

## Supplementary Material Files

### Title:

***Mrakia panshiensis* sp. nov. a new member of the Cystofilobasidiales from soil in China, and description of the teleomorphic-stage of *M. arctica***

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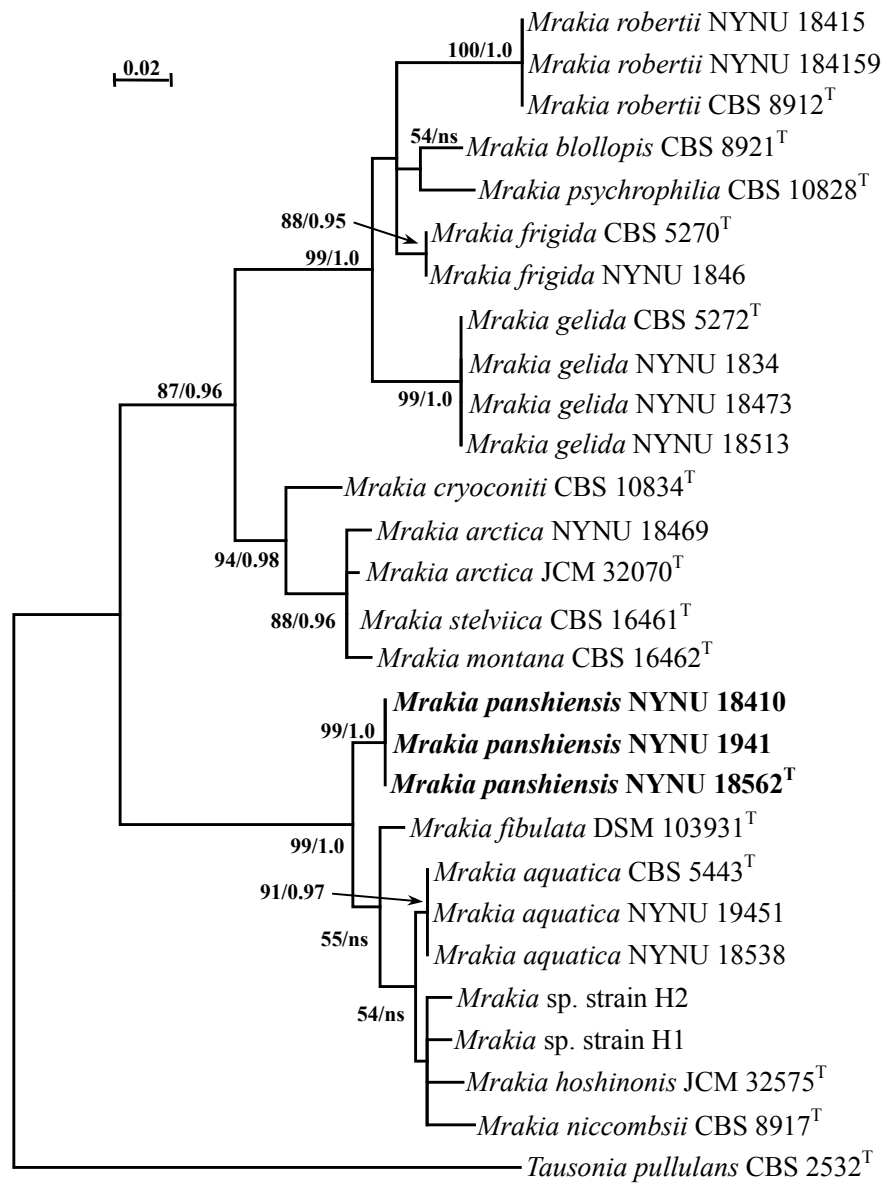


Fig. S1 Phylogenetic tree derived from the maximum-likelihood based on the ITS sequences, *Mrakia panshiensis* strains investigated in this study are highlighted in bold font. *Tausonia pullulans* CBS 2532<sup>T</sup> was designated as the outgroup. The tree backbone was constructed by maximum likelihood analysis with MEGA7. Bootstrap percentages of maximum likelihood over 50% from 1000 bootstrap replicates and posterior probabilities of Bayesian inference above 0.9 are shown from left on the branches. The scale bar represents 0.02 substitutions per nucleotide.

