

Supplementary materials

Characterization of the *Castanopsis carlesii* deadwood mycobiome by Pacbio sequencing of the full-length fungal nuclear ribosomal internal transcribed spacer (ITS)

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Appendix 1: Community composition, richness, and taxonomic identification of the *Castanopsis carlesii* deadwood mycobiome based on the ITS1, ITS2, and full-length ITS sequences

Table S1. Taxonomic information of all wood-inhabiting fungi identified at species level based on Pacbio

Full ITS (36 OTUs identified at species level)	ITS1 (46 OTUs identified at species level)	ITS2 (41 OTUs identified at species level)
<i>Alternaria alternata</i>	<i>Acremoniopsis suttonii</i>	<i>Campylocarpon fasciculare</i>
<i>Campylocarpon fasciculare</i>	<i>Colacogloea terpenoidalis</i>	<i>Colacogloea terpenoidalis</i>
<i>Colacogloea terpenoidalis</i>	<i>Devriesia strelitziicola</i>	<i>Devriesia strelitziicola</i>
<i>Coprinellus disseminatus</i>	<i>Dictyochaeta simplex</i>	<i>Dichomitus albidofuscus</i>
<i>Devriesia strelitziicola</i>	<i>Erythromyces crocicreas</i>	<i>Erythromyces crocicreas</i>
<i>Dichomitus squalens</i>	<i>Erythromyces crocicreas</i>	<i>Erythromyces crocicreas</i>
<i>Dictyochaeta simplex</i>	<i>Hawksworthiomyces crousii</i>	<i>Fusarium oxysporum</i>
<i>Erythromyces crocicreas</i>	<i>Hymenochaete tongbiguanensis</i>	<i>Ganoderma tsugae</i>
<i>Hawksworthiomyces crousii</i>	<i>Nakazawaea ishiwadae</i>	<i>Hawksworthiomyces crousii</i>
<i>Hymenochaete tongbiguanensis</i>	<i>Pestalotiopsis palustris</i>	<i>Hymenochaete tongbiguanensis</i>
<i>Jianyunia sakaguchii</i>	<i>Pestalotiopsis vismiae</i>	<i>Hymenochaete xerantica</i>
<i>Meliniomyces bicolor</i>	<i>Pilidium eucalyptorum</i>	<i>Jianyunia sakaguchii</i>
<i>Nectria aurantiaca</i>	<i>Piskurozyma taiwanensis</i>	<i>Nakazawaea ishiwadae</i>
<i>Pestalotiopsis maculiformans</i>	<i>Porogramme albocincta</i>	<i>Neopestalotiopsis javaensis</i>
<i>Pilidium concavum</i>	<i>Pseudohyphozyma bogoriensis</i>	<i>Pestalotiopsis microspora</i>
<i>Pilidium eucalyptorum</i>	<i>Scytalidium cuboideum</i>	<i>Pilidium acerinum</i>
<i>Pilidium pseudoconcavum</i>	<i>Scytalidium lignicola</i>	<i>Pilidium eucalyptorum</i>

Full ITS (36 OTUs identified at species level)	ITS1 (46 OTUs identified at species level)	ITS2 (41 OTUs identified at species level)
<i>Porogramme albocincta</i>	<i>Scytalidium lignicola</i>	<i>Piskurozyma taiwanensis</i>
<i>Pseudohyphozyma bogoriensis</i>	<i>Scytalidium lignicola</i>	<i>Porogramme albocincta</i>
<i>Rhodotorula cycloclastica</i>	<i>Scytalidium lignicola</i>	<i>Rhodotorula cycloclastica</i>
<i>Scytalidium lignicola</i>	<i>Scytalidium lignicola</i>	<i>Scytalidium lignicola</i>
<i>Scytalidium lignicola</i>	<i>Sistotremastrum guttuliferum</i>	<i>Sistotremastrum guttuliferum</i>
<i>Scytalidium lignicola</i>	<i>Sistotremastrum guttuliferum</i>	<i>Sistotremastrum guttuliferum</i>
<i>Sistotremastrum guttuliferum</i>	<i>Sistotremastrum guttuliferum</i>	<i>Sugiyamaella chiloensis</i>
<i>Sistotremastrum guttuliferum</i>	<i>Sugiyamaella smithiae</i>	<i>Sugiyamaella smithiae</i>
<i>Subulicystidium perlongisporum</i>	<i>Symbiotaphrina kochii</i>	<i>Symbiotaphrina kochii</i>
<i>Sugiyamaella novakii</i>	<i>Tinctoporellus epimiltinus</i>	<i>Tremella foliacea</i>
<i>Symbiotaphrina kochii</i>	<i>Tremella foliacea</i>	<i>Trichoderma harzianum</i>
<i>Tinctoporellus epimiltinus</i>	<i>Trichoderma harzianum</i>	<i>Trichoderma harzianum</i>
<i>Tremella fuciformis</i>	<i>Trichoderma harzianum</i>	<i>Trichoderma harzianum</i>
<i>Trichoderma harzianum</i>	<i>Trichoderma harzianum</i>	<i>Trichoderma harzianum</i>
<i>Trichoderma virens</i>	<i>Trichoderma harzianum</i>	<i>Trichoderma harzianum</i>
<i>Trichosphaerella ceratophora</i>	<i>Trichoderma harzianum</i>	<i>Trichoderma harzianum</i>
<i>Xenasmatella ardosiacae</i>	<i>Trichoderma harzianum</i>	<i>Trichoderma harzianum</i>
<i>Xenoacremonium falcatum</i>	<i>Trichoderma harzianum</i>	<i>Trichoderma harzianum</i>

Full ITS (36 OTUs identified at species level)	ITS1 (46 OTUs identified at species level)	ITS2 (41 OTUs identified at species level)
<i>Xenoacremonium recifei</i>	<i>Trichoderma harzianum</i>	<i>Trichoderma harzianum</i>
	<i>Trichoderma harzianum</i>	<i>Trichoderma lixii</i>
	<i>Trichoderma harzianum</i>	<i>Trichoderma virens</i>
	<i>Trichoderma harzianum</i>	<i>Trichosphaerella ceratophora</i>
	<i>Trichoderma harzianum</i>	<i>Xenasmatella ardosiaca</i>
	<i>Trichoderma inhamatum</i>	<i>Xenoacremonium falcatum</i>
	<i>Trichoderma virens</i>	
	<i>Veronaea botryosa</i>	
	<i>Xenasmatella ardosiaca</i>	
	<i>Xenasmatella ardosiaca</i>	
	<i>Xenoacremonium falcatum</i>	

***Dark green highlight = detected using Pacbio based on the ITS1, ITS2, and full-length ITS. Light green highlight = detected using Pacbio based on the full-length ITS and ITS1 or ITS2. Red highlight = only detected using Pacbio based on the full-length ITS.





































Table S2. Comparison of fungal taxonomic information of 36 wood-inhabiting fungi identified at species level based on Pacbio sequencing alone and Pacbio sequencing incorporated with phylogenetic analysis based on Randomized Axelerated Maximum Likelihood (RAxML) of the complete internal transcribed spacer (ITS) sequence.

ID	Taxonomy based on ITS1 phylogeny	Bootstrap	Taxonomy based on ITS2 phylogeny	Bootstrap	Taxonomy based on Pacbio	Taxonomy based on Pacbio and phylogeny	Bootstrap
<i>Devriesia</i> OTU219	<i>Devriesia strelitzicola</i>	100%	<i>Devriesia strelitzicola</i>	100%	<i>Devriesia strelitzicola</i>	<i>Devriesia strelitzicola</i>	100%
<i>Alternaria</i> OTU741	Multiple taxa including <i>Alternaria</i> spp.	-	Multiple taxa including <i>Alternaria</i> spp.	-	<i>Alternaria alternata</i>	<i>Pleospora herbarum</i>	88%
<i>Pilidium</i> OTU445	<i>Pilidium pseudoconcavum</i>	33%	<i>Pilidium eucalyptorum</i>	59%	<i>Pilidium concavum</i>	<i>Pilidium eucalyptorum</i>	90%
<i>Pilidium</i> OTU479	<i>Pilidium pseudoconcavum</i>	33%	<i>Pilidium eucalyptorum</i>	59%	<i>Pilidium pseudoconcavum</i>	<i>Pilidium eucalyptorum</i>	90%
<i>Pilidium</i> OTU632	<i>Pilidium pseudoconcavum</i>	33%	<i>Pilidium eucalyptorum</i>	59%	<i>Pilidium eucalyptorum</i>	<i>Pilidium eucalyptorum</i>	90%
<i>Scytalidium</i> OTU182	Multiple taxa including <i>Scytalidium</i> spp.	-	<i>Scytalidium lignicola</i>	56%	<i>Scytalidium lignicola</i>	<i>Scytalidium lignicola</i>	<60%
<i>Scytalidium</i> OTU235	Multiple taxa including <i>Scytalidium</i> spp.	-	<i>Scytalidium lignicola</i>	56%	<i>Scytalidium lignicola</i>	<i>Scytalidium lignicola</i>	<60%
<i>Scytalidium</i> OTU260	Multiple taxa including <i>Scytalidium</i> spp.	-	<i>Scytalidium lignicola</i>	56%	<i>Scytalidium lignicola</i>	<i>Scytalidium lignicola</i>	<60%
<i>Meliniomyces</i> OTU283	Multiple taxa including <i>Meliniomyces</i> spp.	-	Multiple taxa including <i>Meliniomyces</i> spp.	-	<i>Meliniomyces bicolor</i>	Separate from existing <i>Meliniomyces</i> sp.	100%
<i>Sugiyamaella</i> OTU730	<i>Sugiyamaella</i> sp.	17%	Multiple taxa including <i>Sugiyamaella</i> spp.	44%	<i>Sugiyamaella novakii</i>	<i>Sugiyamaella</i> spp.	77%
<i>Campylocarpon</i> OTU403	<i>Campylocarpon pseudofasciculare</i>	75%	<i>Campylocarpon fasciculare</i>	69%	<i>Campylocarpon fasciculare</i>	<i>Campylocarpon fasciculare</i>	100%
<i>Trichosphaerella</i> OTU525	<i>Trichosphaerella ceratophora</i>	86%	<i>Trichosphaerella ceratophora</i>	100%	<i>Trichosphaerella ceratophora</i>	<i>Trichosphaerella ceratophora</i>	100%
<i>Hawksworthiomyces</i> OTU676	<i>Hawksworthiomyces crousii</i>	74%	<i>Hawksworthiomyces crousii</i>	100%	<i>Hawksworthiomyces crousii</i>	<i>Hawksworthiomyces crousii</i>	100%
<i>Pestalotiopsis</i> OTU124	<i>Pestalotiopsis</i> spp.	14%	<i>Pestalotiopsis australis</i>	26%	<i>Pestalotiopsis maculiformans</i>	<i>Pestalotiopsis adusta</i>	87%
<i>Trichoderma</i> OTU425	<i>Trichoderma aureoviride</i>	50%	<i>Trichoderma</i> spp.	62%	<i>Trichoderma harzianum</i>	<i>Trichoderma harzianum</i>	74%
<i>Trichoderma</i> OTU432	<i>Trichoderma aureoviride</i>	50%	<i>Trichoderma</i> spp.	21%	<i>Trichoderma virens</i>	<i>Trichoderma harzianum</i>	74%
<i>Xenoacremonium</i> OTU524	<i>Xenoacremonium recifei</i> <i>Xenoacremonium falcatus</i>	37%	<i>Xenoacremonium recifei</i>	48%	<i>Xenoacremonium recifei</i>	<i>Xenoacremonium recifei</i>	62%
<i>Dictyochaeta</i> OTU98	Multiple taxa including <i>Dictyochaeta</i> spp.	-	<i>Codinaea pini</i>	53%	<i>Dictyochaeta simplex</i>	<i>Dictyochaeta simplex</i>	60%
<i>Nectria</i> OTU266	<i>Xenoacremonium recifei</i> <i>Xenoacremonium falcatus</i>	38%	<i>Xenoacremonium recifei</i>	26%	<i>Nectria aurantiaca</i>	<i>Nectria pseudotrichia</i>	<60%

