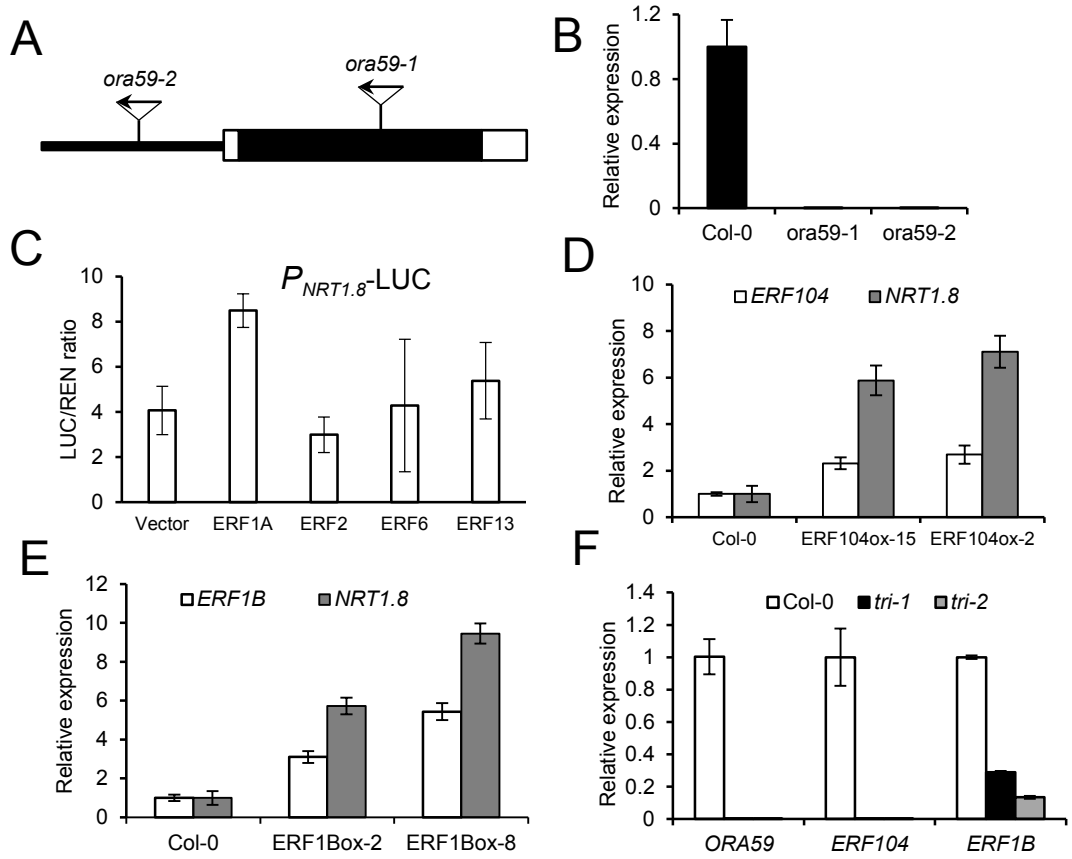


Supplemental Figure 1. ERF family members function redundantly in the regulation of *NRT1.8* expression

