

Figure S198

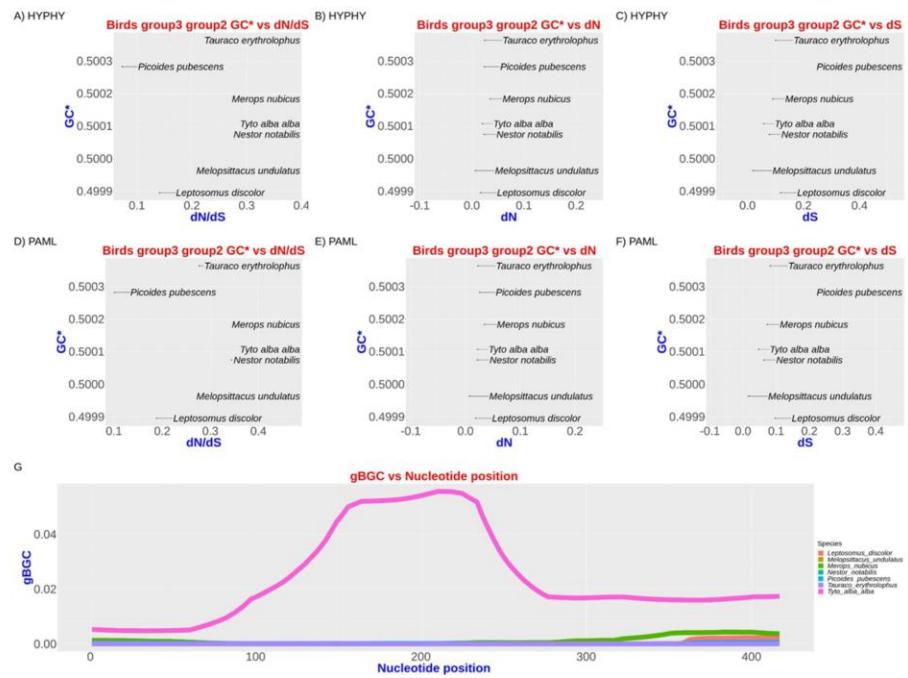


Figure S198: Values of GC* in birds are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S199

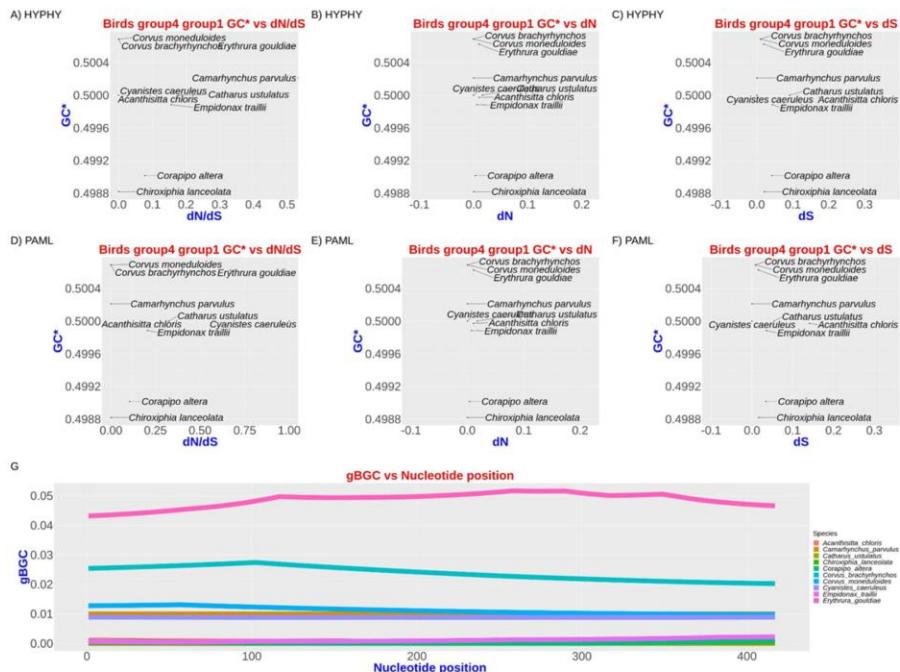


Figure S199: Values of GC* in birds are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S200

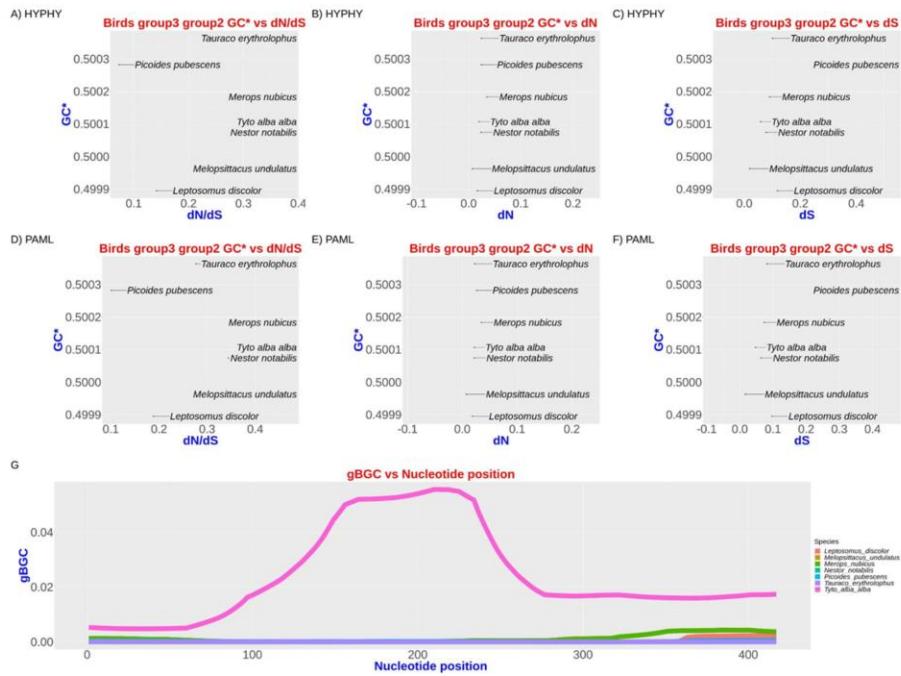


Figure S200: Values of GC* in birds are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S201

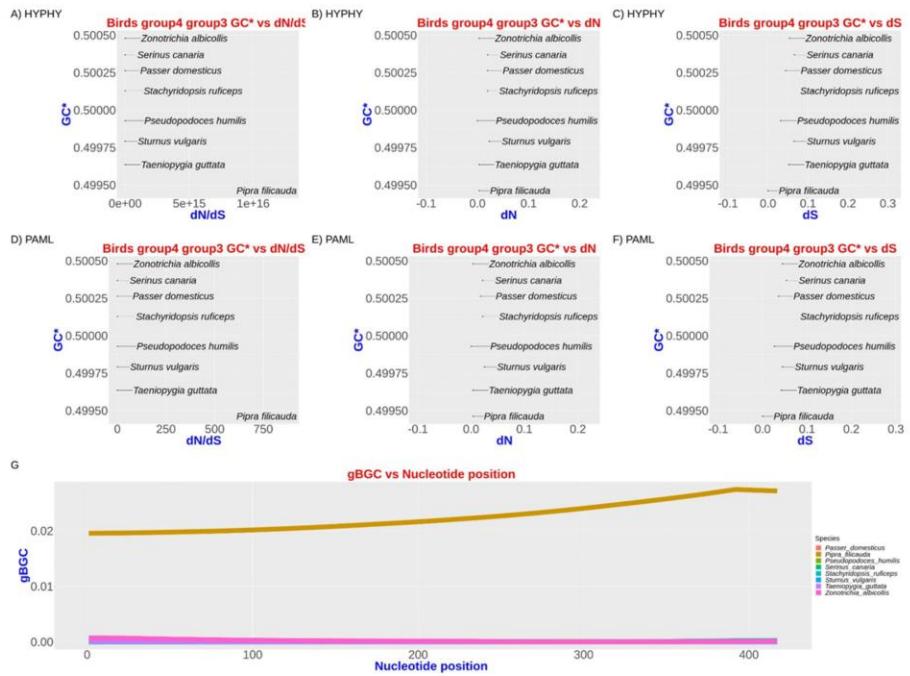


Figure S201: Values of GC* in birds are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S202

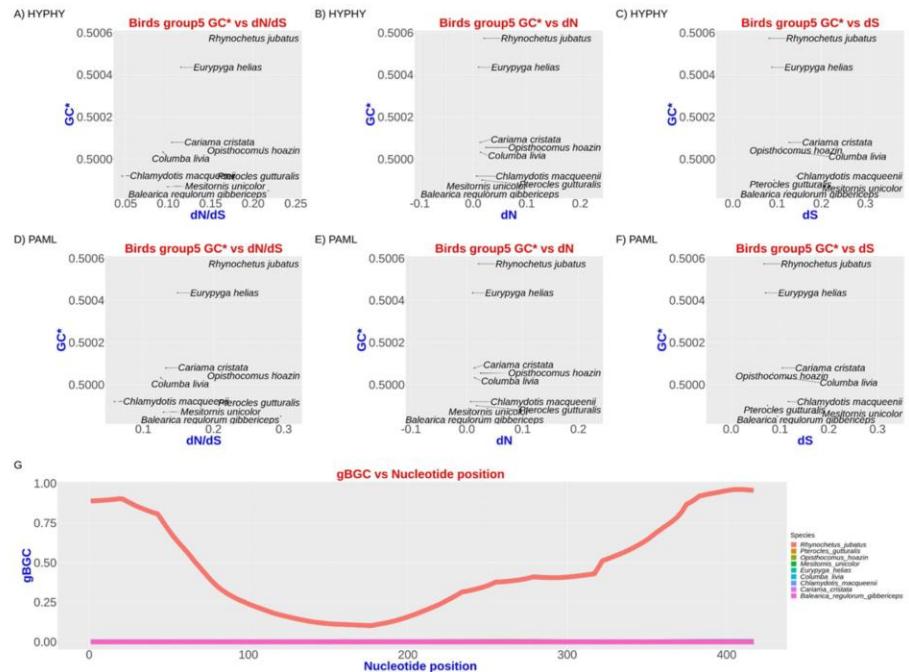


Figure S202: Values of GC* in birds are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias. *Rhynochetus jubatus* has a significant gBGC in *COA1*.

Figure S203

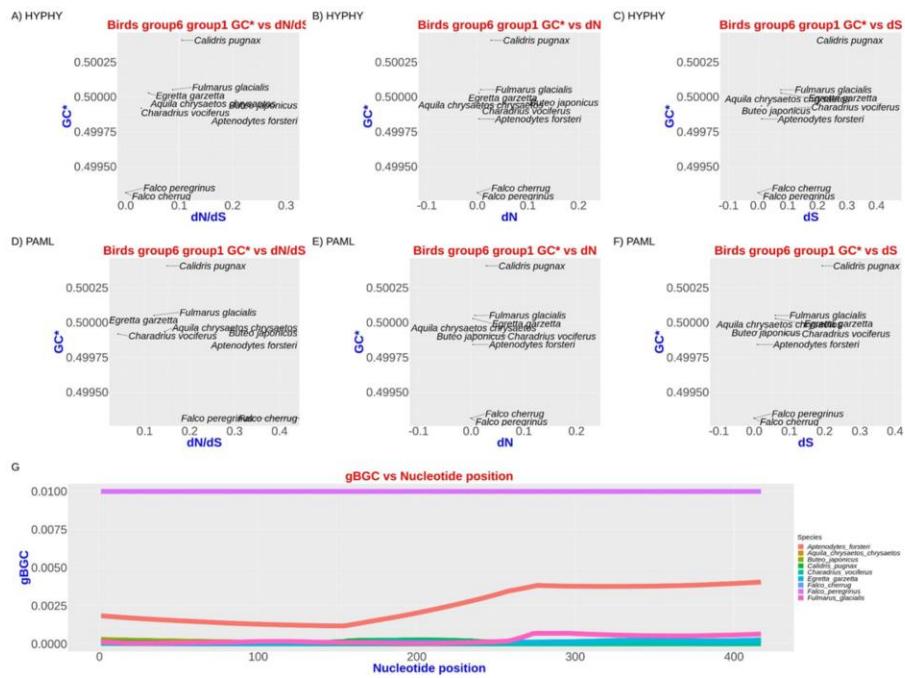


Figure S203: Values of GC* in birds are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S204

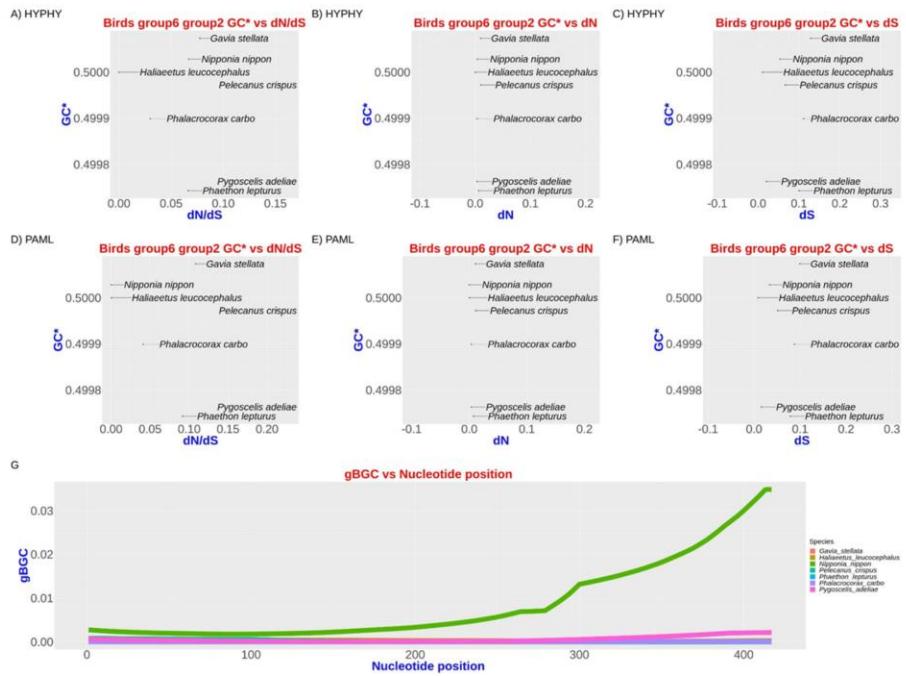


Figure S204: Values of GC* in birds are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S205

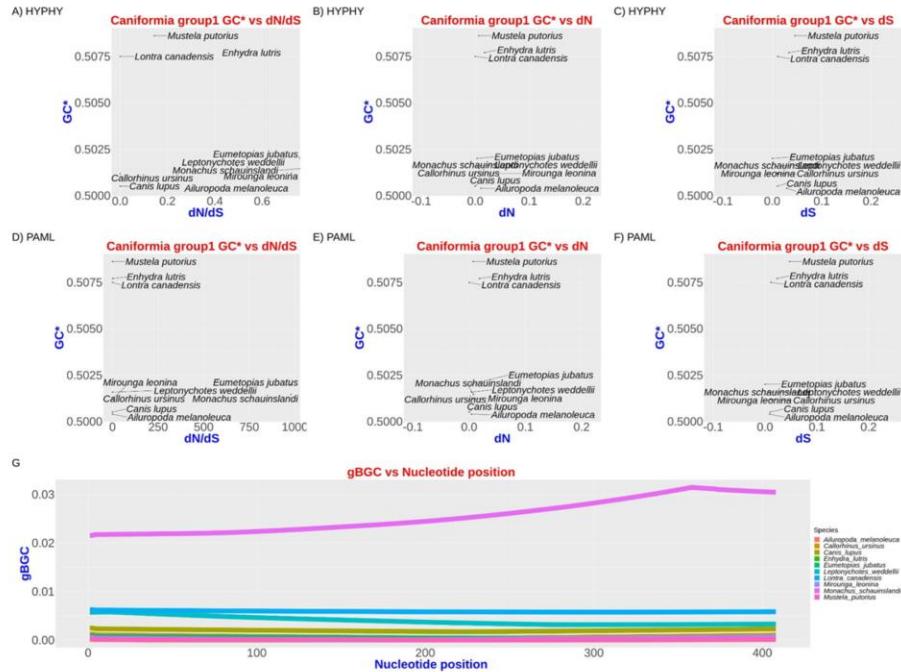


Figure S205: Values of GC* in Caniformia are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S206

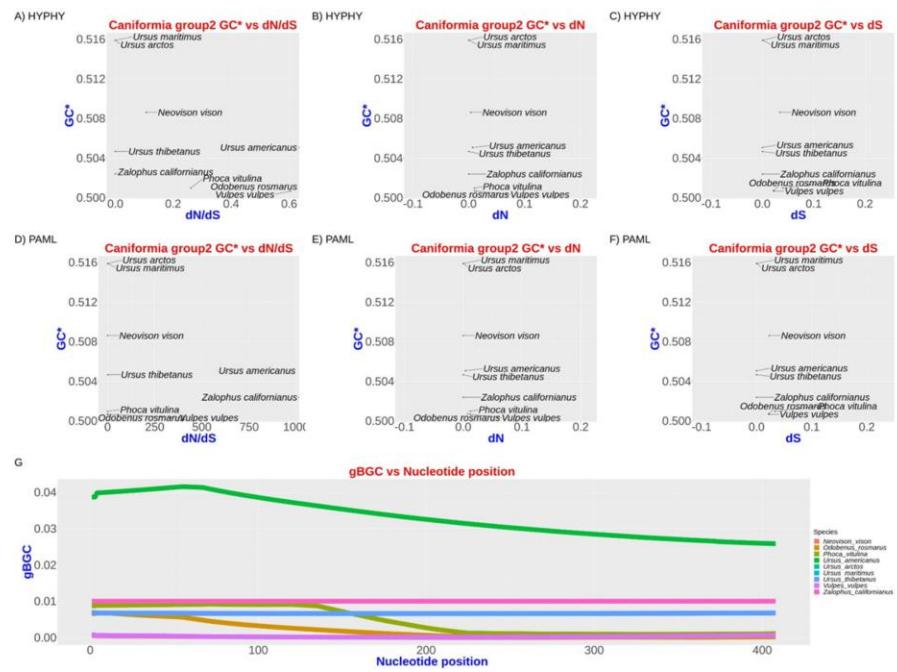


Figure S206: Values of GC* in Caniformia are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S207

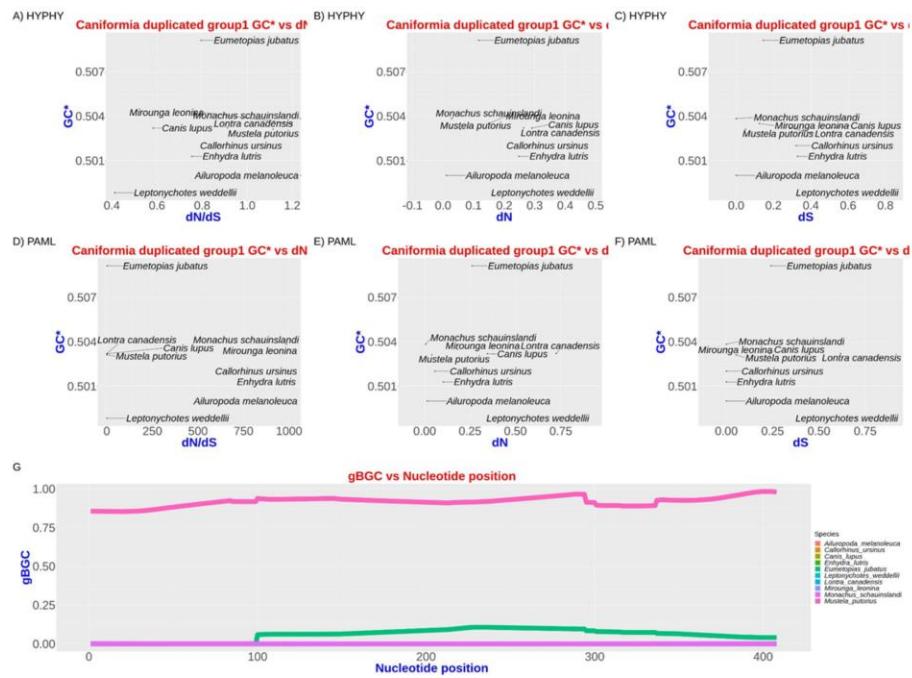


Figure S207: Values of GC* in Caniformia duplicated *COA1* are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias. *Mustela putorius* has a significant gBGC across *COA1*.

Figure S208

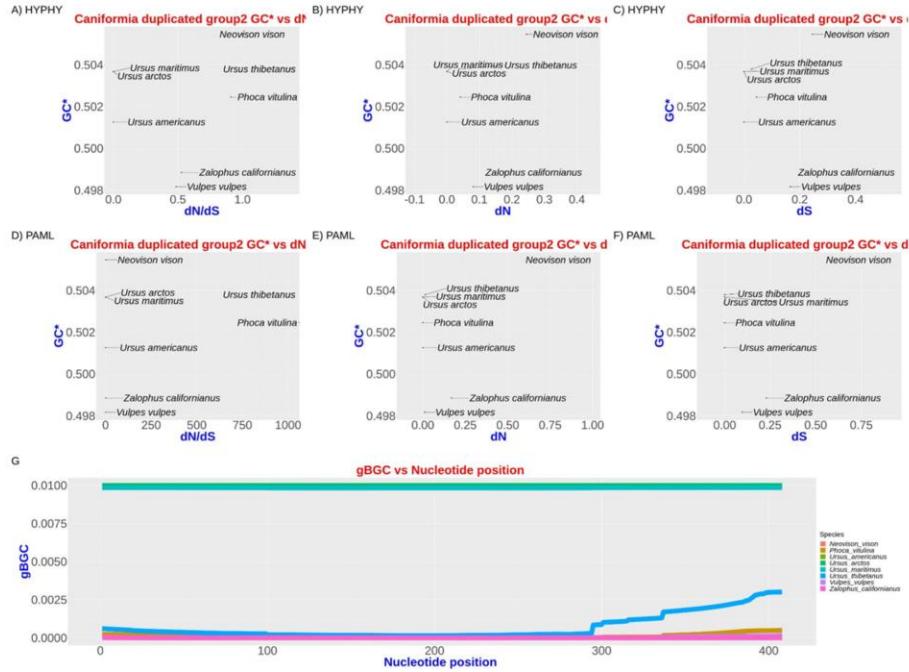


Figure S208: Values of GC* in Caniformia duplicated *COA1* are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S209

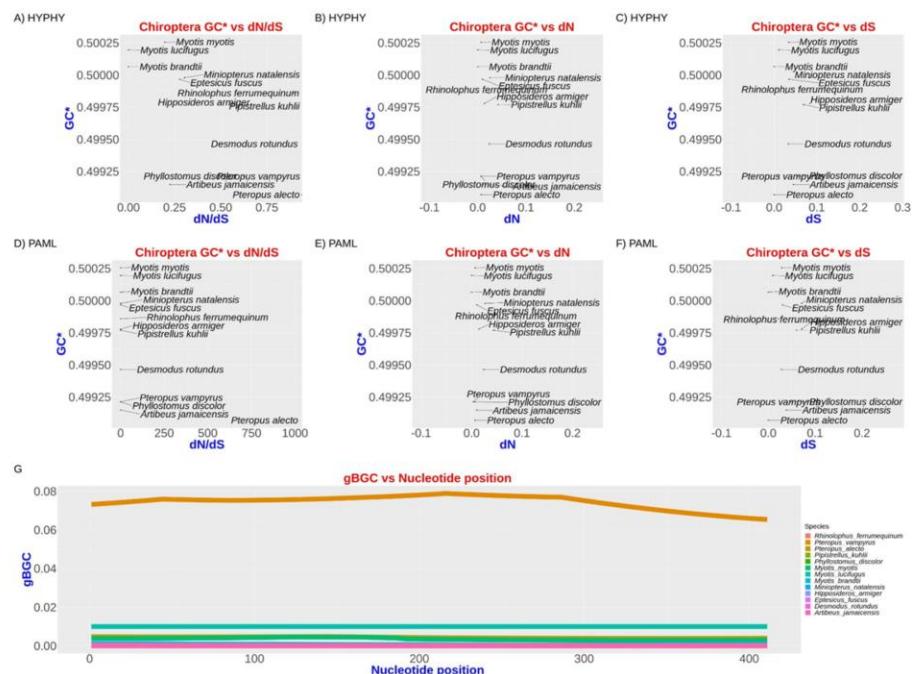


Figure S209: Values of GC* in Chiroptera are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S210

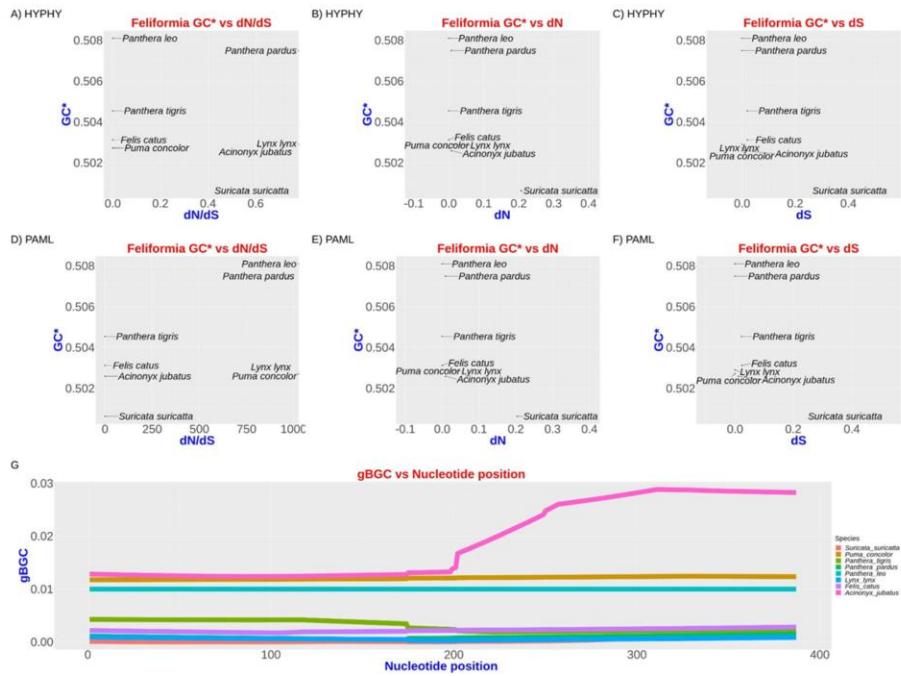


Figure S210: Values of GC* in Feliformia are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S211

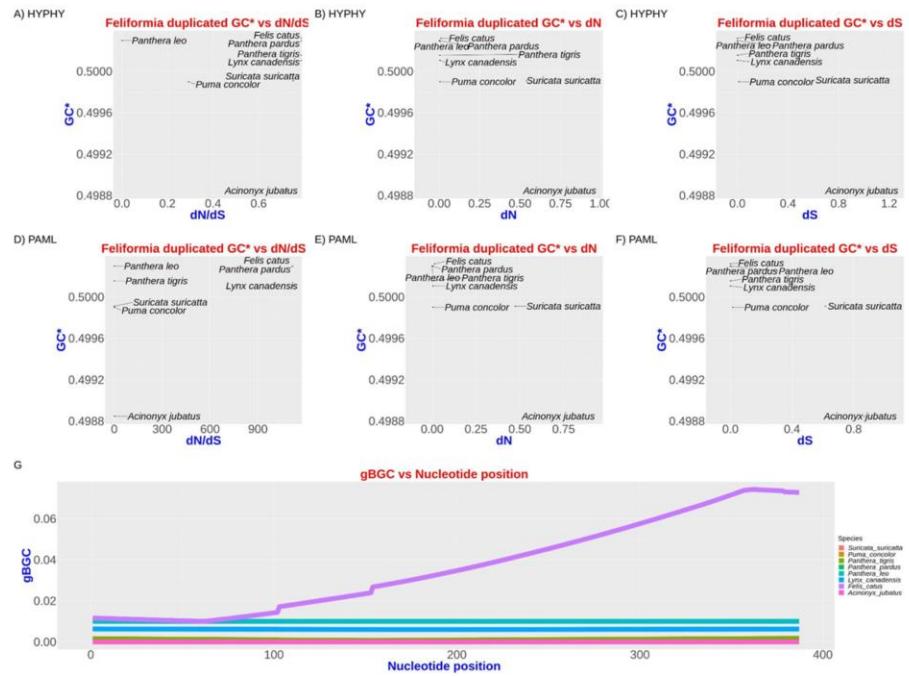


Figure S211: Values of GC* in Feliformia duplicated *COA1* are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

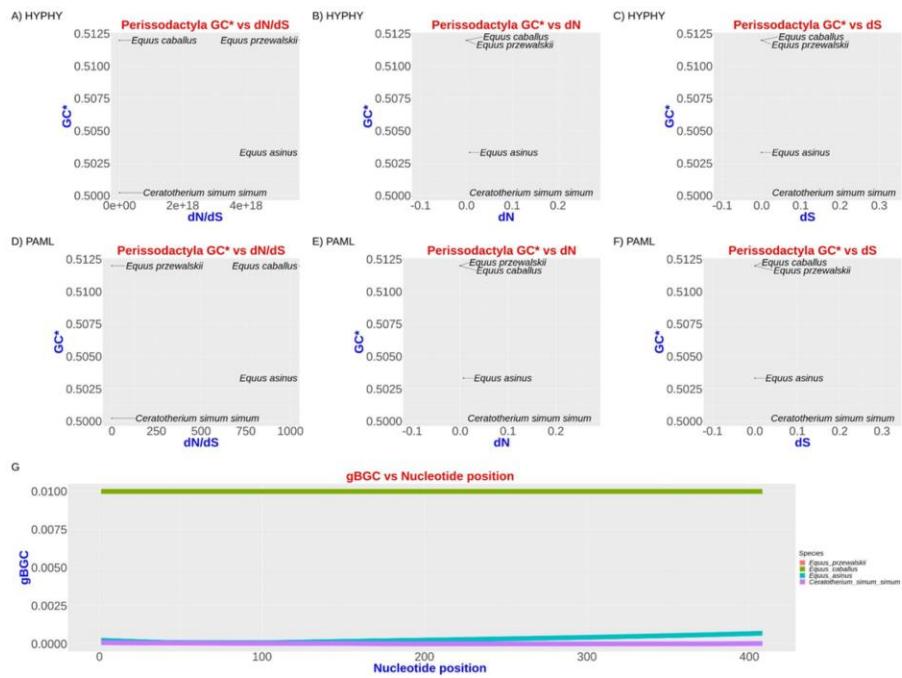
Figure S212

Figure S212: Values of GC* in Perissodactyla are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S213

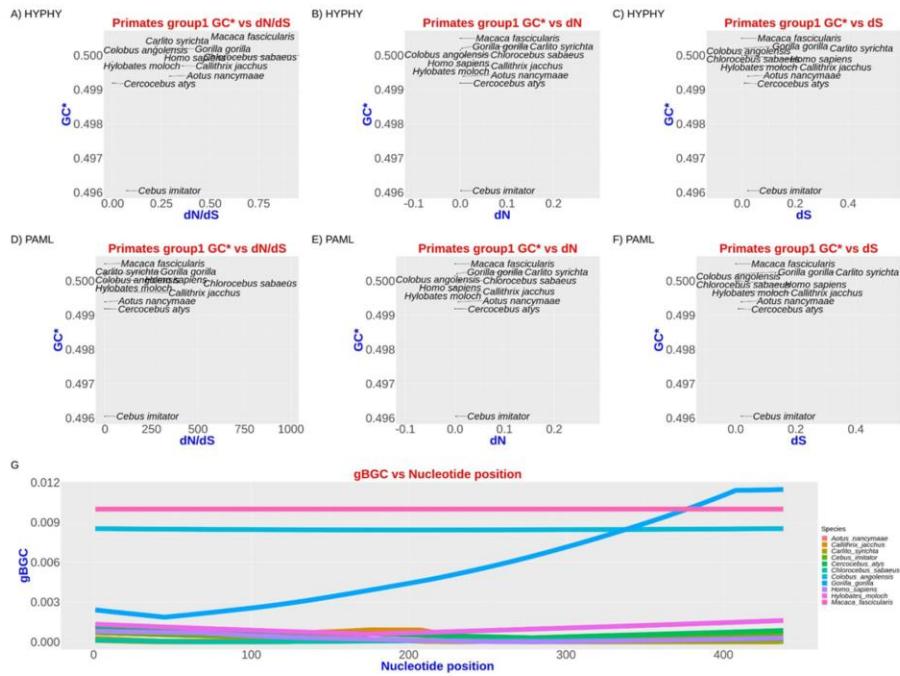


Figure S213: Values of GC* in Primates *COA1* are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S214

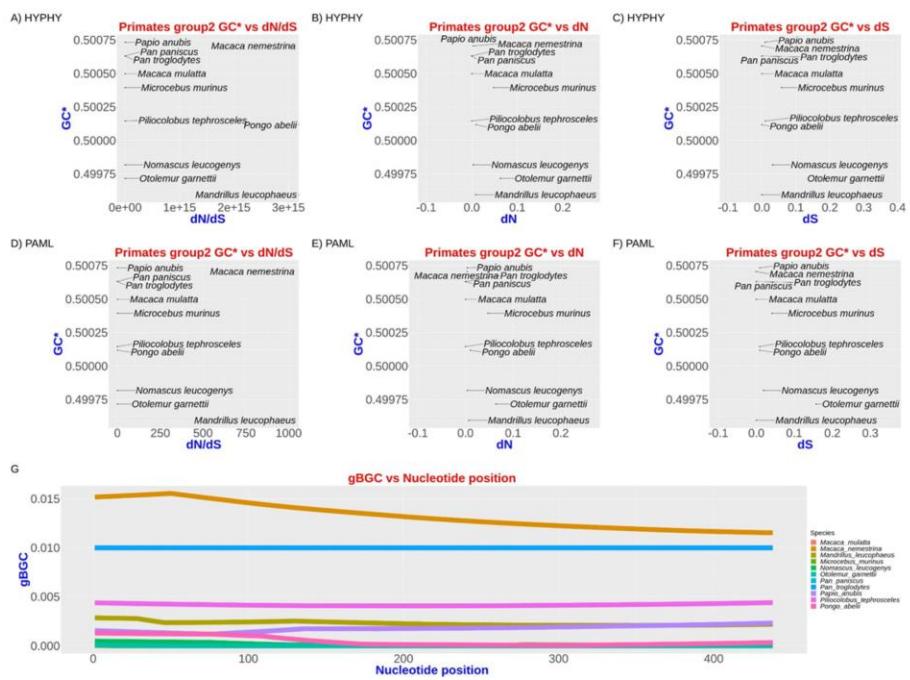


Figure S214: Values of GC* in Primates *COA1* are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S215

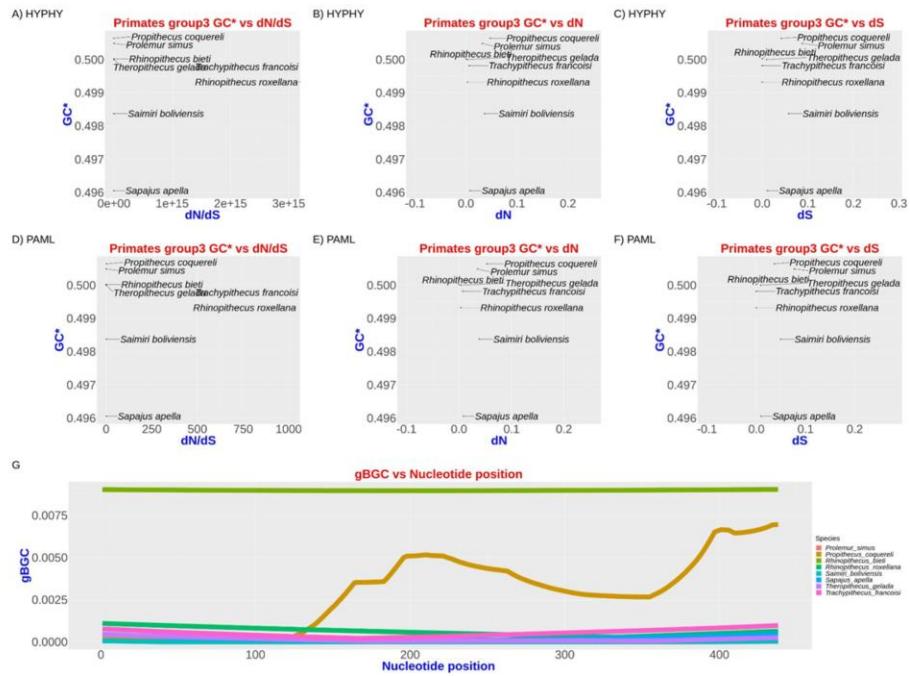


Figure S215: Values of GC* in Primates *COA1* are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S216

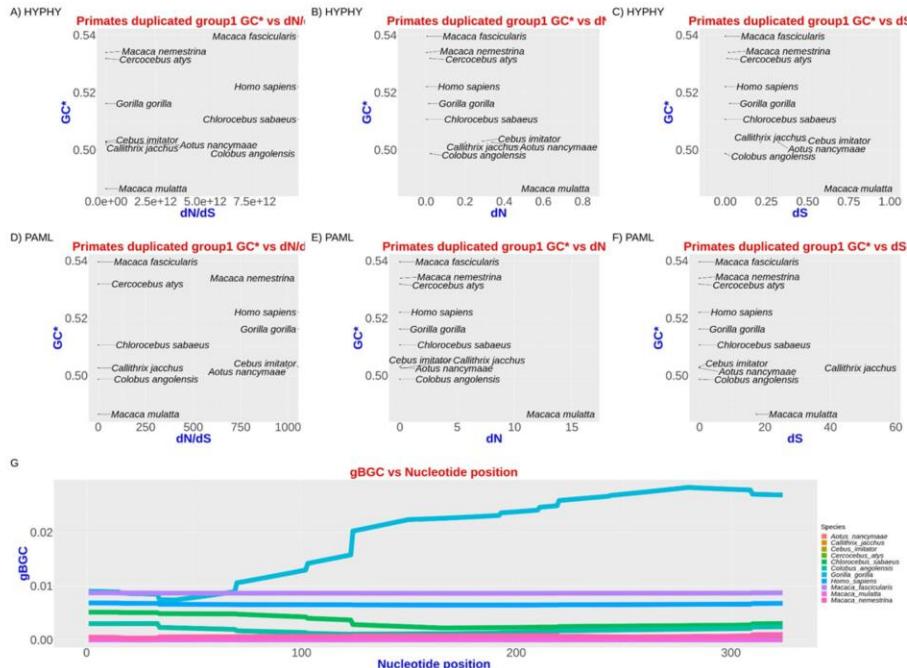


Figure S216: Values of GC* in Primates duplicated COA1 are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S217

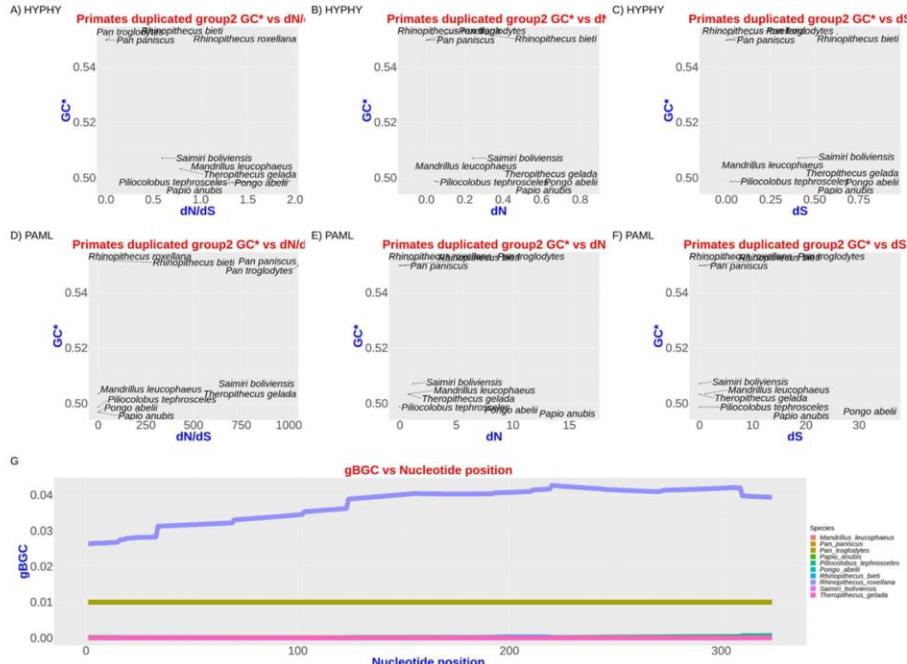


Figure S217: Values of GC* in Primates duplicated COA1 are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S218

