

Figure S1. Phylogenetic tree of *Amanita* sect. *Vaginatae* inferred from maximum likelihood analyses based on the nrLSU sequences. Bootstrap values over 50% are shown along the branches. Sequences from type collections are indicated with (T), and new species are in boldface.

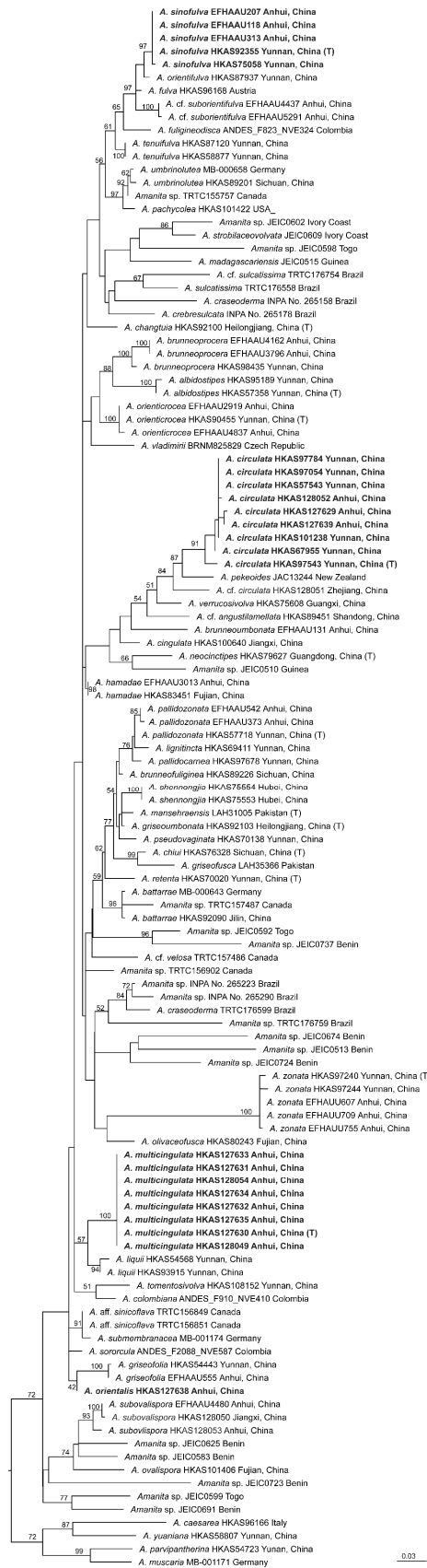


Figure S2. Phylogenetic tree of *Amanita* sect. *Vaginatae* inferred from maximum likelihood analyses based on the *tef1-α* sequences. Bootstrap values over 50% are shown along the branches. Sequences from type collections are indicated with (T), and new species are in boldface.