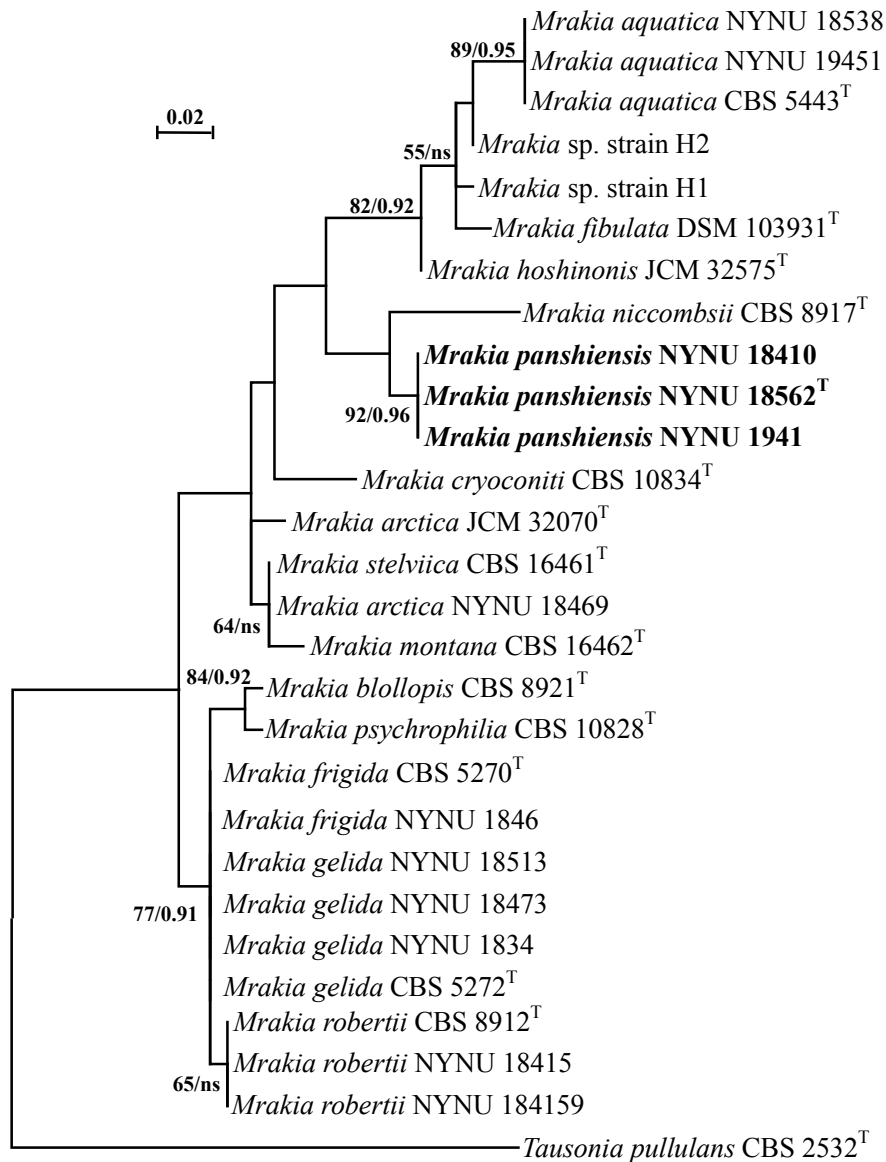


Fig. S2 Phylogenetic tree derived from the maximum-likelihood based on the the gene sequences of nuc 28S rDNA gene, *Mrakia panshiensis* strains investigated in this study are highlighted in bold font. *Tausonia pullulans* CBS 2532<sup>T</sup> was designated as the outgroup. The tree backbone was constructed by maximum likelihood analysis with MEGA7. Bootstrap percentages of maximum likelihood over 50% from 1000 bootstrap replicates and posterior probabilities of Bayesian inference above 0.9 are shown from left on the branches. The scale bar represents 0.02 substitutions per nucleotide.