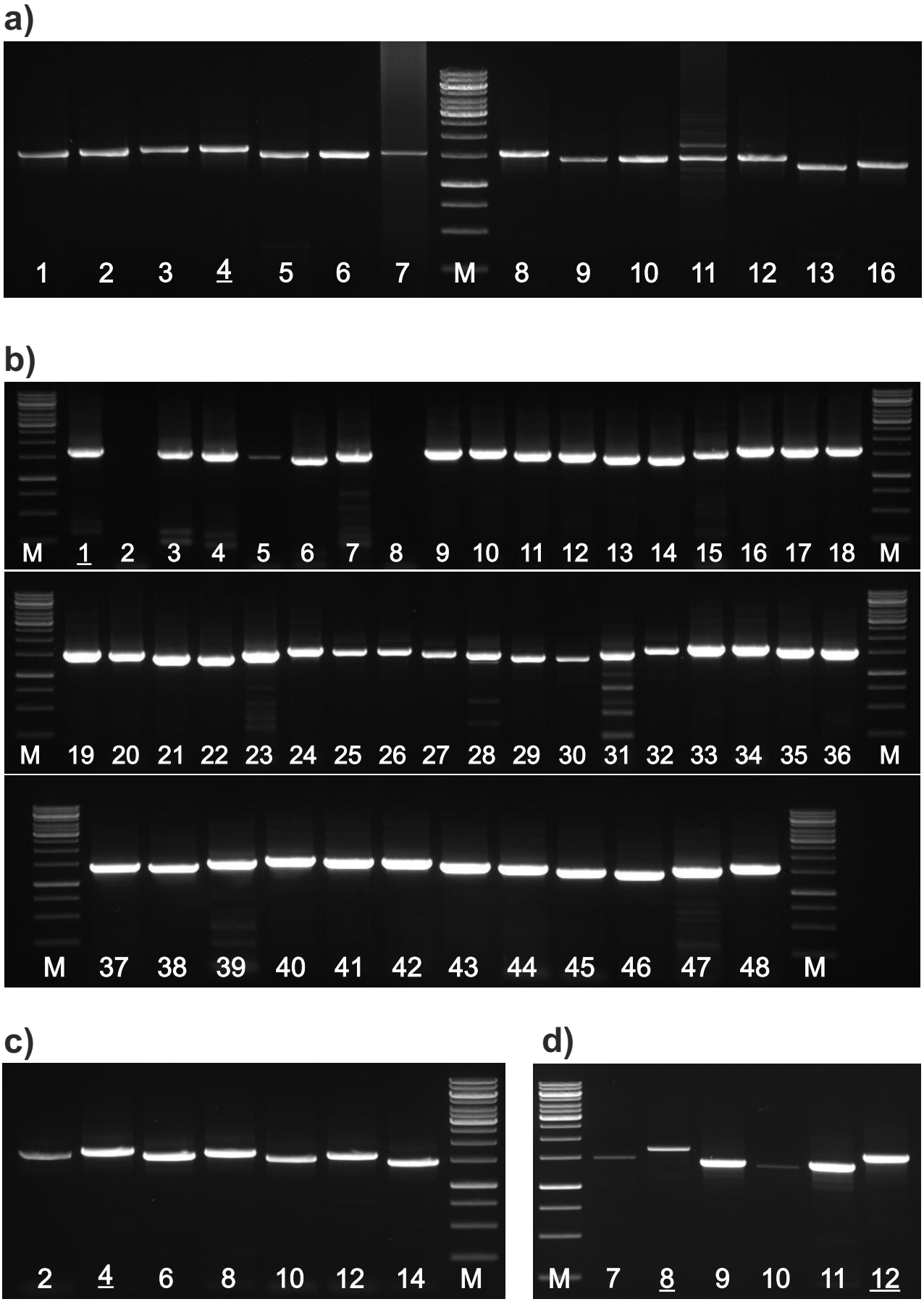


Figure S1. Representative cropped agarose gels of CR1/CR2 amplicons obtained for *Struthio camelus* (a), *Rhea pennata* (b), *Rhea americana* (c) and *Crypturellus tataupa* (d). The numbering of amplicons separated in the agarose gel corresponds to the reaction numbered in Table S1. The numbers of PCR fragments, which were finally sequenced, are underlined. Lane M - GeneRuler 1 kb DNA Ladder (Thermo Scientific). Original uncropped and unprocessed gels are presented in Fig. S13a-d.

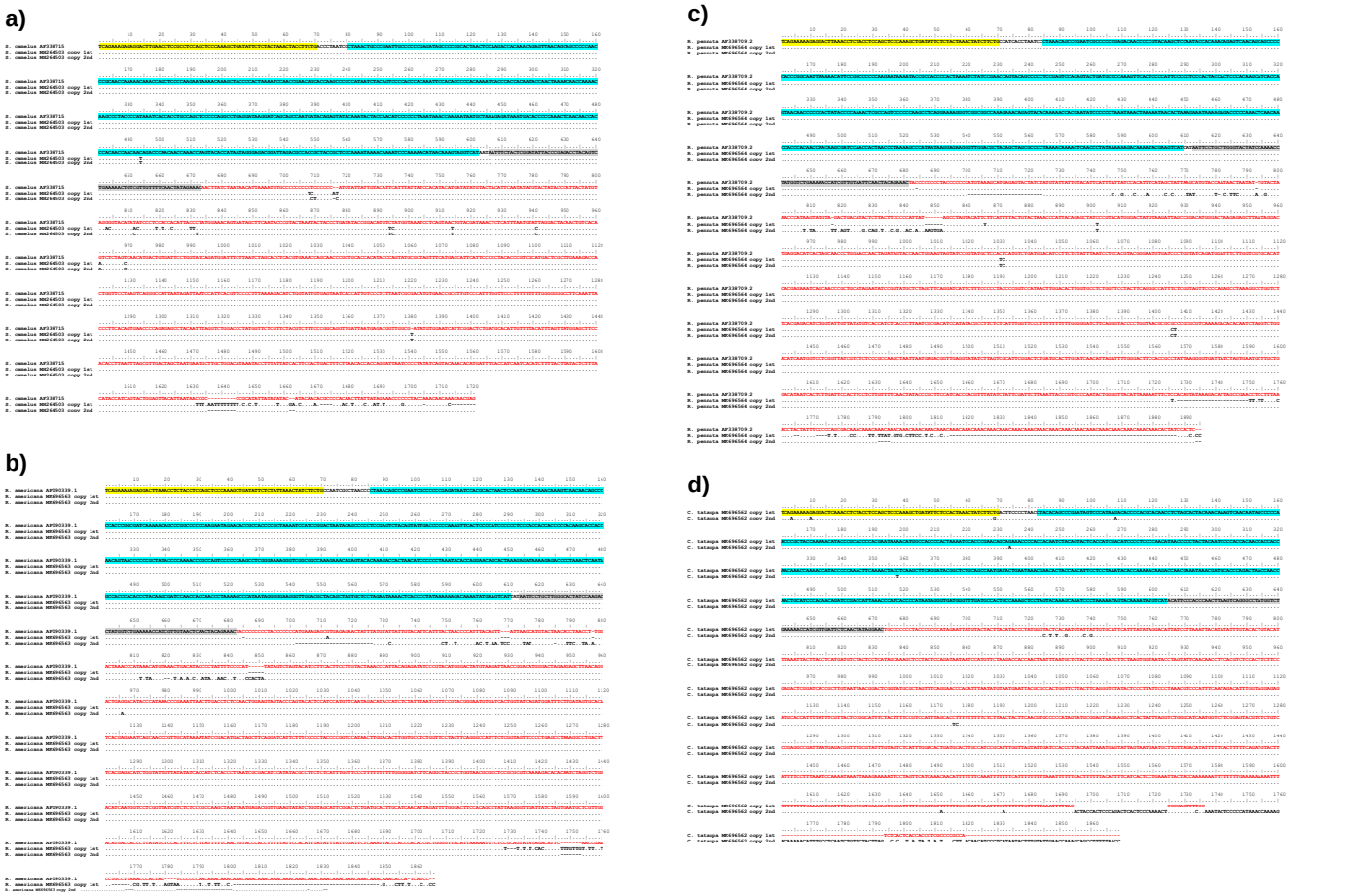
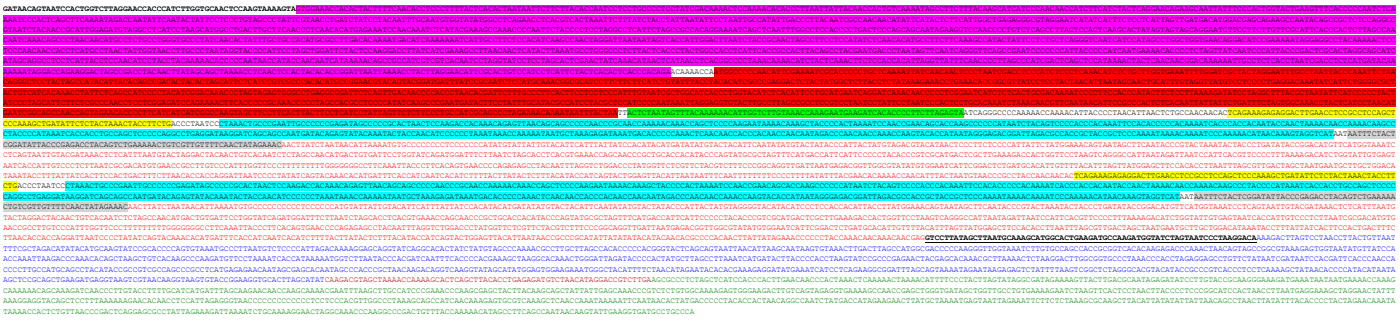


Figure S2. Sequence comparison of two copies of *tRNA-Pro*, *ND6*, *tRNA-Glu* genes and control region, found in this study as duplicated, with appropriate sequences of mitogenomes previously deposited in GenBank and showing a typical avian gene order. The alignments are shown for *Struthio camelus* (a), *Rhea americana* (b), *Rhea pennata* (c) and *Crypturellus tataupa* (d). Dots indicate residues identical in the obtained copies with those in the single sequence previously published. Genes for tRNA-Pro are marked in yellow coloring, NADH dehydrogenase subunit 6 in cyan coloring, tRNA-Glu in grey shading, and control regions in red fonts. In the case of *Crypturellus tataupa* only two obtained copies are compared to each other because the previously published mitogenome of these taxa is incomplete and it does not contain any of the analyzed genes or the control region. The sequences were aligned with MUSCLE [125] in MEGA [124].

***Struthio camelus*: tRNA-Leu/16S rRNA (MH264503)**



***Rhea americana*: ND5/16S rRNA (MK696563)**

***Rhea pennata*: ND5/16S rRNA (MK696564)**

***Crypturellus tataupa*: ND5/12S rRNA (MK696562)**

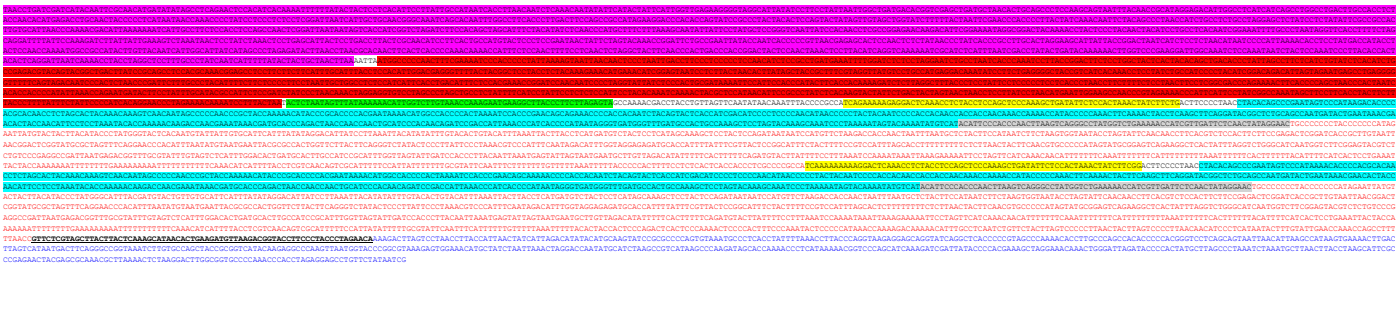


Figure S3. Sequences of mitogenomic fragments amplified and sequenced in this study for *Struthio camelus* (MH264503), *Rhea americana* (MK696563), *Rhea pennata* (MK696564) and *Crypturellus tataupa* (MK696562). **Genes for tRNA-Leu are marked in bold**, NADH dehydrogenase subunit 5 in magenta coloring, cytochrome b in red coloring, tRNA-Thr in green coloring, tRNA-Pro in yellow coloring, NADH dehydrogenase subunit 6 in cyan coloring, tRNA-Glu in grey shading, 12S rRNA in blue fonts, tRNA-Val in brown fonts, 16S rRNA in green fonts, **tRNA-Phe are in bold and underlined**, and control regions in red fonts.

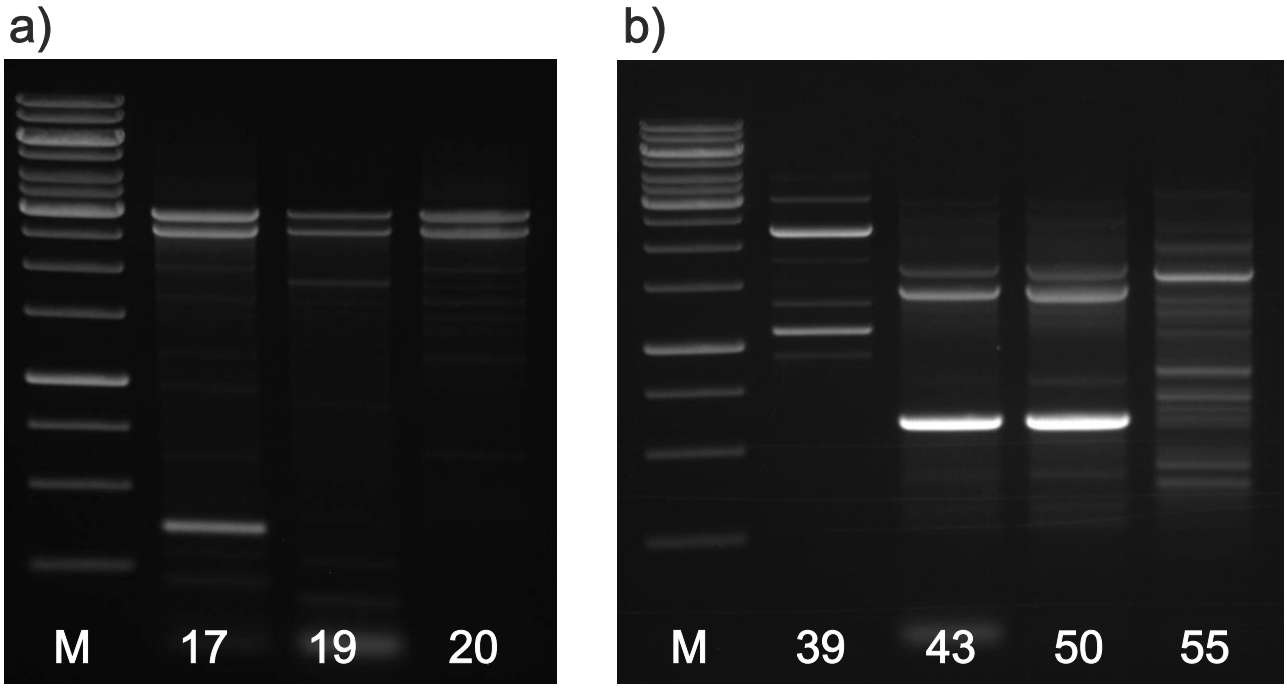


Figure S4. Cropped agarose gels of potential NUMTs amplified for *Dromaius novaehollandiae* (a) and *Casuarius casuarius* (b) with the use of primers designed for detection of CR1/CR2 fragments. The numbering of lanes corresponds to the reaction numbered in Table S1. Lane M - GeneRuler 1 kb DNA Ladder (Thermo Scientific). Original uncropped and unprocessed gels are presented in Fig. S13e and f.

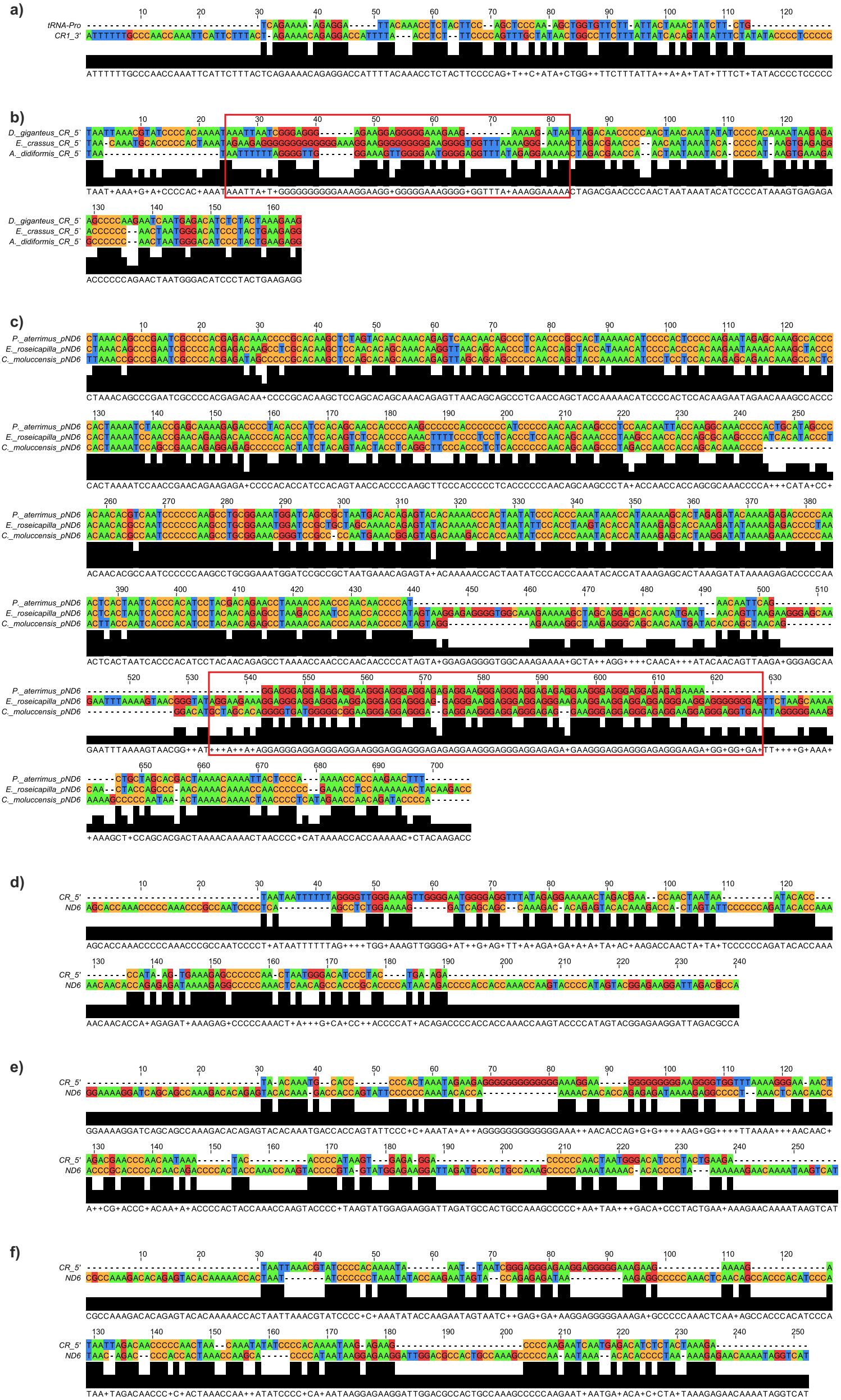


Figure S5. Comparison of selected sequence associated with reannotation of Palaeognathae mitogenomes. *Eudromia elegans* gene for tRNA-Pro with the last 200 nucleotides of the control region (a); *Emeus crassus*, *Dinornis giganteus* and *Anomalopteryx didiformis* control region 5' spacers (b); *Prosobsciger aterrinus* (MH133970.1), *Eolophus roseicapilla* (MH133971.1) and *Cacatua moluccensis* (MH133972.1) *ND6* pseudogenes (c); *Anomalopteryx didiformis ND6* gene with control region 5' spacer (d); *Emeus crassus ND6* gene with control region 5' spacer (e); *Dinornis giganteus ND6* gene with control region 5' spacer (f). Sequences rich in G and A residues are marked in a red box. The sequences in b and c were aligned with MUSCLE [125] in MEGA [124], whereas those in a, d, e and f using the optimal global:local algorithm (glsearch) form FASTA package version 36.3.8g[127].

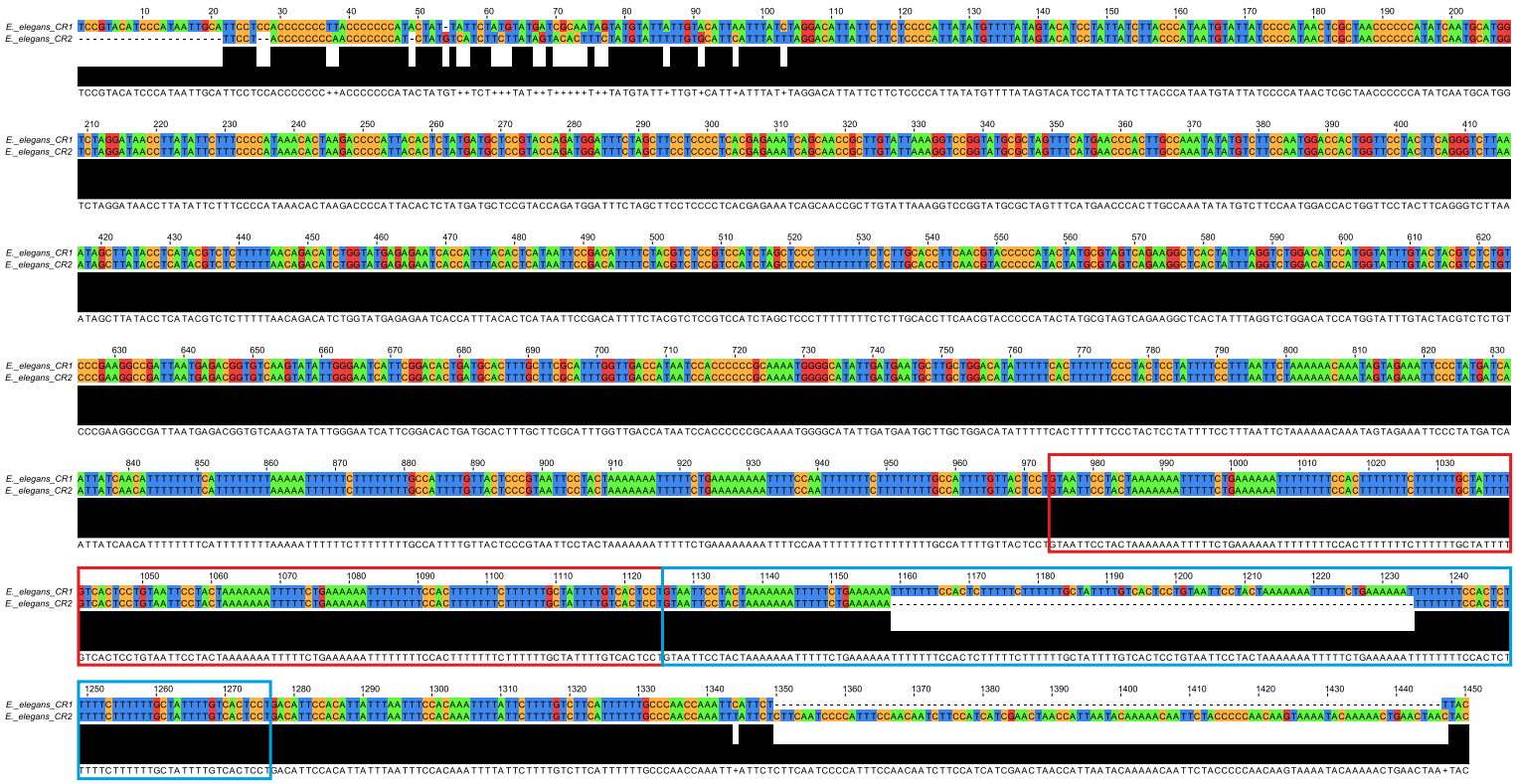


Figure S6. Sequence comparison of two *Eudromia elegans* control regions. Dots indicate residues identical in the compared copies. Dots indicate residues identical in the compared sequences. Sequence repeats present in both control regions are marked in red and blue boxes.The sequences were aligned with MUSCLE[125] in MEGA[124].

