



Figure S6: Phylogenetic tree of orthologues of QDE-2-like AGO-1 and AGO-2 proteins of *C. zeina* using representative fungal species from different orders in the class *Dothideomycetes*. *C. zeina* AGO-1 (PKR99617) and AGO-2 (PKS00983) are shown with black dots. The tree was constructed using the Maximum Likelihood method in Mega-X, and was rooted using *Fusarium graminearum* and *Neurospora crassa* (class, *Sordariomycetes*) as an out-group. Bootstrap values greater than 50% are shown (1000 bootstraps). The scale bars indicate substitutions per site.