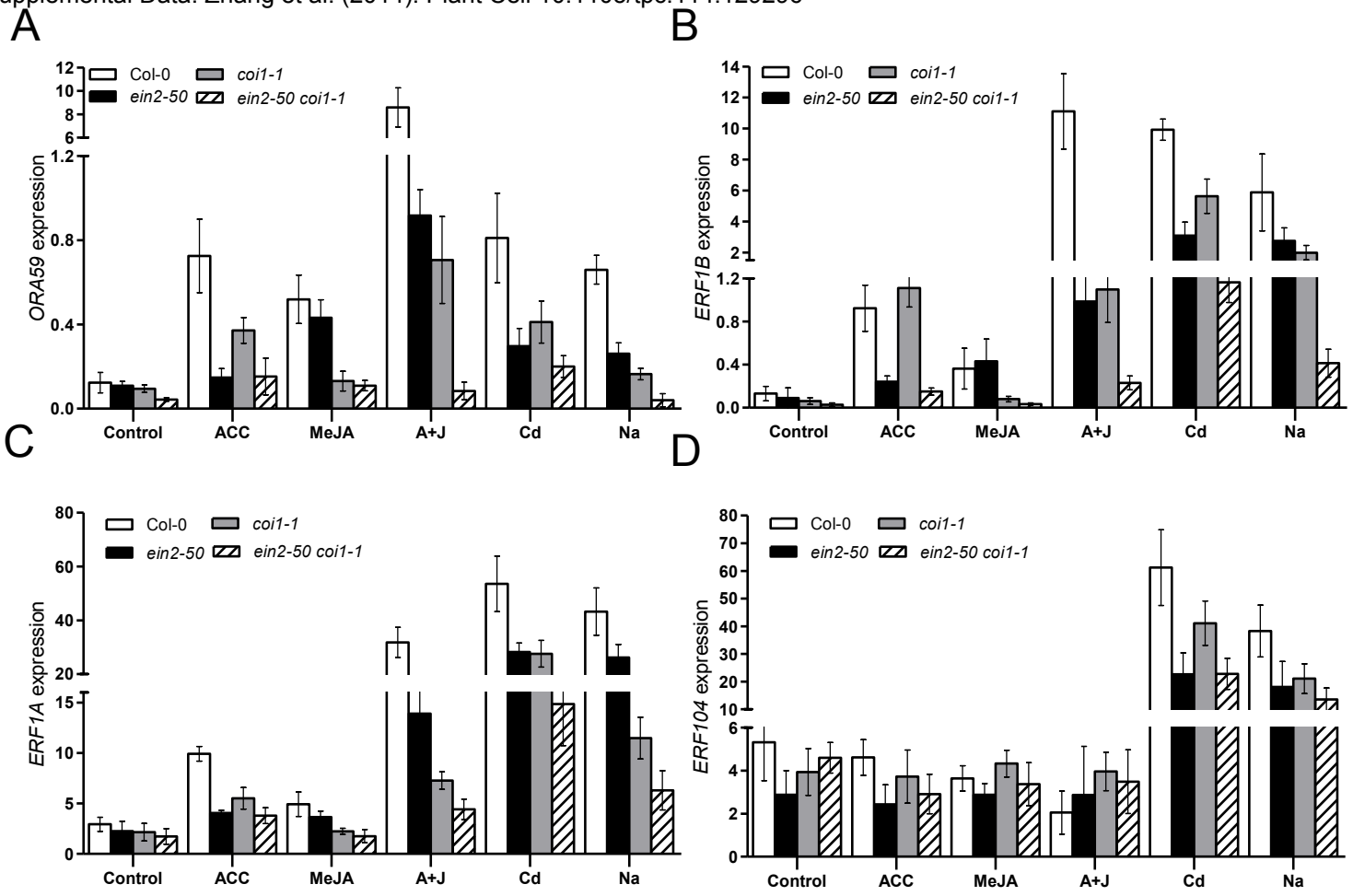
(A) Schematic map of the T-DNA insertion sites in *ora59-1* and *ora59-2* mutants. Closed box and open boxes represent coding region and untranslated regions (UTRs), respectively.

(B) Quantitative RT-PCR analysis of *ORA59* expression in *ora59* mutant plants. Values are mean ± SD, n = 3.

(C) Transient transcriptional activity assay of $P_{NRT1.8}$:LUC expression. The $P_{NRT1.8}$*:LUC-35S:REN* reporter construct was transiently expressed in *Arabidopsis* protoplasts together with the control vector, 35S:ERF1A, 35S:ERF2, 35S:ERF6 or 35S:ERF13 effectors, respectively. The expression of REN was used as an internal control. LUC/REN ratio represents the relative activity of the *NRT1.8* promoter. Values are mean ± SD, n = 3.

