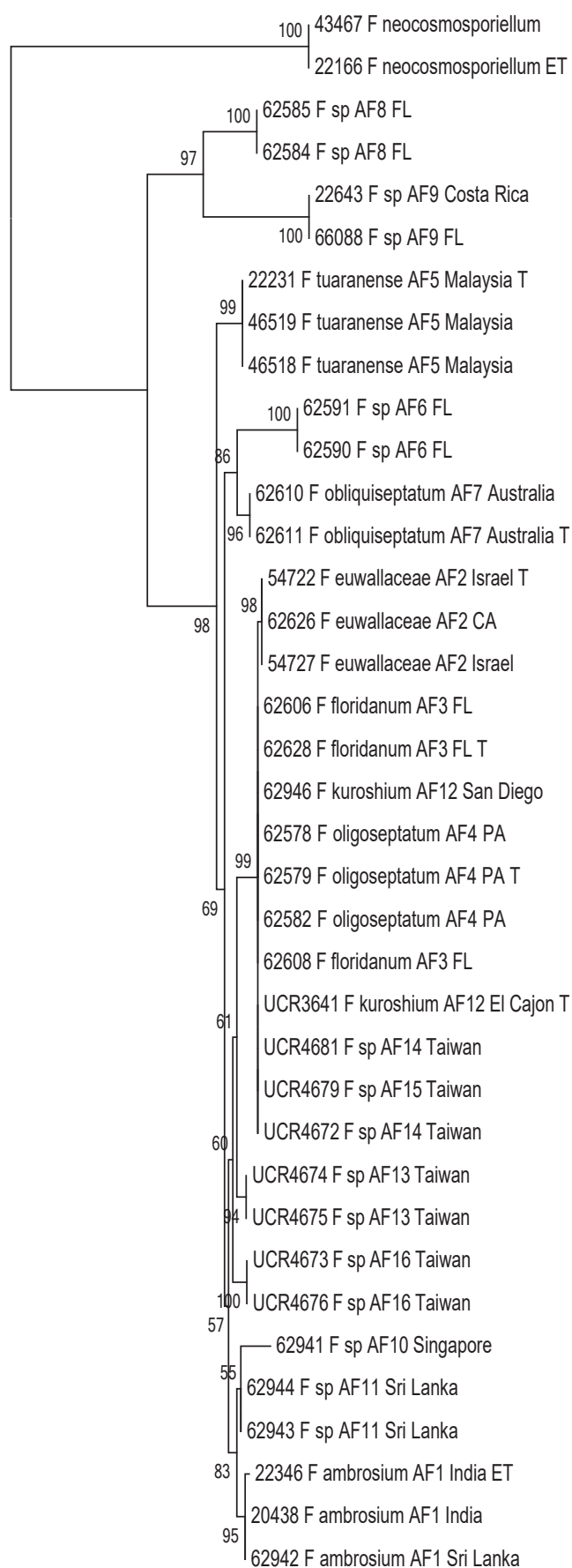
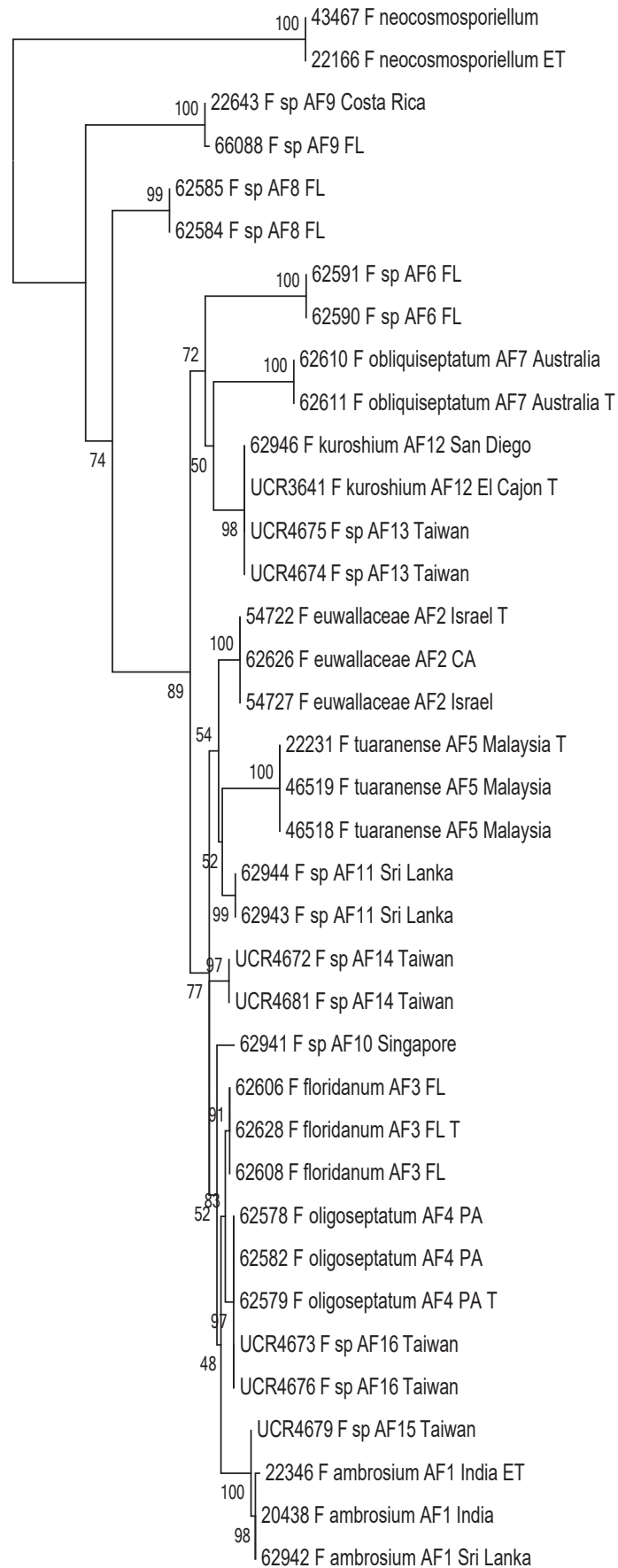