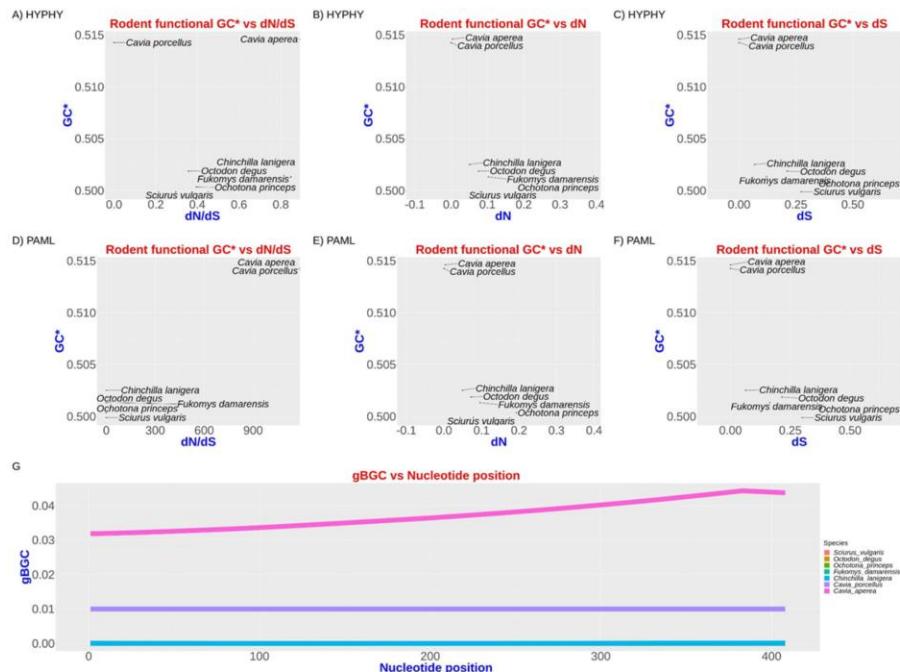


Figure S218: Values of GC* in rodents *COA1* are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S219

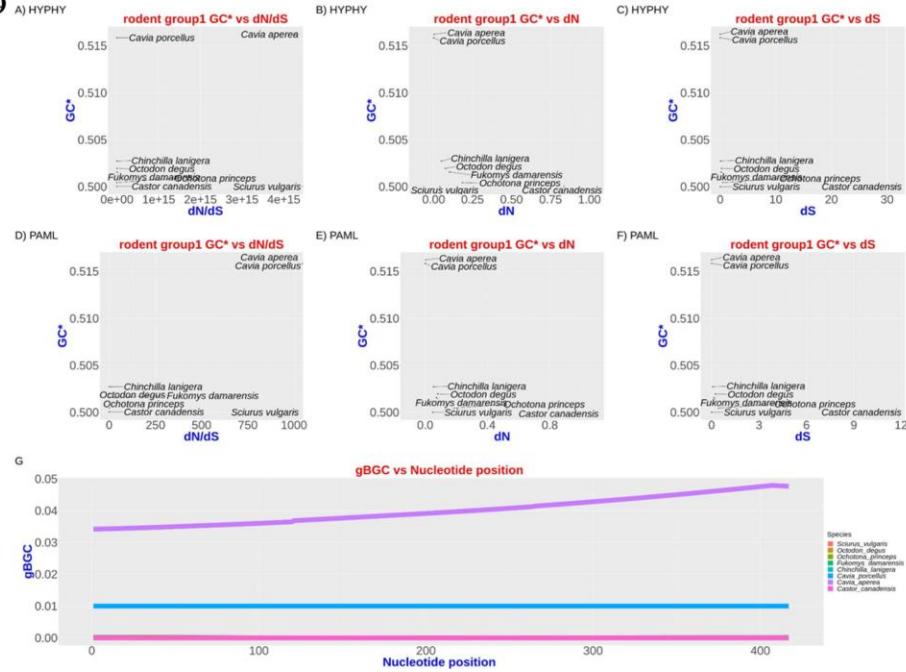


Figure S219: Values of GC^* in rodents unsaturated group are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S220

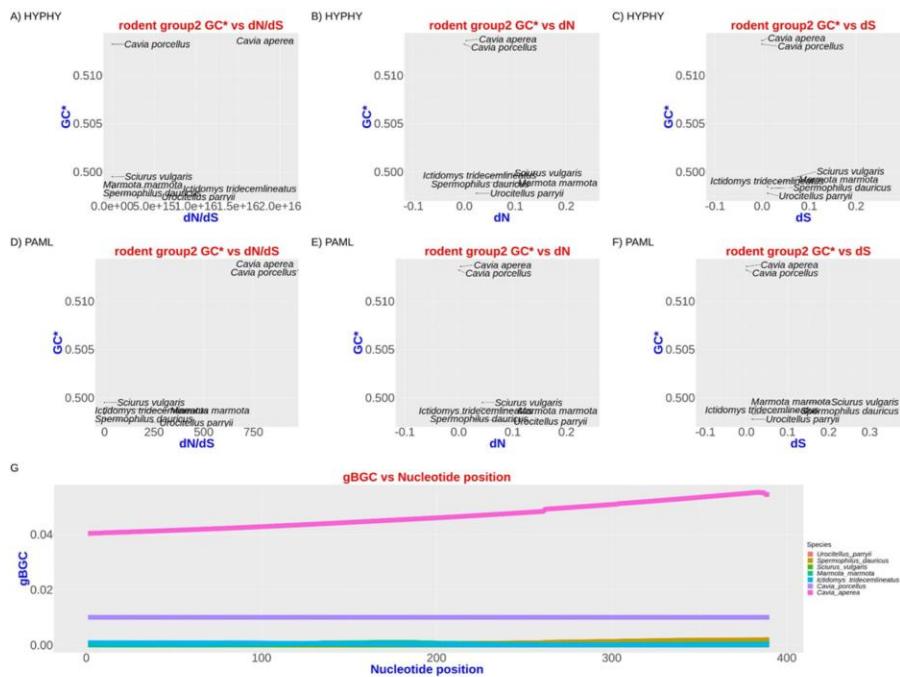


Figure S220: Values of GC* in rodents unsaturated group are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S221

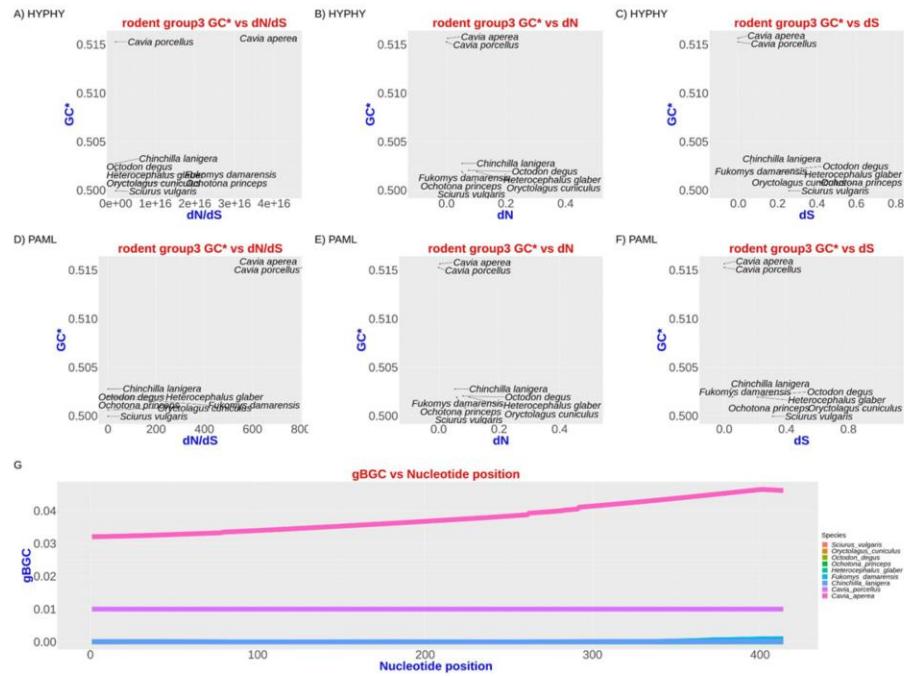


Figure S221: Values of GC* in rodents unsaturated group are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S222

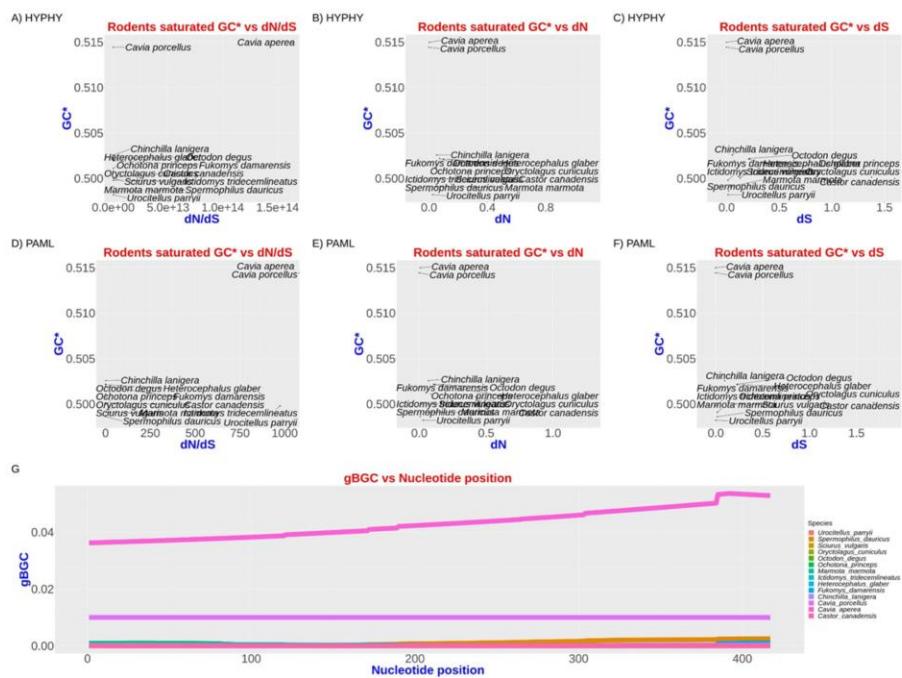


Figure S222: Values of GC* in rodents saturated group are plotted with dN and dS which is calculated using mapNH. dN and dS were calculated using PAML and HyPhy both. gBGC across nucleotide position were calculated using PhastBias.

Figure S223

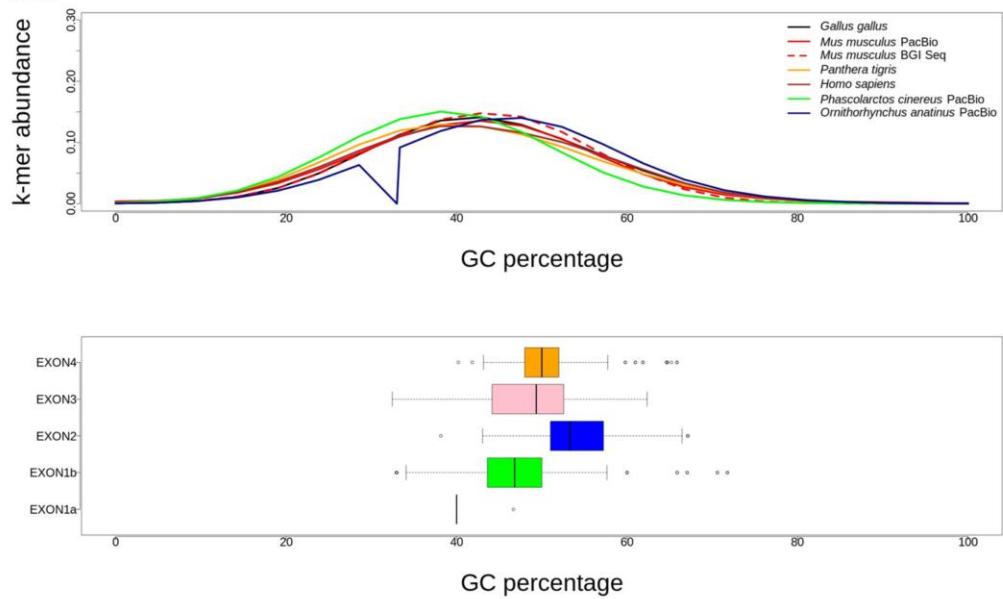


Figure S223: GC% versus K-mer plot using different data platforms like Illumina and PacBio, Each colour defines the species. Box plot of GC% of exon-1a, exon-1b, exon-2, exon-3, and exon-4 in the various group as one.

Figure S224

Variation in GC % in Exon1a in Primates species



Figure S224: Box plot of GC% of exon-1a for primates group along with pairwise Wilcox test.

Figure S225

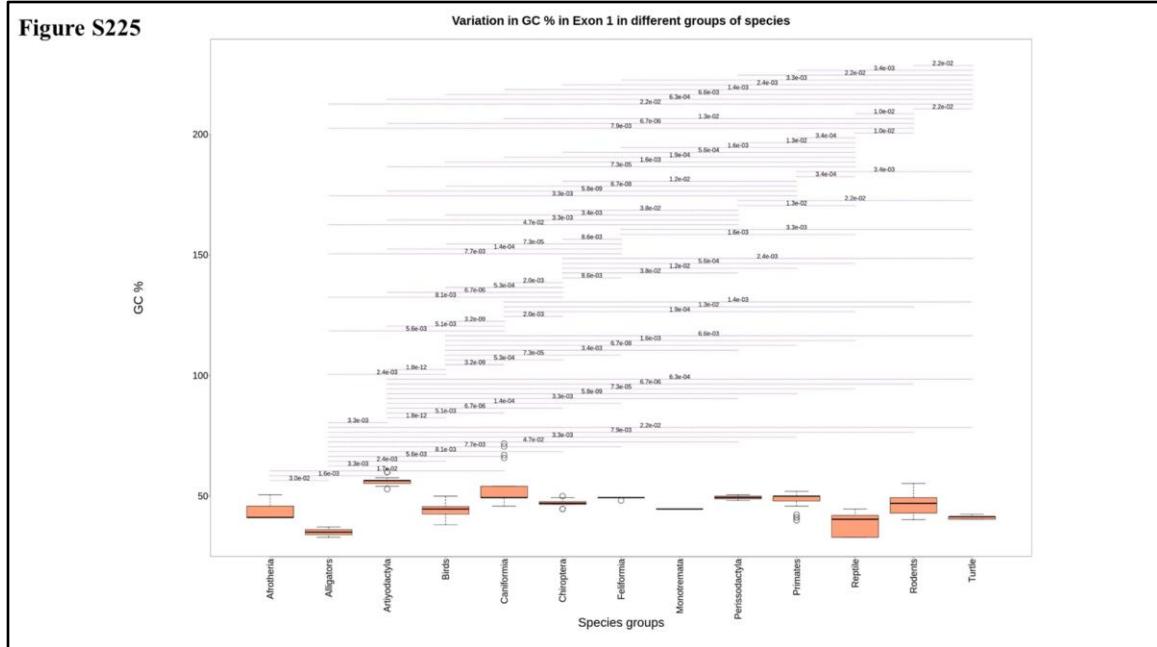


Figure S225: Box plot of GC% of exon-1 for various groups along with pairwise Wilcox test.

Figure S226

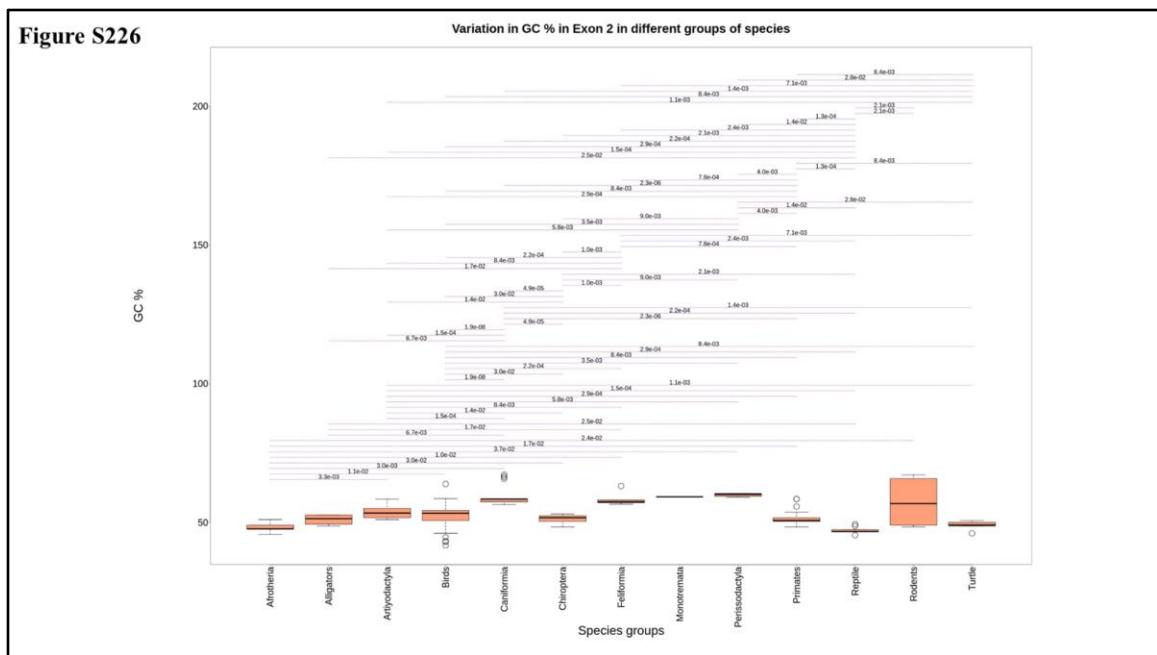


Figure S226: Box plot of GC% of exon-2 for various groups along with pairwise Wilcox test.

Figure S227

Variation in GC % in Exon 3 in different groups of species

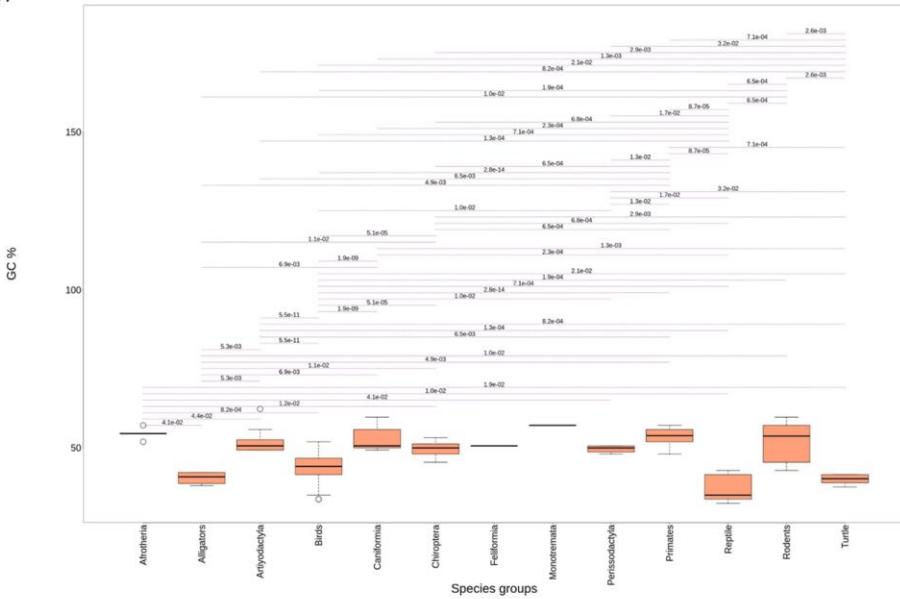


Figure S227: Box plot of GC% of exon-3 for various groups along with pairwise Wilcoxon test.

Figure S228

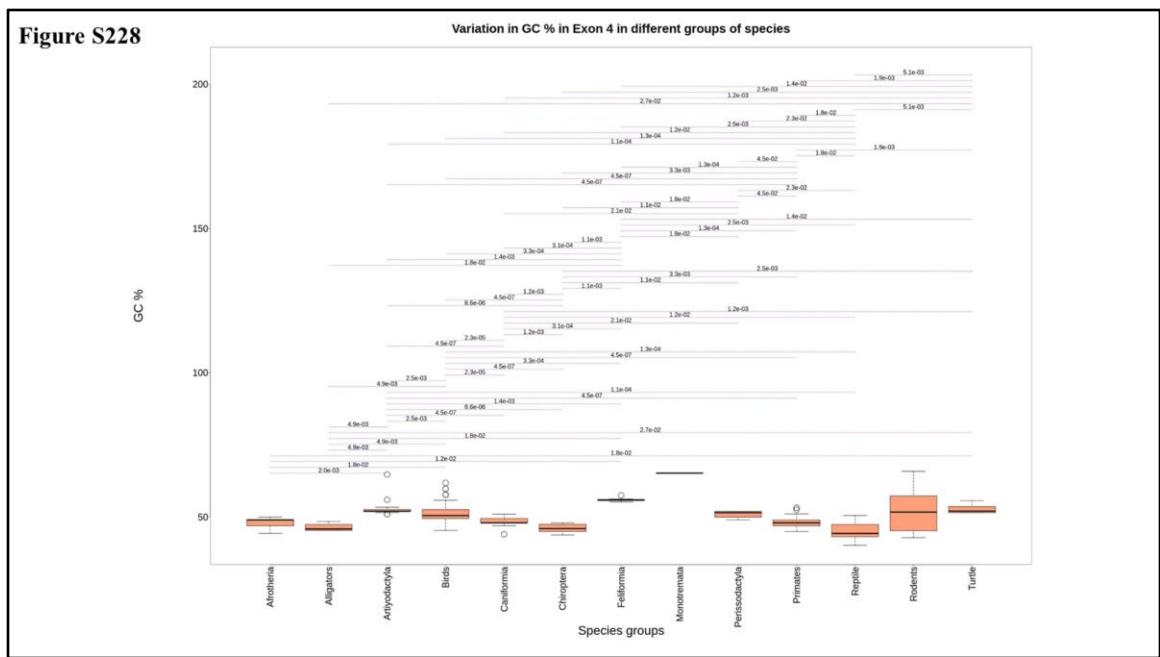


Figure S228: Box plot of GC% of exon-4 for various groups along with pairwise Wilcoxon test.

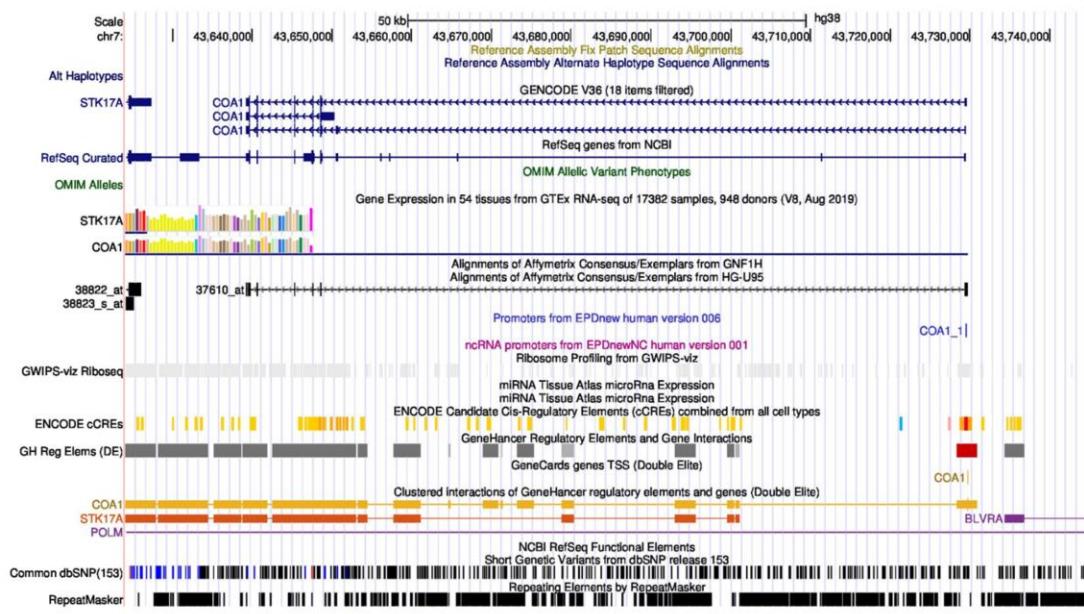
Figure S229*Homo sapiens***Figure S229:** Screenshot of UCSC genome browser of the *COA1* in human (*Homo sapiens*).

Figure S230

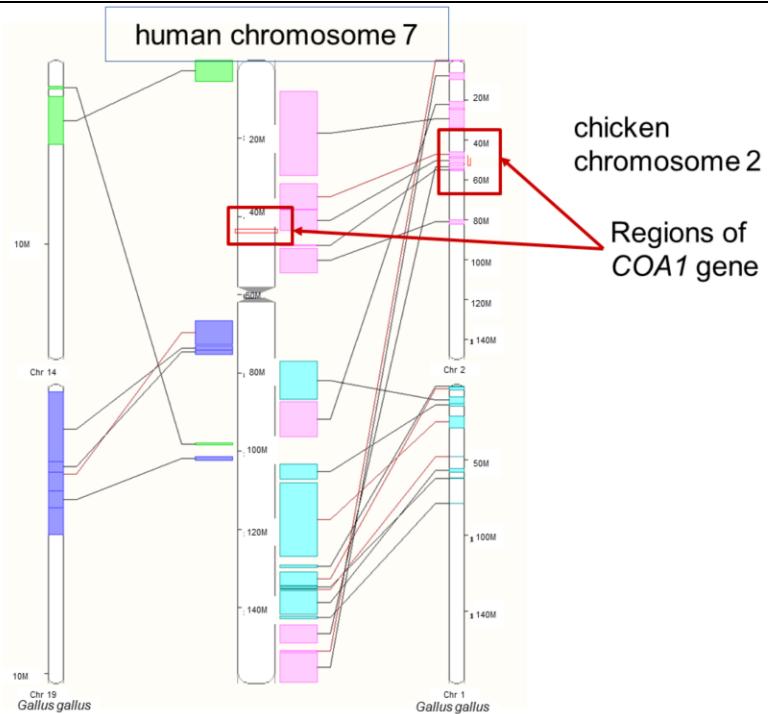


Figure S230: Conserved synteny in the *COA1* region of human chromosome 7 and chicken chromosome 2. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to chicken chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S231

birds group

Gallus gallus

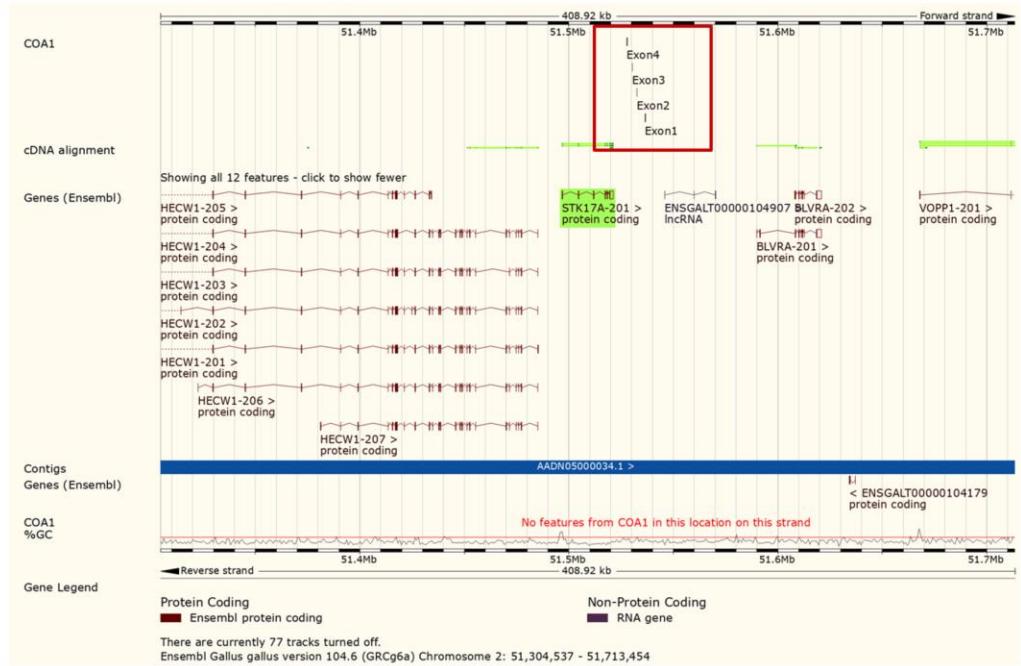


Figure S231: Gene order near *COA1* gene in the chicken (*Gallus gallus*) genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the $>$ or $<$ symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S232

human chromosome 7

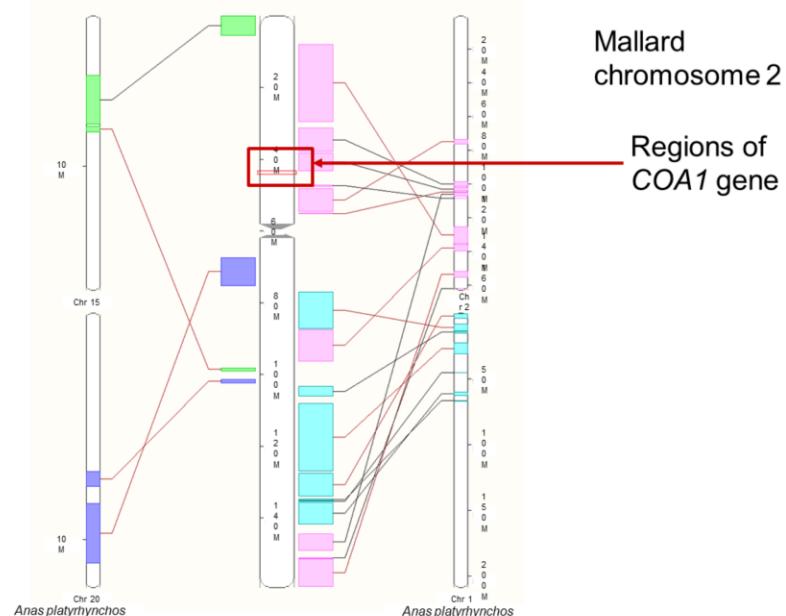


Figure S232: Conserved synteny in the *COA1* region of human chromosome 7 and mallard chromosome 2. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to mallard chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S233

human chromosome 7

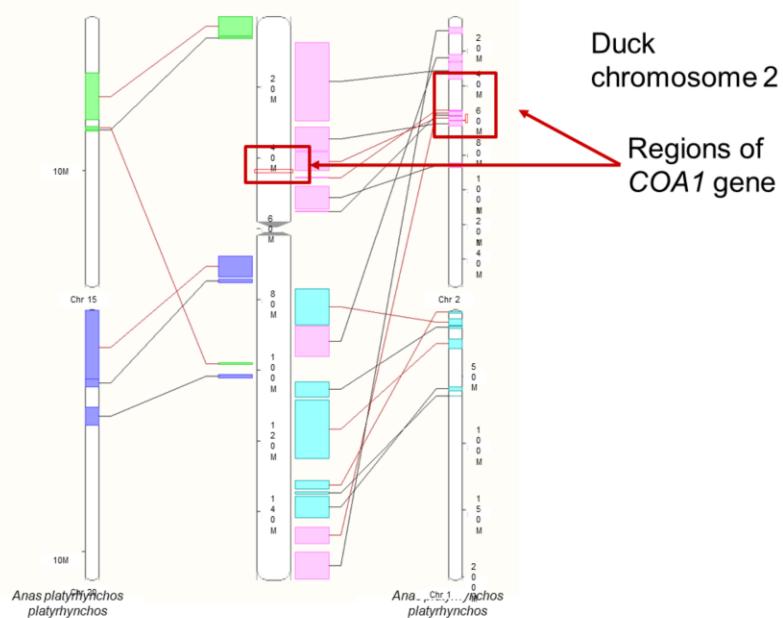


Figure S233: Conserved synteny in the *COA1* region of human chromosome 7 and duck chromosome 2. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to duck chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S234

human chromosome 7

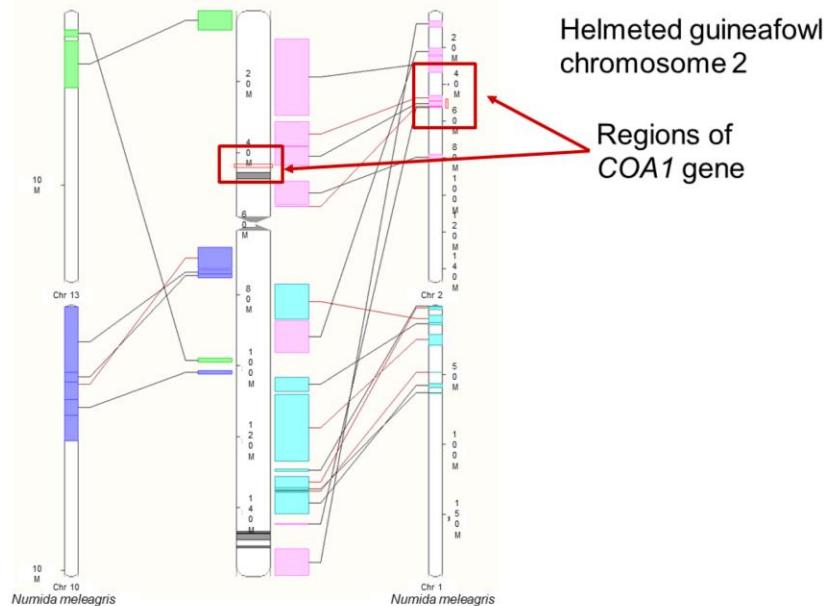


Figure S234: Conserved synteny in the *COA1* region of human chromosome 7 and helmeted guineafowl chromosome 2. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to helmeted guineafowl chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S235

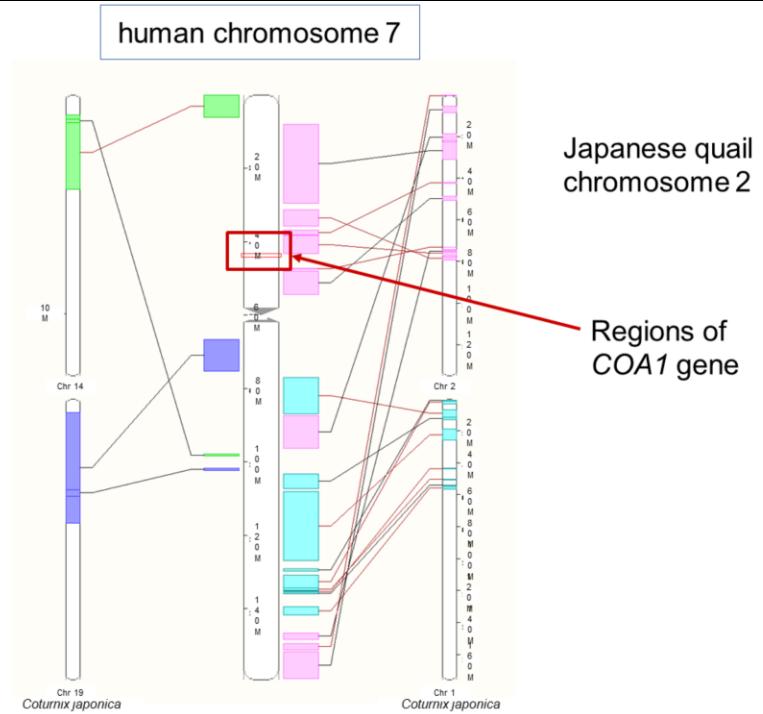


Figure S235: Conserved synteny in the *COA1* region of human chromosome 7 and Japanese quail chromosome 2. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to Japanese quail chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S236

human chromosome 7

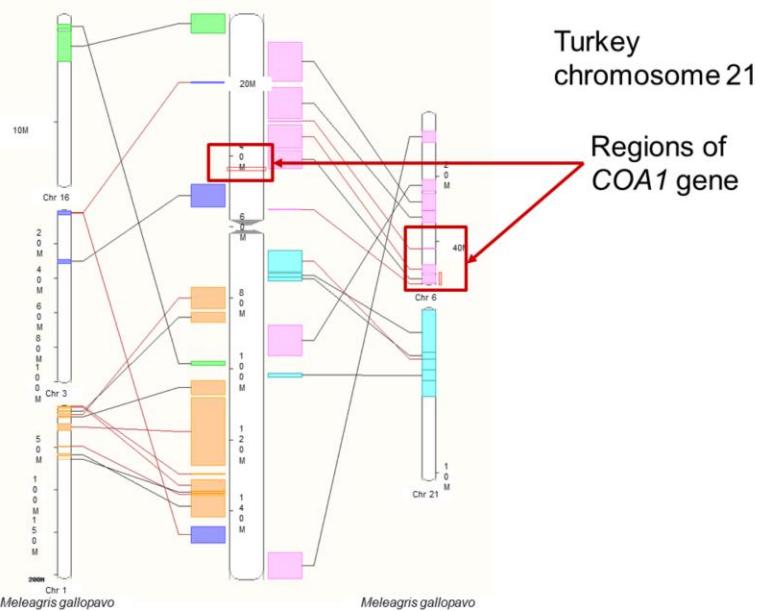


Figure S236: Conserved synteny in the *COA1* region of human chromosome 7 and turkey chromosome 21. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to turkey chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S237

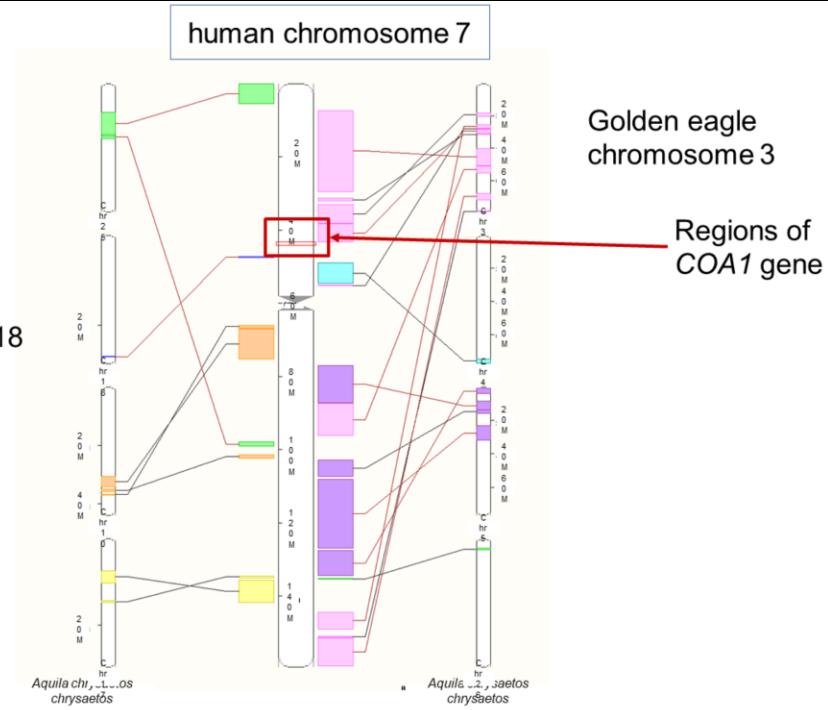


Figure S237: Conserved synteny in the *COA1* region of human chromosome 7 and golden eagle chromosome 3. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to golden eagle chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S238

human chromosome 7

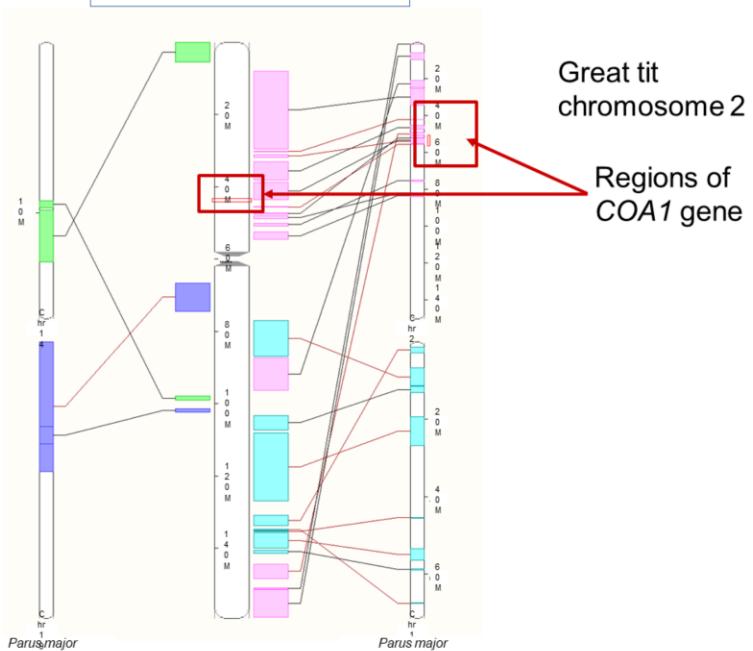


Figure S238: Conserved synteny in the *COA1* region of human chromosome 7 and great tit chromosome 2. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to great tit chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S239

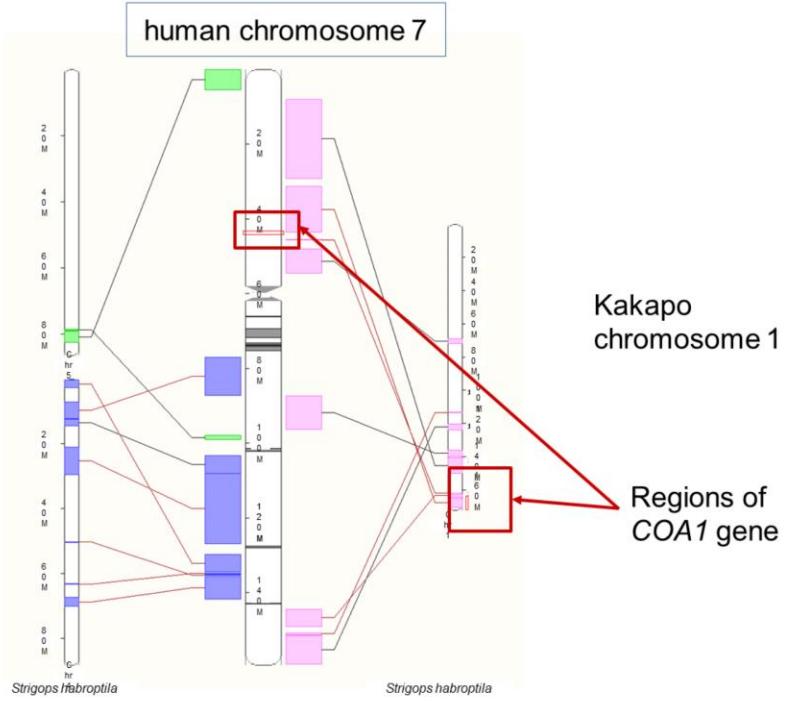


Figure S239: Conserved synteny in the *COA1* region of human chromosome 7 and kakapo chromosome 1. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to kakapo chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S240