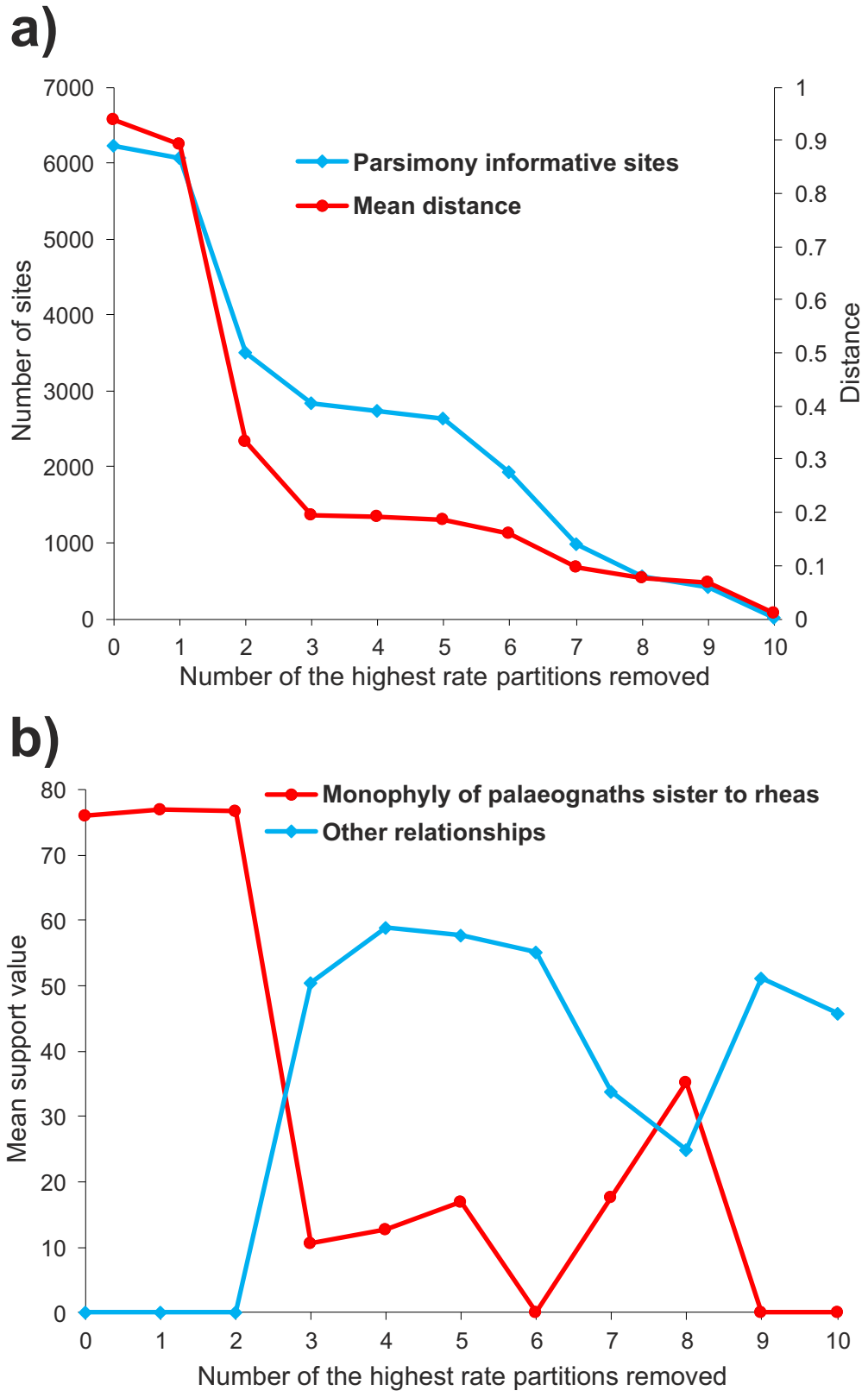


Figure S7. Influence of removing partitions with the highest substitution rate on alignment and tree parameters: the number of parsimony informative sites and mean distance (a) as well as mean support values (b). The mean phylogenetic distance was obtained from MrBayes tree. The mean support values were calculated from posterior probabilities received in MrBayes and PhyloBayes as well as SH-aLRT and non-parametric bootstrap percentages obtained in IQ-TREE. The posterior probabilities were scaled to 100%.

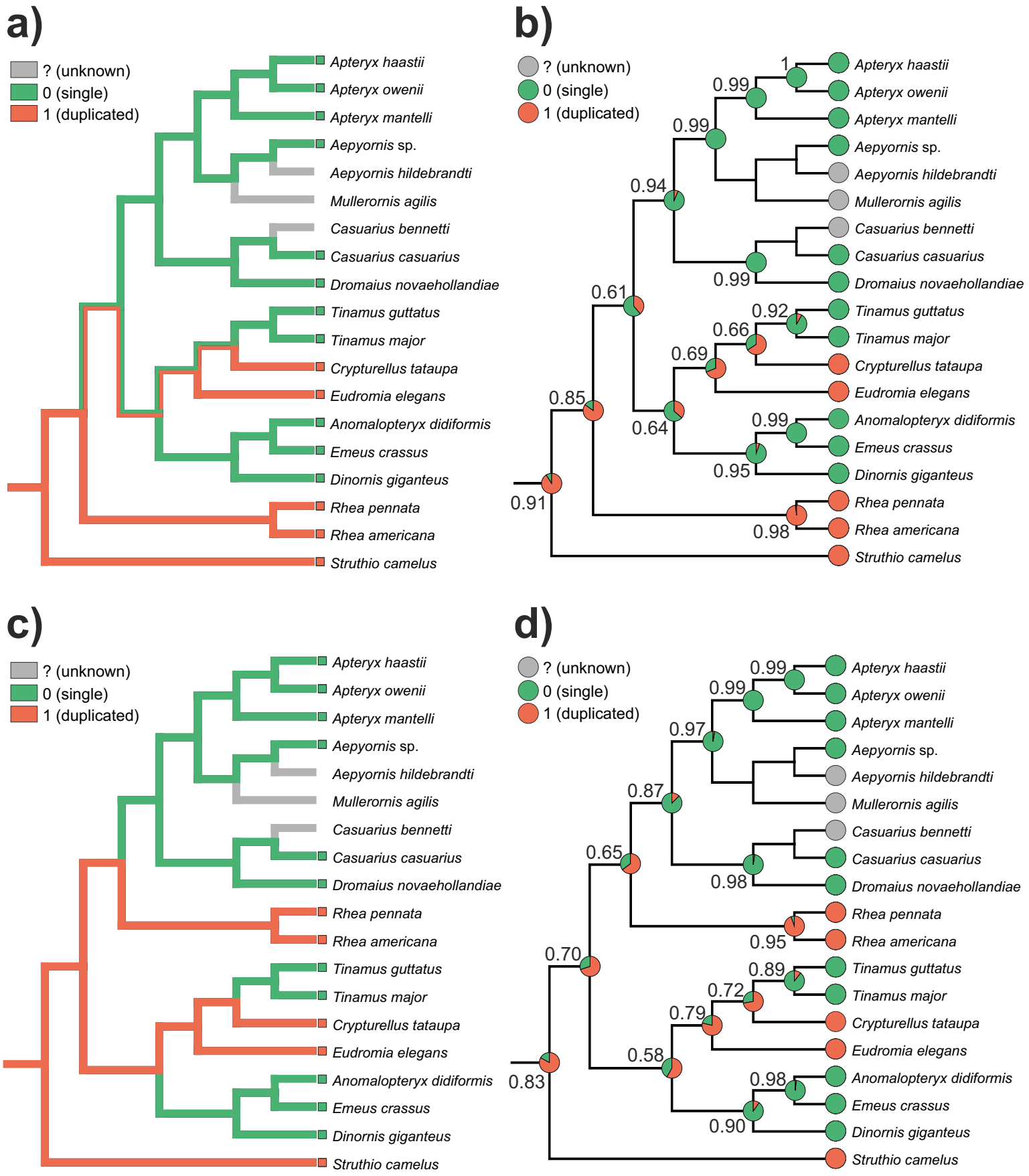
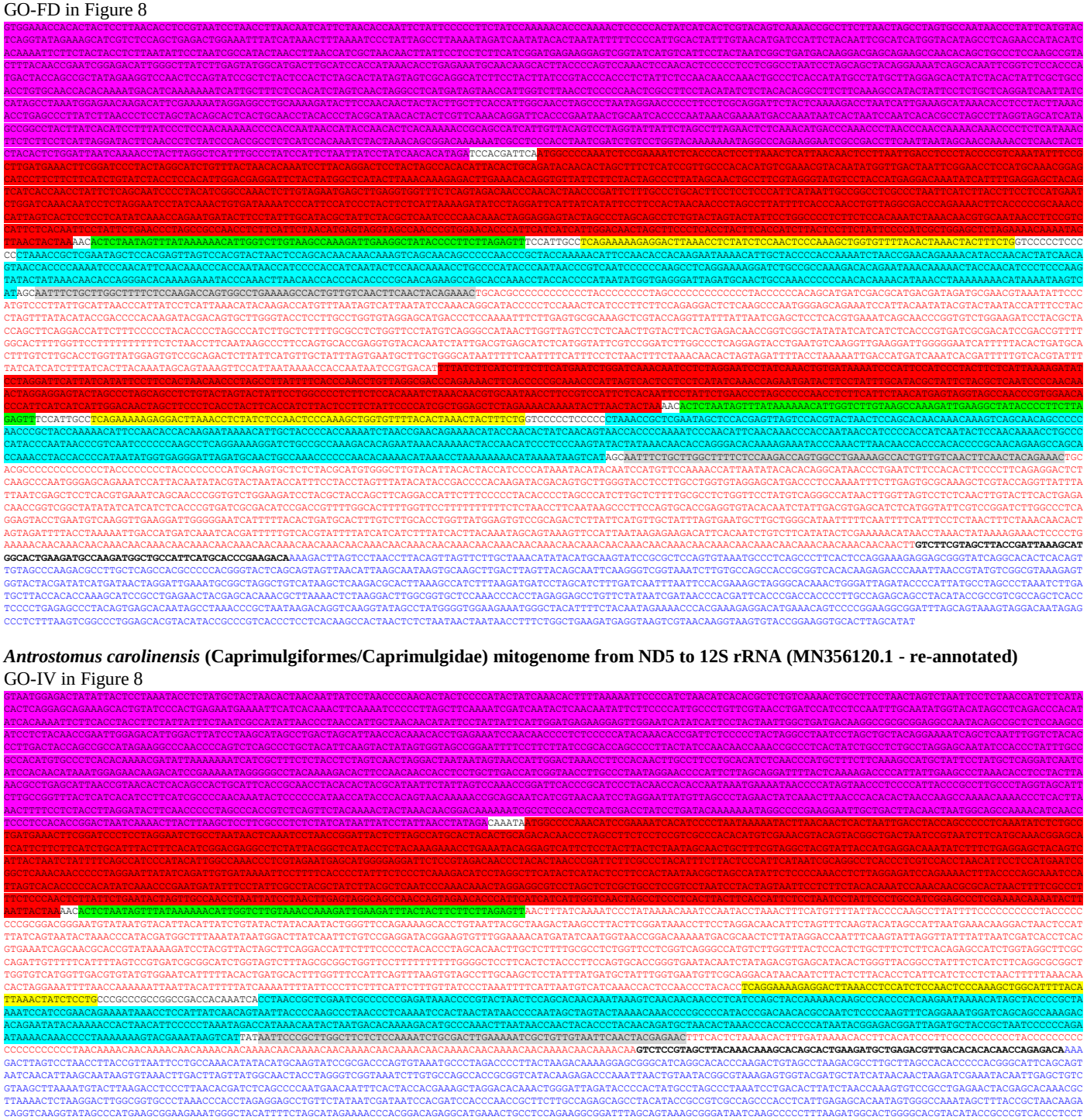


Figure S8. Maximum parsimony (a, c) and maximum likelihood (b, d) reconstruction of ancestral states and mapping of mitogenomic duplications onto the Palaeognathae tree topology t1 based on sequences of mitochondrial genes (a, b) and the Palaeognathae tree topology t2 supported by nuclear markers in coalescent-based approaches (c, d). In contrast to Fig. 6, this approach assumes that *Anomalopteryx didiformis*, *Emeus crassus* and *Dinornis giganteus* already lost mitogenomic duplication. The area of colors at nodes in b and d corresponds to the probability of the given state, single or duplicated region. Two-colored branches correspond to the equal probability of two states, single or duplicated region. The probability value for a more likely state was also given at these nodes. Mk1 model was applied for ML approach.

Figure S9. Annotated and reannotated duplicated gene orders in mitogenomes of Neoaves and Galloanserae deposited in GenBank for: *Alca torda* (CM018102.1), *Antrostomus carolinensis* (MN356120.1), *Calypte anna* (CM016612.1), *Cariama cristata* (CM020379.1), *Catharus ustulatus* (CM020378.1), *Colius striatus* (MN356125.1), *Ketupa blackistoni* (LC099104), *Ketupa flavipes* (LC099100.1), *Leptosomus discolour* (MN356135.1), *Merops nubicus* (CM020464.1), *Melanereps aurifrons* (CM022134.1), *Morus serrator* (GU071056.1), *Nyctibius grandis* (CM023771.1), *Pterocles burchelli* (MN356340.1), *Pterocles gutturalis* (CM020177.1, MN356147.1), *Puffinus lherminieri* (MH206162.1), *Rynchops niger* (MN356248.1), *Sterna hirundo* (CM020500.1), *Thalassarche chlororhynchos* (MN356342.1), *Uria aalge* (MN356418.1) and *Urocolius indicus* (MN356373.1). Genes for NADH dehydrogenase subunit 5 are marked in magenta coloring, cytochrome b in red coloring, tRNA-Thr in green coloring, tRNA-Pro in yellow coloring, NADH dehydrogenase subunit 6 in cyan coloring, tRNA-Glu in grey shading, 12S rRNA in blue fonts, **tRNA-Phe in bold fonts**, and control regions in red fonts. *Pseudogenes are in italics and underlined*. Microsatellites present within *Pterocles gutturalis* mitogenomes between *tRNA-Thr* gene and *tRNA-Pro* pseudogene or *tRNA-Thr* gene and *ND6* pseudogene are marked in brown.

***Alca torda* (Charadriiformes/Alcidae) mitogenome from ND5 to 12S rRNA (CM018102.1 - annotated)**

GO-FD in Figure 8

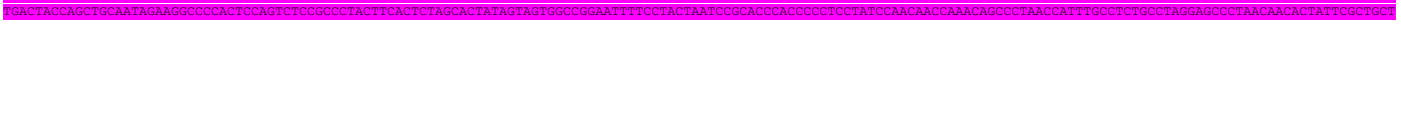


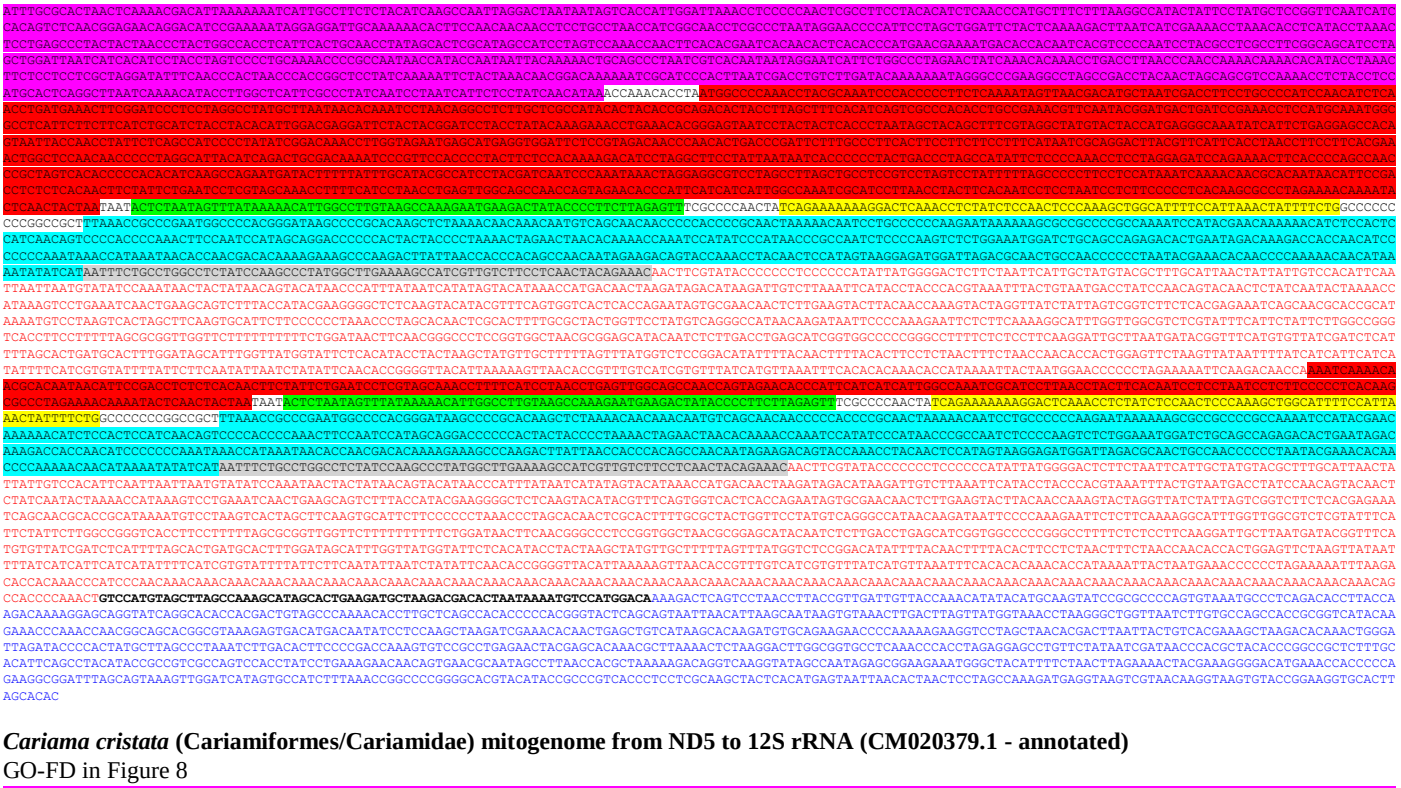
***Antrostomus carolinensis* (Caprimulgiformes/Caprimulgidae) mitogenome from ND5 to 12S rRNA (MN356120.1 - re-annotated)**

GO-IV in Figure 8

***Calypte anna* (Caprimulgiformes/Trochilidae) mitogenome from ND5 to 12S rRNA (CM016612.1 - annotated)**

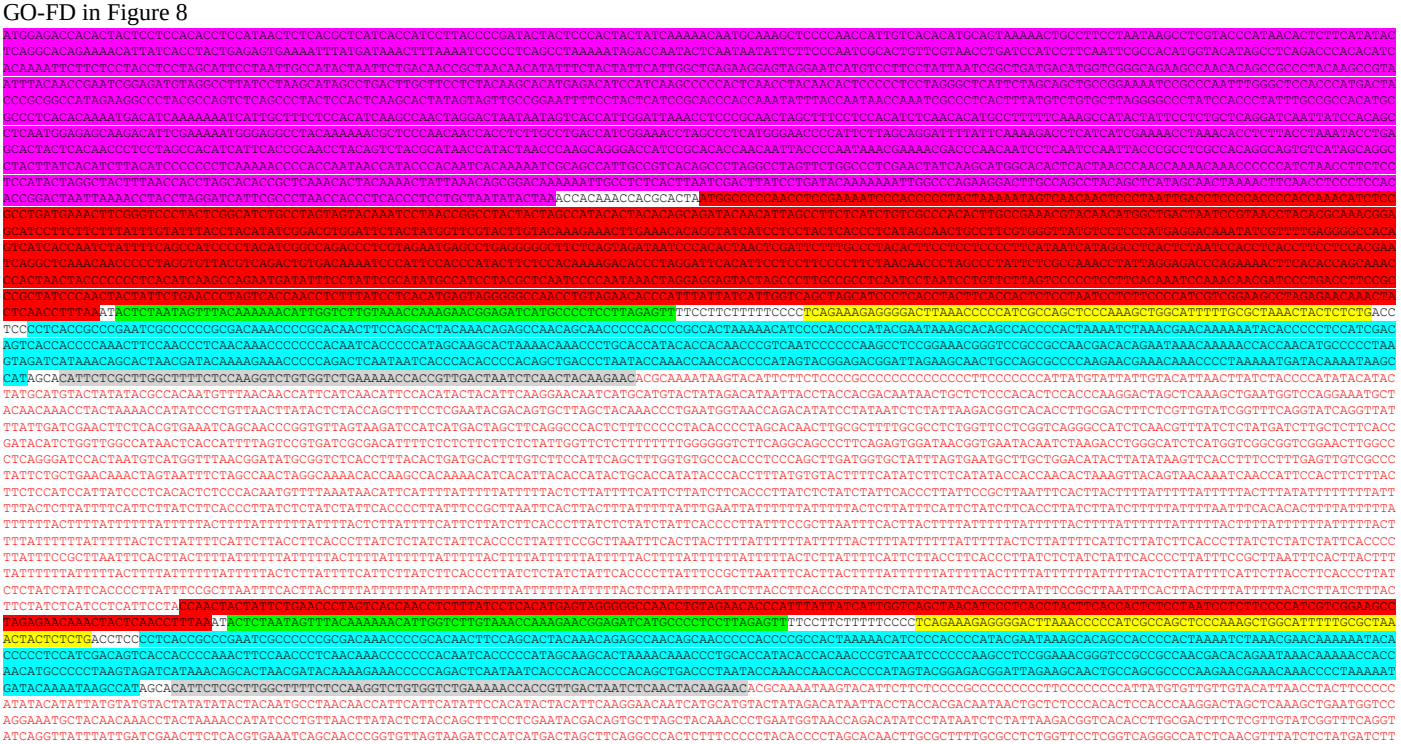
GO-FD in Figure 8





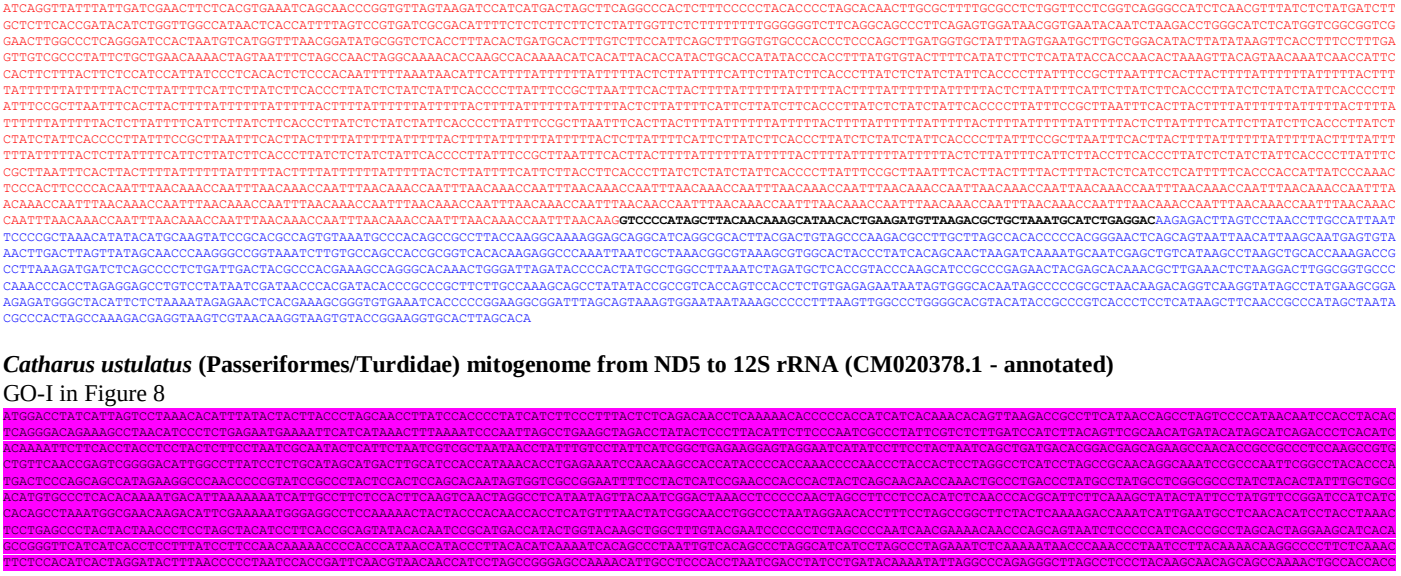
Cariama cristata (Cariamiformes/Cariamidae) mitogenome from ND5 to 12S rRNA (CM020379.1 - annotated)