ID	Taxonomy based on ITS1 phylogeny	Bootstrap	Taxonomy based on ITS2 phylogeny	Bootstrap	Taxonomy based on Pacbio	Taxonomy based on Pacbio and phylogeny	Bootstrap
<i>Xenoacremonium</i> OTU522	<i>Xenoacremonium recifei</i> <i>Xenoacremonium falcatus</i>	38%	<i>Xenoacremonium recifei</i> <i>Xenoacremonium falcatus</i>	56%	<i>Xenoacremonium falcatus</i>	<i>Xenoacremonium falcatus</i>	<60%
<i>Symbiotaphrina</i> OTU423	<i>Symbiotaphrina kochii</i>	57%	<i>Symbiotaphrina kochii</i>	100%	<i>Symbiotaphrina kochii</i>	<i>Symbiotaphrina kochii</i>	100%
<i>Coprinellus</i> OTU515	<i>Coprinellus disseminatus</i>	92%	<i>Coprinellus disseminatus</i>	100%	<i>Coprinellus disseminatus</i>	<i>Coprinellus disseminatus</i>	100%
<i>Erythromyces</i> OTU623	<i>Erythromyces crocicreas</i>	72%	<i>Erythromyces crocicreas</i>	100%	<i>Erythromyces crocicreas</i>	<i>Erythromyces crocicreas</i>	100%
<i>Hymenochaete</i> OTU500	<i>Hymenochaete tongbiguanensis</i>	96%	<i>Hymenochaete tongbiguanensis</i>	93%	<i>Hymenochaete tongbiguanensis</i>	<i>Hymenochaete tongbiguanensis</i>	100%
<i>Subulicystidium</i> OTU541	<i>Subulicystidium perlongisporum</i>	94%	<i>Subulicystidium perlongisporum</i>	93%	<i>Subulicystidium perlongisporum</i>	<i>Subulicystidium perlongisporum</i>	100%
<i>Sistotremastrum</i> OTU194	<i>Sistotremastrum guttuliferum</i>	86%	<i>Sistotremastrum spp.</i>	-	<i>Sistotremastrum guttuliferum</i>	<i>Sistotremastrum guttuliferum</i>	99%
<i>Sistotremastrum</i> OTU493	<i>Sistotremastrum spp.</i>	-	<i>Sistotremastrum spp.</i>	-	<i>Sistotremastrum guttuliferum</i>	<i>Sistotremastrum guttuliferum</i>	99%
<i>Xenasmatella</i> OTU488	<i>Xenasmatella ardosiacae</i>	72%	<i>Xenasmatella ardosiacae</i>	59%	<i>Xenasmatella ardosiacae</i>	<i>Xenasmatella ardosiacae</i>	90%
<i>Dichomitus</i> OTU309	Multiple taxa including <i>Porogramme albocincta</i> and <i>Tinctoporellus spp.</i>	-	Multiple taxa including <i>Porogramme albocincta</i> and <i>Tinctoporellus spp.</i>	-	<i>Dichomitus squalens</i>	<i>Tinctoporellus sp. and</i> <i>Porogramme sp. clade</i>	74%
<i>Porogramme</i> OTU377	Multiple taxa including <i>Porogramme albocincta</i> and <i>Tinctoporellus spp.</i>	-	Multiple taxa including <i>Porogramme albocincta</i> and <i>Tinctoporellus spp.</i>	-	<i>Porogramme albocincta</i>	<i>Tinctoporellus sp. and</i> <i>Porogramme sp. clade</i>	74%
<i>Tinctoporellus</i> OTU512	Multiple taxa including <i>Porogramme albocincta</i> and <i>Tinctoporellus spp.</i>	-	Multiple taxa including <i>Porogramme albocincta</i> and <i>Tinctoporellus spp.</i>	-	<i>Tinctoporellus epimiltinus</i>	<i>Tinctoporellus sp. and</i> <i>Porogramme sp. clade</i>	74%
<i>Jianyunia</i> OTU49	<i>Jianyunia sakaguchii</i> <i>Bensingtonia sakaguchii</i>	38%	<i>Jianyunia sakaguchii</i> <i>Bensingtonia sakaguchii</i>	87%	<i>Jianyunia sakaguchii</i>	<i>Jianyunia sakaguchii</i>	78%
<i>Colacogloea</i> OTU48	<i>Colacogloea terpenoidalis</i>	43%	<i>Colacogloea terpenoidalis</i>	85%	<i>Colacogloea terpenoidalis</i>	<i>Colacogloea terpenoidalis</i>	100%
<i>Colacogloea</i> OTU50	<i>Colacogloea cycloclastica</i>	97%	<i>Colacogloea cycloclastica</i>	100%	<i>Colacogloea cycloclastica</i>	<i>Colacogloea cycloclastica</i>	100%
<i>Pseudohyphozyma</i> OTU45	Multiple taxa including <i>Pseudohyphozyma bogoriensis</i>	-	<i>Pseudohyphozyma bogoriensis</i>	100%	<i>Pseudohyphozyma bogoriensis</i>	<i>Pseudohyphozyma bogoriensis</i>	100%
<i>Tremella</i> OTU709	<i>Tremella spp.</i>	66%	<i>Tremella foliacea</i>	51%	<i>Tremella fuciformis</i>	<i>Tremella spp.</i>	100%

***Green highlight = identical identification at species level (bold letters indicate 99 – 100% Bootstrap support).
Orange highlight = identical identification at genus level. Red highlight = different identification at genus level.

Figure S16. Information on similarity of community composition in *Castanopsis carlesii* deadwood mycobiomes subjected to different bioinformatics parameters (rarified and rarified with singletons removed).

Parameter	Full-length ITS		ITS1		ITS2	
	Bray-Curtis similarity	Jaccard similarity	Bray-Curtis similarity	Jaccard similarity	Bray-Curtis similarity	Jaccard similarity
Replicate: 1 and 2						
Rarify	 0.38	 0.30	 0.37	 0.25	 0.38	 0.25
Rarify and singletons removed	 0.39	 0.61	 0.38	 0.47	 0.39	 0.52
Replicate: 1 and 3						
Rarify	 0.30	 0.23	 0.30	 0.24	 0.27	 0.22
Rarify and singletons removed	 0.30	 0.43	 0.30	 0.43	 0.28	 0.40
Replicate: 2 and 3						
Rarify	 0.16	 0.23	 0.14	 0.19	 0.17	 0.22
Rarify and singletons removed	 0.16	 0.41	 0.14	 0.32	 0.17	 0.40

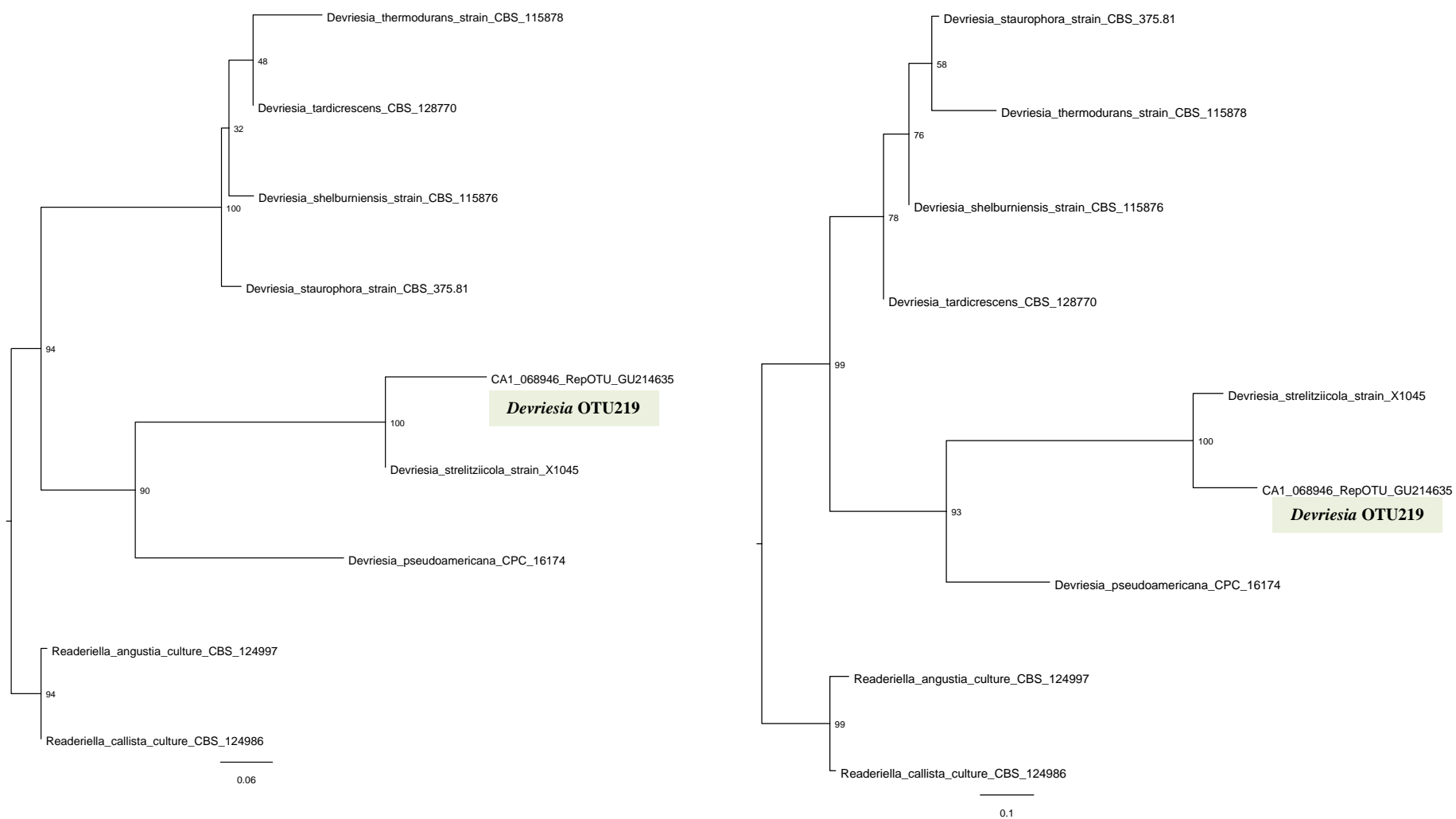


Figure S17. Phylograms of *Devriesia* OTU219 (Dothideomycetes) generated from Randomized Axelerated Maximum Likelihood (RAxML) analysis based on internal transcribed spacer 1 (ITS1, left) or on internal transcribed spacer 2 (ITS2; right) sequence.

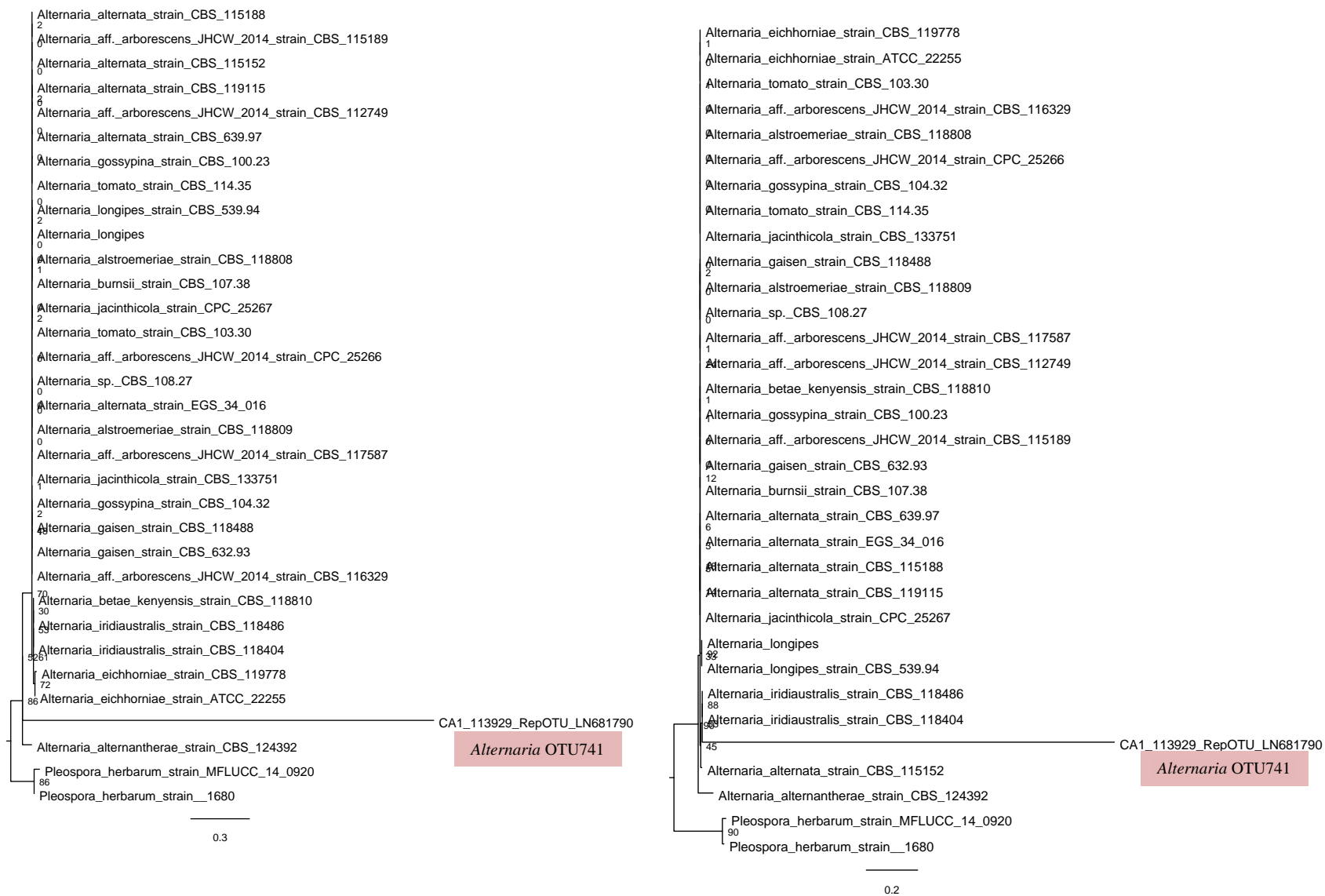


Figure S18. Phylograms of *Alternaria* OTU741 (Dothideomycetes) generated from Randomized Axelerated Maximum Likelihood (RAxML) analysis based on internal transcribed spacer 1 (ITS1, left) or on internal transcribed spacer 2 (ITS2; right) sequence.

