

Supplementary files

Fig. S1 Phylogenetic tree based on maximum likelihood (ML) analysis of *ACT* sequence alignments for *Calonectria* spp. Bootstrap values $\geq 70\%$ for ML analyses and posterior probabilities values ≥ 0.95 obtained from Bayesian inference (BI) are indicated at the nodes as ML/BI. Bootstrap values $< 70\%$ or probabilities values < 0.95 are marked with “*”, and nodes lacking the support values are marked with “-”. Isolates representing ex-type material are marked with “T”. *Curviciadiella cigneae* (isolate CBS 109167 and CBS 109168) represents the outgroup.

Fig. S2 Phylogenetic tree based on maximum likelihood (ML) analysis of *CMDA* sequence alignments for *Calonectria* spp. Bootstrap values $\geq 70\%$ for ML analyses and posterior probabilities values ≥ 0.95 obtained from Bayesian inference (BI) are indicated at the nodes as ML/BI. Bootstrap values $< 70\%$ or probabilities values < 0.95 are marked with “*”, and nodes lacking the support values are marked with “-”. Isolates representing ex-type material are marked with “T”. *Curviciadiella cigneae* (isolate CBS 109167 and CBS 109168) represents the outgroup.

Fig. S3 Phylogenetic tree based on maximum likelihood (ML) analysis of *HIS3* sequence alignments for *Calonectria* spp. Bootstrap values $\geq 70\%$ for ML analyses and posterior probabilities values ≥ 0.95 obtained from Bayesian inference (BI) are indicated at the nodes as ML/BI. Bootstrap values $< 70\%$ or probabilities values < 0.95 are marked with “*”, and nodes lacking the support values are marked with “-”. Isolates representing ex-type material are marked with “T”. *Curviciadiella cigneae* (isolate CBS 109167 and CBS 109168) represents the outgroup.

Fig. S4 Phylogenetic tree based on maximum likelihood (ML) analysis of *RPB2* sequence alignments for *Calonectria* spp. Bootstrap values $\geq 70\%$ for ML analyses and posterior

probabilities values ≥ 0.95 obtained from Bayesian inference (BI) are indicated at the nodes as ML/BI. Bootstrap values $< 70\%$ or probabilities values < 0.95 are marked with “*”, and nodes lacking the support values are marked with “–”. Isolates representing ex-type material are marked with “T”. *Curviciadiella cigneae* (isolate CBS 109167 and CBS 109168) represents the outgroup.

Fig. S5 Phylogenetic tree based on maximum likelihood (ML) analysis of *TEF1* sequence alignments for *Calonectria* spp. Bootstrap values $\geq 70\%$ for ML analyses and posterior probabilities values ≥ 0.95 obtained from Bayesian inference (BI) are indicated at the nodes as ML/BI. Bootstrap values $< 70\%$ or probabilities values < 0.95 are marked with “*”, and nodes lacking the support values are marked with “–”. Isolates representing ex-type material are marked with “T”. *Curviciadiella cigneae* (isolate CBS 109167 and CBS 109168) represents the outgroup.

Fig. S6 Phylogenetic tree based on maximum likelihood (ML) analysis of *TUB2* sequence alignments for *Calonectria* spp. Bootstrap values $\geq 70\%$ for ML analyses and posterior probabilities values ≥ 0.95 obtained from Bayesian inference (BI) are indicated at the nodes as ML/BI. Bootstrap values $< 70\%$ or probabilities values < 0.95 are marked with “*”, and nodes lacking the support values are marked with “–”. Isolates representing ex-type material are marked with “T”. *Curviciadiella cigneae* (isolate CBS 109167 and CBS 109168) represents the outgroup.