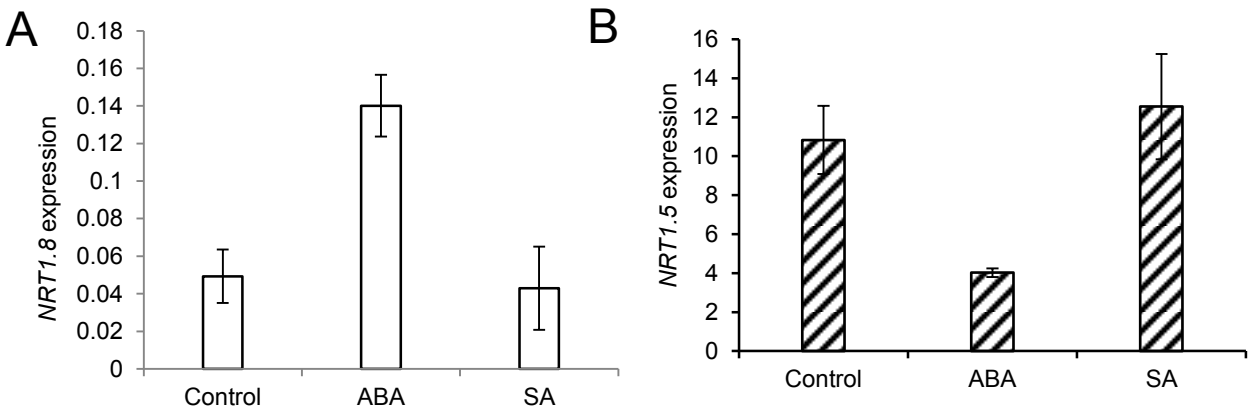
(D) and **(E)** Quantitative RT-PCR analysis of *NRT1.8* expression in roots of 4-week-old *ERF104*-overexpressing **(D)** or *ERF1B*-overexpressing **(E)** plants grown in hydroponics. Values are mean ± SD, n = 3.

(F) Characterization of the triple mutant lines *tri-1* and *tri-2,* in which *ORA59* and *ERF104* showed undetectable mRNA, while *ERF1B* showed essentially reduced mRNA level. Values are mean ± SD, n = 3.



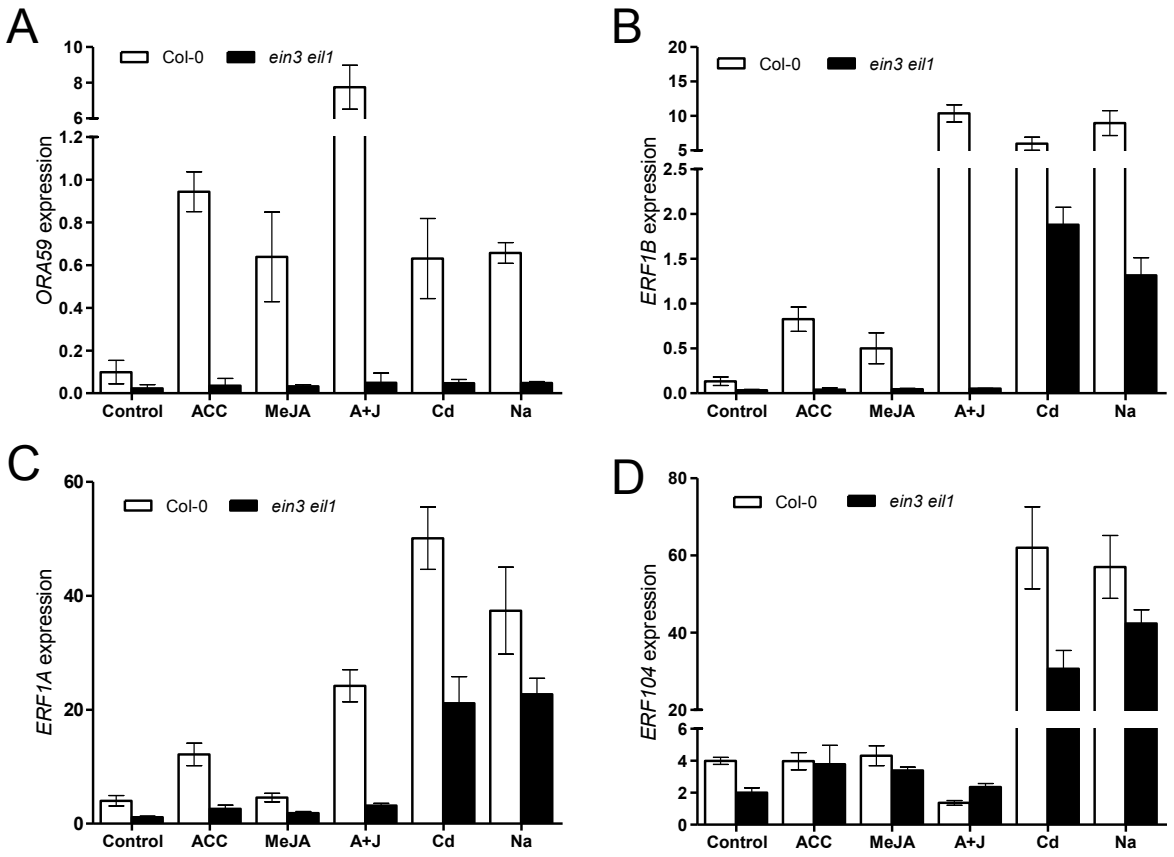
Supplemental Figure 2. *ERF* expression upon stress/hormone treatment in the ET/JA mutants