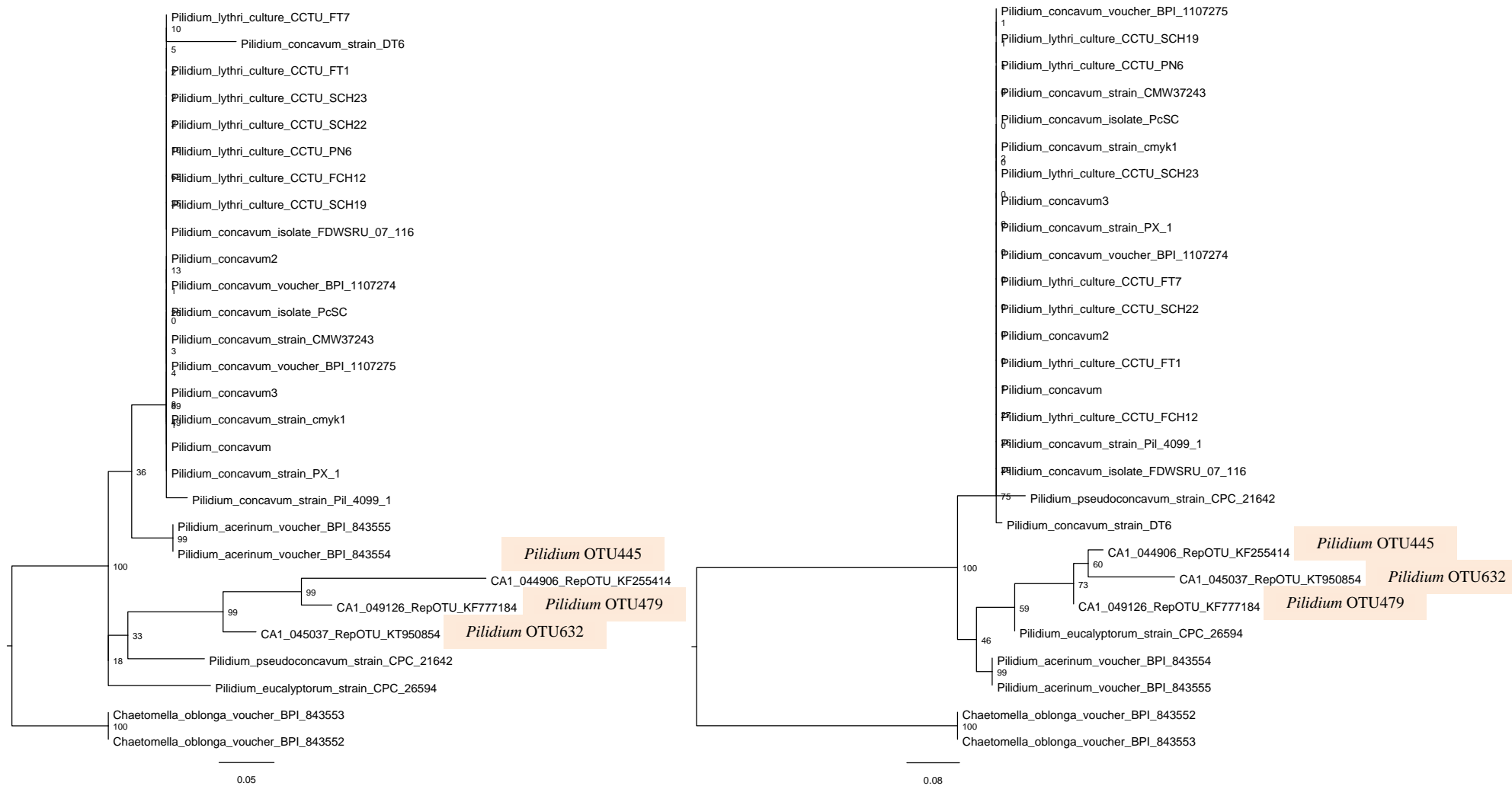


Figure S19. Phylograms of *Pilidium* OTU445, OTU479, OTU632 (Leotiomycetes) generated from Randomized Axelerated Maximum Likelihood (RAxML) analysis based on internal transcribed spacer 1 (ITS1, left) or on internal transcribed spacer 2 (ITS2; right) sequence.

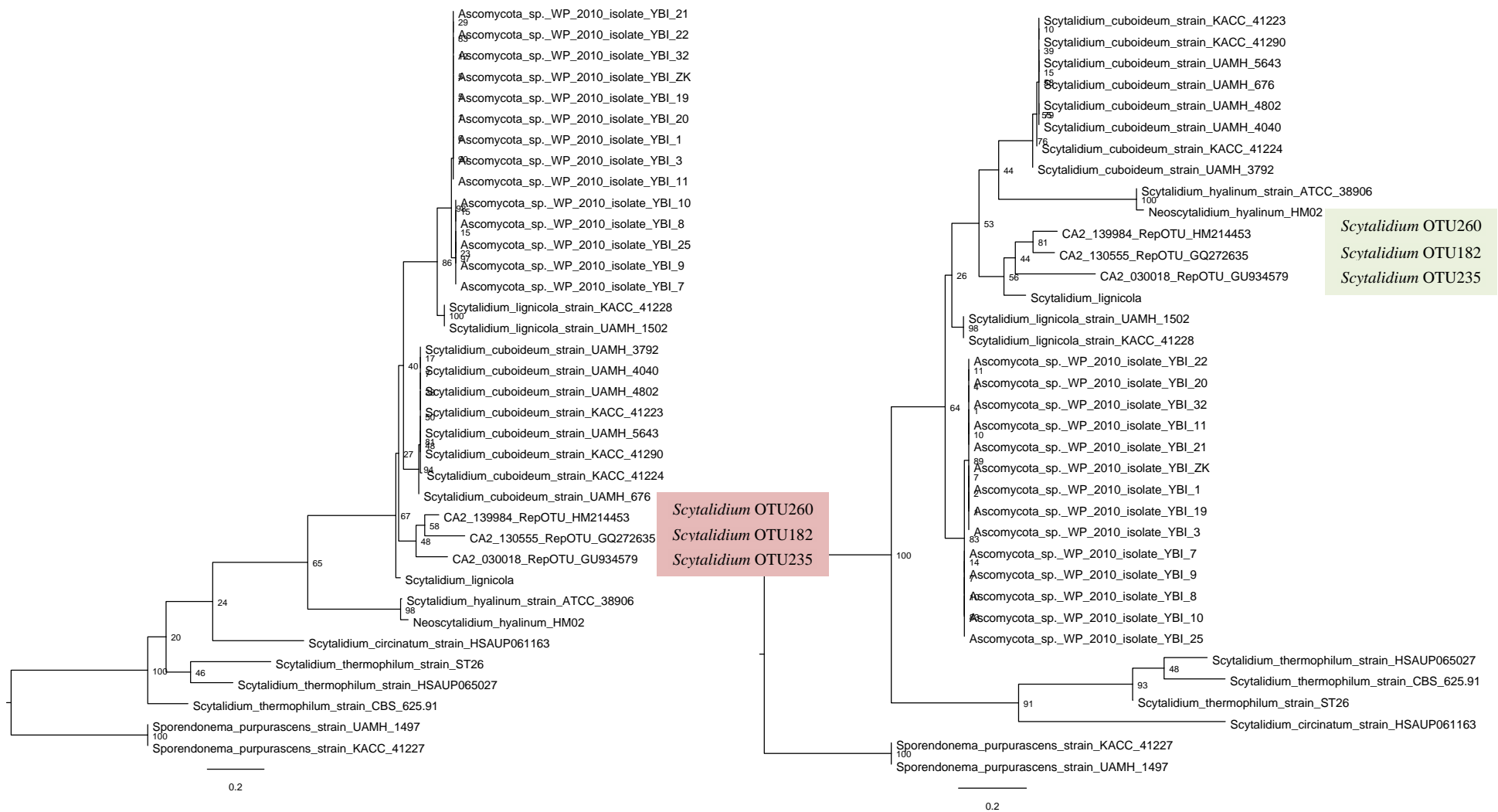


Figure S20. Phylograms of *Scytalidium* OTU182, OTU235, OTU260 (Leotiomycetes) generated from Randomized Axelerated Maximum Likelihood (RAxML) analysis based on internal transcribed spacer 1 (ITS1; left) or on internal transcribed spacer 2 (ITS2; right) sequence.

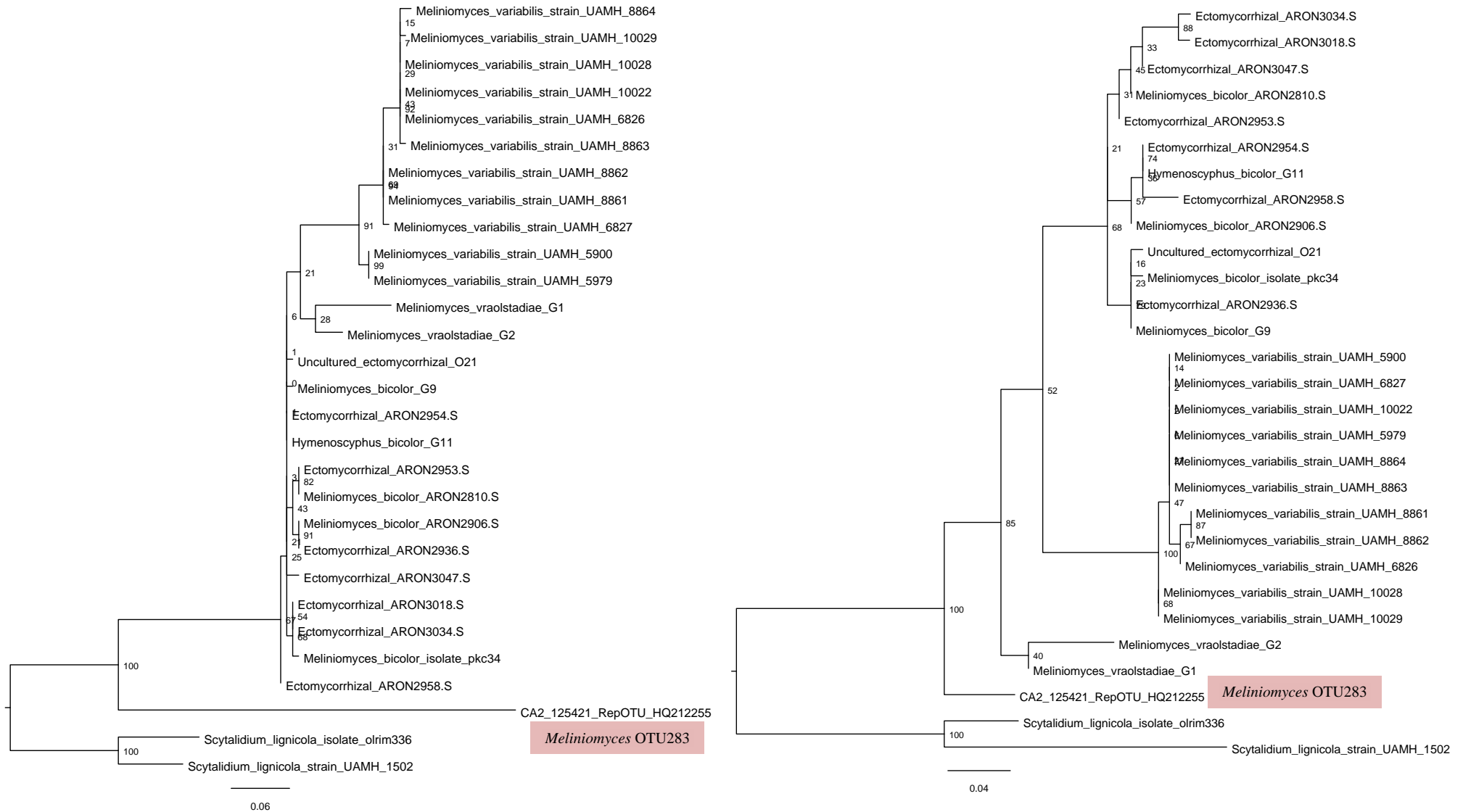


Figure S21. Phylograms of *Meliniomyces* OTU283 (Leotiomycetes) generated from Randomized Axelerated Maximum Likelihood (RAXML) analysis based on internal transcribed spacer 1 (ITS1, left) or on internal transcribed spacer 2 (ITS2; right) sequence.

