Supplemental Figure 1. Phylogenetic Analysis of small GTPase from E. festucae and Ascomycota fungi. The tree was prepared by the neighbor-joining method (Saitou and Nei, 1987) using MEGA ver. 6.06 (Tamura et al., 2013). The scale bar corresponds to 5 estimated amino acid substitutions per site. Numbers at the nodes indicate the percentage of 1000 bootstrap replicates that supported each labeled interior branch.