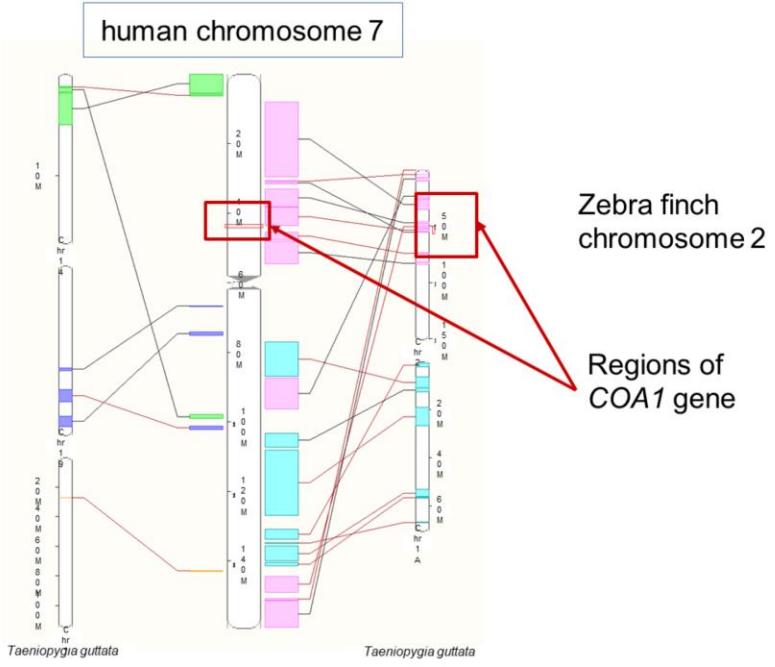


Figure S240 Conserved synteny in the *COA1* region of human chromosome 7 and zebra finch chromosome 2. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to zebra finch chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S241

human chromosome 7

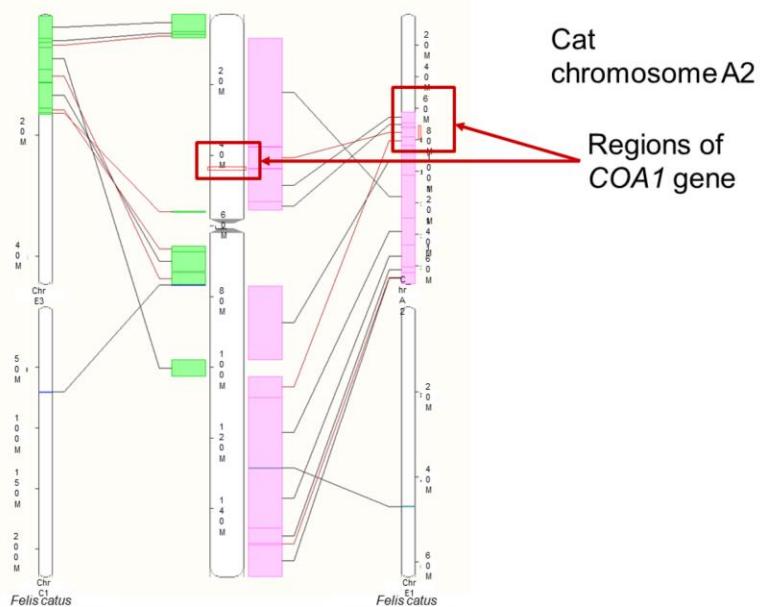


Figure S241: Conserved synteny in the *COA1* region of human chromosome 7 and cat chromosome A2. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to cat chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S242

human chromosome 7

dog
chromosome 18

Regions of
COA1 gene

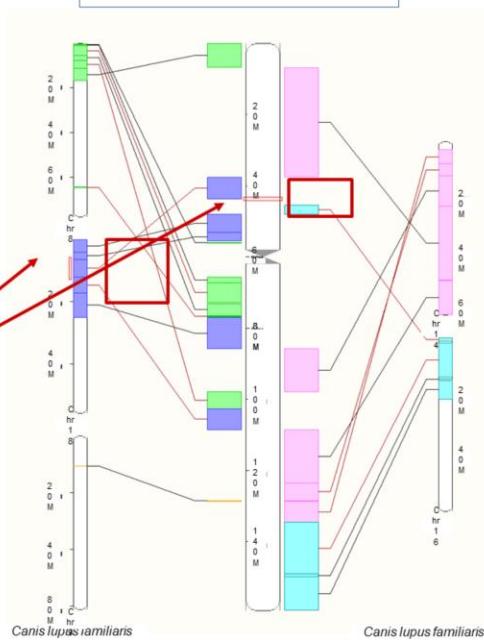


Figure S242: Conserved synteny in the *COA1* region of human chromosome 7 and dog chromosome 18. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to dog chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S243

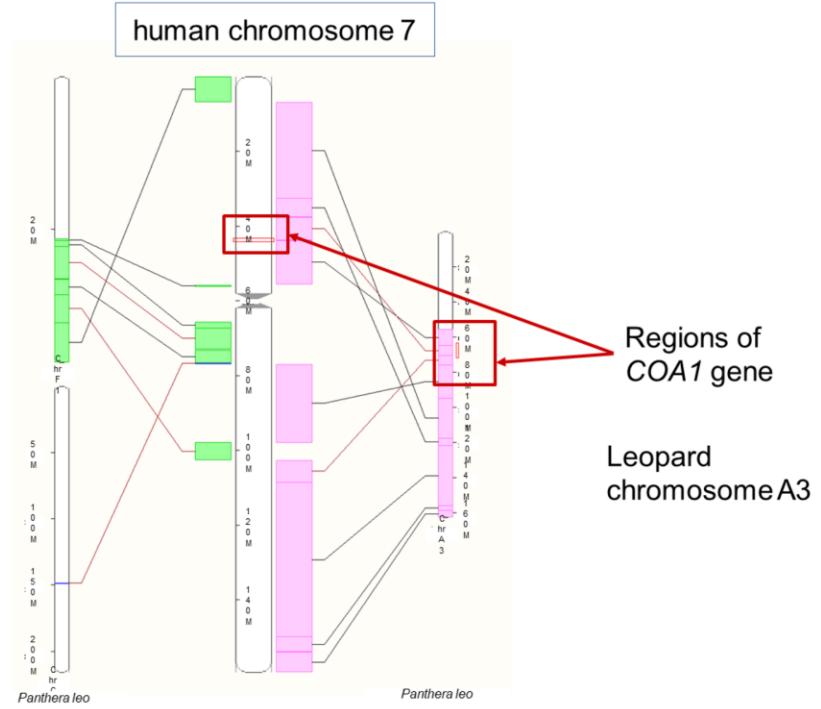


Figure S243: Conserved synteny in the *COA1* region of human chromosome 7 and leopard chromosome A3. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to leopard chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S244

human chromosome 7

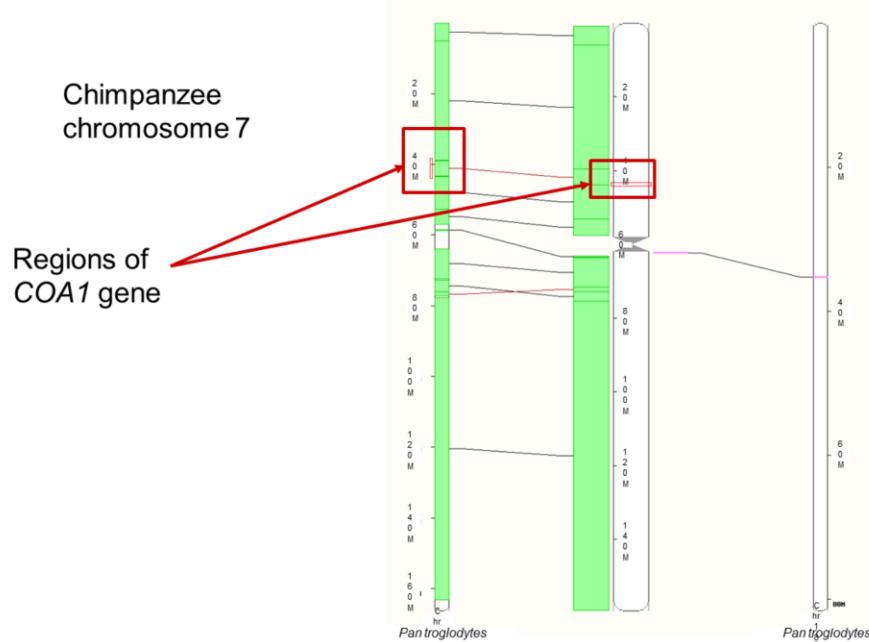


Figure S244: Conserved synteny in the *COA1* region of human chromosome 7 and chimpanzee chromosome 7. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to chimpanzee chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S245

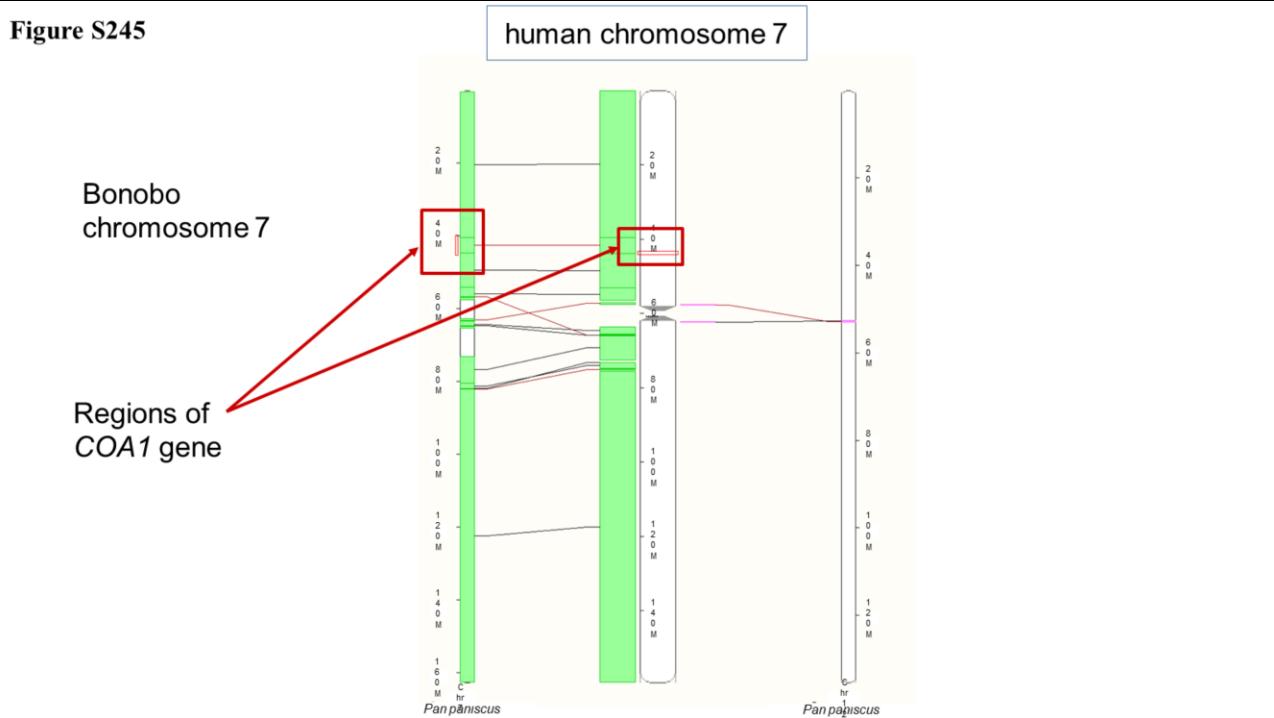


Figure S245: Conserved synteny in the *COA1* region of human chromosome 7 and bonobo chromosome 7. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to bonobo chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S246

human chromosome 7

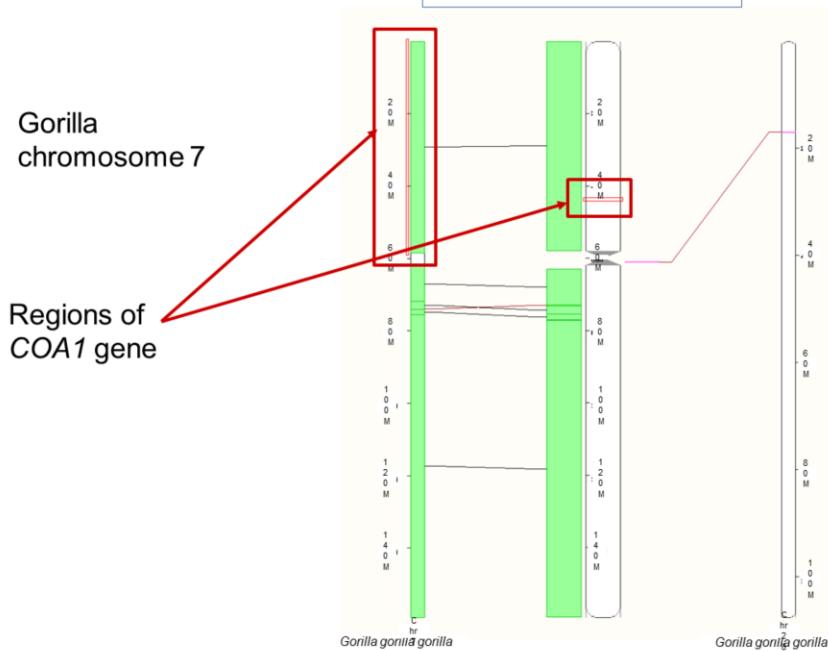


Figure S246: Conserved synteny in the *COA1* region of human chromosome 7 and gorilla chromosome 7. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to gorilla chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S247

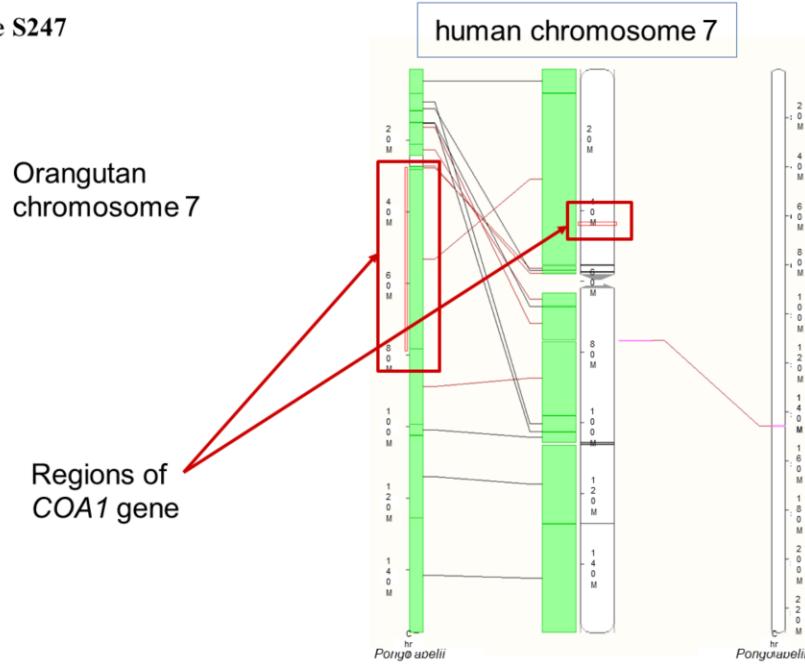


Figure S247: Conserved synteny in the *COA1* region of human chromosome 7 and orangutan chromosome 7. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to orangutan chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S248

human chromosome 7

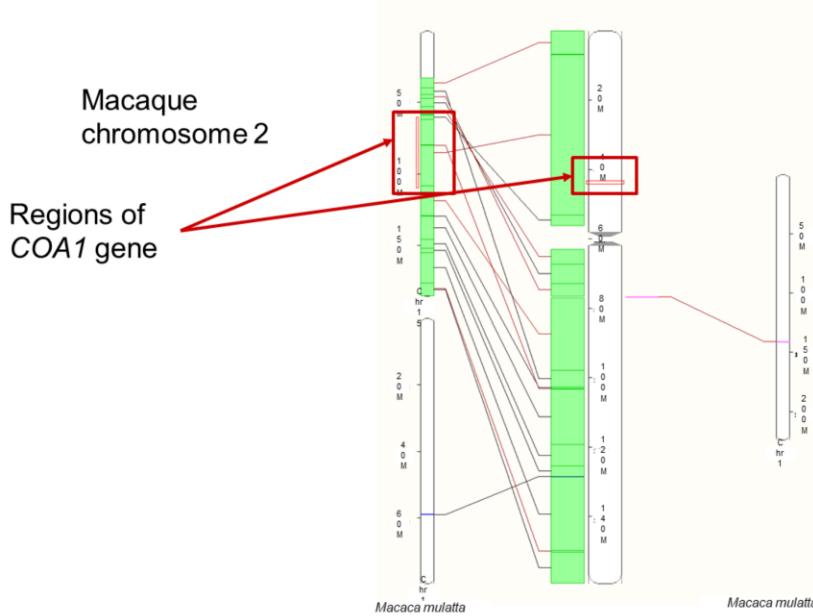


Figure S248: Conserved synteny in the *COA1* region of human chromosome 7 and macaque chromosome 2. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to macaque chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S249

human chromosome 7

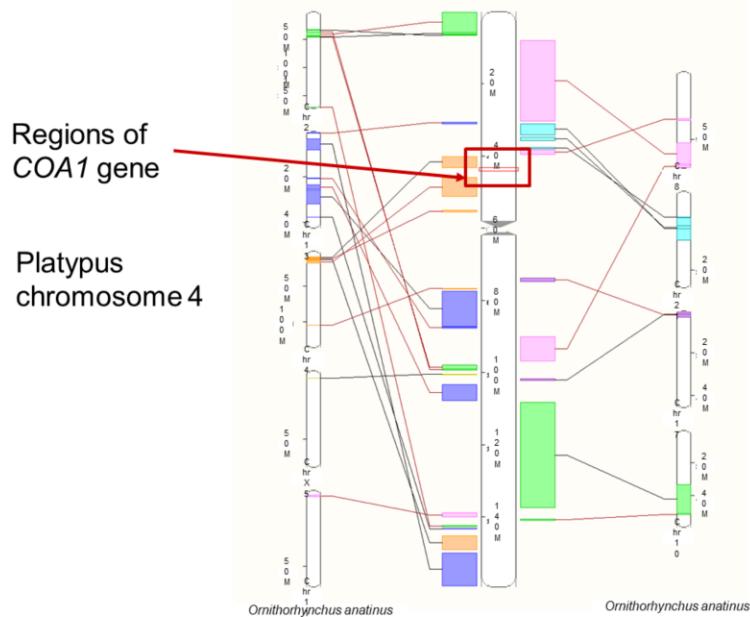


Figure S249: Conserved synteny in the *COA1* region of human chromosome 7 and platypus chromosome 4. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to platypus chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S250

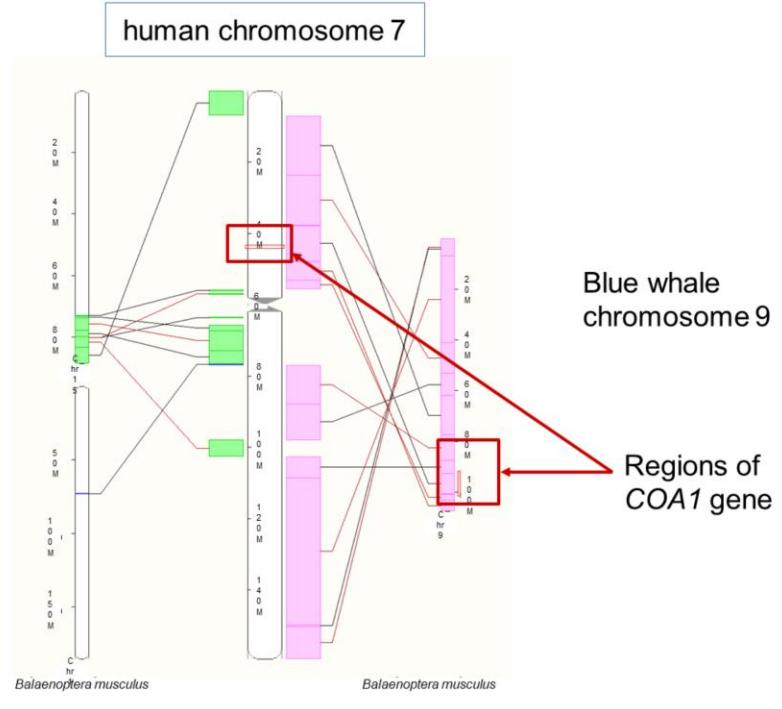


Figure S250: Conserved synteny in the *COA1* region of human chromosome 7 and blue whale chromosome 9. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to blue whale chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S251

human chromosome 7

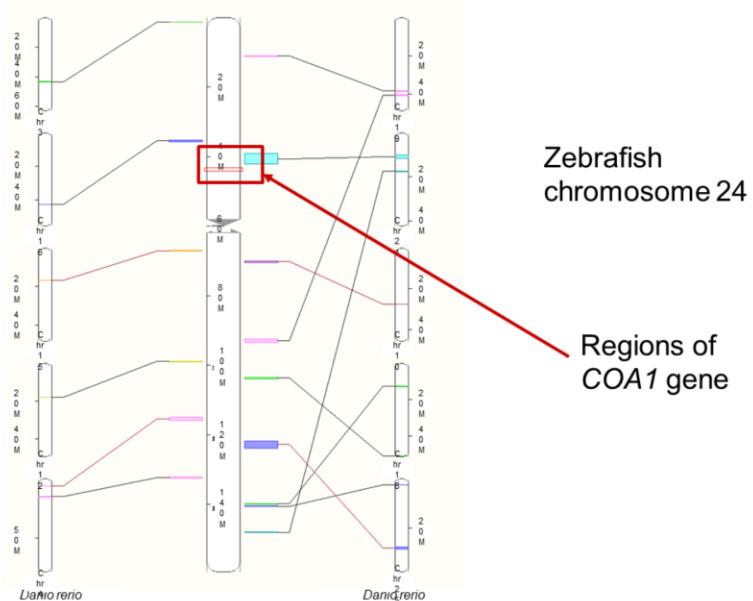


Figure S251: Conserved synteny in the *COA1* region of human chromosome 7 and zebrafish chromosome 24. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to zebrafish chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S252

human chromosome 7

Common wall
lizard
chromosome 15

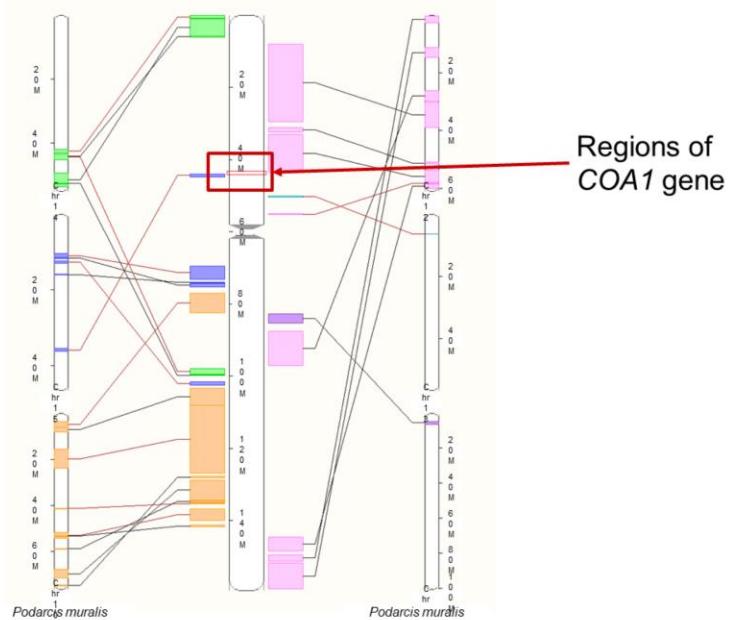


Figure S252: Conserved synteny in the *COA1* region of human chromosome 7 and common wall lizard chromosome 15. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to common wall lizard chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S253

human chromosome 7

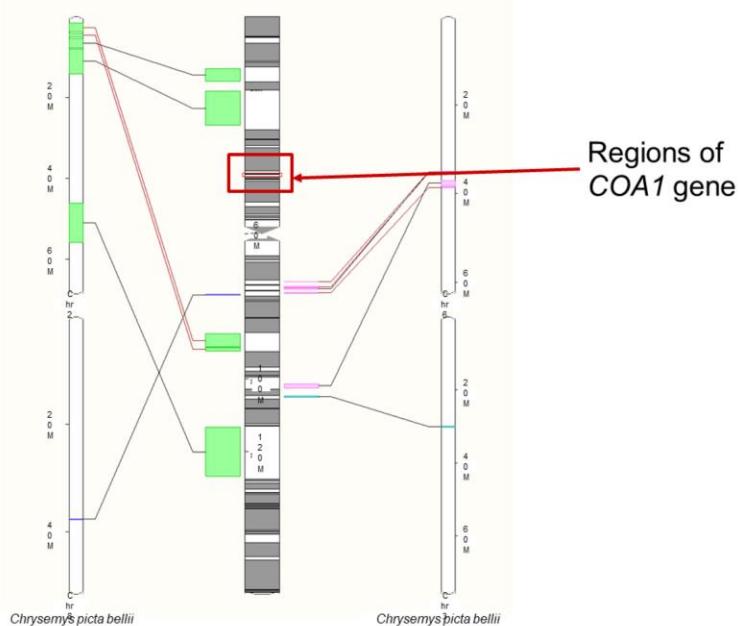


Figure S253: Conserved synteny in the *COA1* region of human chromosome 7 and painted turtle chromosome 2. Each of the synteny blocks is depicted by different colors and connected by lines that go from the human chromosome to painted turtle chromosomes. Exact location of the *COA1* gene is depicted by a red box within the chromosome representations.

Figure S254

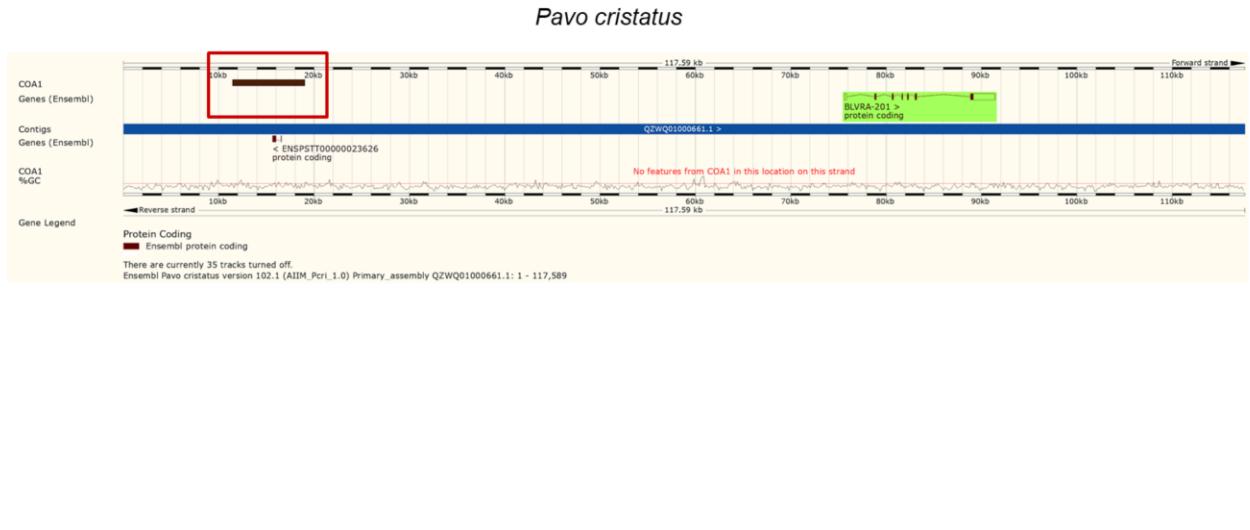


Figure S254: Gene order near *COA1* gene in the Indian peafowl genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S255

Meleagris gallopavo



Figure S255: Gene order near *COA1* gene in the turkey genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S256

Coturnix japonica

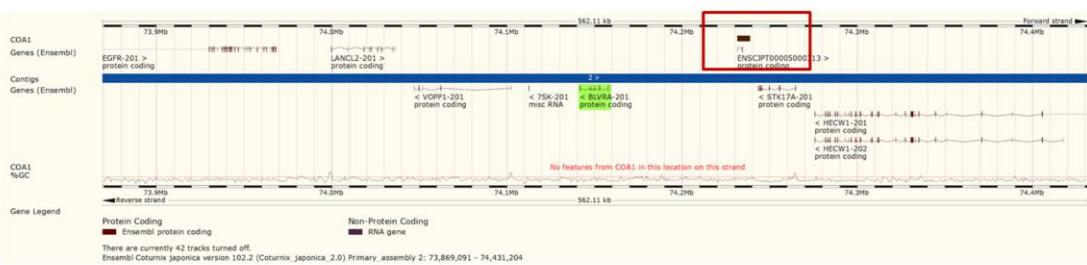


Figure S256: Gene order near *COA1* gene in the Japanese quail genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. Chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S257

Numida meleagris

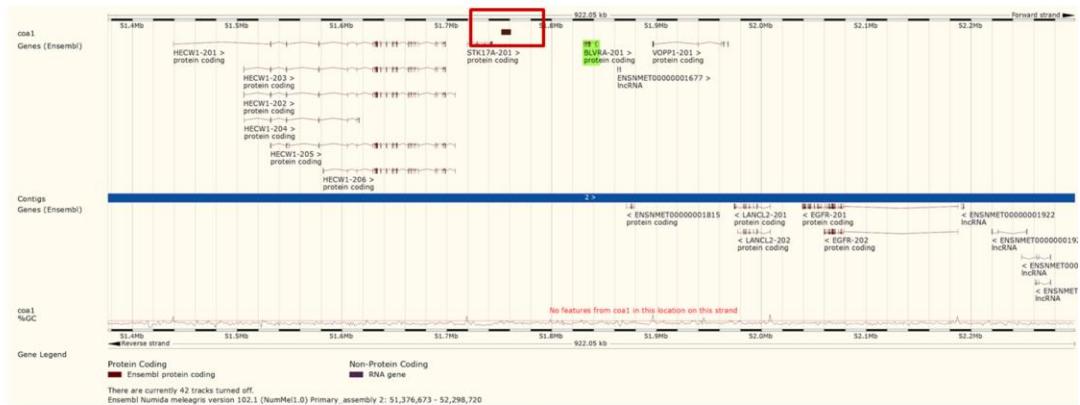


Figure S257: Gene order near *COA1* gene in the helmeted guineafowl genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S258

Anas platyrhynchos

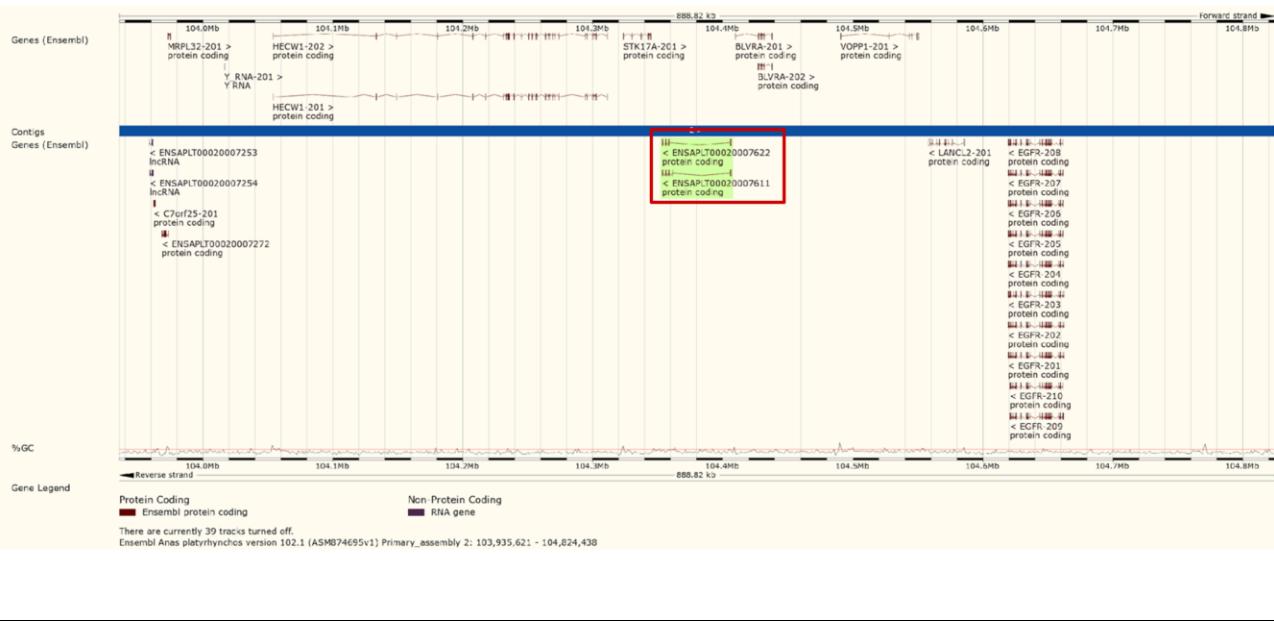


Figure S258: Gene order near *COA1* gene in the mallard genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S259

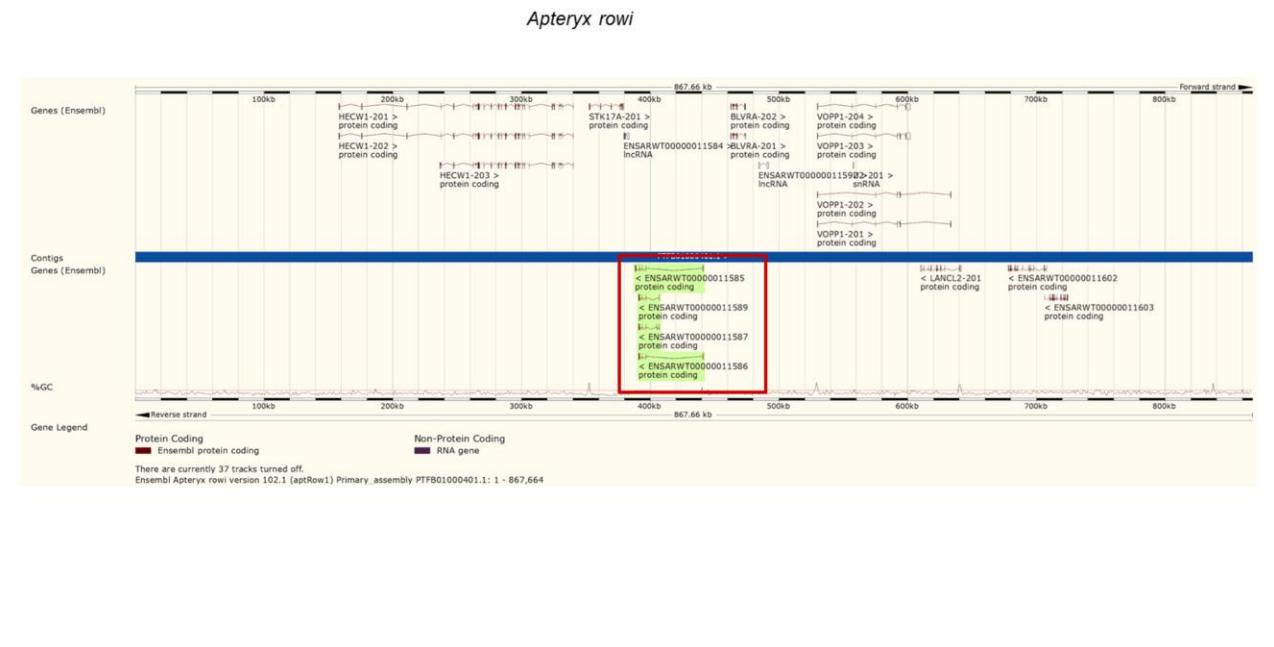


Figure S259: Gene order near *COA1* gene in the Okarito brown kiwi genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S260

Dromaius novaehollandiae

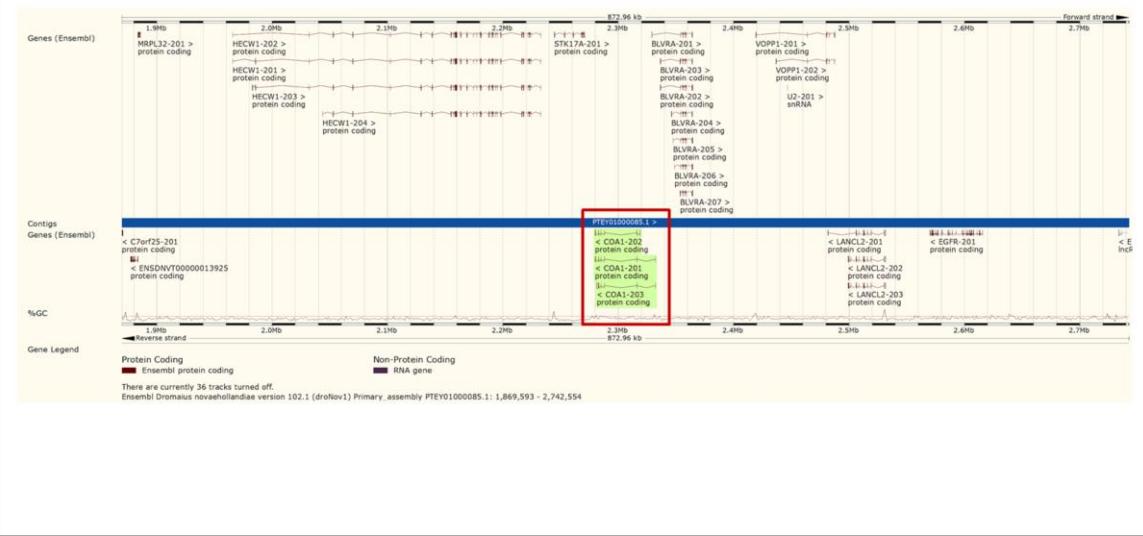


Figure S260: Gene order near *COA1* gene in the emu genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S261

Nothoprocta perdicaria

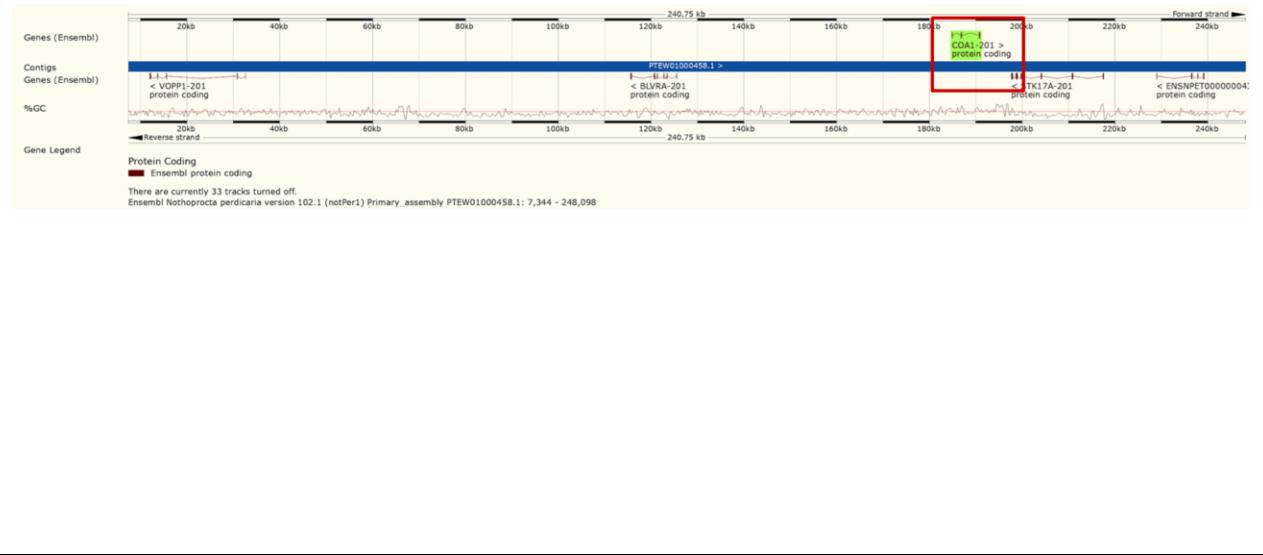


Figure S261: Gene order near *COA1* gene in the Chilean tinamou genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S262

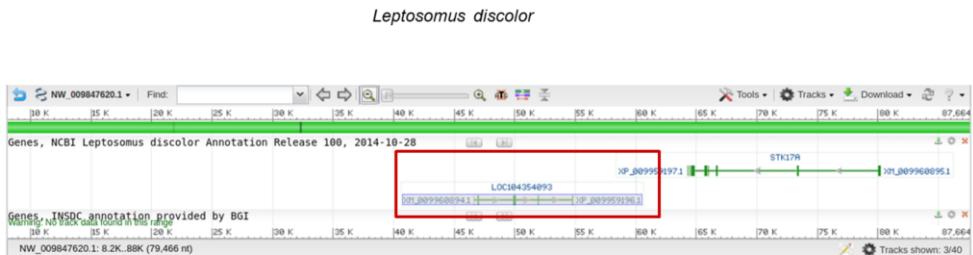


Figure S262: Gene order near *COA1* gene in the cuckoo roller genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S263

