Figure S1

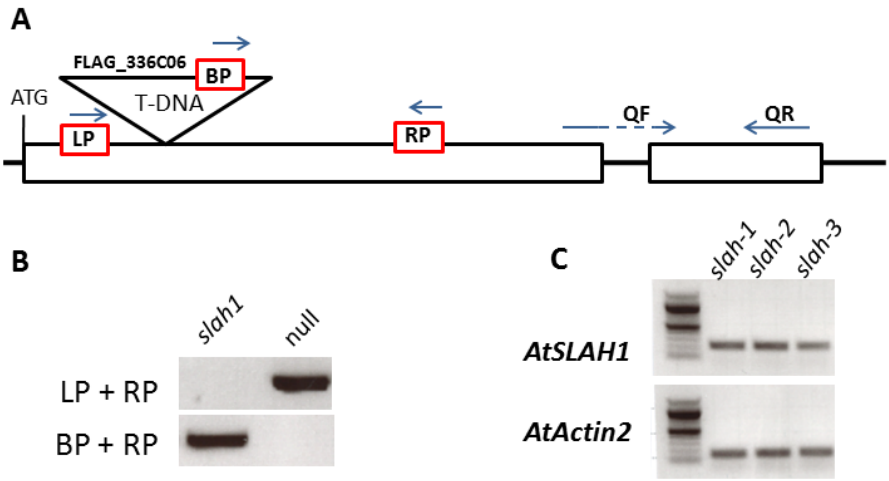

Figure S1 *AtSLAH1* is still expressed in the slah1 homozygous T-DNA insertion line FLAG_336C06. (A) Map of the *slah1*T-DNA insertions in AtSLAH1 (At1g62280). LP, T-DNA left border primer; RP, T-DNA right border primer; BP, T-DNA border primer; QF, *AtSLAH1* q-RT-PCR forward primer; QR, q-RT-PCR reverse primer; (B) RT-PCR detection of T-DNA insertion in *slah1* mutant gDNA. Primers used were listed in Supplementary Table S1; (C) RT-PCR suggested that *AtSLAH1*'s expression is still detectable in mutant's cDNA, bands in upper panel were sequenced and showed that the amplified PCR products are *AtSLAH1* rather than non-specific bands. Primers used for detecting *AtSLAH1* expression were listed in Supplementary Table S1.

