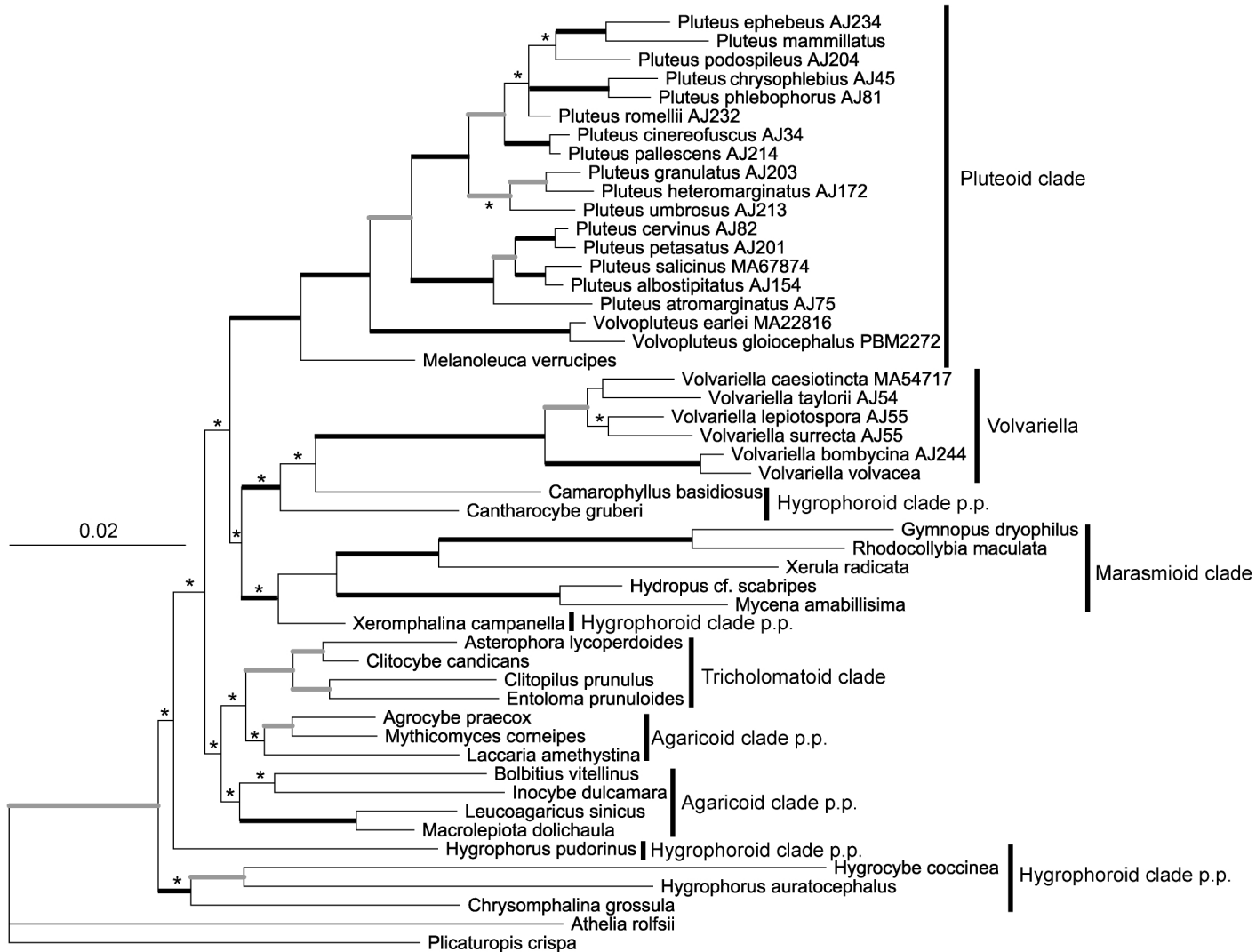


Supplementary Information

Analyses of the combined nSSU+ITS+nLSU dataset: Main lineages of the Agaricales

The dataset includes sixteen species of *Pluteus*, two of *Volvopluteus* and *Melanoleuca verrucipes* (as representatives of the Pluteoid clade), six species of *Volvariella* and a representation of the Hygrophoroid, Tricholomatoid, Agaricoid and Marasmioid clades sensu Matheny *et al.* (2006), taking into account the results of Binder *et al.* (2010), and excluding other lineages of the Agaricales placed outside these major clades (*Clavariaceae* Chevall., *Lachnellaceae* Boud., *Pterulaceae* Corner, *Schizophyllaceae* Quél., *Stephanosporaceae* Oberw. & E. Horak). *Athelia rolfsii* and *Plicaturopsis crispa* were used as an outgroup. The final dataset consists of 50 combined sequences (nSSU+ITS+nLSU) of 3276 characters (gaps included), of which 406 are parsimony informative. In the MP analysis, 24 MPT were recovered (Length = 1922; CI = 0.40; RI = 0.57). The fifty percent majority rule Bayesian phylogram is shown here.

