



S4 Fig: Species tree of the 31 fungal species analyzed in Fig. 1. The species tree was constructed using the concatenated alignment (S2 Dataset) of the 20 best scoring single-copy genes (S7 Table). Numbers at nodes represent the bootstrap values of Maximum Likelihood (left), Neighbor-Joining (middle), and the Bayesian posterior probabilities (right). A hyphen (-) indicates no support value in the corresponding method.