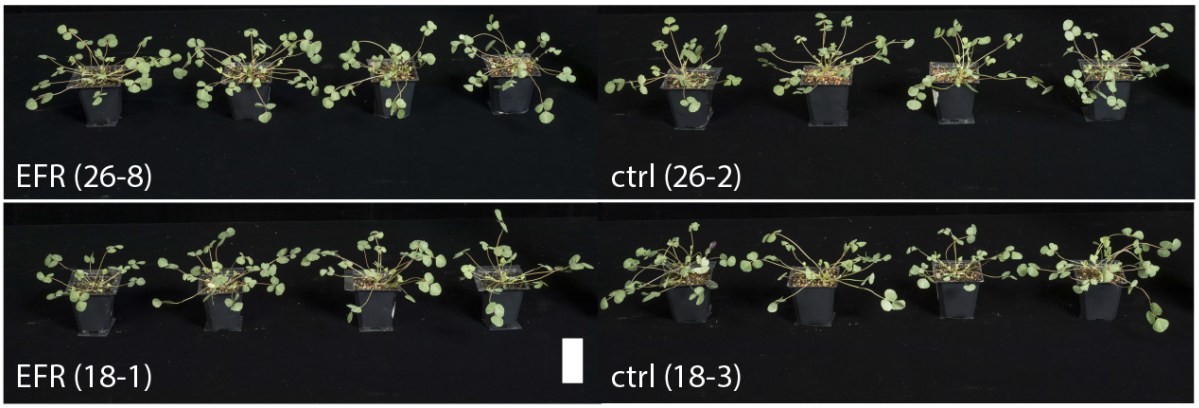

Fig S1. *EFR* expression does not affect development of *M. truncatula*. Phenotype of two independent stable *EFR*-expressing *M. truncatula* lines, 26-8 and 18-1, and their null segregant control lines 26-2 and 18-3, respectively. White scale bar, 5 cm.

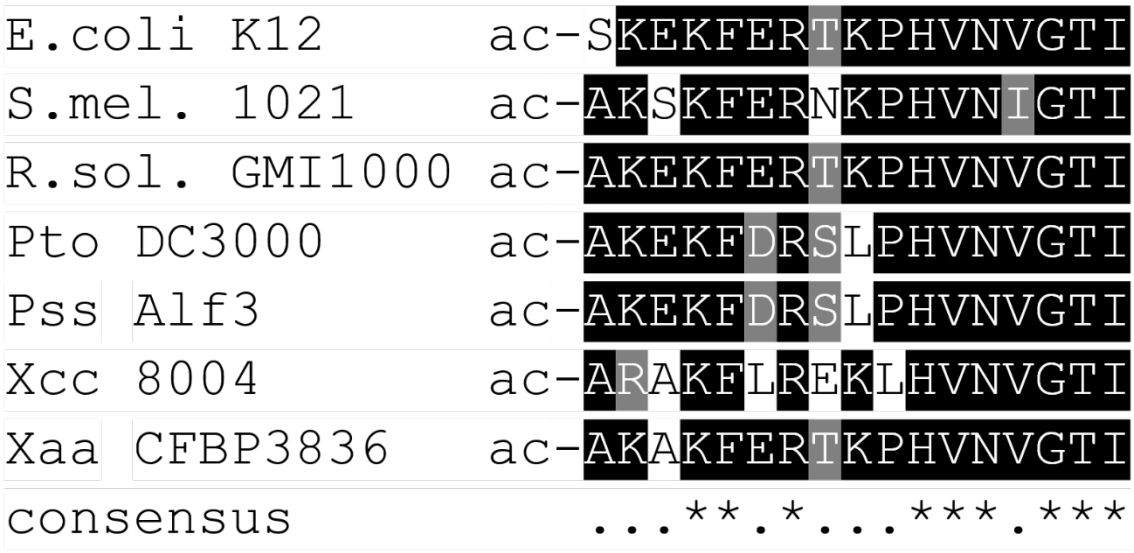

Fig S2. Alignment of elf18 peptide sequences. Peptide sequences are displayed with N-terminal acetylation (ac-) from following species: *Xanthomonas alfalfae* subsp. *alfalfae* CFBP3836, *X. campestris* pv. *campestris* 8004, *S. meliloti* 1021, *Escherichia coli* K12, *R. solanacearum* GMI1000, *Pseudomonas syringae* pv. *syringae* ALF3, *P. syringae* pv. *tomato* DC3000. Elf18 peptide sequences belong to seven groups with different eliciting activity according to Lacombe *et al.* 2010. Multiple sequence alignment has been created with Boxshade v3.21. Shadings indicate different degrees of conservation. Asterisk (*) in consensus indicates identity across all sequences.