Lonchura striata domestica

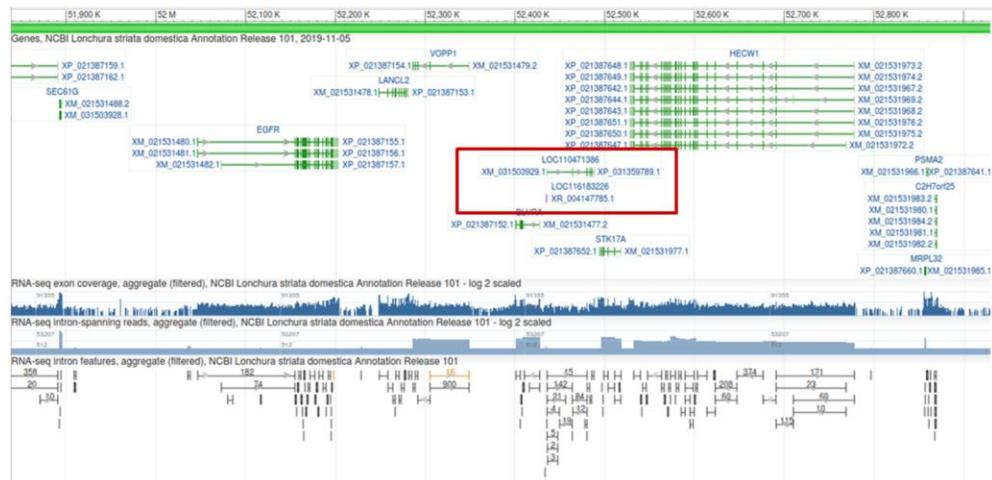


Figure S263: Gene order near *COA1* gene in the Bengalese finch genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S264

Erythrura gouldiae

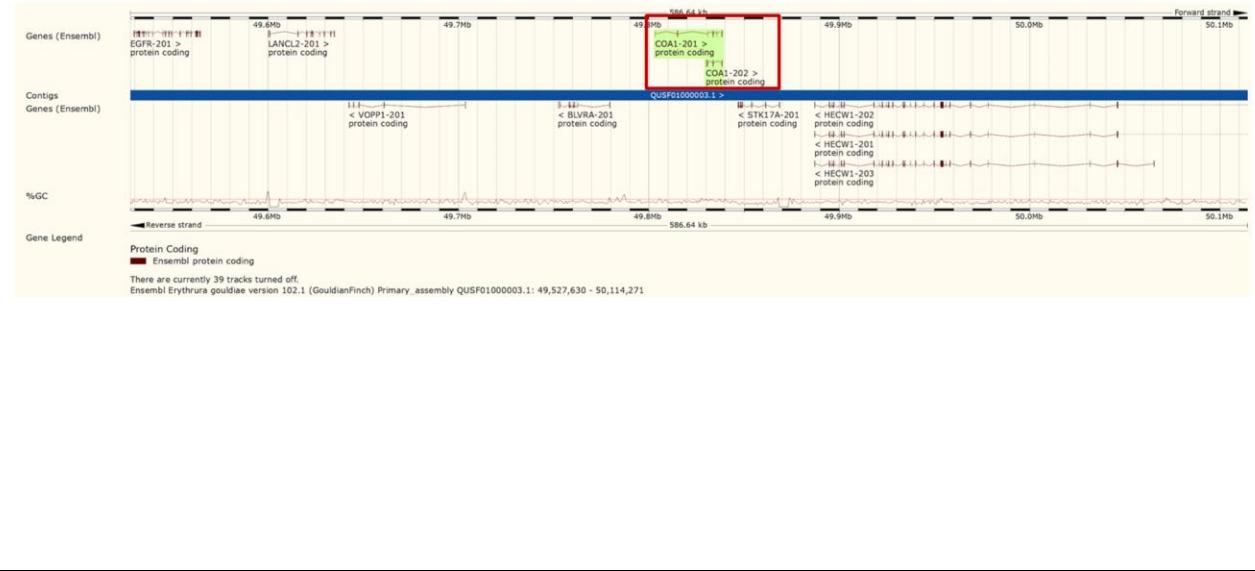


Figure S264: Gene order near *COA1* gene in the Gouldian finch genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S265

Geospiza fortis

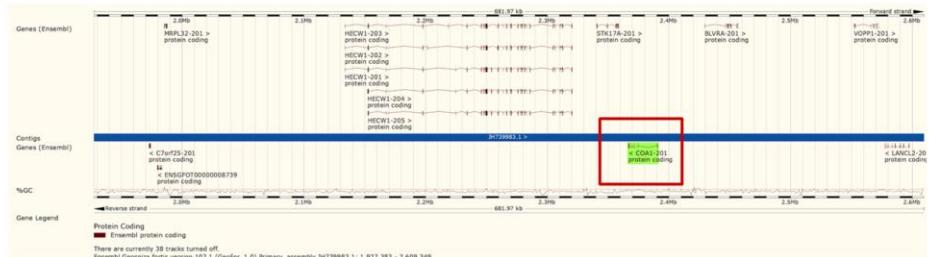


Figure S266: Gene order near *COA1* gene in the medium ground-finches genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. Chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S266

Corvus monedulaoides

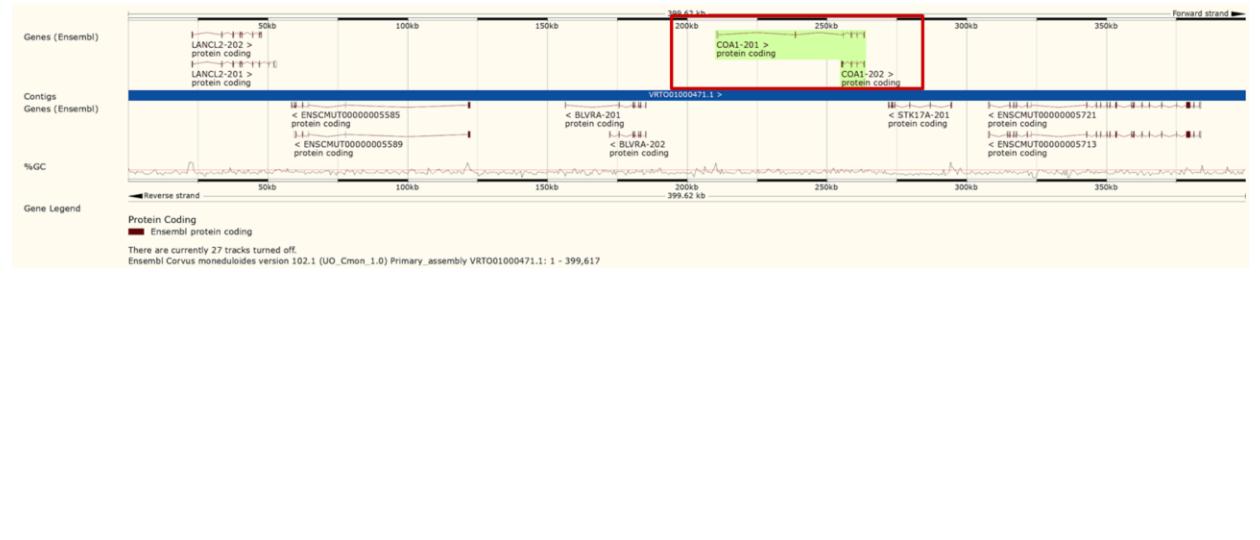


Figure S266: Gene order near *COA1* gene in the new Caledonian crow genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S267

Manacus vitellinus

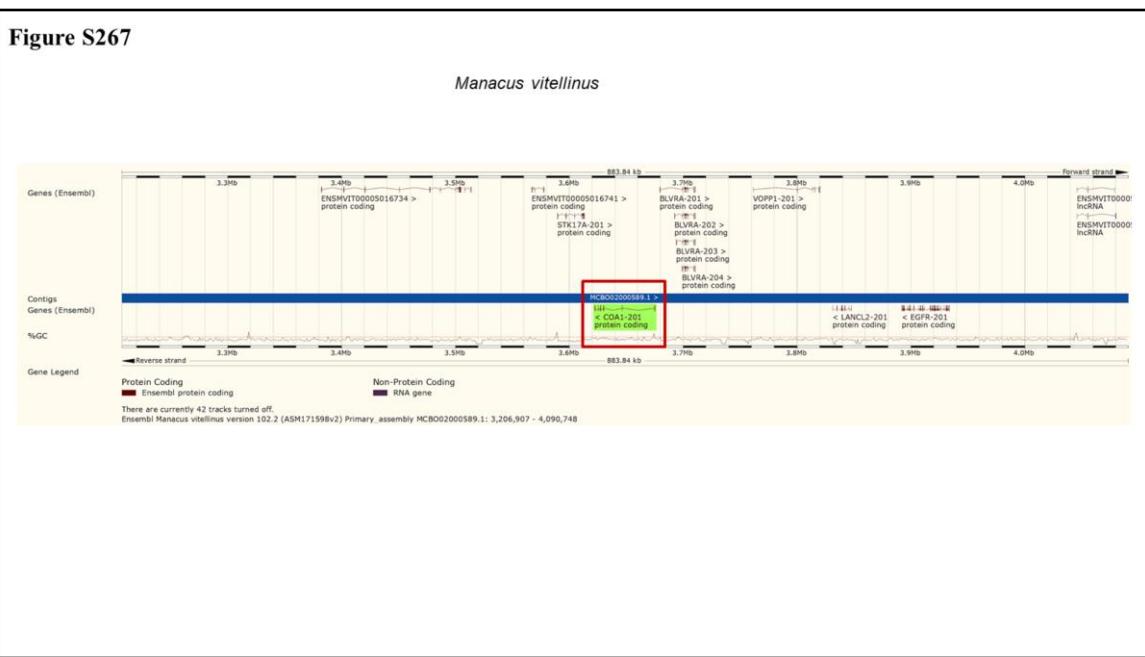


Figure S267: Gene order near *COA1* gene in the golden-collared manakin genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

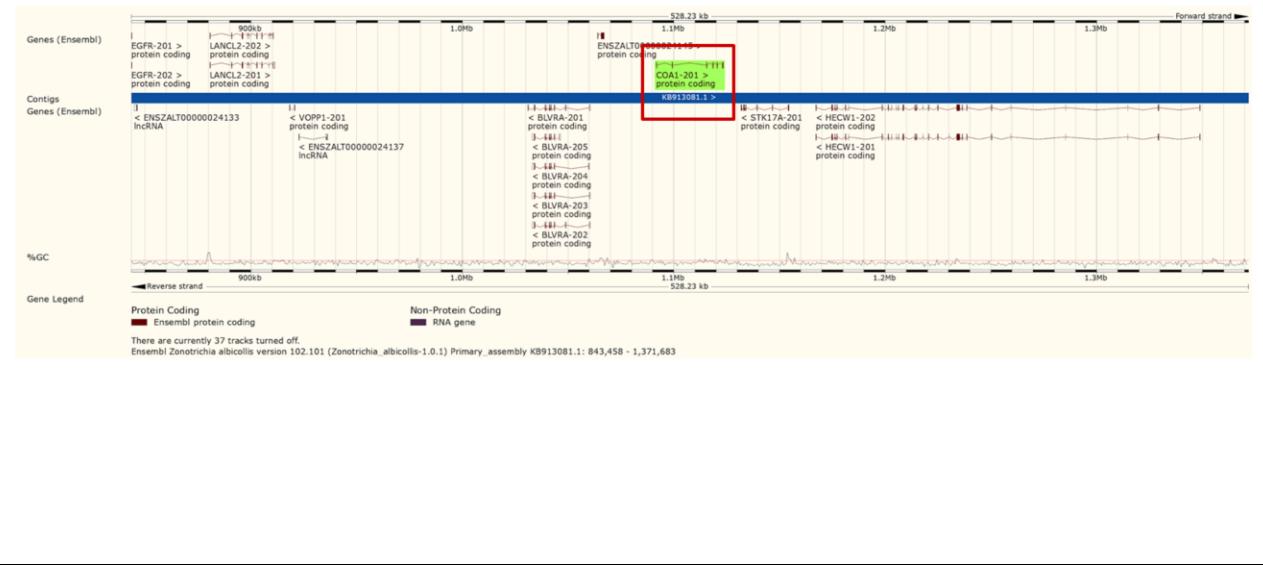
Figure S268*Zonotrichia albicollis*

Figure S268: Gene order near *COA1* gene in the white-throated sparrow genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S269

Cyanoderma ruficeps

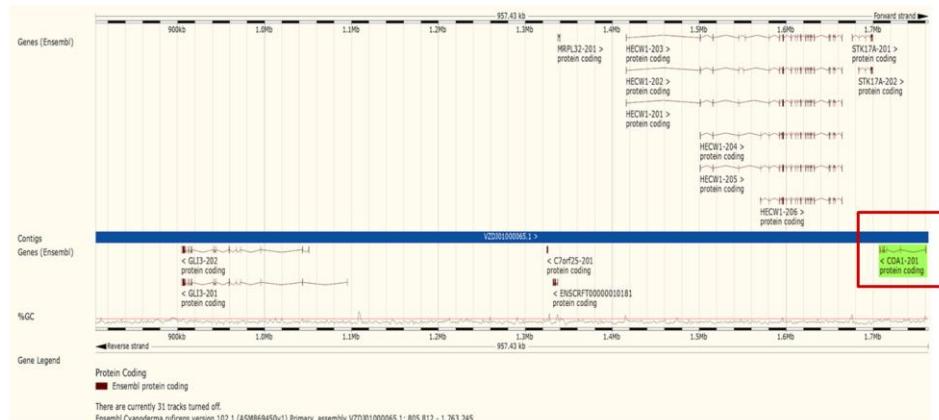


Figure S269: Gene order near *COA1* gene in the rufous-capped babbler genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S270

Struthio camelus australis

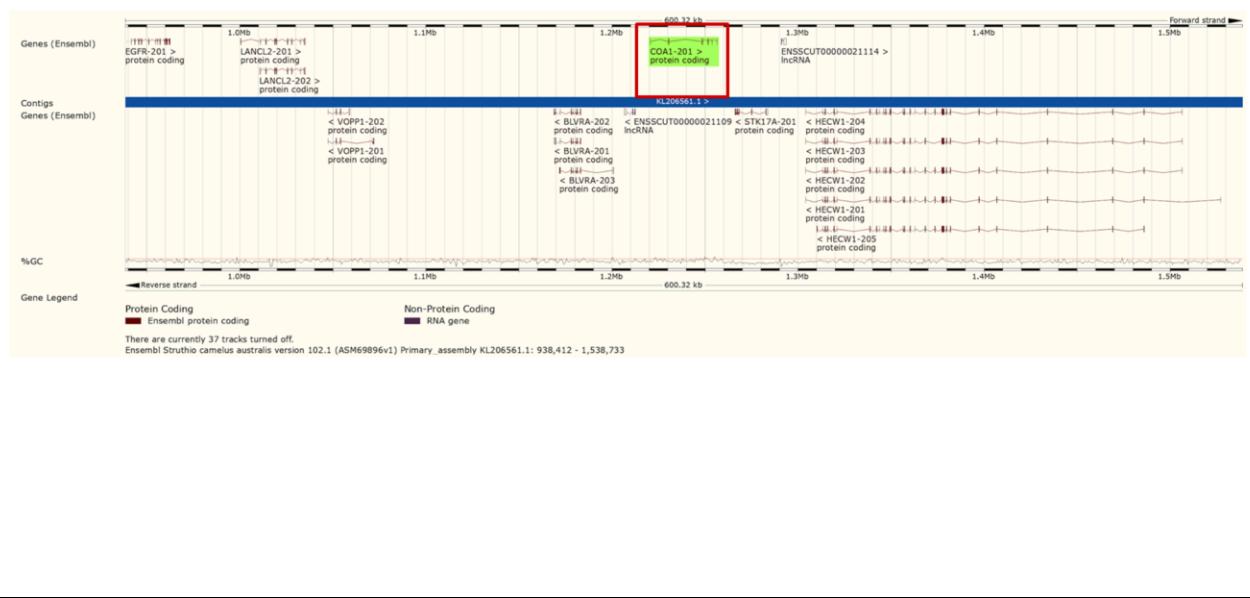


Figure S270: Gene order near *COA1* gene in the African ostrich genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S271

Ficedula albicollis

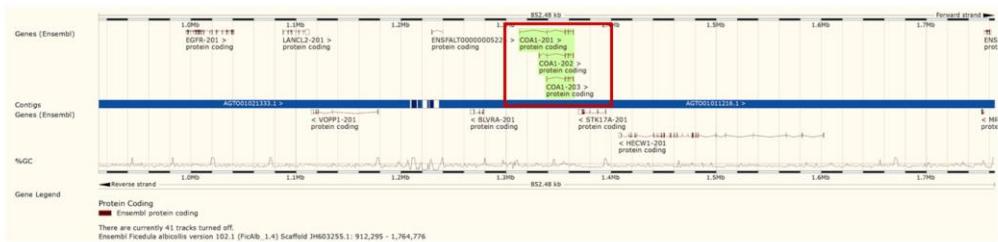


Figure S271: Gene order near *COA1* gene in the flycatcher genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S272

Taeniopygia guttata

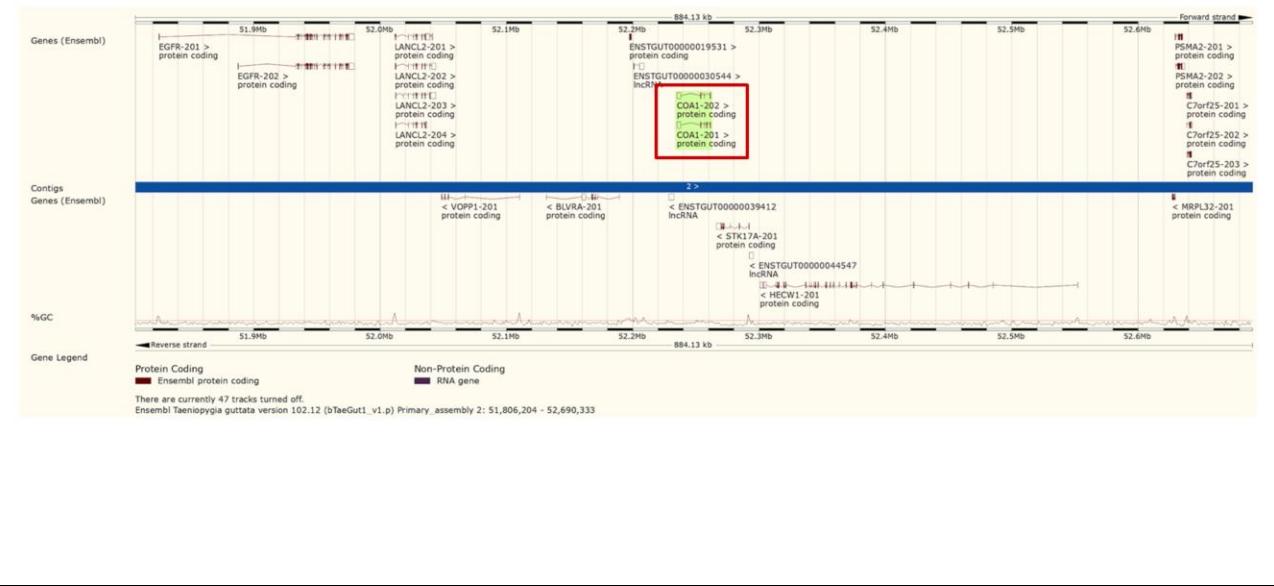


Figure S272: Gene order near *COA1* gene in the zebra finch genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S273

Camarhynchus parvulus



Figure S273: Gene order near *COA1* gene in the small tree finch genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S274

Strigops habroptila

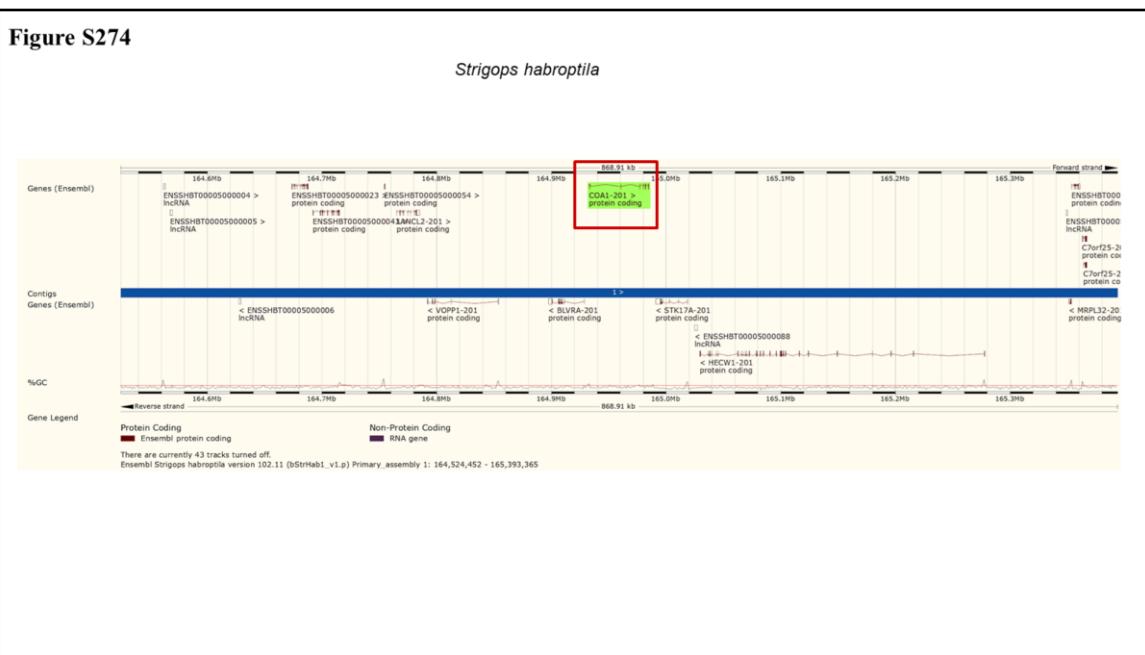


Figure S274: Gene order near *COA1* gene in the kakapo genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S275

Parus major

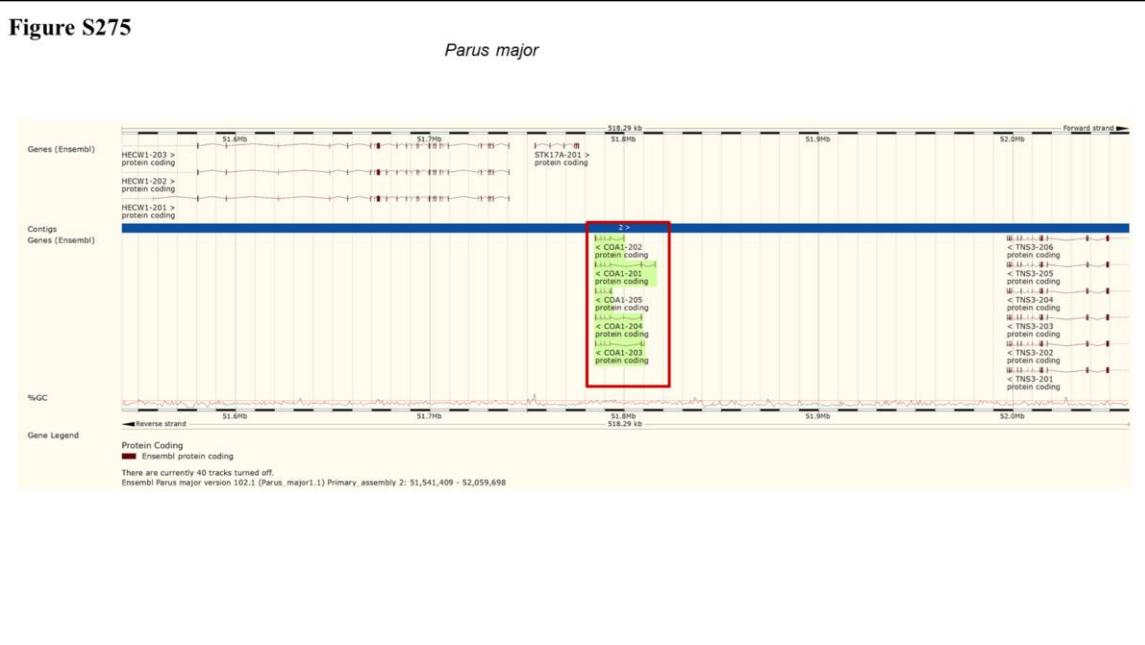


Figure S275: Gene order near *COA1* gene in the great tit genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosomal bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S276

Aquila chrysaetos chrysaetos

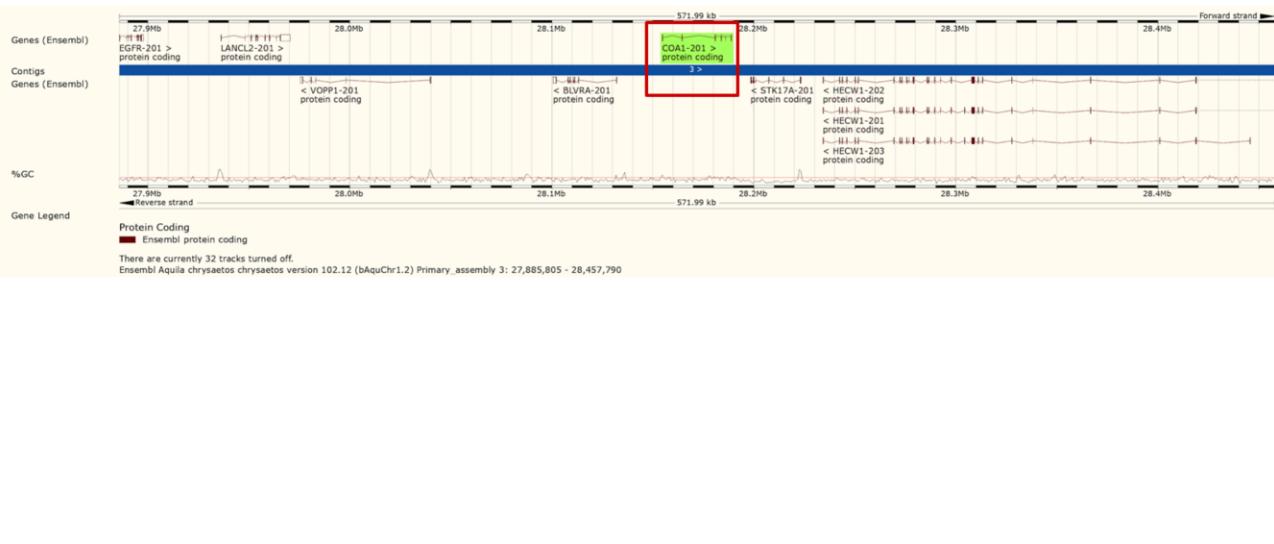


Figure S276: Gene order near *COA1* gene in the golden eagle genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. Chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S277

Acanthisitta chloris

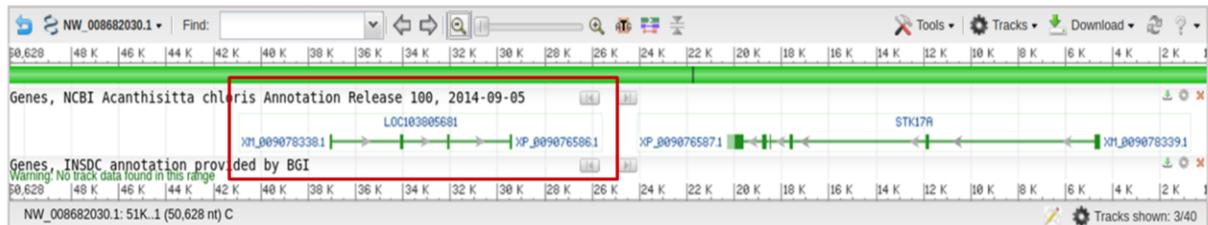


Figure S277: Gene order near *COA1* gene in the rifleman genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S278

Anser cygnoides



Figure S278: Gene order near *COA1* gene in the swan goose genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S279

Calidris pugnax

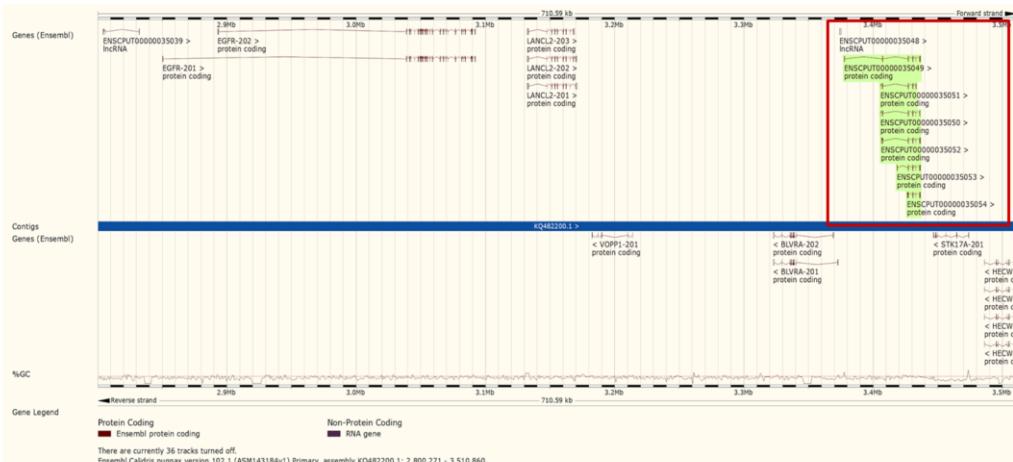


Figure S279: Gene order near *COA1* gene in the ruff genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S280

Antrostomus carolinensis

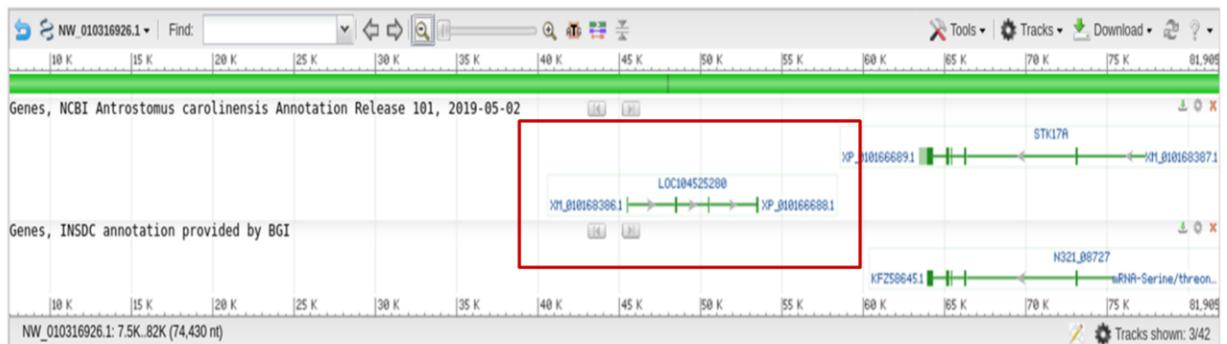


Figure S280: Gene order near *COA1* gene in the chuck-will-widow genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S281

Apaloderma vittatum

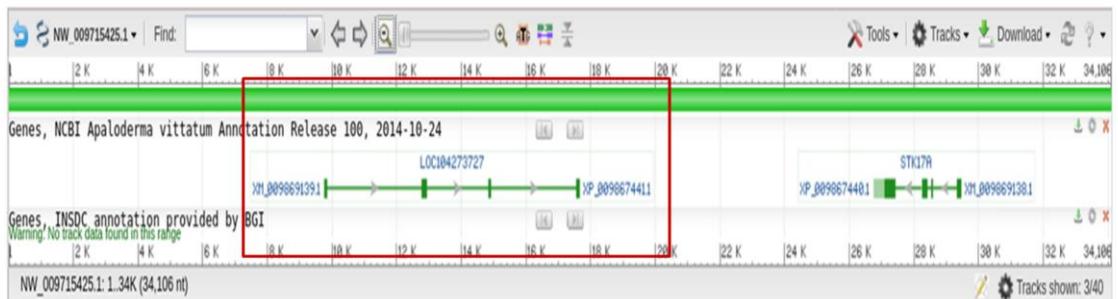


Figure S281: Gene order near *COA1* gene in the bar-tailed trogon genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S282

Aptenodytes forsteri

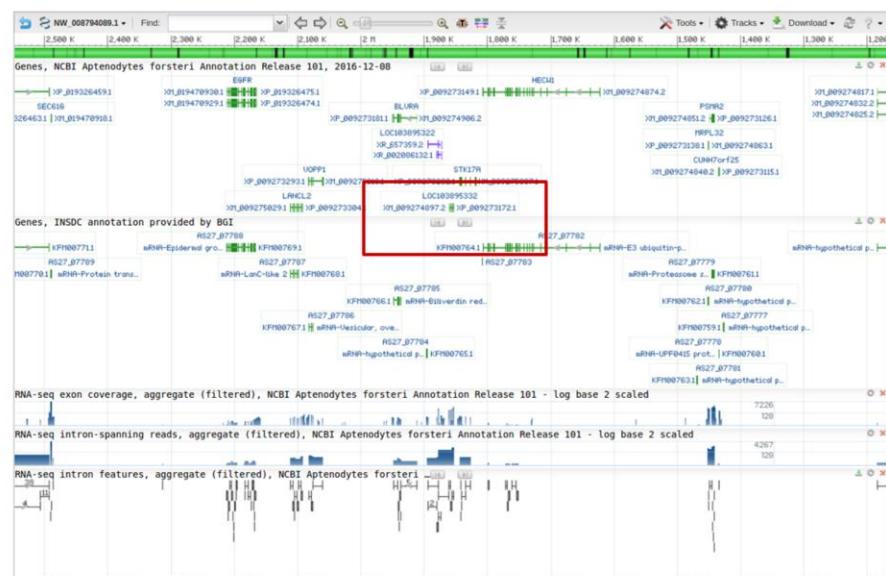


Figure S282: Gene order near *COA1* gene in the emperor penguin genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S283

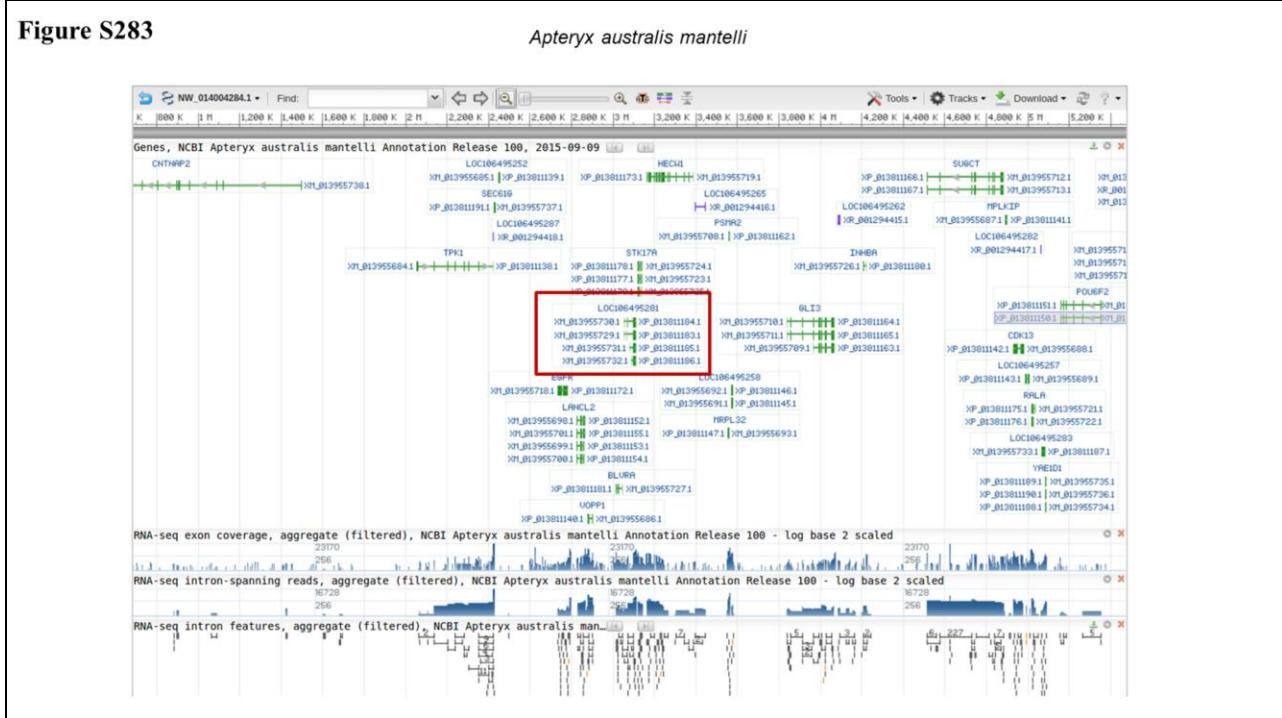


Figure S283: Gene order near *COA1* gene in the North Island brown kiwi genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S284

Aythya fuligula



Figure S284: Gene order near *COA1* gene in tufted duck genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S285

Balearica regulorum gibbericeps

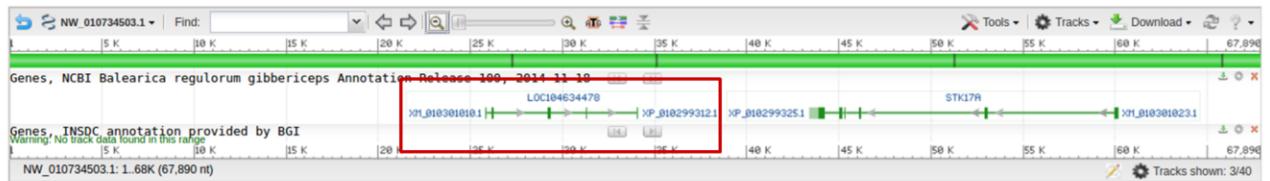


Figure S285: Gene order near *COA1* gene in the East African gray crowned-crane genome.

