Supplementary figure legends

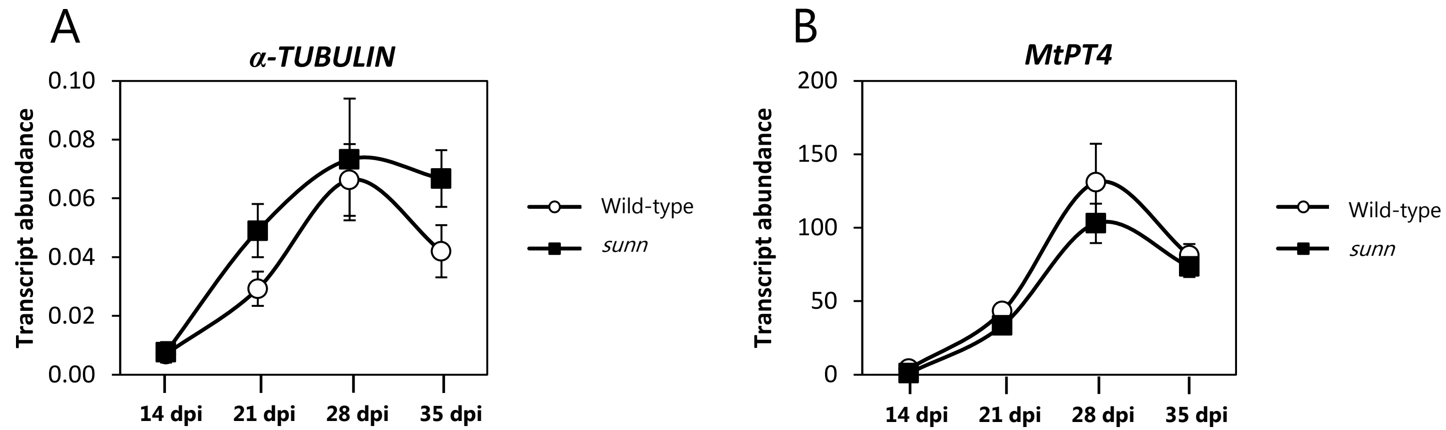
Fig. S1. (A,B) Transcript abundances of the AMF marker genes *MtPT4* (plant) and *α-TUBULIN* (fungus) in wild-type and *sunn*. Marks are averages ± standard errors (n=3). There were no significant differences in transcript levels between wild-type and *sunn* at any time point based on two-way ANOVA ($p < 0.05$). (C) Representative pictures of colonized roots of wild-type, *sunn* and *rdn1* at the four different time-points (days post inoculation (dpi)).

Fig. S2. Arbuscule and vesicle intensity in colonized roots of wild-type, *sunn* and *rdn1*. Number of vesicles (A) and arbuscules (B) were counted within a predefined square of 0.08 mm^2 in individual root segments of four biological replicates in wild-type, *sunn* and *rdn1* at three different time points (days post inoculation (dpi)). 100 observations were made per replicate. Bars are averages + standard errors (n = 100). Different letters indicate significant differences within genotypes at each time point as calculated by one-way ANOVA followed by Tukey´s posthoc test ($p<0.05$).

Fig. S3. Gene expression analyses and phosphate contents. (A) Relative gene expression levels of *PHOSPHATE STARVATION INDUCED* (*MtPSI*) and *MtPT4* at sufficient phosphorus (High P), phosphorus deficiency (Low P) and Low P plants colonized with arbuscular mycorrhiza (AMF). Expression levels were analyzed with RT-qPCR using the delta-delta Ct method (n=4). (B) Shoot phosphate (Pi) content (mg $plant^{-1}$) measured using the Malachite-green assay (n = 3). (C) Total root length colonization by arbuscules in wild-type and *mtpt4* plants derived from (Watts-Williams *et al.*, 2015) (n = 3). (D,E) Gene expression levels of *MtCLE53* and *MtPSI* in Low P roots re-supplied or not with Pi for 48 hours and 72 hours (n = 4). (F) Shoot Pi content (mg $plant^{-1}$) in Low P plants re-supplied with Pi or not for 48 hours and 72 hours (n = 4). (G) *MtCLE53* expression levels in composite plants overexpressing *p35S::CLE53*, *p35S::DsRed* or a mutated version of *MtCLE53* where the prolines in positions four and seven were modified to glycines *p35S::CLE53ΔPro4,7* (n = 4). Statistically significant differences were calculated based on one-way ANOVA followed by Tukey´s posthoc test ($p < 0.05$) and are marked with letters, while significant differences calculated based on two-sided Student´s t-test ($p < 0.05$) are marked with an asterisk (*). Non-significant differences are denoted “ns”.

Fig. S4. KEGG pathway analysis. Enriched pathways were identified among all DEGs in roots of wild-type and *sunn*, and are marked with an X to indicate in which genotype they were enriched. Gene ratios, i.e. number of enriched DEGs divided by the total number of genes associated with a given pathway, were calculated for pathways enriched in at least one genotype. Circle sizes refer to the number of DEGs enriched in the individual pathways.