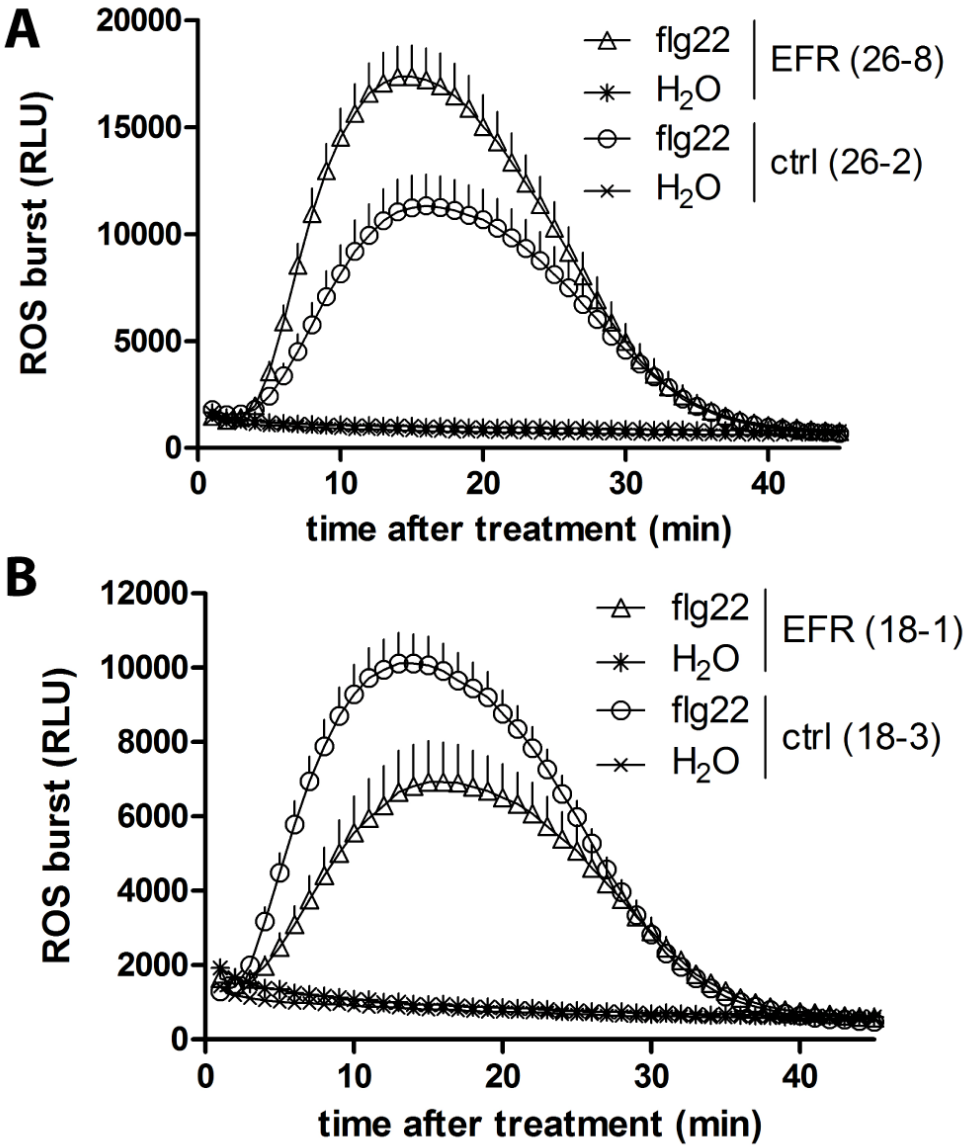

Fig S3. *M. truncatula* responds to flg22 peptide. ROS burst was monitored in root segments from line 26-8 and 26-2 (A) and from line 18-1 and 18-3 (B) after application of 100 nM flg22 peptide and displayed as relative light units (RLU). Values are means ± standard error (*n*=8). Experiment was performed twice.

