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Quartet Multispecies Coalescent & Incomplete Lineage Sorting Across 1,064 Gene Trees (28.66 Million Quartets): 4-Stage Native Quartet MSC & ABBA-BABA Engine vs. ASTRAL v5.7.8

Head-to-Head Calibration of a 4-Stage Native Rust Quartet Multispecies Coalescent, Bayesian Local Posterior Probability, and ABBA-BABA Introgression Engine Against ASTRAL v5.7.8 Across Four Multi-Locus Vertebrate Cohorts

When ancestral populations diverge across rapid evolutionary intervals, ancestral polymorphisms frequently persist across successive speciation events -- a population-genetic process known as Incomplete Lineage Sorting (ILS) that causes individual gene trees to conflict with the overarching species phylogeny. We benchmark our 4-Stage Native Rust Quartet Multispecies Coalescent (MSC), Bayesian Local Posterior Probability (LPP), and ABBA-BABA Introgression Engine against ASTRAL v5.7.8 across four multi-locus cohorts comprising 1,064 gene trees and 28,656,824 quartets (with upstream sequence alignment, substitution model selection, and ML gene-tree inference executed exclusively via native engines). Across all four cohorts, the native quartet engine achieves 100.00% topological concordance (Robinson-Foulds distance $RF = 0$ across all 138 internal bipartitions), exact quartet-score identity (ratio = 1.000000), Pearson $r(q_1) = 1.0000$ on quartet support frequencies, and $r(\tau) = 0.9873$ on coalescent branch lengths at a 3.49x to 37.73x (mean 23.79x) wall-clock speedup.

1. Gene-Tree Discordance, the Anomaly Zone, and Quartet Consistency Under the Multispecies Coalescent

In multi-locus phylogenomics, concatenating hundreds of loci into a single supermatrix implicitly assumes that every genomic region shares an identical genealogical history. Under Kingman's coalescent and the Multispecies Coalescent (MSC) model (Degnan & Rosenberg 2009), the probability that two lineages sampled from sister species A and B coalesce within their shared ancestral internode of length $\tau = \Delta t / (2N_e)$ (measured in Coalescent Units, CU) is $1 - e^{-\tau}$. With probability $e^{-\tau}$, the two lineages fail to coalesce before reaching the deeper ancestral population ABC, where all three lineages coalesce at equal probability (1/3 each) into one of the three possible rooted topologies:

* Concordant Quartet Topology (q_1): $q_1 = 1 - (2/3)e^{-\tau}$, which exceeds 1/3 for every positive internode length $\tau > 0$.

* Discordant Quartet Topologies (q_2, q_3): $q_2 = q_3 = (1/3)e^{-\tau}$; under strictly neutral panmictic incomplete lineage sorting without post-speciation gene flow.

Crucially, while rooted 5-taxon and larger trees exhibit an anomaly zone ($\tau < 0.156$ CU) in which the most probable rooted gene tree is discordant with the species

tree -- causing concatenation and greedy consensus methods to converge on an incorrect topology as more genes are added -- unrooted 4-taxon quartets have no anomaly zone . For any four species $\{a, b, c, d\}$, the true unrooted species quartet $ab|cd$ is strictly the most probable quartet topology across gene trees whenever the internal branch $\tau > 0$ (Mirarab et al. 2014 ; Zhang et al. 2018).

To evaluate species-tree inference within our self-contained bioinformatics architecture, we implemented a 4-Stage Native Rust Quartet Multispecies Coalescent Engine and benchmarked it head-to-head against ASTRAL v5.7.8 across four multi-locus cohorts spanning 1,064 gene trees and 28,656,824 quartets:

* Stage 1 -- 64-Bit Clade-Mask Decomposition & Search-Space Completion: Parses unrooted or rooted Newick gene trees into 64-bit integer leaf masks, extracts all observed gene-tree clade bipartitions, and completes the candidate cluster lattice $\mathcal{X}$; via weighted co-occurrence UPGMA hierarchy completion and sparse anomaly-zone symmetric differences.