Figure S2

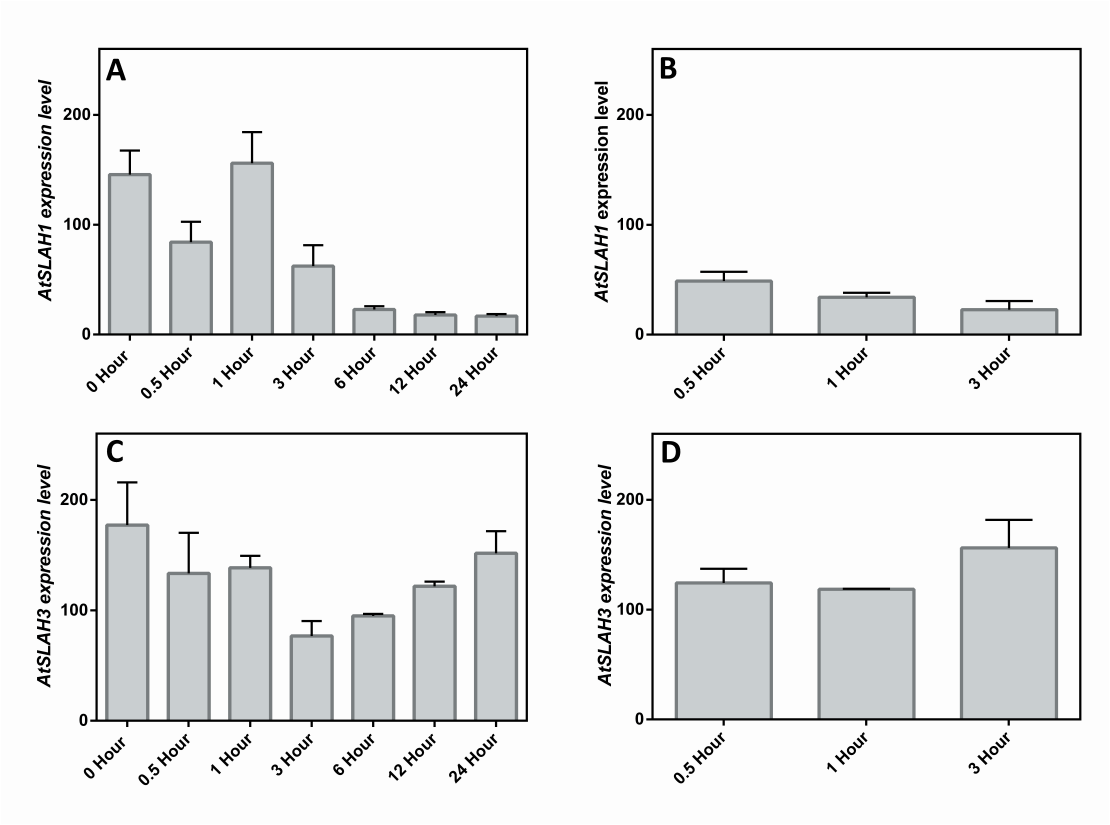

Figure S2 The transcript level changes of *AtSLAH1* and *AtSLAH3* upon NaCl or ABA treatments. For NaCl treatment, 150 mM NaCl was applied for 0-24 hours and for ABA treatment, 20 µM ABA was applied for 0.5-3 hours. (A) and (B) *AtSLAH1*, (C) and (D) *AtSLAH3*. Data was extracted from Arabidopsis eFP Browser database. Results were presented as mean + SD (n = 3). Y axis: GCOS signal (adapted from Kilian *et al*., 2007).

