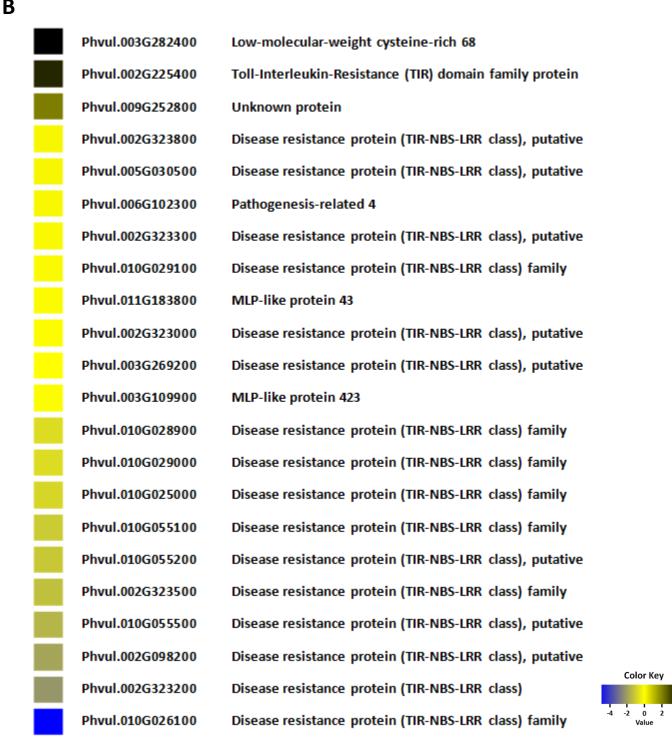
S5 Fig

Gene

Transcript ID

•	
Phvul.004G139700	Disease resistance protein (TIR-NBS-LRR class) family
Phvul.010G132200	Disease resistance protein (TIR-NBS-LRR class) family
Phvul.005G084100	Toll-Interleukin-Resistance (TIR) domain family protein
Phvul.010G027300	Disease resistance protein (TIR-NBS-LRR class) family
Phvul.004G140800	TIR-NBS-LRR class, putative transmembrane receptors; ATP binding
Phvul.004G140100	Disease resistance protein (TIR-NBS-LRR class), putative
Phvul.010G132000	Disease resistance protein (TIR-NBS-LRR class) family
Phvul.004G139800	TIR-NBS-LRR class, putative transmembrane receptors;ATP binding
Phvul.008G220600	Polyketide cyclase/dehydrase and lipid transport superfamily protein
Phvul.004G140700	Disease resistance protein (TIR-NBS-LRR class), putative
Phvul.010G054400	Disease resistance protein (TIR-NBS-LRR class) family
Phvul.003G109200	MLP-like protein 423
Phvul.010G101200	Disease resistance protein (TIR-NBS-LRR class), putative
Phvul.004G046400	Disease resistance protein (TIR-NBS-LRR class), putative
Phvul.010G136700	Disease resistance protein (TIR-NBS-LRR class), putative
Phvul.011G195800	Disease resistance protein (TIR-NBS-LRR class), putative
Phvul.010G025200	Disease resistance protein (TIR-NBS-LRR class) family
Phvul.001G093900	Disease resistance protein (TIR-NBS-LRR class), putative
Phvul.003G070900	Transmembrane receptors; ATP binding
Phvul.011G181400	Disease resistance protein (TIR-NBS-LRR class), putative
Phvul.010G065400	PYR1-like 4
Phvul.003G109000	MLP-like protein 423
Phvul.008G265900	Disease resistance protein (TIR-NBS-LRR class), putative
Phvul.010G026900	Disease resistance protein (TIR-NBS-LRR class) family
Phvul.008G195100	Disease resistance protein (TIR-NBS-LRR class), putative
Phvul.008G267700	Disease resistance protein (TIR-NBS-LRR class), putative
Phvul.010G026600	Disease resistance protein (TIR-NBS-LRR class) family
Phvul.011G140400	Disease resistance protein (TIR-NBS-LRR class), putative
Phvul.009G077200	PYR1-like 2
	Phvul.010G132200 Phvul.005G084100 Phvul.010G027300 Phvul.004G140800 Phvul.004G140100 Phvul.010G132000 Phvul.004G139800 Phvul.008G220600 Phvul.004G140700 Phvul.010G054400 Phvul.010G101200 Phvul.010G101200 Phvul.010G136700 Phvul.011G195800 Phvul.011G195800 Phvul.011G195800 Phvul.011G195800 Phvul.011G093900 Phvul.003G070900 Phvul.011G181400 Phvul.010G055400 Phvul.010G055400 Phvul.010G055900 Phvul.008G265900 Phvul.008G265900 Phvul.008G267700 Phvul.010G026600 Phvul.010G026600





S5 Fig. DEGs of defense-responsive genes during root symbioses. Expression profile of unique defense-responsive genes in P. vulgaris roots colonized by (A) AMF and (B) rhizobia. Expression profile showing upregulated and downregulated DEGs obtained form GO analysis. Statistically significant DEGs were identified using an unpaired t-test (p<0.05) in symbiont treatment over controls (S3 Table). Fold-change values (over control) were used to plot heat maps. Color bar scale shows the fold-change range with red and green representing downregulation and upregulation, respectively.