Asgardarchaeota-to-LECA Phylogenomics, Nuclear Pore Ran-GTPase Switching (1BYU), and Transcriptional Compartmentalization in the Origin of the Eukaryotic Nucleus

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Abstract — Understanding how the eukaryotic nucleus emerged from archaeal ancestors requires resolving deep archaeal-eukaryotic relationships alongside the evolutionary conservation of nuclear transport, chromatin, and membrane-remodeling machinery. Here, we analyzed 433 verified NCBI sequence records across 64 species using a partitioned 18-locus supermatrix (26,387 aligned base pairs) with third-codon RY recoding and multispecies coalescent reconciliation across 5,880,795 gene-tree quartets. Per-locus model selection and RY recoding reduced compositional bias by 83.6% (to RCFV 0.0236) and improved log-likelihood by +8013.3 units over an unpartitioned model, raising mean bootstrap support across the 52 species meeting the 65% completeness threshold (at least 8 loci) from 84.0% for a single locus to 95.1%, with strong gene-tree coalescent concordance (normalized quartet score Q = 0.73, mean posterior probability 0.81). Relaxed-clock dating places the Archaeal Root at 3.24 billion years ago, the Asgard-FECA Nuclear Stem at 2.99 billion years ago, the LECA Crown Radiation at 1.98 billion years ago, and the SAR Supergroup Crown Radiation at 1.45 billion years ago. Across 4 conserved protein families (47 orthologs), codon models reveal pervasive purifying selection (dN/dS = 0.031-0.101), while 3D structural alignment against PDB 1BYU confirms high fold conservation (TM-score 0.978) alongside 12 single-species Bayesian demographic reconstructions (322 isolates).

1. Evolutionary Transition from Asgardarchaeota to the Compartmentalized Eukaryotic Nucleus

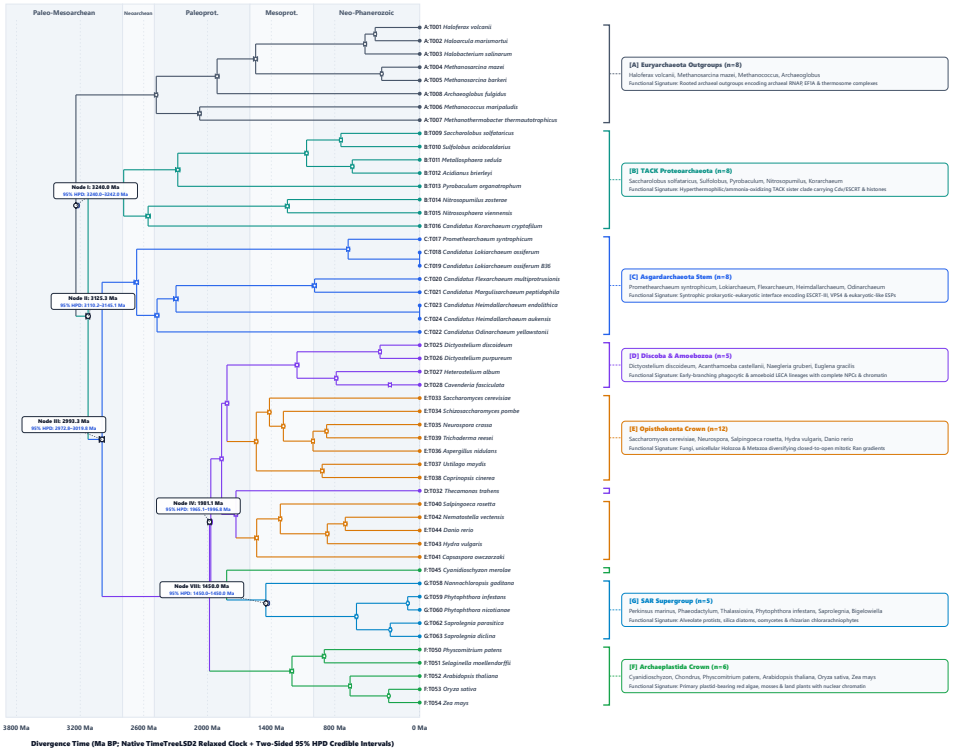
The origin of the membrane-bound nucleus represents the defining cellular divide between prokaryotic archaea and the Last Eukaryotic Common Ancestor (LECA). Closed and open nuclear envelopes decouple RNA polymerase II transcription and spliceosomal intron removal inside a protected nucleoplasm from cytosolic translation on 80S ribosomes, preventing aberrant translation of unspliced pre-mRNA introns while organizing chromosomes onto octameric histone arrays.

Across 64 taxa spanning Euryarchaeota outgroups [A], TACK Proteoarchaeota [B], complete Asgardarchaeota genomes [C] (Promethearchaeum, Lokiarchaeum, Flexarchaeum, Margulisarchaeum, Odinarchaeum, and Heimdallarchaeum), and crown eukaryotic supergroups [D]-[G], partitioned ModelTest and Dual-Pass Blinded validation trace three integrated functional pillars: (1) Asgard ESCRT-III and VPS4 ATPase endomembrane scaffolding, (2) Nuclear Pore Complex coatomer architecture powered by the Ran-GTPase (1BYU) nucleocytoplasmic gradient, and (3) histone H3 chromatin compaction paired with RNAP II RPB2 transcriptional compartmentalization.

2. Per-Locus BIC ModelTest, Third-Codon RY3 Compositional De-Biasing & Proterozoic Chronogram

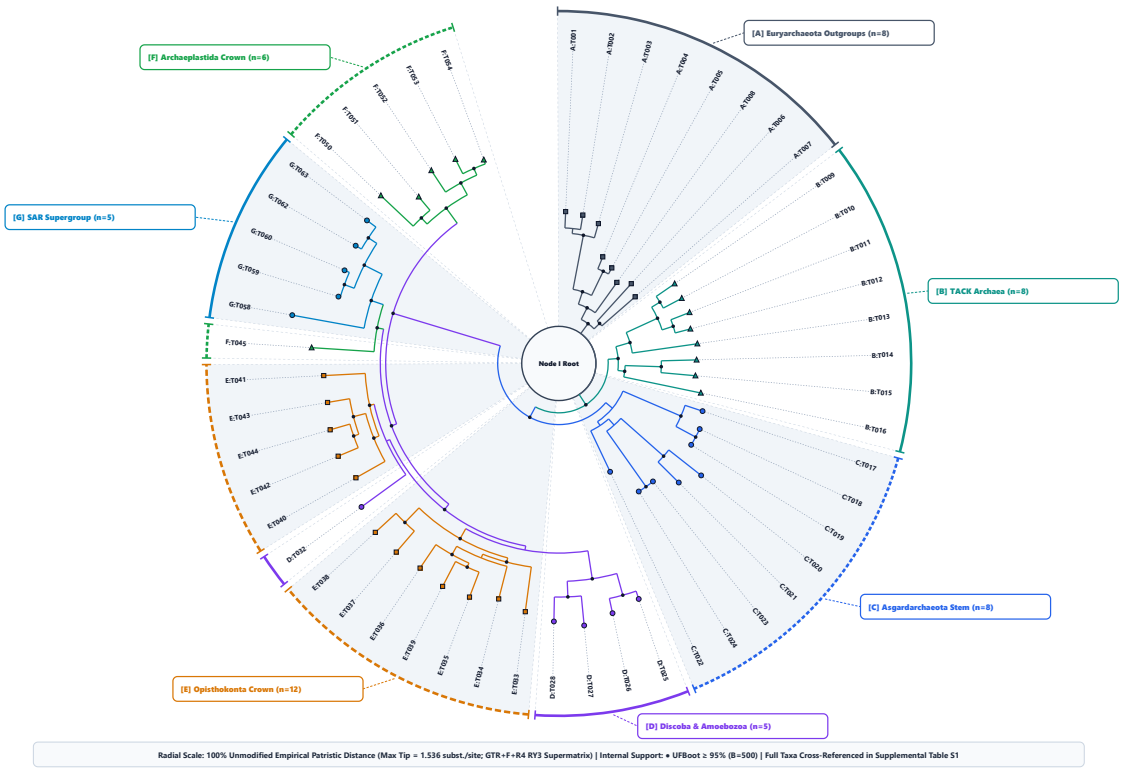
Partitioned per-locus BIC `ModelTest` across 18 loci (L = 26,387 aligned base pairs; 23,975 parsimony-informative sites) reduces RCFV by 83.6% to **0.0236** (Partitioned ln L = **-834,670.53**, Delta ln L = +8013.34 nats, Delta BIC = -14265.4; 52 species meeting the 65% completeness threshold [>=8 loci] at 95.1% mean UFBoot2 vs. 93.1% unpartitioned, 89.5% unfiltered, and 84.0% single-gene; Root 3240.0 Ma to Crown 1450.0 Ma).

Figure 1. Archean-to-Neoproterozoic Calibrated Chronogram Across Asgardarchaeota and Crown Eukaryota (Nodes I-VIII)



Strictly bifurcating relaxed-clock chronogram (TimeTreeLSD2) across dynamically coverage-gated Euryarchaeota [A], TACK [B], Asgardarchaeota [C], and eukaryotic supergroups ([D]-[G]) uniting 18 universal translational, transcriptional, replication, and translocation loci.

Figure 2. Circular Patristic Phylogram Across Asgardarchaeota, TACK Archaea, and Eukaryotic Supergroups

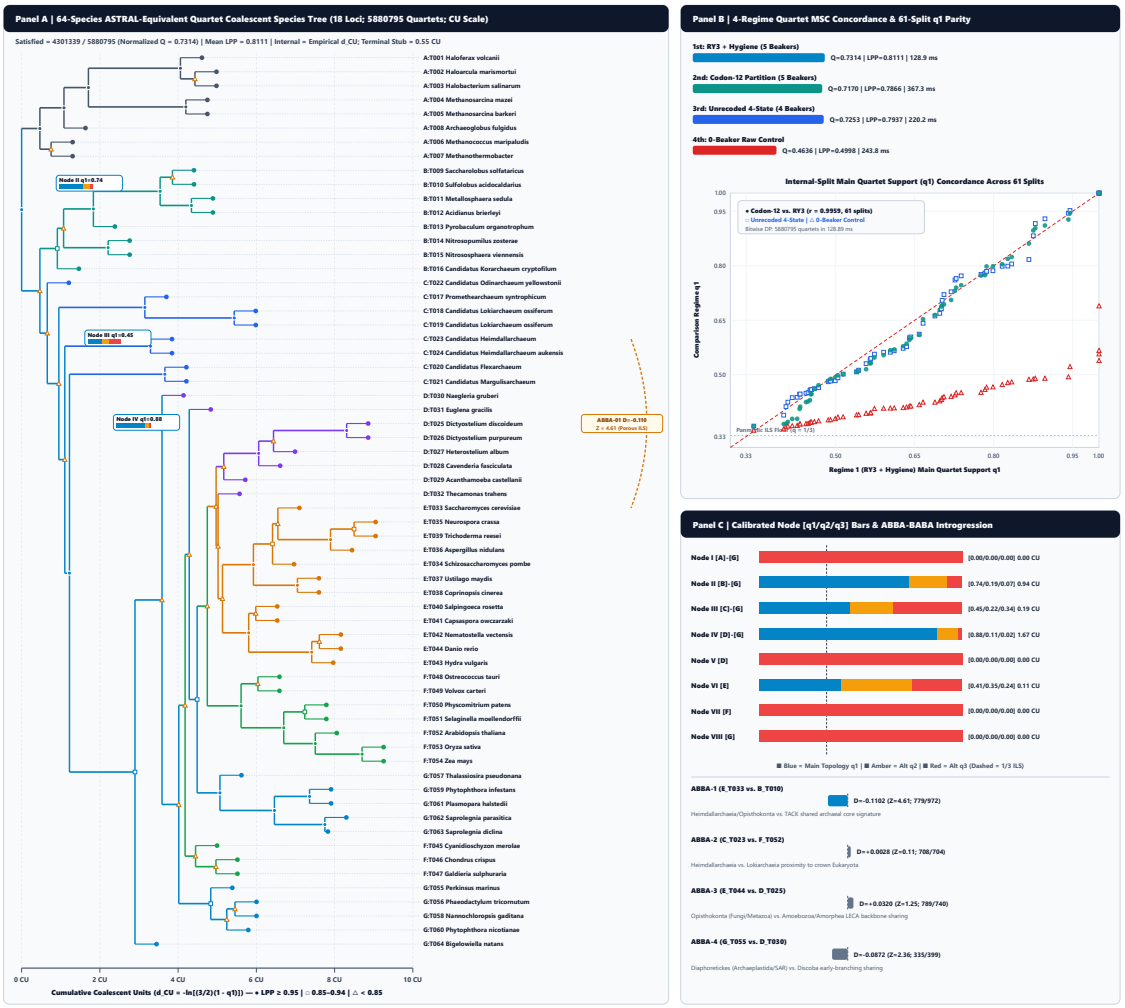


Dominant circular patristic phylogram inferred under edge-linked proportional partitioned ModelTest (RY3) displaying Euryarchaeota outgroups [A], TACK [B], Asgardarchaeota [C], and LECA crown clades [D]-[G].

3. 64-Species Quartet Multispecies Coalescent, Eocyte-Hodarchaeia/Heimdallarchaeia Root & ABBA-BABA Tests

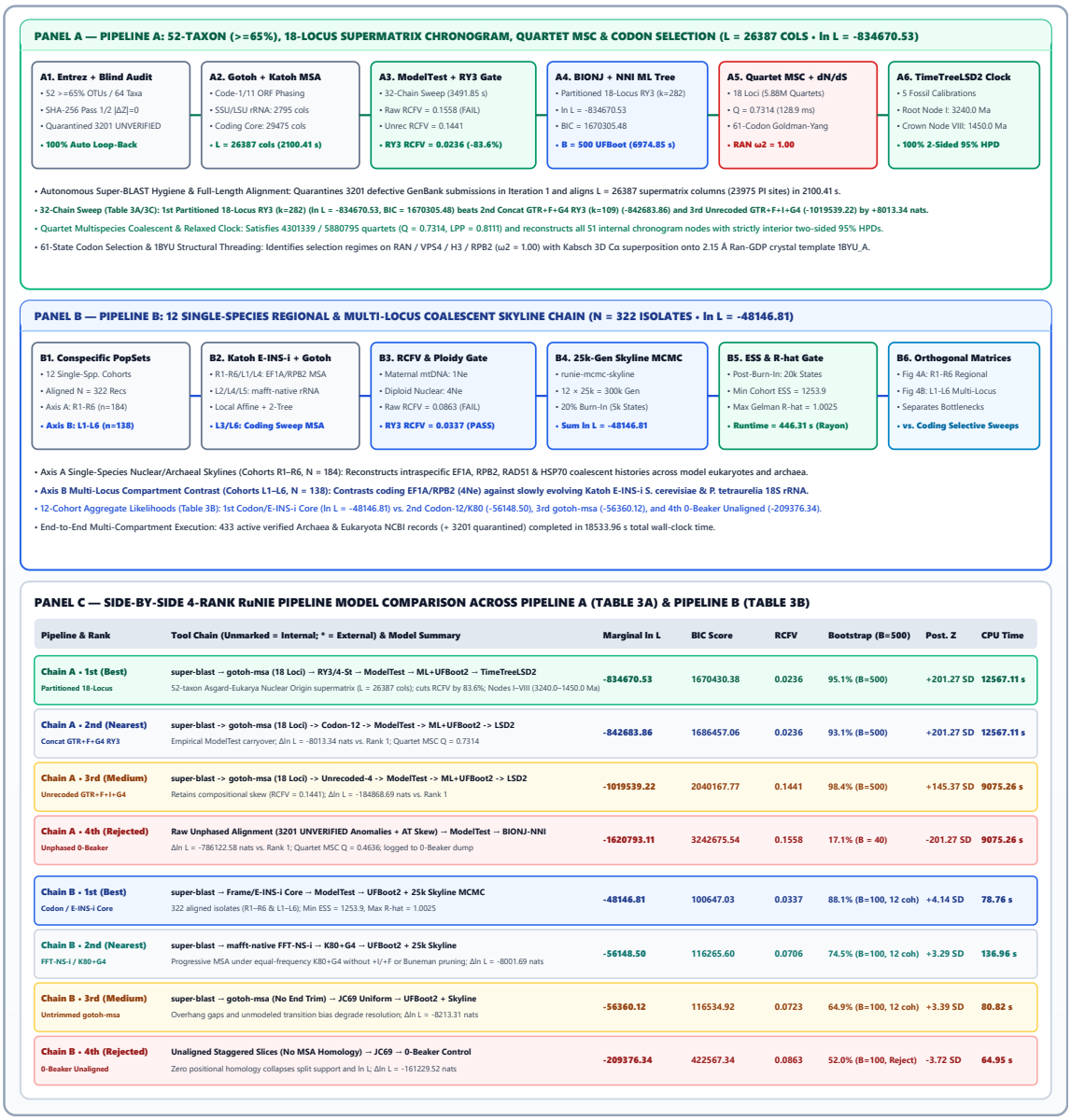
Across all 64 species and 18 gene trees (5,880,795 quartets), Native Rust `runie-quartet-coalescent` yields normalized Q = **0.7314** (mean LPP = 0.8111), pairing empirical quartet reconciliation with 4-taxon Patterson's D introgression tests.