Figure S3

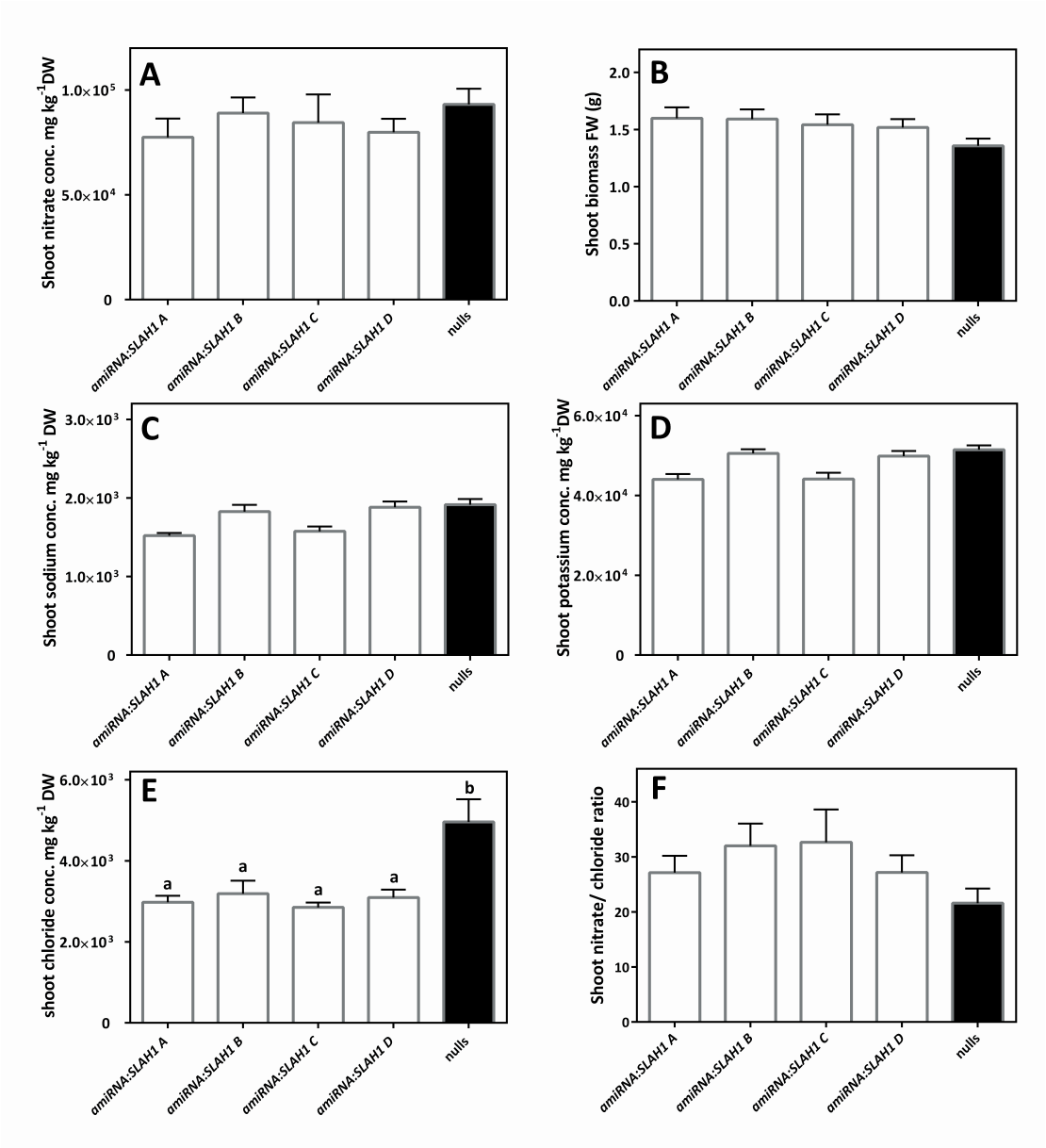

Figure S3 Under low Cl^- conditions, the shoot NO_3^-, Na^+, K^+ concentrations and biomass were detected in all *amiRNA:AtSLAH1* mutants and null segregants (nulls). Hydroponically grown plants (6 weeks old) supplied with BNS containing 2 mM NaCl (low Cl^- conditions) were harvested at the same time point. (A) Shoot NO_3^- accumulation of amiRNA:*AtSLAH1* mutants and nulls under low Cl^- conditions. (B) Shoot biomass of amiRNA:*AtSLAH1* mutants and nulls under low Cl^- conditions. (C) Shoot Na^+ accumulation of amiRNA:*AtSLAH1* mutants and nulls under low Cl^- conditions. (D) Shoot K^+ accumulation of amiRNA:*AtSLAH1* mutants and nulls under low Cl^- conditions. (E) Shoot Cl^- accumulation of amiRNA:*AtSLAH1* mutants and nulls under low Cl^- conditions in a replicate experiment. (F) Shoot NO_3^-/Cl^- ratio of amiRNA:*AtSLAH1* mutants and nulls under low Cl^- conditions in a replicate experiment. Results are presented as mean + SEM (n > 8). Statistically significant differences were determined by one-way ANOVA ($P \leq 0.005$). Letters a and b denote data groups that are statistically significantly different from each other.

Figure S4

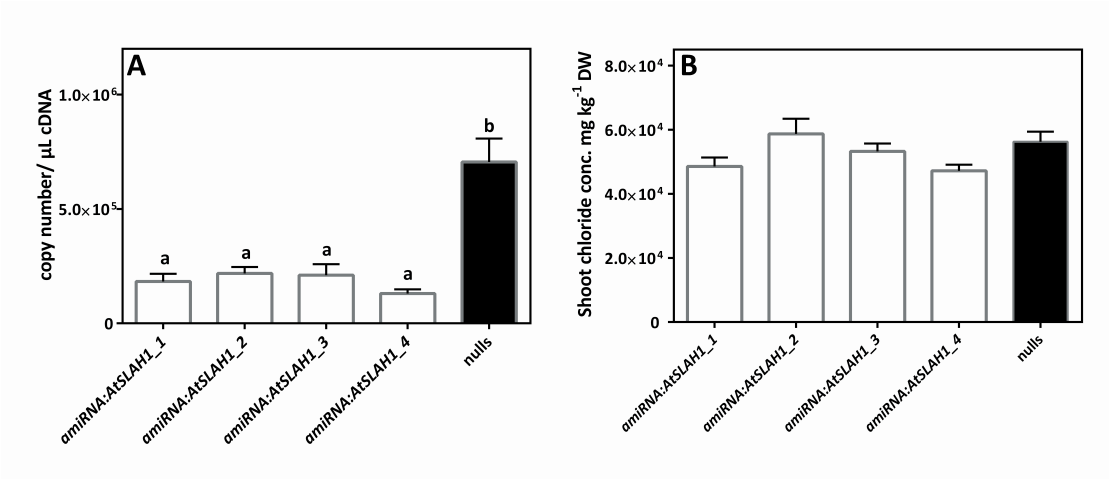

Figure S4 Transcript abundance of *AtSLAH1* amiRNA containing lines (T_2) and shoot Cl^- concentration under high Cl^- stress. Hydroponically grown plants (5 weeks old) were treated with BNS containing 75 mM NaCl (high Cl^- stress) for 7 days before harvest. (A) *AtSLAH1* transcript levels were determined in the root of all amiRNA-*AtSLAH1* mutants (amiRNA-*AtSLAH1*_1, 2, 3 and 4) and null segregants. (B) Shoot Cl^- accumulation of amiRNA-*AtSLAH1* mutants and null segregants under high Cl^- conditions. Results are presented as mean + SEM (n > 10). Statistically significant differences were determined by one-way ANOVA ($P \leq 0.005$). Letters a and b denote data groups that are statistically significantly different from each other.

