**Supplementary File 1.** This file is the six-gene dataset in nexus format and includes both the RAxML bipartitions ML tree and the BI .con tree.

**Supplementary Figure 1**. Best ML tree of the Inocybaceae based on phylogenetic analyses of *rpb1* coding regions and partial *rpb1*-intron 2. The seven major lineages of Inocybaceae are labeled. Whole numbers above or below branches represent bootstrap proportions. The tree is rooted between the families Crepidotaceae and Inocybaceae.

**Supplementary Figure 2**. Best ML tree of the Inocybaceae based on phylogenetic analyses of *rpb2* coding regions. The seven major lineages of Inocybaceae are labeled. Whole numbers above or below branches represent bootstrap proportions. The tree is rooted between the families Crepidotaceae and Inocybaceae.

**Supplementary Figure 3**. Best ML tree of the Inocybaceae based on phylogenetic analyses of *tef1* coding regions. The seven major lineages of Inocybaceae are labeled. Whole numbers above or below branches represent bootstrap proportions. The tree is rooted between the families Crepidotaceae and Inocybaceae.

**Supplementary Figure 4**. Best ML tree of the Inocybaceae based on phylogenetic analyses of combined rRNA gene regions 18S, 28S, and 5.8S. The seven major lineages of Inocybaceae are labeled. Whole numbers above or below branches represent bootstrap proportions. The tree is rooted between the families Crepidotaceae and Inocybaceae.

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