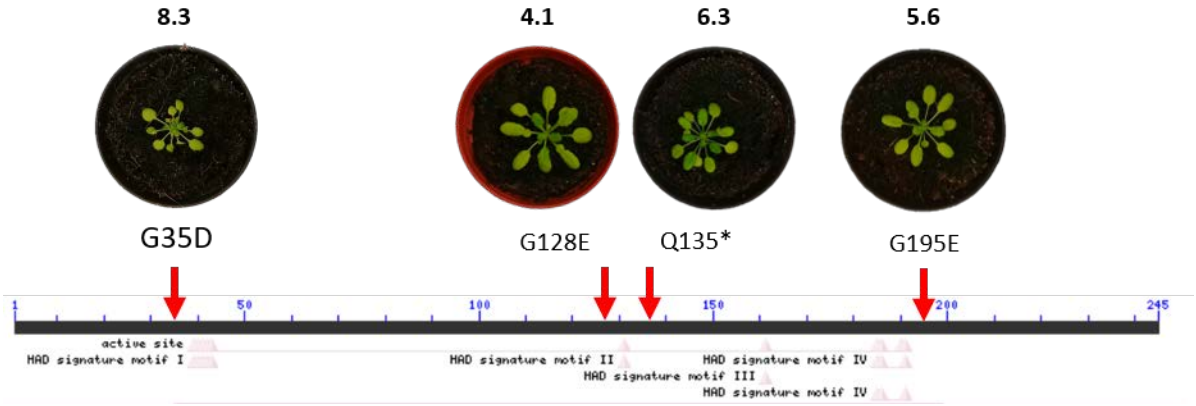
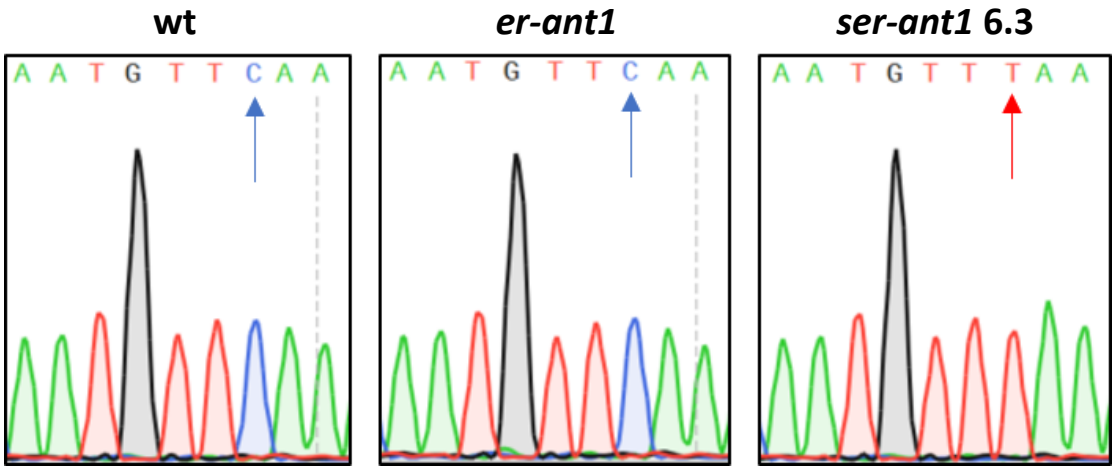
