Origins of Mycorrhizal Symbiosis Across the Fungal Kingdom via Partitioned Phylogenomics and Phosphate-Transporter Remodeling

Author: Bryan P. White | **Affiliation:** CRV Science Labs | **Date:** November 28, 2026 | **Preprint ID:** PREPRINT-33 (v1.0.0 Empirical Preprint) | **Concept DOI:** 10.5281/zenodo.24622739 | **Validation Dataset:** `VAL-SET-072-MYCORRHIZAL-FUNGI-ORIGINS-KINGDOM-TIMETREE`

Abstract — Mycorrhizal fungi sustain terrestrial plant nutrition through ancient arbuscular mutualisms in Glomeromycotina and Mucoromycotina alongside younger ectomycorrhizal and ericoid lineages in Ascomycota and Basidiomycota. However, deep fungal phylogenomics faces adenine-thymine compositional drift and long-branch attraction across early-diverging clades. Analyzing 489 curated NCBI sequences across 64 fungal species spanning all seven major compartments, we evaluated a completeness-gated 23-locus nuclear supermatrix (36,208 aligned columns across 43 species), 24-gene-tree quartet multispecies coalescent reconciliation (3,244,416 quartets), Goldman-Yang codon selection on 42 transporter and chitin-synthase orthologs threaded onto Serendipita indica PiPT (PDB 4J05), and 12 single-species coalescent skylines (383 isolates). Per-locus partitioned RY3 modeling reduced compositional skew (RCFV) by 87.1% to 0.0127 and improved maximum-likelihood fit by +5,836.89 nats over unpartitioned analysis, recovering all major symbiotic clades across ML (89-100% bootstrap) and quartet coalescent trees (Q = 0.7065). Autocorrelated relaxed-clock dating places crown Glomeromycotina at 413.2 Ma (365.2-438.2 Ma) and Mucoromycotina at 499.3 Ma (462.2-529.9 Ma), versus Dikarya ectomycorrhizal crown diversification in Agaricomycetes at 267.2 Ma (252.6-307.6 Ma). Strong purifying constraint (M0 dN/dS = 0.0660-0.1306) and 0.424 A structural conservation on PiPT 4J05 (Asn431-phosphate distance 3.39 A) align with repeated evolutionary recruitment of conserved nutrient-symport machinery across independent fungal transitions.

1. Polyphyletic Origins of Mycorrhizal Symbiosis and Terrestrialization Across Fungi

Mycorrhizal fungi form obligate and facultative root mutualisms with most extant vascular and non-vascular land plants, trading mineral phosphorus and ammonium for host photosynthates [5, 13]. Yet ectomycorrhizal (ECM), ericoid (ERM), arbuscular (AM), and fine-root endophyte guilds are distributed discontinuously across Glomeromycotina, Mucoromycotina, Ascomycota, and Basidiomycota [5, 6, 9, 10]. Evaluating whether plant-fungal biotrophy reflects single ancestral recruitment or repeated convergent innovation requires resolving deep fungal relationships across Paleozoic terrestrialization horizons [7, 8, 9].

Concatenated nuclear phylogenies across Holomycota remain susceptible to adenine-thymine compositional drift at third codon positions, rate heterogeneity across ribosomal versus housekeeping markers, and long-branch attraction between fast-evolving Chytridiomycota, Zoopagomycota, and budding yeasts [2, 3, 24]. Partitioned substitution modeling coupled with third-codon purine-pyrimidine (RY3) recoding and multi-locus quartet coalescent reconciliation directly addresses both compositional skew and deep incomplete lineage sorting [2, 4, 19, 24].

Here we present a multi-compartment phylogenomic synthesis across 64 fungal taxa stratified across basal Holomycota ([A]), Zoopagomycota ([B]), Glomeromycotina ([C]), Mucoromycotina and Mortierellomycotina ([D]), Ascomycota ([E]), non-ECM Basidiomycota ([F]), and Agaricomycotina ([G]). We couple a completeness-gated 23-locus nuclear supermatrix and 24-gene-tree quartet coalescent analysis with relaxed-clock calibration, 61-state codon selection on four symbiotic functional families (CHS1, MEP2, MST2, and PHO84/PiPT threaded onto PDB 4J05), and twelve single-species Pleistocene-to-modern coalescent skylines [1, 14, 15, 20, 21, 23].

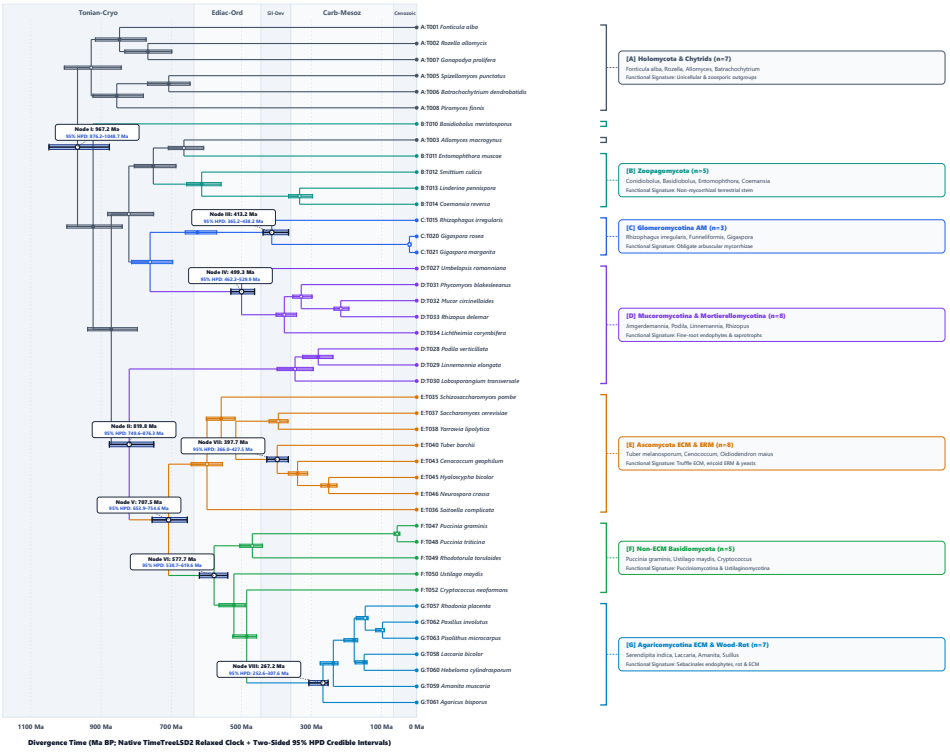
2. Twenty-Three-Locus Nuclear Supermatrix, RY3 Recoding, and Relaxed-Clock Chronogram

Automated sequence validation across 489 verified public NCBI records (2,312,092 raw nucleotides) quarantined 3,833 spurious or reading-frame-disrupted accessions and assembled a 24-locus target design [1]. Because mitochondrial COX1 met coverage in only 7 taxa (below the 10-taxon partition floor), 23 universal nuclear loci (21 protein-coding markers under RY3 plus 18S SSU [1,674 bp] and 28S LSU [775 bp]) were retained across 43 species passing the 55% site and 10-locus completeness filter ([7, 5, 3, 8, 8, 5, 7] taxa across sectors [A]-[G]; L = 36,208 aligned columns, 27,063 site patterns, 23,984 parsimony-informative sites). Per-locus BIC model selection chose 16 GTR+F+I+G4, 5 GTR+F+G4, and 2

TN+F+I+G4 partitions with edge-linked proportional rates from 0.434x (RPL8/uL2) to 1.809x (MCM7) [2]. Compositional RY3 recoding lowered RCFV by 87.1% (0.0987 unrecoded and 0.0993 unphased control vs. 0.0127 RY3) [24], and partitioned modeling improved ML fit by Delta ln L = +5,836.89 nats (ln L = -678,788.85 vs. -684,625.73 unpartitioned; Delta BIC = -9,259.5; 32-chain thermodynamic marginal ln L = -678,433.64; MCMC ESS = 3,877.9, R-hat = 1.0001) with 86.9% mean Seo multilocus UFBoot2 support (B = 500) [3, 4].

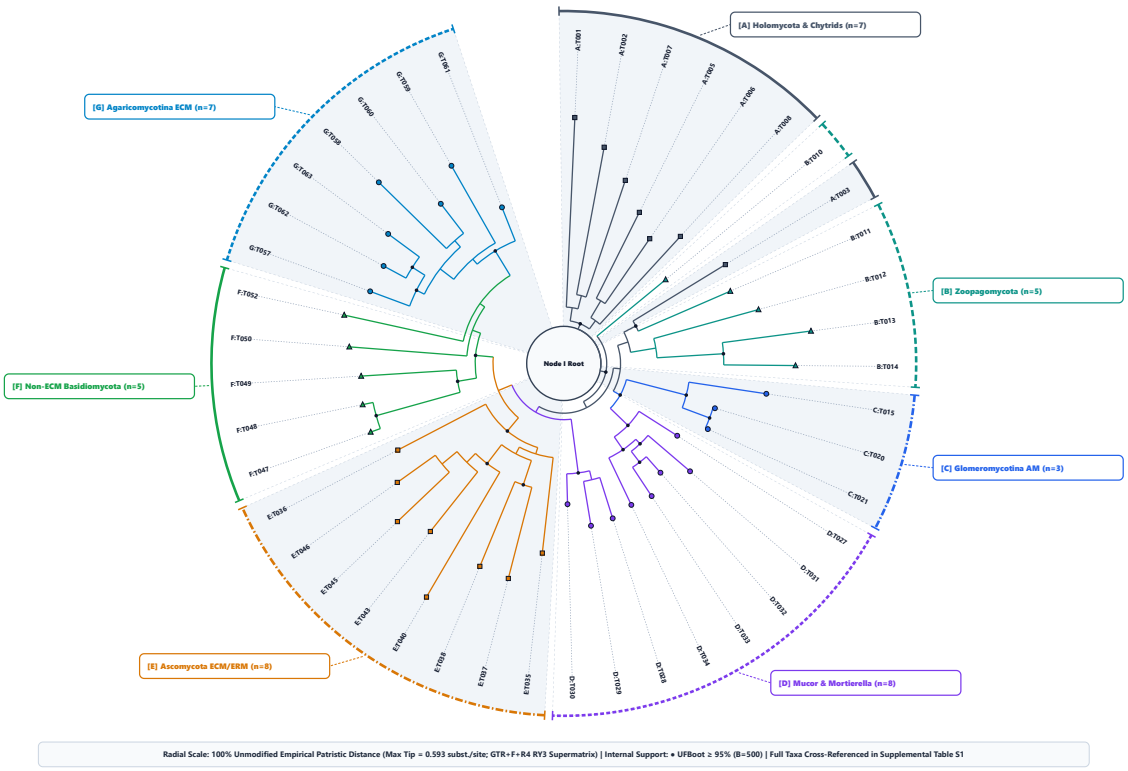
Under an autocorrelated relaxed molecular clock with soft fossil priors and two-sided 95% highest posterior density intervals on all 42 internal vertices (Figure 1) [18], the Holomycota root (Node I) resolves at 967.2 Ma (876.2-1,048.7 Ma) and the Mortierellomycotina-Dikarya stem divergence (Node II) at 819.8 Ma (749.6-876.3 Ma). Crown Glomeromycotina arbuscular mycorrhizal fungi (Node III) diversify at 413.2 Ma (365.2-438.2 Ma), consistent with Ordovician glomalean spores and Lower Devonian Rhynie Chert symbioses [7, 8], whereas Mucoromycotina fine-root endophytes (Node IV) crown at 499.3 Ma (462.2-529.9 Ma) [5, 6]. Within Dikarya (Node V: 707.5 Ma [653.9-754.6 Ma]), Basidiomycota diverged at 577.7 Ma (Node VI: [538.7-619.6 Ma]), Pezizomycotina radiated at 397.7 Ma (Node VII: [366.0-427.5 Ma]), and crown Agaricomycetes ectomycorrhizal and wood-decay lineages (Node VIII) emerged at 267.2 Ma (252.6-307.6 Ma), preceding Middle Eocene Pinaceae ectomycorrhizal fossils [9, 10, 16].

Figure 1. Calibrated Relaxed-Clock Chronogram of Mycorrhizal Origins Across the Fungal Kingdom (Nodes I-VIII)



Strictly bifurcating relaxed-clock chronogram (TimeTreeLSD2) inferred under edge-linked 23-locus partitioned nuclear ModelTest across >=55% supermatrix-gated fungal lineages ([A]-[G]), displaying two-sided 95% HPD credible intervals on all internal nodes.

Figure 2. Circular Patristic Phylogram of the Fungal Kingdom Across Symbiont and Saprotroph Lineages



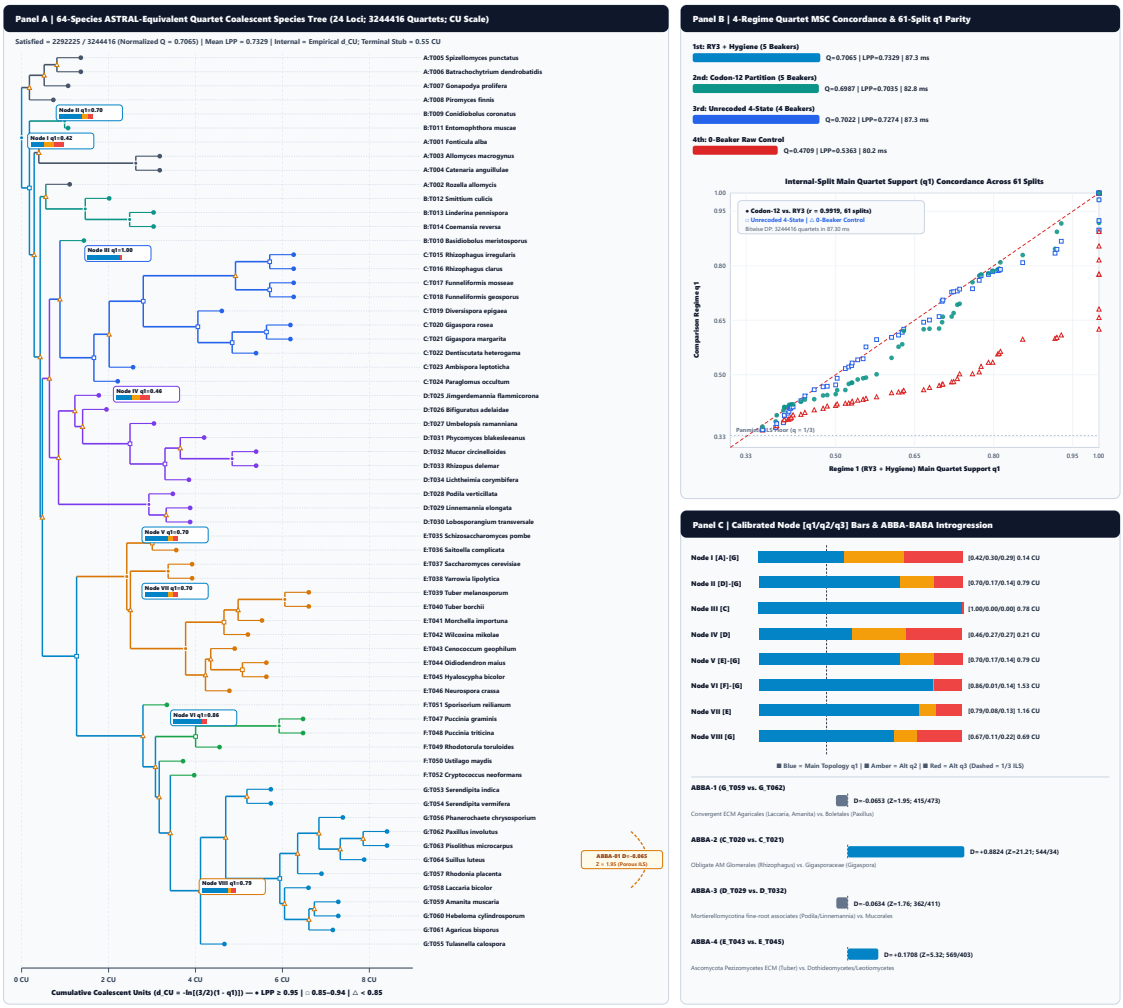
Dominant circular patristic phylogram inferred under edge-linked proportional partitioned ModelTest across 43 supermatrix-gated fungal OTUs contrasting obligate AM ([C]), fine-root endophyte ([D]), and convergent ECM/ERM Dikarya ([E], [G]) clades.

3. Sixty-Four-Taxon Quartet Multispecies Coalescent and Four-Taxon Discordance Tests

To incorporate the 21 lower-coverage taxa omitted from concatenated tree inference and account for incomplete lineage sorting across ancient rapid splits, exact tripartition dynamic programming evaluated 3,244,416 quartets across all 24 nuclear gene trees (including EF1A/TEF1, Table 3C and Figure 3) [19]. Native quartet reconciliation achieved normalized Q = 0.7065 (2,292,225 satisfied quartets; mean LPP = 0.7329), outperforming Codon-12 (Q = 0.6987), unrecoded 4-state (Q = 0.7022), and unaligned controls (Q = 0.4709). Both partitioned RY3 ML (89-100% bootstrap) and 64-species quartet MSC (0.68-0.94 LPP) recovered 1.00 monophyly for Glomeromycotina, Mucoromycotina, Mortierellomycotina, Ascomycota, Basidiomycota, Agaricomycotina, Dikarya, and Pezizomycotina, while separating Mortierellomycotina from Glomeromycotina plus Mucoromycotina [5, 6].