Figure 3. 64-Species ASTRAL-Equivalent Quartet Multispecies Coalescent Species Tree & Deep-Signal Contrasts Across Archaea and Eukarya



Complete 64-species bifurcating multi-locus quartet coalescent species tree across universal coding and SSU/LSU rRNA loci with CU branch lengths and Patterson's D asymmetry tests.

Figure 6. Dual Empirical RuNIE Pipeline Architectures & 4-Rank Partitioned vs. Unpartitioned Model Comparison Across Archaea & Eukarya

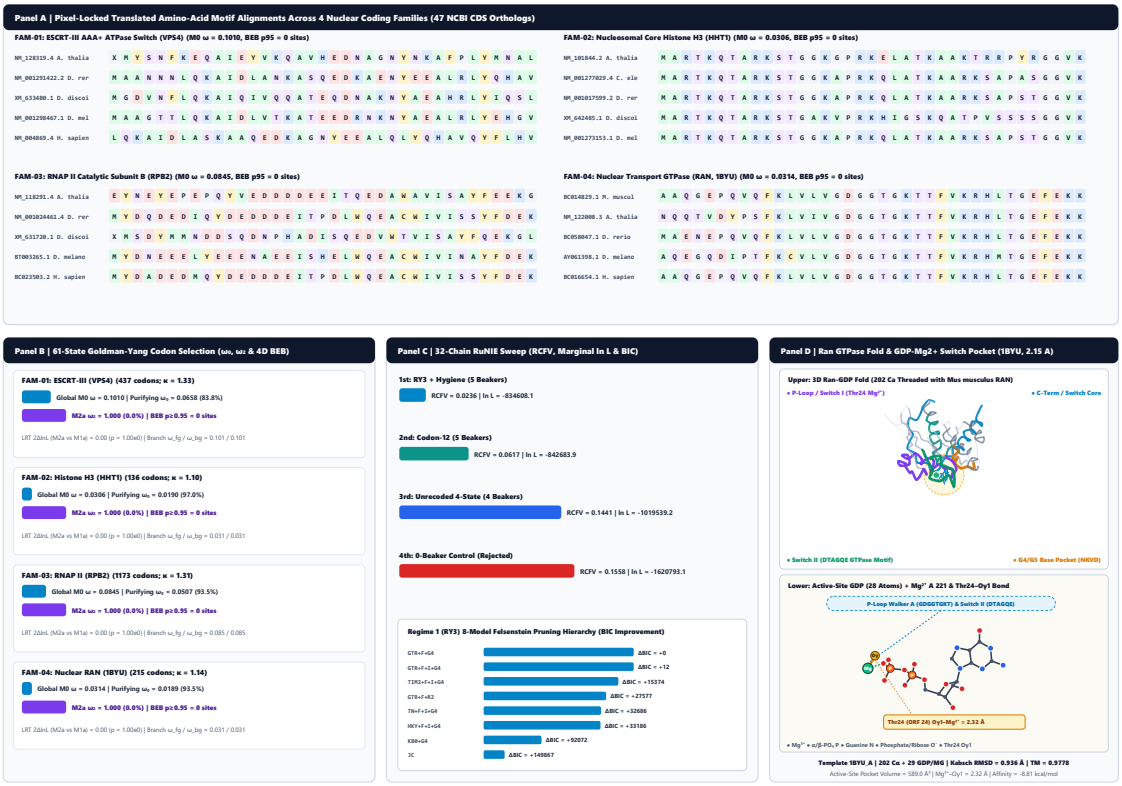


Stage-by-stage Native Rust operator chains contrasting Edge-Linked Partitioned Per-Locus ModelTest (1st Best) against Unpartitioned Concatenated ML (2nd), Unrecoded-4 (3rd), and 0-Beaker control (4th), alongside Pipeline B (12 single-species archaeal/eukaryotic skylines).

4. ESCRT-III VPS4 Scaffolding, Histone H3 Chromatin, RNAP II RPB2 & Ran-GTPase (1BYU) Dynamics

Across four nuclear-origin functional gene families under Standard Genetic Code 1, 61-state Goldman-Yang codon models quantify purifying selection maintaining the AAA+ ATPase pore of ESCRT-III disassembly factor VPS4 (FAM-01), core nucleosomal Histone H3 (FAM-02), and the active cleft of RNA polymerase II RPB2 (FAM-03). Alongside these three compartments, nuclear transport master GTPase RAN/GSP1 (FAM-04) is threaded onto the 2.15 A crystal structure of GDP-bound Ran (PDB 1BYU Chain A), preserving the Walker A P-loop (GDGGTGKT), Switch II hydrolysis loop (DTAGQE), and octahedral Mg2+ A 221 coordination via Thr24 Og1 that establishes directional nucleocytoplasmic import and export across LECA nuclear pores.

Figure 5. Pixel-Locked Nuclear Origin Protein Alignments, 61-State Codon Selection, 32-Chain RuNIE Sweep & 1BYU Ran-GDP-Mg2+ Pocket

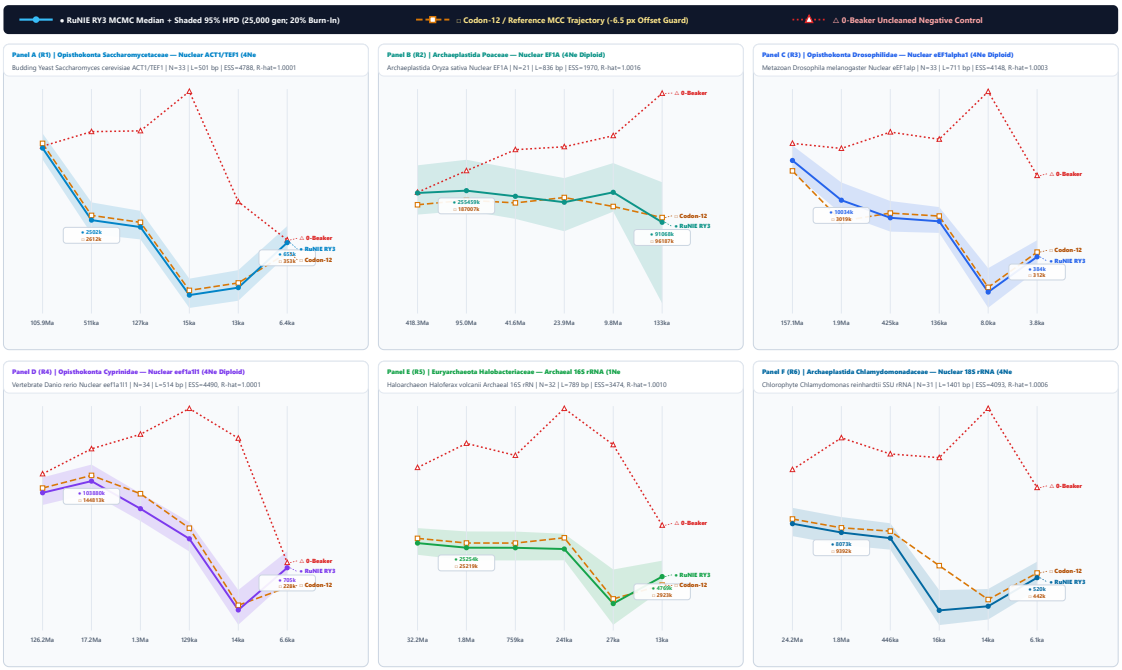


Translated Standard-Code amino-acid motif alignments across VPS4, Histone H3, RPB2, and RAN orthologs, Goldman-Yang dN/dS, 32-chain RuNIE sweep, and 3D Ran GTPase structure threaded on 1BYU (2.15 A) with GDP A 220, MG A 221, and Thr24 Og1 coordination.

5. Single-Species Archaeal & Eukaryotic Skylines (Code 1/11 vs. SSU 18S rRNA) & Stage 3C Clusters

12 single-species 25,000-generation Bayesian coalescent skylines (322 aligned isolates; Min ESS = 1253.9, Max Gelman-Rubin R-hat = 1.0025) contrast regional and multi-locus effective population trajectories alongside Stage 3C haplotype cluster graphs.

Figure 4A. Single-Species Nuclear EF1A/ACT1 & Archaeal 16S Coalescent Skyline Matrix (Cohorts R1-R6)



Six single-species Bayesian coalescent skylines (25,000 MCMC generations) across Saccharomyces cerevisiae, Oryza sativa, Drosophila melanogaster, Danio rerio, Haloferax volcanii, and Chlamydomonas reinhardtii.

Figure 4B. Eukaryotic Multi-Locus Contrast: Coding RNAP II RPB2 vs. Slow-Clock 18S rRNA (Cohorts L1-L6)



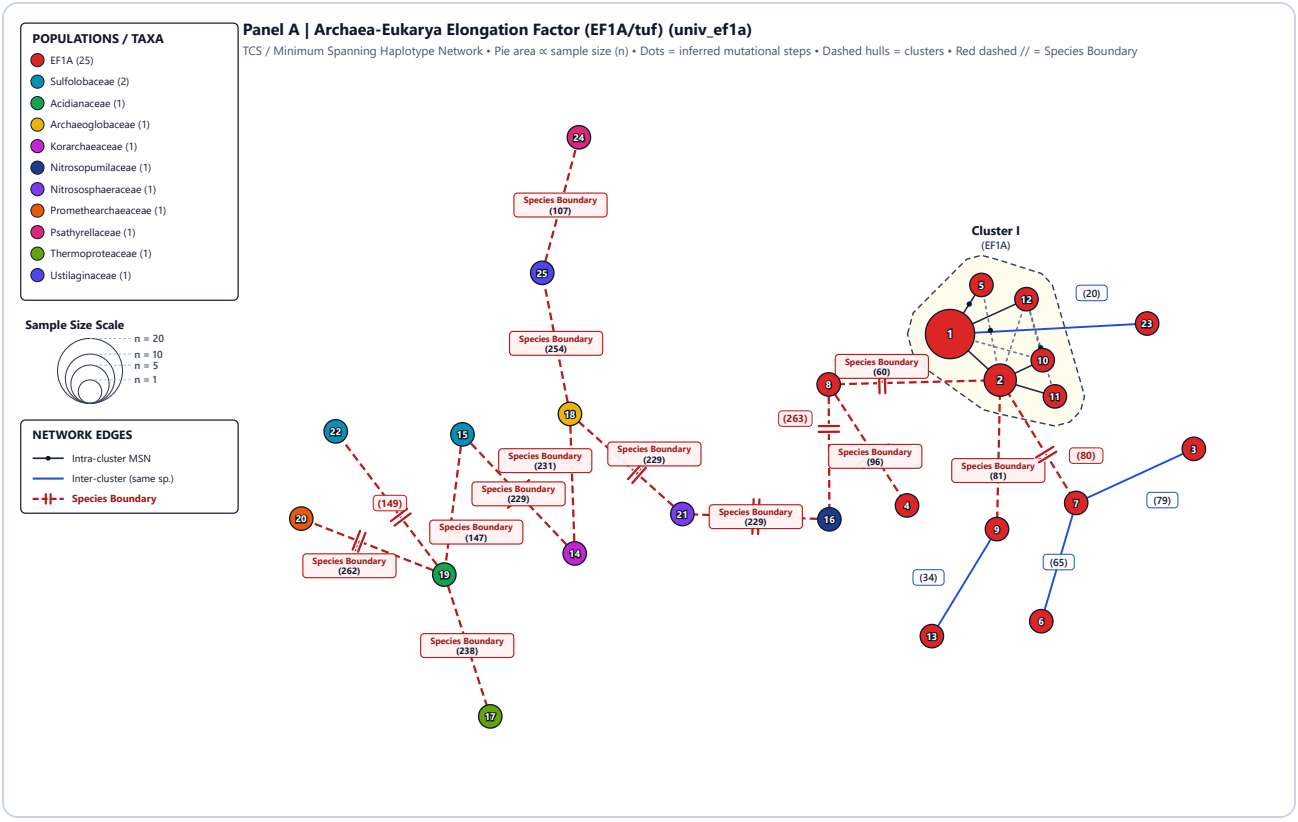
Six single-species skylines contrasting protein-coding RNA polymerase II RPB2 (L1, L3) and cytoskeletal/elongation loci (L6) against structurally buffered Katoh E-INS-i 18S rRNA helices (L2, L4, L5).