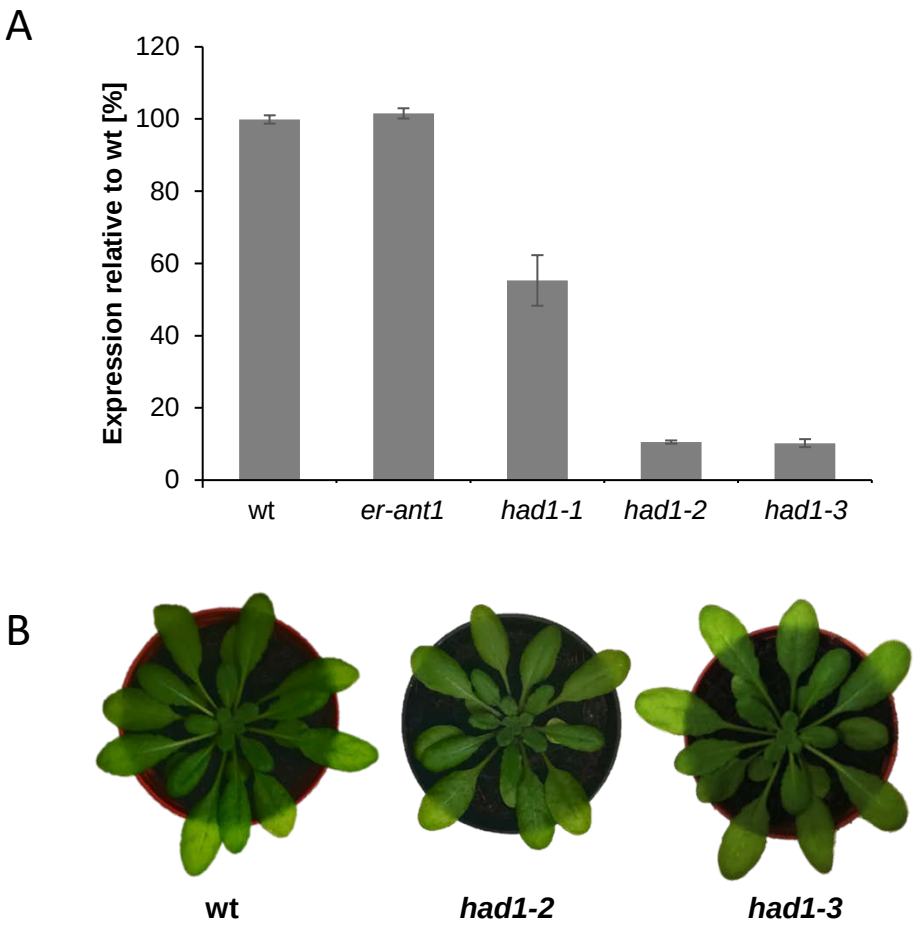