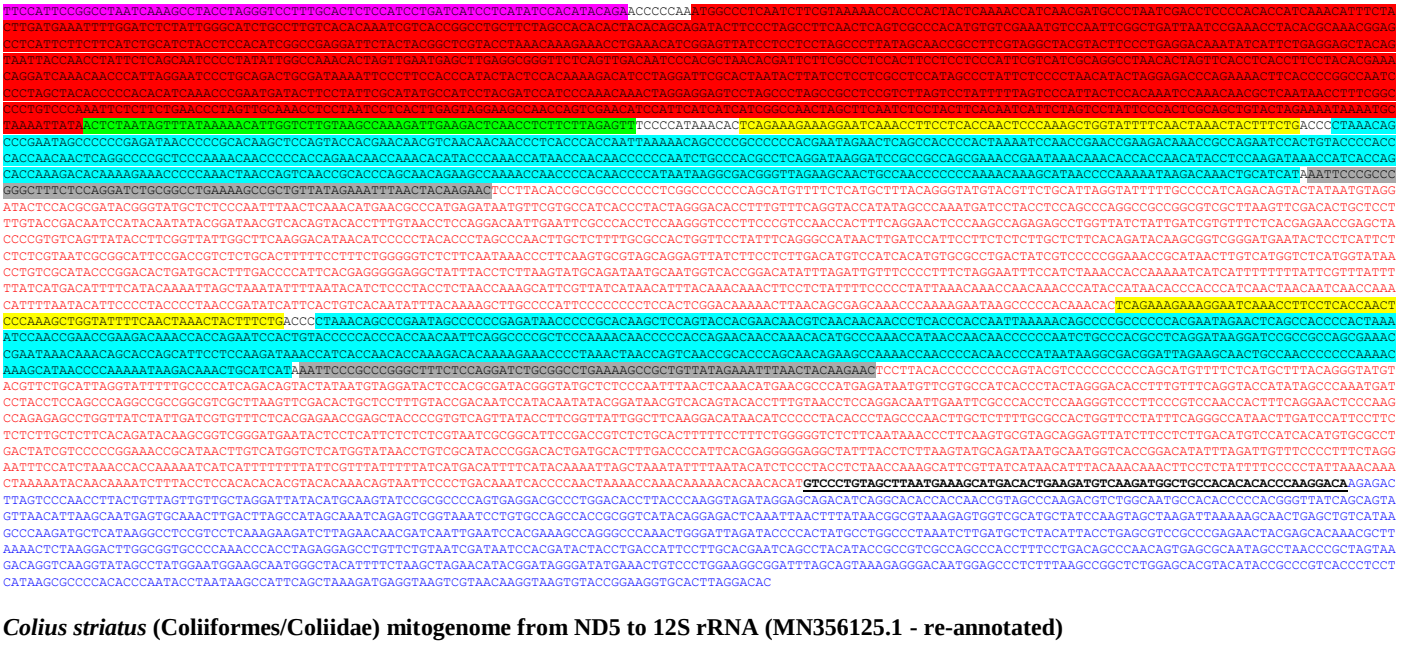
GO-FD in Figure 8



Catharus ustulatus (Passeriformes/Turdidae) mitogenome from ND5 to 12S rRNA (CM020378.1 - annotated)

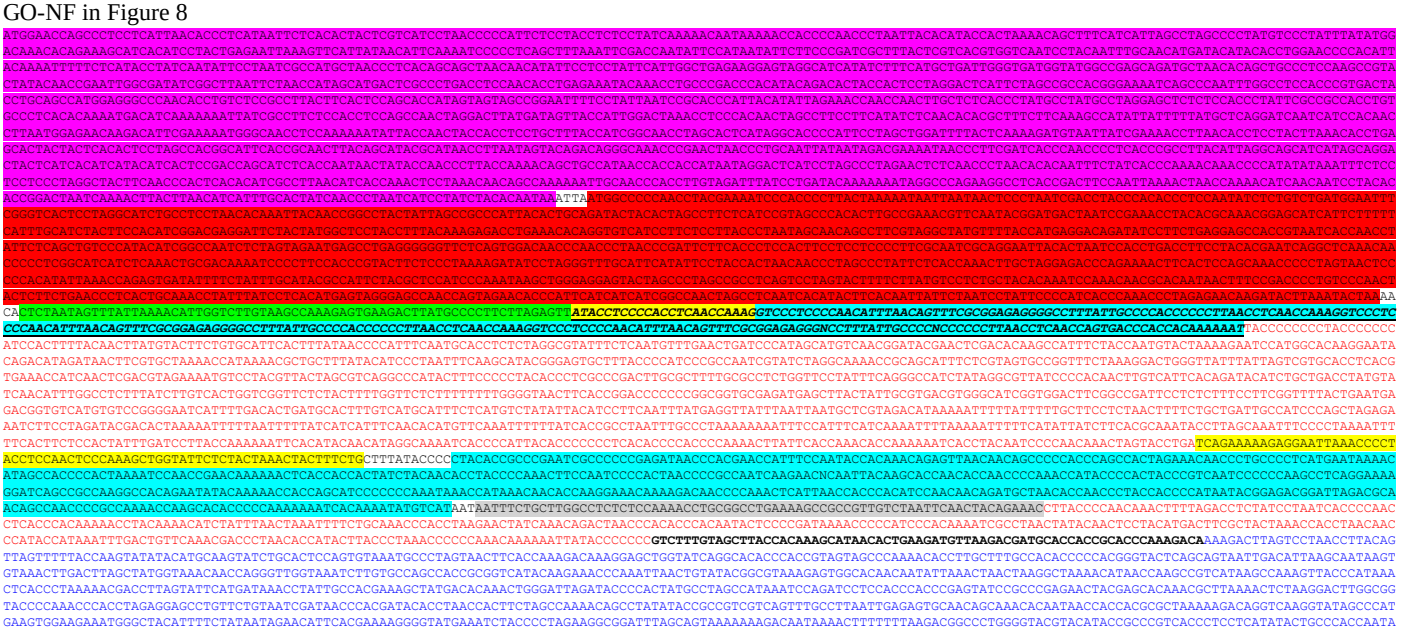
GO-I in Figure 8





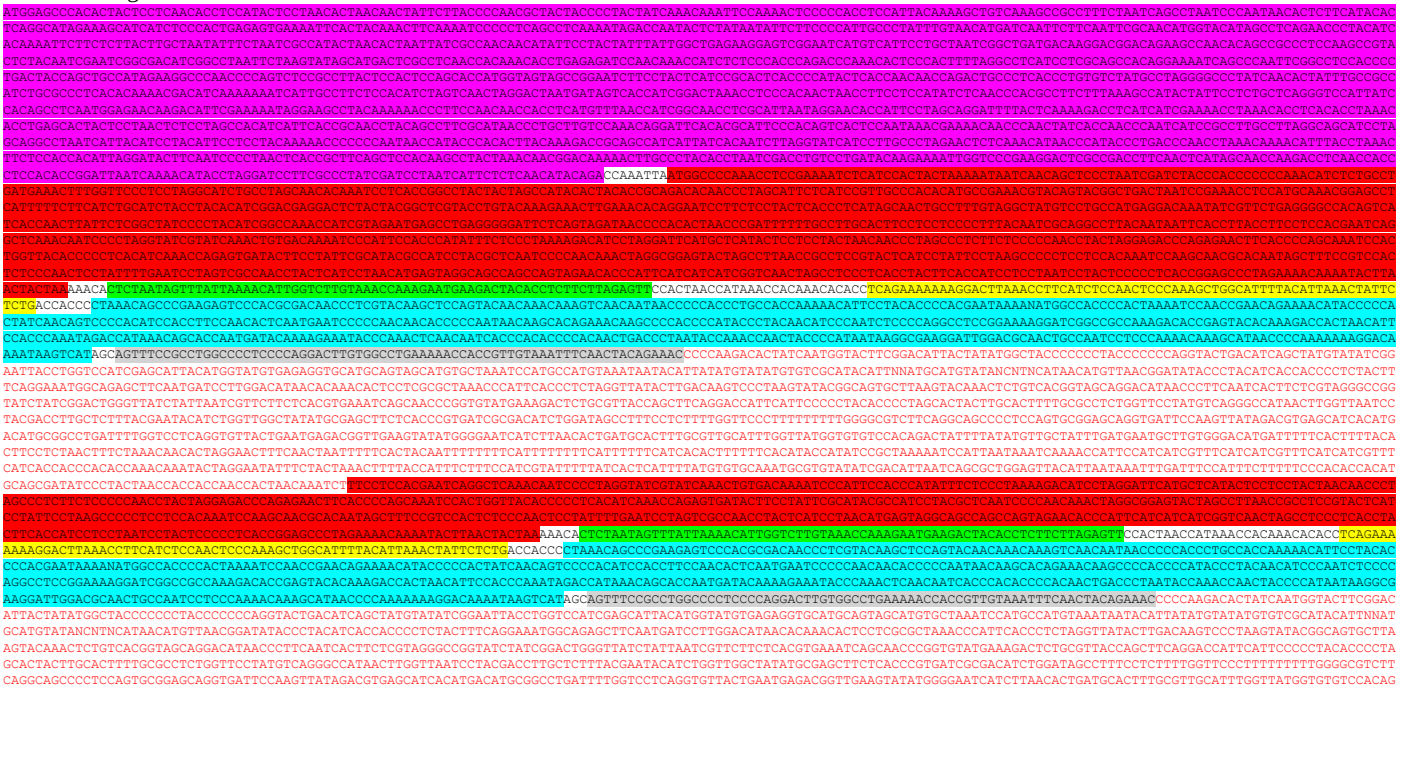
Colius striatus (Coliiformes/Coliidae) mitogenome from ND5 to 12S rRNA (MN356125.1 - re-annotated)

GO-NF in Figure 8



Fregetta grallaria (Procellariiformes/ Oceanitidae) mitogenome from ND5 to 12S rRNA (MN356296.1 - re-annotated)

GO-FD in Figure 8



[illegible]

Ketupa blackistoni (Strigiformes/Strigidae) mitogenome from ND5 to 12S rRNA (LC099104 - re-annotated)

GO-FD in Figure 8

[illegible]

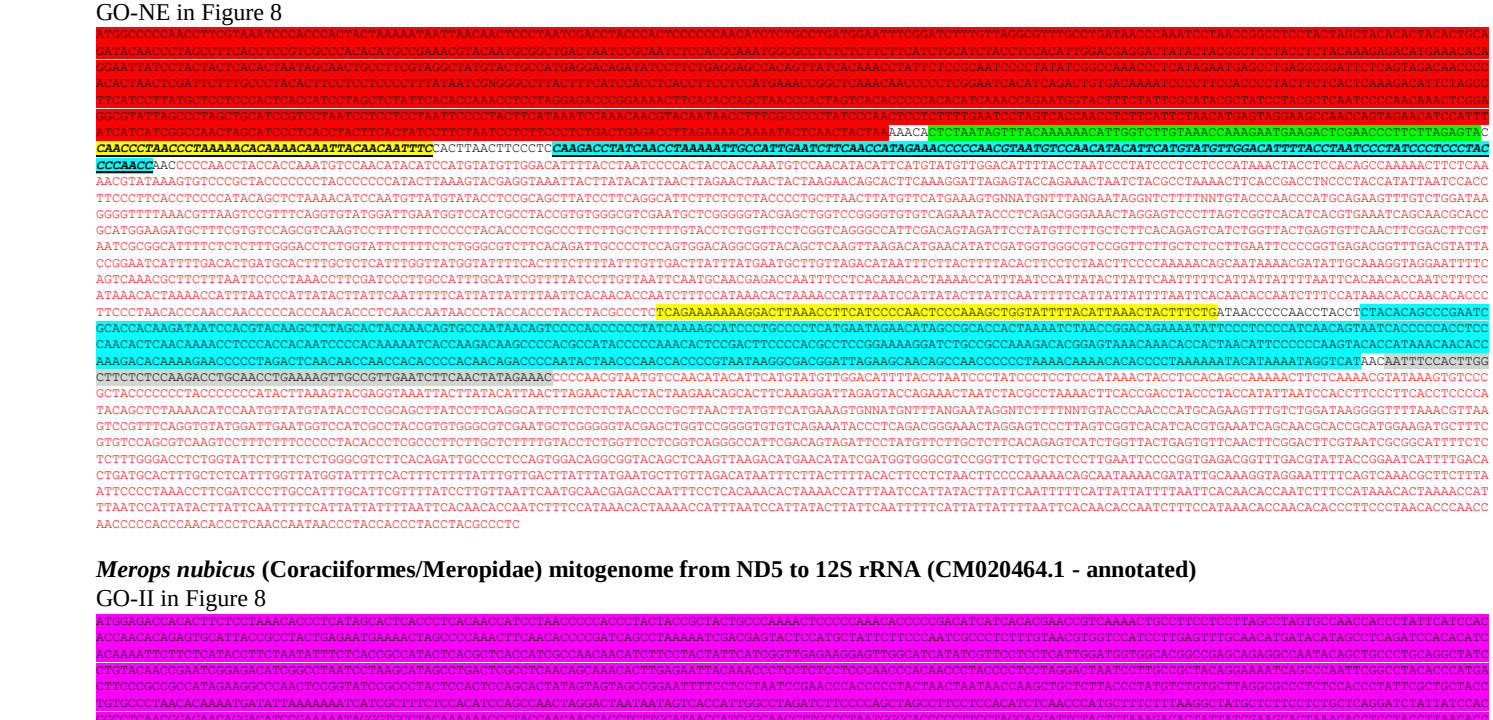
Ketupa flavipes (Strigiformes/Strigidae) mitogenome from ND5 to 12S rRNA (LC099100.1 - re-annotated)

GO-FD in Figure 8

[illegible]

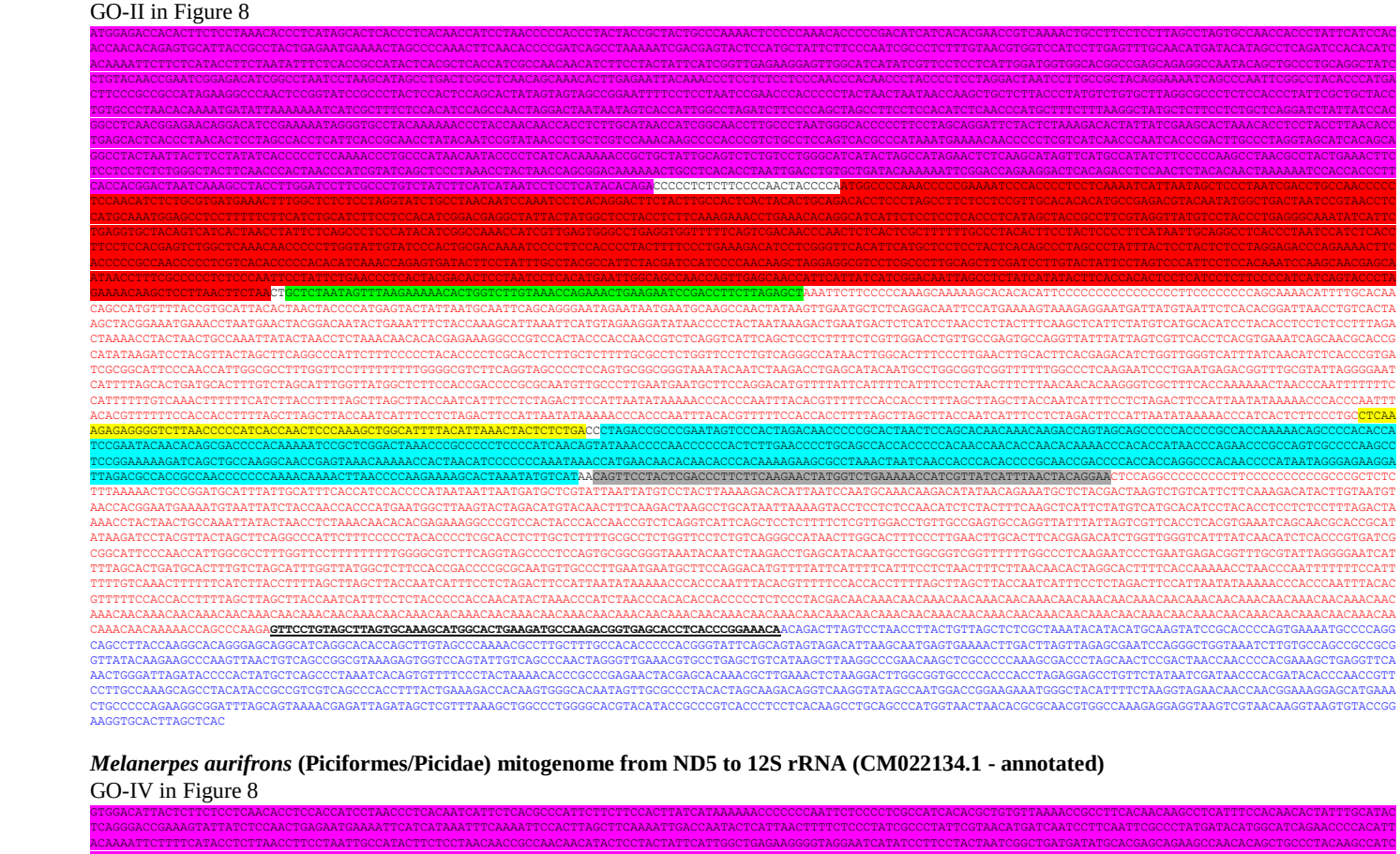
Leptosomus discolor **(Leptosomiformes/Leptosomidae) mitogenome from CYTB to CR2 (MN356135.1 - re-annotated)**

GO-NE in Figure 8



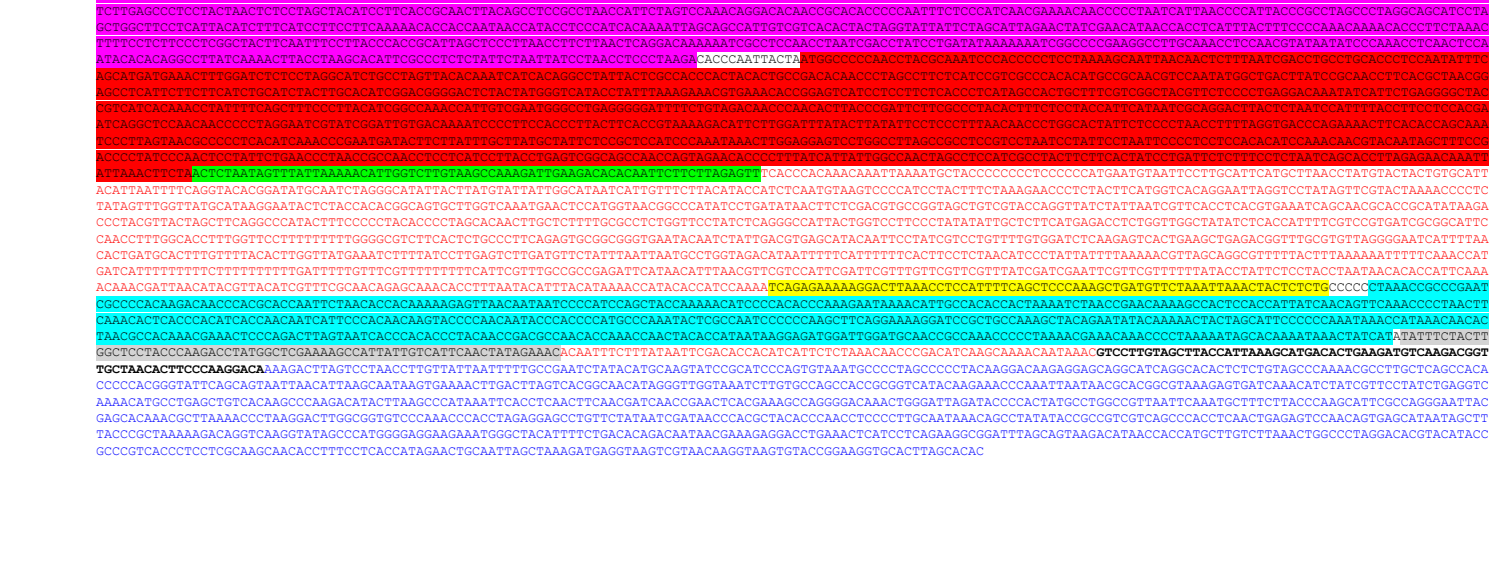
Merops nubicus **(Coraciiformes/Meropidae) mitogenome from ND5 to 12S rRNA (CM020464.1 - annotated)**

GO-II in Figure 8



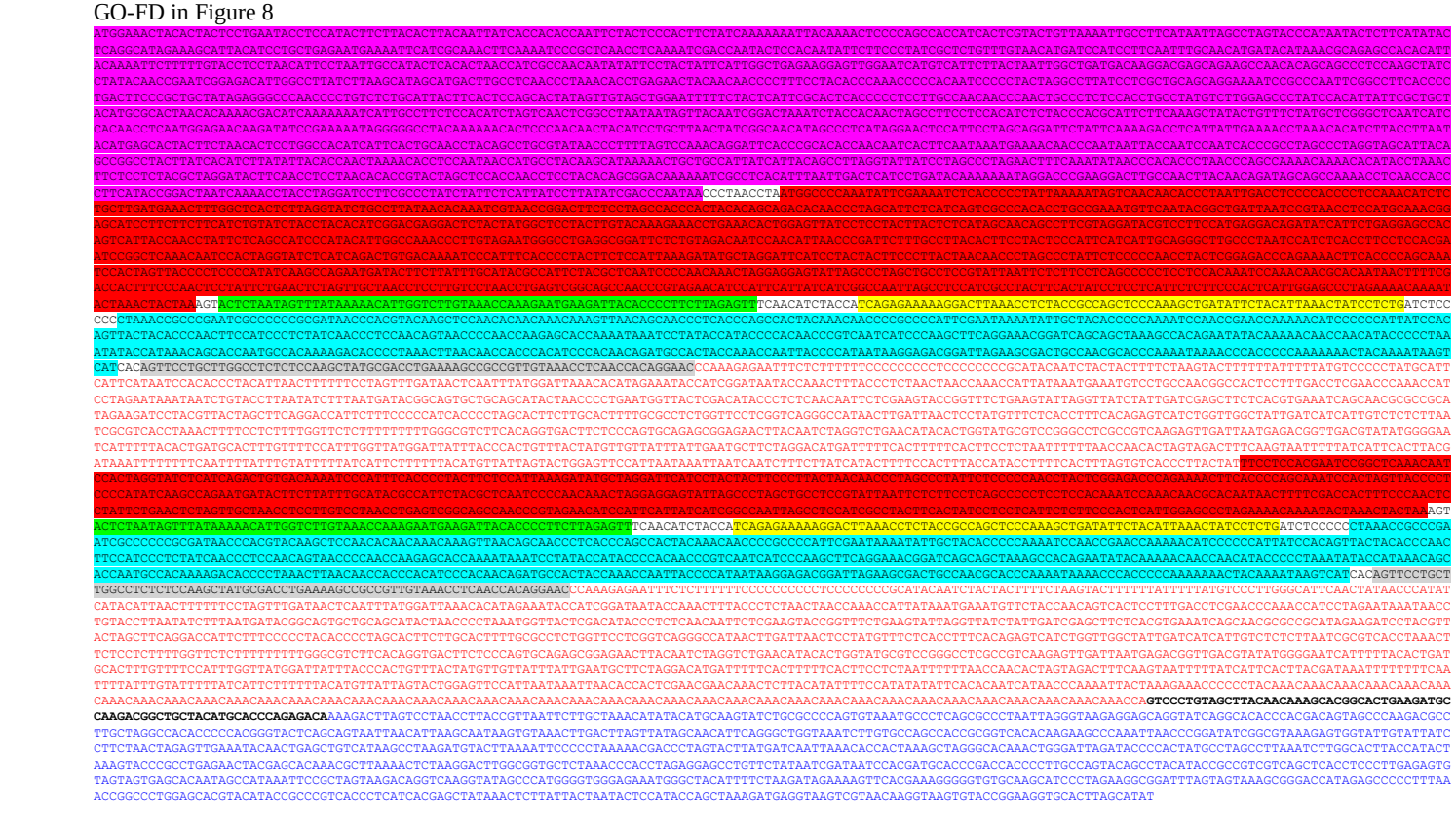
Melanerpes aurifrons **(Piciformes/Picidae) mitogenome from ND5 to 12S rRNA (CM022134.1 - annotated)**

