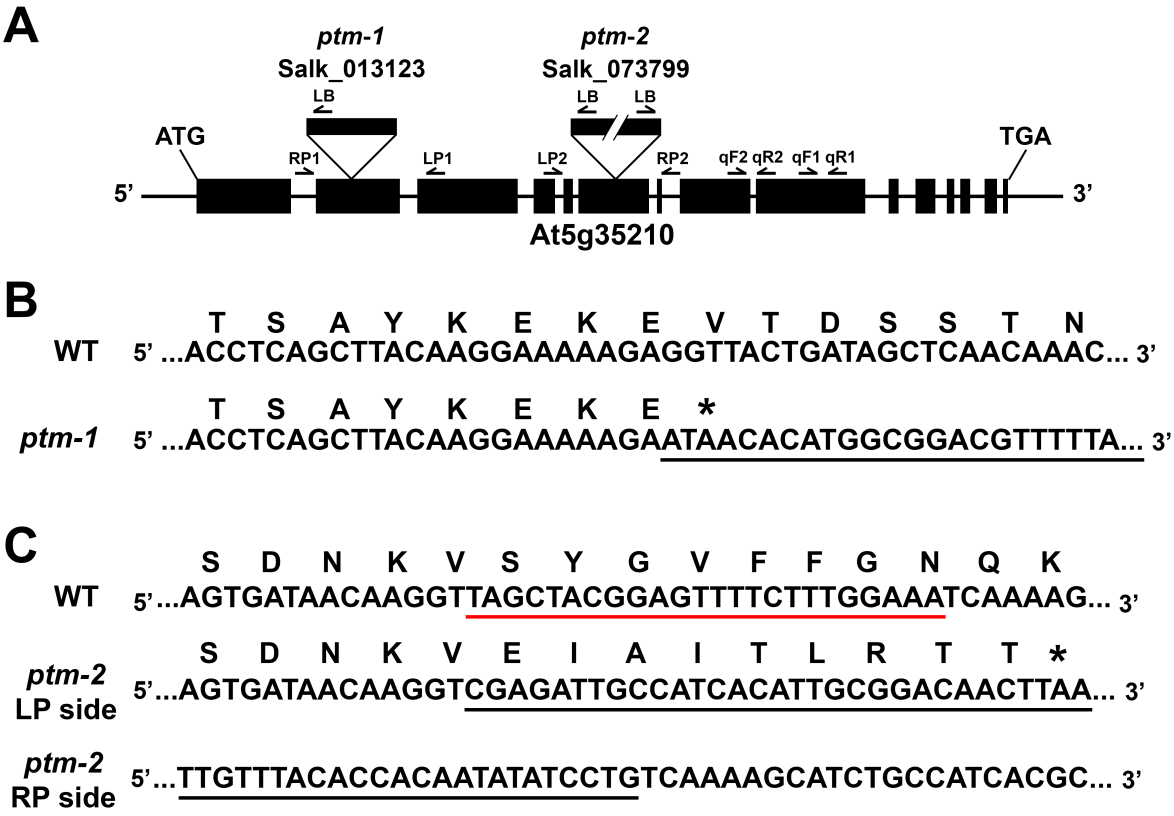

Supplemental Fig. S1. Characterisation of the *ptm* T-DNA insertion mutants. (A) *PTM* gene structure, with black boxes representing exons. The approximate location of the Salk_013123 (*ptm-1*) and Salk_073799 (*ptm-2*) T-DNA inserts, genotyping primers (LB, LP, RP) and qRT-PCR primers (qF, qR) are indicated. The *ptm-2* mutant has tandem T-DNA insertions with a 24 bp deletion, in which the LB primer binding site is located at each end of the tandem insertion. Precise T-DNA insertion sites in (B) *ptm-1* and (C) *ptm-2* as revealed by sequencing. For (B) and (C) amino acid single letter codes are given above DNA sequences, with the T-DNA sequences underlined in black. Sequence is given from the LP and RP sides of the *ptm-2* T-DNA insertion in (C), to demonstrate the site of the 24 bp deletion (underlined in red in the WT sequence). (D) PCR genotyping of *ptm-1* and *ptm-2* mutants. Primers shown in (A) were used to amplify the following: *ptm-1* - WT band (LP1 + RP1, predicted size 1,098 bp) and mutant band (LB + RP1, predicted size 687 bp); *ptm-2* - WT band (LP2 + RP2, predicted size 1,142 bp) and two mutant bands (LB + RP2, predicted size 661 bp, and LB + LP2, predicted size 904 bp). MW = molecular weight marker. (E) Expression of *PTM* in WT and *ptm-1* seedlings as determined by qRT-PCR. This analysis was repeated under the three conditions used in this study: growth condition 1 (GC1, white bars), GC2 (grey bars) and GC3 (black bars), all in the absence of NF. Expression is relative to WT for each GC and normalised to *ACTIN DEPOLYMERISING FACTOR 2* (*ADF2*, At3g46000). Data represent the mean + SEM of three independent biological replicates, asterisks indicate a significant difference *vs*. WT ($p < 0.05$, Student's *t*-test).