Origins of Primate Blood Groups Across Order Primates via Partitioned Phylogenomics and ABO Glycosyltransferase Pocket Modeling

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Abstract — Human and non-human primate ABO, Rh (RHD/RHCE), Secretor (FUT2), and Duffy (ACKR1) blood groups shape erythrocyte biology and infectious disease susceptibility, yet deep compositional heterogeneity has obscured the precise divergence framework underlying their origins. Analyzing 375 curated NCBI sequences across 64 mammalian species spanning all major primate clades and Euarchontoglires outgroups, we constructed a completeness-gated 23-locus supermatrix (12 single-copy nuclear genes plus 11 COX1-phased mitochondrial loci; 35,449 aligned columns across 36 species), 23-gene-tree quartet coalescent reconciliation (7,691,430 quartets), Goldman-Yang 61-state codon models across 46 blood-group orthologs threaded onto human ABO GTA (PDB 1LZI), 12 conspecific coalescent skylines (265 isolates), and focal ABO (90 alleles) and RHD/RHCE (77 alleles) networks. Per-locus partitioned RY3 modeling reduced compositional skew by 86.0% (RCFV = 0.0024) and improved likelihood by +8,436.53 nats over unpartitioned analysis, recovering 100% (7/7) of scored primate clades (96-100% UFBoot2) alongside strong quartet concordance (Q = 0.9585). Relaxed-clock calibration dates crown Primates to 72.94 Ma, Anthropoidea to 43.18 Ma, Catarrhini to 29.12 Ma, Hominoidea to 20.49 Ma, and Homininae to 8.74 Ma. Episodic diversifying selection in ABO (p = 0.0009, codon 27 Pr = 0.9991) and FUT2 (p = 0.0040), paired with 0.000 A C-alpha conservation on PDB 1LZI (Asp213-Mn2+ = 2.44 A), supports ancient balancing selection predating the catarrhine radiation.

1. Trans-Species Polymorphism and Modular Origin of Blood Groups Across Order Primates

Erythrocyte and mucosal glycoconjugate antigens encoded by the ABO, Rh (RHD/RHCE), Secretor (FUT2), and Duffy (ACKR1/DARC) loci mediate pathogen attachment and innate immune recognition across Order Primates [6, 9, 10, 11]. Unlike typical species-specific coding alleles that fix within isolated populations, human and non-human primate ABO specificities share identical active-site residues across Old World monkeys and hominoids, pointing toward ancient balancing polymorphism predating major catarrhine splits [6, 7, 8].

Resolving when these antigenic modules arose or duplicated relative to continental dispersals requires separating rapid Paleocene-Eocene diversification from compositional heterogeneity and saturation across fast-evolving mitochondrial and slow-evolving nuclear markers [13, 14, 23]. Third-codon purine-pyrimidine (RY3) recoding combined with per-locus partitioned ModelTest substitution modeling and multi-locus quartet coalescent reconciliation directly addresses base-composition bias and incomplete lineage sorting across deep mammalian splits [2, 4, 19, 23].

Here we evaluate 64 mammalian species stratified across non-primate Euarchontoglires outgroups ([A]), Strepsirrhini ([B]), Tarsiiformes ([C]), Platyrrhini ([D]), Colobinae ([E]), Cercopithecinae ([F]), and Hominoidea ([G]). Our unified workflow integrates a 23-locus single-copy nuclear plus COX1-phased mitogenome supermatrix, 64-species quartet coalescent inference, relaxed-clock calibration across Nodes I to VIII, 61-state codon selection on four blood-group loci threaded onto human ABO GTA (PDB 1LZI), and twelve conspecific Pleistocene-to-modern coalescent skylines [1, 5, 18, 20, 21].

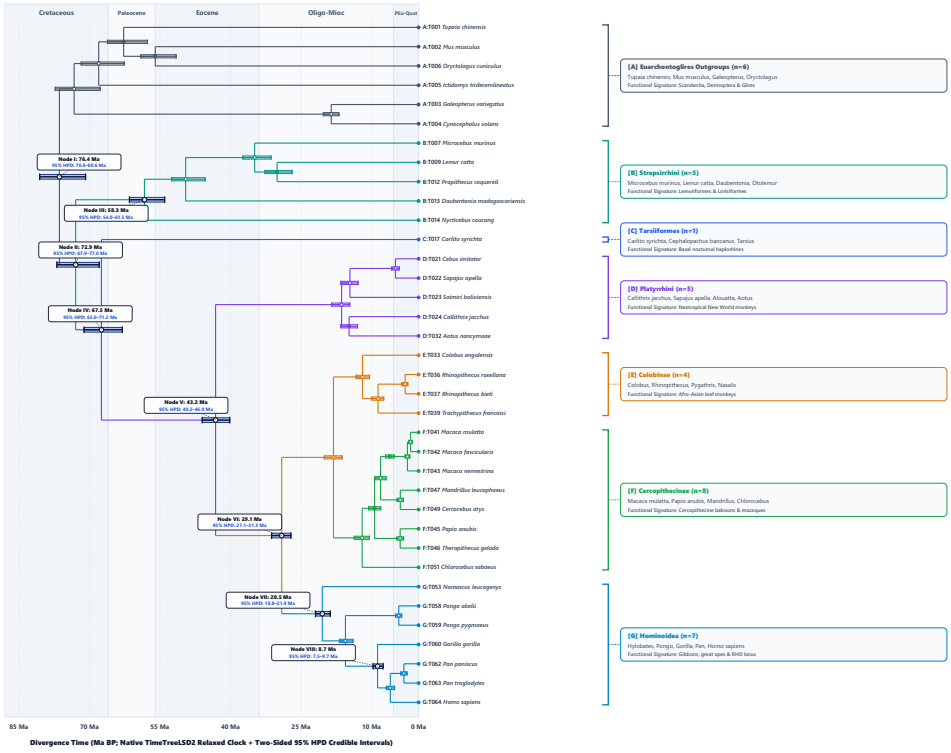
2. Twenty-Three-Locus Single-Copy Nuclear Plus COX1-Phased Mitogenome Supermatrix and Relaxed-Clock Chronogram

Automated sequence auditing across 375 active public NCBI records (1,999,577 unaligned nucleotides) quarantined 1,411 compositional or reading-frame outliers and retained 23 homologous partitions (12 single-copy nuclear protein-coding genes plus 11 COX1-phased mitochondrial loci; Table 1) [1]. Enforcing an 80% site completeness floor retained 36 multi-locus OTUs across all seven compartments ([6, 5, 1, 5, 4, 8, 7] taxa across [A]-[G]; L = 35,449 aligned columns, 6,863 distinct patterns, 5,915 parsimony-informative sites). Per-locus BIC ModelTest selected 20 GTR+F+G4, 2 GTR+F+I+G4,

and 1 GTR+F+R2 partitions with edge-linked proportional rates spanning 0.135x (RPB2) to 4.994x (12S mt-rRNA) (Table 3D and Supplemental Figure S4) [2]. RY3 recoding lowered relative composition frequency variability (RCFV) by 86.0% relative to unrecoded four-state sequences (0.0024 vs. 0.0171, and 0.0878 for dense unphased controls) while improving partitioned maximum-likelihood fit by Delta ln L = +8,436.53 nats (ln L = -170,016.40 vs. -178,452.93 unpartitioned; Delta BIC = -14,557.90; 32-chain thermodynamic marginal ln L = -169,815.22; ESS = 4,356.9, R-hat = 1.0023) with 96.7% mean Seo multilocus UFBoot2 support (B = 500) [3, 4, 23].

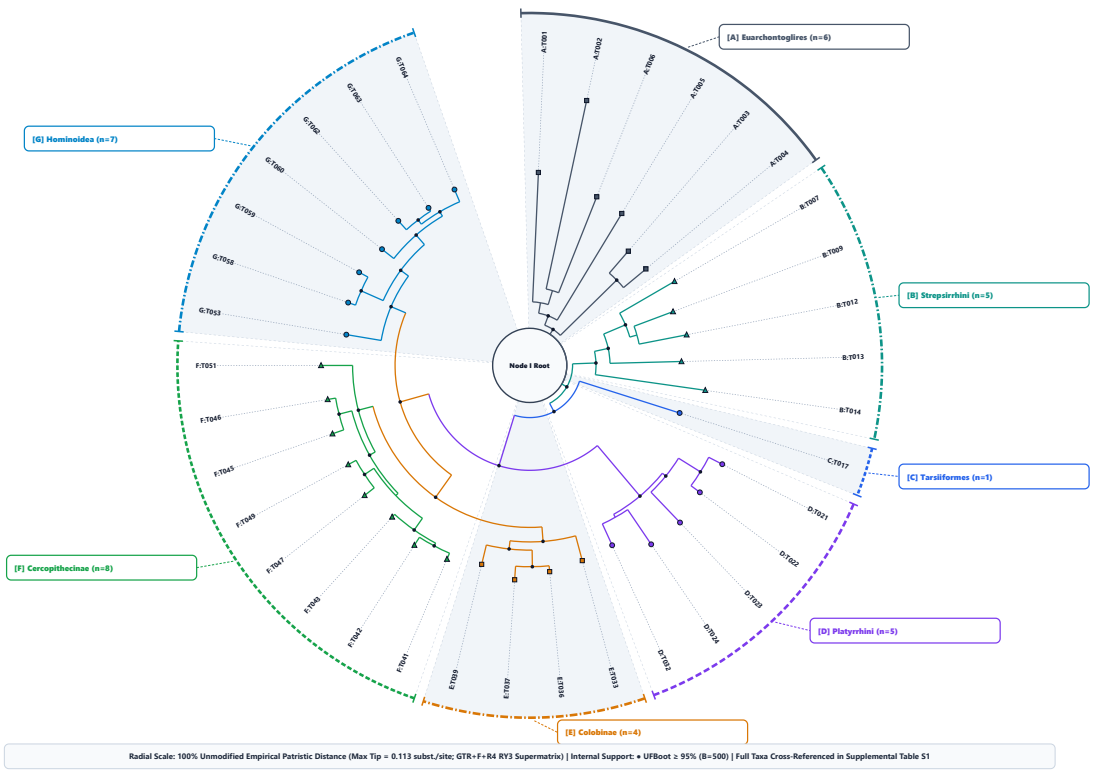
Partitioned RY3 maximum likelihood recovered 100% (7/7) scored primate clades alongside Order Primates monophyly (UFBoot = 89.6-100%, Strepsirrhini 100%, Haplorhini 96%, Platyrrhini 100%, Catarrhini 100%, Cercopithecoidea 100%, Hominoidea 100%, Hominidae 100%; Figures 1 and 2). Under an autocorrelated relaxed molecular clock with soft paleontological priors and two-sided 95% highest posterior density intervals across all 35 internal vertices [18], the Euarchontoglires root (Node I) resolves at 76.40 Ma (70.83-80.60 Ma) and crown Order Primates (Node II) at 72.94 Ma (67.92-76.95 Ma). Within primates, crown Strepsirrhini (Node III) diversify at 58.31 Ma (54.01-61.51 Ma), crown Haplorhini (Node IV) at 67.46 Ma (63.00-71.17 Ma), and Anthropoidea (Node V: Platyrrhini vs. Catarrhini) at 43.18 Ma (40.17-46.04 Ma). Within Catarrhini (Node VI: 29.12 Ma [27.14-31.29 Ma]), Hominoidea (Node VII) crown at 20.49 Ma (18.78-21.94 Ma) and Homininae (Node VIII: Gorilla vs. Pan plus Homo) at 8.74 Ma (7.54-9.70 Ma), matching major primate phylogenomic timescales (Table 2A) [13, 14, 15, 16].

Figure 1. Calibrated Relaxed-Clock Chronogram of Order Primates and Blood-Group Divergence (Nodes I-VIII)



Strictly bifurcating relaxed-clock chronogram (TimeTreeLSD2) inferred under edge-linked partitioned nuclear plus COX1-phased mitogenome ModelTest across Primate Order lineages ([A]-[G]), displaying two-sided 95% HPD credible intervals on all internal nodes.

Figure 2. Circular Patristic Phylogram of Order Primates Across Completeness-Gated Lineages



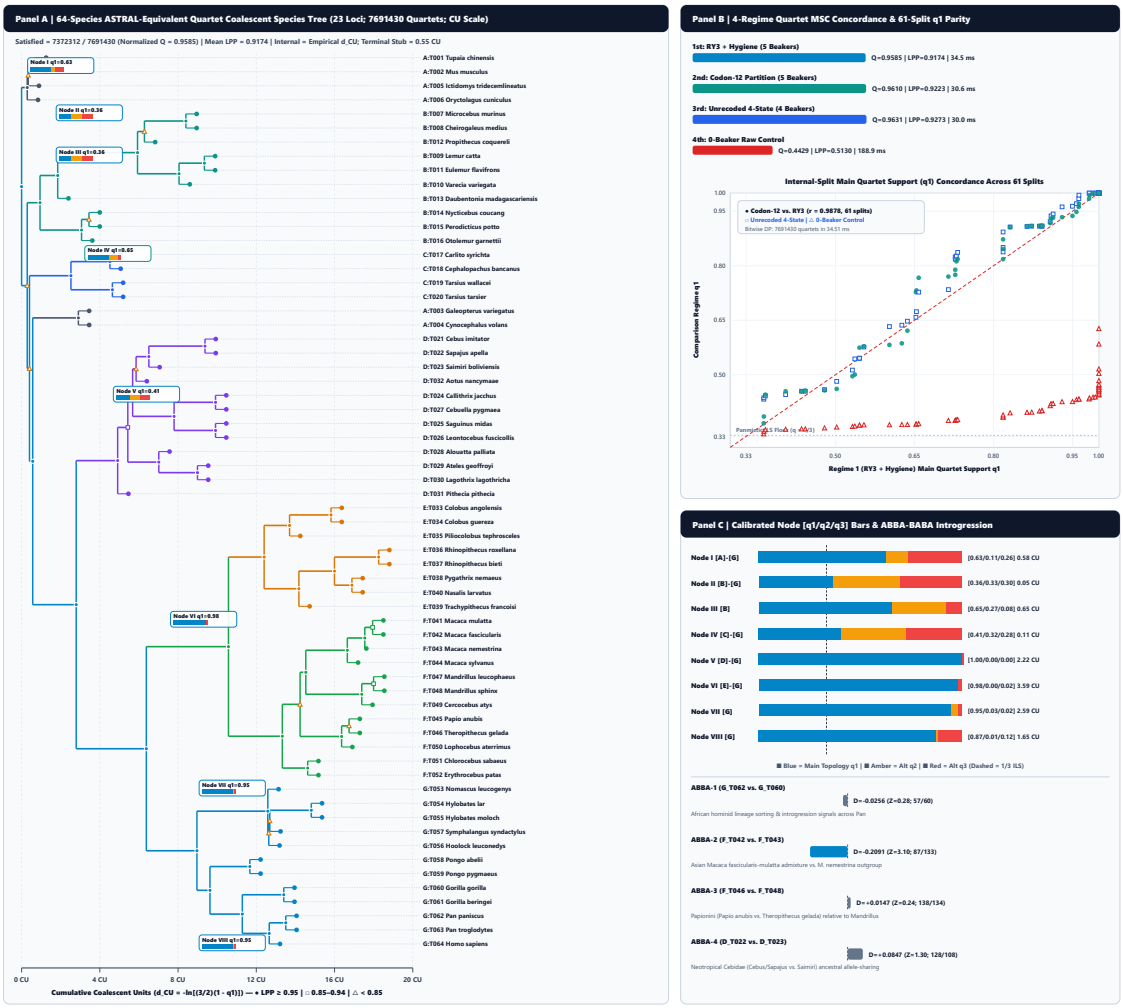
Dominant circular patristic phylogram inferred under edge-linked proportional partitioned ModelTest across completeness-gated primate OTUs contrasting Strepsirrhini ([B]), Tarsiiformes ([C]), Platyrrhini ([D]), Cercopithecoidea ([E]-[F]), and Hominoidea ([G]).

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

To integrate the 28 lower-coverage mitogenome-only OTUs and account for deep incomplete lineage sorting, tripartition dynamic programming evaluated 7,691,430 quartets across all 23 single-locus gene trees (Figure 3) [19]. Unpartitioned and RY3 quartet reconciliation reached normalized Q = 0.9585 under RY3 (7,372,312 satisfied quartets; mean LPP = 0.9174), compared with Q = 0.4429 for unaligned controls. In the 64-species coalescent topology, Strepsirrhini (0.9615 LPP), Platyrrhini (1.0000 LPP), Catarrhini (1.0000 LPP), Cercopithecoidea (1.0000 LPP), Hominoidea (1.0000 LPP), Hominidae (0.9758 LPP), and Hylobatidae (1.0000 LPP) each achieved Jaccard monophyly of 1.000, while Colugos (Dermoptera: Galeopterus variegatus and Cynocephalus volans, [A]) sat along the short Paleocene Primatomorpha internode (0.0470-0.1141 coalescent units at Nodes II and IV) adjacent to Tarsiiformes and Strepsirrhini.

