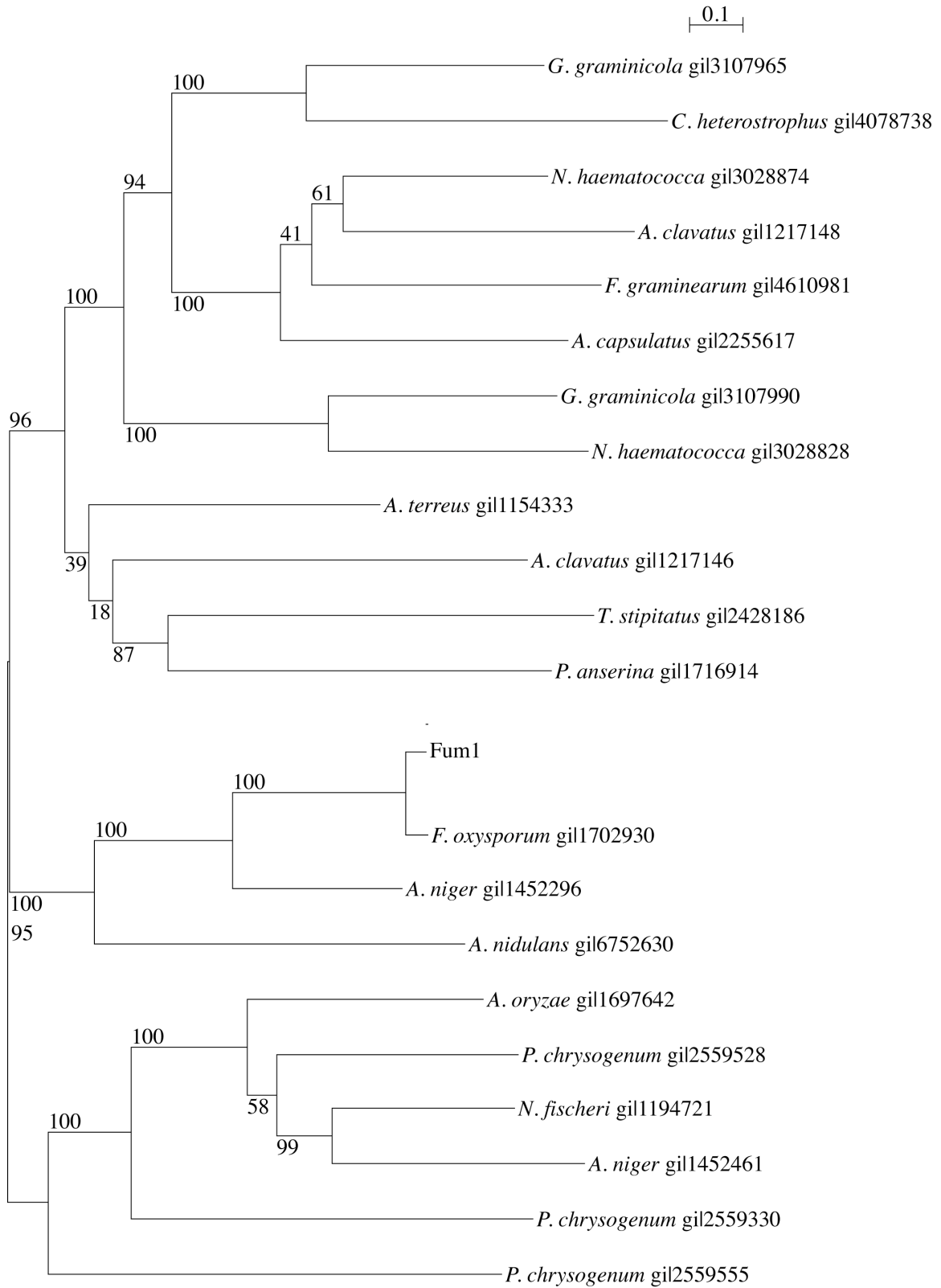


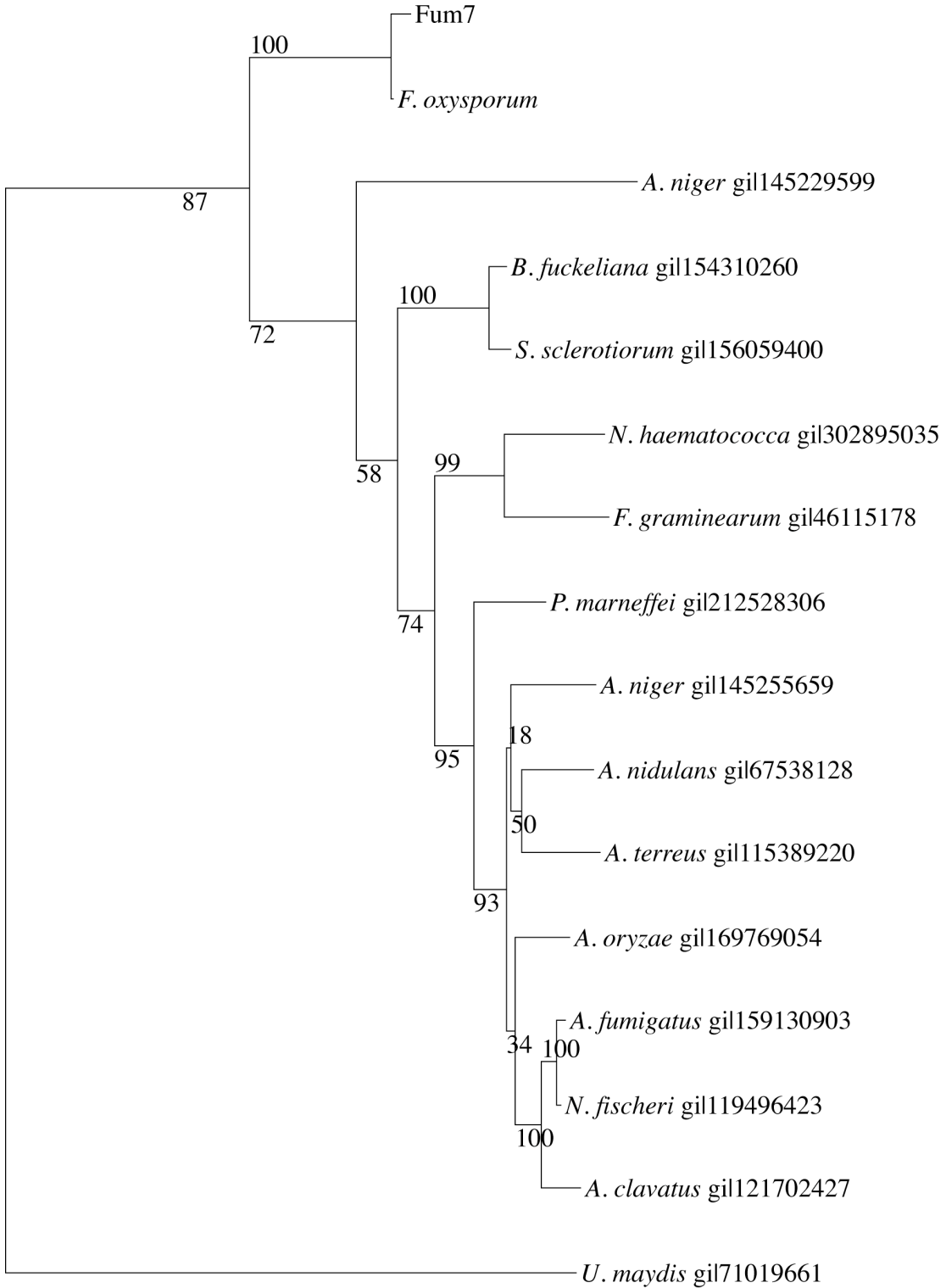
Supplementary 1. Maximum likelihood trees for the common fumonisin proteins between *F. verticillioides* and *A. niger* and their homologs. The species name and the NCBI ID are provided on each branch. Bootstrap percentages are shown for all nodes. Trees were constructed from amino acid sequences as described in Methods using PHYML after alignment with ClustalW.