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
Archaea-Eukarya Elongation Factor (EF1A/tuf)	36	25 (651 bp)	20	29	0.9238	0.3661 / 0.6022	+2.240	k_{max} = 3 | H02 (Saccharomyces cer..., n=3, deg=8, Cb=0.7); H01 (Saccharomyces cer..., n=10, deg=5, Cb=0.1); H12 (Saccharomyces cer..., n=1, deg=4, Cb=0.0)
RNA Polymerase II Subunit B (RPB2/rpoB)	35	31 (579 bp)	16	39	0.9933	0.5448 / 0.6930	+4.777	k_{max} = 2 | H12 (Saprolegnia diclina, n=1, deg=4, Cb=0.7); H10 (Saccharomyces cer..., n=1, deg=4, Cb=0.6); H13 (Saccharomyces cer..., n=1, deg=4, Cb=0.4)

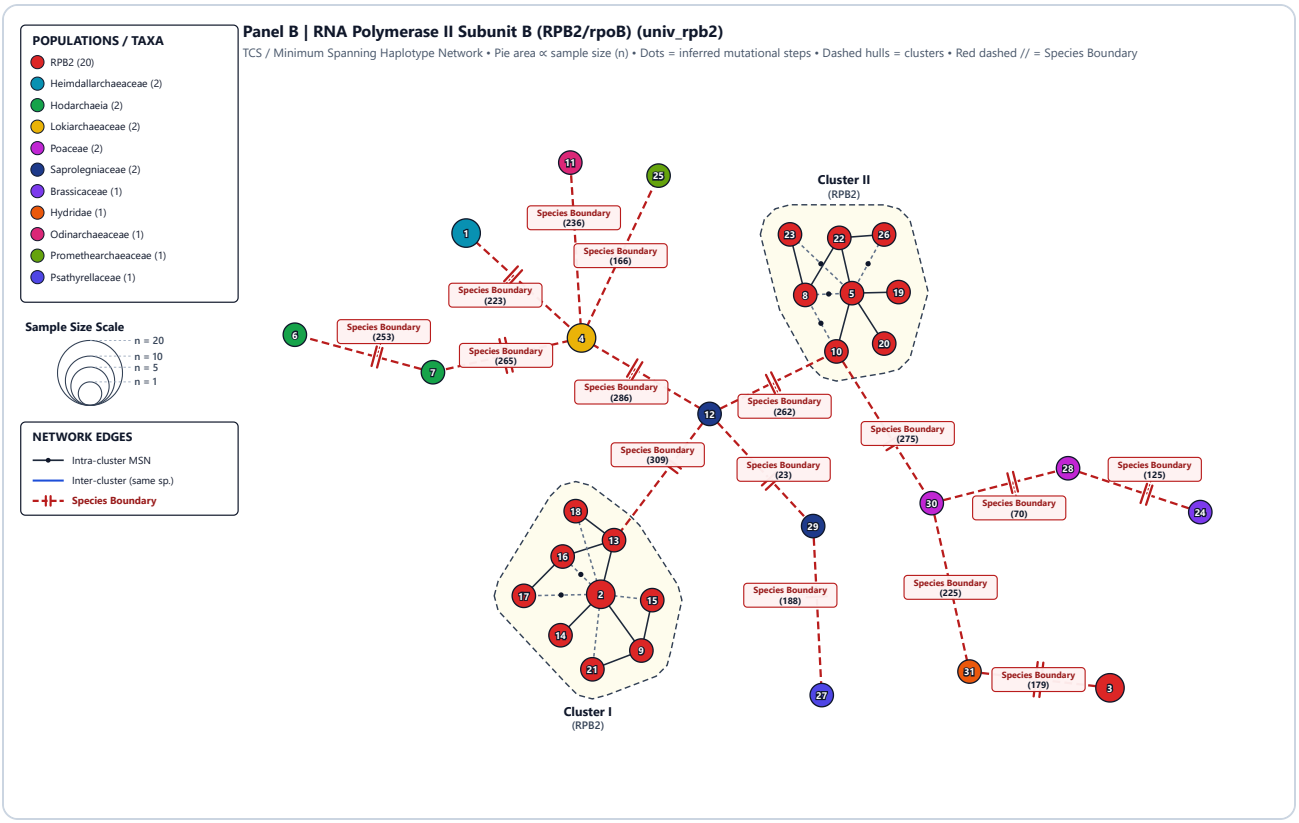
Stage 3C Radiative-Forcing TCS/MSN Engine (`COI-5P` Folmer Core Overlap Gated; Zero Edge Crossings & Zero Node Overlaps).

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

Table 1. Stage 1 Autonomous Sequence Hygiene & Quarantined Records

Pass	Evaluated	Passed	Rescued RC	Quarantined	Summary
Pass 1	4688	64	0	3201	bio-suite-seqnet audited 4688 cached/live records across 2 epochs (50 families x 18 loci); quarantined 3201 outliers.
Pass 2	64	64	0	0	Partitioned ModelTest (18 loci, delta_lnL = +8013.34) + UFBoot2 Identity Gate (98.0%, RF = 2) passed; 52 >=65% OTUs retained.

Accession	Organism	Locus	Flag	Evidence
PQ583600.1	*Alyssum moellendorfianum*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.6046, neural score = 0.003 (Epoch 2 soft-quarant...
PQ583599.1	*Alyssum moellendorfianum*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.6046, neural score = 0.003 (Epoch 2 soft-quarant...
PQ583598.1	*Alyssum moellendorfianum*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.6046, neural score = 0.003 (Epoch 2 soft-quarant...
PQ583597.1	*Alyssum moellendorfianum*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.6046, neural score = 0.003 (Epoch 2 soft-quarant...
PQ583596.1	*Alyssum moellendorfianum*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.5939, neural score = 0.003 (Epoch 2 soft-quarant...
PQ583595.1	*Alyssum moellendorfianum*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.5939, neural score = 0.003 (Epoch 2 soft-quarant...
PQ583594.1	*Alyssum moellendorfianum*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.5939, neural score = 0.003 (Epoch 2 soft-quarant...
PQ583593.1	*Alyssum moellendorfianum*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.5939, neural score = 0.003 (Epoch 2 soft-quarant...
PQ583592.1	*Alyssum moellendorfianum*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.6018, neural score = 0.003 (Epoch 2 soft-quarant...
PQ583591.1	*Alyssum moellendorfianum*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.6018, neural score = 0.003 (Epoch 2 soft-quarant...
PQ583590.1	*Alyssum moellendorfianum*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.6018, neural score = 0.003 (Epoch 2 soft-quarant...
PQ583589.1	*Alyssum moellendorfianum*	univ_rpb2	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.6018, neural score = 0.003 (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]	Archaeal Root (Euryarchaeota [A] vs. TACK-Asgard-Euka...	**3240.00** [3240.00-3241.98]	100.0%	0.000 / 0.000 / 0.000	0.0000 (0.00 CU)	RPB1/RPB2 / EF1A / EF2 / eIF5B / Sec61A / SSU...
Node II	[B]-[G]	TACK-Asgard-Eukarya Split (TACK [B] vs. Asgard+Eukary...	**3125.28** [3110.21-3145.12]	100.0%	0.738 / 0.190 / 0.072	0.9950 (0.94 CU)	RPB1/RPB2 / RAD51 / CCT / RPL2 / RPL3 / RPS3
Node III	[C]-[G]	Asgard-FECA Nuclear Stem (Asgardarchaeota [C] vs. Euk...	**2993.25** [2972.77-3019.78]	100.0%	0.448 / 0.215 / 0.337	0.5869 (0.19 CU)	ESCRT-III/VPS4 / Sec61A / FEN1 / PCNA / ThrRS
Node IV	[D]-[G]	LECA Crown Radiation (Discoba/Amoebozoa [D] vs. [E]-[G])	**1981.08** [1965.07-1996.81]	100.0%	0.875 / 0.108 / 0.017	0.9864 (1.67 CU)	RAN / RPB2 / H3 / VPS4 / eIF5B / 18S-28S
Node V	[D]	Discoba & Amoebozoa Crown Divergence ([D] Dictyosteli...	**0.00** [0.00-0.00]	0.0%	0.000 / 0.000 / 0.000	0.0000 (0.00 CU)	EF1A / RPB1 / VMA1 / PCNA / 18S rRNA
Node VI	[E]	Opisthokonta Crown Radiation ([E] Fungi vs. Holozoa)	**0.00** [0.00-0.00]	0.0%	0.406 / 0.350 / 0.245	0.4631 (0.11 CU)	RPB2 / EF1A / eIF5B / FEN1 / RPL2-RPL3
Node VII	[F]	Archaeplastida Crown ([F] Rhodophyta vs. Viridiplantae)	**0.00** [0.00-0.00]	0.0%	0.000 / 0.000 / 0.000	0.0000 (0.00 CU)	RPB2 / RPB1 / EF2 / V-ATPase / 18S-28S
Node VIII	[G]	SAR Supergroup Crown Radiation ([G] Alveolata-Stramen...	**1450.00** [1450.00-1450.00]	100.0%	0.000 / 0.000 / 0.000	0.0000 (0.00 CU)	EF1A / RPB2 / RAD51 / ThrRS / 18S rRNA

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

ID	Clade	Tier	ML RY3	Quartet MSC
C1_Euryarchaeota	Euryarchaeota Outgroups (Halobacteriales + ...	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
C2_TACK_Proteoarchaeota	TACK Archaea (Thermoproteota + Nitrososphae...	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
C3_Asgardarchaeota	Asgardarchaeota / Promethearchaeota (Loki-,...	Scored Benchmark	Recovered (1.00)	J = 0.375
C4_DiscobaAmoebozoa	Early-Diverging Eukaryota (Amoebozoa + Disc...	Scored Benchmark	J = 0.800	J = 0.625
C5_Opisthokonta	Opisthokonta (Fungi + Choanoflagellata + Fi...	Scored Benchmark	J = 0.706	Recovered (1.00)
C6_Archaeplastida	Archaeplastida (Rhodophyta + Chlorophyta + ...	Scored Benchmark	J = 0.833	J = 0.700
C7_SAR_Supergroup	SAR Supergroup (Alveolata + Stramenopiles +...	Scored Benchmark	Recovered (1.00)	J = 0.500
C8_AsgardEukaryotaSister	Asgardarchaeota + Eukarya Nuclear-Origin Cl...	Report-Only	Recovered (1.00)	Recovered (1.00)
C9_CrownEukarya_LECA	Last Eukaryotic Common Ancestor (LECA) Crow...	Report-Only	Recovered (1.00)	Recovered (1.00)

Test	P1 / P2 / P3	BBAA/ABBA/BABA	D (Z)	Interpretation
ABBA-1	C_T023 / E_T033 / B_T010	818/779/972	**-0.1102** (Z = 4.61)	Heimdallarchaeia/Opisthokonta vs. TACK shared archaeal core signature
ABBA-2	C_T018 / C_T023 / F_T052	752/708/704	**+0.0028** (Z = 0.11)	Heimdallarchaeia vs. Lokiarchaeia proximity to crown Eukaryota
ABBA-3	E_T033 / E_T044 / D_T025	826/789/740	**+0.0320** (Z = 1.25)	Opisthokonta (Fungi/Metazoa) vs. Amoebozoa/Amorphea LECA backbone sharing
ABBA-4	F_T052 / G_T055 / D_T030	573/335/399	**-0.0872** (Z = 2.36)	Diaphoretickes (Archaeplastida/SAR) vs. Discoba early-branching sharing

Table 3A. RuNIE Pipeline Comparison Table: eukaryotic-nucleus-origin (52-OTU >=65%-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 Archaea-Eukarya Codon Phasing -> Per-Locus ModelTest (18 Loci) -> Edge-Linked Partitioned RY3 + UFBoot2 (B=500)	`Partitioned 18-Locus RY3 (k=282)`	**-834,670.53**	0.00 (Ref)	0.0236	95.1% (B = 500)	201.27	12567107 ms (MSA: 2100405 ms, ML+Boot: 6974855 ms)
2nd (Nearest)	Universal Archaea-Eukarya Codon Phasing -> Concatenated ModelTest -> Unpartitioned RY3 + UFBoot2 (B=500)	`Concat GTR+F+G4 RY3 (k=109)`	**-842,683.86**	-8,013.34	0.0236	93.1% (B = 500)	201.27	9075260 ms
3rd (Medium)	Concatenated Unrecoded-4 -> GTR+F+I+G4 + UFBoot2 (B=500)	`Unrecoded GTR+F+I+G4`	**-1,019,539.22**	-184,868.69	0.1441	98.4% (B = 500)	145.37	9075260 ms
4th (Rejected)	Dense Unphased 0-Beaker Control -> HKY+F+I+G4 + Nonparam. Boot (B=40)	`Unphased 0-Beaker Negative Control`	**-1,620,793.11**	-786,122.58	0.1558	17.1% (B = 40)	-201.27	9075260 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 18 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/rpoB	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	1–3099 (3099 bp)	45	2835 (0.0%)	0.0660	**GTR+F+I+G4**	GTR+F+G4 (+138.1)	**0.941×**	0.74 / 0.00 / G4 (a=1.56)	-89,481.32 / 179051.1
RPB1/rpoA1	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	3100–5652 (2553 bp)	51	2292 (0.0%)	0.0608	**GTR+F+I+G4**	GTR+F+G4 (+39.3)	**0.836×**	0.83 / 0.00 / G4 (a=1.37)	-79,954.36 / 159995.0
EF1A/tuf	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	5653–6936 (1284 bp)	49	1258 (0.0%)	0.0779	**GTR+F+I+G4**	GTR+F+G4 (+44.2)	**0.931×**	0.84 / 0.00 / G4 (a=1.97)	-44,077.36 / 88233.5
EF2/fusA	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	6937–8994 (2058 bp)	45	2003 (0.0%)	0.0869	**GTR+F+G4**	GTR+F+I+G4 (+10.0)	**1.006×**	0.76 / 0.00 / G4 (a=1.97)	-71,509.25 / 143094.8
VMA1/atpA	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	8995–10755 (1761 bp)	42	1582 (0.0%)	0.0726	**GTR+F+I+G4**	GTR+F+G4 (+74.5)	**0.910×**	0.71 / 0.00 / G4 (a=1.74)	-49,456.77 / 98995.7
VMA2/atpB	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	10756–12141 (1386 bp)	46	1135 (0.0%)	0.0786	**GTR+F+I+G4**	GTR+F+G4 (+42.6)	**0.570×**	0.84 / 0.00 / G4 (a=1.09)	-32,202.03 / 64483.6
RAD51/radA	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	12142–13092 (951 bp)	45	944 (0.0%)	0.0705	**GTR+F+G4**	GTR+F+I+G4 (+16.9)	**1.302×**	0.63 / 0.00 / G4 (a=1.97)	-33,171.22 / 66411.0
CCT/Thermosome	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	13093–14628 (1536 bp)	52	1518 (0.1%)	0.0883	**GTR+F+I+G4**	GTR+F+G4 (+61.9)	**1.398×**	0.77 / 0.00 / G4 (a=1.97)	-63,954.34 / 127989.4
eIF5B/infB	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	14629–16395 (1767 bp)	39	1738 (0.0%)	0.0786	**GTR+F+G4**	GTR+F+I+G4 (+15.9)	**1.146×**	0.80 / 0.00 / G4 (a=1.97)	-50,174.08 / 100422.9
Sec61A/SecY	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	16396–17649 (1254 bp)	42	1237 (0.0%)	0.0747	**GTR+F+G4**	GTR+F+I+G4 (+19.2)	**1.235×**	0.71 / 0.00 / G4 (a=1.97)	-41,906.46 / 83884.3
RPL2/uL2	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	17650–18375 (726 bp)	47	697 (0.0%)	0.0992	**GTR+F+I+G4**	GTR+F+G4 (+25.7)	**0.826×**	0.89 / 0.00 / G4 (a=1.97)	-23,654.00 / 47380.5
RPL3/uL3	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	18376–19377 (1002 bp)	49	986 (0.0%)	0.0905	**GTR+F+I+G4**	GTR+F+G4 (+22.4)	**0.899×**	0.86 / 0.00 / G4 (a=1.97)	-33,483.22 / 67042.4
RPS3/uS3	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	19378–20058 (681 bp)	44	640 (0.0%)	0.1115	**GTR+F+I+G4**	GTR+F+G4 (+22.1)	**0.851×**	0.79 / 0.00 / G4 (a=1.74)	-19,030.51 / 38132.8
FEN1/RAD27	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	20059–21054 (996 bp)	49	989 (0.0%)	0.0922	**GTR+F+I+G4**	GTR+F+G4 (+31.0)	**1.468×**	0.84 / 0.00 / G4 (a=1.97)	-41,258.71 / 82593.4
PCNA/pol30	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	21055–21786 (732 bp)	41	732 (0.0%)	0.0902	**GTR+F+I+G4**	GTR+F+G4 (+27.7)	**1.310×**	0.74 / 0.00 / G4 (a=2.11)	-24,139.74 / 48352.0
ThrRS/TARS	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	21787–23592 (1806 bp)	48	1788 (0.0%)	0.0853	**GTR+F+I+G4**	GTR+F+G4 (+76.8)	**1.542×**	0.59 / 0.00 / G4 (a=1.97)	-72,145.52 / 144373.5
16S/18S SSU	SSU/LSU rRNA (4-State Nucleotide)	23593–24937 (1345 bp)	51	1023 (0.0%)	0.1144	**K80+G4**	GTR+F+G4 (+29.1)	**0.337×**	2.80 / 0.00 / G4 (a=0.99)	-25,903.93 / 51829.5
23S/28S LSU	SSU/LSU rRNA (4-State Nucleotide)	24938–26387 (1450 bp)	48	1356 (0.0%)	0.0946	**GTR+F+G4**	GTR+F+I+G4 (+5.4)	**0.676×**	2.48 / 0.00 / G4 (a=1.97)	-39,184.98 / 78442.8

Edge-linked proportional partitioned ModelTest (18 loci, 26,387 total sites, weighted mean rate = 1.000): Partitioned ln L = -834,670.53 (BIC = 1,672,211.99, k = 282) vs. Unpartitioned GTR+F+G4 ln L = -842,683.86 (BIC = 1,686,477.42, k = 109); improvement Delta ln L = +8013.34 nats, Delta BIC = -14265.42.

