

Legend Figure S1

Figure S1. TME3 differential expressed protein interactions at 67 dpi. **(a)** STRING protein-protein interaction network functional enrichment analysis of over-expressed proteins with p -value $< 1.0\text{e-}16$. Network Settings: Full network; Confidence edge; Text mining; Experiments; Databases; Co-expression Interaction sources; Confidence of 0.7; More than 50 interactors 1st and 2nd shell; Hide disconnected nodes in the network **(b)** KEGG pathways analysis of over-expressed and under-expressed proteins with false discovery rate (FDR) < 0.05 .