Supplementary Fig. 1A



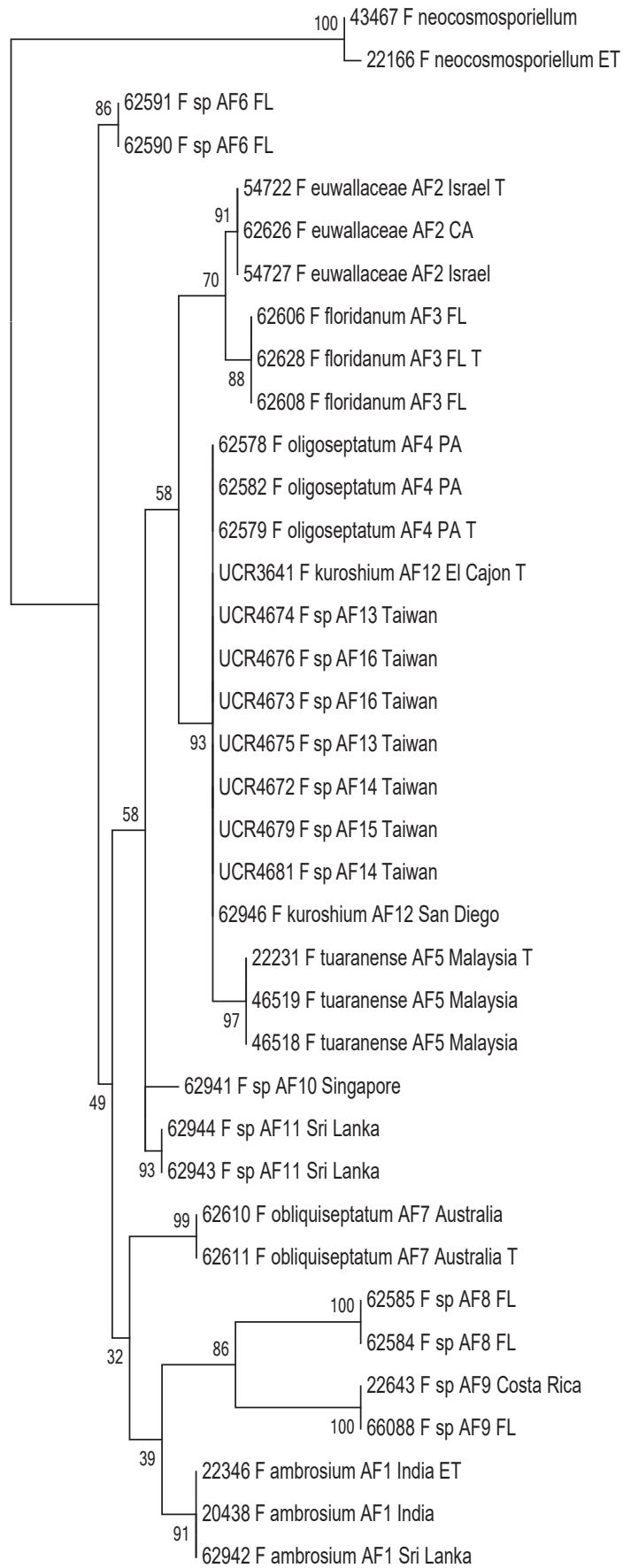
H
0.0010

Supplementary Fig. 1B



H
0.0020

Supplementary Fig. 1C



0.0020

Supplementary Fig. 1D

Supplementary Fig. 1A–D. Maximum likelihood bootstrap (ML-BS) analyses of the four individual partitions. The 16 ingroup Ambrosia Fusarium Clade (AFC) species are distinguished by an informal ad hoc nomenclature (AF-1 through AF-16). Eight of the ambrosia fusaria possess Latin binomials. The 4.35 kb 4-locus dataset included portions of **A:** ITS rDNA (445 bp alignment), **B:** *RPB1* (1588 bp alignment), **C:** *RPB2* (1635 bp alignment) and **D:** *TEF1* (684 bp alignment). The ingroup was rooted on sequences of *F. neocosmosporiellum* based on more inclusive analyses (O'Donnell et al. 2013). Numbers above nodes represent ML-BS support based on 5000 pseudoreplicates of the data implemented in IQ-tree (Nguyen et al. 2015). Twenty-nine of the strains are identified by the 5-digit ARS Culture Collection number (NRRL); sequences of eight UCR isolates were downloaded from GenBank (Na et al. 2018).