Figure S5

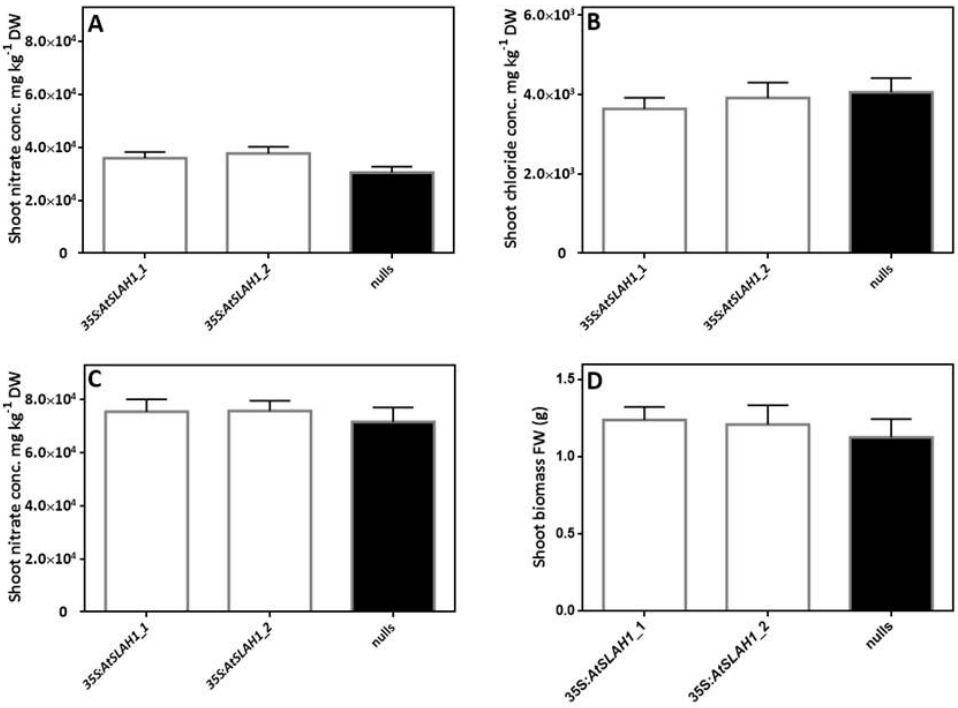

Figure S5 The shoot NO_3^-, Cl^- concentrations and shoot biomass were detected under high and low Cl^- supply in both *35S:AtSLAH1-1* and *35S:AtSLAH1_2*, and null segregants (nulls). Hydroponically grown plants (6 weeks old) supplied with BNS containing 2 mM or 75 mM NaCl (low or high Cl^- conditions) for 7 days were harvested at the same time point. (A) Shoot NO_3^- accumulation of *35S:AtSLAH1* overexpression and null segregant lines under high Cl^- conditions (75 mM NaCl). (B) Shoot Cl^- accumulation of *35S:AtSLAH1* overexpression and null segregant lines under low Cl^- conditions (2 mM NaCl). (C) Shoot NO_3^- accumulation of *35S:AtSLAH1* overexpression and null segregant lines under low Cl^- conditions (2 mM NaCl). (D) Whole shoot biomass of *35S:AtSLAH1* overexpression and null segregant lines under low Cl^- conditions (2 mM NaCl). Results are presented as mean + SEM ($n > 9$). No significant differences were found using one-way ANOVA analysis or unpaired students t-tests.