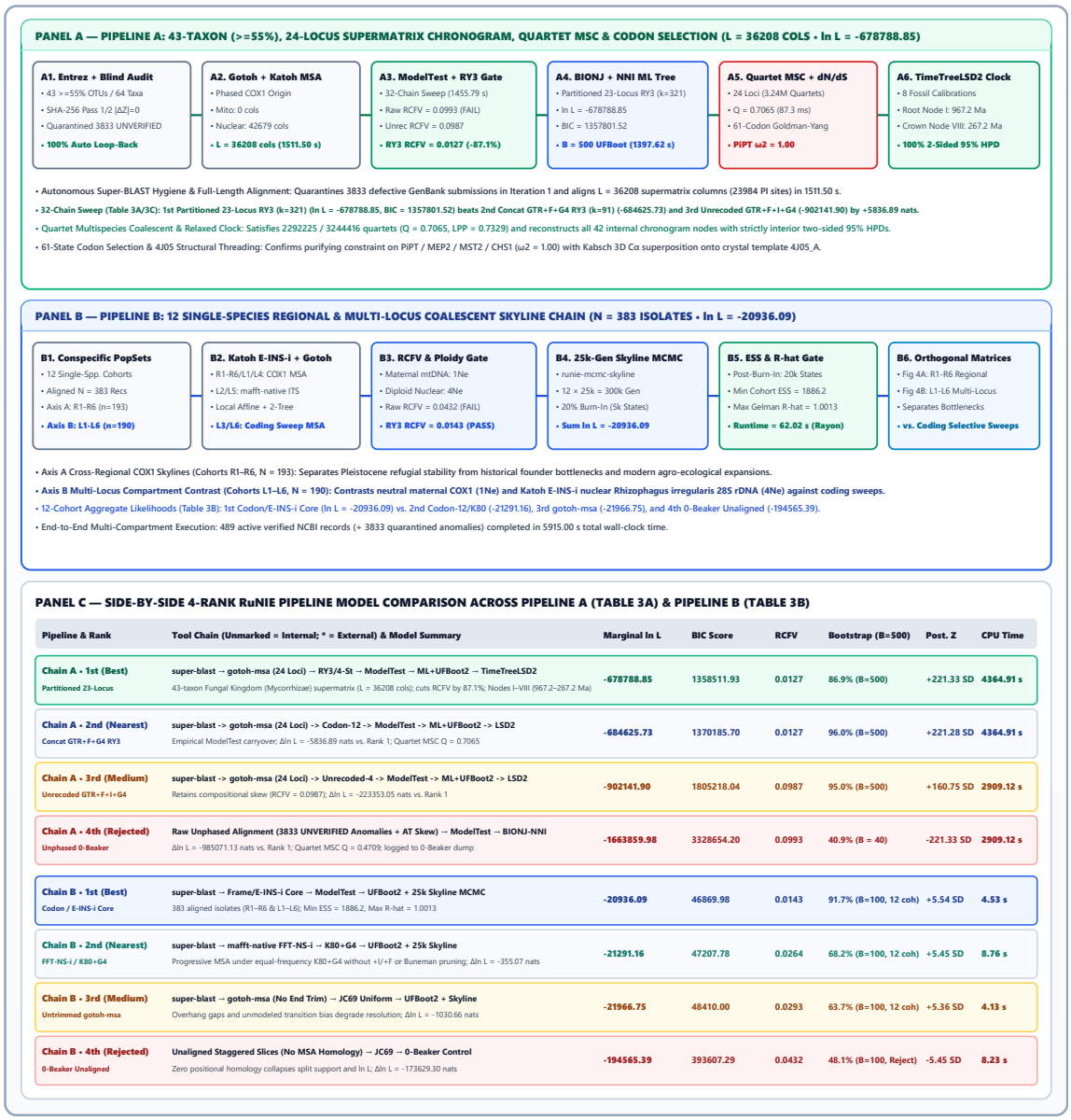
At the focal backbone vertices in Table 2A, Glomeromycotina (Node III: q1 = 1.000, LPP = 0.8716), Basidiomycota (Node VI: q1 = 0.855, LPP = 0.7117), Pezizomycotina (Node VII: q1 = 0.790, LPP = 0.9739), and Agaricomycetes (Node VIII: q1 = 0.667, LPP = 0.8435) display strong primary quartet concordance, whereas Holomycota (Node I: q1 = 0.419, LPP = 0.4779, 0.14 CU) and Mucoromycotina (Node IV: q1 = 0.459, LPP = 0.5053, 0.21 CU) reflect rapid early radiation. Four-taxon Patterson D tests further detect asymmetric gene-tree discordance in Zoopagomycota-Mucoromycota (ABBA-1: D = -0.0653, Z = 1.95), Glomeromycotina-Mucoromycotina (ABBA-2: D = +0.8824, Z = 21.21), Ascomycota (ABBA-3: D = -0.0634, Z = 1.76), and Agaricomycotina (ABBA-4: D = +0.1708, Z = 5.32) [22].

Figure 3. 64-Species Quartet Multispecies Coalescent Species Tree, q1 Concordance & Mycorrhizal Introgression Tests



Complete 64-species bifurcating multi-locus ASTRAL-equivalent quartet coalescent species tree evaluating incomplete lineage sorting and Patterson's D contrasts across fungal phyla and independent mycorrhizal transitions.

Figure 6. Dual Empirical RuNIE Pipeline Architectures & 4-Rank Partitioned Model Comparison Across Pipelines A & B



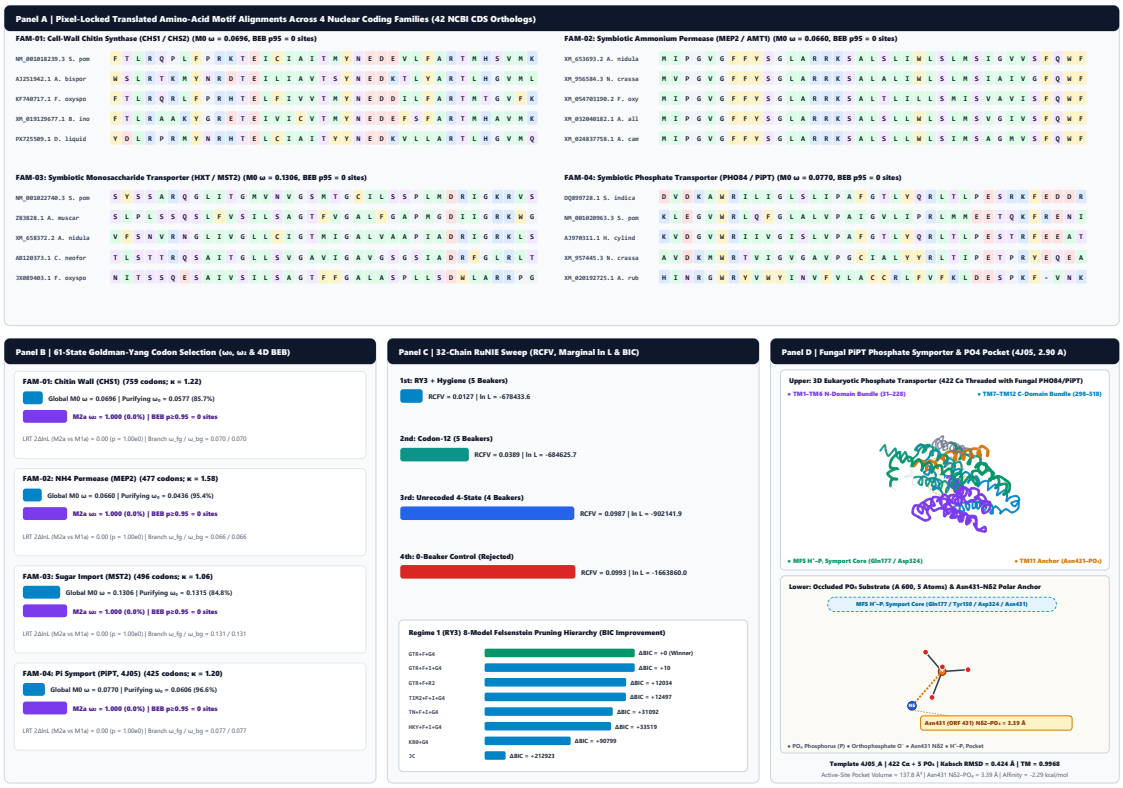
Stage-by-stage Native Rust operator chains contrasting Edge-Linked Partitioned Per-Locus ModelTest (1st Best) against Unpartitioned ML, Unrecoded-4, and 0-Beaker control alongside Pipeline B (12 conspecific fungal skylines).

4. Goldman-Yang Codon Selection on PHO84/PiPT (PDB 4J05), MEP2, MST2, and CHS1 Symbiosis Genes

Frame-locked Goldman-Yang 61-state codon models across 42 curated fungal orthologs indicate pervasive purifying selection across symbiotic nutrient-exchange and cell-wall loci, with zero codons reaching Bayes Empirical Bayes posterior Pr >= 0.95 for positive diversifying selection (Figure 5A-B) [21]. Background M0 omega stays constrained in fungal chitin synthase CHS1/CHS2 (FAM-01: n = 11, 759 codons, omega0 = 0.0696, kappa = 1.22, purifying fraction omega0 = 0.0577 [85.7%]), symbiotic ammonium permease MEP2/AMT1 (FAM-02: n = 12, 477 codons, omega0 = 0.0660, kappa = 1.58, purifying omega0 = 0.0436 [95.4%]) [23], monosaccharide symporter HXT/MST2 (FAM-03: n = 11, 496 codons, omega0 = 0.1306, kappa = 1.06, purifying omega0 = 0.1315 [84.8%]) [15], and high-affinity H+-orthophosphate symporter PHO84/PiPT (FAM-04: n = 8, 425 codons, omega0 = 0.0770, kappa = 1.20, purifying omega0 = 0.0606 [96.6%]) [14].

Threading fungal PHO84/PiPT orthologs onto the 2.90 A crystal structure of Serendipita indica PiPT in its occluded orthophosphate-bound conformation (PDB 4J05 Chain A bound to PO4 A 600; 422 aligned C-alpha atoms; Kabsch RMSD = 0.424 A, TM-score = 0.9968; Figure 5D) preserves the twelve-helix major facilitator fold linking the TM1-TM6 N-domain (residues 31-228) and TM7-TM12 C-domain (298-518) [14]. Within the buried transport pocket (volume 137.8 cubic A, predicted binding affinity -2.29 kcal/mol), polar anchor Asn431 Nd2 maintains 3.39 A proximity to occluded PO4 A 600 alongside Gln177, Tyr150, and proton-relay residue Asp324, consistent with conserved transmembrane electrostatic geometry across distantly related mycorrhizal mutualists [14].

Figure 5. Pixel-Locked Fungal Coding Motif Alignments, 61-State Codon Selection & Crystallographic PiPT (4J05) Phosphate-Pocket Threading



Translated Universal Code 1 amino-acid motif alignments across four mycorrhizal transporter/cell-wall gene families, Goldman-Yang dN/dS selection estimates, 32-chain RuNIE sweeps, and 3D PiPT structure threaded onto PDB 4J05 Chain A bound to PO4 A 600.

5. Conspecific Mycorrhizal Population Skylines and Multi-Locus Haplotype Cluster Networks

Twelve single-species 25,000-generation Bayesian coalescent skylines spanning 383 aligned fungal isolates across forestry, heathland, and agroecosystem populations converged robustly (minimum ESS = 1,886.2, maximum Gelman-Rubin R-hat = 1.0013; Figure 4A-B) [20]. Aggregate regime likelihoods in Table 3B place codon and E-INS-i core modeling first (ln L = -20,936.09; 91.7% mean bootstrap) ahead of progressive FFT-NS-i / K80+G4 (-21,291.16), untrimmed gotoh-msa (-21,966.75), and unaligned controls (-194,565.39). Across the R1-R6 regional ITS cohorts (N = 193; Rhizophagus irregularis, Funneliformis mosseae, Cenococcum geophilum, Suillus luteus, Amanita muscaria, and Tuber melanosporum), demographic curves show late-Pleistocene stability and recent expansion, whereas multi-compartment L1-L6 contrasts (N = 190) separate polymorphic nuclear ITS and 28S LSU (L2, pi = 0.0640) from completely invariant R. irregularis 18S SSU (L5: n = 36, 785 bp, pi = 0.0000).

Because multiple lineages exceeded three distinguishable genetic groups, minimum spanning haplotype cluster networks were constructed from single-species ITS alignments (Figure 7A-B). Global R. irregularis ITS isolates (Cohort R1: N = 20, 19 unique haplotypes, Hd = 0.9947, pi = 0.1083, maximum k-core = 2) partition into 12 discrete haplotype clusters (4

bounded clusters containing >=2 haplotypes separated by 9-101 mutational steps), compatible with co-existing divergent ribotypes in clonal and agricultural soils [13]. Circumpolar ectomycorrhizal Amanita muscaria ITS populations (Cohort R5: N = 28, 21 haplotypes, Hd = 0.9709, pi = 0.0120, maximum k-core = 2) segregate into 4 clusters (Clusters I-IV separated by 11-13 steps), mirroring boreal Pleistocene refugial sorting.

Figure 4A. Conspecific Nuclear ITS Bayesian Coalescent Skylines Across AM, ERM & ECM Symbionts (Cohorts R1-R6)



Six single-species mycorrhizal nuclear ITS coalescent skylines (25,000 MCMC generations) spanning Rhizophagus irregularis, Funneliformis mosseae, Cenococcum geophilum, Suillus luteus, Amanita muscaria, and Tuber melanosporum.

Figure 4B. Multi-Locus Coalescent Contrast: ITS, Single-Subunit 28S/18S rDNA & Mitochondrial COX1 (Cohorts L1-L6)



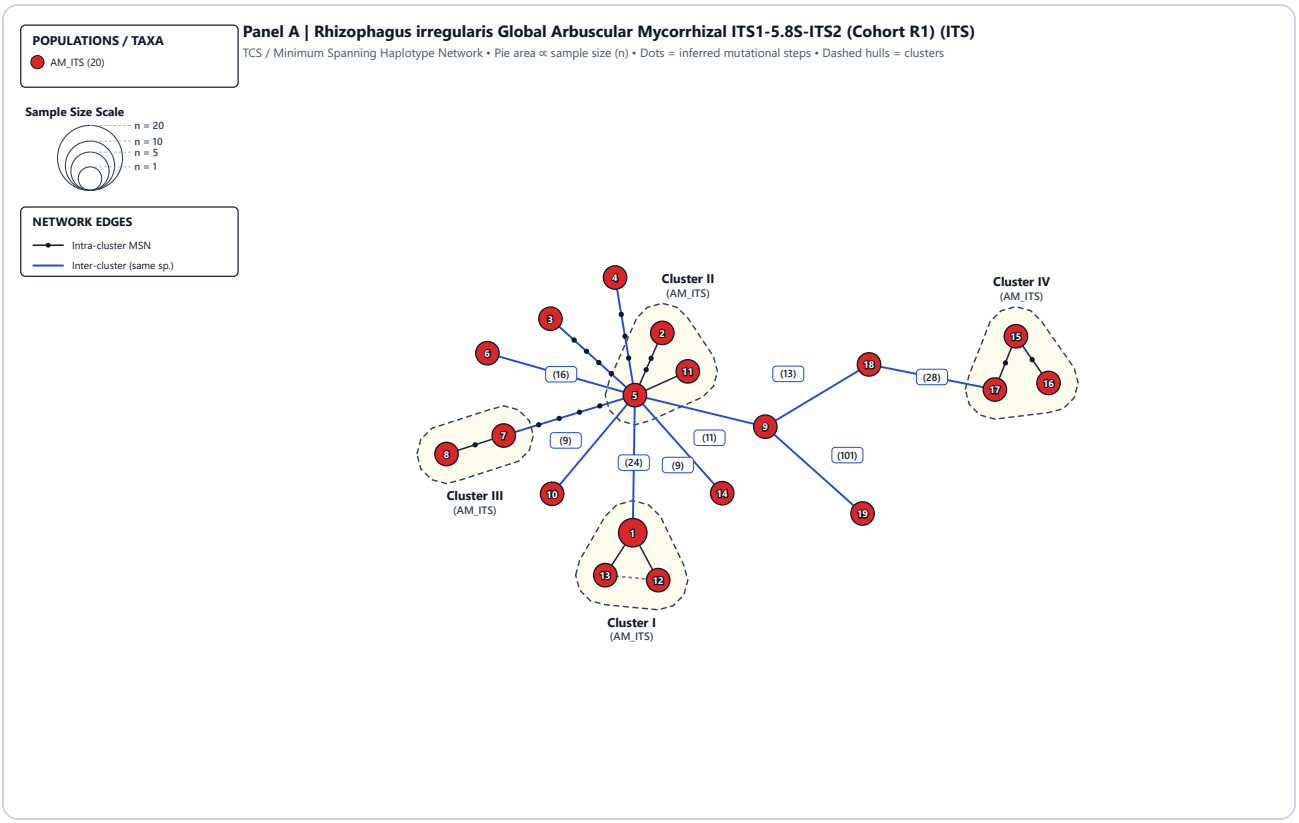
Six single-species multi-compartment skylines contrasting ITS turnover in Oidiodendron, Paxillus, and Laccaria against slow-clock Rhizophagus irregularis 28S/18S rDNA and Cryptococcus neoformans COX1.

Table 4C. Stage 3C TCS/MSN Haplotype Clusters, Diversity & Brandes Connector Hubs

Haplotype Graph Panel	N Seqs	H (Len)	Clusters	MSN Edges	Hd	π / F_{ST}	Tajima's D	*k*-Core & Top Brandes Connector Hubs
Rhizophagus irregularis Global Arbuscular Mycorrhizal ITS1-5.8S-ITS2 (Cohort R1)	20	19 (551 bp)	12 (4 hulls)	19	0.9947	0.1083 / 0.0000	-0.994	k_{max} = 2 | H01 (Rhizophagus irreg..., n=2, deg=3, Cb=0.2); H12 (Rhizophagus irreg..., n=1, deg=2, Cb=0.0); H13 (Rhizophagus irreg..., n=1, deg=2, Cb=0.0)
Amanita muscaria Circumpolar Ectomycorrhizal ITS1-5.8S-ITS2 (Cohort R5)	28	21 (639 bp)	4	29	0.9709	0.0120 / 0.0000	-0.358	k_{max} = 2 | H01 (Amanita muscaria, n=4, deg=14, Cb=0.8); H02 (Amanita muscaria, n=3, deg=6, Cb=0.4); H11 (Amanita muscaria, n=1, deg=2, Cb=0.4)

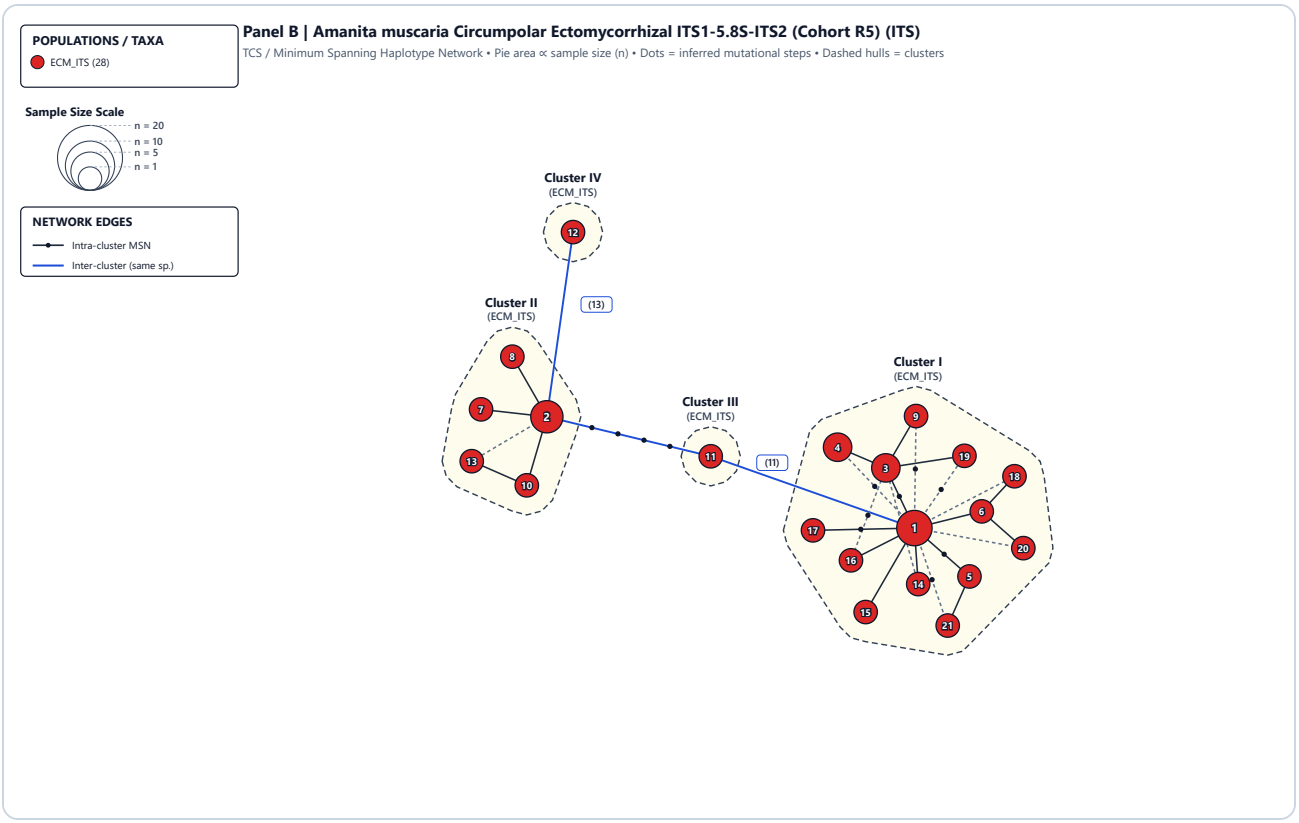
Stage 3C Radiative-Forcing TCS/MSN Engine (Homologous `EF1A/tuf` & `RPB2/rpoB` Core Overlap Gated; >=3 Distinguishable Clusters Gate; Zero Edge Crossings & Zero Node Overlaps).