* Stage 2 -- Deduplicated Degree-3 Closed-Form Quartet Dynamic Programming: Compresses all internal nodes across the K input gene trees into unique sorted tripartition tuples with multiplicity weights, evaluating the exact tripartition quartet weight $W(Y, Z, S \setminus X)$ via hardware POPCNT instructions across the dynamic-programming recurrence $V(X) = \max_{Y \subseteq X} [V(Y) + V(X \setminus Y) + W(Y, X \setminus Y, S \setminus X)]$.

* Stage 3 -- Quartet-Polished Nearest-Neighbor Interchange (NNI) Verification: Performs exact quadripartition quartet evaluation around every internal species-tree branch to verify global optimality across adjacent NNI topologies.

* Stage 4 -- Bayesian Local Posterior Probability (LPP), Coalescent Units (τ), & Nucleotide ABBA-BABA Screening: Computes per-branch quartet frequencies (q_1, q_2, q_3), quartet weights (f_1, f_2, f_3), Gene Concordance Factors (gCF), Sayyari & Mirarab (2016) Beta-integral Bayesian Local Posterior Probabilities (LPP = pp_1), Laplace-smoothed coalescent branch lengths $\tau = -\ln((3/2)(1 - q_1))$ CU, discordance asymmetry χ^2 , and nucleotide ABBA-BABA Patterson's D - statistics .

2. Four-Cohort Head-to-Head Calibration: Native Quartet MSC vs. ASTRAL v5.7.8

We evaluated both engines across four distinct phylogenomic regimes: (1) a 16-specimen Carnivora sub-locus window cohort generated from raw NCBI RefSeq mitochondrial COX1 sequences using exclusively native upstream stages (Native Gotoh alignment -> Native Felsenstein ModelTest -> 16 window ML gene trees via Native 4-Stage BIONJ+NNI), (2) the 14-taxon Primate and Euarchontoglires 424-nuclear-gene benchmark (Song et al. 2012), (3) the 37-taxon Amniote and Placental Mammal 424-nuclear-gene radiation benchmark (28,003,080 quartets; Song et al. 2012), and (4) a 200-gene-tree 14-taxon deep-coalescent 5x ILS anomaly-zone cohort.

| Cohort ID | Taxonomic & Evolutionary Scope | Taxa | Internal Splits | Gene Trees | Total Quartets | Native Quartet Score | ASTRAL Quartet Score | Normalized Q-Score | RF Distance | Split Match (%) | $r(q_1)$ | $r(CU)$ | Native Time (ms) | ASTRAL Time (ms) | Speedup (x) |

| COHORT-01 || Carnivora 16-Window Native Chain (COX1) || 16 || 13 || 16 ||
29120 || 27482 || 27482 || 0.943800 || 0 || 100.00 || 1.0000 || 0.9525 ||
5.18 || 195.49 || 37.73 |

| COHORT-02 || Euarchontoglires & Primates (Song et al. 2012) || 14 || 11 || 424
|| 424424 || 389734 || 389734 || 0.918300 || 0 || 100.00 || 1.0000 || 0.9993
|| 20.27 || 482.83 || 23.82 |

| COHORT-03 || Placental Mammal Radiation (Song et al. 2012) || 37 || 34 || 424
|| 28003080 || 25526915 || 25526915 || 0.911600 || 0 || 100.00 || 1.0000 ||
0.9974 || 333.58 || 1165.15 || 3.49 |

| COHORT-04 || Deep Coalescent 5x ILS Anomaly Zone || 14 || 11 || 200 || 200200
|| 118477 || 118477 || 0.591800 || 0 || 100.00 || 1.0000 || 1.0000 || 15.45
|| 465.49 || 30.12 |

| CUMULATIVE / MEAN || All 4 Multi-Locus Phylogenomic Cohorts || 81 || 69 (138) |
| 1064 || 28656824 || 26062608 || 26062608 || 0.841375 || 0 || 100.00 ||
1.0000 || 0.9873 || 374.48 || 2308.96 || 23.79 |

Generated by: Native Rust Quartet Multispecies Coalescent Engine (coalescent.rs) *
ASTRAL v5.7.8 (Mirarab et al.)

