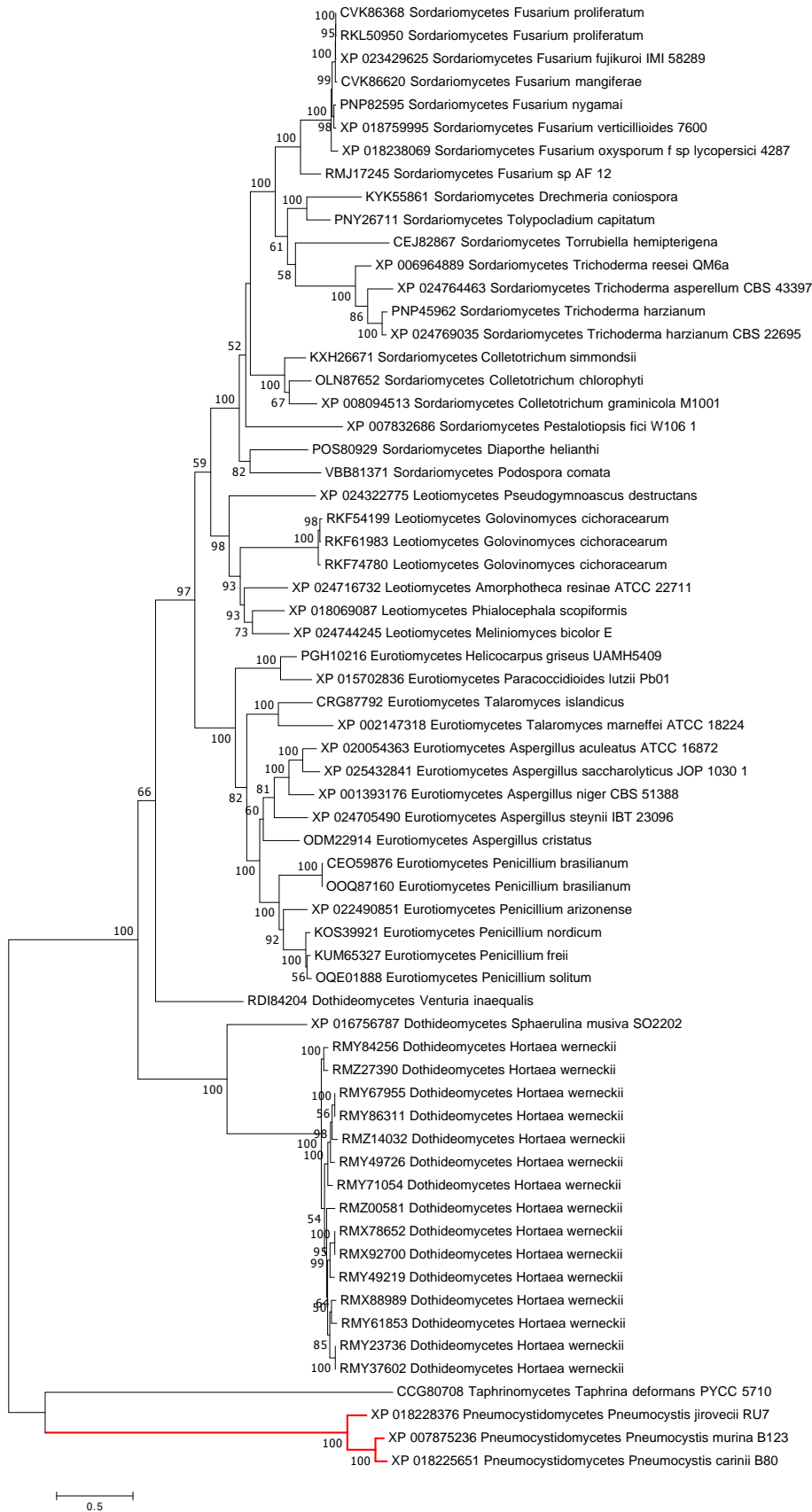
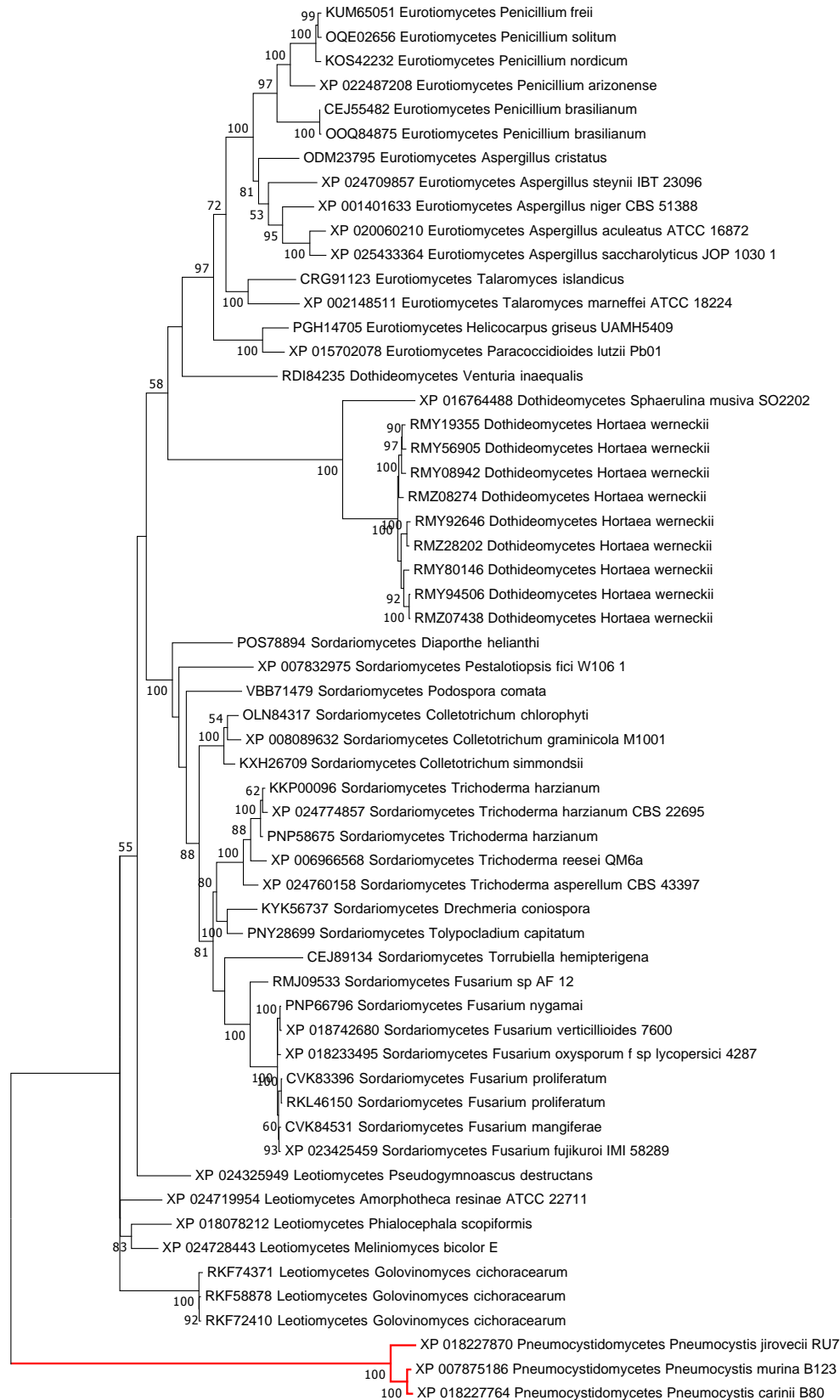


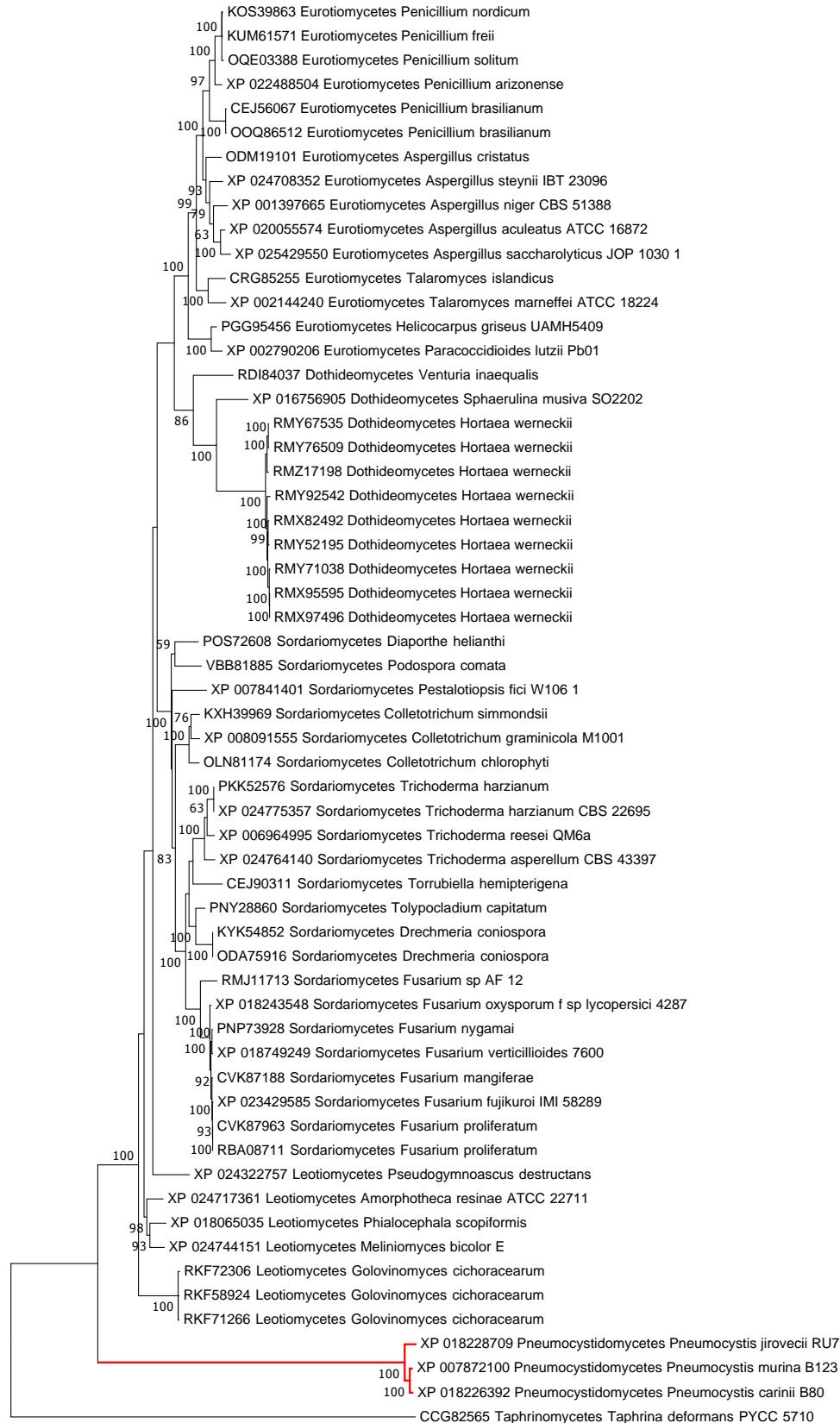
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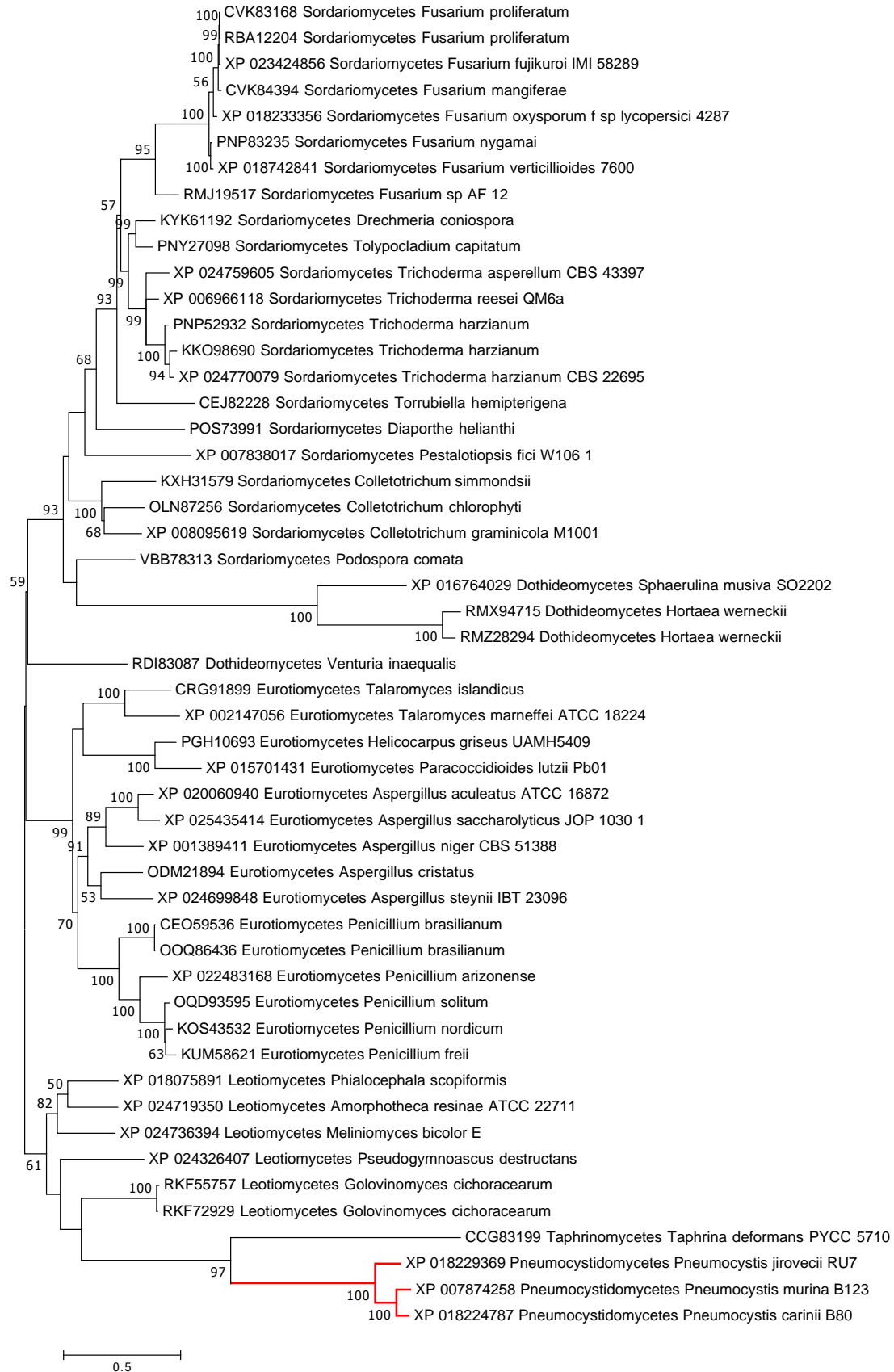
