Table 1 Suppl. Primer sequences.

Primer	Sequences
BR6OX2 F	ATGGCGGCGATGAAATACAAAGGA
BR6OX2 R	TGTTCCTCCATCAATCTTCTTCTC
AtActin2 F	TCCAAGCTGTTCTCTCCTTG
AtActin2 R	GAGGGCTGGAACAAGACTTC
AtAMT1;1 F	TGGGTAAGTGCGACCATG
AtAMT1;1 R	GTGTAGTATTAGCACCAG
AtAMT1;2 F	GTAACTATGGGACCGTTG
AtAMT1;2 R	CAGTCAAGGTCGGTGTAG
AtAMT1;3 F	CTGTTGGGAGCACAATTG
AtAMT1;3 R	GAGGAGTAGCTGATCGAG
BES1 F	TGTCTCCAAACACAGCAG
BES1 R	AGCTTTACCATTTCCAAG
GLUT2 F	ACTTGGGAAAGTTGGTAG
GLUT2 R	CTTCATCTCCTGTGGTTG
FDGS F	TAGCTTACCTTCTTGATG
FDGS R	ACTCGGTGGAACCAGTTG
GLT1 F	CGAATGTGACAACAGGTC
GLT1 R	CATCTGGTTAAGGTCTTG
GLN1;2 F	TACGGTGAAGGAAACGAG
GLN1;2 R	AGAGGAGTGTAGTCTCTG
GLN2 F	CTGAAGCCCTTGCAGCTC
GLN2 R	GGACATGCTCTAACAGTC
FPGS2 F	CAGGTTGCTAAAGAGATG
FPGS2 R	TAAGTGGAGGGTTCTCAC
P1 F	AATTTCGCTGCCATTTCC
P1 R	AAGAAGGAAGCTAAAGGC
P2 F	GAGTTTAGTTCTTTTGAC
P2 R	AAACCTAGGAAATTGATG
P3 F	TTGGAAAAATAGACATAC
P3 R	CGTTTAGTGTTTGAATCG
P4 F	CATATTTGTTTGATTAAC
P4 R	TGTGATATAGGGGGCAAG
P5 F	GTTGTTACGTCACATAAC
P5 R	GAGATACGGAGAAGAAAG
P6 F	TGTTTTGGTATAAACGTG
P6 R	CAAGCAAGAGATATATAC

