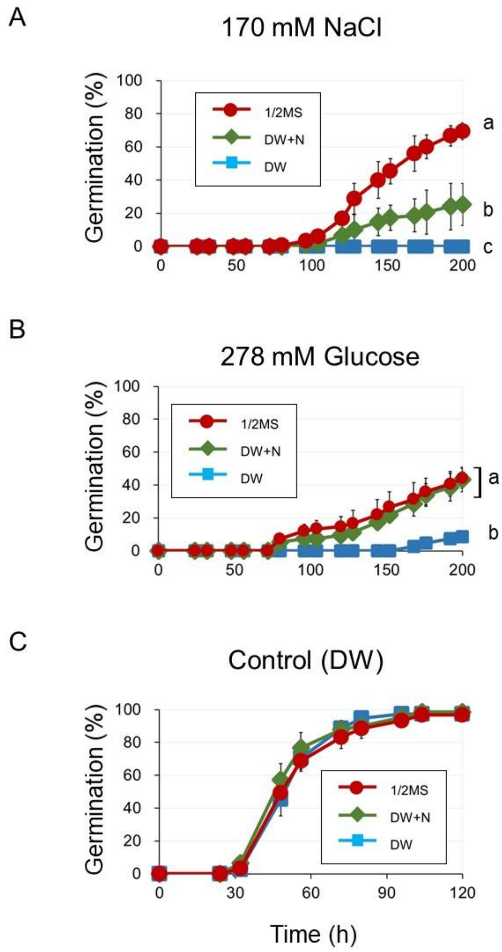

Figure S1. Seed germination on 1/2 MS, nitrogen components of 1/2 MS (DW+N), and DW in the presence of (**A**) 170 mM NaCl, (**B**) 278 mM glucose, and (**C**) no additional compounds (control). Freshly harvested seeds were incubated at 23 °C without stratification. Data are means ± SD for three replicates. Each replicate containing 50 seeds. Different letters indicate significant differences in germination at the final time point. (ANOVA and Tukey's test, $p < 0.05$).

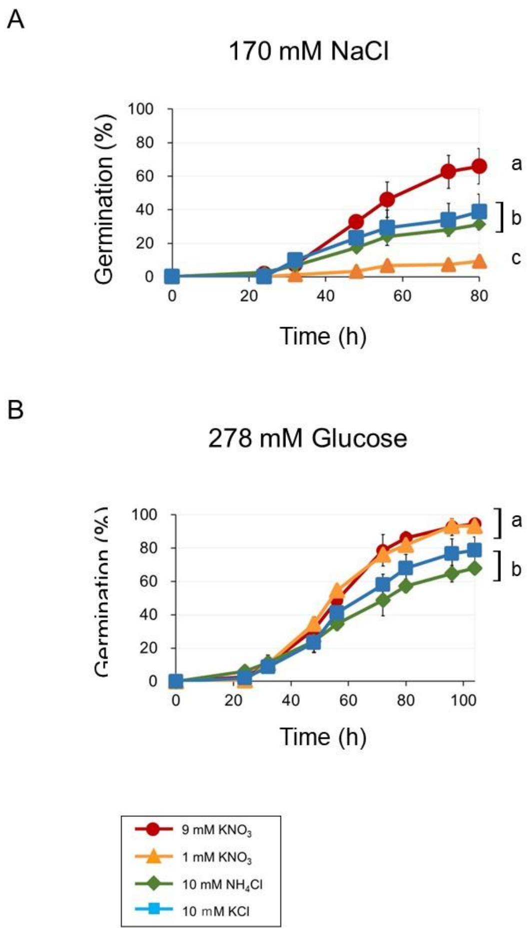

Figure S2. The effect of KCl and NH_4Cl on seed germination in the presence of (**A**) 170 mM NaCl and (**B**) 278 mM Glucose. Seeds were stratified for three days before incubation at 23 °C. Germination was scored after transferred to 23 °C. Data are means ± SD for three replicates. Each replicate containing 50 seeds. Different letters indicate significant differences in germination at the final time point. (ANOVA and Tukey's test, $p < 0.05$).

