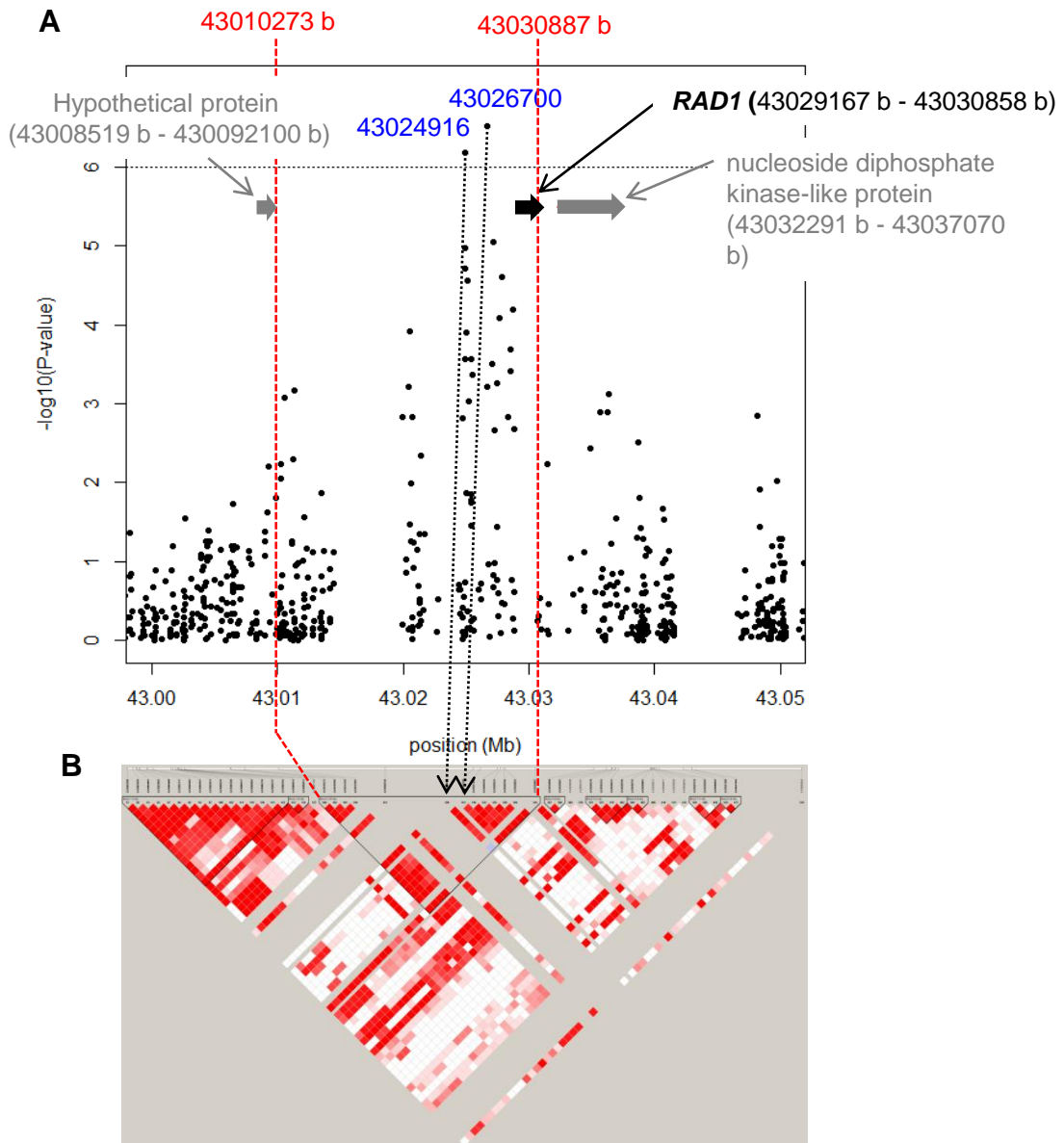
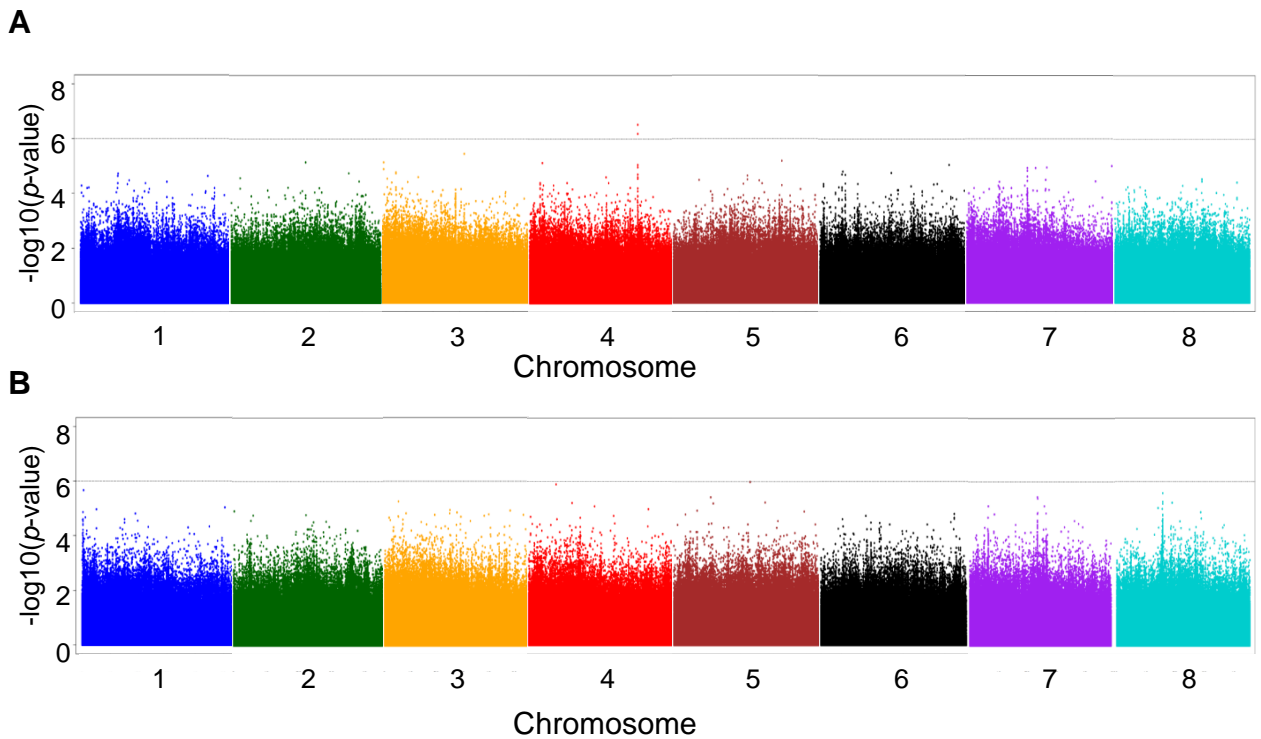