FUM1



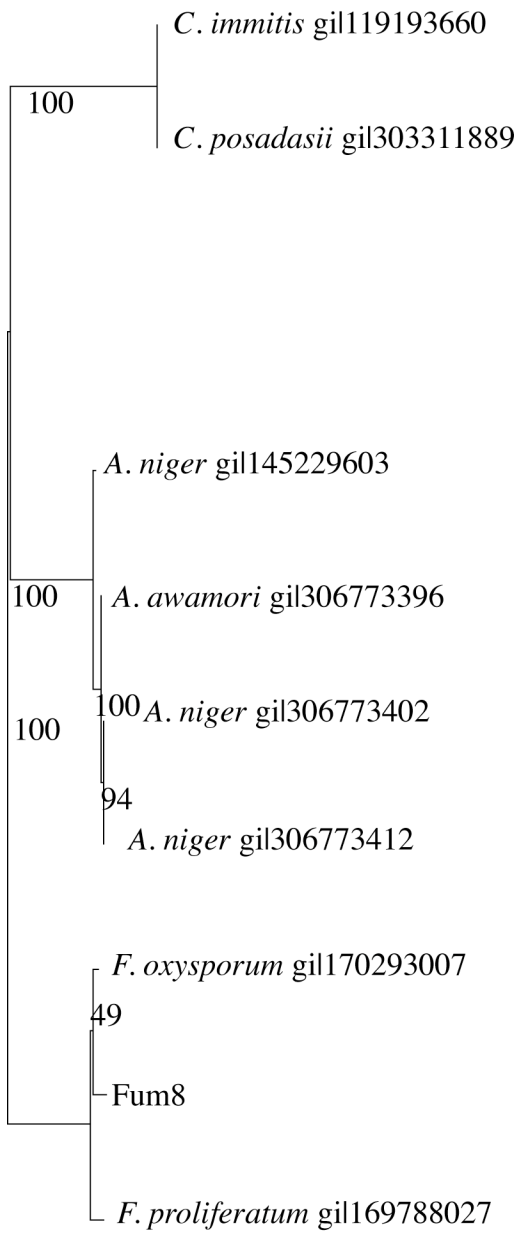
FUM7

0.5

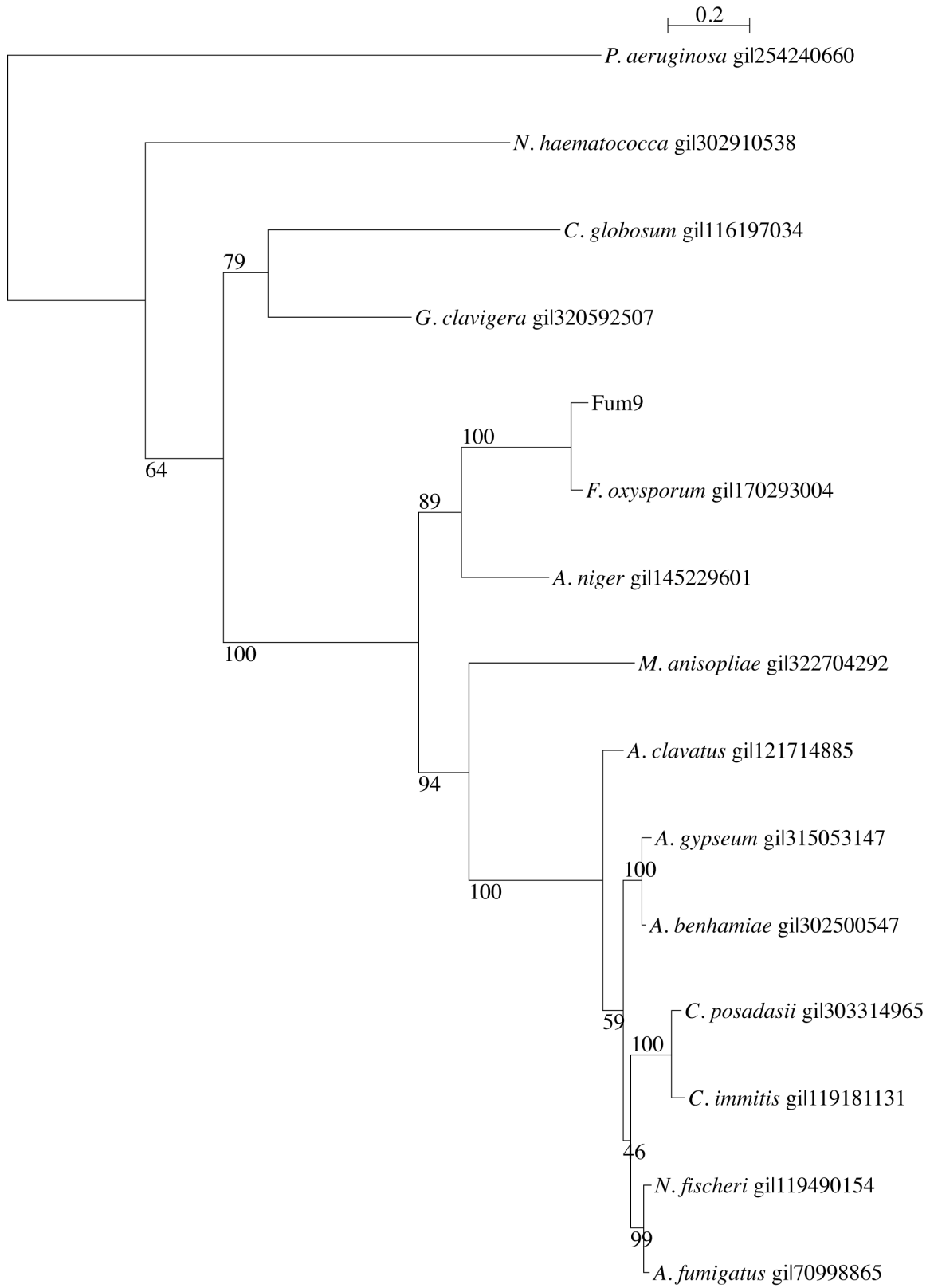