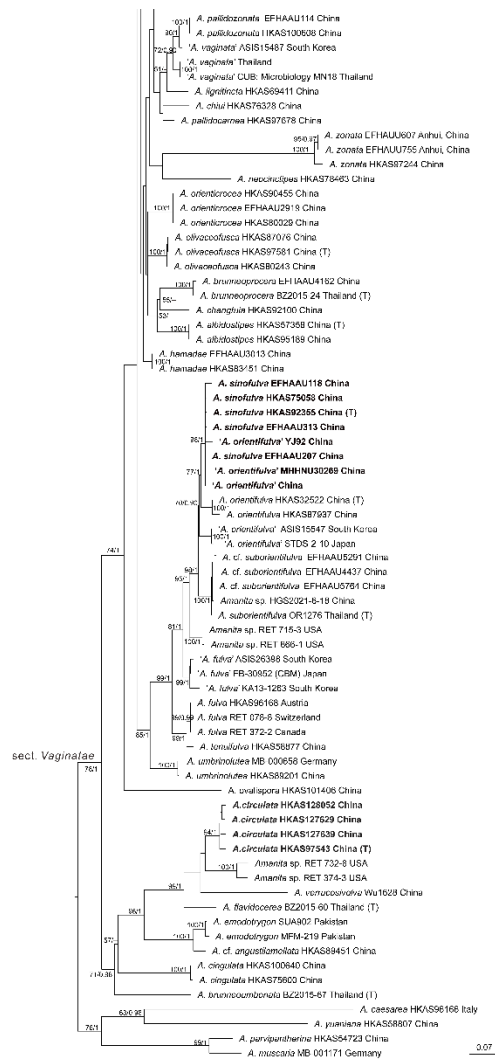
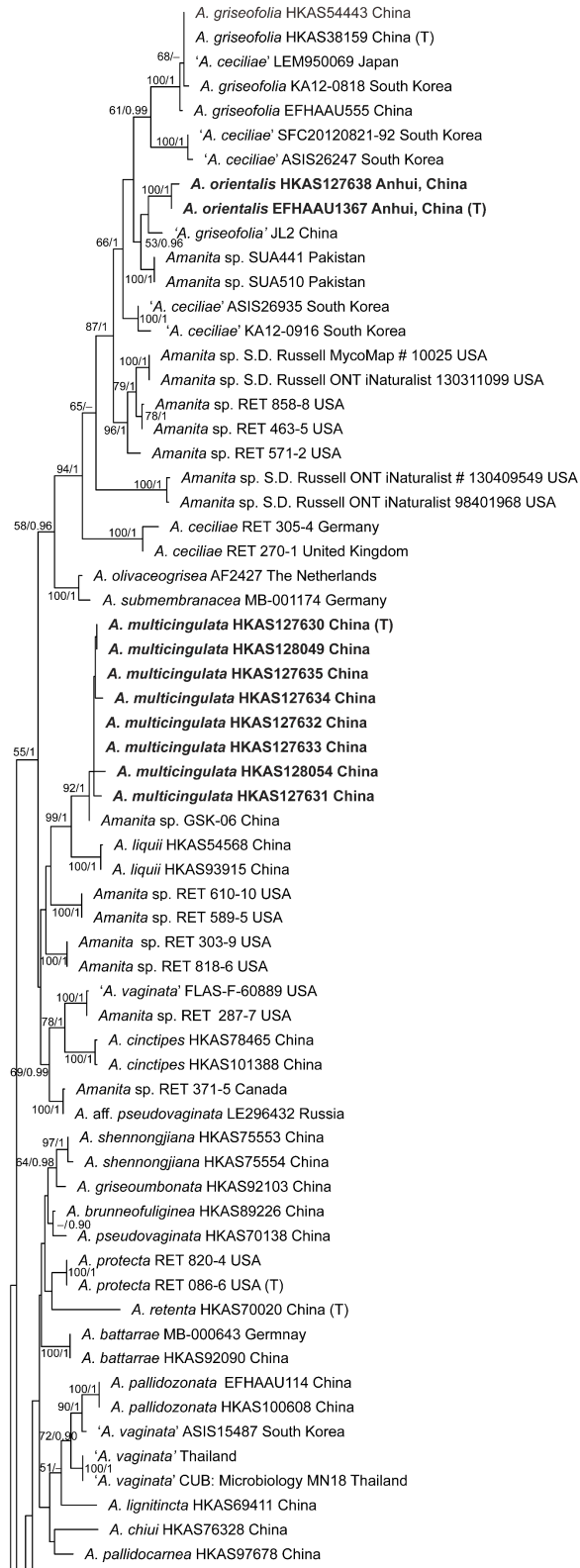


Figure S3. Phylogenetic tree of *Amanita* sect. *Vaginatae* inferred from maximum likelihood analyses based on the *rpb2* sequences. Bootstrap values over 50% are shown along the branches. Sequences from type collections are indicated with (T), and new species are in boldface.