The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the $>$ or $<$ symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S286

Cyanistes caeruleus

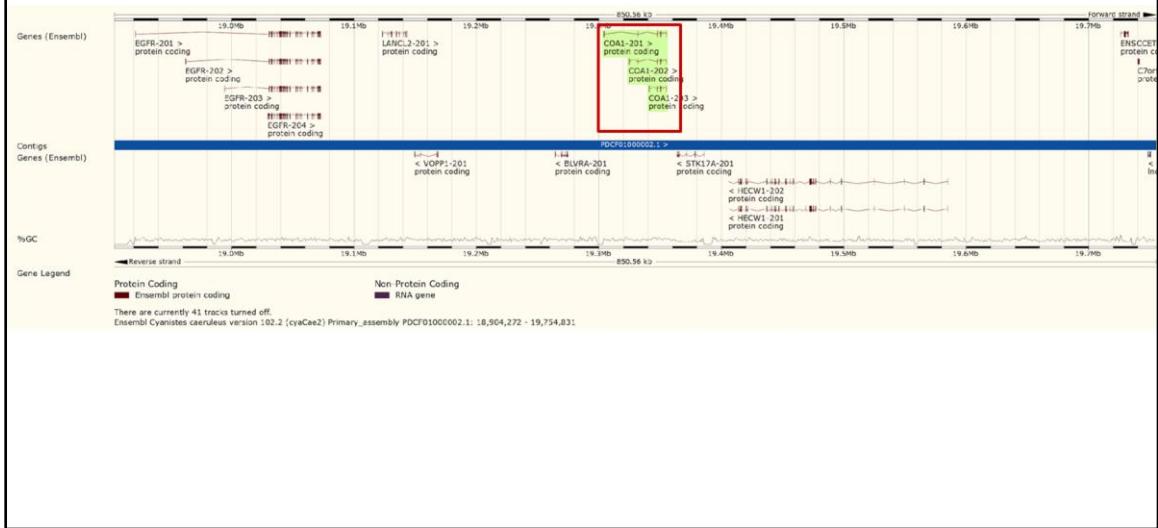


Figure S286: Gene order near *COA1* gene in the blue tit genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S287

Lepidothrix coronata

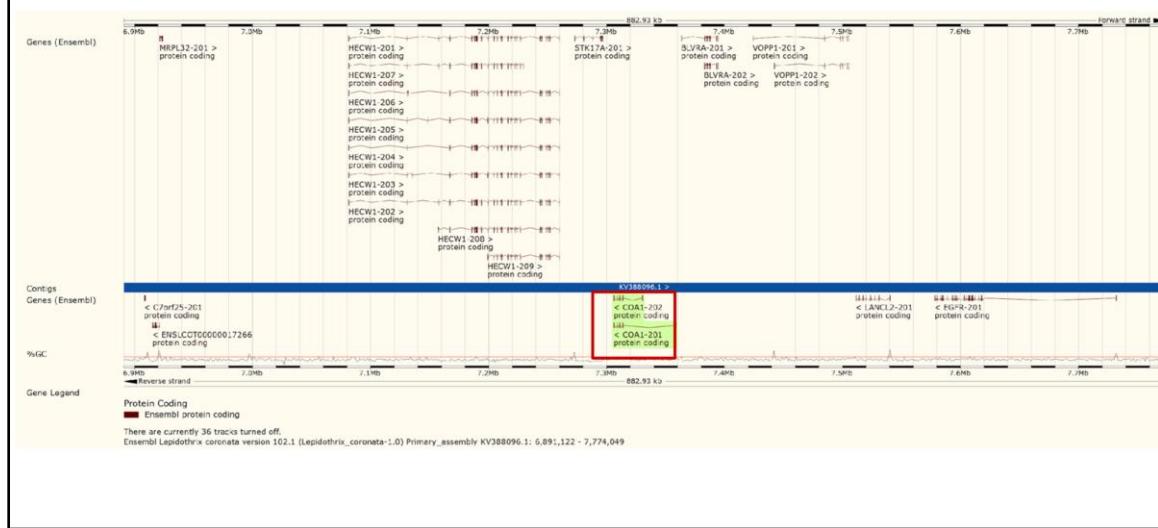


Figure S287: Gene order near *COA1* gene in the blue-crowned manakin genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S288

Buceros rhinoceros silvestris

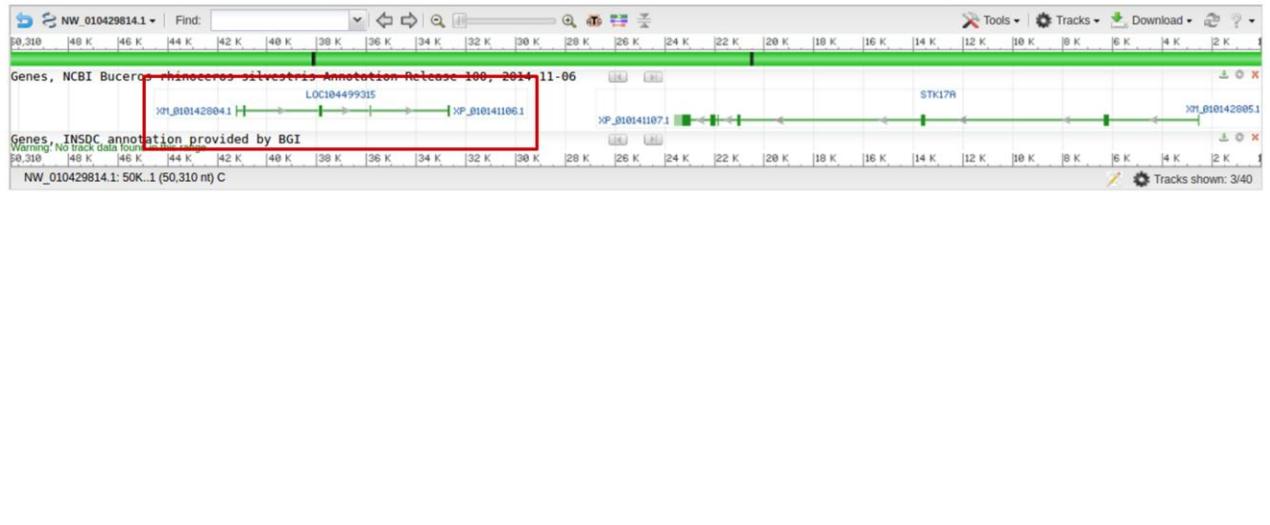


Figure S288: Gene order near *COA1* gene in the rhinoceros hornbill genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S289

Athene cunicularia

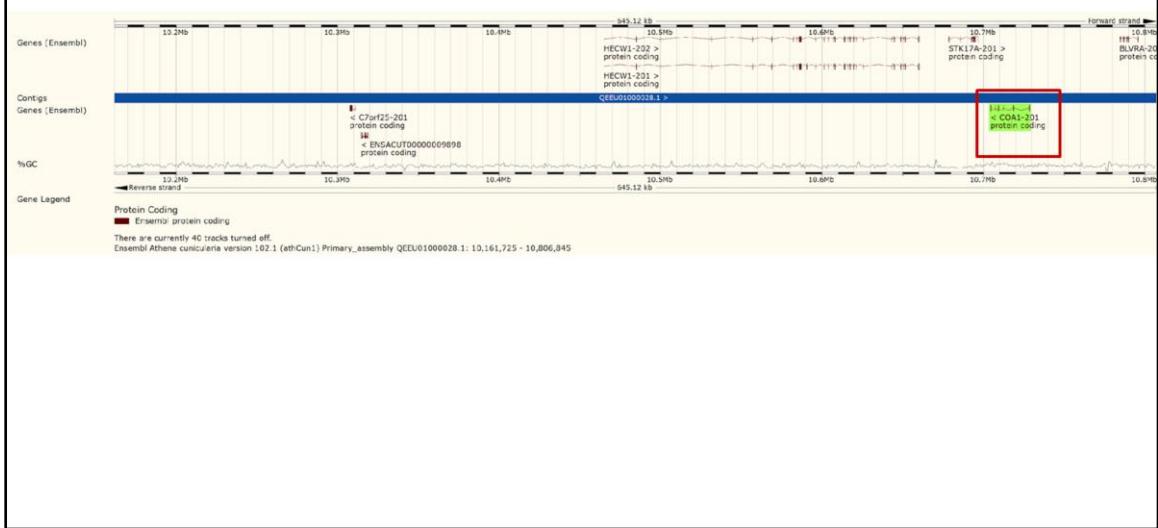


Figure S289: Gene order near *COA1* gene in the burrowing owl genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S290*Calypte anna*

Figure S290: Gene order near *COA1* gene in the Anna's hummingbird genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S291

Cariama cristata

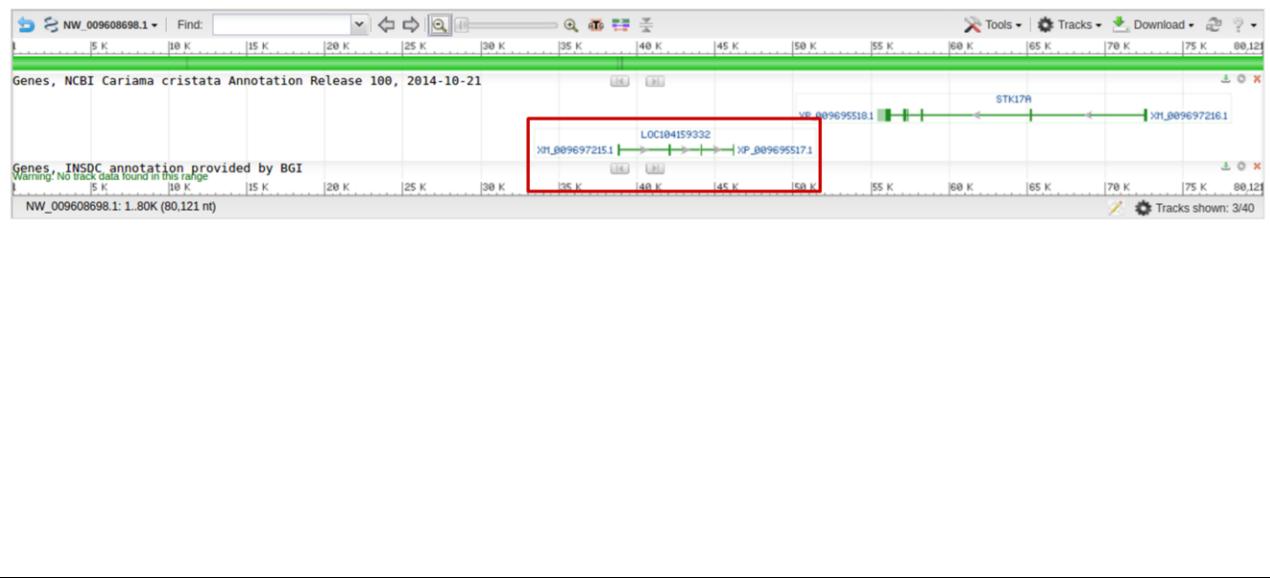


Figure S291: Gene order near *COA1* gene in the red-legged seriema genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S292

Chaetura pelagica

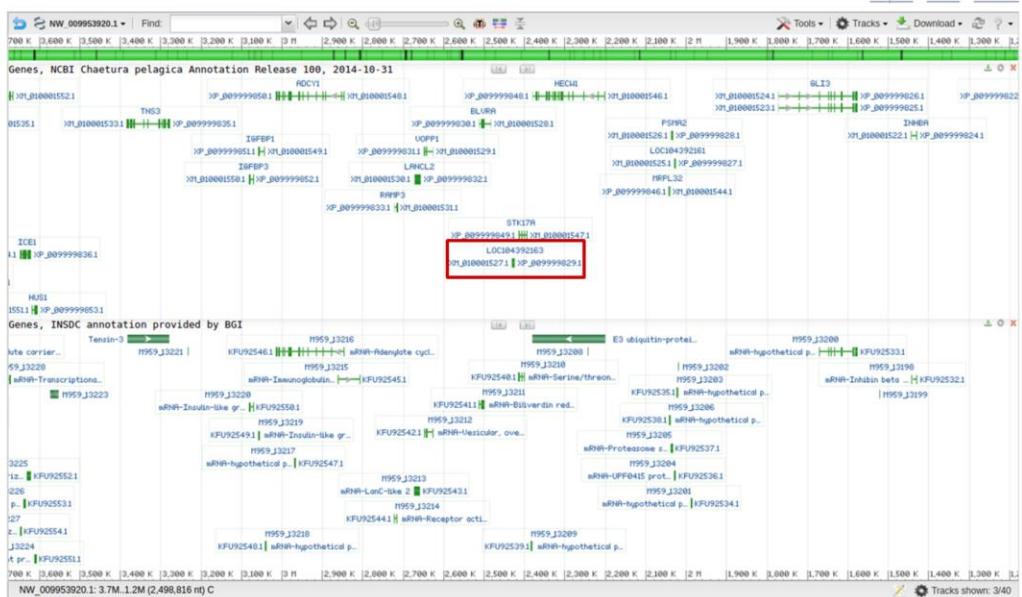


Figure S292: Gene order near *COA1* gene in the chimney swift genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosomal bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

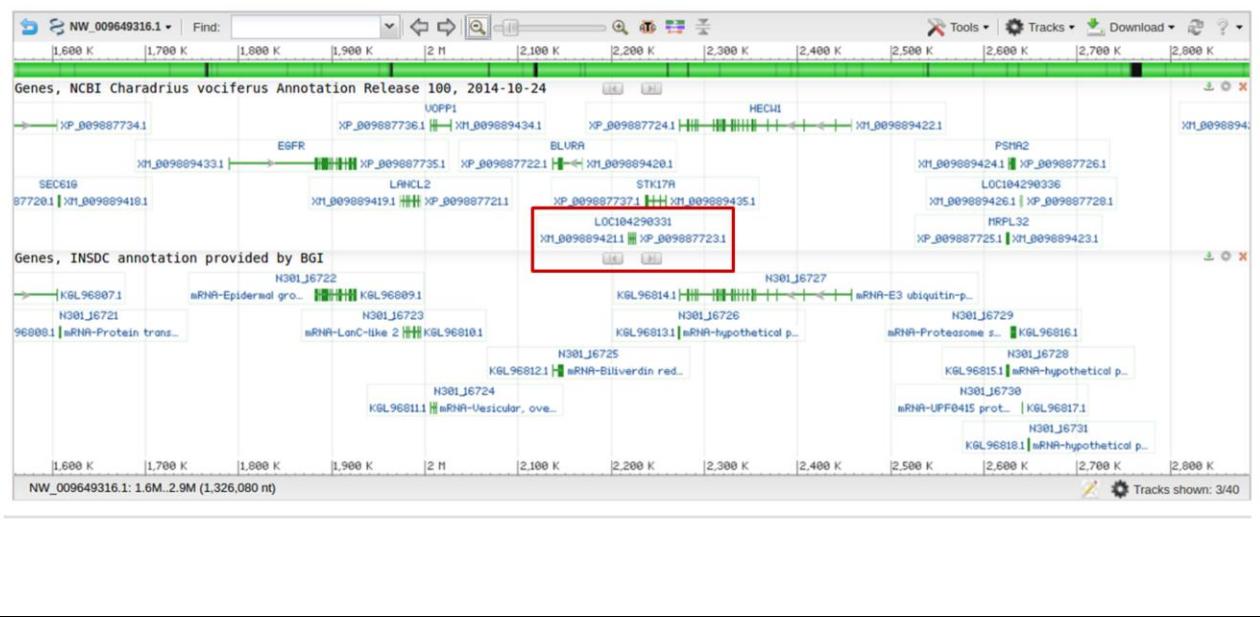
Figure S293*Charadrius vociferus*

Figure S293: Gene order near *COA1* gene in the killdeer genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. Chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S294



Figure S294: Gene order near *COA1* gene in the lance-tailed manakin genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. Chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S295

Chlamydotis macqueenii



Figure S295: Gene order near *COA1* gene in the MacQueen's bustard genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S296

Colius striatus



Figure S296: Gene order near *COA1* gene in the speckled mousebird genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S297

Columba livia

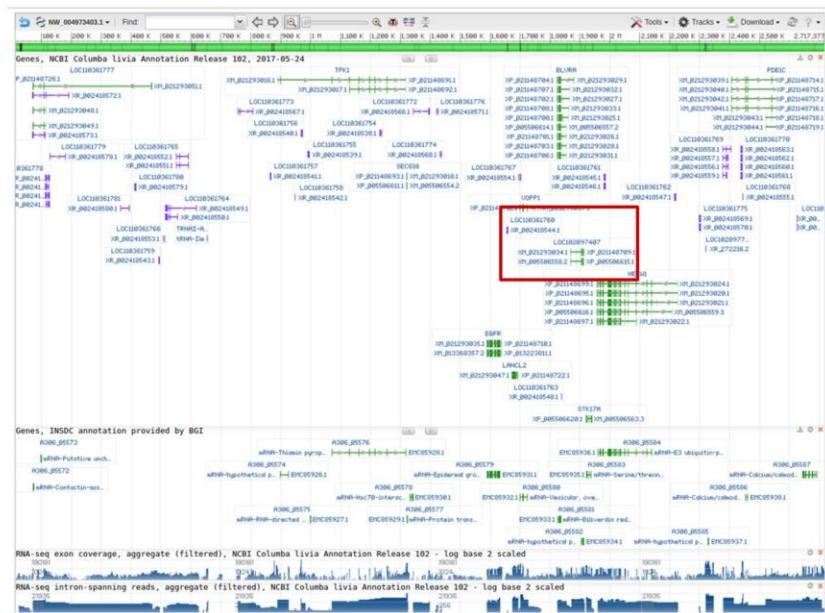


Figure S297: Gene order near *COA1* gene in the rock pigeon genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S298

Serinus canaria



Figure S298: Gene order near *COA1* gene in the common canary genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S299

Falco tinnunculus

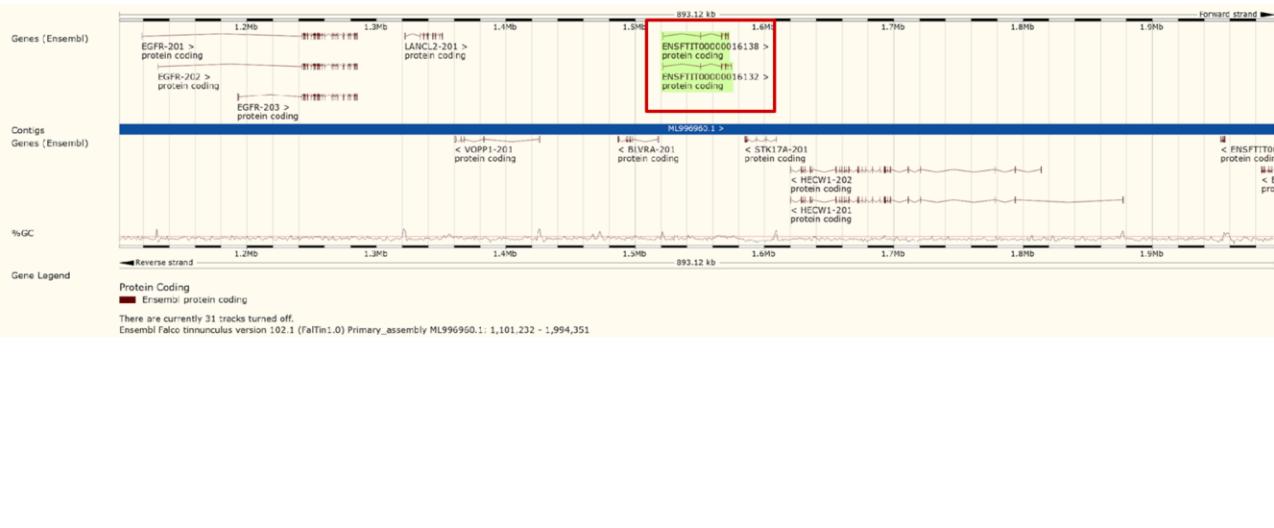


Figure S299: Gene order near *COA1* gene in the common kestrel genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S300

Corapipo altera



Figure S300: Gene order near *COA1* gene in the white-ruffed manakin genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S301

Corvus brachyrhynchos

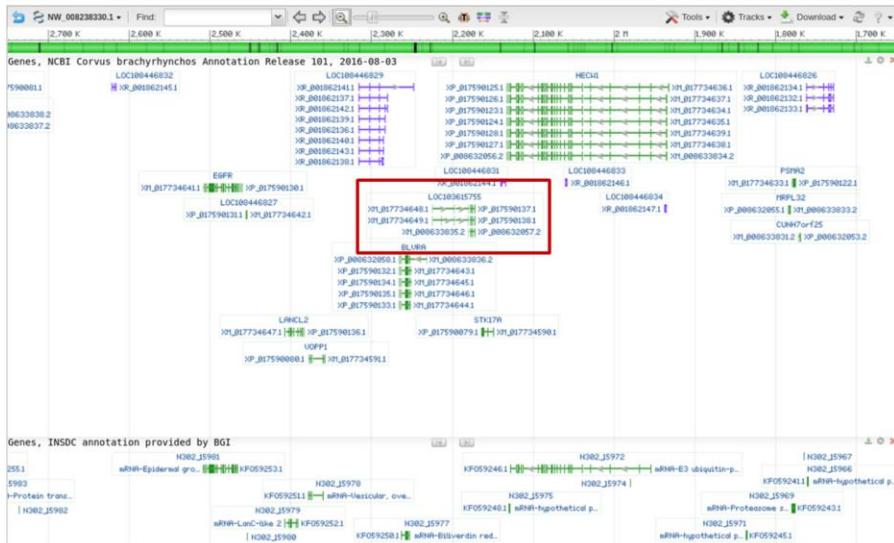


Figure S301: Gene order near *COA1* gene in the American crow genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S302

Corvus cornix cornix



Figure S302: Gene order near *COA1* gene in the hooded crow genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S303

Cuculus canorus

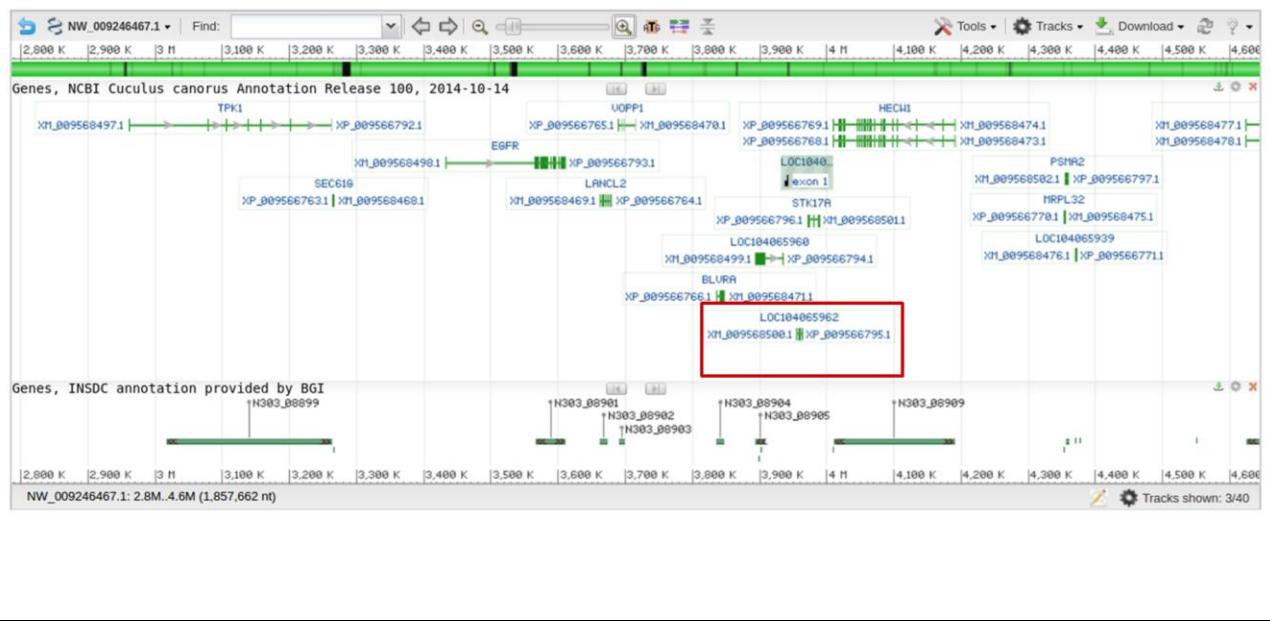


Figure S303: Gene order near *COA1* gene in the common cuckoo genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S304

Cygnus atratus

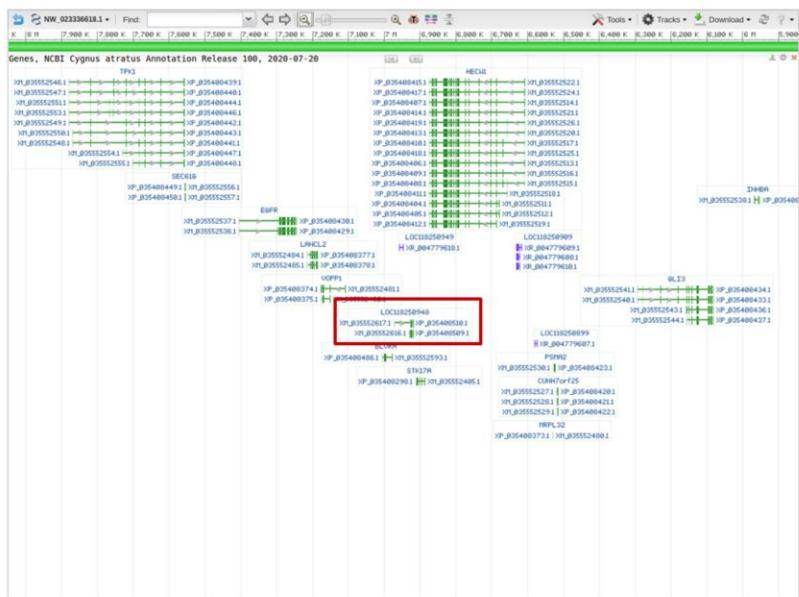


Figure S304: Gene order near *COA1* gene in the black swan genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

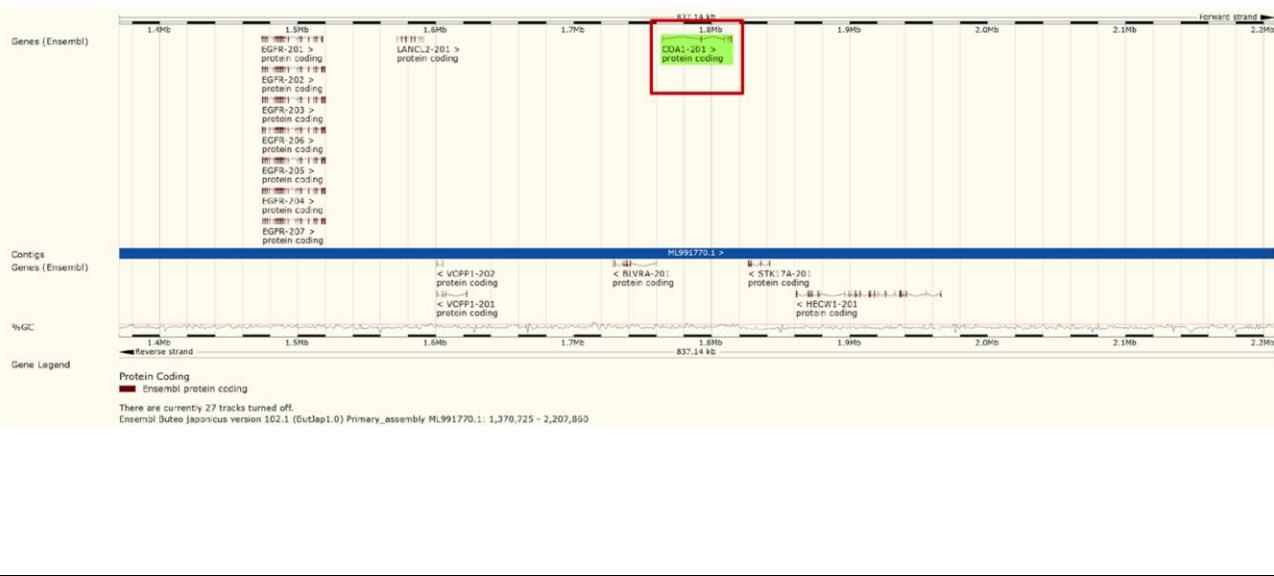
Figure S305*Buteo japonicus*

Figure S305: Gene order near *COA1* gene in the eastern buzzard genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the *>* or *<* symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S306

Egretta garzetta

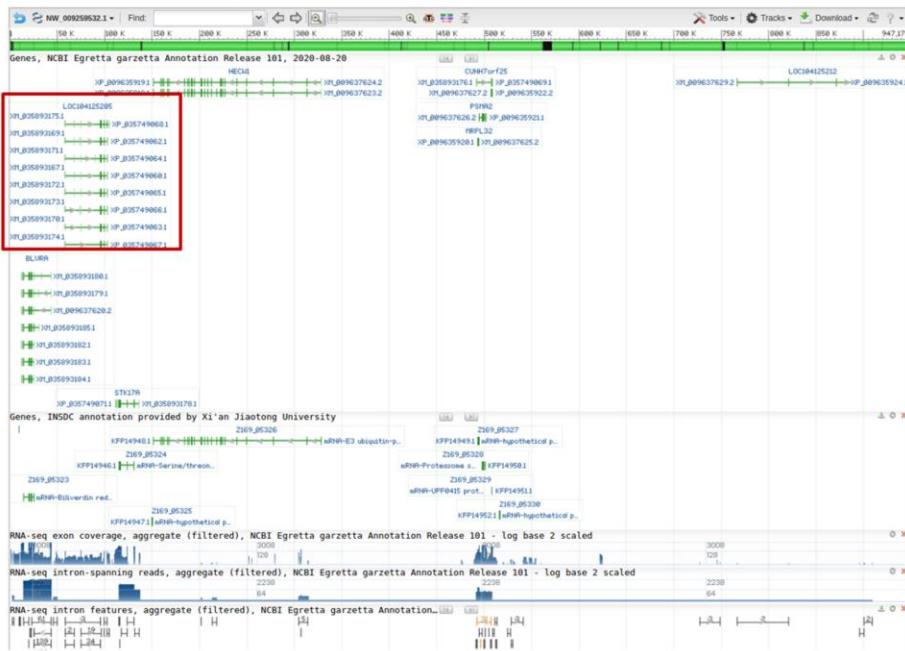


Figure S306: Gene order near *COA1* gene in the little egret genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

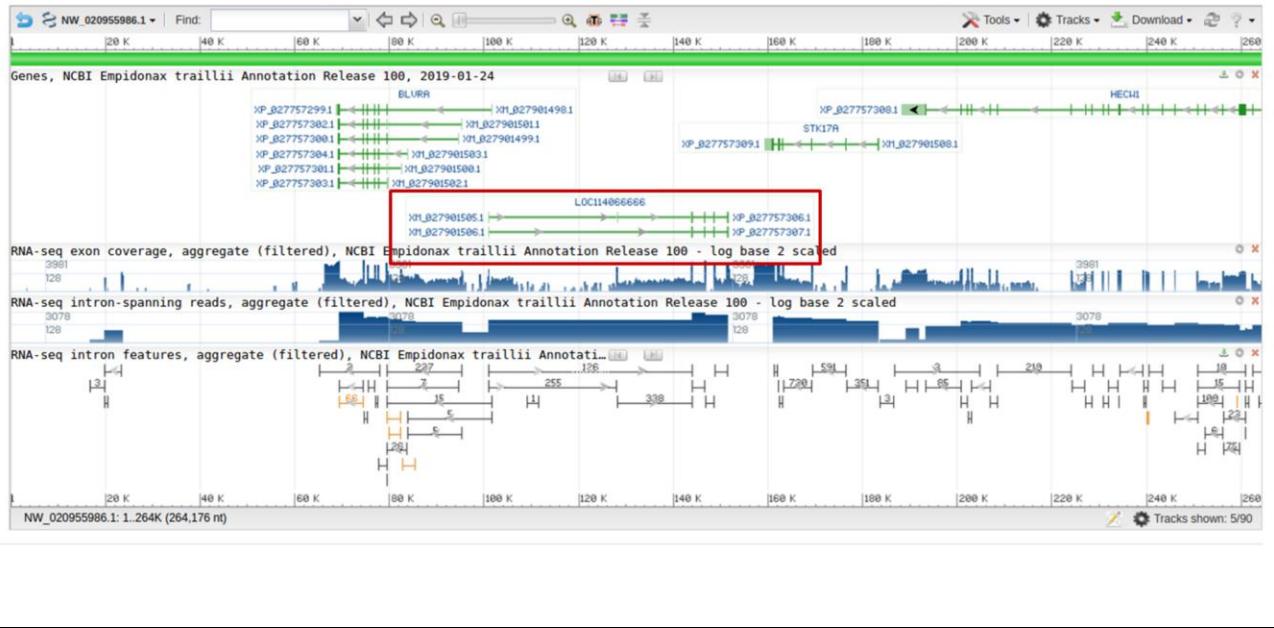
Figure S307*Empidonax traillii*

Figure S307: Gene order near *COA1* gene in the willow flycatcher genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S308

Eurypyga helias



Figure S308: Gene order near *COA1* gene in the sunbittern genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. Chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S309

Falco cherrug



Figure S309: Gene order near *COA1* gene in the saker falcon genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

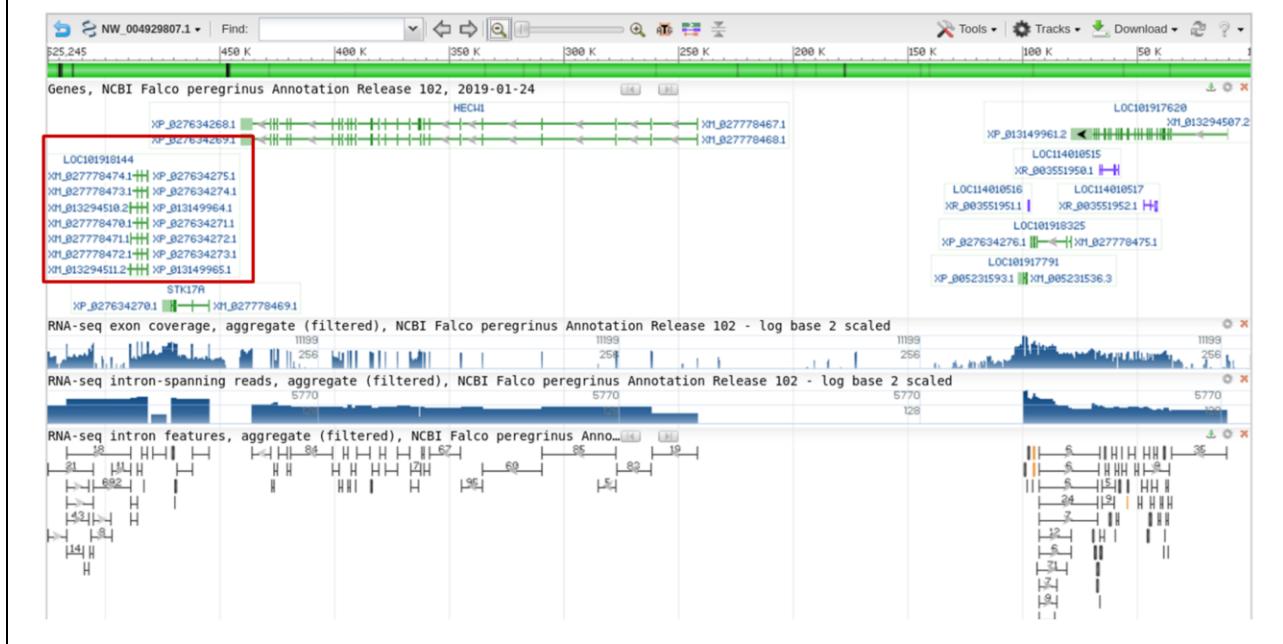
Figure S310*Falco peregrinus*

Figure S310: Gene order near *COA1* gene in the peregrine falcon genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S311

Falco rusticolus



Figure S311: Gene order near *COA1* gene in the gyrfalcon genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S312

Fulmarus glacialis

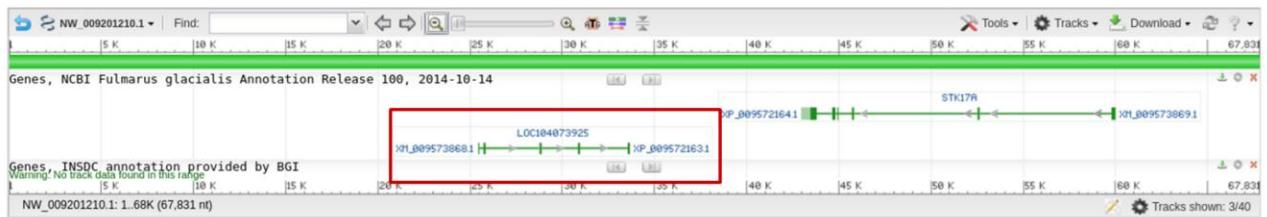


Figure S312: Gene order near *COA1* gene in the Northern fulmar genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S313

Gavia stellata



Figure S313: Gene order near *COA1* gene in the red-throated loon genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S314

Haliaeetus albicilla

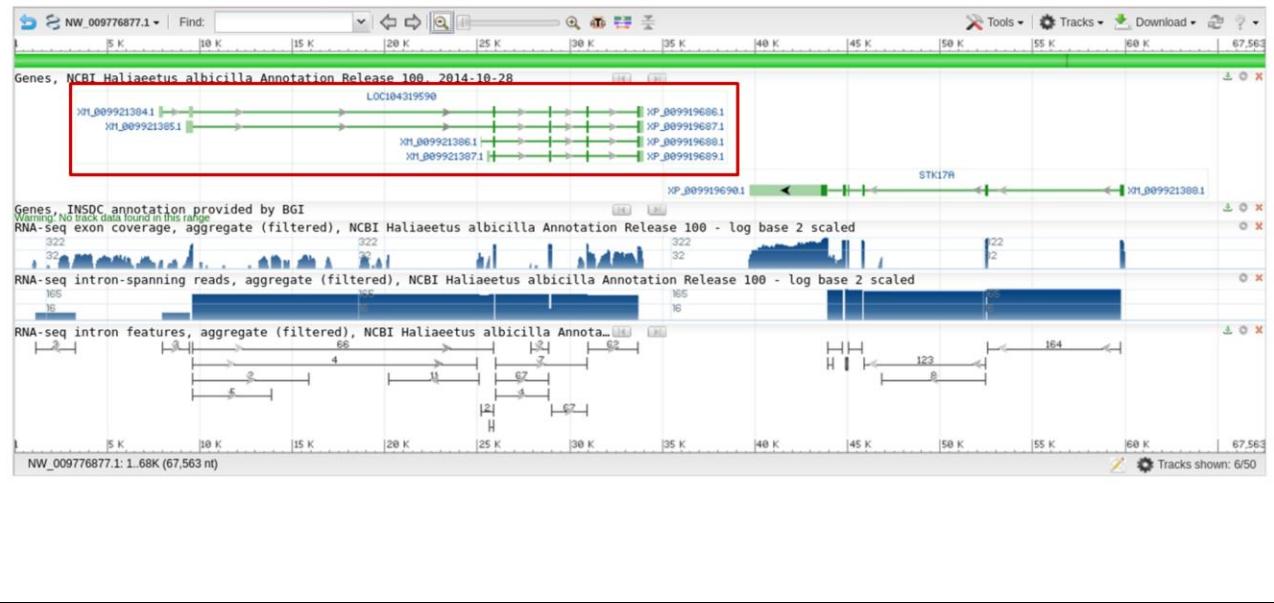


Figure S314: Gene order near *COA1* gene in the white-tailed eagle genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S315

Haliaeetus leucocephalus

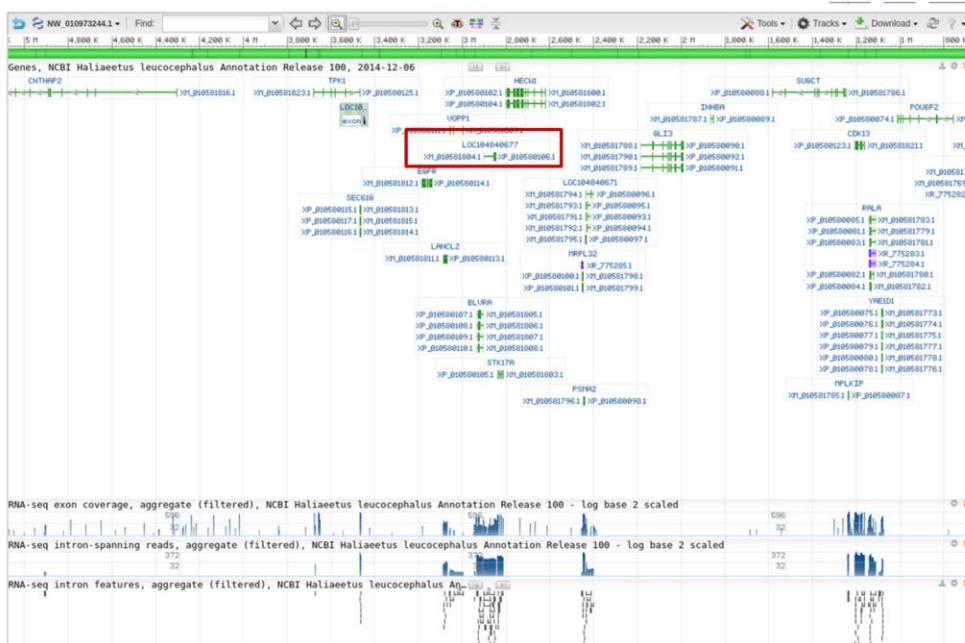


Figure S315: Gene order near *COA1* gene in the bald eagle genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S316*Melopsittacus undulatus*

Figure S316: Gene order near *COA1* gene in the budgerigar genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. Chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S317

Merops nubicus



Figure S317: Gene order near *COA1* gene in the carmine bee-eater genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S318

Mesitornis unicolor

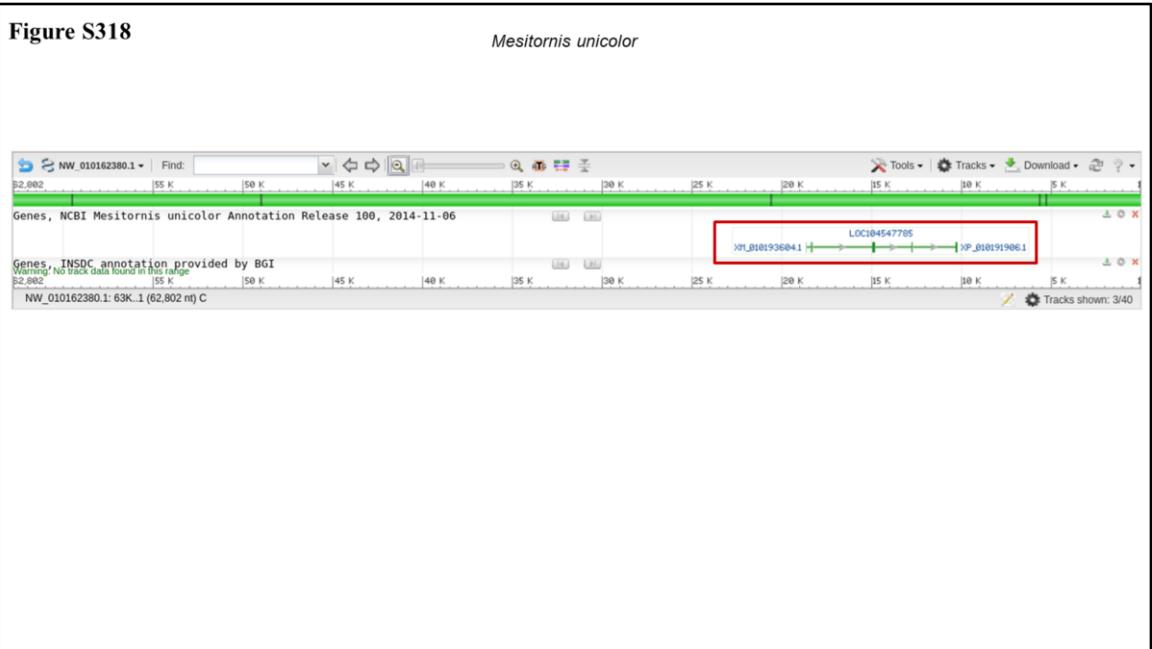


Figure S318: Gene order near *COA1* gene in the brown roatelo genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S319*Molothrus ater*