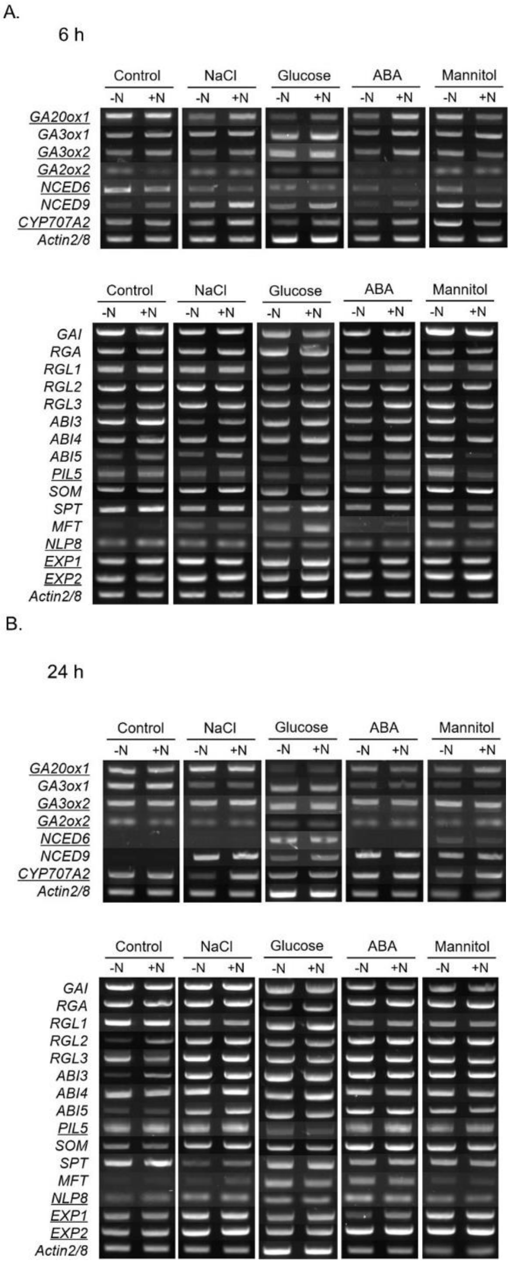

Figure S3. Expression of genes involved in the regulation of seed germination in the presence in the presence (+N) or absence (-N) of 10 mM KNO_3. Seeds were imbibed in the presence of 170 mM NaCl, 278 mM Glucose, 5 mM ABA, and 500 mM Mannitol for (**A**) 6 and (**B**) 24 h. The gene expression was analyzed by semi-quantitative RT-PCR. The Actin 2/8 gene was used as control. The gene amplification reactions were carried out for 30 PCR cycles or 35 PCR cycles (underlined genes).

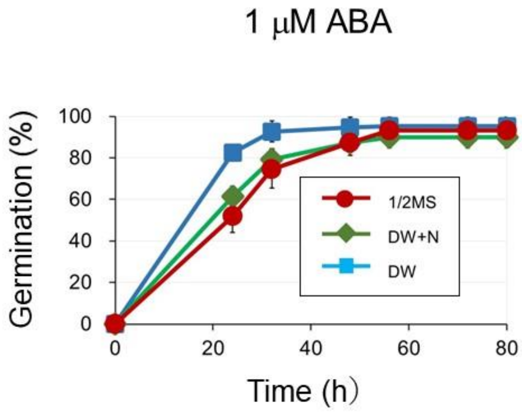

Figure S4. Seed germination on 1/2 MS, nitrogen components of 1/2 MS (DW + N), and DW in the presence of 1 μM ABA. Seeds were stratified for two days before incubation at 23 °C. Data are means ± SD for three replicates. Each replicate containing 50 seeds.

Table S1. List of genes used in this study.