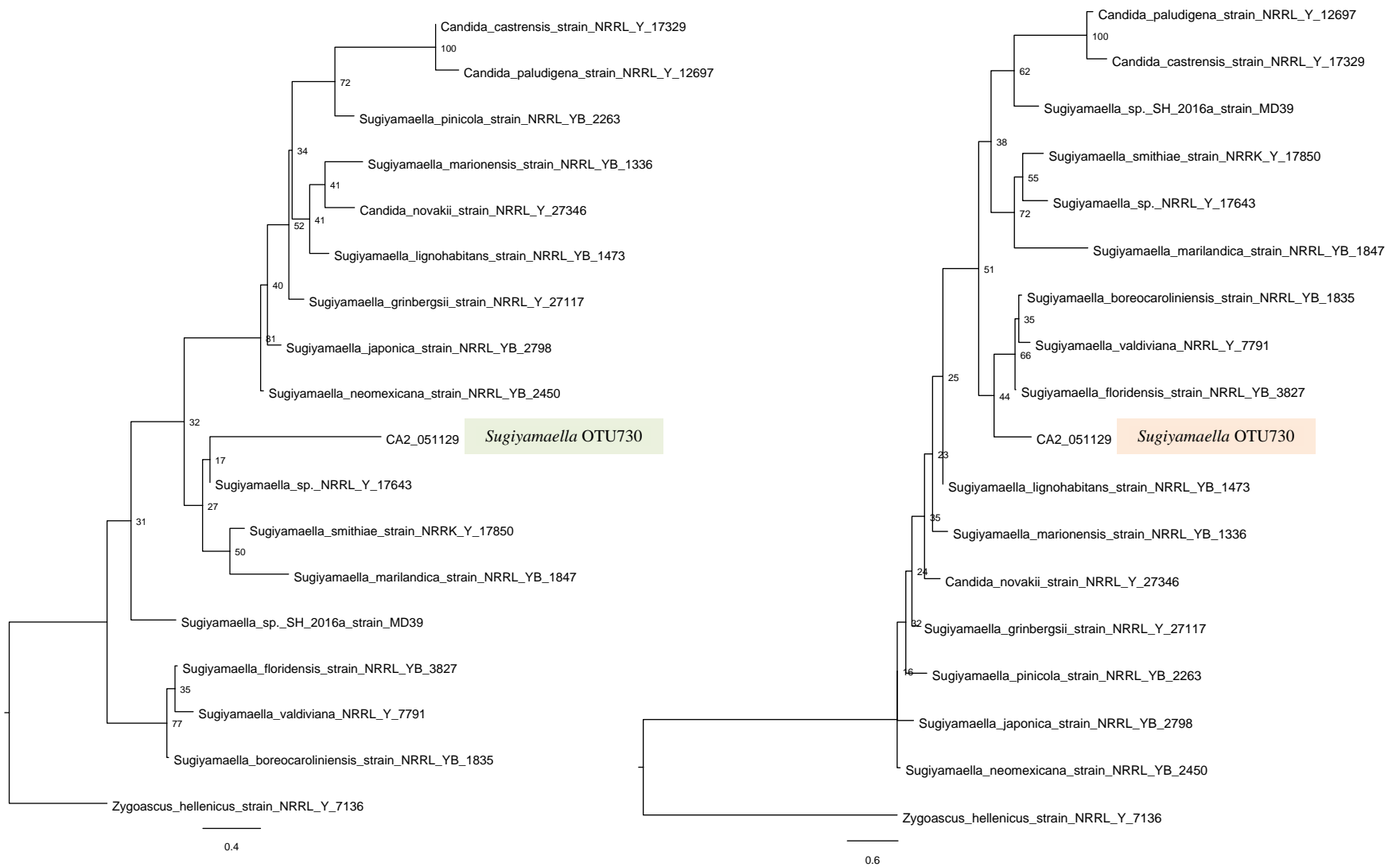


Figure S22. Phylograms of *Sugiyamaella* OTU730 (Saccharomycetes) generated from Randomized Axelerated Maximum Likelihood (RAxML) analysis based on internal transcribed spacer 1 (ITS1, left) or on internal transcribed spacer 2 (ITS2; right) sequence.

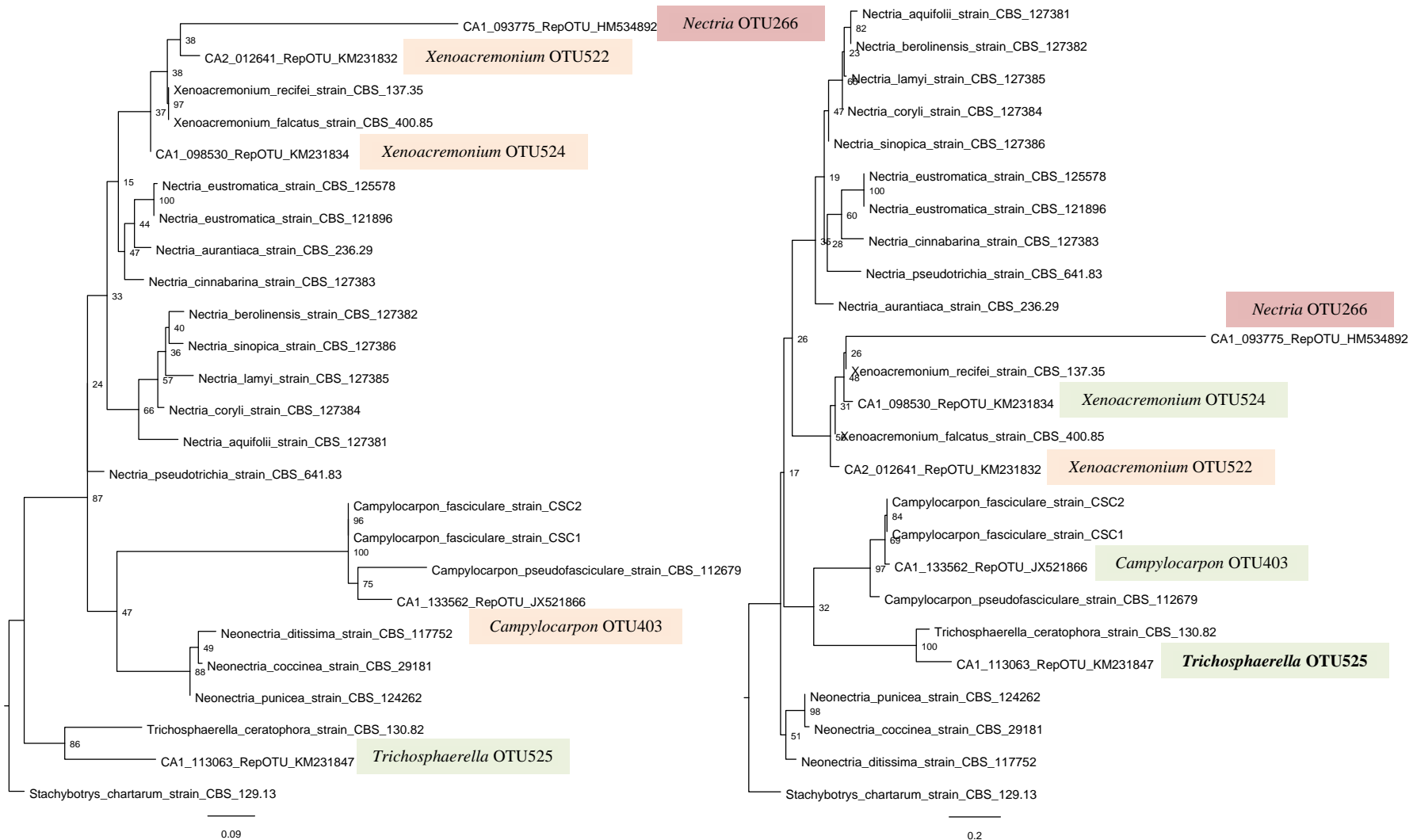


Figure S23. Phylograms of *Campylocarpon* OTU403 (Sordariomycetes), *Xenoacremonium* OTU524, OTU522 (Sordariomycetes), *Nectria* OTU266 (Sordariomycetes), *Trichosphaerella* OTU525 (Sordariomycetes) generated from Randomized Axelerated Maximum Likelihood (RAxML) analysis based on internal transcribed spacer 1 (ITS1, left) or on internal transcribed spacer 2 (ITS2; right) sequence.

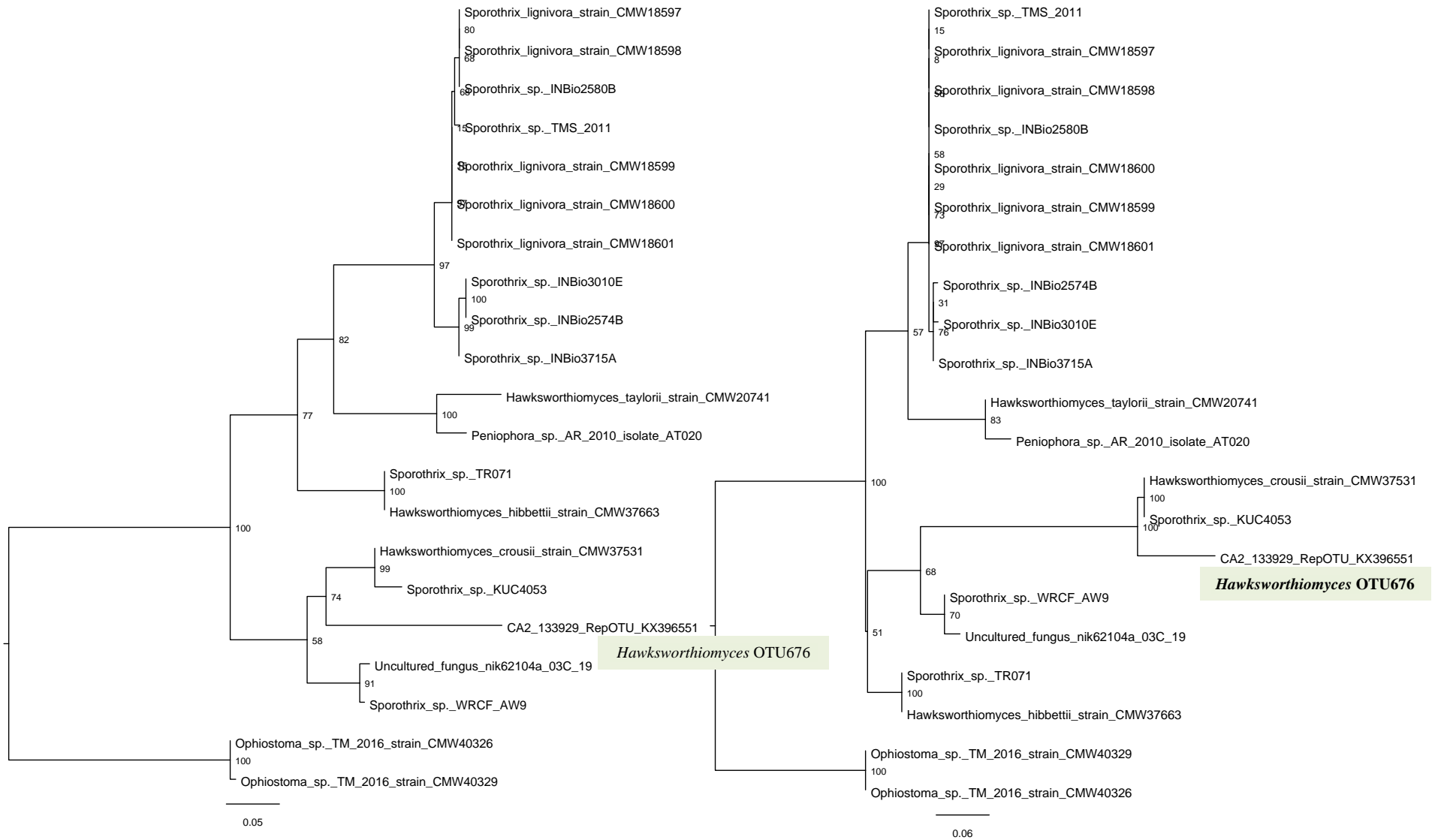


Figure S24. Phylograms of *Hawksworthiomyces* OTU666 (Sordariomycetes) generated from Randomized Axelerated Maximum Likelihood (RAxML) analysis based on internal transcribed spacer 1 (ITS1, left) or on internal transcribed spacer 2 (ITS2; right) sequence.