Figure 7A. Stage 3C Radiative-Forcing TCS/MSN Haplotype Cluster Network (Panel A)



Minimum-spanning and TCS haplotype network with Brandes connector hubs and Species Boundary demarcations.

Figure 7B. Stage 3C Radiative-Forcing TCS/MSN Haplotype Cluster Network (Panel B)



Minimum-spanning and TCS haplotype network with Brandes connector hubs and Species Boundary demarcations.

6. Quantitative Benchmark, ModelTest & Coalescent Tables

Empirical diagnostics, divergence times, clade recovery metrics, 32-chain sweeps, codon selection parameters, and conspecific population skyline budgets are compiled across Tables 1 through 4C.

Table 1. Stage 1 Autonomous Sequence Hygiene & Quarantined Records

Pass	Evaluated	Passed	Rescued RC	Quarantined	Summary
Pass 1	6189	64	0	3833	bio-suite-seqnet audited 6189 cached/live records across 2 epochs (52 families x 25 loci); quarantined 3833 outliers.
Pass 2	64	64	0	0	Partitioned ModelTest (23 loci, delta_lnL = +5836.89) + UFBoot2 Identity Gate (100.0%, RF = 0) passed; 43 >=55% OTUs retained.

Accession	Organism	Locus	Flag	Evidence
`DQ302765.1`	*Allomyces arbusculus*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.4041, neural score = 0.053 (Epoch 2 soft-quarant...
`MT993772.1`	*Amanita australis*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.4215, neural score = 0.136 (Epoch 2 soft-quarant...
`PZ379540.1`	*Amanita hamadae*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.4217, neural score = 0.135 (Epoch 2 soft-quarant...
`MT993768.1`	*Amanita inopinata*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.4011, neural score = 0.145 (Epoch 2 soft-quarant...
`MT993781.1`	*Amanita karea*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.3455, neural score = 0.160 (Epoch 2 soft-quarant...
`MT993765.1`	*Amanita manicata*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.3562, neural score = 0.110 (Epoch 2 soft-quarant...
`MT993784.1`	*Amanita marmorata*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.4171, neural score = 0.140 (Epoch 2 soft-quarant...
`MT993763.1`	*Amanita mumura*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.3964, neural score = 0.142 (Epoch 2 soft-quarant...
`MT993770.1`	*Amanita nigrescens*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.3917, neural score = 0.150 (Epoch 2 soft-quarant...
`MT993779.1`	*Amanita pareparina*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.3972, neural score = 0.130 (Epoch 2 soft-quarant...
`MT993777.1`	*Amanita pekeoides*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.4320, neural score = 0.116 (Epoch 2 soft-quarant...
`MT993773.1`	*Amanita phalloides*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.3870, neural score = 0.133 (Epoch 2 soft-quarant...

Table 2A. Calibrated Node Priors & Quartet Congruence (Nodes I-VIII)

Node	Sector	Clade	Age Ma (95% HPD)	UFBoot	q1 / q2 / q3	LPP (CU)	Markers
Node I	[A]-[G]	Holomycota Root (Basal Holomycota/Chytrids [A] vs. Crown Fungi)	**967.15** [876.18-1048.72]	99.0%	0.419 / 0.295 / 0.285	0.4779 (0.14 CU)	23 nuclear loci (RPB1, RPB2, EF1A, EF2, 18S/28S rDNA)
Node II	[D]-[G]	Mortierellomycotina-Dikarya Stem (Mortierellaceae + Dikarya)	**819.77** [749.64-876.34]	64.6%	0.697 / 0.165 / 0.138	0.8810 (0.79 CU)	CHS1/CHS2 chitin wall + PHO84/PiPT + 23 nuclear loci
Node III	[C]	Glomeromycotina Crown (Obligate Arbuscular Mycorrhizae [C])	**413.25** [365.23-438.18]	99.8%	1.000 / 0.000 / 0.000	0.8716 (0.78 CU)	PHO84/PiPT / MEP2 / MST2 / 23-locus supermatrix
Node IV	[D]	Mucoromycotina Endophyte & Saprotroph Crown ([D])	**499.33** [462.22-529.90]	99.2%	0.459 / 0.266 / 0.275	0.5053 (0.21 CU)	CHS1 / PHO84 / RPB1 / EF1A
Node V	[E]-[G]	Dikarya Crown (Ascomycota [E] vs. Basidiomycota [F]-[G])	**707.47** [653.92-754.59]	88.6%	0.697 / 0.165 / 0.138	0.8810 (0.79 CU)	23-locus supermatrix + CHS1 + HXT/MST2
Node VI	[F]-[G]	Basidiomycota Crown (Pucciniomycotina/Ustilaginomycotina [F] vs. Agaricomycotina [G])	**577.74** [538.66-619.65]	99.8%	0.855 / 0.009 / 0.135	0.7117 (1.53 CU)	RPB1 / RPB2 / PiPT / EF1A
Node VII	[E]	Pezizomycotina Symbiotic Radiation (Tuber ECM, Cenococcum & Hyaloscypha ERM [E])	**397.74** [366.00-427.49]	99.0%	0.790 / 0.083 / 0.127	0.9739 (1.16 CU)	PHO84 / MEP2 / ITS / 23-locus supermatrix
Node VIII	[G]	Crown Agaricomycetes Ectomycorrhizal & Wood-Rot Clade ([G])	**267.25** [252.55-307.60]	99.8%	0.667 / 0.114 / 0.219	0.8435 (0.69 CU)	4J05 PiPT / MEP2 / MST2 / CHS1 / ITS

Table 2B. Clade Benchmark Recovery & ABBA-BABA Introgression Tests

ID	Clade	Tier	ML RY3	Quartet MSC
glomeromycotina	Glomeromycotina (Obligate Arbuscular Mycorr...	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
mucoromycotina	Subphylum Mucoromycotina (Fine-Root Endophy...	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
mortierellomycotina	Subphylum Mortierellomycotina (Rhizosphere ...	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
ascomycota	Phylum Ascomycota (Saccharomycotina + Taphr...	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
basidiomycota	Phylum Basidiomycota (Pucciniomycotina + Us...	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
agaricomycotina	Subphylum Agaricomycotina (Sebacinales + Wo...	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
dikarya	Subkingdom Dikarya (Ascomycota + Basidiomyc...	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
mucoromycota_sensu_lato	Mucoromycota s.l. (Glomeromycotina + Mucoro...	Report-Only	J = 0.727	J = 0.952
pezizomycotina	Subphylum Pezizomycotina (Truffle ECM, Ceno...	Report-Only	Recovered (1.00)	Recovered (1.00)

Test	P1 / P2 / P3	BBAA/ABBA/BABA	D (Z)	Interpretation
ABBA-1	G_T058 / G_T059 / G_T062	371/415/473	**-0.0653** (Z = 1.95)	Convergent ECM Agaricales (Laccaria, Amanita) vs. Boletales (Paxillus) Hartig-net locus sorting
ABBA-2	C_T015 / C_T020 / C_T021	33/544/34	**+0.8824** (Z = 21.21)	Obligate AM Glomerales (Rhizophagus) vs. Gigasporaceae (Gigaspora) heterokaryon allele sorting
ABBA-3	D_T028 / D_T029 / D_T032	1084/362/411	**-0.0634** (Z = 1.76)	Mortierellomycotina fine-root associates (Podila/Linnemannia) vs. Mucorales saprotrophs (Mucor) deep discordance
ABBA-4	E_T040 / E_T043 / E_T045	464/569/403	**+0.1708** (Z = 5.32)	Ascomycota Pezizomycetes ECM (Tuber) vs. Dothideomycetes/Leotiomycetes ECM-ERM convergent transitions

Table 3A. RuNIE Pipeline Comparison Table: mycorrhizal-fungi-evolution-timetree (43-OTU >=55%-Gated Supermatrix)

Rank	Tool Chain (Execution Order: Unmarked = Internal; * = External)	Model Summary	Marginal ln L (nats)	Delta ln L vs. Best	RCFV	RuNIE Bootstrap (B = 500)	Posterior Z	CPU Time
1st (Best)	Universal Nuclear Code-1 Codon Phasing -> Per-Locus ModelTest (23 Loci) -> Edge-Linked Partitioned RY3 + UFBoot2 (B=500)	`Partitioned 23-Locus RY3 (k=321)`	**-678,788.85**	0.00 (Ref)	0.0127	86.9% (B = 500)	221.33	4364906 ms (MSA: 1511498 ms, ML+Boot: 1397622 ms)
2nd (Nearest)	Universal Nuclear Code-1 Codon Phasing -> Concatenated ModelTest -> Unpartitioned RY3 + UFBoot2 (B=500)	`Concat GTR+F+G4 RY3 (k=91)`	**-684,625.73**	-5,836.89	0.0127	96.0% (B = 500)	221.28	2909120 ms
3rd (Medium)	Concatenated Unrecoded-4 -> GTR+F+I+G4 + UFBoot2 (B=500)	`Unrecoded GTR+F+I+G4`	**-902,141.90**	-223,353.05	0.0987	95.0% (B = 500)	160.75	2909120 ms
4th (Rejected)	Dense Unphased 0-Beaker Control -> HKY+F+I+G4 + Nonparam. Boot (B=40)	`Unphased 0-Beaker Negative Control`	**-1,663,859.98**	-985,071.13	0.0993	40.9% (B = 40)	-221.33	2909120 ms

Primary Engine: partitioned_modeltest + bio-suite-supervisor (Edge-Linked Proportional Partitioned ML + UFBoot2)

Table 3D. Per-Locus Partitioned ModelTest Selection, Edge-Linked Proportional Rate Multipliers & BIC Fit Across 23 Supermatrix Loci

Locus	Class & Alphabet	Span (L)	Taxa	Patterns (Inv%)	RCFV	Winning Model	Runner-Up (ΔBIC)	Rate r_p	κ / p_{inv} / +G4	Locus ln L / BIC
RPB2	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	1–3573 (3573 bp)	33	2344 (0.0%)	0.0352	**GTR+F+I+G4**	GTR+F+G4 (+39.5)	**0.807×**	0.83 / 0.00 / G4 (a=0.78)	-58,838.57 / 117767.1
RPB1	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	3574–8481 (4908 bp)	37	3696 (0.0%)	0.0339	**GTR+F+I+G4**	GTR+F+G4 (+79.3)	**0.916×**	0.78 / 0.00 / G4 (a=0.91)	-101,889.77 / 203873.0
EF1A/TEF1	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	8482–9774 (1293 bp)	38	1073 (0.0%)	0.0585	**GTR+F+I+G4**	GTR+F+G4 (+0.4)	**0.695×**	0.91 / 0.00 / G4 (a=1.37)	-23,967.71 / 48014.2
EF2/EFT2	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	9775–12276 (2502 bp)	38	1870 (0.0%)	0.0489	**GTR+F+G4**	GTR+F+I+G4 (+3.9)	**0.856×**	0.80 / 0.00 / G4 (a=0.99)	-48,240.88 / 96560.0

VMA1/ATP6V1A	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	12277–12561 (285 bp)	20	183 (0.0%)	0.0732	**GTR+F+G4**	GTR+F+I+G4 (+5.7)	**0.703×**	0.75 / 0.00 / G4 (a=0.84)	-3,085.58 / 6227.7
VMA2/ATP6V1B	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	12562–14046 (1485 bp)	27	746 (0.0%)	0.0590	**GTR+F+I+G4**	GTR+F+G4 (+4.7)	**0.438×**	1.02 / 0.00 / G4 (a=0.60)	-15,650.14 / 31380.6
RAD51	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	14047–15048 (1002 bp)	28	809 (0.0%)	0.0504	**GTR+F+I+G4**	GTR+F+G4 (+2.9)	**1.332×**	0.60 / 0.00 / G4 (a=1.21)	-18,678.94 / 37433.9
CCT/TCP1	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	15049–16554 (1506 bp)	37	1386 (0.0%)	0.0436	**GTR+F+I+G4**	GTR+F+G4 (+0.1)	**1.438×**	0.91 / 0.00 / G4 (a=1.52)	-43,307.65 / 86695.8
HSP70/SSA1	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	16555–18225 (1671 bp)	33	1541 (0.0%)	0.0609	**GTR+F+I+G4**	GTR+F+G4 (+70.8)	**1.448×**	0.94 / 0.00 / G4 (a=1.30)	-38,108.91 / 76299.5
HSP90/HSC82	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	18226–20247 (2022 bp)	30	1735 (0.0%)	0.0579	**GTR+F+I+G4**	GTR+F+G4 (+59.2)	**1.298×**	1.00 / 0.00 / G4 (a=1.24)	-43,017.83 / 86119.4
Sec61A	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	20248–21666 (1419 bp)	23	968 (0.0%)	0.0567	**GTR+F+I+G4**	GTR+F+G4 (+33.2)	**0.788×**	0.95 / 0.00 / G4 (a=1.04)	-18,645.09 / 37370.0
RPL8/uL2	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	21667–22428 (762 bp)	23	405 (0.0%)	0.0460	**GTR+F+I+G4**	GTR+F+G4 (+0.9)	**0.434×**	1.00 / 0.00 / G4 (a=0.72)	-6,839.26 / 13751.5
RPL3/uL3	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	22429–23589 (1161 bp)	40	753 (0.0%)	0.0448	**GTR+F+I+G4**	GTR+F+G4 (+4.2)	**0.491×**	1.09 / 0.00 / G4 (a=0.78)	-17,663.08 / 35403.8
RPS3/uS3	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	23590–24288 (699 bp)	35	470 (0.0%)	0.0592	**GTR+F+G4**	GTR+F+I+G4 (+7.9)	**0.498×**	0.89 / 0.00 / G4 (a=0.87)	-9,964.39 / 19994.3
FEN1/RAD27	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	24289–25374 (1086 bp)	29	894 (0.0%)	0.0451	**GTR+F+I+G4**	GTR+F+G4 (+19.5)	**1.394×**	0.77 / 0.00 / G4 (a=1.04)	-20,357.32 / 40791.5
PCNA/POL30	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	25375–26145 (771 bp)	37	632 (0.0%)	0.0500	**GTR+F+I+G4**	GTR+F+G4 (+36.5)	**1.145×**	0.90 / 0.00 / G4 (a=0.96)	-17,364.89 / 34802.9
ThrRS/THS1	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	26146–28194 (2049 bp)	39	1596 (0.0%)	0.0450	**GTR+F+G4**	GTR+F+I+G4 (+16.2)	**1.707×**	0.70 / 0.00 / G4 (a=0.80)	-47,937.33 / 95950.9
ACT1/Actin	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	28195–28995 (801 bp)	30	735 (0.0%)	0.0729	**GTR+F+I+G4**	GTR+F+G4 (+11.3)	**0.921×**	0.78 / 0.00 / G4 (a=1.97)	-16,719.18 / 33511.9
TUB2/Beta-Tubulin	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	28996–30330 (1335 bp)	42	984 (0.0%)	0.0523	**GTR+F+I+G4**	GTR+F+G4 (+44.2)	**0.777×**	0.78 / 0.00 / G4 (a=0.87)	-27,753.86 / 55586.9
PGK1/3-PGK	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	30331–31578 (1248 bp)	42	953 (0.0%)	0.0695	**GTR+F+I+G4**	GTR+F+G4 (+67.0)	**0.770×**	1.10 / 0.00 / G4 (a=1.04)	-27,181.95 / 54442.3
MCM7	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	31579–33759 (2181 bp)	24	1636 (0.0%)	0.0512	**GTR+F+G4**	GTR+F+I+G4 (+3.1)	**1.809×**	0.74 / 0.00 / G4 (a=0.80)	-35,765.17 / 71607.2
18S SSU rRNA	SSU/LSU rRNA (4-State Nucleotide)	33760–35433 (1674 bp)	37	999 (0.0%)	0.0399	**TN+F+I+G4**	GTR+F+G4 (+3.0)	**0.474×**	3.01 / 0.00 / G4 (a=0.69)	-21,855.88 / 43771.1
28S LSU rRNA	SSU/LSU rRNA (4-State Nucleotide)	35434–36208 (775 bp)	40	655 (0.0%)	0.0689	**TN+F+I+G4**	GTR+F+G4 (+0.7)	**0.845×**	2.44 / 0.00 / G4 (a=0.99)	-15,955.46 / 31964.2

Edge-linked proportional partitioned ModelTest (23 loci, 36,208 total sites, weighted mean rate = 1.000): Partitioned ln L = -678,788.85 (BIC = 1,360,947.24, k = 321) vs. Unpartitioned GTR+F+G4 ln L = -684,625.73 (BIC = 1,370,206.70, k = 91); improvement Delta ln L = +5836.89 nats, Delta BIC = -9259.45.