Quantitative RT-PCR analysis of *ORA59* **(A)**, *ERF1B* **(B)**, *ERF1A* **(C)** and *ERF104* **(D)** expression in the roots of 4-week-old WT, *ein2-50*, *coi1-1* and *ein2-50 coi1-1* plants treated with 20 μM ACC, 50 μM MeJA, 20 μM ACC+50 μM MeJA (A+J), 200 μM $CdCl_2$ and 150 mM NaCl for 6 h. Data were normalized to those of *SAND*. Values are mean ± SD, n = 3.



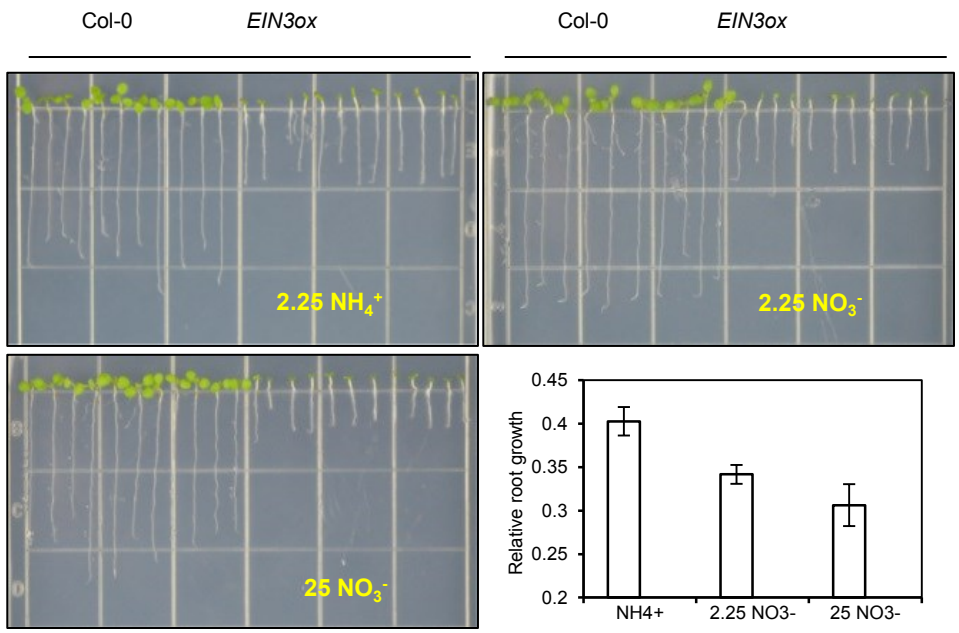
Supplemental Figure 3. *NRT1.5* and *NRT1.8* expression in response to SA or ABA treatment

Quantitative RT-PCR analysis of *NRT1.8* **(A)** and *NRT1.5* **(B)** expression in roots of 4-week-old Col-0 exposed to 50 μM ABA or 1 mM SA for 6 h. Data were normalized to those of *SAND*. Values are mean ± SD, n = 3.