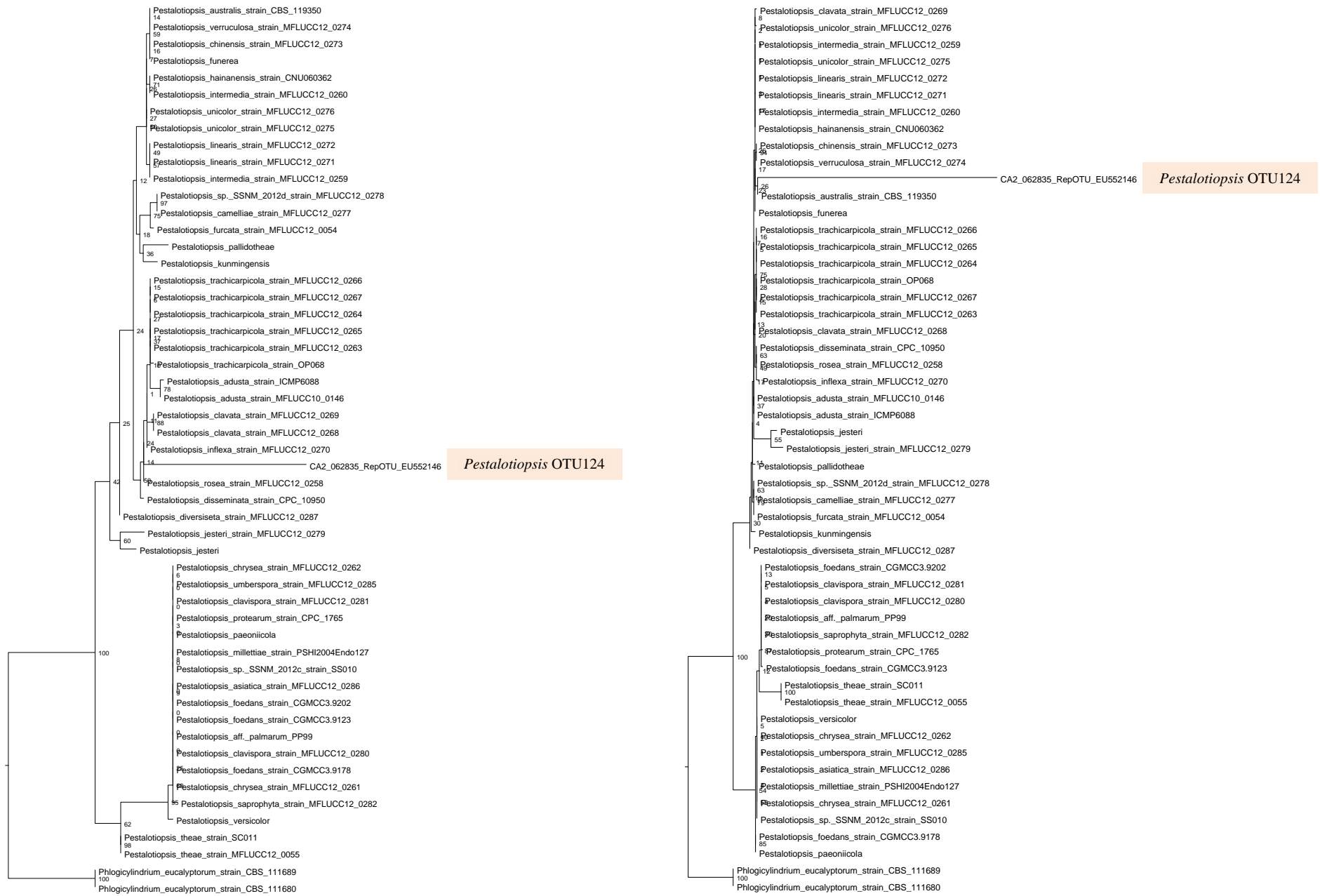


Figure S25. Phylograms of *Pestalotiopsis* OTU124 (Sordariomycetes) generated from Randomized Axelerated Maximum Likelihood (RAxML) analysis based on internal transcribed spacer 1 (ITS1, left) or on internal transcribed spacer 2 (ITS2; right) sequence.

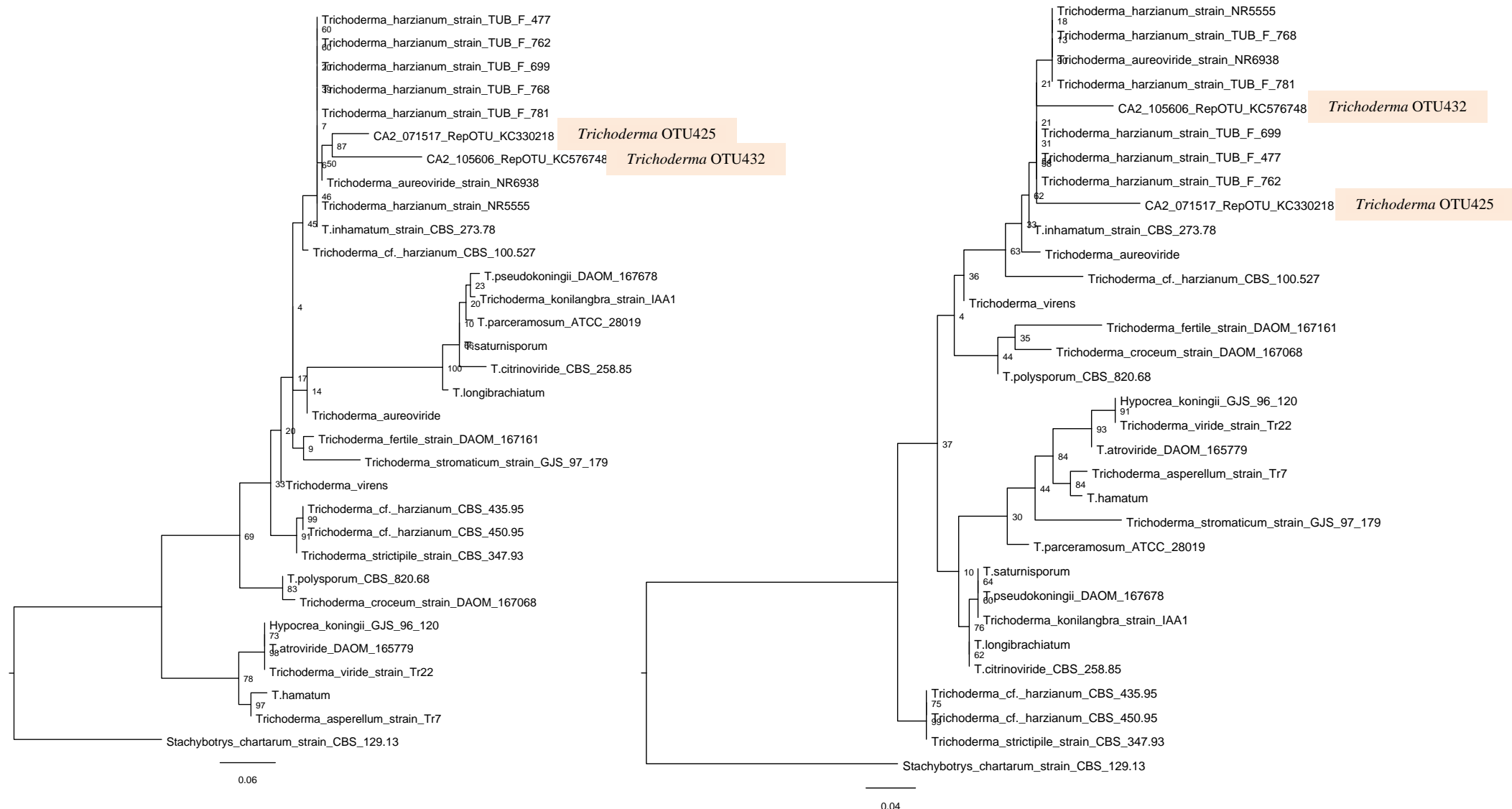


Figure S26. Phylograms of *Trichoderma* OTU425, OTU432 (Sordariomycetes) generated from Randomized Axelerated Maximum Likelihood (RAxML) analysis based on internal transcribed spacer 1 (ITS1, left) or on internal transcribed spacer 2 (ITS2; right) sequence.

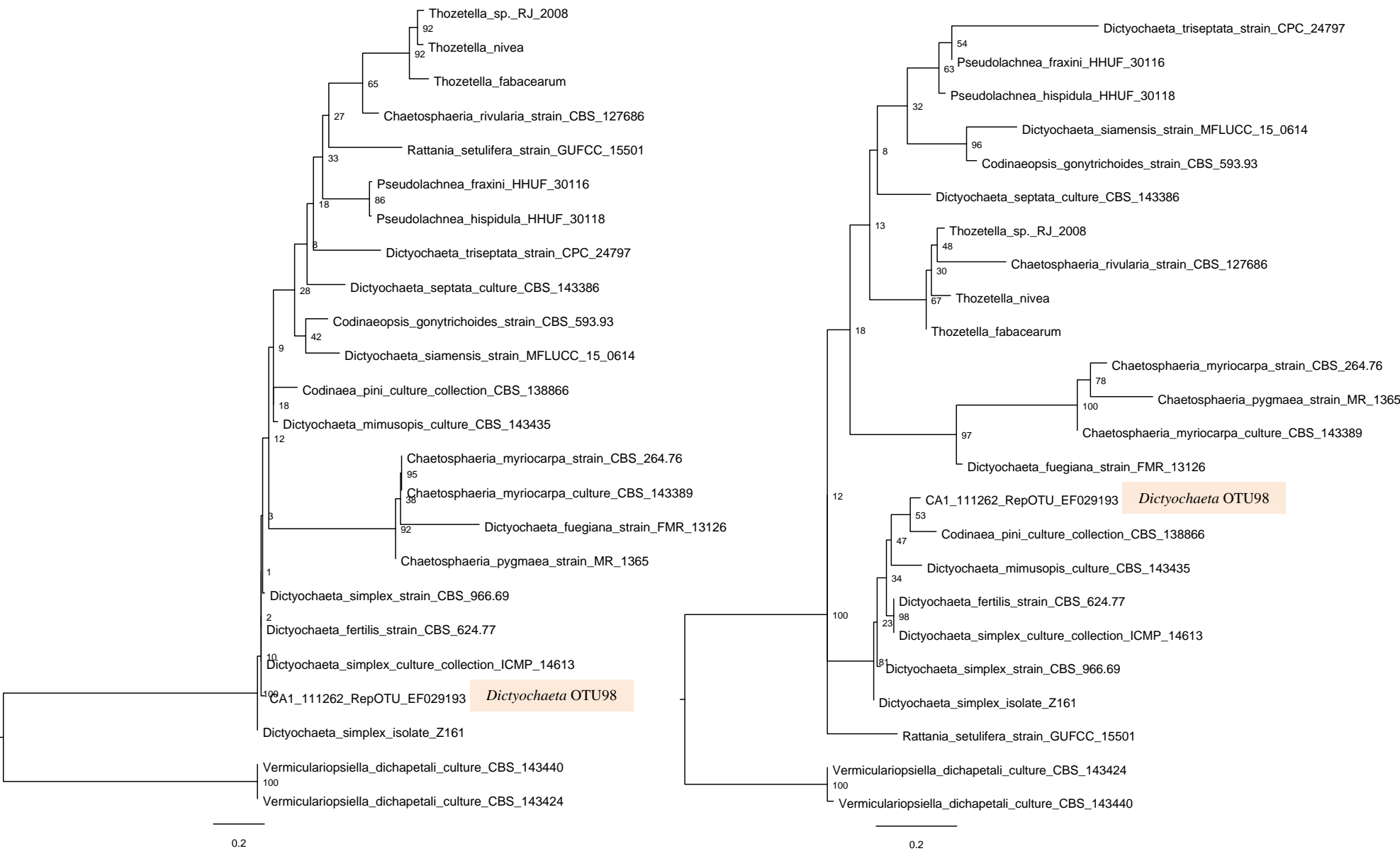


Figure S27. Phylograms of *Dictyochoeta* OTU98 (Sordariomycetes) generated from Randomized Axelerated Maximum Likelihood (RAxML) analysis based on internal transcribed spacer 1 (ITS1, left) or on internal transcribed spacer 2 (ITS2; right) sequence.