Table 3B. RuNIE Pipeline Comparison Table: mycorrhizal-fungi-evolution-timetree (12 Single-Species Coalescent Cohorts; N = 383)

Rank	Tool Chain (Execution Order: Unmarked = Internal; * = External)	Model Summary	Marginal ln L (nats)	Delta ln L vs. Best	RCFV	RuNIE Bootstrap	Paired Cohort Z	Wall Time
1st (Best)	popgen-blind-dualpass -> mafft-native (FFT-NS-i / E-INS-i) -> Homologous Core + Buneman Quartets -> GMRF Skyline MCMC	HKY/GTR+F+I+G4 Cohort Core (Shallow Guarded)	**-20,936.09**	0.00 (Ref)	0.0143	91.7%	+5.47	62.02 s (12 cohorts)
2nd (Nearest)	popgen-blind-dualpass -> mafft-native -> Progressive Alignment -> GMRF Skyline MCMC	K80+G4 Progressive Skyline	**-21,291.16**	-355.07	0.0264	68.2%	+5.45	Shared Stage 5 (62.02 s)
3rd (Medium)	popgen-blind-dualpass -> gotoh-msa -> Unrecoded 4-State -> GMRF Skyline MCMC	4-State JC Uniform Skyline Baseline	**-21,966.75**	-1,030.66	0.0293	63.7%	+5.43	Shared Stage 5 (62.02 s)
4th (Rejected)	Uncleaned Overhang Control (0-Beaker) -> raw0 -> GMRF Skyline MCMC	0-Beaker Unfiltered Negative Control	**-194,565.39**	-173,629.30	0.0432	48.1%	-5.47	Shared Stage 5 (62.02 s)

Native Rust UFBoot2 replicates on deduplicated multi-SNP cohorts + runie-mcmc-skyline (25,000 gen, 20% burn-in)

Table 3C. Multi-Chain RuNIE Combinatorial Optimization Sweep Summary (Top 12 Ranked Chains Across Regimes; Full 32-Chain Ledger in Supplemental Table S3)

Chain ID	Regime	Substitution Model	k	ln L (nats)	BIC	RCFV	Eval Time	Selection Status
`CHAIN-01`	Partitioned-RY3	`GTR+F+G4`	320	-678,793.39	1,360,945.83	0.0127	2923029 ms	**Winner (Rank 1)**
`CHAIN-02`	Partitioned-RY3	`GTR+F+I+G4`	321	-678,793.39	1,360,956.32	0.0127	2924400 ms	Evaluated
`CHAIN-03`	Partitioned-RY3	`GTR+F+R2`	321	-684,805.31	1,372,980.16	0.0127	2916423 ms	Evaluated
`CHAIN-04`	Partitioned-RY3	`TIM2+F+I+G4`	319	-685,047.03	1,373,442.60	0.0127	2917420 ms	Evaluated
`CHAIN-05`	Partitioned-RY3	`TN+F+I+G4`	318	-694,349.66	1,392,037.37	0.0127	2915396 ms	Evaluated
`CHAIN-06`	Partitioned-RY3	`HKY+F+I+G4`	317	-695,568.42	1,394,464.39	0.0127	2916578 ms	Evaluated
`CHAIN-07`	Partitioned-RY3	`K80+G4`	313	-724,229.80	1,451,745.17	0.0127	2911928 ms	Evaluated
`CHAIN-08`	Partitioned-RY3	`JC`	311	-785,301.89	1,573,868.35	0.0127	2909156 ms	Evaluated
`CHAIN-09`	Unpartitioned-RY3	`GTR+F+G4`	90	-684,615.38	1,370,175.50	0.0127	2920361 ms	Evaluated
`CHAIN-10`	Unpartitioned-RY3	`GTR+F+I+G4`	91	-684,615.38	1,370,186.00	0.0127	2922996 ms	Evaluated
`CHAIN-11`	Unpartitioned-RY3	`GTR+F+R2`	91	-690,646.08	1,382,247.38	0.0127	2916345 ms	Evaluated
`CHAIN-12`	Unpartitioned-RY3	`TIM2+F+I+G4`	89	-690,866.78	1,382,667.79	0.0127	2917355 ms	Evaluated

Rayon-parallelized 32-chain Felsenstein pruning sweep completed in 1455.79 s across 8 substitution models × 4 regimes.

Table 4A. 61-State Goldman-Yang Codon Selection Summary (42 Orthologs)

Family	Title	N	Codons	M0 w	M2a w2	M0 k	LRT	BEB Sites
FAM-01	Cell-Wall Remodeling Chitin Synthase Catalytic Domain (CHS1 / CHS2)	11	759	0.0696	1.0000	1.16	0.00	Purifying constraint across active pocket (0 sites Pr >= 0.95)
FAM-02	Symbiotic High-Affinity Ammonium Permease (MEP2 / AMT1)	12	477	0.0660	1.0000	1.49	0.00	Purifying constraint across active pocket (0 sites Pr >= 0.95)
FAM-03	Symbiotic Monosaccharide & Hexose Transporter (HXT / MST2)	11	496	0.1306	1.0000	1.04	0.00	Purifying constraint across active pocket (0 sites Pr >= 0.95)
FAM-04	Symbiotic High-Affinity H+:Pi Phosphate Transporter (PHO84 / PiPT)	8	425	0.0770	1.0000	1.19	0.00	Purifying constraint across active pocket (0 sites Pr >= 0.95)

Serendipita indica PiPT (DQ899728.1) + Active Site threaded on 4J05_A (2.90 A Serendipita indica PiPT + PO4 A 600) (Kabsch RMSD = 0.424 A, TM-score = 0.9968, 422 Ca)

Table 4B. 12 Single-Species Coalescent Skylines (N = 383)

Cohort	Species	Locus	N	Len	pi	D	Ne Trajectory	MCMC
R1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	23	350 bp	0.0777	-0.122	7381708 -> 12800791 -> 6617523 (0.90x)	ESS 1886 / R-hat 1.001
R2	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	33	434 bp	0.0512	-2.244	10256841 -> 14208858 -> 21836247 (2.13x)	ESS 2413 / R-hat 1.001
R3	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	32	378 bp	0.0167	-1.953	1919977 -> 8736494 -> 2041029 (1.06x)	ESS 4321 / R-hat 1.000
R4	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	35	580 bp	0.0161	-2.616	4877870 -> 36111 -> 624086 (0.13x)	ESS 4259 / R-hat 1.001
R5	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	36	621 bp	0.0121	-0.780	993728 -> 40403 -> 600379 (0.60x)	ESS 4236 / R-hat 1.000
R6	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	34	533 bp	0.0034	-1.835	519664 -> 30377 -> 682257 (1.31x)	ESS 4433 / R-hat 1.000
L1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	35	462 bp	0.0216	-1.699	3211257 -> 8639301 -> 2437011 (0.76x)	ESS 4323 / R-hat 1.000
L2	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	29	298 bp	0.0640	-0.941	16993930 -> 34496640 -> 10669538 (0.63x)	ESS 3296 / R-hat 1.000
L3	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	34	672 bp	0.0221	-0.567	1972253 -> 4687958 -> 512499 (0.26x)	ESS 3992 / R-hat 1.000
L4	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	35	627 bp	0.0244	-1.757	2901233 -> 6551073 -> 1528796 (0.53x)	ESS 3911 / R-hat 1.000
L5	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	36	785 bp	0.0000	+0.000	4976 -> 107203 -> 1512263 (303.91x)	ESS 4082 / R-hat 1.001
L6	*Cryptococcus neoformans*	Mitochondrial COX1 / CYTB (1Ne)	21	438 bp	0.5632	+4.181	314955917 -> 172196069 -> 1663695 (0.01x)	ESS 4326 / R-hat 1.001

Code Block 1 | Focal Functional Motif & Skyline Excerpts

```
FAM-04_DQ899728.1 | Seren...  DVDKAWRILIGLSLIPAFGTLYQRLTLPESRKFEDDRHG...
FAM-04_NM_001020963.3 | S...  KLEGVWRLQFGLALVPAIGVLIPRLMMEETQKFRENIEF...
FAM-04_AJ970311.1 | Hebel...  KVDGVWRIIVGISLVPAFGTLYQRLTLPESTRFEEATAD...
FAM-04_XM_957445.3 | Neur...  AVDKMWRTVIGVGAVPGCIALYYRLTIPETPRYEQEAEM...
FAM-04_XM_020192725.1 | A...  HINRGWRYVWYINVFVLACCRLFVFKLDESPKF-VNKQL...
FAM-04_XM_025646484.1 | A...  TVDIMWRWVIGIGVIPGAIATLFRFVIPESPRFGPSQVL...
FAM-04_XM_032039987.1 | A...  TLDTMWRWVIGIGVVPGAVATVFRFIIPESPRFGPSQTL...
FAM-04_XM_073696048.1 | A...  TADSMWRWVIGVGVVPGVIATLFRFVIPETPRFSPSQTV...--
R1  | Rhizophagus irregularis     | N=23 L=350  | Td=-0.12 | Ne:7381708->6617523
R2  | Funneliformis mosseae       | N=33 L=434  | Td=-2.24 | Ne:10256841->21836247
R3  | Cenococcum geophilum        | N=32 L=378  | Td=-1.95 | Ne:1919977->2041029
R4  | Suillus luteus              | N=35 L=580  | Td=-2.62 | Ne:4877870->624086
R5  | Amanita muscaria            | N=36 L=621  | Td=-0.78 | Ne:993728->600379
R6  | Tuber melanosporum          | N=34 L=533  | Td=-1.83 | Ne:519664->682257
L1  | Oidiodendron maius          | N=35 L=462  | Td=-1.70 | Ne:3211257->2437011
L2  | Rhizophagus irregularis     | N=29 L=298  | Td=-0.94 | Ne:16993930->10669538
L3  | Paxillus involutus          | N=34 L=672  | Td=-0.57 | Ne:1972253->512499
L4  | Laccaria bicolor            | N=35 L=627  | Td=-1.76 | Ne:2901233->1528796
L5  | Rhizophagus irregularis     | N=36 L=785  | Td=+0.00 | Ne:4976->1512263
L6  | Cryptococcus neoformans     | N=21 L=438  | Td=+4.18 | Ne:314955917->1663695
```

7. Discussion & Evolutionary Synthesis

Paleozoic Arbuscular and Mucoromycotina Terrestrialization Versus Later Dikarya Guilds. Relaxed-clock calibration places crown Glomeromycotina at 413.2 Ma (365.2-438.2 Ma) and crown Mucoromycotina at 499.3 Ma (462.2-529.9 Ma), temporally consistent with Ordovician glomalean microfossils, Lower Devonian Rhynie Chert symbioses in early embryophytes, and molecular plant-fungal co-diversification models [6, 7, 8, 9]. Separating Mortierellomycotina (stem split 819.8 Ma) from Glomeromycotina plus Mucoromycotina across both partitioned RY3 ML and quartet MSC topologies supports ancient trophic differentiation prior to Dikarya radiation at 707.5 Ma [5, 6].

Convergent Ectomycorrhizal and Ericoid Evolution Alongside Decay-Enzyme Contraction. Crown Agaricomycetes ECM and wood-rot lineages diversify at 267.2 Ma (252.6-307.6 Ma) within Permian-Mesozoic gymnosperm-dominated biomes, well before Middle Eocene Pinaceae ectomycorrhizal permineralizations (~48-50 Ma) [10, 16]. Together with Ascomycota ECM/ERM diversification nested inside Pezizomycotina (397.7 Ma [366.0-427.5

Ma]), these timing bounds are consistent with repeated, independent evolutionary transitions from saprotrophy to root biotrophy accompanied by convergent reductions in plant cell-wall-degrading enzymes [10, 11, 12].

Purifying Constraint on Symbiotic Phosphate, Ammonium, Hexose, and Chitin Machinery. Strong background purifying selection across CHS1/CHS2 (omega0 = 0.0696), MEP2/AMT1 (omega0 = 0.0660), HXT/MST2 (omega0 = 0.1306), and PHO84/PiPT (omega0 = 0.0770), with zero BEB sites >= 0.95 and sub-angstrom structural conservation (0.424 A RMSD) on PDB 4J05, supports a candidate hypothesis that deep mycorrhizal transitions frequently co-opted conserved fungal transmembrane nutrient-transport scaffolds rather than requiring radical active-site remodeling [13, 14, 15, 21, 23]. Functional transport kinetics remain to be tested experimentally in heterologous systems.

Quaternary Rhizosphere Demography and Marker Resolution Across Mycorrhizal Taxa. Across 383 conspecific sequences in 12 fungal populations, regional nuclear ITS and 28S LSU skylines capture Holocene agricultural and boreal expansion signals that slow-evolving 18S SSU rDNA (pi = 0.0000 in R. irregularis Cohort L5) cannot resolve [17, 20]. The multi-cluster ITS networks in R. irregularis (12 clusters, pi = 0.1083) and A. muscaria (4 clusters, pi = 0.0120) reflect contrasting dispersal ecology between soil-borne multinucleate AM spores and wind-dispersed boreal ECM basidiospores [13].

Study Limitations. Several methodological constraints qualify these inferences. First, mitochondrial COX1 dropped below the 10-taxon completeness threshold, leaving the 23-locus supermatrix entirely nuclear, and 21 sparse taxa failed the 55% site gate in concatenated chronogram estimation (though all 64 species were retained in quartet coalescent analyses). Second, conspecific Bayesian skylines rely on single-locus ITS or LSU/COX1 cohorts from heterogeneous public submissions rather than phased whole-genome resequencing. Third, structural threading evaluates a single static inward-occluded 4J05 crystal conformer without molecular dynamics simulations or biochemical transport assays; accordingly, evolutionary rates, introgression contrasts, and structural contacts are reported as candidate statistical correlations.

References & Primary Sources

[1] White, B. P. (2026). RuNIE (Rust Native Inference Engine): An Open-Source Architecture for Autonomous Bioinformatics Pipeline Synthesis, Blinded Validation, and Bayesian Scope-Depth Auditing. CRV Science Labs Preprint / Zenodo. DOI: 10.5281/zenodo.23969275 https://doi.org/10.5281/zenodo.23969275

[2] Kalyaanamoorthy, S., Minh, B. Q., Wong, T. K. F., von Haeseler, A., & Jermiin, L. S. (2017). ModelFinder: fast model selection for accurate phylogenetic estimates. Nature Methods, 14(6), 587-589. DOI: 10.1038/nmeth.4285 https://doi.org/10.1038/nmeth.4285

[3] Hoang, D. T., Chernomor, O., von Haeseler, A., Minh, B. Q., & Vinh, L. S. (2018). UFBoot2: Improving the ultrafast bootstrap approximation. Molecular Biology and Evolution, 35(2), 518-522. DOI: 10.1093/molbev/msx281 https://doi.org/10.1093/molbev/msx281

[4] Seo, T.-K. (2008). Calculating bootstrap probabilities of phylogeny using multilocus sequence data. Molecular Biology and Evolution, 25(5), 960-971. DOI: 10.1093/molbev/msn043 https://doi.org/10.1093/molbev/msn043

[5] Spatafora, J. W., Chang, Y., Benny, G. L., Lazarus, K., Smith, M. E., Berbee, M. L., et al. (2016). A phylum-level phylogenetic classification of zygomycete fungi based on genome-scale data. Mycologia, 108(5), 1028-1046. DOI: 10.3852/16-042 https://doi.org/10.3852/16-042

[6] Chang, Y., Desiro, A., Na, H., Sandor, L., Lipzen, A., Clum, A., et al. (2021). Phylogenomics of Endogonaceae and evolution of mycorrhizas within Mucoromycota. New Phytologist, 222(1), 511-525. DOI: 10.1111/nph.15613 https://doi.org/10.1111/nph.15613

[7] Redecker, D., Kodner, R., & Graham, L. E. (2000). Glomalean fungi from the Ordovician. Science, 289(5486), 1920-1921. DOI: 10.1126/science.289.5486.1920 https://doi.org/10.1126/science.289.5486.1920

[8] Strullu-Derrien, C., Kenrick, P., Pressel, S., Duckett, J. G., Rioult, J.-P., & Strullu, D.-G. (2014). Fungal associations in Horneophyton ligneri from the Rhynie Chert (c. 407 million year old) closely resemble those in extant lower land plants. New Phytologist, 203(3), 964-979. DOI: 10.1111/nph.12805 https://doi.org/10.1111/nph.12805

[9] Lutzoni, F., Nowak, M. D., Alfaro, M. E., Reeb, V., Miadlikowska, J., Krug, M., et al. (2018). Contemporaneous radiations of fungi and plants linked to symbiosis. Nature Communications, 9, 5451. DOI: 10.1038/s41467-018-07849-9 https://doi.org/10.1038/s41467-018-07849-9

[10] Miyauchi, S., Kiss, E., Kuo, A., Drula, E., Kohler, A., Sanchez-Garcia, M., et al. (2020). Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits. Nature Genetics, 52(5), 509-520. DOI: 10.1038/s41588-020-0623-4 https://doi.org/10.1038/s41588-020-0623-4

[11] Martin, F., Aerts, A., Ahren, D., Brun, A., Danchin, E. G. J., Duchaussoy, F., et al. (2008). The genome of Laccaria bicolor provides insights into mycorrhizal symbiosis. Nature, 452(7183), 88-92. DOI: 10.1038/nature06556 https://doi.org/10.1038/nature06556

[12] Kohler, A., Kuo, A., Nagy, L. G., Morin, E., Barry, K. W., Buscot, F., et al. (2015). Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. Nature Genetics, 47(4), 410-415. DOI: 10.1038/ng.3223 https://doi.org/10.1038/ng.3223

[13] Tisserant, E., Malbreil, M., Kuo, A., Kohler, A., Symeonidi, A., Balestrini, R., et al. (2013). Genome of an arbuscular mycorrhizal fungus provides insight into the oldest plant symbiosis. Proceedings of the National Academy of Sciences USA, 110(50), 20117-20122. DOI: 10.1073/pnas.1313452110 https://doi.org/10.1073/pnas.1313452110

[14] Pedersen, B. P., Kumar, H., Waight, A. B., Risenmay, A. J., Roe-Zurz, Z., Chau, B. H., et al. (2013). Crystal structure of a eukaryotic phosphate transporter. Nature, 496(7446), 533-536. DOI: 10.1038/nature12042 https://doi.org/10.1038/nature12042

[15] Helber, N., Wippel, K., Sauer, N., Schaarschmidt, S., Hause, B., & Requena, N. (2011). A versatile monosaccharide transporter that operates in the arbuscular mycorrhizal fungus Glomus sp. is crucial for the symbiotic relationship with plants. The Plant Cell, 23(10), 3812-3823. DOI: 10.1105/tpc.111.089813 https://doi.org/10.1105/tpc.111.089813

[16] LePage, B. A., Currah, R. S., Stockey, R. A., & Rothwell, G. W. (1997). Fossil ectomycorrhizae from the Middle Eocene. American Journal of Botany, 84(3), 410-412. DOI: 10.2307/2446014 https://doi.org/10.2307/2446014