Fig. S1

ACT

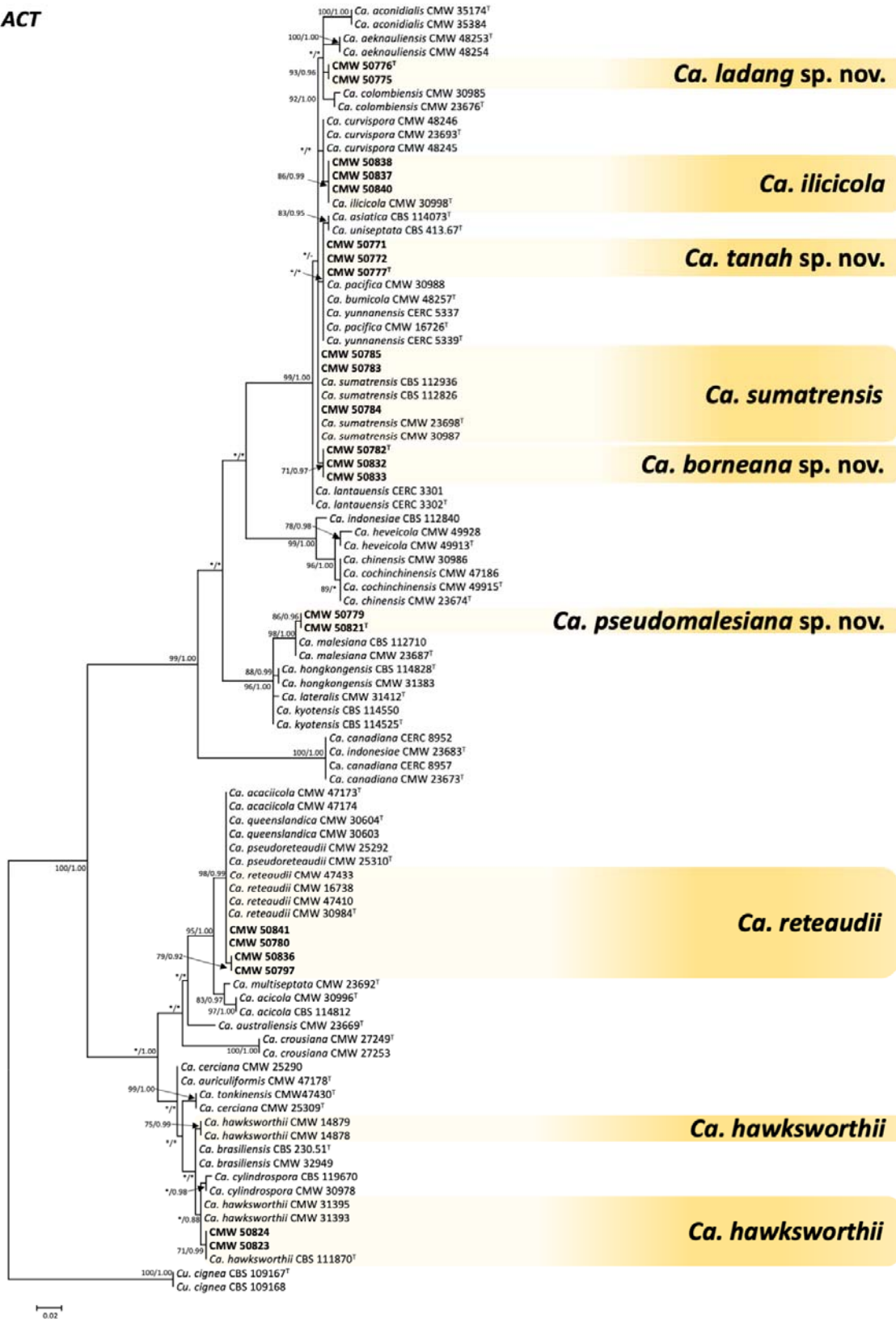