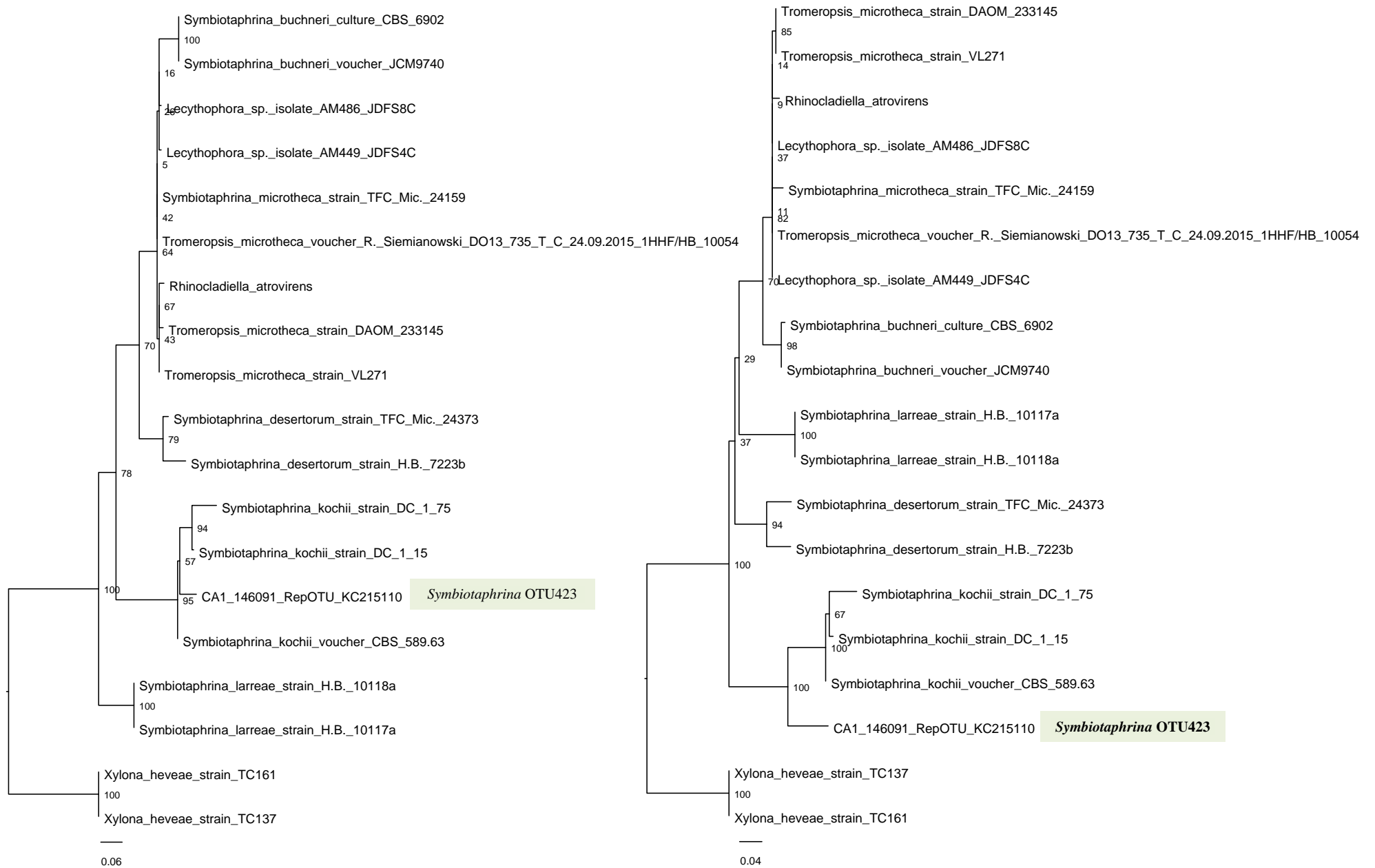


Figure S28. Phylograms of *Symbiotaphrina* OTU423 (Xylonomycetes) generated from Randomized Axelerated Maximum Likelihood (RAxML) analysis based on internal transcribed spacer 1 (ITS1, left) or on internal transcribed spacer 2 (ITS2; right) sequence.

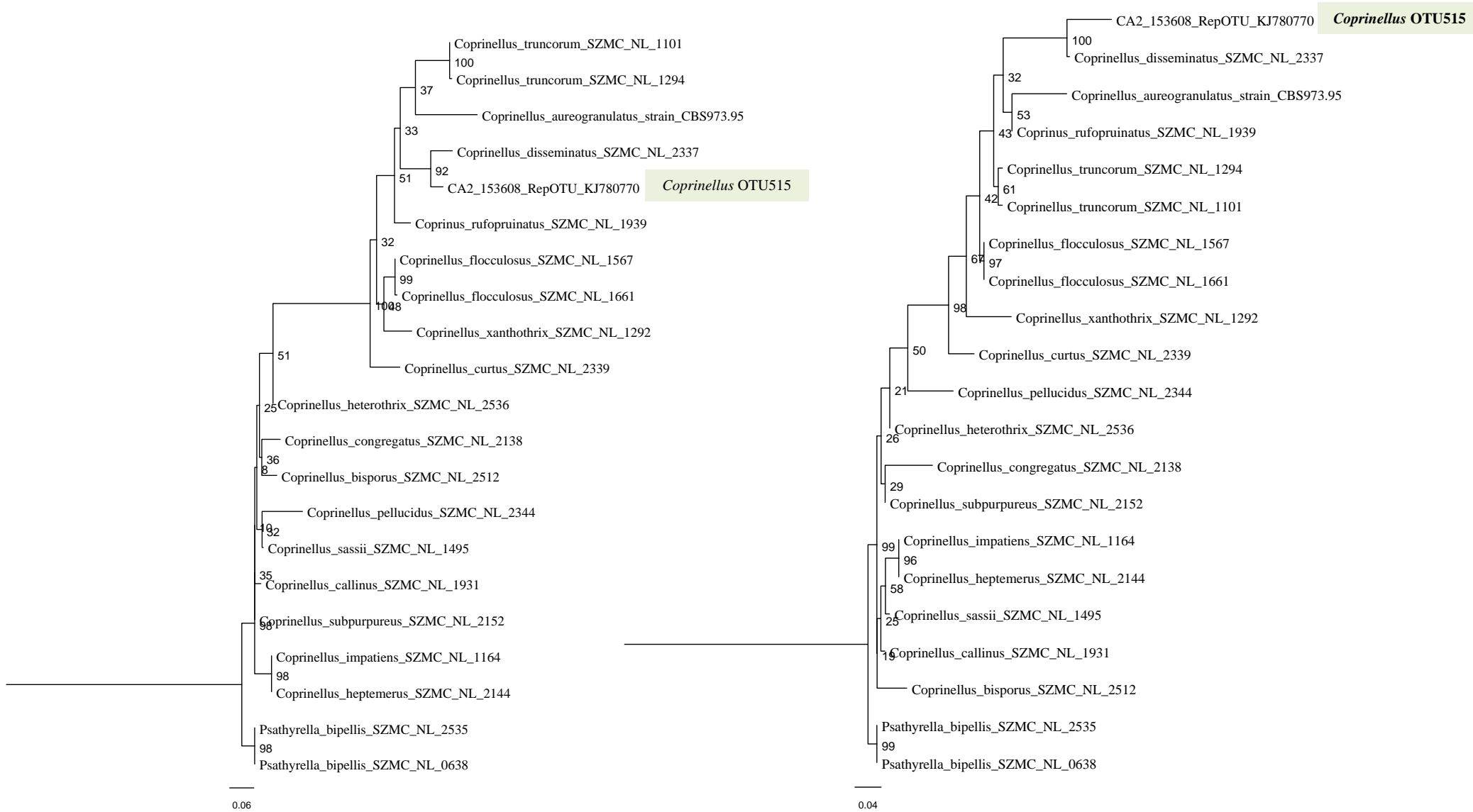


Figure S29. Phylograms of *Coprinellus OTU515* (Agaricomycetes) generated from Randomized Axelerated Maximum Likelihood (RAxML) analysis based on internal transcribed spacer 1 (ITS1, left) or on internal transcribed spacer 2 (ITS2; right) sequence.

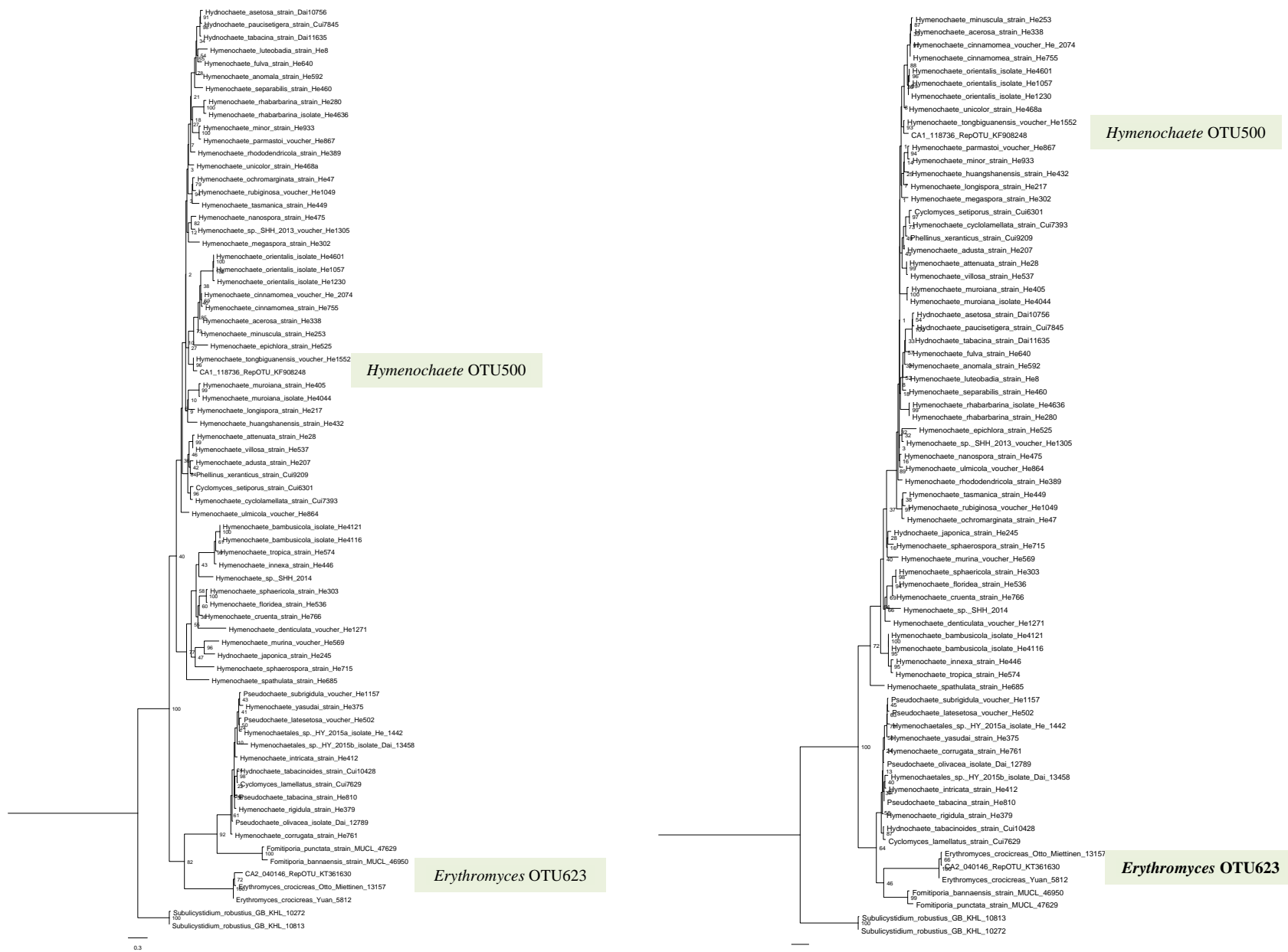


Figure S30. Phylograms of *Hymenochaete* OTU500 (Agaricomycetes), *Erythromyces* OTU623 (Agaricomycetes) generated from Randomized Axelerated Maximum Likelihood (RAxML) analysis based on internal transcribed spacer 1 (ITS1, left) or on internal transcribed spacer 2 (ITS2; right) sequence.

