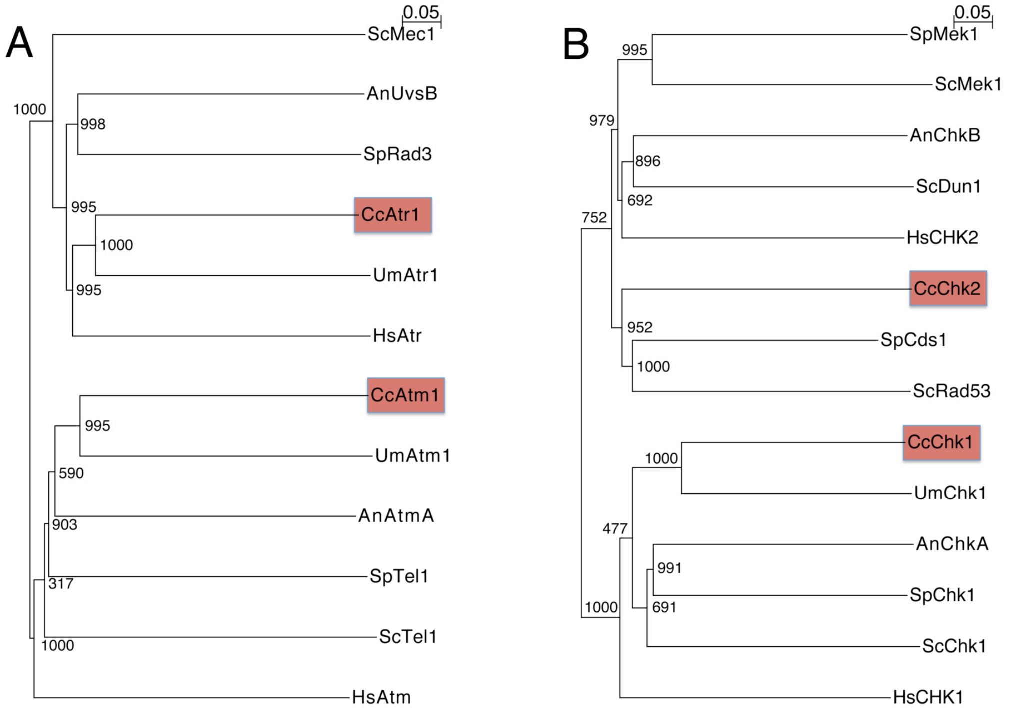

Figure S2 Dendrograms of DDR kinases from *C. cinerea*. (A) Dendrogram of characterized Atm and Atr1-like proteins. The proteins utilized were *Homo sapiens* ATR (CAA70298.1) and ATM (AAB38309.1); *Schizosaccharomyces pombe*; Rad3 (SPBC216.05), and Tel1 (SPCC23B6.03c); *Saccharomyces cerevisiae* Mec1 (YBR136W), and Tel1 (YBL088C); *Aspergillus nidulans* AtmA (AN0038.2) and UvsB (AN6975.2); and *Ustilago maydis* Atm1 (um15011) and Atr1 (um01110) (B) Dendrogram of characterized Chk1 and Rad53/Chk2-like proteins. The proteins utilized were *Homo* sapiens CHK1 (AAP36685.1) and CHK2 (EAW59756.1); *Schizosaccharomyces pombe*; Chk1 (NP588070.1), Cds1 (NP587941.1) and Mek1 (NP594908.1); *Saccharomyces cerevisiae* Chk1 (EDN64882.1), Rad53 (EDV11072.1), Dun1 (NP010182.1) and Mek1 (NP014996.1); *Aspergillus nidulans* ChkA (XP663098.1) and ChkB (XP661883.1); and *Ustilago maydis* Chk1 (XP759637.1).

In both phylogenetic analyses, proteins from diverse fungi (Sc, *Saccharomyces cerevisiae*; Sp, *Schizosaccharomyces pombe*; An, *Aspergillus nidulans*; Um, *Ustilago maydis*) as well as human (Hs) and putative proteins from *C. cinerea* (Cc) were aligned using the distance-based minimum-evolution method, based on 1000 replicates. Bootstrap values are given, and branching points and the scale bar denote substitutions per site.