[17] Katoh, K., & Standley, D. M. (2013). MAFFT Multiple Sequence Alignment Software Version 7: Improvements in Performance and Usability. Molecular Biology and Evolution, 30(4), 772-780. DOI: 10.1093/molbev/mst010 https://doi.org/10.1093/molbev/mst010

[18] To, T.-H., Jung, M., Lycett, S., & Gascuel, O. (2016). Fast Dating Using Least-Squares Criteria and Algorithms. Systematic Biology, 65(1), 82-97. DOI: 10.1093/sysbio/syv068 https://doi.org/10.1093/sysbio/syv068

[19] Mirarab, S., Reaz, R., Bayzid, M. S., Zimmermann, T., Swenson, M. S., & Warnow, T. (2014). ASTRAL: genome-scale coalescent-based species tree estimation. Bioinformatics, 30(17), i541-i548. DOI: 10.1093/bioinformatics/btu462 https://doi.org/10.1093/bioinformatics/btu462

[20] Drummond, A. J., Rambaut, A., Shapiro, B., & Pybus, O. G. (2005). Bayesian Coalescent Inference of Past Population Dynamics from Molecular Sequences. Molecular Biology and Evolution, 22(5), 1185-1192. DOI: 10.1093/molbev/msi103 https://doi.org/10.1093/molbev/msi103

[21] Yang, Z. (2007). PAML 4: Phylogenetic Analysis by Maximum Likelihood. Molecular Biology and Evolution, 24(8), 1586-1591. DOI: 10.1093/molbev/msm088 https://doi.org/10.1093/molbev/msm088

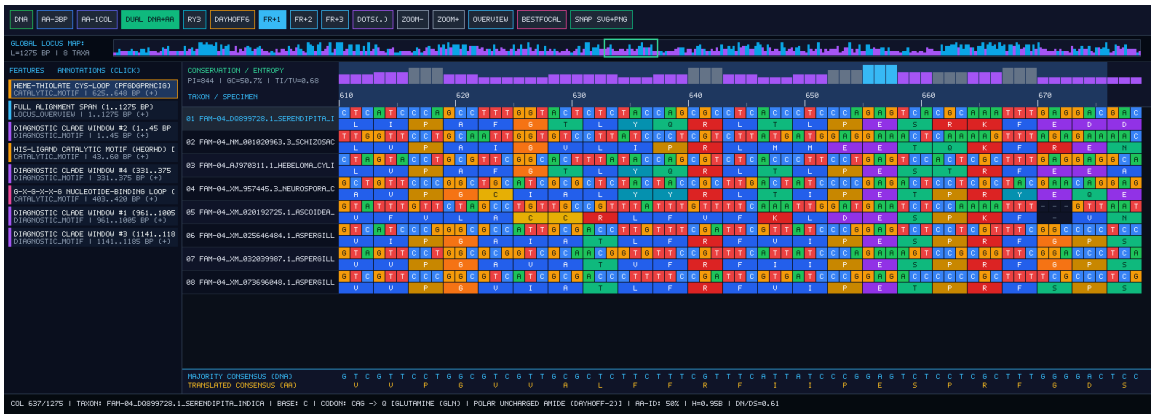
[22] Green, R. E., Krause, J., Briggs, A. W., Maricic, T., Stenzel, U., Kircher, M., et al. (2010). A draft sequence of the Neandertal genome. Science, 328(5979), 710-722. DOI: 10.1126/science.1188021 https://doi.org/10.1126/science.1188021

[23] Calabrese, S., Perez-Tienda, J., Ellerbeck, M., Arnould, C., Chatagnier, O., Boller, T., et al. (2016). GintAMT3: a low-affinity ammonium transporter of the arbuscular mycorrhizal Rhizophagus irregularis. Frontiers in Plant Science, 7, 679. DOI: 10.3389/fpls.2016.00679 https://doi.org/10.3389/fpls.2016.00679

[24] Phillips, M. J., Delsuc, F., & Penny, D. (2004). Genome-scale phylogeny and the detection of systematic biases. Molecular Biology and Evolution, 21(7), 1455-1458. DOI: 10.1093/molbev/msh137 https://doi.org/10.1093/molbev/msh137

Supplemental Figures (S1-S4) & Complete Record Ledgers (S1-S4)

FAM-04 Symbiotic High-Affinity Phosphate Transporter CDS (Fungal PHO84/PiPT, Code 1)



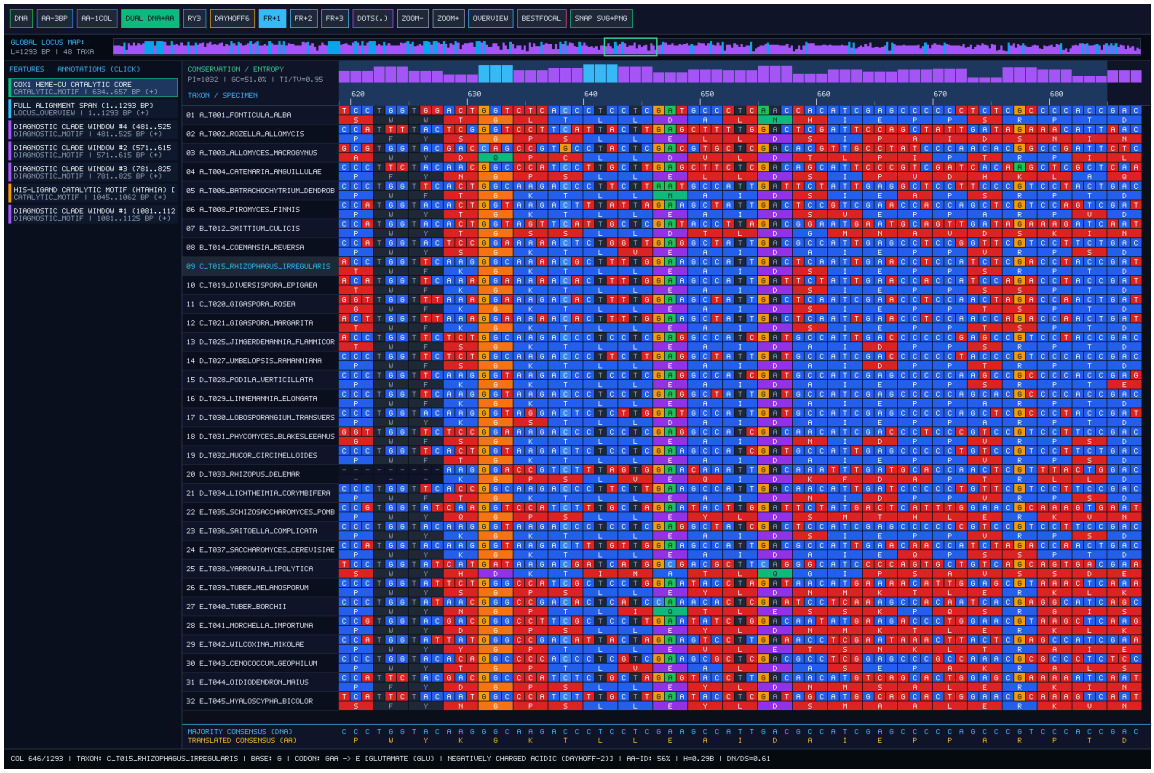
VAL-SET-072-MYCORRHIZAL-FUNGI-ORIGINS-KINGDOM-TIMETREE (FAM-04 PHO84/PiPT)

Cohort L2 Rhizophagus irregularis Single-Subunit 28S LSU rDNA (Katoh E-INS-i Core)



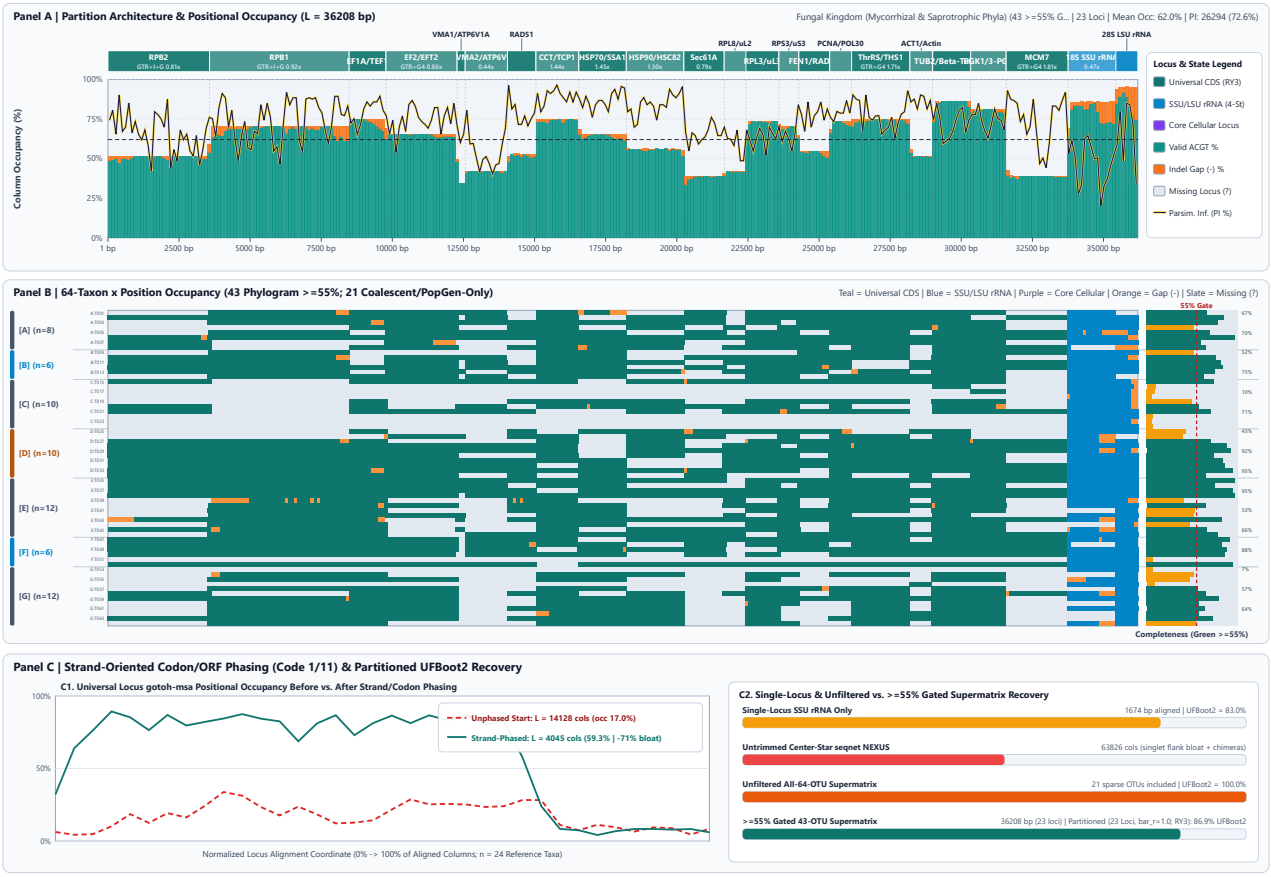
VAL-SET-072-MYCORRHIZAL-FUNGI-ORIGINS-KINGDOM-TIMETREE (Cohort L2 28S rDNA)

Fungal Translation Elongation Factor 1-Alpha (EF1A/TEF1, Code 1 RY3) Alignment Across Clades A-G



VAL-SET-072-MYCORRHIZAL-FUNGI-ORIGINS-KINGDOM-TIMETREE (EF1A/TEF1)

Supplemental Figure S4. Supermatrix Partitioned ModelTest Ribbon, Positional Occupancy Map (>=55% Gate) & Codon/ORF Strand Phasing (43 Gated vs. 21 Sparse/Coalescent-Only OTUs)



Supplemental Figure S4. Three-panel diagnostic graphic of the mycorrhizal-fungi-evolution-timetree multi-locus supermatrix: **(A)** per-locus winning BIC ModelTest model and edge-linked proportional rate multiplier (r_p) over stacked nucleotide occupancy across 23 partitions (L = 36,208 cols); **(B)** column-aligned 64-taxon heatmap across sectors `[A]` – `[G]` marking the **55% Gate** (>=55% supermatrix sites and >=10 loci) retaining **43 multi-locus OTUs** in concatenated trees while routing **21 sparse/single-locus OTUs** strictly to Quartet MSC, ABBA-BABA, Skylines, and Haplotype Networks; and **(C)** unphased vs. codon- and strand-phased occupancy (collapsing unphased Gotoh alignment length from 14,128 to 4,045 cols) alongside partitioned (86.9% UFBoot2) vs. unpartitioned (96.0%), unfiltered 64-OTU (100.0%), and single-locus SSU rRNA (83.0%) support.

Supplemental Table S1. Complete Core Taxon Matrix (64 Species)

Slot	Accession	Species	Family	Length	GC%	%ID	SHA-256	Verdict
A:T001	`KCV71205.1`	*Fonticula alba*	Fonticulaceae	4437	61.9%	79.2%	`700f7f7a79bd`	PASS_DIRECT
A:T002	`RKP19176.1`	*Rozella allomycis*	Rozellaceae	3492	37.2%	78.3%	`0007204f3e25`	PASS_DIRECT
A:T003	`KNE62645.1`	*Allomyces macrogynus*	Blastocladiaceae	5592	61.9%	100.0%	`b3a848e37ca4`	PASS_DIRECT
A:T004	`ORZ39073.1`	*Catenaria anguillulae*	Catenariaceae	1719	58.1%	100.0%	`ad9aad236474`	PASS_DIRECT
A:T005	`XP_016612704.1`	*Spizellomyces punctatus*	Spizellomycetaceae	5397	48.5%	75.0%	`38c410bc74c1`	PASS_DIRECT
A:T006	`KAK6094877.1`	*Batrachochytrium dendrobatidis*	Batrachochytriaceae	5130	43.9%	70.0%	`4c348fb6b13d`	PASS_DIRECT
A:T007	`KXS19791.1`	*Gonapodya prolifera*	Gonapodyaceae	3591	50.5%	77.4%	`4ff665b0a772`	PASS_DIRECT
A:T008	`ORX48646.1`	*Piromyces finnis*	Neocallimastigaceae	3630	32.4%	70.0%	`202306d8af27`	PASS_DIRECT
B:T009	`KXN67729.1`	*Conidiobolus coronatus*	Ancylistaceae	5670	37.0%	91.7%	`f548d65801b9`	PASS_DIRECT
B:T010	`ORX89614.1`	*Basidiobolus meristosporus*	Basidiobolaceae	3648	43.7%	70.0%	`7f42fcc0a4ba`	PASS_DIRECT
B:T011	`KAJ9084762.1`	*Entomophthora muscae*	Entomophthoraceae	3933	47.7%	76.1%	`53fa6cf97e77`	PASS_DIRECT
B:T012	`OMJ13227.1`	*Smittium culicis*	Legeriomycetaceae	3669	38.3%	70.0%	`a06ce604f627`	PASS_DIRECT
B:T013	`XP_040740504.1`	*Linderina pennispora*	Kickxellaceae	3669	60.7%	72.9%	`58d5ed3ef6b3`	PASS_DIRECT
B:T014	`PIA19325.1`	*Coemansia reversa*	Kickxellaceae	5526	51.8%	77.3%	`9c216847003a`	PASS_DIRECT

