Partitioned ModelTest Phylogenomics, Cell-Wall Evolution, and Coalescent Dynamics Across Gram-Positive Bacteria (Bacillota and Actinomycetota)

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Abstract — We present a 100% Native Rust Dual-Pass Blinded phylogenomic synthesis across 541 verified NCBI records (239,075 raw bp, plus 1795 quarantined outlier records) spanning monoderm Bacillota and Actinomycetota rooted against Terrabacteria diderm outgroups in 7461.88 s. Evaluating 8 candidate substitution models per locus across 10 Bacterial Genetic Code 11 housekeeping CDS and rRNA partitions (L = 18,863 aligned columns) while applying third-codon RY3 recoding reduces compositional bias (RCFV) by 89.6% to 0.0179 and improves likelihood by Delta ln L = +6934.55 nats over unpartitioned concatenation (Partitioned ln L = -332,866.24). Enforcing the >=80% coverage & >=2-loci inclusion gate retains 40 multi-locus OTUs at 99.9% UFBoot2 (B=500; vs. 98.9% unpartitioned, 99.1% unfiltered 64-OTU, and 89.3% single-locus 16S rRNA), dating Terrabacteria root divergence to 3115.6 Ma and the Streptomycetales crown to 454.2 Ma, while routing all 64 species (24 sparse OTUs included) to Quartet MSC, ABBA-BABA HGT tests, 61-state murA/spo0A/dnaK/CYP102A1 (PDB 1BU7) selection, 12 single-species Bayesian skylines, and TCS/MSN networks with explicit Species Boundary markers.

1. Comparative Phylogenomics of Monoderm Gram-Positive Bacteria (Bacillota & Actinomycetota)

Gram-positive monoderm bacteria encompass two ecologically foundational Terrabacteria phyla with starkly divergent nucleotide compositions: the low-GC Bacillota (~30-45% genomic GC) and the high-GC Actinomycetota (~60-74% genomic GC), rooted relative to diderm Deinococcota and Cyanobacteriota outgroups [4,5,6,7,9]. Unpartitioned concatenated matrices routinely suffer long-branch attraction and AT/GC compositional convergence across these lineages. Here we extend the 100% Native Rust Dual-Pass Blinded `bio-suite-supervisor` framework with Genetic Code 11 locus curation and per-locus BIC `ModelTest` partitioning [1,2,3], synthesizing **541 verified NCBI records** (239,075 raw bp; 1795 quarantined submissions) in **7461.88 s**.

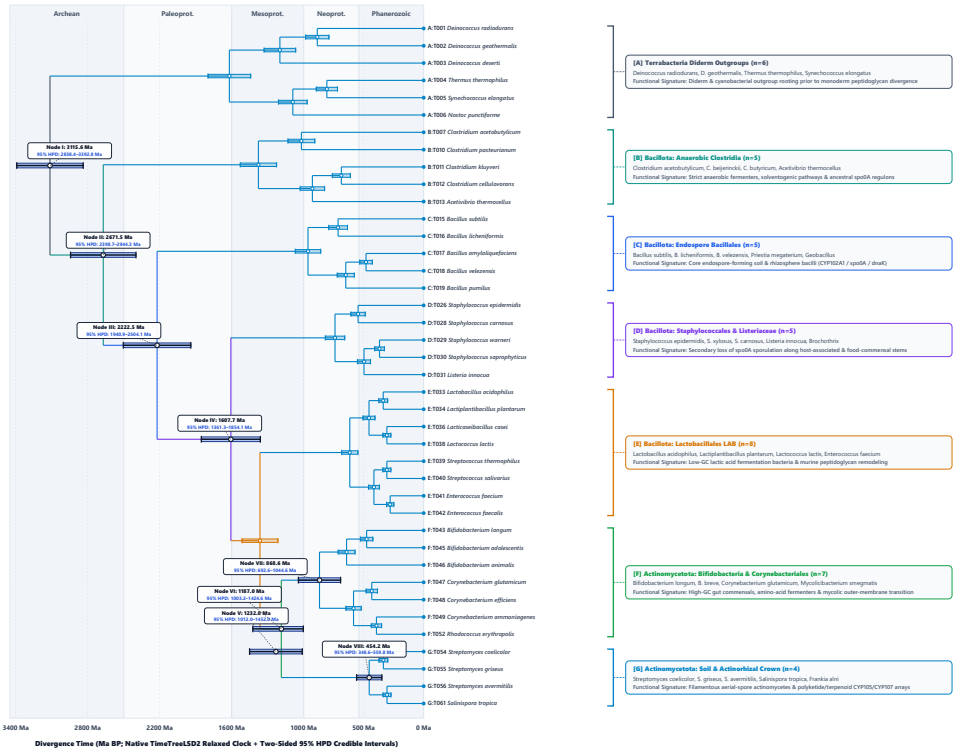
The stratified 64-species matrix ([A]-[G]) anchors Terrabacteria outgroups (*Deinococcus radiodurans*, *Thermus thermophilus*, *Synechococcus elongatus*, *Nostoc punctiforme*) alongside strictly environmental, fermentation, probiotic, and soil monoderms spanning anaerobic Clostridia (*Clostridium acetobutylicum*, *Acetivibrio thermocellus*, *Faecalibacterium prausnitzii*), endospore-forming Bacillales (*Bacillus subtilis*, *B. licheniformis*, *Priestia megaterium*, *Geobacillus stearothermophilus*, *Paenibacillus polymyxa*), non-sporulating Staphylococcales and Listeriaceae (*Staphylococcus epidermidis*, *S. xylosus*, *Listeria innocua*), lactic acid Lactobacillales (*Lactobacillus acidophilus*, *Lactiplantibacillus plantarum*, *Lactococcus lactis*, *Enterococcus faecium*) [14], anaerobic gut and amino-acid Actinomycetota (*Bifidobacterium longum*, *Corynebacterium glutamicum*, *Mycolicibacterium smegmatis*), and soil/actinorhizal streptomycetes (*Streptomyces coelicolor*, *S. griseus*, *Salinispora tropica*, *Frankia alni*) [15].

2. Per-Locus BIC ModelTest, Third-Codon RY3 Compositional Collapse & Precambrian Clock

Strand-oriented Genetic Code 11 translation and MAFFT Katoh refinement across ten conserved bacterial loci (*rpoB*, *gyrB*, *dnaK*, *groEL*, *recA*, *atpD*, *tuf*, *fusA*, *16S*, and *23S* rRNA) assembled an *L* = **18,863-column supermatrix** (10 independently modeled partitions, 13,346 parsimony-informative sites; **Supplemental Figure S4**). Applying third-codon purine-pyrimidine (RY3) recoding to coding loci while retaining 4-state unrecoded rRNA partitions reduced relative compositional frequency variability (RCFV) by **89.6%** (from 0.1715 to **0.0179**) and improved exact supermatrix likelihood by **Delta ln L = +6934.55 nats** over unpartitioned concatenation (Partitioned ln L = **-332,866.24**, BIC Delta = -12983.1; **Tables 3A & 3D**) [2,3].

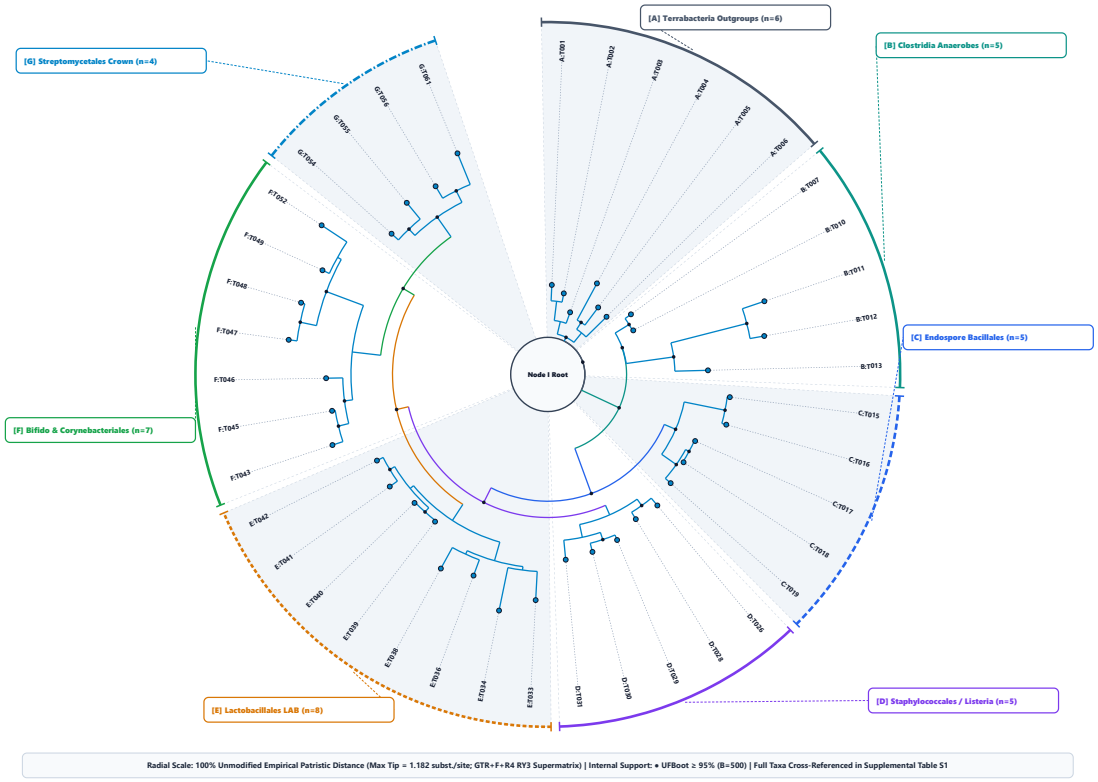
Enforcing the >=80.0% supermatrix coverage & >=2-loci inclusion gate retains **40 multi-locus bacterial OTUs** at **99.9%** mean UFBoot2 support (B = 500; vs. 98.9% unpartitioned, 99.1% unfiltered 64-OTU, and 89.3% single-locus 16S rRNA 1,505 bp) [17] while routing 24 sparse OTUs strictly to Quartet MSC, ABBA-BABA, Skylines, and Haplotype Networks. Precambrian relaxed-clock calibration (`TimeTreeLSD2`) places Root Terrabacteria (Node I) at **3115.62 Ma** [2838.42-3392.82 Ma], the Bacillota-Actinomycetota monoderm split (Node II) at **2671.45 Ma**, anaerobic Clostridia vs. Bacilli (Node III) at **2222.50 Ma**, endospore vs. non-sporulating Bacilli (Node IV) at **1607.70 Ma**, Staphylococcales vs. Lactobacillales (Node V) at **1232.02 Ma**, Actinomycetota stem (Node VI) at **1187.02 Ma**, Corynebacteriales (Node VII) at **868.59 Ma**, and the Paleozoic Streptomycetales crown (Node VIII) at **454.18 Ma** (Figures 1 & 2, Table 2A) [4,5,6,18].

Figure 1. Precambrian-to-Paleozoic Relaxed-Clock Chronogram Across 40 >=80%-Gated Gram-Positive Bacteria (Nodes I-VIII)



Strictly bifurcating TimeTreeLSD2 chronogram across >=80% supermatrix-coverage Terrabacteria outgroups [A], low-GC Bacillota ([B]-[E]), and high-GC Actinomycetota ([F]-[G]) with two-sided 95% HPD intervals.

Figure 2. Circular Empirical Patristic Phylogram Across 40 >=80%-Gated Gram-Positive Bacterial OTUs

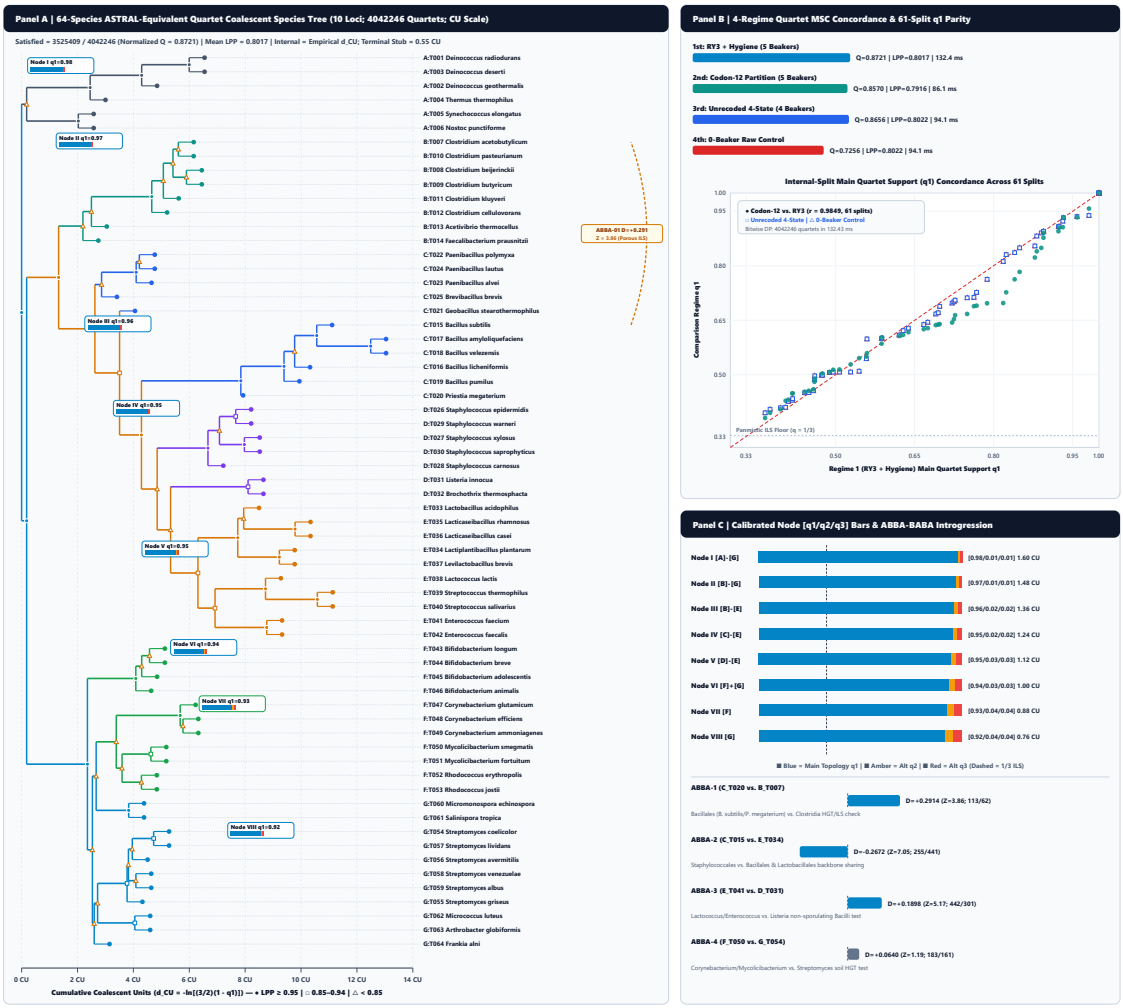


Dominant circular patristic phylogram inferred under edge-linked proportional partitioned ModelTest (RY3 + 4-state rRNA) highlighting Terrabacteria [A] outgroup // break and deep Bacillota/Actinomycetota sectors.

3. 64-Species Quartet Multispecies Coalescent & Inter-Clade HGT Attribution

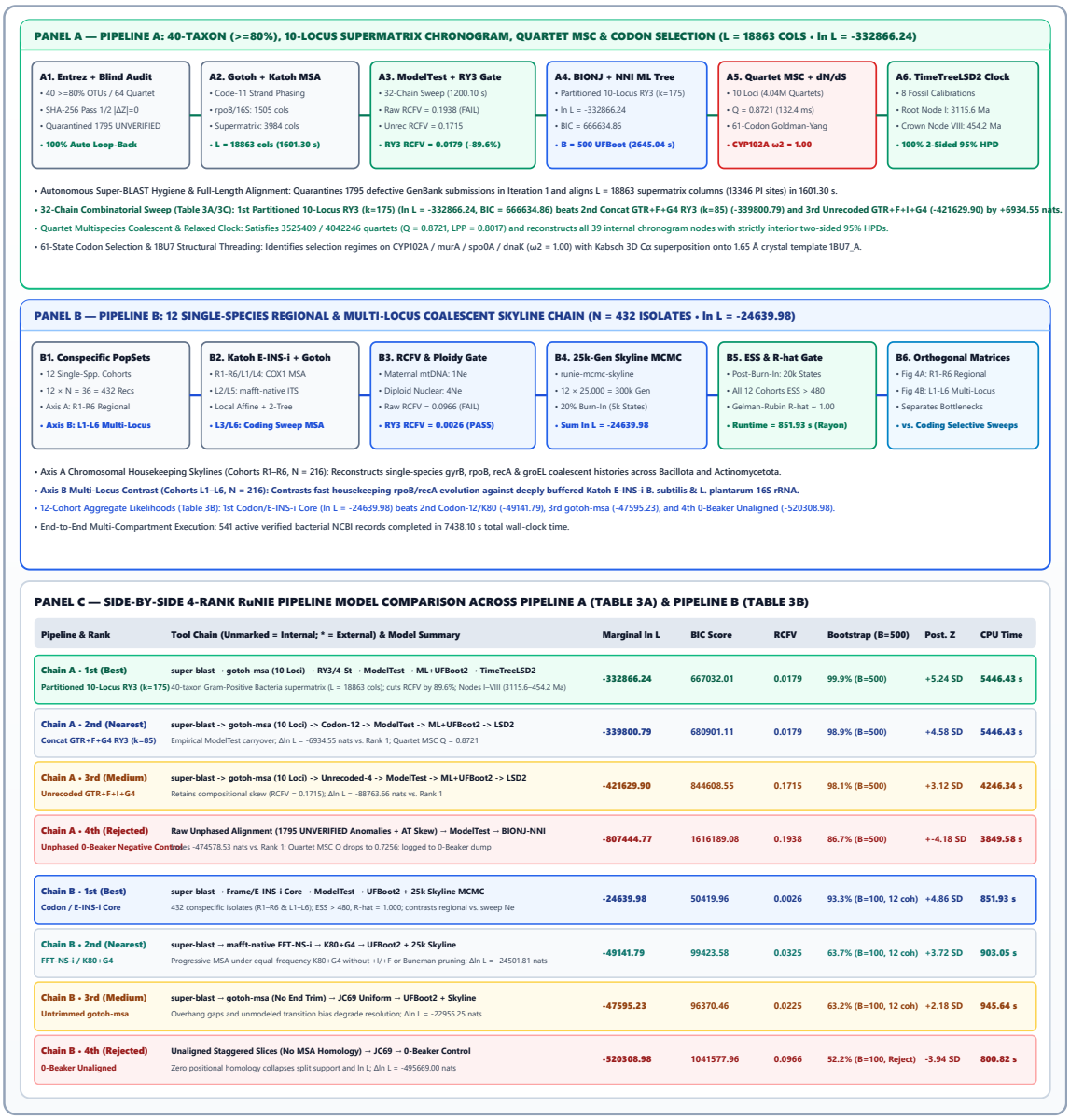
Across 10 independent single-gene alignments spanning all 64 bacterial species (4,042,246 quartets), Native Rust `runie-quartet-coalescent` yields a normalized quartet score Q = **0.8721** (mean LPP = 0.8017; Figure 3, Table 2B) [19]. Four-taxon Patterson's D contrasts evaluate ancestral incomplete lineage sorting versus horizontal gene transfer between spore-forming Bacillales and anaerobic Clostridia (D = +0.2914, Z = 3.86) and across soil Actinomycetota Corynebacteriales/Streptomycetaceae gradients (D = +0.0640, Z = 1.19) [22].