Supplementary Figure 1. Fifty per cent majority rule Bayesian phylogram for the nSSU + ITS + nLSU dataset including the main lineages of Agaricales. Thick black branches are supported by BS values $\geq 90\%$ in both ML and MP analyses and PP ≥ 0.95 . Thick grey branches are supported in at least two of the analyses with BS $\geq 70\%$ and/or PP ≥ 0.90 . An asterisk (*) indicates that the branch collapses in the strict consensus tree of the MP analysis.



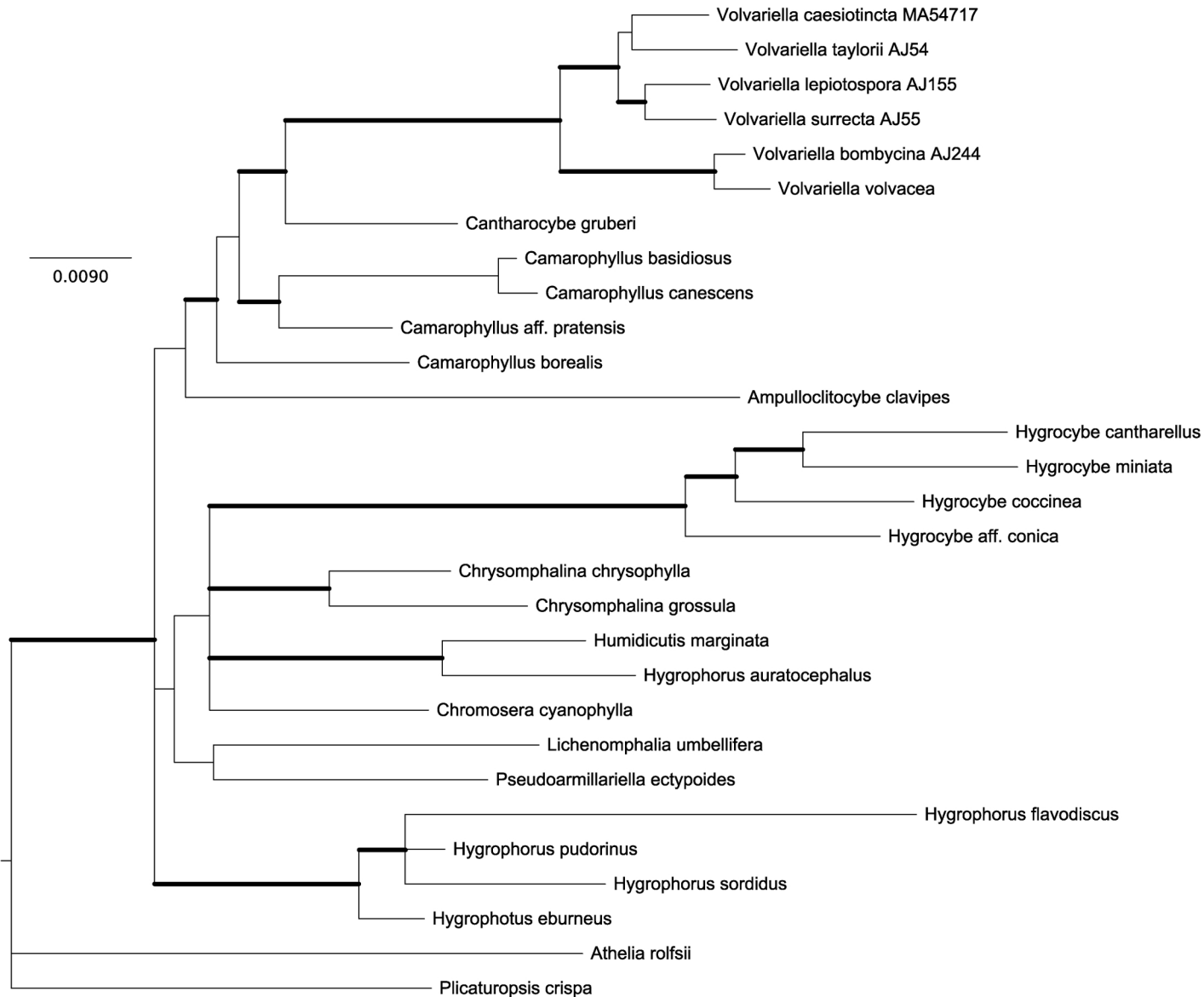
Supplementary Figure 1

Analyses of the combined nSSU+ITS+nLSU dataset: *Volvariella* and Hygrophoroid clade

The dataset includes six species of *Volvariella* and a wide representation of the Hygrophoroid clade sensu Matheny *et al.* (2006), and it takes into account the results of Binder *et al.* (2010).

Athelia rolfsii and *Plicaturopsis crispa* were used as an outgroup. The final dataset consists of 29 combined sequences (nSSU+ITS+nLSU) of 3278 characters (gaps included), of which 374 are parsimony informative. In the MP analysis, one MPT was recovered (Length = 1427; CI = 0.50; RI = 0.57). The best tree from the ML analysis is shown here

Supplementary Figure 2. Fifty per cent majority rule Bayesian phylogram for the nSSU + ITS + nLSU dataset of *Volvariella* and the Hygrophoroid clade. Thick branches are supported by PP \geq 0.90.