GO-IV in Figure 8



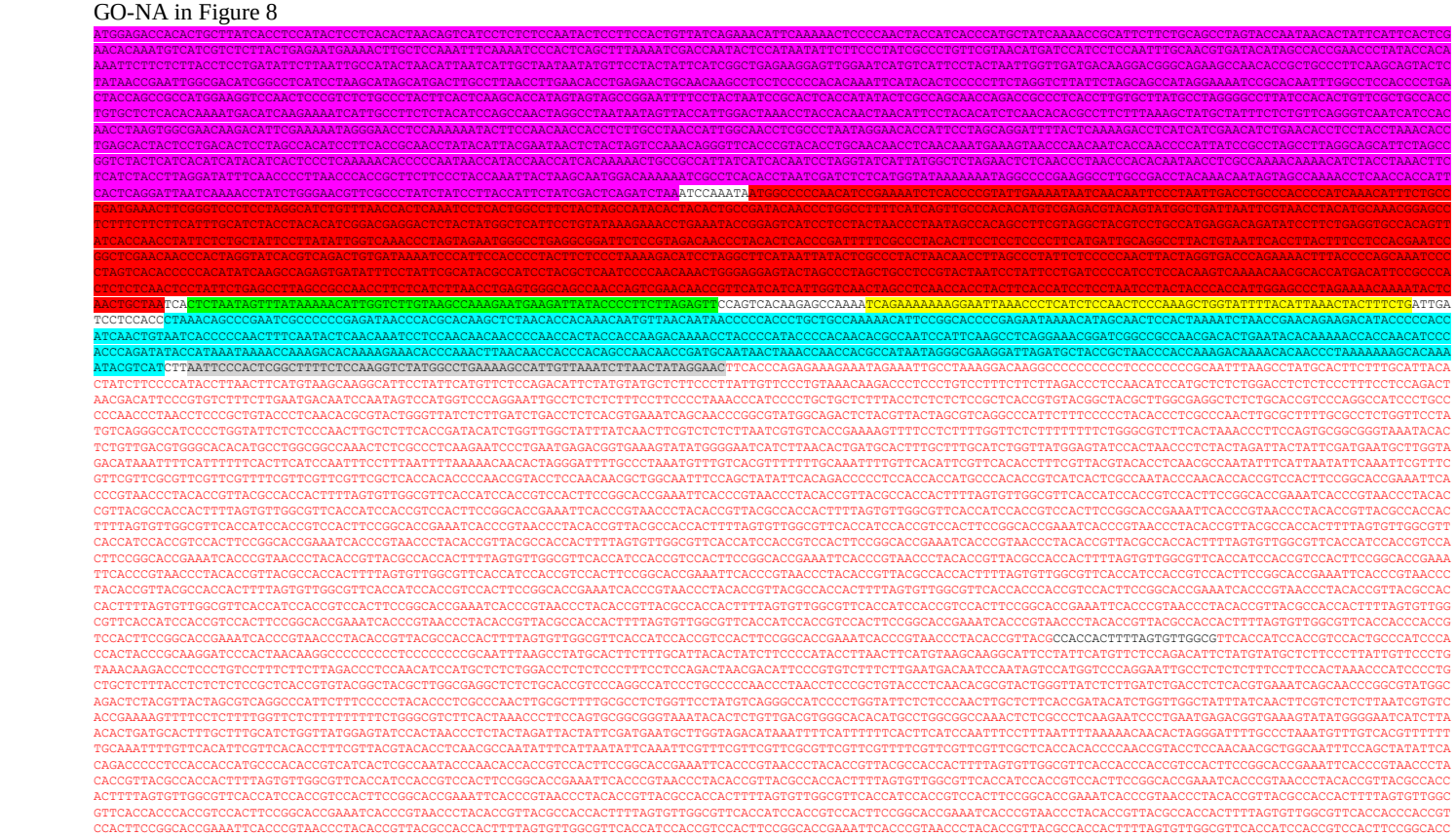
Morus serrator **(Suliformes/Sulidae) mitogenome from ND5 to 12S rRNA (GU071056.1 - re-annotated)**

GO-FD in Figure 8



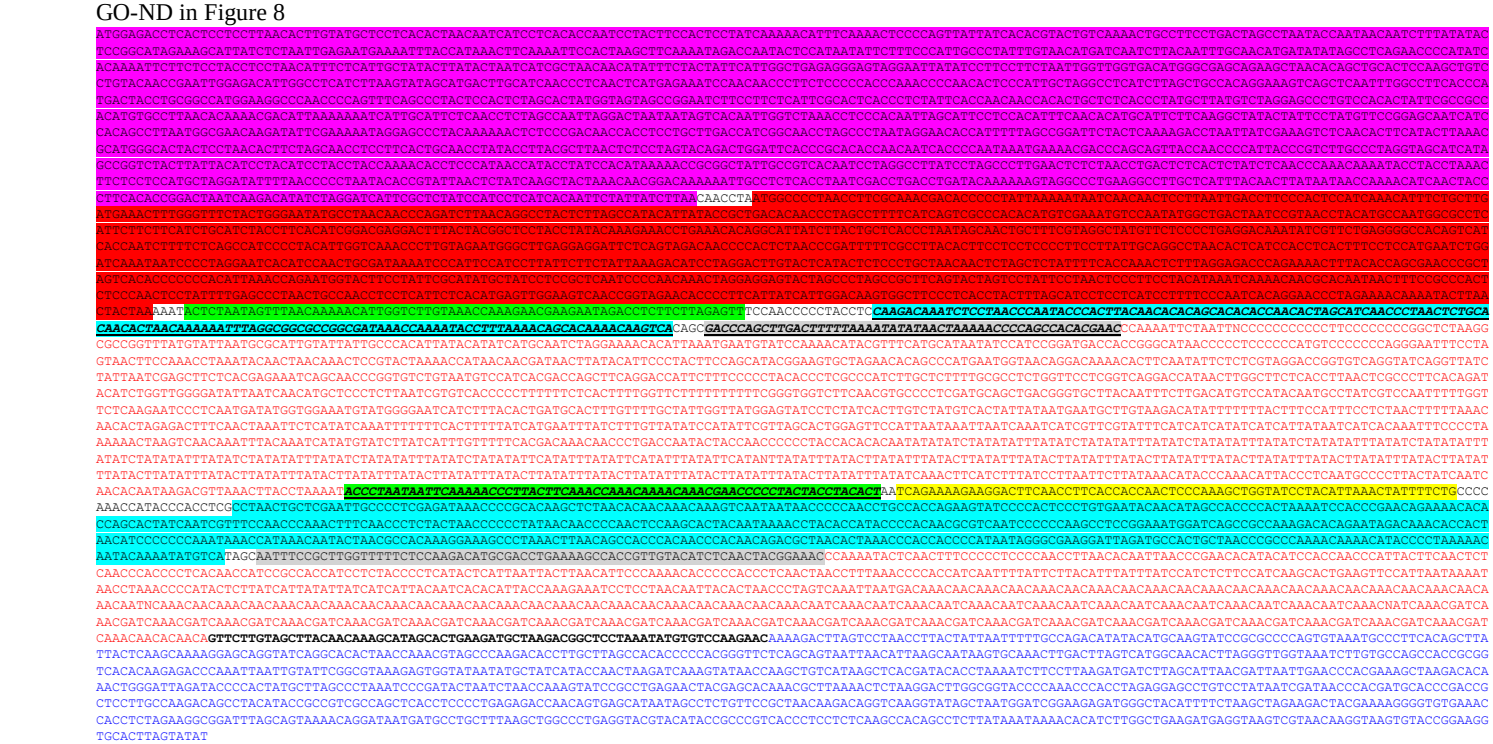
Nyctibius grandis **(Caprimulgiformes/Nyctibiidae) mitogenome from ND5 to 12S rRNA (CM023771.1 - annotated)**

GO-NA in Figure 8



Pterocles burchelli **(Pterocliformes/Pteroclidae) mitogenome from ND5 to 12S rRNA (MN356340.1 - re-annotated)**

GO-ND in Figure 8



Pterocles gutturalis **(Pterocliformes/Pteroclidae) mitogenome from ND5 to 12S rRNA (CM020177.1 - annotated)**

GO-NB in Figure 8

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Pterocles gutturalis (Pteroclifformes/Pteroclidae) mitogenome from ND5 to 12S rRNA (MN356147.1 - re-annotated)

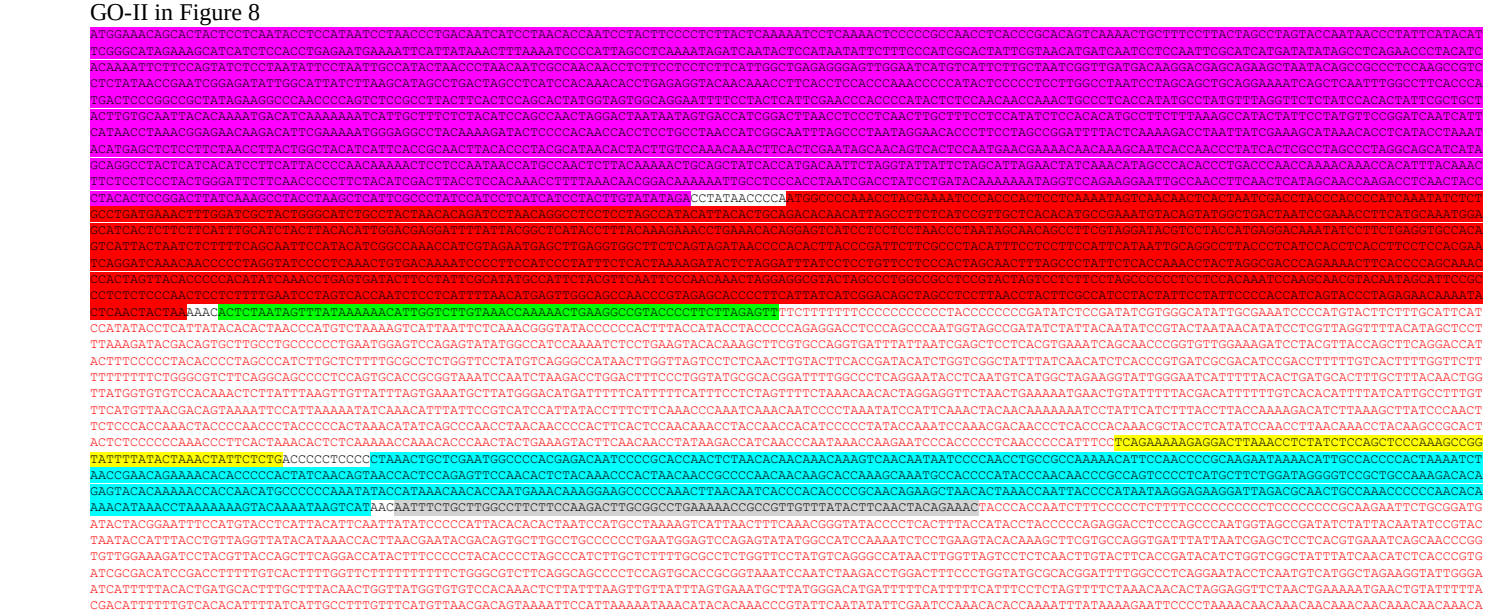
GO-NC in Figure 8

Puffinus lherminieri (Procellariiformes/Procellariidae) mitogenome from ND5 to 12S rRNA (MH206162.1 - re-annotated)

GO-FD in Figure 8

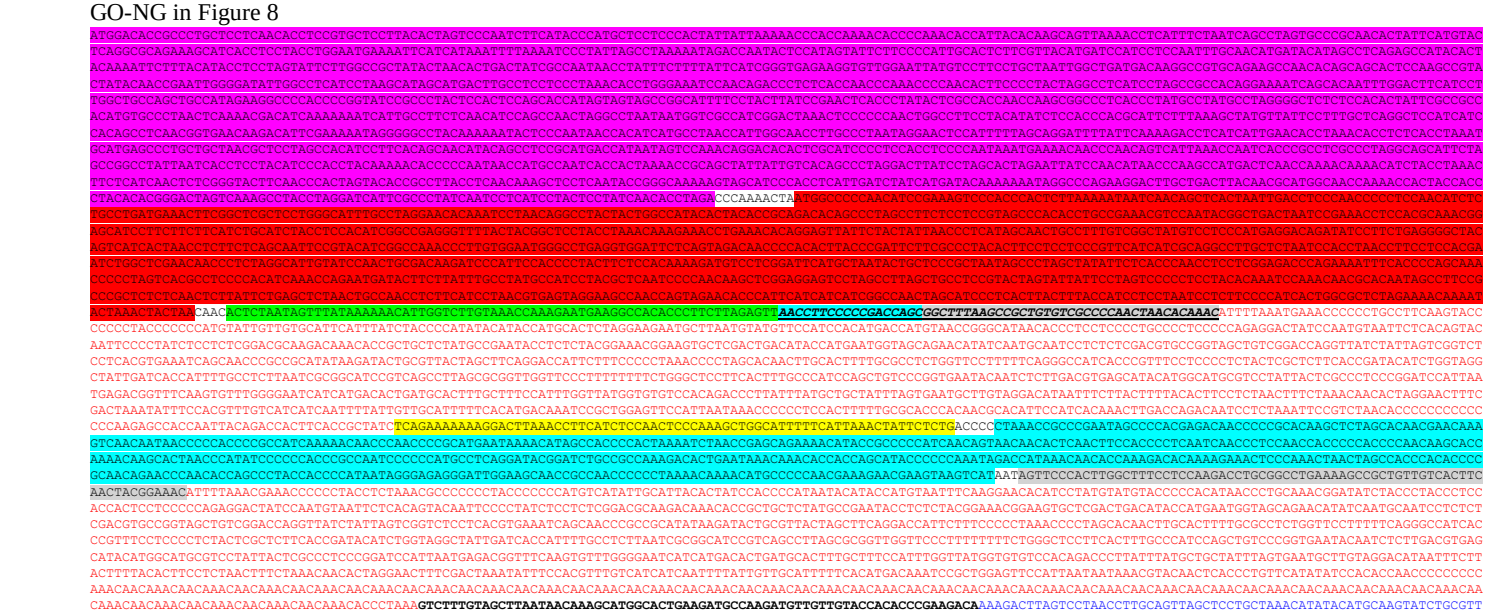
Rynchops niger **(Charadriiformes/Laridae) mitogenome from ND5 to 12S rRNA (MN356248.1 - re-annotated)**

GO-II in Figure 8



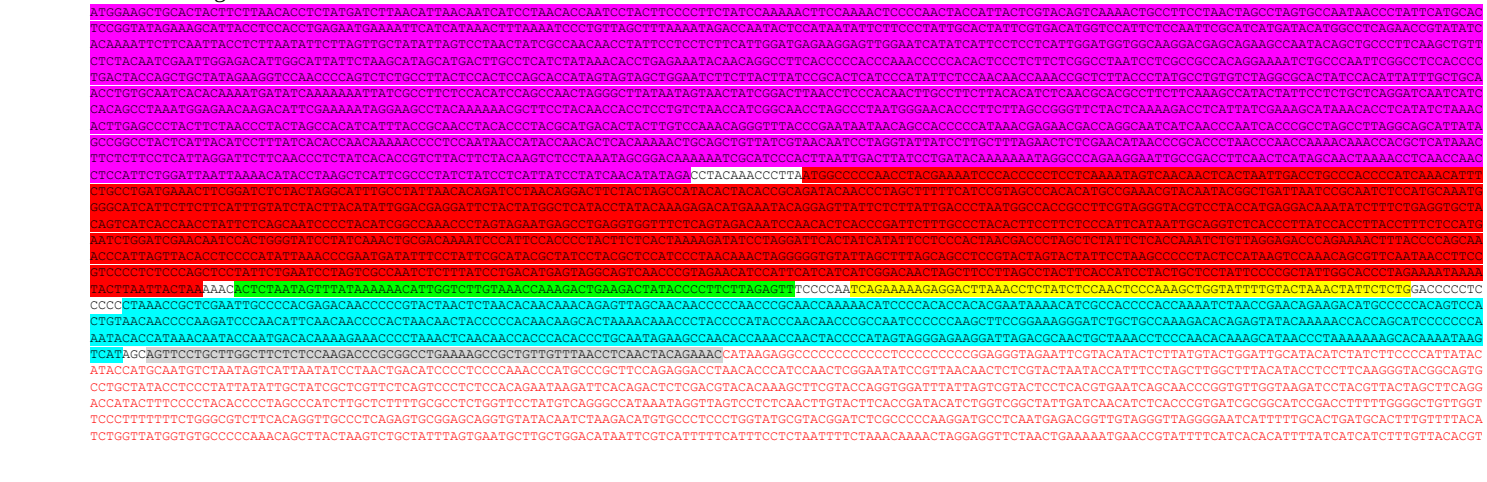
Scopus umbretta **(Pelecaniformes/Scopidae) mitogenome from ND5 to 12S rRNA (MN356281.1 - re-annotated)**

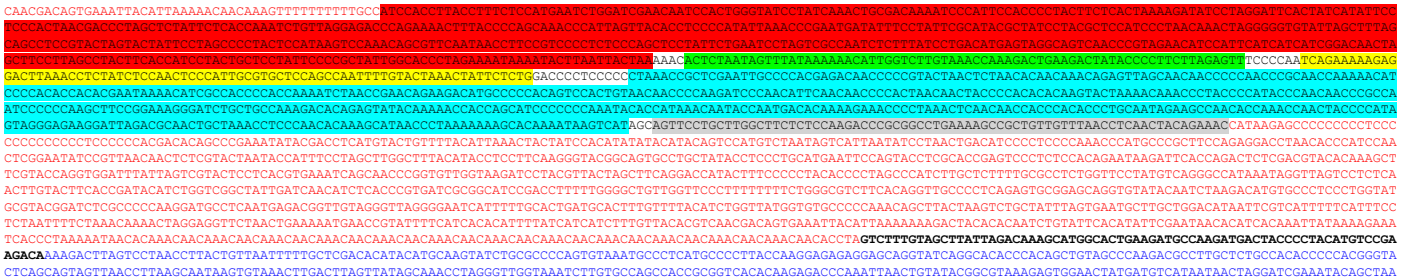
GO-NG in Figure 8



Sterna hirundo **(Charadriiformes/Laridae) mitogenome from ND5 to 12S rRNA (CM020500.1 - annotated)**

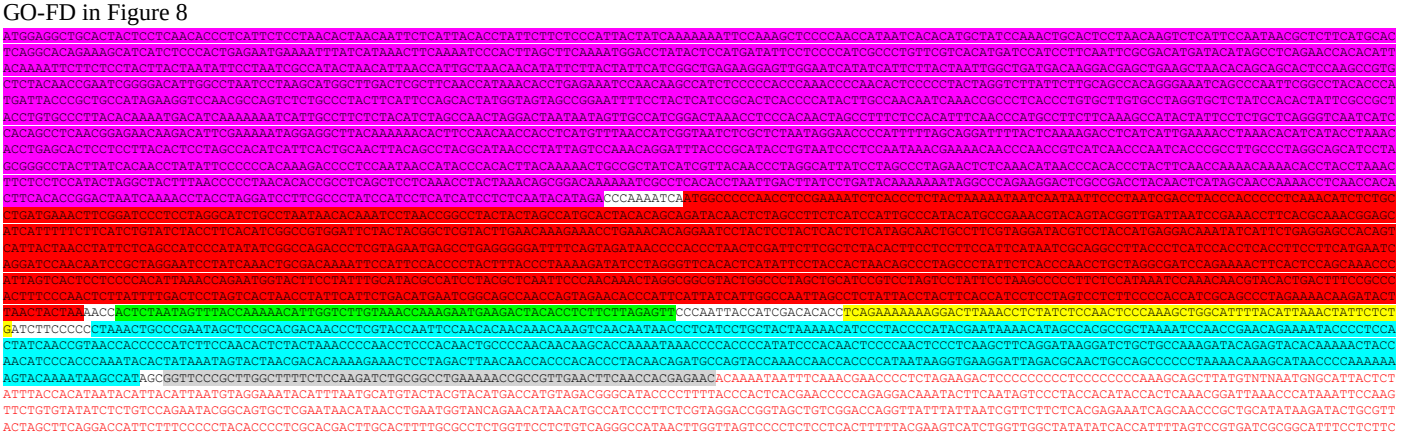
GO-FD in Figure 8





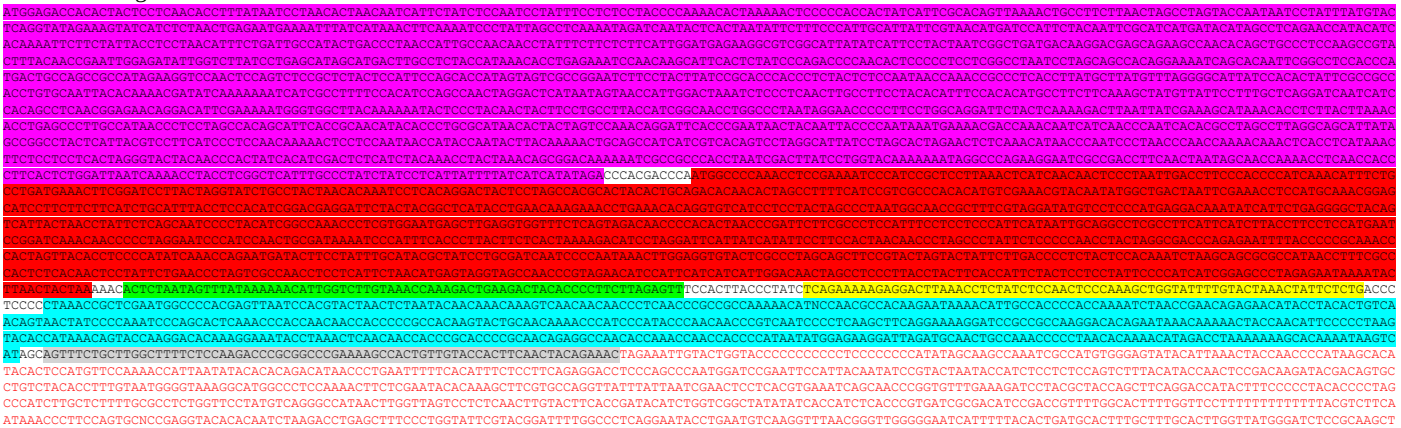
Thalassarche chlororhynchos (Procellariiformes/Diomedeidae) mitogenome from ND5 to 12S rRNA (MN356342.1 - re-annotated)

GO-FD in Figure 8



Uria aalge (Charadriiformes/Alcidae) mitogenome from ND5 to 12S rRNA (MN356418.1 - re-annotated)