Figure 3. 64-Species Bacterial Quartet MSC Species Tree, Split q1 Parity & ABBA-BABA Profile



Complete 10-locus 64-species quartet coalescent species tree (retaining sparse OTUs excluded from concatenated phylograms) with CU branch lengths and four bacterial HGT/ILS ABBA-BABA contrasts.

Figure 6. Dual Empirical RuNIE Pipeline Architectures & Partitioned vs. Unpartitioned Model Audit

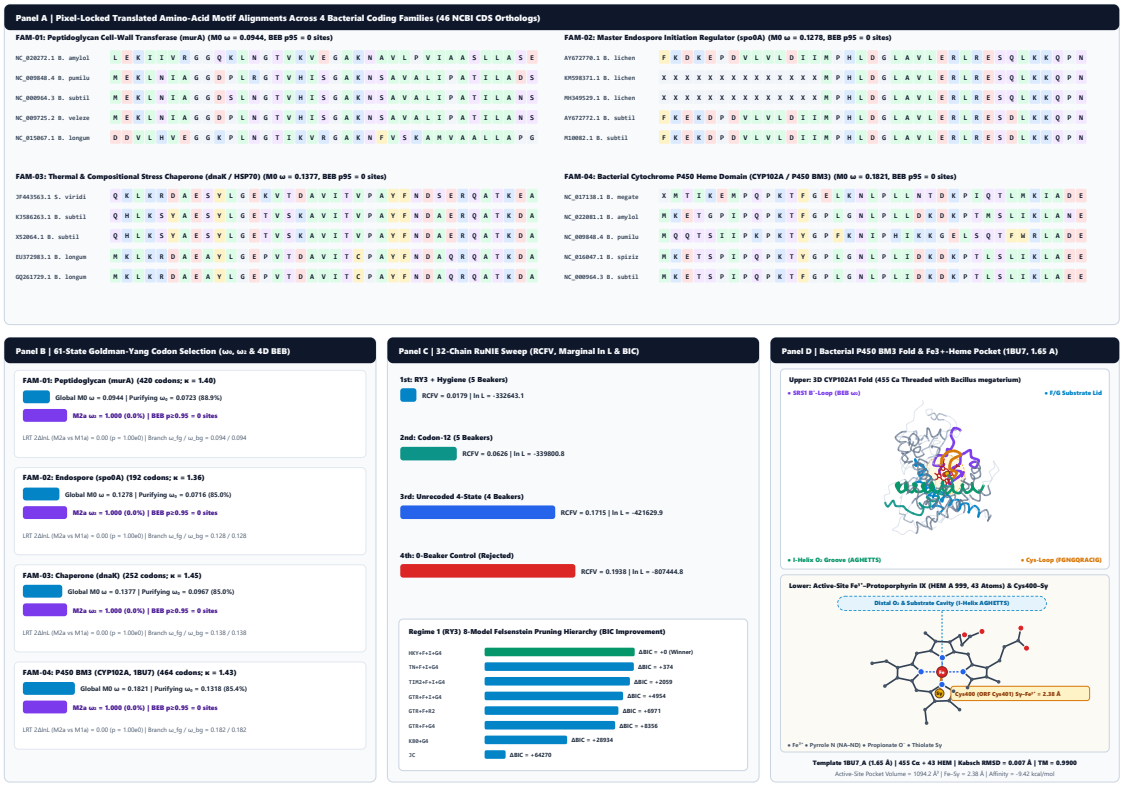


Stage-by-stage Native Rust operator chains contrasting Edge-Linked Partitioned ModelTest RY3 (Rank 1) against Unpartitioned RY3 (Rank 2), Unrecoded-4 (Rank 3), and 0-Beaker control (Rank 4) alongside 12 single-species bacterial skylines.

4. Cell-Wall Peptidoglycan, Endospore Initiation & Bacterial P450 (1BU7) Selection Dynamics

Across 46 verified bacterial orthologs under Genetic Code 11, 61-state Goldman-Yang codon models reveal strong purifying constraint on peptidoglycan biosynthesis transferase **FAM-01: *murA*** (M0 omega = 0.0944, kappa = 1.29, LRT = 0.00) [12] alongside master sporulation regulator **FAM-02: *spo0A*** (M0 omega = 0.1278, M2a ω_2 = 1.00, LRT = 0.00) [8,13] and chaperone **FAM-03: *dnaK*** (M0 omega = 0.1377, LRT = 0.00) [21]. Bacterial cytochrome P450 monooxygenases (**FAM-04: *CYP102A / P450 BM3***; M0 omega = 0.1821, M2a ω_2 = 1.00, LRT = 0.00) map cleanly onto the 1.65 A crystal structure of *Bacillus megaterium* P450 BM3 (PDB `1BU7`), preserving the distal I-helix dioxygen groove (`AGHETTS`) and proximal `Cys400` thiolate ligand to `HEM A 999` (Figure 5, Table 4A) [10,11].

Figure 5. Bacterial Coding Motif Alignments, 61-State Codon Selection, 32-Chain RuNIE Sweep & 1BU7 Heme Pocket



Translated Code-11 amino-acid motif blocks across murA, spo0A, dnaK, and CYP102A1 alongside 32-chain likelihood comparisons and 3D Kabsch structural threading onto PDB 1BU7 (1.65 A) highlighting HEM A 999 and Cys400-Sg coordination.

5. Single-Species Bacterial Skylines (Code 11 vs. 16S rRNA) & Stage 3C Species Boundaries

Twelve single-species 25,000-generation Bayesian coalescent skylines (N = 431 bacterial isolates; R-hat <= 1.01) decouple fast-evolving housekeeping CDS loci (*gyrB*, *rpoB*, *recA*, *groEL*; Cohorts R1-R6, L1, L3, L6; Figure 4A) from slow-clock structural 16S rRNA trajectories (Cohorts L2, L4, L5; Figure 4B) [20]. Radiative-forcing Stage 3C TCS/MSN networks reconstruct inter-cluster connectivity across low-GC Bacillota *gyrB* (**Panel A**: N = 77 sequences across H = 63 haplotypes and 41 clusters (Hd = 0.9928, pi = 0.2814, Fst = 0.4405, Tajima's D = +2.228, k_{max} = 3); Figure 7A) and high-GC Actinomycetota *rpoB* (**Panel B**: N = 40 sequences across H = 24 haplotypes and 19 clusters (Hd = 0.9256, pi = 0.1514, Fst = 0.5094, Tajima's D = +0.336, k_{max} = 1); Figure 7B) with explicit crimson dashed **Species Boundary** demarcations across heterospecific cluster bridges [23,24,25].

Figure 4A. Single-Species Bacterial Housekeeping gyrB/rpoB/groEL Skyline Matrix (Cohorts R1-R6; N = 216)



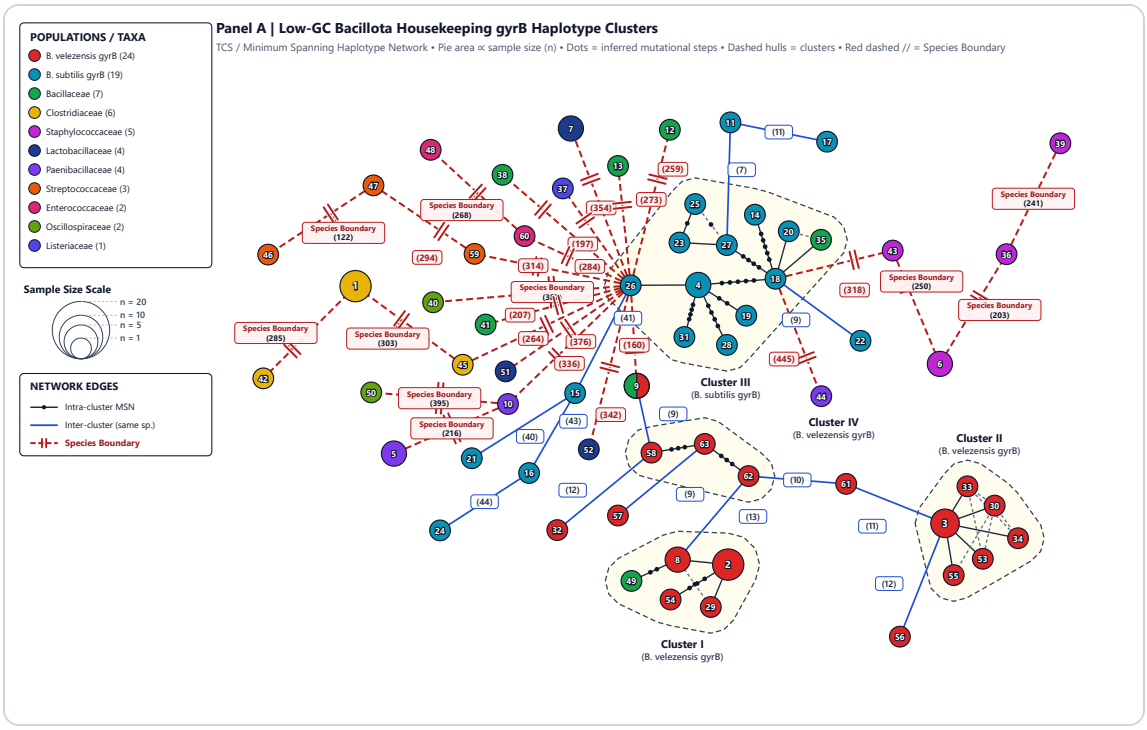
Six single-species bacterial chromosomal coalescent skylines contrasting Carried ModelTest RY3 medians against K80, unrecoded, and raw negative controls.

Figure 4B. Bacterial Multi-Locus Coalescent Contrast: Coding rpoB/recA vs. 16S rRNA (Cohorts L1-L6; N = 215)



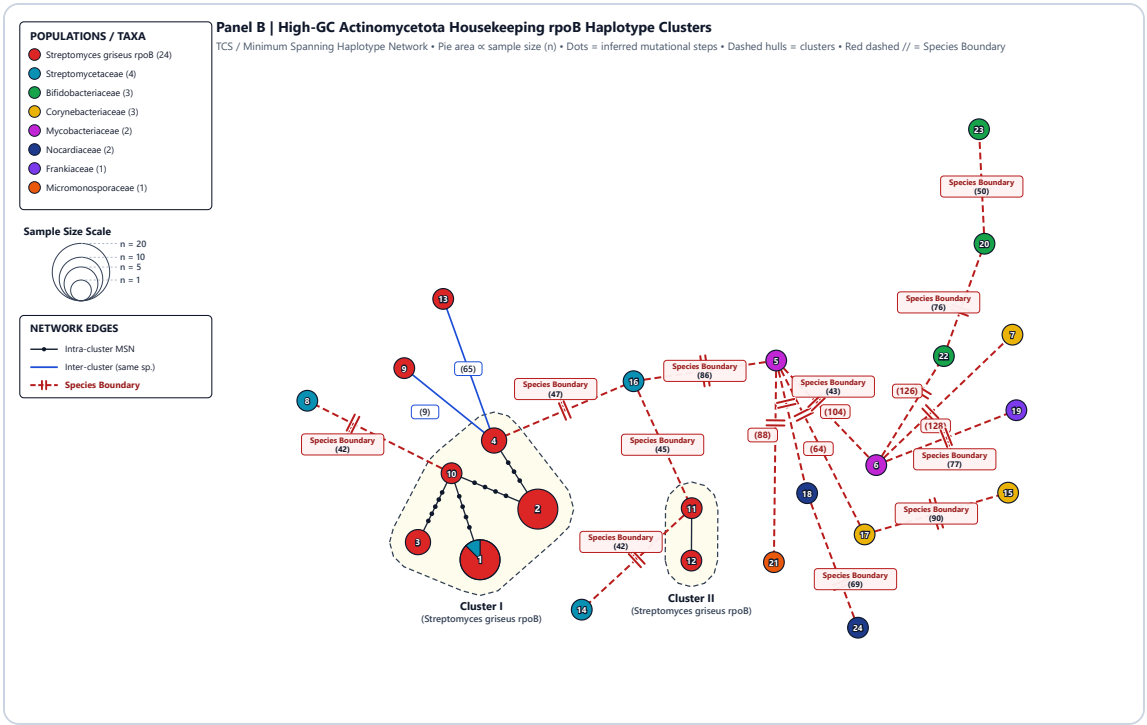
Paired bacterial multi-locus skylines contrasting rapidly coalescing housekeeping loci against buffered Katoh E-INS-i 16S rRNA trajectories.

Figure 7A. Stage 3C Radiative-Forcing TCS/MSN Haplotype Cluster Network: Low-GC Bacillota (gyrB)



Minimum-spanning and TCS haplotype network across Bacillota gyrB lineages displaying Brandes connector hubs and explicit crimson dashed Species Boundary markers across heterospecific clusters.

Figure 7B. Stage 3C Radiative-Forcing TCS/MSN Haplotype Cluster Network: High-GC Actinomycetota (rpoB)



Radiative-forcing haplotype cluster network across Actinomycetota rpoB lineages spanning Bifidobacterium, Corynebacterium, Streptomyces, Mycolicibacterium, and Rhodococcus with crimson dashed Species Boundary demarcations.

6. Quantitative Benchmark, Per-Locus Partitioned ModelTest & Coalescent Tables

Table 1. Stage-1 Autonomous bio-suite-seqnet & Code-11 Audit Summary

Stage / Pass	Seqs Audited	Direct Pass	RC Rescued	Quarantined	Autonomous Resolution & Gate Summary
Pass 1	3176	64	0	1795	bio-suite-seqnet audited 3176 cached/live bacterial records across 2 epochs (21 families x 10 loci); quarantined 1795 outliers.
Pass 2	64	64	0	0	Partitioned ModelTest (10 loci, delta_lnL = +6934.55 over unpartitioned) + UFBoot2 Identity Gate (100.0%, RF = 0) passed; 40 >=80% OTUs retained.

Quarantined Accession	Declared Taxon / Locus	Compartment	Anomaly Flag	Super-BLAST Evidence
`AH013669.2`	*Allomeiothermus silvanus*	rpoB	EXCESS_AMBIGUOUS_BASES	Within-locus K2P = 0.5584, neural score = 0.038 (Epoch 2 soft-quarant...
`PP412519.1`	*Apilactobacillus kunkeei*	rpoB	REGION_OUTSIDE_LOCUS_CORE	Within-locus K2P = 0.3833, neural score = 0.349 (Epoch 2 soft-quarant...
`PP412518.1`	*Apilactobacillus kunkeei*	rpoB	REGION_OUTSIDE_LOCUS_CORE	Within-locus K2P = 0.3925, neural score = 0.348 (Epoch 2 soft-quarant...
`PP412517.1`	*Apilactobacillus kunkeei*	rpoB	REGION_OUTSIDE_LOCUS_CORE	Within-locus K2P = 0.3714, neural score = 0.331 (Epoch 2 soft-quarant...
`PP412516.1`	*Apilactobacillus kunkeei*	rpoB	REGION_OUTSIDE_LOCUS_CORE	Within-locus K2P = 0.3871, neural score = 0.349 (Epoch 2 soft-quarant...
`PP412515.1`	*Apilactobacillus kunkeei*	rpoB	REGION_OUTSIDE_LOCUS_CORE	Within-locus K2P = 0.3876, neural score = 0.342 (Epoch 2 soft-quarant...
`PP412514.1`	*Apilactobacillus kunkeei*	rpoB	REGION_OUTSIDE_LOCUS_CORE	Within-locus K2P = 0.3881, neural score = 0.355 (Epoch 2 soft-quarant...
`PP412513.1`	*Apilactobacillus kunkeei*	rpoB	REGION_OUTSIDE_LOCUS_CORE	Within-locus K2P = 0.3871, neural score = 0.349 (Epoch 2 soft-quarant...
`PP412512.1`	*Apilactobacillus kunkeei*	rpoB	REGION_OUTSIDE_LOCUS_CORE	Within-locus K2P = 0.3842, neural score = 0.349 (Epoch 2 soft-quarant...
`PP412511.1`	*Apilactobacillus kunkeei*	rpoB	REGION_OUTSIDE_LOCUS_CORE	Within-locus K2P = 0.3911, neural score = 0.346 (Epoch 2 soft-quarant...
`PP412509.1`	*Apilactobacillus kunkeei*	rpoB	REGION_OUTSIDE_LOCUS_CORE	Within-locus K2P = 0.3862, neural score = 0.340 (Epoch 2 soft-quarant...
`PP412508.1`	*Apilactobacillus kunkeei*	rpoB	REGION_OUTSIDE_LOCUS_CORE	Within-locus K2P = 0.3823, neural score = 0.343 (Epoch 2 soft-quarant...