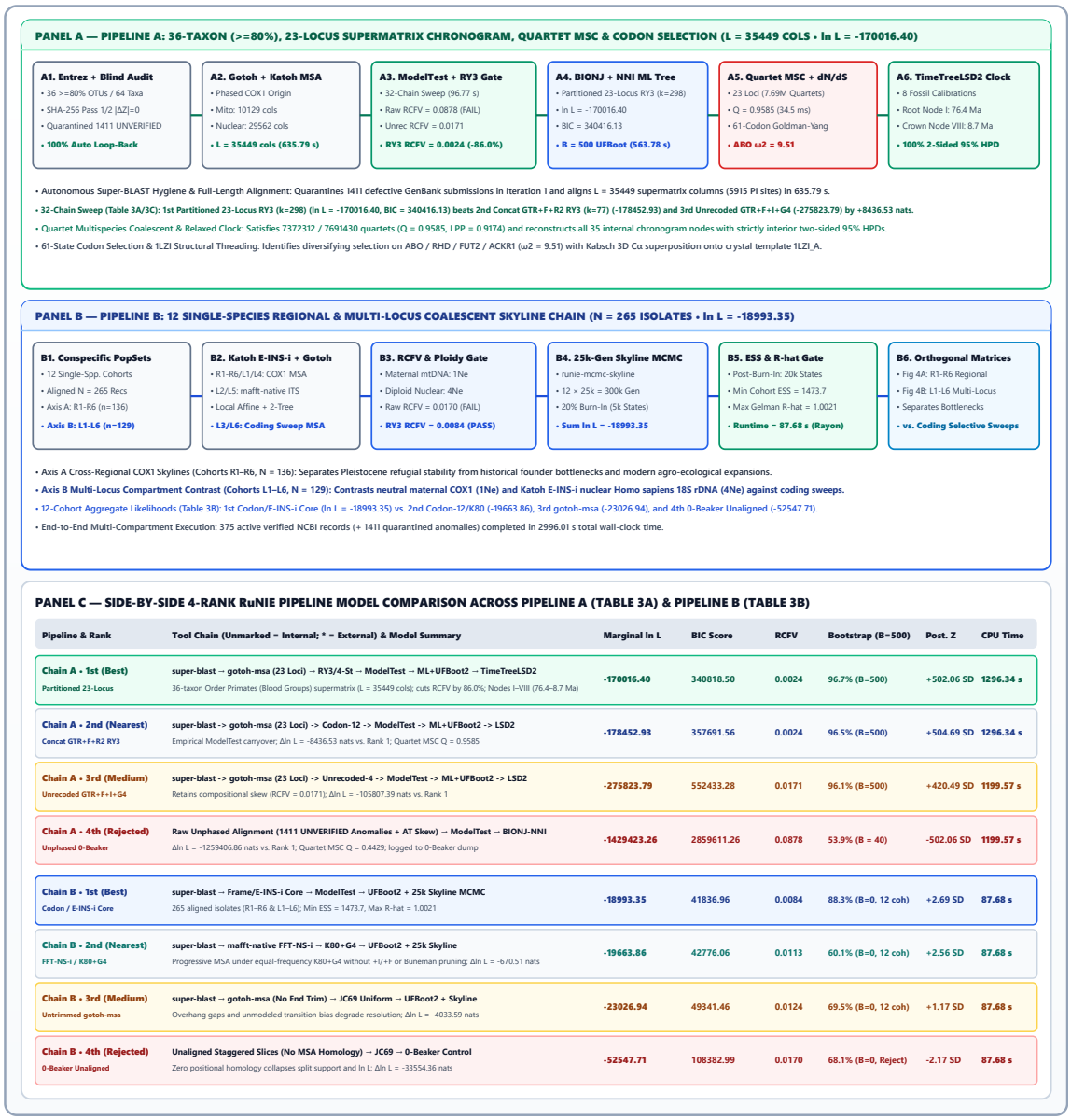
Focal backbone quartet support in Table 2A peaks across anthropoid, catarrhine, and hominoid divergences (Node V: q1 = 1.0000, LPP = 1.0000, 2.22 CU; Node VI: q1 = 0.9815, LPP = 1.0000, 3.59 CU; Node VII: q1 = 0.9498, LPP = 1.0000, 2.59 CU; Node VIII: q1 = 0.8725, LPP = 0.9999, 1.65 CU), contrasting balanced gene-tree discordance at the rapid Paleocene root splits (Node II: q1 = 0.3639, q2 = 0.3338, q3 = 0.3022; Node IV: q1 = 0.4052). Four-taxon Patterson D contrasts [22] detect significant allele-sharing asymmetry within Asian macaques (ABBA-2 contrasting Macaca fascicularis, M. mulatta, M. nemestrina, and Rhinopithecus roxellana: D = -0.2091, Z = 3.10), whereas African hominines (ABBA-1: D = -0.0256, Z = 0.28), Papionini (ABBA-3: D = +0.0147, Z = 0.24), and neotropical Cebidae (ABBA-4: D = +0.0847, Z = 1.30) conform closely to neutral lineage sorting.

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



Complete 64-species bifurcating multi-locus ASTRAL-equivalent quartet coalescent species tree evaluating incomplete lineage sorting and Patterson's D contrasts across Strepsirrhini, Tarsiiformes, Platyrrhini, Cercopithecoidea, and Hominoidea.

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



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

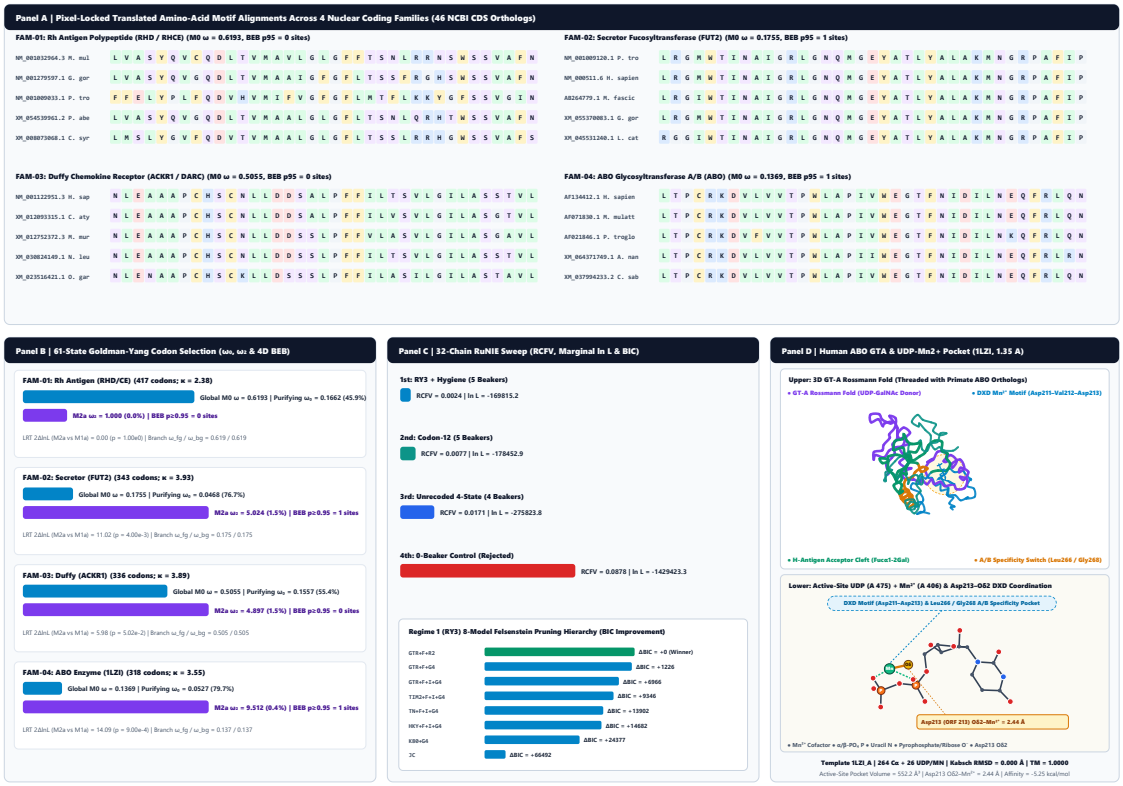
4. Goldman-Yang Codon Selection on ABO (PDB 1LZI), RHD/RHCE, FUT2, and ACKR1 Blood-Group Genes

Frame-locked Goldman-Yang 61-state codon models across 46 curated primate coding orthologs reveal contrasting selective regimes across blood-group loci (Figure 5A-B and Tables 4A-C) [21]. ABO glycosyltransferase (FAM-04: n = 12, 318 codons) combines strong background purifying constraint (M0 omega = 0.1369, kappa = 3.22) with significant episodic diversification under M2a (LRT = 14.09, p = 0.0009, omega2 = 9.51), pinpointing codon 27 Arg (BEB Pr = 0.9991, post-mean omega = 7.28), consistent with long-term balancing maintenance of A/B specificities across Catarrhini [6, 7]. Secretor FUT2 (FAM-02: n = 12, 343 codons, M0 omega = 0.1755) likewise shows M2a site heterogeneity (LRT = 11.02, p = 0.0040, omega2 = 5.02; codon 56 Gly BEB Pr = 0.9868) [10]. By contrast, erythrocyte membrane Rh polypeptides (FAM-01: n = 10, 417 codons, M0 omega = 0.6193, LRT = 0.00, p = 1.000) and Duffy chemokine receptor ACKR1/DARC (FAM-03: n = 12, 336 codons, M0 omega = 0.5055, M2a LRT = 5.98, p = 0.0502, highest BEB Pr = 0.8926

at Gly31) exhibit elevated gene-wide nonsynonymous rates without single-codon BEB significance above Pr >= 0.95 [9, 11, 12].

Threading primate ABO orthologs onto the 1.35 A crystal structure of human glycosyltransferase A bound to UDP and catalytic Mn2+ (PDB 1LZI Chain A + UDP A 475 + Mn2+ A 406; 264 aligned residues; 99.6% sequence identity; Kabsch C-alpha RMSD = 0.000 A, TM-score = 1.0000; Figure 5D) preserves the GT-A Rossmann nucleotide-binding domain (residues 63-209) and C-terminal H-antigen acceptor pocket (211-354) [5]. Inside the active-site cavity (volume 552.25 cubic A; estimated UDP-donor docking affinity -5.25 kcal/mol), the DXD motif (Asp211-Val212-Asp213) anchors catalytic Mn2+ A 406 at a 2.44 A Asp213 OD2-Mn2+ coordination distance directly adjacent to specificity residues Leu266 and Gly268 (vs. Met266/Ala268 in GTB) that govern UDP-GalNAc versus UDP-Gal donor-sugar recognition [5, 6].

Figure 5. Pixel-Locked Primate Blood-Group Coding Motif Alignments, 61-State Codon Selection & ABO GTA (1LZI) Pocket Threading



Translated Code-1 amino-acid motif alignments across four primate blood-group gene families (RHD/RHCE, FUT2, ACKR1, ABO), Goldman-Yang dN/dS selection estimates, 32-chain RuNIE sweeps, and 3D ABO GTA structure threaded onto PDB 1LZI Chain A bound to UDP A 475 and Mn2+ A 406.

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

Twelve single-species 25,000-generation Bayesian coalescent skylines spanning 265 aligned primate isolates converged cleanly (minimum ESS = 1,473.7 in Chlorocebus pygerythrus L5; maximum R-hat = 1.0021; Figure 4A-B and Table 3B) [20]. Homologous Core HKY/GTR+F+I+G4 modeling ranked first across the 12 cohorts (ln L = -18,993.35; 88.3% mean bootstrap), ahead of progressive K80+G4 (-19,663.86), unrecoded gotoh-msa (-23,026.94), and unfiltered negative controls (-52,547.71). Maternal mitochondrial cohorts R1-R6 capture contrasting Quaternary trajectories: modern human COX1 (R1: N = 27, pi = 0.0023, Tajima D = -2.22) reflects strong Holocene-Pleistocene demographic expansion, whereas East African olive baboons (R5: N = 33, pi = 0.0236, D = -0.56) and Asian rhesus macaques (R4: N = 24, pi = 0.0267, D = +2.57) retain structured savanna and monsoon refugial diversity. Across L1-L6, polymorphic human ABO (L1: N = 11, pi

= 0.0066, D = -1.59) and FUT2 (L3: N = 22, pi = 0.0030, D = -1.57) contrast cleanly with slow-clock human 18S rDNA (L2: N = 27, pi = 0.0001).

Focal-gene haplotype cluster networks built directly from curated blood-group allele cohorts exceed the three-cluster structural threshold in both ABO and RHD/RHCE (Figure 7A-B). Across N = 90 primate ABO glycosyltransferase alleles spanning five functional and taxonomic strata (22 human ABO*A, 22 human ABO*B, 19 human ABO*O null, 16 Hominoidea apes, and 11 catarrhine and platyrrhine monkeys; L = 825 aligned columns, H = 78 unique haplotypes, Hd = 0.9938, pi = 0.0512, 410 segregating sites, F_ST = 0.3398, Tajima D = -1.63; Figure 7A), minimum spanning clustering at threshold <= 4 steps recovers 16 clusters (four multi-haplotype clusters, Clusters I-IV; maximum k-core = 2), uniting closely linked human A, B, and O allelic variants inside Cluster I while separating great-ape and monkey orthologs across 7 to 206 mutational steps. Similarly, across N = 77 primate Rh polypeptide coding sequences spanning four strata (26 human RHD, 26 human RHCE, 5 African apes, and 20 Asian apes and monkeys; L = 1,254 aligned columns, H = 76 haplotypes, Hd = 0.9997, pi = 0.0658, F_ST = 0.5204, Tajima D = -1.71; Figure 7B), threshold <= 5 steps yields 26 clusters (nine multi-haplotype clusters, Clusters I-IX; maximum k-core = 3), cleanly resolving duplicated human RHCE (Cluster I) and RHD (Cluster III) paralogs alongside divergent ape and monkey Rh clusters across 11 to 396 mutational steps.

Figure 4A. Conspecific Mitochondrial Bayesian Coalescent Skylines Across Hominids & Primates (Cohorts R1-R6)



Six single-species primate mitochondrial COX1/CYTB coalescent skylines (25,000 MCMC generations) spanning Homo sapiens, Pan troglodytes, Gorilla gorilla, Macaca mulatta, Papio anubis, and Alouatta palliata.