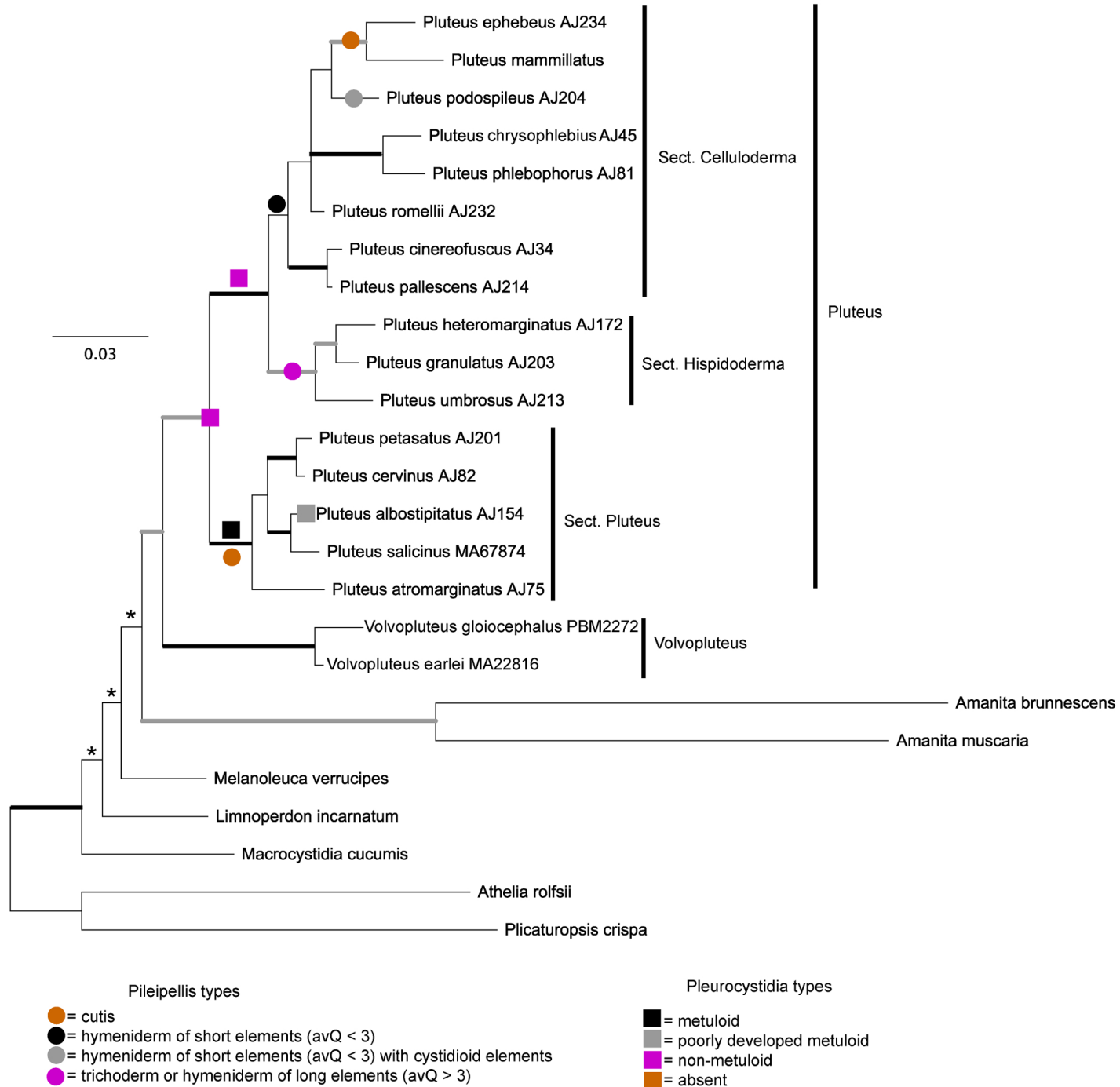


Supplementary Figure 2

Analyses of the combined nSSU+ITS+nLSU dataset: Pluteoid clade

The dataset includes 16 species of *Pluteus*, two of *Volvopluteus* and other members of the Pluteoid clade (*Amanita*, *Limnoperdon*, *Macrocystidia* and *Melanoleuca*). *Athelia rolfsii* (Curzi) C.C. Tu & Kimbr. and *Plicaturopsis crispa* were used as an outgroup. The final dataset consists of 25 combined sequences (nSSU+ITS+nLSU) of 3199 characters (gaps included), of which 230 are parsimony informative. In the MP analysis, two MPT were recovered (Length = 811; CI = 0.60; RI = 0.61). The best tree from the ML analysis is shown here.

Supplementary Figure 3. Best tree from the ML analysis for the nSSU + ITS + nLSU dataset of the Pluteoid clade. Thick black branches are supported by BS values $\geq 90\%$ in both ML and MP analyses and PP ≥ 0.95 . Thick grey branches are supported in at least two of the analyses with BS $\geq 70\%$ and/or PP ≥ 0.90 . An asterisk (*) indicates that the branch collapses in the strict consensus tree of the MP analysis.



Supplementary Figure 3