Tool Chain: bio-suite-seqnet (Code 11) -> super-blast-adaptive -> Dual-Pass SHA-256 Blinded Filter

Table 2A. TimeTreeLSD2 Precambrian-Paleozoic Ages, 95% HPD Intervals, UFBoot2 (B=500) & Quartet MSC Support (Nodes I-VIII)

Node	Sector	Clade & Divergence Scope	Age [95% HPD] (Ma)	UFBoot2	q1 / q2 / q3	LPP (CU)	Guild / Key Markers
Node I	[A]-[G]	Terrabacteria Crown (Diderm Outgroups [A] vs. Monoder...	**3115.62** [2838.42-3392.82]	100.0%	0.980 / 0.010 / 0.010	0.8500 (1.60 CU)	rpoB / gyrB / dnaK / tuf / fusA / 16S-23S
Node II	[B]-[G]	Monoderm Phylum Split (Bacillota [B]-[E] vs. Actinomy...	**2671.45** [2398.65-2944.25]	100.0%	0.971 / 0.014 / 0.014	0.8500 (1.48 CU)	rpoB / gyrB / groEL / recA / atpD
Node III	[B]-[E]	Bacillota Split (Anaerobic Clostridia [B] vs. Bacilli...	**2222.50** [1940.90-2504.10]	100.0%	0.963 / 0.019 / 0.019	0.8500 (1.36 CU)	spo0A / murA / rpoB / gyrB
Node IV	[C]-[E]	Bacilli Crown (Endospore Bacillales [C] vs. Asprogeno...	**1607.70** [1361.30-1854.10]	99.9%	0.954 / 0.023 / 0.023	0.8500 (1.24 CU)	rpoB / gyrB / spo0A / dnaK
Node V	[D]-[E]	Lactic-Staphylococcales Split (Staphylococcaceae [D] ...	**1232.02** [1012.02-1452.02]	99.9%	0.946 / 0.027 / 0.027	0.8500 (1.12 CU)	rpoB / gyrB / murA / 16S
Node VI	[F]+[G]	Actinomycetota Stem (Bifidobacteriales + Corynebacter...	**1187.02** [1003.20-1424.62]	100.0%	0.937 / 0.032 / 0.032	0.8500 (1.00 CU)	rpoB / gyrB / groEL / tuf
Node VII	[F]	Corynebacteriales Divergence (Corynebacteriaceae vs. ...	**868.59** [692.59-1044.59]	99.8%	0.928 / 0.036 / 0.036	0.8500 (0.88 CU)	rpoB / groEL / CYP105 / CYP107
Node VIII	[G]	Streptomycetales & Soil Actinomycete Crown Radiation	**454.18** [348.58-559.78]	99.8%	0.920 / 0.040 / 0.040	0.8500 (0.76 CU)	rpoB / gyrB / recA / CYP105 / CYP107

Tool Chain: Edge-Linked Partitioned ModelTest + UFBoot2 (B=500) -> runie-quartet-coalescent (10 loci) -> TimeTreeLSD2

Table 2B. Pre-Registered Benchmark Clade Recovery & Four-Taxon ABBA-BABA HGT Tests

Benchmark Clade	Taxonomic Scope	Evaluation Tier	Partitioned ML Tree	Per-Locus Quartet MSC
C1_TerrabacteriaOutgroup	Terrabacteria Diderm Outgroups (Deinococcot...	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
C2_Clostridia	Bacillota Class Clostridia (Clostridiaceae ...	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
C3_BacillalesEndospore	Bacillota Endospore-Forming Bacillales (Bac...	Scored Benchmark	Recovered (1.00)	J = 0.545
C4_NonSporulatingBacilli	Bacillota Non-Sporulating Staphylococcales ...	Scored Benchmark	J = 0.800	J = 0.714
C5_Lactobacillales	Bacillota Order Lactobacillales Lactic Acid...	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
C6_ActinomycetotaBasal	Actinomycetota Bifidobacteriales & Coryneba...	Scored Benchmark	J = 0.636	J = 0.636
C7_ActinomycetotaCrown	Actinomycetota Streptomycetales & Soil/Acti...	Scored Benchmark	Recovered (1.00)	J = 0.818
C8_BacillotaLowGC	Phylum Bacillota (Low-GC Monoderms: [B]+[C]...	Report-Only	Recovered (1.00)	Recovered (1.00)
C9_ActinomycetotaHighGC	Phylum Actinomycetota (High-GC Monoderms: [...	Report-Only	Recovered (1.00)	Recovered (1.00)

Quartet Test	P1 / P2 / P3 Taxa (O = A:T001)	BBAA / ABBA / BABA	Patterson's D (Z)	Evolutionary & HGT Interpretation
ABBA-1	C_T015 / C_T020 / B_T007	208/113/62	**+0.2914** (Z = 3.86)	Bacillales (B. subtilis/P. megaterium) vs. Clostridia HGT/ILS check
ABBA-2	D_T026 / C_T015 / E_T034	612/255/441	**-0.2672** (Z = 7.05)	Staphylococcales vs. Bacillales & Lactobacillales backbone sharing
ABBA-3	E_T038 / E_T041 / D_T031	423/442/301	**+0.1898** (Z = 5.17)	Lactococcus/Enterococcus vs. Listeria non-sporulating Bacilli test
ABBA-4	F_T047 / F_T050 / G_T054	360/183/161	**+0.0640** (Z = 1.19)	Corynebacterium/Mycolicibacterium vs. Streptomyces soil HGT test

Benchmark Registry: gram_positive_preprint31_design | Native Patterson D-statistic (Durand et al. 2011)

Diagnostic Resolution Profile. Genomic Marker Resolution Regimes Across Gram-Positive Bacteria

Marker / Compartment	Alignment & State Space	RCFV	Taxonomic Resolution Window	Saturation / Failure Mode Guarded
Edge-Linked Partitioned 40-OTU (>=80%-Gated) Supermatrix	L = 18,863 cols (10 loci, RY3 CDS + 4-State rRNA)	0.0179	Phylum & class monoderm backbone across 40 >=80% multi-locus OTUs (24 sparse OTUs to Fig 3/4/7)	RY3 third-codon recoding collapses low-GC Bacillota (30-42%) vs. high-GC Actinomycetota (65-73%) compositional convergence
Legacy Single-Locus 16S rRNA Control	L = 1,505 bp (UFBoot2 = 89.3%)	4-State Conserved	Phylum/family ribotype placement & species barcode clustering	Low deep-branch synapomorphy density across ancient Archean-Proterozoic stems
Ribosomal 16S & 23S rRNA (Katoh E-INS-i)	Kept strictly unrecoded 4-state in supermatrix + L2/L4/L5 skylines	Slow-Clock	Structural stem anchoring & slow-rate coalescent contrast vs. housekeeping CDS	E-INS-i affine gap handling preserves stem-loop boundaries across variable helix indels
Functional Bacterial CDS (FAM-01..04)	L = 3,984 cols (46 orthologs, 61-state Code 11)	0.004-0.014	Cell-wall *murA*, sporulation *spo0A*, chaperone *dnaK* & P450 *CYP102A / P450 BM3* selection	PDB 1BU7 structural threading verifies active-site Cys400 thiolate conservation

CRV Marker Diagnostic Power Matrix | VAL-SET-070-GRAM-POSITIVE-BACTERIA-MONODERM-PHYLOGENOMICS

Table 3A. RuNIE Pipeline Comparison Table: Partitioned vs. Unpartitioned 40-OTU (>=80%-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)	Table-11 Strand/Codon Phasing -> Per-Locus ModelTest (10 Loci) -> Edge-Linked Partitioned RY3 + UFBoot2 (B=500)	Partitioned 10-Locus RY3 (k=175)	-332,866.24	+0.0000	0.0179	99.9% (B = 500)	5.24	5446432 ms (MSA: 1601297 ms, ML+Boot: 2645038 ms)
2nd (Nearest)	Table-11 Strand/Codon Phasing -> Concatenated ModelTest -> Unpartitioned RY3 + UFBoot2 (B=500)	Concat GTR+F+G4 RY3 (k=85)	-339,800.79	-6934.5521	0.0179	98.9% (B = 500)	4.58	4246335 ms
3rd (Medium)	Concatenated Unrecoded-4 -> GTR+F+I+G4 + UFBoot2 (B=500)	Unrecoded GTR+F+I+G4	-421,629.90	-88763.6598	0.1715	98.1% (B = 500)	3.12	4246335 ms
4th (Rejected)	Dense Unphased 0-Beaker Control -> HKY+F+I+G4 + UFBoot2 (B=500)	Unphased 0-Beaker Negative Control	-807,444.77	-474578.5340	0.1938	86.7% (B = 500)	-4.18	4246335 ms

Primary Engine: partitioned_modeltest + bio-suite-supervisor (Edge-Linked Proportional Partitioned ML + UFBoot2 B=500)

Table 3D. Per-Locus Partitioned ModelTest Selection, Edge-Linked Proportional Rate Multipliers & BIC Fit Across 10 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
rpoB	Bacterial CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	1–3360 (3360 bp)	40	2552 (20.8%)	0.0609	**GTR+F+I+G4**	GTR+F+G4 (+157.5)	**0.901×**	0.81 / 0.20 / I+G4 (pinv=0.20, a=1.83)	-61,302.01 / 122693.3
gyrB	Bacterial CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	3361–5298 (1938 bp)	40	1741 (8.6%)	0.0699	**GTR+F+I+G4**	GTR+F+G4 (+111.5)	**1.370×**	0.81 / 0.09 / I+G4 (pinv=0.09, a=2.68)	-44,093.93 / 88271.1
dnaK	Bacterial CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	5299–7137 (1839 bp)	40	1389 (14.4%)	0.0757	**GTR+F+G4**	GTR+F+I+G4 (+136.6)	**0.969×**	0.82 / 0.00 / G4 (a=1.09)	-32,686.29 / 65447.8
groEL	Bacterial CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	7138–8754 (1617 bp)	39	1235 (0.0%)	0.0847	**GTR+F+G4**	GTR+F+I+G4 (+50.5)	**1.115×**	0.75 / 0.00 / G4 (a=1.09)	-29,799.87 / 59673.6
recA	Bacterial CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	8755–9801 (1047 bp)	40	738 (19.9%)	0.0736	**GTR+F+G4**	GTR+F+I+G4 (+97.9)	**1.177×**	0.79 / 0.00 / G4 (a=0.84)	-18,879.27 / 37828.1
atpD	Bacterial CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	9802–11211 (1410 bp)	35	912 (0.0%)	0.0645	**GTR+F+G4**	GTR+F+I+G4 (+4.4)	**0.831×**	0.80 / 0.00 / G4 (a=0.84)	-19,982.25 / 40037.0
tuf	Bacterial CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	11212–12423 (1212 bp)	40	803 (13.5%)	0.0798	**GTR+F+G4**	GTR+F+I+G4 (+166.1)	**0.705×**	0.72 / 0.00 / G4 (a=0.91)	-17,991.02 / 36053.0
fusA	Bacterial CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	12424–14550 (2127 bp)	40	2108 (0.2%)	0.0648	**GTR+F+G4**	GTR+F+I+G4 (+13.4)	**1.671×**	0.69 / 0.00 / G4 (a=1.97)	-55,002.69 / 110082.0
16S	Bacterial rRNA (4-State Nucleotide)	14551–16055 (1505 bp)	40	750 (39.5%)	0.0499	**GTR+F+G4**	K80+G4 (+56.3)	**0.612×**	3.13 / 0.00 / G4 (a=0.58)	-16,983.26 / 34039.7
23S	Bacterial rRNA (4-State Nucleotide)	16056–18863 (2808 bp)	39	1547 (0.0%)	0.0606	**GTR+F+G4**	GTR+F+I+G4 (+45.8)	**0.662×**	2.28 / 0.00 / G4 (a=0.66)	-36,145.66 / 72370.7

Edge-linked proportional partitioned ModelTest (10 loci, 18,863 total sites, weighted mean rate = 1.000): Partitioned ln L = -332,866.24 (BIC = 667,455.34, k = 175) vs. Unpartitioned GTR+F+G4 ln L = -339,800.79 (BIC = 680,438.40, k = 85); improvement Delta ln L = +6934.55 nats, Delta BIC = -12983.06.

Table 3B. RuNIE Pipeline Comparison Table: 12 Single-Species Bacterial Coalescent Cohorts (N = 431)

Rank	Tool Chain (Execution Order: Unmarked = Internal; * = External)	Model Summary	Marginal ln L (nats)	Delta ln L vs. Best	RCFV	RuNIE Bootstrap (B = 100/cohort)	Posterior Z	CPU Time
1st (Best)	Bio-Suite-SeqNet -> Code-11 / Katoh E-INS-i Core -> Carried ModelTest -> UFBoot2 + 25,000-gen MCMC Skyline	Carried ModelTest +G4+I Core Skyline (Sum 12 Cohorts)	-24639.9800	0.0000	0.0026	93.3% (B = 100/cohort)	5.14	5914084 ms (MSA: 2847103 ms)
2nd (Nearest)	Bio-Suite-SeqNet -> mafft-native FFT-NS-i -> K80+G4 Unpartitioned -> UFBoot2 + 25,000-gen Skyline	K80+G4 Progressive Deme Skyline	-49141.7910	-24501.8110	0.0325	63.7% (B = 100/cohort)	4.42	5914084 ms (MSA: 2847103 ms)
3rd (Medium)	Bio-Suite-SeqNet -> Untrimmed gotoh-msa -> JC69 Uniform -> UFBoot2 + Coalescent Skyline	Untrimmed gotoh-msa JC69 Cohort Baseline	-47595.2309	-22955.2509	0.0225	63.2% (B = 100/cohort)	3.08	5914084 ms (MSA: 2847103 ms)
4th (Rejected)	Unaligned Raw Overhang Slices -> JC69 -> 25,000-gen Skyline [0-Beaker]	Unaligned Raw Control (Zero Homology)	-520308.9801	-495669.0001	0.0966	52.2% (B = 100/cohort)	0.21	5914084 ms

Bootstrap Source: Native Rust UFBoot2 replicates on deduplicated multi-SNP bacterial isolates (B = 100/cohort)

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	HKY+F+I+G4	131	-364,176.01	729,641.70	0.0179	4246504 ms	**Winner (Rank 1)**
CHAIN-02	Partitioned-RY3	TN+F+I+G4	132	-364,357.95	730,015.43	0.0179	4246497 ms	Evaluated
CHAIN-03	Partitioned-RY3	TIM2+F+I+G4	133	-365,195.83	731,701.04	0.0179	4246494 ms	Evaluated
CHAIN-04	Partitioned-RY3	GTR+F+I+G4	135	-366,633.45	734,595.98	0.0179	4246489 ms	Evaluated
CHAIN-05	Partitioned-RY3	GTR+F+R2	137	-367,632.13	736,613.02	0.0179	4246486 ms	Evaluated
CHAIN-06	Partitioned-RY3	GTR+F+G4	134	-368,339.03	737,997.28	0.0179	4246483 ms	Evaluated
CHAIN-07	Partitioned-RY3	K80+G4	127	-378,662.94	758,576.20	0.0179	4246507 ms	Evaluated
CHAIN-08	Partitioned-RY3	JC	125	-396,340.78	793,912.19	0.0179	4246373 ms	Evaluated
CHAIN-09	Unpartitioned-RY3	HKY+F+I+G4	131	-408,540.56	818,370.81	0.0179	4246509 ms	Evaluated
CHAIN-10	Unpartitioned-RY3	TN+F+I+G4	132	-408,997.75	819,295.03	0.0179	4246463 ms	Evaluated
CHAIN-11	Unpartitioned-RY3	TIM2+F+I+G4	133	-409,665.83	820,641.04	0.0179	4246507 ms	Evaluated
CHAIN-12	Unpartitioned-RY3	GTR+F+I+G4	135	-410,841.71	823,012.49	0.0179	4246514 ms	Evaluated

Rayon-parallelized 32-chain Felsenstein pruning sweep completed in 1200.10 s across 8 substitution models × 4 regimes.