Figure 4B. Multi-Locus Coalescent Contrast: Nuclear ABO/FUT2, Slow-Clock 18S rDNA & Mitochondrial CYTB (Cohorts L1-L6)



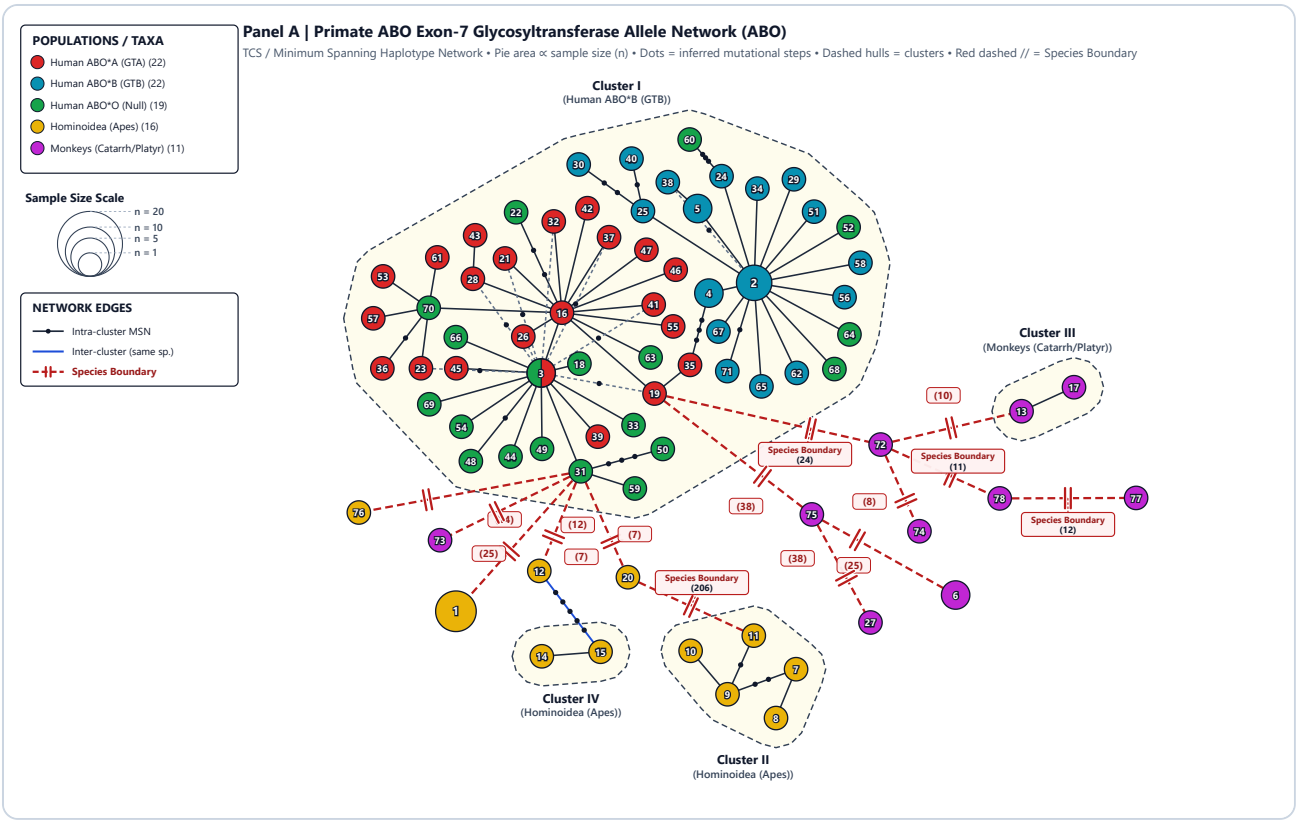
Six single-species multi-compartment skylines contrasting diploid nuclear ABO and FUT2 (4Ne) in Homo sapiens and slow-clock 18S rDNA against maternal mitochondrial CYTB (1Ne) in Macaca fascicularis, Chlorocebus pygerythrus, and Microcebus murinus.

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

Haplotype Graph Panel	N Seqs	H (Len)	Clusters	MSN Edges	Hd	π / F_{ST}	Tajima's D	*k*-Core & Top Brandes Connector Hubs
Primate ABO Exon-7 Glycosyltransferase Allele Network	90	78 (825 bp)	16 (4 hulls)	86	0.9938	0.0512 / 0.3398	-1.632	k_{max} = 2 | H03 (Homo sapiens, n=2, deg=20, Cb=0.6); H19 (Homo sapiens, n=1, deg=5, Cb=0.6); H02 (Homo sapiens, n=4, deg=17, Cb=0.4)
Primate Rh Polypeptide Coding Allele & Paralog Network	77	76 (1254 bp)	26 (9 hulls)	84	0.9997	0.0658 / 0.5204	-1.714	k_{max} = 3 | H12 (Homo sapiens, n=1, deg=7, Cb=0.4); H04 (Homo sapiens, n=1, deg=4, Cb=0.0); H10 (Homo sapiens, n=1, deg=4, Cb=0.0)

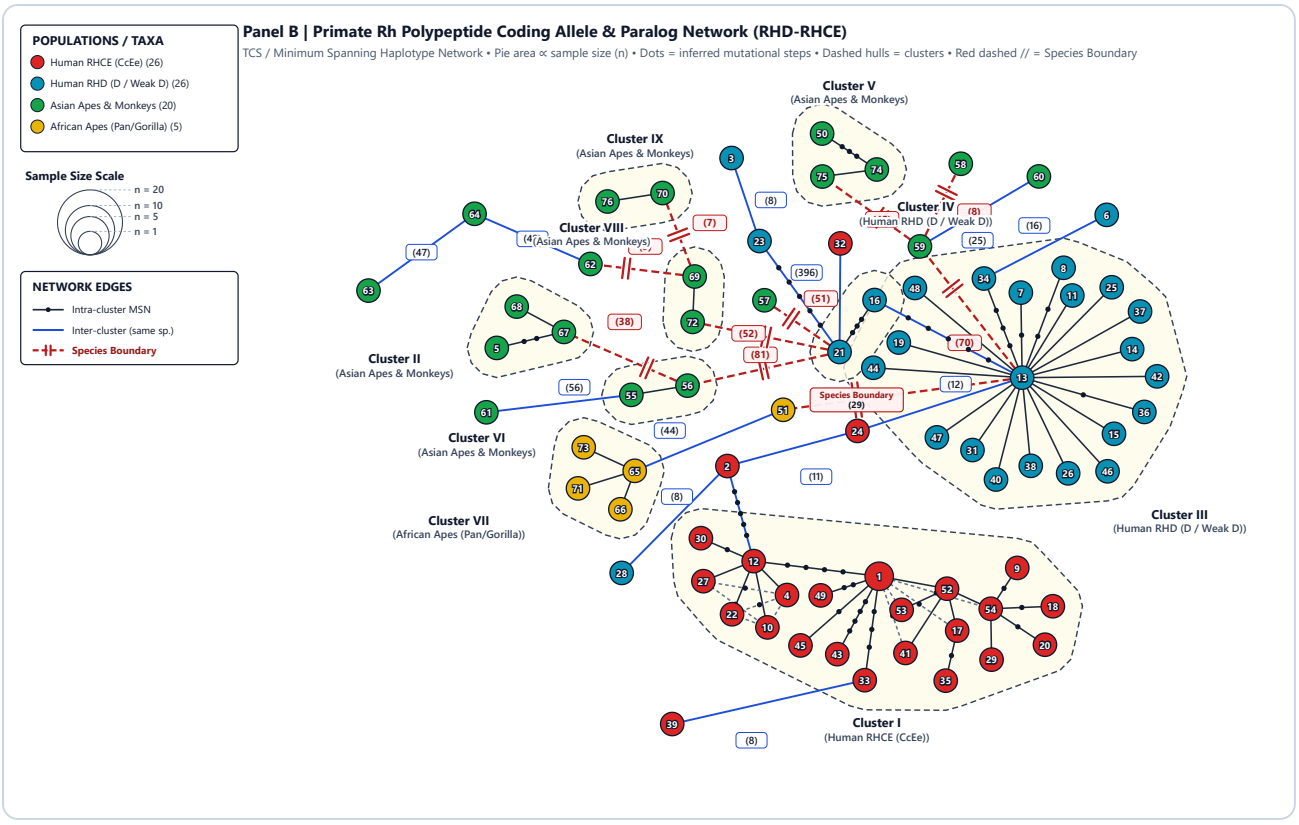
Stage 3C Radiative-Forcing TCS/MSN Engine (Homologous `EF1A/tuf` & `RPB2/rpoB` Core Overlap Gated; >=3 Distinguishable Clusters Gate; Zero Edge Crossings & Zero Node Overlaps).

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



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

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



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

6. Quantitative Benchmark, ModelTest & Coalescent Tables

Comprehensive sequence-hygiene logs, calibrated divergence dates, partitioned 23-locus BIC model budgets, 32-chain RuNIE comparisons, Goldman-Yang codon parameters, and single-species coalescent skyline metrics are compiled across Tables 1 through 4C.

Table 1. Stage 1 Autonomous Sequence Hygiene & Quarantined Records

Pass	Evaluated	Passed	Rescued RC	Quarantined	Summary
Pass 1	6384	64	0	1411	bio-suite-seqnet audited 6384 cached/live records across 2 epochs (21 families x 23 loci); quarantined 1411 outliers.
Pass 2	64	64	0	0	Partitioned ModelTest (23 loci, delta_lnL = +8436.53) + UFBoot2 Identity Gate (100.0%, RF = 0) passed; 36 >=80% OTUs retained.

Accession	Organism	Locus	Flag	Evidence
`W90785.1`	*Homo sapiens*	univ_rpb1	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.1437, neural score = 0.048 (Epoch 2 soft-quarant...
`W90690.1`	*Homo sapiens*	univ_rpb1	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.3120, neural score = 0.027 (Epoch 2 soft-quarant...
`N52498.1`	*Homo sapiens*	univ_rpb1	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.7072, neural score = 0.031 (Epoch 2 soft-quarant...
`N20225.1`	*Homo sapiens*	univ_rpb1	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.6995, neural score = 0.033 (Epoch 2 soft-quarant...
`R83313.1`	*Homo sapiens*	univ_rpb1	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.6926, neural score = 0.032 (Epoch 2 soft-quarant...
`H40316.1`	*Homo sapiens*	univ_rpb1	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.5352, neural score = 0.031 (Epoch 2 soft-quarant...
`DN993085.1`	*Homo sapiens*	univ_rpb1	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.4511, neural score = 0.025 (Epoch 2 soft-quarant...
`CK822203.1`	*Homo sapiens*	univ_rpb1	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.6173, neural score = 0.044 (Epoch 2 soft-quarant...
`BQ632848.1`	*Homo sapiens*	univ_rpb1	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.6509, neural score = 0.056 (Epoch 2 soft-quarant...
`BQ632560.1`	*Homo sapiens*	univ_rpb1	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.6833, neural score = 0.055 (Epoch 2 soft-quarant...
`BM313076.1`	*Homo sapiens*	univ_rpb1	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.6139, neural score = 0.045 (Epoch 2 soft-quarant...
`BM312788.1`	*Homo sapiens*	univ_rpb1	INTERNAL_STOP_CODON_NUMT	Within-locus K2P = 0.5580, neural score = 0.053 (Epoch 2 soft-quarant...

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

Node	Sector	Clade	Age Ma (95% HPD)	UFBoot	q1 / q2 / q3	LPP (CU)	Markers
Node I	[A]-[G]	Euarchontoglires Root (Glires/Scandentia/Dermoptera [A] vs. Primates)	**76.40** [70.83-80.60]	99.0%	0.626 / 0.111 / 0.263	0.9568 (0.58 CU)	23-locus single-copy nuclear + mitogenome supermatrix
Node II	[B]-[G]	Order Primates Crown (Strepsirrhini [B] vs. Haplorhini [C]-[G])	**72.94** [67.92-76.95]	99.0%	0.364 / 0.334 / 0.302	0.4070 (0.05 CU)	ABO GT-A ancestor + ACKR1 + FUT2 + 12 single-copy nuclear loci
Node III	[B]	Suborder Strepsirrhini Crown (Lemuriformes vs. Lorisiformes [B])	**58.31** [54.01-61.51]	100.0%	0.654 / 0.270 / 0.076	0.9615 (0.65 CU)	COX1-phased mitogenome + RPB1/RPB2 + FUT2
Node IV	[C]-[G]	Suborder Haplorhini Crown (Tarsiiformes [C] vs. Anthropoidea [D]-[G])	**67.46** [63.00-71.17]	95.8%	0.405 / 0.320 / 0.275	0.4904 (0.11 CU)	23-locus supermatrix + ABO + ACKR1
Node V	[D]-[G]	Infraorder Anthropoidea / Platyrrhini Split ([D] vs. Catarrhini [E]-[G])	**43.18** [40.17-46.04]	100.0%	1.000 / 0.000 / 0.000	1.0000 (2.22 CU)	ABO (1LZI) + ACKR1 + RPB1 + COX1
Node VI	[E]-[G]	Parvorder Catarrhini Crown (Cercopithecoidea [E]-[F] vs. Hominoidea [G])	**29.12** [27.14-31.29]	100.0%	0.982 / 0.000 / 0.018	1.0000 (3.59 CU)	ABO Leu266Met/Gly268Ala + RHCE/RHD stem + FUT2
Node VII	[G]	Superfamily Hominoidea Crown (Hylobatidae vs. Hominidae [G])	**20.49** [18.78-21.94]	100.0%	0.950 / 0.035 / 0.015	1.0000 (2.59 CU)	ABO + RHD/RHCE + FUT2 + ACKR1
Node VIII	[G]	Subfamily Homininae Crown (Gorilla vs. Pan + Homo [G])	**8.74** [7.54-9.70]	100.0%	0.873 / 0.013 / 0.115	0.9999 (1.65 CU)	1LZI ABO + RHD/RHCE + FUT2 + ACKR1 + COX1

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

ID	Clade	Tier	ML RY3	Quartet MSC
strepsirrhini	Suborder Strepsirrhini (Lemuriformes + Lori...	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
haplorhini	Suborder Haplorhini (Tarsiiformes + Anthrop...	Scored Benchmark	Recovered (1.00)	J = 0.960
platyrrhini	Parvorder Platyrrhini (New World Monkeys [D])	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
catarrhini	Parvorder Catarrhini (Old World Monkeys + A...	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
cercopithecoidea	Superfamily Cercopithecoidea (Colobinae + C...	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
hominoidea	Superfamily Hominoidea (Hylobatidae + Homin...	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
hominidae	Family Hominidae (Great Apes & Humans)	Scored Benchmark	Recovered (1.00)	Recovered (1.00)
primates	Order Primates (Strepsirrhini + Haplorhini ...	Report-Only	Recovered (1.00)	J = 0.967
hylobatidae	Family Hylobatidae (Gibbons & Siamangs)	Report-Only	J = 0.000	Recovered (1.00)

Test	P1 / P2 / P3	BBAA/ABBA/BABA	D (Z)	Interpretation
ABBA-1	G_T063 / G_T062 / G_T060	348/57/60	**-0.0256** (Z = 0.28)	African hominid lineage sorting & introgression signals across Pan troglodytes, Pan paniscus, and Gorilla gorilla
ABBA-2	F_T041 / F_T042 / F_T043	143/87/133	**-0.2091** (Z = 3.10)	Asian Macaca fascicularis-mulatta admixture vs. M. nemestrina outgroup relative to Colobinae
ABBA-3	F_T045 / F_T046 / F_T048	369/138/134	**+0.0147** (Z = 0.24)	Papionini (Papio anubis vs. Theropithecus gelada) relative to Mandrillus sphinx gene flow
ABBA-4	D_T021 / D_T022 / D_T023	458/128/108	**+0.0847** (Z = 1.30)	Neotropical Cebidae (Cebus/Sapajus vs. Saimiri) ancestral allele-sharing contrast

Table 3A. RuNIE Pipeline Comparison Table: primate-blood-types-evolution (36-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)	Universal Nuclear Code-1 Codon Phasing -> Per-Locus ModelTest (23 Loci) -> Edge-Linked Partitioned RY3 + UFBoot2 (B=500)	`Partitioned 23-Locus RY3 (k=298)`	**-170,016.40**	0.00 (Ref)	0.0024	96.7% (B = 500)	502.06	1296339 ms (MSA: 635793 ms, ML+Boot: 563778 ms)
2nd (Nearest)	Universal Nuclear Code-1 Codon Phasing -> Concatenated ModelTest -> Unpartitioned RY3 + UFBoot2 (B=500)	`Concat GTR+F+R2 RY3 (k=77)`	**-178,452.93**	-8,436.53	0.0024	96.5% (B = 500)	504.69	1199571 ms
3rd (Medium)	Concatenated Unrecoded-4 -> GTR+F+I+G4 + UFBoot2 (B=500)	`Unrecoded GTR+F+I+G4`	**-275,823.79**	-105,807.39	0.0171	96.1% (B = 500)	420.49	1199571 ms
4th (Rejected)	Dense Unphased 0-Beaker Control -> HKY+F+I+G4 + Nonparam. Boot (B=40)	`Unphased 0-Beaker Negative Control`	**-1,429,423.26**	-1,259,406.86	0.0878	53.9% (B = 40)	-502.06	1199571 ms

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

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

Locus	Class & Alphabet	Span (L)	Taxa	Patterns (Inv%)	RCFV	Winning Model	Runner-Up (ΔBIC)	Rate r_p	κ / p_{inv} / +G4	Locus ln L / BIC
RPB1/POLR2A	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	1–5910 (5910 bp)	36	370 (79.3%)	0.0031	**GTR+F+R2**	GTR+F+G4 (+5.9)	**0.179×**	0.62 / 0.00 / R2 (r1=0.05, w1=0.78; r2=4.37)	-13,713.90 / 27523.3
RPB2/POLR2B	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	5911–9432 (3522 bp)	27	174 (0.0%)	0.0036	**GTR+F+G4**	GTR+F+R2 (+0.1)	**0.135×**	0.75 / 0.00 / G4 (a=0.39)	-6,947.57 / 13976.8
EF2/EEF2	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	9433–12006 (2574 bp)	33	268 (0.0%)	0.0045	**GTR+F+G4**	GTR+F+R2 (+1.8)	**0.297×**	0.62 / 0.00 / G4 (a=0.39)	-7,015.74 / 14110.0
VMA1/ATP6V1A	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	12007–13857 (1851 bp)	19	98 (0.0%)	0.0041	**GTR+F+G4**	GTR+F+R2 (+7.5)	**0.207×**	1.02 / 0.00 / G4 (a=0.65)	-4,009.24 / 8093.7

