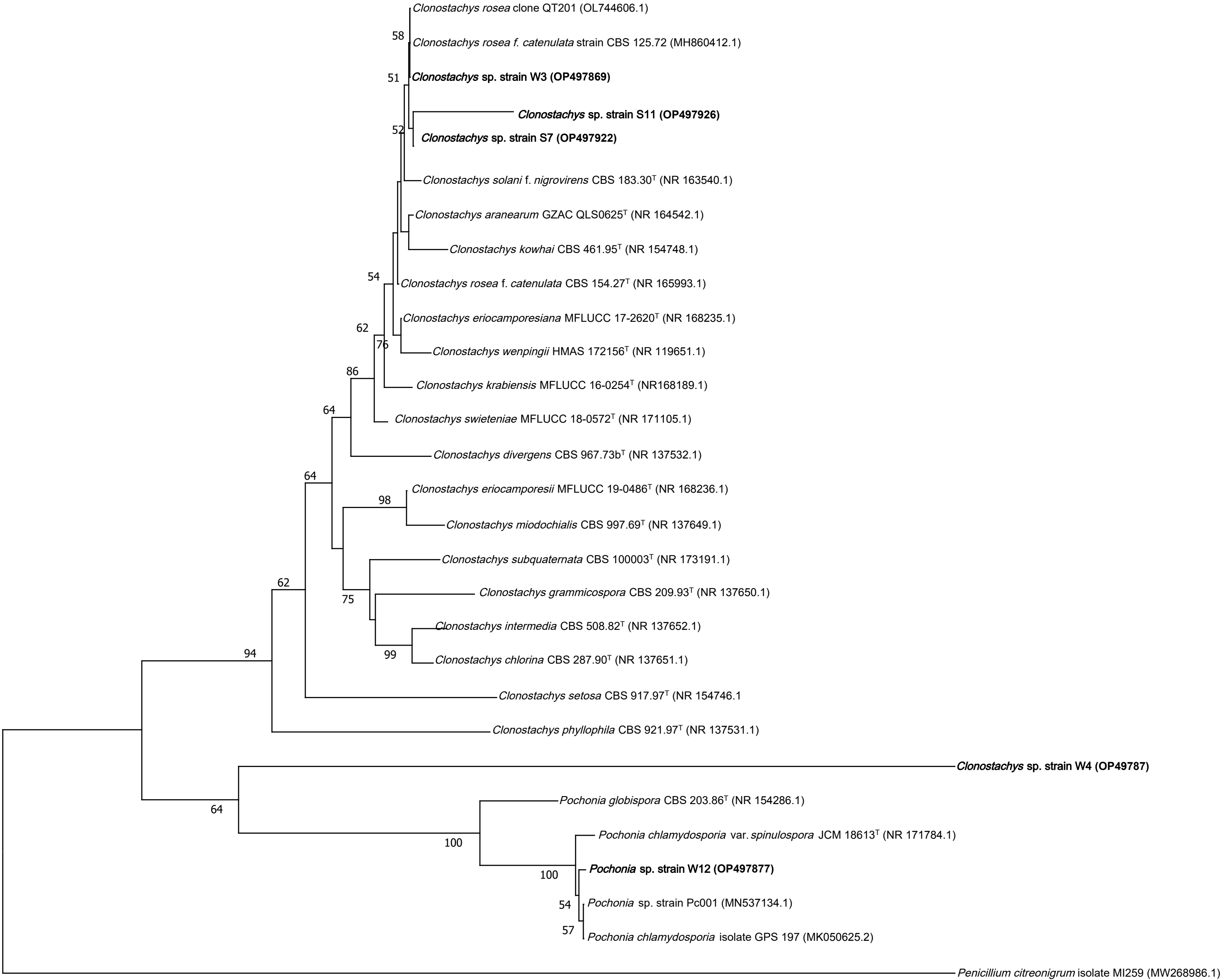
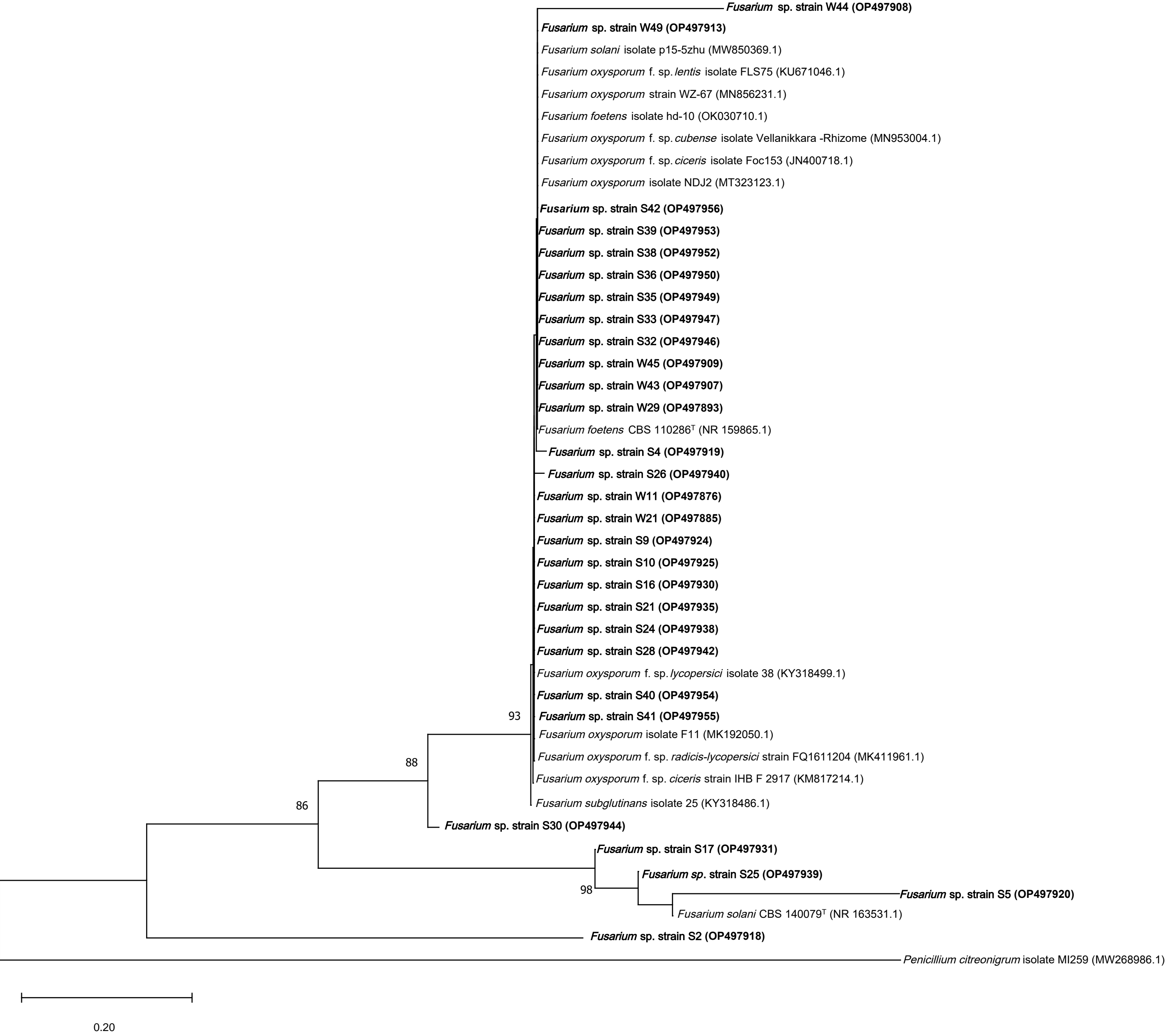


Supplementary Figure __: Neighbour-joining phylogenetic tree based on the internal transcribed spacer (ITS) gene of fungal strains in this study and their closest relatives. Bootstrap values (expressed as percentages of 1000 replications) are shown at the nodes (only values > 50% are shown).