Fum8

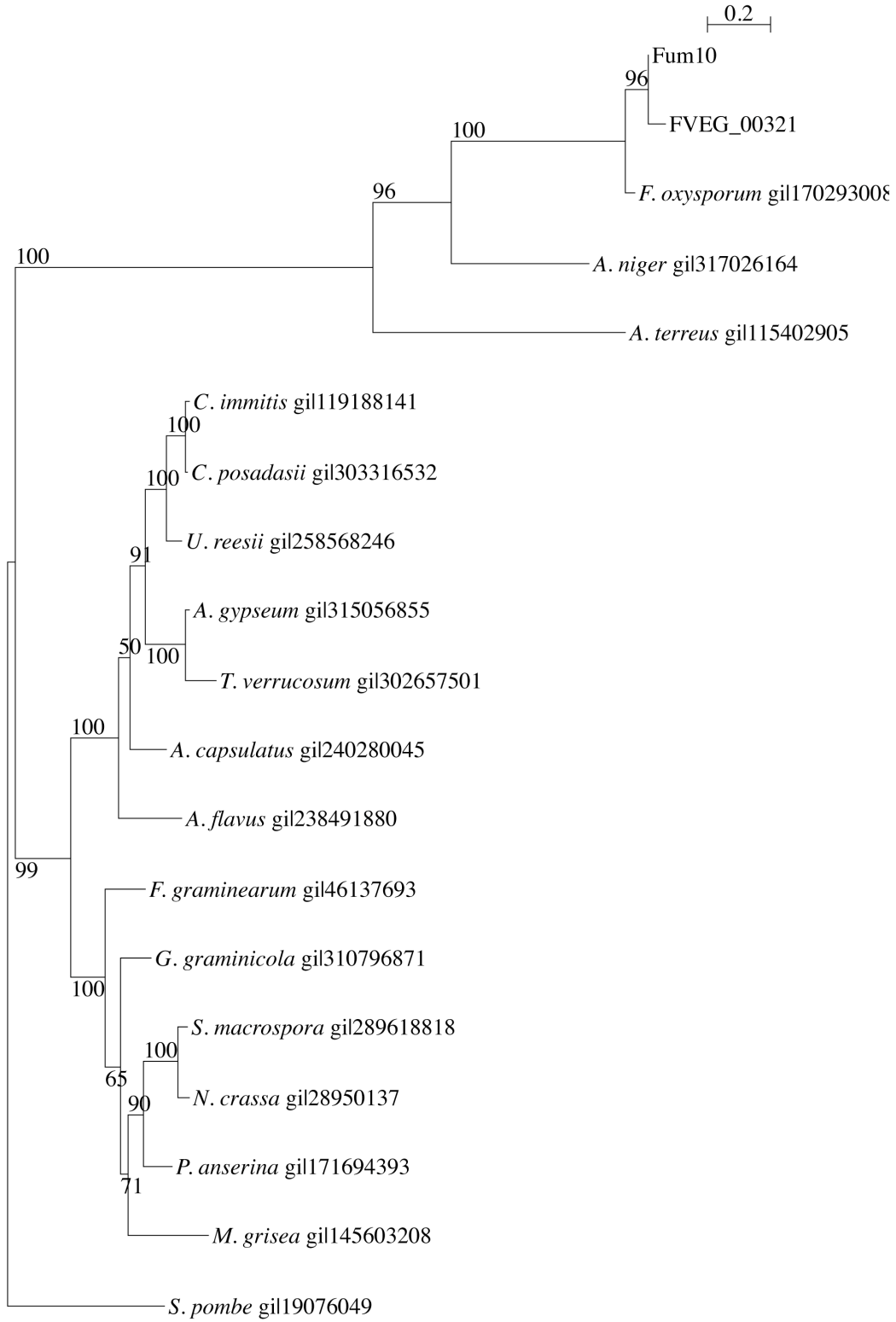
