

S1 Fig. Midrooted phylogenetic tree of *rnpb* genes. *Rnpb* genes were manually retrieved from annotated ascomycete mt genomes publicly available in GenBank. Phylogenetic analysis was performed using maximum likelihood method implemented in RAxML with HKY model of selection. Branch support was calculated using 1000 bootstrap replicates. Green boxes depict *atp6* gene, red; small sub-unit of ribosomal RNA (*rns*) and dark red; *rnpb*, gold; *cob*, yellow; *cox* genes and lawn green boxes; *nad* genes. Accession numbers of mt genomes in which annotated *rnpb* genes were retrieved are NC_016187 (*Penicillium solitum*), KR952335 (*Penicillium roqueforti*), NC_016955 (*Peltigera malacea*), NC_025200 (*Sclerotinia borealis*), NC_018044 (*Saccharomyces paradoxus*), JQ435097 (*Aspergillus nidulans*).