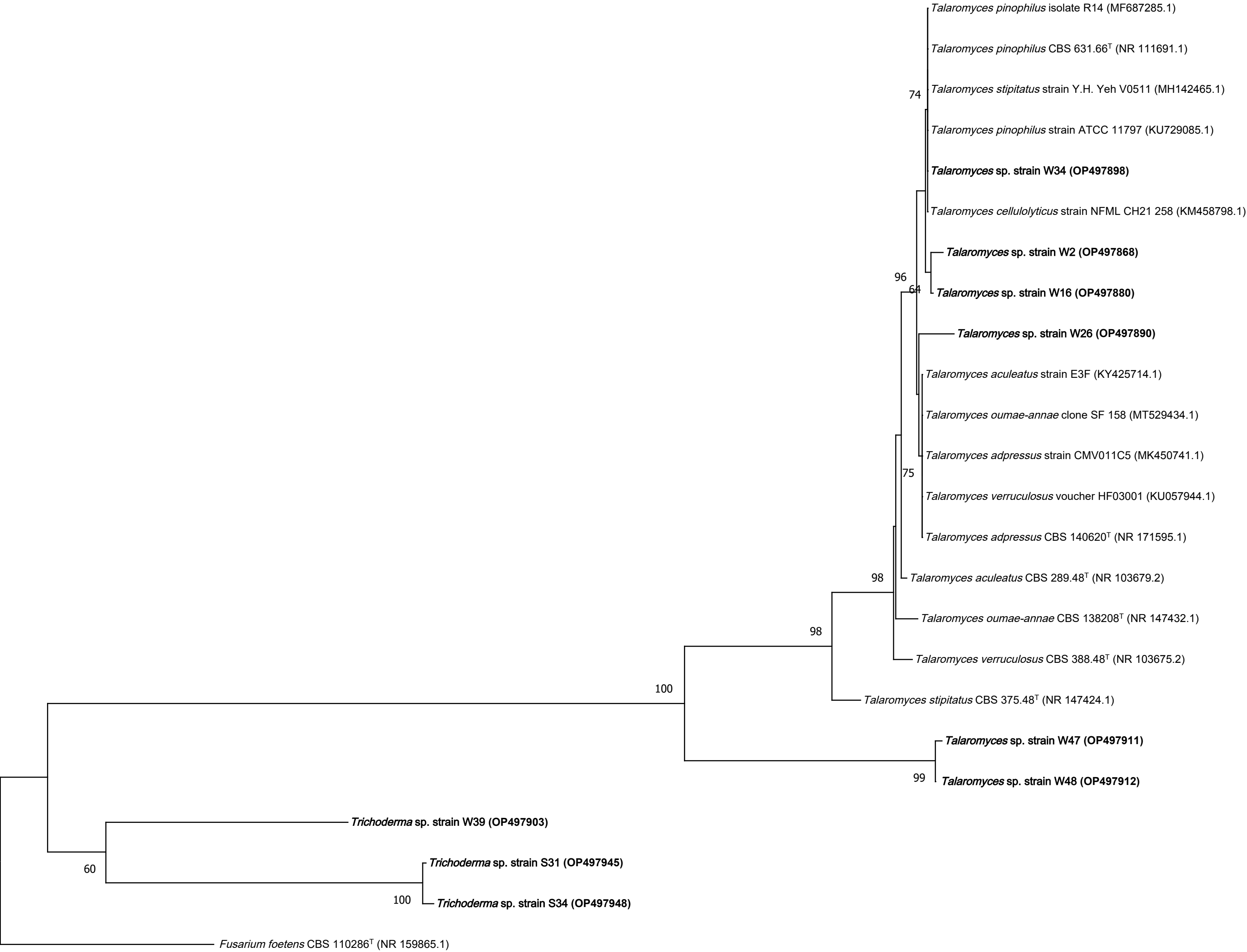




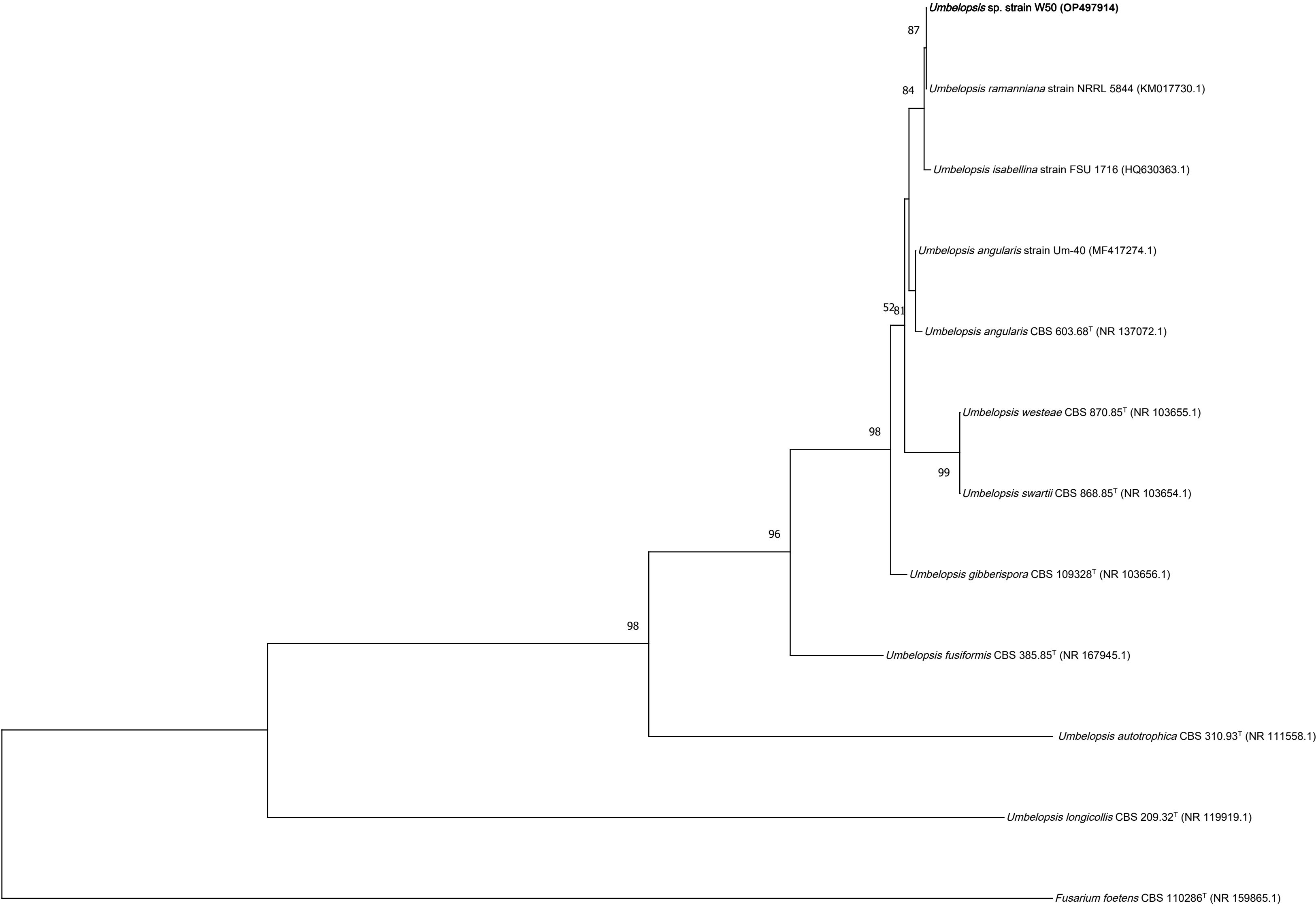




0.050

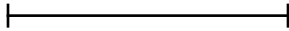
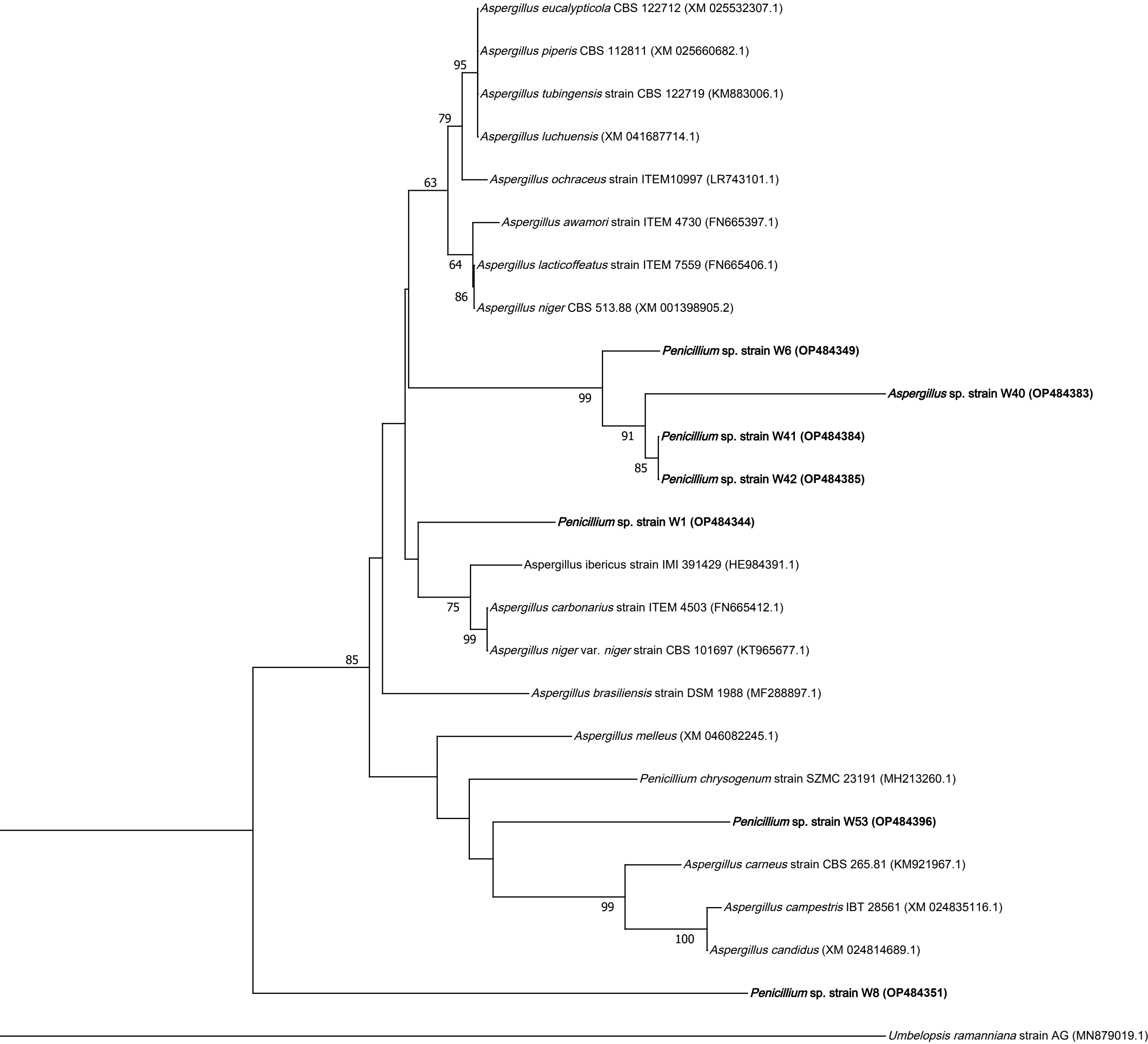