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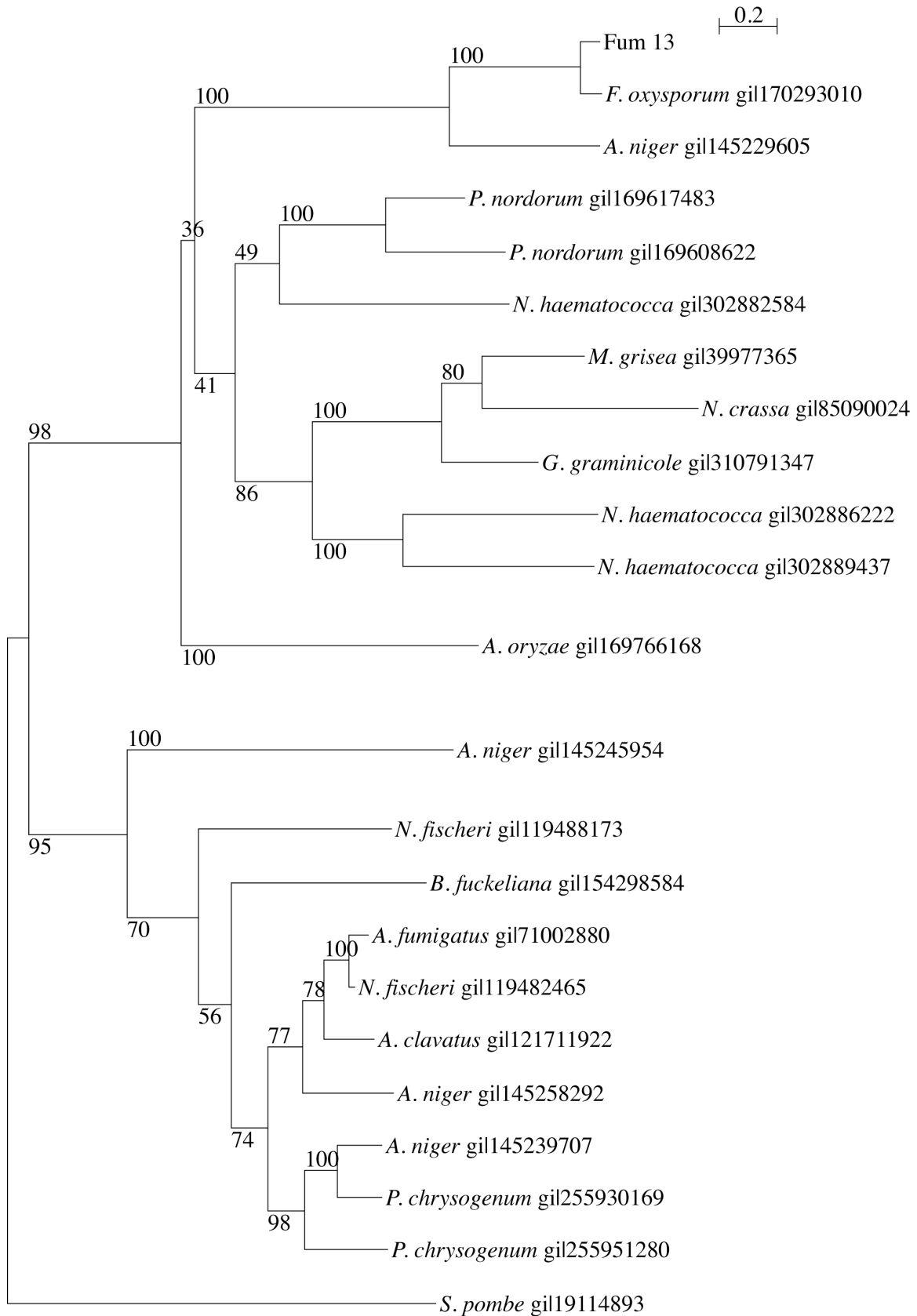
Fum9