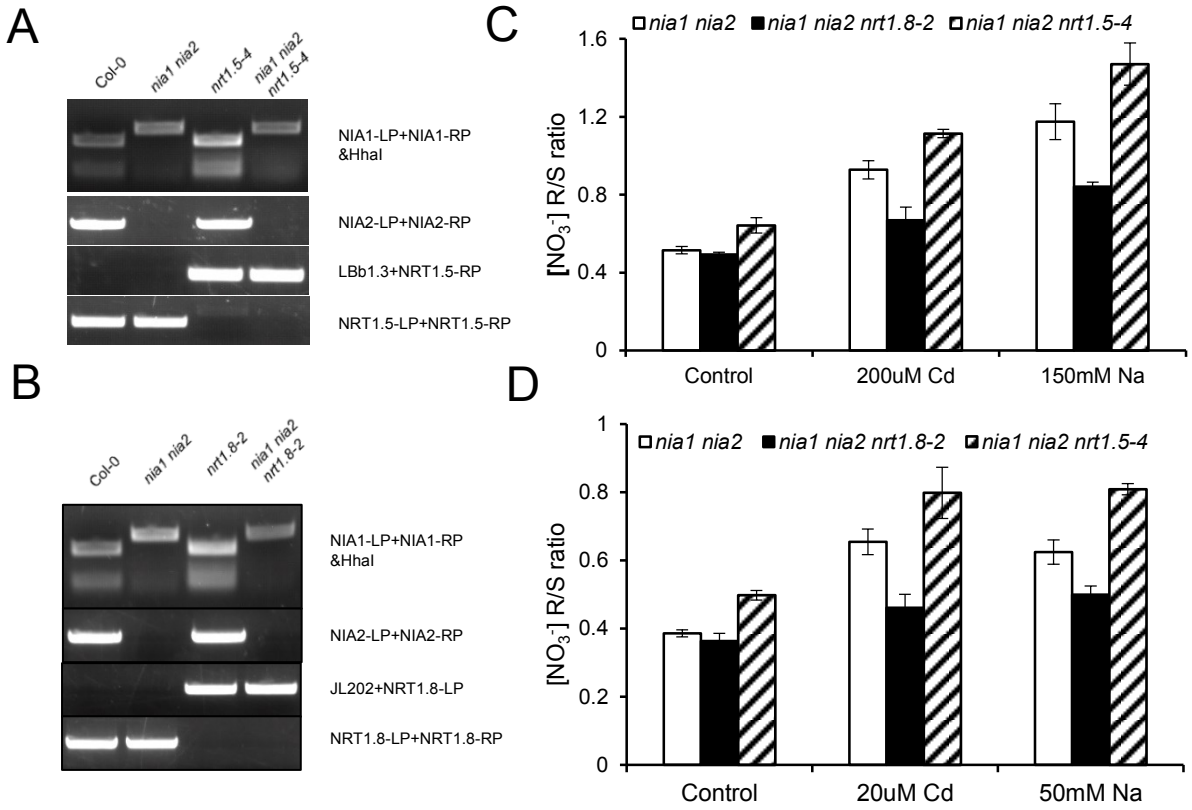
Supplemental Figure 4. The expression of *ERFs* in the *ein3 eil1* mutant in response to different treatments

Quantitative RT-PCR analysis of *ORA59* **(A)**, *ERF1B* **(B)**, *ERF1A* **(C)** and *ERF104* **(D)** expression in the roots of 4-week-old WT, *ein3 eil1* plants treated with 20 μM ACC, 50 μM MeJA, 20 μM ACC+50 μM MeJA (A+J), 200 μM $CdCl_{2\ or}$ 150 mM NaCl for 6 h. Data were normalized to those of *SAND*. Values are mean ± SD, n = 3.



Supplemental Figure 5. Root growth of *EIN3* overexpressing lines under non-stressed conditions

Seedlings were germinated and allowed to grow as described in Figure 8. Relative root growth was defined as the root elongation of *EIN3* overexpressing line *EIN3ox* plants against those of wild type control Col-0.Values are mean ± SE, n = 5.



Supplemental Figure 6. Nitrate reallocation upon stresses in *nrt1.8* and *nrt1.5* mutants in the *nia1 nia2* background

(A) and **(B)** PCR-based genotyping of *nrt1.5-4 nia1 nia2* **(A)** and *nrt1.8-2 nia1 nia2* **(B)** mutant plants. A region containing the nucleotide mutation (G to A) of *nia1* was amplified and further digested with *HhaI* to identify *nia1* mutants. Specific primers located in the deleted region of *NIA2* were designed to identify *nia2* mutants. Both *nrt1.5-4* and *nrt1.8-2* contain T-DNA insertion and were identified as described (Krysan et al., 1999). Primer sequence information is available in Supplemental Table 1 online.

(C) and **(D)** Nitrate reallocation to roots as determined by the root/shoot nitrate ratio. Plants in the *nia1nia2* background were grown hydroponically with NH_4HCO_3 as the only nitrogen source. At 4 weeks of age, plants were transferred to 2.25 mM NO_3^- solution and subjected to 200 μM $CdCl_2$ or 150 mM NaCl for 12h **(C)**, or 20 μM $CdCl_2$ or 50 mM NaCl for 72h **(D)**. Tissues were then sampled and nitrate was extracted and determined. Data were normalized to fresh weight and ratio between roots and shoots (R/S) were calculated. Values are mean ± SD, n = 3.

