Supplementary Material

S - materials and methods

Northern blot analysis

For northern blot analysis, equal amounts (10 µg) of total RNA for each sample were separated on an 0.8% agarose formaldehyde gel and transferred to a positively charged nylon filter (Amersham Biosciences). About 50 ng of an *Asg1* DNA fragment corresponding to the first 154 bp of *Asg1* coding sequence were PCR amplified (For primer, 5'- ATGGATCCTCAAGCTTTCATTCGT -3', Rev primer 5'- TTTGAACAGGAAAGCCTCGT -3') and labelled with [α-^{32}P] dCTP using the Ready-To-Go DNA labelling beads (Amersham Biosciences) following manufacturer's instructions. The hybridization was performed at 42°C in Perfect Hyb buffer (Sigma). The filters were washed at 42°C three times with 2X, 1X and 0.5X SSC, 0.1% SDS for 15 min.

ABA extraction and quantification

ABA was extracted from 1g of plant material per sample using water as described by Gomez-Cadenas and colleagues (2002) quantified using the Phytodetek ABA immunoassay kit (Idetek, Inc., Sunnyvale, CA).

Table S1. Primers used in this study

Primer Name	**Sequence (5'-3')**
LP	CTGTCCCAACCCTGAGAAGTC
RP	CATGCTCACTTGGAAATCTCG
N2.1 ST1	GTATGCGAGATCCGTCTTCGAGGTT
N2.1ST2	GGCAGTGGGGTGAGTCCTGG
AtN2.1 For	GAATTGCGGTGTTGGTGGCA
AtN2.1 Rev	GACACTGTGGGACAGAGACG
18S1	TAGATAAAAGGTCGACGCGG
18S2	CCCAAAGTCCAACTACGAGC
18S2 At	CCCAAGGTTCAACTACGAGC
Act For	GGCTCCTCTTAACCCAAAGG
Act Rev	GAACCACCGATCCAGACACT
N2.1 ATG	GGAGCTCTGACTAGAATGGATCCTCAGGC
N2.1 STOP	TATACATCACCAGGAATGGCG
CH11	GAAACTGATGCATTGAACTTG
AtN2.1DONRFor	GGGGACAAGTTTGTACAAAAAAGCAGGCTATATGGATCCTCAAGCTTTCATTC
AtN2.1DONRevnostop	GGGGACCACTTTGTACAAGAAAGCTGGGTTCCAGGAGTAATGCCGGAAC
N2.1 Prom left	CCCAAGCTTTTAGAAGAAACAAATAATTG
N2.1 Prom right	CCGGAATTCTAAATGTCAGAAATGTTTCC

Figure S1. Quantification of ABA levels in wild-type potato (WT) and a transgenic line over-expressing Asg1(15A8) in control (0 mM NaCl) and salt stress (50 mM NaCl and 100 mM NaCl) conditions.

Figure S2. Expression analyses of Arabidopsis transgenic plants over-expressing *Asg1* (A) and *asg1* knockout mutants (SALK_059272, *asg1*). A) Northern blot analysis of *Asg1* expression in T-3 homozygous single copy transgenic lines. A ^{32}P labeled *Asg1* fragment (1-150 of the coding sequence) was used as probe. b) RT-PCR analysis to confirm that the expression of *Asg1* is abolished in the mutant. The primers used were AtN2.1For + AtN2.1Rev. 18S ribosomal RNA was amplified as internal standard of the RT-PCR reaction.