Supplementary data: genotyping of *int1*, *int2* and *int4* mutant lines

Two *int1* mutant alleles were previously described by Schneider *et al*. (2008). However, when we attempted to obtain the corresponding seed stocks, the ABRC database indicated that SALK_085400 (designated *int1.1* in Schneider *et al*. 2008) carries an additional polymorphism associated with a second T-DNA insertion at At2g22370, in addition to the insertion at At2g43330, which encodes inositol transporter 1 (INT1). At2g22370 encodes Mediator 18 (MED18), a subunit of the mediator complex implicated in the regulation of flowering time and floral organ development through FLOWERING LOCUS C (FLC) and AGAMOUS (AG). In conjunction with MED20, MED18 has also been proposed to modulate the balance between salicylic acid- and jasmonate-associated defense pathways. Given the likely involvement of this locus in stress signaling, we excluded SALK_085400 from further analysis and instead selected SALK_018591 (designated *int1.2* in the same study), which exhibits fewer pleiotropic phenotypic defects, while still lacking detectable full-length *INT1* transcript. For subsequent analysis, we ordered CS859776, the ABRC-listed homozygous stock derived from SALK_018591. Genotyping was performed using two primer sets, one specific for the wild-type allele and the other specific for the mutant allele. In 10 randomly selected plants, amplification was detected exclusively with the mutant-specific primers, whereas no band was observed with the wild-type-specific primers (Fig. S1A). These results confirm that CS859776 is homozygous for the *int1* mutation.

There was one *int2* mutant line described by Schneider *et al*. (2007), SAIL_1264_A07, which carries a T-DNA insertion at At1g30220. We ordered CS879026, the ABRC-listed homozygous stock derived from SAIL_1264_A07. All seedlings exhibited a Basta- and hygromycin-resistant phenotype, and genotyping showed amplification exclusively with the mutant-specific primers in 10 randomly selected plants (Fig. S1B). These results confirm that CS879026 is homozygous for the *int2* mutation.

The *int4* mutant line described by Schneider *et al*. (2006) was SALK_082661, which carries a T-DNA insertion at At4g16480. We ordered CS859802, the ABRC-listed homozygous stock derived from SALK_082661. However, kanamycin resistance and T-DNA insertion were not detected in any of the seedlings tested. We therefore used SALK_082661 for genotyping with the wild type- and mutant-specific primers as described by Schneider *et al*. (2006). The results revealed three genotypes among the SALK_082661 seedlings. Lane 1 was a wild-type plant lacking the T-DNA insertion, whereas Lane 2 and Lane 3 were heterozygous and homozygous plants, respectively (Fig. S1C). Seeds were collected from homozygous plant and genotyping of 8 randomly selected progeny showed mutant phenotype (Fig. S1D), which confirmed that all were homozygous *int4* plants.

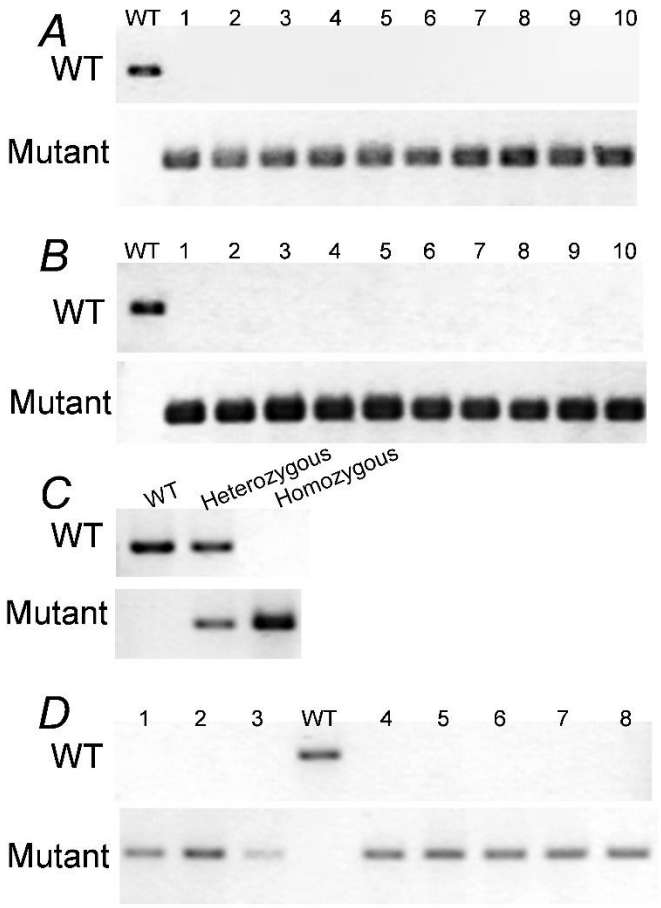


Figure S1. Genotyping of *int1*, *int2* and *int4* mutant plants.
(A) Characterization of the homozygous *int1* mutant. Genomic DNA from ten randomly selected CS859776 plants (numbered 1 to 10 at the top) was analyzed by PCR using wild type-specific (int1/-945 and int1/557r) or mutant-specific (LBb1 and int1/557r) primer pairs, as described by Schneider *et al*. (2008). All 10 plants showed bands with the mutant-specific primers, whereas no bands were detected with the wild type-specific primers. Genomic DNA from Col-0 (WT) served as the control.
(B) Characterization of the homozygous *int2* mutant. Genomic DNA from ten randomly selected CS879026 plants (numbered 1 to 10 at the top) was analyzed by PCR using wild type-specific (int2-1/108 and int2-1/1226r) or mutant-specific (LB3 and int2-1/1226r) primer pairs, as described by Schneider *et al*. (2007). All 10 plants showed bands with the mutant-specific primers, whereas no bands were detected with the wild type-specific primers. Genomic DNA from Col-0 (WT) served as the control.
(C) Genotype screening of SALK_082661 using wild type-specific (int4-802 and int4-1826r) or mutant-specific (LBb1 and int4-802) primers, as described by Schneider *et al*. (2006). Three genotypes were identified among the SALK_082661 seedlings: wild type (lacking the mutant band), heterozygous (showing both wild type and mutant bands), and homozygous (showing only the mutant band).
(D) Characterization of the homozygous *int4* mutant. Genomic DNA from eight randomly selected homozygous SALK_082661 plants (numbered 1 to 8 at the top) was analyzed by PCR using wild type-specific (int4-802 and int4-1826r) or mutant-specific (LBb1 and int4-802) primer pairs, as described by Schneider *et al*. (2006). All 8 plants showed bands with the mutant-specific primers, whereas no bands were detected with the wild type-specific primers. Genomic DNA from Col-0 (WT) served as the control.