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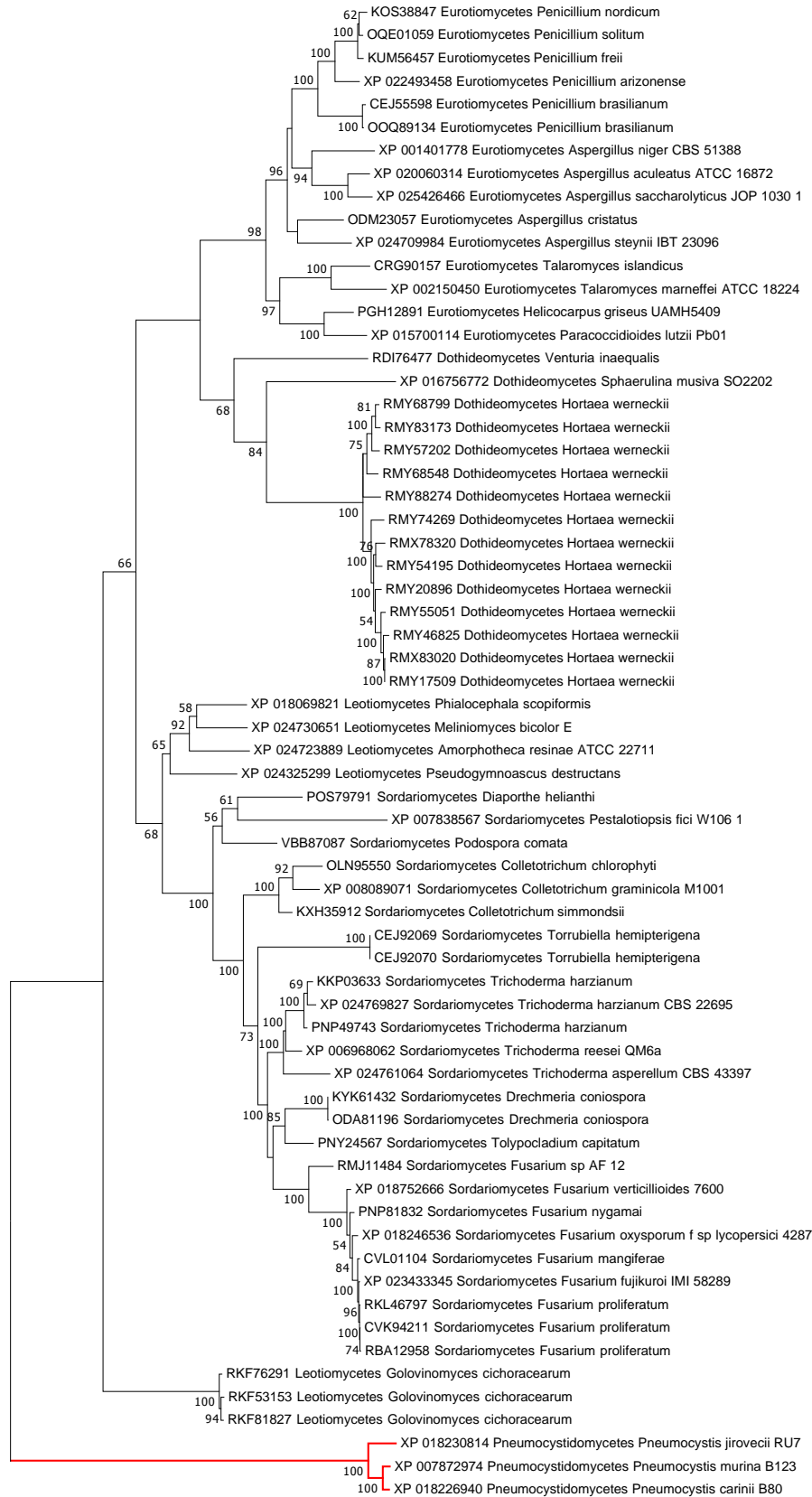
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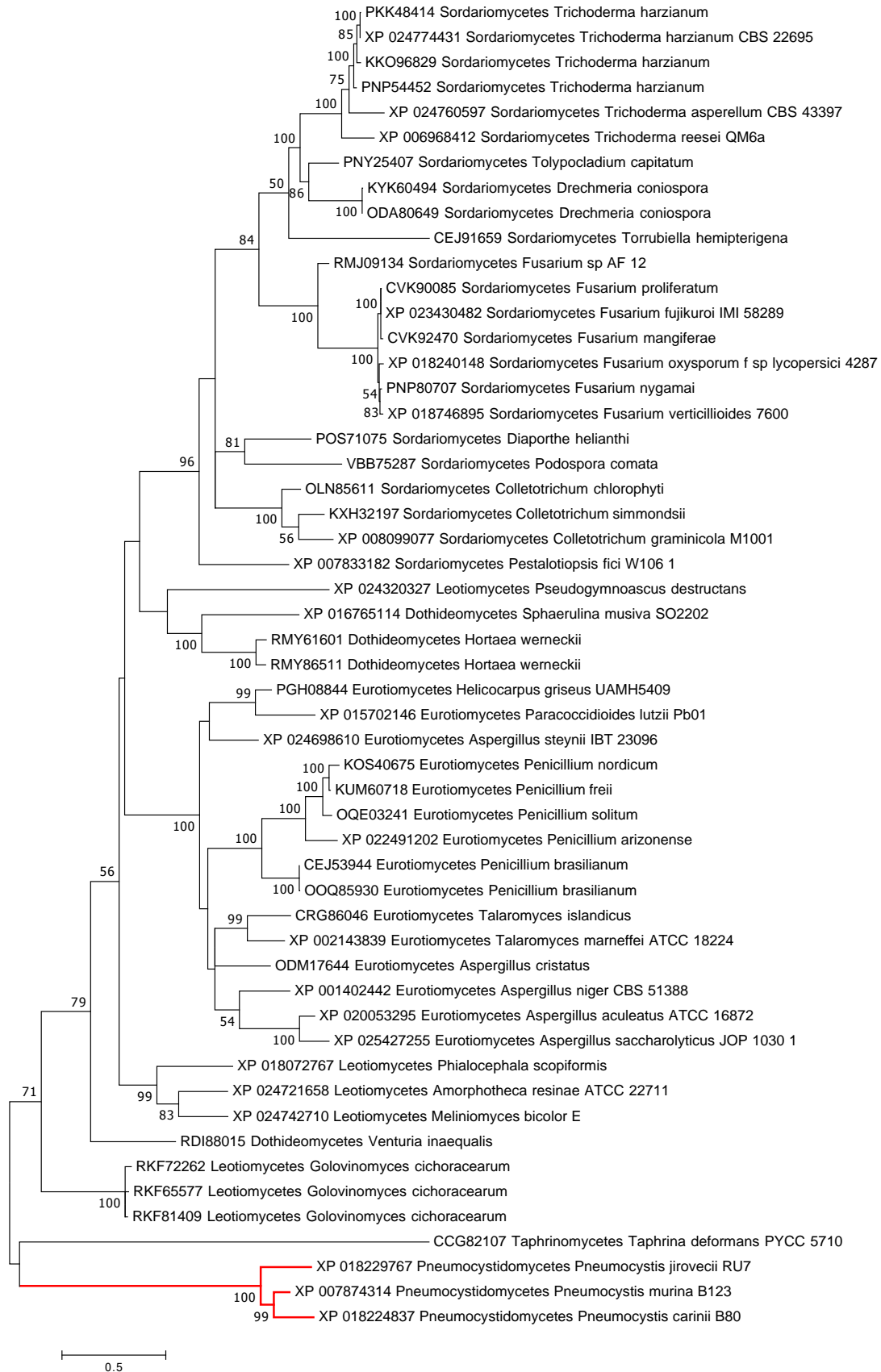


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