Gene Name	Protein	Key role	References
GA20ox1 (*At4g25420*) *GA20-OXIDASE 1*	gibberellin 20-oxidase	GA biosynthesis	[47,48]
GA3ox1 (*At1g15550*) *GA3-OXIDASE 1*	Gibberellin 3-b-dioxygenase	GA biosynthesis	[49] [50]
GA3ox2 (AT1G80340) GA3-OXIDASE 2	Gibberellin 3-b-dioxygenase	GA biosynthesis	[49]
GA2ox2 (AT1G30040) GA2-OXIDASE 2	Gibberellin 2-b-dioxygenase	GA cabatolism	[51,52]
NCED6 (AT3G24220) NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 6	9-cis-epoxycarotenoid dioxygenase	ABA biosynthesis	[53]
NCED9 (AT1G78390) NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 9	9-cis-epoxycarotenoid dioxygenase	ABA biosynthesis	[53]
CYP707A2 (AT2G29090) ABA 8′-HYDROXYLASE CYTOCHROME P450-2	Abscisic acid 8'-hydroxylase	ABA degradation	[54,55]
GAI (AT1G14920) GA INSENSITIVE	DELLA transcription factor	GA signaling	[56]
RGA (AT2G01570) REPRESSOR OF GA1-3	DELLA transcription factor	GA signaling	[57]
RGL1 (AT1G66350) RGA-LIKE 1	DELLA transcription factor	GA signaling	[58]
RGL2 (AT3G03450) RGA-LIKE 2	DELLA transcription factor	GA signaling	[59]
RGL3 (AT5G17490) RGA-LIKE 3	DELLA transcription factor	GA signaling	[60]
ABI3 (AT3G24650) ABA INSENSITIVE 3	b-ZIP transcription factor	ABA signaling	[60]
ABI4 (AT2G40220) ABA INSENSITIVE 4	AP2 transcription factor	ABA signaling	[61]
ABI5 (AT2G36270) ABA INSENSITIVE 5	b-ZIP transcription factor	ABA signaling	[60]
PIL5 (AT2G20180) PHYTOCHROME INTERACTING FACTOR 3-LIKE 5	PIF1, bHLH transcription factor	light signaling	[62,63]
SOM (AT1G03790) SOMNUS	zinc finger CCCH-type transcription factor	seed germination	[12]
SPT (AT4G36930) SPATULA	bHLH transcription factor	floral organogenesis.seed germination	[64]
MFT (AT1G18100) MOTHER OF FT AND TFL1	phosphatidylethanolamine-binding protein	seed dormancy, germination	[65]
NLP8 (AT2G43500) NIN-LIKE PROTEIN 8	NIN-like transcription factor	nitrate signaling	[19]
EXP1 (AT1G69530) EXPANSIN 1	expansin	loosening and extension of plant cell walls	[66]
EXP2 (AT5G05290) EXPANSIN 2	expansin	loosening and extension of plant cell walls	[67]

Table S2. Primers used in this study.