Figure S6

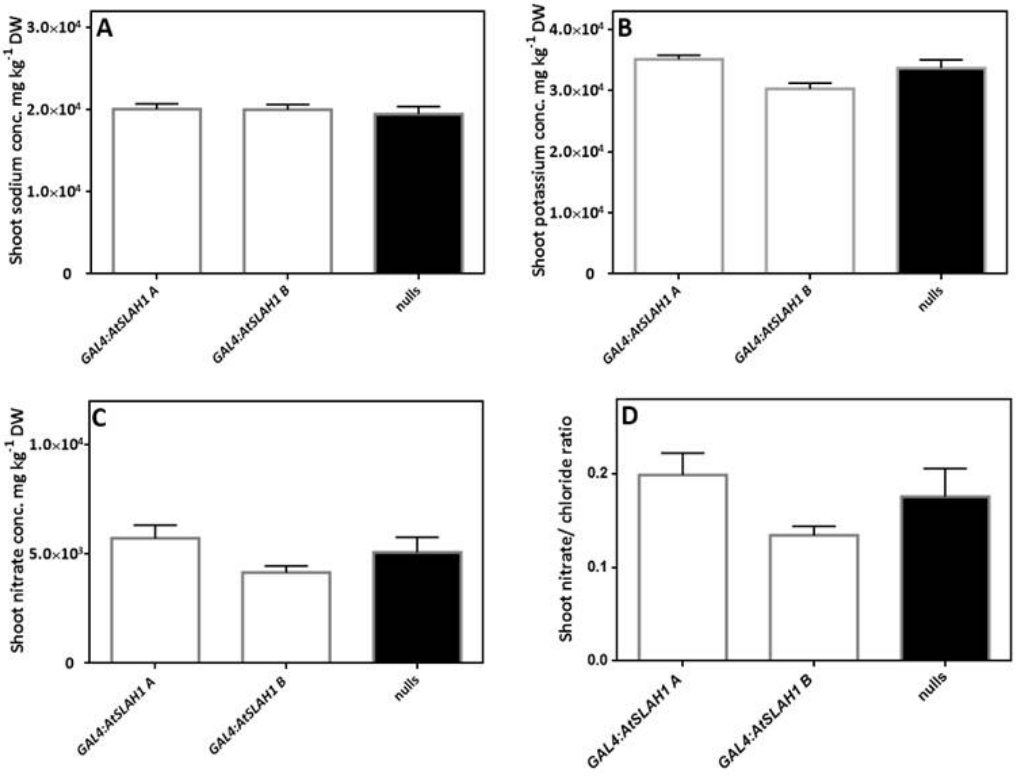

Figure S6 Under high Cl^- conditions, the shoot Na^+, K^+ and NO_3^- concentrations were detected in all *GAL4:AtSLAH1* overexpression and null segregant (nulls) lines. Hydroponically grown plants (6 weeks old) supplied with BNS containing 75 mM NaCl (high Cl^- conditions) were harvested at the same time point. (A) Shoot Na^+ accumulation of GAL4:*AtSLAH1* mutants and nulls under high Cl^- conditions. (B) Shoot K^+ of GAL4:*AtSLAH1* overexpression and null lines under high Cl^- conditions. (C) Shoot NO_3^- accumulation of GAL4:*AtSLAH1* overexpression and null lines under high Cl^- conditions. (D) Shoot NO_3^-/Cl^- ratio of GAL4:*AtSLAH1* overexpression and null lines under high Cl^- conditions. Results are presented as mean + SEM (n > 9). No significant differences were found using one-way ANOVA analysis or unpaired students t-tests.