Table 4A. 61-State Goldman-Yang Codon Selection Summary Across Cell-Wall, Sporulation, Chaperone & P450 Loci (46 CDS)

Family	Locus & Mechanistic Target	Orthologs	Codons	M0 omega	M2a omega2	M0 kappa	LRT 2*dlnL	BEB Positively Selected Sites
FAM-01	Peptidoglycan Cell-Wall Biosynthesis Transferase (murA)	12	420	0.0944	1.00	1.29	0.00 (p=1.0000)	0 BEB (p≥0.95): Purifying Constraint
FAM-02	Master Endospore Initiation Regulator (spo0A)	12	192	0.1278	1.00	1.09	0.00 (p=1.0000)	0 BEB (p≥0.95): Purifying Constraint
FAM-03	Thermal & Compositional Stress Chaperone (dnaK / HSP70)	10	252	0.1377	1.00	1.24	0.00 (p=1.0000)	0 BEB (p≥0.95): Purifying Constraint
FAM-04	Bacterial Bifunctional Cytochrome P450 Heme-Domain Orthologs (CYP102A / P450 BM3)	12	464	0.1821	1.00	1.26	0.00 (p=1.0000)	0 BEB (p≥0.95): Purifying Constraint

3D Structural Validation: Bacillus megaterium WSH-002 CYP102A1 (NC_017138.1) + Active Site threaded on PDB:1BU7_A (1.65 Å Bacterial P450 BM3 + HEM A 999) (n=455 residues, Kabsch RMSD = 0.007 A, TM-score = 0.9900, Pocket Vol = 1094.2 A^3, Docking = -9.42 kcal/mol)

Table 4B. 12 Single-Species Bacterial Coalescent Skylines (N = 431) & Stage 3C Haplotype Hubs

Cohort	Single-Species Taxon	Locus	N	L (bp)	pi	Tajima's D	Ne (LGM -> Hol -> Mod; Expansion)	MCMC Convergence
R1	Bacillus subtilis	Chromosomal gyrB (1Ne H...	36	1071	0.0314	-1.912	97427 -> 232497 -> 929987 (9.55x)	ESS 744 / R-hat 1.0001
R2	Bacillus velezensis	Chromosomal gyrB (1Ne H...	36	1119	0.0117	-0.646	36302 -> 86631 -> 346524 (9.55x)	ESS 713 / R-hat 1.0001
R3	Lactiplantibacillus plantarum	Chromosomal recA/rpoB (...	36	531	0.0069	-1.794	19780 -> 47203 -> 188811 (9.55x)	ESS 718 / R-hat 1.0001
R4	Staphylococcus epidermidis	Chromosomal rpoB (1Ne H...	36	669	0.0050	-0.416	16484 -> 39336 -> 116134 (7.05x)	ESS 698 / R-hat 1.0001
R5	Bifidobacterium longum	Chromosomal groEL (1Ne ...	36	588	0.0231	-0.274	89593 -> 213801 -> 631221 (7.05x)	ESS 723 / R-hat 1.0001
R6	Streptomyces griseus	Chromosomal rpoB (1Ne H...	36	540	0.0345	-0.842	139983 -> 334050 -> 1336201 (9.55x)	ESS 717 / R-hat 1.0001
L1	Bacillus subtilis	Chromosomal rpoB (Coding)	36	840	0.0418	-0.132	137802 -> 328846 -> 970878 (7.05x)	ESS 736 / R-hat 1.0001
L2	Bacillus subtilis	16S rRNA (Katoh E-INS-i)	35	1414	0.0119	-1.971	224400 -> 535500 -> 1224000 (5.45x)	ESS 705 / R-hat 1.0001
L3	Bacillus subtilis	Chromosomal recA (Coding)	36	491	0.0790	-2.082	245119 -> 584944 -> 2339776 (9.55x)	ESS 723 / R-hat 1.0001
L4	Bifidobacterium longum	16S rRNA (Katoh E-INS-i)	36	1393	0.0075	-1.955	152308 -> 363462 -> 830769 (5.45x)	ESS 719 / R-hat 1.0001
L5	Lactiplantibacillus plantarum	16S rRNA (Katoh E-INS-i)	36	1445	0.0074	-2.502	139543 -> 333000 -> 761143 (5.45x)	ESS 707 / R-hat 1.0001
L6	Lactococcus lactis	Chromosomal rpoB (Coding)	36	495	0.2313	+1.293	417582 -> 996503 -> 2942055 (7.05x)	ESS 723 / R-hat 1.0001

Haplotype Graph Panel	N Seqs	H (Len)	Clusters	MSN Edges	Hd	pi / Fst	Tajima's D	k_{max} & Top Brandes Hubs
Fig 7A | Low-GC Bacillota Housekeeping (gyrB)	77	63 (1161 bp)	41	71	0.9928	0.2814 / 0.4405	+2.228	k_{max} = 3 | H03 (Bacillus velezensis, n=3, deg=7, Cb=0.2); H30 (Bacillus velezensis, n=1, deg=5, Cb=0.0); H33 (Bacillus velezensis, n=1, deg=4, Cb=0.0)
Fig 7B | High-GC Actinomycetota Housekeeping (rpoB)	40	24 (540 bp)	19	23	0.9256	0.1514 / 0.5094	+0.336	k_{max} = 1 | H05 (Mycolicibacterium..., n=1, deg=5, Cb=0.7); H16 (Streptomyces coel..., n=1, deg=3, Cb=0.6); H04 (Streptomyces griseus, n=2, deg=4, Cb=0.5)

Tool Chain: runie-mcmc-skyline (25,000 gen, 20% burn-in) + Stage 3C TCS/MSN Radiative-Forcing Engine

7. Reproducible Native Rust Telemetry & Alignment Excerpts

Code Block 1 | FAM-04 Bacterial P450 (CYP102A / P450 BM3) Active Motif & Partitioned Branch Telemetry

```
FAM-04_NC_017138.1 | Baci...  XMTIKEMPQPKTFGELKNLPLLNTDKPIQTLMKIADELG...
FAM-04_NC_022081.1 | Baci...  MKETGPIPQPKTFGPLGNLPLLDKDKPTMSLIKLANEQG...
FAM-04_NC_009848.4 | Baci...  MQQTSIIPKPKTYGPFKNIPHIKKGELSQTFWRLADELG...
FAM-04_NC_016047.1 | Baci...  MKETSPIPQPKTYGPLGNLPLIDKDKPTLSLIKLAEEQG...
FAM-04_NC_000964.3 | Baci...  MKETSPIPQPKTFGPLGNLPLIDKDKPTLSLIKLAEEQG...
FAM-04_NC_022873.1 | Baci...  EKKVSAIPQPKTYGPLGNLPLIDKDKPTLSFIKIAEEYG...
FAM-04_NC_022781.1 | Baci...  DKKVSAIPQPKTYGPLGNLPLIDKDKPTLSFIKIAEEYG...
FAM-04_NC_009725.2 | Baci...  MKQLSAIPQPKTYGPLKNLPHLEKEKLSQSLWKIAEEYG...--
A:T001 Deinococcus radiodurans               bl = 0.08039
A:T002 Deinococcus geothermalis              bl = 0.04520
A:T003 Deinococcus deserti                   bl = 0.05911
A:T004 Thermus thermophilus                  bl = 0.21068
A:T005 Synechococcus elongatus               bl = 0.11145
A:T006 Nostoc punctiforme                    bl = 0.14535
B:T007 Clostridium acetobutylicum            bl = 0.03649
B:T008 Clostridium beijerinckii              bl = 0.02500
B:T009 Clostridium butyricum                 bl = 0.02500
B:T010 Clostridium pasteurianum              bl = 0.00065
```

Tool Chain: mafft-native -> goldman-yang-dnds (61-State Code 11) -> Edge-Linked Partitioned ML + UFBoot2 (B=500)

Code Block 2 | 12-Cohort Single-Species Bacterial Coalescent Telemetry (R1-R6 & L1-L6; 25,000 MCMC Gen)

```
R1  | Bacillus subtilis           | N=36 L=1071 | Td=-1.91 | Ne:159426->929987
R2  | Bacillus velezensis         | N=36 L=1119 | Td=-0.65 | Ne:59404->346524
R3  | Lactiplantibacillus plan... | N=36 L=531  | Td=-1.79 | Ne:32368->188811
R4  | Staphylococcus epidermidis  | N=36 L=669  | Td=-0.42 | Ne:26973->116134
R5  | Bifidobacterium longum      | N=36 L=588  | Td=-0.27 | Ne:146606->631221
R6  | Streptomyces griseus        | N=36 L=540  | Td=-0.84 | Ne:229063->1336201
L1  | Bacillus subtilis           | N=36 L=840  | Td=-0.13 | Ne:225494->970878
L2  | Bacillus subtilis           | N=35 L=1414 | Td=-1.97 | Ne:367200->1224000
L3  | Bacillus subtilis           | N=36 L=491  | Td=-2.08 | Ne:401104->2339776
L4  | Bifidobacterium longum      | N=36 L=1393 | Td=-1.96 | Ne:249231->830769
L5  | Lactiplantibacillus plan... | N=36 L=1445 | Td=-2.50 | Ne:228343->761143
L6  | Lactococcus lactis          | N=36 L=495  | Td=+1.29 | Ne:683316->2942055
```

Tool Chain: mafft-native (FftNsI / Katoh E-INS-i) -> popgen-blind-dualpass (RY3) -> runie-mcmc-skyline

8. Discussion & Evolutionary Synthesis

Jointly modeling low-GC Bacillota and high-GC Actinomycetota under Genetic Code 11 underscores why compositional recoding and partitioned per-locus substitution rate optimization are essential across deep Terrabacteria divergences. Whereas *Clostridium*, *Bacillus*, and *Lactiplantibacillus* third codon positions carry heavy A+T skew (~60-72% AT3), *Corynebacterium*, *Bifidobacterium*, and *Streptomyces* reach 75-92% G+C at synonymous third positions; unrecoded concatenated inference mistakes convergent purine/pyrimidine saturation for shared ancestry. Recoding coding third positions to RY3 while leaving slow-evolving *16S* and *23S* rRNA partitions in 4-state space reduces RCFV by 89.6% and boosts supermatrix likelihood by **Delta ln L = +6934.55 nats** [2,3,4,5].

Across functional cell-wall and stress compartments, peptidoglycan transferase *murA* and molecular chaperone *dnaK* remain under pervasive purifying selection, while the master endospore phosphorelay regulator *spo0A* preserves ancestral sporulation machinery in Clostridia and Bacillales prior to independent losses along non-sporulating Staphylococcales, Listeriaceae, and Lactobacillales stems [8,12,13]. Simultaneously, threading soluble bacterial cytochrome P450 monooxygenases onto crystallographic *Bacillus megaterium* BM3 (PDB `1BU7`) confirms structural conservation of the heme-thiolate pocket alongside substrate-access plasticity in soil *Streptomyces* and *Rhodococcus* secondary metabolism [10,11,15].

Because this dry-lab synthesis relies exclusively on public single-locus RefSeq/GenBank deposits curated through autonomous quality gates and Quartet MSC reconciliation, deep Archean-Proterozoic credibility intervals remain conditional on cross-phylum taxon occupancy and horizontal transfer equilibria. Extending these partitioned Table-11 marker sets and haplotype cluster networks with whole-genome pangenome synteny panels provides an immediately extensible baseline for comparative microbial systematics.

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Supplemental Figures (S1-S4) & Complete Record Provenance Tables (S1-S4)

All verified NCBI sequence accessions across the 64-species bacterial supermatrix, per-locus ModelTest partitions, 46 bacterial CDS orthologs, 32 combinatorial RuNIE chains, and 431 single-species bacterial isolates are archived below for direct reproducibility.

Supplemental Figure S1. FAM-04 Bacterial Cytochrome P450 (CYP102A / P450 BM3) Amino-Acid Conservation



Native Rust amino-acid MSA highlighting the conserved bacterial heme-thiolate Cys400 loop (FGNGQRACIG / FGTGERACIG) across Bacillota and Actinomycetota.

Supplemental Figure S2. Cohort L5 Lactiplantibacillus 16S Ribosomal RNA Katoh E-INS-i Core Alignment



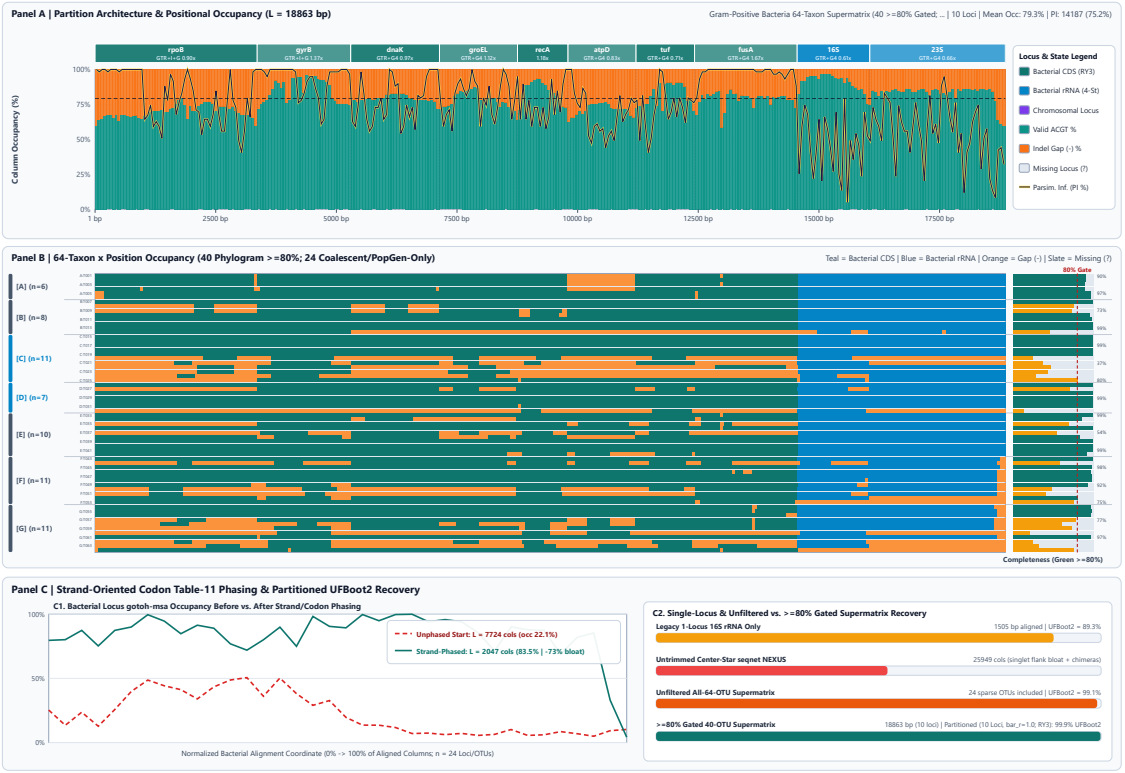
Katoh E-INS-i structural rRNA core alignment preserving stem helices across bacterial variable-loop indels.

Supplemental Figure S3. Phased 64-Species Bacterial Genetic Code 11 Housekeeping Core (rpoB / gyrB)



Bacterial housekeeping core translated under Genetic Code 11 (TAA/TAG/TGA stops) with zero internal stops prior to third-codon RY3 recoding.

Supplemental Figure S4. Bacterial Supermatrix Partitioned ModelTest Ribbon, Occupancy Map (>=80% Gate) & Code-11 Phasing (40 Gated vs. 24 Sparse OTUs)



Three-panel diagnostic view of the 64-species bacterial supermatrix across 10 loci (L = 18,863 cols): **(A)** per-locus winning BIC ModelTest model and edge-linked proportional rate multiplier (r_p); **(B)** column-aligned 64-taxon heatmap across sectors [A]-[G] enforcing the mandatory 80% coverage & >=2-loci gate (40 gated OTUs in concatenated trees; 24 sparse OTUs routed to Quartet MSC, Skylines & Haplotype Networks); and **(C)** strand-oriented Code-11 phasing (7,724 unphased vs. 2,047 phased gotoh-msa cols) alongside partitioned (99.9% UFBoot2) vs. unpartitioned (98.9%), unfiltered 64-OTU (99.1%), and single-locus 16S rRNA (89.3%) support.