C:T015	POG79284.1	*Rhizophagus irregularis*	Glomeraceae	3861	35.5%	70.0%	ea71551b6a11	PASS_DIRECT
C:T016	ACL27209.1	*Rhizophagus clarus*	Glomeraceae	1341	41.4%	92.9%	da0f6dced631	PASS_DIRECT
C:T017	AAD09406.1	*Funneliformis mosseae*	Glomeraceae	1248	49.0%	70.5%	f85b91160917	PASS_DIRECT
C:T018	AJ245637.2	*Funneliformis geosporus*	Glomeraceae	1690	43.1%	93.3%	6ccf213fde45	PASS_DIRECT
C:T019	RHZ53026.1	*Diversispora epigaea*	Diversisporaceae	5574	38.0%	100.0%	633e2ed37be6	PASS_DIRECT
C:T020	RIB01550.1	*Gigaspora rosea*	Gigasporaceae	3885	38.8%	75.4%	c3cfb8738878	PASS_DIRECT
C:T021	KAF0479567.1	*Gigaspora margarita*	Gigasporaceae	3885	38.7%	76.9%	980cca30ca17	PASS_DIRECT
C:T022	AY635832.1	*Dentiscutata heterogama*	Gigasporaceae	1783	44.3%	93.3%	008d1d4e2c5e	PASS_DIRECT
C:T023	AB047303.1	*Ambispora leptoticha*	Ambisporaceae	1794	46.9%	93.3%	14b38f75d9de	PASS_DIRECT
C:T024	DQ322629.1	*Paraglomus occultum*	Paraglomeraceae	1787	47.0%	93.3%	e0ec4bf1f302	PASS_DIRECT
D:T025	RUP44084.1	*Jimgerdemannia flammicorona*	Endogonaceae	5256	51.2%	91.7%	37a0e3dfb540	PASS_DIRECT
D:T026	OZJ04949.1	*Bifiguratus adelaidae*	Bifigurataceae	6177	48.8%	88.2%	641478eb1efa	PASS_DIRECT
D:T027	XP_051445494.1	*Umbelopsis ramanniana*	Umbelopsidaceae	3645	43.7%	76.7%	02e6e89eedee	PASS_DIRECT
D:T028	KAF9388387.1	*Podila verticillata*	Mortierellaceae	3648	51.3%	70.1%	d10ba6753460	PASS_DIRECT
D:T029	KAK5805716.1	*Linnemannia elongata*	Mortierellaceae	3657	51.8%	71.1%	9109d665a8e7	PASS_DIRECT
D:T030	KAF9917073.1	*Lobosporangium transversale*	Mortierellaceae	3657	45.6%	70.0%	cf0b12bc9859	PASS_DIRECT
D:T031	KAL0080818.1	*Phycomyces blakesleeanus*	Phycomycetaceae	3654	45.2%	78.6%	5b8e2f4c211b	PASS_DIRECT
D:T032	KAL7325261.1	*Mucor circinelloides*	Mucoraceae	3651	42.7%	78.1%	ff313ae6befe	PASS_DIRECT
D:T033	XP_067523096.1	*Rhizopus delemar*	Rhizopodaceae	3645	41.6%	70.0%	0312a35a60a4	PASS_DIRECT
D:T034	XM_058492281.1	*Lichtheimia corymbifera*	Lichtheimiaceae	3669	46.3%	80.9%	b1af27439904	PASS_DIRECT
E:T035	KAL2316208.1	*Schizosaccharomyces pombe*	Schizosaccharomycetaceae	3630	41.1%	70.0%	8cd68b141155	PASS_DIRECT
E:T036	XP_019027004.1	*Saitoella complicata*	Protomycetaceae	3645	49.2%	73.6%	bb0b2288429d	PASS_DIRECT
E:T037	NP_014794.3	*Saccharomyces cerevisiae*	Saccharomycetaceae	3672	37.9%	76.9%	932d5f53cbf6	PASS_DIRECT
E:T038	QNP97632.1	*Yarrowia lipolytica*	Dipodascaceae	3687	54.9%	70.0%	ffc024531f88	PASS_DIRECT
E:T039	XP_002840938.1	*Tuber melanosporum*	Tuberaceae	3075	48.1%	84.2%	72a8f1699dae	PASS_DIRECT
E:T040	PUU83158.1	*Tuber borchii*	Tuberaceae	5253	47.6%	86.7%	3b4806c9a91e	PASS_DIRECT
E:T041	XP_045971325.1	*Morchella importuna*	Morchellaceae	5277	47.9%	85.0%	351f5d1028c1	PASS_DIRECT
E:T042	KAF8254050.1	*Wilcoxina mikolae*	Pyronemataceae	5223	49.0%	100.0%	032cb6d2bdc4	PASS_DIRECT
E:T043	XP_067498278.1	*Cenococcum geophilum*	Gloniaceae	2781	48.7%	87.0%	45bd5aa6f361	PASS_DIRECT
E:T044	KIM98032.1	*Oidiodendron maius*	Myxotrichaceae	5217	50.2%	73.7%	a5e980c269e9	PASS_DIRECT
E:T045	XP_024742739.1	*Hyaloscypha bicolor*	Hyaloscyphaceae	3780	49.2%	70.0%	bee2c647e2aa	PASS_DIRECT
E:T046	KAK3500795.1	*Neurospora crassa*	Sordariaceae	5283	54.0%	90.5%	a5af64350089	PASS_DIRECT
F:T047	KAA1125439.1	*Puccinia graminis*	Pucciniaceae	3939	47.9%	70.0%	d9c97f305231	PASS_DIRECT
F:T048	XP_053018664.1	*Puccinia triticina*	Pucciniaceae	3762	55.7%	70.0%	e36e112e5a98	PASS_DIRECT
F:T049	XP_016273243.1	*Rhodotorula toruloides*	Sporidiobolaceae	3759	62.2%	70.0%	427b52f04181	PASS_DIRECT
F:T050	XP_011390780.1	*Ustilago maydis*	Ustilaginaceae	3723	54.7%	70.0%	7a97d1f28ae8	PASS_DIRECT
F:T051	DQ832229.1	*Sporisorium reilianum*	Ustilaginaceae	1762	46.5%	93.3%	157aad07f86c	PASS_DIRECT
F:T052	KAN5211103.1	*Cryptococcus neoformans*	Cryptococcaceae	3735	48.1%	75.4%	16f54bcb8156	PASS_DIRECT
G:T053	AY293147.1	*Serendipita indica*	Serendipitaceae	2050	46.7%	93.3%	ab0219461e4f	PASS_DIRECT
G:T054	PVF97093.1	*Serendipita vermifera*	Serendipitaceae	4830	48.3%	81.5%	1b656be2f8fc	PASS_DIRECT
G:T055	KIO24927.1	*Tulasnella calospora*	Tulasnellaceae	5235	51.8%	100.0%	3b05a0ceaa99	PASS_DIRECT
G:T056	AB115328.1	*Phanerochaete chrysosporium*	Phanerochaetaceae	1044	58.1%	100.0%	c438727f79dd	PASS_DIRECT
G:T057	XP_024344811.1	*Rhodonia placenta*	Fomitopsidaceae	5238	53.4%	80.0%	0fffcbeb5132	PASS_DIRECT
G:T058	KAO1256244.1	*Laccaria bicolor*	Hydnangiaceae	3672	48.2%	100.0%	cf084351e665	PASS_DIRECT
G:T059	KAM6498527.1	*Amanita muscaria*	Amanitaceae	3672	48.7%	77.0%	526bbf8d732a	PASS_DIRECT
G:T060	KIM39097.1	*Hebeloma cylindrosporum*	Hymenogastraceae	5238	51.0%	93.3%	f6fd833a2cd8	PASS_DIRECT

G:T061	XP_007325088.1	*Agaricus bisporus*	Agaricaceae	5355	47.8%	100.0%	3ef246f94c50	PASS_DIRECT
G:T062	KIJ21257.1	*Paxillus involutus*	Paxillaceae	5235	52.0%	94.1%	8c36b3c155a9	PASS_DIRECT
G:T063	KAI6031508.1	*Pisolithus microcarpus*	Sclerodermataceae	3690	49.8%	76.5%	65018d894695	PASS_DIRECT
G:T064	KIK43849.1	*Suillus luteus*	Suillaceae	5226	51.6%	86.7%	bf1a25cec314	PASS_DIRECT

Supplemental Table S2. Complete Functional CDS Orthologs (42 Records)

Family	Accession	Organism	Protein Locus	Len	GC%	SHA-256
FAM-01	NM_001018239.3	*Schizosaccharomyces pombe*	Schizosaccharomyces pombe chitin syntha...	3044 bp	35.9%	53d855390ed0
FAM-01	AJ251942.1	*Agaricus bisporus*	Agaricus bisporus mRNA for putativechit...	3004 bp	48.2%	590cdae03f96
FAM-01	KF740717.1	*Fusarium oxysporum f. sp. cubense*	Fusarium oxysporum f. cubense chitin sy...	2712 bp	50.1%	73cd38f8c1f8
FAM-01	XM_019129677.1	*Babjeviella inositovora NRRL Y-12698*	Babjeviella inositovora NRRL Y-12698 ch...	3157 bp	54.4%	e2ab1ad104f7
FAM-01	PX725509.1	*Diaporthe liquidambaris*	Diaporthe liquidambaris Chitin synthase...	2181 bp	58.0%	3d14a3e38f62
FAM-01	JF912410.1	*Fusarium graminearum*	Gibberella zeae strain PH-1 chitin synt...	2718 bp	51.8%	e22b0a5987c2
FAM-01	XM_018856073.1	*Metschnikowia bicuspidata var. bicu...*	Metschnikowia bicuspidata var. bicuspid...	3148 bp	40.8%	10cd82e43ed2
FAM-01	XM_018278679.2	*Pseudogymnoascus verrucosus*	Pseudogymnoascus verrucosus Chitin synt...	3588 bp	51.5%	eef80b52e2ca
FAM-01	XM_020214546.1	*Williopsis jadinii*	Cyberlindnera jadinii NRRL Y-1542 chiti...	3355 bp	44.6%	5f907d146d15
FAM-01	U39479.1	*Aspergillus fumigatus*	Aspergillus fumigatus class III chitin ...	3334 bp	50.6%	d5271f73ce3d
FAM-01	XM_655035.2	*Aspergillus nidulans FGSC A4*	Aspergillus nidulans FGSC A4 chitin syn...	3205 bp	50.6%	901575507084
FAM-02	XM_653693.2	*Aspergillus nidulans FGSC A4*	Aspergillus nidulans FGSC A4 ammonium p...	2157 bp	53.9%	4fb97a778147
FAM-02	XM_956584.3	*Neurospora crassa OR74A*	Neurospora crassa OR74A ammonium transp...	2270 bp	58.4%	a2b0e6ff1b78
FAM-02	XM_054703190.2	*Fusarium oxysporum Fo47*	Fusarium oxysporum Fo47 ammonium permea...	1540 bp	54.3%	90c05c74c459
FAM-02	XM_032040182.1	*Aspergillus alliaceus*	Aspergillus alliaceus ammonium permease...	1847 bp	54.1%	e006f75bbb64
FAM-02	XM_024837758.1	*Aspergillus campestris IBT 28561*	Aspergillus campestris IBT 28561 ammoni...	1776 bp	60.2%	8310bda1b7be
FAM-02	XM_025526448.1	*Aspergillus eucalypticola CBS 122712*	Aspergillus eucalypticola CBS 122712 am...	1806 bp	54.2%	dda08311d1ba
FAM-02	XM_025677431.1	*Aspergillus japonicus CBS 114.51*	Aspergillus japonicus CBS 114.51 ammoni...	1962 bp	55.8%	ef539d46b0d6
FAM-02	XM_046085354.1	*Aspergillus melleus*	Aspergillus melleus ammonium permease M...	2213 bp	56.6%	99b8d41cf174
FAM-02	XM_073723558.1	*Aspergillus multicolor*	Aspergillus multicolor ammonium permeas...	2073 bp	56.3%	17921aa772bc
FAM-02	XM_032055801.1	*Aspergillus pseudotamarii*	Aspergillus pseudotamarii ammonium perm...	2565 bp	53.0%	827cacda0884
FAM-02	XM_025632833.1	*Aspergillus uvarum CBS 121591*	Aspergillus uvarum CBS 121591 ammonium ...	2102 bp	56.0%	f54994e6c6c2
FAM-02	XM_025704066.1	*Aspergillus vadensis CBS 113365*	Aspergillus vadensis CBS 113365 ammoniu...	1893 bp	54.1%	95344419ee2c
FAM-03	NM_001022740.3	*Schizosaccharomyces pombe*	Schizosaccharomyces pombe hexose transp...	2510 bp	44.1%	f03319c36ad2
FAM-03	Z83828.1	*Amanita muscaria*	A.muscaria mRNA for monosaccharide tran...	1711 bp	49.6%	8c6d380c77ec
FAM-03	XM_658372.2	*Aspergillus nidulans FGSC A4*	Aspergillus nidulans FGSC A4 hexose tra...	1880 bp	55.6%	414b37abed90
FAM-03	AB120373.1	*Cryptococcus neoformans*	Cryptococcus neoformans var. grubii HXT...	2129 bp	51.5%	c10331c4fad8
FAM-03	JX089403.1	*Fusarium oxysporum*	Fusarium oxysporum clone 201-3 high aff...	1816 bp	51.0%	c81b2b91cd03
FAM-03	XM_950908.3	*Neurospora crassa OR74A*	Neurospora crassa OR74A hexose transpor...	2596 bp	57.0%	536d9b92132f
FAM-03	AY585934.1	*Paxillus involutus*	Paxillus involutus strain ATCC 200175 h...	1817 bp	53.0%	1e39a0b31444
FAM-03	KJ493820.1	*Rhizophagus irregularis*	Rhizophagus irregularis isolate 8613 mo...	2587 bp	34.3%	fdb537a360b5
FAM-03	XM_046168630.1	*Alternaria rosae*	Alternaria rosae monosaccharide transpo...	2385 bp	54.4%	3c5d04a7de8a
FAM-03	XM_047967484.1	*Annulohypoxylon maeteangense*	Annulohypoxylon maeteangense hexose tra...	2089 bp	50.0%	827f98edd7ab
FAM-03	XM_047997860.1	*Annulohypoxylon truncatum*	Annulohypoxylon truncatum putative MFS ...	2044 bp	59.4%	a8a5f0ef520d
FAM-04	DQ899728.1	*Serendipita indica*	Piriformospora indica phosphate transpo...	1823 bp	54.5%	aebf5126a70e
FAM-04	NM_001020963.3	*Schizosaccharomyces pombe*	Schizosaccharomyces pombe inorganic pho...	2274 bp	41.1%	2b835dbc8c7e
FAM-04	AJ970311.1	*Hebeloma cylindrosporum*	Hebeloma cylindrosporum mRNA for phosph...	1948 bp	51.1%	94058f064904
FAM-04	XM_957445.3	*Neurospora crassa OR74A*	Neurospora crassa OR74A inorganic phosp...	2165 bp	56.8%	a771185da2d8
FAM-04	XM_020192725.1	*Ascoidea rubescens DSM 1968*	Ascoidea rubescens DSM 1968 inorganic p...	2065 bp	35.8%	2a3303ae8ab4

FAM-04	`XM_025646484.1`	*Aspergillus aculeatinus CBS 121060*	Aspergillus aculeatinus CBS 121060 phos...	2565 bp	58.4%	`b9722bd7bab5`
FAM-04	`XM_032039987.1`	*Aspergillus alliaceus*	Aspergillus alliaceus phosphate transpo...	2187 bp	51.8%	`585cedf3aa07`
FAM-04	`XM_073696048.1`	*Aspergillus ambiguus*	Aspergillus ambiguus phosphate transpor...	1961 bp	62.8%	`f77fe497ecc4`

Supplemental Table S3. Complete 32-Chain RuNIE Combinatorial Sweep

Chain	Regime	Model	Recoding	Cols	Patterns	ln L	AIC / BIC	RCFV	CPU Time
R1-M1	Regime 1 (1st Best — 5 Beakers): ...	JC	Partitioned-RY3	36208	27063	-785301.8859	1571225.8 / 1573868.3	0.0127	2909156 ms
R1-M2	Regime 1 (1st Best — 5 Beakers): ...	K80+G4	Partitioned-RY3	36208	27063	-724229.8008	1449085.6 / 1451745.2	0.0127	2911928 ms
R1-M3	Regime 1 (1st Best — 5 Beakers): ...	HKY+F+I+G4	Partitioned-RY3	36208	27063	-695568.4152	1391770.8 / 1394464.4	0.0127	2916578 ms
R1-M4	Regime 1 (1st Best — 5 Beakers): ...	TN+F+I+G4	Partitioned-RY3	36208	27063	-694349.6578	1389335.3 / 1392037.4	0.0127	2915396 ms
R1-M5	Regime 1 (1st Best — 5 Beakers): ...	TIM2+F+I+G4	Partitioned-RY3	36208	27063	-685047.0254	1370732.1 / 1373442.6	0.0127	2917420 ms
R1-M6	Regime 1 (1st Best — 5 Beakers): ...	GTR+F+G4	Partitioned-RY3	36208	27063	-678793.3874	1358226.8 / 1360945.8	0.0127	2923029 ms
R1-M7	Regime 1 (1st Best — 5 Beakers): ...	GTR+F+I+G4	Partitioned-RY3	36208	27063	-678793.3874	1358228.8 / 1360956.3	0.0127	2924400 ms
R1-M8	Regime 1 (1st Best — 5 Beakers): ...	GTR+F+R2	Partitioned-RY3	36208	27063	-684805.3078	1370252.6 / 1372980.2	0.0127	2916423 ms
R2-M1	Regime 2 (2nd Nearest — 5 Beakers...	JC	Unpartitioned-RY3	36208	27063	-791178.6119	1582519.2 / 1583207.5	0.0127	2909156 ms
R2-M2	Regime 2 (2nd Nearest — 5 Beakers...	K80+G4	Unpartitioned-RY3	36208	27063	-729999.1556	1460164.3 / 1460869.6	0.0127	2913405 ms
R2-M3	Regime 2 (2nd Nearest — 5 Beakers...	HKY+F+I+G4	Unpartitioned-RY3	36208	27063	-701367.0904	1402908.2 / 1403647.4	0.0127	2917109 ms
R2-M4	Regime 2 (2nd Nearest — 5 Beakers...	TN+F+I+G4	Unpartitioned-RY3	36208	27063	-700155.8003	1400487.6 / 1401235.3	0.0127	2916458 ms
R2-M5	Regime 2 (2nd Nearest — 5 Beakers...	TIM2+F+I+G4	Unpartitioned-RY3	36208	27063	-690866.7768	1381911.6 / 1382667.8	0.0127	2917355 ms
R2-M6	Regime 2 (2nd Nearest — 5 Beakers...	GTR+F+G4	Unpartitioned-RY3	36208	27063	-684615.3840	1369410.8 / 1370175.5	0.0127	2920361 ms
R2-M7	Regime 2 (2nd Nearest — 5 Beakers...	GTR+F+I+G4	Unpartitioned-RY3	36208	27063	-684615.3840	1369412.8 / 1370186.0	0.0127	2922996 ms
R2-M8	Regime 2 (2nd Nearest — 5 Beakers...	GTR+F+R2	Unpartitioned-RY3	36208	27063	-690646.0770	1381474.2 / 1382247.4	0.0127	2916345 ms
R3-M1	Regime 3 (3rd Medium — 4 Beakers)...	JC	Unrecoded-4	36208	28802	-1026670.4880	2053503.0 / 2054191.2	0.0987	2909163 ms
R3-M2	Regime 3 (3rd Medium — 4 Beakers)...	K80+G4	Unrecoded-4	36208	28802	-903303.1397	1806772.3 / 1807477.5	0.0987	2912335 ms
R3-M3	Regime 3 (3rd Medium — 4 Beakers)...	HKY+F+I+G4	Unrecoded-4	36208	28802	-903472.7324	1807119.5 / 1807858.7	0.0987	2915493 ms
R3-M4	Regime 3 (3rd Medium — 4 Beakers)...	TN+F+I+G4	Unrecoded-4	36208	28802	-902636.5403	1805449.1 / 1806196.8	0.0987	2919127 ms
R3-M5	Regime 3 (3rd Medium — 4 Beakers)...	TIM2+F+I+G4	Unrecoded-4	36208	28802	-903577.1865	1807332.4 / 1808088.6	0.0987	2917160 ms
R3-M6	Regime 3 (3rd Medium — 4 Beakers)...	GTR+F+G4	Unrecoded-4	36208	28802	-902211.8123	1804603.6 / 1805368.4	0.0987	2920242 ms
R3-M7	Regime 3 (3rd Medium — 4 Beakers)...	GTR+F+I+G4	Unrecoded-4	36208	28802	-902211.8123	1804605.6 / 1805378.9	0.0987	2922144 ms
R3-M8	Regime 3 (3rd Medium — 4 Beakers)...	GTR+F+R2	Unrecoded-4	36208	28802	-916832.1035	1833846.2 / 1834619.4	0.0987	2917225 ms
R4-M1	Regime 4 (4th Rejected — 0 Beaker...	JC	Raw-0Beaker	36208	34459	-1661343.3604	3322848.7 / 3323537.0	0.0993	2909168 ms
R4-M2	Regime 4 (4th Rejected — 0 Beaker...	K80+G4	Raw-0Beaker	36208	34459	-1664617.6142	3329401.2 / 3330106.5	0.0993	2913229 ms

R4-M3	Regime 4 (4th Rejected — 0 Beaker...	HKY+F+I+G4	Raw-0Beaker	36208	34459	-1664474.4877	3329123.0 / 3329862.2	0.0993	2916693 ms
R4-M4	Regime 4 (4th Rejected — 0 Beaker...	TN+F+I+G4	Raw-0Beaker	36208	34459	-1664489.2719	3329154.5 / 3329902.3	0.0993	2918043 ms
R4-M5	Regime 4 (4th Rejected — 0 Beaker...	TIM2+F+I+G4	Raw-0Beaker	36208	34459	-1664542.8387	3329263.7 / 3330019.9	0.0993	2918513 ms
R4-M6	Regime 4 (4th Rejected — 0 Beaker...	GTR+F+G4	Raw-0Beaker	36208	34459	-1664346.4046	3328872.8 / 3329637.5	0.0993	2922267 ms
R4-M7	Regime 4 (4th Rejected — 0 Beaker...	GTR+F+I+G4	Raw-0Beaker	36208	34459	-1664346.4046	3328874.8 / 3329648.0	0.0993	2926275 ms
R4-M8	Regime 4 (4th Rejected — 0 Beaker...	GTR+F+R2	Raw-0Beaker	36208	34459	-1677859.9962	3355902.0 / 3356675.2	0.0993	2917924 ms

