHX3Mq	TCTTTTGTGGTATTGTTATGCTCATTATACCTGGCATAACGTGACCGAGAGTTCAAGAA	900
NHX1Mq	TCTTTTGTGGGATTGTATGCTCATTATACCTGGCATAATGTGACTGAGAGTTCAAGAA	899

NHX3Mq	TCACTACCAAGCATTCTTTTGCAACCTTGTCATTGTTGCTGAGATCTTTATCTTCCTTT	960
NHX1Mq	TCACTACCAAGCATTCTTTTGCAACCTTGTCATTGTTGCTGAGATCTTTATCTTCCTTT	959

NHX3Mq	ATGTTGGTATGGATGCCTTGGACATTGAAAAATG - -GAAATTCGTCAGTGATAGCCCTGG	1018
NHX1Mq	ATGTTGGTATGGATGCCTTGGACATTGAAAAATGAAAAATTTGTCAGTGATAGCCCTGA	1019

NHX3Mq	AACATCTGTAGCAACTAGTGGAGTATTGTTGGGTCTAATTCT - TCTTGGAAAGAGCAGCTT	1077
NHX1Mq	AACATCTGTAGCAACTAGTTCAGTATTGTTGGGGTCTAATTCTTCTTGGAAAAAGCAGCT	1079

NHX3Mq	TTGT - - - TTTCCCTTA - TCCTTCATATCCAACCTTGGCTAAAAATCACCA - - - AATGA	1129
NHX1Mq	TTTTGTTTCCCCCTTATCCTTCCTATCCAACCTTGGGCTAAAAAATCACCAAAATGAA	1139
	* * * * *	
NHX3Mq	GAAAATCAGCTTCAG - -ACAGCAA - -GTTATCATTTGGTTGGGCTGGCCCTTATGAAAAG	1185
NHX1Mq	GAAAATCAGCTTTCAGAACAGCAAGTTAATCATTTTGGTGGGCTGGTTCCTTATGAGAAG	1199

NHX3Mq	GTGCTGTTTC - -CATCGCCACTTGCCATATAAATCAGTTTCACCATGGTCGGGGGCACACT	1243
NHX1Mq	GTGCTGTTTTCATCCGCACCTTGCCATATAAATCAATTTACCATGGTCGGGGGCACCT	1259

NHX3Mq	TTCCTGGCGAAACAATGGCAATCCTGAATCCCAAGCCCCATCCACGGTTGTGGCTTTT	1303
NHX1Mq	TTCCCTTAAGAAGCCAGGCAATCATGATCACAAG---CACCATCACTGTT---GTGCT	1311

NHX3Mq	TCACCACAAGGGGTGTTTGGGCCCGTTAACAAGCCACTATAAGGCTTTTACTGCCCCA	1363
NHX1Mq	TTTCAGCACAGTGGTGTGGTCTGTGACTAAGCCACTAATAAGGCTTTTACTGCCCCA	1371
	* * * * *	
NHX3Mq	TACTCCACATCATAAAGAATCAAGCATCACGATAATCACAGATCCATCTACTCCAAGTCC	1423
NHX1Mq	TACTCCACATCATAAAGAATCAAGCATCACGATAACCACAGATCCATCTACTCCAAGTCC	1431

NHX3Mq	AAAATCAGTCACTATCCCACCTTCTGGGAGTGCCCAAGAATCTGAAGTTGATATTGATGG	1483
NHX1Mq	AAAATCAGTCACTGTCCCACCTTCTGGGAGTGCCCAAGAATCTGAAGTCGATATTGATGG	1491

NHX3Mq	CCATGATATCCATCGTCCAAGCAGTATTCGTGCCTTGCTTACGACTCCAACACACACTGT	1543
NHX1Mq	CCATGATATTCATTGTCCAAGCAGCATCCGTGCTTTACTTTCCACTCCAACACACACTGT	1551

NHX3Mq	TCATCGTTTGTGGCGTAAGTTTGTATGATGCATTATGCGTCCCTGTTTTTGGTGGCAGGG	1603
NHX1Mq	TCATCGCTTGTGGCGTAAGTTTGTATGATGCATTATGCGTCCCTGTTTTTGGTGGCAGGG	1611

NHX3Mq	GTTTTGTCTTTAGAACCTGTCCCTACATTTACCCCGGCCATCAATGGCGTTGA	1657
NHX1Mq	TGA-GTCCTTAGAAACCGATCACAAAA---ATGTCGGCCATCAATGGCGTTGA	1661
	* * * * *	

Fig. 3B Suppl. Alignment between cDNAs of *GmNHX3* and *GmNHX1* (Munasqa): 93% similarity (BLASTN 2 sequences).