Figure S1



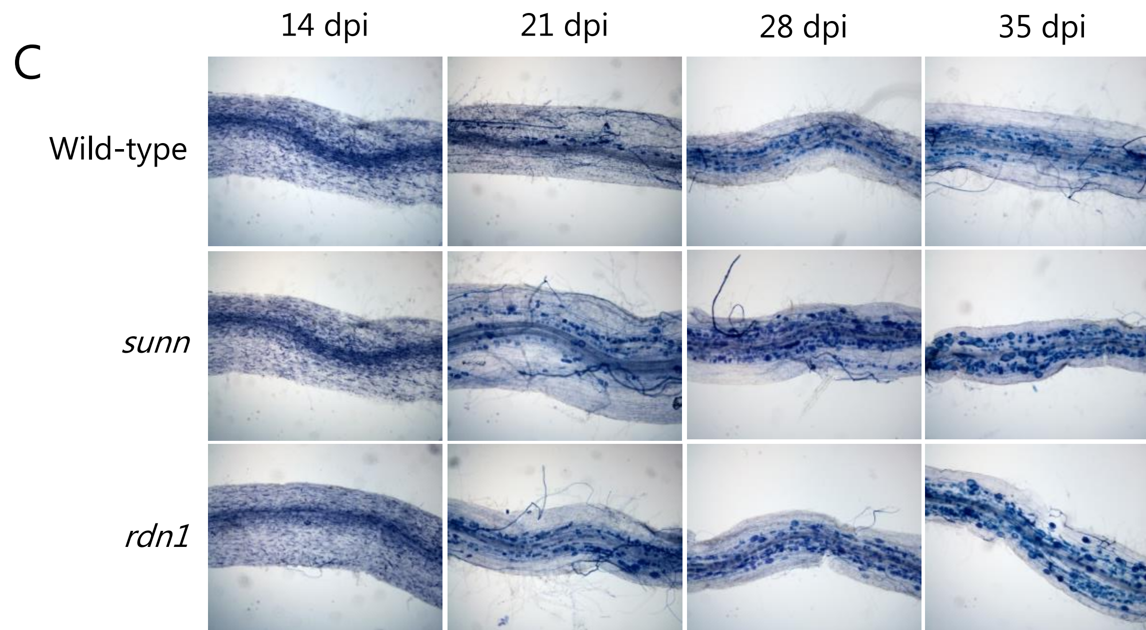
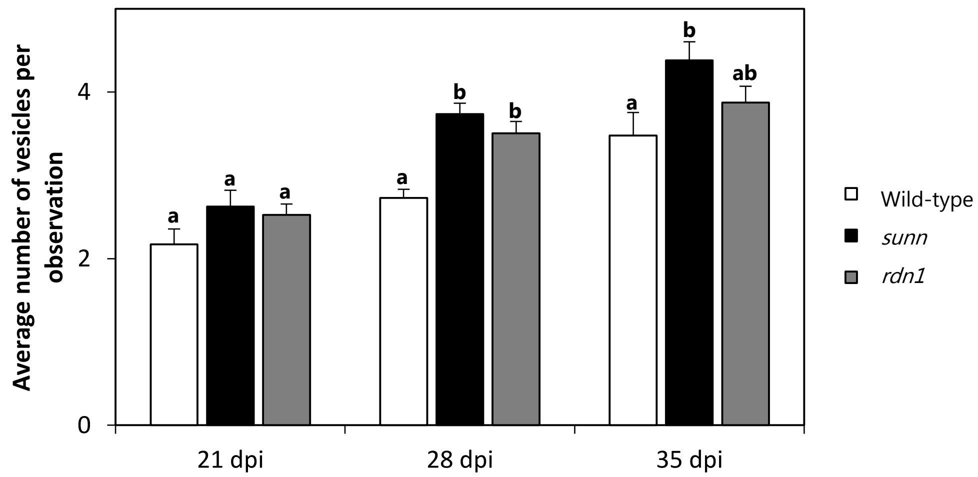