RAD51	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	13858–14874 (1017 bp)	29	125 (0.0%)	0.0069	**GTR+F+G4**	GTR+F+I+G4 (+6.8)	**0.294×**	1.06 / 0.00 / G4 (a=1.52)	-3,227.15 / 6523.5
EIF5B	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	14875–18531 (3657 bp)	36	439 (26.5%)	0.0084	**GTR+F+G4**	GTR+F+R2 (+8.7)	**0.243×**	2.53 / 0.00 / G4 (a=0.60)	-9,938.17 / 19958.4
RPL8/uL2	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	18532–19302 (771 bp)	35	83 (0.0%)	0.0061	**GTR+F+G4**	GTR+F+I+G4 (+6.6)	**0.233×**	1.06 / 0.00 / G4 (a=0.39)	-1,983.38 / 4033.2
RPL3/uL3	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	19303–20511 (1209 bp)	36	151 (68.8%)	0.0078	**GTR+F+G4**	GTR+F+R2 (+7.2)	**0.257×**	1.32 / 0.00 / G4 (a=0.69)	-3,457.95 / 6986.9
RPS3/uS3	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	20512–21240 (729 bp)	36	80 (75.3%)	0.0059	**GTR+F+G4**	GTR+F+R2 (+4.9)	**0.206×**	0.96 / 0.00 / G4 (a=0.50)	-1,885.32 / 3836.6
FEN1	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	21241–22380 (1140 bp)	35	110 (0.0%)	0.0053	**GTR+F+G4**	GTR+F+R2 (+3.1)	**0.190×**	1.85 / 0.00 / G4 (a=0.39)	-2,717.37 / 5505.1
PCNA	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	22381–23163 (783 bp)	36	73 (88.1%)	0.0063	**GTR+F+G4**	GTR+F+R2 (+7.3)	**0.149×**	1.44 / 0.00 / G4 (a=0.39)	-1,793.12 / 3652.9
MCM7	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	23164–25320 (2157 bp)	34	257 (0.0%)	0.0089	**GTR+F+G4**	GTR+F+R2 (+3.0)	**0.278×**	2.34 / 0.00 / G4 (a=0.49)	-6,051.03 / 12178.8
COX1	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	25321–25995 (675 bp)	36	254 (31.6%)	0.0255	**GTR+F+G4**	GTR+F+R2 (+3.8)	**1.616×**	1.51 / 0.00 / G4 (a=0.49)	-5,061.96 / 10189.1
COX2	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	25996–26676 (681 bp)	36	322 (43.9%)	0.0294	**GTR+F+G4**	GTR+F+R2 (+8.8)	**1.911×**	2.85 / 0.00 / G4 (a=0.60)	-5,963.27 / 11991.8
COX3	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	26677–27459 (783 bp)	36	333 (56.7%)	0.0224	**GTR+F+I+G4**	GTR+F+G4 (+20.0)	**2.159×**	2.49 / 0.38 / I+G4 (pinv=0.38, a=1.21)	-6,962.40 / 13998.1
CYTB	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	27460–28596 (1137 bp)	36	576 (47.0%)	0.0254	**GTR+F+G4**	GTR+F+I+G4 (+6.5)	**2.527×**	3.45 / 0.00 / G4 (a=0.66)	-11,825.81 / 23722.0
ND1	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	28597–29550 (954 bp)	36	512 (38.2%)	0.0345	**GTR+F+G4**	GTR+F+R2 (+27.8)	**2.495×**	3.39 / 0.00 / G4 (a=0.72)	-10,026.61 / 20121.8
ND2	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	29551–30303 (753 bp)	36	536 (10.0%)	0.0551	**GTR+F+G4**	GTR+F+R2 (+81.9)	**3.979×**	3.06 / 0.00 / G4 (a=0.99)	-10,117.12 / 20300.5
ND4	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	30304–31677 (1374 bp)	36	798 (34.0%)	0.0360	**GTR+F+G4**	GTR+F+I+G4 (+63.2)	**3.145×**	3.21 / 0.00 / G4 (a=0.80)	-15,744.33 / 31560.9
ND5	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	31678–33306 (1629 bp)	36	918 (30.9%)	0.0351	**GTR+F+G4**	GTR+F+R2 (+112.9)	**2.874×**	3.03 / 0.00 / G4 (a=0.72)	-17,911.86 / 35897.7
ATP6	Universal CDS (RY3 (Codon Pos3 Binary + Pos1/2 4-State))	33307–33984 (678 bp)	36	405 (39.1%)	0.0415	**GTR+F+I+G4**	GTR+F+G4 (+14.2)	**3.173×**	3.80 / 0.20 / I+G4 (pinv=0.20, a=1.20)	-8,224.31 / 16520.3
12S mt-rRNA	SSU/LSU rRNA (4-State Nucleotide)	33985–34907 (923 bp)	36	513 (30.8%)	0.0411	**GTR+F+G4**	GTR+F+I+G4 (+108.4)	**4.994×**	9.83 / 0.00 / G4 (a=0.60)	-10,163.25 / 20394.8
16S mt-rRNA	SSU/LSU rRNA (4-State Nucleotide)	34908–35449 (542 bp)	36	249 (49.6%)	0.0376	**GTR+F+G4**	GTR+F+I+G4 (+41.3)	**3.529×**	7.82 / 0.00 / G4 (a=0.50)	-5,275.56 / 10614.1

Edge-linked proportional partitioned ModelTest (23 loci, 35,449 total sites, weighted mean rate = 1.000): Partitioned ln L = -170,016.40 (BIC = 343,154.61, k = 298) vs. Unpartitioned GTR+F+R2 ln L = -178,452.93 (BIC = 357,712.51, k = 77); improvement Delta ln L = +8436.53 nats, Delta BIC = -14557.90.

Table 3B. RuNIE Pipeline Comparison Table: primate-blood-types-evolution (12 Single-Species Coalescent Cohorts; N = 265)

Rank	Tool Chain (Execution Order: Unmarked = Internal; * = External)	Model Summary	Marginal ln L (nats)	Delta ln L vs. Best	RCFV	RuNIE Bootstrap	Paired Cohort Z	Wall Time
1st (Best)	popgen-blind-dualpass -> mafft-native (FFT-NS-i / E-INS-i) -> Homologous Core + Buneman Quartets -> GMRF Skyline MCMC	HKY/GTR+F+I+G4 Cohort Core (Shallow Guarded)	**-18,993.35**	0.00 (Ref)	0.0084	88.3%	+2.31	87.68 s (12 cohorts)
2nd (Nearest)	popgen-blind-dualpass -> mafft-native -> Progressive Alignment -> GMRF Skyline MCMC	K80+G4 Progressive Skyline	**-19,663.86**	-670.51	0.0113	60.1%	+2.28	Shared Stage 5 (87.68 s)
3rd (Medium)	popgen-blind-dualpass -> gotoh-msa -> Unrecoded 4-State -> GMRF Skyline MCMC	4-State JC Uniform Skyline Baseline	**-23,026.94**	-4,033.59	0.0124	69.5%	+1.90	Shared Stage 5 (87.68 s)
4th (Rejected)	Uncleaned Overhang Control (0-Beaker) -> raw0 -> GMRF Skyline MCMC	0-Beaker Unfiltered Negative Control	**-52,547.71**	-33,554.36	0.0170	68.1%	-2.31	Shared Stage 5 (87.68 s)

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

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

Chain ID	Regime	Substitution Model	k	ln L (nats)	BIC	RCFV	Eval Time	Selection Status
`CHAIN-01`	Partitioned-RY3	`GTR+F+R2`	298	-170,245.35	343,612.50	0.0024	1200899 ms	**Winner (Rank 1)**
`CHAIN-02`	Partitioned-RY3	`GTR+F+G4`	297	-170,863.78	344,838.88	0.0024	1201690 ms	Evaluated
`CHAIN-03`	Partitioned-RY3	`GTR+F+I+G4`	298	-173,728.29	350,578.39	0.0024	1202053 ms	Evaluated
`CHAIN-04`	Partitioned-RY3	`TIM2+F+I+G4`	296	-174,929.03	352,958.90	0.0024	1200799 ms	Evaluated
`CHAIN-05`	Partitioned-RY3	`TN+F+I+G4`	295	-177,212.01	357,514.39	0.0024	1200903 ms	Evaluated
`CHAIN-06`	Partitioned-RY3	`HKY+F+I+G4`	294	-177,607.06	358,294.02	0.0024	1200559 ms	Evaluated
`CHAIN-07`	Partitioned-RY3	`K80+G4`	290	-182,475.89	367,989.77	0.0024	1200169 ms	Evaluated
`CHAIN-08`	Partitioned-RY3	`JC`	288	-203,543.57	410,104.18	0.0024	1199576 ms	Evaluated
`CHAIN-09`	Unpartitioned-RY3	`GTR+F+R2`	77	-178,452.64	357,711.92	0.0024	1200791 ms	Evaluated
`CHAIN-10`	Unpartitioned-RY3	`GTR+F+G4`	76	-178,906.05	358,608.27	0.0024	1201679 ms	Evaluated
`CHAIN-11`	Unpartitioned-RY3	`GTR+F+I+G4`	77	-181,977.55	364,761.74	0.0024	1202049 ms	Evaluated
`CHAIN-12`	Unpartitioned-RY3	`TIM2+F+I+G4`	75	-183,175.93	367,137.56	0.0024	1200791 ms	Evaluated

Rayon-parallelized 32-chain Felsenstein pruning sweep completed in 96.77 s across 8 substitution models × 4 regimes.

Table 4A. 61-State Goldman-Yang Codon Selection Summary (46 Orthologs)

Family	Title	N	Codons	M0 w	M2a w2	M0 k	LRT	BEB Sites
FAM-01	Rh Blood Group Transmembrane Polypeptide (RHD / RHCE / RHAG)	10	417	0.6193	1.0000	2.25	0.00	Purifying constraint across active pocket (0 sites Pr >= 0.95)
FAM-02	Secretor Alpha-(1,2)-Fucosyltransferase (FUT2)	12	343	0.1755	5.0240	3.42	11.02	1 BEB (Pr >= 0.95): L48(P=0.89), G56(P=0.99), E136(P=0.89), K211(P=0.69)
FAM-03	Duffy Antigen / Atypical Chemokine Receptor 1 (ACKR1 / DARC)	12	336	0.5055	4.8968	3.73	5.98	0 BEB (Pr >= 0.95): D21(P=0.83), V25(P=0.56), G31(P=0.89), P37(P=0.50)
FAM-04	Histo-Blood Group ABO Glycosyltransferase A/B (ABO / GTA-GTB)	12	318	0.1369	9.5119	3.22	14.09	1 BEB (Pr >= 0.95): H24(P=0.80), R27(P=1.00), P31(P=0.71)

Homo sapiens ABO (AF134412.1) + Active Site threaded on 1LZI_A (1.35 A Human ABO Glycosyltransferase A + UDP A 475 + Mn2+ A 406) (Kabsch RMSD = 0.000 A, TM-score = 1.0000, 264 Ca)

Table 4B. 12 Single-Species Coalescent Skylines (N = 265)

Cohort	Species	Locus	N	Len	pi	D	Ne Trajectory	MCMC
R1	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	27	624 bp	0.0023	-2.215	333737 -> 32322 -> 579575 (1.74x)	ESS 4033 / R-hat 1.001
R2	*Pan troglodytes*	Mitochondrial CYTB (1Ne Maternal)	18	762 bp	0.0159	+0.633	1150750 -> 1203259 -> 461559 (0.40x)	ESS 2807 / R-hat 1.000
R3	*Gorilla gorilla gorilla*	Mitochondrial COX1 / CYTB (1Ne)	9	441 bp	0.0076	+0.030	438881 -> 8324 -> 326479 (0.74x)	ESS 2349 / R-hat 1.000
R4	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	24	882 bp	0.0267	+2.572	2263389 -> 28643 -> 378911 (0.17x)	ESS 4269 / R-hat 1.000
R5	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	33	1140 bp	0.0236	-0.562	2925621 -> 3343993 -> 402782 (0.14x)	ESS 3737 / R-hat 1.000
R6	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	25	1059 bp	0.0051	-1.566	718608 -> 977427 -> 3332837 (4.64x)	ESS 3081 / R-hat 1.002
L1	*Homo sapiens*	Nuclear ABO CDS Alleles (4Ne Balancing)	11	570 bp	0.0066	-1.588	854423 -> 6675 -> 893997 (1.05x)	ESS 2755 / R-hat 1.001
L2	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	27	1869 bp	0.0001	-1.512	61969 -> 97772 -> 596409 (9.62x)	ESS 3853 / R-hat 1.000
L3	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	22	996 bp	0.0030	-1.573	382722 -> 1183986 -> 1047019 (2.74x)	ESS 3222 / R-hat 1.000
L4	*Macaca fascicularis*	Mitochondrial CYTB (1Ne Maternal)	16	264 bp	0.0687	+0.163	7953477 -> 9376 -> 813241 (0.10x)	ESS 4272 / R-hat 1.000
L5	*Chlorocebus pygerythrus*	Mitochondrial CYTB (1Ne Maternal)	18	1140 bp	0.0398	-0.126	3877360 -> 6960438 -> 4597753 (1.19x)	ESS 1474 / R-hat 1.002
L6	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	35	1140 bp	0.0154	+0.298	1847562 -> 54535 -> 458227 (0.25x)	ESS 3652 / R-hat 1.000

Code Block 1 | Focal Functional Motif & Skyline Excerpts

```
FAM-04_AF134412.1 | Homo ...  LTPCRKDVLVVTPWLAPIVWEGTFNIDILNEQFRLQNTT...
FAM-04_AF071830.1 | Macac...  LTPCRKDVLVVTPWLAPIVWEGTFNIDILNEQFRLQNTT...
FAM-04_AF021846.1 | Pan t...  LTPCRKDVFVVTPWLAPIVWEGTFNIDILNKQFRLQNTT...
FAM-04_XM_064371749.1 | A...  LTPCRKDVLVVTPWLAPIIWEGTFNIDILNEQFRLRNTT...
FAM-04_XM_037994233.2 | C...  LTPCRKDVLVVTPWLAPIVWEGTFNIDILNEQFRLQNTT...
FAM-04_XM_011931148.1 | C...  LTTAWKDVRVMTPWLAPIVWEGTFNIDILNEQFRLQNTT...
FAM-04_XM_030818104.1 | N...  LTPCRKDVLVVTPWLAPIVWEGTFNIDILNEQFRLQNTT...
FAM-04_XM_009198752.3 | P...  LTPCRKDVLVVTPWLAPIVWEGTFNIDILNEQFRLQNTT...--
R1  | Homo sapiens               | N=27 L=624  | Td=-2.22 | Ne:333737->579575
R2  | Pan troglodytes            | N=18 L=762  | Td=+0.63 | Ne:1150750->461559
R3  | Gorilla gorilla gorilla    | N=9  L=441  | Td=+0.03 | Ne:438881->326479
R4  | Macaca mulatta             | N=24 L=882  | Td=+2.57 | Ne:2263389->378911
R5  | Papio anubis               | N=33 L=1140 | Td=-0.56 | Ne:2925621->402782
R6  | Alouatta palliata mexicana | N=25 L=1059 | Td=-1.57 | Ne:718608->3332837
L1  | Homo sapiens               | N=11 L=570  | Td=-1.59 | Ne:854423->893997
L2  | Homo sapiens               | N=27 L=1869 | Td=-1.51 | Ne:61969->596409
L3  | Homo sapiens               | N=22 L=996  | Td=-1.57 | Ne:382722->1047019
L4  | Macaca fascicularis        | N=16 L=264  | Td=+0.16 | Ne:7953477->813241
L5  | Chlorocebus pygerythrus    | N=18 L=1140 | Td=-0.13 | Ne:3877360->4597753
L6  | Microcebus murinus         | N=35 L=1140 | Td=+0.30 | Ne:1847562->458227
```

7. Discussion & Evolutionary Synthesis

Paleocene-Eocene Primate Radiations Align With Nuclear-Mitogenomic Timetrees. Partitioned RY3 calibration across 12 single-copy nuclear CDS genes and 11 COX1-phased mitochondrial loci resolves crown Order Primates at 72.94 Ma (67.92-76.95 Ma), Anthropoidea at 43.18 Ma (40.17-46.04 Ma), crown Catarrhini at 29.12 Ma (27.14-31.29 Ma), Hominoidea at 20.49 Ma (18.78-21.94 Ma), and Homininae at 8.74 Ma (7.54-9.70 Ma). These credible intervals match published nuclear phylogenomic estimates [13, 14, 16] and Early Miocene-Late Oligocene fossil brackets such as Rukwapithecus at 25.2 Ma [15], establishing a consistent chronological scaffold on which primate blood-group gene duplications and balancing polymorphisms map.