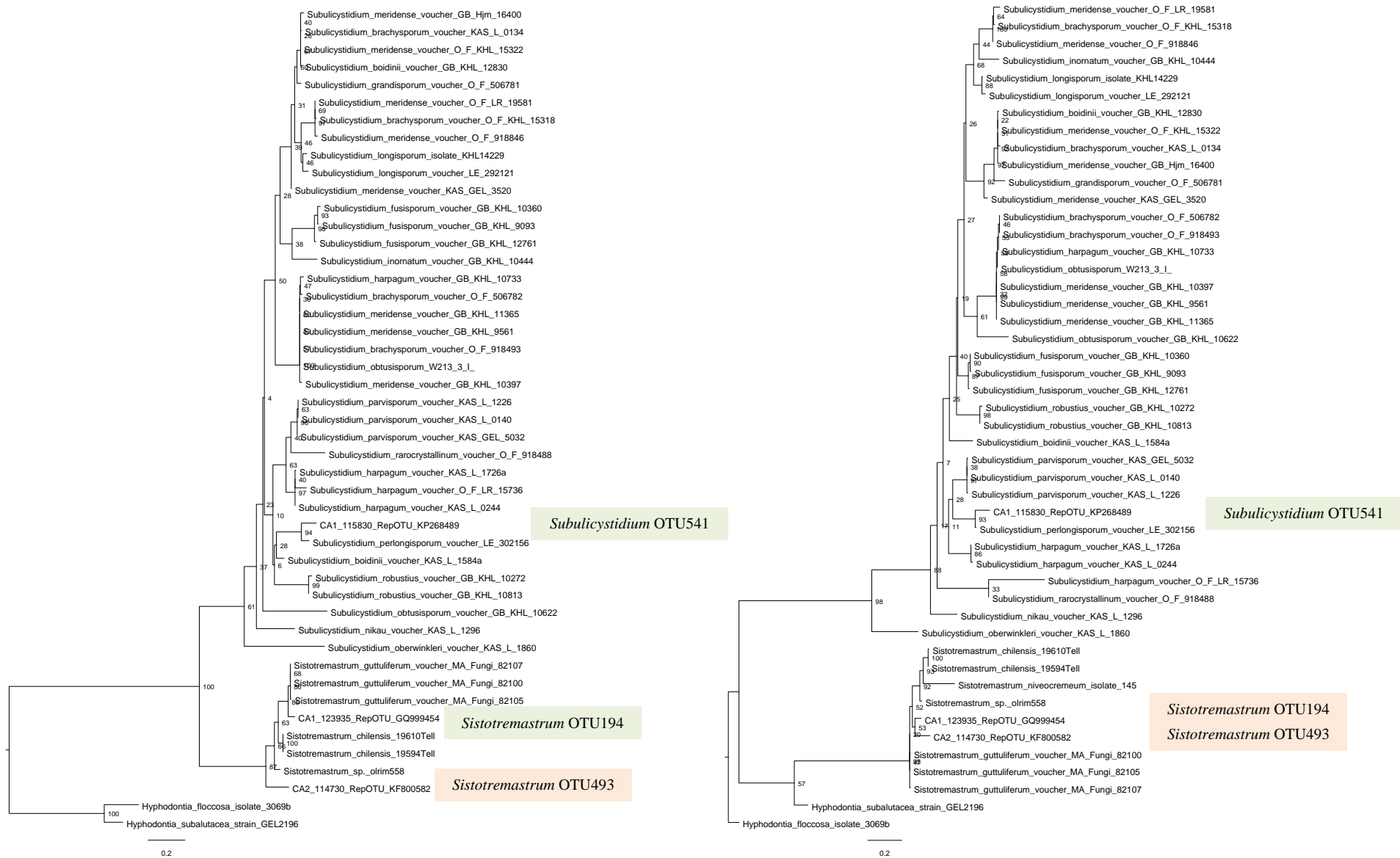


Figure S31. Phylograms of *Subulicystidium* OTU541, *Sistotremastrum* OTU194, OTU493 (Agaricomycetes) generated from Randomized Axelerated Maximum Likelihood (RAxML) analysis based on internal transcribed spacer 1 (ITS1, left) or on internal transcribed spacer 2 (ITS2; right) sequence.

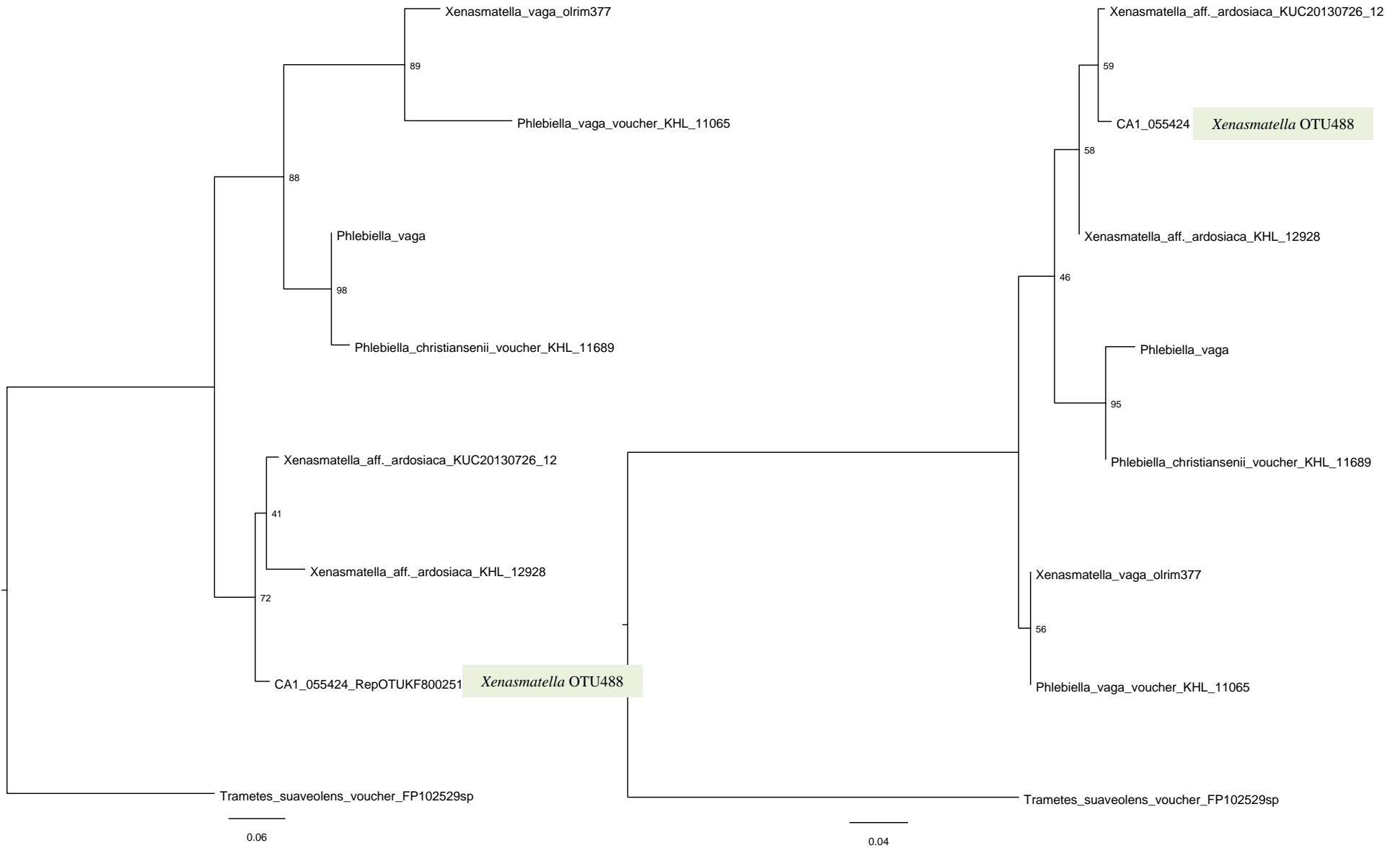


Figure S32. Phylograms of *Xenasmatella* OTU488 (Agaricomycetes) generated from Randomized Axelerated Maximum Likelihood (RAxML) analysis based on internal transcribed spacer 1 (ITS1, left) or on internal transcribed spacer 2 (ITS2; right) sequence.

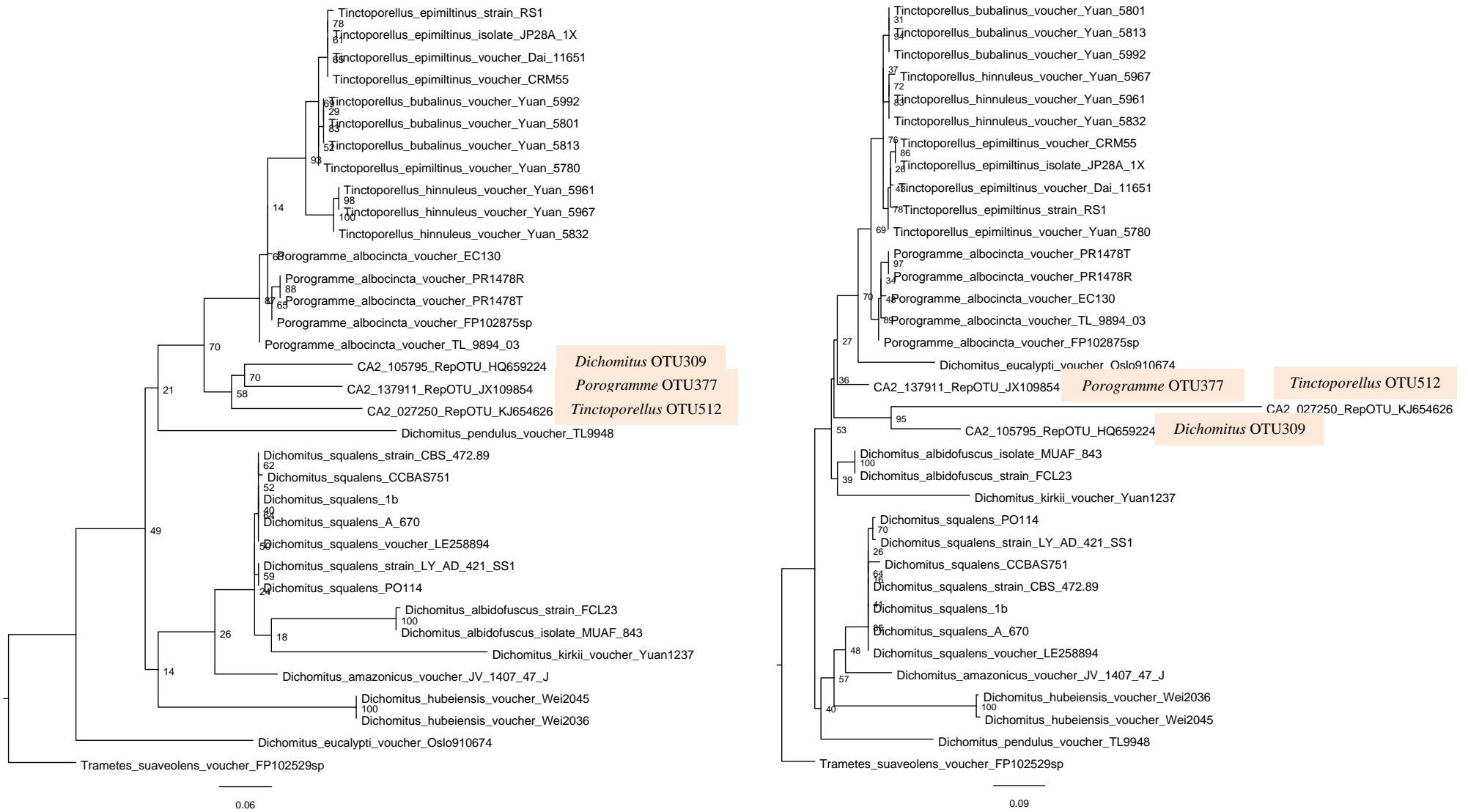


Figure S33. Phylograms of *Dichomitrus* OTU309 (Agaricomycetes), *Porogramme* OTU377 (Agaricomycetes), *Tinctoporellus* OTU512 (Agaricomycetes) generated from Randomized Axelerated Maximum Likelihood (RAxML) analysis based on internal transcribed spacer 1 (ITS1, left) or on internal transcribed spacer 2 (ITS2; right) sequence.