Semi-quantitative RT-PCR (GA/ABA metabolism)	
GA20ox1 F	ATGGCCGTAAGTTTCGTAAC
GA20ox1 R	TTAGATGGGTTTGGTGAGCC
GA3ox1 F	ATGCCTGCTATGTTAACAG
GA3ox1 R	TCATTCTTCTCTGTGATTTC
GA3ox2 F	ATGAGTTCAACGTTGAGCG
GA3ox2 R	TTAATTTCTAATAATGGAAAG
GA2ox2 F	ATGGTGGTTTTGCCACAGCC
GA2ox2 R new	TCATACAAGGGTTTTATGATTG
NCED6 F	ATGCAACACTCTCTTCGTTC
NCED6 R	TCAGAAAACTTGTTCCTTCAAC
NCED9 3rd ATG- F	ATGGCTTCTACTACCTTACT
NCED9 R	CTAACACAAAGCTTGCTTCG
CYP707A2 F	ATGCAAATCTCATCTTCATC
CYP707A2 R	TTAAATCGGGGTTACTCTTATTG
Semi-quantitative RT-PCR (GA/ABA signaling)	
Y GAI EcoRI F	GGAATTCATGAAGAGAGATCATC
Y GAI BamHI R	GGGATCCCTAATTGGTGGAGAGTTTCC
RGA1 XbaI F	GTCTAGAATGAAGAGAGATCATCACCAATTCCAAG
RGA1 BamHI R	GGGATCCTCAGTACGCCGCCGTCGAGAGTTTCCAAGC
Y RGL1 BamHI F	GGGATCCCGATGAAGAGAGAGCACAACCAC
Y RGL1 SalI R	GGTCGACTTATTCCACACGATTGATTC
Y RGL2 SalI F	GGTCGACCGATGAAGAGAGGATACGGAGAAAC
Y RGL2 PstI R	GCTGCAGTCAGGCGAGTTTCCACGCCG
Y RGL3 SalI F	GGTCGACGATGAAACGAAGCCATCAAG
Y RGL3 PstI R	GCTGCAGCTACCGCCGCAACTCCGCCG
ABI3 XbaI F	GTCTAGAATGAAAAGCTTGCATGTGGC
ABI3 BamHI R	GGGATCCTCATTTAACAGTTTGAGAAG
ABI4 XbaI F for effector	GTCTAGAATGGACCCTTTAGCTTCCC
ABI4 KpnI R for effector	GGGTACCTTAATAGAATTCCCCCAAG
ABI5 BamHI F	GGGATCCATGGTAACTAGAGAAACGAAG
ABI5 KpnI R	GGGTACCTTAGAGTGGACAACTCGGGTTC
SPATULA KpnI F	CGGTACCATGATATCACAGAGAGAAG
SPATULA EcoRI R	GGAATTCTCAAGTAATTCGATCTTTTAG
Y MFT EcoRI F	GGAATTCATGGCGGCTTCTGTTGATCC
Y MFT SalI R	GGTCGACCTAGCGTCTGCGTGAAGCAG
PIL5 XbaI F	GTCTAGAATGCATCATTTTGTCCCTG
PIL5 KpnI R	GGGTACCTTAACCTGTTGTGTGGTTTC
SOMNUS BamHI F	GGGATCCATGGATGTCGTTTGTACGG
SOMNUS KpnI R	GGGTACCTCAAGTCAAGAGATCATTG
EXP1 F	ATGGCTCTTGTCACCTTCTTG
EXP1 R new	TCAAGCACTCGAAGCACCAC
EXP2 F	ATGAATCTTACAGAATATTC
EXP2 R	CTAAAATTGTCCGCCTTC
NLP8_1500bp_F	TTTGAGAACTGTTTCAGAAG
NLP8_2000bp_R	TCGCCAGTTGCTGAGTCGAAC
Actin2/8 F	CTGGTGATGGTGTGTCTCAC
Actin2/8 R	GACCTTAATCTTCATGCTGC
Quantitative RT-PCR	
Real-time GA20ox1(Roche) F	CATGGGTTTCAGCCATTTG
Real-time GA20ox1(Roche) R	CTCTAAAGTAGTCCCGTTTTACGC
Real-time GA2ox2(Roche) F	CTCCTCCTCAATGCTAATCCTC
Real-time GA2ox2(Roche) R	CTCCTCCACCGACTCACG
Real-time NCED6(Roche) F	TAGCAATAGCCGATCCTTGG
Real-time NCED6(Roche) R	GCCGTTTTGTATATCTACCTTCG
Real-time NCED9(Roche) F	AAAGTATATTTACGGAGAGGGGAAAT
Real-time NCED9(Roche) R	CGTCACCGGAAGGTAGAAAC
Real-time CYP707A2(Roche) F	GCTTCTCAAGTACTTACACGACCA
Real-time CYP707A2(Roche) R	TGTCGAATGCTGAATTGCTC
Real-time PIL5 (Roche) F	AGCGAGGAAACAAAACAAGC

Real-time PIL5 (Roche) R	TCATTGATCCTATCTCTCCGTTTT
Real-time SOM (Roche) F	GAGAACGTTTCCGGTGTCTC
Real-time SOM (Roche) R	CAAGCAACATGGATTCTTCG
Real-time SPT (Roche) F	GCAGAGCTGCTGAAGTTCATAAT
Real-time SPT (Roche) R	TTTGAATTAGGGATGAGACTTTGTAA
Real-time MFT F (Xi et al. 2010)	CGAGCCGAACATGAGAGAAT
Real-time MFT R (Xi et al. 2010)	AAGTATCTCTTTTCCTCTTGAGGG
Real-time ABI3 (Roche) F	GCTGGCTCAGCTTCTGCTAT
Real-time ABI3 (Roche) R	AAATTCTTTTCTGGTTTCCATCC
Real-time ABI4 (Roche) F	CCGCTTCTTCTCCTTCCAC
Real-time ABI4 (Roche) R	GAGGGAGGAGAGGTCTTAGGG
Real-time ABI5 (Roche) F	TGGAGAGAAGACAGAGGAGGA
Real-time ABI5 (Roche) R	GTTCAGCTTCCAATTCCACTG
Real-time RGL2 (Roche) F	CTTTCTGCGTTTCCAAAGGA
Real-time RGL2 (Roche) R	TCGGATCCTCTTGCTGCTA
Real-time NLP8 (Roche) F	AGGCACTTTGGAGCAGGA
Real-time NLP8 (Roche) R	GCTCACATTTTTCTCTGTAGTGCT
Real-time EF1aA4 (Roche) F	CTTGGTGTCAAGCAGATGATTT
Real-time EF1aA4 (Roche) R	CGTACCTAGCCTTGGAGTATTTG

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