GO-FDr in Figure 8



***Urocolius indicus* (Coliiformes/Coliidae) mitogenome from ND5 to 12S rRNA (MN356373.1 - re-annotated)**

GO-NH in Figure 8

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TTACTCATCACCTCATATATTACCCCTGCCAACACTACCCCAATAACAATACCCCCTATCACCAAAATAGCTGCAATAATCGTCACTATCCTAGGCCTCATACTAGCCCTAGAACTCTCAAATATAACACATAACCTCTTCACCCTAAACAAACCCCACATCAAAACTTTTCC
TCCTCCCTAGGCTACTTCAACCTACTTATACACCGCCCTAACACTACCAAACTCTTAAGCAACTGTCAAAAAATTGCAACCCATCTCATTGATCTCTCCTGATACAAAAAAATAGGTCCCGAAGGTATCACTGACCTTCAACTAATCTTAACCAAAACATCACAGCCCTACAC
ACCGGACTAATCAAAACCTACCTAACATCATTTGCACTATCAATCCTAATCATCCTGTCCACACAATAAATTATAATGGCCCCAAACCTACGAAAATCCCACCCGCTACTAAAAATAATTAATAACTCCTTAATCGACCTACCTACGCCTCCCAACATTTCAGCCTGATGAAACTT
TGGATCACTCCTAGGCATCTGCCTCATAACTCAAATCCTAACAGGCCTATTACTAGCCGCCCACTACACCGCAGATACAAGCCTAGCCTTCTCATCCGTCGCTCATACCTGCCGGAACGTCCAATATGGCTGACTAATCCGCAACCTTCACGCAAACGGAGCATCTCTATTCTT
TATTTGCATCTACCTTCACATCGGACGAGGGTTCTACTACGGCTCATACCTTTACAAAGAAACCTGAAACACAGGCATCATCCTCCTCCTCACCCTAATAGCAACAGCCTTCGTAGGCTATGTCCTACCATGAGGACAAATATCCTTCTGAGGCGCTACCGTCATCACCAACTT
ATTCTCAGCCGTCCCCTACATTGGACAAACCTTAGTAGAATGAGCCTGAGGGGGATTCTCGGTAGATAACCCAACTCTAACCCGATTCTTCACCCTCCACTTCCTACTCCCCTTCATAATTGCCGGACTCACATTAATCCACCTAACCTTCCTTCACGAATCAGGCTCAAACAA
CCCCCTAGGCATCATCTCAAGCTGCGACAAAATCCCATTCCACCCCTACTTCTCTCTAAAAGACATCCTAGGATTCGGCACTCATAATCTTCCCCCTAACATCTCTAGCCCTATTTTCCCCAAACCTCCTAGGAGACCCAGAAAACTTCACACCAGCAAACCCCTTAGTAACCCC
TCCCCACATTAAACCAGAGTGGTATTTCCTATTCGCATACGCCATCCTACGCTCCATCCCAAACAAATTGGGAGGAGTACTAGCCTTAGCTGCATCAGTCCTCGTACTATTCCTTTGTCCACTACTCCACAAATCCAAACAACGCACAATAACCTTCCGACCCCTATCCCAAGT
ACTATTTTGAACCCTCACCGCAAACCTATTTATCCTAACATGGGTAGGCAGCCAACCAGTAGAACACCCCTTATCATCATTGGCCAACTAGCCTCAATCACCTACTTCACAATCATCCTTATCCTCTTCCTATCATCGGAACACTAGAAAACAAAATACTCAAATACTAAAA
TACTCTAATAGTTTATTAAAACATTGGTCTTGTAAACCAAAGAATGAAGACTTATACCTCTTCTTAGAGTTCC***CTATAATAACCAAACCAAATAAAACCTTTCCCCTAACCCATGGCCCTCCCCCTAGCAAAGGAAGGGCCATTATTGCCTTACCTTTTTCCTCCCTAACCCAT***
GGCCCTCCCCCTAGCAAAGGAAGGGTCATTATTGCCTTACCCTTCCCCCCACCCCCACTCATGGTCCACAACAAAATTTCTCAATCTGGAAAGAAAAAAGACCCCATACTACCACTATTATTATCTCCCCCCCCCCCCTACCCCCCCCTATGTACTTCTGTACATTAAACCCAT
AACCCCATATCAATGCACCTCTCTAGGCGTAAATCCAAATGATTGAACTGATCCCATAACATGAAAACGGATACGAACTCAAGACAATCCATTTTTGCCGGCAGACTAACAAATCCATGCACACACGGTTTAACAATCTATATAACTTCGGACTAAACCCATAAAATGTCTCTT
TATACATCCCTAATTTCAAGCATACGGAAGTGCTTTAACACATACCATCAATGGTAACCGGACAAATCAATGTAATCTGATTTCTCGTCGGACCTATTTCTAAAGGACTGGGTTATTTATTGATCGCGCCCCTCACGTGAAATCAGCAACTCGACGTATTACGGATCCTACGTT
ACTAGCGTCAGGCCCATTCTTTCCCCCTAAACCCTCGCCCAACTTGCGCTTTTGCGCCTCTGGTTCCTATTTCAGGGCCATTCATAAGCTTGACTCCCCCAACTTGTTATTCACAGATACATCTGGTTACTTATATCTCAACCATTTGGCCTCTTTATCGCGTCACTGGCCGG
TTCTCTACTTTTGGTTCTCTTTTTTTTCTGGGTAATTTCAACGGACCCTCCAGGCGGCTGGAGCCGGAGCATACTATCGCGTGACGTGGGCACCGGTGGACTTCGTCCAATTCCTCTCTTTCCTTCGGTTAACTCAATGAGACGGAGTCAAGTGTCCTCGGAATCATTTTTAC
ACTGATGCACTTTGTCATGCATTTCTCATGCCTGTCTTGCTTACTTAAACTGTCAGGGGTAATTAAAGCAATGCTCGAAAGACATAAATTTTCACACTTTCAATACTCCTAACTTTCCTGCTATTTAAAAAATTTTAGCAGGAATTTTCCCAAGTCTGACACCAAAATTTTTGT
CATTTTTTGTCATTTTTTGTCATCAAATCAACACTTGTTTGCACTTGTTGTCACGGCCTGATTTCCCCTTAAACAACAAAATCGTTTCACAAAAATTTTTTCAAATCATTAACACAAATTTTACACATACATTCCTCTGACTTTTCCCATAAAATTCTTTCATCATTCACCATT
CATTTTTTTTCACCAAAATTAACTAACAACAGTAGCCAAAAACCCCGTAAACCTTCTAAGAAGGGGACCCCCCCCCCATTTGTTCAACCAACCAAACAAAAACACCCACCTAATCCCCTACCACTCTCAGAAAAAGAGGGATCAAACCTCTGCCTCCAGCTCCCAAAGCTGATG
CTCTGCATTAAACTATTTTCTGCCCCCTAAACCGCCCGAATAGCACCACGAGATAACCCTCGAACCAACTCCAACACTACAAACAATGTTAACAATAACCCCCACCCCGCCACCCAAGAACAACCCCACCCCCCCACGAATAAAACATAGCTACTCCACTAAAATCTAAACGCAC
AAAAAATCCCCCACCACTATCCACAACATCAACCCCAAACCCCAAACCACCAAACCCTCCAACCAAAATACCAACAATAAGCACCAACAACAGCCCCAACCCATAACCAACTACCCGTCAATCCCCTCAAGTCTCAGGAAAAGGGTCCGCCGCCAAAGCAACAGAATATACAAA
AACCACCAACATCCCCCCTAAGTACACCATAAATAGTACCAAAGACACAAAAGACAACCCCAAACTCATCAACCACCCACACCCAACAACAGACGCCAACACCAACCCAACAACTCCATAATATGGAGAAGGATTAGATGCAACCGCCAACCCCCCTAAAACAAAACACACCCC
TAAAAAAAATATAAAATATACCATAATAGTTTCTGCTTGGCCTCTCTCCAAAACCTACGACCTGAAAAGCCGCCGTTGTACTCAATTCAACTACAGAAACATCCTACCCTAAAACCAACCCTCAACCATTTTCACAAAACCAATCACAAACCATTTATCCTGCCAAATTAACCC
CCAAGCCCTATTATAAATGACCAAATAAACAATCCCACACACTTCCCCACCTAAACTACTATACACCAACCACTTAAATCCAAACCCACTCAAACAACACACAACACAAAACTACAAAGCCACTTAACCAACCAAGACCCCATATAAGTTTACTTACAAACAACCCAACAAACG
ACAACACAAATTAGACTATTCAAGCACAAAGTTTTCCCCT**GTCTTTGTAGCTTAAACAAAGCATAACACTGAAGATGTTAAGATGTTGTTAACTACACCCAAAGAC**AAAAGACTTAGTCCTAACCTTGCAGTTAGTTCTTACCTAGTATATACATGCAAGTATCCGCGCCCCAG
TGTAAATGCCCTAACCTCTTTACTAAAGATATAGGAGCTGGTATCAGGCACACCCACCATAGTAGCCCACAACACCTTGCTTCGCCACACCCACACGGGCTTTCAGCAGTAATTGACATTAAGCAATAAGTGTAAACTTGACTTAGCTACGGTAAAACCCAGGGTCGGTAAATC
TTGTGCCAGCCACCGCGGTCATACAAGAGACCCAAATTAACTGCACCCGGCGTAAAGAGTGGTACAATGATATCATAACAACTAAGACTGAAACACAACCAAGCCGTCATAAGCTAAAGTTGAACTTAAAACCATCCTAAAAATGGTCCTAGTATATTAGATTAACTTAACACC
ACGAAAGCTAAGACACAAACTGGGATTAGATACCCCACTATGCCTAGCCATAAATCCAGATTCTCCCCTCACTAGAGAATCCGCCCGAGAACTACGAGCACAAACGCTTAAAACTCTAAGGACTTGGCGGTGCCCCAAACCCACCTAGAGGAGCCTGTTCTGTAATCGATAACC
CACGATCCACCTAACCACTTCTTGCCCAAACAGCCTACATACCGCCGTCCCCAGCTCGCCTTAACTGAAAGCACAATAGCAAGCATAACAGCCACAACCCACGCTAGTAAGACAGGTCAAGGTATAGCCTATGAAGTGGAAGAAATGGGCTACATTTTCTAACCATAGAACACT
CACGAAAAGAGGAGTGAAACCCTCCCCTAGAAGGCGGATTTAGCAGTAAAGAAAGGTAATTAAACTTCCTTTAAGACGGCCCTGGAGCACGTACATACCGCCCGTCACCCTCCTCACGCACTACCCATCAACAATACATAATACAAGTACCAACCACAAGACGAGGTAAGTCGT
AACAAGGTAAGTGTACTGGAAAGTGCACTTAGCACA

Figure S10. Sequences of mitogenomic fragments in Neoaves and Galloanserae mitogenomes amplified and sequenced for: *Alca torda* (MK263222), *Apus apus* (MW151827), *Cathartes aura* (MN629891), *Chrysolophus pictus* (MW151829), *Ciconia nigra* (MH264509), *Corythaixoides personatus* (MW082596), *Gavia arctica* (MK263210), *Gavia stellata* (MK263209), *Eurypyga helias* (MW208859), *Podiceps cristatus* (MN629890), *Podiceps grisegena* (MK263194), *Scopus umbretta* (MW151828), *Spheniscus demersus* (MH264510) and *Uria aalge* (MK263188). Genes for NADH dehydrogenase subunit 5 are marked in magenta coloring, cytochrome b in red coloring, tRNA-Thr in green coloring, tRNA-Pro in yellow coloring, NADH dehydrogenase subunit 6 in cyan coloring, tRNA-Glu in grey shading, 12S rRNA in blue fonts, **tRNA-Phe in bold fonts**, and control regions in red fonts. *Pseudogenes are in italics and underlined*.

Alca torda (Charadriiformes/Alcidae) mitogenome from CR1 to CR2 (MK263222)

GO-FD in Figure 8

GTTCCTATGTCAGGGCCATAACTTGGTTAGTCCTCTCAACTTGTACTTCACTGAGACAACCGGTCGGCTATATATCATCATCTCACCCGTGATCGCACATCCGACCGTTTTGGCACTTTTGGTTCCTTTTTTTTTTCTCTAACCTTCAATAAGCCCTTCCAGTGCACCGAGGTG
TACACAATCTATTGACGTGAGCATCTCATGGTATTCGTCCGGATCTTGGCCCTCAGGAGTACCTGAATGTCAAGGTTGAAGGATTGGGGGAATCATTTTTACACTGATGCACTTTGTCTTGCACCTGGTTATGGAGTGTCCGCAGACTCTTATTCATGTTGCTATTTAGTGAAT
GCTTGTTGGGCATAATTTTTCAATTTTCATTTCCTCTAACTTTCTAAACAACACTAGTAGATTTTACCTAAAAATTGACCATGATCAAATCACGATTTTTGTCACGTATTTTATCATCATCTTTATCACTTACAAATAGCAGTAAAGTTCCATTAATAAAACCACCAATAATCC
GTGACATTTTATCTTCATCTTTCTTCATGAATCTGGATCAAACAATCCTCTAGGAATCCTATCAAACTGTGACAAAATCCCATTCCATCCCTACTTCTCATTAAAAGATATCCTAGGATTCATTATCATATTCCTTCCACTAACAACCCTAGCCTTATTTTCACCCAACCTGTT
AGGCGACCCAGAAAACTTCACCCCCGCAAACCCATTAGTCACTCCTCCTCATATCAAACCAGAATGATACTTCCTATTTGCATACGCTATTCTACGCTCAATCCCCAACAAACTAGGAGGAGTACTAGCCCTAGCAGCCTCTGTACTAGTACTATTCCTGGCCCCTCTTCTCCA
CAAATCCAAACAACGTGCAATAACCTTCCGTCCATTCTCACAATTCCTATTCTGAACCCTAGCCGCCAACCTCTTCATTCTAACATGAGTAGGTAGCCAACCCGTGGAACACCCATTCATCATCATTGGACAACTAGCTTCCCTCACCTACTTCACCATCTTACTCCTTCTATT
CCCCATCGCTGGAGCTCTAGAAAACAAAATACTTAACTACTAAAACACTCTAATAGTTTATAAAAAACATTGGTCTTGTAAGCCAAAGATTGAAGGCTATACCCCTTCTTAGAGTTTCCATTGCCTCAGAAAAAGAGGACTTAAACCTCTATCTCCAACTCCCAAAGCTGGTGT
TTTACACTAAACTACTTTCTGGTCCCCCTCCCCCTAAACCGCTCGAATAGCTCCACGAGTTAGTCCACGTACTAACTCCAGCACAACAAACAAAGTCAGCAACAGCCCCCAACCCGCTACCAAAACATTCCAACACCACAAGAATAAAACATTGCTACCCCACCAAAATCTA
ACCGAACAGAAAACATACCGACACTATCAACAGTAACCACCCCAAAATCCCAACATTCAACAAACCCACCAATAACCATCCCCATCATCAATACTCCAACAAAACCTGCCCCATACCCAATAACCCGTCAATCCCCCCAAGCCTCAGGAAAAGGATCTGCCGCCAAAGACACAG
AATAAACAAAAACTACCAACATCCCTCCCAAGTATACTATAAACAACACCAGGGACACAAAAGAAATACCCAAACTTAACAACCACCCACACCCCGCAACAGAAGCCAGCACCAAACCTACCACCCCATAATATGGTGAGGGATTAGATGCAACTGCCAAACCCCCCAACACAA
AACATAAACCTAAGAAAAACATAAAATAAGTCATAGCAATTTCTGCTTGGCTTTTCTCCAAGACCAGTGGCCTGAAAAGCCACTGTTGTCAACTTCAACTACAGAAACTGCACGCCCCCCCCCCCCCCCCATGCAAGTGCTCTCTACGCATGTGGGCTTGTACATTACACTACC
ATCCCCATAAATACATACAATCCATGTTCCAAAACCATTAATATACACACAGGCATAACCCTGAATTTTCCACACTTCCCCTTCAGAGGACTCTCAAGCCCAATGGGAGCAGAAATCCATTACAATATACGTACTAATACCATTTCCTACCTAGCTTATACATACCAACCCCAC
AAGATACGACAGTGCTTGGGTACCTCCTTGCCTGGTGTAGGAGCATGACCCTCCAAAATTTCTTGAGTGCGCAAAGCTCGTACCAGGTTATTTATTAATCGAGCTCCTCACGTGAAATCAGCAACCCGGTGTCTGGAAGATCCTACGCTACCAGCTTCAGGAC

Apus apus (Caprimulgiformes/Apodidae) mitogenome from CR1 to CR2 (MW151827)

GO-FD in Figure 8

CATGAACATTCTATGACATGCGTCCTGTTTTTTGGCCTTCAGGAGTAGCTGAATGAGACGGTTTGCGTATAACGGGAATCATTTTGACACTGATGCACTTGCTACCGCATTTGGTTATGGAGTATCCACTAACTACTTATATATGTTGCTTTTTAGTTCATGCTTGTTAGACAT
AATTTTCCAGCTATTTTACATTCCTCTAAATTCCCTTAATATTGCAAATCGACACCAGTAACTTTTCTACTAATCTTCCCAAACACACCATCATCATAATTTTTTCATTTTTTCAATTTTTTTCATCACACCATCACTTAACATTACCACTGAAATTACATTAATAATCTAATT
AACATTTTTCAACATTTATCATGTTAATTTTTTCATAAAAACACCATAATTTACTAAAGCAACCCTACTAGAACAAATTTATACATCATCCATCACCAAAAAACCACATCACATTTAATGACTTACCAGCAAAACACCTAATCATCATCGGCCAACTAGCCTCCCTCACCTACT
TCACTATTCTCCTAATCCTCTTCCCCCTTATCGGAGCTCTAGAAAACAAAATACTTAACTACTAAAATACTCTAATAGTTTATTAAAACATTGGTCTTGTAAGCCAAAGAATGAAGACTCCACCCCTTCTTAGAGTTACCCCAACCCAAATATCAGAAAAAAAGGACTTAAACC
TCTATCTCCAACTCCCAAAGCTGGCATTTTCATTAAACTATTCTCTGACACCCCCCTAACTGCCCGAATTGCACCACGAGAAAGTCCCCGCACAAGCTCCAATACAACAAACAGAGTCAACAGTAAACCCCACCCACCCATCAAAAACATCCCCACCCCCCAAGAATAGAACAT
AGCCACACCACCAAAATCCAACCGAACAGAAAGCATCCCCCCACTATCAACTGCTACCACCCCTCACTCCCACCCCTTAACAAAGCCACCCACCACTACCCCCAAAATCAGCACTAAGGCAAACCCAACCCCATACCCTATAACACGCCAATCTCCCCATGCCTCAGGAAAAGG
ATCAGCTGCCAACGACACAGAGTACACAAAACTACTAACATCCCCCCCAAATACACCATAAACAAAACCAACGACACAAAAGAAAGGCCAAGACTTACCAATCACCCACATCCAACAACAGAAGCAACTACCAAACCAACCACCCCATAATATGGTGAAGGATTAGATGCAAC
TGCTAATCCCCCTAACACAAAACACACCGCTAAAAAAACAATGAAATAGGTCATAAAAGTTCCTACTTGGCTTTTCTCCAAGACCTACGGCCTGAAAAGCCGTCGTTGTTACTTCAACCATAGAAACACAGCCTACACAAACACCATTAGCCCTATGACGTATGCCCCCCTACC
CCCCATAATACAGGGATGTTCCTAGAATCATTATGAGTTCTATTGGCTTTATGTCATACTAGCATTCATCTATATACCCCATTACATTAAATGATACCTAGGGCATACACCTTAATACCCGTACTAAAACCATAAGCTGTTAACCAGGGCAGGCAAAAACACTCTACGAATATG
ACACCACAGGGATTAAGAATGTAATGCTCTACCACCATAACCTAAAACCCTCGTACTAAAACCATTAGAACCCTCGGTTATGCATAAACCTATCACCCCTACGAGAGAGTATCTCAGGTACCAAAGGAATCCATGTTAGGCAGACTGAACTTGCCACTATCTCTTGAAGTGCCG
GTAGCTGTCGTATTGGGTTATTTATTGATCGTACCTCTCACGCGAGACAGCTACGCACCGTAGGTTCCTAATTACGTGACCAGCTTCAGGCCCATTTACTGCCCCTATAGCTTAATTATACACACCGGTGAGCCTTGCTCTTTTGCGCCTCGGGCTGTTTCTTCATGAGCATAG
CATGGCTCCTCCCTTTCCTTTTCTCTTCACGAGACCTTTGGTTCGTTATATTCGTTCTTCTCACCCGTAATCGCGGCATCTGTATTGCT

Cathartes aura (Cathartiformes/Cathartidae) mitogenome from ND5 to 12S rRNA (MN629891)