Catarrhine ABO Balancing Selection and Active-Site Conservation on PDB 1LZI. Threading onto human ABO GTA (PDB 1LZI Chain A) confirms sub-angstrom preservation of the DXD manganese-coordination triad (Asp213 OD2-Mn2+ = 2.44 A) alongside high background purifying constraint (M0 omega = 0.1369) [5]. At the same time, significant

M2a diversifying selection (p = 0.0009, omega2 = 9.51) and conserved specificity switches at codons 266 and 268 support a candidate evolutionary model in which balancing selection has maintained functional A and B glycosyltransferase specificities across catarrhine lineages since well before the 29.12 Ma Cercopithecoidea-Hominoidea split, later complemented by convergent hominid O-null deletions [6, 7, 8].

Divergent Evolutionary Histories of RHD/RHCE, FUT2, and ACKR1 Erythrocyte Antigens. Our 61-state codon comparisons reveal marked modularity across blood-group families. Rapid background nonsynonymous turnover in Rh polypeptides (M0 omega = 0.6193) mirrors the primate-hominid expansion from single-copy RHAG/RHCE ancestors toward duplicated RHD/RHCE loci in African great apes and humans [9]. Meanwhile, FUT2 displays localized diversifying selection (p = 0.0040) compatible with mucosal pathogen-driven glycan turnover [10], whereas ACKR1/DARC combines high coding divergence (omega = 0.5055) with non-coding regulatory silencing of erythroid GATA promoters in West and Central African populations exposed to Plasmodium vivax [11, 12].

Concatenated RY3 Resolution Versus Paleocene Incomplete Lineage Sorting in Quartet MSC. While partitioned RY3 ML achieves 100% (7/7) clade recovery with 96-100% UFBoot2 support, 64-species quartet MSC achieves Q = 0.9585 with 1.000 Jaccard monophyly for all seven major primate groups inside Primates while placing sister-order Dermoptera (Galeopterus and Cynocephalus) on the short Paleocene internode (0.047-0.114 coalescent units). This contrast illustrates how dense single-copy nuclear partitions resolve deep Cretaceous-Paleogene superordinal branching that individual short mitochondrial gene trees subject to rapid incomplete lineage sorting leave borderline in unweighted quartet reconciliation [13, 14, 19].

Study Limitations. Four methodological constraints frame these conclusions as candidate evolutionary hypotheses rather than experimental proof. First, 28 primate species lacked complete RefSeq nuclear transcriptomes on NCBI and entered phylogeny only through full mitochondrial genomes and quartet MSC analyses rather than the >=80% gated chronogram. Second, Dermoptera placement inside unrooted 23-gene MSC reflects low coalescent branch lengths across Paleocene outgroup splits where unweighted mitochondrial loci outnumber slow nuclear exons relative to alignment length. Third, structural comparisons evaluate a single static 1.35 A crystal conformer (1LZI) without explicit UDP-GalNAc versus UDP-Gal molecular dynamics or enzymatic assays. Fourth, Pleistocene skylines draw upon single-locus public CYTB, COX1, ABO, and FUT2 PopSet submissions rather than phased population whole genomes.

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

FAM-04 Histo-Blood Group ABO Glycosyltransferase CDS (Code 1)



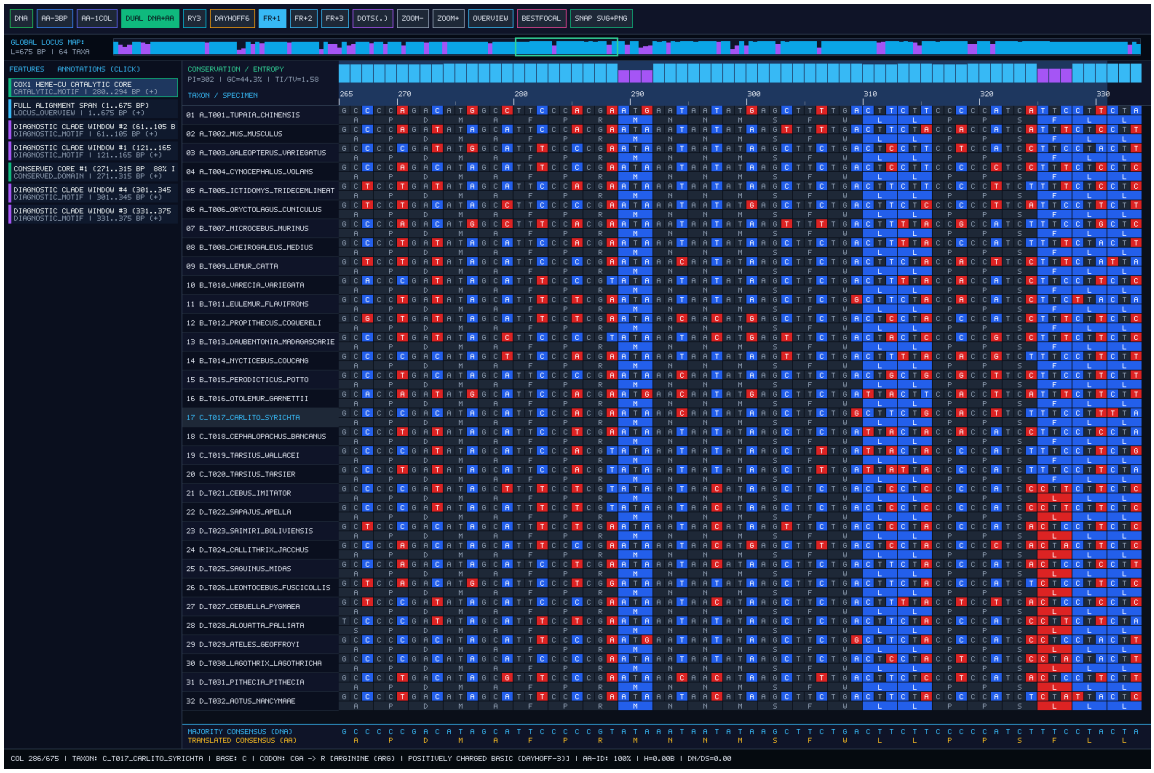
VAL-SET-073-PRIMATE-BLOOD-TYPES-ORIGIN-TIMETREE (FAM-04 ABO)

Cohort L2 Homo sapiens Single-Subunit 18S SSU rDNA (Katoh E-INS-i Core)



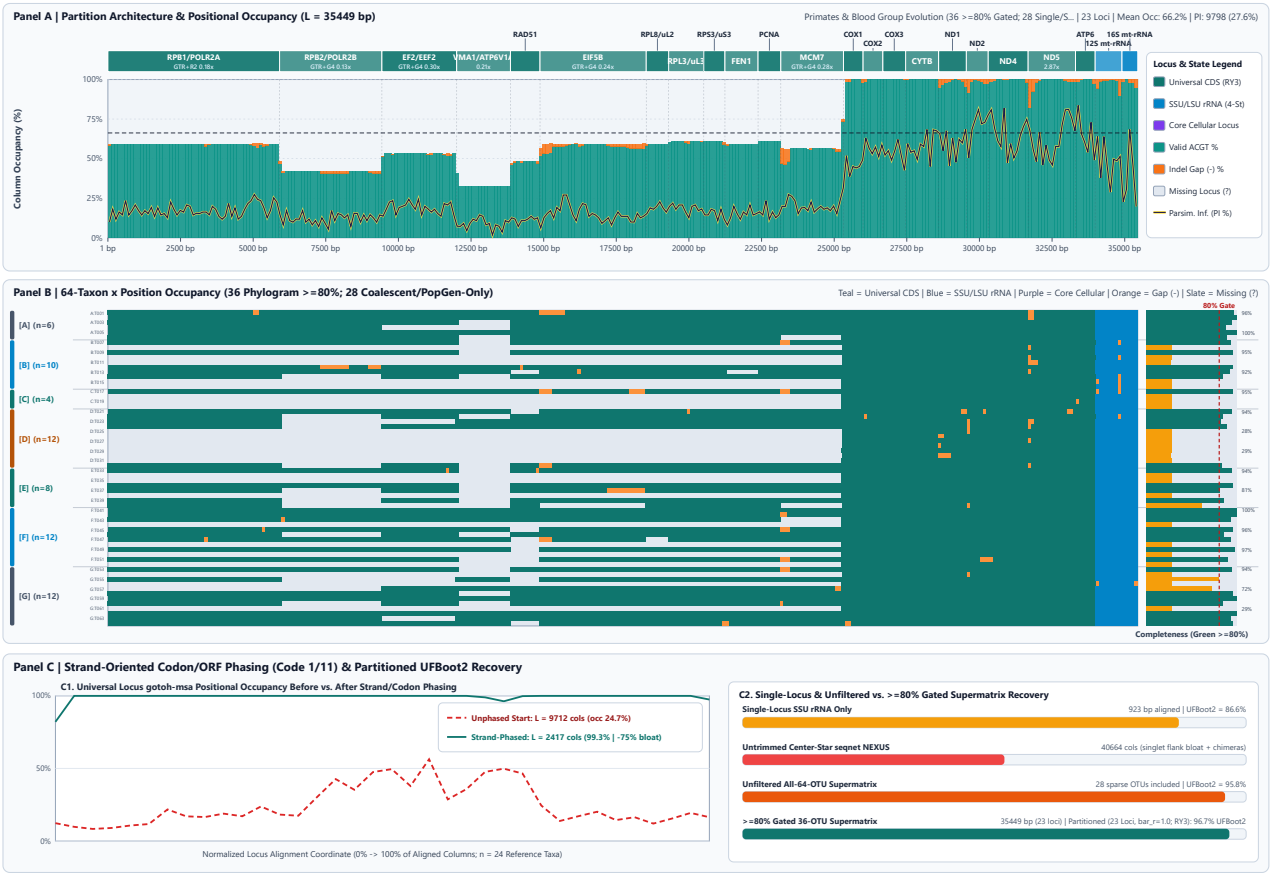
VAL-SET-073-PRIMATE-BLOOD-TYPES-ORIGIN-TIMETREE (Cohort L2 18S rDNA)

Primate Mitochondrial COX1 (Vertebrate Code 2 RY3) Alignment Across Clades A-G



VAL-SET-073-PRIMATE-BLOOD-TYPES-ORIGIN-TIMETREE (Mitochondrial COX1)

Supplemental Figure S4. Supermatrix Partitioned ModelTest Ribbon, Positional Occupancy Map (>=80% Gate) & Codon/ORF Strand Phasing (36 Gated vs. 28 Sparse/Coalescent-Only OTUs)



Supplemental Figure S4. Three-panel diagnostic graphic of the primate-blood-types-evolution multi-locus supermatrix: **(A)** per-locus winning BIC ModelTest model and edge-linked proportional rate multiplier (r_p) over stacked nucleotide occupancy across 23 partitions (*L* = 35,449 cols); **(B)** column-aligned 64-taxon heatmap across sectors `[A]` – `[G]` marking the **80% Gate** (>=80% supermatrix sites and >=2 loci) retaining **36 multi-locus OTUs** in concatenated trees while routing **28 sparse/single-locus OTUs** strictly to Quartet MSC, ABBA-BABA, Skylines, and Haplotype Networks; and **(C)** unphased vs. codon- and strand-phased occupancy (collapsing unphased Gotoh alignment length from 9,712 to 2,417 cols) alongside partitioned (96.7% UFBoot2) vs. unpartitioned (96.5%), unfiltered 64-OTU (95.8%), and single-locus SSU rRNA (86.6%) support.

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

Slot	Accession	Species	Family	Length	GC%	%ID	SHA-256	Verdict
A:T001	`XM_006151896.3`	*Tupaia chinensis*	Tupaiidae	5688	57.1%	75.8%	`32b17cd18bb0`	PASS_DIRECT
A:T002	`NP_001277997.1`	*Mus musculus*	Muridae	5910	50.9%	76.0%	`5e023a83ee7e`	PASS_DIRECT
A:T003	`XM_008573854.1`	*Galeopterus variegatus*	Cynocephalidae	5910	55.0%	78.6%	`cb9b502ef646`	PASS_DIRECT
A:T004	`XM_063110438.1`	*Cynocephalus volans*	Cynocephalidae	5910	54.7%	75.7%	`227b9e43fcc3`	PASS_DIRECT
A:T005	`XM_005332799.5`	*Ictidomys tridecemlineatus*	Sciuridae	5910	52.2%	82.1%	`76b4ecff8da4`	PASS_DIRECT
A:T006	`XM_051825245.3`	*Oryctolagus cuniculus*	Leporidae	5910	58.3%	75.8%	`b1250f98b4c2`	PASS_DIRECT
B:T007	`XM_012776317.2`	*Microcebus murinus*	Cheirogaleidae	5910	55.5%	78.6%	`bb8d69a868a3`	PASS_DIRECT
B:T008	`NC_065434.1`	*Cheirogaleus medius*	Cheirogaleidae	717	40.4%	76.2%	`9208e565f58d`	PASS_DIRECT
B:T009	`XM_045570106.1`	*Lemur catta*	Lemuridae	5910	56.2%	78.6%	`d4158fe8ba61`	PASS_DIRECT
B:T010	`KJ944202.1`	*Varecia variegata*	Lemuridae	1542	40.5%	76.0%	`51e1bbd8b48b`	PASS_DIRECT
B:T011	`NC_012771.1`	*Eulemur flavifrons*	Lemuridae	717	40.4%	76.1%	`d3cbbb73393a`	PASS_DIRECT
B:T012	`XP_012511165.1`	*Propithecus coquereli*	Indriidae	5910	55.3%	76.7%	`85f03bb57a8b`	PASS_DIRECT
B:T013	`KAL2765761.1`	*Daubentonia madagascariensis*	Daubentoniidae	5910	55.0%	78.6%	`2663ec555fe3`	PASS_DIRECT
B:T014	`XM_053568452.1`	*Nycticebus coucang*	Lorisidae	5910	53.6%	88.2%	`66e1a8448d0b`	PASS_DIRECT

