



Supplementary Fig. 1. Neighbor-joining phylogenetic tree based on the concatenated sequences of the internal transcribed spacer region and *tef1* and *tub2* genes. *Neofusicoccum parvum* (ATCC 58191) was used as an outgroup. Bootstrap values are based on 1,000 resamples, and values below 70 are not shown. The scale bar represents 0.010 substitutions per nucleotide position. All isolates from the current study were grouped into the *Botryosphaeria sinensis* and *B. kuwatsukai* clades, only reference sequences are outside of them.