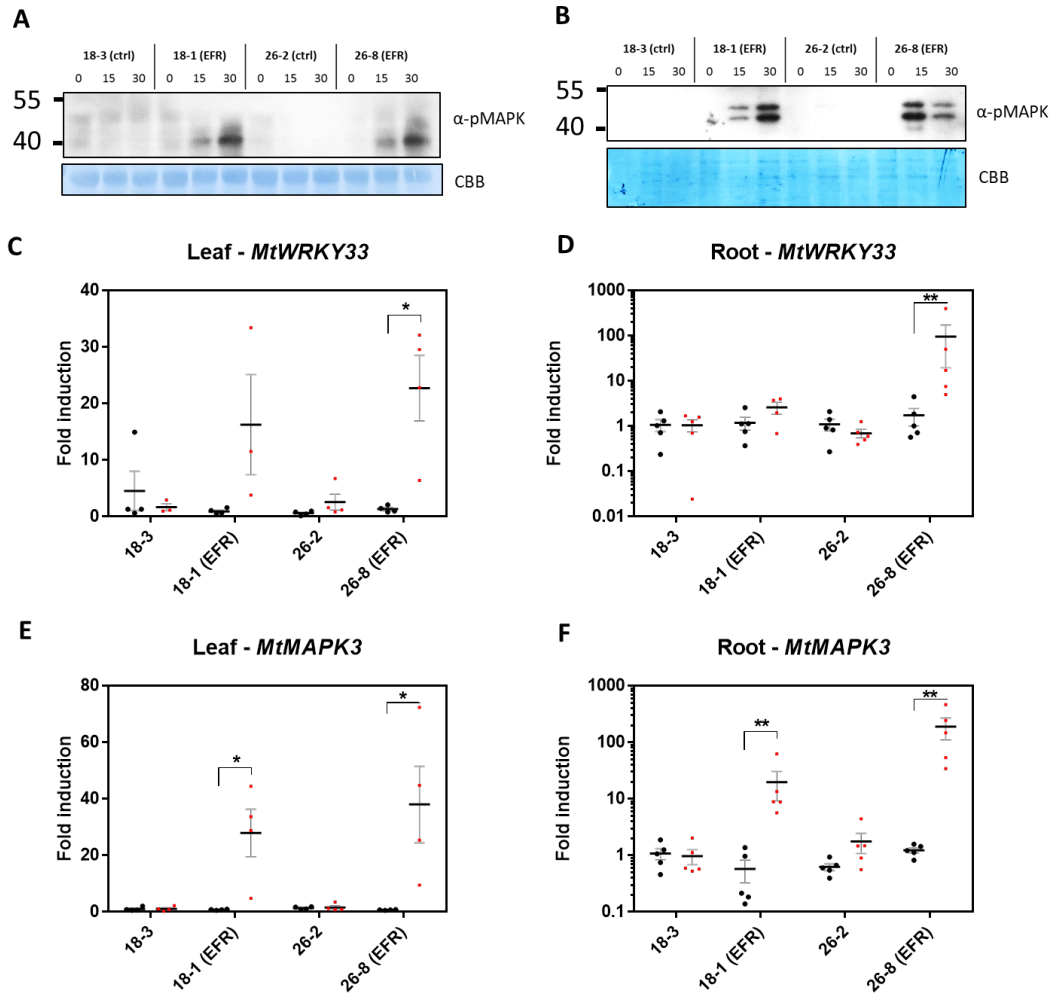

Fig S4. MAPK activation and marker gene induction is induced upon elf18 treatment in *EFR*-expressing lines . (A,B) Leaves (A) or roots (B) of *M. truncatula* were treated with 1 µM elf18 for 0, 15 or 30 minutes. Immunoblot analysis was performed using anti-phosho-p44/42 MAPK antibody. CBB staining was used as a loading control. This experiment was repeated three times with similar results. (C-F) Quantitative RT-PCR analysis of immune-related genes after 1h treatment with 1 µM elf18 (red symbols) or water (black symbols). *MtWRKY33* (C,D) and *MtMAPK3* transcripts (E,F) were analysed independently in leaf (C,E) and root tissues (D,F). Values represented are relative to water treatment at time 0 of each experiment. At least three experiments were performed with similar results. Means and SEM are shown by horizontal and vertical bars, respectively. Stars indicate significant differences determined by Wilcoxon test (* p≤0.05, ** p≤0.01).