Supplemental Figure S1: SNP induced changes in the *At2g33255* gene product.
The individual positions in the amino acid sequence (taken from BLAST: https://blast.ncbi.nlm.nih.gov/Blast.cgi) are indicated by red arrows. The resulting amino acid changes and photos of representative plants are displayed above the arrows. Stop codon (*). Plants were grown under standard growth conditions (diurnally for 10 h at 22°C and 120 µmol photons m^{-2} s^{-1} light intensity followed by 14 h at 18°C without light, CO_2 levels around 400 ppm).

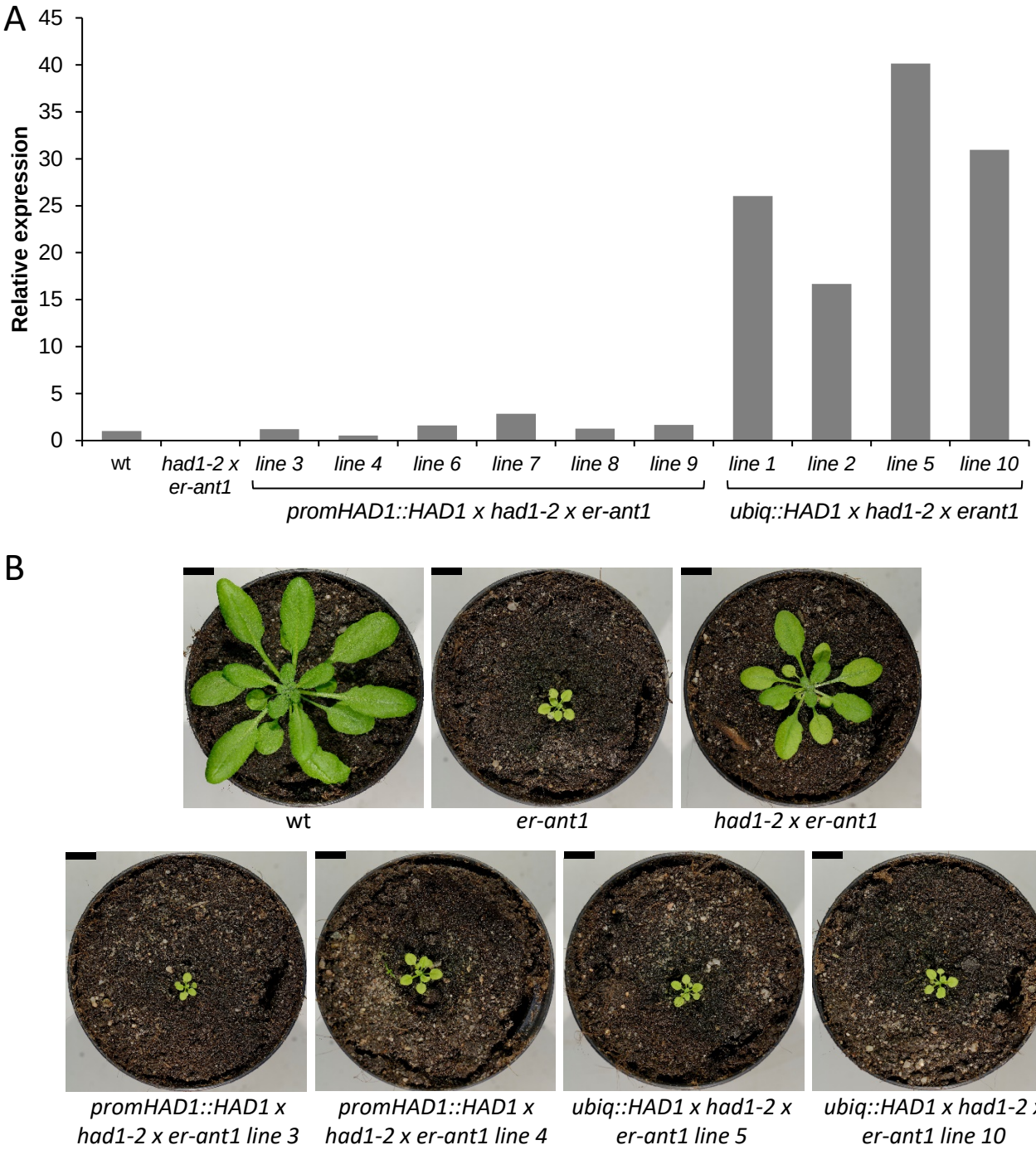


Supplemental Figure S2: Confirmation of the candidate SNP in *At2g33255* of *ser-ant1* line 6.3.

Comparison of the sequences determined by Sanger sequencing of genomic DNA (gDNA) from the wild type (wt), *er-ant1* and the *ser-ant1* M_3 line 6.3. Blue arrows highlight nucleotides identical to the reference genome at TAIR10. The red arrow highlights the confirmed candidate single nucleotide polymorphism (SNP).