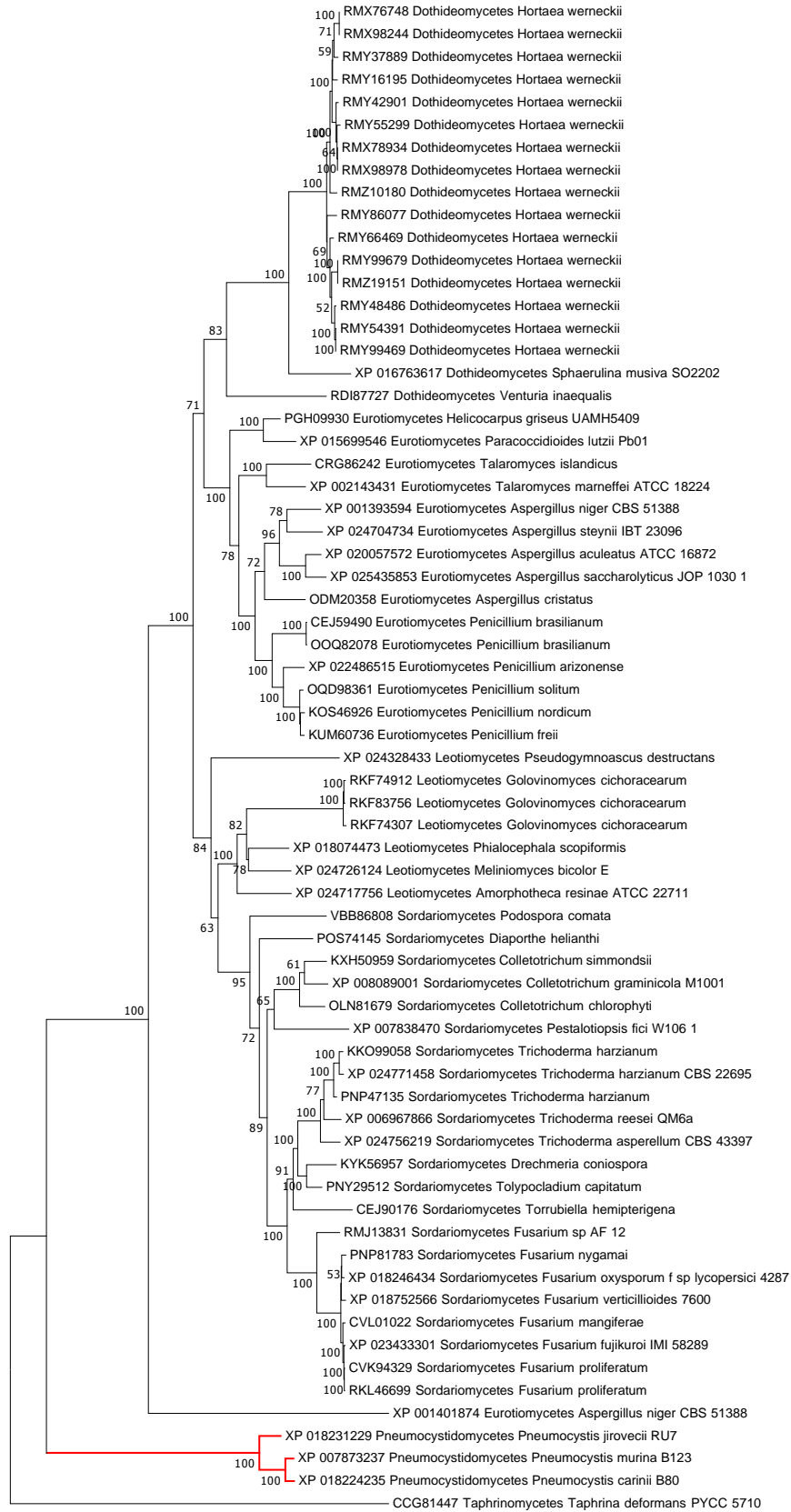


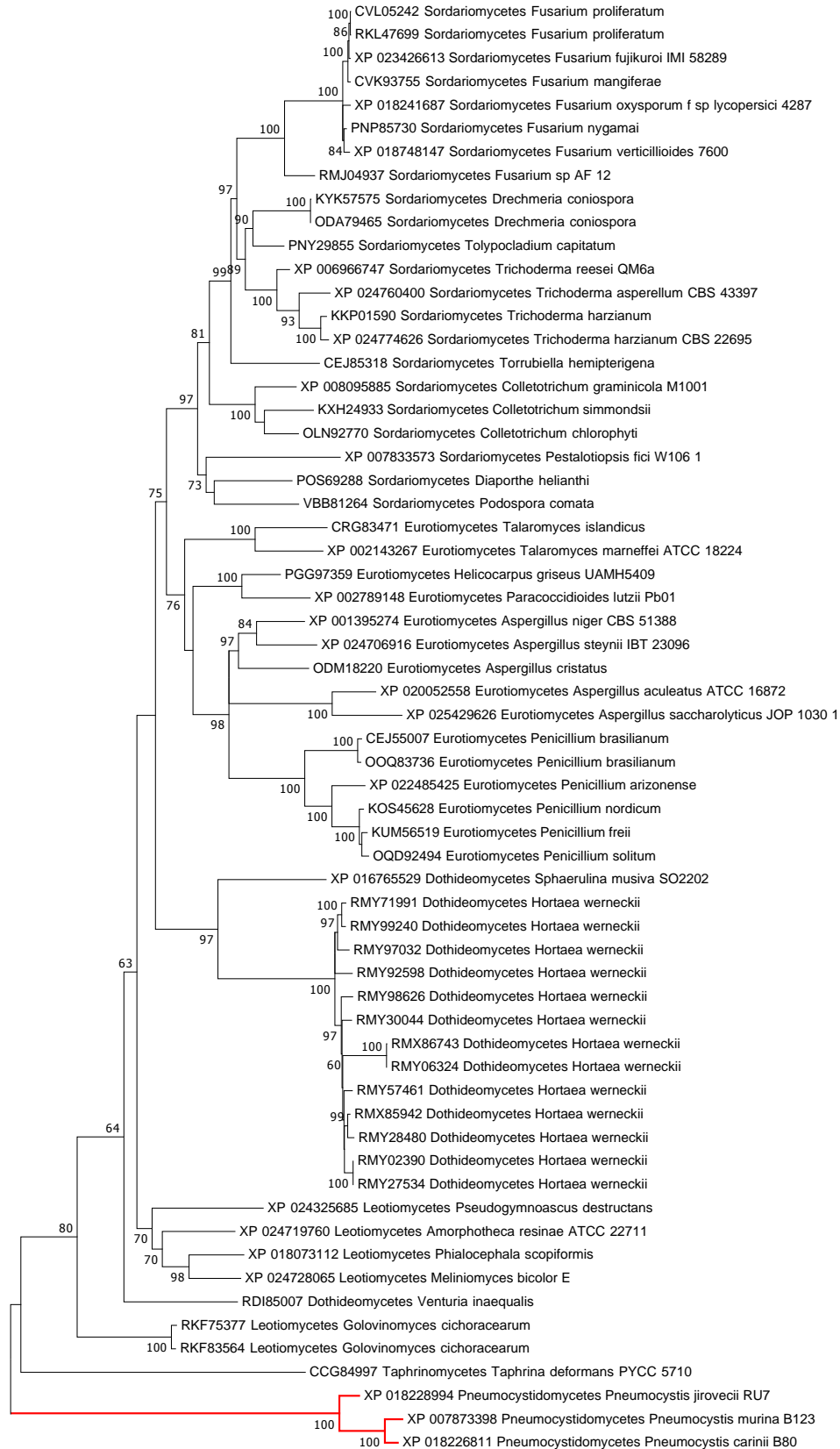
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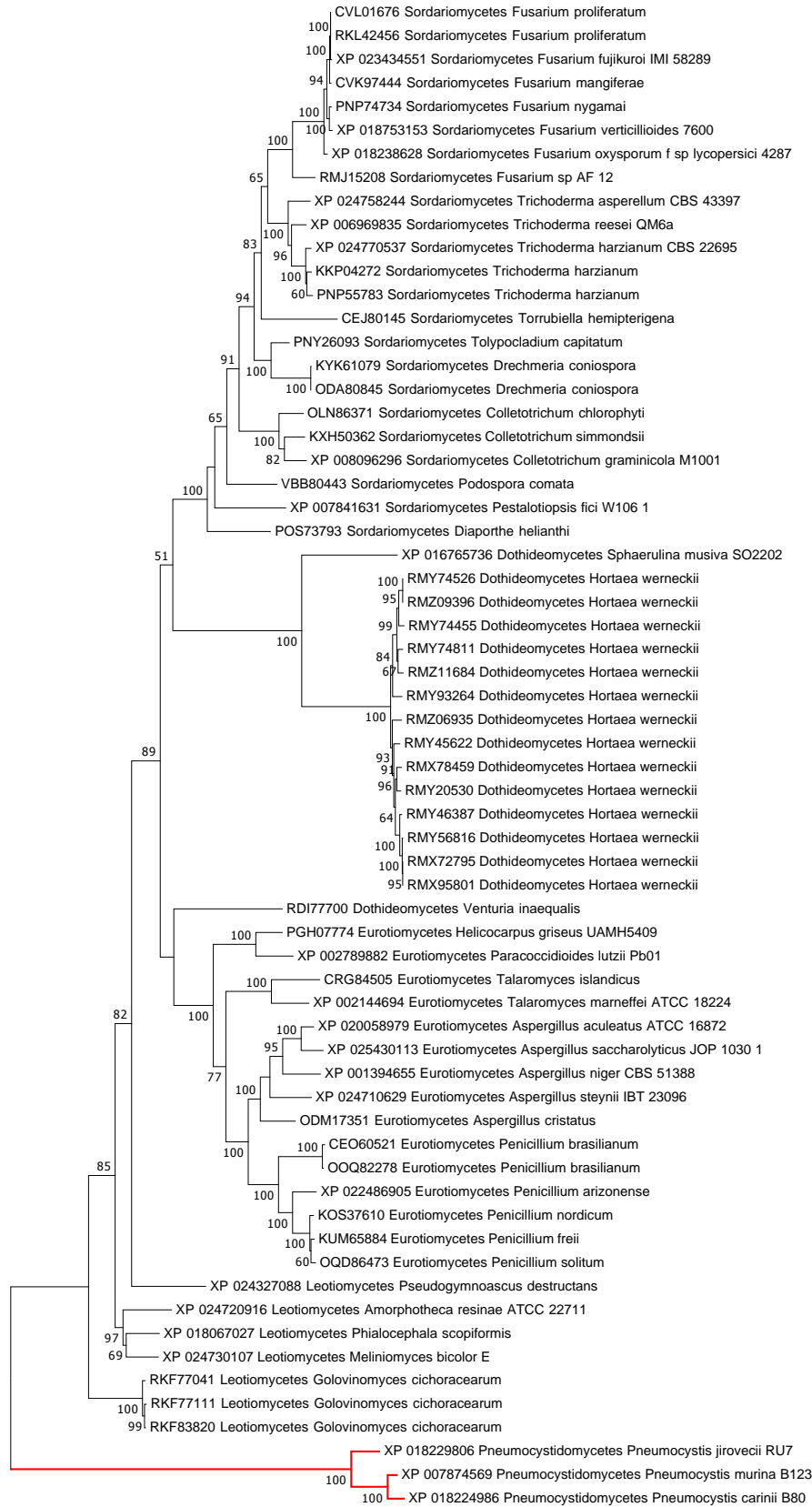
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