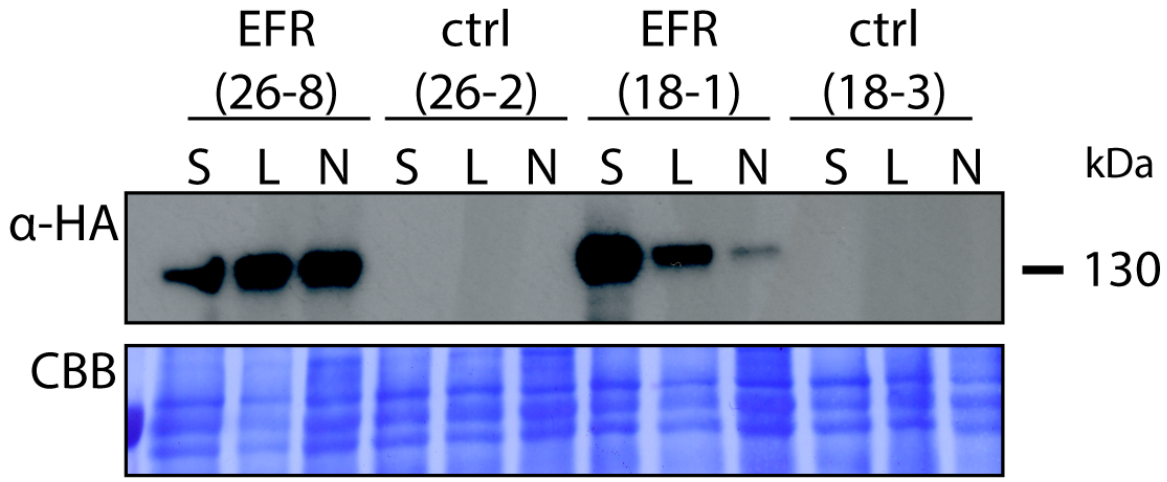

Fig S5. Transgenic EFR-*Medicago* roots and nodules accumulate EFR. Accumulation of EFR can be detected in stem root (S), lateral roots (L) and nodules (N) by western blot using α-HA antibody. Root material and nodules were harvested after inoculation with *Sm*1021-*lacZ* at 28 dpi. Membrane was stained with Coomassie Brilliant Blue (CBB) as loading control. Experiment was performed twice.

