

Figure S4 Functional annotation of the DEGs in rhizobia-inoculated and mycorrhized PvRbohB-RNAi roots, relative to the control. The bars show the percentages of upregulated (\mathbf{a} , \mathbf{c} , \mathbf{e}) and downregulated (\mathbf{b} , \mathbf{d} , \mathbf{f}) DEGs annotated with GO terms of the functional categories of biological processes (\mathbf{a} - \mathbf{b}), molecular functions (\mathbf{c} - \mathbf{d}), and cellular components (\mathbf{e} - \mathbf{f}). A cutoff threshold of Log2FC ≥ 1.5 and P-adj/FDR ≤ 0.05 was used, and GO terms were assigned using a GO-Slim analysis against the UniProt database in Blast2GO.