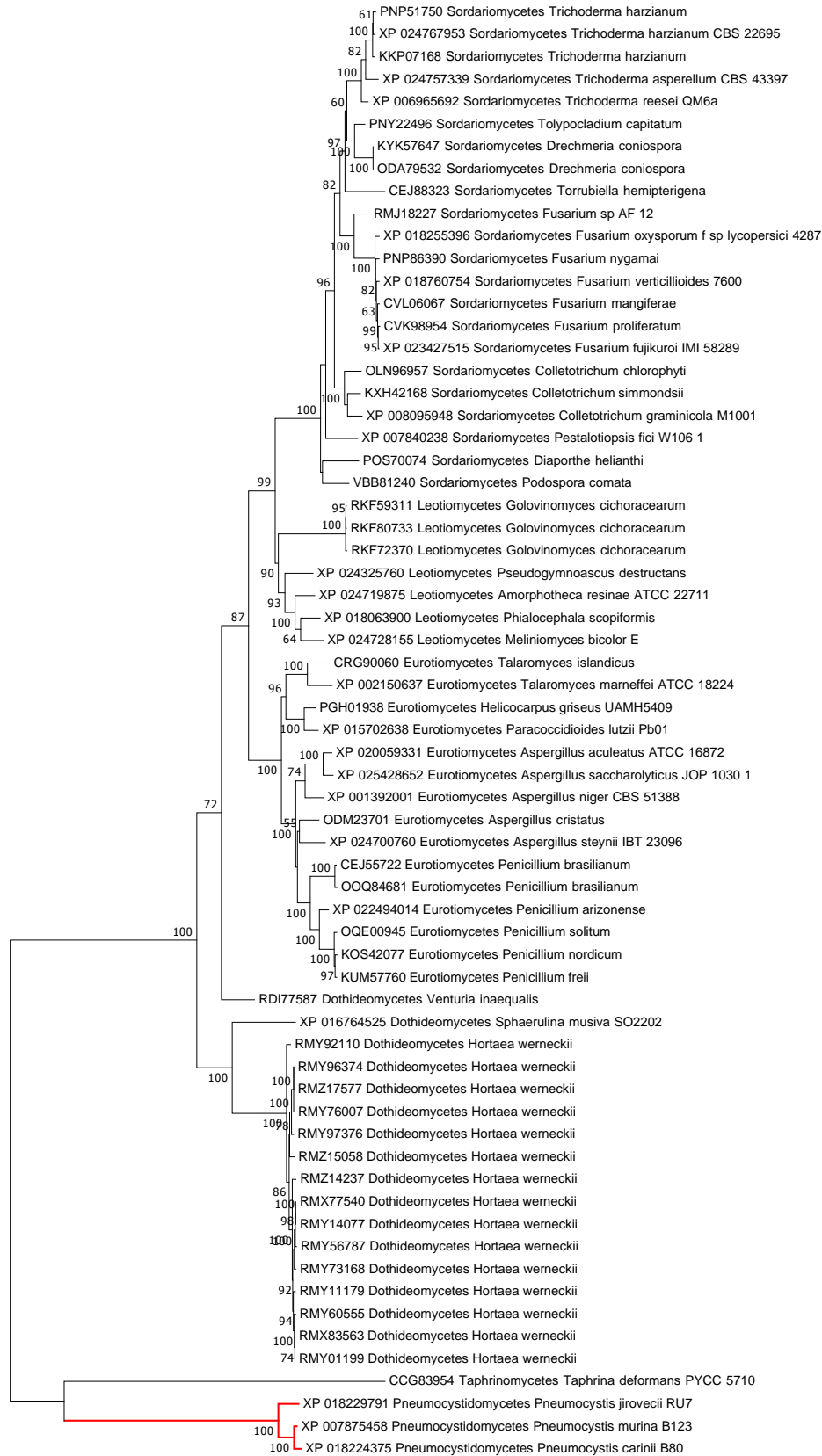
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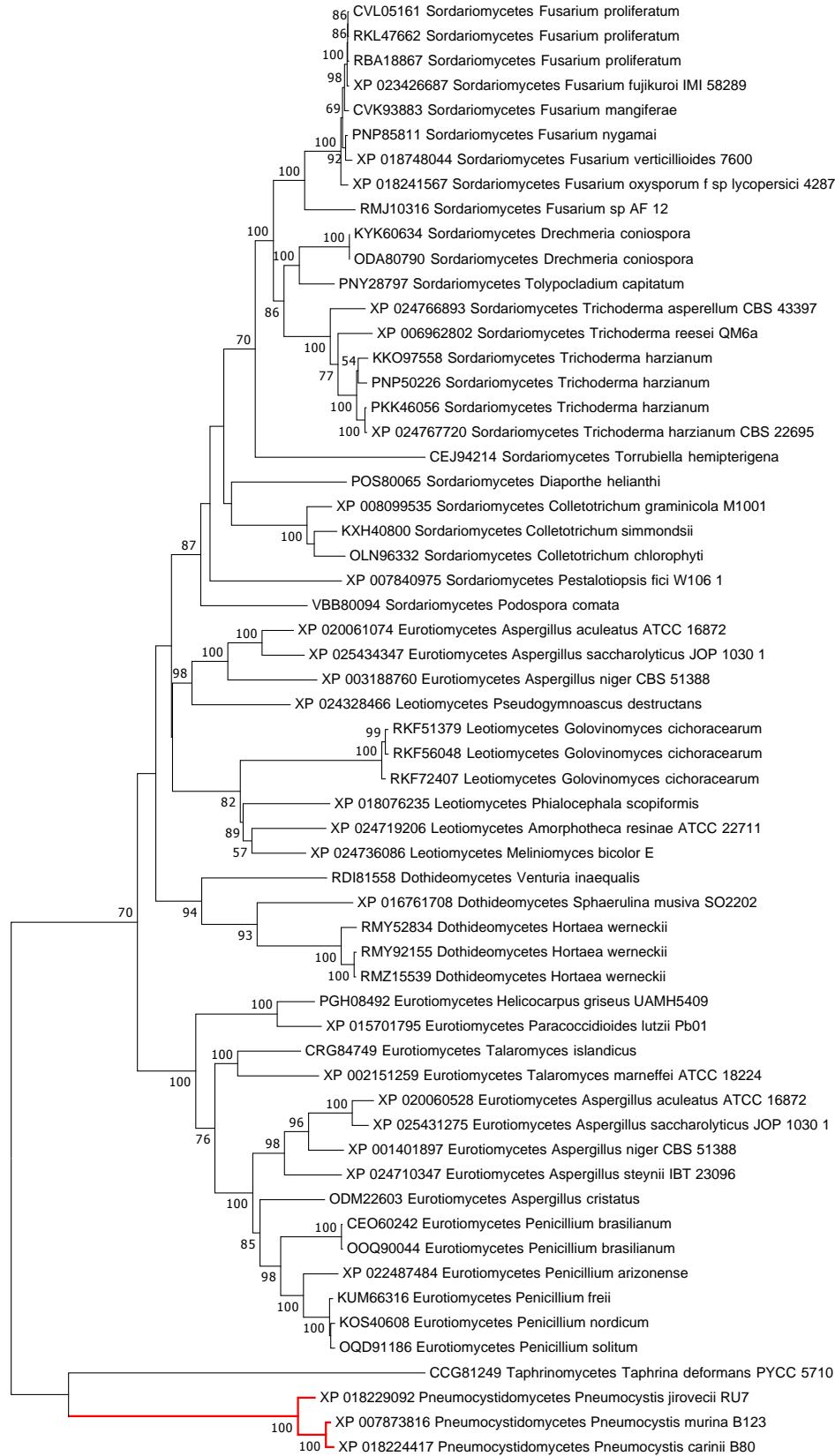
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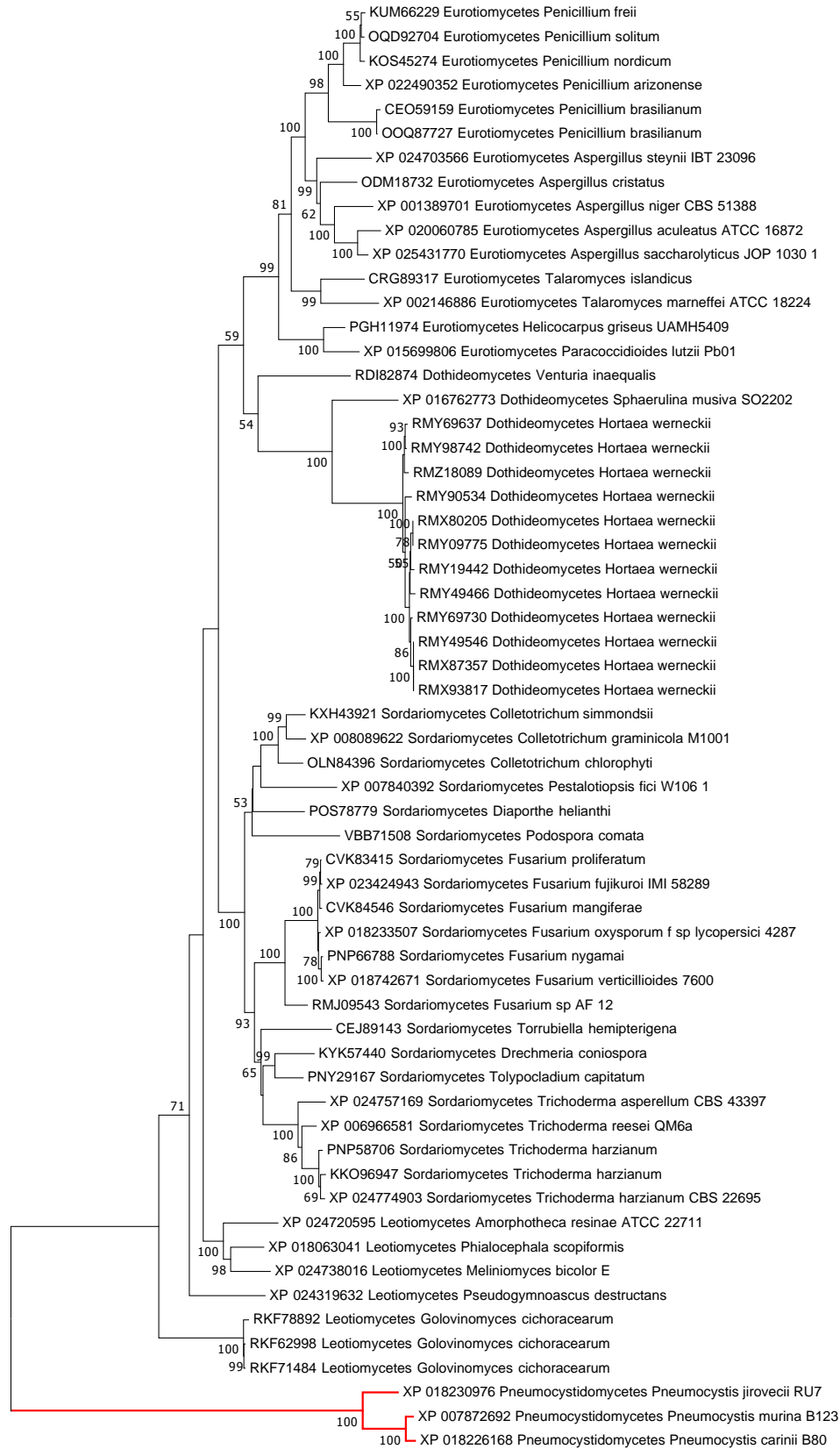
