

Supplementary Figure S3

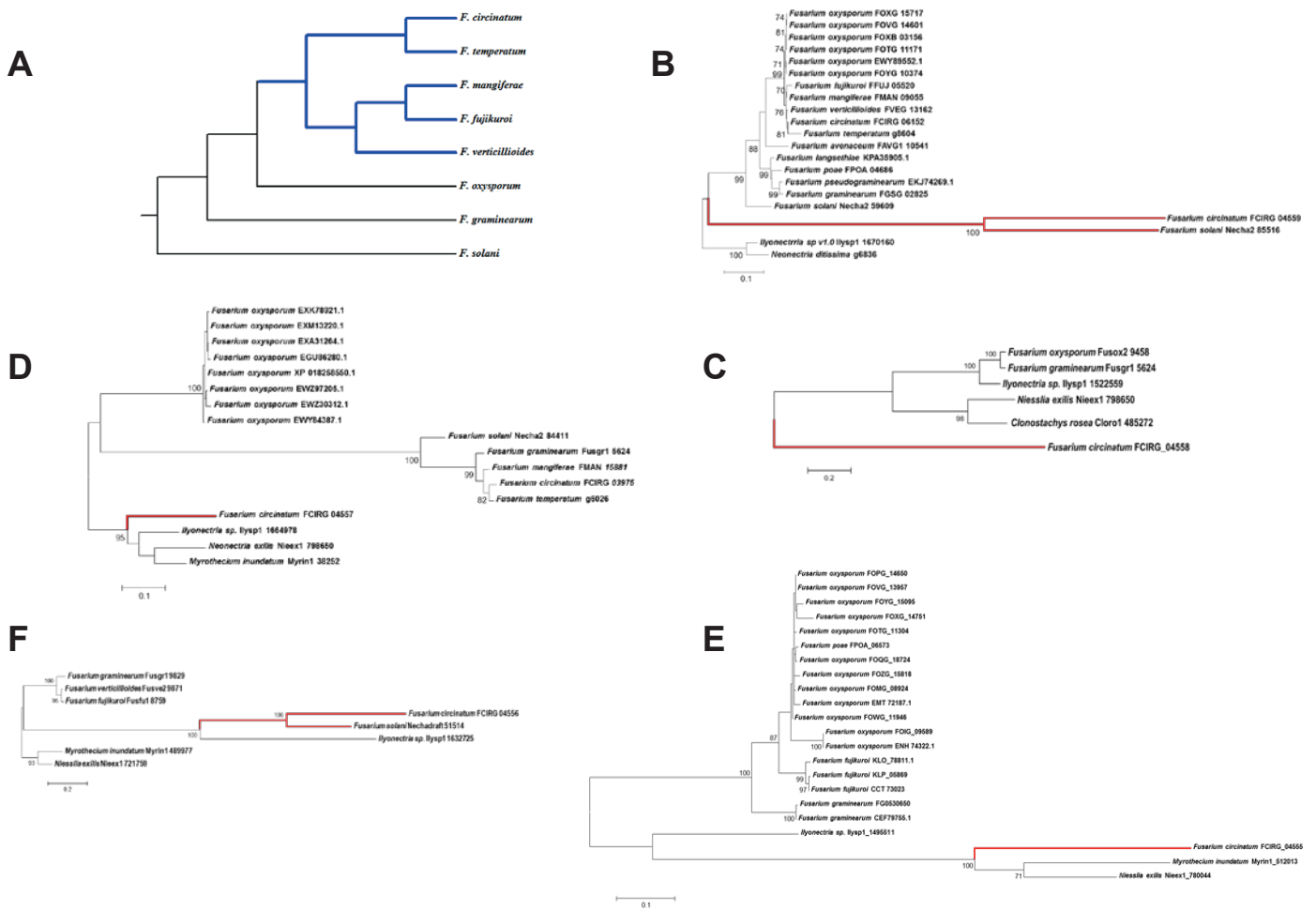


Fig. S3. Incongruence between the FFSC species tree (A) and the maximum likelihood phylogenies of the five genes encoded on the 12000 bp region specific to *F. circinatum* (B-F). Bootstrap values above 70 % (1000 replicates) are indicated at nodes and the nodes indicate substitutions per site. Branches indicated in red show the position and closest relative of the respective *F. circinatum* sequence in the trees. The relevant sequences from one or more of *Myrothecium inundatum*, *Clonostachys rosea*, *Niesslia exilis*, *Neonectria ditissima* and *Ilyonectria* sp. were included for comparison or as outgroups. (A) Cladogram illustrating expected phylogenetic relationships amongst diverse *Fusarium* species investigated in this study. (B) Tree constructed from the alignment containing FCIRG_04559 and its homologs in the genomes of other *Fusarium* species. (C) Tree inferred from the alignment of FCIRG_04558, its two *Fusarium* homologs and other homologs. (D) Tree inferred from the alignment of FCIRG_04557 and its homologs in the genomes of other *Fusarium* species. (E) Tree inferred from the alignment of FCIRG_04556 and its homologs in the genomes of other *Fusarium* species and taxa. (F) Tree inferred from the alignment of FCIRG_04555 its homologs in the genomes of other *Fusarium* species.