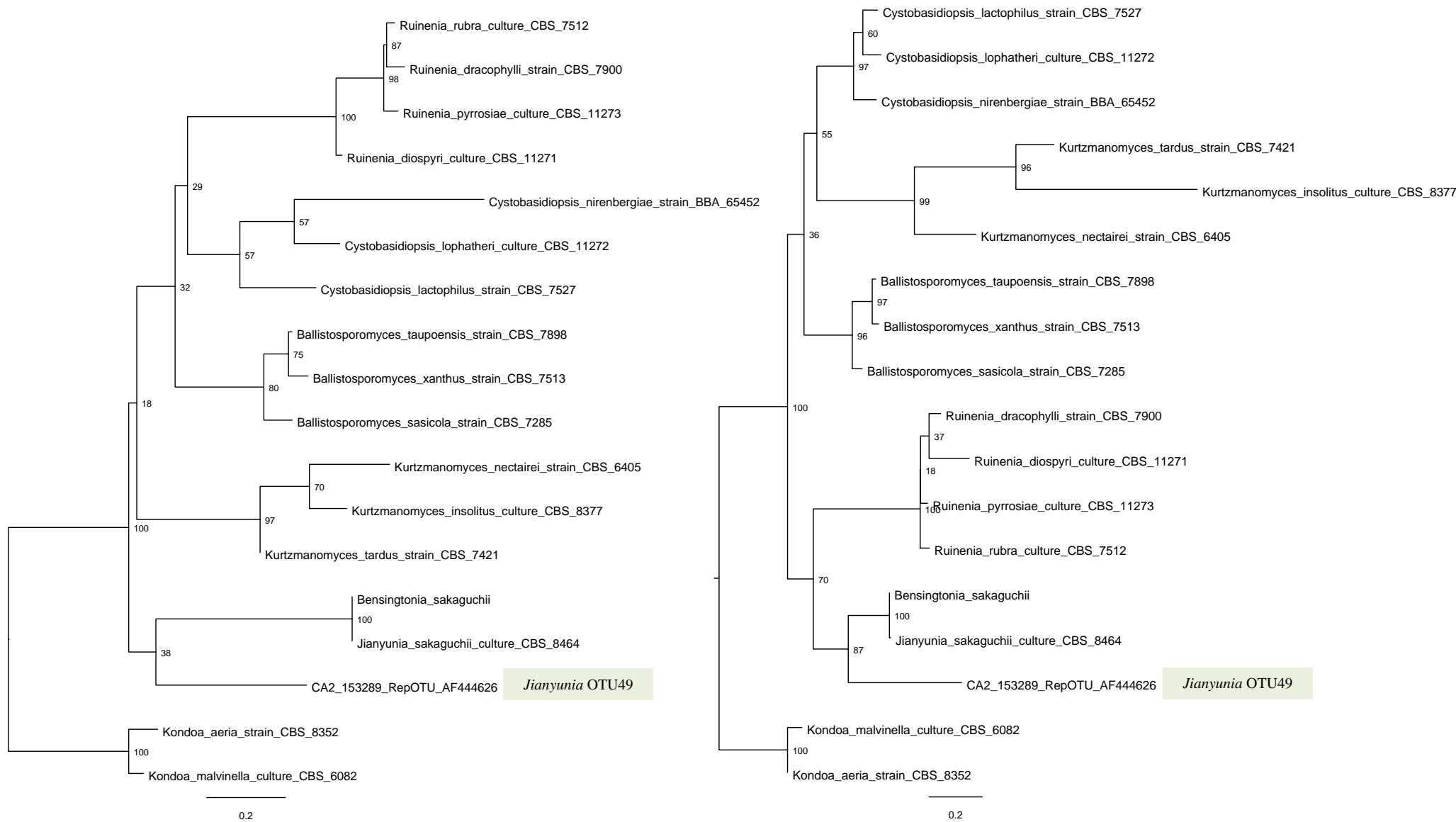


Figure S34. Phylograms of *Jianyunia* OTU49 (Agaricomycetes) generated from Randomized Axelerated Maximum Likelihood (RAxML) analysis based on internal transcribed spacer 1 (ITS1, left) or on internal transcribed spacer 2 (ITS2; right) sequence.

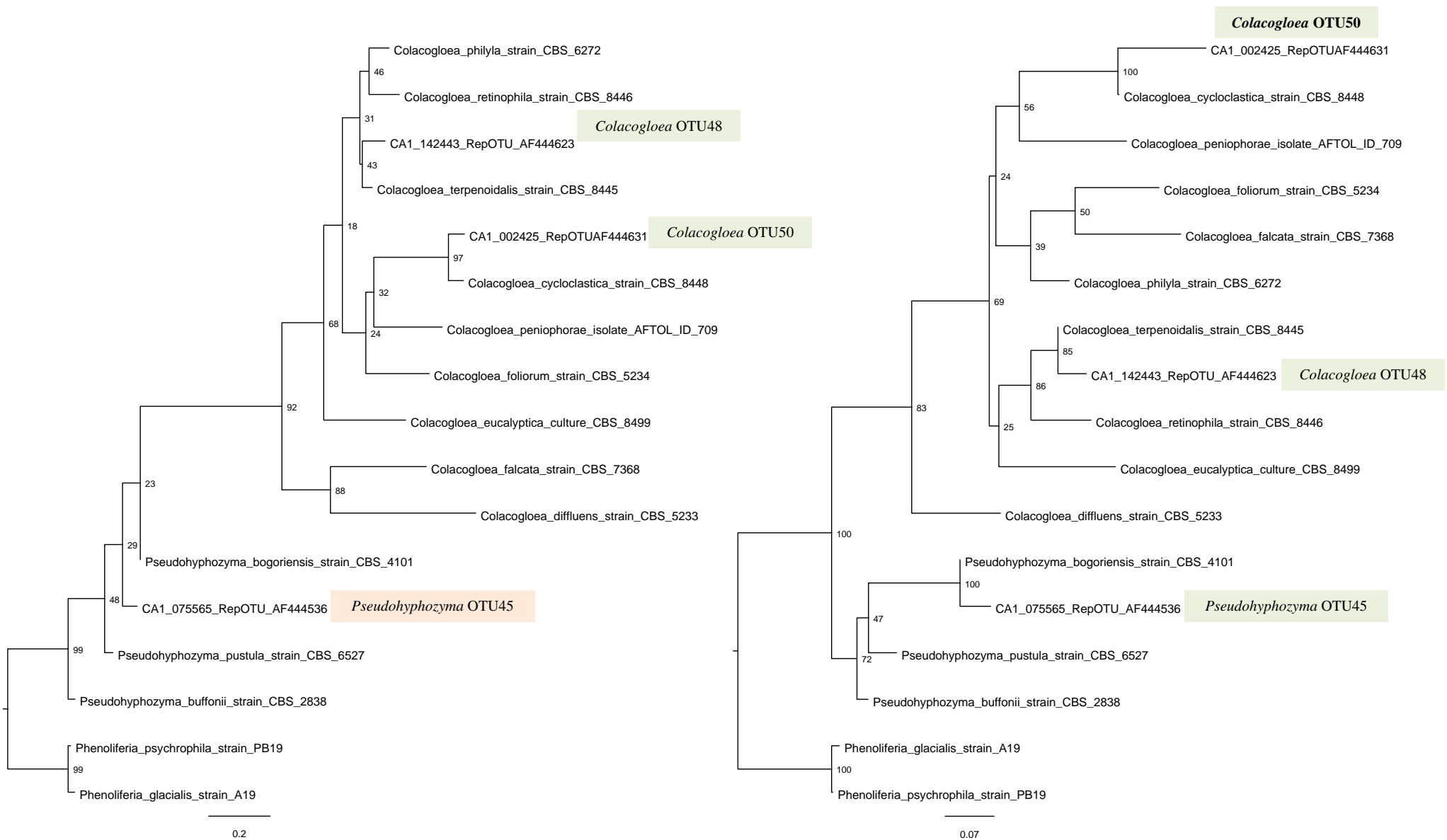


Figure S35. Phylograms of *Colacogloea* OTU48, OTU50 (Microbotryomycetes), *Pseudohyphozyma* OTU45 (Microbotryomycetes) generated from Randomized Axelerated Maximum Likelihood (RAXML) analysis based on internal transcribed spacer 1 (ITS1, left) or on internal transcribed spacer 2 (ITS2; right) sequence.

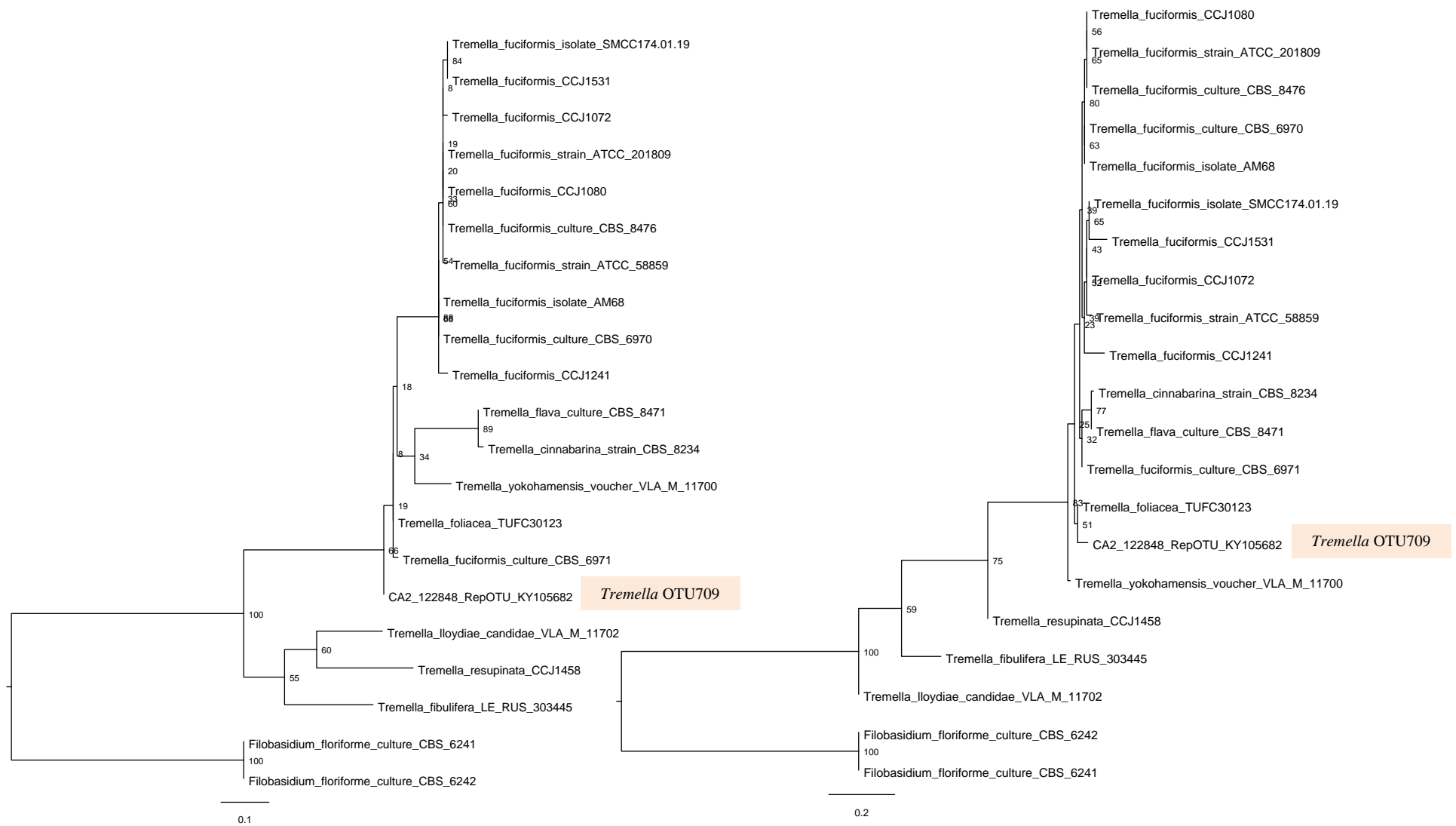


Figure S36. Phylograms of *Tremella* OTU709 (Tremellomycetes) generated from Randomized Axelerated Maximum Likelihood (RAxML) analysis based on internal transcribed spacer 1 (ITS1, left) or on internal transcribed spacer 2 (ITS2; right) sequence.