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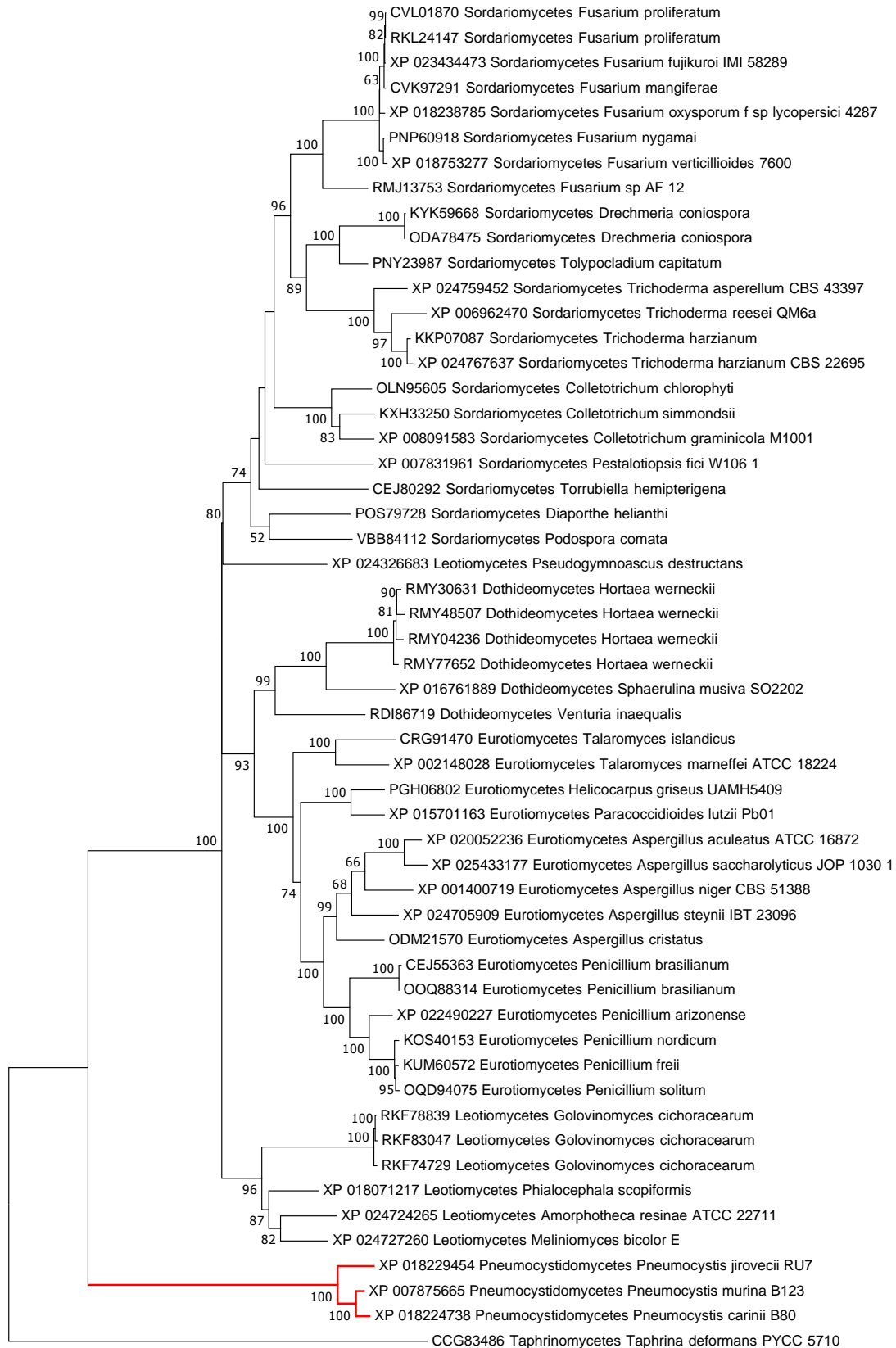


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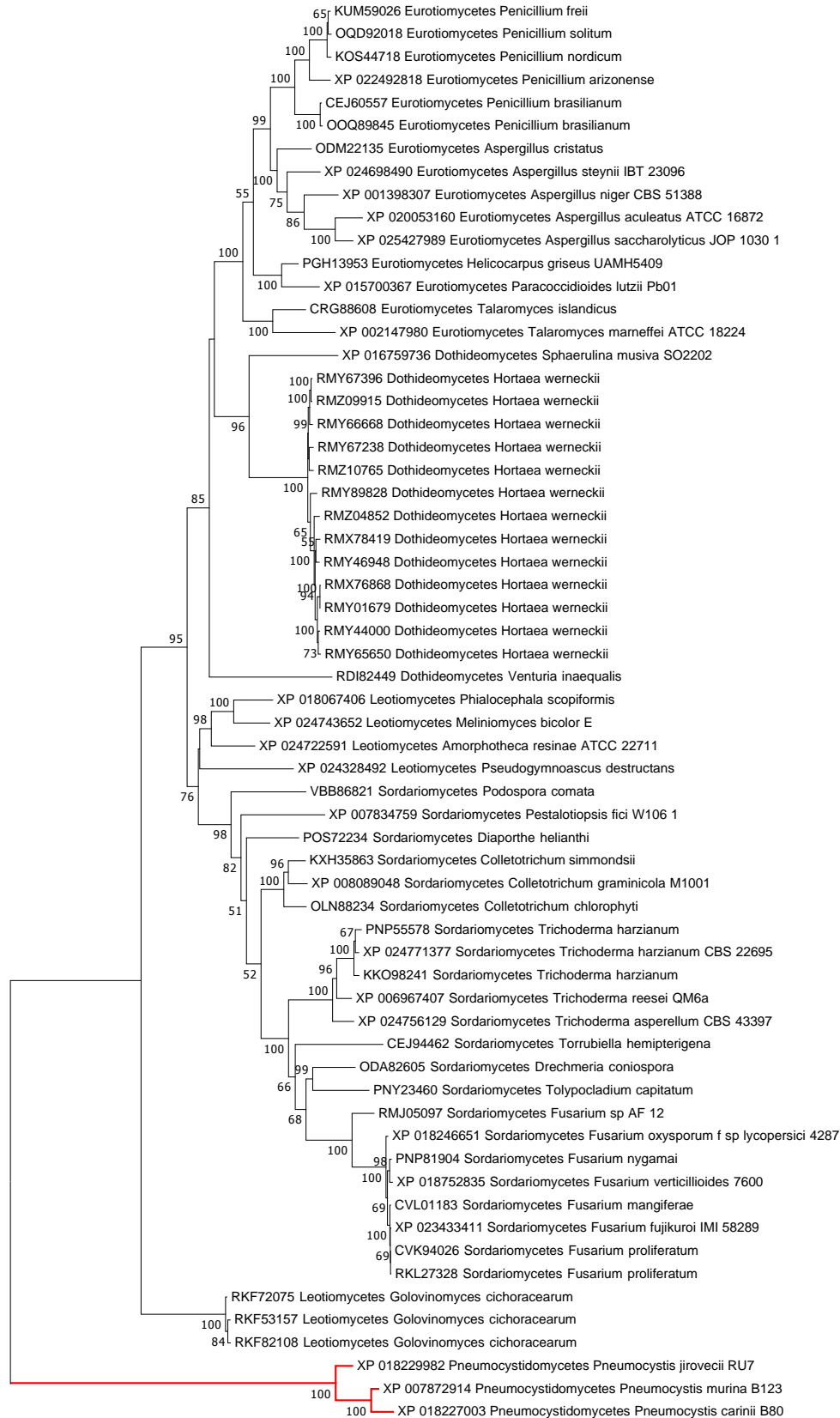
GWT1



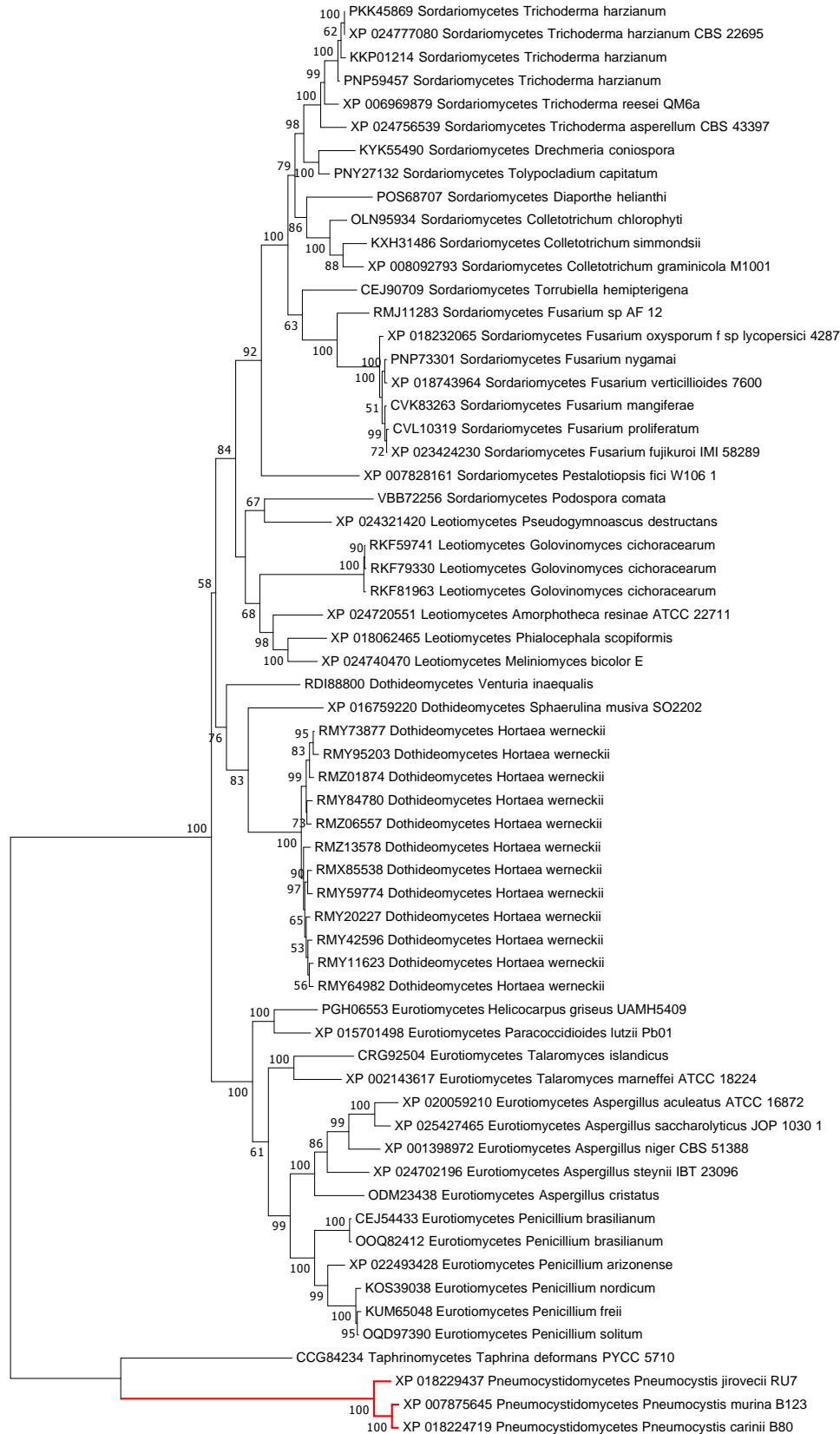