Across all 28,656,824 evaluated quartets, the native Rust engine and ASTRAL v5.7.8 recover the exact same optimal quartet score on every cohort -- including 25,526,915 / 28,003,080 satisfied quartets (91.1575%) on the 37-taxon mammalian radiation and 118,477 / 200,200 satisfied quartets (59.1793%) in the 5x ILS anomaly-zone cohort -- with zero Robinson-Foulds split discrepancies (RF = 0/26, 0/22, 0/68, and 0/22). Deduplicating internal gene-tree tripartitions reduces the 424-gene primate search to 20.27 ms (23.82x faster than ASTRAL v5.7.8 at 482.83 ms) and completes the 28-million-quartet 37-taxon mammalian search in 333.58 ms (3.49x faster than ASTRAL v5.7.8 at 1,165.15 ms).

3. Resolving the Five Classic Incomplete Lineage Sorting Zones of the Placental Mammal Radiation

The diversification of placental mammals (Eutheria) near the Cretaceous-Paleogene (K-Pg) transition is a textbook example of rapid evolutionary radiation accompanied by deep incomplete lineage sorting (Song et al. 2012). Examining the per-branch quartet frequencies (q_1 , q_2 , q_3), quartet weights (f_1 , f_2 , f_3 out of 424 nuclear orthologs), Bayesian Local Posterior Probabilities (LPP), and coalescent branch lengths (τ ; in CU) across the 37-taxon amniote phylogeny highlights five classic rapid-radiation internodes alongside high-concordance crown clades:

| Evolutionary Clade / Internode || q_1 (Main) || q_2 (Alt 1) || q_3 (Alt 2) || f_1 (Loci) || f_2 (Loci) || f_3 (Loci) || gCF (%) || Native LPP || ASTRAL LPP || Native CU || ASTRAL CU || Asymmetry Chi2 || Coalescent Regime Classification |

| ILS Zone #1: Atlantogenata (Xenarthra + Afrotheria) || 0.4082 || 0.2811 || 0.3107 || 173.08 || 119.18 || 131.74 || 34.67 || 0.9977 || 0.9977 || 0.1175 || 0.1175 || 0.63 || Deep Rapid-Radiation Polytomy Zone (τ ; < 0.20 CU) |

| ILS Zone #2: Scrotifera (Chiroptera + Fereuungulata) || 0.4068 || 0.3131 || 0.2800 || 172.50 || 132.77 || 118.73 || 33.96 || 0.9972 || 0.9972 || 0.1152 |

| 0.1152 || 0.78 || Deep Rapid-Radiation Polytomy Zone (τ ; < 0.20 CU) |

| ILS Zone #3: Fereuungulata (Zooamata vs. Cetartiodactyla) || 0.3756 || 0.3172 |
 | 0.3072 || 159.26 || 134.49 || 130.25 || 33.02 || 0.9056 || 0.9044 || 0.0641
 | 0.0641 || 0.07 || Extreme Anomaly-Zone Short Internode (τ ; $= 0.0641$ CU) |

| ILS Zone #4: Euarchontoglires / Scandentia (Tree Shrew + Glires) || 0.3893 ||
 0.3604 || 0.2503 || 165.04 || 152.81 || 106.15 || 28.54 || 0.9096 || 0.9084 |
 | 0.0876 || 0.0861 || 8.41 || Short Internode + Asymmetric Discordance (χ ; [2
 $= 8.41$) |

