



Figure S1: Phylogenetic relationships of *F. circinatum* isolates investigated in this study. The tree was constructed from the concatenated β -tubulin and TEF1 α sequences obtained from representatives of the *Fusarium fujikuroi* species complex [10]. Briefly, this involved alignment of the sequences using MAFFT v. 7 [31], followed by determining the best-fit nucleic acid substitution model using jModelTest v.2 [32] and the Akaike Information criterium (AIC). Phylogenetic relationships were inferred using maximum likelihood analyses in MEGA v7.0.26 [33]. Bootstrap values above 95% are indicated at branch node as determined for 1000 pseudo-replicates. The red coloured branch depicts the phylogenetic relationship of the newly sequenced *F. circinatum* strains FSOR, FFRA, UG27, and CMWF567, relative to that of the *F. circinatum* strains that were investigated in this study.