Supplemental Information







Supplemental Figure S2. Time for 50% of chimeric receptor seeds to germinate in response to NaCl. The time for 50% germination on 150 mM NaCl was calculated for each seed line from the data in figure 5. aStatistically different from the wild-type seeds under the same conditions (P < 0.05). bMutant transgene different from c*ETR1* under the same condition. cStatistically slower germination from the triple mutant caused by the transgene (P < 0.05). All *P* values were calculated using Student's *t* test.



Supplemental Figure S3. Time for 50% of select point mutant seeds to germinate in response to

ABA. The time for 50% germination on 150 mM NaCl was calculated for each seed line from the data in figure 6. NR denotes that 50% germination was not reached in the time-frame of the experiment. ^aStatistically different from the wild-type seeds under the same conditions (P < 0.05). ^bMutant transgene different from *gETR1* under the same condition. ABA caused a significant increase (P < 0.05) in the time for 50% seed germination for all seed lines. ^cStatistically slower germination from the triple mutant caused by the transgene (P < 0.05). All P values were calculated using Student's *t* test.



Supplemental Figure S4. Change in transcript abundance of *RAB18* and *CRA1* in response to NaCl and norflorazon. The levels of transcript for *CRA1* and *RAB18* were measured using qRT-PCR. For this, seeds were germinated for 2d in the indicated conditions and mRNA extracted from wild-type and *etr1-6;etr2-3;ein4-4* triple mutants. Data were normalized to the levels of At3g12210 in each seed line to determine the relative transcript level for each gene. These were then normalized to levels of the transcript in untreated wild-type seeds. The average \pm SEM for two biological replicates with three technical replicates each is shown. All *P* values were calculated by *t* test. **A**) Seeds were germinated in the absence or presence of 150 mM NaCl and data normalized to wild-type seeds in the absence of salt. Salt caused a statistically significant (*P* < 0.05) lower levels of each gene transcript compared to wild-type in both the presence and absence of salt. **B**) Seeds were germinated on 150 mM NaCl in absence of 100 μ M norflurazon and data normalized to wild-type seeds in the absence or absence of a significant decrease (*P* < 0.05) in *CRA1* transcript levels in both wild-type and triple mutant seeds and in the *RAB18* trancript levels in wild-type seeds.



Supplemental Figure S5. Time for 50% of select point mutant seeds to germinate on NaCl in response to norflurazon. The time for 50% germination on 150 mM NaCl was calculated for each seed line from the data in figure 8. NR denotes that 50% germination was not reached in the time-frame of the experiment. ^aStatistically different from the wild-type seeds under the same conditions (P < 0.05). ^bMutant transgene different from *gETR1* under the same condition. The application of both 10 µM and 100 µM norflurazon caused a significant decrease (P < 0.05) in the time for 50% seed germination for all seed lines. All *P* values were calculated using Student's *t* test.

Supplemental	Table S1.	Primers used	for site-directe	l mutagenesis
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Primer Name	Primer Sequence 5' to 3'a	
etr1-silent-F	CAGCCATTCCtaGgCAcagtAATTTCACTGGACTTAAGG	
etr1-silent-R	CAGTGAAATTactgTGcCtaGGAATGGCTGGAACTTTCG	
E617A F	CATGGATGetAACGGGTTAGTATAAGC	
E617A R	ACCCGTTagCATCCATGACAAGAACCT	
N618A F	ATGAGgctGGGTTAGTATAAGCTT	
N618A R	AACCCagcCTCATCCATGACAA	
C661A F	CATGGACGTGgctATGCCCGGGGTCGAAAAC	
C661A R	CGGGCATagcCACGTCCATGAAGACCAC	
V665A F	GCCCGGGGctGAAAACTACCAAATCGCTCT	
V665A R	AGTTTTCagCCCCGGGCATGCACACGTCCATG	
E666A F	CGGGGTCGctAACTACCAAATCGCTCTCCGTAT	
E666A R	TGGTAGTTagCGACCCCGGGCATGCACACG	
N667A F	GTCGAAgctTACCAAATCGCTCTCCGTAT	
N667A R	ATTTGGTAagcTTCGACCCCGGGCATGC	
Q681A F	TCACAAAAgctCGCCACCAACGGCCACTAC	
Q681A R	TGGTGGCGagcTTTTGTGAATTTCTCGTGAAT	
R682A F	CAAAACAAgetCACCAACGGCCACTAC	
R682A R	CGTTGGTGagcTTGTTTTGTGAATTTCTCG	
Q684A F	CGCCACCAAgctCCACTACTTGTGGCA	
Q684A R	GTAGTGGCCGagcGTGGCGTTGTTTTGTG	
E730A F	TTCTCGctCCCCGGGTACTGT	
E730A R	TACCCGGGGagCGAGAAGAT	
L734A F	CCGGGTAgetTACGAGGGCATGTAAAG	
L734A R	TGCCCTCGTAagcTACCCGGGGGCTCGAGAA	

^a Lower case denotes sites of mutations being introduced.