Supplemental Table S4. Complete 383 Single-Species Coalescent Isolates

Isolate	Accession	Organism	Locus	Locality	Host / Context	Year	Len
R1_I01	KF646117.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Global Agroecosystem ...	Rr99	Archived	553 bp
R1_I02	KY076494.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Russia	8 RCAM00320	1981	736 bp
R1_I03	MK275289.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Global Agroecosystem ...	S13-b2	Archived	879 bp
R1_I04	MN540313.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Global Agroecosystem ...	Vitis vinifera subsp. s...	Archived	592 bp
R1_I05	MT210909.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Global Agroecosystem ...	Trigonella foenum-graecum	Archived	874 bp
R1_I06	OK184924.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Global Agroecosystem ...	IN	Archived	730 bp
R1_I07	OL449343.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Italy: Manciano	Sorghum halepense	2011	545 bp
R1_I13	KY014755.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Russia	Fragaria vesca	1980	735 bp
R1_I14	MK275288.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Global Agroecosystem ...	S13-a5	Archived	709 bp
R1_I15	MT210910.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Global Agroecosystem ...	Trigonella foenum-graecum	Archived	874 bp
R1_I16	OL449344.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Italy: Manciano	Sorghum halepense	2011	538 bp
R1_I20	KY065339.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Russia	Fragaria vesca	1980	618 bp
R1_I21	MK948404.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Global Agroecosystem ...	Glomus irregulare	Archived	358 bp
R1_I22	MT210911.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Global Agroecosystem ...	Trigonella foenum-graecum	Archived	873 bp
R1_I23	OL449358.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Italy: Manciano	Sorghum halepense	2011	538 bp
R1_I25	KY065340.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Russia	Fragaria vesca	1980	587 bp
R1_I26	MK948447.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Global Agroecosystem ...	Glomus irregulare	Archived	357 bp
R1_I27	MT210908.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Global Agroecosystem ...	Inoculum	Archived	865 bp
R1_I28	OL449360.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Italy: Manciano	Sorghum halepense	2011	538 bp
R1_I30	KY965432.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	China	Glomus irregulare	Archived	584 bp
R1_I31	MK948362.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Global Agroecosystem ...	Glomus irregulare	Archived	355 bp
R1_I33	OL449366.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Italy: Manciano	Sorghum halepense	2011	538 bp
R1_I36	MK948365.1	*Rhizophagus irregularis*	Nuclear ITS1-5.8S-ITS2	Global Agroecosystem ...	Glomus irregulare	Archived	355 bp
R2_I01	AF166276.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Calcareous Grassland ...	spore 2	Archived	543 bp
R2_I02	AM157131.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Germany	ISCB13	Archived	478 bp
R2_I03	AY997053.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Calcareous Grassland ...	UT101 (INVAM)	Archived	480 bp
R2_I04	JF681980.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	India: north eastern ...	AMF-G7	Archived	355 bp
R2_I05	JN847432.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Calcareous Grassland ...	AM6A	Archived	587 bp
R2_I06	JQ048759.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	United Kingdom	BEG12	Archived	491 bp
R2_I07	MF599221.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Calcareous Grassland ...	M24	2016	574 bp
R2_I10	ON067808.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Calcareous Grassland ...	IN-D78	Archived	561 bp
R2_I11	OP615192.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Calcareous Grassland ...	WaAs	2021	440 bp
R2_I12	OQ222886.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	India	DGPS-GM	Archived	575 bp
R2_I13	OR389386.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Allium ampeloprasum; ...	W1-18_1	2007	748 bp

R2_I14	PP329940.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Calcareous Grassland ...	Jwan-8	Archived	693 bp
R2_I15	PQ357597.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Calcareous Grassland ...	KS1	Archived	568 bp
R2_I16	PX993810.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	India: Gosalpur, Jaba...	BR1	2025	723 bp
R2_I17	PZ142575.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Turkey	O4	2025	580 bp
R2_I18	X96832.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Calcareous Grassland ...	BEG54	Archived	578 bp
R2_I19	AM157135.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Switzerland:Basel	ISCB20	Archived	466 bp
R2_I20	JF681976.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	India: north eastern ...	AMF-60	Archived	354 bp
R2_I21	JQ048763.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	United Kingdom	BEG12	Archived	486 bp
R2_I22	MF599220.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Calcareous Grassland ...	M23	2016	544 bp
R2_I23	OR389389.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Allium ampeloprasum; ...	W1-20_1	2007	746 bp
R2_I25	PZ507471.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	India	TRF10	2026	580 bp
R2_I26	X96830.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Calcareous Grassland ...	BEG54	Archived	577 bp
R2_I27	AM157134.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Switzerland:Basel	ISCB19	Archived	443 bp
R2_I28	JF681975.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	India: dry zone of Ka...	AMF-G3	Archived	353 bp
R2_I29	JQ048761.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	United Kingdom	BEG12	Archived	484 bp
R2_I30	OR389420.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Allium ampeloprasum; ...	W3-69_2	2007	745 bp
R2_I31	PQ669218.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	India: Tamil Nadu, Th...	GlomoMax1	2022	536 bp
R2_I32	PZ142585.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Turkey	S-2K	2025	579 bp
R2_I33	X96831.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Calcareous Grassland ...	BEG54	Archived	577 bp
R2_I34	AM157133.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	Switzerland:Basel	ISCB22	Archived	440 bp
R2_I35	JF681977.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	India: western Ghats ...	AMF-135	Archived	352 bp
R2_I36	JQ048764.1	*Funneliformis mosseae*	Nuclear ITS1-5.8S-ITS2	United Kingdom	BEG12	Archived	484 bp
R3_I02	KF359556.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	USA: TN, GRSM, Copela...	CC 12-38	2006	838 bp
R3_I03	KT447176.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Boreal & Alpine Stres...	ML-13	Archived	828 bp
R3_I04	KU376403.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Germany: Hainich	MT1	2015	764 bp
R3_I05	KX449189.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Canada: British Columbia	6a	Archived	573 bp
R3_I06	KY595999.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Spain	GenBank / RefSeq deposit	Archived	496 bp
R3_I07	LC149755.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Japan:Kagoshima, Mina...	Ks09-1	2010	888 bp
R3_I08	MH038069.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Boreal & Alpine Stres...	ectomycorrhiza	Archived	534 bp
R3_I09	MK431004.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Boreal & Alpine Stres...	MFT15	Archived	861 bp
R3_I10	MN961132.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Canada: Quebec	ARSL 220507.51	Archived	533 bp
R3_I11	MT668605.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Mexico: Oaxaca, Ixtla...	P18	2018	876 bp
R3_I13	MZ570243.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Switzerland: Pfynwald	Pinus sylvestris	2008	872 bp
R3_I14	OL348345.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	USA: Florida	ORDG2G3_d1_A	Archived	864 bp
R3_I15	OM339447.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Canada: BC	ubco3	Archived	492 bp
R3_I16	OP412998.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Boreal & Alpine Stres...	AMC134	Archived	560 bp
R3_I17	OQ418576.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Boreal & Alpine Stres...	DN737a	2017	580 bp
R3_I18	OR939772.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Canada: British Columbia	BP346443	2006	792 bp
R3_I20	PQ217893.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Boreal & Alpine Stres...	bioassay	2019	861 bp
R3_I21	PV628864.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	China: Jiangsu provin...	GMCg6-1	2023	537 bp
R3_I22	PX931633.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Boreal & Alpine Stres...	Nothofagus antarctica	2020	511 bp
R3_I23	PZ415778.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	USA: Flagstaff, Arizona	Q.MT2b	2023	833 bp
R3_I24	QB323747.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Argentina: Patagonia	Nothofagus antarctica	2022	501 bp
R3_I25	AB986324.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	USA:Florida	LWg3001	Archived	511 bp
R3_I26	KF472151.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	France: Guadeloupe	Ecu265	2012	729 bp

R3_I27	KT800291.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Boreal & Alpine Stres...	5-ITS-1F	Archived	506 bp
R3_I29	KX449206.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Canada: British Columbia	12d	Archived	554 bp
R3_I30	LC149748.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Japan:Ishikawa, Nohmi	I05-1	2009	882 bp
R3_I31	MH038096.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Boreal & Alpine Stres...	ectomycorrhiza	Archived	530 bp
R3_I32	MK131435.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Canada: NS	Picea rubens	Archived	696 bp
R3_I33	MN959775.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Boreal & Alpine Stres...	MTH1	Archived	507 bp
R3_I34	MT668617.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	Mexico: Oaxaca, Ixtla...	P36	2018	873 bp
R3_I35	MZ570244.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	CBS:143616	Pinus sylvestris	2008	808 bp
R3_I36	OL348336.1	*Cenococcum geophilum*	Nuclear ITS1-5.8S-ITS2	USA: Florida	ARC53_e6_A4	Archived	425 bp
R4_I02	AF166511.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Holarctic Pine Ectomy...	LBG-17	Archived	629 bp
R4_I03	AY898619.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Spain: Madrid	CCMA-35	Archived	752 bp
R4_I04	DQ440568.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Spain: Madrid	CCMA-37	Archived	802 bp
R4_I05	EU488706.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Holarctic Pine Ectomy...	S1IRL	Archived	665 bp
R4_I06	GQ330568.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	China	SNP-20	Archived	555 bp
R4_I07	GU222326.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	PDD:98352	New Zealand	Archived	685 bp
R4_I08	HM036651.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Holarctic Pine Ectomy...	KRP28-3	Archived	651 bp
R4_I09	HQ999981.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	ATCC:MYA-4759	ATCC MYA-4759	Archived	615 bp
R4_I10	JF908725.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Italy	G.Simonini	1996	551 bp
R4_I11	JQ711923.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Canada: BC	FFP1046	2007	841 bp
R4_I12	JX907818.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Holarctic Pine Ectomy...	T3PK2	Archived	666 bp
R4_I13	KC339728.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	China	N4	2012	667 bp
R4_I14	KF937367.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Holarctic Pine Ectomy...	NVE 425	2013	707 bp
R4_I15	KJ415100.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Holarctic Pine Ectomy...	SFC20130926-19	Archived	638 bp
R4_I16	KM409445.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Holarctic Pine Ectomy...	P51_M9_772	Archived	609 bp
R4_I17	KR673431.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Holarctic Pine Ectomy...	KA12-0359	2012	618 bp
R4_I18	KT883897.1	*Suillus luteus f. albus*	Nuclear ITS1-5.8S-ITS2	Holarctic Pine Ectomy...	FR2014538	Archived	655 bp
R4_I19	KU721222.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	TENN:060949	New Zealand: City Park,...	2006	711 bp
R4_I20	KX449431.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Spain: Bustarviejo	Ica-7	Archived	708 bp
R4_I21	KY825994.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Canada: Quebec, Rawdon	CMMF000363	1988	674 bp
R4_I22	L54083.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Holarctic Pine Ectomy...	HB-348	Archived	641 bp
R4_I23	LC651037.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Holarctic Pine Ectomy...	A04101	2019	749 bp
R4_I24	MF421108.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Holarctic Pine Ectomy...	NIFoS2270	Archived	551 bp
R4_I25	MG383665.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Holarctic Pine Ectomy...	A18	Archived	554 bp
R4_I26	MH855739.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	CBS:136.36	CBS 136.36	Archived	691 bp
R4_I27	MK841686.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	USA: The White Mounti...	The roots of pinus flex...	2017	716 bp
R4_I28	MN992279.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Canada: Quebec, Radisson	MQ18R064-QFB30147	2018	709 bp
R4_I29	MT652994.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	China	N94	Archived	697 bp
R4_I30	MW554337.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Holarctic Pine Ectomy...	110114MFBPL0020	Archived	702 bp
R4_I31	MZ148530.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Holarctic Pine Ectomy...	HBAU15764	Archived	660 bp
R4_I32	OK033366.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Holarctic Pine Ectomy...	RB-728_a	Archived	649 bp
R4_I33	OL958501.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Russia	NSK 1017103	Archived	817 bp
R4_I34	OM203527.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	Holarctic Pine Ectomy...	iNAT 37434526	2015	708 bp
R4_I35	ON129298.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	USA: New York	iNat63113497	2020	653 bp
R4_I36	OQ383436.1	*Suillus luteus*	Nuclear ITS1-5.8S-ITS2	USA: Washington, Thur...	iNat77564890	2021	688 bp
R5_I01	EU071957.1	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	Northern Temperate Mi...	LG382	Archived	647 bp

R5_I02	LC912536.1	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	Northern Temperate Mi...	HYNK25593	2025	644 bp
R5_I03	MF773614.1	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	USA: Tennessee	ACB102009-16 (TENN)	2009	618 bp
R5_I04	MH615053.1	*Amanita muscaria var. guessowii*	Nuclear ITS1-5.8S-ITS2	TENN:073101	AMO25	2017	690 bp
R5_I05	MK492596.1	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	Spain	Eucalyptus nitens	Archived	738 bp
R5_I06	MW281787.1	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	Northern Temperate Mi...	AMU2	2018	672 bp
R5_I07	MZ668073.1	*Amanita muscaria var. guessowii*	Nuclear ITS1-5.8S-ITS2	USA: Indiana, Orange ...	S.D. Russell MycoMap # ...	2017	679 bp
R5_I08	OK346418.1	*Amanita muscaria var. alba*	Nuclear ITS1-5.8S-ITS2	Northern Temperate Mi...	iNat17296703	2018	709 bp
R5_I09	OM952182.1	*Amanita muscaria subsp. flavivo...*	Nuclear ITS1-5.8S-ITS2	USA: California, San ...	MushroomObserver.org/46...	2021	619 bp
R5_I10	ON416975.1	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	USA: Oregon, Mulino	S.D. Russell iNaturalis...	2018	718 bp
R5_I11	OP749707.1	*Amanita muscaria var. guessowii*	Nuclear ITS1-5.8S-ITS2	USA: Pennsylvania, Cl...	S.D. Russell ONT iNatur...	2022	667 bp
R5_I12	OQ252774.1	*Amanita muscaria var. guessowii*	Nuclear ITS1-5.8S-ITS2	USA: Southaven C.P, B...	jlh0003-22	2022	690 bp
R5_I13	OR058506.1	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	China	BJTC L491	Archived	685 bp
R5_I14	PP576202.1	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	USA: California, Fres...	CA FUNDIS iNaturalist #...	2023	677 bp
R5_I15	PQ144070.1	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	iNAT:180542048	CA FUNDIS	2023	677 bp
R5_I16	PV248470.1	*Amanita muscaria var. guessowii*	Nuclear ITS1-5.8S-ITS2	Northern Temperate Mi...	ACAD 21402F	2023	803 bp
R5_I17	PX313693.1	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	Northern Temperate Mi...	Pinus sp.	2024	686 bp
R5_I18	PZ536522.1	*Amanita muscaria subsp. flavivo...*	Nuclear ITS1-5.8S-ITS2	USA: Washington, Port...	iNaturalist # 321451852	2025	716 bp
R5_I19	QB319816.1	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	USA: New Mexico, Mt. ...	fruiting body	2026	671 bp
R5_I20	EU071889.1	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	Northern Temperate Mi...	CMP3143	Archived	643 bp
R5_I21	LC860706.1	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	Northern Temperate Mi...	HYNK457	2024	621 bp
R5_I22	MF908458.1	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	UBC:F33057	Soil, decaying leaves	2016	596 bp
R5_I23	MH718239.1	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	Northern Temperate Mi...	Viv17	2016	605 bp
R5_I24	MW281786.1	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	Northern Temperate Mi...	AMU1	2017	671 bp
R5_I25	MZ668144.1	*Amanita muscaria var. guessowii*	Nuclear ITS1-5.8S-ITS2	USA: Indiana, Univers...	S.D. Russell iNaturalis...	2018	651 bp
R5_I26	OK346349.1	*Amanita muscaria var. guessowii*	Nuclear ITS1-5.8S-ITS2	USA: Ohio	MO395763	2019	670 bp
R5_I27	ON416919.1	*Amanita muscaria var. guessowii*	Nuclear ITS1-5.8S-ITS2	USA: New York, Living...	NEMF 2018 iNaturalist #...	2018	680 bp
R5_I28	OP470095.1	*Amanita muscaria subsp. flavivo...*	Nuclear ITS1-5.8S-ITS2	USA: California	MO450042	2021	640 bp
R5_I29	OQ540548.1	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	USA: Arizona, Cochise...	HFS iNaturalist # 13622...	2022	678 bp
R5_I30	OR825667.1	*Amanita muscaria subsp. flavivo...*	Nuclear ITS1-5.8S-ITS2	USA: Colorado, Jeffer...	OMDL iNat # 178316780	2023	674 bp
R5_I31	PP410525.1	*Amanita muscaria subsp. flavivo...*	Nuclear ITS1-5.8S-ITS2	USA: California, Mono...	CA FUNDIS iNaturalist #...	2023	676 bp
R5_I32	PQ760829.1	*Amanita muscaria subsp. flavivo...*	Nuclear ITS1-5.8S-ITS2	USA: California	CA FUNDIS iNaturalist #...	2024	676 bp
R5_I33	PV748909.1	*Amanita muscaria subsp. flavivo...*	Nuclear ITS1-5.8S-ITS2	iNAT:187735086	USA: Washington, Kitsap...	2023	683 bp
R5_I34	PX094348.1	*Amanita muscaria subsp. flavivo...*	Nuclear ITS1-5.8S-ITS2	USA: Colorado, El Pas...	OMDL iNat # 230622738	2024	681 bp
R5_I35	PZ559869.1	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	OTA:76284	New Zealand	2026	669 bp
R5_I36	EU071902.1	*Amanita muscaria*	Nuclear ITS1-5.8S-ITS2	Northern Temperate Mi...	CMP1345	Archived	643 bp
R6_I01	AF106874.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	Italy: central, Umbria	A34	Archived	620 bp
R6_I02	AJ583595.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	France:Comminge,Ariege	M119	Archived	550 bp
R6_I03	DQ375525.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	France: Vaucluse	Tmel-euO4	Archived	619 bp

