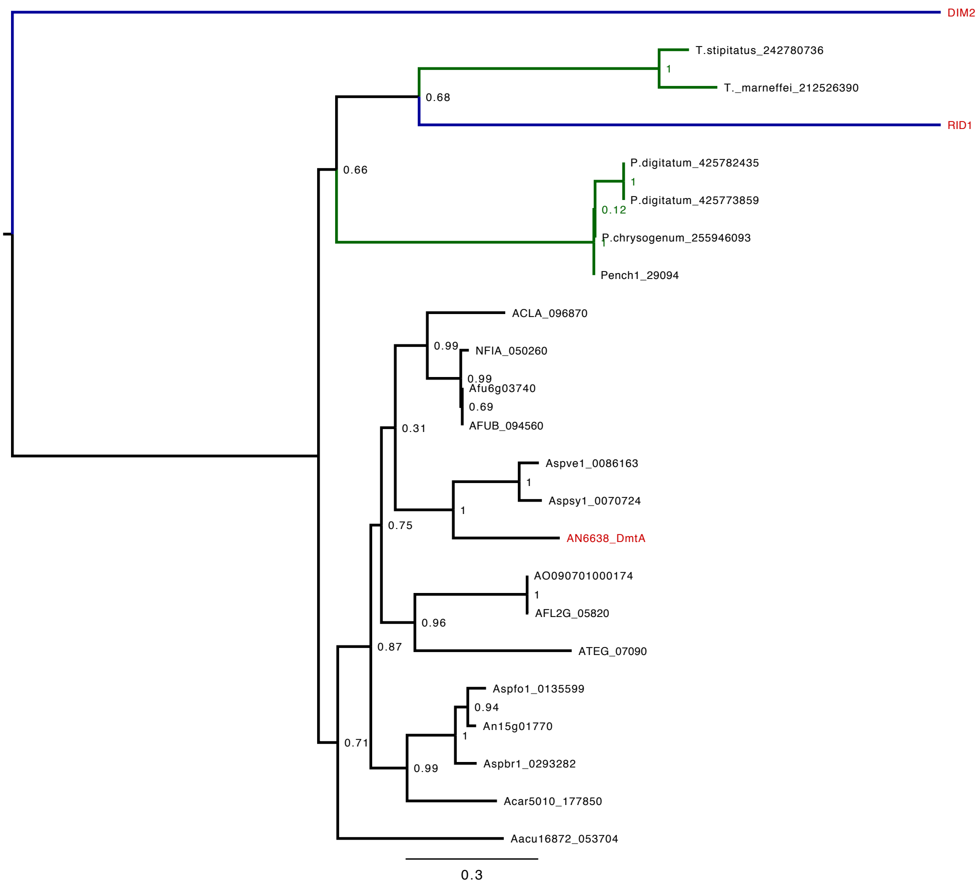

Additional.File.35.Maximum likelihood phylogeny of MASC1/RID1 orthologs.

Alignment carried out with MAFFT (G-ins-i), curation with BMGE with default settings, version-1, phylogeny with PhyML. Digits at the nodes are aLTR (approximate likelihood ratio test values). Names in red, proteins encoded by experimentally characterised genes. Blue branches, *N. crassa*, green branches *Penicillium* and *Talaromyces*, black branches *Aspergillus*. Using different curation algorithms gave essentially the same topology.