Figure S4  Phylogenetic tree showing the evolutionary relationships among eukaryotic orthologs of nbs1 from animals, fungi, plants and protists. C. cinereus Nbs1 groups with its closest relative Laccaria and other Basidiomycete fungi. Branch support is indicated by numbers at the base of branches, the percent bootstrap support ≥ 50%. The scale bar represents the distance of 0.5 amino acid substitutions per site. 186 aligned amino acid sites were analyzed using the LG+25γ substitution model implemented in RAxML version 7.3.1, resulting in this tree with an optimized LnL=−41564.91. The parameter describing the γ-distributed amino acid substitution frequencies is α=1.58. The GenInfo Identifier numbers for each sequence from Genbank are indicated.