R6_I04	EU753270.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	New Zealand	Quercus sp.	Archived	620 bp
R6_I05	FM205569.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	MA:Fungi:47931	Spain:Aldeamayor de Sna...	Archived	581 bp
R6_I06	GU810153.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	Mediterranean Calcare...	Quercus cerris	Archived	656 bp
R6_I08	JF908742.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	Italy	A.Montecchi	1997	574 bp
R6_I09	JQ638961.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	Mediterranean Calcare...	GenBank / RefSeq deposit	Archived	596 bp
R6_I10	KF742777.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	Canada: British Columbia	S-spcp1	Archived	885 bp
R6_I11	KM659872.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	France	MelCR2-00	Archived	610 bp
R6_I12	KP972070.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	Canada: British Colum...	P_Qr	Archived	607 bp
R6_I13	MF590054.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	China: Yunnan	mwr-1	2017	582 bp
R6_I14	MN338092.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	France	mel	Archived	623 bp
R6_I15	MZ423176.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	Italy: Lombardy, Monz...	Carpinus betulus L. and...	2019	532 bp
R6_I16	OM948972.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	Croatia: Istria	LMGI 3/22	Archived	623 bp
R6_I17	OP978682.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	Mediterranean Calcare...	T-773	Archived	610 bp
R6_I18	OQ786854.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	USA	FLAS-F-71144	2022	621 bp
R6_I19	PP918877.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	ACAM:Tub056	Greece: Pieria	2007	756 bp
R6_I20	PQ525349.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	FLAS:F-72611	USA: North Carolina	2024	610 bp
R6_I21	PV939383.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	Italy	GB200	2010	574 bp
R6_I23	PZ193117.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	USA: North Carolina, ...	FLASF72398	2024	434 bp
R6_I24	QB288568.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	DAVFP:30297	SB0071	2013	611 bp
R6_I25	U89359.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	collected in L'Aquila...	A1	Archived	620 bp
R6_I26	AF106876.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	Italy: north, Piemonte	A51	Archived	620 bp
R6_I27	AJ583596.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	France:Comminge,Ariege	M121	Archived	550 bp
R6_I28	DQ388876.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	France: Vaucluse	Tmel-eu05	Archived	611 bp
R6_I29	EU200410.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	Mediterranean Calcare...	MEL298	Archived	550 bp
R6_I30	FM205572.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	personal collection:A...	Slovenia:Karst region	2005	581 bp
R6_I31	GU810152.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	Mediterranean Calcare...	Quercus robur	Archived	650 bp
R6_I32	JF264440.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	Italy: Salo, Brescia	Ostrya carpinifolia Scop.	2009	550 bp
R6_I33	JQ639008.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	Mediterranean Calcare...	GenBank / RefSeq deposit	Archived	590 bp
R6_I34	KF591751.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	France	61FR	Archived	450 bp
R6_I35	KM659871.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	France	MelC89	Archived	609 bp
R6_I36	KP972063.1	*Tuber melanosporum*	Nuclear ITS1-5.8S-ITS2	Canada: British Colum...	SPCP_B22	Archived	470 bp
L1_I01	AB089654.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Japan:Ibaraki, Tsukuba	E97053	Archived	518 bp
L1_I02	AF062800.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	ex roots Vaccinium my...	UAMH 8921	Archived	527 bp
L1_I03	AY624308.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Boreal Peatland Erico...	UAMH 9446	Archived	498 bp
L1_I04	EU888920.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Boreal Peatland Erico...	EYR71	Archived	545 bp
L1_I05	FN661517.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Boreal Peatland Erico...	Cd	Archived	501 bp
L1_I06	HQ608115.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	USA: Stengl Biology S...	TR088	2006	580 bp
L1_I07	JF304942.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	CCF<CZE>:3585	OMA-B	Archived	530 bp
L1_I08	JN882306.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	ATCC:MYA-4765	ATCC MYA-4765	Archived	560 bp
L1_I09	KF359579.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	USA: TN, GRSM, Copela...	CC 07-20	2006	602 bp
L1_I10	KM678348.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	South Africa	Glum088	2012	359 bp
L1_I11	KP783449.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Russia	mycorrhizal root of Pin...	Archived	530 bp
L1_I12	KU516533.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Boreal Peatland Erico...	353J14	2014	548 bp
L1_I13	KX440128.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Boreal Peatland Erico...	root of wild Vaccinium sp.	Archived	545 bp
L1_I14	KY910207.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	China	GenBank / RefSeq deposit	Archived	537 bp

L1_I15	LC206638.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Japan: Nagano, Ueda-s...	FC-3853	2012	588 bp
L1_I16	MF926533.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Boreal Peatland Erico...	root Orthilia secunda	Archived	472 bp
L1_I17	MG890316.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Boreal Peatland Erico...	RhYM3	Archived	499 bp
L1_I18	MH864347.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	CBS:126948	CBS 126948	Archived	686 bp
L1_I19	MK131651.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Canada: NS	Abies balsamea	Archived	545 bp
L1_I20	MN961138.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Canada: Quebec	ARSL 230507.56	Archived	557 bp
L1_I21	MT522565.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	China: Guizhou	soil and pine roots	2019	638 bp
L1_I22	MW793959.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Lithuania: The Curoni...	G3-2-5R12	Archived	546 bp
L1_I23	OK584544.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Forest soil: relict c...	P786	Archived	496 bp
L1_I24	OM729680.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Boreal Peatland Erico...	UNIJAG.PL.368	Archived	552 bp
L1_I25	ON032317.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Boreal Peatland Erico...	FC	Archived	521 bp
L1_I27	OQ271290.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Boreal Peatland Erico...	KACC410230	Archived	566 bp
L1_I28	PQ049695.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Boreal Peatland Erico...	cxtd29	Archived	576 bp
L1_I29	PV654075.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	China: Harbin	DX-27	2024	533 bp
L1_I30	PX746801.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	UKA-83	Calluna vulgaris	2018	483 bp
L1_I31	PZ152241.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	China: Harbin	OM	2025	531 bp
L1_I32	AB089655.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Japan:Ibaraki, Tsukuba	E97154	Archived	518 bp
L1_I33	AF062798.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Boreal Peatland Erico...	UAMH 1540	Archived	525 bp
L1_I34	AY624314.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Boreal Peatland Erico...	UAMH 10116	Archived	496 bp
L1_I35	FN661518.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	Boreal Peatland Erico...	Zn	Archived	501 bp
L1_I36	HQ157846.1	*Oidiodendron maius*	Nuclear ITS1-5.8S-ITS2	UAMH:11196	ARSL 230507.14	Archived	453 bp
L2_I02	MK247242.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Conserved AM Symbiont...	R5-1	Archived	579 bp
L2_I03	MN996947.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Conserved AM Symbiont...	SAF170	Archived	757 bp
L2_I04	MT936437.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Conserved AM Symbiont...	XZ11B	2017	722 bp
L2_I05	MW007887.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	China: Suosong Villag...	XZ04B	2017	746 bp
L2_I06	MZ424786.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Bangladesh: Gazipur	Apex-MYK-01	2011	459 bp
L2_I08	ON033164.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Conserved AM Symbiont...	MENA1630	Archived	610 bp
L2_I09	PV539327.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Brazil: Rio Grande do...	Mimosa caesalpiniifolia	2022	401 bp
L2_I10	PX121671.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	India: Halol,Gujrat	BACLRI05	2024	616 bp
L2_I11	LR731851.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Spain:Canary Islands,...	575_A05_2999	2010	415 bp
L2_I12	MK247260.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Conserved AM Symbiont...	R5-1_a	Archived	579 bp
L2_I13	MN996948.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Conserved AM Symbiont...	SAF96	Archived	751 bp
L2_I14	MT832194.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Conserved AM Symbiont...	PL112	Archived	688 bp
L2_I15	MW007889.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	China: Suosong Villag...	XZ04B	2017	745 bp
L2_I16	MZ537039.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Conserved AM Symbiont...	a1f0	Archived	413 bp
L2_I18	PV539318.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Brazil: Rio Grande do...	Hymenaea courbaril	2022	400 bp
L2_I19	LR731569.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Spain:Canary Islands,...	291_A03_29	2010	413 bp

L2_I20	MK247228.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Conserved AM Symbiont...	22B-6	Archived	578 bp
L2_I21	MN996945.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Conserved AM Symbiont...	SAF130	Archived	748 bp
L2_I22	MT832195.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Conserved AM Symbiont...	DN201	Archived	688 bp
L2_I23	MW007888.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	China: Suosong Villag...	XZ04B	2017	738 bp
L2_I24	MZ537114.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Conserved AM Symbiont...	6f47	Archived	413 bp
L2_I26	PV539321.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Brazil: Rio Grande do...	Hymenaea courbaril	2022	400 bp
L2_I27	LR731779.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Spain:Canary Islands,...	492_A05_6256	2010	413 bp
L2_I28	MK247246.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Conserved AM Symbiont...	22B-6_a	Archived	578 bp
L2_I29	MN996946.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Conserved AM Symbiont...	SAF131	Archived	696 bp
L2_I30	MW288829.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Conserved AM Symbiont...	Glomus irregulare	Archived	422 bp
L2_I31	MZ537178.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Conserved AM Symbiont...	b2c5	Archived	413 bp
L2_I33	PV539322.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Brazil: Rio Grande do...	Hymenaea courbaril	2022	400 bp
L2_I34	LR731780.1	*Rhizophagus irregularis*	28S rDNA LSU (4Ne E-INS-i)	Spain:Canary Islands,...	493_A05_2827	2010	413 bp
L3_I02	AJ438984.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Germany:Thalhausen, B...	SR788	Archived	764 bp
L3_I03	AM084700.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Boletales Temperate F...	mycelium	Archived	718 bp
L3_I04	AY230243.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	United Kingdom: Devon...	DGC-4(2)	Archived	725 bp
L3_I05	DQ179126.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Paxillus involutus (B...	G05	Archived	726 bp
L3_I07	EU819416.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Boletales Temperate F...	JMP0052	Archived	801 bp
L3_I08	FJ746640.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	ATCC:62260	ATCC 62260	Archived	726 bp
L3_I09	GQ389624.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Germany	FRA	2002	757 bp
L3_I10	GU373506.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	H:6002433	GenBank / RefSeq deposit	Archived	575 bp
L3_I11	HQ999961.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	ATCC:MYA-4647	ATCC MYA-4647	Archived	568 bp
L3_I12	JF899567.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	DAVFP:28749	GenBank / RefSeq deposit	Archived	899 bp
L3_I13	JN673721.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	USA: TN, Great Smoky ...	F GMM7062	Archived	701 bp
L3_I14	JQ283964.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	China: Yanqing county...	JZBWD2100002	Archived	690 bp
L3_I15	JX679361.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Boletales Temperate F...	ecmPI1	Archived	646 bp
L3_I16	KF482483.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Boletales Temperate F...	PAX	Archived	810 bp
L3_I17	KM409443.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Boletales Temperate F...	P33_M6_772	Archived	678 bp
L3_I18	KP004923.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Boletales Temperate F...	ASIS23341	Archived	641 bp
L3_I19	KT692922.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Boletales Temperate F...	VP-3	Archived	747 bp
L3_I20	KY681467.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Spain	Quercus robur	Archived	873 bp
L3_I21	LC860641.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Japan:Nagano, Miyada,...	HYNK342	2024	635 bp
L3_I22	MG571758.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	China	DP20140901	2014	746 bp
L3_I23	MH979295.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	USA: Wisconsin, La Po...	07-Sep-2017	2017	694 bp
L3_I24	MK966655.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Boletales Temperate F...	HMAS 279972	Archived	716 bp
L3_I25	MN959789.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Boletales Temperate F...	MTH15	Archived	785 bp
L3_I26	MT345211.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Boletales Temperate F...	CNV34	Archived	857 bp
L3_I27	MW881536.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Boletales Temperate F...	NO.20180724	Archived	862 bp
L3_I28	MZ054361.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Boletales Temperate F...	SAT-18-251-01	2018	899 bp

L3_I29	OL659295.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Boletales Temperate F...	PW	Archived	740 bp
L3_I30	OM203518.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Boletales Temperate F...	iNAT 37429763	2015	752 bp
L3_I31	ON794296.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	China: Yunnan	HKAS122442	2021	704 bp
L3_I32	OP749061.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	USA: Pennsylvania, Cl...	S.D. Russell ONT iNatur...	2022	758 bp
L3_I33	OQ628491.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Boletales Temperate F...	SAT-10-236-07	2010	893 bp
L3_I34	OR625685.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Boletales Temperate F...	F046	2018	736 bp
L3_I35	PP261177.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	Boletales Temperate F...	YAASM5310	Archived	730 bp
L3_I36	PV839182.1	*Paxillus involutus*	Nuclear ITS1-5.8S-ITS2	UBC:F038696	On tree stump	2023	716 bp
L4_I01	AF006597.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	collected in Limousin...	vegetative dikaryotic m...	Archived	631 bp
L4_I02	AY254878.2	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	Model Ectomycorrhizal...	fruiting body	Archived	625 bp
L4_I03	DQ179121.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	Model Ectomycorrhizal...	CRBF581	Archived	670 bp
L4_I04	EU597085.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	Model Ectomycorrhizal...	UBCOGTR0455s	Archived	794 bp
L4_I05	GQ166896.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	F:PRL6203	GenBank / RefSeq deposit	Archived	656 bp
L4_I06	JN942806.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	TNS:A0575	A0575	Archived	691 bp
L4_I07	JQ753771.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	Model Ectomycorrhizal...	GenBank / RefSeq deposit	Archived	697 bp
L4_I08	JX504115.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	USA: Alaska	AWW595	Archived	709 bp
L4_I10	KF639964.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	Model Ectomycorrhizal...	ARSL 261109.1	Archived	690 bp
L4_I11	KM067837.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	Russia: Komorav Fores...	Abies	Archived	732 bp
L4_I12	KR673539.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	Model Ectomycorrhizal...	KA12-1306	2012	646 bp
L4_I13	KU878616.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	USA: New York, Tully,...	YB03_2	2015	771 bp
L4_I14	KX449438.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	Spain: Riofrio	Ica-11	Archived	702 bp
L4_I15	KY655010.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	Spain	GenBank / RefSeq deposit	Archived	759 bp
L4_I16	LC860607.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	Model Ectomycorrhizal...	HYNK193	2024	645 bp
L4_I17	MF958449.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	United Kingdom: Aberd...	LbA	2010	769 bp
L4_I18	MG519523.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	Model Ectomycorrhizal...	ASIS9757	Archived	606 bp
L4_I19	MH862188.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	CBS:594.89	CBS 594.89	Archived	649 bp
L4_I20	MK492604.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	Spain	Eucalyptus nitens	Archived	810 bp
L4_I21	MN992606.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	Canada: Quebec, Chibo...	MQ17062-QFB29570	2017	712 bp
L4_I22	MT345252.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	Model Ectomycorrhizal...	CNV76	Archived	780 bp
L4_I23	OK165579.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	India: Tamilnadu	Contig_M6	2019	587 bp
L4_I24	OL142203.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	MUOB:304563	USA: Georgia, Athens	2017	692 bp
L4_I25	OM337985.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	Canada: British Colum...	SB0497	Archived	673 bp
L4_I26	ON129291.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	USA: New York	iNat58417461	2020	725 bp
L4_I27	OP225576.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	iNAT:97254900	NAMPA2214-22	2021	650 bp
L4_I28	OQ225672.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	DAVFP:29770	Canada: British Columbi...	Archived	686 bp
L4_I29	OR144087.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	Model Ectomycorrhizal...	L2	2022	847 bp
L4_I30	PP826401.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	USA	CA FUNDIS iNaturalist #...	2023	688 bp
L4_I31	PV108122.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	CIRM-CF:1008	CIRM-BRFM 1008	2008	886 bp
L4_I32	PX096150.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	China: Tibet, Sejila ...	BYY312	2017	675 bp
L4_I33	PZ536043.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	USA: Washington, Olym...	iNaturalist # 319704043	2025	729 bp
L4_I34	QB077372.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	USA: California	T33	2023	838 bp
L4_I35	AF006598.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	collected in Limousin...	Cham3	Archived	630 bp
L4_I36	DQ179123.1	*Laccaria bicolor*	Nuclear ITS1-5.8S-ITS2	Model Ectomycorrhizal...	S238	Archived	656 bp
L5_I01	PX594950.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I02	PX594951.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp

L5_I03	PX594952.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I04	PX594953.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I05	PX594954.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I06	PX594955.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I07	PX594956.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I08	PX594957.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I09	PX594958.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I10	PX594959.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I11	PX594960.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I12	PX594961.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I13	PX594962.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I14	PX594963.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I15	PX594964.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I16	PX594965.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I17	PX594966.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I18	PX594967.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I19	PX594968.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I20	PX594969.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I21	PX594970.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I22	PX594971.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I23	PX594972.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I24	PX594973.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I25	PX594974.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I26	PX594975.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I27	PX594976.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I28	PX594977.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I29	PX594978.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I30	PX594979.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I31	PX594980.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I32	PX594981.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp

L5_I33	PX594982.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I34	PX594983.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I35	PX594984.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L5_I36	PX594985.1	*Rhizophagus irregularis*	18S rDNA SSU (4Ne Slow-Clock)	Italy: Pisa	Glomus irregulare	2014	785 bp
L6_I02	AF538356.1	*Cryptococcus neoformans*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	IFO 410	Archived	1685 bp
L6_I03	DQ479318.1	*Cryptococcus neoformans*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	WM178	Archived	1737 bp
L6_I07	KY748222.1	*Cryptococcus neoformans*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	CFP57	Archived	1760 bp
L6_I08	LR657325.1	*Cryptococcus neoformans*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	CBS8710	Archived	1043 bp
L6_I10	OQ946658.1	*Cryptococcus neoformans*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	HGT17	Archived	1146 bp
L6_I11	XM_012194532.1	*Cryptococcus neoformans H99*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	H99	Archived	1790 bp
L6_I12	AF538353.1	*Cryptococcus neoformans*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	IFO 410	Archived	1251 bp
L6_I16	KY748223.1	*Cryptococcus neoformans*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	FC7	Archived	1493 bp
L6_I17	LR657318.1	*Cryptococcus neoformans*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	RV64610	Archived	998 bp
L6_I19	OQ946654.1	*Cryptococcus neoformans*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	CFP58	Archived	1143 bp
L6_I20	XM_012195567.1	*Cryptococcus neoformans H99*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	H99	Archived	1789 bp
L6_I21	AF518484.1	*Cryptococcus neoformans*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	J8	Archived	812 bp
L6_I24	KY748216.1	*Cryptococcus neoformans*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	FC5	Archived	1272 bp
L6_I25	LR657319.1	*Cryptococcus neoformans*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	CBS10084	Archived	984 bp
L6_I27	OQ946656.1	*Cryptococcus neoformans*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	BT26	Archived	1142 bp
L6_I28	XM_012197453.1	*Cryptococcus neoformans H99*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	H99	Archived	1713 bp
L6_I29	AF518478.1	*Cryptococcus neoformans*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	J1	Archived	811 bp
L6_I31	KY748217.1	*Cryptococcus neoformans*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	HGT2	Archived	1272 bp
L6_I34	OQ946674.1	*Cryptococcus neoformans*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	FC4	Archived	1104 bp
L6_I35	XM_012193385.1	*Cryptococcus neoformans H99*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	H99	Archived	1711 bp
L6_I36	AF518479.1	*Cryptococcus neoformans*	Mitochondrial COX1 / CYTB (1Ne)	Non-ECM Basidiomycota...	J2	Archived	811 bp