Figure S7

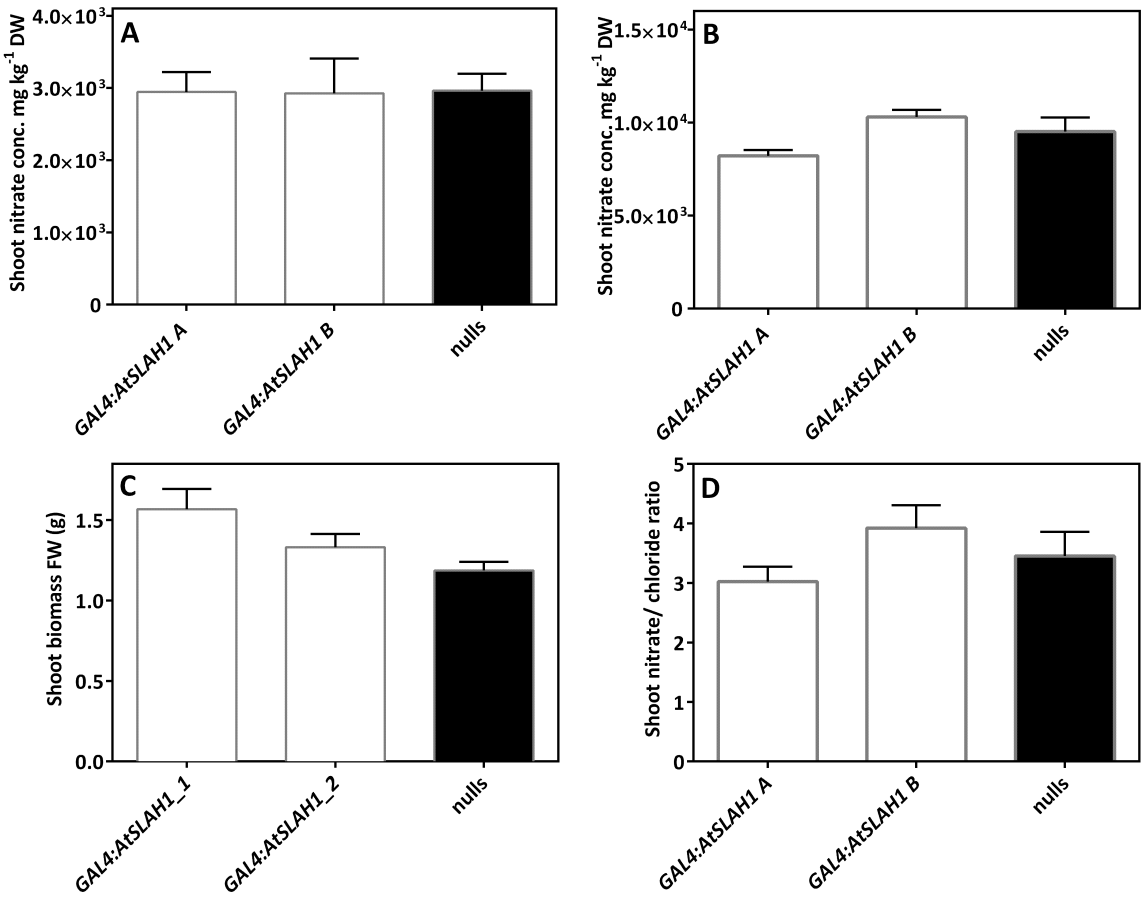

Figure S7 Under low Cl^- conditions, shoot Cl^-, NO_3^- concentrations and whole shoot biomass were detected in all GAL4:*AtSLAH1* overexpression and null segregant (null) lines. Hydroponically grown plants (7 weeks old) supplied with BNS containing 2 mM NaCl (low Cl^- conditions) were harvested at the same time point. (A) Shoot Cl^- accumulation of GAL4:*AtSLAH1* overexpression and null lines under low Cl^- conditions. (B) Shoot NO_3^- accumulation of GAL4:*AtSLAH1* overexpression and null lines under low Cl^- conditions. (C) Whole shoot biomass of GAL4:*AtSLAH1* overexpression and null lines under low Cl^- conditions. (D) Shoot NO_3^-/Cl^- ratio of GAL4:*AtSLAH1* overexpression and null lines under low Cl^- conditions. Results are mean + SEM (n > 6). No significant differences were found using one-way ANOVA analysis or unpaired students t-tests.