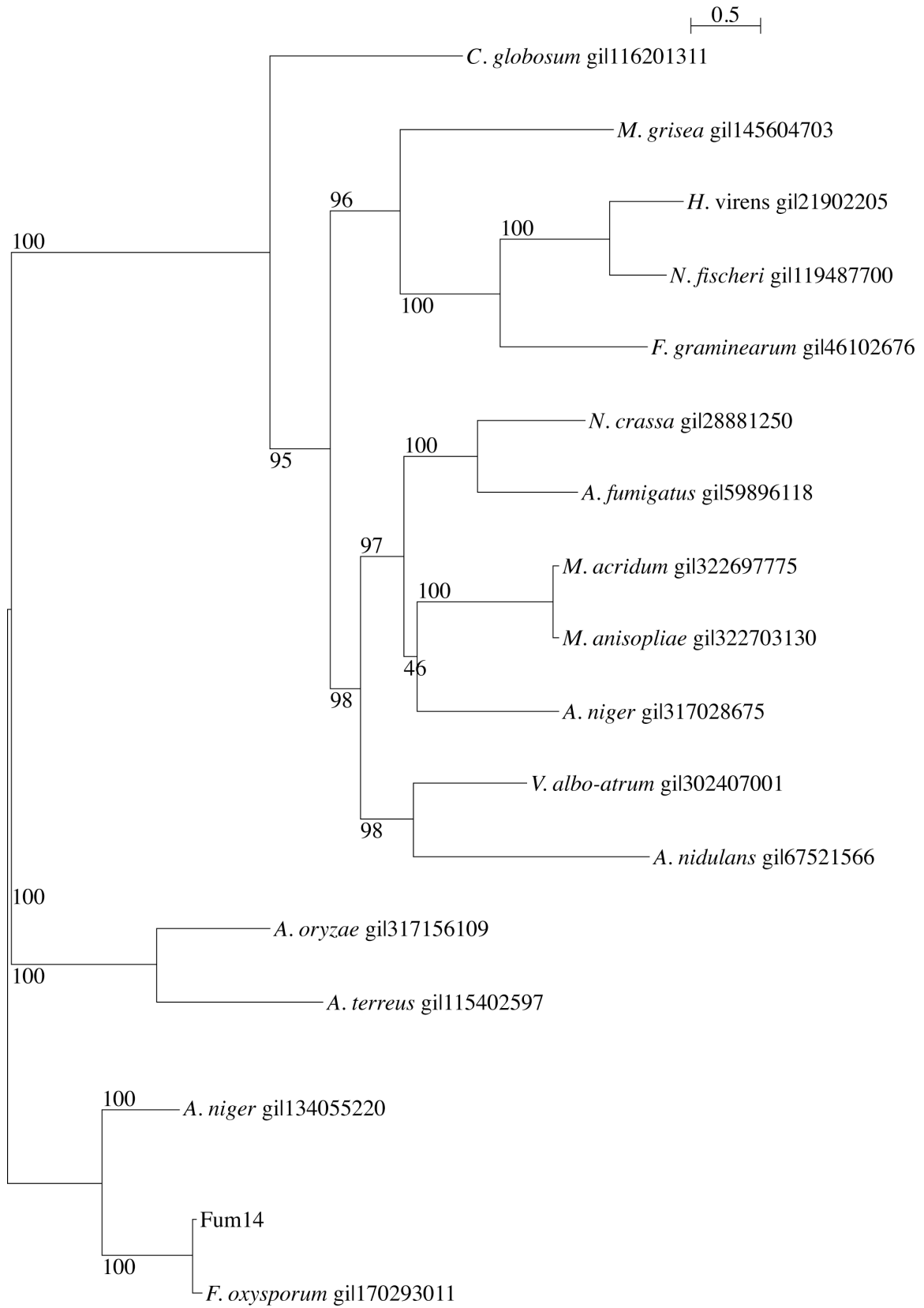
FUM10



FUM13



Fum14



Fum19