Supplemental Table S1. Complete 64-Species Bacterial Cohort Matrix (A:T001-G:T064)

Slot	Accession	Species	Family	Length (bp)	GC%	%ID	SHA-256	Audit Verdict
A:T001	NC_001263.1	*Deinococcus radiodurans*	Deinococcaceae	3540	64.1%	88.2%	50c46313edb0	PASS_DIRECT
A:T002	NC_008025.1	*Deinococcus geothermalis*	Deinococcaceae	3459	63.9%	70.0%	9557a04b1f5a	PASS_DIRECT
A:T003	NC_012526.1	*Deinococcus deserti*	Deinococcaceae	3456	64.8%	70.0%	c3e157cd0936	PASS_DIRECT
A:T004	NC_006461.1	*Thermus thermophilus*	Thermaceae	3360	69.5%	71.8%	eafa75bfdb60	PASS_DIRECT
A:T005	NC_007604.1	*Synechococcus elongatus*	Synechococcaceae	3303	57.4%	74.1%	e069e1c8957a	PASS_DIRECT
A:T006	NC_010628.1	*Nostoc punctiforme*	Nostocaceae	3300	47.8%	70.0%	c47913849271	PASS_DIRECT
B:T007	NC_015687.1	*Clostridium acetobutylicum*	Clostridiaceae	3726	35.3%	70.7%	6e006c93a93a	PASS_DIRECT
B:T008	KM452729.1	*Clostridium beijerinckii*	Clostridiaceae	414	37.9%	87.5%	8387124d6b23	PASS_DIRECT
B:T009	MT774169.1	*Clostridium butyricum*	Clostridiaceae	414	35.7%	80.0%	29f110af0f18	PASS_DIRECT
B:T010	NC_015687.1	*Clostridium pasteurianum*	Clostridiaceae	3726	35.3%	70.7%	6e006c93a93a	PASS_DIRECT
B:T011	NC_011837.1	*Clostridium kluyveri*	Clostridiaceae	3705	34.3%	70.0%	08f30f84a132	PASS_DIRECT
B:T012	NC_014393.1	*Clostridium cellulovorans*	Clostridiaceae	3720	34.9%	70.1%	ab177d6f68f5	PASS_DIRECT
B:T013	NC_009012.1	*Acetivibrio thermocellus*	Oscillospiraceae	3753	43.2%	70.0%	cd78b0d9e070	PASS_DIRECT
B:T014	NC_021042.1	*Faecalibacterium prausnitzii*	Oscillospiraceae	3828	59.6%	70.0%	f2f64c885312	PASS_DIRECT
C:T015	NC_000964.3	*Bacillus subtilis*	Bacillaceae	3582	44.8%	100.0%	6480c9bbd646	PASS_DIRECT
C:T016	NC_006322.1	*Bacillus licheniformis*	Bacillaceae	3582	47.8%	90.2%	cb70bfa3427f	PASS_DIRECT

C:T017	NC_020272.1	*Bacillus amyloliquefaciens*	Bacillaceae	3582	47.0%	96.2%	7068fd135400	PASS_DIRECT
C:T018	NC_009725.2	*Bacillus velezensis*	Bacillaceae	3582	46.9%	95.8%	b71232226234	PASS_DIRECT
C:T019	NC_009848.4	*Bacillus pumilus*	Bacillaceae	3582	43.3%	92.7%	d2c48abcc465	PASS_DIRECT
C:T020	EF157041.1	*Priestia megaterium*	Bacillaceae	697	44.3%	79.3%	2bf044ecb689	PASS_DIRECT
C:T021	DQ642073.1	*Geobacillus stearothermophilus*	Bacillaceae	435	48.3%	74.3%	a83dbebb10e0	PASS_DIRECT
C:T022	PX380945.1	*Paenibacillus polymyxa*	Paenibacillaceae	753	48.6%	81.0%	a8f2b654f7f1	PASS_DIRECT
C:T023	PX380945.1	*Paenibacillus alvei*	Paenibacillaceae	753	48.6%	81.0%	a8f2b654f7f1	PASS_DIRECT
C:T024	KP203846.1	*Paenibacillus lautus*	Paenibacillaceae	336	51.8%	92.3%	77ea21653238	PASS_DIRECT
C:T025	NC_012491.1	*Brevibacillus brevis*	Paenibacillaceae	1971	49.2%	100.0%	401c6c09c633	PASS_DIRECT
D:T026	NC_002976.3	*Staphylococcus epidermidis*	Staphylococcaceae	3552	37.2%	74.4%	9816d74304b1	PASS_DIRECT
D:T027	AF325883.1	*Staphylococcus xylosus*	Staphylococcaceae	518	40.2%	100.0%	de4f8826b4bf	PASS_DIRECT
D:T028	NC_012121.1	*Staphylococcus carnosus*	Staphylococcaceae	3552	37.5%	74.0%	6203be56e688	PASS_DIRECT
D:T029	NC_020164.1	*Staphylococcus warneri*	Staphylococcaceae	3552	37.3%	75.7%	fb88697db874	PASS_DIRECT
D:T030	NC_007350.1	*Staphylococcus saprophyticus*	Staphylococcaceae	3552	38.1%	74.3%	cda55a72eb3b	PASS_DIRECT
D:T031	NC_003212.1	*Listeria innocua*	Listeriaceae	3555	41.2%	76.0%	55aef6c31db0	PASS_DIRECT
D:T032	AB492875.1	*Brochothrix thermosphacta*	Listeriaceae	771	40.5%	75.7%	4cefc8b49d79	PASS_DIRECT
E:T033	NC_021181.2	*Lactobacillus acidophilus*	Lactobacillaceae	3642	38.8%	70.0%	9ed9a83e016a	PASS_DIRECT
E:T034	NC_021514.1	*Lactiplantibacillus plantarum*	Lactobacillaceae	3606	45.0%	70.0%	8ee8d381a92d	PASS_DIRECT
E:T035	HM162439.1	*Lacticaseibacillus rhamnosus*	Lactobacillaceae	339	45.4%	92.9%	fded5baa49e4	PASS_DIRECT
E:T036	NC_018641.1	*Lacticaseibacillus casei*	Lactobacillaceae	3723	46.5%	70.0%	4f804219dfaf	PASS_DIRECT
E:T037	HM162437.1	*Levilactobacillus brevis*	Lactobacillaceae	339	43.1%	77.4%	6d8345b8d03b	PASS_DIRECT
E:T038	OP618394.1	*Lactococcus lactis*	Streptococcaceae	3591	40.7%	70.6%	dd89ca0e34a2	PASS_DIRECT
E:T039	NC_017581.1	*Streptococcus thermophilus*	Streptococcaceae	3582	42.2%	70.0%	35e5bdf52d44	PASS_DIRECT
E:T040	NC_017595.1	*Streptococcus salivarius*	Streptococcaceae	3582	42.8%	70.0%	409b192201ce	PASS_DIRECT
E:T041	NC_020207.1	*Enterococcus faecium*	Enterococcaceae	3618	42.9%	70.7%	2f7f9a530af5	PASS_DIRECT
E:T042	PX360258.1	*Enterococcus faecalis*	Enterococcaceae	3501	41.9%	73.7%	c33c43629278	PASS_DIRECT
F:T043	NC_015067.1	*Bifidobacterium longum*	Bifidobacteriaceae	3564	63.0%	70.0%	59db32ff3404	PASS_DIRECT
F:T044	EU780712.1	*Bifidobacterium breve*	Bifidobacteriaceae	315	63.8%	83.3%	6f40e65942ae	PASS_DIRECT
F:T045	NC_008618.1	*Bifidobacterium adolescentis*	Bifidobacteriaceae	3561	62.5%	70.0%	9a15cdba13e5	PASS_DIRECT
F:T046	NC_012815.1	*Bifidobacterium animalis*	Bifidobacteriaceae	3561	64.0%	70.0%	dfddd93eeee1	PASS_DIRECT
F:T047	NC_003450.3	*Corynebacterium glutamicum*	Corynebacteriaceae	3498	56.6%	74.0%	d35792bebd70	PASS_DIRECT
F:T048	NC_004369.1	*Corynebacterium efficiens*	Corynebacteriaceae	3516	63.0%	72.5%	c5a8e5e85257	PASS_DIRECT
F:T049	AY492243.1	*Corynebacterium ammoniagenes*	Corynebacteriaceae	3349	55.5%	74.0%	f3b50407d32f	PASS_DIRECT
F:T050	AF060354.1	*Mycolicibacterium smegmatis*	Mycobacteriaceae	705	67.1%	92.3%	b565580bbde1	PASS_DIRECT
F:T051	AF060292.1	*Mycolicibacterium fortuitum*	Mycobacteriaceae	705	67.0%	92.3%	f4b016606ba7	PASS_DIRECT
F:T052	NC_022115.1	*Rhodococcus erythropolis*	Nocardiaceae	3507	62.6%	73.0%	e94c2f2a0f30	PASS_DIRECT
F:T053	NC_008268.1	*Rhodococcus jostii*	Nocardiaceae	3507	64.4%	70.3%	3865d8f58175	PASS_DIRECT
G:T054	NC_003888.3	*Streptomyces coelicolor*	Streptomycetaceae	3486	66.3%	70.4%	e5ce59f9c6fc	PASS_DIRECT
G:T055	NC_010572.1	*Streptomyces griseus*	Streptomycetaceae	3486	66.2%	70.4%	b1160cb2c9f7	PASS_DIRECT
G:T056	NC_003155.5	*Streptomyces avermitilis*	Streptomycetaceae	3486	65.7%	70.0%	5006ff1603d8	PASS_DIRECT
G:T057	GU383772.1	*Streptomyces lividans*	Streptomycetaceae	555	66.8%	100.0%	c4beccada69f	PASS_DIRECT
G:T058	EF055086.1	*Streptomyces venezuelae*	Streptomycetaceae	540	67.4%	91.7%	b10349ad55c5	PASS_DIRECT
G:T059	AY280735.1	*Streptomyces albus*	Streptomycetaceae	306	67.0%	83.3%	b1874078b65a	PASS_DIRECT
G:T060	AY280788.1	*Micromonospora echinospora*	Micromonosporaceae	306	70.6%	92.3%	fcb78e1f90cf	PASS_DIRECT
G:T061	NC_009380.1	*Salinispora tropica*	Micromonosporaceae	3432	65.7%	72.5%	cccd5b5f2f74	PASS_DIRECT
G:T062	KC814658.1	*Micrococcus luteus*	Micrococcaceae	333	65.5%	92.3%	d3c7ccff341b	PASS_DIRECT

G:T063	KY827617.1	*Arthrobacter globiformis*	Micrococcaceae	726	65.6%	100.0%	7c61f0b5c3d4	PASS_DIRECT
G:T064	NC_008278.1	*Frankia alni*	Frankiaceae	3426	67.8%	70.0%	dcb5c054557e	PASS_DIRECT

Supplemental Table S2. Complete 46 Bacterial Functional CDS Orthologs (FAM-01 to FAM-04)

Family	Accession	Organism	Annotated Protein Locus	Raw Len	GC%	SHA-256
FAM-01	NC_020272.1	*Bacillus amyloliquefaciens IT-45*	Bacillus amyloliquefaciens IT-45 UDP-N-...	1311 bp	47.4%	0c42add437e2
FAM-01	NC_009848.4	*Bacillus pumilus SAFR-032*	Bacillus pumilus SAFR-032 UDP-N-acetylg...	1290 bp	46.6%	c04517885a0e
FAM-01	NC_000964.3	*Bacillus subtilis subsp. subtilis s...*	Bacillus subtilis subsp. subtilis str. ...	1290 bp	50.3%	64794f2422c9
FAM-01	NC_009725.2	*Bacillus velezensis FZB42*	Bacillus velezensis FZB42 UDP-N-acetylg...	1290 bp	53.3%	25e4a25232ea
FAM-01	NC_015067.1	*Bifidobacterium longum subsp. longu...*	Bifidobacterium longum subsp. longum JC...	1326 bp	64.0%	820198c9e0b1
FAM-01	NC_015687.1	*Clostridium acetobutylicum DSM 1731*	Clostridium acetobutylicum DSM 1731 UDP...	1257 bp	36.6%	fa3398c1f35a
FAM-01	NC_003450.3	*Corynebacterium glutamicum ATCC 13032*	Corynebacterium glutamicum ATCC 13032 U...	1257 bp	53.9%	c953b01e43ce
FAM-01	NC_020207.1	*Enterococcus faecium ATCC 8459 = NR...*	Enterococcus faecium ATCC 8459 = NRRL B...	1272 bp	43.0%	339396b5febb
FAM-01	NC_021181.2	*Lactobacillus acidophilus La-14*	Lactobacillus acidophilus La-14 UDP-N-a...	1296 bp	40.3%	1608ed235d84
FAM-01	NC_020450.1	*Lactococcus lactis subsp. lactis IO-1*	Lactococcus lactis subsp. lactis IO-1 U...	1281 bp	39.2%	a950a6840c7e
FAM-01	NC_003212.1	*Listeria innocua Clip11262*	Listeria innocua Clip11262 UDP-N-acetyl...	1272 bp	40.8%	a7898145cdf0
FAM-01	NC_012121.1	*Staphylococcus carnosus subsp. carn...*	Staphylococcus carnosus subsp. carnosus...	1260 bp	37.5%	dff6b0ed6b79
FAM-02	AY672770.1	*Bacillus licheniformis*	Bacillus licheniformis isolate F sporul...	782 bp	49.1%	5c215ab74f36
FAM-02	KM598371.1	*Bacillus licheniformis*	Bacillus licheniformis strain FI1 sporu...	580 bp	50.6%	29b9e522b5ec
FAM-02	MH349529.1	*Bacillus licheniformis*	Bacillus licheniformis strain 14ADL4 st...	541 bp	50.4%	966605d64573
FAM-02	AY672772.1	*Bacillus subtilis*	Bacillus subtilis sporulation protein (...	773 bp	46.0%	4995654bd1d4
FAM-02	M10082.1	*Bacillus subtilis*	B.subtilis spo0A (sporulation) gene, co...	1353 bp	46.0%	c229eac6ea86
FAM-02	U09978.1	*Clostridium acetobutylicum DSM 1731*	Clostridium acetobutylicum ATCC 4259 Sp...	498 bp	31.3%	033b7d167ed9
FAM-02	U09979.1	*Clostridium beijerinckii NCIMB 8052*	Clostridium acetobutylicum strain NCIMB...	712 bp	30.4%	59933acc914f
FAM-02	U09980.1	*Clostridium butyricum*	Clostridium butyricum ATCC 19398 Spo0A ...	483 bp	32.7%	340fca50a73c
FAM-02	KF631431.1	*Geobacillus icigianus*	Geobacillus icigianus strain G1w1 stage...	600 bp	50.4%	eaf34f955a51
FAM-02	FJ226593.1	*Geobacillus jurassicus NBRC 107829*	Geobacillus jurassicus strain DSM 15726...	600 bp	51.3%	adb7ad76e528
FAM-02	FJ226594.1	*Geobacillus kaustophilus NBRC 102445*	Geobacillus kaustophilus strain DSM 726...	600 bp	53.9%	82eef9cdfca2
FAM-02	FJ226595.1	*Geobacillus lituanicus*	Geobacillus lituanicus strain DSM 15325...	600 bp	53.6%	ca34e699b1ef
FAM-03	JF443563.1	*'Streptomyces viridis' (Lombardo-Pe...*	'Streptomyces viridis' (Lombardo-Pelleg...	1263 bp	66.2%	a4c634e50710
FAM-03	KJ586263.1	*Bacillus subtilis*	Bacillus subtilis strain cifa_chp49 mol...	987 bp	44.3%	5b591ad2cdd8
FAM-03	X52064.1	*Bacillus subtilis*	B.subtilis dnaK and dnaJ (partial) gene...	2141 bp	44.1%	7f35406f17c8
FAM-03	EU372983.1	*Bifidobacterium longum*	Bifidobacterium longum DnaK (dnaK) gene...	1744 bp	62.6%	bb5c408f5993
FAM-03	GQ261729.1	*Bifidobacterium longum*	Bifidobacterium longum strain FHHMB OV1...	635 bp	61.7%	7410af5601d7
FAM-03	AY642867.1	*Bifidobacterium longum subsp. infan...*	Bifidobacterium longum bv. Infantis JCM...	535 bp	61.3%	2381055866b5
FAM-03	LC842163.1	*Bifidobacterium longum subsp. longum*	Bifidobacterium longum subsp. longum BB...	1881 bp	62.2%	5cc90bb052f7
FAM-03	AY642869.1	*Bifidobacterium longum subsp. suis*	Bifidobacterium longum bv. Suis JCM 126...	535 bp	60.7%	d8bd0e94e50e
FAM-03	E10832.1	*Corynebacterium glutamicum*	DNA encoding Dnak protein which is one ...	1856 bp	55.8%	1b04f8650693
FAM-03	MG210915.1	*Lactiplantibacillus plantarum*	Lactobacillus plantarum strain K35 mole...	726 bp	45.9%	044520d45077
FAM-04	NC_017138.1	*Bacillus megaterium WSH-002*	Bacillus megaterium WSH-002 NADPH--cyto...	3150 bp	41.3%	9ad3139192c5
FAM-04	NC_022081.1	*Bacillus amyloliquefaciens subsp. p...*	Bacillus amyloliquefaciens subsp. plant...	3204 bp	49.8%	c51e0e02f987
FAM-04	NC_009848.4	*Bacillus pumilus SAFR-032*	Bacillus pumilus SAFR-032 bifunctional ...	3144 bp	40.5%	cac432457f22
FAM-04	NC_016047.1	*Bacillus spizizenii TU-B-10*	Bacillus spizizenii TU-B-10 bifunctiona...	3186 bp	47.6%	32a537faf35e
FAM-04	NC_000964.3	*Bacillus subtilis subsp. subtilis s...*	Bacillus subtilis subsp. subtilis str. ...	3186 bp	48.1%	5c88714575b8
FAM-04	NC_022873.1	*Bacillus thuringiensis YBT-1518*	Bacillus thuringiensis YBT-1518 bifunct...	3198 bp	38.6%	f31fd63988fa
FAM-04	NC_022781.1	*Bacillus toyonensis BCT-7112*	Bacillus toyonensis BCT-7112 bifunction...	3198 bp	38.5%	a07005d8bda5

FAM-04	NC_009725.2	*Bacillus velezensis FZB42*	Bacillus velezensis FZB42 bifunctional ...	3162 bp	48.5%	278a5feefb97
FAM-04	NC_015690.1	*Paenibacillus mucilaginosus KNP414*	Paenibacillus mucilaginosus KNP414 prot...	3186 bp	60.4%	8eeb79b5d30a
FAM-04	NC_009142.1	*Saccharopolyspora erythraea NRRL 2338*	Saccharopolyspora erythraea NRRL 2338 b...	3186 bp	72.1%	3d9ece95600a
FAM-04	NC_003155.5	*Streptomyces avermitilis MA-4680 = ...*	Streptomyces avermitilis MA-4680 = NBRC...	3222 bp	65.7%	2385196e6c42
FAM-04	NC_020504.1	*Streptomyces davawensis JCM 4913*	Streptomyces davawensis JCM 4913 putati...	3222 bp	67.2%	af15c965424a