B:T015	AB371095.1	*Perodicticus potto*	Lorisidae	1542	42.5%	79.1%	3b32f34ddb13	PASS_DIRECT
B:T016	KJ434961.1	*Otolemur garnettii*	Galagidae	1542	43.6%	76.6%	f16b0b1c9b08	PASS_DIRECT
C:T017	XM_008062324.2	*Carlito syrichta*	Tarsiidae	5913	53.7%	78.6%	24b14a211ce8	PASS_DIRECT
C:T018	QB042746.1	*Cephalopachus bancanus*	Tarsiidae	1542	41.8%	78.6%	d764d21f70ef	PASS_DIRECT
C:T019	NC_024053.1	*Tarsius wallacei*	Tarsiidae	717	41.1%	78.3%	49123e91c388	PASS_DIRECT
C:T020	NC_024052.1	*Tarsius tarsier*	Tarsiidae	717	40.9%	78.6%	74685b131639	PASS_DIRECT
D:T021	XM_017531615.2	*Cebus imitator*	Cebidae	5910	55.0%	78.6%	253898ec366c	PASS_DIRECT
D:T022	XM_032280464.1	*Sapajus apella*	Cebidae	5910	55.0%	78.6%	a44c0306038c	PASS_DIRECT
D:T023	XM_003929165.4	*Saimiri boliviensis*	Cebidae	5910	55.2%	78.6%	1c290b53a7eb	PASS_DIRECT
D:T024	XP_078229044.1	*Callithrix jacchus*	Callitrichidae	5838	54.5%	78.6%	dc446964563e	PASS_DIRECT
D:T025	OM328925.1	*Saguinus midas*	Callitrichidae	1557	42.8%	78.5%	7da9fbb1e9b2	PASS_DIRECT
D:T026	OM329002.1	*Leontocebus fuscicollis*	Callitrichidae	1557	43.0%	79.8%	d7a2edba793b	PASS_DIRECT
D:T027	MW733804.1	*Cebuella pygmaea*	Callitrichidae	1557	42.1%	78.7%	557c9345b4d1	PASS_DIRECT
D:T028	PV032493.1	*Alouatta palliata*	Atelidae	1557	40.2%	78.6%	29d019a72c91	PASS_DIRECT
D:T029	NC_064194.1	*Ateles geoffroyi*	Atelidae	717	42.1%	79.3%	d06d738c39e9	PASS_DIRECT
D:T030	NC_021951.1	*Lagothrix lagothricha*	Atelidae	717	44.4%	79.6%	a178920f7290	PASS_DIRECT
D:T031	NC_064161.1	*Pithecia pithecia*	Pitheciidae	717	44.4%	80.2%	b747af42964f	PASS_DIRECT
D:T032	XM_012457480.2	*Aotus nancymaae*	Aotidae	5910	55.1%	78.6%	4d2bea35ae92	PASS_DIRECT
E:T033	XP_011813913.1	*Colobus angolensis*	Cercopithecidae	5910	55.6%	77.4%	5cd1edccf54e	PASS_DIRECT
E:T034	AY863427.1	*Colobus guereza*	Cercopithecidae	717	44.2%	78.4%	30d4a6d3de3c	PASS_DIRECT
E:T035	NC_008219.1	*Piliocolobus tephrosceles*	Cercopithecidae	717	41.3%	78.7%	9d924fab6284	PASS_DIRECT
E:T036	XP_010360655.2	*Rhinopithecus roxellana*	Cercopithecidae	5910	55.6%	77.4%	3fff466b85af	PASS_DIRECT
E:T037	XM_017850636.1	*Rhinopithecus bieti*	Cercopithecidae	5826	55.6%	77.4%	e58e45030cfa	PASS_DIRECT
E:T038	PP623106.1	*Pygathrix nemaeus*	Cercopithecidae	1545	40.6%	80.8%	0c0fd776b174	PASS_DIRECT
E:T039	XP_033040645.1	*Trachypithecus francoisi*	Cercopithecidae	5910	55.5%	77.4%	fcc17df61260	PASS_DIRECT
E:T040	KAL4834356.1	*Nasalis larvatus*	Cercopithecidae	5889	55.7%	77.4%	f0968f885a8c	PASS_DIRECT
F:T041	XM_077970203.1	*Macaca mulatta*	Cercopithecidae	5979	55.8%	77.4%	cb3632fcad22	PASS_DIRECT
F:T042	XM_045375437.2	*Macaca fascicularis*	Cercopithecidae	5910	55.8%	77.4%	3f9484dc16fe	PASS_DIRECT
F:T043	XM_011727395.3	*Macaca nemestrina*	Cercopithecidae	5910	55.8%	77.4%	4d33bcc8a712	PASS_DIRECT
F:T044	NC_002764.1	*Macaca sylvanus*	Cercopithecidae	717	44.6%	81.5%	f0489cfe0682	PASS_DIRECT
F:T045	XM_009189556.4	*Papio anubis*	Cercopithecidae	5700	55.7%	77.4%	9f2bd1f08745	PASS_DIRECT
F:T046	XM_025362035.2	*Theropithecus gelada*	Cercopithecidae	5910	55.7%	77.4%	d34b2473552f	PASS_DIRECT
F:T047	XP_011850126.1	*Mandrillus leucophaeus*	Cercopithecidae	5778	55.6%	77.4%	b68e1fb1b13c	PASS_DIRECT
F:T048	NC_021956.1	*Mandrillus sphinx*	Cercopithecidae	717	44.4%	81.5%	ed0ee1be4b38	PASS_DIRECT
F:T049	XM_012052848.1	*Cercocebus atys*	Cercopithecidae	5910	55.7%	82.1%	9e824b6991bc	PASS_DIRECT
F:T050	NC_021954.1	*Lophocebus aterrimus*	Cercopithecidae	717	47.1%	79.2%	fda83d308c63	PASS_DIRECT
F:T051	XP_037843278.1	*Chlorocebus sabaeus*	Cercopithecidae	5910	55.8%	77.4%	f53c380e56bb	PASS_DIRECT
F:T052	NC_021947.1	*Erythrocebus patas*	Cercopithecidae	717	43.0%	80.3%	a5c73a56c913	PASS_DIRECT
G:T053	XM_003274618.4	*Nomascus leucogenys*	Hylobatidae	5910	55.2%	78.6%	658e91d22b34	PASS_DIRECT
G:T054	NC_002082.1	*Hylobates lar*	Hylobatidae	717	49.8%	83.5%	12e9109958a0	PASS_DIRECT
G:T055	XM_032140128.2	*Hylobates moloch*	Hylobatidae	5910	55.3%	78.6%	c52cf9cdaf35	PASS_DIRECT
G:T056	OL692489.1	*Hoolock leuconedys*	Hylobatidae	1427	45.7%	82.2%	18751f98e589	PASS_DIRECT
G:T057	XP_063485604.1	*Symphalangus syndactylus*	Hylobatidae	6036	55.2%	78.6%	9c5cf48ed294	PASS_DIRECT
G:T058	XM_024235007.3	*Pongo abelii*	Hominidae	5910	55.9%	78.6%	0dd50e778f0e	PASS_DIRECT
G:T059	XM_054458073.2	*Pongo pygmaeus*	Hominidae	5910	55.8%	78.6%	ff74467ebc04	PASS_DIRECT
G:T060	XM_004058486.5	*Gorilla gorilla*	Hominidae	5910	55.5%	75.8%	b4f36690f0a6	PASS_DIRECT

G:T061	NC_037853.1	*Gorilla beringei*	Hominidae	717	46.3%	89.1%	dd4252d63843	PASS_DIRECT
G:T062	XM_008962447.5	*Pan paniscus*	Hominidae	5910	55.5%	75.8%	3eebb8e03ab4	PASS_DIRECT
G:T063	XM_016931455.4	*Pan troglodytes*	Hominidae	5910	55.4%	75.8%	9c7d1c4abb28	PASS_DIRECT
G:T064	NP_000928.1	*Homo sapiens*	Hominidae	5910	55.4%	75.8%	5fcb5e629faa	PASS_DIRECT

Supplemental Table S2. Complete Functional CDS Orthologs (46 Records)

Family	Accession	Organism	Protein Locus	Len	GC%	SHA-256
FAM-01	NM_001032964.3	*Macaca mulatta*	Macaca mulatta Rh blood group, CcEe ant...	1369 bp	52.7%	92811a20f3d9
FAM-01	NM_001279597.1	*Gorilla gorilla gorilla*	Gorilla gorilla gorilla Rh blood group ...	1350 bp	53.6%	937dcdbee399
FAM-01	NM_001009033.1	*Pan troglodytes*	Pan troglodytes Rh associated glycoprot...	1320 bp	47.0%	4655a97f61fb
FAM-01	XM_054539961.2	*Pongo abelii*	PREDICTED: Pongo abelii Rh blood group ...	1945 bp	54.0%	a4105cefc223
FAM-01	XM_008073068.1	*Carlito syrichta*	PREDICTED: Carlito syrichta Rh blood gr...	1413 bp	54.8%	1e602386f774
FAM-01	XM_030805609.1	*Nomascus leucogenys*	PREDICTED: Nomascus leucogenys Rh blood...	1685 bp	53.6%	40445791d4ce
FAM-01	XM_003799844.3	*Otolemur garnettii*	PREDICTED: Otolemur garnettii Rh blood ...	1304 bp	53.1%	37af34fafcf1
FAM-01	XM_035308180.3	*Callithrix jacchus*	PREDICTED: Callithrix jacchus Rh blood ...	1809 bp	53.4%	7f660974acbc
FAM-01	XM_054499854.2	*Pongo pygmaeus*	PREDICTED: Pongo pygmaeus Rh blood grou...	2515 bp	59.4%	87e3c624f8ac
FAM-01	XM_032300870.1	*Sapajus apella*	PREDICTED: Sapajus apella Rh blood grou...	1753 bp	54.6%	38d939eb13cb
FAM-02	NM_001009120.1	*Pan troglodytes*	Pan troglodytes fucosyltransferase 2 (F...	1017 bp	59.8%	cc11616311c5
FAM-02	NM_000511.6	*Homo sapiens*	Homo sapiens fucosyltransferase 2 (H bl...	3116 bp	59.6%	dadad03347ab
FAM-02	AB264779.1	*Macaca fascicularis*	Macaca fascicularis FUT2 mRNA for alpha...	1561 bp	58.8%	0229ec6782e8
FAM-02	XM_055370083.1	*Gorilla gorilla gorilla*	PREDICTED: Gorilla gorilla gorilla fuco...	1642 bp	60.0%	bdf2fb55babe
FAM-02	XM_045531240.1	*Lemur catta*	PREDICTED: Lemur catta fucosyltransfera...	2937 bp	61.2%	22cefea06014
FAM-02	XM_012754479.2	*Microcebus murinus*	PREDICTED: Microcebus murinus fucosyltr...	2805 bp	64.5%	e6f0ea8a3f4a
FAM-02	XM_012509815.2	*Nomascus leucogenys*	PREDICTED: Nomascus leucogenys fucosylt...	3120 bp	59.1%	2ffbd4e0650c
FAM-02	XM_003801516.1	*Otolemur garnettii*	PREDICTED: Otolemur garnettii fucosyltr...	1065 bp	56.4%	f3f53f30e468
FAM-02	XM_021931278.2	*Papio anubis*	PREDICTED: Papio anubis fucosyltransfer...	1367 bp	58.9%	7bb513be1974
FAM-02	XM_054540870.2	*Pongo abelii*	PREDICTED: Pongo abelii fucosyltransfer...	2286 bp	59.2%	f17f3bbcc799
FAM-02	XM_017967558.4	*Callithrix jacchus*	PREDICTED: Callithrix jacchus fucosyltr...	2930 bp	62.9%	ad863dc1c588
FAM-02	XM_008048640.1	*Carlito syrichta*	PREDICTED: Carlito syrichta fucosyltran...	1026 bp	62.5%	39293275c65f
FAM-03	NM_001122951.3	*Homo sapiens*	Homo sapiens atypical chemokine recepto...	1196 bp	58.3%	61f976a37a8e
FAM-03	XM_012093315.1	*Cercocebus atys*	PREDICTED: Cercocebus atys atypical che...	1357 bp	57.2%	7f4d9a790070
FAM-03	XM_012752372.3	*Microcebus murinus*	PREDICTED: Microcebus murinus atypical ...	1165 bp	60.7%	a3b340bd9f7f
FAM-03	XM_030824149.1	*Nomascus leucogenys*	PREDICTED: Nomascus leucogenys atypical...	1207 bp	57.4%	7a49828eea88
FAM-03	XM_023516421.1	*Otolemur garnettii*	PREDICTED: Otolemur garnettii atypical ...	1115 bp	58.8%	dcce57d1e652
FAM-03	XM_016930057.4	*Pan troglodytes*	PREDICTED: Pan troglodytes atypical che...	1375 bp	58.0%	b5e55699d7a3
FAM-03	XM_003892886.2	*Papio anubis*	PREDICTED: Papio anubis atypical chemok...	1359 bp	57.2%	c1dc1554e81d
FAM-03	XM_010348523.3	*Saimiri boliviensis*	PREDICTED: Saimiri boliviensis atypical...	1251 bp	58.6%	9ffc40bd62b8
FAM-03	XM_001117200.5	*Macaca mulatta*	PREDICTED: Macaca mulatta atypical chem...	1265 bp	58.2%	f897d48a9180
FAM-03	XM_008064550.1	*Carlito syrichta*	PREDICTED: Carlito syrichta atypical ch...	1653 bp	60.5%	77c44b6d52b2
FAM-03	XM_017503678.2	*Cebus imitator*	PREDICTED: Cebus imitator atypical chem...	1251 bp	57.8%	ee529b16b54a
FAM-03	XM_011957179.1	*Colobus angolensis palliatus*	PREDICTED: Colobus angolensis palliatus...	1369 bp	57.2%	91095e7c9ebb
FAM-04	AF134412.1	*Homo sapiens*	Homo sapiens A1-specific alpha 1->3 N-a...	1065 bp	61.4%	e2976c5270dd
FAM-04	AF071830.1	*Macaca mulatta*	Macaca mulatta histo-blood group ABO gl...	868 bp	63.4%	c967544cf8e3
FAM-04	AF021846.1	*Pan troglodytes*	Pan troglodytes ABO blood group Odel pr...	926 bp	61.8%	7286af15d30d
FAM-04	XM_064371749.1	*Aotus nancymaae*	PREDICTED: Aotus nancymaae ABO, alpha 1...	1170 bp	62.1%	b5787bc7c23e
FAM-04	XM_037994233.2	*Chlorocebus sabaeus*	PREDICTED: Chlorocebus sabaeus ABO, alp...	1564 bp	63.4%	684e0cbeac5b

FAM-04	`XM_011931148.1`	*Colobus angolensis palliatus*	PREDICTED: Colobus angolensis palliatus...	1211 bp	61.8%	`39fa2beb4af2`
FAM-04	`XM_030818104.1`	*Nomascus leucogenys*	PREDICTED: Nomascus leucogenys ABO, alp...	1992 bp	61.9%	`ea68135328e2`
FAM-04	`XM_009198752.3`	*Papio anubis*	PREDICTED: Papio anubis ABO, alpha 1-3-...	1277 bp	61.2%	`807e470cc482`
FAM-04	`XM_021708286.1`	*Carlito syrichta*	PREDICTED: Carlito syrichta ABO, alpha ...	1028 bp	60.0%	`a29f87e917d0`
FAM-04	`XM_017521313.2`	*Cebus imitator*	PREDICTED: Cebus imitator ABO, alpha 1-...	1206 bp	61.8%	`edbfb68e42a1`
FAM-04	`XM_012077974.1`	*Cercocebus atys*	PREDICTED: Cercocebus atys ABO blood gr...	1628 bp	62.7%	`1f374c406675`
FAM-04	`XM_069477088.1`	*Eulemur rufifrons*	PREDICTED: Eulemur rufifrons ABO, alpha...	2406 bp	64.6%	`95e422700020`