Fig. S2

CMDA

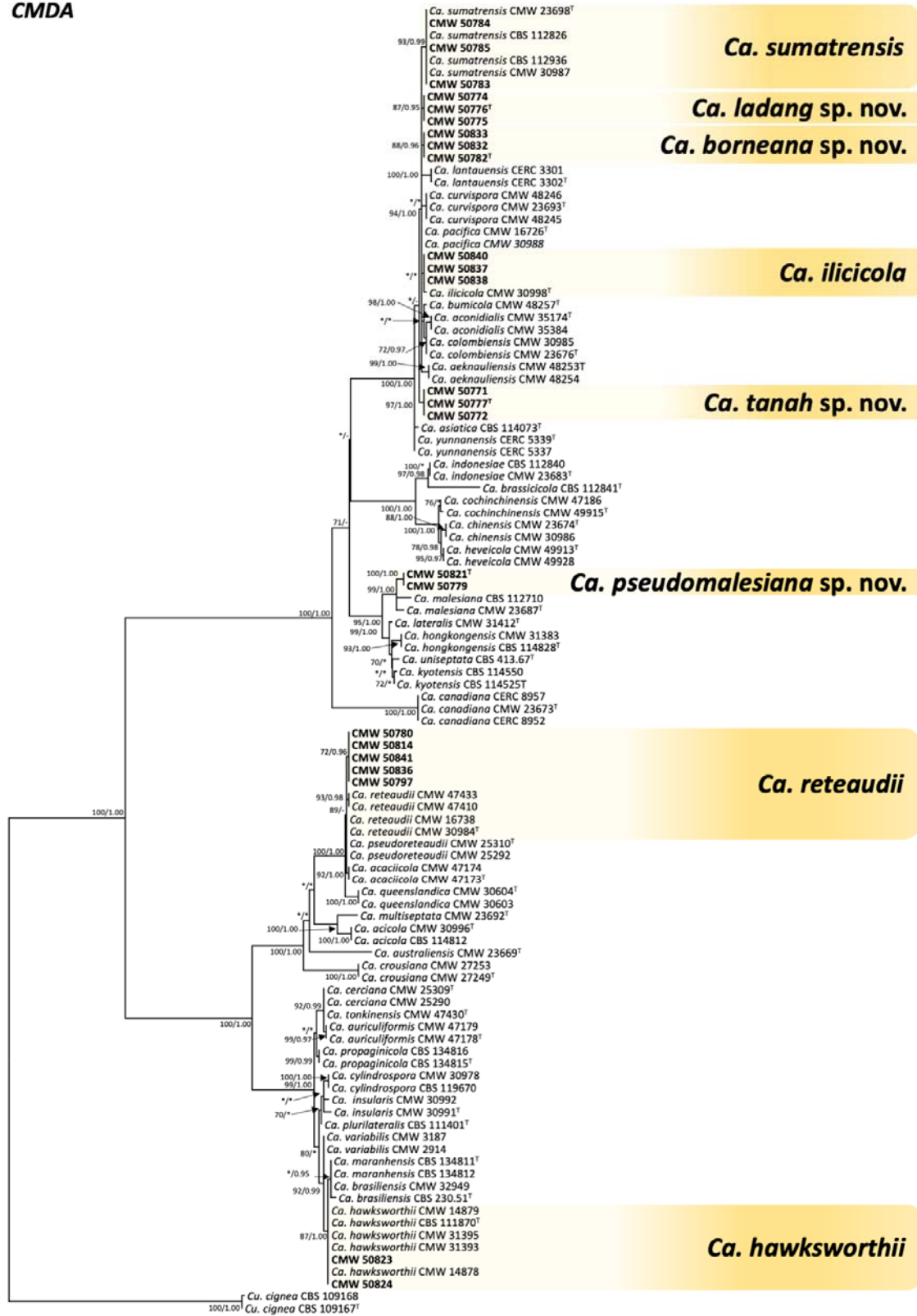


Fig. S3