ILS Zone #5: Hominini (Homo sapiens + Pan troglodytes vs. Gorilla)		0.6512												
0.1841		0.1647		276.12		78.06		69.82		63.68		1.0000		1.0000
0.6479		0.6435		0.46		Classic ~35% Great-Ape Incomplete Lineage Sorting								

| Rodentia Sub-Clade (Cavia + Dipodomys + Murinae) || 0.4267 || 0.2941 || 0.2792
 || 180.93 || 124.71 || 118.36 || 38.92 || 0.9999 || 0.9999 || 0.1492 ||
 0.1492 || 0.17 || Early Rodent Radiation Short Internode (τ ; $= 0.1492$ CU) |

| Superorder Laurasiatheria (Eulipotyphla + Scrotifera) || 0.5680 || 0.2312 ||
 0.2007 || 240.84 || 98.04 || 85.11 || 48.82 || 1.0000 || 1.0000 || 0.4308 ||
 0.4308 || 0.91 || Moderate Incomplete Lineage Sorting (0.20-1.00 CU) |

| Haplorhini (Tarsius + Anthropeidea) || 0.6539 || 0.1706 || 0.1755 || 277.26 |
 | 72.33 || 74.41 || 62.26 || 1.0000 || 1.0000 || 0.6556 || 0.6512 || 0.03 ||
 Moderate Incomplete Lineage Sorting (0.20-1.00 CU) |

| Cetancodontamorpha + Suina (Sus + [Tursiops + Bos]) || 0.6497 || 0.1854 ||
 0.1649 || 275.48 || 78.59 || 69.92 || 63.92 || 1.0000 || 1.0000 || 0.6392 ||
 0.6392 || 0.51 || Moderate Incomplete Lineage Sorting (0.20-1.00 CU) |

| Paenungulata (Procavia Hyrax + Loxodonta Elephant) || 0.8543 || 0.0893 ||
 0.0563 || 362.24 || 37.88 || 23.88 || 84.91 || 1.0000 || 1.0000 || 1.5072 ||
 1.5072 || 3.17 || High-Concordance Coalescent Split (> 1.00 CU) |

| Chiroptera (Myotis Microbat + Pteropus Megabat) || 0.8609 || 0.0814 || 0.0577
 || 365.04 || 34.49 || 24.46 || 84.43 || 1.0000 || 1.0000 || 1.5530 || 1.5530
 || 1.70 || High-Concordance Coalescent Split (> 1.00 CU) |

| Boreoeutheria (Laurasiatheria + Euarchontoglires) || 0.9093 || 0.0482 || 0.0425
 || 385.54 || 20.43 || 18.02 || 80.90 || 1.0000 || 1.0000 || 1.9714 || 1.9714
 || 0.15 || High-Concordance Coalescent Split (> 1.00 CU) |

| Homininae (Gorilla + [Homo + Pan]) || 0.9378 || 0.0227 || 0.0396 || 397.61
 || 9.61 || 16.79 || 91.27 || 1.0000 || 1.0000 || 2.3711 || 2.3363 || 1.95 |
 | High-Concordance Coalescent Split (> 1.00 CU) |

| Ferae / Carnivora (Canis Dog + Felis Cat) || 0.9658 || 0.0177 || 0.0165 ||
 409.50 || 7.50 || 7.00 || 96.46 || 1.0000 || 1.0000 || 2.9058 || 2.9058 ||
 0.02 || High-Concordance Coalescent Split (> 1.00 CU) |

| Afrotheria (Tenrec + [Hyrax + Elephant]) || 0.9702 || 0.0248 || 0.0051 ||
 411.34 || 10.50 || 2.16 || 96.23 || 1.0000 || 1.0000 || 3.0324 || 3.0324 ||
 5.50 || High-Concordance Coalescent Split (> 1.00 CU) |

| Lagomorpha (Oryctolagus Rabbit + Ochotona Pika) || 0.9811 || 0.0164 || 0.0025

|| 416.00 || 6.93 || 1.07 || 97.64 || 1.0000 || 1.0000 || 3.4494 || 3.4494 |
 | 4.30 || High-Concordance Coalescent Split (> 1.00 CU) |

| Cetartiodactyla Crown (Vicugna + Suina + Cetancodonta) || 0.9836 || 0.0085 ||
 0.0079 || 417.04 || 3.62 || 3.33 || 97.41 || 1.0000 || 1.0000 || 3.5728 ||
 3.5728 || 0.01 || High-Concordance Coalescent Split (> 1.00 CU) |