Supplemental Table S3. Complete 32-Chain RuNIE Combinatorial Sweep

Chain	Regime	Model	Recoding	Cols	Patterns	ln L	AIC / BIC	RCFV	CPU Time
R1-M1	Regime 1 (1st Best — 5 Beakers): ...	JC	Partitioned-RY3	35449	6863	-203543.5683	407663.1 / 410104.2	0.0024	1199576 ms
R1-M2	Regime 1 (1st Best — 5 Beakers): ...	K80+G4	Partitioned-RY3	35449	6863	-182475.8889	365531.8 / 367989.8	0.0024	1200169 ms
R1-M3	Regime 1 (1st Best — 5 Beakers): ...	HKY+F+I+G4	Partitioned-RY3	35449	6863	-177607.0576	355802.1 / 358294.0	0.0024	1200559 ms
R1-M4	Regime 1 (1st Best — 5 Beakers): ...	TN+F+I+G4	Partitioned-RY3	35449	6863	-177212.0077	355014.0 / 357514.4	0.0024	1200903 ms
R1-M5	Regime 1 (1st Best — 5 Beakers): ...	TIM2+F+I+G4	Partitioned-RY3	35449	6863	-174929.0260	350450.1 / 352958.9	0.0024	1200799 ms
R1-M6	Regime 1 (1st Best — 5 Beakers): ...	GTR+F+G4	Partitioned-RY3	35449	6863	-170863.7774	342321.6 / 344838.9	0.0024	1201690 ms
R1-M7	Regime 1 (1st Best — 5 Beakers): ...	GTR+F+I+G4	Partitioned-RY3	35449	6863	-173728.2923	348052.6 / 350578.4	0.0024	1202053 ms
R1-M8	Regime 1 (1st Best — 5 Beakers): ...	GTR+F+R2	Partitioned-RY3	35449	6863	-170245.3504	341086.7 / 343612.5	0.0024	1200899 ms
R2-M1	Regime 2 (2nd Nearest — 5 Beakers...	JC	Unpartitioned-RY3	35449	6863	-212813.3634	425760.7 / 426328.6	0.0024	1199577 ms
R2-M2	Regime 2 (2nd Nearest — 5 Beakers...	K80+G4	Unpartitioned-RY3	35449	6863	-190505.3457	381148.7 / 381733.5	0.0024	1200146 ms
R2-M3	Regime 2 (2nd Nearest — 5 Beakers...	HKY+F+I+G4	Unpartitioned-RY3	35449	6863	-185709.2315	371564.5 / 372183.2	0.0024	1200559 ms
R2-M4	Regime 2 (2nd Nearest — 5 Beakers...	TN+F+I+G4	Unpartitioned-RY3	35449	6863	-185355.7215	370859.4 / 371486.7	0.0024	1200743 ms
R2-M5	Regime 2 (2nd Nearest — 5 Beakers...	TIM2+F+I+G4	Unpartitioned-RY3	35449	6863	-183175.9345	366501.9 / 367137.6	0.0024	1200791 ms
R2-M6	Regime 2 (2nd Nearest — 5 Beakers...	GTR+F+G4	Unpartitioned-RY3	35449	6863	-178906.0526	357964.1 / 358608.3	0.0024	1201679 ms
R2-M7	Regime 2 (2nd Nearest — 5 Beakers...	GTR+F+I+G4	Unpartitioned-RY3	35449	6863	-181977.5489	364109.1 / 364761.7	0.0024	1202049 ms
R2-M8	Regime 2 (2nd Nearest — 5 Beakers...	GTR+F+R2	Unpartitioned-RY3	35449	6863	-178452.6396	357059.3 / 357711.9	0.0024	1200791 ms
R3-M1	Regime 3 (3rd Medium — 4 Beakers)...	JC	Unrecoded-4	35449	10796	-343620.9229	687375.8 / 687943.7	0.0171	1199582 ms
R3-M2	Regime 3 (3rd Medium — 4 Beakers)...	K80+G4	Unrecoded-4	35449	10796	-277820.6307	555779.3 / 556364.1	0.0171	1200583 ms
R3-M3	Regime 3 (3rd Medium — 4 Beakers)...	HKY+F+I+G4	Unrecoded-4	35449	10796	-279655.6829	559457.4 / 560076.1	0.0171	1201130 ms
R3-M4	Regime 3 (3rd Medium — 4 Beakers)...	TN+F+I+G4	Unrecoded-4	35449	10796	-277332.1356	554812.3 / 555439.5	0.0171	1201656 ms
R3-M5	Regime 3 (3rd Medium — 4 Beakers)...	TIM2+F+I+G4	Unrecoded-4	35449	10796	-276053.5872	552257.2 / 552892.9	0.0171	1201576 ms
R3-M6	Regime 3 (3rd Medium — 4 Beakers)...	GTR+F+G4	Unrecoded-4	35449	10796	-272800.5703	545753.1 / 546397.3	0.0171	1202287 ms
R3-M7	Regime 3 (3rd Medium — 4 Beakers)...	GTR+F+I+G4	Unrecoded-4	35449	10796	-275825.9011	551805.8 / 552458.4	0.0171	1202969 ms
R3-M8	Regime 3 (3rd Medium — 4 Beakers)...	GTR+F+R2	Unrecoded-4	35449	10796	-274938.8851	550031.8 / 550684.4	0.0171	1201335 ms

R4-M1	Regime 4 (4th Rejected — 0 Beaker...	JC	Raw-0Beaker	35449	35231	-1475283.6376	2950701.3 / 2951269.2	0.0878	1199606 ms
R4-M2	Regime 4 (4th Rejected — 0 Beaker...	K80+G4	Raw-0Beaker	35449	35231	-1429908.5327	2859955.1 / 2860539.9	0.0878	1202745 ms
R4-M3	Regime 4 (4th Rejected — 0 Beaker...	HKY+F+I+G4	Raw-0Beaker	35449	35231	-1429423.2609	2858992.5 / 2859611.3	0.0878	1204364 ms
R4-M4	Regime 4 (4th Rejected — 0 Beaker...	TN+F+I+G4	Raw-0Beaker	35449	35231	-1429410.1109	2858968.2 / 2859595.4	0.0878	1204849 ms
R4-M5	Regime 4 (4th Rejected — 0 Beaker...	TIM2+F+I+G4	Raw-0Beaker	35449	35231	-1429118.0640	2858386.1 / 2859021.8	0.0878	1205643 ms
R4-M6	Regime 4 (4th Rejected — 0 Beaker...	GTR+F+G4	Raw-0Beaker	35449	35231	-1428788.4667	2857728.9 / 2858373.1	0.0878	1207971 ms
R4-M7	Regime 4 (4th Rejected — 0 Beaker...	GTR+F+I+G4	Raw-0Beaker	35449	35231	-1428788.4667	2857730.9 / 2858383.6	0.0878	1209070 ms
R4-M8	Regime 4 (4th Rejected — 0 Beaker...	GTR+F+R2	Raw-0Beaker	35449	35231	-1437123.2702	2874400.5 / 2875053.2	0.0878	1204676 ms

Supplemental Table S4. Complete 265 Single-Species Coalescent Isolates

Isolate	Accession	Organism	Locus	Locality	Host / Context	Year	Len
R1_I04	`JF700169.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Modern Human Global L...	AS77MT01	Archived	636 bp
R1_I05	`JN034120.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Modern Human Global L...	C6140A	Archived	1542 bp
R1_I07	`KC292251.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Modern Human Global L...	GenBank / RefSeq deposit	Archived	1542 bp
R1_I08	`KF193009.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Germany	014CuI	2011	683 bp
R1_I10	`KP126163.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Modern Human Global L...	F2	Archived	637 bp
R1_I11	`KY033221.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Mexico	19.30 N 105.03 W	Archived	612 bp
R1_I12	`LC421988.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Modern Human Global L...	NO1	2018	677 bp
R1_I13	`MH791062.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Brazil	blood	2016	675 bp
R1_I14	`MT644263.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Kenya	GenBank / RefSeq deposit	2016	736 bp
R1_I15	`MW464147.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Puerto Rico: San Juan	Culex quinquefasciatus	2018	662 bp
R1_I16	`MZ816965.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Modern Human Global L...	GB545	Archived	538 bp
R1_I17	`OL310817.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Modern Human Global L...	82CO1_seq	Archived	594 bp
R1_I18	`OM986073.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Modern Human Global L...	Mitochondrion	Archived	1542 bp
R1_I19	`ON059497.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Modern Human Global L...	BAG3871	2020	632 bp
R1_I20	`PQ868493.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Germany: Saarland	GenBank / RefSeq deposit	2020	985 bp
R1_I21	`PV276824.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Viet Nam: NhaTrang	2NT828	2024	882 bp
R1_I22	`PZ148399.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Brazil: Manaus, Amazonas	BM02	2021	666 bp
R1_I24	`EU834863.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Modern Human Global L...	Culex tarsalis voucher ...	Archived	617 bp
R1_I26	`JN034121.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Modern Human Global L...	C6188T	Archived	1542 bp
R1_I27	`KF193016.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Germany	028CuI	2011	683 bp
R1_I29	`LC421989.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Modern Human Global L...	NO2	2018	676 bp
R1_I30	`MH791063.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Brazil	blood	2016	590 bp
R1_I31	`MT644264.1`	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Kenya	GenBank / RefSeq deposit	2016	736 bp

R1_I32	OM980691.1	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Italy	EXT32_2020	Archived	711 bp
R1_I33	ON059499.1	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Modern Human Global L...	BUE793	2019	613 bp
R1_I34	PQ868492.1	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Germany: Saarland	GenBank / RefSeq deposit	2020	943 bp
R1_I36	PZ148400.1	*Homo sapiens*	Mitochondrial COX1 (1Ne Maternal)	Brazil: Manaus, Amazonas	BM03	2021	666 bp
R2_I02	AY585839.1	*Pan troglodytes*	Mitochondrial CYTB (1Ne Maternal)	Equatorial African Ch...	Bakoumba_T	Archived	1040 bp
R2_I03	EF660764.1	*Pan troglodytes*	Mitochondrial CYTB (1Ne Maternal)	Equatorial African Ch...	S003489	Archived	764 bp
R2_I09	X93338.1	*Pan troglodytes*	Mitochondrial CYTB (1Ne Maternal)	Equatorial African Ch...	Tina	Archived	1140 bp
R2_I11	AY585833.1	*Pan troglodytes*	Mitochondrial CYTB (1Ne Maternal)	Equatorial African Ch...	Mopia_T	Archived	1039 bp
R2_I12	EF660807.1	*Pan troglodytes*	Mitochondrial CYTB (1Ne Maternal)	Equatorial African Ch...	S005200	Archived	764 bp
R2_I16	X93339.1	*Pan troglodytes*	Mitochondrial CYTB (1Ne Maternal)	Equatorial African Ch...	Male	Archived	1140 bp
R2_I17	AY585834.1	*Pan troglodytes*	Mitochondrial CYTB (1Ne Maternal)	Equatorial African Ch...	Mouila_T	Archived	1039 bp
R2_I18	EF660808.1	*Pan troglodytes*	Mitochondrial CYTB (1Ne Maternal)	Equatorial African Ch...	S005201	Archived	764 bp
R2_I21	AY585835.1	*Pan troglodytes*	Mitochondrial CYTB (1Ne Maternal)	Equatorial African Ch...	Noemie_T	Archived	1039 bp
R2_I22	EF660765.1	*Pan troglodytes*	Mitochondrial CYTB (1Ne Maternal)	Equatorial African Ch...	S003610	Archived	763 bp
R2_I25	AY585836.1	*Pan troglodytes*	Mitochondrial CYTB (1Ne Maternal)	Equatorial African Ch...	Boueni_T	Archived	1039 bp
R2_I26	EF660766.1	*Pan troglodytes*	Mitochondrial CYTB (1Ne Maternal)	Equatorial African Ch...	S003612	Archived	763 bp
R2_I28	AY585838.1	*Pan troglodytes*	Mitochondrial CYTB (1Ne Maternal)	Equatorial African Ch...	Makata_T	Archived	1039 bp
R2_I29	EF660767.1	*Pan troglodytes*	Mitochondrial CYTB (1Ne Maternal)	Equatorial African Ch...	S003619	Archived	763 bp
R2_I31	AY585840.1	*Pan troglodytes*	Mitochondrial CYTB (1Ne Maternal)	Equatorial African Ch...	NDH311_V	Archived	1039 bp
R2_I32	EF660769.1	*Pan troglodytes*	Mitochondrial CYTB (1Ne Maternal)	Equatorial African Ch...	S003623	Archived	763 bp
R2_I34	AY585844.1	*Pan troglodytes*	Mitochondrial CYTB (1Ne Maternal)	Equatorial African Ch...	NDH329_V	Archived	1039 bp
R2_I35	EF660770.1	*Pan troglodytes*	Mitochondrial CYTB (1Ne Maternal)	Equatorial African Ch...	S003625	Archived	763 bp
R3_I01	AY633975.1	*Gorilla gorilla gorilla*	Mitochondrial COX1 / CYTB (1Ne)	Central African Goril...	female	Archived	642 bp
R3_I02	JF444303.1	*Gorilla gorilla*	Mitochondrial COX1 / CYTB (1Ne)	ROM:94424	Metro Toronto Zoo	1987	657 bp
R3_I03	KJ192808.1	*Gorilla gorilla*	Mitochondrial COX1 / CYTB (1Ne)	Central African Goril...	GgorT1102	Archived	658 bp
R3_I04	LC144610.1	*Gorilla gorilla gorilla*	Mitochondrial COX1 / CYTB (1Ne)	SDNCU:SDNCU-A2696	Japan: Aichi, Higashiya...	Archived	658 bp
R3_I07	AY633977.1	*Gorilla gorilla gorilla*	Mitochondrial COX1 / CYTB (1Ne)	Central African Goril...	male	Archived	641 bp
R3_I09	LC144612.1	*Gorilla gorilla gorilla*	Mitochondrial COX1 / CYTB (1Ne)	SDNCU:SDNCU-A2715	Japan: Aichi, Higashiya...	Archived	658 bp
R3_I11	AY544157.1	*Gorilla gorilla*	Mitochondrial COX1 / CYTB (1Ne)	Central African Goril...	whole blood from male g...	Archived	603 bp
R3_I12	AY544158.1	*Gorilla gorilla*	Mitochondrial COX1 / CYTB (1Ne)	Central African Goril...	PR00573	Archived	603 bp
R3_I13	AY544159.1	*Gorilla gorilla*	Mitochondrial COX1 / CYTB (1Ne)	Central African Goril...	PR00107	Archived	603 bp
R4_I01	PP028193.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh23_BR	Archived	886 bp
R4_I02	PQ815885.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh862_WB-S	Archived	889 bp
R4_I04	PP028194.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh26_BR	Archived	886 bp
R4_I05	PQ815886.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh863_WB-S	Archived	889 bp
R4_I07	PP028195.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh30_BR	Archived	886 bp
R4_I08	PQ815887.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh864_WB-S	Archived	889 bp
R4_I10	PP028196.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh36_BR	Archived	886 bp

R4_I11	PQ815888.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh866_WB-S	Archived	889 bp
R4_I13	PP028197.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh38_TL	Archived	886 bp
R4_I14	PQ815889.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh867_WB-S	Archived	889 bp
R4_I16	PP028198.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh39_TL	Archived	886 bp
R4_I17	PQ815890.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh876_D	Archived	889 bp
R4_I19	PP028199.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh41_TL	Archived	886 bp
R4_I20	PQ815891.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh877_D	Archived	889 bp
R4_I22	PP028200.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh42_TL	Archived	886 bp
R4_I23	PQ815892.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh878_D	Archived	889 bp
R4_I25	PP028201.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh43_TL	Archived	886 bp
R4_I26	PQ815893.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh879_D	Archived	889 bp
R4_I28	PP028202.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh44_TL	Archived	886 bp
R4_I29	PQ815894.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh880_D	Archived	889 bp
R4_I31	PP028203.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh46_TL	Archived	886 bp
R4_I32	PQ815895.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh881_D	Archived	889 bp
R4_I34	PP028204.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh47_TL	Archived	886 bp
R4_I35	PQ815896.1	*Macaca mulatta*	Mitochondrial CYTB (1Ne Maternal)	South & East Asian Rh...	ZSI/SRC Rh882_D	Archived	889 bp
R5_I01	EU885420.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	GenBank / RefSeq deposit	Archived	1141 bp
R5_I02	KM267338.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	0077PAHay	Archived	1140 bp
R5_I03	KU871123.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	Tanzania	0295PANgo	Archived	1140 bp
R5_I06	EU885421.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	GenBank / RefSeq deposit	Archived	1141 bp
R5_I07	KM267340.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	0194PAHad	Archived	1140 bp
R5_I08	KU871124.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	0341PAWen	Archived	1140 bp
R5_I10	EU885422.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	GenBank / RefSeq deposit	Archived	1141 bp
R5_I11	KM267341.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	0200PAHay	Archived	1140 bp
R5_I12	KU871125.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	0343PAWen	Archived	1140 bp
R5_I13	EU885423.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	GenBank / RefSeq deposit	Archived	1141 bp
R5_I14	KM267358.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	0332PAAda	Archived	1140 bp
R5_I15	KU871126.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	Tanzania	0351PANi2	Archived	1140 bp
R5_I16	EU885424.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	GenBank / RefSeq deposit	Archived	1141 bp
R5_I17	KM267359.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	0334PAAda	Archived	1140 bp
R5_I18	KU871127.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	Uganda	0444PAKb1	Archived	1140 bp
R5_I19	EU885425.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	GenBank / RefSeq deposit	Archived	1141 bp
R5_I20	KM267360.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	0335PAAda	Archived	1140 bp
R5_I21	KU871128.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	0509PACFr	Archived	1140 bp
R5_I22	EU885426.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	GenBank / RefSeq deposit	Archived	1141 bp