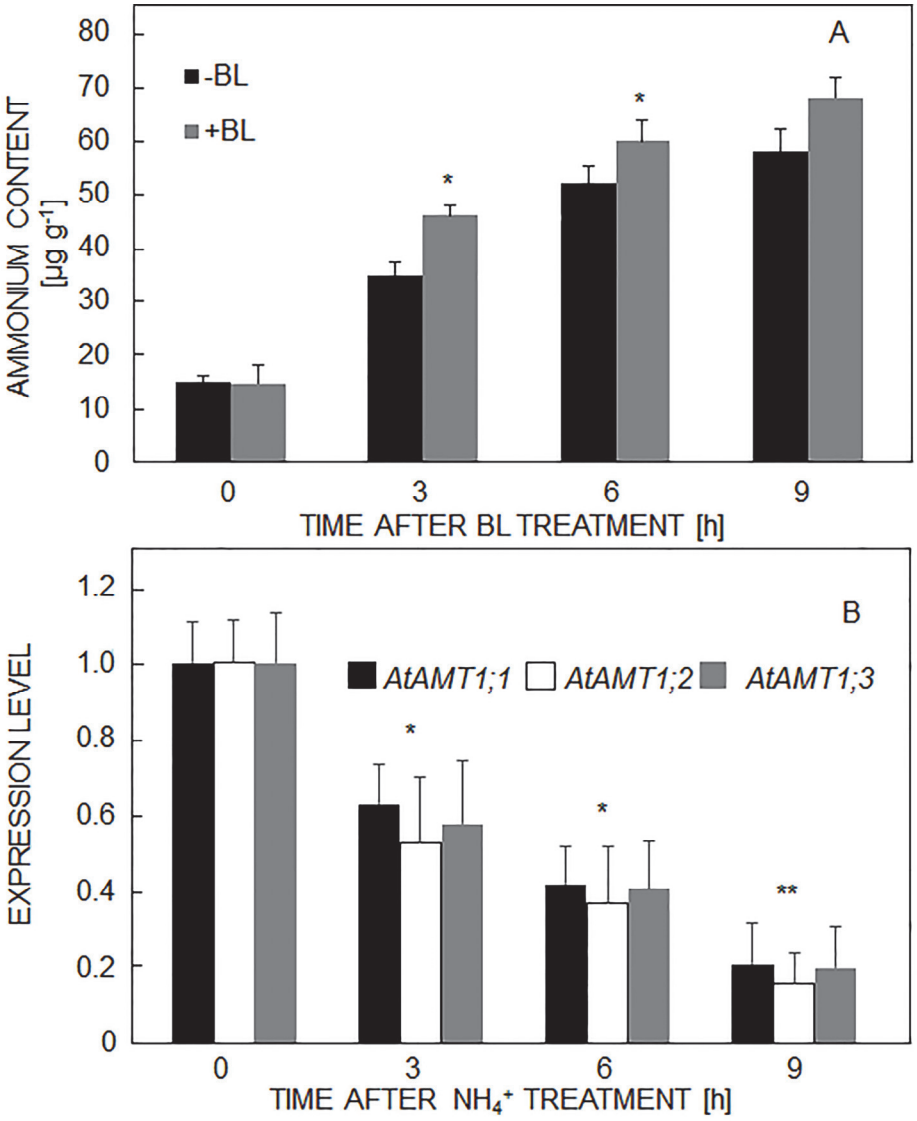

Fig. 1 Suppl. The effects of brassinosteroids on cellular NH_4^+ accumulation, and NH_4^+ dependent down-regulation of *AtAMT1* expression. *A* - Plants grown for 10 d in a modified-MS medium containing 10 mM KNO_3 as sole nitrogen source were transferred to a MS medium containing 0 and 100 nM brassinolide (BL). Cellular ammonium content was measured. Data represent means ± SEs ($n > 10$). * - significant difference between samples with or without BL treatment at $P < 0.05$. *B* - Plants were supplied with a 0.5× MS for 7 d, deprived of N for 3 d, and then transferred to a medium containing 2.5 mM $(NH_4)_2SO_4$. Real time qPCR analysis shows that the relative expressions of *AtAMT1;1*, *AtAMT1;2*, and *AtAMT1;3* were reduced by NH_4^+. *Actin* was used as reference gene. The expressions of *AtAMT1;1*, *AtAMT1;2*, and *AtAMT1;3* in a wild-type (Col-0) before NH_4^+ treatment (0 h) were defined as "1". Data represent means ± SEs ($n = 3$). *, ** - significant differences of samples at 3, 6, and 9 h with respect to 0 h at $P < 0.05$ and $P < 0.01$, respectively.