Supplemental Table 1. List of primer sequences.

Destination	Forward primer	Reverse primer
RT-PCR		
SAND expression	GATGAGGATGATGCTTCTACG	CCTGAGCGTTGTATCTTGGT
ORA59 expression	CAATCCTTCCTTTTATCTAGCCCTAC	CAGCACCTAAATCCTCAAGAACC
ERF1B expression	GAATTCATGGATCCATTTTTAATTC	GTCGACTCACCAAGTCCCACTATTTTC
ERF104 expression	ATGGCAACTAAACAAGAAGC	TGAAGTGACGGAGATAACGGAAAAGTTG
NRT1.8 expression	TCTTTGCTTGGTGCTTTCCT	ATCCGCTCTCTACTTTCTCAGC
qRT-PCR		
SAND expression	ATATGACACCCTTGCTTGGAGGGA	TGAGAATAAGACACCAGACGCGCA
ORA59 expression	AAGGGATAAGAGTGTGGCTTGGGA	CTTTCAAAGCGAAAGCCGCCTGAT
ERF1B expression	GAGGAAACACTCGATGAGACG	GGAGCGGTGATCAAAGTCAC
ERF104 expression	GAACCATCACCAACCAATCC	GTCCCAAGCCAGATCCTACA
ERF1A expression	TCCGGTCAAGAAGGAGAAGA	GCCGTCTCAAACGTTCCTAA
NRT1.8 expression	TCTTCATCTTCGCATACAGGCGGT	GCCATTATCGCAATCACAAGCCCA
NRT1.5 expression	TGGAGCGTTTCTCAGCGATT	TCCATCATGGAATGTGAACCAC
Genotyping		
Genotyping of *ora59-1*	ATGCTGCAGACGGTAACAAAC	CTTCAAGCTCATGGAGCTCAC
Genotyping of *ora59-2*	GCCACACTCTTATCCCTTTCC	TTACTTTGGGATTGGTTGCAG
Genotyping of *erf104*	CCTCTTGCTCAGTTGCTTGAC	GAAACAGGCCCTAGAACCATC
Genotyping of *nrt1.5-4*	TGAAAATTGTGTATACGAAACGAGA	GGTGTCGATCATATATTTTCCTCC
Genotyping of *nrt1.8-2*	AGTTAGACAGTTTGAGGTTTGCACTCAAG	GTAGAATCTCTCCAAGTGTCCTTTGTTGA
Genotyping of *ein3-1*	TACCAAGTATCAAGCGGAG	AGGCCACCAATCCTCTTTC
Genotyping of *eil1-1*	GGGAATGGTGGAAAGATAAG	CTTTCGCCGTCATCTTATCC
Genotyping of *nia1*	TACGACGACTCCTCAAGCGAC	GGCTATAGATCCCGCATCGAC
Genotyping of *nia2*	GTTCTTACAAACCTCCCGTTCC	CTCTGTTGTCCTTGAAATGGTAG
Genotyping of *ctr1-8*	AGAGTCCACGACATATCTTG	AGGAATCAGGCTCCCATAAG
Genotyping of *eto1-1*	GCAACACAACTTGACCCTCTT	GGGAGAATCCCTCAGAAAGG
Protein expression and EMSA		
pET-30a(+) ORA59	GGATCC ATGGAATATCAAACTAACTTC	AAGCTT TCAAGAACATGATCTCATAAGC
pET-30a(+) ERF1B	GAATTC ATGGATCCATTTTTAATTC	GTCGAC TCACCAAGTCCCACTATTTTC
pET-30a(+) ERF104	GTCGAC TCATGGCAACTAAACAAGAAGC	GCGGCCGC TCAAGTGACGGAGATAAC GGAAAAGTTG
pGEX 4T-1 EIN3 (N)	GGATCC ATGATGTTTAATGAGATGGGAATG	GAATTC ACCAGACAGAGAAAGAGGTGGAC
NRT1.8 promoter WT probe	GATTTTATCAGTCTCTTCCAGCAG	CAATTTAATTGTAAAGGTTTTGAAACG