HIS3

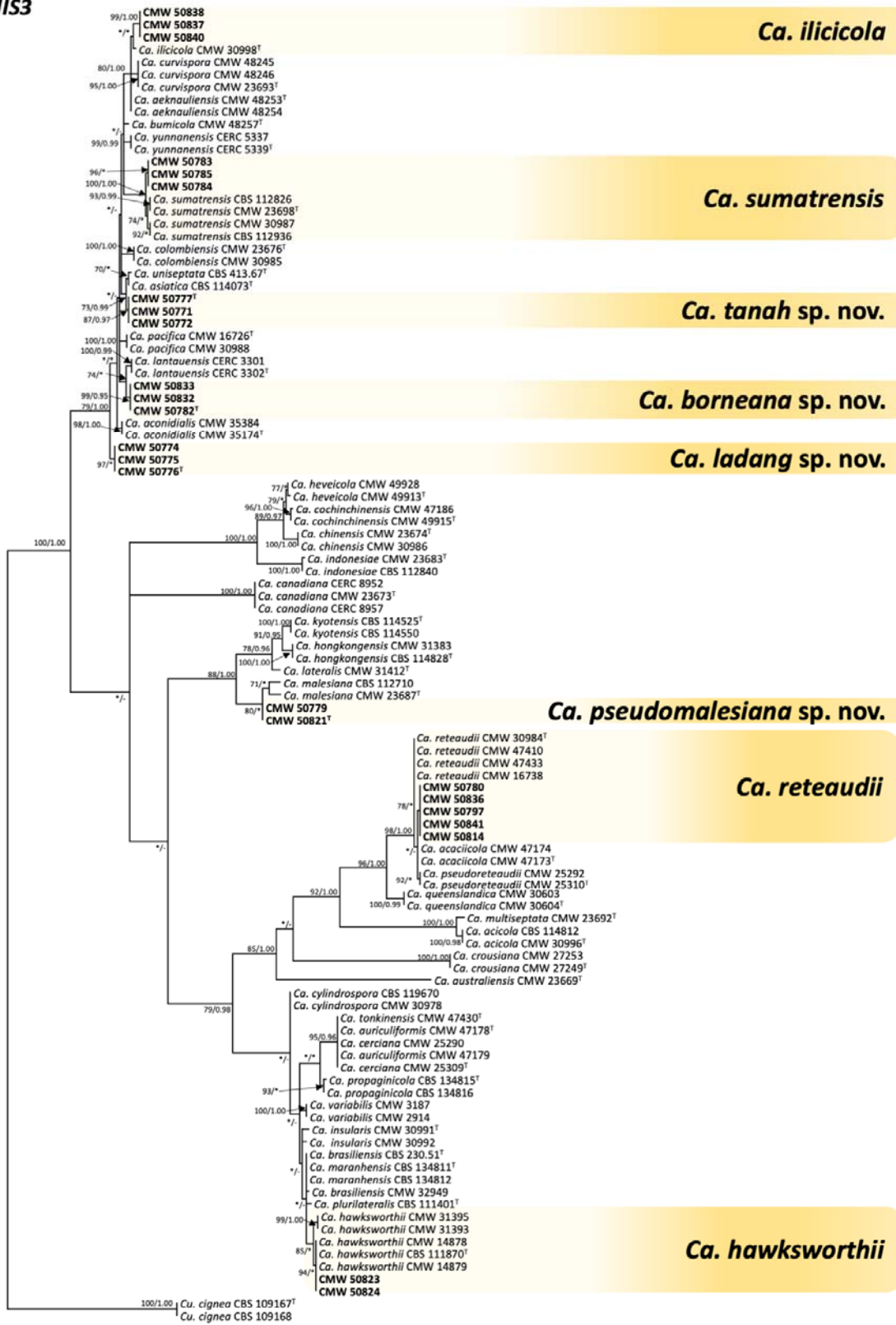


Fig. S4