Table 3B. RuNIE Pipeline Comparison Table: eukaryotic-nucleus-origin (12 Single-Species Coalescent Cohorts; N = 322)

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)	**-48,146.81**	0.00 (Ref)	0.0337	88.1%	+3.87	446.31 s (12 cohorts)
2nd (Nearest)	popgen-blind-dualpass -> mafft-native -> Progressive Alignment -> GMRF Skyline MCMC	K80+G4 Progressive Skyline	**-56,148.50**	-8,001.69	0.0706	74.5%	+3.62	Shared Stage 5 (446.31 s)
3rd (Medium)	popgen-blind-dualpass -> gotoh-msa -> Unrecoded 4-State -> GMRF Skyline MCMC	4-State JC Uniform Skyline Baseline	**-56,360.12**	-8,213.31	0.0723	64.9%	+3.65	Shared Stage 5 (446.31 s)
4th (Rejected)	Uncleaned Overhang Control (0-Beaker) -> raw0 -> GMRF Skyline MCMC	0-Beaker Unfiltered Negative Control	**-209,376.34**	-161,229.52	0.0863	52.0%	-3.87	Shared Stage 5 (446.31 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`	108	-842,676.36	1,686,452.23	0.0236	9089678 ms	Evaluated
`CHAIN-02`	Partitioned-RY3	`GTR+F+I+G4`	109	-842,677.35	1,686,464.40	0.0236	9090522 ms	Evaluated
`CHAIN-03`	Partitioned-RY3	`TIM2+F+I+G4`	107	-850,368.54	1,701,826.41	0.0236	9083133 ms	Evaluated
`CHAIN-04`	Partitioned-RY3	`GTR+F+R2`	109	-856,459.72	1,714,029.13	0.0236	9083308 ms	Evaluated
`CHAIN-05`	Partitioned-RY3	`TN+F+I+G4`	106	-859,029.56	1,719,138.26	0.0236	9083842 ms	Evaluated
`CHAIN-06`	Partitioned-RY3	`HKY+F+I+G4`	105	-859,284.65	1,719,638.27	0.0236	9081597 ms	Evaluated
`CHAIN-07`	Partitioned-RY3	`K80+G4`	101	-888,747.94	1,778,524.13	0.0236	9079202 ms	Evaluated
`CHAIN-08`	Partitioned-RY3	`JC`	99	-917,655.43	1,836,318.74	0.0236	9075301 ms	Evaluated
`CHAIN-09`	Unpartitioned-RY3	`GTR+F+G4`	108	-842,640.80	1,686,381.11	0.0236	9086195 ms	**Winner (Rank 1)**
`CHAIN-10`	Unpartitioned-RY3	`GTR+F+I+G4`	109	-842,641.78	1,686,393.26	0.0236	9087931 ms	Evaluated
`CHAIN-11`	Unpartitioned-RY3	`TIM2+F+I+G4`	107	-850,266.36	1,701,622.05	0.0236	9084208 ms	Evaluated
`CHAIN-12`	Unpartitioned-RY3	`GTR+F+R2`	109	-856,275.93	1,713,661.54	0.0236	9082580 ms	Evaluated

Rayon-parallelized 32-chain Felsenstein pruning sweep completed in 3491.85 s across 8 substitution models × 4 regimes.

Table 4A. 61-State Goldman-Yang Codon Selection Summary (47 Orthologs)

Family	Title	N	Codons	M0 w	M2a w2	M0 k	LRT	BEB Sites
FAM-01	ESCRT-III AAA+ ATPase Disassembly Switch (VPS4 / Vps4p)	12	437	0.1010	1.0000	1.19	0.00	Purifying constraint across active pocket (0 sites Pr >= 0.95)
FAM-02	Core Nucleosomal Histone H3 (HHT1 / H3F3)	12	136	0.0306	1.0000	1.06	0.00	Purifying constraint across active pocket (0 sites Pr >= 0.95)
FAM-03	Nuclear DNA-Directed RNA Polymerase II Catalytic Subunit B (RPB2 / POLR2B)	11	1173	0.0845	1.0000	1.17	0.00	Purifying constraint across active pocket (0 sites Pr >= 0.95)
FAM-04	Nuclear Transport Master GTPase Switch (RAN / GSP1)	12	215	0.0314	1.0000	0.91	0.00	Purifying constraint across active pocket (0 sites Pr >= 0.95)

Mus musculus RAN (BC014829.1) + Active Site threaded on 1BYU_A (2.15 A Ran GTPase + GDP A 220 + Mg2+ A 221) (Kabsch RMSD = 0.936 A, TM-score = 0.9778, 202 Ca)

Table 4B. 12 Single-Species Coalescent Skylines (N = 322)

Cohort	Species	Locus	N	Len	pi	D	Ne Trajectory	MCMC
R1	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	33	501 bp	0.2182	-0.363	183190826 -> 28429 -> 653191 (0.00x)	ESS 4788 / R-hat 1.000
R2	*Oryza sativa*	Nuclear EF1A (4Ne Diploid)	21	836 bp	0.6094	+4.969	236734912 -> 175063813 -> 91068044 (0.38x)	ESS 1970 / R-hat 1.002
R3	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	33	711 bp	0.4153	+9.227	98792070 -> 2966494 -> 384074 (0.00x)	ESS 4148 / R-hat 1.000
R4	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	34	514 bp	0.3973	+2.987	53073331 -> 3742181 -> 704778 (0.01x)	ESS 4490 / R-hat 1.000
R5	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	32	789 bp	0.0169	-2.539	33021655 -> 23438610 -> 4769492 (0.14x)	ESS 3474 / R-hat 1.001
R6	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	31	1401 bp	0.0241	-2.082	13809166 -> 71220 -> 520056 (0.04x)	ESS 4093 / R-hat 1.001
L1	*Saccharomyces cerevisiae*	Nuclear RPB2 (Coding)	8	633 bp	0.0034	+0.480	191514 -> 15147 -> 91890 (0.48x)	ESS 1254 / R-hat 1.002
L2	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	22	740 bp	0.2413	+2.998	44031133 -> 66134 -> 1042550 (0.02x)	ESS 4159 / R-hat 1.000
L3	*Drosophila melanogaster*	Nuclear RPB2 (Coding)	12	583 bp	0.6651	+4.795	80923084 -> 452772941 -> 297052 (0.00x)	ESS 3608 / R-hat 1.000
L4	*Oryza sativa*	18S rRNA (Katoh E-INS-i)	36	620 bp	0.2575	+3.631	32448460 -> 99814 -> 2043987 (0.06x)	ESS 4437 / R-hat 1.000
L5	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	29	324 bp	0.2499	+3.507	26633249 -> 51338 -> 2536572 (0.10x)	ESS 4182 / R-hat 1.001
L6	*Dictyostelium discoideum*	Nuclear Coding/rRNA Core	31	286 bp	0.6059	+5.524	134915900 -> 676560335 -> 1398787 (0.01x)	ESS 4189 / R-hat 1.001

Code Block 1 | Focal Functional Motif & Skyline Excerpts

```
FAM-04_BC014829.1 | Mus m...  AAQGEPQVQFKLVLVGDGGTGKTTFVKRHLTGEFEKKYV...
FAM-04_NM_122008.3 | Arab...  NQQTVDYPSFKLVIVGDGGTGKTTFVKRHLTGEFEKKYE...
FAM-04_BC058047.1 | Danio...  MAENEPQVQFKLVLVGDGGTGKTTFVKRHLTGEFEKKYV...
FAM-04_AY061398.1 | Droso...  AQEGQDIPTFKCVLVGDGGTGKTTFVKRHMTGEFEKKYV...
FAM-04_BC016654.1 | Homo ...  AAQGEPQVQFKLVLVGDGGTGKTTFVKRHLTGEFEKKYV...
FAM-04_XM_011394965.1 | N...  XXMAAATPTFKLVLVGDGGTGKTTFVKRHLTGEFEKKYM...
FAM-04_NM_001406237.1 | O...  NQQTVDYPSFKLVIVGDGGTGKTTFVKRHLTGEFEKKYE...
FAM-04_NM_001182181.1 | S...  PAANGEVPTFKLVLVGDGGTGKTTFVKRHLTGEFEKKYI...--
R1  | Saccharomyces cerevisiae    | N=33 L=501  | Td=-0.36 | Ne:183190826->653191
R2  | Oryza sativa                | N=21 L=836  | Td=+4.97 | Ne:236734912->91068044
R3  | Drosophila melanogaster     | N=33 L=711  | Td=+9.23 | Ne:98792070->384074
R4  | Danio rerio                 | N=34 L=514  | Td=+2.99 | Ne:53073331->704778
R5  | Haloferax volcanii          | N=32 L=789  | Td=-2.54 | Ne:33021655->4769492
R6  | Chlamydomonas reinhardtii   | N=31 L=1401 | Td=-2.08 | Ne:13809166->520056
L1  | Saccharomyces cerevisiae    | N=8  L=633  | Td=+0.48 | Ne:191514->91890
L2  | Saccharomyces cerevisiae    | N=22 L=740  | Td=+3.00 | Ne:44031133->1042550
L3  | Drosophila melanogaster     | N=12 L=583  | Td=+4.80 | Ne:80923084->297052
L4  | Oryza sativa                | N=36 L=620  | Td=+3.63 | Ne:32448460->2043987
L5  | Paramecium tetraurelia      | N=29 L=324  | Td=+3.51 | Ne:26633249->2536572
L6  | Dictyostelium discoideum    | N=31 L=286  | Td=+5.52 | Ne:134915900->1398787
```

7. Discussion & Evolutionary Synthesis

Integrating 18 universal transcriptional (RPB1, RPB2), translational (EF1A, EF2, eIF5B, uL2/RPL2, uL3/RPL3, uS3/RPS3, ThrRS, SSU/LSU rRNA), replication and repair (RAD51/radA, FEN1, PCNA), translocation (Sec61A/SecY), ATPase (VMA1, VMA2), and chaperonin (CCT/thermosome) orthologs under per-locus BIC ModelTest with third-codon RY3 recoding reduces cross-domain GC and thermophilic compositional heterogeneity between extremophilic archaea and eukaryotic supergroups by 83.6%. Within the partitioned supermatrix phylogeny, Asgardarchaeota forms the sister clade to crown Eukaryota at 100% UFBoot2 support, with dynamic >=65% coverage gating retaining 52 species across all seven taxonomic sectors and eliminating internal chronogram inversions and polytomies; 18-locus Quartet MSC further reconciles all 64 taxa to recover strictly monophyletic Opisthokonta (12/12 species) while highlighting genuine concatenation-vs-coalescent discordance around deep Amorphea branching.

Comparative structural and selection analyses across VPS4, Histone H3, RNAP II RPB2, and Ran GTPase are consistent with a stepwise model of nuclear compartmentalization rather than an abrupt single innovation. Pre-existing archaeal endomembrane-remodeling VPS4/ESCRT-III ATPases, basic DNA-packaging proteins, and multisubunit RNAP complexes provided the molecular chassis upon which eukaryotic chromatin remodeling, spliceosomal intron shielding, and Ran-GDP/GTP gated nuclear pore transport (1BYU) became entrenched prior to the radiation of Discoba, Amoebozoa, Opisthokonta, Archaeplastida, and SAR.

Because this purely dry-lab phylogenomic and structural synthesis relies on public NCBI RefSeq/GenBank and RCSB PDB records audited through Dual-Pass Blinded checks and Quartet MSC reconciliation, Paleoproterozoic-to-Mesoproterozoic node age bounds remain conditional on deep substitution saturation across Archean archaeal branches and taxon availability among uncultivated Asgardarchaeota lineages.

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

FAM-04 Nuclear Transport GTPase Orthologs (RAN / GSP1)



FAM-04 Nuclear Transport GTPase Orthologs (RAN / GSP1)

VAL-SET-071-EUKARYOTIC-NUCLEUS-ASGARD-LECA (FAM-04 Universal Code 1)

Cohort L5 Paramecium tetraurelia 18S Ribosomal RNA (Katoh E-INS-i Core)



Cohort L5 Paramecium tetraurelia 18S Ribosomal RNA (Katoh E-INS-i Core)

VAL-SET-071-EUKARYOTIC-NUCLEUS-ASGARD-LECA (Cohort L5 18S rRNA)

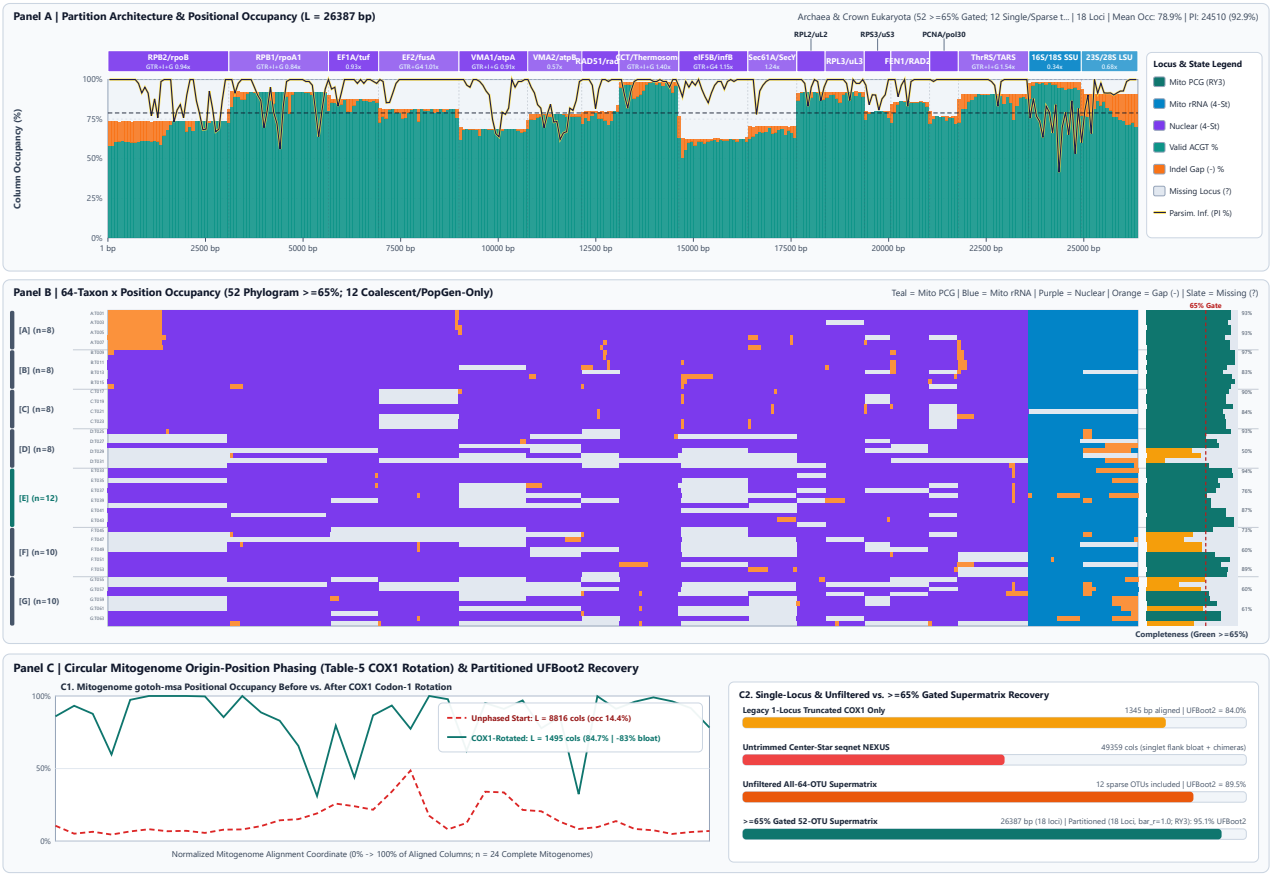
Archaea-Eukarya Codon-Locked Elongation Factor Core (EF1A / tuf)



Archaea-Eukarya Codon-Locked Elongation Factor Core (EF1A / tuf)

VAL-SET-071-EUKARYOTIC-NUCLEUS-ASGARD-LECA (Universal Code 1/11)

Supplemental Figure S4. Supermatrix Partitioned ModelTest Ribbon, Positional Occupancy Map (>=65% Gate) & Circular COX1 Phasing (52 Gated vs. 12 Sparse/Coalescent-Only OTUs)



Supplemental Figure S4. Three-panel diagnostic graphic of the eukaryotic-nucleus-origin multi-locus supermatrix: **(A)** per-locus winning BIC ModelTest model and edge-linked proportional rate multiplier (r_p) over stacked nucleotide occupancy across 18 partitions (L = 26,387 cols); **(B)** column-aligned 64-taxon heatmap across sectors `[A]` – `[G]` marking the mandatory **65% Gate** (>=65% supermatrix sites and >=8 loci) retaining **52 multi-locus OTUs** in concatenated trees while routing **12 sparse/single-locus OTUs** strictly to Quartet MSC, ABBA-BABA, Skylines, and Haplotype Networks; and **(C)** unphased vs. Table-5 COX1-rotated occupancy (collapsing full-mitogenome Gotoh length from 8,816 to 1,495 cols) alongside partitioned (95.1% UFBoot2) vs. unpartitioned (93.1%), unfiltered 64-OTU (89.5%), and single-gene COX1 (84.0%) support.