0.050

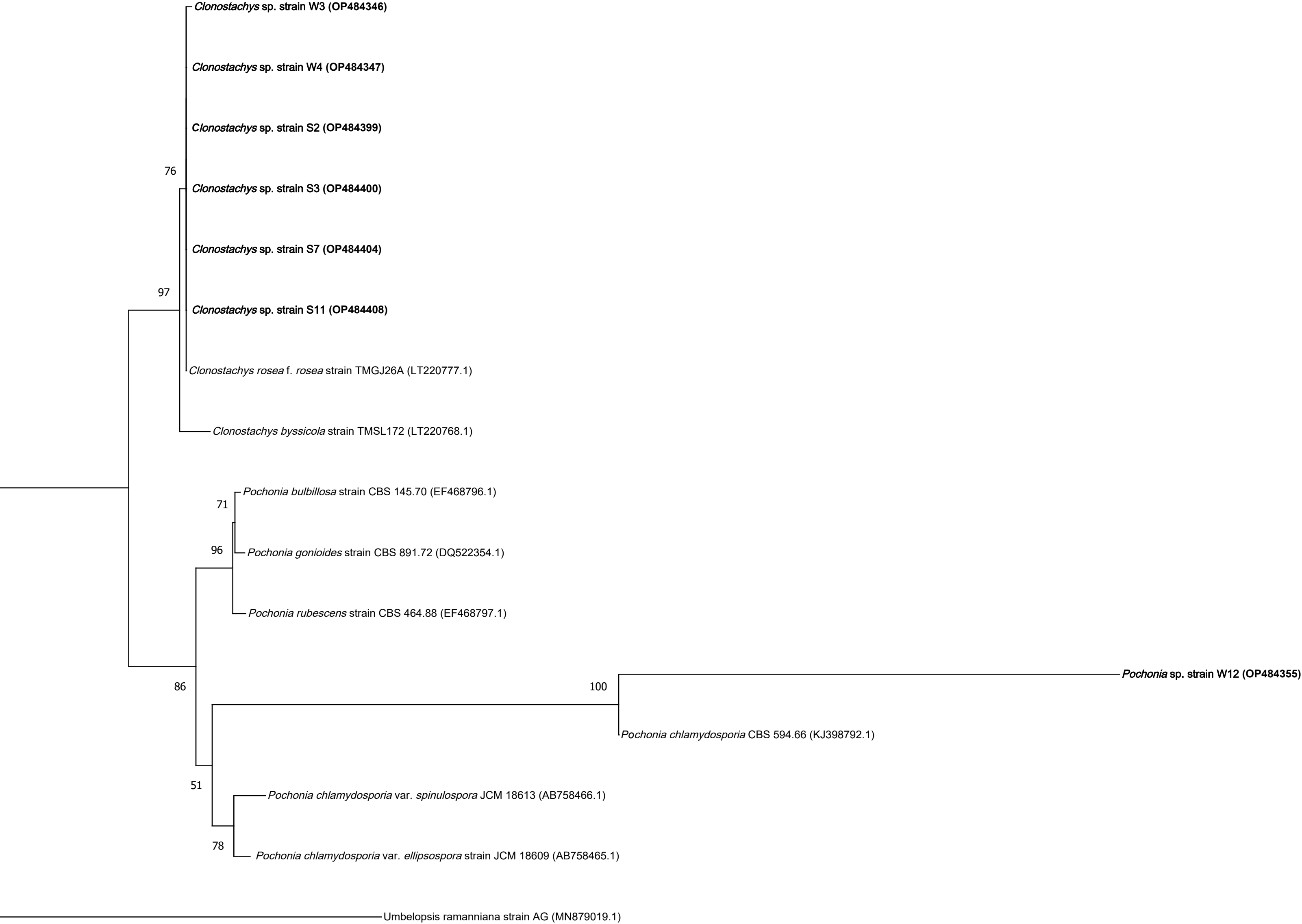


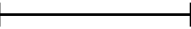
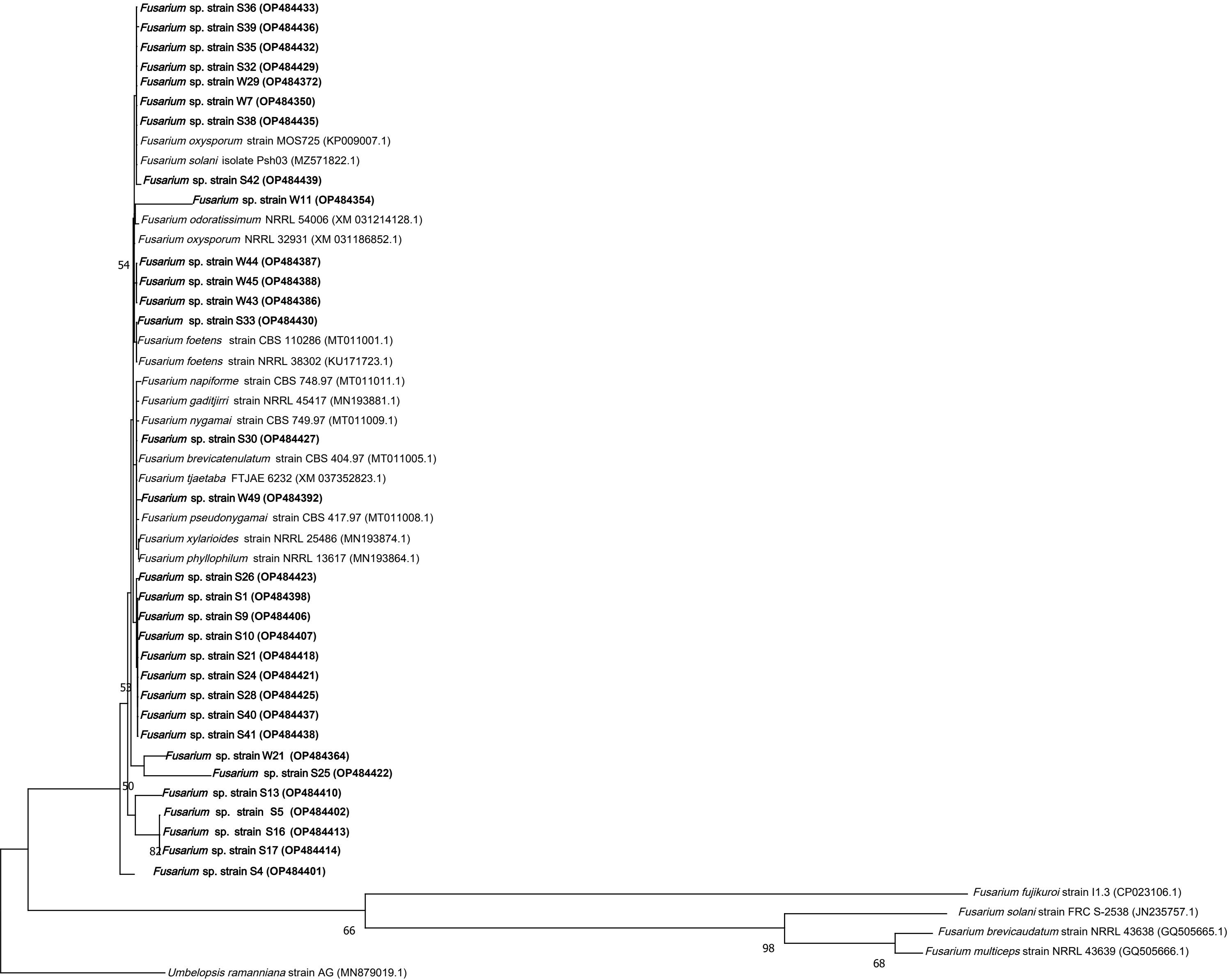
0.10

Supplementary Figure __: Neighbour-joining phylogenetic tree based on the translation elongation factor I-alpha (TEF1) gene of fungal strains in this study and their closest relatives. Bootstrap values (expressed as percentages of 1000 replications) are shown at the nodes (only values > 50% are shown).

