

Figure_S1.pdf Supplementary image file:

Supplementary Figure:

Assessment of genome assembly and annotation completeness for the *A. rabiei* ArME14 reference genome assembly and comparison with the published ArD2 *A. rabiei* assembly, using BUSCO. BUSCO was run using annotated protein files with graphical output within BUSCO by implementation of ggplot in R. For benchmarking of ArME14 annotated assemblies against the BUSCO Ascomycota database of 1315 genes, 1300 proteins were matched, 12 annotations were fragmented and 3 proteins were missing. By comparison, the draft *A. rabiei* ArD2 genome assembly had 37 proteins missing and 17 fragmented genes.