RPB2

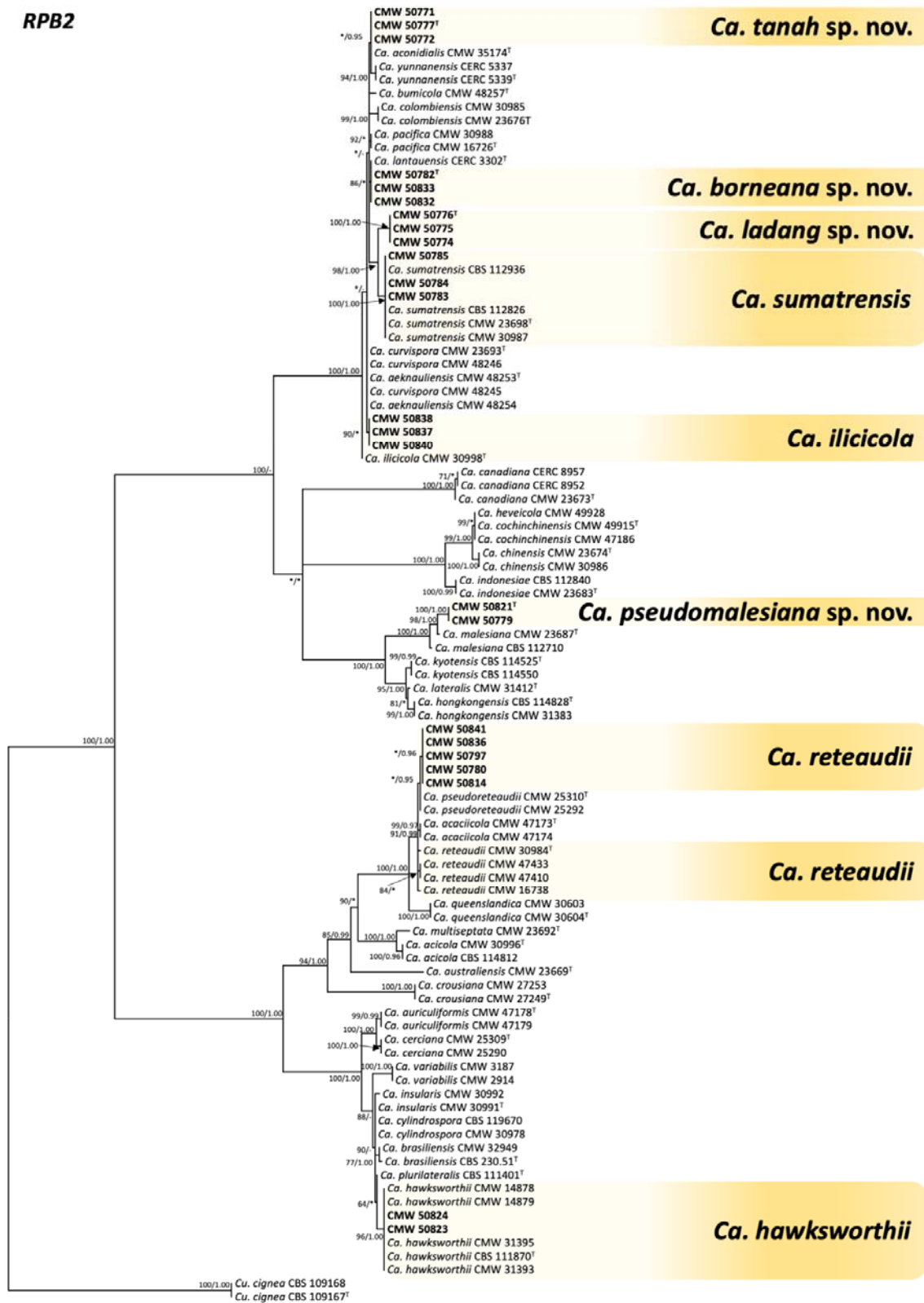


Fig. S5

TEF1