| Xenarthra (Choloepus Sloth + Dasypus Armadillo) || 0.9936 || 0.0041 || 0.0023
 || 421.28 || 1.75 || 0.97 || 99.06 || 1.0000 || 1.0000 || 4.3332 || 4.3332 |
 | 0.22 || High-Concordance Coalescent Split (> 1.00 CU) |

| Metatheria / Marsupialia (Monodelphis + Macropus) || 0.9976 || 0.0000 ||
 0.0024 || 423.00 || 0.00 || 1.00 || 99.76 || 1.0000 || 1.0000 || 4.9535 ||
 4.9535 || 0.00 || Deep Crown Marsupial Split (423/424 Loci Concordant) |

| Murinae (Mus musculus + Rattus norvegicus) || 0.9981 || 0.0019 || 0.0001 ||
 423.18 || 0.79 || 0.03 || 99.76 || 1.0000 || 1.0000 || 5.0459 || 5.0459 ||
 0.00 || Near-Complete Lineage Sorting (> 5.00 CU) |

Generated by: Native Rust Quartet Multispecies Coalescent Engine (coalescent.rs) *
 ASTRAL v5.7.8 (Mirarab et al.)

Several biological patterns stand out in Table 2:

* Great-Ape Incomplete Lineage Sorting (Homininae): Across the 424 nuclear orthologs, the Human + Chimpanzee sister split exhibits $q_1 = 0.6512$ ($f_1 = 276.12$ loci) versus $q_2 = 0.1841$ ((Chimp, Gorilla), Human; $f_2 = 78.06$ loci) and $q_3 = 0.1647$ ((Human, Gorilla), Chimp; $f_3 = 69.82$ loci), yielding a coalescent internode of $\tau = 0.6435$ CU (LPP = 1.0000) and symmetric alternative quartet frequencies ($\chi^2 [2] = 0.46$). This matches whole- genome primate comparative estimates indicating that ~34.9% of the human nuclear genome sorts more closely with Gorilla than with Chimpanzee due to ancestral effective population size in the Miocene Homininae ancestor (Scally et al. 2012).

* Near-Polytomy Diversification in Laurasiatheria (Fereuungulata & Scrotifera): Within Laurasiatheria, the divergence of Perissodactyla (Horse) + Ferae (Dog + Cat) from Cetartiodactyla occurs across an internode of just $\tau = 0.0641$ CU , where the main quartet topology ($q_1 = 0.3756$, $f_1 = 159.26$ loci) barely exceeds the two discordant alternatives ($q_2 = 0.3172$, $q_3 = 0.3072$). Even at $\tau = 0.0641$ CU, integrating quartet counts across 424 independent loci yields a Bayesian Local Posterior Probability of LPP = 0.9056 (ASTRAL LPP = 0.9044).

* Asymmetric Discordance in Scandentia (Tree Shrew): Whereas Atlantogenata, Scrotifera, Fereuungulata, and Hominini display symmetric discordant quartet frequencies ($q_2 \sim q_3$, $\chi^2 [2] \leq 0.78$), the placement of Scandentia (Tupaia belangeri) sister to Glires exhibits $q_1 = 0.3893$ (Tree Shrew + Glires), $q_2 = 0.3604$ (Tree Shrew + Primates), and $q_3 = 0.2503$ (Primates + Glires), producing a quartet asymmetry score of $\chi^2 [2] = 8.41$ that flags this branch as a candidate locus of ancient post-divergence gene flow or substitution-rate heterogeneity across Euarchontoglires.

4. Visual Species Cladogram & Newick Topologies

Below is the 37-taxon Amniota and Placental Mammal coalescent species cladogram annotated with exact quartet support (q_1 , q_2 , q_3), Bayesian Local Posterior Probability (LPP), and coalescent branch lengths (τ ; in CU), followed by the machine-readable Newick species trees for COHORT-02 (Primates) and COHORT-03 (Mammals).

Generated by: Native Rust Quartet Multispecies Coalescent Engine (`coalescent.rs`) *
 ASTRAL v5.7.8 (Mirarab et al.)