GF*NQFCCFHNLRVSTSDHASVVS MNLFVALLCGCIVLGHLLEENRWMNESITALLIGV
 CTGVVILLFSGGKSSHILVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIG
 TLISCTIITLGATQIFKRLDVGPLELGDFLAIGAIFAATDSVCTLQVLNQDETPLLYSLV
 FGEGVVNDATSVVLFNAIQSFDLNQIDSSIAVHFLGNFLYLFIASMTLGVLTGLLSAYII
 KKL YIGRHST DREVALMMLMAYLSYMLAELCYLSGILTVFFCGIVMSHYTWHNVTESSRI
 TTKHSFATLSFVAEIFIFLYVGMDALDIEKWKFYSDSPGTSVATSGVLLGLILLGRAAFV
 FPLSFISNLAKKSPNEKISFROQVIWLGWPL *KGA VSIATCL*ISFTMVGGTSLAKQW
 QS*IPSPHRLWLFHHKGCLGPLTKPLIRLLPHTPHHKESSITIITDPSTPSPKSVTIP
 LLGSAQSEVDIDGHDHHRPSSIRALLTPTHTVHRLWRKFDDAFMRPCFWWQGFCL*NL
 SPTFTPAINGV

Complete NHX3 protein sequence (367 amino acids)

WFLKSVLLFPYCNRVST*DHASVVS MNLFVALLCGCIVLGHLLEENRWMNESITALLIGV
 CTGIVILLFSGGKSSHILVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIG
 TLISCTIITLGATQIFKRLDVGPLELGDFLAIGAIFAATDSVCTLQVLNQDETPLLYSLV
 FGEGVVNDATSVVLFNAIQSFDLNQIDPSIAGHFLGNFLYLFIASMTLGVLTGLLSAYII
 KKL YIGRHST DREVALMMLMAYLSYMLAELSYLSGILTVFFCGIVMSHYTWHNVTESSRI
 TTKHSFATLSFVAEIFIFLYVGMDALDIEKMENLSVIALKHL *QLVQYCWGLILLGKSSF
 LFSPLSFPIQLGLKKSPK*RKSAFRTAS*SFWWGWFL*EGAVFNPHFAYKSISPWGATF
 PLRSQAIMITSTITVVFGLLTKPLIRLLPHTPHHKESSITITDPSTPSPKSV
 TVPLLGSAQSEVDIDGHDHICPSSIRALLSTPTHTVHRLWRKFDDAFMRPVFGGRGESL
 ETDHKKCRPSMAL

Complete NHX1 protein sequence (317 amino acids)

Fig. 3C Suppl. Complete amino acid sequences for NHX3 and NHX1 of soybean cultivar MUNASQA. Functional proteins are highlighted in green according to most probable ORFs analysis (*ExPASy*, <https://web.expasy.org/translate/>)

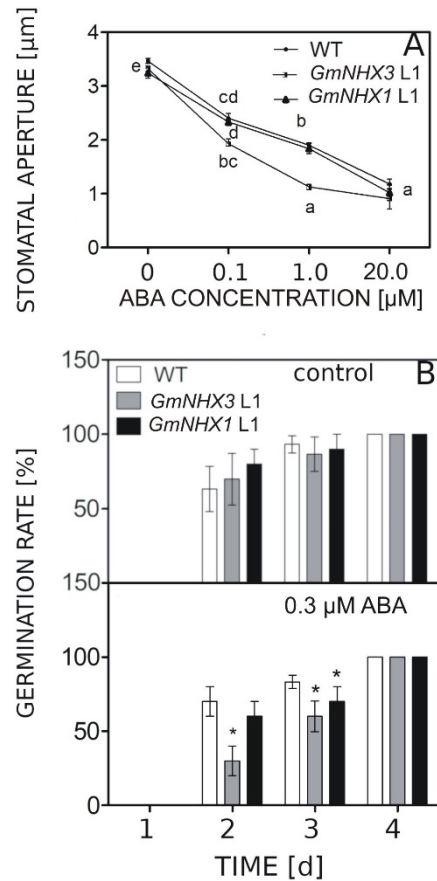


Fig. 5 Suppl. *A* - Stomatal apertures of *Arabidopsis thaliana* wild-type (WT) and transgenic epidermis after incubation with 0.1, 1, and 20 μ M ABA for 1.5 h; *B* - Seed germination rates of WT and transgenic lines on MS medium (control) or supplemented with 0.3 μ M ABA. Results are represented as the average from 120 and 30 measurements per WT and transgenic lines, collected from three independent experiments (n=40 per trial) for (*A*) and (n=10) for (*B*). Error bars represent SE for (*A*) and SD for (*B*). Different letters indicate significant differences at $P < 0.05$ for (*A*) two-way ANOVA, Bonferroni's test. In (*B*) significant differences were determined according to Student's test, $P < 0.05$.