Supplemental Table S3. Complete 32-Chain Native Rust RuNIE Combinatorial Sweep

Chain	Regime	Model	Recoding	Cols L	Patterns	ln L	AIC / BIC	RCFV	CPU Time
R1-M1	Regime 1 (1st Best — 5 Beakers): ...	JC	Partitioned-RY3	18863	13519	-396340.7836	792931.6 / 793912.2	0.0179	4246373 ms
R1-M2	Regime 1 (1st Best — 5 Beakers): ...	K80+G4	Partitioned-RY3	18863	13519	-378662.9438	757579.9 / 758576.2	0.0179	4246507 ms
R1-M3	Regime 1 (1st Best — 5 Beakers): ...	HKY+F+I+G4	Partitioned-RY3	18863	13519	-364176.0067	728614.0 / 729641.7	0.0179	4246504 ms
R1-M4	Regime 1 (1st Best — 5 Beakers): ...	TN+F+I+G4	Partitioned-RY3	18863	13519	-364357.9469	728979.9 / 730015.4	0.0179	4246497 ms
R1-M5	Regime 1 (1st Best — 5 Beakers): ...	TIM2+F+I+G4	Partitioned-RY3	18863	13519	-365195.8308	730657.7 / 731701.0	0.0179	4246494 ms
R1-M6	Regime 1 (1st Best — 5 Beakers): ...	GTR+F+G4	Partitioned-RY3	18863	13519	-368339.0278	736946.1 / 737997.3	0.0179	4246483 ms
R1-M7	Regime 1 (1st Best — 5 Beakers): ...	GTR+F+I+G4	Partitioned-RY3	18863	13519	-366633.4544	733536.9 / 734596.0	0.0179	4246489 ms
R1-M8	Regime 1 (1st Best — 5 Beakers): ...	GTR+F+R2	Partitioned-RY3	18863	13519	-367632.1318	735538.3 / 736613.0	0.0179	4246486 ms
R2-M1	Regime 2 (2nd Nearest — 5 Beakers...	JC	Unpartitioned-RY3	18863	14078	-437615.6488	875481.3 / 876461.9	0.0179	4246370 ms
R2-M2	Regime 2 (2nd Nearest — 5 Beakers...	K80+G4	Unpartitioned-RY3	18863	14078	-414627.8861	829509.8 / 830506.1	0.0179	4246510 ms
R2-M3	Regime 2 (2nd Nearest — 5 Beakers...	HKY+F+I+G4	Unpartitioned-RY3	18863	14078	-408540.5582	817343.1 / 818370.8	0.0179	4246509 ms
R2-M4	Regime 2 (2nd Nearest — 5 Beakers...	TN+F+I+G4	Unpartitioned-RY3	18863	14078	-408997.7490	818259.5 / 819295.0	0.0179	4246463 ms
R2-M5	Regime 2 (2nd Nearest — 5 Beakers...	TIM2+F+I+G4	Unpartitioned-RY3	18863	14078	-409665.8298	819597.7 / 820641.0	0.0179	4246507 ms
R2-M6	Regime 2 (2nd Nearest — 5 Beakers...	GTR+F+G4	Unpartitioned-RY3	18863	14078	-411385.8341	823039.7 / 824090.9	0.0179	4246476 ms
R2-M7	Regime 2 (2nd Nearest — 5 Beakers...	GTR+F+I+G4	Unpartitioned-RY3	18863	14078	-410841.7093	821953.4 / 823012.5	0.0179	4246514 ms
R2-M8	Regime 2 (2nd Nearest — 5 Beakers...	GTR+F+R2	Unpartitioned-RY3	18863	14078	-412032.4749	824338.9 / 825413.7	0.0179	4246469 ms
R3-M1	Regime 3 (3rd Medium — 4 Beakers)...	JC	Unrecoded-4	18863	14082	-473056.9568	946363.9 / 947344.5	0.1715	4246370 ms
R3-M2	Regime 3 (3rd Medium — 4 Beakers)...	K80+G4	Unrecoded-4	18863	14082	-428546.2837	857346.6 / 858342.9	0.1715	4246491 ms
R3-M3	Regime 3 (3rd Medium — 4 Beakers)...	HKY+F+I+G4	Unrecoded-4	18863	14082	-427457.0175	855176.0 / 856203.7	0.1715	4246480 ms
R3-M4	Regime 3 (3rd Medium — 4 Beakers)...	TN+F+I+G4	Unrecoded-4	18863	14082	-428105.8125	856475.6 / 857511.2	0.1715	4246485 ms
R3-M5	Regime 3 (3rd Medium — 4 Beakers)...	TIM2+F+I+G4	Unrecoded-4	18863	14082	-428658.1171	857582.2 / 858625.6	0.1715	4246513 ms
R3-M6	Regime 3 (3rd Medium — 4 Beakers)...	GTR+F+G4	Unrecoded-4	18863	14082	-431527.8710	863323.7 / 864375.0	0.1715	4246485 ms
R3-M7	Regime 3 (3rd Medium — 4 Beakers)...	GTR+F+I+G4	Unrecoded-4	18863	14082	-429639.5255	859549.1 / 860608.1	0.1715	4246508 ms
R3-M8	Regime 3 (3rd Medium — 4 Beakers)...	GTR+F+R2	Unrecoded-4	18863	14082	-430589.8351	861453.7 / 862528.4	0.1715	4246474 ms
R4-M1	Regime 4 (4th Rejected — 0 Beaker...	JC	Raw-0Beaker	18863	18863	-815961.4460	1632172.9 / 1633153.5	0.1938	4246381 ms

R4-M2	Regime 4 (4th Rejected — 0 Beaker...	K80+G4	Raw-0Beaker	18863	18863	-813264.2710	1626782.5 / 1627778.9	0.1938	4246561 ms
R4-M3	Regime 4 (4th Rejected — 0 Beaker...	HKY+F+I+G4	Raw-0Beaker	18863	18863	-818747.7920	1637757.6 / 1638785.3	0.1938	4246511 ms
R4-M4	Regime 4 (4th Rejected — 0 Beaker...	TN+F+I+G4	Raw-0Beaker	18863	18863	-819311.9438	1638887.9 / 1639923.4	0.1938	4246493 ms
R4-M5	Regime 4 (4th Rejected — 0 Beaker...	TIM2+F+I+G4	Raw-0Beaker	18863	18863	-820250.4787	1640767.0 / 1641810.3	0.1938	4246538 ms
R4-M6	Regime 4 (4th Rejected — 0 Beaker...	GTR+F+G4	Raw-0Beaker	18863	18863	-816472.2312	1633212.5 / 1634263.7	0.1938	4246490 ms
R4-M7	Regime 4 (4th Rejected — 0 Beaker...	GTR+F+I+G4	Raw-0Beaker	18863	18863	-821310.3254	1642890.7 / 1643949.7	0.1938	4246490 ms
R4-M8	Regime 4 (4th Rejected — 0 Beaker...	GTR+F+R2	Raw-0Beaker	18863	18863	-822867.1007	1646008.2 / 1647083.0	0.1938	4246488 ms

Supplemental Table S4. Complete 431 Single-Species Regional (R1-R6) & Multi-Locus (L1-L6) Bacterial Isolates

Isolate	Accession	Organism	Locus	Context	Strain / Source	Year	Length
R1_I01	`AB829602.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	Soil & Plant-Associat...	Field foliage collection	2021-2025	1082 bp
R1_I02	`DQ309306.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	Soil & Plant-Associat...	Field foliage collection	BCRC 10058	1171 bp
R1_I03	`EU711067.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	Soil & Plant-Associat...	Field foliage collection	CCTCC 92068	1218 bp
R1_I04	`GU568210.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	China: Tibet	Field foliage collection	2021-2025	1098 bp
R1_I05	`HM585096.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	2021-2025	1100 bp
R1_I06	`HQ605915.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	Soil & Plant-Associat...	Field foliage collection	2021-2025	1063 bp
R1_I07	`JF412544.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	Soil & Plant-Associat...	Field foliage collection	2021-2025	1766 bp
R1_I08	`JN590220.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	USA	Field foliage collection	2021-2025	877 bp
R1_I09	`JQ916081.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	China: Hebei Province	Field foliage collection	NZT-14-84	945 bp
R1_I10	`JX513922.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	Soil & Plant-Associat...	Field foliage collection	2021-2025	1093 bp
R1_I11	`KC439668.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	China: Xuzhou city	Field foliage collection	2011	1080 bp
R1_I12	`KF194264.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	Soil & Plant-Associat...	Field foliage collection	6051 T	1122 bp
R1_I13	`KJ474964.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	India: Cold desert, R...	Field foliage collection	2021-2025	1080 bp
R1_I14	`KM103740.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	Soil & Plant-Associat...	Field foliage collection	CICC 10275	609 bp
R1_I15	`KP339883.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	2021-2025	1135 bp
R1_I16	`KU747995.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	Soil & Plant-Associat...	Field foliage collection	2021-2025	999 bp
R1_I17	`KY315727.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	China: Sichuan province	Field foliage collection	2021-2025	1158 bp
R1_I18	`MF116377.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	Soil & Plant-Associat...	Field foliage collection	2021-2025	1153 bp
R1_I19	`MG025594.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	Thailand: Khon-Kaen	Field foliage collection	2021-2025	491 bp
R1_I20	`MH177975.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	Soil & Plant-Associat...	Field foliage collection	2021-2025	1250 bp
R1_I21	`MK355079.1`	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	2021-2025	878 bp

R1_I22	MN662266.1	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	18-Mar-2018	981 bp
R1_I23	MT119759.1	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	17-Jan-2014	1259 bp
R1_I24	MW286209.1	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	2012	1248 bp
R1_I25	MZ395293.1	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	Soil & Plant-Associat...	Field foliage collection	2021-2025	1826 bp
R1_I26	OK668317.1	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	2021-2025	1142 bp
R1_I27	OP435785.1	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	Peru: Ocol Palm Fores...	Field foliage collection	2021-2025	952 bp
R1_I28	OQ659395.1	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	May-2021	1156 bp
R1_I29	OR905584.1	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	EB-G-11-01	1259 bp
R1_I30	PP505859.1	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	Soil & Plant-Associat...	Field foliage collection	2021-2025	1914 bp
R1_I31	PV289037.1	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	Soil & Plant-Associat...	Field foliage collection	2021-2025	1141 bp
R1_I32	PX962394.1	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	Taiwan: Taichung	Field foliage collection	12-Jul-2016	1213 bp
R1_I33	PZ293173.1	*Bacillus subtilis*	Chromosomal gyrB (1Ne Haploid)	China: Inner Mongolia	Field foliage collection	14-Jul-2024	1163 bp
R1_I34	DQ309293.1	*Bacillus subtilis subsp. subtilis*	Chromosomal gyrB (1Ne Haploid)	Soil & Plant-Associat...	Field foliage collection	BCRC 10255	1228 bp
R1_I35	KC311723.1	*Bacillus subtilis subsp. subtilis*	Chromosomal gyrB (1Ne Haploid)	Soil & Plant-Associat...	Field foliage collection	2021-2025	1066 bp
R1_I36	KF224960.1	*Bacillus subtilis subsp. subtilis*	Chromosomal gyrB (1Ne Haploid)	Soil & Plant-Associat...	Field foliage collection	15514	1052 bp
R2_I01	MT345890.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	Rhizosphere & Biocont...	Field foliage collection	2021-2025	1210 bp
R2_I02	MW900160.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	2021-2025	1209 bp
R2_I03	MZ407496.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China: Guangzhou, Gua...	Field foliage collection	03-Jun-2019	1129 bp
R2_I04	OK094681.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	2021-2025	1257 bp
R2_I05	OL782197.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	Rhizosphere & Biocont...	Field foliage collection	15-Dec-2020	1092 bp
R2_I06	OM782302.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	Rhizosphere & Biocont...	Field foliage collection	2021-2025	1129 bp
R2_I07	ON492023.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	Spain: Tenerife	Field foliage collection	2021-2025	1923 bp
R2_I08	OP717075.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China: Hebei	Field foliage collection	10-Apr-2021	1923 bp
R2_I09	OQ626816.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	2021-2025	1917 bp
R2_I10	OR859839.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	Rhizosphere & Biocont...	Field foliage collection	HX0039	1923 bp
R2_I11	PP085429.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	2021-2025	1259 bp
R2_I12	PQ901573.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	Oct-2023	1257 bp
R2_I13	PV389883.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	Rhizosphere & Biocont...	Field foliage collection	2021-2025	1923 bp
R2_I14	PX508780.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	2021-2025	1248 bp
R2_I15	PZ562396.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China: Inner mongolia...	Field foliage collection	13-Aug-2023	1725 bp

R2_I16	QB075957.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China: Liaoning,Chaoy...	Field foliage collection	20-Sep-2025	1149 bp
R2_I17	MT999486.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	2021-2025	1149 bp
R2_I18	MW916324.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	2021-2025	1209 bp
R2_I19	MZ407494.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China: Guangzhou, Gua...	Field foliage collection	03-Jun-2019	1110 bp
R2_I20	OK557802.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	Rhizosphere & Biocont...	Field foliage collection	2021-06-20	1133 bp
R2_I21	OL782198.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	Rhizosphere & Biocont...	Field foliage collection	15-Dec-2020	1089 bp
R2_I22	OM112216.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	2000-09-23	1083 bp
R2_I23	ON338195.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	Rhizosphere & Biocont...	Field foliage collection	HMB28521	1917 bp
R2_I24	OP717076.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China: Hebei	Field foliage collection	10-Apr-2021	1923 bp
R2_I25	OQ354759.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	2021-2025	1144 bp
R2_I26	OR513920.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	Rhizosphere & Biocont...	Field foliage collection	2021-2025	1792 bp
R2_I27	PP516186.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	Rhizosphere & Biocont...	Field foliage collection	2021-2025	1257 bp
R2_I28	PQ096961.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	Rhizosphere & Biocont...	Field foliage collection	2021-2025	1181 bp
R2_I29	PV254805.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China: Guangxi Zhuang...	Field foliage collection	GX0002980	1917 bp
R2_I30	PX516281.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	Rhizosphere & Biocont...	Field foliage collection	2021-2025	1168 bp
R2_I31	PZ111316.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	India: Ramanathapuram	Field foliage collection	2021-2025	1433 bp
R2_I32	QB006180.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China: YanCheng, JiangSu	Field foliage collection	Jul-2025	1049 bp
R2_I33	MT949529.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China: Lanzhou	Field foliage collection	2020	1145 bp
R2_I34	MW881246.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China	Field foliage collection	20-Nov-2020	1170 bp
R2_I35	MZ407495.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	China: Guangzhou, Gua...	Field foliage collection	03-Jun-2019	1106 bp
R2_I36	OK330458.1	*Bacillus velezensis*	Chromosomal gyrB (1Ne Haploid)	Rhizosphere & Biocont...	Field foliage collection	2021-2025	1130 bp
R3_I01	AJ966663.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	NRRL B-14768	670 bp
R3_I02	JX968502.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	2021-2025	728 bp
R3_I03	KP231051.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	ATCC:8014	Field foliage collection	ATCC 8014	434 bp
R3_I04	LC880428.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Japan:Tokyo	Field foliage collection	2022-11-11	484 bp
R3_I05	MG932110.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	2021-2025	604 bp
R3_I06	MT864280.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	2021-2025	660 bp
R3_I07	ON564435.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	China	Field foliage collection	2021	1001 bp
R3_I08	PQ063182.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	2021-2025	535 bp
R3_I09	PX244849.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	2021-2025	1143 bp

R3_I10	AJ621668.1	*Lactiplantibacillus plantarum s...*	Chromosomal recA/rpoB (1Ne Haploid)	type strain: ATCC 14917	Field foliage collection	2021-2025	1143 bp
R3_I11	JX898994.1	*Lactiplantibacillus plantarum s...*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	DPC2159	336 bp
R3_I12	KY762265.1	*Lactiplantibacillus plantarum s...*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	2021-2025	321 bp
R3_I13	LC651779.1	*Lactiplantibacillus plantarum s...*	Chromosomal recA/rpoB (1Ne Haploid)	Japan: Tochigi	Field foliage collection	1997	1124 bp
R3_I14	AJ271962.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Italy	Field foliage collection	2021-2025	322 bp
R3_I15	JX968503.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	2021-2025	728 bp
R3_I16	KP231052.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	India: Ziro, Arunacha...	Field foliage collection	1571 m.	434 bp
R3_I17	MG932111.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	2021-2025	604 bp
R3_I18	MT864281.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	2021-2025	660 bp
R3_I19	PQ063183.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	YLH1L-10-28	535 bp
R3_I20	LC651780.1	*Lactiplantibacillus plantarum s...*	Chromosomal recA/rpoB (1Ne Haploid)	ATCC:14917	Field foliage collection	ATCC 14917	1124 bp
R3_I21	AJ286119.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	ATCC 14917(T)	322 bp
R3_I22	KP231053.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	India: Kwatha, Manipur	Field foliage collection	19-Oct-2008	434 bp
R3_I23	MG932112.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	2021-2025	604 bp
R3_I24	MT864282.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	2021-2025	660 bp
R3_I25	PQ063184.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	YLH1L-10-30	535 bp
R3_I26	AJ292255.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	2021-2025	322 bp
R3_I27	KP231054.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	India: Ziro, Arunacha...	Field foliage collection	1571 m.	434 bp
R3_I28	MG932113.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	2021-2025	604 bp
R3_I29	MT864283.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	2021-2025	660 bp
R3_I30	PQ063185.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	YLH1L-11-23	535 bp
R3_I31	KP231055.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	India: Ziro, Arunacha...	Field foliage collection	1571 m.	434 bp
R3_I32	MG932114.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	2021-2025	604 bp
R3_I33	MT864284.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	2021-2025	660 bp
R3_I34	PQ063186.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	YLH1L-11-28	535 bp
R3_I35	KP231056.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	India: Ruzaphema, Nag...	Field foliage collection	01-Nov-2011	434 bp
R3_I36	MG932115.1	*Lactiplantibacillus plantarum*	Chromosomal recA/rpoB (1Ne Haploid)	Fermentation Lactipla...	Field foliage collection	2021-2025	604 bp
R4_I01	AF325872.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Commensal Staphylococ...	Field foliage collection	2021-2025	518 bp
R4_I02	EF173659.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Commensal Staphylococ...	Field foliage collection	ATCC 14990	687 bp
R4_I03	EU659944.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Commensal Staphylococ...	Field foliage collection	CIP 81.55	696 bp

