

Supplemental Information File 9 – The phylogenetic relationship of the M35 gene family across the Fungi

Phylogenetic relationships of the M35 protein family were determined via a bayesian analysis (Mr.Bayes) of the GBLOCKS-pruned amino acid sequence alignment of each M35 Pfam-domain found in the following fungi (formal names followed by species identifiers): *Sclerotinia sclerotiorum* (sscl), *Botrytis cinerea* (bcin), *Laccaria bicolor* (lbic), *Neurospora crassa* (ncre), *Trichoderma reesii* (tree), *Magnaporthe grisea* (mgri), *Coccidioides immitis* (cimm), *C. posadasii* (cpos), *Uncinocarpus reesii* (uree), *Stagonospora nodorum* (snod), *Aspergillus oryzae* (aory), *Aspergillus fumigatus* (afum), *Aspergillus nidulans* (anid), *Coprinopsis cinerea* (ccin), *Batrachochytrium dendrobatidis* (bden). Terminal lineages are described by species identifiers concatenated to the M35 domain-containing annotated gene identifiers. The expanded clade of *Coccidioides* and *Uncinocarpus* M35 domain-containing proteins is highlighted in the blue box.