Figure S319: Gene order near *COA1* gene in the brown-headed cowbird genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

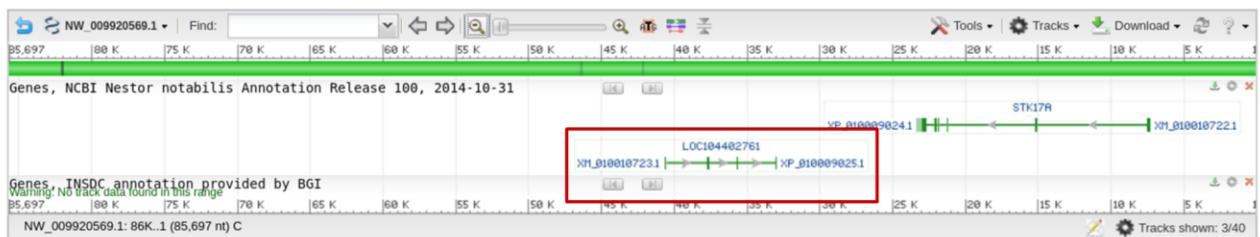
Figure S320*Nestor notabilis*

Figure S320: Gene order near *COA1* gene in the *kea* genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

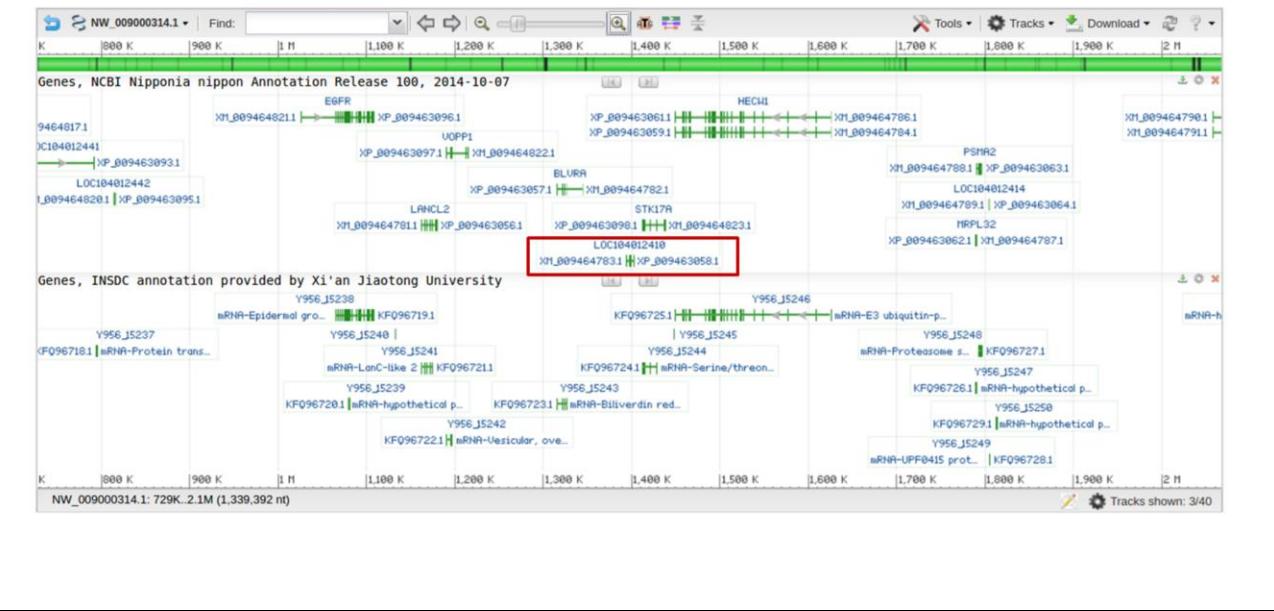
Figure S321*Nipponia nippon*

Figure S321: Gene order near *COA1* gene in the crested ibis genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

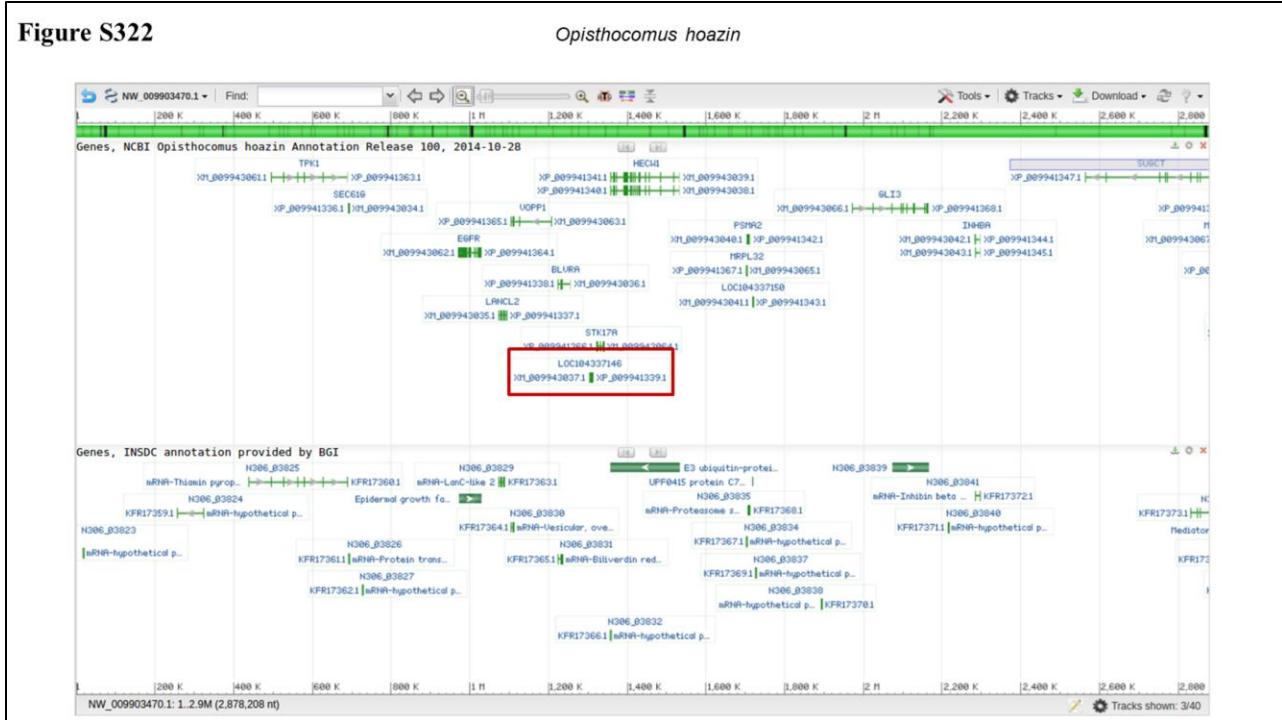
Figure S322*Opisthocomus hoazin*

Figure S322: Gene order near *COA1* gene in the hoatzin genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

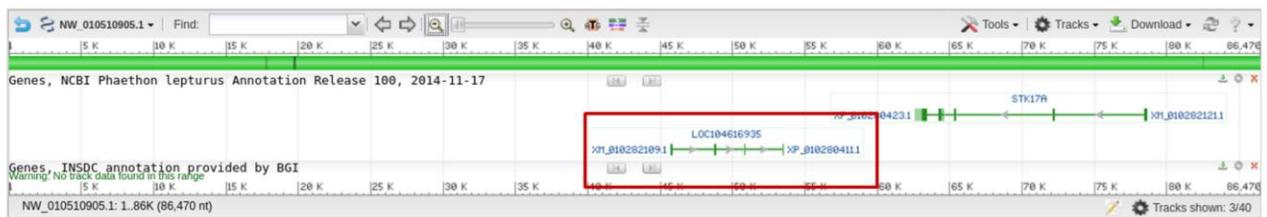
Figure S323*Phaethon lepturus*

Figure S323: Gene order near *COA1* gene in the white-tailed tropicbird genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S324

Phalacrocorax carbo

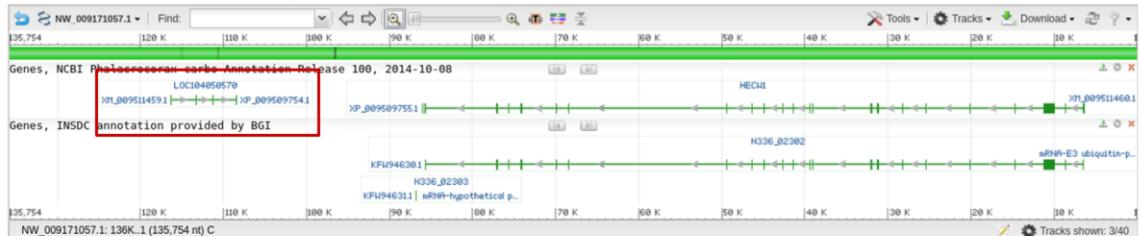


Figure S324: Gene order near *COA1* gene in the great cormorant genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

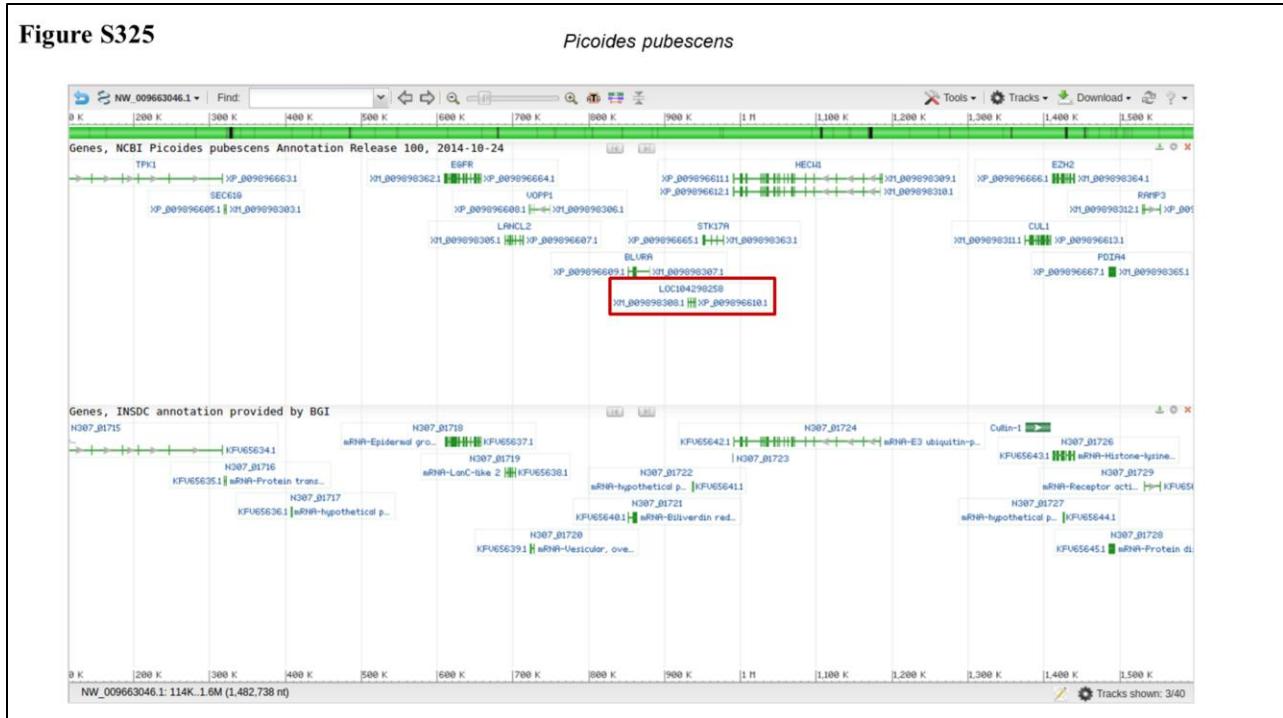
Figure S325*Picoides pubescens*

Figure S325: Gene order near *COA1* gene in the downy woodpecker genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S326*Pterocles gutturalis*

Figure S326: Gene order near *COA1* gene in the yellow-throated sandgrouse genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. Chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S327

Pygoscelis adeliae

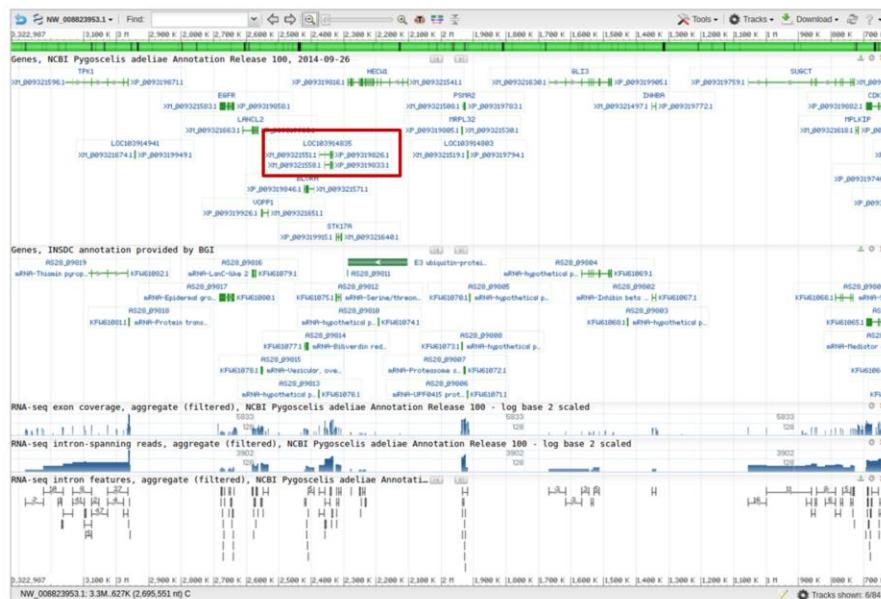


Figure S327: Gene order near *COA1* gene in the Adelie penguin genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

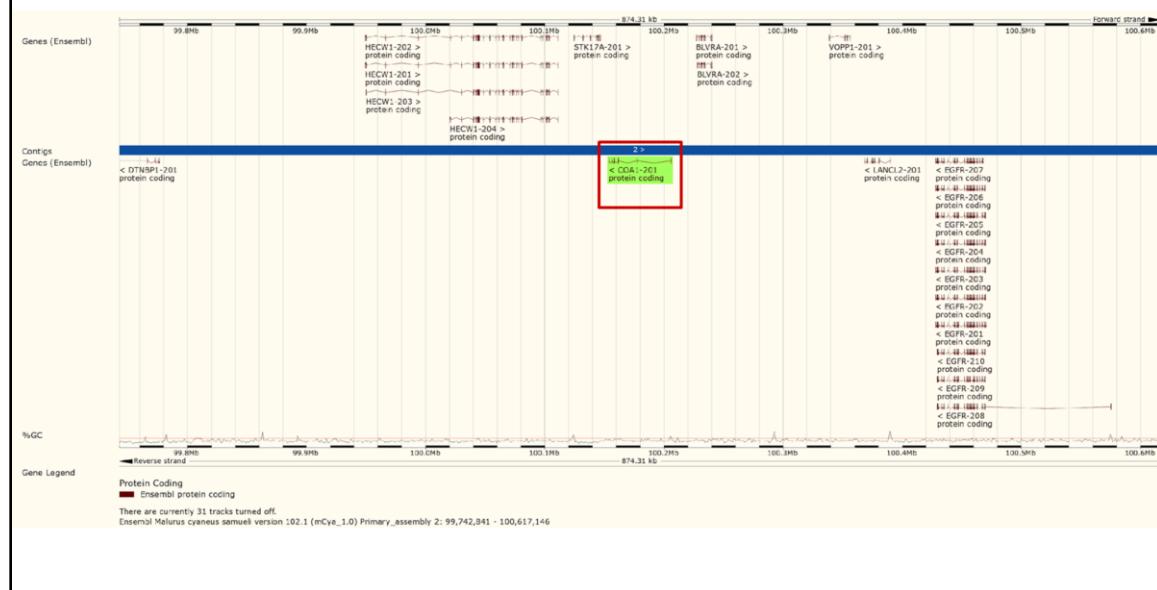
Figure S328*Malurus cyaneus samueli*

Figure S328: Gene order near *COA1* gene in the superb fairywren genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. Chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S329

Catharus ustulatus

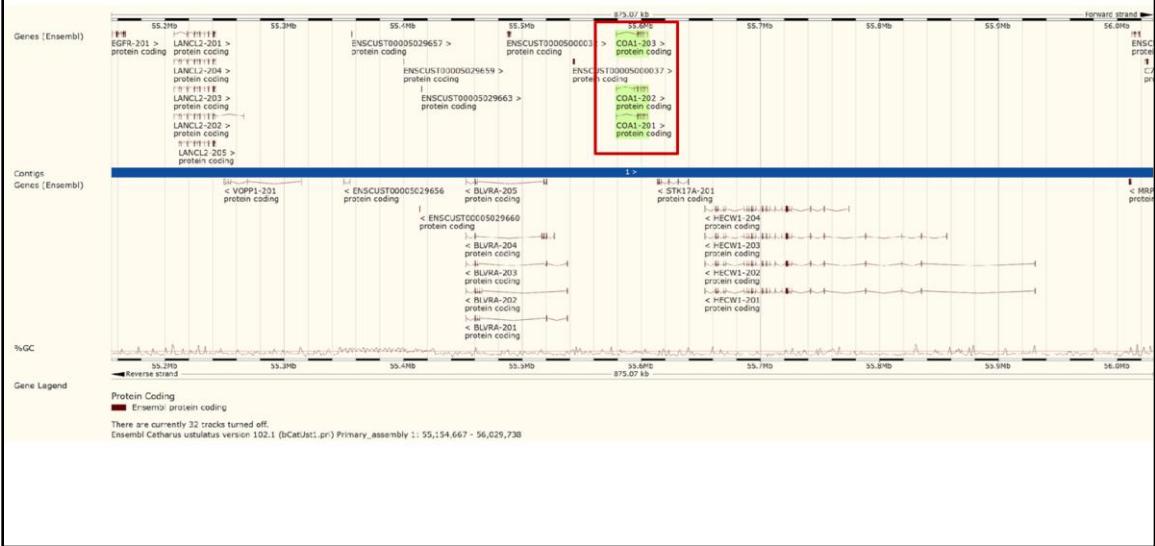


Figure S329: Gene order near *COA1* gene in the Swainson's thrush genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S330

Tauraco erythrolophus



Figure S330: Gene order near *COA1* gene in the red-crested turaco genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

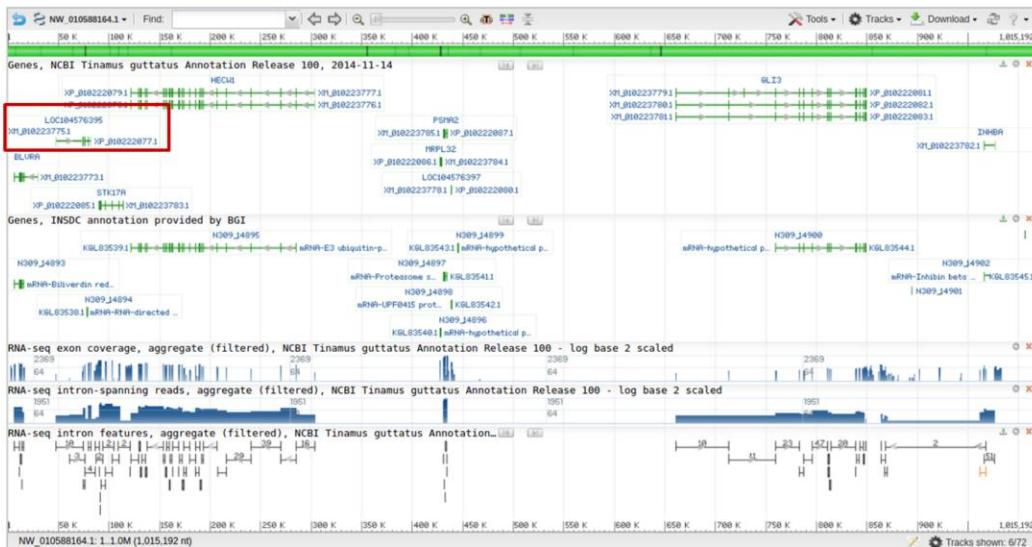
Figure S331*Tinamus guttatus*

Figure S331: Gene order near *COA1* gene in the white-throated tinamou genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S332*Tyto alba*

Figure S332: Gene order near *COA1* gene in the barn owl genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosomal bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S333

Oxyura jamaicensis

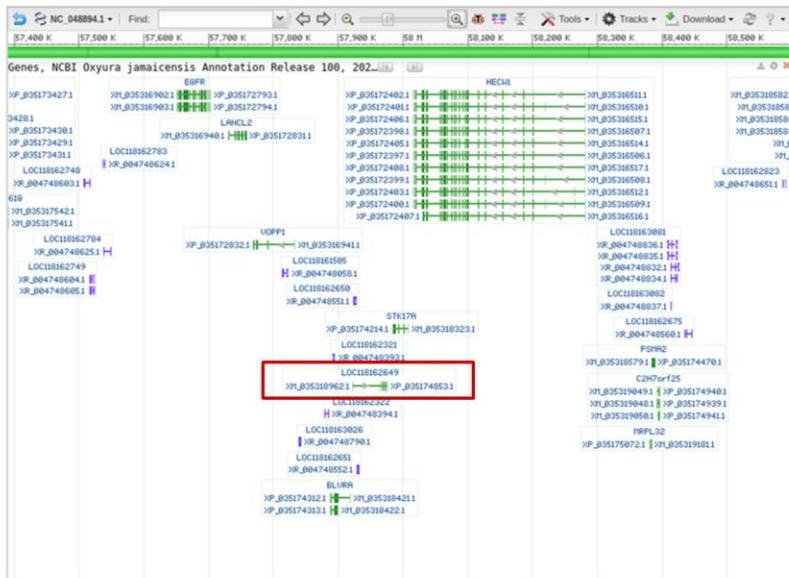


Figure S333: Gene order near *COA1* gene in the ruddy duck genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S334*Pipra filicauda*

Figure S334: Gene order near *COA1* gene in the wire-tailed manakin genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S335

Neopelma chrysocephalum

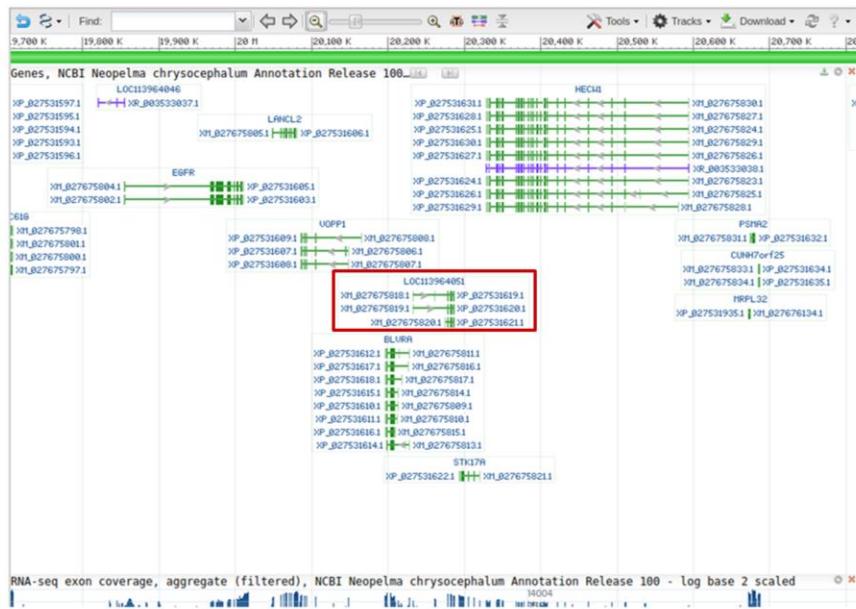


Figure S335: Gene order near *COA1* gene in the saffron-crested tyrant-manakin genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. Chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

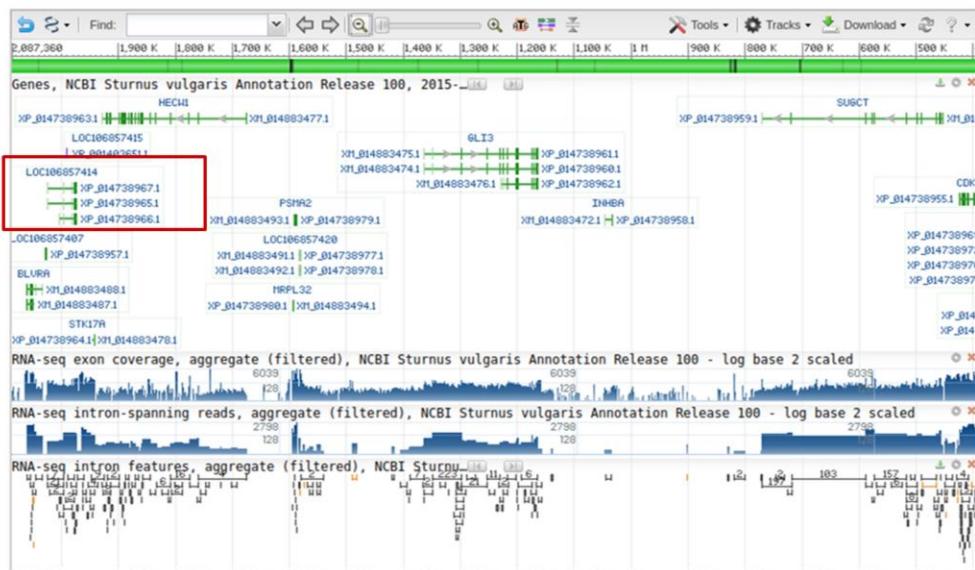
Figure S336*Sturnus vulgaris*

Figure S336: Gene order near *COA1* gene in the common starling genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

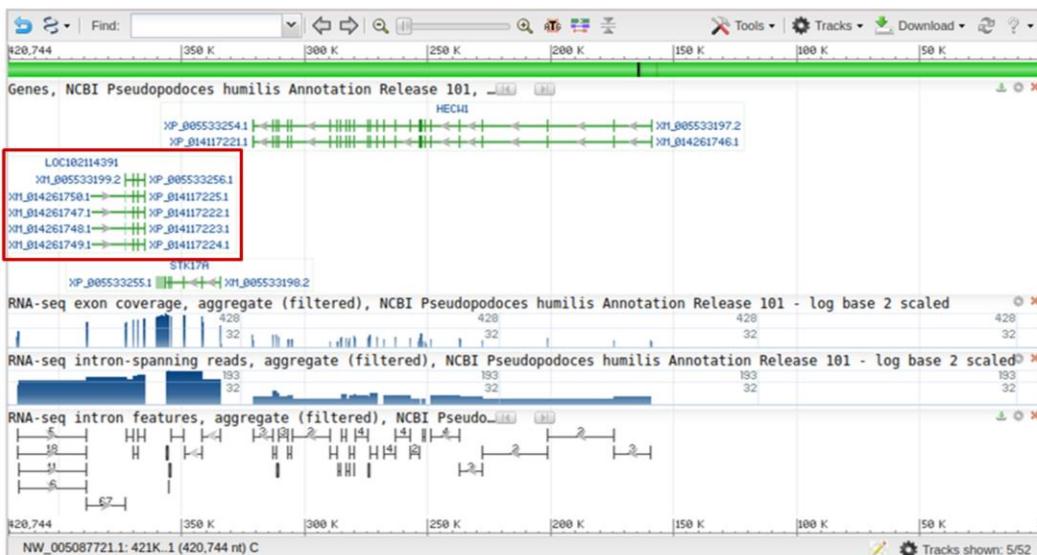
Figure S337*Pseudopodoces humilis*

Figure S337: Gene order near *COA1* gene in the Tibetan ground-tit genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S338

Pelecanus crispus

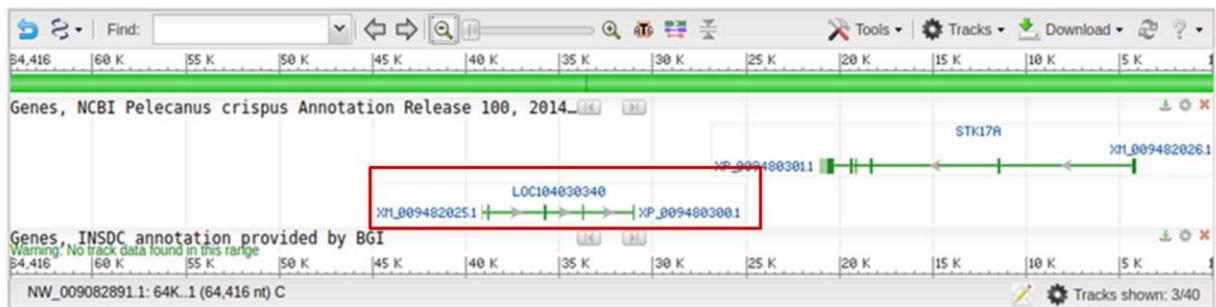


Figure S338: Gene order near *COA1* gene in the Dalmatian pelican genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S339

Rodents group

Ochotona princeps

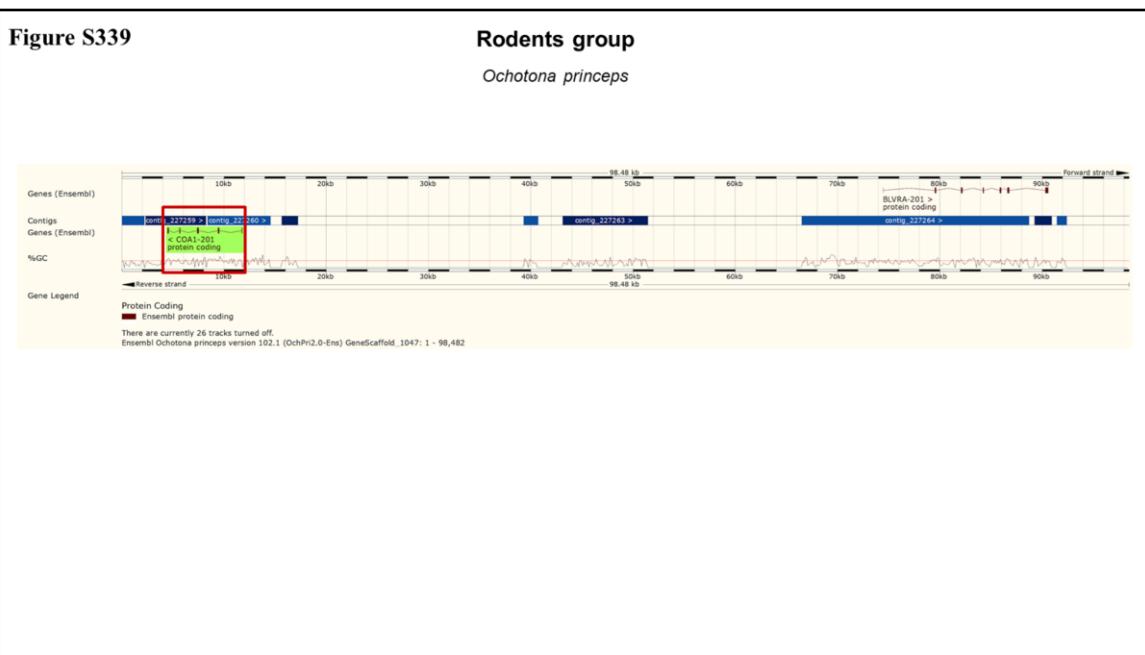


Figure S339: Gene order near *COA1* gene in the American pika (*Ochotona princeps*) genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S340

Fukomys damarensis

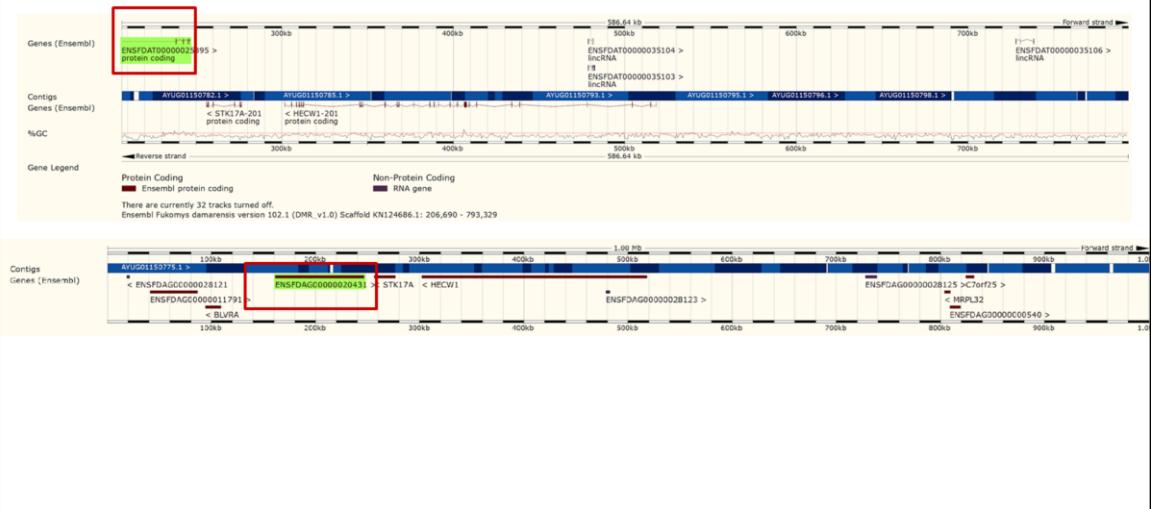


Figure S340: Gene order near *COA1* gene in the damara mole-rat genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S341

Cavia porcellus



Figure S341: Gene order near *COA1* gene in the domestic guinea pig genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

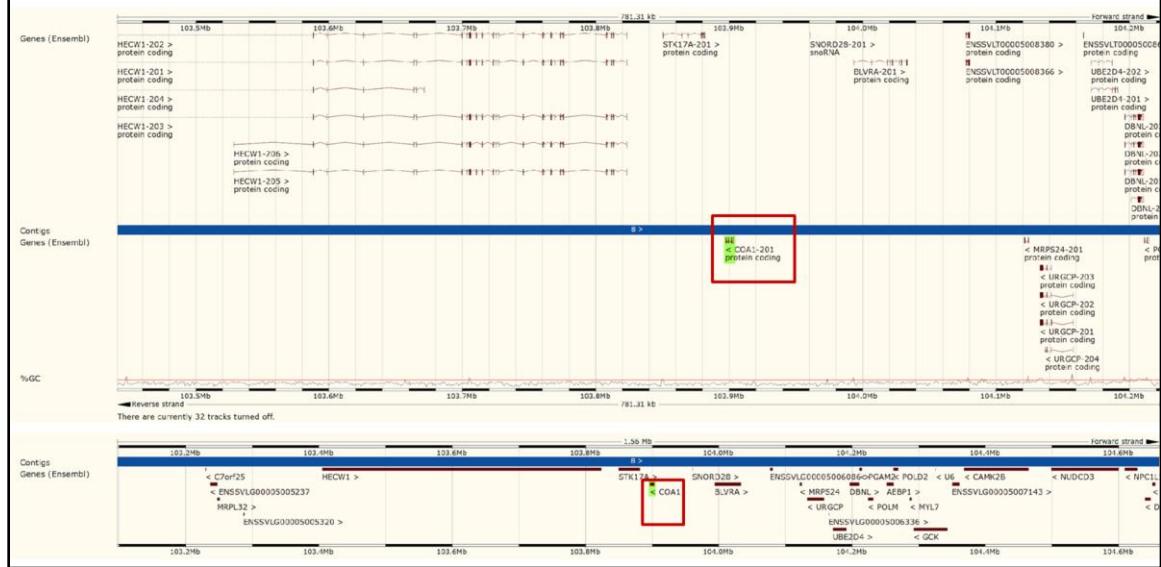
Figure S342*Sciurus vulgaris*

Figure S342: Gene order near *COA1* gene in the Eurasian red squirrel genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S343

Chinchilla lanigera

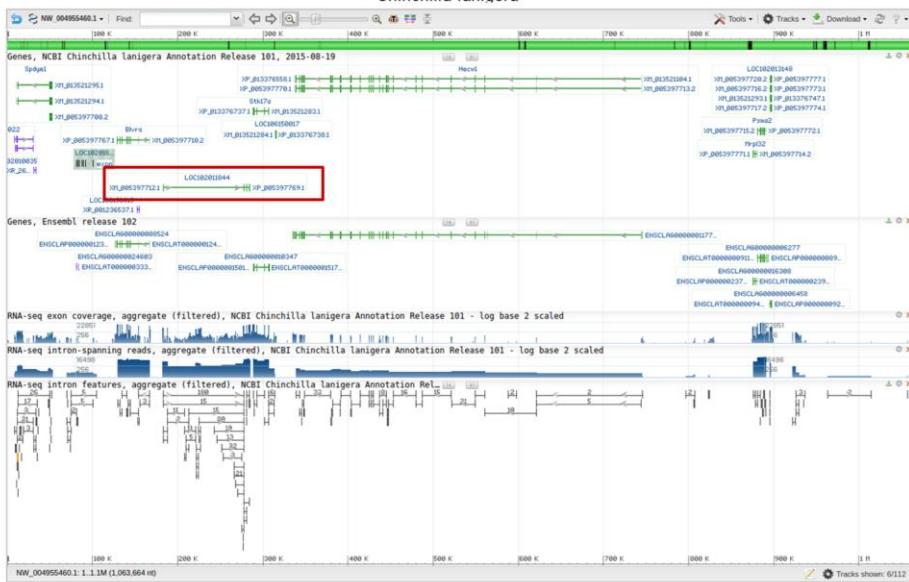


Figure S343: Gene order near *COA1* gene in the long-tailed chinchilla genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S344

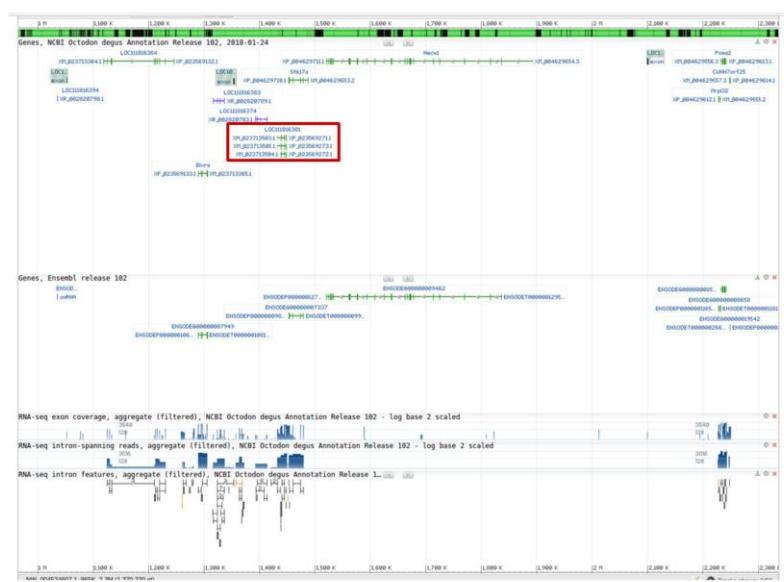


Figure S344: Gene order near *COA1* gene in the degu genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S345

Heterocephalus glaber

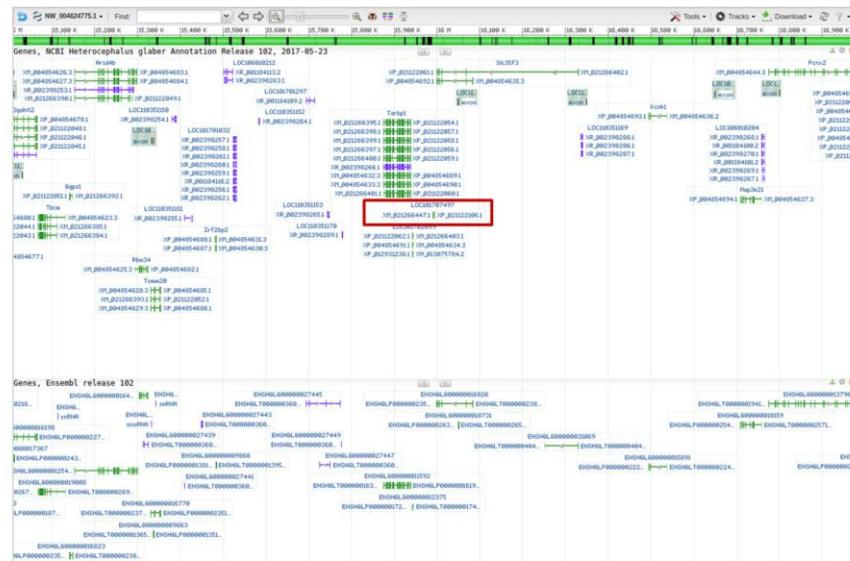


Figure S345: Gene order near *COA1* gene in the naked mole-rat genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosomal bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S346