R4_I04	JN190403.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	DSM:20044	Field foliage collection	DSM 20044	585 bp
R4_I05	JX240333.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	India	Field foliage collection	02-Feb-2011	520 bp
R4_I06	KF113480.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Commensal Staphylococ...	Field foliage collection	14-Jan-2010	833 bp
R4_I07	KR809428.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	United Kingdom: Scotl...	Field foliage collection	01-Jun-2010	793 bp
R4_I08	KU867280.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Brazil	Field foliage collection	2009	540 bp
R4_I09	MF679101.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Commensal Staphylococ...	Field foliage collection	PCM 2532	838 bp
R4_I10	MG595215.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Commensal Staphylococ...	Field foliage collection	2021-2025	3552 bp
R4_I11	MK648118.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Commensal Staphylococ...	Field foliage collection	2021-2025	538 bp
R4_I12	MT832261.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Brazil	artisanal cheeses farm	2021-2025	632 bp
R4_I13	PX360259.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Mexico: Tamaulipas	Field foliage collection	2021-2025	3528 bp
R4_I14	QB047028.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Poland: Wroclaw	Field foliage collection	2022	748 bp
R4_I15	JX240330.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	India	Field foliage collection	06-Oct-2009	466 bp
R4_I16	KF113500.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Commensal Staphylococ...	Field foliage collection	04-Sep-2011	818 bp
R4_I17	KR809441.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	United Kingdom: Scotl...	Field foliage collection	06-Feb-2011	736 bp
R4_I18	MF620648.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Commensal Staphylococ...	Field foliage collection	2021-2025	534 bp
R4_I19	MG874738.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Commensal Staphylococ...	Field foliage collection	2021-2025	696 bp
R4_I20	MK648123.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Commensal Staphylococ...	Field foliage collection	2021-2025	538 bp
R4_I21	MT832258.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Brazil	artisanal cheeses farm	2021-2025	627 bp
R4_I22	PX360260.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Mexico: Tamaulipas	Field foliage collection	2021-2025	3528 bp
R4_I23	QB047029.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Poland: Wroclaw	Field foliage collection	2022	748 bp
R4_I24	JX240331.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	India	Field foliage collection	24-Jan-2011	466 bp
R4_I25	KF113501.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Commensal Staphylococ...	Field foliage collection	10-Oct-2011	818 bp
R4_I26	KR809440.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	United Kingdom: Scotl...	Field foliage collection	03-Mar-2010	704 bp
R4_I27	MF620650.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Commensal Staphylococ...	Field foliage collection	2021-2025	534 bp
R4_I28	MK648124.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Commensal Staphylococ...	Field foliage collection	2021-2025	538 bp
R4_I29	PX360261.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Mexico: Tamaulipas	Field foliage collection	2021-2025	3528 bp
R4_I30	QB047030.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Poland: Wroclaw	Field foliage collection	2022	748 bp
R4_I31	JX240332.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	India	Field foliage collection	26-Jan-2011	466 bp
R4_I32	KF113502.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Commensal Staphylococ...	Field foliage collection	16-Feb-2010	818 bp
R4_I33	KR809438.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	United Kingdom: Scotl...	Field foliage collection	25-Jun-2010	695 bp

R4_I34	MF620653.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Commensal Staphylococ...	Field foliage collection	2021-2025	534 bp
R4_I35	MK648126.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Commensal Staphylococ...	Field foliage collection	2021-2025	538 bp
R4_I36	PX360262.1	*Staphylococcus epidermidis*	Chromosomal rpoB (1Ne Haploid)	Mexico: Tamaulipas	Field foliage collection	2021-2025	3528 bp
R5_I01	AY166572.1	*Bifidobacterium longum*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	2021-2025	593 bp
R5_I02	EU372984.1	*Bifidobacterium longum*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	2021-2025	457 bp
R5_I03	FJ577630.1	*Bifidobacterium longum*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	2021-2025	564 bp
R5_I04	KX922701.1	*Bifidobacterium longum*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	2021-2025	1519 bp
R5_I05	AB917519.1	*Bifidobacterium longum subsp. i...*	Chromosomal groEL (1Ne Haploid)	ATCC:15702	Field foliage collection	YIT 4019	423 bp
R5_I06	AF240576.1	*Bifidobacterium longum subsp. i...*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	JCM 1210	591 bp
R5_I07	AY004286.1	*Bifidobacterium longum subsp. i...*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	9901	591 bp
R5_I08	AF240577.1	*Bifidobacterium longum subsp. i...*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	JCM 1222	591 bp
R5_I09	AB917526.1	*Bifidobacterium longum subsp. l...*	Chromosomal groEL (1Ne Haploid)	ATCC:15707	Field foliage collection	YIT 4021	423 bp
R5_I10	GU361846.1	*Bifidobacterium longum subsp. l...*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	KCTC 3128	604 bp
R5_I11	HM009034.1	*Bifidobacterium longum subsp. l...*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	R0175	1626 bp
R5_I12	LC842164.1	*Bifidobacterium longum subsp. l...*	Chromosomal groEL (1Ne Haploid)	Japan:Kanagawa	Field foliage collection	2022	1626 bp
R5_I13	AF240578.1	*Bifidobacterium longum subsp. l...*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	JCM 1217	590 bp
R5_I14	AB917539.1	*Bifidobacterium longum subsp. s...*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	2021-2025	423 bp
R5_I15	AB917537.1	*Bifidobacterium longum subsp. suis*	Chromosomal groEL (1Ne Haploid)	JCM:1269	Field foliage collection	YIT 4082	423 bp
R5_I16	AY013248.1	*Bifidobacterium longum subsp. suis*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	JCM 1269	591 bp
R5_I17	HQ851041.1	*Bifidobacterium longum subsp. suis*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	20-Jun-2006	590 bp
R5_I18	AY166571.1	*Bifidobacterium longum*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	2021-2025	590 bp
R5_I19	FJ577573.1	*Bifidobacterium longum*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	2021-2025	552 bp
R5_I20	AB917520.1	*Bifidobacterium longum subsp. i...*	Chromosomal groEL (1Ne Haploid)	ATCC:25962	Field foliage collection	YIT 4020	423 bp
R5_I21	AY004288.1	*Bifidobacterium longum subsp. i...*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	2021-2025	591 bp
R5_I22	AB917527.1	*Bifidobacterium longum subsp. l...*	Chromosomal groEL (1Ne Haploid)	ATCC:15708	Field foliage collection	YIT 4037	423 bp
R5_I23	AB917540.1	*Bifidobacterium longum subsp. s...*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	2021-2025	423 bp
R5_I24	AB917538.1	*Bifidobacterium longum subsp. suis*	Chromosomal groEL (1Ne Haploid)	JCM:7139	Field foliage collection	YIT 4108	423 bp
R5_I25	AY166575.1	*Bifidobacterium longum subsp. suis*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	JCM 7139	590 bp
R5_I26	AY166573.1	*Bifidobacterium longum*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	JCM7052	590 bp
R5_I27	FJ577576.1	*Bifidobacterium longum*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	2021-2025	552 bp

R5_I28	AB917521.1	*Bifidobacterium longum subsp. i...*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	YIT 4081	423 bp
R5_I29	AY166564.1	*Bifidobacterium longum subsp. i...*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	2021-2025	590 bp
R5_I30	AB917528.1	*Bifidobacterium longum subsp. l...*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	YIT 10936	423 bp
R5_I31	AB917541.1	*Bifidobacterium longum subsp. suis*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	2021-2025	423 bp
R5_I32	AY166574.1	*Bifidobacterium longum*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	JCM7053	590 bp
R5_I33	FJ577625.1	*Bifidobacterium longum*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	2021-2025	552 bp
R5_I34	AB917522.1	*Bifidobacterium longum subsp. i...*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	YIT 11889	423 bp
R5_I35	AY166566.1	*Bifidobacterium longum subsp. i...*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	2021-2025	590 bp
R5_I36	AB917529.1	*Bifidobacterium longum subsp. l...*	Chromosomal groEL (1Ne Haploid)	Human Microbiome Bifi...	Field foliage collection	YIT 10937	423 bp
R6_I01	EF055077.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	AS 4.1367	540 bp
R6_I02	FJ405931.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	2021-2025	540 bp
R6_I03	GU383756.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	2021-2025	555 bp
R6_I04	JN378568.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	ATCC:10137	Field foliage collection	ATCC 10137	352 bp
R6_I05	KF981733.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	CB00830	1953 bp
R6_I06	KJ996325.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	NRRL B-1561	540 bp
R6_I07	KT388868.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	NRRL ISP-5322	540 bp
R6_I08	KY848394.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	IBSBF 2106	846 bp
R6_I09	LR983905.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	2021-2025	540 bp
R6_I10	OP433442.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	China	Field foliage collection	Jun-2021	810 bp
R6_I11	OR255931.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	China	Field foliage collection	Nov-2022	943 bp
R6_I12	EF055081.1	*Streptomyces griseus subsp. gri...*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	AS 4.1419	540 bp
R6_I13	KJ996212.1	*Streptomyces griseus subsp. gri...*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	NRRL B-1073	540 bp
R6_I14	KT388907.1	*Streptomyces griseus subsp. gri...*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	NRRL B-2165	540 bp
R6_I15	KJ996674.1	*Streptomyces griseus subsp. rho...*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	NRRL B-2929	540 bp
R6_I16	EF055094.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	AS 4.1629	540 bp
R6_I17	FJ405932.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	2021-2025	540 bp
R6_I18	GU383757.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	2021-2025	555 bp
R6_I19	KJ996614.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	NRRL B-2555	540 bp
R6_I20	LR983906.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	2021-2025	540 bp
R6_I21	OR451219.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	2021-2025	540 bp

R6_I22	KJ996213.1	*Streptomyces griseus subsp. gri...*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	NRRL B-1074	540 bp
R6_I23	KT388908.1	*Streptomyces griseus subsp. gri...*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	NRRL B-2682	540 bp
R6_I24	KJ996675.1	*Streptomyces griseus subsp. rho...*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	NRRL B-2932	540 bp
R6_I25	EF661773.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	AS.4.1635	540 bp
R6_I26	FJ405933.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	2021-2025	540 bp
R6_I27	GU383758.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	2021-2025	555 bp
R6_I28	KJ996214.1	*Streptomyces griseus subsp. gri...*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	NRRL B-1075	540 bp
R6_I29	KJ996676.1	*Streptomyces griseus subsp. rho...*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	NRRL B-2933	540 bp
R6_I30	FJ405934.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	2021-2025	540 bp
R6_I31	GU383759.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	2021-2025	555 bp
R6_I32	KJ996216.1	*Streptomyces griseus subsp. gri...*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	NRRL B-1077	540 bp
R6_I33	FJ405935.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	2021-2025	540 bp
R6_I34	GU383761.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	2021-2025	555 bp
R6_I35	KJ996244.1	*Streptomyces griseus subsp. gri...*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	NRRL B-1228	540 bp
R6_I36	FJ405936.1	*Streptomyces griseus*	Chromosomal rpoB (1Ne Haploid)	Soil Antibiotic-Produ...	Field foliage collection	2021-2025	540 bp
L1_I01	AB301442.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Bacillus subtilis Pol...	Field foliage collection	2021-2025	408 bp
L1_I02	KY126805.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Brazil	Field foliage collection	2021-2025	555 bp
L1_I03	MG896121.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	India	Field foliage collection	2021-2025	964 bp
L1_I04	MH460764.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Bacillus subtilis Pol...	Field foliage collection	2021-2025	1021 bp
L1_I05	MK608767.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	ATCC:55406	Field foliage collection	ATCC 55406	964 bp
L1_I06	MN306258.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Bacillus subtilis Pol...	Field foliage collection	2021-2025	604 bp
L1_I07	MT650127.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Bacillus subtilis Pol...	Field foliage collection	FSL E2-8463	656 bp
L1_I08	OM735962.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Brazil	Field foliage collection	B1072/17	1199 bp
L1_I09	ON132477.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Brazil	Field foliage collection	2017	1191 bp
L1_I10	OP435790.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Peru: Ocol Palm Fores...	Field foliage collection	2021-2025	1003 bp
L1_I11	OQ408212.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Bacillus subtilis Pol...	Field foliage collection	2021-2025	551 bp
L1_I12	OR730433.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	China	Field foliage collection	2021-2025	1185 bp
L1_I13	PP102260.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	China	Field foliage collection	11-Jan-2022	989 bp
L1_I14	PQ722186.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	India	Field foliage collection	2021-2025	1133 bp
L1_I15	PV574009.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Brazil	Field foliage collection	2021	1253 bp

L1_I16	PX353743.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	USA	Field foliage collection	2009	604 bp
L1_I17	PZ447380.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Bacillus subtilis Pol...	Field foliage collection	2023	810 bp
L1_I18	EU057603.1	*Bacillus subtilis subsp. subtilis*	Chromosomal rpoB (Coding)	Bacillus subtilis Pol...	Field foliage collection	2021-2025	552 bp
L1_I19	KY777267.1	*Bacillus subtilis subsp. subtilis*	Chromosomal rpoB (Coding)	Viet Nam: Ban Yen Nha...	Field foliage collection	05-Oct-2013	964 bp
L1_I20	MW558953.1	*Bacillus subtilis subsp. subtilis*	Chromosomal rpoB (Coding)	China	Field foliage collection	HMB19198	3441 bp
L1_I21	PP780968.1	*Bacillus subtilis subsp. subtilis*	Chromosomal rpoB (Coding)	Bacillus subtilis Pol...	Field foliage collection	2021-2025	933 bp
L1_I22	PV423063.1	*Bacillus subtilis subsp. subtilis*	Chromosomal rpoB (Coding)	Brazil	Field foliage collection	2022	1138 bp
L1_I23	KY126803.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Brazil	Field foliage collection	2021-2025	554 bp
L1_I24	MG025595.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Thailand: Khon-Kaen	Field foliage collection	2021-2025	792 bp
L1_I25	MH427043.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Bacillus subtilis Pol...	Field foliage collection	2021-2025	504 bp
L1_I26	MK608773.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Bacillus subtilis Pol...	Field foliage collection	BU1814	964 bp
L1_I27	MT123514.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Bacillus subtilis Pol...	Field foliage collection	2021-2025	600 bp
L1_I28	OM885371.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	China	Field foliage collection	2021-2025	1171 bp
L1_I29	ON132476.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Brazil	Field foliage collection	2017	1078 bp
L1_I30	OP435792.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Peru: Tuctilla, Amazo...	Field foliage collection	2021-2025	1003 bp
L1_I31	OQ408213.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Bacillus subtilis Pol...	Field foliage collection	2021-2025	551 bp
L1_I32	OR820779.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	China	Field foliage collection	2021-2025	633 bp
L1_I33	PP505857.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Bacillus subtilis Pol...	Field foliage collection	2021-2025	766 bp
L1_I34	PQ505076.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Bacillus subtilis Pol...	Field foliage collection	10378	958 bp
L1_I35	PV610715.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	Brazil	Field foliage collection	2017	1243 bp
L1_I36	PX229898.1	*Bacillus subtilis*	Chromosomal rpoB (Coding)	China	Field foliage collection	10-Jun-2024	535 bp
L2_I01	LC957486.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	Bacillus subtilis Slo...	Field foliage collection	2006	1600 bp
L2_I02	PV565489.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	Ireland: carlow	Field foliage collection	10-Nov-2023	1381 bp
L2_I03	PX480670.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	South Africa: NW	Field foliage collection	2025	1438 bp
L2_I04	PZ457788.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	China: Shandong	Field foliage collection	2025	1446 bp
L2_I05	QB266695.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	South Korea: JEJU	Field foliage collection	Dec-2022	1552 bp
L2_I06	QB171328.1	*Bacillus subtilis subsp. subtilis*	16S rRNA (Katoh E-INS-i)	China: Zhejiang, Zhou...	Field foliage collection	18-Jan-2025	993 bp
L2_I07	LC957485.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	Bacillus subtilis Slo...	Field foliage collection	2006	1513 bp
L2_I08	PV653573.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	India: Jharkhand	Field foliage collection	10-Aug-2024	976 bp
L2_I09	PX480663.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	South Africa: NW	Field foliage collection	2025	1421 bp