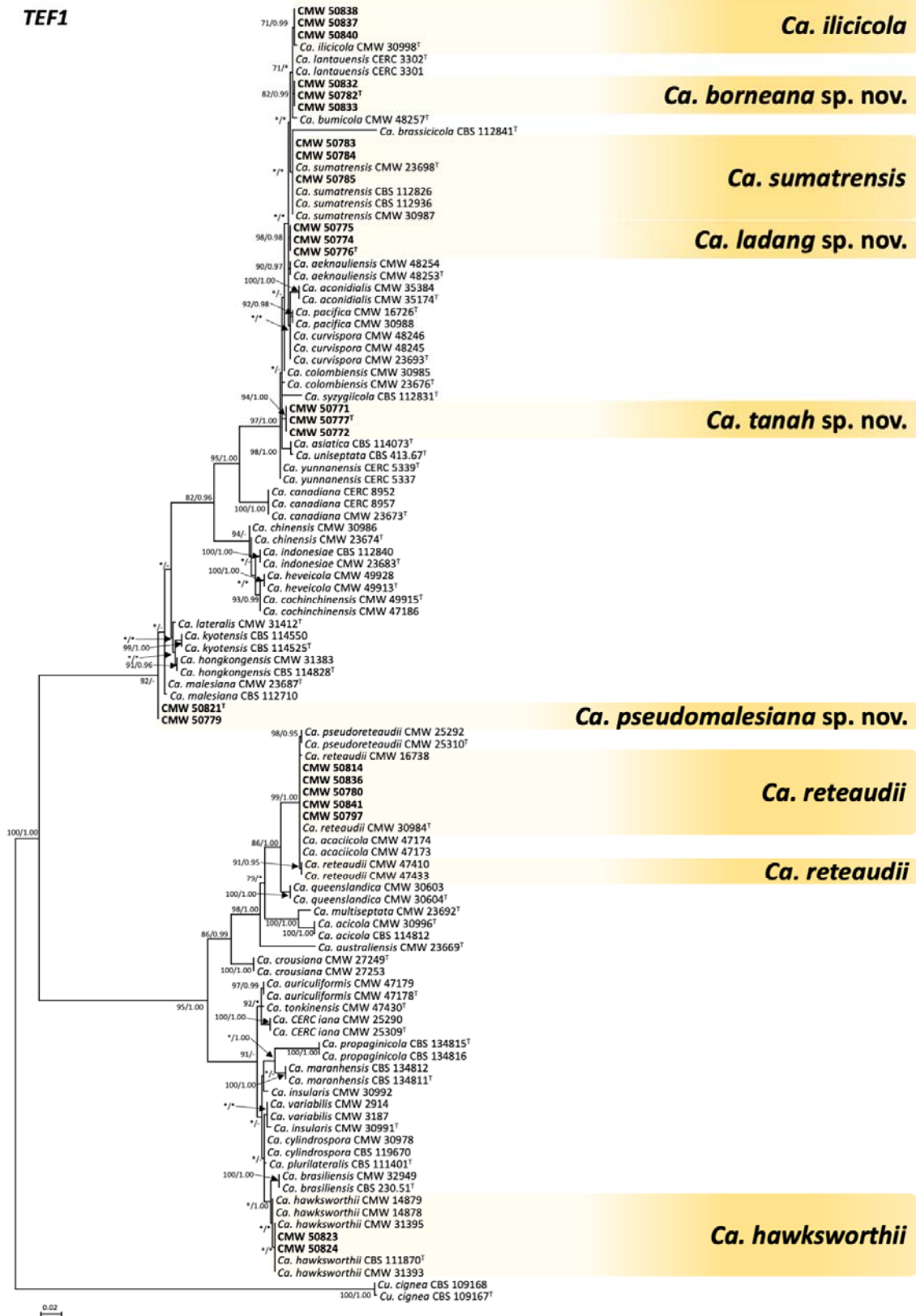


Fig. S6

TUB2

