

Figure S1. Quantitative PCR analysis of *EIL1*, *EIN3* and *ORA59* mRNA levels in unchallenged plants mis-expressing TOC1. Leaf tissue was harvested at ZT18 from fourweek-old plants grown under a 16 h light and 8h dark cycle. Relative expression of *EIL1*, *EIN3* and *ORA59* was determined by qPCR with normalisation to the geometric mean of *ACTIN2* (AT3G18780) and *MON1* (AT2G28390) expression. Plant genotype had a significant effect on mRNA levels of all three genes (*EIL1* F = 31.4, p <0.001, partial η^2 = 0.92, *EIN3* F = 87.1, p <0.001, partial η^2 = 0.97 and ORA59 F = 11.2, p =0.003, partial η^2 = 0.81) in one-way ANOVA. Mean expression values with different letters are significantly different (p <0.05) as determined by Fisher LSD post-hoc test. The data presented are mean values ± SEM from three biological replicates.

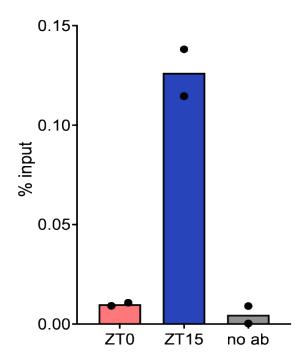


Figure S2. TOC1 occupies a G-box containing region of the *CCA1* **promoter at ZT15.** Two-week old *TMG* seedlings were cross-linked at ZT0 or ZT15 and chromatin immuno-precipitated with an anti-GFP antibody. ChIP-qPCR analysis of TOC1 occupancy of a G-box containing region of the *CCA1* promoter (a known binding site for TOC1) was performed. A no antibody control (no ab) was performed for the ZT15 samples. Values shown are mean percentage input from two independent experiments.

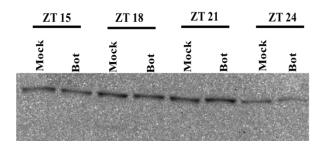


Figure S3. TOC1 protein levels do not change following *B. cinerea* infection. Two-week old *TMG* seedlings grown under a 16 h light and 8 h dark cycle were spray-inoculated with *B. cinerea* spore suspension (Bot) or mock-inoculated with half-strength grape juice (Mock) at ZT0. Samples were collected every three hours from ZT15 to ZT24 for extraction of total protein. TOC1-YFP fusion protein was detected using anti-GFP antibody. Protein bands were detected with Enhanced Chemiluminescent (ECL) reagent and visualised using the ChemiDoc™ XRS+ system and Image Lab software (version 5.2). This experiment was repeated twice with similar results.