GO-FD in Figure 8

CGAATCGGGGACATTGGCCTCATCCTAAGCATGGCATGACTTGCCACAACCATAAACACATGAGAAATTCAACAAGCCTTCTCCCCCACCCAAACTCCAACTCTCCCTCTACTCGGCCTCATCTTAGCTGCCACAGGAAAATCAGCCCAATTTGGCCTCCACCCATGACTACCA
GCTGCCATAGAAGGCCCAACCCAGTTTCCGCCTTACTCCACTCCAGCACAATAGTTGTTGCTGGAATTTTCCTACTCATCCGCACTCACCCCATACTCTCCAACAACCAAACTGCCCTCACCTCCTGTTTATGCTTAGGAGCTCTATCCACACTATTCGCTGCCACATGTGCA
CTCACACAAAATGACATCAAAAAAATCATTGCCTTCTCAACCTCTAGCCAACTAGGGCTAATAATAGTCACCATCGGACTAAACCTCCCACAATTAGCCTTCCTTCACATCTCAATACATGCATTCTTCAAAGCCATATTATTCCTCTGCTCAGGCTCAATCATCCACAATCTC
AACGGAGAGCAAGACATTCGAAAAATAGGGGGACTACAAAAAACACTCCCAACAACAACCTCATGCCTAACCATCGGCAATCTAGCCCTAACAGGAACCCCATTCCTAGCGGGCTTCTACTCGAAAGACCTCATCATTGAAAGCCTAAATACCTCTTACCTAAACACCTGAGCA
CTACTGCTAACACTCCTAGCCACCTCATTCACTGCAACCTACAGCCTGCGTATAACCCTAATAGTCCAAACAGGATTCACCCGCACCCCAACAATCACCCCCATAAACGAAAACAATCCAACGATCATCAACCCAATCATCCGCCTTGCTCTAGGTAGCATCCTAGCTGGCCTA
TTCATCACATCATACACTATCCCCACAAAAACACCCCCCATAACCATGCCCACACTCACAAAAACTGCAGCAATCATCGCCACAATCCTAGGAGCGATCCTAGCCTTAGAGCTCTTAAACATAACACACACTCTAACCCAACCAAAACAAAACCCCCTCCTAAACTTCTCATCC
ACATTAGGATACTTCAACCCATTAACACACCGCCTTACCTCCACAAAACTTCTAAACAACGGACAAAAAATTGCCTCACACCTAATTGACCTATCTTGGTACAAAAAAGTAGGCCCTGAGGGACTCGCTGACCTACAACTCCTAGCAACCAAAACCTCAACTACCCTCCACACC
GGATTAATCAAAACCTACCTTGGATCCTTCGCCCTATCCATCCTCATTATCCTATCAACACACAGAACCAAGACTAATGGCCCCTAACATCCGAAAATCACACCCCCTACTAAAAGTAATCAACAACTCCCTGATCGACTTACCCACTCCCTCAAACATCTCTGCCTGATGAAA
CTTCGGATCCCTACTAGGCATCTGCCTAGTGACCCAAATCCTAACCGGCTTACTACTAGCCATACATTATACTGCAGACACAACACTAGCCTTTTCGTCCGTCGCTCACACATGTCGAAACGTACAATATGGCTGACTAATCCGCAACCTACATGCAAACGGAGCTTCATTCTT
CTTCATCTGTATTTACCTACATATCGGACGAGGACTCTACTATGGCTCATACCTGTACAAAGAAACATGAAACACAGGTGTCATCCTCCTACTCACCCTCATAGCAACTGCTTTCGTGGGCTACGTCCTACCATGAGGACAAATATCATTCTGGGGTGCCACAGTAATTACTAA
CCTATTCTCAGCTATCCCTTACATCGGCCAAACCCTTGTAGAATGAGCATGAGGGGGATTTTCAGTAGACAACCCCACTCTGACCCGATTCTTTGCCTTACACTTCCTCCTCCCCTTCGCAATTGCAGGCCTTACCTTAATCCACCTCACCTTCCTACACGAATCAGGTTCAAA
CAACCCTTTGGGCATCGTATCAAGCTGTGACAAAATCCCATTCCATCCCTACTTCACCCTAAAAGATGTCCTAGGATTCATGCTCATATTTCTCCCCCTAACAACCCTAGCCCTATTCTCACCTAATTTATTAGGAGACCCAGAAAACTTCACACCCGCAAACCCTCTAGTCAC
ACCACCCCATATCAAGCCAGAGTGATATTTCCTGTTCGCCTATGCCATTCTCCGCTCAATCCCCAACAAACTAGGAGGAGTACTAGCCCTAGCTGCCTCCGTACTAATCCTATTCCTAATACCTTTCCTCCATAAATCTAAACAACGTACAATAACCTTTCGCCCACTCTCCCA
ACTCCTATTCTGAACACTAGCAGCCAACCTTCTCATCCTAACATGAGTGGGCAGCCAACCAGTAGAACATCCCTTCATCATCATCGGCCAACTAGCCTCCCTCACCTACTTCACCATCCTCCTTATCCTCTTCCCTATCCTCGGAGCCCTAGAAAACAAAATACTCCATCAAAA
ATACTCTAATAGTTTATAAAAACATTGGCCTTGTAAGCCAAAGAATGAAGACTACGCCCCTTCTTAGAGTTTAAACCACACCAACCCTCCCACCAAAACACCTCAGAAAAAGAGGACTTAAACCTCTATCCCCAGCTCCCAAAGCTGGTATTTTACACTAAACTATTCTCTGAC
GTCCACCCTAAACCGCCCGAATTGCCCCACGAGACAACCCCCGCACAAGCTCTAACACAACAAACAAAGTCAACAACAACCCCCACCCAGCCACTAAAAATATTCCGGCCCCGCGCGAATAAAATATTGCTGCACCACTAAAATCCAACCGAATTGAAAACAACCCCACACTAT
CAACAGTGACTACTCCCCACTCCCAACCCCCTACAACTCCTACAACCCCCACACCCACAACAAGTACTAAAACCAGCCCCGCCCCATATCCTACTACACGCCGATCCCCCCAAGCTTCCGGAAAAGGATCGGCCGCCAAAGACACAGAGTACACAAATACCACCAACATTCCGC
CCAAATAGACCATAAATAGTACCAAAGATACAAAAGAAACCCCCAAACTCAACAACCACCCGCAACCCATGACAGATGCCAGTACTAAGCCAACCACCCCATAATATGGAGAAGGGTTGGATGCTACTGCCAGCCCCCCTAAAACAAAACATACCCCTAGAAAAAGCACAAAAT
AAGTCATCAGCAGTTTCTGCTTGGCTTTTCTCCAAGGTCTATGGCTTGAAAAGCCATCGTTGAAACTATCTCAACCACAGAAACACTGGAAATACATTAAAAAAGGCTACCCCCCCTACCCCCCCATAATAAATTAATCTACCTATGTATTACTGTGCATTAATATATTTACCC
CATATACATTACATTCATGCTAGGAAAACACATTCAATGCATGTACTATGTACATCAACATTTTACGGGCAATCATCACTCCCACCACACTCCCCCCACAAGGACAATTTAATCAATGATCTACGGACAAGCCTCCTAACTCCAAGTACTAAAACCAGTTAAATGTTAGCTTAT
ACCTACCTCAATCTCCCGAATACGACAGTGCTTGAACACATAACATTAATGGTATCCGGACAAACCATGCATCCTTTCTCGTAGTGCCTGCGTCTGAAGGACCAGGTTATCTATTAATCGTTCTTCTCACGTGAAATCAGCAACCCGCCGCATATAAGACCCAACACGACCAGC
TTCAGGACCATTCTTTCCCCCTACACCCCTAGCCCTACTTGCACTTTTGCGCCTCTGGTTCCTATATCAGGGCCATTCCTTGATTCATCCTCTCAACTTGCTCTTCACAGAAACATCTGGTAGGCTATATATTAGCATCTCACCCGTGATCGCGGCATCTGGATAGCCTTAGCA
CTTTTGGTTCCCTTTTTTTTTGGGGCGTCTTCACAGGTCACCCTTCCAGTGCGGCGGGAAATAACAATCTAAGACCTGAGCATACACTGCGTTGCGTCCTAATTTTGGCCCTCAAGAATTACTGAATGAGACGGTTTGCGTATATGGGGAATCATTTTGACACTGATGCACTTG
CTGTTACATTTGGTTATGGTATCCCCGCAAGCTCTAACTTATGTGGCTATTTAGTGAATGCTTGTTGGACATGTTTTCTTACCTTTACACTTCCTCTAACTTTTCAACCAACACTAGAGGCTTTTCGACCAAATACCTATCGTATGCTAGTCACGAATTTTATTCACACTTTTT
TTACACAACATCACCGCTGAAATTACATTAACAAAGCTAACCTTTGCCATCTTTCATATCTTCTTCTTAACATCACAAAACCTTCCGCTAAAATCTCAACTAAATTCTCCTACACAAACTCGAACCCCAAACCAGGTTCAAACAACCCTTTGGGCATCGTATCAAGCTGTGACA
AAATCCCATTCCATCCCTACTTCACCCTAAAAGATGTCCTAGGATTCATGCTCATATTTCTCCCCCTAACAACCCTAGCCCTATTCTCACCTAATTTATTAGGAGACCCAGAAAACTTCACACCCGCAAACCCTCTAGTCACACCACCCCATATCAAGCCAGAGTGATATTTCC
TGTTCGCCTATGCCATTCTCCGCTCAATCCCCAACAAACTAGGAGGAGTACTAGCCCTAGCTGCCTCCGTACTAATCCTATTCCTAATACCTTTCCTCCATAAATCTAAACAACGTACAATAACCTTTCGCCCACTCTCCCAACTCCTATTCTGAACACTAGCAGCCAACCTTC
TCATCCTAACATGAGTGGGCAGCCAACCAGTAGAACATCCCTTCATCATCATCGGCCAACTAGCCTCCCTCACCTACTTCACCATCCTCCTTATCCTCTTCCCTATCCTCGGAGCCCTAGAAAACAAAATACTCCATCAAAAATACTCTAATAGTTTATAAAAACATTGGCCTT
GTAAGCCAAAGAATGAAGACTACGCCCCTTCTTAGAGTTTAAACCACACCAACCCTCCCACCAAAACACCTCAGAAAAAGAGGACTTAAACCTCTATCCCCAGCTCCCAAAGCTGGTATTTTACACTAAACTATTCTCTGACGTCCACCCTAAACCGCCCGAATTGCCCCACGA
GACAACCCCCGCACAAGCTCTAACACAACAAACAAAGTCAACAACAACCCCCACCCAGCCACTAAAAATATTCCGGCCCCGCGCGAATAAAATATTGCTGCACCACTAAAATCCAACCGAATTGAAAACAACCCCACACTATCAACAGTGACTACTCCCCACTCCCAACCCCCT
ACAACTCCTACAACCCCCACACCCACAACAAGTACTAAAACCAGCCCCGCCCCATATCCTACTACACGCCGATCCCCCCAAGCTTCCGGAAAAGGATCGGCCGCCAAAGACACAGAGTACACAAATACCACCAACATTCCGCCCAAATAGACCATAAATAGTACCAAAGATACA
AAAGAAACCCCCAAACTCAACAACCACCCGCAACCCATGACAGATGCCAGTACTAAGCCAACCACCCCATAATATGGAGAAGGGTTGGATGCTACTGCCAGCCCCCCTAAAACAAAACATACCCCTAGAAAAAGCACAAAATAAGTCATCAGCAGTTTCTGCTTGGCTTTTCTC
CAAGGTCTATGGCTTGAAAAGCCATCGTTGAAACTATCTCAACCACAGAAACACTGGAAATACATTAAAAAAGGCTACCCCCCCTACCCCCCCATAATAATTTGCCCTACCCATGTATGGTTTACATTAATATACCCACCCCATATACATTATATCCATGCTAGGAAAACATA
TTTAATCCATGTACTATACACATAACAATGTATGTACTATAAGCATTATAATGTATGCAGCACGTCCATCAAACTTATACCCGGATATACTTAAACCAACAGACCATTTCTCCCACAAGGACAATTTAATCAATGATCTACGGACAAGCCTCCTAACTCCAAGTACTAAAACCA
GTTAAATGTTAGCTTATACCTACCTCAATCTCCCGAATACGACAGTGCTTGAACACATAACATTAATGGTATCCGGACAAACCATGCATCCTTTCTCGTAGTGCCTGCGTCTGAAGGACCAGGTTATCTATTAATCGTTCTTCTCACGTGAAATCAGCAACCCGCCGCATATAA
GACCCAACACGACCAGCTTCAGGACCATTCTTTCCCCCTACACCCCTAGCCCTACTTGCACTTTTGCGCCTCTGGTTCCTATATCAGGGCCATTCCTTGATTCATCCTCTCAACTTGCTCTTCACAGAAACATCTGGTAGGCTATATATTAGCATCTCACCCGTGATCGCGGCA
TCTGGATAGCCTTAGCACTTTTGGTTCCCTTTTTTTTTGGGGCGTCTTCACAGGTCACCCTTCCAGTGCGGCGGGAAATAACAATCTAAGACCTGAGCATACACTGCGTTGCGTCCTAATTTTGGCCCTCAAGAATTACTGAATGAGACGGTTTGCGTATATGGGGAATCATTT
TGACACTGATGCACTTGCTGTTACATTTGGTTATGGTATCCCCGCAAGCTCTAACTTATGTGGCTATTTAGTGAATGCTTGTTGGACATGTTTTCTTACCTTTACACTTCCTCTAACTTTTCAACCAACACTAGAGGCTTTTCGACCAAATACCTATCGTATGCTAGTCACGAA
TTTTATTCACACTTTTTTTACACAACATCACCGCTGAAATTACATTAACAAAAGAAAGAACCAACATGCACGCACACACCGGCGCGCAGCGCCAAAACTTTTAAAGAATATCCTAACTAACAACACCAACACAACACAACACAACACCACCAACACCAACCACCAACCACCAACAC
AACACAACACAAAACCACAAACAACAAACAACAAACAACAAACAACAAACAACAAACAACAAACAACAAACAACAAACAACAAACAACAAACAACAAACAACAAACAACAAACAACAAACAACAAACAACAAACAACAAACAACGCCAAATCGTT**GTTTTCGTAGCTTAACAAT**
AAAGCGTGGCACTGAAGATGCCAAGATGGCCTACCACATGCCCGATGACAAAAGACTTAGTCCTAACCTTACCGTTAATTCTTGCTAAACATATACATGCAAGTATCCGCGTCCCAGTGTAAATGCCCCTAATCTCTTACCAAGACAAAAGGAGCGGGTATCAGGCACACCCAC
GACTAGTAGCCCAAGACACCTTGCCCAGCCACACCCCCACGGGTACTCAGCAGTAATTAACATTAAGCAATAAGTGTAAACTTGACTTAGTTATAGCAATTATTCAGGGTTGGTAAATCTTGTGCCAGCCGCCGCGGTCATACAAGAGACCCAAATTAACCGTACACGGCGTAA
AGAGTGGGATTAGTACTATCACAGCAACTAAGATCAAAGCGCAACTAAGCCGTCATAAGCCCAAGATGCACCTAAGACCATCCTTAAGATGATCTTAGCGCCTCACGATTAATCAAACCCCACGAAAGCTTGGACACAAACTGGGATTAGATACCCCACTATGCCTGGCCCTAA
ATCTCGATGCTTAGCTCACCAAAGCATCCGCCTGAGAACTACGAGCACAAACGCTTAAAACTCTAAGGACTTGGCGGTGCCCCAAACCCACCTAGAGGAGCCTGTTCTATAATCGATAATCCACGATACACCCGACCGTTCCTTGCCAAAGCAGCCTACATACCGCCGTCGCCA
GCTCACCTTTCCTGAAAGCACAACAGTGGGCACAATAGCATTAACCTCGCTAACAAGACAGGTCAAGGTATAGCCCATGGGGCGGAAGAAATGGGCTACATTTTCTAAGTTAGAAAACTCCACGAAAAGAGGTGTGAAACCACCCCTAAAAGGCGGATTTAGTAGTAAAGTGGG
ATAATAGAGCCCCCTTTAAACTGGCCCTGGGGTACGTACATACCGCCCGTCACCCTCCTCACAAGCTCCAACTTCTTATAACTAATCCACCTATTAGCTGAAGATGAGGTAAGTCGTAACAAGGTAAGTGTACCGGAAG

Chrysolophus pictus (Galliformes/Phasianidae) mitogenome from CR1 to CR2 (MW151829)

GO-GA in Figure 8

CTATATAGTGAATGCTTGTCGGACATATTTTTACAAATTTTCACTTCCTCTATTTTCTCCACAAAACTAGGAGATTTACCACAATTTTTTCTTTGTTATTTTGTTATTTTTTTTAAAAACATTTTTAAAAAACTAAATTAAACTAAAACTACCGCATAAAAACCCTCAAACCAA
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TCAGGCACACCCATGAGTAGCCCAAAACACCTTGCCACAGCCACACCCCCACGGGTATTCAGCAGTAATTAACCTTAAGCAATAAGTGTAAACTTGACTTAGCCATAGCAATCCTCAGGGTTGGTAAATCTTGTGCCAGCCACCGCGGTCATACAAGAAACCCGAATCAATAGC
CAACCGGCGTAAAGAGTGGCCATATGTTATCCTCATTACCTAAGATCGAAGTGCAACTAAGCTGTCATAAGCCCAAGATCCACTTAAGGCCCCCTCCCAACCATCTTAGCCTAACGACTAATTTCACCCCACGAAAGCCAGGACACAAACTGGGATTAGATACCCCACTATGCC
TGGCCCTAAATCTAGATGCCTGCATACCCATGCATCCGCCCGAGAACTACGAGCACAAACGCTTAAAACTCTAAGGACTTGGCGGTGCCCCAAACCCACCTAGAGGAGCCTGTTCTGTAATCGATAGTCCACGATTCACCCAACCACCCCTTGCCAACACAGCCTACATACCGC
CGTCGCCAGCTCACCTAAAATGAAAGACCAACAGTGGGCCCAACAGTCATACCACTAGCAAGACAGGTCAAGGTATAGCCCATGGGGTGGAAGAAATGGGCTACATTTTCTAACATAGAATAAACGAAAAAGGGCGTGAGTTAGATGCCACAGCCAAAACCCCTAACATAAAAC
*AAACCCCAAGAAAAATCACAAAATAGGTCAT*ATATTCCCGCTTGGATAGACCCCAAGGACTACGGCTTGAAAAGCCATTGTTGTTCTCAACTACGGGAACAACAAACTTTTTTAACTCAACTCCCCTATTGAATGTACCCCCCCCTTCCCCCCCAGGGGGGGTATACTATGCAT
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AACTTCCAGGTCCCCATATTCATGAATGGTTACAGGACATACATGTAATACTAGGTATTTCCCCATTTGGTTATGCTCGACGTACCAGATGGATTTATTGATCGTACACCTCACGAGAGATCAGCAACCCCTGCCTGTAATGTACTCTATGACTAGCTTCAGGCCCATTCTTTC
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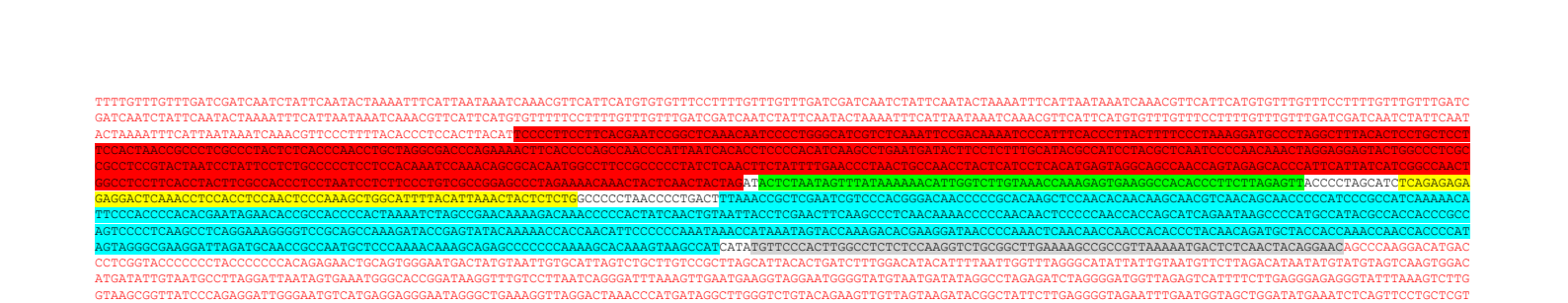
Ciconia nigra (Ciconiiformes/Ciconiidae) mitogenome from CR1 to CR2 (MH264509)

GO-FD in Figure 8

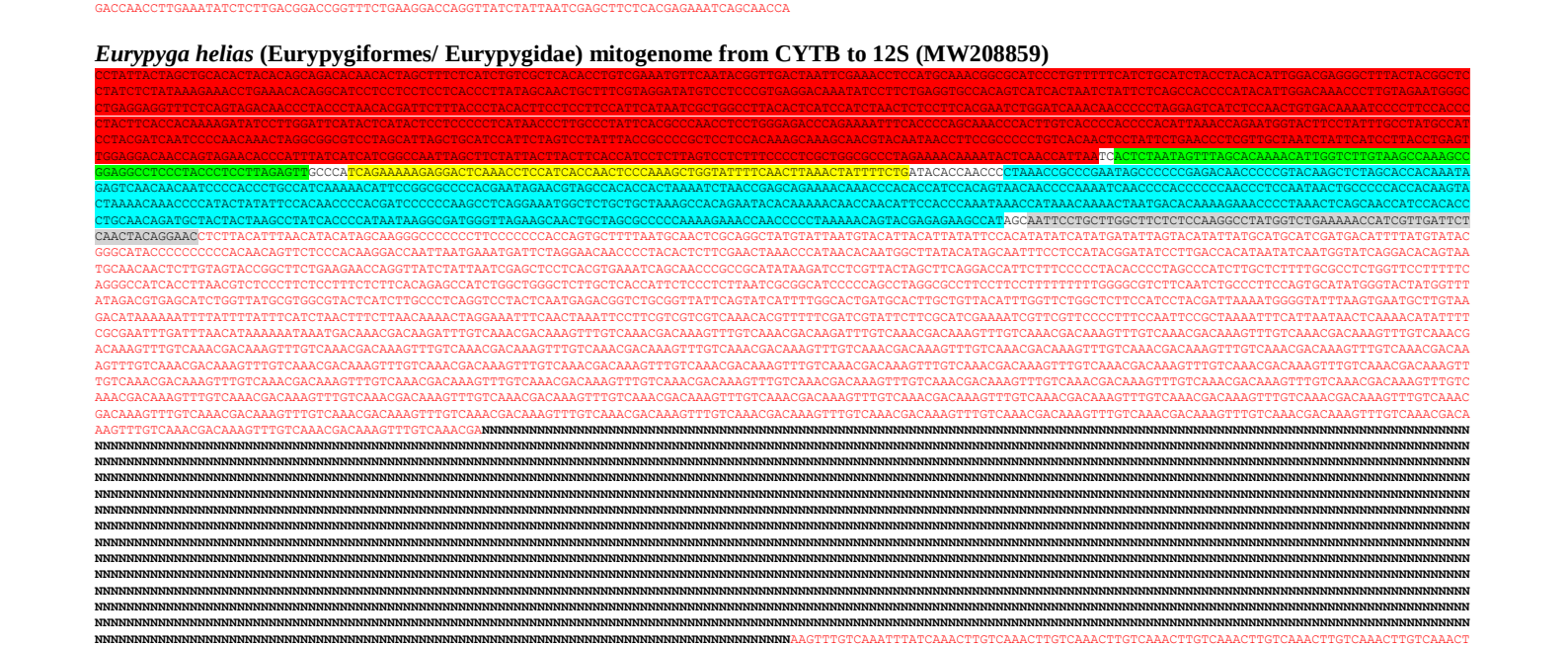
CTGAATGAGACGGTTGGCGTATATGGGGAATCATCTTAACACTGATGCACTTTGGTTTCCATTTAGTTATGGCGTATCCACAGACTCTTTAAAGTGTTACTATTTAGTGAATGCTTGTTGGACATGCTATTCTACTTTTACACTTCCTCTAACTTTCTAAACAACACTAGGAAC
TTTTACTTAAATCCATTTTTATCGTTCACACATATTTTCATTCGTTCTTTCATCGTTCGTTCGATCAATCTATTCAATACTAAAATTTCATTAATAAATCAAACGTTCATTCATGTGTTTGTTTCCTTTTGTTTGTTTGATCGATCAATCTATTCAATACTAAAATTTCATTAA
TAAATCAAACGTTCATTCATGTGTTTGTTTCCTTTTGTTTGTTTGATCGATCAATCTATTCAATACTAAAATTTCATTAATAAATCAAACGTTCATTCATGTGTGTTTCCTTTTGTTTGTTTGATCGATCAATCTATTCAATACTAAAATTTCATTAATAAATCAAACGTTCAT
TCATGTGTTTGTTTCCTTTTGTTTGTTTGATCGATCAATCTATTCAATACTAAAATTTCATTAATAAATCAAACGTTCATTCATGTGTTTTTCCTTTTGTTTGTTTGATCGATCAATCTATTCAATACTAAAATTTCATTAATAAATCAAACGTTCATTCATGTGTTTGTTTCC



Corythaixoides personatus (Musophagiformes/Musophagidae) mitogenome from CR1 to CR2 (MW082596)

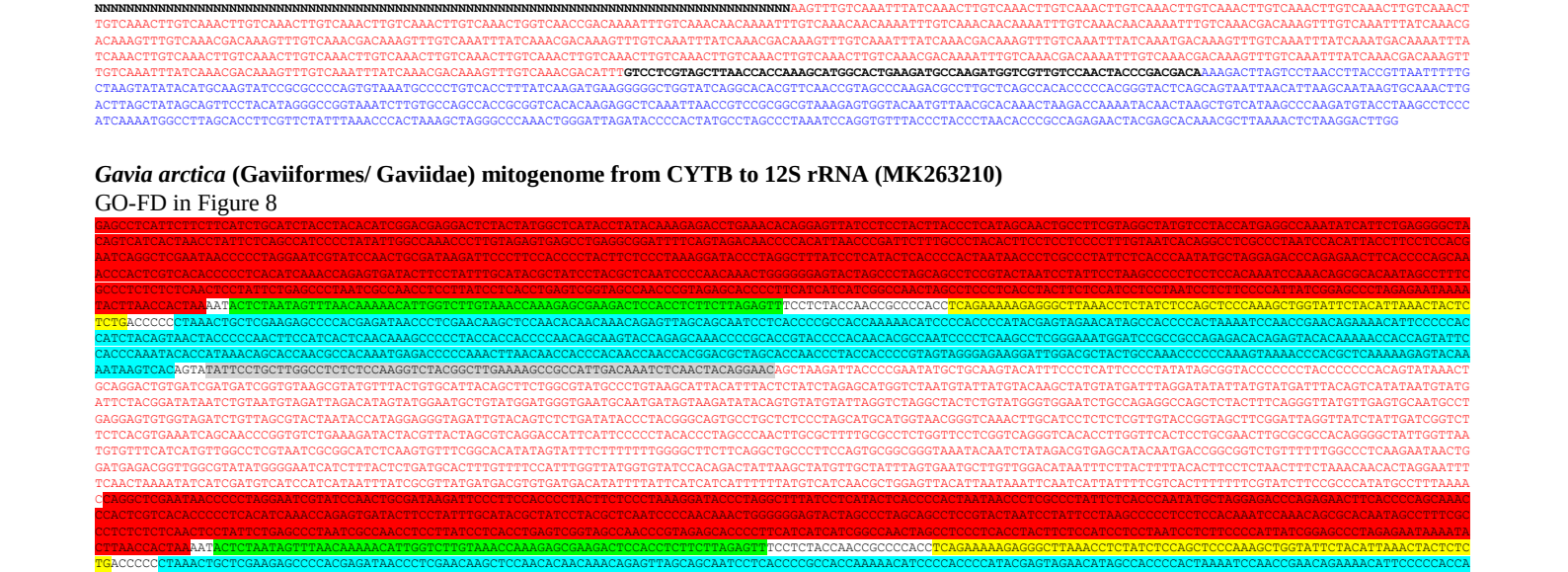
GO-FD in Figure 8

Eurypyga helias (Eurypygiformes/ Eurypygidae) mitogenome from CYTB to 12S (MW208859)



Gavia arctica (Gaviiformes/ Gaviidae) mitogenome from CYTB to 12S rRNA (MK263210)

GO-FD in Figure 8



Gavia stellata **(Gaviiformes/Gaviidae) mitogenome from CYTB to 12S rRNA (MK263209)**

GO-FD in Figure 8

[illegible]

Podiceps cristatus **(Podicipediformes/ Podicipedidae) mitogenome from Cytb to CR2 (MN629890)**

GO-FD in Figure 8

[illegible]

Podiceps grisegena **(Podicipediformes/Podicipedidae) mitogenome from ND6-1 to CR2 (MK263194)**

GO-FD in Figure 8

[illegible]

Scopus umbretta **(Pelecaniformes/Scopidae) mitogenome from CR1 to CR2 (MW151828)**

GO-NG in Figure 8

[illegible]

AATCCTCTCTCGACGTGCCGGTAGCTGTCGGACCAGGTTATCTATTAGTCGGTCTCCTCACGTGAAATCAGCAACCCGCCGCATATAAGATACTGCGTTACTAGCTTCAGGACCATTCTTTCCCCCTAAACCCCTAGCACAACTTGCACTTTTGCGCCTCTGGTTCCTTTTTCA
GGGCCATCACCCGTTTCCTCCCCTCTACTCGCTCTTCACCGATACATCTGGTTGGCTATATATCAC

Spheniscus demersus (Sphenisciformes/Spheniscidae) mitogenome from CR1 to CR2 (MH264510)