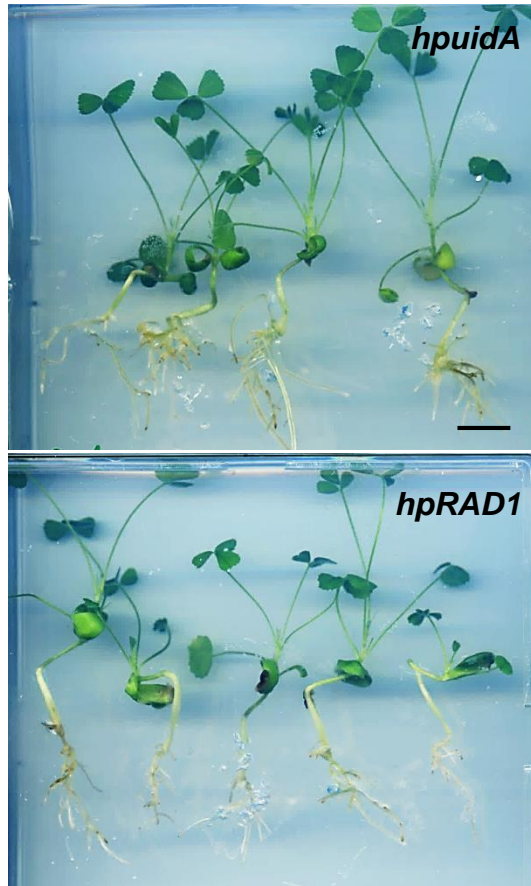
Supplementary Figure S1. Time course of *P. palmivora* AJ-td infection in *M. truncatula* A17. (A) microscopic assessment of colonisation. Filled arrowheads depict cortical biotrophic hyphae, empty arrow heads point to vascular colonisation (bar = 100µm). (B) Disease symptom development (root browning).