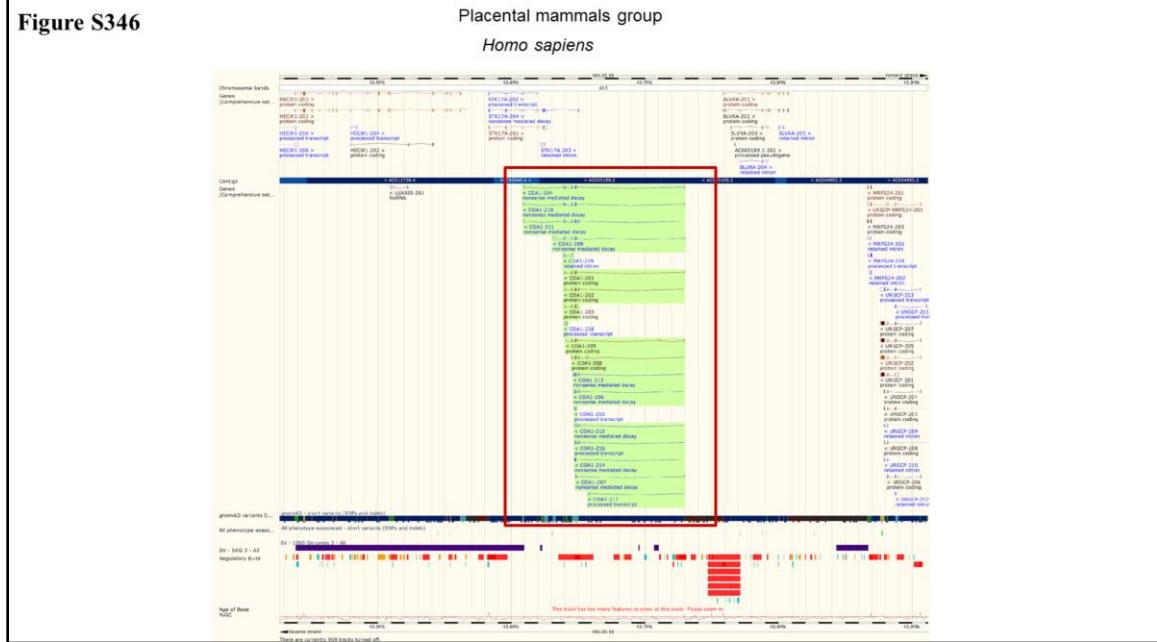


Figure S346: Gene order near *COA1* gene in the *human* genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S347

Macaca mulatta

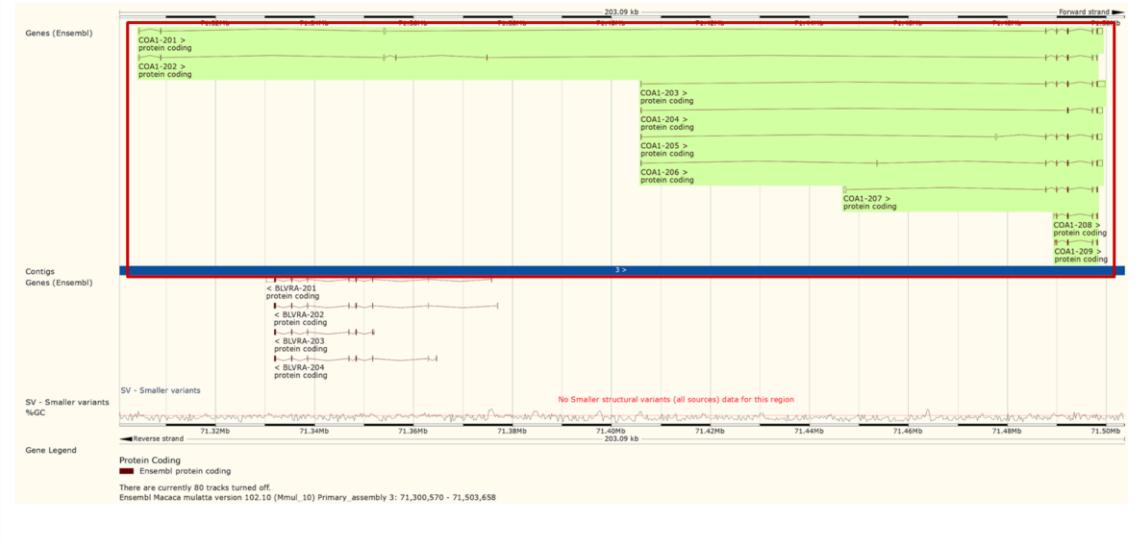


Figure S347: Gene order near *COA1* gene in the macaque genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

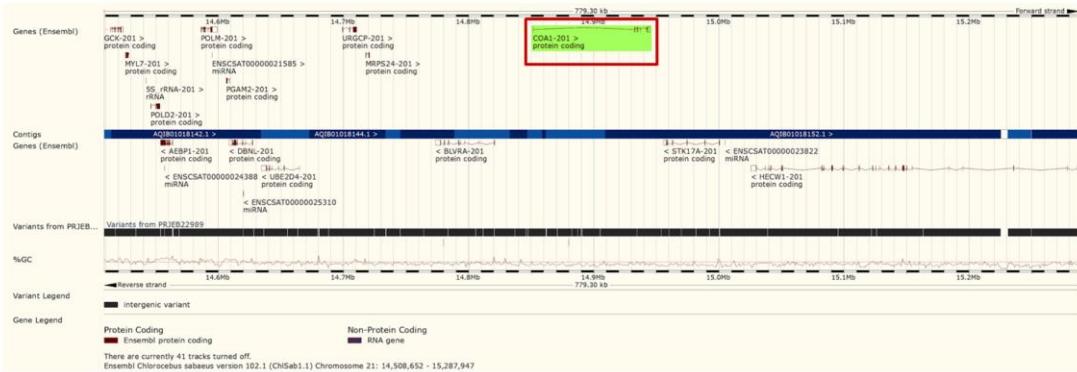
Figure S348*Chlorocebus sabaeus*

Figure S348: Gene order near *COA1* gene in the velvet-AGM genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S349

Nomascus leucogenys

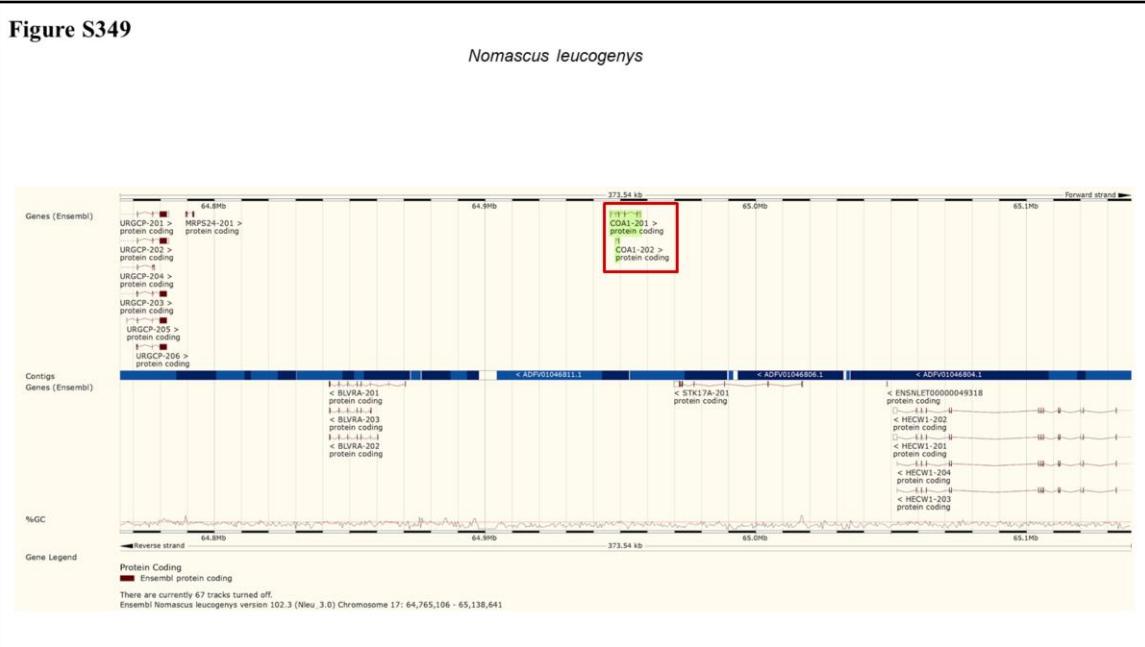


Figure S349: Gene order near *COA1* gene in the gibbon genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S350

Pan troglodytes

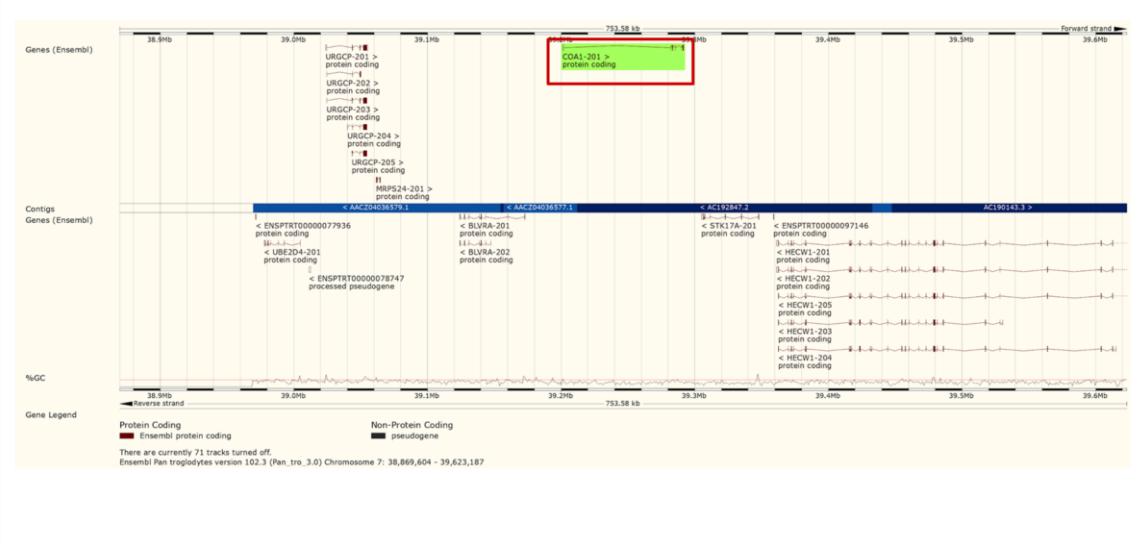


Figure S350: Gene order near *COA1* gene in the chimpanzee genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S351

Colobus angolensis palliatus

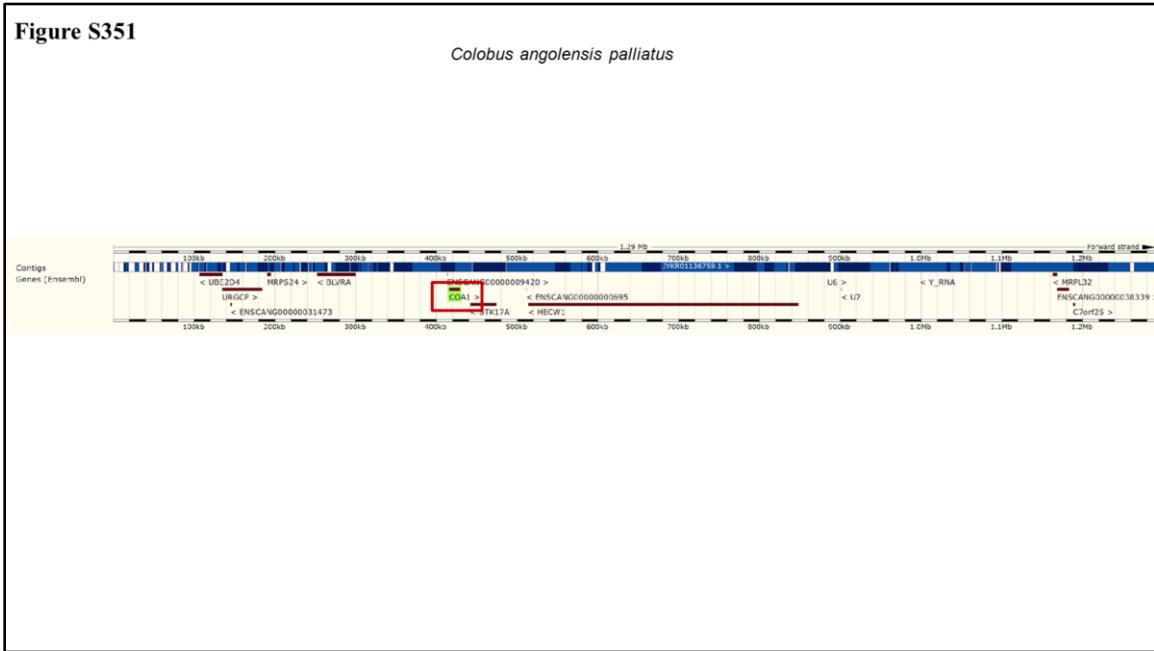


Figure S351: Gene order near *COA1* gene in the Angola colobus genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

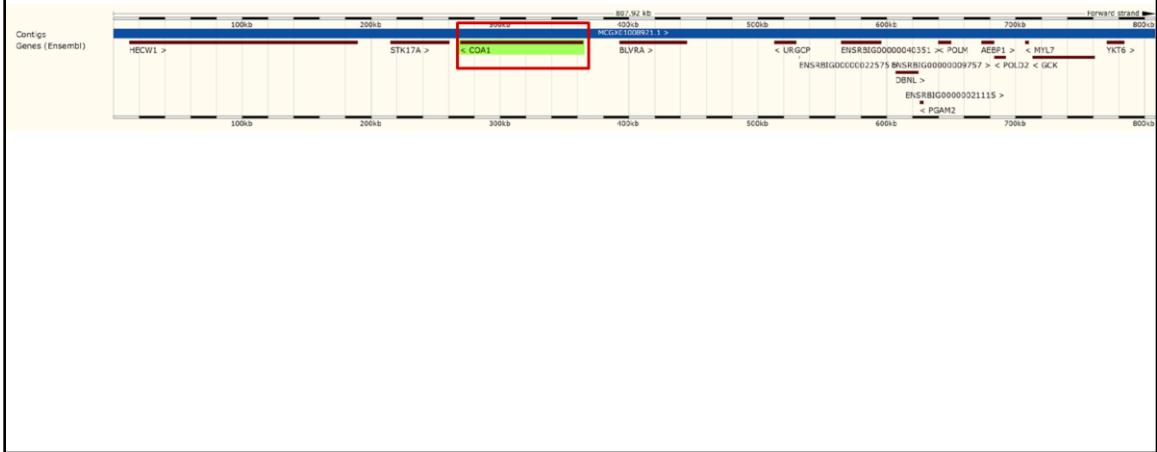
Figure S352*Rhinopithecus bieti*

Figure S352: Gene order near *COA1* gene in the black snub-nosed monkey genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S353

Saimiri boliviensis boliviensis

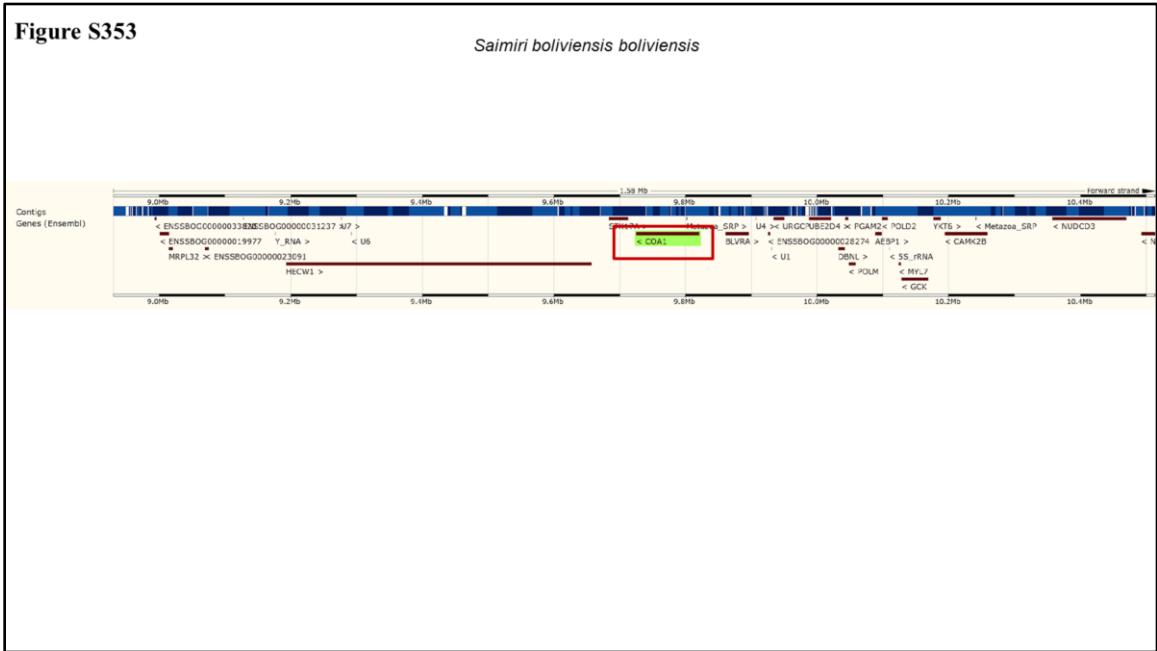


Figure S353: Gene order near *COA1* gene in the Bolivian squirrel monkey genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. Chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S354

Otolemur garnettii

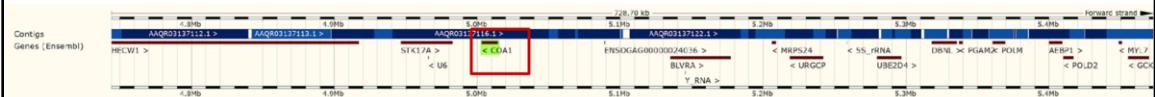


Figure S354: Gene order near *COA1* gene in the bushbaby genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S355

Pongo abelii

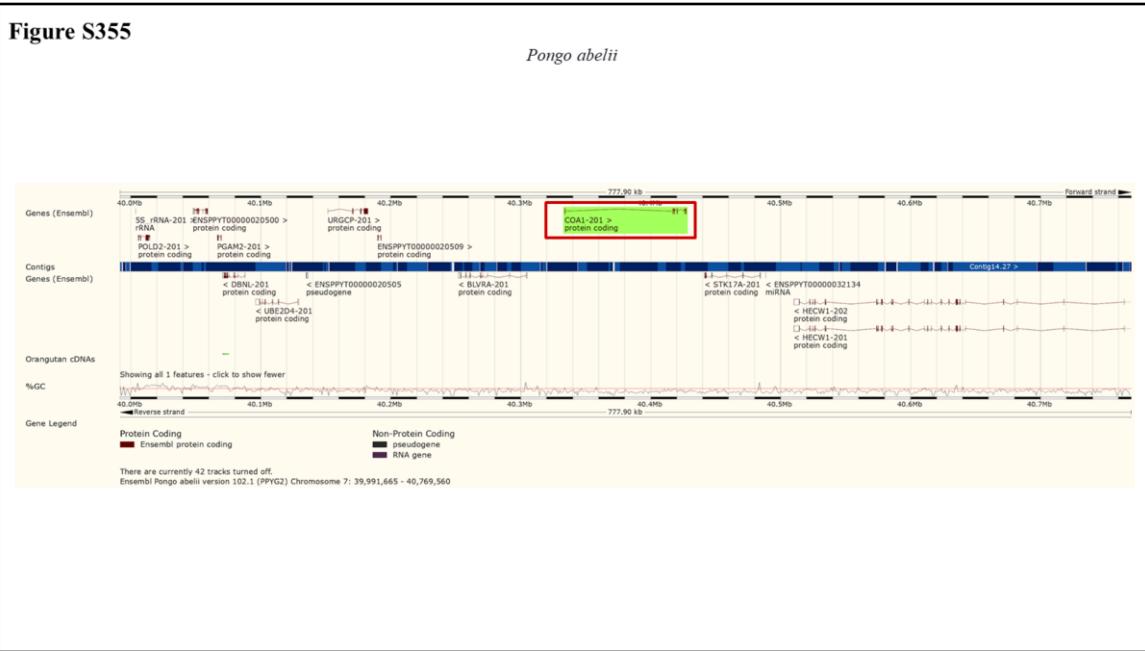


Figure S355: Gene order near *COA1* gene in the orangutan genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S356

Cebus capucinus imitator

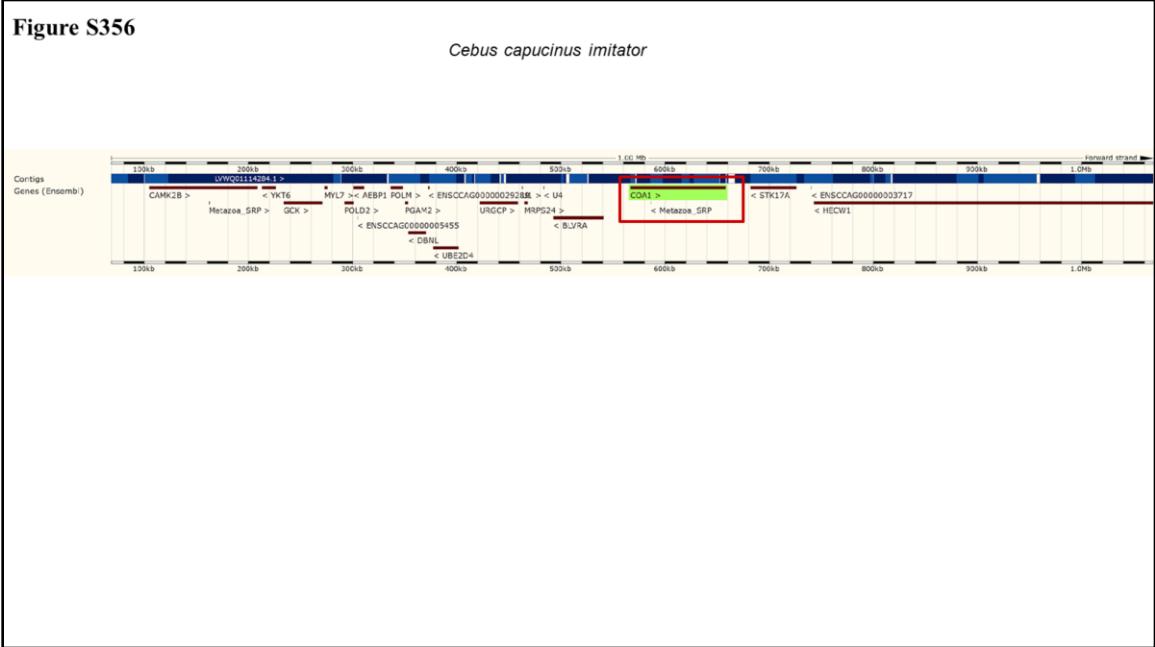


Figure S356: Gene order near *COA1* gene in the capuchin genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S357

Propithecus coquereli

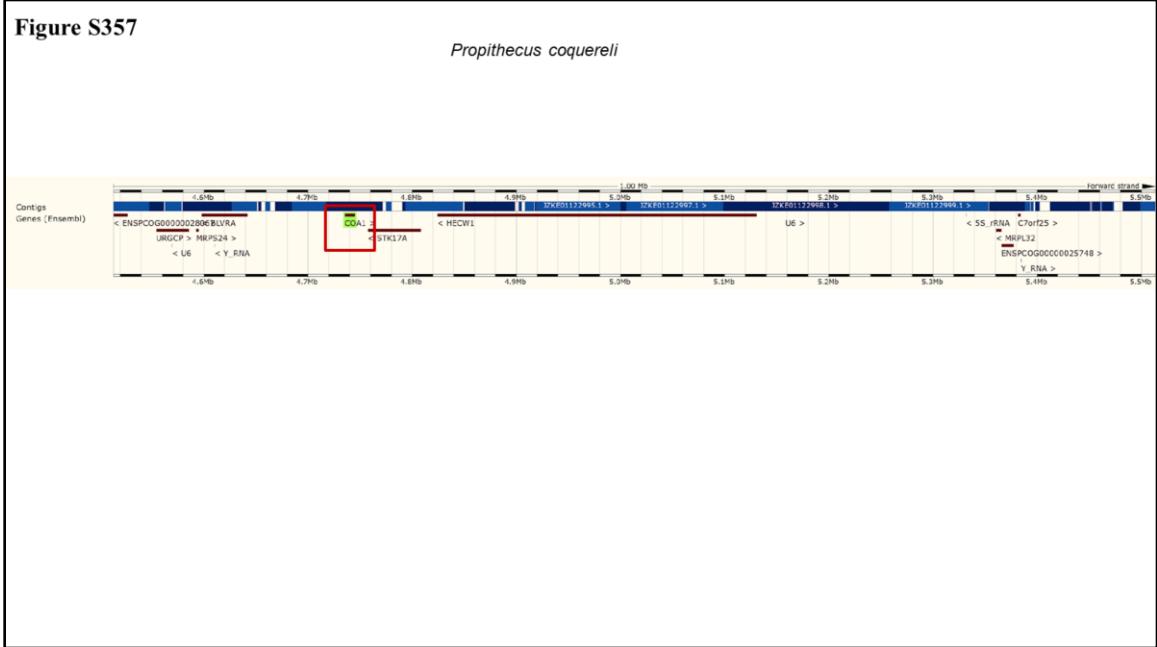


Figure S357: Gene order near *COA1* gene in the Coquerel's sifaka genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S358

Macaca fascicularis

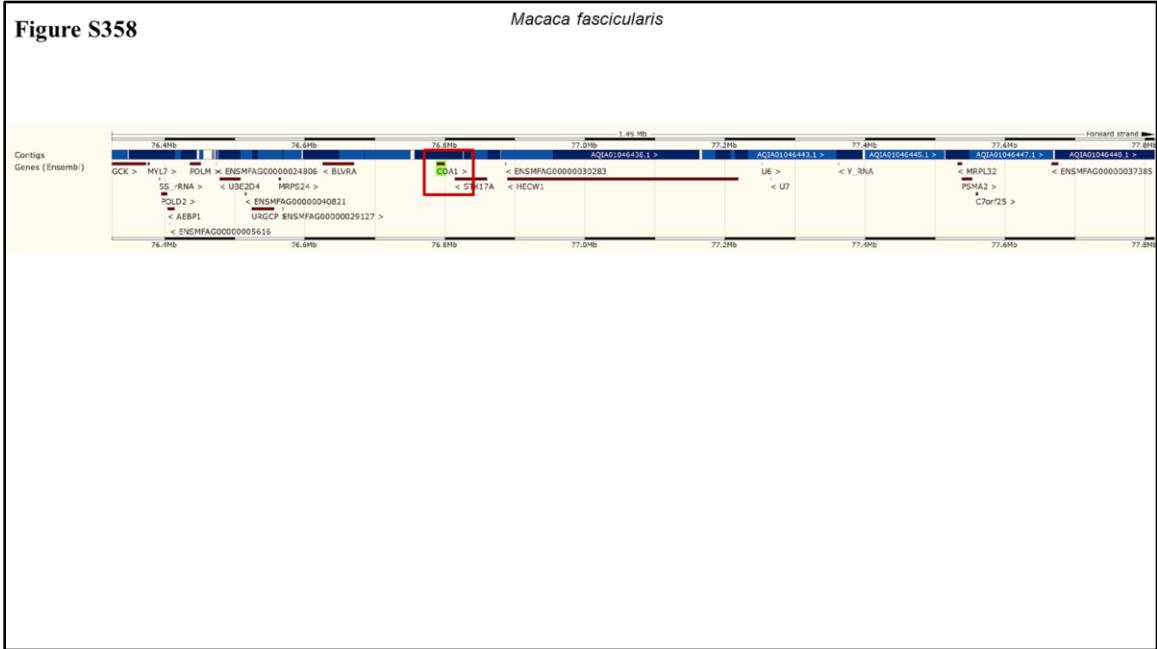


Figure S358: Gene order near *COA1* gene in the crab-eating macaque genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

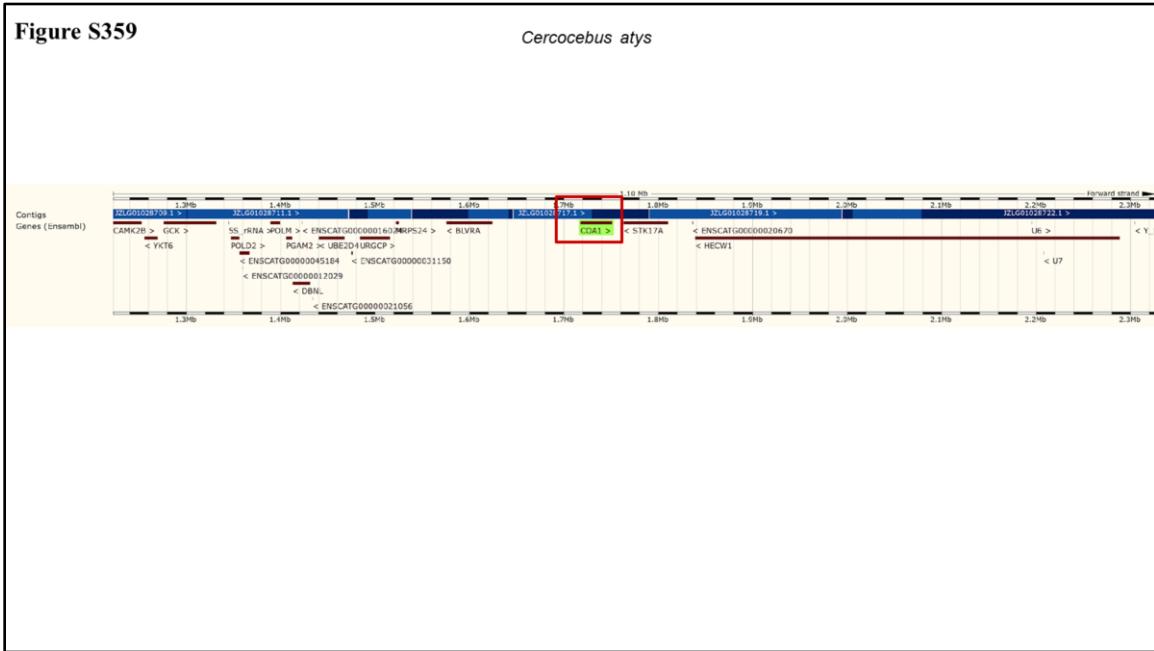
Figure S359*Cercocebus atys*

Figure S359: Gene order near *COA1* gene in the sooty mangabey genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S360

Piliocolobus tephrosceles

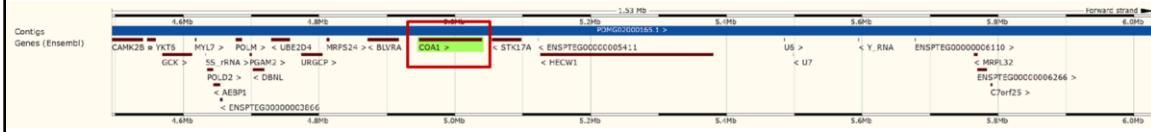


Figure S360: Gene order near *COA1* gene in the Ugandan red colobus genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S361

Mandrillus leucophaeus

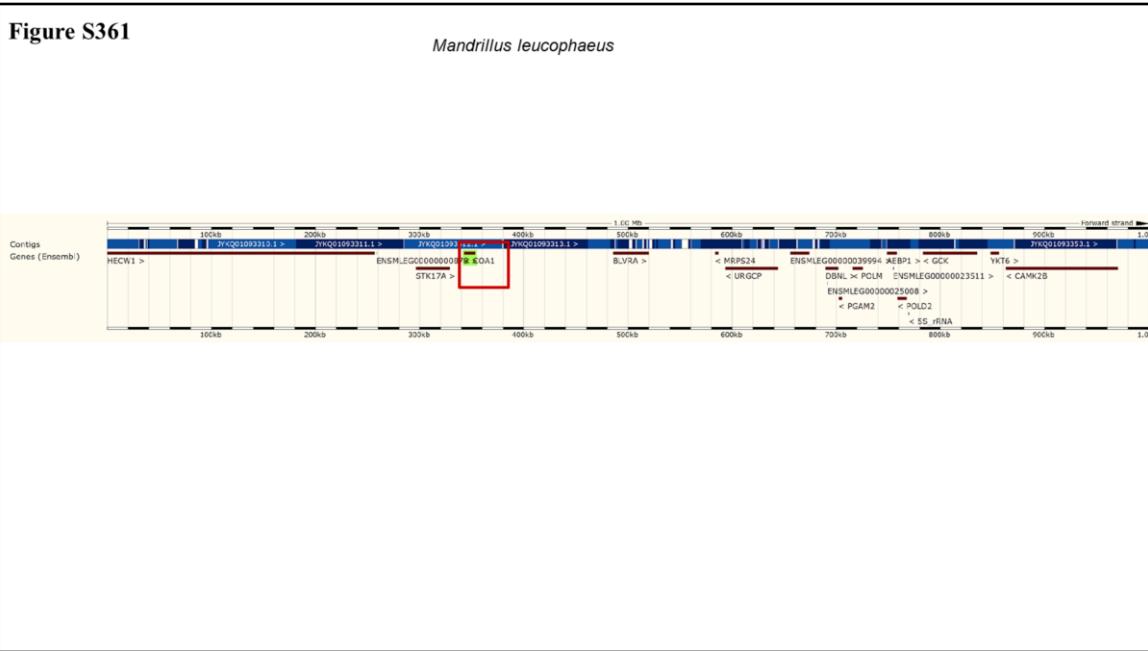


Figure S361: Gene order near *COA1* gene in the drill genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. Chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S362

Theropithecus gelada

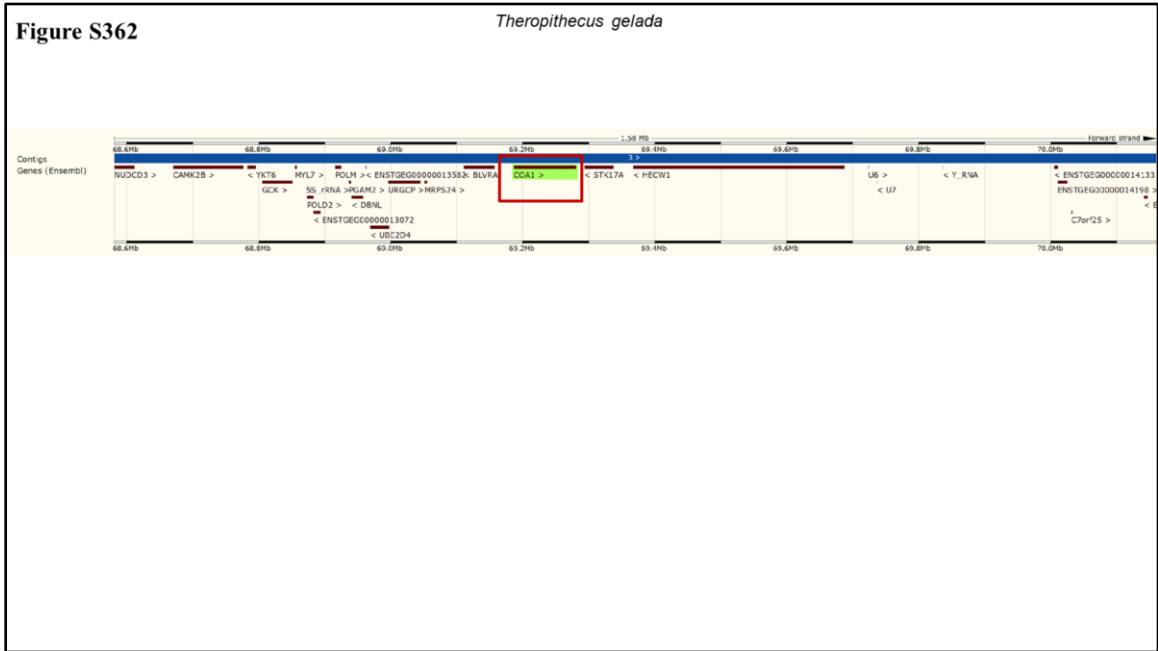


Figure S362: Gene order near *COA1* gene in the *gelada* genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S363

Gorilla gorilla gorilla

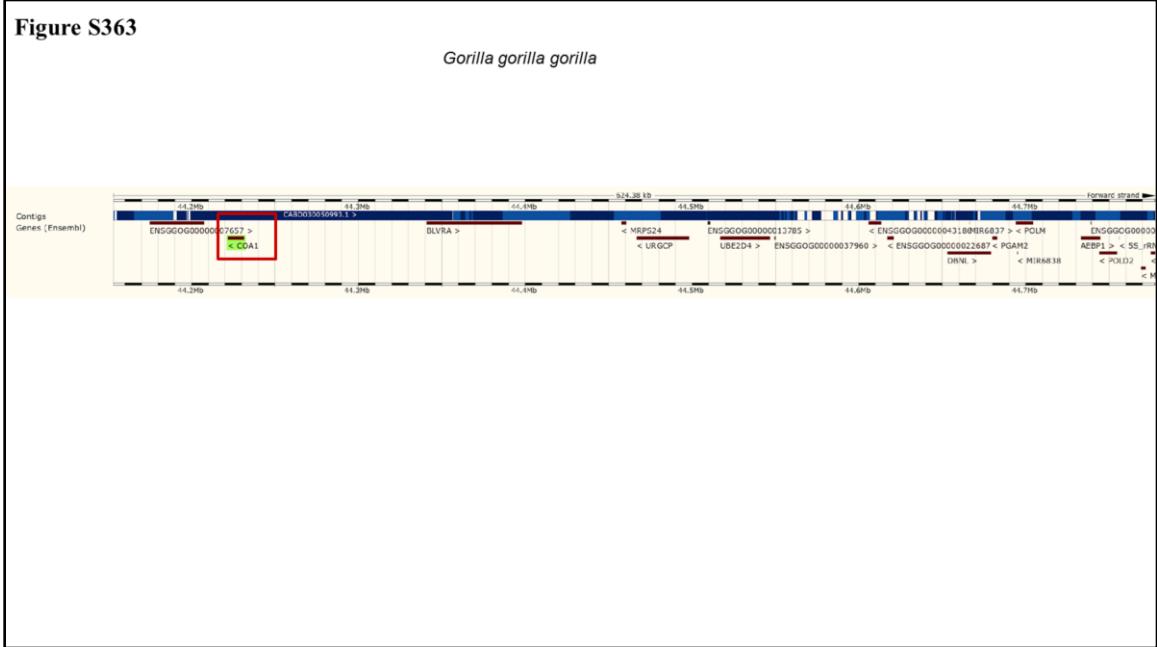


Figure S363: Gene order near *COA1* gene in the gorilla genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S364

Prolemur simus

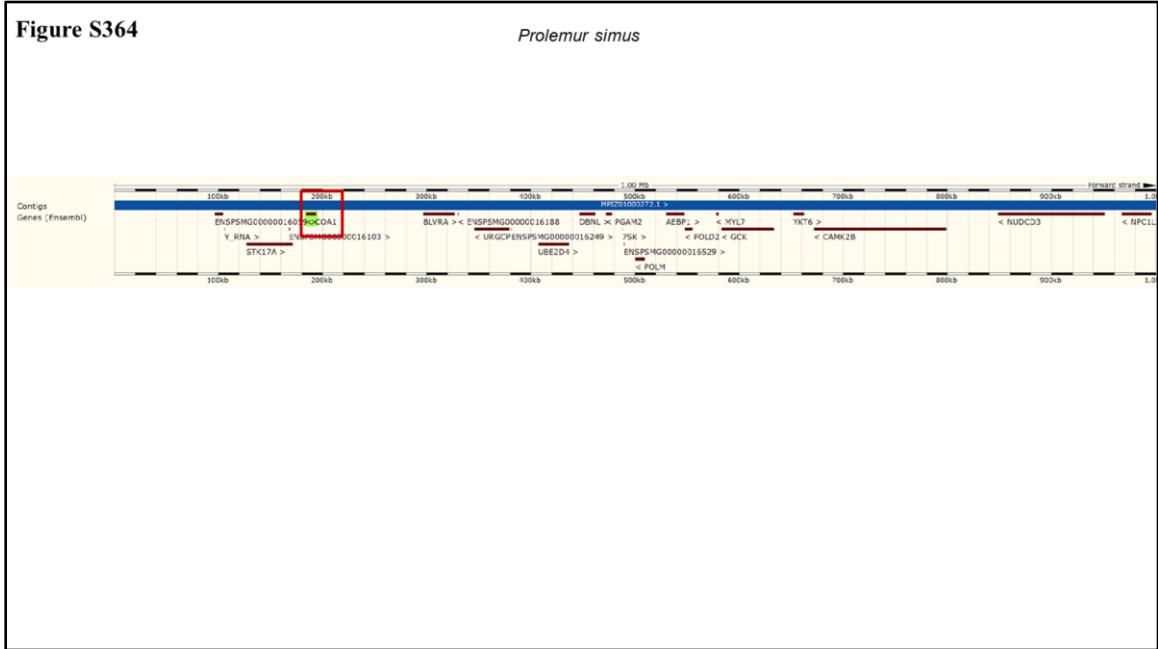


Figure S364: Gene order near *COA1* gene in the greater bamboo lemur genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. Chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