GO-FD in Figure 8

ATACTATTGGTTGACATGAGCATCACATGGGTCACGGTCGTTCCTAGCCTTCAAGAATACCTGAATGAGACGGTTTGAGGTATTAGGGGAATCATCTTAACACTGATGCACTTTGGTTTGCATTTAGTTATGGTGTATTTACTTGCTTTTAGATATGTTGCTATTTGTTGAATG
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GCCATAACTTGAATAACTCCTTCTATCTTGCTCTTCACAGAGCCATTTGGTTGATGTGTTTCATCATTTTCGTC

Uria aalge (Charadriiformes/Alcidae) mitogenome from CR1 to CR2 (MK263188)

GO-FD in Figure 8

TAACTTGGTTAGTCCTCTCAACTTGTACTTCACCGATACATCTGGTCGGCTATATATCACCATCTCACCCGTGATCGCGACATCCGACCGTTTTGGCACTTTTGGTTCCTTTTTTTTTTTTTACGTCTTCAATAAACCCTTCCAGTGCACCGAGGTACACACAATCTAAGACCT
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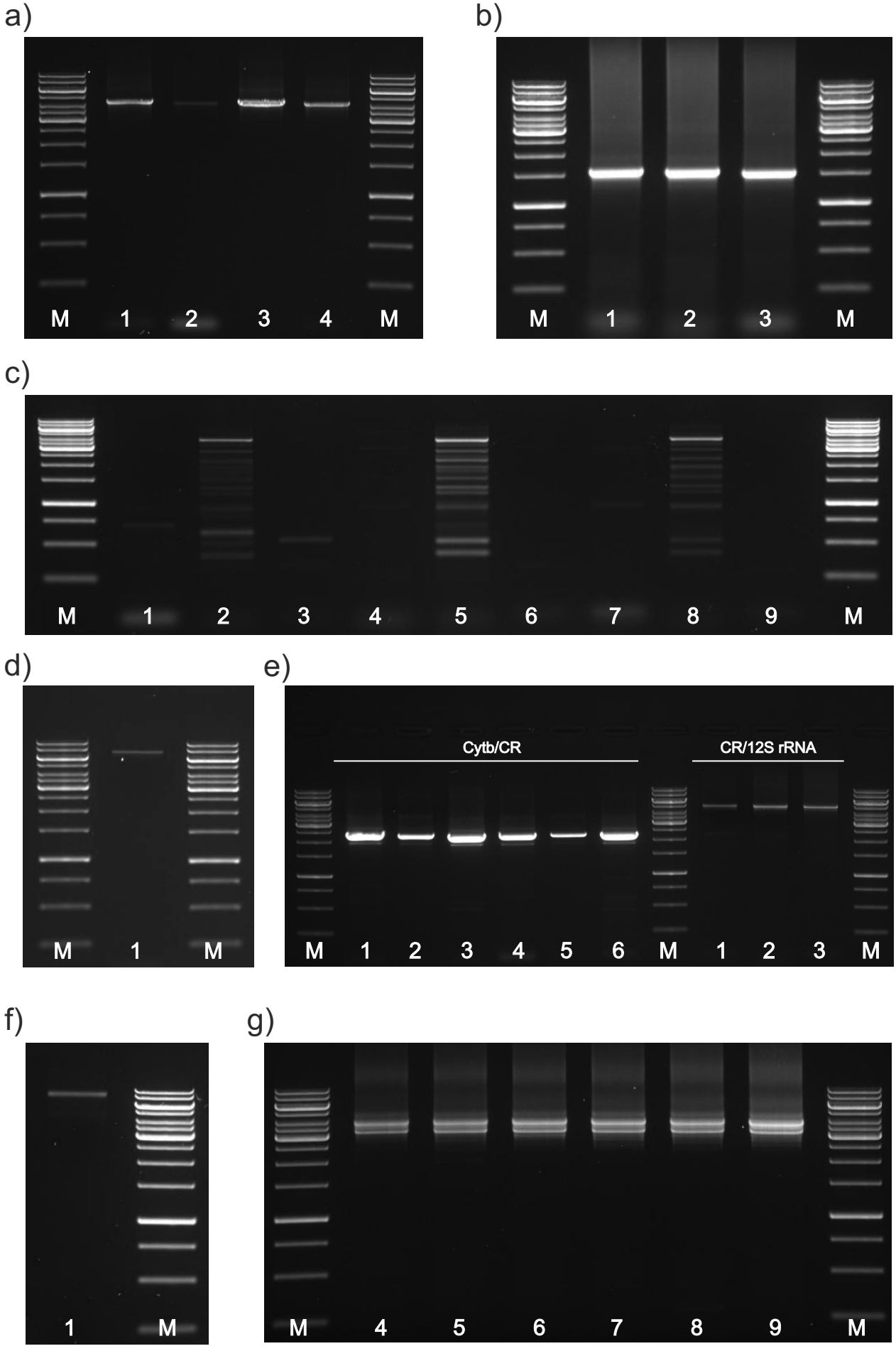


Figure S11. Representative cropped agarose gels of the following amplicons: *cytb*/12S rRNA obtained *for Rhynochetos jubatus* (a), *Eurypyga helias* (d) and *Trogon collaris* (f); CR1/CR2 obtained for *Rhynochetos jubatus* (c) and *Trogon collaris* (g); CR/12S rRNA obtained for *Rhynochetos jubatus* (b) and *Eurypyga helias* (e); *cytb*/CR obtained for *Eurypyga helias* (e). The numbering of amplicons separated in the agarose gel corresponds to the reaction numbered in Table S9. Lane M - GeneRuler 1 kb DNA Ladder (Thermo Scientific).

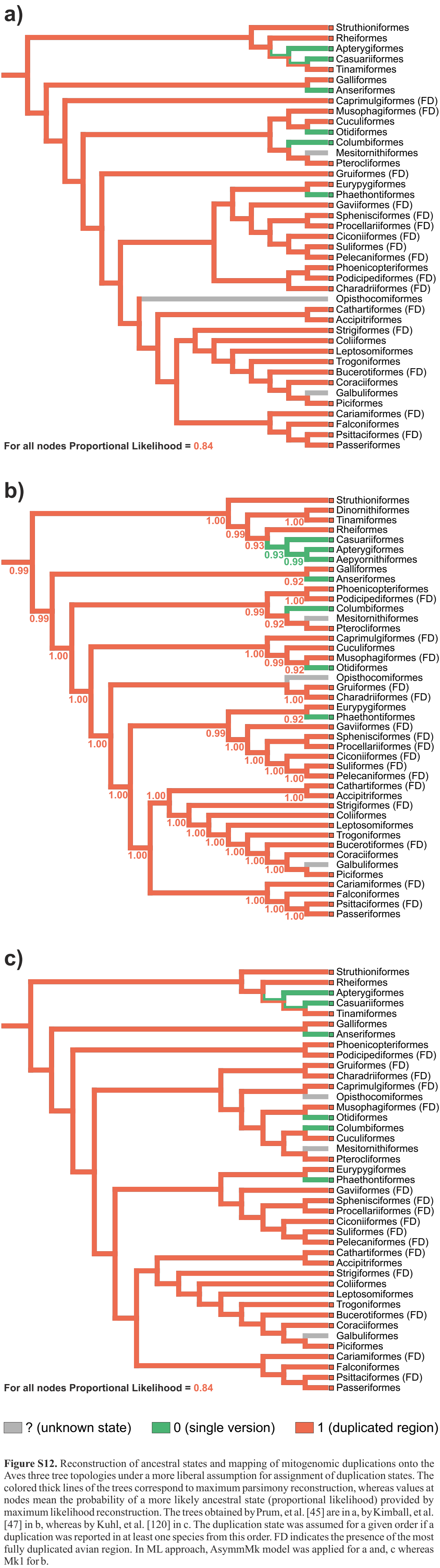
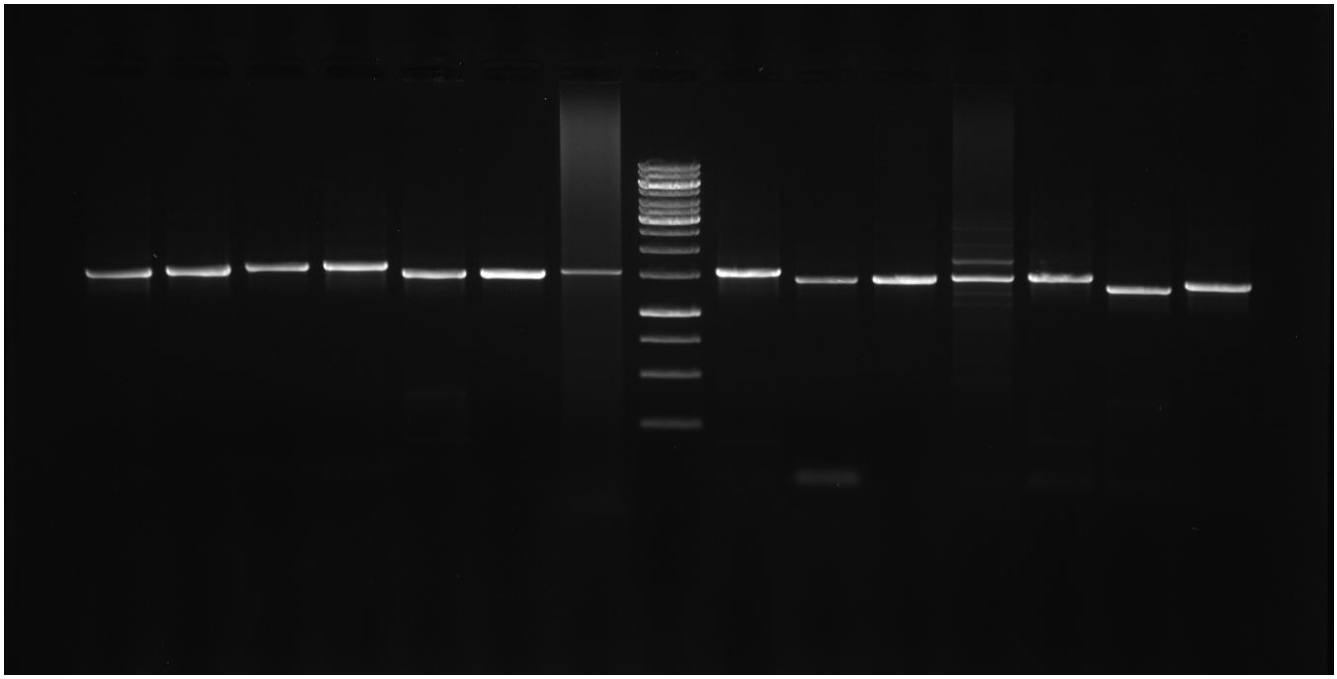


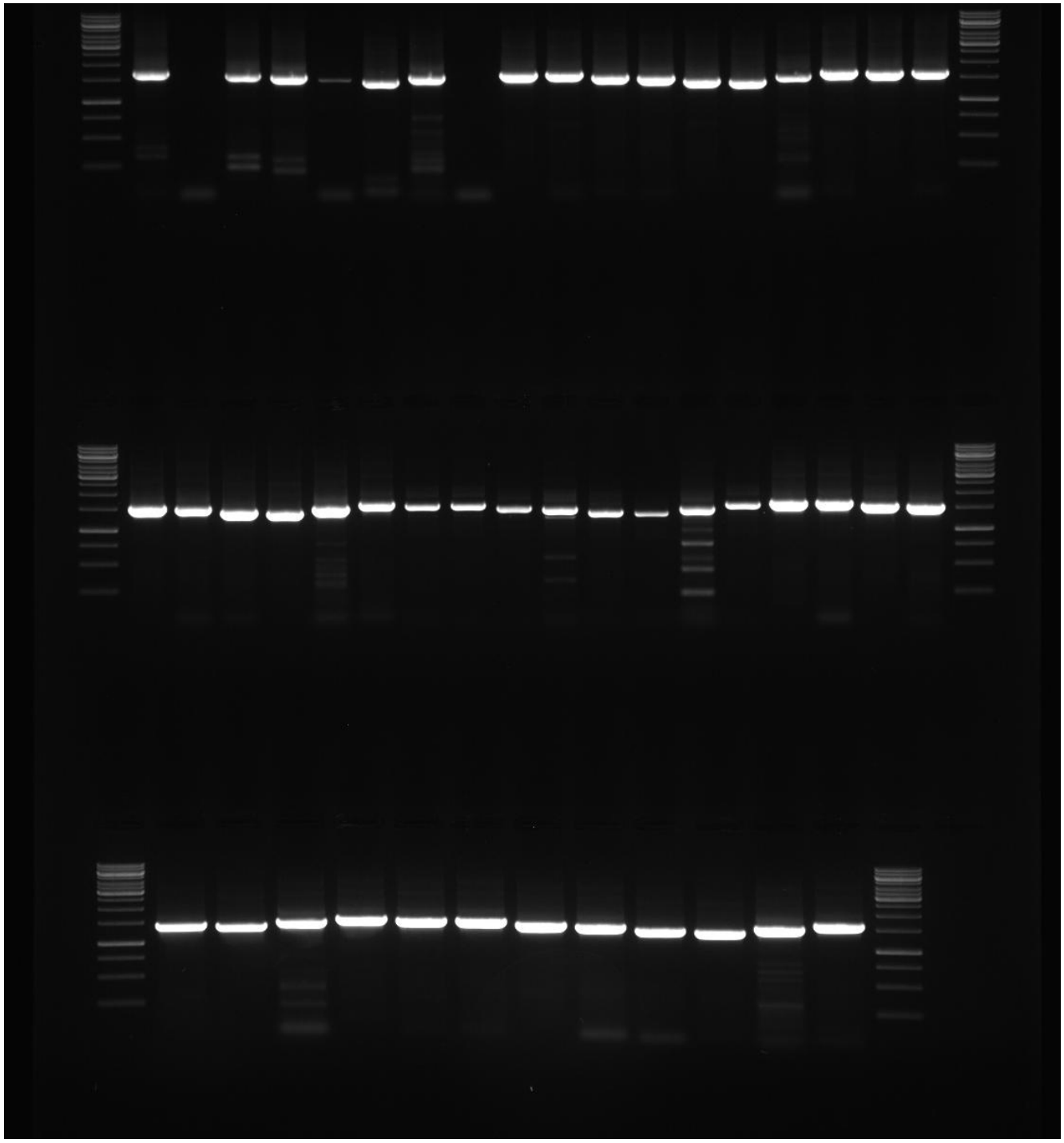
Figure S12. Reconstruction of ancestral states and mapping of mitogenomic duplications onto the Aves three tree topologies under a more liberal assumption for assignment of duplication states. The colored thick lines of the trees correspond to maximum parsimony reconstruction, whereas values at nodes mean the probability of a more likely ancestral state (proportional likelihood) provided by maximum likelihood reconstruction. The trees obtained by Prum, et al. [45] are in a, by Kimball, et al. [47] in b, whereas by Kuhl, et al. [120] in c. The duplication state was assumed for a given order if a duplication was reported in at least one species from this order. FD indicates the presence of the most fully duplicated avian region. In ML approach, AsymmMk model was applied for a and, c whereas Mk1 for b.

Figure S13. Original uncropped and unprocessed agarose gels of: CR1/CR2 amplicons obtained for *Struthio camelus* (a), which were also shown in the Fig. S1a; CR1/CR2 amplicons obtained for *Rhea pennata* (b) which were also shown in the Fig. S1b; CR1/CR2 amplicons obtained for *Rhea americana* (7 lanes to the left of DNA Ladder) (c), which were also shown in the Fig. S1c; CR1/CR2 amplicons obtained for *Crypturellus tataupa* (6 lanes to the right of the DNA Ladder) (d), which were also shown in the Fig. S1d; potential NUMTs amplified for *Dromaius novaehollandiae* (e), which were also shown in the Fig. S4a; potential NUMTs amplified for *Casuarius casuarius* (f), which were also shown in the Fig. S4b; *cytb*/*12S rRNA* amplicons obtained for *Rhynochetos jubatus* (g), which were shown in the Fig. S11a; CR/*12S rRNA* amplicons obtained for *Rhynochetos jubatus* (h), which were shown in the Fig. S11b; CR1/CR2 amplicons (potential NUMTs) obtained for *Rhynochetos jubatus* (i), which were shown in the Fig. S11c; *cytb*/*12S rRNA* amplicon obtained for *Eurypyga helias* (j), which was shown in the Fig. S11d; *cytb*/CR and CR/*12S rRNA* amplicons obtained for *Eurypyga helias* (k), which were shown in the Fig. S11e; *cytb*/*12S rRNA* amplicon obtained for *Trogon collaris* (the first lane prior the first DNA Ladder) (l), which was shown in the Fig. S11f; CR1/CR2 amplicons obtained for *Trogon collaris* (m), which were shown in the Fig. S11g.

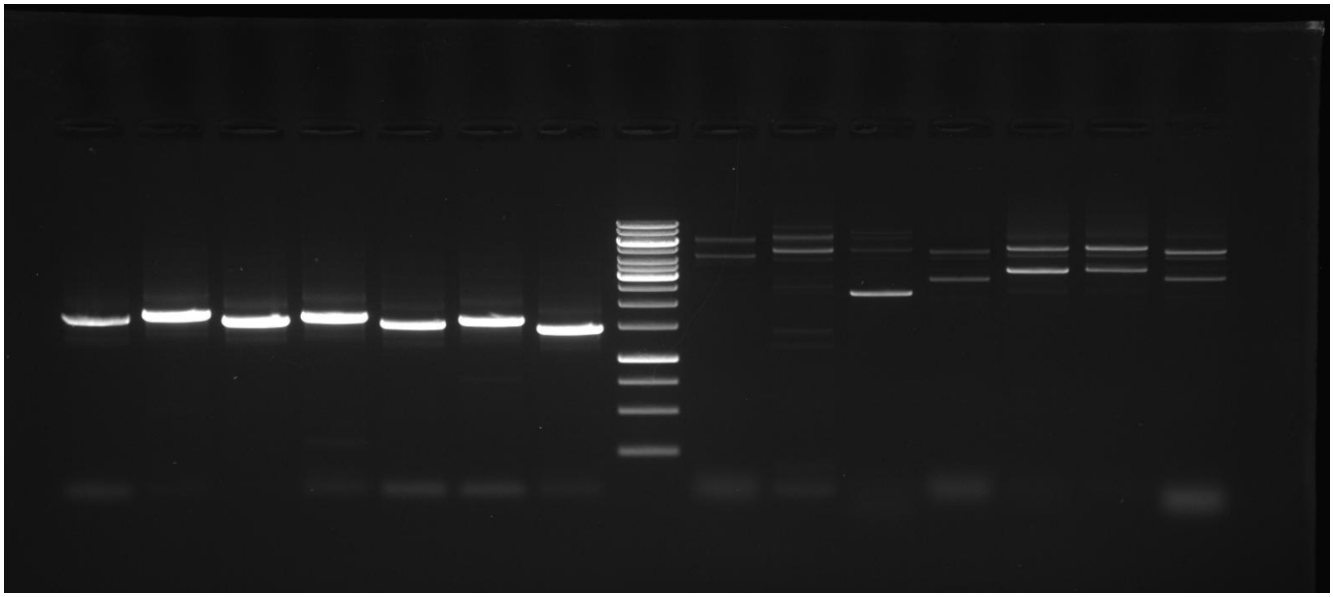
a)



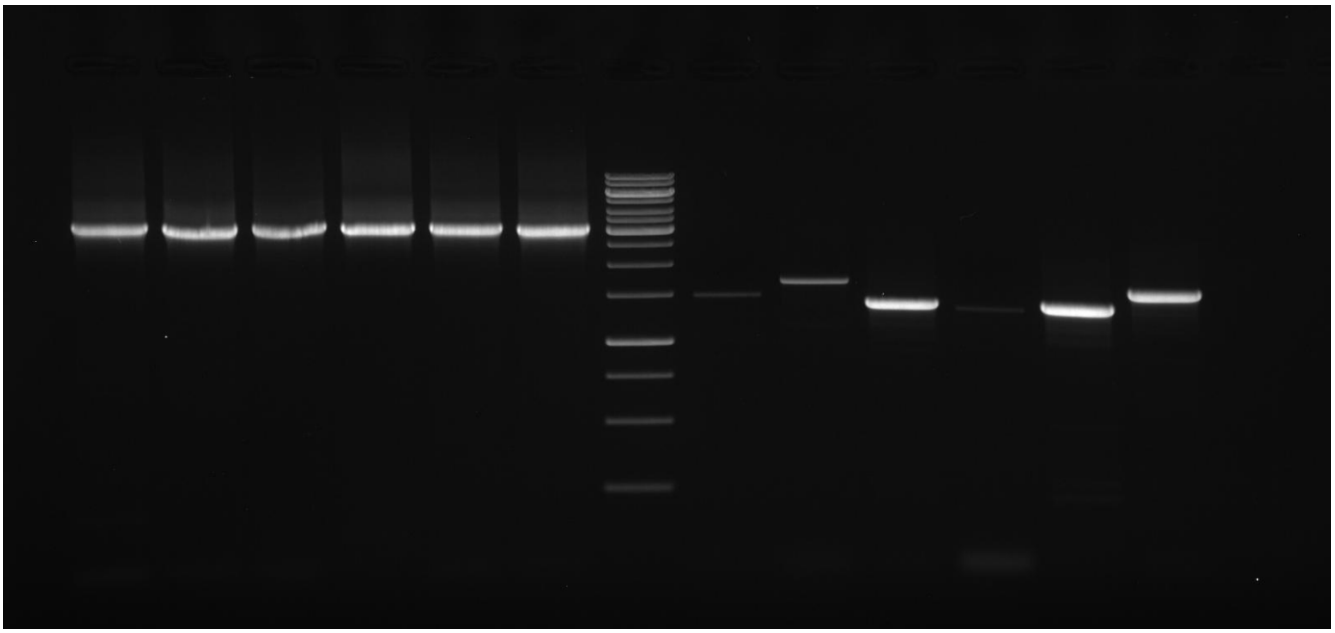
b)



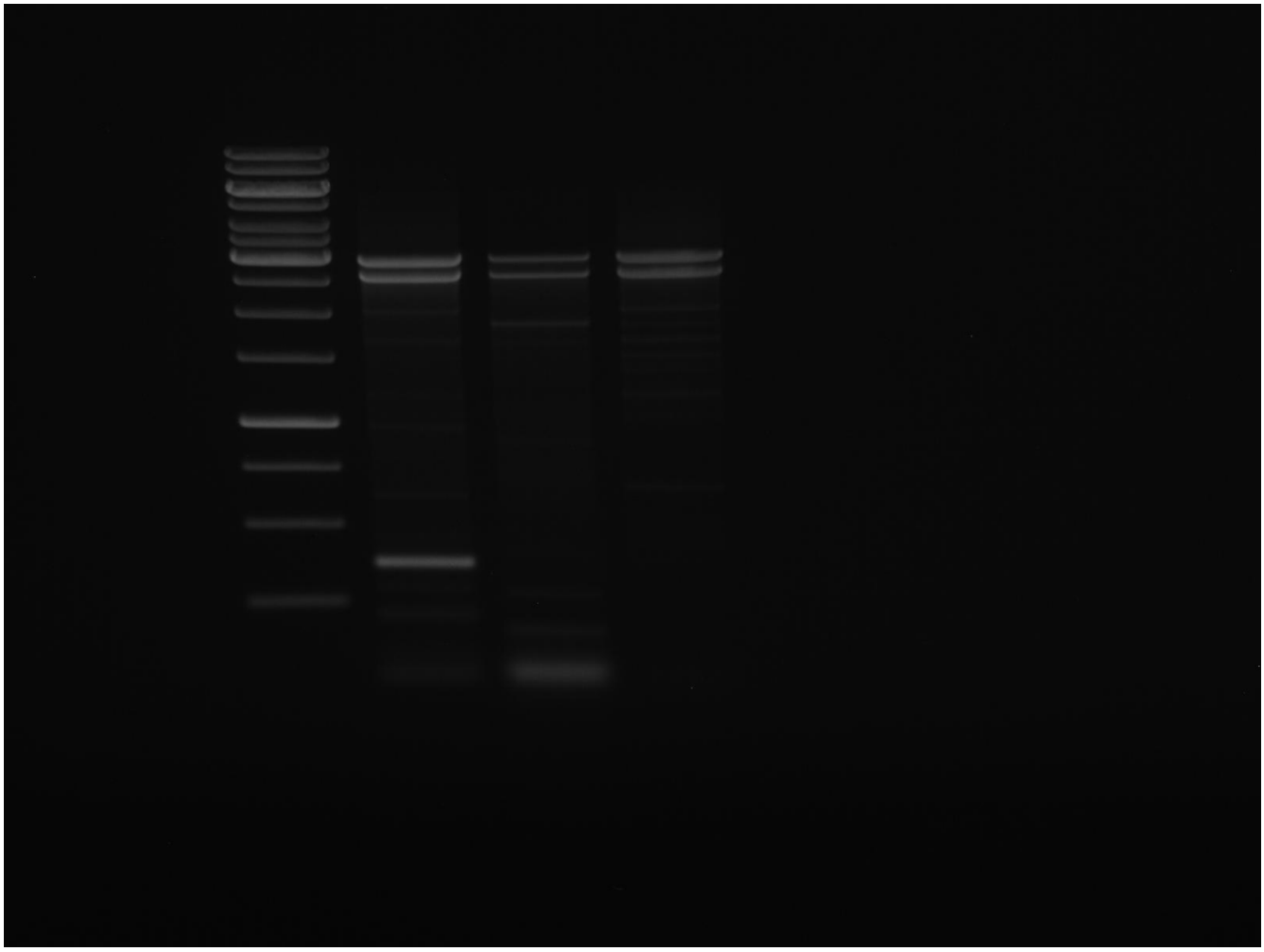
c)



