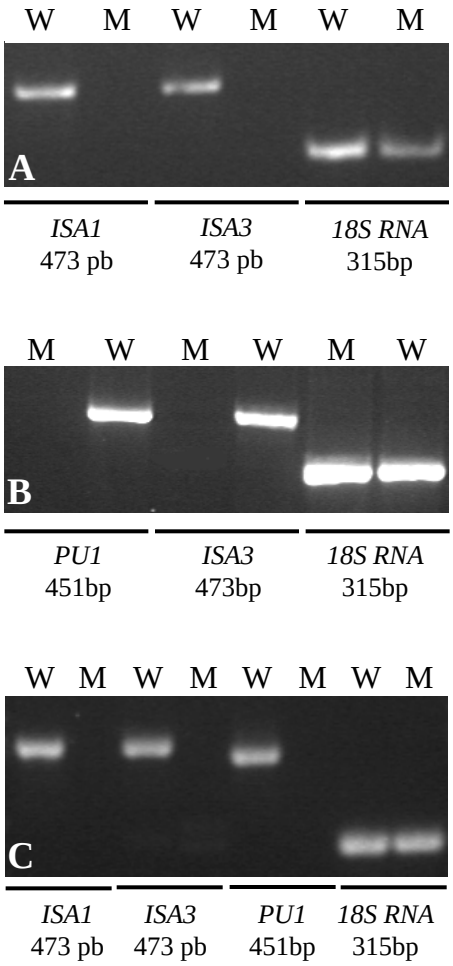

Supplemental figure 1: Genotyping of mutant lines selected after crosses. After crosses, plants were confirmed mutant by RT-PCR amplifications carried out on total RNA extracted from leaves. Reverse transcription reaction and PCR amplification cycles were as described in Methods. Used primers were designed in the way to span the reported insertion site of the T-DNA in the nuclear genome of the plant. W and M letters above the gels correspond to Wild-type and Mutant allele respectively. The expected size of the amplified fragment is indicated below the gel. RT-PCR amplification of a 315 bp region of the 18S RNA was used as a control in both Wild-type and Mutant plant and loaded on the same gel. A, B and C: selection of *isa1-1 isa3-1*, *isa3-1 pu1-1* and *isa1-1 isa3-1 pu1-1* mutant lines respectively.