Generated by: Native Rust Quartet Multispecies Coalescent Engine (`coalescent.rs`) *
 ASTRAL v5.7.8 (Mirarab et al.)

5. Nucleotide ABBA-BABA (Patterson's D) Introgression Screening on Carnivora Quartets

While quartet tree frequencies (q_1 , q_2 , q_3) summarize topological discordance at the locus level, site-level ABBA-BABA tests (Green et al. 2010 ; Patterson et al. 2012) directly count biallelic parsimony-informative sites across four aligned sequences (((P_1 , P_2) , P_3) , O) where the outgroup O carries ancestral allele A and a derived allele B is shared either by (P_1 , P_2) (concordant BBAA), (P_2 , P_3) (discordant ABBA), or (P_1 , P_3) (discordant BABA). Table 3 reports the nucleotide ABBA-BABA tests computed on our 16-specimen Carnivora mitogenome alignment alongside focal sequence alignment windows illustrating informative biallelic columns.

Quartet ID	P1 Taxon	P2 Taxon	P3 Taxon	Outgroup (O)	BBAA Sites	ABBA Sites	BABA Sites	Patterson D	Z-Score	Evolutionary & Genealogical Interpretation
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ABBA-01-URSIDAE	Ursus americanus (NC_003426)	Ursus arctos (NC_003427)	Ursus maritimus (NC_003428)	Ursus thibetanus (NC_009971)	4	70	2	0.9444	8.0139	Strong derived site sharing between U. arctos and U. maritimus (70 ABBA vs. 2 BABA), reflecting their sister-clade relationship and documented Pleistocene mitochondrial introgression across Holarctic bears.
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ABBA-02-FELIDAE	Panthera tigris (NC_010642)	Panthera pardus (NC_010641)	Felis catus (NC_001700)	Meles anakuma (NC_009677)	36	27	24	0.0588	0.4201	High BBAA concordance (36 sites) uniting Panthera relative to Felis , with balanced ABBA (27) vs. BABA (24) counts ($D = +0.0588$, $Z = 0.42$) consistent with symmetric neutral sorting and third-codon homoplasy.
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ABBA-03-CANIDAE	Canis lupus (NC_008092)	Canis l. familiaris (NC_002008)	Vulpes vulpes (NC_008434)	Ursus arctos (NC_003427)	88	0	0	0.0000	0.0000	Complete BBAA synapomorphic concordance (88 BBAA vs. 0 ABBA / 0 BABA; $D = 0.0000$) uniting Gray wolf and Domestic dog relative to Red fox.
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Generated by: Native Rust Nucleotide ABBA-BABA Patterson's D Engine (`coalescent.rs`)

Generated by: Native Rust Nucleotide ABBA-BABA Patterson's D Engine (`coalescent.rs`) * Native Rust Column-Compressed Felsenstein ModelTest Engine (`modeltest.rs`) *

Native Rust Gotoh 3-State Affine-Gap & 9-mer Anchor Multiple Sequence Aligner (phylo.rs)

6. Discussion & Key Takeaways

This four-cohort calibration establishes that our 4-Stage Native Rust Quartet Multispecies Coalescent Engine achieves exact mathematical and topological parity with ASTRAL v5.7.8 across 1,064 gene trees and 28,656,824 quartets while executing 3.49x to 37.73x faster. Within a computational bioinformatics and molecular systematics workflow, these results highlight three practical takeaways:

* Why Quartet Coalescent Inference Complements Supermatrix ML: When internodes span fewer than 0.20 coalescent units -- such as the K-Pg placental mammal splits in *Fereuungulata* (0.0641 CU), *Scandentia* (0.0861 CU), *Scrotifera* (0.1152 CU), and *Atlantogenata* (0.1175 CU) -- more than 59% of individual nuclear gene trees conflict with the species tree. Evaluating unrooted gene-tree quartets avoids the multi-taxon concatenation anomaly zone and provides calibrated Bayesian Local Posterior Probabilities (LPP) and coalescent branch lengths (τ).

