



Figure S6. RNASeq analysis revealed transcriptional difference in four different growth stages of *P. megakarya* (*Pmeg*) isolate Pm1. (A) Heatmap showing Euclidean distances among the 16 libraries, calculated from Variance stabilized transformed count data. Color key indicates level of similarity between libraries. (B) Principal Component Analysis (PCA) of the first two principal components (PC1, PC2) of the 16 libraries. (C-D) Scatter MA-plot showing differential expression for the *Pmeg* genes in mycelia, zoospore and in planta (36 h post inoculation). Red-colored dots represent DEGs with \log_2 -fold changes.