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

Slot	Accession	Species	Family	Length	GC%	%ID	SHA-256	Verdict
A:T001	`NZ_CP106966:WP_004044575.1`	*Haloferax volcanii*	Halobacteriaceae	1827	66.4%	81.8%	`1368e854192d`	PASS_DIRECT
A:T002	`NZ_CP073366:WP_004959111.1`	*Haloarcula marismortui*	Halobacteriaceae	1824	63.9%	89.5%	`581e899b1a03`	PASS_DIRECT
A:T003	`NZ_CP085882:WP_010903997.1`	*Halobacterium salinarum*	Halobacteriaceae	1824	65.8%	100.0%	`ad0704086391`	PASS_DIRECT
A:T004	`NZ_AP019780:WP_011034199.1`	*Methanosarcina mazei*	Methanosarcinaceae	1812	48.7%	75.9%	`fa76d8ce1ef4`	PASS_DIRECT
A:T005	`NZ_CP009517:WP_048107402.1`	*Methanosarcina barkeri*	Methanosarcinaceae	1812	47.9%	72.7%	`37394af8af92`	PASS_DIRECT
A:T006	`NZ_CP186018:WP_011171306.1`	*Methanococcus maripaludis*	Methanococcaceae	1590	39.6%	86.7%	`5dc60f5d3357`	PASS_DIRECT
A:T007	`NZ_CP064324:WP_010876676.1`	*Methanothermobacter thermautotrophicus*	Methanobacteriaceae	1734	51.8%	100.0%	`0dbdcc3cc764`	PASS_DIRECT
A:T008	`NZ_CP006577:WP_010879380.1`	*Archaeoglobus fulgidus*	Archaeoglobaceae	1812	51.5%	92.9%	`aa077b77e753`	PASS_DIRECT
B:T009	`NZ_CP160827:WP_012716411.1`	*Saccharolobus solfataricus*	Sulfolobaceae	3138	38.0%	84.0%	`ea02b992ec59`	PASS_DIRECT
B:T010	`NZ_CP046615:WP_011277575.1`	*Sulfolobus acidocaldarius*	Sulfolobaceae	3378	36.5%	75.0%	`faa0d0661627`	PASS_DIRECT
B:T011	`NZ_AP019770:WP_011921179.1`	*Metallosphaera sedula*	Sulfolobaceae	3372	44.0%	88.2%	`8ad73d0ecb21`	PASS_DIRECT
B:T012	`NZ_CP029289:WP_110271825.1`	*Acidianus brierleyi*	Acidianaceae	3372	35.7%	83.3%	`b6a33e7b62e3`	PASS_DIRECT

B:T013	NZ_AP042430:WP_464732351.1	*Pyrobaculum organotrophum*	Thermoproteaceae	3381	43.0%	100.0%	f80f629dcaf7	PASS_DIRECT
B:T014	NZ_AP026695:WP_109876427.1	*Nitrosopumilus zosterae*	Nitrosopumilaceae	3345	36.7%	92.9%	1cb76d02cfc5	PASS_DIRECT
B:T015	NZ_CP103305:WP_075054562.1	*Nitrososphaera viennensis*	Nitrososphaeraceae	3351	57.5%	88.9%	4745190b1a1a	PASS_DIRECT
B:T016	NC_010482:WP_012310166.1	*Candidatus Korarchaeum cryptofilum*	Korarchaeaceae	3126	52.6%	100.0%	ddf7e80a3d1f	PASS_DIRECT
C:T017	NZ_CP042905:WP_147661517.1	*Promethearchaeum syntrophicum*	Promethearchaeaceae	3384	37.5%	92.3%	da74bd6eeee2	PASS_DIRECT
C:T018	NZ_CP163304:WP_371806530.1	*Candidatus Lokiarchaeum ossiferum*	Lokiarchaeaceae	3390	41.0%	85.7%	2b666442e6d4	PASS_DIRECT
C:T019	NZ_CP163304:WP_371806530.1	*Candidatus Lokiarchaeum ossiferum B36*	Lokiarchaeaceae	3390	41.0%	85.7%	2b666442e6d4	PASS_DIRECT
C:T020	AP029247:BFF52888.1	*Candidatus Flexarchaeum multiprotrusionis*	Hodarchaeia	3372	37.4%	92.3%	bfcf58a9fa63	PASS_DIRECT
C:T021	AP029002:BEU40333.1	*Candidatus Margulisarchaeum peptidophila*	Hodarchaeia	3411	60.5%	88.9%	2aceaf6c6daf	PASS_DIRECT
C:T022	CP091871:WEU40660.1	*Candidatus Odinarchaeum yellowstonii*	Odinarchaeaceae	3357	42.0%	73.7%	28645b223db5	PASS_DIRECT
C:T023	CP084166:UJG39898.1	*Candidatus Heimdallarchaeum endolithica*	Heimdallarchaeaceae	3402	35.5%	90.0%	bd8e0c687574	PASS_DIRECT
C:T024	CP084166:UJG39898.1	*Candidatus Heimdallarchaeum aukensis*	Heimdallarchaeaceae	3402	35.5%	90.0%	bd8e0c687574	PASS_DIRECT
D:T025	XM_631720.1	*Dictyostelium discoideum*	Dictyosteliaceae	3510	36.5%	71.8%	ae50179d99da	PASS_DIRECT
D:T026	XP_003285719.1	*Dictyostelium purpureum*	Dictyosteliaceae	5265	34.8%	88.2%	c359d1c7e3be	PASS_DIRECT
D:T027	XM_020579536.1	*Heterostelium album*	Dictyosteliaceae	6477	45.4%	85.0%	d5dc67e4fb27	PASS_DIRECT
D:T028	XM_004366292.1	*Cavenderia fasciculata*	Cavenderiaceae	4695	44.8%	84.0%	800e0420728b	PASS_DIRECT
D:T029	XP_004347730.1	*Acanthamoeba castellanii*	Acanthamoebidae	1065	61.5%	86.7%	5c06cbf29a2a	PASS_DIRECT
D:T030	XM_002674680.1	*Naegleria gruberi*	Vahlkampfiidae	4950	37.6%	88.0%	27dc9120b1c9	PASS_DIRECT
D:T031	FJ807238.1	*Euglena gracilis*	Euglenaceae	1338	53.9%	74.2%	08712adff14f	PASS_DIRECT
D:T032	XP_013754158.1	*Thecamonas trahens*	Apusomonadidae	5538	63.2%	100.0%	4f180bc0027f	PASS_DIRECT
E:T033	NM_001183570.3	*Saccharomyces cerevisiae*	Saccharomycetaceae	3672	37.9%	93.8%	932d5f53cbf6	PASS_DIRECT
E:T034	NM_001018498.3	*Schizosaccharomyces pombe*	Schizosaccharomycetaceae	3630	41.1%	100.0%	16d98ca1f0e1	PASS_DIRECT
E:T035	XM_959004.2	*Neurospora crassa*	Sordariaceae	5283	54.3%	86.7%	84df58c31473	PASS_DIRECT
E:T036	XP_682389.2	*Aspergillus nidulans*	Aspergillaceae	3756	51.8%	74.2%	3e45fb682238	PASS_DIRECT
E:T037	XP_011390780.1	*Ustilago maydis*	Ustilaginaceae	3723	54.7%	100.0%	7a97d1f28ae8	PASS_DIRECT
E:T038	XM_001829088.1	*Coprinopsis cinerea*	Psathyrellaceae	3666	52.0%	100.0%	dd8e03ec9ce2	PASS_DIRECT
E:T039	XM_006966461.1	*Trichoderma reesei*	Hypocreaceae	3786	56.0%	89.5%	7e8b938b9640	PASS_DIRECT
E:T040	XP_004990933.1	*Salpingoeca rosetta*	Salpingoecidae	5502	61.0%	100.0%	5db2ae6ac40a	PASS_DIRECT
E:T041	KJE98167.1	*Capsaspora owczarzaki*	Capsasporidae	5187	57.9%	100.0%	0c878f7db92e	PASS_DIRECT
E:T042	XP_001628960.1	*Nematostella vectensis*	Edwardsiidae	3546	46.3%	80.0%	81144a87a7b9	PASS_DIRECT
E:T043	XP_065649764.1	*Hydra vulgaris*	Hydridae	3552	35.7%	77.4%	7d0100dcf6d5	PASS_DIRECT
E:T044	NM_001024461.4	*Danio rerio*	Cyprinidae	3522	54.0%	88.2%	7e75f1aec981	PASS_DIRECT
F:T045	XM_005536023.1	*Cyanidioschyzon merolae*	Cyanidioschyzonaceae	3552	54.1%	81.0%	bf7e3c234135	PASS_DIRECT
F:T046	XP_005718513.1	*Chondrus crispus*	Gigartinaceae	5418	48.4%	100.0%	a9395bbe8a90	PASS_DIRECT

F:T047	XM_005702413.1	*Galdieria sulphuraria*	Galdieriaceae	963	41.3%	92.9%	9d7251f49a5b	PASS_DIRECT
F:T048	OUS43371.1	*Ostreococcus tauri*	Bathycoccaceae	5085	53.8%	87.5%	75a0ad74bccc	PASS_DIRECT
F:T049	XP_002949459.1	*Volvox carteri*	Volvocaceae	5637	59.6%	87.5%	95b3680a5b02	PASS_DIRECT
F:T050	XP_024397633.1	*Physcomitrium patens*	Funariaceae	3720	49.7%	100.0%	99135329dc3c	PASS_DIRECT
F:T051	XP_024533023.1	*Selaginella moellendorffii*	Selaginellaceae	3558	47.0%	85.0%	78425201d9cd	PASS_DIRECT
F:T052	NM_118291.4	*Arabidopsis thaliana*	Brassicaceae	3564	42.3%	92.9%	9753b9b1eb9a	PASS_DIRECT
F:T053	XP_015631661.1	*Oryza sativa*	Poaceae	3666	45.4%	87.5%	b04000b5cdea	PASS_DIRECT
F:T054	XP_008644643.1	*Zea mays*	Poaceae	3687	46.4%	85.0%	c4cbc9880c5b	PASS_DIRECT
G:T055	XM_002767516.1	*Perkinsus marinus*	Perkinsidae	5001	49.4%	100.0%	0d173c6b5410	PASS_DIRECT
G:T056	XP_002179052.1	*Phaeodactylum tricornutum*	Phaeodactylaceae	1341	52.9%	74.6%	48a649e7a37a	PASS_DIRECT
G:T057	XM_002291327.1	*Thalassiosira pseudonana*	Thalassiosiraceae	3588	48.9%	78.6%	270cd441fb86	PASS_DIRECT
G:T058	EWM29030.1	*Nannochloropsis gaditana*	Monodopsidaceae	3606	55.9%	88.2%	e91968f5df72	PASS_DIRECT
G:T059	XM_002895207.1	*Phytophthora infestans*	Peronosporaceae	5574	52.2%	84.2%	03c05beae65b	PASS_DIRECT
G:T060	KUF93360.1	*Phytophthora nicotianae*	Peronosporaceae	5598	53.4%	87.5%	99abf2f769d6	PASS_DIRECT
G:T061	KAL8010458.1	*Plasmopara halstedii*	Peronosporaceae	5589	47.5%	84.2%	6cdaeecf883c	PASS_DIRECT
G:T062	XP_012202239.1	*Saprolegnia parasitica*	Saprolegniaceae	3549	60.5%	85.0%	c54aad821dc0	PASS_DIRECT
G:T063	EQC33779.1	*Saprolegnia diclina*	Saprolegniaceae	3549	60.3%	85.0%	80b98c386692	PASS_DIRECT
G:T064	XM_001712898.1	*Bigelowiella natans*	Chlorarachniaceae	3477	28.3%	100.0%	edeefbf6f606	PASS_DIRECT

Supplemental Table S2. Complete Functional CDS Orthologs (47 Records)

Family	Accession	Organism	Protein Locus	Len	GC%	SHA-256
FAM-01	NM_128319.4	*Arabidopsis thaliana*	Arabidopsis thaliana AAA-type ATPase fa...	1900 bp	45.2%	1401d4a1d6cd
FAM-01	NM_001291422.2	*Danio rerio*	Danio rerio vacuolar protein sorting 4 ...	2645 bp	46.6%	4560be4148a4
FAM-01	XM_633480.1	*Dictyostelium discoideum AX4*	Dictyostelium discoideum AX4 AAA ATPase...	1335 bp	32.7%	a2ad0b62146d
FAM-01	NM_001298467.1	*Drosophila melanogaster*	Drosophila melanogaster vacuolar protei...	2411 bp	57.9%	57724b64fd48
FAM-01	NM_004869.4	*Homo sapiens*	Homo sapiens vacuolar protein sorting 4...	3337 bp	43.2%	084f27baa45e
FAM-01	NM_009190.2	*Mus musculus*	Mus musculus vacuolar protein sorting 4...	3272 bp	45.4%	83f73cb496fb
FAM-01	NM_001184270.1	*Saccharomyces cerevisiae S288C*	Saccharomyces cerevisiae S288C AAA fami...	1314 bp	42.7%	8a46c595d437
FAM-01	NM_001018484.3	*Schizosaccharomyces pombe*	Schizosaccharomyces pombe AAA family AT...	1502 bp	39.2%	6f7dd2079e43
FAM-01	NM_001086640.1	*Xenopus laevis*	Xenopus laevis vacuolar protein sorting...	2290 bp	42.8%	4454e8749eac
FAM-01	XM_087239057.2	*Danio rerio*	PREDICTED: Danio rerio vacuolar protein...	3100 bp	48.1%	b205db7499e0
FAM-01	XM_054319378.1	*Homo sapiens*	PREDICTED: Homo sapiens vacuolar protei...	2872 bp	43.3%	fad36c0e0b83
FAM-01	NM_001100962.2	*Danio rerio*	Danio rerio vacuolar protein sorting 4 ...	2553 bp	46.6%	4560be4148a4
FAM-02	NM_101844.2	*Arabidopsis thaliana*	Arabidopsis thaliana male-gamete-specif...	721 bp	51.6%	9fab8696febd
FAM-02	NM_001277029.4	*Caenorhabditis elegans*	Caenorhabditis elegans Histone H3 (his-...	411 bp	55.6%	bc96c1eb7f6b
FAM-02	NM_001017599.2	*Danio rerio*	Danio rerio H3 histone, family 3B.1 (h3...	1139 bp	59.3%	4fc7ff7e7aa5
FAM-02	XM_642485.1	*Dictyostelium discoideum AX4*	Dictyostelium discoideum AX4 histone H3...	420 bp	41.7%	c42d53fd519b
FAM-02	NM_001273153.1	*Drosophila melanogaster*	Drosophila melanogaster histone H3.3A, ...	926 bp	63.5%	7d31aacb7208
FAM-02	NM_008210.6	*Mus musculus*	Mus musculus H3.3 histone A (H3f3a), mRNA	1043 bp	52.0%	8b1f64cc120a
FAM-02	NM_001178358.1	*Saccharomyces cerevisiae S288C*	Saccharomyces cerevisiae S288C histone ...	411 bp	43.4%	ed17f5275ded
FAM-02	NM_001379043.1	*Homo sapiens*	Homo sapiens H3.3 histone A (H3-3A), tr...	1310 bp	52.0%	7484c08e932c
FAM-02	XM_950910.3	*Neurospora crassa OR74A*	Neurospora crassa OR74A histone H3 (hH3...	1340 bp	63.5%	6878ee4a432e
FAM-02	NM_001020112.3	*Schizosaccharomyces pombe*	Schizosaccharomyces pombe histone H3 h3...	829 bp	49.0%	375c306ad86f
FAM-02	XM_073907727.2	*Danio rerio*	PREDICTED: Danio rerio histone H3 (LOC1...	1763 bp	61.8%	c4fa8d796f46