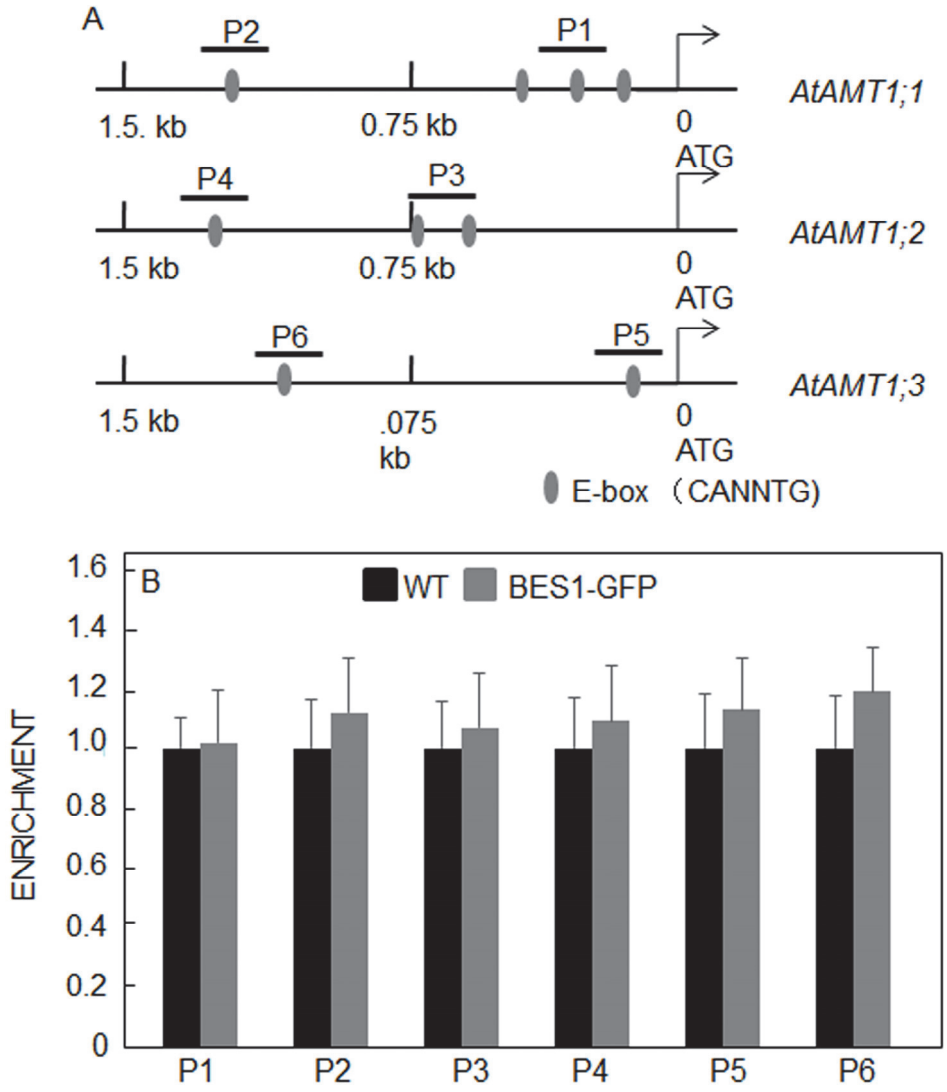

Fig. 2 Suppl. BES1 affinity for the *AtAMT1* promoter in transgenic plants. *A* - Schematically indicated locations of the E-box and chromatin immunoprecipitation (ChIP)-assay probes. *B* - Immunoprecipitated DNA fragments (P1 - P6) were amplified to detect E-box regions in the *AtAMT1* promoter; relative ratios of immunoprecipitated DNA and input DNA were measured by ChIP-PCR; input DNA was used to normalize the data. Data represent means ± SEs (n = 3). Wild-type plants (Col-0) were used as control.