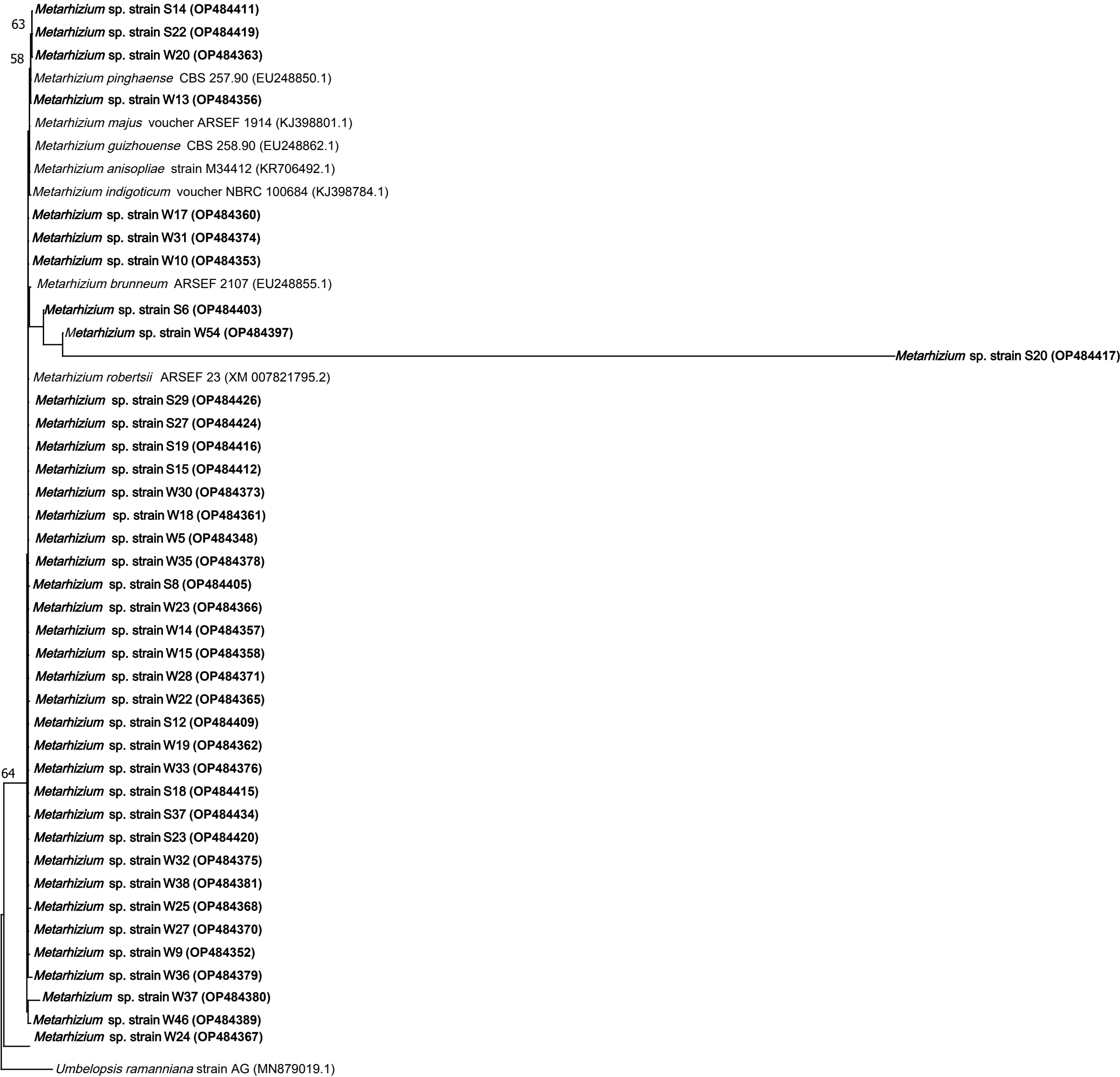


0.020





0.02

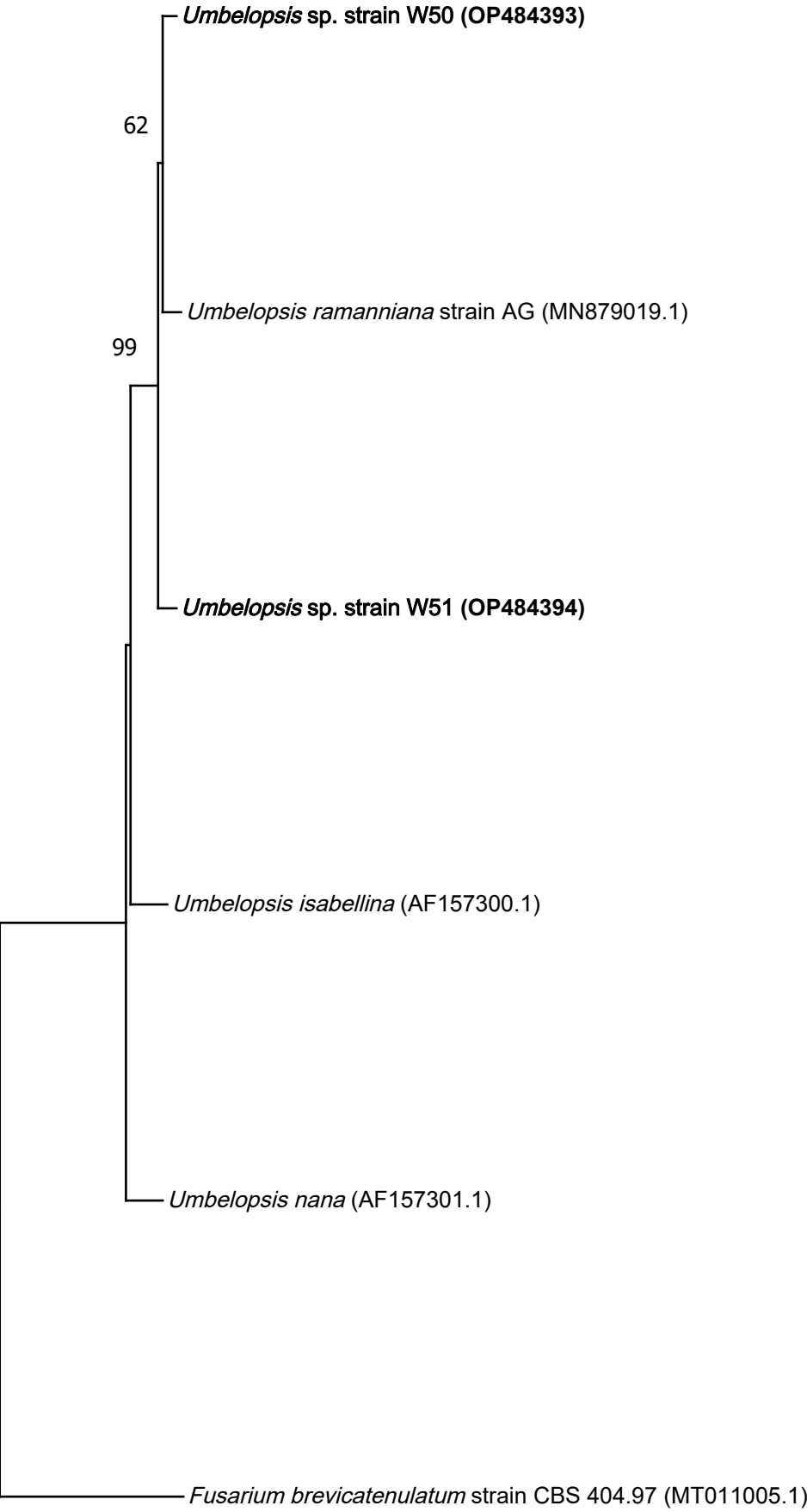


0.20



H

0.020



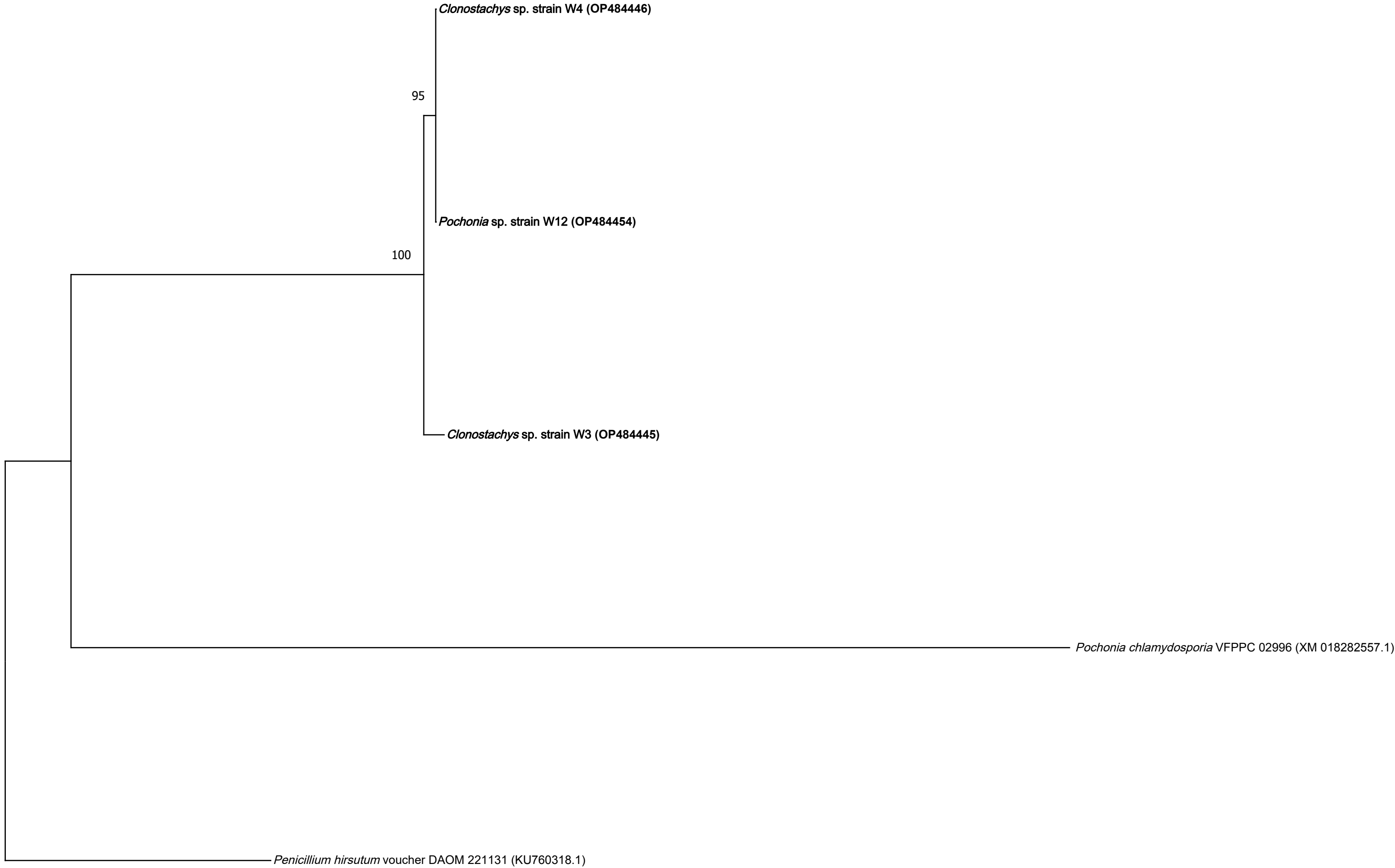
H

0.020

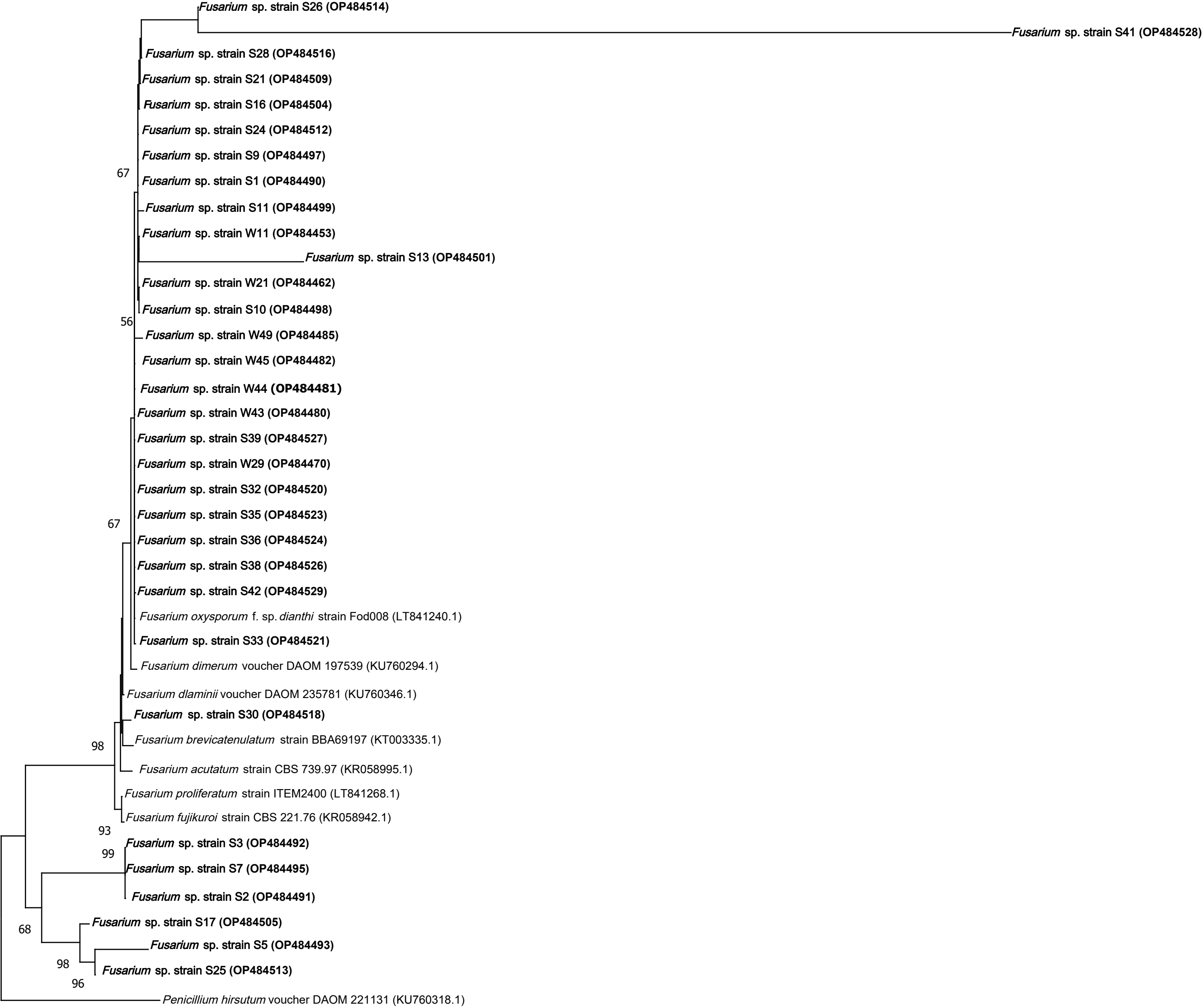
Supplementary Figure __: Neighbour-joining phylogenetic tree based on the DNA topoisomerase I (TOP1) gene of fungal strains in this study and their closest relatives. Bootstrap values (expressed as percentages of 1000 replications) are shown at the nodes (only values > 50% are shown).