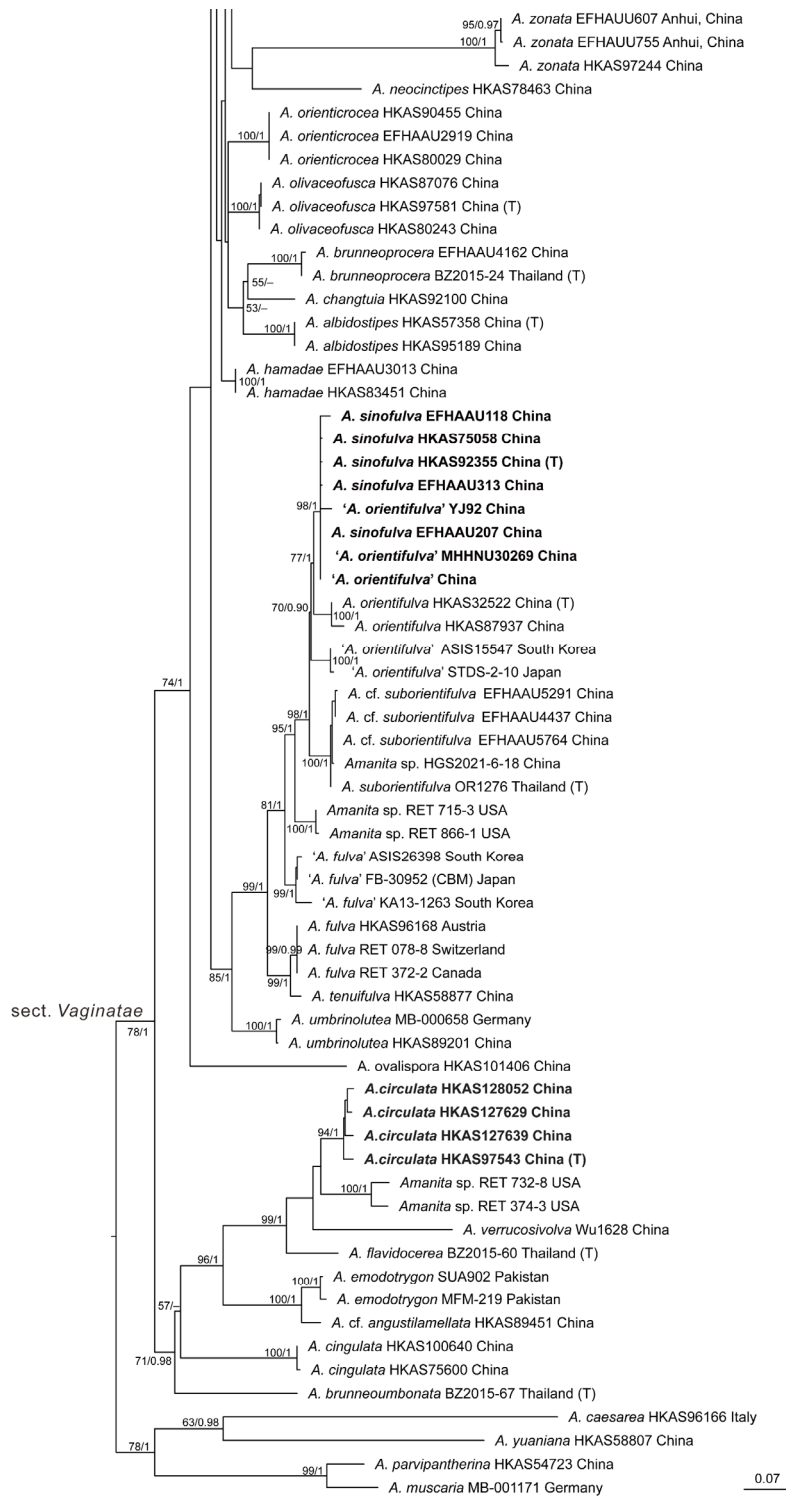


Figure S4. Phylogenetic tree of *Amanita* sect. *Vaginatae* inferred from maximum likelihood analyses based on the ITS sequences. Bootstrap values over 50% and Bayesian posterior probabilities over 0.90 are shown along the branches. Sequences from type collections are indicated with (T), and new species are in boldface.