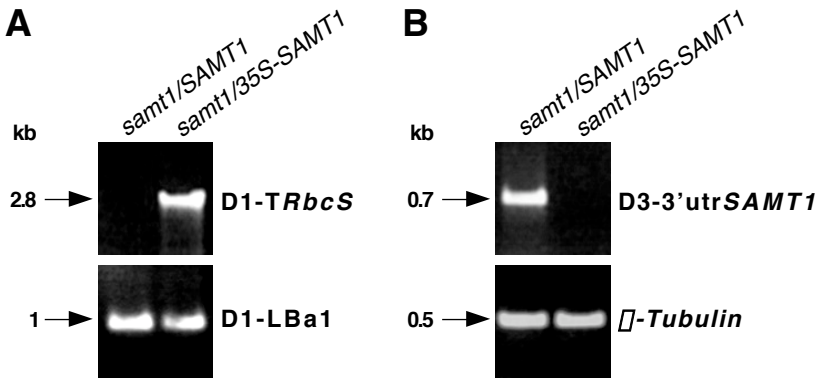

Supplemental Figure 4. Functional Complementation of *samt1* with *SAMT1.*

Samt1 was complemented in an heterozygous background (*samt1/SAMT1*) using a *35SSAMT1* construct.

(**A**) For detecting the transgene (*35S-SAMT1)* in the complemented lines (*samt1*/*35S-SAMT1*), the forward primer (D1) and the reverse primer (T*RbcS*) representing a fragment of the pea Rubisco small subunit terminator that is present in the pKYLX71-35S2 vector, were used for PCR amplification. The T*Rbcs* primer hybridizes only to the transgene. The native *samt1* was detected using the forward (D1) and the reverse (left border LBa1) primers.

(**B**) The absence of native SAMT1 in the complemented lines (*samt1*/*35S-SAMT1*) was analyzed by RT-PCR using the forward primer (D3) and the reverse primer (3'untranslated region of *SAMT1* (3'utr *SAMT1*)). The 3'utr *SAMT1* primer is not present in the *35S-SAMT1* transgene. Amplification of -*tubulin* mRNA was used as a positive control. PCR was performed for 35 cycles (*SAMT1*) and 27 cycles *(*-*tubulin*). PCR fragments derived from the different primers are indicated. Numbers refer to the lengths of amplified products.