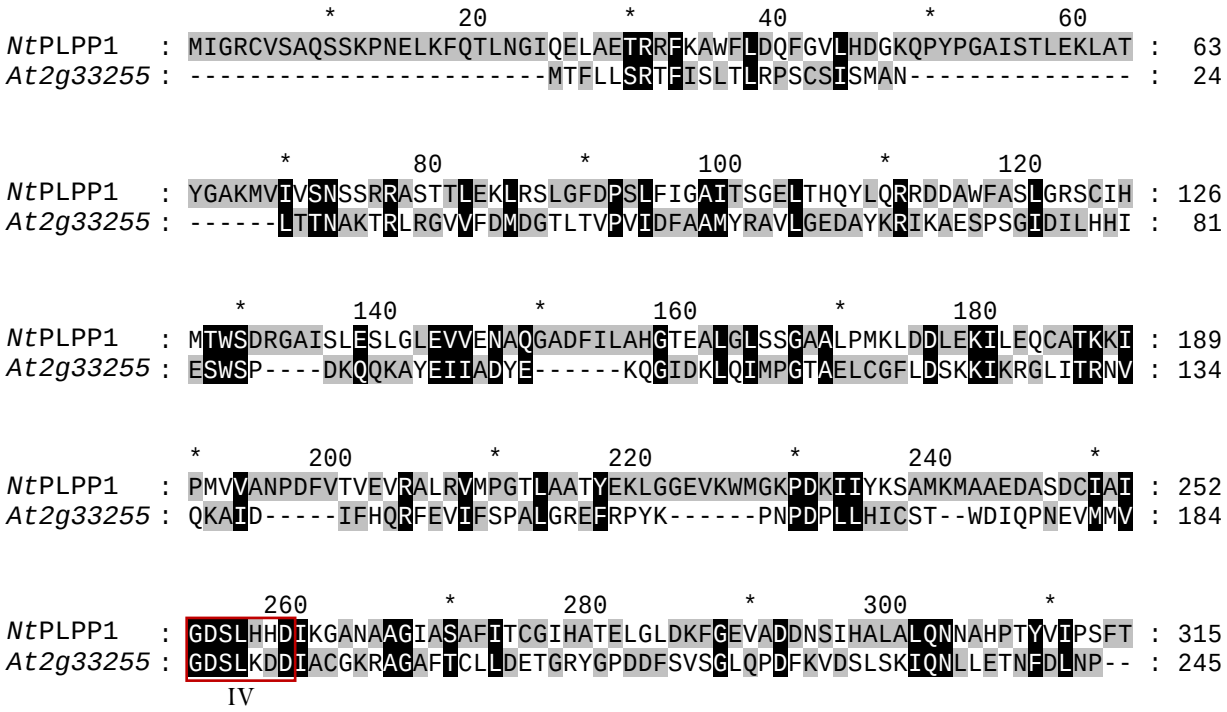


Supplemental Figure S3: Analysis of *At2g33255* T-DNA insertion lines.
(A) Expression of *At2g33255* in *er-ant1* and three *had* transfer-DNA (T-DNA) insertion lines relative to the wild type (wt). Expression levels were determined by qRT-PCR. RNA for cDNA synthesis was extracted from leaves of three weeks old plants. Data were normalized to the SAND (*At2g28390)* housekeeping gene. Shown are mean values of the expression in at least four plants ± SE. Line *had1-1* still contains about 50% of the transcript whereas the level in *had1-2* and *had1-3* is at the detection limit. Therefore, we considered *had1-1* as a knock-down and *had1-2* and *had1-3* as knock-out plants. (B) Phenotype of four weeks old plants grown under standard growth conditions (diurnally for 10 h at 22°C and 120 µmol photons m^{-2} s^{-1} light intensity followed by 14 h at 18°C without light, CO_2 levels around 400 ppm). Images of panel B were digitally extracted for comparison.



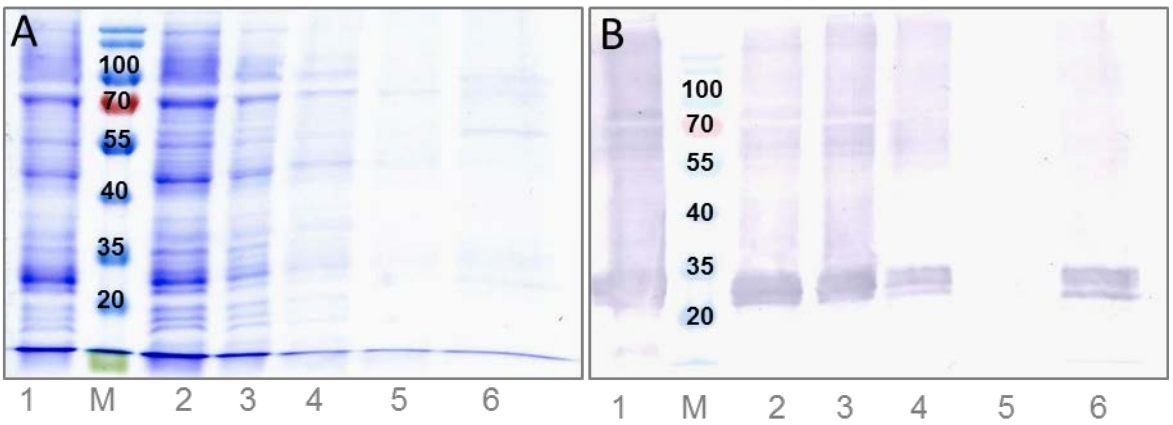
Supplemental Figure S4: Analysis of *promHAD1::HAD1 x had1-2 x er-ant1* and *ubiq::HAD1 x had1-2 x erant1 lines*.