* Distinguishing Neutral ILS from Introgression Candidates: Under panmictic incomplete lineage sorting alone, the two discordant quartet topologies around any internal branch are expected to occur at equal frequencies ($q_2 \sim q_3$). Combining branch-level quartet asymmetry (χ^2) with site-level nucleotide ABBA-BABA Patterson's D -statistics surfaces candidate branches (such as the *Scandentia*/*Glires* split at χ^2 = 8.41 or Holarctic *Ursus* mitochondrial capture) that merit deeper demographic or pangenomic investigation.

* Self-Contained Native Execution: By chaining Native Gotoh alignment, Native Felsenstein ModelTest, Native 4-Stage ML gene-tree inference, and Native Quartet MSC species-tree reconstruction in pure Rust, multi-locus phylogenomic pipelines can run end-to-end without external Java VM subprocess overhead while preserving on-demand --coalescent astral cross-validation.

7. Provenance Ledger & Benchmark Dataset Verification

#	Cohort / Taxonomic Group	Accession / Dataset ID	Organism / Clade	Loci / Length	Quartets	Database Verification
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1	COHORT-01 (Ursidae)	NC_003427.1 / AP012578.1	<i>Ursus arctos</i> (Brown bear -- Eurasian & Hokkaido)	16 windows (1,545 bp)	29120	NCBI RefSeq / GenBank Verified
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2	COHORT-01 (Ursidae)	NC_003428.1 / GU573490.1	<i>Ursus maritimus</i> (Polar bear -- RefSeq & Isolate 495)	16 windows (1,545 bp)	29120	NCBI RefSeq / GenBank Verified
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3	COHORT-01 (Ursidae)	NC_003426.1 / JX196366.1	<i>Ursus americanus</i> (American black bear)	16 windows (1,545 bp)	29120	NCBI RefSeq / GenBank Verified
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4	COHORT-01 (Ursidae)	NC_009971.1	<i>Ursus thibetanus</i> (Asian black bear)	16 windows (1,545 bp)	29120	NCBI RefSeq Verified
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5	COHORT-01 (Felidae)	NC_010642.1 / EF551003.1	<i>Panthera tigris</i> (Tiger)			
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-- RefSeq & Amur) || 16 windows (1,545 bp) || 29120 || NCBI RefSeq / GenBank Verified |

| 6 || COHORT-01 (Felidae) || NC_010641.1 / NC_001700.1 || Panthera pardus & Felis catus || 16 windows (1,545 bp) || 29120 || NCBI RefSeq Verified |

| 7 || COHORT-01 (Canidae) || NC_008092.1 / NC_002008.4 / NC_008434.1 || Canis lupus , C. l. familiaris , & Vulpes vulpes || 16 windows (1,545 bp) || 29120 || NCBI RefSeq Verified |

| 8 || COHORT-01 (Mustelidae) || NC_009677.1 / NC_020638.1 || Meles anakuma & Mustela putorius || 16 windows (1,545 bp) || 29120 || NCBI RefSeq Verified |

| 9 || COHORT-02 (Euarchontoglires) || song_primates.424.gene.tre || 14-Taxon Primate & Euarchontoglires Ortholog Panel (Song et al. 2012) || 424 nuclear genes | 424424 || PNAS / ASTRAL Benchmark Verified |

| 10 || COHORT-03 (Mammalia) || song_mammals.424.gene.tre || 37-Taxon Amniote & Placental Mammal Radiation Panel (Song et al. 2012) || 424 nuclear genes || 28003080 || PNAS / ASTRAL Benchmark Verified |

| 11 || COHORT-04 (5x ILS Anomaly Zone) || simulated_primates_5X.10.bootstrap || 14-Taxon Controlled 5x ILS Short-Internode Coalescent Ensemble || 200 gene trees | 200200 || ASTRAL Coalescent Benchmark Verified |

Generated by: NCBI Entrez E-Utilities (efetch.fcgi) * CRV Science Labs
PoliteCacheManager (fetch.rs) * Native Rust Quartet Multispecies Coalescent Engine
(coalescent.rs) * ASTRAL v5.7.8 (Mirarab et al.)

8. Primary Literature & Methodological References

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