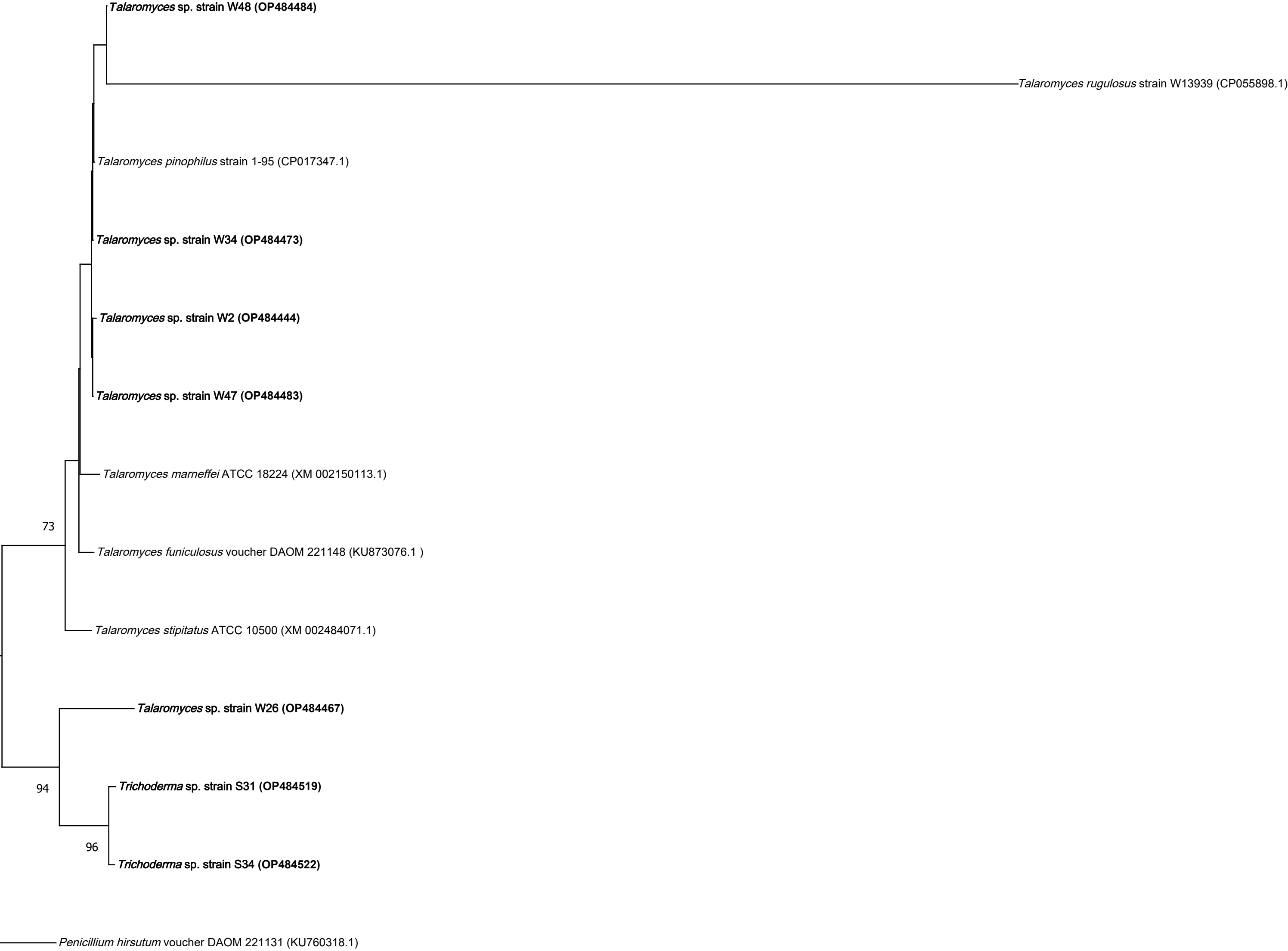
0.20



0.050

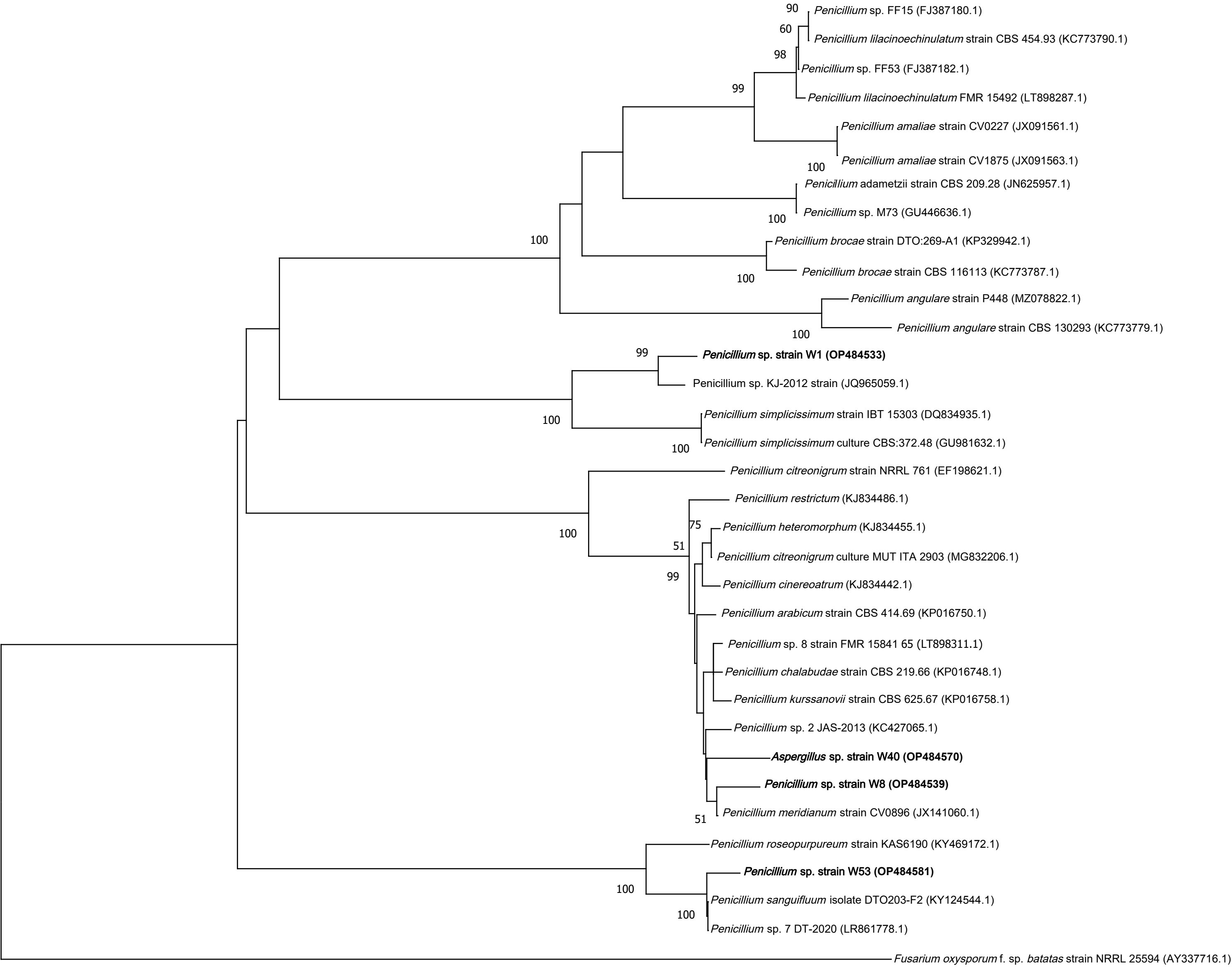


0.20

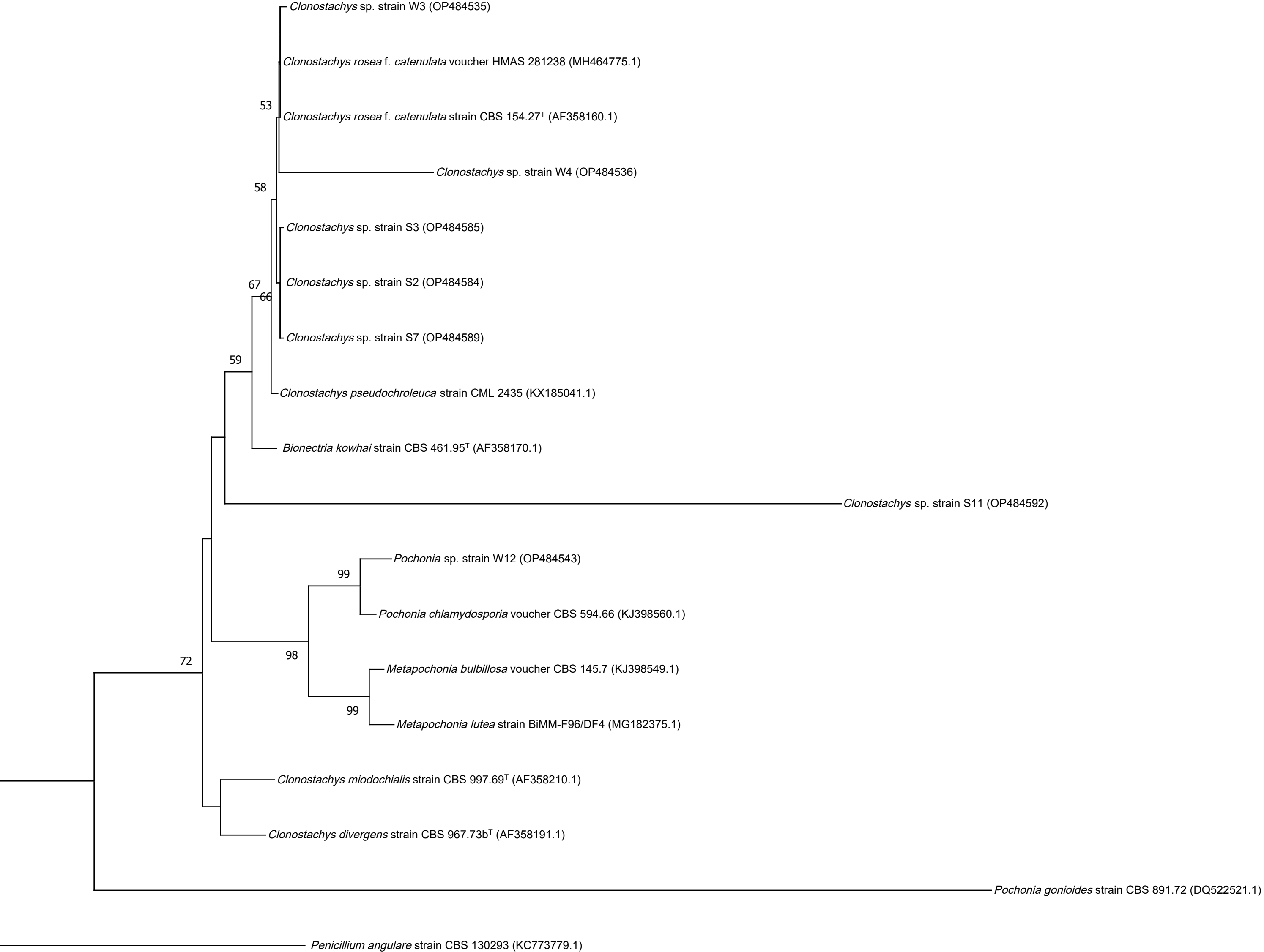


0.50

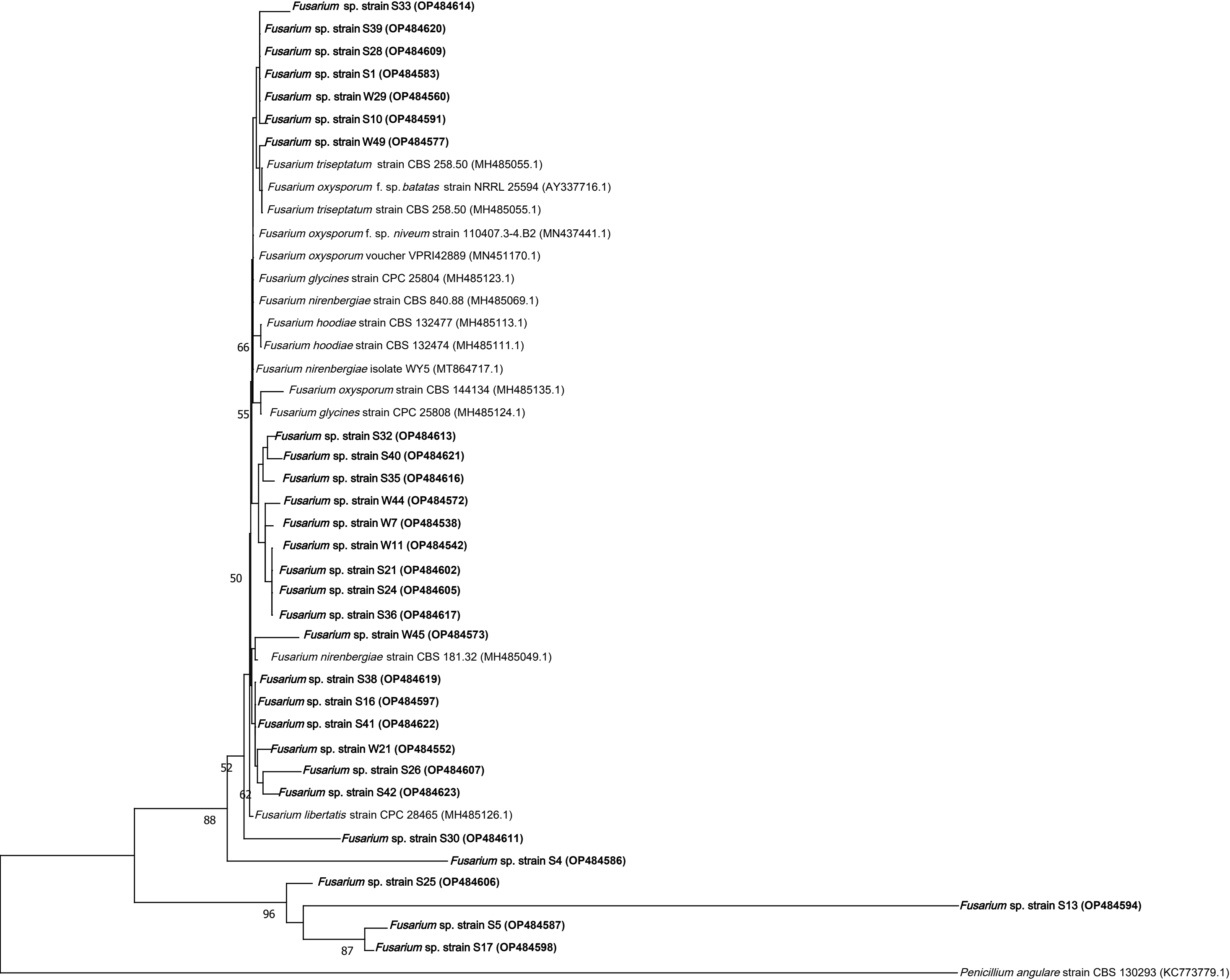
Supplementary Figure __: Neighbour-joining phylogenetic tree based on the β -tubulin II (BTUB) gene of fungal strains in this study and their closest relatives. Bootstrap values (expressed as percentages of 1000 replications) are shown at the nodes (only values > 50% are shown).