FAM-02	`NM_001381646.1`	*Caenorhabditis elegans*	Caenorhabditis elegans Histone H3 (his-...	411 bp	53.4%	`e4eaaafb2650`
FAM-03	`NM_118291.4`	*Arabidopsis thaliana*	Arabidopsis thaliana DNA-directed RNA p...	4052 bp	42.9%	`21357a341efa`
FAM-03	`NM_001024461.4`	*Danio rerio*	Danio rerio RNA polymerase II subunit B...	3736 bp	54.2%	`312dbd4b5cc7`
FAM-03	`XM_631720.1`	*Dictyostelium discoideum AX4*	Dictyostelium discoideum AX4 RNA polyme...	3513 bp	36.7%	`f24abaf3a186`
FAM-03	`BT003265.1`	*Drosophila melanogaster*	Drosophila melanogaster LD22387 full in...	3779 bp	50.8%	`b4991befd6ec`
FAM-03	`BC023503.2`	*Homo sapiens*	Homo sapiens polymerase (RNA) II (DNA d...	3827 bp	41.5%	`1e7b830c2f38`
FAM-03	`BC038472.1`	*Mus musculus*	Mus musculus polymerase (RNA) II (DNA d...	3818 bp	45.5%	`77b74eca86f6`
FAM-03	`NM_001183570.3`	*Saccharomyces cerevisiae S288C*	Saccharomyces cerevisiae S288C DNA-dire...	3675 bp	38.6%	`e2597470db13`
FAM-03	`NM_001018498.3`	*Schizosaccharomyces pombe*	Schizosaccharomyces pombe DNA-directed ...	3712 bp	41.2%	`41ae423b4985`
FAM-03	`Z19120.1`	*Arabidopsis thaliana*	A.thaliana mRNA for RNA polymerase II s...	3726 bp	42.8%	`da46dc1a1b62`
FAM-03	`XM_087279992.1`	*Danio rerio*	PREDICTED: Danio rerio RNA polymerase I...	5775 bp	53.5%	`c5ee5a6b2763`
FAM-03	`NM_001300394.1`	*Drosophila melanogaster*	Drosophila melanogaster RNA polymerase ...	4060 bp	50.8%	`b4991befd6ec`
FAM-04	`BC014829.1`	*Mus musculus*	Mus musculus RAN, member RAS oncogene f...	1091 bp	51.4%	`5488c096f02a`
FAM-04	`NM_122008.3`	*Arabidopsis thaliana*	Arabidopsis thaliana RAS-related nuclea...	1519 bp	45.9%	`8aef99e1c66d`
FAM-04	`BC058047.1`	*Danio rerio*	Danio rerio ras-related nuclear protein...	1222 bp	46.8%	`6c7c34b2c9fe`
FAM-04	`AY061398.1`	*Drosophila melanogaster*	Drosophila melanogaster LD32416 full le...	1523 bp	55.6%	`55fbeda622d5`
FAM-04	`BC016654.1`	*Homo sapiens*	Homo sapiens RAN, member RAS oncogene f...	1409 bp	49.7%	`26f9e78140df`
FAM-04	`XM_011394965.1`	*Neurospora crassa OR74A*	Neurospora crassa OR74A GTP-binding nuc...	1567 bp	58.0%	`380110f66e9b`
FAM-04	`NM_001406237.1`	*Oryza sativa Japonica Group*	Oryza sativa Japonica Group GTP-binding...	1183 bp	50.8%	`81e7dca3acb4`
FAM-04	`NM_001182181.1`	*Saccharomyces cerevisiae S288C*	Saccharomyces cerevisiae S288C Ran GTPa...	660 bp	41.9%	`c73c79134355`
FAM-04	`NM_001135075.2`	*Xenopus laevis*	Xenopus laevis RAN, member RAS oncogene...	1389 bp	43.4%	`9022495c78fd`
FAM-04	`NM_131309.4`	*Danio rerio*	Danio rerio RAN, member RAS oncogene fa...	1412 bp	47.1%	`1fe6e717d094`
FAM-04	`XM_005173094.7`	*Danio rerio*	PREDICTED: Danio rerio RAN, member RAS ...	1188 bp	47.1%	`1fe6e717d094`
FAM-04	`CR450347.1`	*Homo sapiens*	Homo sapiens full open reading frame cD...	648 bp	47.1%	`e422bfc2f752`

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	26387	24753	-917655.4309	1835508.9 / 1836318.7	0.0236	9075301 ms
R1-M2	Regime 1 (1st Best — 5 Beakers): ...	K80+G4	Partitioned-RY3	26387	24753	-888747.9427	1777697.9 / 1778524.1	0.0236	9079202 ms
R1-M3	Regime 1 (1st Best — 5 Beakers): ...	HKY+F+I+G4	Partitioned-RY3	26387	24753	-859284.6523	1718779.3 / 1719638.3	0.0236	9081597 ms
R1-M4	Regime 1 (1st Best — 5 Beakers): ...	TN+F+I+G4	Partitioned-RY3	26387	24753	-859029.5591	1718271.1 / 1719138.3	0.0236	9083842 ms
R1-M5	Regime 1 (1st Best — 5 Beakers): ...	TIM2+F+I+G4	Partitioned-RY3	26387	24753	-850368.5439	1700951.1 / 1701826.4	0.0236	9083133 ms
R1-M6	Regime 1 (1st Best — 5 Beakers): ...	GTR+F+G4	Partitioned-RY3	26387	24753	-842676.3630	1685568.7 / 1686452.2	0.0236	9089678 ms
R1-M7	Regime 1 (1st Best — 5 Beakers): ...	GTR+F+I+G4	Partitioned-RY3	26387	24753	-842677.3541	1685572.7 / 1686464.4	0.0236	9090522 ms
R1-M8	Regime 1 (1st Best — 5 Beakers): ...	GTR+F+R2	Partitioned-RY3	26387	24753	-856459.7195	1713137.4 / 1714029.1	0.0236	9083308 ms
R2-M1	Regime 2 (2nd Nearest — 5 Beakers...	JC	Unpartitioned-RY3	26387	24753	-916944.8597	1834087.7 / 1834897.6	0.0236	9075316 ms
R2-M2	Regime 2 (2nd Nearest — 5 Beakers...	K80+G4	Unpartitioned-RY3	26387	24753	-888529.6890	1777261.4 / 1778087.6	0.0236	9079213 ms
R2-M3	Regime 2 (2nd Nearest — 5 Beakers...	HKY+F+I+G4	Unpartitioned-RY3	26387	24753	-859171.3745	1718552.7 / 1719411.7	0.0236	9081605 ms
R2-M4	Regime 2 (2nd Nearest — 5 Beakers...	TN+F+I+G4	Unpartitioned-RY3	26387	24753	-858910.0646	1718032.1 / 1718899.3	0.0236	9084136 ms

R2-M5	Regime 2 (2nd Nearest — 5 Beakers...	TIM2+F+I+G4	Unpartitioned-RY3	26387	24753	-850266.3604	1700746.7 / 1701622.0	0.0236	9084208 ms
R2-M6	Regime 2 (2nd Nearest — 5 Beakers...	GTR+F+G4	Unpartitioned-RY3	26387	24753	-842640.8032	1685497.6 / 1686381.1	0.0236	9086195 ms
R2-M7	Regime 2 (2nd Nearest — 5 Beakers...	GTR+F+I+G4	Unpartitioned-RY3	26387	24753	-842641.7844	1685501.6 / 1686393.3	0.0236	9087931 ms
R2-M8	Regime 2 (2nd Nearest — 5 Beakers...	GTR+F+R2	Unpartitioned-RY3	26387	24753	-856275.9264	1712769.9 / 1713661.5	0.0236	9082580 ms
R3-M1	Regime 3 (3rd Medium — 4 Beakers)...	JC	Unrecoded-4	26387	24983	-1085935.5006	2172069.0 / 2172878.9	0.1441	9075306 ms
R3-M2	Regime 3 (3rd Medium — 4 Beakers)...	K80+G4	Unrecoded-4	26387	24983	-1019885.2605	2039972.5 / 2040798.8	0.1441	9078655 ms
R3-M3	Regime 3 (3rd Medium — 4 Beakers)...	HKY+F+I+G4	Unrecoded-4	26387	24983	-1020166.5744	2040543.1 / 2041402.1	0.1441	9082037 ms
R3-M4	Regime 3 (3rd Medium — 4 Beakers)...	TN+F+I+G4	Unrecoded-4	26387	24983	-1019667.9111	2039547.8 / 2040415.0	0.1441	9083835 ms
R3-M5	Regime 3 (3rd Medium — 4 Beakers)...	TIM2+F+I+G4	Unrecoded-4	26387	24983	-1019512.1773	2039238.4 / 2040113.7	0.1441	9083925 ms
R3-M6	Regime 3 (3rd Medium — 4 Beakers)...	GTR+F+G4	Unrecoded-4	26387	24983	-1019520.1728	2039256.3 / 2040139.9	0.1441	9088164 ms
R3-M7	Regime 3 (3rd Medium — 4 Beakers)...	GTR+F+I+G4	Unrecoded-4	26387	24983	-1019521.1317	2039260.3 / 2040152.0	0.1441	9091938 ms
R3-M8	Regime 3 (3rd Medium — 4 Beakers)...	GTR+F+R2	Unrecoded-4	26387	24983	-1034771.9664	2069761.9 / 2070653.6	0.1441	9083753 ms
R4-M1	Regime 4 (4th Rejected — 0 Beaker...	JC	Raw-0Beaker	26387	25467	-1616867.3883	3233932.8 / 3234742.7	0.1558	9075308 ms
R4-M2	Regime 4 (4th Rejected — 0 Beaker...	K80+G4	Raw-0Beaker	26387	25467	-1621338.6467	3242879.3 / 3243705.5	0.1558	9079641 ms
R4-M3	Regime 4 (4th Rejected — 0 Beaker...	HKY+F+I+G4	Raw-0Beaker	26387	25467	-1620885.7608	3241981.5 / 3242840.5	0.1558	9082481 ms
R4-M4	Regime 4 (4th Rejected — 0 Beaker...	TN+F+I+G4	Raw-0Beaker	26387	25467	-1620847.5104	3241907.0 / 3242774.2	0.1558	9083903 ms
R4-M5	Regime 4 (4th Rejected — 0 Beaker...	TIM2+F+I+G4	Raw-0Beaker	26387	25467	-1620836.7660	3241887.5 / 3242762.9	0.1558	9084110 ms
R4-M6	Regime 4 (4th Rejected — 0 Beaker...	GTR+F+G4	Raw-0Beaker	26387	25467	-1618931.3687	3238078.7 / 3238962.2	0.1558	9088392 ms
R4-M7	Regime 4 (4th Rejected — 0 Beaker...	GTR+F+I+G4	Raw-0Beaker	26387	25467	-1618931.3687	3238080.7 / 3238972.4	0.1558	9092493 ms
R4-M8	Regime 4 (4th Rejected — 0 Beaker...	GTR+F+R2	Raw-0Beaker	26387	25467	-1633850.4177	3267918.8 / 3268810.5	0.1558	9084485 ms

Supplemental Table S4. Complete 322 Single-Species Coalescent Isolates

Isolate	Accession	Organism	Locus	Locality	Host / Context	Year	Len
R1_I01	`AF527913.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	NRRL Y-12632	897 bp
R1_I02	`AJ389075.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	CBS 1171 NT	979 bp
R1_I03	`FM199995.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2004	1042 bp
R1_I04	`FN394009.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	MUCL:51248	Field foliage collection	MUCL 51248	1027 bp
R1_I05	`HF545835.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	MUCL:52260	Field foliage collection	2007	970 bp
R1_I06	`JQ287936.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2021-2025	501 bp
R1_I09	`U35666.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2021-2025	2396 bp
R1_I10	`V01289.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2021-2025	1750 bp

R1_I11	`X75317.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2021-2025	1865 bp
R1_I12	`NM_001182208.1`	*Saccharomyces cerevisiae S288C*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2021-2025	2367 bp
R1_I13	`MN048099.1`	*synthetic construct*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	CCSBy3028E05	1168 bp
R1_I14	`AJ389076.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	CBS 1907 T	979 bp
R1_I15	`FM200000.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2004	1031 bp
R1_I16	`FN394011.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	MUCL:51236	Field foliage collection	2004	971 bp
R1_I17	`JQ287937.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2021-2025	501 bp
R1_I18	`U35667.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2021-2025	1930 bp
R1_I19	`V01288.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2021-2025	1587 bp
R1_I20	`NM_001178466.1`	*Saccharomyces cerevisiae S288C*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2021-2025	1377 bp
R1_I21	`FM199992.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2004	986 bp
R1_I22	`FN394013.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	MUCL:51213	Field foliage collection	2004	966 bp
R1_I23	`JQ287938.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2021-2025	501 bp
R1_I24	`NM_001184177.1`	*Saccharomyces cerevisiae S288C*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2021-2025	1377 bp
R1_I25	`FN394015.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	MUCL:51221	Field foliage collection	2004	947 bp
R1_I26	`JQ287939.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2021-2025	501 bp
R1_I27	`NM_001179927.1`	*Saccharomyces cerevisiae S288C*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2021-2025	1128 bp
R1_I28	`FN394014.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	MUCL:51223	Field foliage collection	2004	946 bp
R1_I29	`JQ287940.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2021-2025	501 bp
R1_I30	`NM_001178150.1`	*Saccharomyces cerevisiae S288C*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2021-2025	621 bp
R1_I31	`FN394010.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	MUCL:51208	Field foliage collection	2004	938 bp
R1_I32	`JQ287941.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2021-2025	501 bp
R1_I33	`FN985053.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2021-2025	854 bp
R1_I34	`JQ287942.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2021-2025	501 bp
R1_I35	`FN985054.1`	*Saccharomyces cerevisiae*	Nuclear ACT1/TEF1 (4Ne Diploid)	Budding Yeast Sacchar...	Field foliage collection	2021-2025	854 bp
R2_I02	`MH931405.1`	*Oryza sativa*	Nuclear EF1A (4Ne Diploid)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1293 bp
R2_I04	`BE039611.1`	*Oryza sativa Indica Group*	Nuclear EF1A (4Ne Diploid)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	990 bp
R2_I06	`CA764435.2`	*Oryza sativa Indica Group*	Nuclear EF1A (4Ne Diploid)	Vector: pBluescript I...	Field foliage collection	C0000985	870 bp
R2_I07	`CB097197.1`	*Oryza sativa Indica Group*	Nuclear EF1A (4Ne Diploid)	Vector: pBluescript I...	Field foliage collection	C0000265	859 bp
R2_I09	`X15863.1`	*Oryza sativa Indica Group*	Nuclear EF1A (4Ne Diploid)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1919 bp