(A) Expression of *At2g33255* in various mutant lines relative to the wild type (wt). Expression levels were determined via RT-qPCR. RNA for cDNA synthesis was extracted from leaves of 3 weeks old plants. Data were normalised to the ubiquitin housekeeping gene (*At4g05320*). (B) Phenotype of four weeks old plants. Plants were grown for 4 weeks under standard growth conditions (diurnally for 10 h at 22°C and 120 µmol photons m^{-2} s^{-1} light intensity followed by 14 h at 18°C without light, CO_2 levels around 400 ppm). Black bars represent 10 mm.



Supplemental Figure S5: ClustalW alignment of the amino acid sequences of the pyridoxal 5'-phosphate phosphatase (PLPP) from *Nicotiana tabacum* (*Nt*PLPP1) and the *At2g33255* gene product.

Residues identical among the two sequences or with similar properties are indicated by black shading. Residues not identical are highlighted by different shading (gray/white). The red box marks the conserved haloacid dehalogenase-like superfamily (HADSF) motif IV (E/DD, GDxxxD, or GDxxxxD). Dashes represent introduced gaps for alignment improvement. Numbers at the right indicate amino acid positions.



Supplemental Figure S6: Purification of the HAD-type hydrolase, *At*2g33255, heterologously expressed in *Escherichia coli* Rosetta cells.

(A) Coomassie stained SDS-PAGE of the purification of the haloacid dehalogenase (HAD)-type hydrolase. Lane 1: Lysate of induced *E. coli* cells; Lane M: Protein marker Pageruler (ThermoFisher), the numbers represent the molecular masses (given in kDa); Lane 2: soluble protein fraction after centrifugation (5000 *g*, 4°C); Lane 3: flow through of Immobilized Metal Ion Affinity Chromatography (IMAC); Lane 4: flow through of the first washing step with binding buffer; Lane 5: flow through of the second washing step with washing buffer; Lane 6: eluate. The calculated molecular mass of the HAD-type hydrolase is 27.5 kDa (http://aramemnon.uni-koeln.de). (B) Immunochemical staining of the same samples as in (A) with the anti-His antibody and the corresponding secondary anti-mouse antibody (alkaline phosphatase conjugate). Colorimetric detection was by NBT/BCIP staining.

Supplemental Table S1: SNP in the coding sequence of *At2g33255* from different *er-ant1* suppressor lines.

Line	AF	Max AF	SNP Position	AA change
8.3	0.86	0.88	14098898	G→D
4.1	0.97	1	14099659	G→E
4.2	0.83	0.94	14099659	G→E
4.4	1	1	14099659	G→E
6.3	0.94	0.97	14099679	Q→*
5.6	0.86	0.92	14100204	G→E
17.1	0.98	0.98	14100204	G→E

Shown are allele frequencies (AF) of the single nucleotide polymorphisms (SNPs) in *At2g33255*, highest allele frequency among all candidate SNPs in the respective line (Max AF), *At2g33255* SNP position on chromosome 2 (SNP position), and the respective amino acid (AA) change caused by the SNP. Lines are sorted by SNP position (5'→3'). Redundant SNPs are highlighted by identical colours.