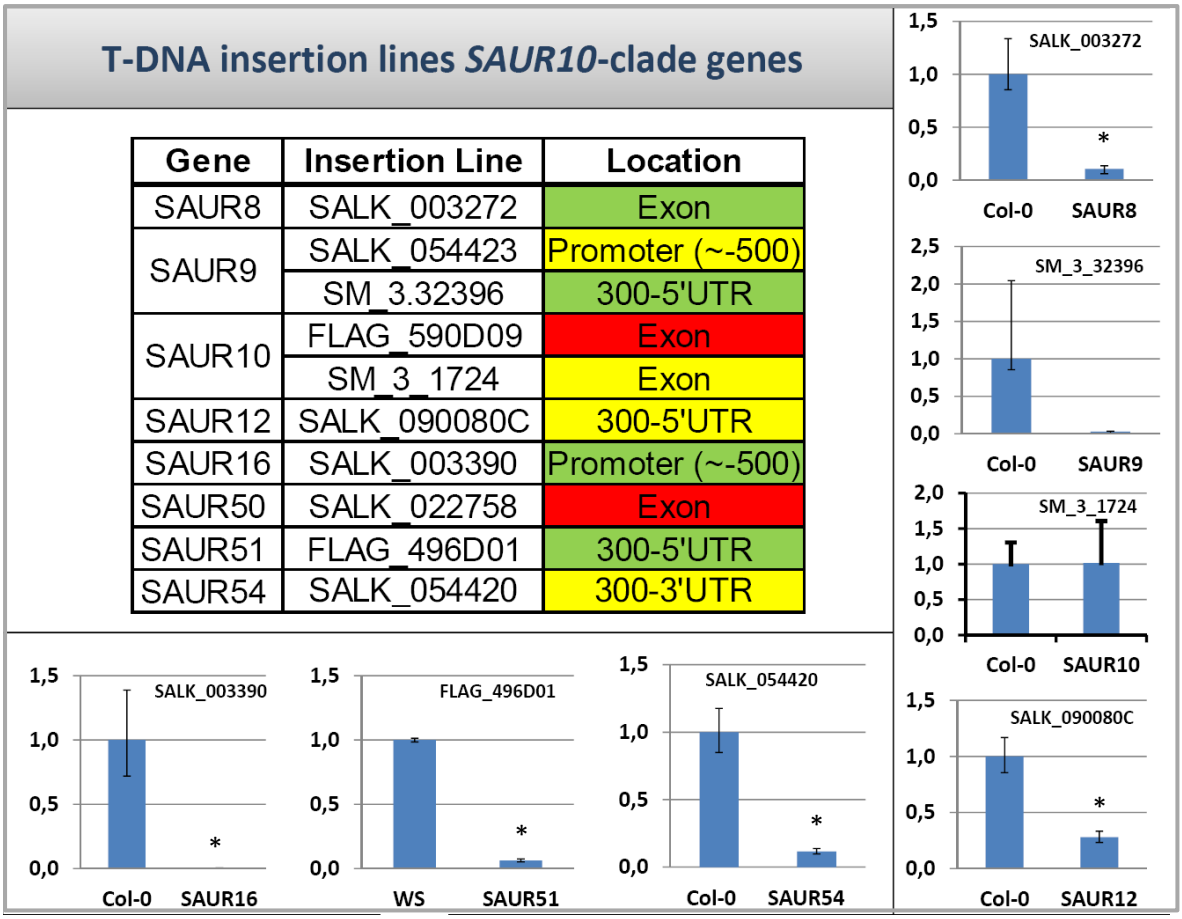

Additional file 3: Figure S2. Analysis of the T-DNA insertion lines. The table shows the different lines that were tested. Insertions could not always be identified in the coding sequence, due to the small size of the intronless *SAUR* genes (~350 bp). Green marked lines could be confirmed by genotyping and are probably knock-out lines. Yellow marked lines could be confirmed by genotyping, but are only partially impaired in expression (T-DNA in upstream region). Red marked lines could not be confirmed and do not appear to contain the insertion. The panels on the side show the expression analysis of the *SAUR10*-clade genes in the corresponding insertion lines. The qPCRs were performed with inflorescence tissue. The graph shows the relative fold change compared with the corresponding wild-type line. Significant differences (T-test, $p<0.05$) are indicated with an asterisk.

The following double and triple mutants were generated: *saur12 saur16; saur50 saur8; saur12 saur16; saur12 saur16 saur54; saur12 saur16 saur50; saur12 saur16 saur8; saur10 saur9*. No aberrant phenotypes were observed in any of these mutants.