R5_I23	KM267361.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	0336PAAda	Archived	1140 bp
R5_I24	KU871129.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	0513PAsBu	Archived	1140 bp
R5_I25	EU885427.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	GenBank / RefSeq deposit	Archived	1141 bp
R5_I26	KM267362.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	0338PHAla	Archived	1140 bp
R5_I27	KU871130.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	0516PAsBu	Archived	1140 bp
R5_I28	EU885450.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	GenBank / RefSeq deposit	Archived	1141 bp
R5_I29	KM267363.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	0340PAWen	Archived	1140 bp
R5_I30	KU871131.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	Kenya	0531PACho	Archived	1140 bp
R5_I31	EU885451.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	GenBank / RefSeq deposit	Archived	1141 bp
R5_I32	KM267407.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	0101PAKoS	Archived	1140 bp
R5_I33	KU871133.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	0940PAKam	Archived	1140 bp
R5_I34	EU885452.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	GenBank / RefSeq deposit	Archived	1141 bp
R5_I35	KU871134.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	0941PAKay	Archived	1140 bp
R5_I36	EU885453.1	*Papio anubis*	Mitochondrial CYTB (1Ne Maternal)	East African Savanna ...	GenBank / RefSeq deposit	Archived	1141 bp
R6_I02	MW452896.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E10	Archived	1063 bp
R6_I03	OK423769.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E95_84UPA	Archived	1063 bp
R6_I06	MW452897.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E29	Archived	1063 bp
R6_I07	OK423770.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E60_156CMLCO	Archived	1063 bp
R6_I10	MW452898.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E40	Archived	1063 bp
R6_I13	MW452899.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E68	Archived	1063 bp
R6_I16	MW452900.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E1	Archived	1063 bp
R6_I19	MW452901.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E18	Archived	1063 bp
R6_I20	MW452902.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E49	Archived	1063 bp
R6_I21	MW452903.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E53	Archived	1063 bp
R6_I22	MW452904.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E105	Archived	1063 bp
R6_I23	MW452905.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E139	Archived	1063 bp
R6_I24	MW452906.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E142	Archived	1063 bp
R6_I25	MW452907.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E47	Archived	1063 bp
R6_I26	MW452908.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E48	Archived	1063 bp
R6_I27	MW452909.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E6	Archived	1063 bp

R6_I28	MW452910.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E12	Archived	1063 bp
R6_I29	MW452911.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E86	Archived	1063 bp
R6_I30	MW452912.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E106	Archived	1063 bp
R6_I31	MW452913.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E116	Archived	1063 bp
R6_I32	MW452914.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E119	Archived	1063 bp
R6_I33	MW452915.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E126	Archived	1063 bp
R6_I34	MW452916.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E128	Archived	1063 bp
R6_I35	MW452917.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E110	Archived	1063 bp
R6_I36	MW452918.1	*Alouatta palliata mexicana*	Mitochondrial CYTB (1Ne Maternal)	Mexico	E109	Archived	1063 bp
L1_I03	AY727862.1	*Homo sapiens*	Nuclear ABO CDS Alleles (4Ne Balancing)	Human ABO Glycosyltra...	9q34.1-q34.2	Archived	826 bp
L1_I04	DQ092379.1	*Homo sapiens*	Nuclear ABO CDS Alleles (4Ne Balancing)	Human ABO Glycosyltra...	9q34.1-q34.2	Archived	798 bp
L1_I07	KU961549.2	*Homo sapiens*	Nuclear ABO CDS Alleles (4Ne Balancing)	Human ABO Glycosyltra...	GenBank / RefSeq deposit	Archived	691 bp
L1_I09	KY094065.1	*Homo sapiens*	Nuclear ABO CDS Alleles (4Ne Balancing)	Human ABO Glycosyltra...	GenBank / RefSeq deposit	Archived	691 bp
L1_I11	MF280401.1	*Homo sapiens*	Nuclear ABO CDS Alleles (4Ne Balancing)	Human ABO Glycosyltra...	GenBank / RefSeq deposit	Archived	691 bp
L1_I15	MN401412.1	*Homo sapiens*	Nuclear ABO CDS Alleles (4Ne Balancing)	Human ABO Glycosyltra...	GenBank / RefSeq deposit	Archived	892 bp
L1_I17	MW821349.1	*Homo sapiens*	Nuclear ABO CDS Alleles (4Ne Balancing)	China	female	Archived	1062 bp
L1_I21	ON720797.1	*Homo sapiens*	Nuclear ABO CDS Alleles (4Ne Balancing)	Human ABO Glycosyltra...	GenBank / RefSeq deposit	Archived	1065 bp
L1_I30	QB261409.1	*Homo sapiens*	Nuclear ABO CDS Alleles (4Ne Balancing)	China	GenBank / RefSeq deposit	2026	1065 bp
L1_I33	AY510089.1	*Homo sapiens*	Nuclear ABO CDS Alleles (4Ne Balancing)	Human ABO Glycosyltra...	9q34.1-q34.2	Archived	798 bp
L1_I34	DQ092380.1	*Homo sapiens*	Nuclear ABO CDS Alleles (4Ne Balancing)	Human ABO Glycosyltra...	9q34.1-q34.2	Archived	798 bp
L2_I01	XR_007085225.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1896 bp
L2_I02	XR_007086113.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1872 bp
L2_I03	XR_007084224.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I04	XR_007084225.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I05	XR_007084226.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I06	XR_007084227.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I07	XR_007084228.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I08	XR_007084229.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I09	XR_007084230.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I10	XR_007084232.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp

L2_I11	XR_007084233.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I12	XR_007084234.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I13	XR_007084235.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I14	XR_007084238.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I15	XR_007084239.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I16	XR_007084240.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I17	XR_007084241.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I18	XR_007084242.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I19	XR_007084243.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I20	XR_007084244.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I21	XR_007084245.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I22	XR_007084246.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I23	XR_007084247.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I24	XR_007084249.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I25	XR_007084250.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I26	XR_007084251.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L2_I27	XR_007084252.1	*Homo sapiens*	18S rDNA SSU (4Ne Slow-Clock Control)	Conserved Primate 18S...	CHM13	Archived	1869 bp
L3_I02	AY751739.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	Human FUT2 Secretor L...	19q13.3	Archived	1038 bp
L3_I04	DQ321371.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	Human FUT2 Secretor L...	9q13.3	Archived	1032 bp
L3_I05	FM180558.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	Austria:Styria	WBC	Archived	1266 bp
L3_I06	KF906451.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	Human FUT2 Secretor L...	FUT2-N1	Archived	999 bp
L3_I08	MN866041.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	Human FUT2 Secretor L...	ZL021	Archived	999 bp
L3_I09	MW036699.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	South Africa	1-1961_Sese	Archived	1032 bp
L3_I10	OM135398.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	Human FUT2 Secretor L...	GenBank / RefSeq deposit	Archived	1146 bp
L3_I11	OR995728.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	Human FUT2 Secretor L...	23WB03114	Archived	1032 bp
L3_I13	PX907523.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	Human FUT2 Secretor L...	GenBank / RefSeq deposit	Archived	1002 bp
L3_I14	PZ258778.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	Brazil	CD01	2025	999 bp
L3_I15	U17894.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	Human FUT2 Secretor L...	19q13.3	Archived	2115 bp
L3_I16	AY402924.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	Human FUT2 Secretor L...	GenBank / RefSeq deposit	Archived	1032 bp
L3_I19	KF906452.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	Human FUT2 Secretor L...	FUT2-N2	Archived	999 bp
L3_I20	MN866042.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	Human FUT2 Secretor L...	ZL031	Archived	999 bp

L3_I21	MW036706.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	South Africa	1-290_Sese	Archived	1032 bp
L3_I22	OM135401.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	Human FUT2 Secretor L...	GenBank / RefSeq deposit	Archived	1146 bp
L3_I23	OR947464.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	China	whole blood	Archived	999 bp
L3_I27	MN866043.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	Human FUT2 Secretor L...	ZL053	Archived	999 bp
L3_I29	OM135402.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	Human FUT2 Secretor L...	GenBank / RefSeq deposit	Archived	1146 bp
L3_I33	MN866044.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	Human FUT2 Secretor L...	ZL058	Archived	999 bp
L3_I35	OM135403.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	Human FUT2 Secretor L...	GenBank / RefSeq deposit	Archived	1146 bp
L3_I36	PZ258781.1	*Homo sapiens*	Nuclear FUT2 Secretor CDS (4Ne)	Brazil	CD05	2025	999 bp
L4_I09	LC093176.1	*Macaca fascicularis*	Mitochondrial CYTB (1Ne Maternal)	Southeast Asian Cynom...	WKC362	Archived	674 bp
L4_I11	LC093177.1	*Macaca fascicularis*	Mitochondrial CYTB (1Ne Maternal)	Southeast Asian Cynom...	WKC361	Archived	674 bp
L4_I13	LC093178.1	*Macaca fascicularis*	Mitochondrial CYTB (1Ne Maternal)	Southeast Asian Cynom...	WKC360	Archived	674 bp
L4_I15	LC093179.1	*Macaca fascicularis*	Mitochondrial CYTB (1Ne Maternal)	Southeast Asian Cynom...	SRY1934	Archived	674 bp
L4_I17	LC093180.1	*Macaca fascicularis*	Mitochondrial CYTB (1Ne Maternal)	Southeast Asian Cynom...	SRY1933	Archived	674 bp
L4_I19	LC093181.1	*Macaca fascicularis*	Mitochondrial CYTB (1Ne Maternal)	Southeast Asian Cynom...	SRY1932	Archived	674 bp
L4_I21	LC093182.1	*Macaca fascicularis*	Mitochondrial CYTB (1Ne Maternal)	Southeast Asian Cynom...	SRY1931	Archived	674 bp
L4_I23	LC093183.1	*Macaca fascicularis*	Mitochondrial CYTB (1Ne Maternal)	Southeast Asian Cynom...	SRY1930	Archived	674 bp
L4_I25	LC093184.1	*Macaca fascicularis*	Mitochondrial CYTB (1Ne Maternal)	Southeast Asian Cynom...	SRI1929	Archived	674 bp
L4_I27	LC093185.1	*Macaca fascicularis*	Mitochondrial CYTB (1Ne Maternal)	Southeast Asian Cynom...	SRI1928	Archived	674 bp
L4_I29	LC093186.1	*Macaca fascicularis*	Mitochondrial CYTB (1Ne Maternal)	Southeast Asian Cynom...	SRI1927	Archived	674 bp
L4_I30	DQ373844.1	*Macaca fascicularis*	Mitochondrial CYTB (1Ne Maternal)	Southeast Asian Cynom...	VietC15593	Archived	838 bp
L4_I31	LC093187.1	*Macaca fascicularis*	Mitochondrial CYTB (1Ne Maternal)	Southeast Asian Cynom...	SRI1925	Archived	674 bp
L4_I33	LC093188.1	*Macaca fascicularis*	Mitochondrial CYTB (1Ne Maternal)	Southeast Asian Cynom...	KRI1950	Archived	674 bp
L4_I35	LC093189.1	*Macaca fascicularis*	Mitochondrial CYTB (1Ne Maternal)	Southeast Asian Cynom...	KRI1949	Archived	674 bp
L4_I36	DQ373847.1	*Macaca fascicularis*	Mitochondrial CYTB (1Ne Maternal)	Southeast Asian Cynom...	VietC15596	Archived	838 bp
L5_I01	JX983763.1	*Chlorocebus pygerythrus*	Mitochondrial CYTB (1Ne Maternal)	West/Central African ...	pygET546	Archived	1140 bp
L5_I02	JX983764.1	*Chlorocebus pygerythrus*	Mitochondrial CYTB (1Ne Maternal)	West/Central African ...	pygET496	Archived	1140 bp
L5_I03	JX983765.1	*Chlorocebus pygerythrus*	Mitochondrial CYTB (1Ne Maternal)	West/Central African ...	pygSO545	Archived	1140 bp
L5_I04	JX983766.1	*Chlorocebus pygerythrus*	Mitochondrial CYTB (1Ne Maternal)	West/Central African ...	pygET421	Archived	1140 bp
L5_I05	JX983767.1	*Chlorocebus pygerythrus*	Mitochondrial CYTB (1Ne Maternal)	Kenya	pygKY504	Archived	1140 bp
L5_I06	JX983768.1	*Chlorocebus pygerythrus*	Mitochondrial CYTB (1Ne Maternal)	Kenya	pygKY540	Archived	1140 bp
L5_I07	JX983769.1	*Chlorocebus pygerythrus*	Mitochondrial CYTB (1Ne Maternal)	South Africa	pygSA64	Archived	1140 bp

L5_I08	JX983770.1	*Chlorocebus pygerythrus*	Mitochondrial CYTB (1Ne Maternal)	South Africa	pygSA65	Archived	1140 bp
L5_I09	JX983771.1	*Chlorocebus pygerythrus*	Mitochondrial CYTB (1Ne Maternal)	South Africa	pygSA75	Archived	1140 bp
L5_I10	JX983772.1	*Chlorocebus pygerythrus*	Mitochondrial CYTB (1Ne Maternal)	South Africa	pygSA78	Archived	1140 bp
L5_I11	JX983773.1	*Chlorocebus pygerythrus*	Mitochondrial CYTB (1Ne Maternal)	Tanzania	pygTZ503	Archived	1140 bp
L5_I12	JX983774.1	*Chlorocebus pygerythrus*	Mitochondrial CYTB (1Ne Maternal)	Tanzania	pygTZ522	Archived	1140 bp
L5_I13	JX983775.1	*Chlorocebus pygerythrus*	Mitochondrial CYTB (1Ne Maternal)	Tanzania	pygTZ524	Archived	1140 bp
L5_I14	JX983776.1	*Chlorocebus pygerythrus*	Mitochondrial CYTB (1Ne Maternal)	Tanzania	pygTZ549	Archived	1140 bp
L5_I15	JX983777.1	*Chlorocebus pygerythrus*	Mitochondrial CYTB (1Ne Maternal)	Tanzania	pygTZ563	Archived	1140 bp
L5_I16	JX983849.1	*Chlorocebus pygerythrus*	Mitochondrial CYTB (1Ne Maternal)	Uganda	pygUG560	Archived	1140 bp
L5_I17	JX983850.1	*Chlorocebus pygerythrus*	Mitochondrial CYTB (1Ne Maternal)	Kenya	pygKY513	Archived	1140 bp
L5_I18	JX983851.1	*Chlorocebus pygerythrus*	Mitochondrial CYTB (1Ne Maternal)	Kenya	pygKY507	Archived	1140 bp
L6_I01	AF285557.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Andranomena	RMR 44	Archived	1140 bp
L6_I02	AY167071.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Berenty	YLE357	Archived	1140 bp
L6_I03	GU327173.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Andranomena	RMR44	Archived	1140 bp
L6_I04	U53572.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Malagasy Strepsirrhin...	GenBank / RefSeq deposit	Archived	1140 bp
L6_I06	AF285558.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Andranomena	YLE74	Archived	1140 bp
L6_I07	AY441460.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Malagasy Strepsirrhin...	GenBank / RefSeq deposit	Archived	1140 bp
L6_I08	GU327174.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Andranomena	RMR47	Archived	1140 bp
L6_I09	AF285559.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Andranomena	RMR 45	Archived	1140 bp
L6_I10	GU327175.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Andranomena	RMR45	Archived	1140 bp
L6_I11	AF285560.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Manamby	RMR 25	Archived	1140 bp
L6_I12	GU327176.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Andranomena	RMR49	Archived	1140 bp
L6_I13	AF285561.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Kirindy	Jorg 37	Archived	1140 bp
L6_I14	GU327177.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Andranomena	RMR46	Archived	1140 bp
L6_I15	AF285562.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Kirindy	Jorg 33	Archived	1140 bp
L6_I16	GU327178.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Kirindy	Jorg64	Archived	1140 bp
L6_I17	AF285563.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Kirindy	Jorg 64	Archived	1140 bp
L6_I18	GU327179.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Kirindy	Jorg147	Archived	1140 bp
L6_I19	AF285564.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Vohimena	RMR 24	Archived	1140 bp
L6_I20	GU327180.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Kirindy	Jorg37	Archived	1140 bp

L6_I21	AF285565.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Mandena	00-016A-8EBC	Archived	1140 bp
L6_I22	GU327181.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Manamby	RMR25	Archived	1140 bp
L6_I23	AF285566.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Mandena	YLE199	Archived	1140 bp
L6_I24	GU327182.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Manamby	RMR26	Archived	1140 bp
L6_I25	GU327183.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Manamby	RMR29	Archived	1140 bp
L6_I26	GU327184.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Manamby	RMR27	Archived	1140 bp
L6_I27	GU327185.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Mandena	00-016A-9347	Archived	1140 bp
L6_I28	GU327186.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Mandena	00-016A-8577	Archived	1140 bp
L6_I29	GU327187.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Mandena	00-016B-A8F9	Archived	1140 bp
L6_I30	GU327188.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Mandena	00-016A-8982	Archived	1140 bp
L6_I31	GU327189.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Mandena	00-016A-875E	Archived	1140 bp
L6_I32	GU327190.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Mandena	00-016A-8A1D	Archived	1140 bp
L6_I33	GU327191.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Mandena	00-016B-A6DE	Archived	1140 bp
L6_I34	GU327192.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Mandena	00-016A-96FO	Archived	1140 bp
L6_I35	GU327193.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Mandena	00-016A-8EBC	Archived	1140 bp
L6_I36	GU327194.1	*Microcebus murinus*	Mitochondrial CYTB (1Ne Madagascar Refugia)	Madagascar: Mandena	00-016A-8DB7	Archived	1140 bp