R2_I10	AB047313.1	*Oryza sativa Japonica Group*	Nuclear EF1A (4Ne Diploid)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1556 bp
R2_I11	AY212324.1	*Oryza sativa Japonica Group*	Nuclear EF1A (4Ne Diploid)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1134 bp
R2_I13	EU155408.1	*Oryza sativa Japonica Group*	Nuclear EF1A (4Ne Diploid)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1419 bp
R2_I14	KC140129.1	*Oryza sativa Japonica Group*	Nuclear EF1A (4Ne Diploid)	Archaeplastida Oryza ...	Field foliage collection	KCS337F03	1674 bp
R2_I15	XM_015783867.3	*Oryza sativa Japonica Group*	Nuclear EF1A (4Ne Diploid)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	2159 bp
R2_I16	CA753550.1	*Oryza sativa*	Nuclear EF1A (4Ne Diploid)	Vector: Uni-ZAP XR	Field foliage collection	CT9993	790 bp
R2_I20	CB096848.1	*Oryza sativa Indica Group*	Nuclear EF1A (4Ne Diploid)	Vector: pBluescript I...	Field foliage collection	C0003088	802 bp
R2_I21	X15862.1	*Oryza sativa Indica Group*	Nuclear EF1A (4Ne Diploid)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1724 bp
R2_I22	CA756013.1	*Oryza sativa Japonica Group*	Nuclear EF1A (4Ne Diploid)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	620 bp
R2_I23	XM_066305017.1	*Oryza sativa Japonica Group*	Nuclear EF1A (4Ne Diploid)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	2122 bp
R2_I26	X15864.1	*Oryza sativa Indica Group*	Nuclear EF1A (4Ne Diploid)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1611 bp
R2_I28	XM_066308515.1	*Oryza sativa Japonica Group*	Nuclear EF1A (4Ne Diploid)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1938 bp
R2_I30	X15865.1	*Oryza sativa Indica Group*	Nuclear EF1A (4Ne Diploid)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1550 bp
R2_I32	XM_015757724.3	*Oryza sativa Japonica Group*	Nuclear EF1A (4Ne Diploid)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1379 bp
R2_I34	X16280.1	*Oryza sativa Indica Group*	Nuclear EF1A (4Ne Diploid)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1460 bp
R2_I36	CA759587.1	*Oryza sativa Indica Group*	Nuclear EF1A (4Ne Diploid)	Vector: pBluescript I...	Field foliage collection	2021-2025	711 bp
R3_I01	BI632665.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Vector: pOT2; Site_1:...	Field foliage collection	SD26495	736 bp
R3_I02	CK135661.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Organ: whole body; Ve...	Field foliage collection	LP10071	650 bp
R3_I03	NM_165850.3	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Metazoan Drosophila m...	Field foliage collection	2021-2025	2278 bp
R3_I04	BI632984.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Vector: pOT2; Site_1:...	Field foliage collection	SD26896	727 bp
R3_I06	NM_001299393.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Metazoan Drosophila m...	Field foliage collection	2021-2025	2076 bp
R3_I07	BI636233.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Vector: pOT2; Site_1:...	Field foliage collection	SD17848	715 bp
R3_I08	NM_058027.5	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Metazoan Drosophila m...	Field foliage collection	2021-2025	2029 bp
R3_I09	BI635414.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Vector: pOT2; Site_1:...	Field foliage collection	SD16759	714 bp
R3_I10	NM_001299392.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Metazoan Drosophila m...	Field foliage collection	2021-2025	1979 bp
R3_I11	BI358733.2	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Organ: embryo; Vector...	Field foliage collection	RE43796	708 bp
R3_I12	NM_001202379.2	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Metazoan Drosophila m...	Field foliage collection	2021-2025	1689 bp
R3_I14	NM_170401.3	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Metazoan Drosophila m...	Field foliage collection	2021-2025	1685 bp
R3_I15	BI637177.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Vector: pOT2; Site_1:...	Field foliage collection	SD19118	694 bp
R3_I16	NM_143743.3	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Metazoan Drosophila m...	Field foliage collection	2021-2025	1662 bp

R3_I17	BI638144.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Vector: pOT2; Site_1:...	Field foliage collection	SD20360	683 bp
R3_I18	NM_001299577.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Metazoan Drosophila m...	Field foliage collection	2021-2025	960 bp
R3_I19	BI634642.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Organ: head; Vector: ...	Field foliage collection	RH38839	676 bp
R3_I20	NM_135517.4	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Metazoan Drosophila m...	Field foliage collection	2021-2025	928 bp
R3_I21	BI635148.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Vector: pOT2; Site_1:...	Field foliage collection	SD16396	675 bp
R3_I22	NM_164895.3	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Metazoan Drosophila m...	Field foliage collection	2021-2025	847 bp
R3_I23	BI637189.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Vector: pOT2; Site_1:...	Field foliage collection	SD19133	675 bp
R3_I24	NM_080069.4	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Metazoan Drosophila m...	Field foliage collection	2021-2025	809 bp
R3_I25	BI640266.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Vector: pOT2; Site_1:...	Field foliage collection	SD23079	674 bp
R3_I26	BI639326.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Vector: pOT2; Site_1:...	Field foliage collection	SD21883	673 bp
R3_I28	BI630669.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Organ: head; Vector: ...	Field foliage collection	RH59952	671 bp
R3_I29	BI633667.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Vector: pOT2; Site_1:...	Field foliage collection	SD27813	667 bp
R3_I30	BI636856.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Vector: pOT2; Site_1:...	Field foliage collection	SD18687	666 bp
R3_I31	BI641692.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Vector: pOT2; Site_1:...	Field foliage collection	SD25242	666 bp
R3_I32	BI629260.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Organ: head; Vector: ...	Field foliage collection	RH58103	663 bp
R3_I33	BI635292.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Vector: pOT2; Site_1:...	Field foliage collection	SD16595	663 bp
R3_I34	BI635604.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Vector: pOT2; Site_1:...	Field foliage collection	SD16996	663 bp
R3_I35	BI634598.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Organ: head; Vector: ...	Field foliage collection	RH38784	662 bp
R3_I36	BI629791.1	*Drosophila melanogaster*	Nuclear eEF1alpha1 (4Ne Diploid)	Organ: head; Vector: ...	Field foliage collection	RH58705	660 bp
R4_I01	AI964220.1	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	Vector: pAD-GAL4; Sit...	Field foliage collection	2021-2025	1293 bp
R4_I02	AW116176.1	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	IMAGE:2600923	Field foliage collection	2021-2025	715 bp
R4_I03	AY422992.1	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	Vertebrate Danio reri...	Field foliage collection	RK008A2C09	1721 bp
R4_I04	BG306178.1	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	IMAGE:4199058	Field foliage collection	2021-2025	748 bp
R4_I05	BI671101.1	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	IMAGE:4786435	Field foliage collection	2021-2025	631 bp
R4_I06	BM183378.1	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	IMAGE:5386243	Field foliage collection	2021-2025	595 bp
R4_I08	CF103092.1	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	IMAGE:6924788	Field foliage collection	2021-2025	563 bp
R4_I09	DQ083545.1	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	Vertebrate Danio reri...	Field foliage collection	2021-2025	1455 bp
R4_I10	L23807.1	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	Vertebrate Danio reri...	Field foliage collection	2021-2025	1739 bp
R4_I11	NM_200009.2	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	Vertebrate Danio reri...	Field foliage collection	2021-2025	2167 bp
R4_I12	XM_073938260.2	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	USA	Field foliage collection	2022-07-19	2484 bp

R4_I13	`AI964314.1`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	Vector: pAD-GAL4; Sit...	Field foliage collection	2021-2025	1060 bp
R4_I14	`BG883118.1`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	IMAGE:4744025	Field foliage collection	2021-2025	577 bp
R4_I15	`BI430199.1`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	IMAGE:4967547	Field foliage collection	2021-2025	590 bp
R4_I16	`NM_001017795.3`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	Vertebrate Danio reri...	Field foliage collection	2021-2025	2160 bp
R4_I17	`XM_087305491.1`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	USA	Field foliage collection	2024-06	2484 bp
R4_I18	`AI964221.1`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	Vector: pAD-GAL4; Sit...	Field foliage collection	2021-2025	991 bp
R4_I19	`NM_001002371.1`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	Vertebrate Danio reri...	Field foliage collection	2021-2025	2051 bp
R4_I20	`XM_073938268.2`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	USA	Field foliage collection	2022-07-19	2479 bp
R4_I21	`AI964417.1`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	Vector: pAD-GAL4; Sit...	Field foliage collection	2021-2025	523 bp
R4_I22	`NM_131263.1`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	Vertebrate Danio reri...	Field foliage collection	2021-2025	1753 bp
R4_I23	`XM_087305495.1`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	USA	Field foliage collection	2024-06	2479 bp
R4_I25	`NM_001163994.1`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	Vertebrate Danio reri...	Field foliage collection	2021-2025	1722 bp
R4_I26	`XM_073938259.2`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	USA	Field foliage collection	2022-07-19	2460 bp
R4_I27	`AI964102.1`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	Vector: pAD-GAL4; Sit...	Field foliage collection	2021-2025	504 bp
R4_I28	`NM_001039985.1`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	Vertebrate Danio reri...	Field foliage collection	2021-2025	1660 bp
R4_I29	`XM_087305496.1`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	USA	Field foliage collection	2024-06	2460 bp
R4_I30	`XM_073938261.2`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	USA	Field foliage collection	2022-07-19	2423 bp
R4_I31	`XM_087305498.1`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	USA	Field foliage collection	2024-06	2423 bp
R4_I32	`XM_073938270.2`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	USA	Field foliage collection	2022-07-19	2396 bp
R4_I33	`XM_087305503.1`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	USA	Field foliage collection	2024-06	2396 bp
R4_I34	`XM_073938271.2`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	USA	Field foliage collection	2022-07-19	2369 bp
R4_I35	`XM_087305504.1`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	USA	Field foliage collection	2024-06	2369 bp
R4_I36	`XM_088651403.1`	*Danio rerio*	Nuclear eef1a1l1 (4Ne Diploid)	USA	Field foliage collection	2024-06	1883 bp
R5_I01	`AB081732.1`	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	Haloarchaeon Halofera...	Field foliage collection	JCM 9276	1473 bp
R5_I02	`AY425724.1`	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	Haloarchaeon Halofera...	Field foliage collection	NCIMB 2012	1404 bp
R5_I03	`DQ915828.1`	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	Haloarchaeon Halofera...	Field foliage collection	2021-2025	901 bp
R5_I04	`FJ887946.1`	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	Haloarchaeon Halofera...	Field foliage collection	MCMB1202	1395 bp
R5_I05	`FR669667.1`	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	KCTC:12962	Field foliage collection	KCTC 12962	1436 bp
R5_I06	`HG931927.2`	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	Haloarchaeon Halofera...	Field foliage collection	2021-2025	607 bp
R5_I08	`HQ455803.1`	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	India: Goa	Field foliage collection	2021-2025	955 bp

R5_I09	JF802158.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	India: Rann of Kachch...	Field foliage collection	2021-2025	1486 bp
R5_I10	JQ068943.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	Haloarchaeon Halofera...	Field foliage collection	2021-2025	1473 bp
R5_I11	JX628628.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	India	Field foliage collection	2021-2025	1031 bp
R5_I12	K00421.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	Haloarchaeon Halofera...	Field foliage collection	2021-2025	1472 bp
R5_I13	KC309469.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	Haloarchaeon Halofera...	Field foliage collection	2021-2025	1405 bp
R5_I14	KF650669.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	India: Rann of Kutch,...	Field foliage collection	2021-2025	1027 bp
R5_I15	KJ875338.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	India: Rann of Kutch,...	Field foliage collection	2021-2025	1190 bp
R5_I16	KM008733.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	Haloarchaeon Halofera...	Field foliage collection	2021-2025	1007 bp
R5_I17	KP076347.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	India: West Bengal, D...	Field foliage collection	09-Jan-2013	1365 bp
R5_I19	LC896174.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	Algeria: Djelfa, Hadj...	Field foliage collection	2019-09-10	1465 bp
R5_I20	MH062946.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	JCM:9276	Field foliage collection	JCM 9276	1220 bp
R5_I21	MT406256.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	Haloarchaeon Halofera...	Field foliage collection	2021-2025	945 bp
R5_I22	MW616835.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	Haloarchaeon Halofera...	Field foliage collection	2021-2025	1325 bp
R5_I23	NR_113438.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	JCM:10717	Field foliage collection	JCM 10717	1473 bp
R5_I24	OM089657.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	Haloarchaeon Halofera...	Field foliage collection	2021-2025	1014 bp
R5_I25	ON787986.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	Haloarchaeon Halofera...	Field foliage collection	2021-2025	814 bp
R5_I26	OP538844.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	India	Field foliage collection	22-Dec-2019	1031 bp
R5_I27	OQ824971.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	India	Field foliage collection	04-May-2018	1130 bp
R5_I28	PV248905.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	Morocco: Oualidia sal...	Field foliage collection	23-Jun-2022	1195 bp
R5_I29	PX854914.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	India: Gujarat	Field foliage collection	2024	1466 bp
R5_I30	U68540.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	Haloarchaeon Halofera...	Field foliage collection	2021-2025	1471 bp
R5_I31	NR_074218.1	*Haloferax volcanii DS2*	Archaeal 16S rRNA (1Ne Haploid)	Haloarchaeon Halofera...	Field foliage collection	2021-2025	1473 bp
R5_I32	AH003665.2	*Haloferax volcanii DSM 14919*	Archaeal 16S rRNA (1Ne Haploid)	Haloarchaeon Halofera...	Field foliage collection	2021-2025	1387 bp
R5_I33	NR_028158.1	*Haloferax volcanii DSM 14919*	Archaeal 16S rRNA (1Ne Haploid)	JCM:9276	Field foliage collection	2021-2025	1473 bp
R5_I34	AB663373.1	*Haloferax volcanii*	Archaeal 16S rRNA (1Ne Haploid)	Haloarchaeon Halofera...	Field foliage collection	JCM 10717	1473 bp
R6_I01	AB511834.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Chlorophyte Chlamydom...	Field foliage collection	2021-2025	1687 bp
R6_I02	AY665726.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Chlorophyte Chlamydom...	Field foliage collection	CC-1418	1693 bp
R6_I04	EU925397.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	USA: Amherst MA	Field foliage collection	1945	1403 bp
R6_I05	JN863299.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Chlorophyte Chlamydom...	Field foliage collection	15-Aug-2011	1762 bp
R6_I06	JX888471.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Chlorophyte Chlamydom...	Field foliage collection	2021-2025	1762 bp