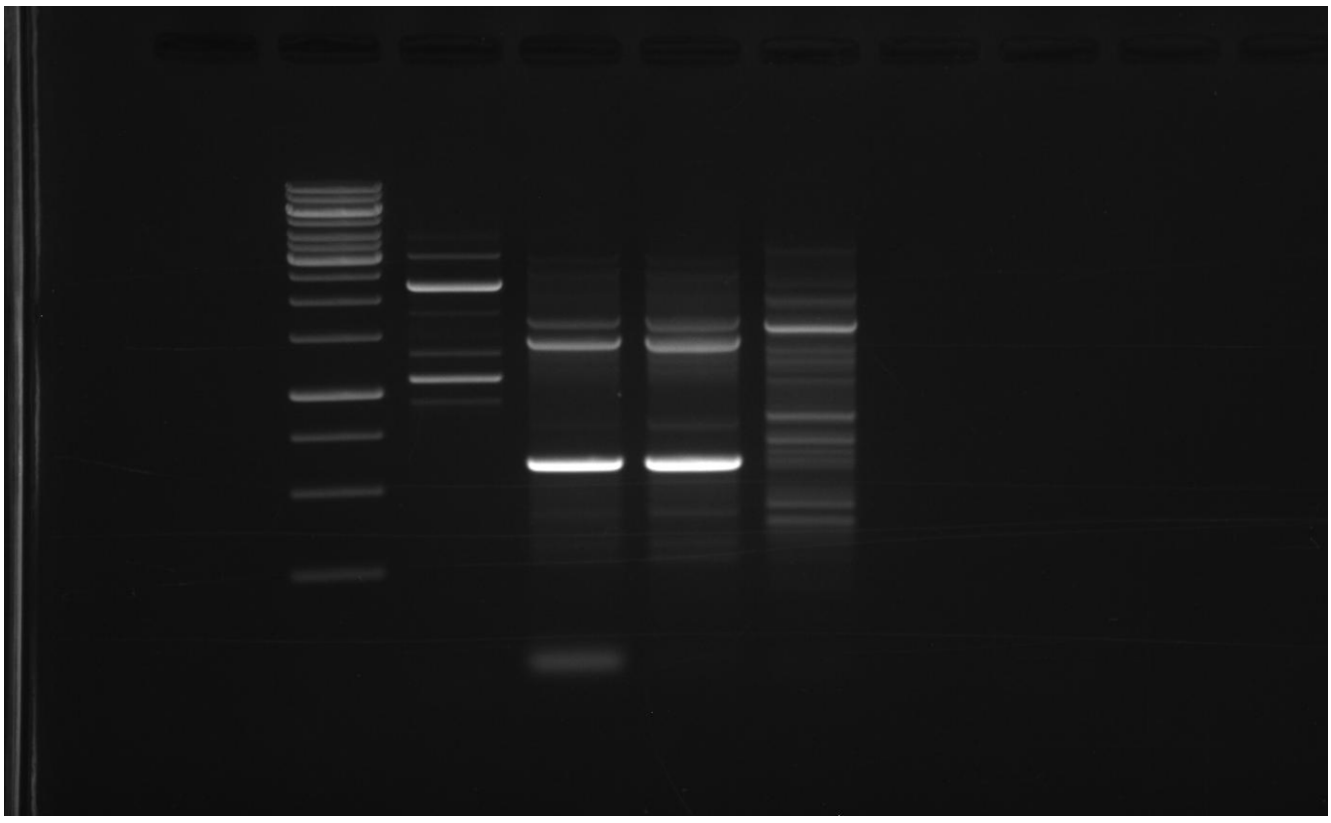
d)



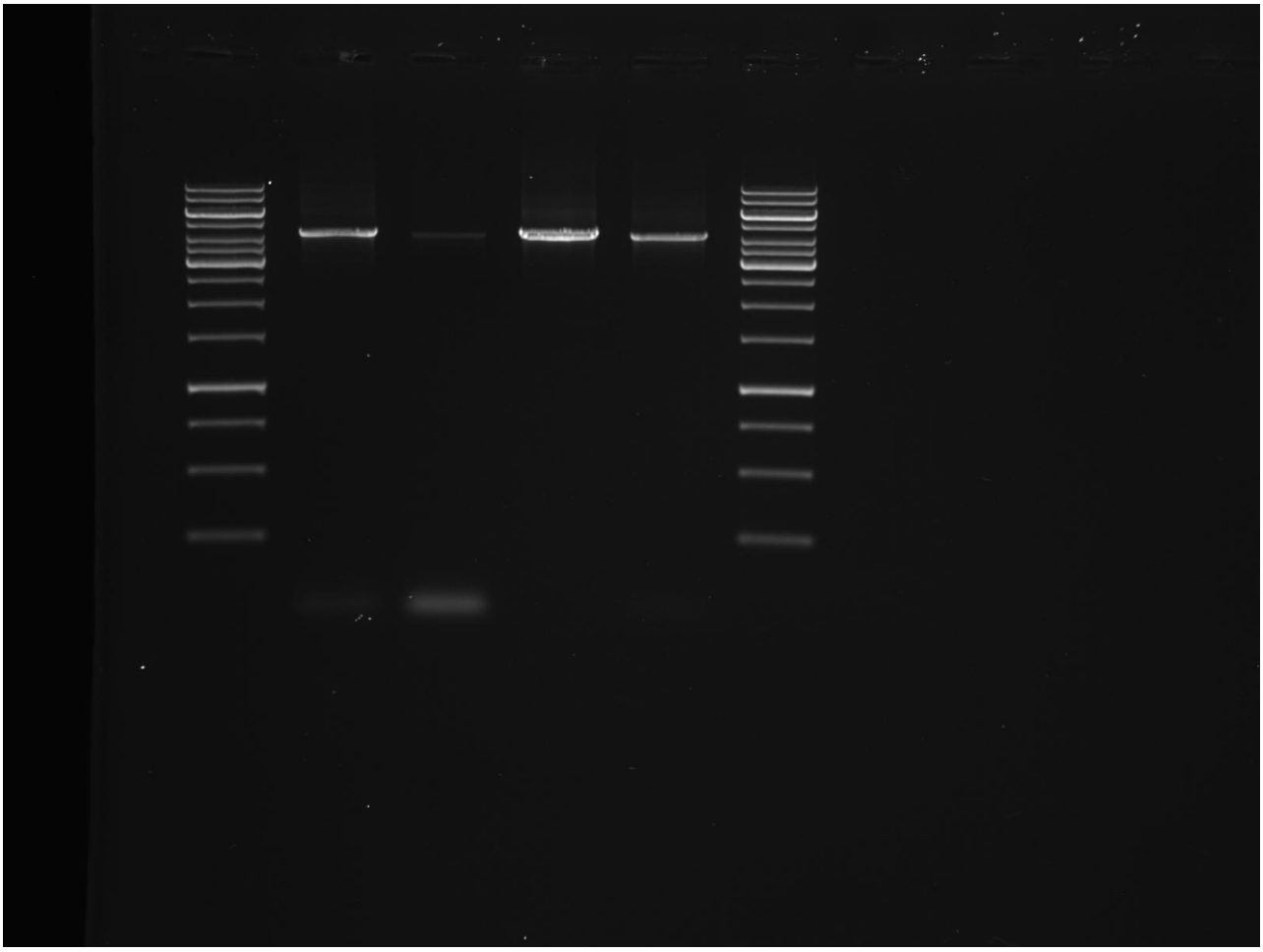
e)



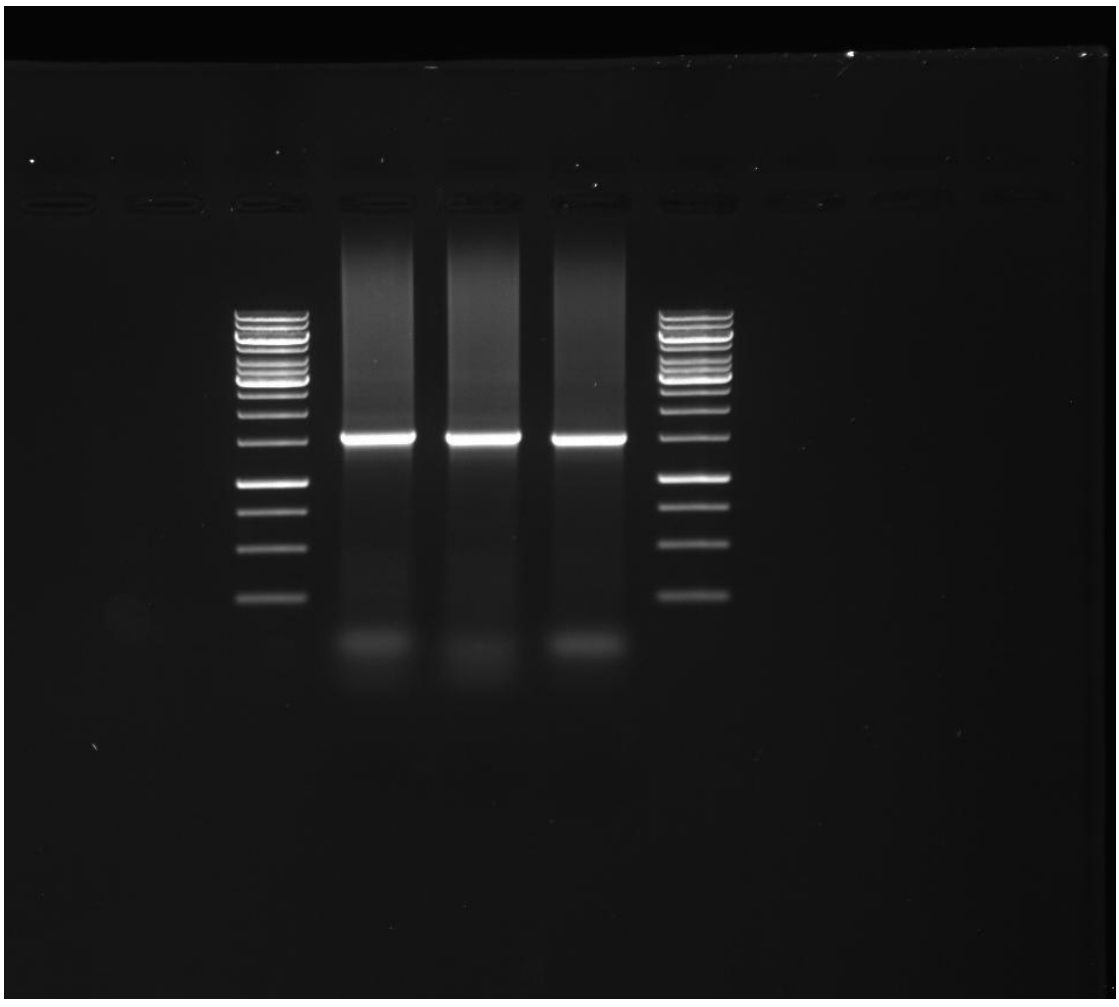
f)



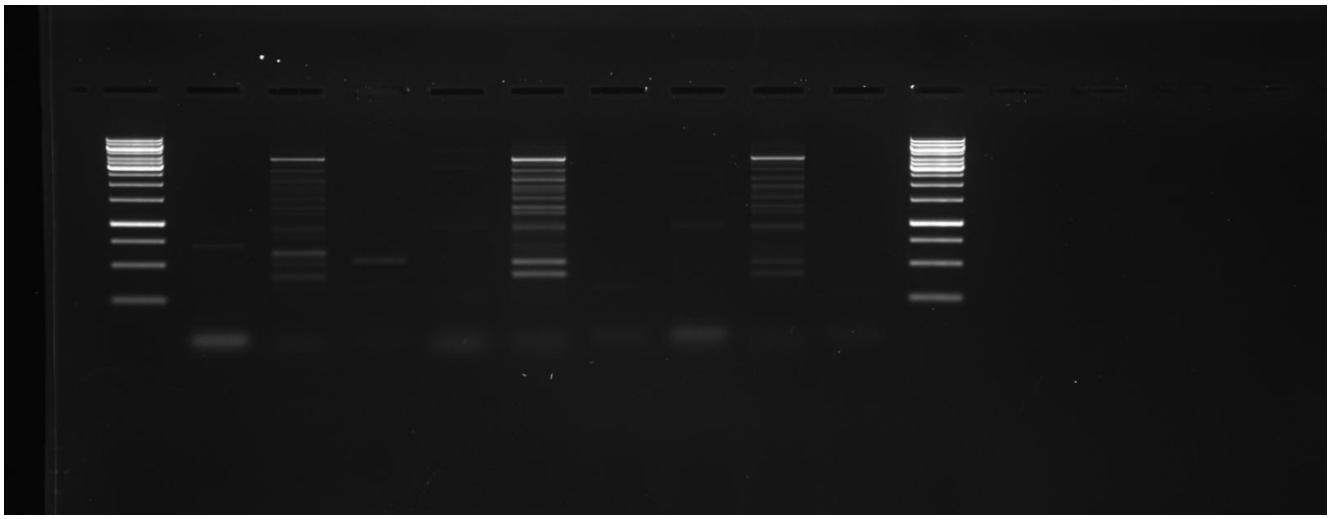
g)



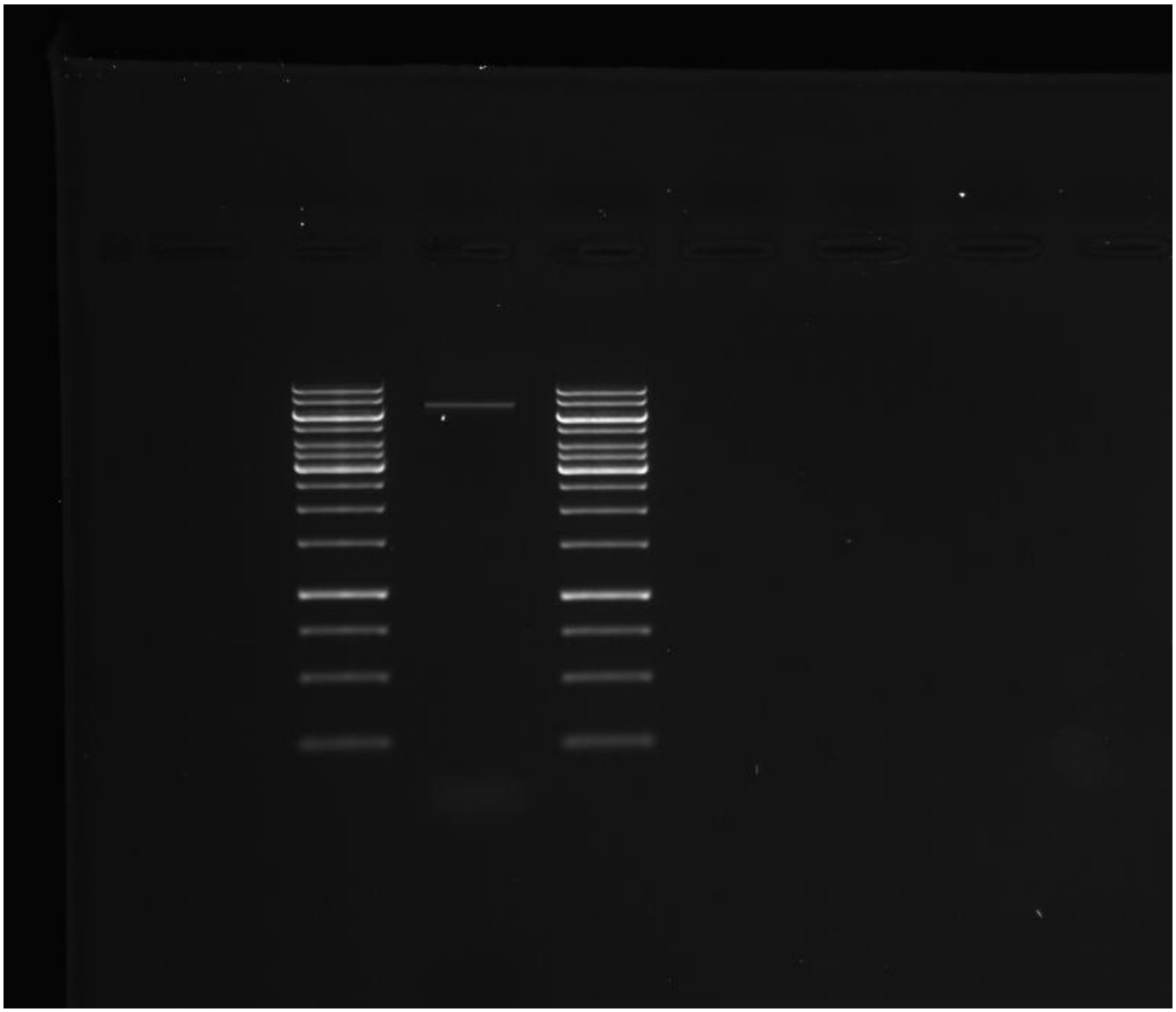
h)



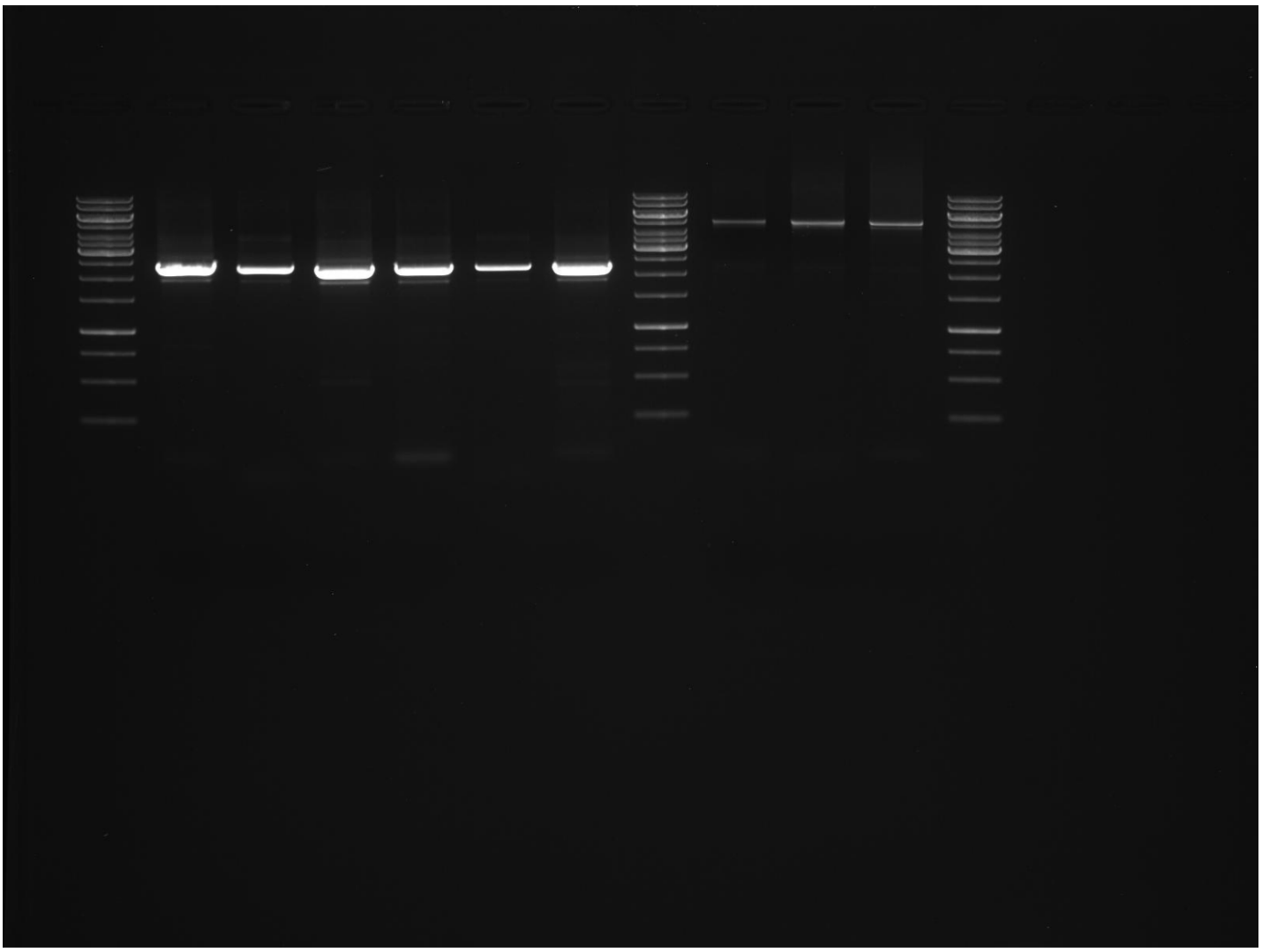
i)



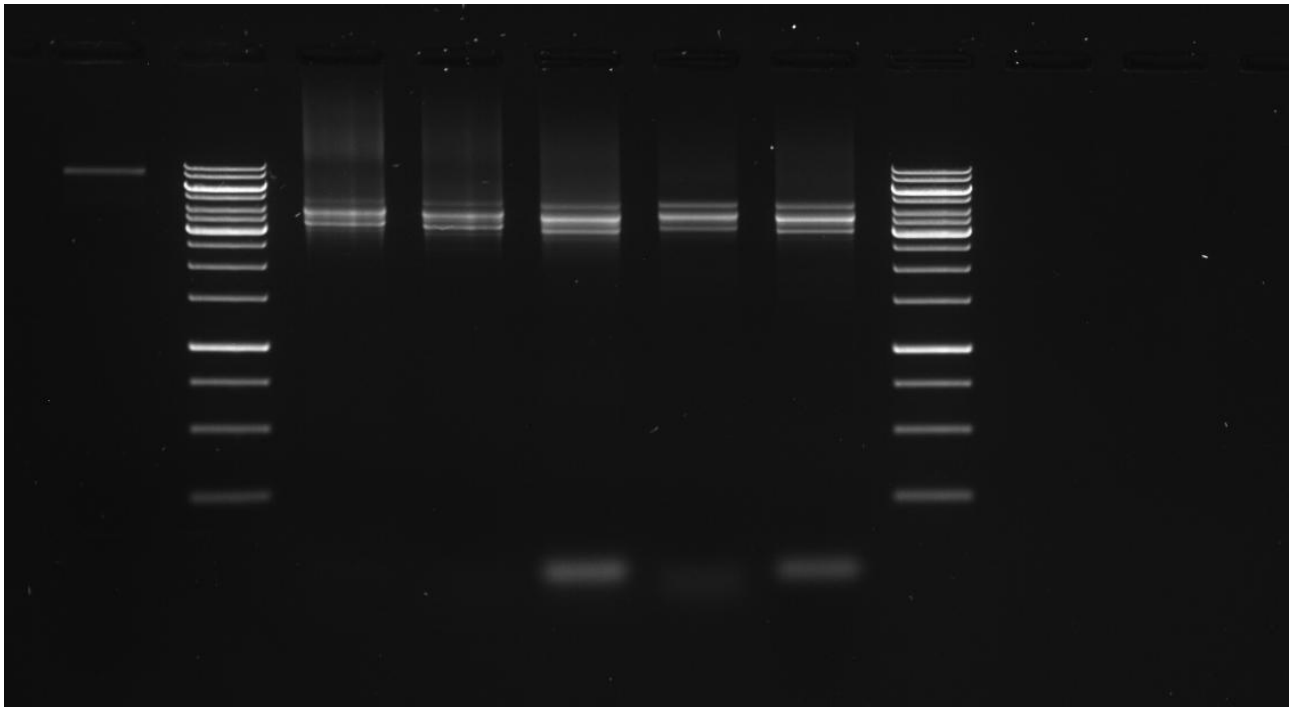
j)



k}



l)



m)