

Supplemental Figure S1. Expression of *MtROP9* and other related genes in MtROP9i and Mtvector transgenic roots after *A. euteiches* (Ae), *G. intraradices* (Gi) and *S. meliloti* (Sm) infection at 3 h and 24 h post inoculation. Representative bands of electrophoretically separated amplification products of RT-PCR. Increased expression relative to that in the water controls is marked with black boxes.



Supplemental Figure S2. PCA analysis of relative expression of *MtROP9* and other related genes in MtROP9i and Mtvector transgenic roots for all single infections (A), and separately after *A. euteiches* (Ae, B), *G. intraradices* (Gi, C) and *S. meliloti* (Sm, D) infection at 3 h and 24 h post inoculation. The scores for the first two principal components are presented in a bi-plot. Arrows: Vectorial alignment for relative gene expression in one direction and graph section indicate co-expression of genes. Red box: co-expression of the genes *Cat*, *RBOH* and *ROP9*. (A) Scores of one infection group are visually separated via dotted lines.