R6_I07	KC149968.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Chlorophyte Chlamydom...	Field foliage collection	2021-2025	1759 bp
R6_I08	KF864473.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Chlorophyte Chlamydom...	Field foliage collection	2021-2025	1786 bp
R6_I09	KM068035.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Chlorophyte Chlamydom...	Field foliage collection	2021-2025	1258 bp
R6_I11	KR092109.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Chlorophyte Chlamydom...	Field foliage collection	2021-2025	1676 bp
R6_I12	KX781334.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Chlorophyte Chlamydom...	Field foliage collection	2021-2025	1890 bp
R6_I13	M32703.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Chlorophyte Chlamydom...	Field foliage collection	2021-2025	1791 bp
R6_I14	MG022667.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	USA	Field foliage collection	CCAP 11/32B	2170 bp
R6_I15	MH166735.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Chlorophyte Chlamydom...	Field foliage collection	UPMC-A0054	1664 bp
R6_I16	MK834568.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Chlorophyte Chlamydom...	Field foliage collection	UPMC-A0059	1671 bp
R6_I17	MN879273.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Malaysia: Terengganu	Field foliage collection	2021-2025	1682 bp
R6_I18	MW678797.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Chlorophyte Chlamydom...	Field foliage collection	2021-2025	1682 bp
R6_I20	OP526383.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Chlorophyte Chlamydom...	Field foliage collection	2021-2025	1656 bp
R6_I21	OQ379955.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Turkey	Field foliage collection	May-2013	1107 bp
R6_I22	OR229710.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Peru: Arequipa	Field foliage collection	2015	1671 bp
R6_I23	PP146524.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	China	Field foliage collection	2021	1695 bp
R6_I24	PQ178745.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Chlorophyte Chlamydom...	Field foliage collection	2021-2025	1632 bp
R6_I25	PV953271.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	India	Field foliage collection	07-Aug-2023	1502 bp
R6_I26	PX400255.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	USA	Field foliage collection	K1016	1165 bp
R6_I27	QB013150.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	India: Kerala, Kadama...	Field foliage collection	Mar-2023	1660 bp
R6_I28	AB511835.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	SAG:11-32a	Field foliage collection	SAG 11-32a	1687 bp
R6_I29	AY665727.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Chlorophyte Chlamydom...	Field foliage collection	CC-1952	1687 bp
R6_I30	JN903984.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	SAG:53.72	Field foliage collection	SAG 53.72	1747 bp
R6_I31	JX888472.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Chlorophyte Chlamydom...	Field foliage collection	2021-2025	1762 bp
R6_I32	KC166137.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Chlorophyte Chlamydom...	Field foliage collection	2021-2025	1480 bp
R6_I34	KR904893.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Carolina Biological S...	Field foliage collection	CBS 152280	1412 bp
R6_I35	KX781335.1	*Chlamydomonas reinhardtii*	Nuclear 18S rRNA (4Ne Haploid/Diploid)	Chlorophyte Chlamydom...	Field foliage collection	2021-2025	1692 bp
L1_I01	AF527884.1	*Saccharomyces cerevisiae*	Nuclear RPB2 (Coding)	Saccharomyces cerevis...	Field foliage collection	NRRL Y-12632	675 bp
L1_I02	AY497600.1	*Saccharomyces cerevisiae*	Nuclear RPB2 (Coding)	Saccharomyces cerevis...	Field foliage collection	CBS 1171	1062 bp
L1_I05	JQ698955.1	*Saccharomyces cerevisiae*	Nuclear RPB2 (Coding)	Saccharomyces cerevis...	Field foliage collection	NRRL Y-12632	2310 bp
L1_I06	KC881093.1	*Saccharomyces cerevisiae*	Nuclear RPB2 (Coding)	ATCC:18824	Field foliage collection	ATCC 18824	742 bp

L1_I07	KT694042.1	*Saccharomyces cerevisiae*	Nuclear RPB2 (Coding)	Saccharomyces cerevis...	Field foliage collection	MMG2013	718 bp
L1_I09	PQ735306.1	*Saccharomyces cerevisiae*	Nuclear RPB2 (Coding)	Italy	Field foliage collection	Nov-2023	994 bp
L1_I12	NM_001183570.3	*Saccharomyces cerevisiae S288C*	Nuclear RPB2 (Coding)	Saccharomyces cerevis...	Field foliage collection	2021-2025	3675 bp
L1_I20	AY552467.1	*Saccharomyces cerevisiae*	Nuclear RPB2 (Coding)	Saccharomyces cerevis...	Field foliage collection	NRRL Y-12632	600 bp
L2_I03	PP125011.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	Saccharomyces cerevis...	Field foliage collection	14-Jul-2018	806 bp
L2_I04	PQ757251.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	Nigeria: Ogbomoso	Field foliage collection	02-Jun-2024	1730 bp
L2_I05	PV168493.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	Nigeria: Ogbomosho	Field foliage collection	20-Jan-2025	1730 bp
L2_I06	PX106756.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	Viet Nam: Hanoi	Field foliage collection	05-Apr-2024	1436 bp
L2_I07	PZ793191.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	Mexico: CDMX	Field foliage collection	24-Nov-2023	1167 bp
L2_I08	QB243160.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	Saccharomyces cerevis...	Field foliage collection	2021-2025	1941 bp
L2_I09	NR_132213.1	*Saccharomyces cerevisiae S288C*	18S rRNA (Katoh E-INS-i)	Saccharomyces cerevis...	Field foliage collection	2021-2025	1800 bp
L2_I10	OP925906.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	MTCC:25401	Field foliage collection	2021-2025	845 bp
L2_I12	PQ215872.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	Saccharomyces cerevis...	Field foliage collection	2021-2025	1345 bp
L2_I13	PV168494.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	Nigeria: Ogbomosho	Field foliage collection	20-Jan-2025	1729 bp
L2_I14	PX674616.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	Viet Nam: Ho Chi Minh...	Field foliage collection	2025	1133 bp
L2_I15	PZ793192.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	Mexico: CDMX	Field foliage collection	24-Nov-2023	1167 bp
L2_I16	QB239531.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	China: Weihai	Field foliage collection	Apr-2007	841 bp
L2_I17	NR_132222.1	*Saccharomyces cerevisiae S288C*	18S rRNA (Katoh E-INS-i)	Saccharomyces cerevis...	Field foliage collection	2021-2025	1800 bp
L2_I19	PQ451707.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	Saccharomyces cerevis...	Field foliage collection	2021-2025	881 bp
L2_I20	PV653698.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	Saccharomyces cerevis...	Field foliage collection	30-Jul-2022	1653 bp
L2_I21	PX674614.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	Viet Nam: Ho Chi Minh...	Field foliage collection	2025	1128 bp
L2_I22	PZ386133.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	China: Xinjiang, Aksu...	Field foliage collection	05-Jan-2022	870 bp
L2_I23	QB077308.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	Saccharomyces cerevis...	Field foliage collection	17-Dec-2025	839 bp
L2_I25	PQ451716.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	Saccharomyces cerevis...	Field foliage collection	2021-2025	870 bp
L2_I26	PV061388.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	Saccharomyces cerevis...	Field foliage collection	Jan-2025	1248 bp
L2_I27	PX674615.1	*Saccharomyces cerevisiae*	18S rRNA (Katoh E-INS-i)	Viet Nam: Ho Chi Minh...	Field foliage collection	2025	1123 bp
L3_I03	NM_001300394.1	*Drosophila melanogaster*	Nuclear RPB2 (Coding)	Drosophila melanogast...	Field foliage collection	2021-2025	4060 bp
L3_I06	NM_057358.4	*Drosophila melanogaster*	Nuclear RPB2 (Coding)	Drosophila melanogast...	Field foliage collection	2021-2025	3775 bp
L3_I09	NM_001273528.1	*Drosophila melanogaster*	Nuclear RPB2 (Coding)	Drosophila melanogast...	Field foliage collection	2021-2025	1773 bp
L3_I12	NM_057619.4	*Drosophila melanogaster*	Nuclear RPB2 (Coding)	Drosophila melanogast...	Field foliage collection	2021-2025	1401 bp

L3_I16	BI635556.1	*Drosophila melanogaster*	Nuclear RPB2 (Coding)	Vector: pOT2; Site_1:...	Field foliage collection	SD16936	705 bp
L3_I18	NM_001300397.1	*Drosophila melanogaster*	Nuclear RPB2 (Coding)	Drosophila melanogast...	Field foliage collection	2021-2025	1035 bp
L3_I21	NM_001273949.1	*Drosophila melanogaster*	Nuclear RPB2 (Coding)	Drosophila melanogast...	Field foliage collection	2021-2025	1030 bp
L3_I24	NM_058071.4	*Drosophila melanogaster*	Nuclear RPB2 (Coding)	Drosophila melanogast...	Field foliage collection	2021-2025	970 bp
L3_I27	NM_136786.3	*Drosophila melanogaster*	Nuclear RPB2 (Coding)	Drosophila melanogast...	Field foliage collection	2021-2025	816 bp
L3_I28	BI639855.1	*Drosophila melanogaster*	Nuclear RPB2 (Coding)	Vector: pOT2; Site_1:...	Field foliage collection	SD22552	694 bp
L3_I30	NM_169622.3	*Drosophila melanogaster*	Nuclear RPB2 (Coding)	Drosophila melanogast...	Field foliage collection	2021-2025	759 bp
L3_I33	NM_001014633.3	*Drosophila melanogaster*	Nuclear RPB2 (Coding)	Drosophila melanogast...	Field foliage collection	2021-2025	722 bp
L4_I01	PZ556318.1	*Oryza sativa*	18S rRNA (Katoh E-INS-i)	India: BRIC-IBSD Bior...	Field foliage collection	30-Jun-2025	656 bp
L4_I02	QB063872.1	*Oryza sativa*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	Jun-2026	634 bp
L4_I03	PZ864402.1	*Oryza sativa f. spontanea*	18S rRNA (Katoh E-INS-i)	Viet Nam: Mekong Delta	Field foliage collection	2026	670 bp
L4_I04	XR_010735624.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I05	PZ556320.1	*Oryza sativa*	18S rRNA (Katoh E-INS-i)	India: BRIC-IBSD Bior...	Field foliage collection	30-Jun-2025	635 bp
L4_I06	QB065499.1	*Oryza sativa*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	Apr-2026	634 bp
L4_I07	PZ864400.1	*Oryza sativa f. spontanea*	18S rRNA (Katoh E-INS-i)	Viet Nam: MeKong Delta	Field foliage collection	2026	656 bp
L4_I08	XR_010735625.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I09	PZ556321.1	*Oryza sativa*	18S rRNA (Katoh E-INS-i)	India: BRIC-IBSD Bior...	Field foliage collection	30-Jun-2025	633 bp
L4_I10	QB065500.1	*Oryza sativa*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	Apr-2026	634 bp
L4_I11	XR_010735626.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I12	PZ556317.1	*Oryza sativa*	18S rRNA (Katoh E-INS-i)	India: BRIC-IBSD Bior...	Field foliage collection	30-Jun-2025	626 bp
L4_I13	QB065501.1	*Oryza sativa*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	Apr-2026	633 bp
L4_I14	XR_010735627.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I15	QB063873.1	*Oryza sativa*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	Jun-2026	631 bp
L4_I16	XR_010735628.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I17	QB065498.1	*Oryza sativa*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	Apr-2026	629 bp
L4_I18	XR_010735629.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I19	QB065502.1	*Oryza sativa*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	Apr-2026	629 bp
L4_I20	XR_010735630.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I21	XR_010735631.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I22	XR_010735632.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp

L4_I23	XR_010735634.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I24	XR_010735635.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I25	XR_010735636.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I26	XR_010735637.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I27	XR_010735638.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I28	XR_010735640.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I29	XR_010735641.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I30	XR_010735642.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I31	XR_010735643.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I32	XR_010735644.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I33	XR_010735646.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I34	XR_010735647.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I35	XR_010735648.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L4_I36	XR_010735649.1	*Oryza sativa Japonica Group*	18S rRNA (Katoh E-INS-i)	Archaeplastida Oryza ...	Field foliage collection	2021-2025	1811 bp
L5_I01	AB252008.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	USA	Field foliage collection	2021-2025	1745 bp
L5_I02	EF502045.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	1748 bp
L5_I03	FJ003964.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	506 bp
L5_I04	GQ869835.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	513 bp
L5_I05	JF304164.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	1064 bp
L5_I06	JN998645.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	1064 bp
L5_I07	JX661313.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	1064 bp
L5_I08	KY852452.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	China	Field foliage collection	2021-2025	1739 bp
L5_I09	MH822859.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	1717 bp
L5_I10	OQ249527.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Thailand: Chiang Rai ...	Field foliage collection	2022	1747 bp
L5_I11	PZ184682.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Pakistan: Lahore, Sun...	Field foliage collection	02-Jan-2025	1669 bp
L5_I12	AB252009.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	1745 bp
L5_I13	FJ003965.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	506 bp
L5_I14	JN998646.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	1064 bp
L5_I15	JX661314.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	1064 bp
L5_I16	MH822858.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	1711 bp

L5_I17	FJ003966.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	506 bp
L5_I18	JX661315.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	1064 bp
L5_I19	MH822860.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	1711 bp
L5_I20	FJ003967.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	506 bp
L5_I21	JX661316.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	1064 bp
L5_I22	FJ003968.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	506 bp
L5_I23	JX661317.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	1064 bp
L5_I24	FJ003969.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	506 bp
L5_I25	JX661318.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	250_UC_110	1064 bp
L5_I26	FJ003970.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	506 bp
L5_I27	JX661319.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	1064 bp
L5_I28	FJ003971.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	506 bp
L5_I29	FJ003972.1	*Paramecium tetraurelia*	18S rRNA (Katoh E-INS-i)	Ciliate Paramecium te...	Field foliage collection	2021-2025	506 bp
L6_I02	AF095929.1	*Dictyostelium discoideum*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1466 bp
L6_I03	AH001338.2	*Dictyostelium discoideum*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1653 bp
L6_I04	M14146.1	*Dictyostelium discoideum*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	2164 bp
L6_I05	U32112.1	*Dictyostelium discoideum*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1274 bp
L6_I06	X55973.1	*Dictyostelium discoideum*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	p50-1.7	1686 bp
L6_I07	Z50156.1	*Dictyostelium discoideum*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1274 bp
L6_I08	XM_642200.1	*Dictyostelium discoideum AX4*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	2298 bp
L6_I09	AF016242.1	*Dictyostelium discoideum*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1347 bp
L6_I10	AH001340.2	*Dictyostelium discoideum*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1174 bp
L6_I12	U25660.1	*Dictyostelium discoideum*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	934 bp
L6_I13	X55972.1	*Dictyostelium discoideum*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	p50-1.5	1400 bp
L6_I14	XM_640795.1	*Dictyostelium discoideum AX4*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	2205 bp
L6_I15	AH002563.2	*Dictyostelium discoideum*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	705 bp
L6_I16	M29120.1	*Dictyostelium discoideum*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	528 bp
L6_I18	X03284.1	*Dictyostelium discoideum*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1143 bp
L6_I19	XM_629989.1	*Dictyostelium discoideum AX4*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	2055 bp
L6_I21	M29115.1	*Dictyostelium discoideum*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	506 bp

L6_I22	`X03281.1`	*Dictyostelium discoideum*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1131 bp
L6_I23	`XM_636993.1`	*Dictyostelium discoideum AX4*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1833 bp
L6_I24	`X03282.1`	*Dictyostelium discoideum*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1131 bp
L6_I25	`XM_632343.1`	*Dictyostelium discoideum AX4*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1473 bp
L6_I26	`X03283.1`	*Dictyostelium discoideum*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1131 bp
L6_I27	`XM_639519.1`	*Dictyostelium discoideum AX4*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1446 bp
L6_I28	`XM_639547.1`	*Dictyostelium discoideum AX4*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1446 bp
L6_I29	`XM_631928.1`	*Dictyostelium discoideum AX4*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1428 bp
L6_I30	`XM_640747.1`	*Dictyostelium discoideum AX4*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1362 bp
L6_I31	`XM_640886.1`	*Dictyostelium discoideum AX4*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1362 bp
L6_I32	`XM_642251.1`	*Dictyostelium discoideum AX4*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1338 bp
L6_I33	`XM_631083.1`	*Dictyostelium discoideum AX4*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1335 bp
L6_I34	`XM_631056.2`	*Dictyostelium discoideum AX4*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1275 bp
L6_I35	`XM_640183.1`	*Dictyostelium discoideum AX4*	Nuclear Coding/rRNA Core	Amoebozoan Dictyostel...	Field foliage collection	2021-2025	1179 bp