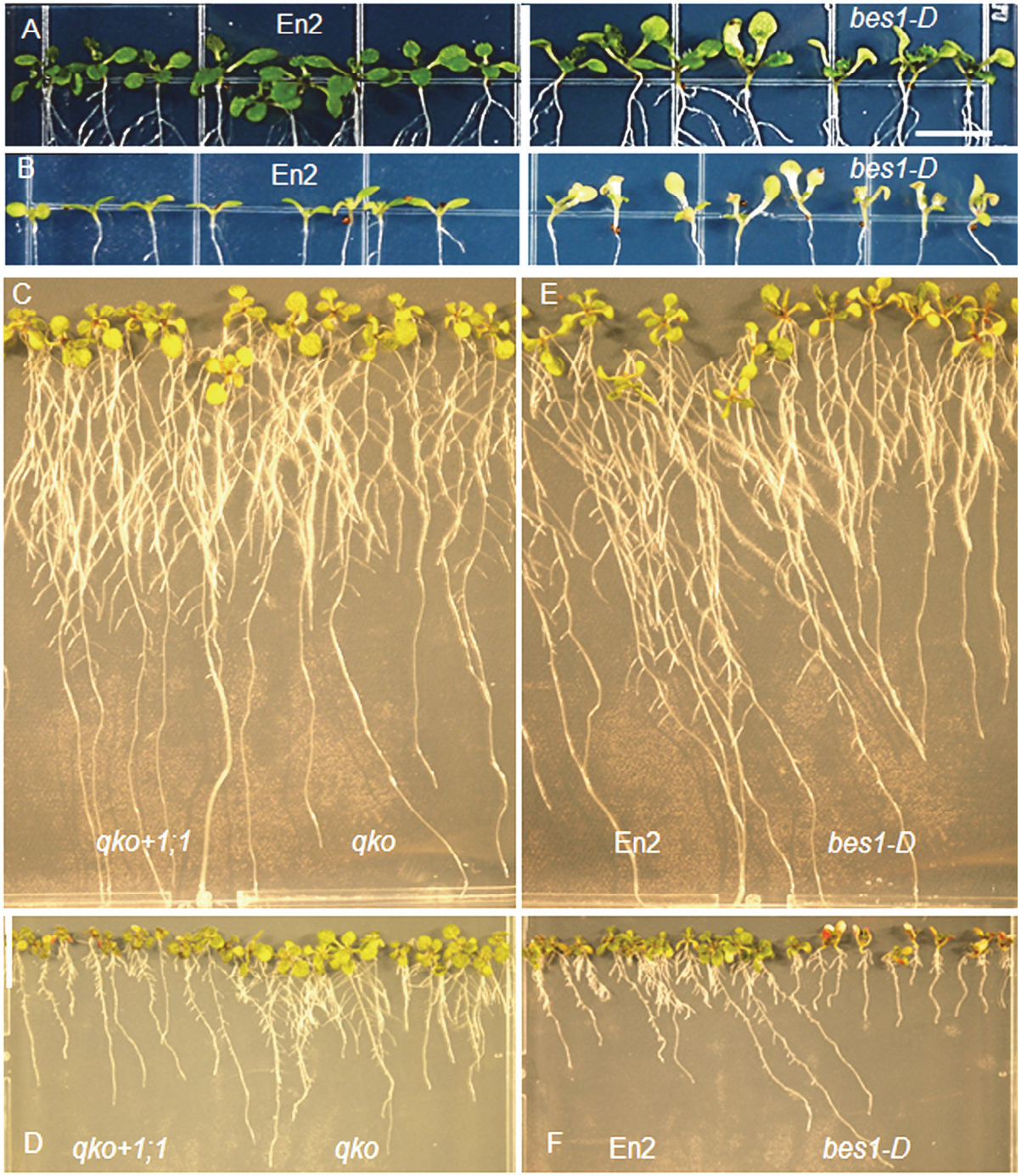

Fig. 3 Suppl. Phenotypic differences of wild-type (En2) and *bes1-D* plants grown in an NH_4^+-containing medium with high methylammonium (MeA) concentrations.. The plants were grown for 7 d in a modified-MS medium containing 1 mM NH_4NO_3 (*A*) and 5 mM MeA (buffered with 1 mM MES) (*B*). NH_4^+-mediated primary root inhibition in the quadruple mutant (*qko*), *qko+AMT1;1*, En2, and *bes1-D*. The plants were grown for 12 d in a modified-MS medium containing 0.5 mM KNO_3 as sole N source (*C*, *E*) and 5 mM NH_4Cl (*D*, *F*); 12-d-old *qko*, *qko+AMT1;1*, En2, and *bes1-D* were photographed. *Bar* = 0.5 cm.