Supplementary Figure S2. Linkage disequilibrium (LD) analysis of the region encompassing *RAD1*. *RAD1* is the only gene within a LD block of ~ 20.6 kb. Red dashed lines in (A) limit a black triangle representing a block of LD in (B) where red squares show LD (D' estimator) between each SNPs. SNPs within the *RAD1*-containing LD block (including the blue highlighted two GWAM significant SNPs) are all in complete or nearly complete LD ($D' = 1$). SNPs used for LD have MAF>0.20 and 90% genotype scoring.



Supplementary Figure S3. Genome-wide association mapping of seedling length on infected and uninfected conditions. $-\log_{10}(\text{p-value})$ are displayed for all SNPs tested. **A Two SNPs are above the significance threshold of $-\log_{10}(6)$ in the association study for root length after *P. palmivora* infection; **B** No significantly associated SNPs were identified in the association study of seedling root length in the absence of an infection**



Supplementary Figure S4. Root expression of *hpRAD1* does not impact root habitus of composite plant. Composite plants expressing hairpin RNAi fragments in their roots grown for 6 weeks in sterile culture prior their inoculation with *P. palmivora* (bar = 1 cm).

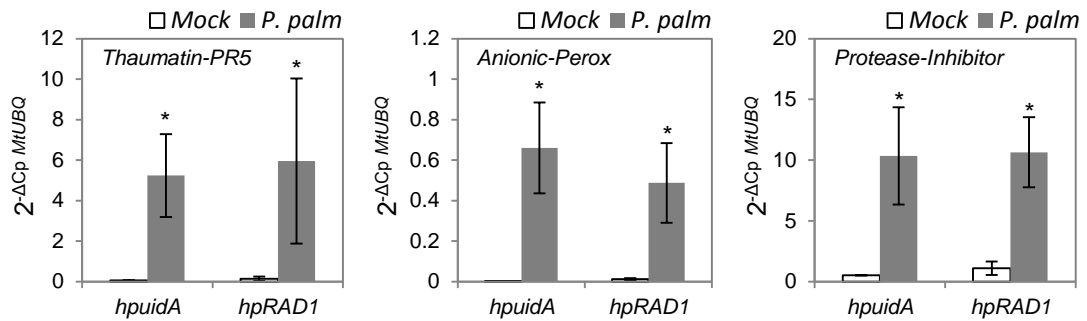


Figure S5. *M. truncatula* A17 roots expressing *hpRAD1* silencing constructs are not impaired in the defence response triggered by *P. palmivora* Lili-YKDEL. Transcript levels of *Thaumatin-PR5* (Mtr.9569.1.S1_at), *Anionic Peroxidase* (Medtr4g083710) and *Protease Inhibitor* (Medtr1g075340) were quantified in control (Mock) conditions (white bars, n=3) or upon infection with *P. palmivora* Lili YKDEL (grey bars, n=4) of composite plants transformed with *hpuidA* or *hpRAD1* constructs. Student's *t*-test was applied to compare gene expression between conditions and between constructs. Defence marker gene expression was standardised using *MtUBQ* (Medtr3g091400) as housekeeping gene and the $2^{-\Delta C_p}$ method (*= $p < 0.05$). Error bars show SEM.