Figure S2



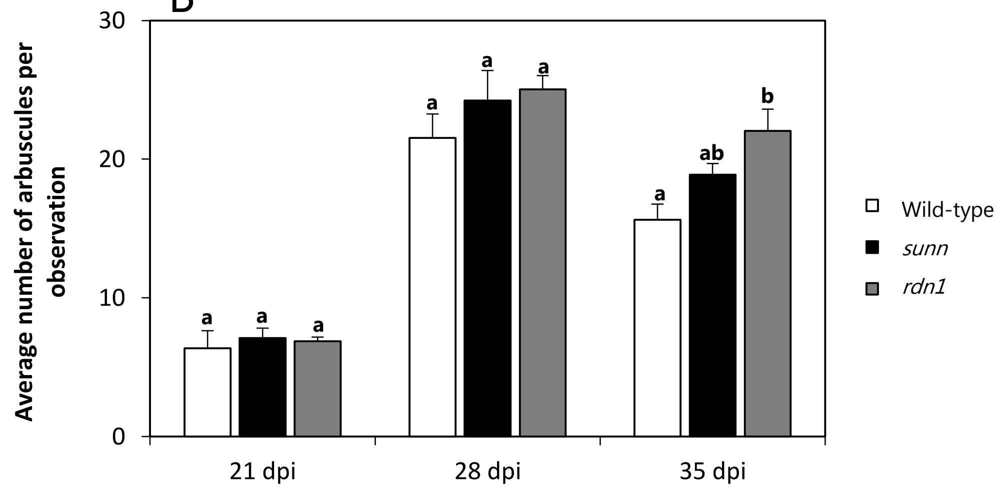


Figure S3

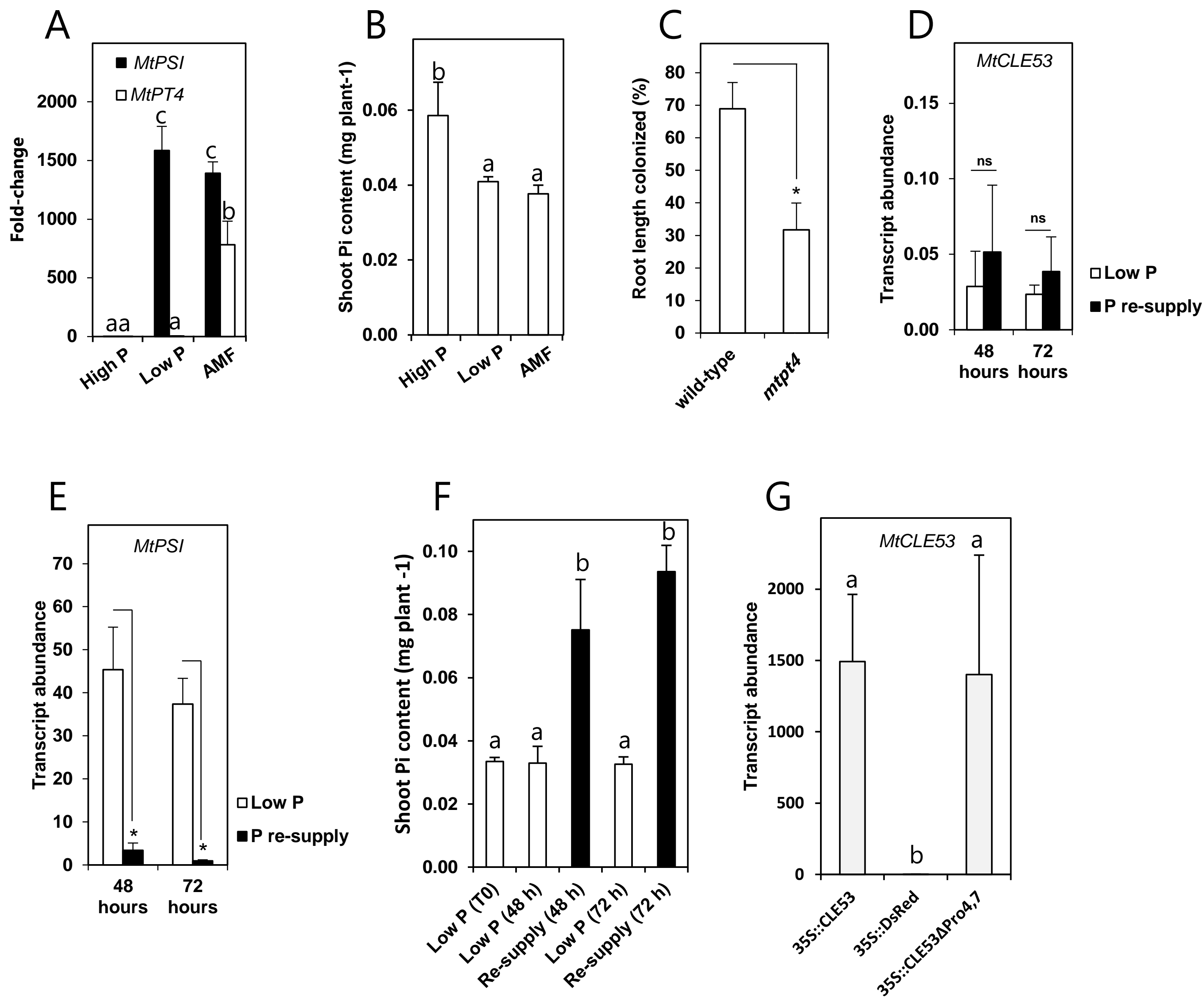


Figure S4