Mutate *NRT1.8* promoter WT probe GCC box B1	TTTATCAGTCTCTTCCATCATCCCTCC AGGTGTAACTGG	
Mutate *NRT1.8* promoter WT probe GCC box B2	AATCCACCGAACATATATTTTATCATCCCGTT TCAAAACCTTTAC	
NRT1.5 P5 fragment	TCTATAAGCATACGCATAAATGGA	CATATTGCCTCACAATCAATCTAG
NRT1.5 P7 fragment	TATTGGTATTTAAACTTTGTTTTACTA	TAAATGATATAAACGTTTAAAGTACTT
ChIP-qPCR		
TUB2 for ChIP normalization	ATCCGTGAAGAGTACCCAGAT	AAGAACCATGCACTCATCAGC
NRT1.8 P1 fragment	CTATTTAAGAACAATTATTTGGGG	CATCCCTAAAATCTATGAAGAAGG
NRT1.8 P2 fragment	GCATATGATTATTATTGAGATAAC	GAGAGCTCAGAAATTGAGTCAG
NRT1.8 P3 fragment	CACTTCTTCACTTTCCTCGA	AGATTCGATTTGGTGTAGAG
ERFs binding sites in *PDF1.2* promoter	TATACTTGTGTAACTATGGCTTGG	TGTTGATGGCTGGTTTCTCCAC
EIN3 binding sites in *EBF2* promoter	TGATGACAATTGGGTTCGGTG	GTTTGTGATATTGAGAAGAAC
NRT1.5 P1 fragment	GGCATGCTTGCGTTTAGTTAGGT	TCACTCAAACTTAAAATCATATTAC
NRT1.5 P2 fragment	GTTGTTTTTAATCATGGGATTTATC	TTACACACTACAATATCTTTCACTAA
NRT1.5 P3 fragment	GTGTTTTGCATAGTAAATCGAATG	GCGGAGTAAAGTTTACATTATATC
NRT1.5 P4 fragment	CAAGGGATTGACCTGTGGTAG	CGATTTCATGAGGTTGCAATATC
NRT1.5 P5 fragment	TCTATAAGCATACGCATAAATGGA	CATATTGCCTCACAATCAATCTAG
NRT1.5 P6 fragment	TAGATTGATTGTGAGGCAATATG	AATCGTTGAGATCTAATTTTAGCT
NRT1.5 P7 fragment	TATTGGTATTTAAACTTTGTTTTACTA	TAAATGATATAAACGTTTAAAGTACTT
NRT1.5 P8 fragment	ACAATGTTGTAGTTCACACAATGC	GTTGTTAGAAAAAAGAGGTACCAC
Transient expression & Plant transformation		
ERF1B RNAi	CCCGGG GGCGCGCC CAATCCACTAAC GATCCCTAAC	TCTAGA ATTTAAAT TTCTCTGACTTTC TTGAGCTTAC
pGreen II 62-SK & pCAMBIA 1300 *ORA59*	CTCGAG GGATCCATGGAATATCAA ACTAACTTC	GTCGAC TGAAGAACATGATCTCATAAGCTC
pGreen II 62-SK & pCAMBIA 1300 *ERF1B*	TCTAGA GAATTC ATGGATCCAT TTTTAATTC	GTCGAC TGACCAAGTCCCACTATTTTC
pGreen II 62-SK &pCAMBIA 1300 *ERF104*	TCTAGA ATGGCAACTAAACAAGAAGC	CCCGGG TGAAGTGACGGAGATAACGGAAAAGTTG
pGreen II 62-SK *ERF1A*	GGATCC ATGTCGATGACGGCGGATTC	CCCGGG TGATAAAACCAATAAACGAT CGCCACG

pGreenII62-SK *ERF2*	GGATCC ATGTACGGACAGTGCA ATATAGAATC	CCCGGG TGATGAAACCAATAACTCAT CAACACG
pGreenII62-SK *ERF6*	GGATCC ATGGCTACACCAAACGAAG TATCAGCTC	CCCGGG TGAAACAACGGTCAATTG TGGATAACC
pGreenII62-SK *ERF13*	TCTAGA GAATTC ATGAGCTCATCTG ATTCCGTTAATAACG	CCCGGG TGATATCCGATTATCAGAA TAAGAACATTC
pGreenII62-SK *ERF15*	GGATCC ATGGAATATTCCCAATC TTCCATGTATTC	CCCGGG TGAACATGAGCTCATAAG AAGTTGTTC
NRT1.8 promoter in pGreenII0800-LUC	AAGCTT CAATGAATCTAGACATTAATTCG	GGATCC AGATTCGATTTGGTGTAG AGATATA