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0.5

THO

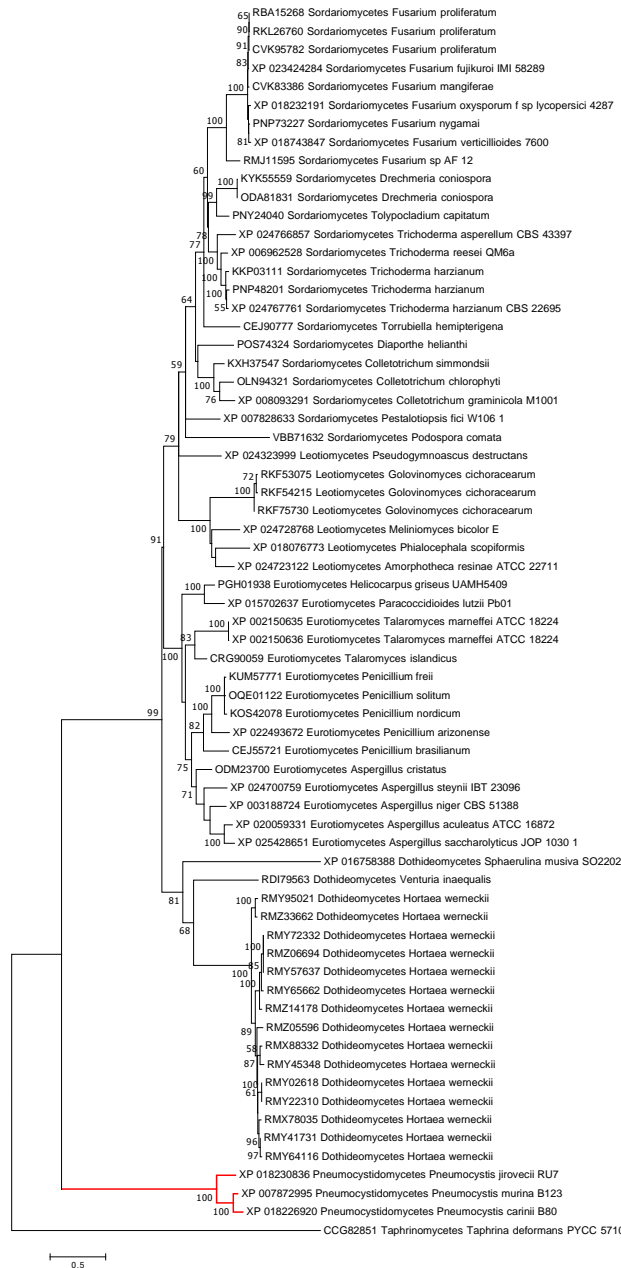


Figure S2 Maximum likelihood phylogenetic trees of genes coding for GPI biosynthesis in *Pneumocystis* and related species. In all cases, the GTR+G+I model of sequence evolution was used with 100 bootstrap replicas (4 rate categories). Sites with GAPS were eliminated from the analysis. In red we show the lineage of *Pneumocystis*. Trees are rooted along the midpoint. Phylogenies prepared with MEGA7 software (Kumar S, Stecher G, Tamura K. MEGA7: Molecular Evolutionary Analysis version 7.0 for bigger datasets. Molecular Biology and Evolution. 2016; 33: 1870-1874).