Figure S8

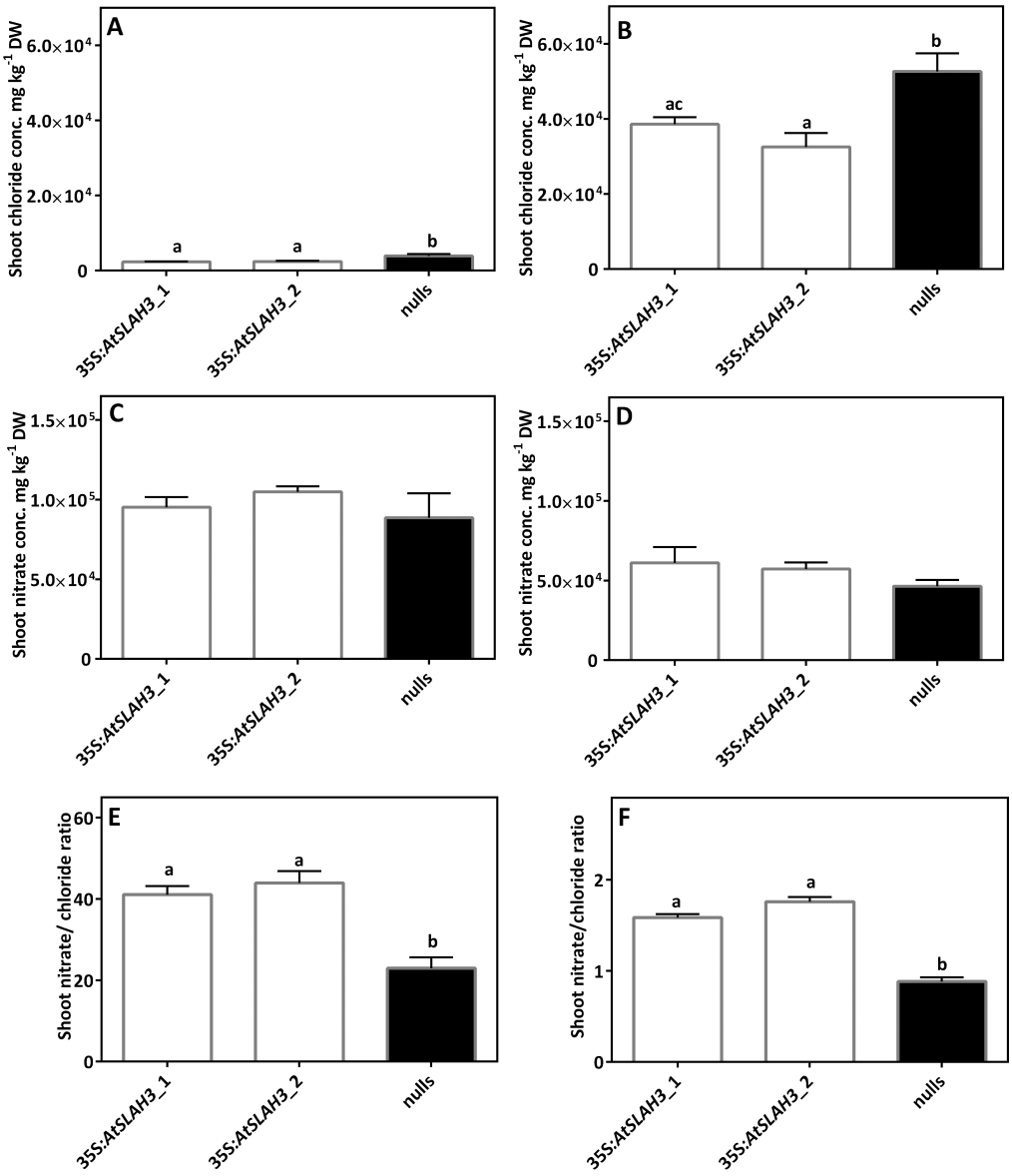

Figure S8 The shoot NO_3^- and Cl^- concentrations were detected under low and high Cl^- supply in both *35S:AtSLAH3-1* and *35S:AtSLAH3_2*, and null segregants (nulls). Hydroponically grown plants (6 weeks old) supplied with BNS containing 2 mM or 75 mM NaCl (low or high Cl^- conditions) for 7 days were harvested at the same time point. (A) Shoot Cl^- accumulation of 35S:*AtSLAH3* overexpression and null lines under low Cl^- (2 mM) conditions. (B) Shoot Cl^- accumulation of 35S:*AtSLAH3* overexpression and null lines under high Cl^- (75 mM) conditions. (C) Shoot NO_3^- accumulation of 35S:*AtSLAH3* overexpression and null lines under low Cl^- conditions. (D) Shoot NO_3^- accumulation of 35S:*AtSLAH3* overexpression and null lines under high Cl^- conditions. (E) The shoot NO_3^-/Cl^- ratio in all 35S:*AtSLAH3* overexpression and null lines grown under low Cl^- conditions. (F) The shoot NO_3^-/Cl^- ratio in all 35S:*AtSLAH3* overexpression and null lines grown under high Cl^- conditions. Results are mean + SEM (n > 6). Statistical significance was determined by

one-way analysis of variance (ANOVA and Tukey test) ($P \leq 0.05$), a, b and c represent data groups that are statistically different from each other.