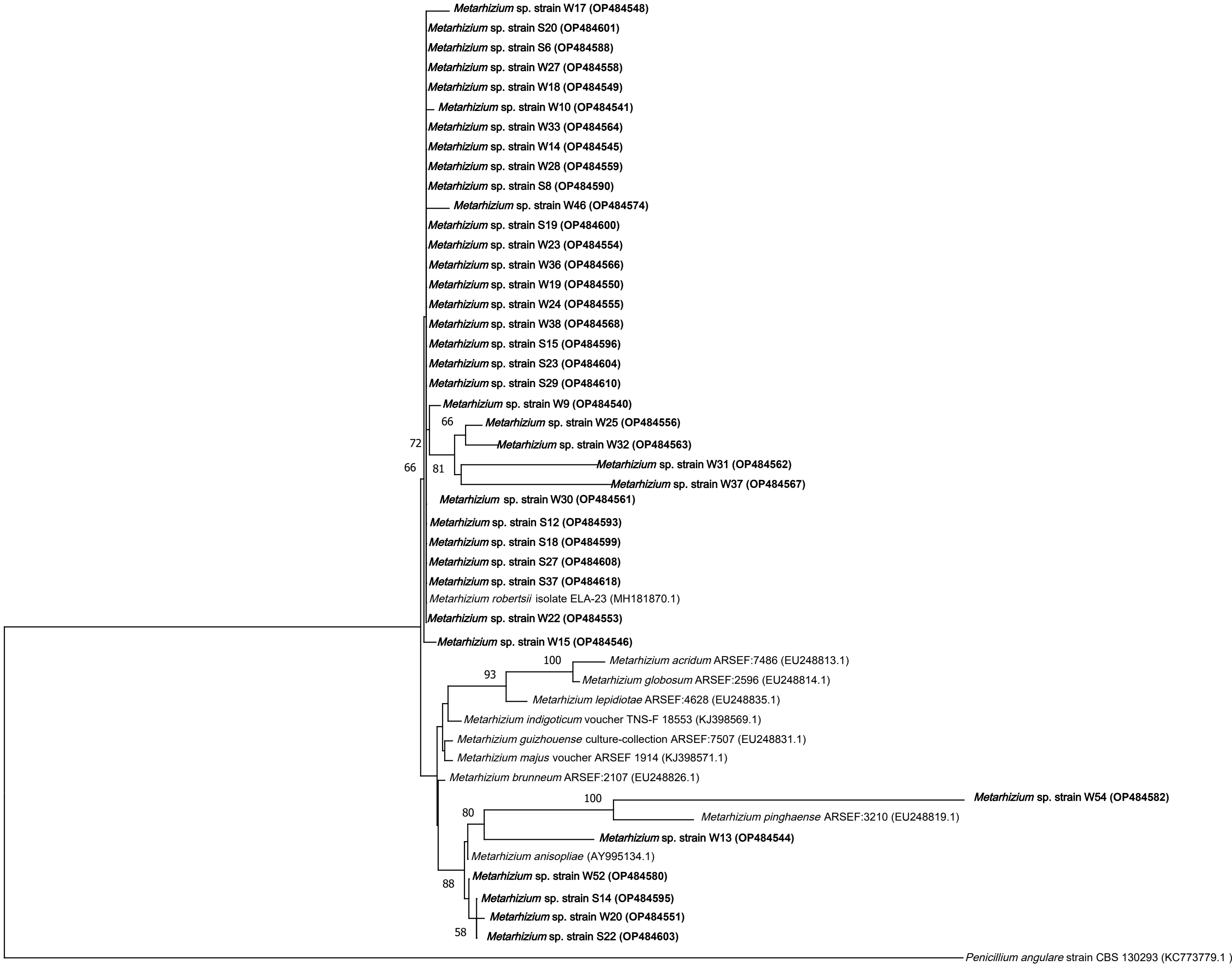


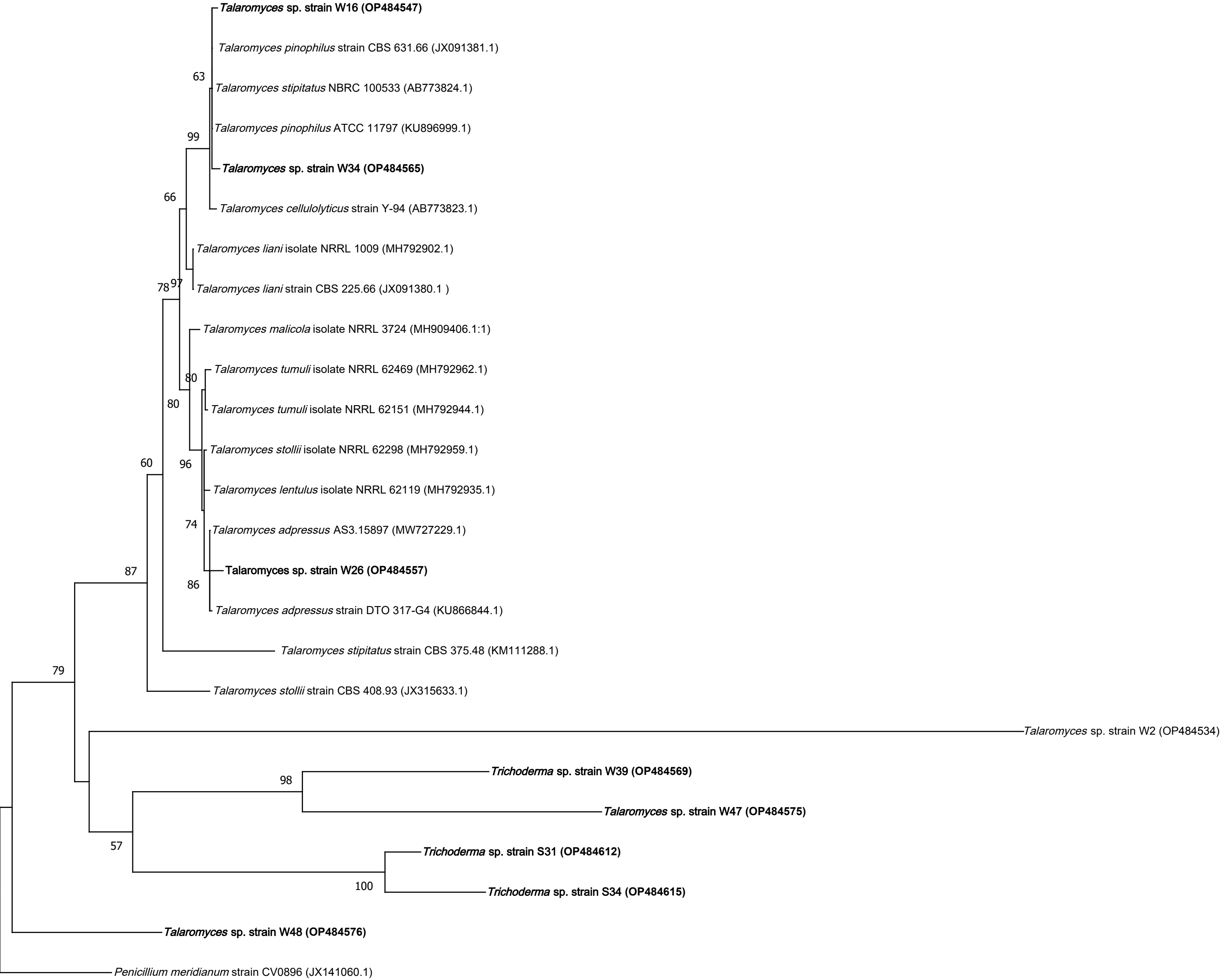
0.050



0.20







0.20