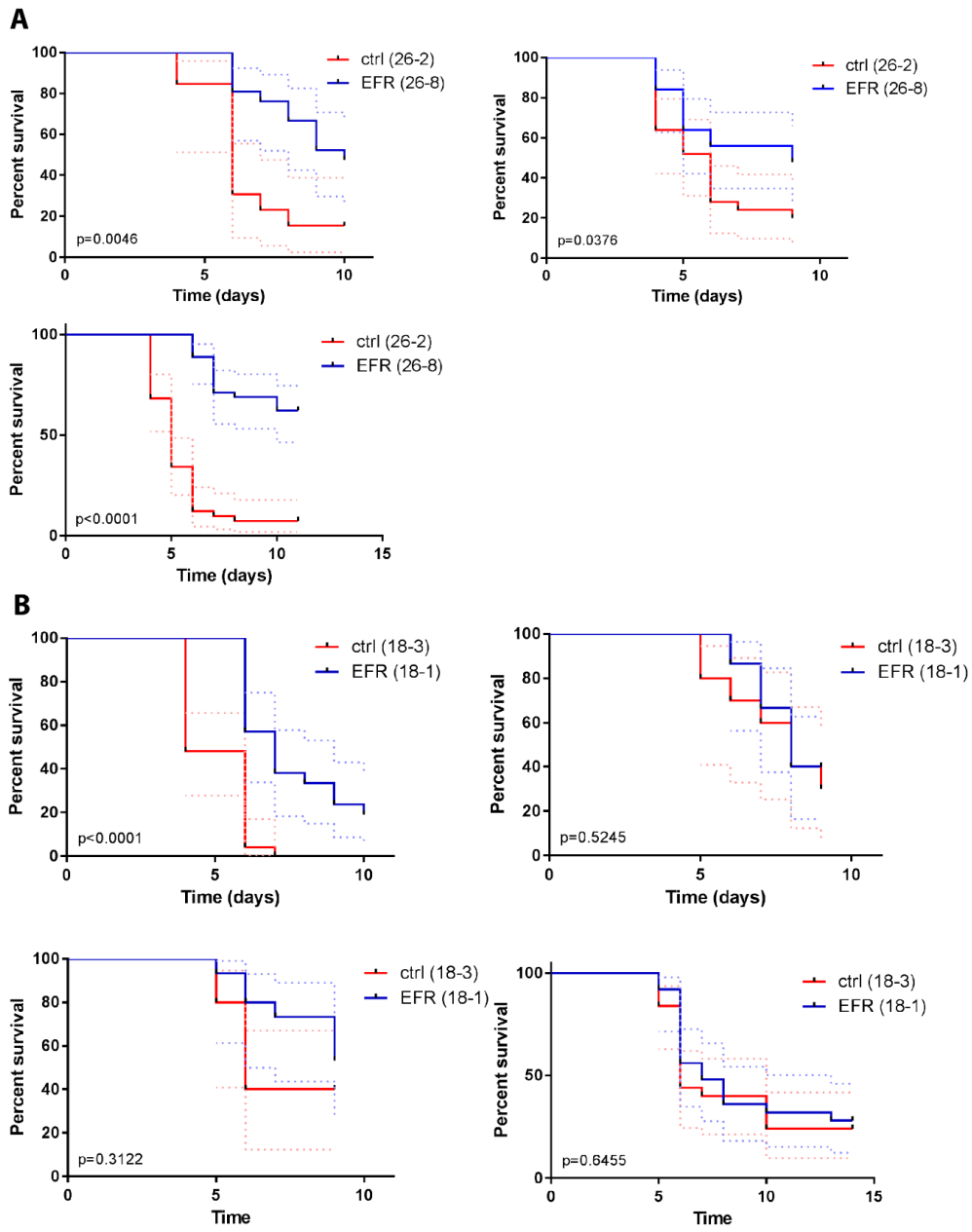

Fig S6. *EFR* expression in *M. truncatula* provides quantitative resistance against the pathogen *R. solanacearum*. (A) *M. truncatula* line expressing *EFR* 26-8 and control line 26-2 (A) and line expressing *EFR* 18-1 and control line 18-3 (B) were infected with *R. solanacearum* GMI1000 and disease symptoms assessed daily. Survival rate is displayed over time and statistical analysis performed with Mantel-Cox test (*n*=25). Dashed lines represent 95% confidence interval.

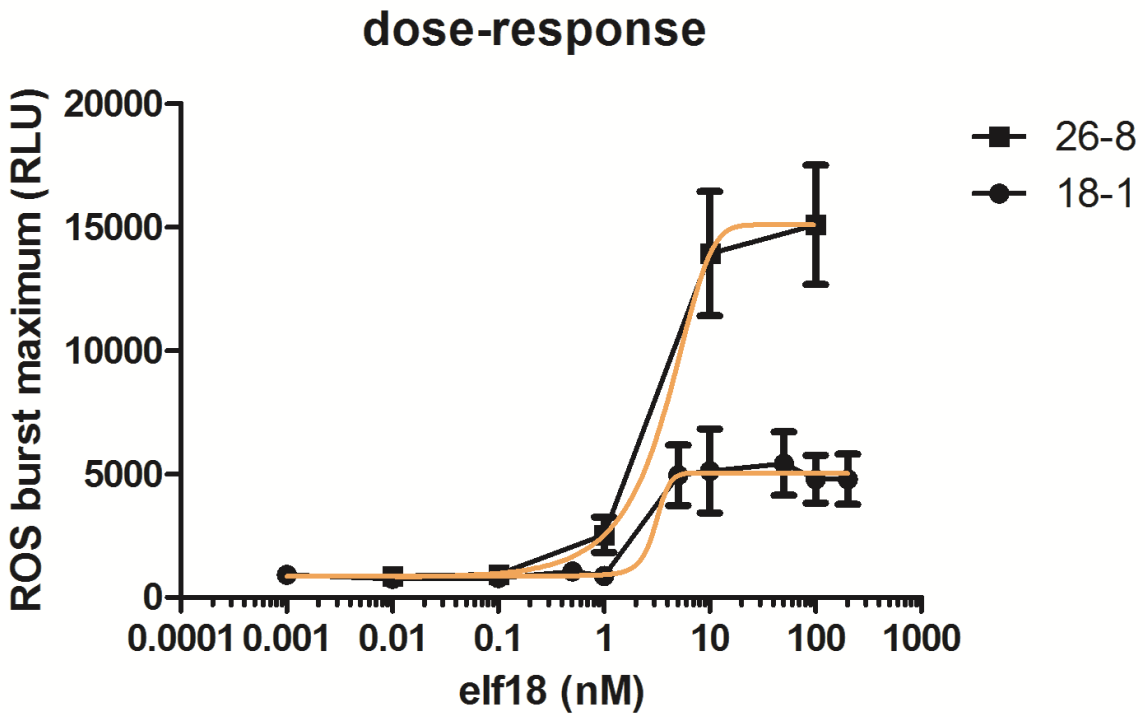

Fig S7. Dose-dependent ROS response of *M. truncatula* roots from *EFR*-expressing lines 26-8 and 18-1 to elf18 peptide. ROS burst maximum (displayed as relative light units) was monitored in root segments of lines 26-8 and 18-1 and plotted against elf18 peptide concentration. Orange line was calculated by the sigmoidal non-linear fit function in GraphPad Prism 5. Values are means ± standard error (*n*=8). Experiment was performed three times.