Figure S9

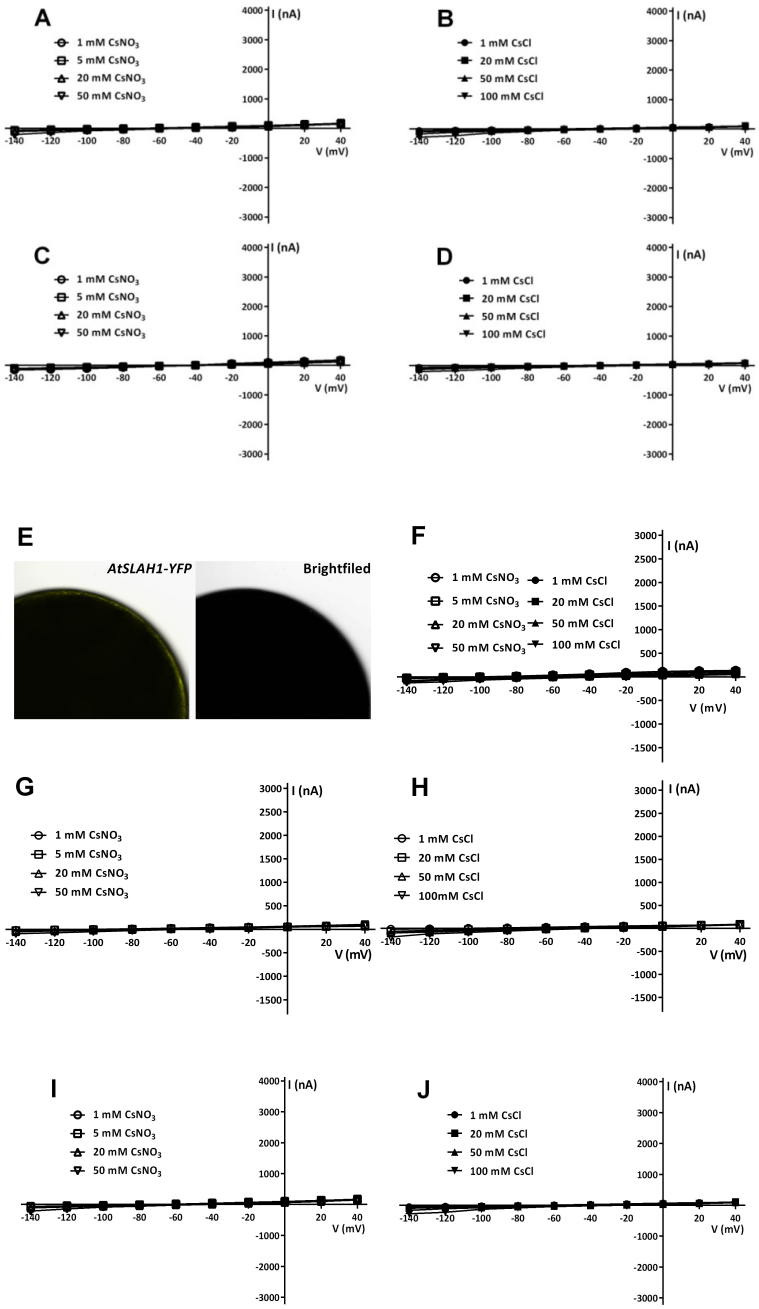

Figure S9 Electrophysiological characterisation of *AtSLAH1* in *X. laevis* oocytes. Whole cell currents (steady state) in response to 3 second voltage pluses from +40 mV to -140 mV for *AtSLAH1* /*AtSLAH1+SnRK2.3* cRNA and nuclease-free water injected oocytes were recorded. (A) water injected oocytes perfused with 1, 5, 20 and 50 mM $CsNO_3$ at pH 7.5 (mean ± SEM, n = 4); (B) water injected oocytes perfused with 1, 20, 50 and 100 mM CsCl at pH 7.5 (mean ± SEM, n = 4); (C) *SLAH1* injected oocytes perfused with 1, 5, 20 and 50 mM $CsNO_3$ at pH 7.5 (mean ± SEM, n = 3); (D) *SLAH1* injected oocytes perfused with 1, 20, 50 and 100 mM CsCl at pH 7.5 (mean ± SEM, n = 4); (E) Transient expression of *AtSLAH1-YFP* in *X. Laevis* oocytes. (F) RNA free water injected oocytes perfused with 1, 5, 20 and 50 mM $CsNO_3$ or with 1, 20, 50 and 100 mM CsCl at pH 7.5 (mean ± SEM, n= 3); (G) *SLAH1-SnRK2.2* injected oocytes perfused with 1, 20, 50 and 100 mM $CsNO_3$ at pH 7.5 (mean ± SEM, n= 5); (H) *SLAH1-SnRK2.2* complex injected oocytes perfused with 1, 5, 20 and 50 mM CsCl at pH 7.5 (mean ± SEM, n= 5); (I) *SLAH1-SnRK2.3* injected oocytes perfused with 1, 20, 50 and 100 mM $CsNO_3$ at pH 7.5 (mean ± SEM, n= 5); (J) *SLAH1-SnRK2.3* complex injected oocytes perfused with 1, 5, 20 and 50 mM CsCl at pH 7.5 (mean ± SEM, n= 5); Data are presented without water subtraction.

Supplementary Table S1

Primers used for generating *amiRNA:AtSLAH1* constructs, for screening homozygous *Atslah1* T-DNA mutant lines and for cloning *AtSLAH1*/*AtSLAH3*/*AtSnRk2.2*/*AtSnRk2.3* from Arabidopsis.

Primers used for generating *amiRNA:AtSLAH1* mutant lines	
Oligos for amiRNA "TAAAACGCTATTTGGTTCCGT"	
I miR-s	5′ gaTAAAACGCTATTTGGTTCCGTtctctcttttgtattcc 3′
II miR-a	5′ gaACGGAACCAAATAGCGTTTTAtcaaagagaatcaatga 3′
III miR*s	5′ gaACAGAACCAAATACCGTTTTTtcacaggtcgtgatatg 3′
IV miR*a	5′ gaAAAAACGGTATTTGGTTCTGTtctacatatatattcct 3′
Oligos for amiRNA "TTATGTCTAGTGTCGAGACTG"	
I miR-s	5′ gaTTATGTCTAGTGTCGAGACTGtctctcttttgtattcc 3′
II miR-a	5′ gaCAGTCTCGACACTAGACATAAtcaaagagaatcaatga 3′
III miR*s	5′ gaCAATCTCGACACTTGACATATtcacaggtcgtgatatg 3′
IV miR*a	5′ gaATATGTCAAGTGTCGAGATTGtctacatatatattcct 3′
Primers used for screening *Atslah1* knockout lines (FLAG_329G06)	
Forward (FP)	5′ TGGCCTACAGACCTGAAAATG 3′
Reverse (RP)	5′ TTGGAATGACTTTGTGTGTGTG 3′
Border (BP)	5′ CTACAAATTGCCTTTTCTTATCGAC 3′
Primers used for detecting *AtSLAH1* expression in *Atslah1* knockout lines (FLAG_329G06)	
Forward (QF)	5′ TCTTCATGTCCCTGGTCTG 3′
Reverse (RF)	5′ ATTGCTGTTTGCTGCTGTC 3′
Primers used for cloning *AtSLAH1*, *AtSLAH3, AtSnRK2.2* and *AtSnRK2.3* from Arabidopsis	
AtSLAH1 (F)	5′ ATGGAAATTCCGAGGCAA 3′
AtSLAH1 (R)	5′ CTAGTTTTGGTTAGTCGCATTG 3′
AtSLAH3 (F)	5′ ATGGAGGAGAAACCAAACTAT 3′
AtSLAH3 (R)	5′ TTATGATGAATCACTCTCTTGAGT 3′
AtSnRK2.2 (F)	5′ ATGGATCCGGCGACTAAT3′
AtSnRK2.2 (R)	5′ TCAGAGAGCATAAACTATCTCTCC3′
AtSnRK2.3 (F)	5′ ATGGATCCGGCGACTAAT3′
AtSnRK2.3 (R)	5′ GAGAGCATAAACTATCTCTCCACT3′