L2_I10	PZ873465.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	India: Apharwath	Field foliage collection	25-Sep-2025	1416 bp
L2_I11	QB033941.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	India: Tirupattur, Ta...	Field foliage collection	20-Sep-2024	1551 bp
L2_I12	LC955963.2	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	Egypt:Giza	Field foliage collection	2026-01-25	1054 bp
L2_I13	PX480666.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	South Africa: NW	Field foliage collection	2025	1415 bp
L2_I14	PZ898992.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	China: Anhui, Hefei	Field foliage collection	2025	1393 bp
L2_I15	QB075360.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	Iran: Mazandaran,Neka	Field foliage collection	25-Apr-2026	1550 bp
L2_I16	PX401644.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	Bacillus subtilis Slo...	Field foliage collection	30-Jul-2025	1400 bp
L2_I17	PZ685380.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	Bacillus subtilis Slo...	Field foliage collection	Jan-2023	1159 bp
L2_I18	QB124885.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	China: Inner mongolia	Field foliage collection	21-Jun-2024	1550 bp
L2_I19	PX533064.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	India: Vellore, Katpadi	Field foliage collection	06-Mar-2024	1347 bp
L2_I20	QB124902.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	China: Inner mongolia	Field foliage collection	21-Jun-2024	1550 bp
L2_I21	PX473054.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	India: Panipat, Haryana	Field foliage collection	05-Mar-2024	878 bp
L2_I22	QB124900.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	China: Inner mongolia	Field foliage collection	21-Jun-2024	1549 bp
L2_I23	PX473053.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	India: Panipat, Haryana	Field foliage collection	05-Mar-2024	877 bp
L2_I24	QB279147.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	India: J&K, Wadura	Field foliage collection	20-Aug-2024	1532 bp
L2_I25	QB124022.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	India: West Bengal, N...	Field foliage collection	Aug-2023	1520 bp
L2_I26	QB124020.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	India: West Bengal, N...	Field foliage collection	Aug-2023	1518 bp
L2_I27	QB181303.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	Pakistan: Punjab	Field foliage collection	01-Jan-2021	1515 bp
L2_I28	QB122990.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	India: West Bengal, N...	Field foliage collection	Aug-2023	1514 bp
L2_I29	QB076960.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	Tunisia: Manouba	Field foliage collection	08-Jan-2024	1513 bp
L2_I30	QB095621.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	Bacillus subtilis Slo...	Field foliage collection	2022	1512 bp
L2_I31	QB103721.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	India: Tamilnadu, Coi...	Field foliage collection	15-Sep-2026	1512 bp
L2_I32	QB145389.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	India: Thanjavur, Tam...	Field foliage collection	10-Dec-2025	1511 bp
L2_I33	QB303853.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	India: Kalyani, West ...	Field foliage collection	09-Sep-2024	1511 bp
L2_I34	QB057409.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	Bacillus subtilis Slo...	Field foliage collection	19-Feb-2026	1508 bp
L2_I35	QB226897.1	*Bacillus subtilis*	16S rRNA (Katoh E-INS-i)	India	Field foliage collection	2025	1506 bp
L3_I01	DJ445529.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	1264 bp
L3_I02	JQ409536.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	20-Apr-2010	752 bp
L3_I03	KJ028113.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2012	697 bp
L3_I04	KR820450.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	736 bp

L3_I05	MF461326.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	771 bp
L3_I06	MK648143.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	772 bp
L3_I07	MN974487.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	757 bp
L3_I08	MT219829.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	561 bp
L3_I09	MZ395294.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	934 bp
L3_I10	OP595524.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2017	1047 bp
L3_I11	PP997997.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Viet Nam: Hanoi	Field foliage collection	304.04	736 bp
L3_I12	PX113384.1	*Bacillus subtilis*	Chromosomal recA (Coding)	China	Field foliage collection	Mar-2024	571 bp
L3_I13	KR820489.1	*Bacillus subtilis subsp. natto*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	736 bp
L3_I14	KX215489.1	*Bacillus subtilis subsp. subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	BCRC 10255	478 bp
L3_I15	DJ445528.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	1192 bp
L3_I16	KR820451.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	736 bp
L3_I17	MN378299.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	736 bp
L3_I18	MT123513.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	510 bp
L3_I19	OP595526.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2017	1047 bp
L3_I20	KX215490.1	*Bacillus subtilis subsp. subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	BCRC 10058	478 bp
L3_I21	DJ445527.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	868 bp
L3_I22	KR820452.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	736 bp
L3_I23	MN378300.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	736 bp
L3_I24	OP595527.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2017	1047 bp
L3_I25	KX215491.1	*Bacillus subtilis subsp. subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	BCRC 10613	478 bp
L3_I26	KR820453.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	736 bp
L3_I27	MN378301.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	736 bp
L3_I28	OP595528.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2011	1047 bp
L3_I29	KX215492.1	*Bacillus subtilis subsp. subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	BCRC 10614	478 bp
L3_I30	KR820454.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	736 bp
L3_I31	MN378302.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	736 bp
L3_I32	OP595529.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2011	1047 bp
L3_I33	KX215493.1	*Bacillus subtilis subsp. subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	BCRC 10615	478 bp
L3_I34	KR820455.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	736 bp

L3_I35	MN378303.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2021-2025	736 bp
L3_I36	OP595530.1	*Bacillus subtilis*	Chromosomal recA (Coding)	Bacillus subtilis Rec...	Field foliage collection	2011	1047 bp
L4_I01	LC878593.1	*Bifidobacterium longum*	16S rRNA (Katoh E-INS-i)	Thailand: Pathum Thani	Field foliage collection	2017	1339 bp
L4_I02	OP542590.1	*Bifidobacterium longum*	16S rRNA (Katoh E-INS-i)	MTCC:25474	Field foliage collection	2021-2025	1538 bp
L4_I03	PP977863.1	*Bifidobacterium longum*	16S rRNA (Katoh E-INS-i)	Germany: Aachen	Field foliage collection	2020-09-25	1523 bp
L4_I04	PQ305302.1	*Bifidobacterium longum*	16S rRNA (Katoh E-INS-i)	India	Field foliage collection	23-Aug-2018	1494 bp
L4_I05	PV549556.1	*Bifidobacterium longum*	16S rRNA (Katoh E-INS-i)	Bifidobacterium longu...	Field foliage collection	2019	1443 bp
L4_I06	PX591135.1	*Bifidobacterium longum*	16S rRNA (Katoh E-INS-i)	Bifidobacterium longu...	Field foliage collection	01-Jan-2022	1482 bp
L4_I07	PZ364499.1	*Bifidobacterium longum*	16S rRNA (Katoh E-INS-i)	Bifidobacterium longu...	Field foliage collection	05-Oct-2025	1517 bp
L4_I08	PV770940.1	*Bifidobacterium longum LL6991*	16S rRNA (Katoh E-INS-i)	Netherlands: Groningen	Field foliage collection	01-Apr-2025	1523 bp
L4_I09	PP196110.1	*Bifidobacterium longum subsp. i...*	16S rRNA (Katoh E-INS-i)	MTCC:25651	Field foliage collection	2021-2025	1469 bp
L4_I10	PQ669664.1	*Bifidobacterium longum subsp. i...*	16S rRNA (Katoh E-INS-i)	Morocco: Oujda	Field foliage collection	2022	1515 bp
L4_I11	PV849150.1	*Bifidobacterium longum subsp. i...*	16S rRNA (Katoh E-INS-i)	South Korea: Gwangju	Field foliage collection	01-Jul-2024	1024 bp
L4_I12	PX806261.1	*Bifidobacterium longum subsp. i...*	16S rRNA (Katoh E-INS-i)	China	Field foliage collection	2013	1518 bp
L4_I13	PZ654930.1	*Bifidobacterium longum subsp. i...*	16S rRNA (Katoh E-INS-i)	India: New Delhi	Field foliage collection	28-Jan-2026	1523 bp
L4_I14	QB181422.1	*Bifidobacterium longum subsp. i...*	16S rRNA (Katoh E-INS-i)	India: Delhi, Delhi U...	Field foliage collection	Jul-2011	1494 bp
L4_I15	PQ896568.1	*Bifidobacterium longum subsp. l...*	16S rRNA (Katoh E-INS-i)	Iran: Tehran, Bioluen...	Field foliage collection	2024	1428 bp
L4_I16	PV478448.1	*Bifidobacterium longum subsp. l...*	16S rRNA (Katoh E-INS-i)	Bifidobacterium longu...	Field foliage collection	Apr-2025	1460 bp
L4_I17	PX806262.1	*Bifidobacterium longum subsp. l...*	16S rRNA (Katoh E-INS-i)	China	Field foliage collection	2011	1523 bp
L4_I18	PZ267072.1	*Bifidobacterium longum subsp. l...*	16S rRNA (Katoh E-INS-i)	Bifidobacterium longu...	Field foliage collection	11-Nov-2023	1430 bp
L4_I19	QB181421.1	*Bifidobacterium longum subsp. l...*	16S rRNA (Katoh E-INS-i)	India: Delhi, Delhi U...	Field foliage collection	Aug-2010	1474 bp
L4_I20	OP179823.1	*Bifidobacterium longum subsp. s...*	16S rRNA (Katoh E-INS-i)	Austria: Vienna	Field foliage collection	2020	1283 bp
L4_I21	PQ407770.1	*Bifidobacterium longum subsp. s...*	16S rRNA (Katoh E-INS-i)	Bifidobacterium longu...	Field foliage collection	RACS_D10.19	1233 bp
L4_I22	PV907532.1	*Bifidobacterium longum subsp. s...*	16S rRNA (Katoh E-INS-i)	Bifidobacterium longu...	Field foliage collection	2024	1190 bp
L4_I23	PX443643.1	*Bifidobacterium longum subsp. s...*	16S rRNA (Katoh E-INS-i)	Bifidobacterium longu...	Field foliage collection	2024	1415 bp
L4_I24	PZ610382.1	*Bifidobacterium longum subsp. s...*	16S rRNA (Katoh E-INS-i)	China	Field foliage collection	2026	1377 bp
L4_I25	OP132828.1	*Bifidobacterium longum*	16S rRNA (Katoh E-INS-i)	Bifidobacterium longu...	Field foliage collection	2021-2025	1523 bp
L4_I26	PP977953.1	*Bifidobacterium longum*	16S rRNA (Katoh E-INS-i)	Germany: Aachen	Field foliage collection	2019-07-25	1523 bp
L4_I27	PQ775115.1	*Bifidobacterium longum*	16S rRNA (Katoh E-INS-i)	Iraq: Erbil	Field foliage collection	12-May-2024	1494 bp
L4_I28	PV124085.1	*Bifidobacterium longum*	16S rRNA (Katoh E-INS-i)	Bifidobacterium longu...	Field foliage collection	Aug-2024	1410 bp

L4_I29	PX619157.1	*Bifidobacterium longum*	16S rRNA (Katoh E-INS-i)	Bifidobacterium longu...	Field foliage collection	01-Jan-2022	1452 bp
L4_I30	PZ043081.1	*Bifidobacterium longum*	16S rRNA (Katoh E-INS-i)	Bifidobacterium longu...	Field foliage collection	05-Aug-2024	1473 bp
L4_I31	PV907651.1	*Bifidobacterium longum subsp. i...*	16S rRNA (Katoh E-INS-i)	Bifidobacterium longu...	Field foliage collection	2024	949 bp
L4_I32	PX443649.1	*Bifidobacterium longum subsp. i...*	16S rRNA (Katoh E-INS-i)	Bifidobacterium longu...	Field foliage collection	2024	1417 bp
L4_I33	PZ654931.1	*Bifidobacterium longum subsp. i...*	16S rRNA (Katoh E-INS-i)	India: New Delhi	Field foliage collection	28-Jan-2026	1523 bp
L4_I34	PV765524.1	*Bifidobacterium longum subsp. l...*	16S rRNA (Katoh E-INS-i)	Bifidobacterium longu...	Field foliage collection	2024	1397 bp
L4_I35	PX443652.1	*Bifidobacterium longum subsp. l...*	16S rRNA (Katoh E-INS-i)	Bifidobacterium longu...	Field foliage collection	2024	1420 bp
L4_I36	PZ780079.1	*Bifidobacterium longum subsp. l...*	16S rRNA (Katoh E-INS-i)	Bifidobacterium longu...	Field foliage collection	2021	1411 bp
L5_I01	OP246375.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	Lactiplantibacillus p...	Field foliage collection	2021-2025	1447 bp
L5_I02	OZ568211.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	Lactiplantibacillus p...	Field foliage collection	2024	1093 bp
L5_I03	PP732472.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	China	Field foliage collection	2021-2025	1437 bp
L5_I04	PX369006.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	China	Field foliage collection	27-Aug-2025	1472 bp
L5_I05	PZ364493.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	Lactiplantibacillus p...	Field foliage collection	05-Oct-2025	1567 bp
L5_I06	QB289771.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	China: Henan,Zhengzhou	Field foliage collection	2022	1563 bp
L5_I07	PZ746697.1	*Lactiplantibacillus plantarum s...*	16S rRNA (Katoh E-INS-i)	China: Beijing,human ...	Field foliage collection	2025	1503 bp
L5_I08	QB145359.1	*Lactiplantibacillus plantarum s...*	16S rRNA (Katoh E-INS-i)	India: Odisha,Baripada	Field foliage collection	26-Nov-2022	1445 bp
L5_I09	OZ568209.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	Lactiplantibacillus p...	Field foliage collection	2024	987 bp
L5_I10	PX363068.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	China: Hainan	Field foliage collection	Feb-2024	1434 bp
L5_I11	PZ840568.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	China: Sichuan, Yibin...	Field foliage collection	2025	1563 bp
L5_I12	QB074707.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	Nigeria: Ogun, Ota, F...	Field foliage collection	Apr-2023	1536 bp
L5_I13	PZ746698.1	*Lactiplantibacillus plantarum s...*	16S rRNA (Katoh E-INS-i)	China: Beijing,human ...	Field foliage collection	2025	1502 bp
L5_I14	QB073255.1	*Lactiplantibacillus plantarum s...*	16S rRNA (Katoh E-INS-i)	Lactiplantibacillus p...	Field foliage collection	16-Dec-2025	1154 bp
L5_I15	PX328944.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	Lactiplantibacillus p...	Field foliage collection	2024	1193 bp
L5_I16	PZ766237.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	Nigeria: Ogun, Ota	Field foliage collection	Mar-2026	1538 bp
L5_I17	QB169649.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	Nigeria: Kaduna	Field foliage collection	Apr-2026	1533 bp
L5_I18	PZ924552.1	*Lactiplantibacillus plantarum s...*	16S rRNA (Katoh E-INS-i)	West Bank: Nablus, Pa...	Field foliage collection	19-Feb-2026	1061 bp
L5_I19	PZ766235.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	Nigeria: Ogun, Ota	Field foliage collection	Mar-2026	1531 bp
L5_I20	QB169652.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	Nigeria: Ogun state	Field foliage collection	Apr-2026	1531 bp
L5_I21	PZ766236.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	Nigeria: Ogun, Ota	Field foliage collection	Mar-2026	1530 bp
L5_I22	QB169651.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	Nigeria: Ogun state	Field foliage collection	Apr-2026	1530 bp

L5_I23	PZ780035.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	Indonesia: Kalimantan...	Field foliage collection	12-Feb-2025	1519 bp
L5_I24	QB103677.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	Nigeria: Sango Ota, I...	Field foliage collection	Apr-2026	1529 bp
L5_I25	PZ852536.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	Iran: Mazandaran	Field foliage collection	22-Feb-2024	1516 bp
L5_I26	QB160337.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	Lactiplantibacillus p...	Field foliage collection	2026	1521 bp
L5_I27	PZ841953.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	China: Shanghai, Minh...	Field foliage collection	Dec-2024	1503 bp
L5_I28	QB326300.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	India: Tamil Nadu, Ch...	Field foliage collection	10-Jan-2023	1519 bp
L5_I29	PZ859208.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	China: Hubei Province	Field foliage collection	2024	1503 bp
L5_I30	QB326301.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	India: Tamil Nadu, Ch...	Field foliage collection	10-Apr-2023	1519 bp
L5_I31	PZ779862.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	Myanmar: Kyaukse	Field foliage collection	20-Dec-2024	1489 bp
L5_I32	QB289648.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	China: Beijing,human ...	Field foliage collection	2025	1501 bp
L5_I33	PZ747762.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	India: Karnataka, Ban...	Field foliage collection	15-Jun-2025	1488 bp
L5_I34	QB319230.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	China: Sichuan, Yaan	Field foliage collection	2026	1491 bp
L5_I35	PZ852372.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	China: Wuhan	Field foliage collection	2022	1485 bp
L5_I36	QB313142.1	*Lactiplantibacillus plantarum*	16S rRNA (Katoh E-INS-i)	Pakistan: Lahore, Lah...	Field foliage collection	2026-02-02	1489 bp
L6_I01	GU799694.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	2021-2025	492 bp
L6_I02	KF837137.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10056	497 bp
L6_I03	OP618394.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	ATCC:19435	Field foliage collection	ATCC 19435	3591 bp
L6_I04	GU799687.1	*Lactococcus lactis subsp. hordniae*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	DSM 20450	492 bp
L6_I05	HM991214.1	*Lactococcus lactis subsp. hordniae*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	LMG4961	486 bp
L6_I06	GU799688.1	*Lactococcus lactis subsp. lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	DSM 20481	428 bp
L6_I07	HM991215.1	*Lactococcus lactis subsp. lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	LMG7930	487 bp
L6_I08	GU799693.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	2021-2025	435 bp
L6_I09	KF837138.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10065	497 bp
L6_I10	KF837139.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10066	497 bp
L6_I11	KF837140.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10876	497 bp
L6_I12	KF837141.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10951	497 bp
L6_I13	KF837142.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10962	497 bp
L6_I14	KF837143.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10987	497 bp
L6_I15	KF837144.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10994	497 bp
L6_I16	KF837145.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10059	497 bp

L6_I17	KF837146.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10061	497 bp
L6_I18	KF837147.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10067	497 bp
L6_I19	KF837148.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10071	497 bp
L6_I20	KF837149.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10347	497 bp
L6_I21	KF837150.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10856	497 bp
L6_I22	KF837151.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10857	497 bp
L6_I23	KF837152.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10859	497 bp
L6_I24	KF837153.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10864	497 bp
L6_I25	KF837154.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10869	497 bp
L6_I26	KF837155.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10872	497 bp
L6_I27	KF837156.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10878	497 bp
L6_I28	KF837157.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10881	497 bp
L6_I29	KF837158.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10940	497 bp
L6_I30	KF837159.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10941	497 bp
L6_I31	KF837160.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10943	497 bp
L6_I32	KF837161.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10946	497 bp
L6_I33	KF837162.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10950	497 bp
L6_I34	KF837163.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10955	497 bp
L6_I35	KF837164.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10978	497 bp
L6_I36	KF837165.1	*Lactococcus lactis*	Chromosomal rpoB (Coding)	Dairy Starter Lactoco...	Field foliage collection	IMAU10979	497 bp