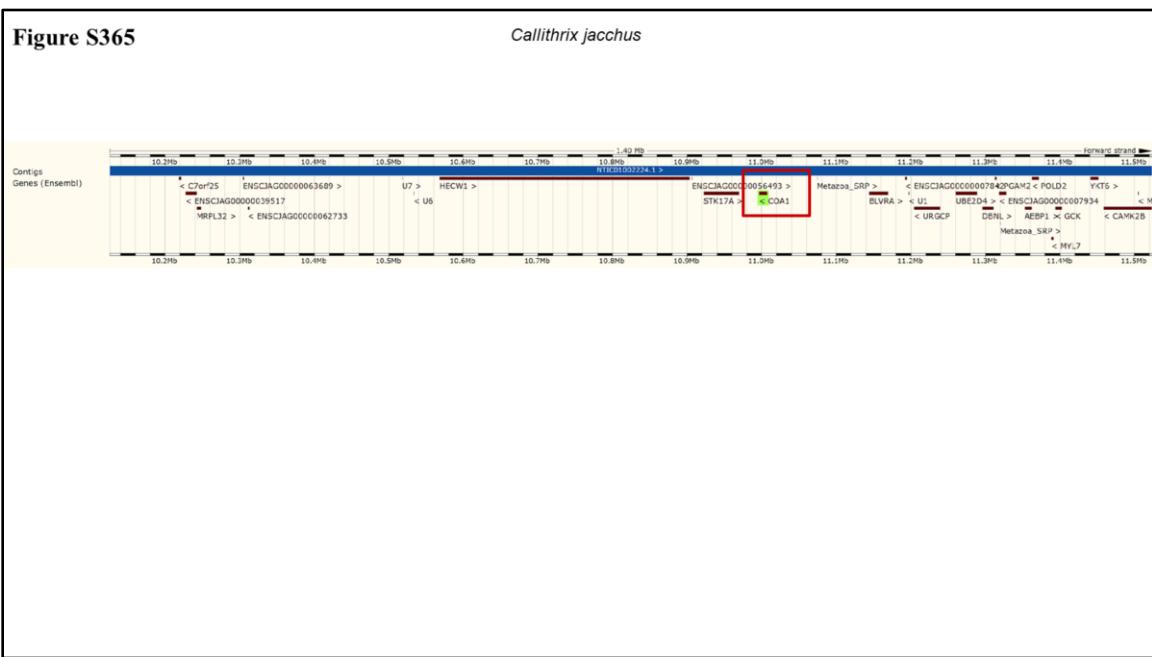
Figure S365*Callithrix jacchus*

Figure S365: Gene order near *COA1* gene in the marmoset genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

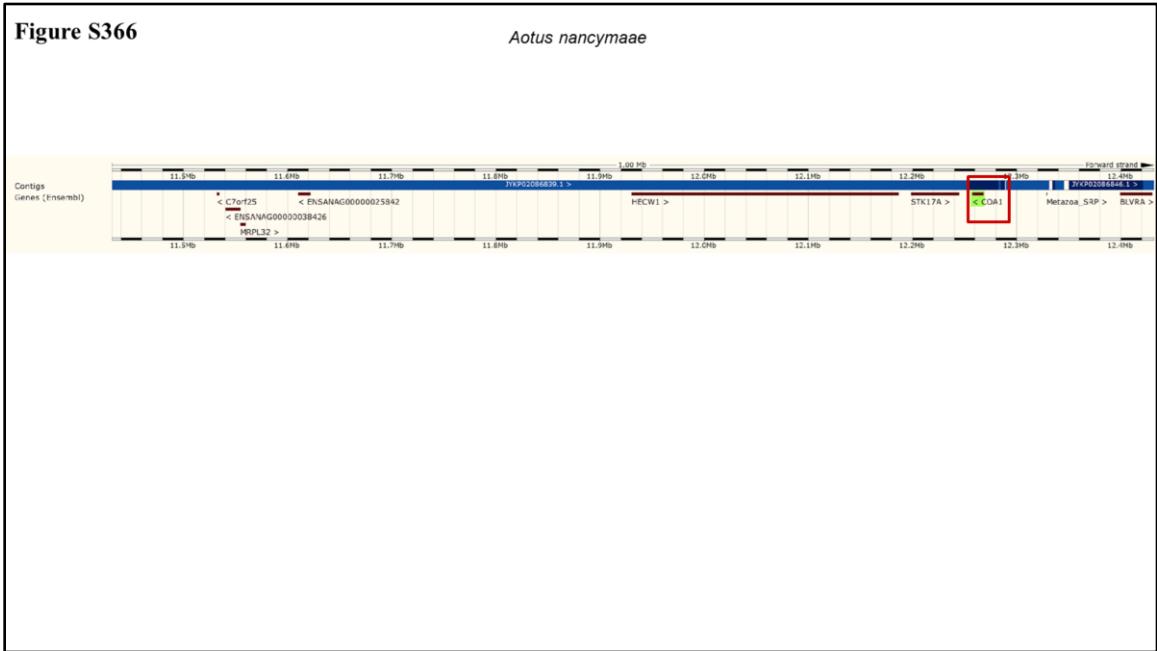
Figure S366*Aotus nancymaae*

Figure S366: Gene order near *COA1* gene in the Ma's night monkey genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

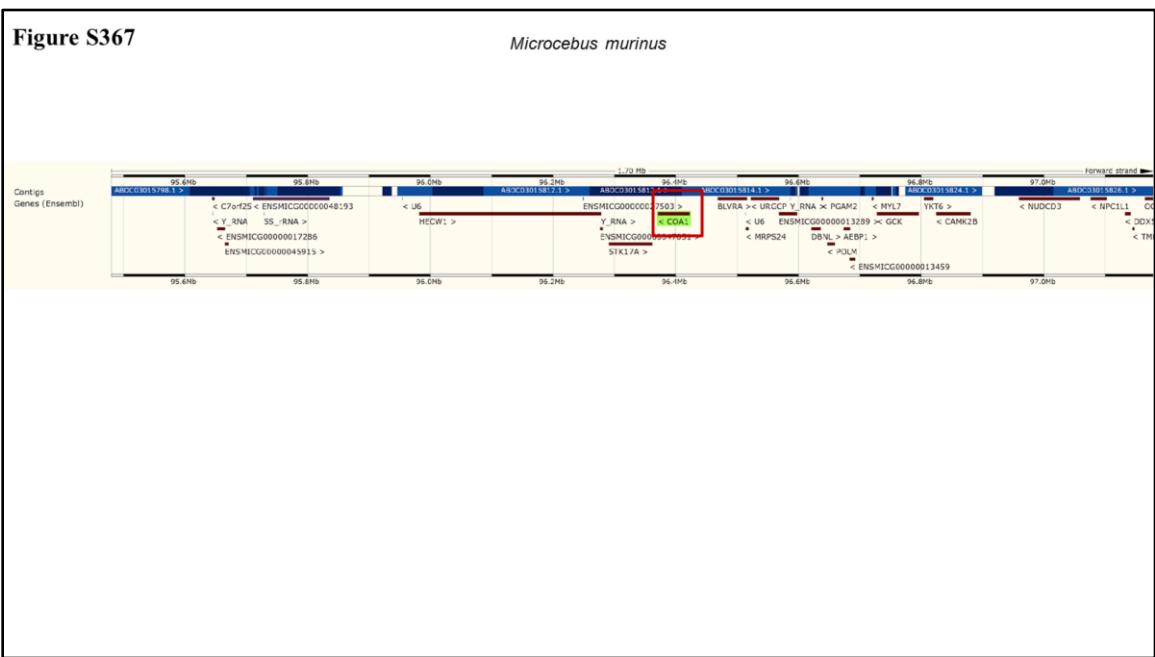
Figure S367*Microcebus murinus*

Figure S367: Gene order near *COA1* gene in the mouse lemur genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S368

Papio anubis

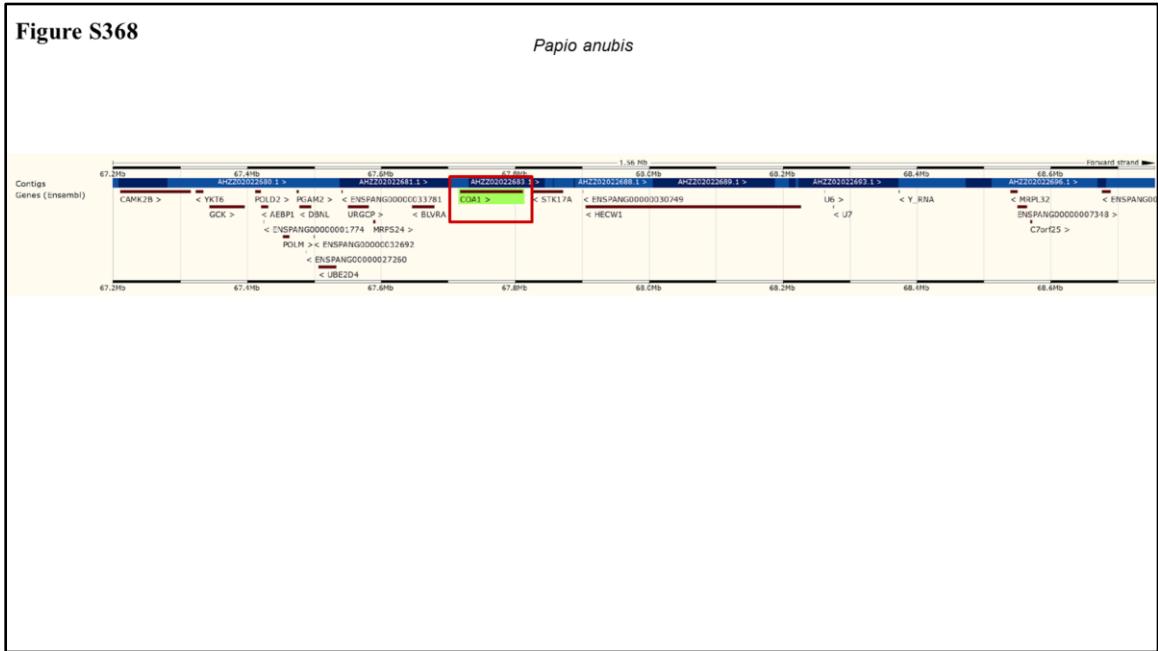


Figure S368: Gene order near *COA1* gene in the olive baboon genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

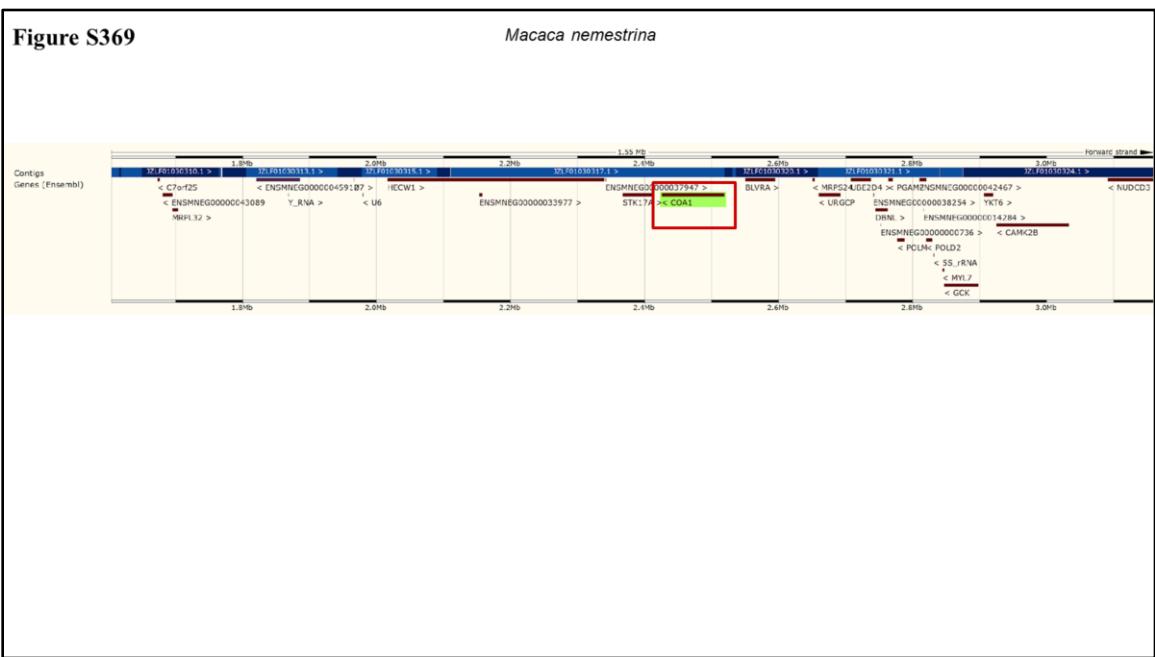
Figure S369*Macaca nemestrina*

Figure S369: Gene order near *COA1* gene in the pig-tailed macaque genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S370

Primates group duplication of COA1 gene

Callithrix jacchus

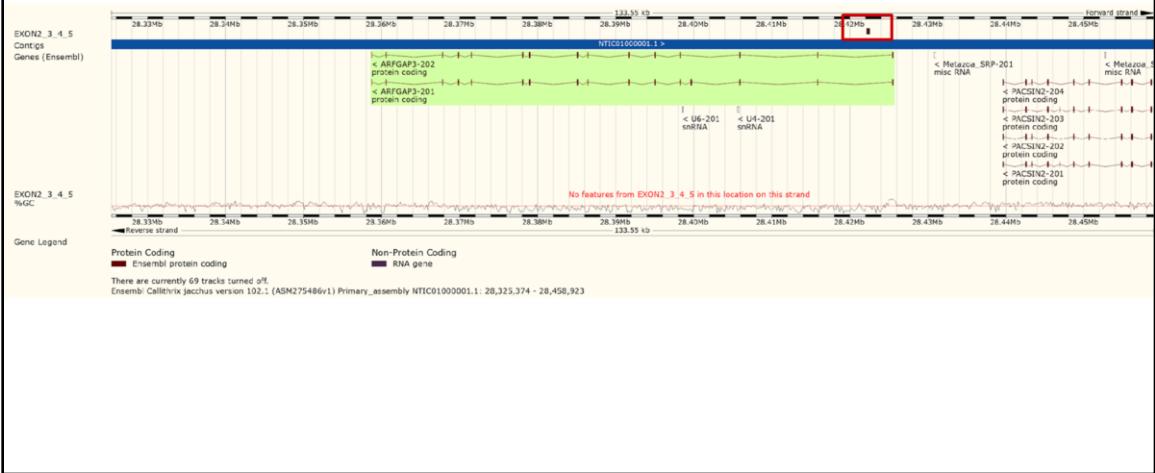


Figure S370: Gene order near *COA1* gene in the marmoset genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the $>$ or $<$ symbols (signify positive and negative strand of transcription respectively) beside the gene names. Chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S371

Aotus nancymaae

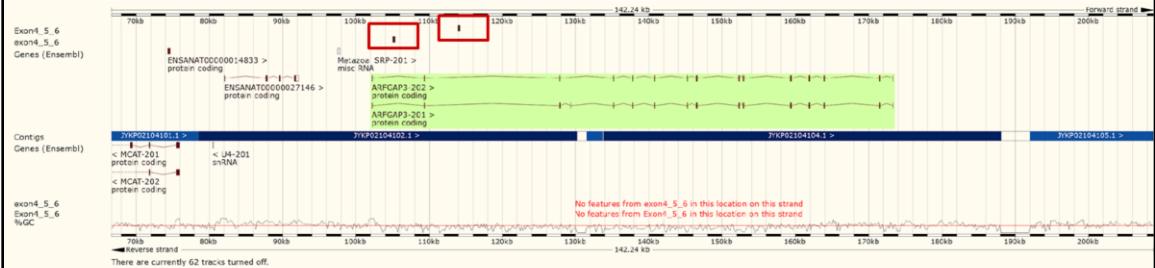


Figure S371: Gene order near *COA1* gene in the Ma's night monkey genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S372

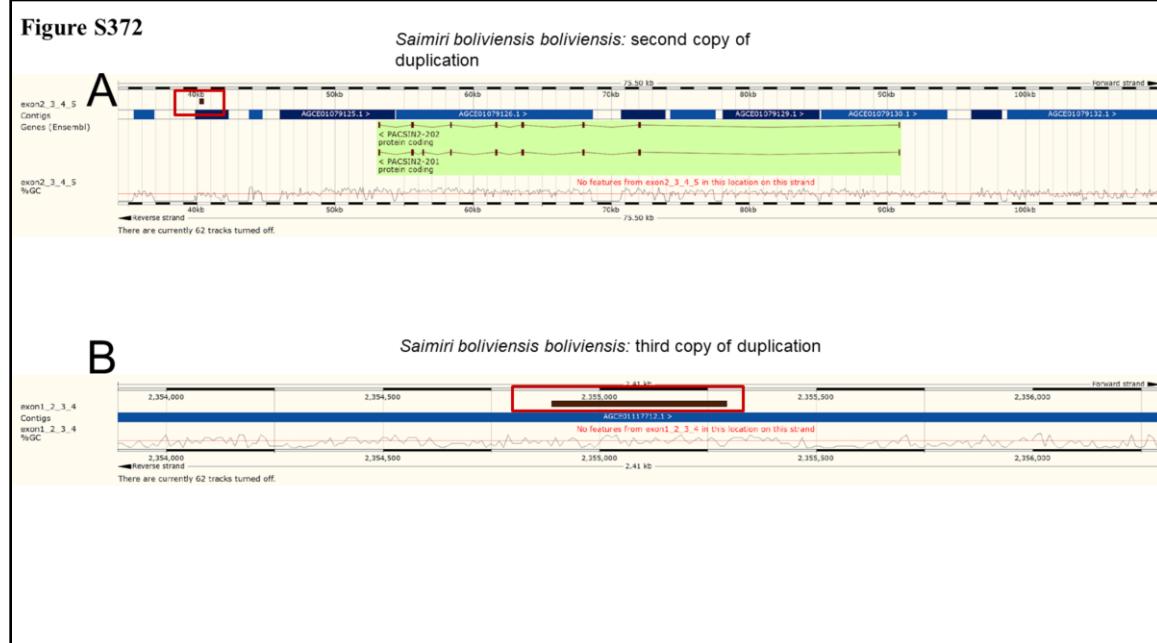
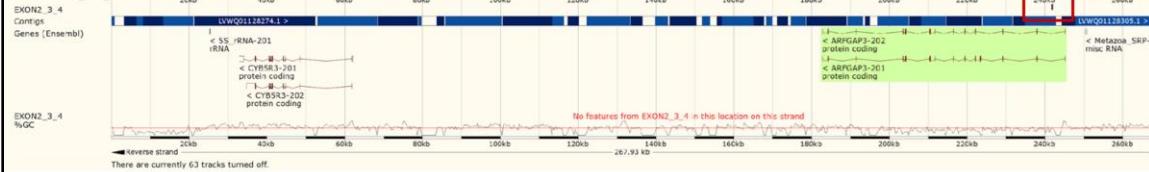


Figure S372: Gene order near *COA1* gene in the Bolivian squirrel monkey genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. Chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S373

Cebus capucinus imitator:second copy of duplication

A



B

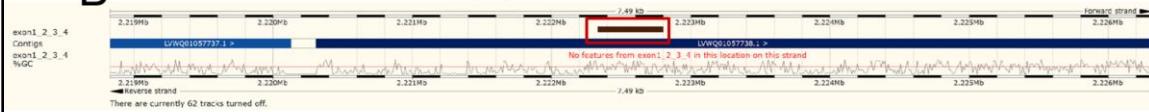


Figure S373: Gene order near *COA1* gene in the capuchin genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S374

Mandrillus leucophaeus

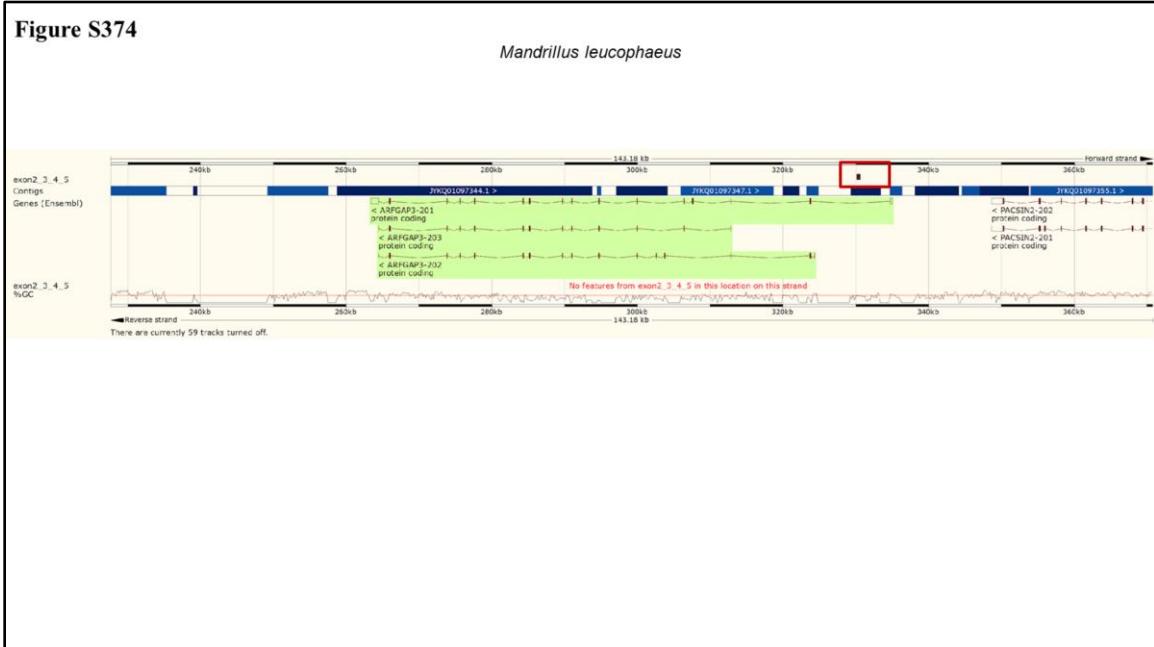


Figure S374: Gene order near *COA1* gene in the drill genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S375

Cercocebus atys

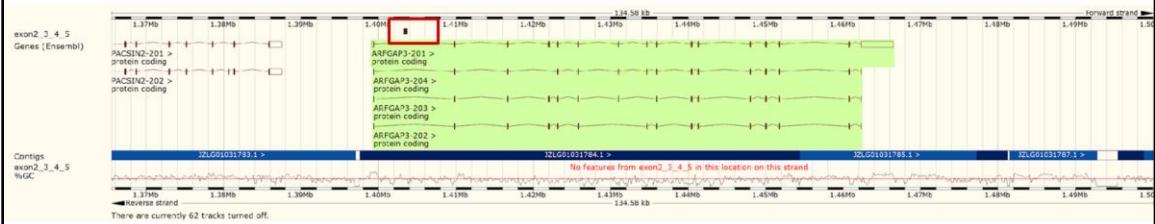


Figure S375: Gene order near *COA1* gene in the sooty mangabey genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the $>$ or $<$ symbols (signify positive and negative strand of transcription respectively) beside the gene names. Chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S376

Papio anubis

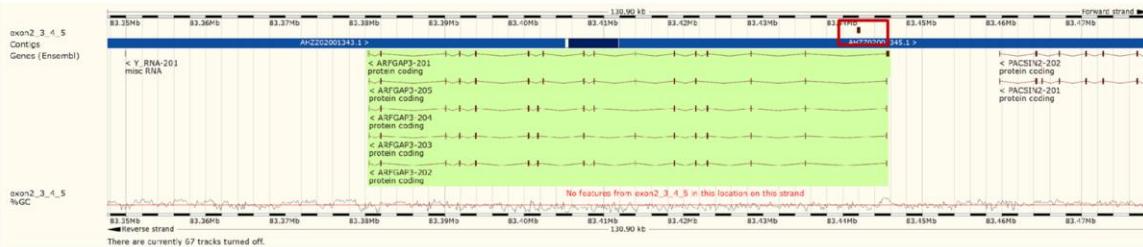


Figure S376: Gene order near *COA1* gene in the olive baboon genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S377

Theropithecus gelada

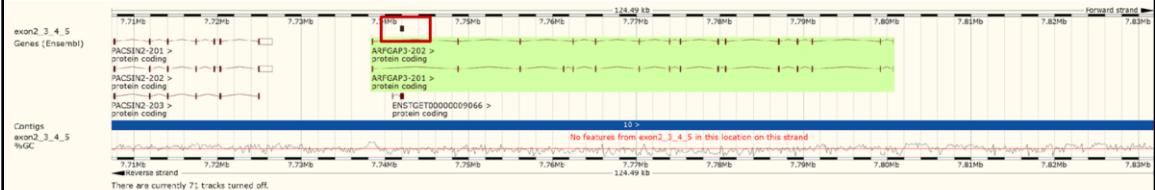


Figure S377: Gene order near *COA1* gene in the **gelada** genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S378

Macaca fascicularis

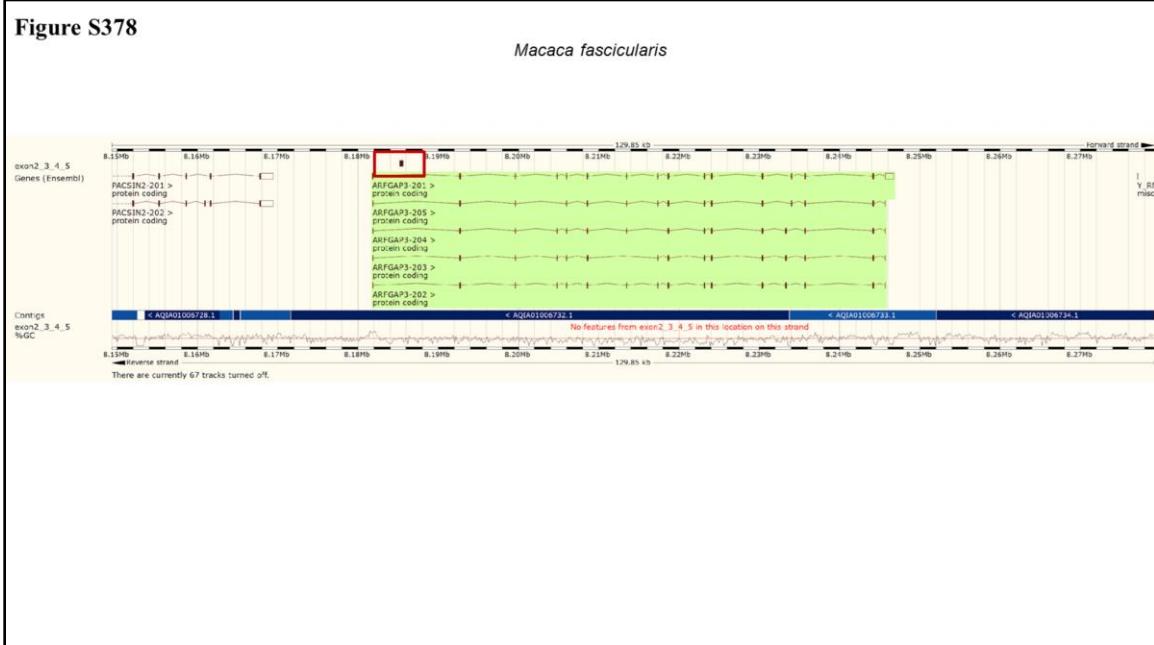


Figure S378: Gene order near *COA1* gene in the crab-eating macaque genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S379

Macaca mulatta

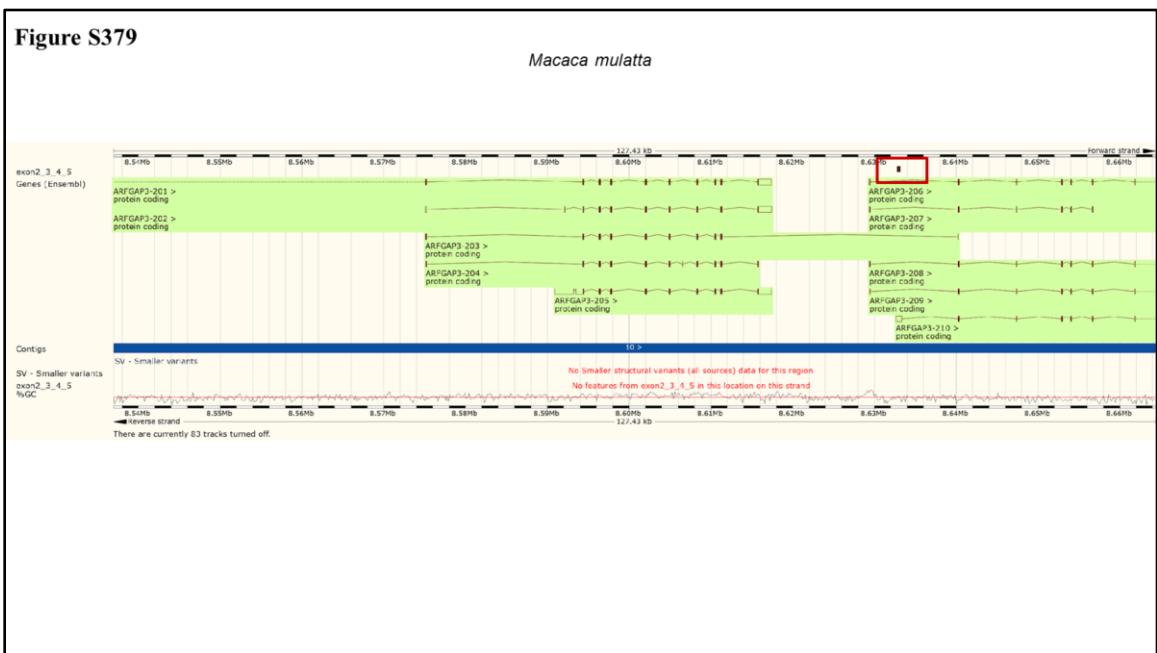


Figure S379: Gene order near *COA1* gene in the macaque genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S380

Macaca nemestrina

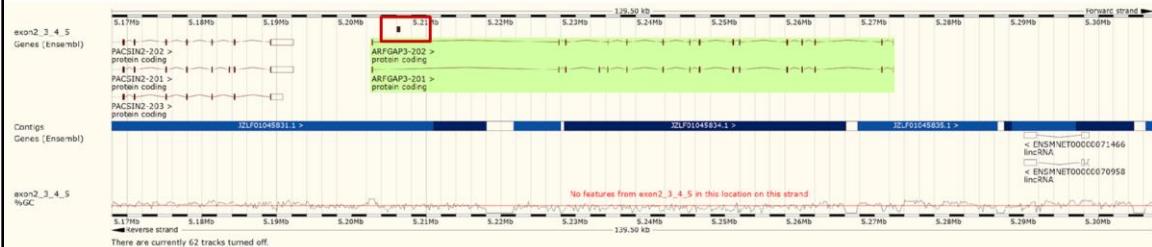


Figure S380: Gene order near *COA1* gene in the pig-tailed macaque genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S381

Chlorocebus sabaeus

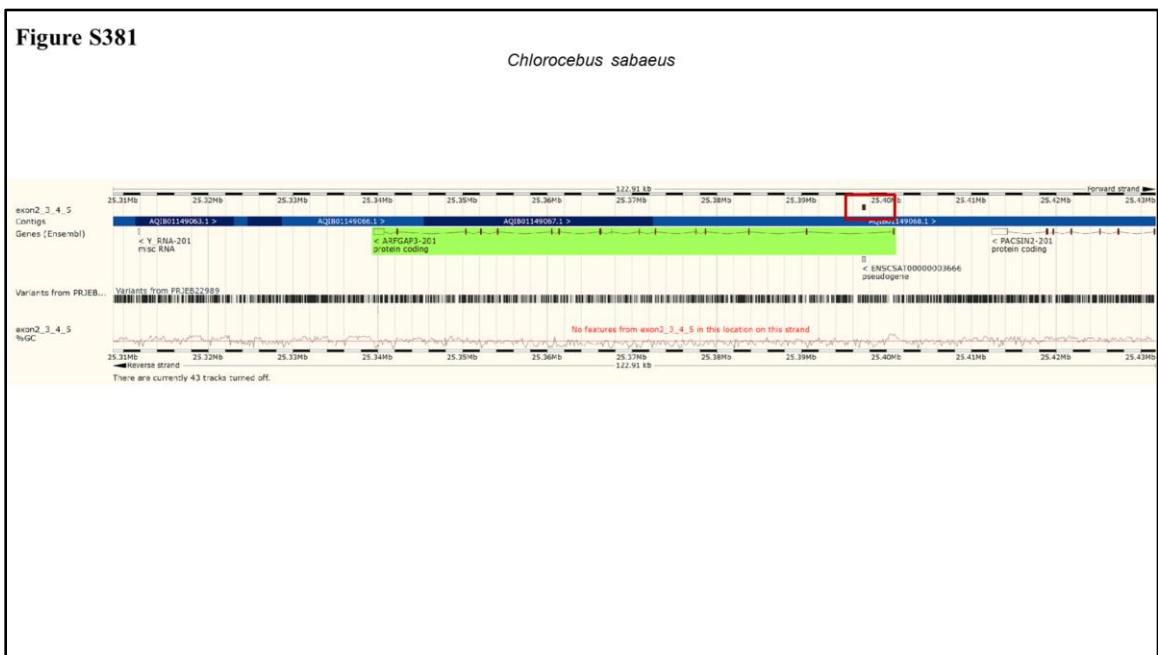


Figure S381: Gene order near *COA1* gene in the *vervet-AGM* genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S382

Rhinopithecus bieti

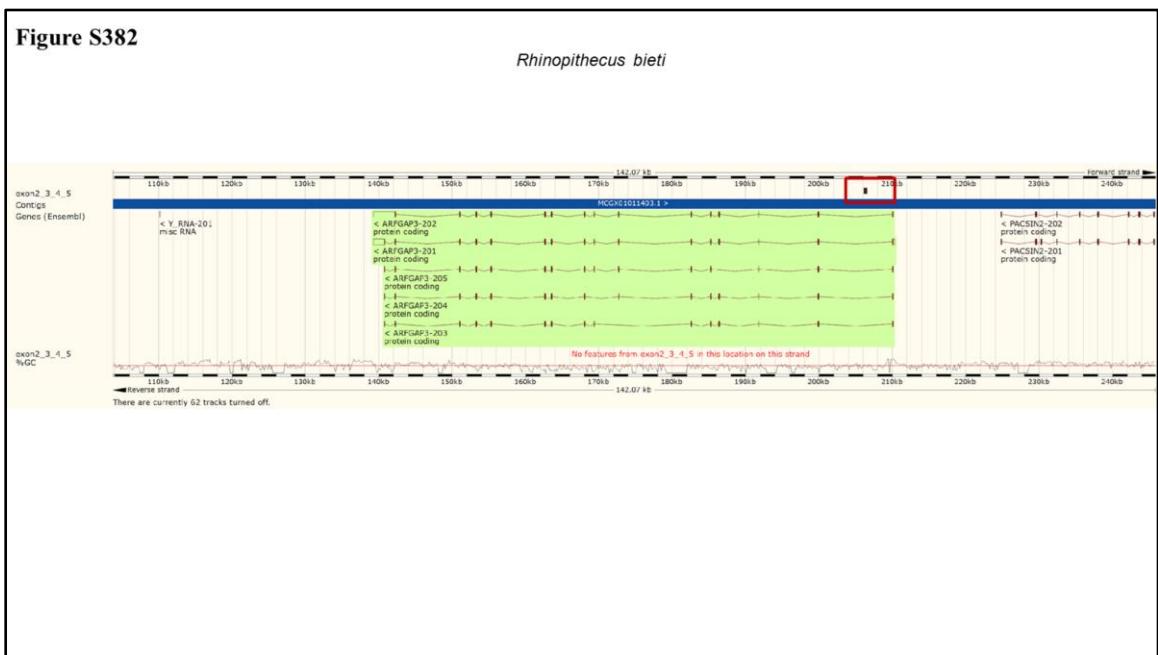


Figure S382: Gene order near *COA1* gene in the black snub-nosed monkey genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S383

Rhinopithecus roxellana

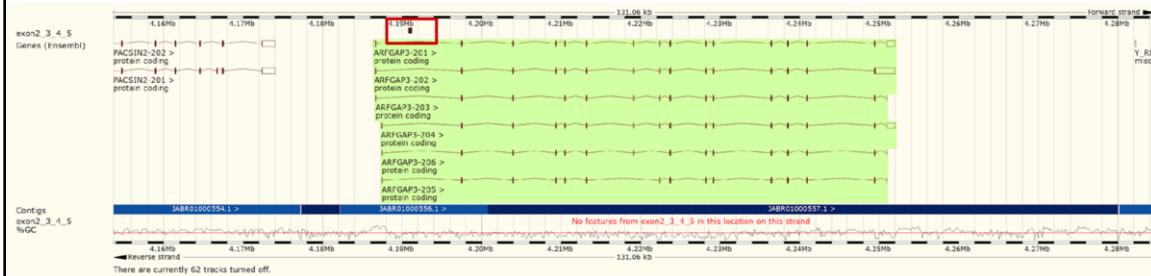


Figure S383: Gene order near *COA1* gene in the golden snub-nosed monkey genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S384

Piliocolobus tephrosceles

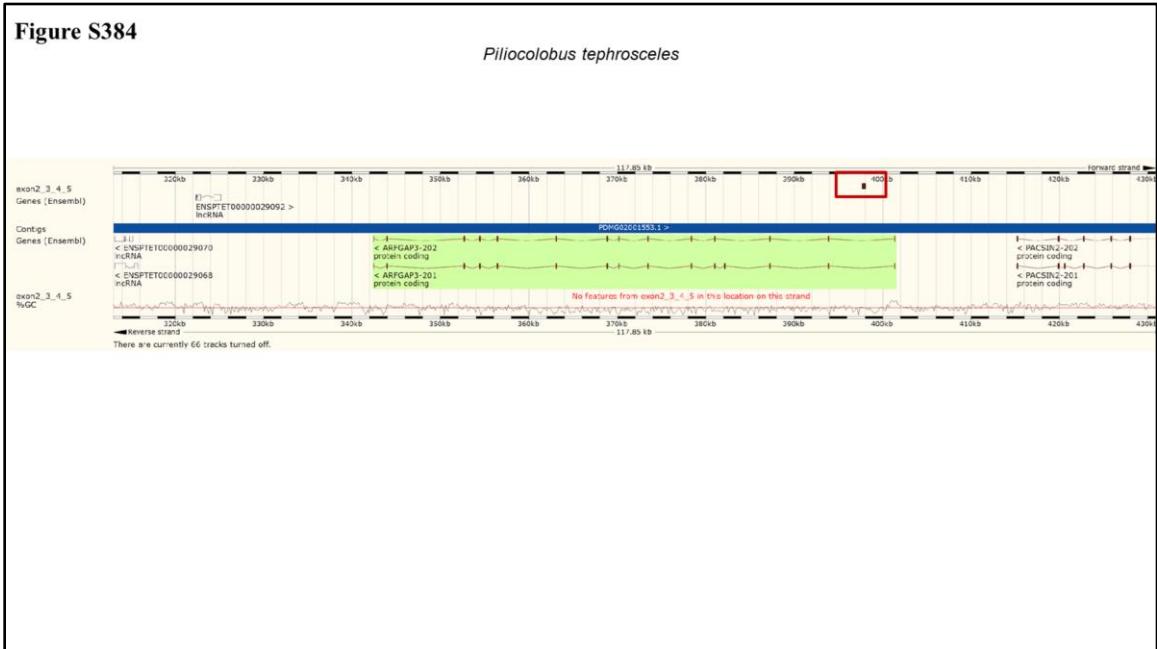


Figure S384: Gene order near *COA1* gene in the Ugandan red colobus genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S385

Colobus angolensis palliatus

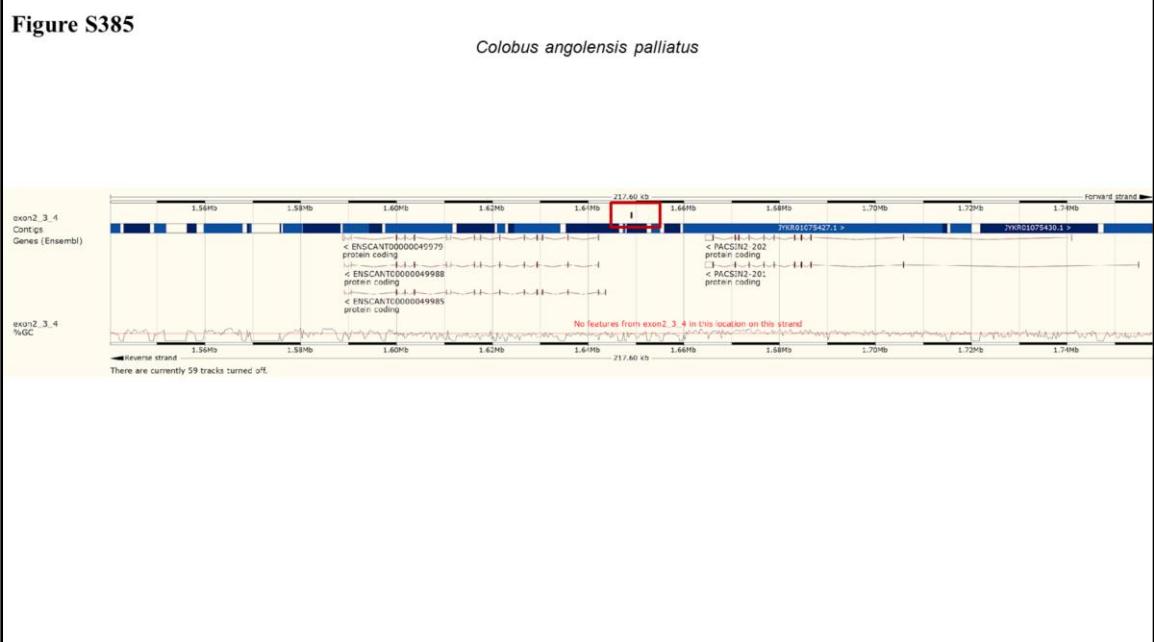


Figure S385: Gene order near *COA1* gene in the Angola colobus genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S386

Nomascus leucogenys

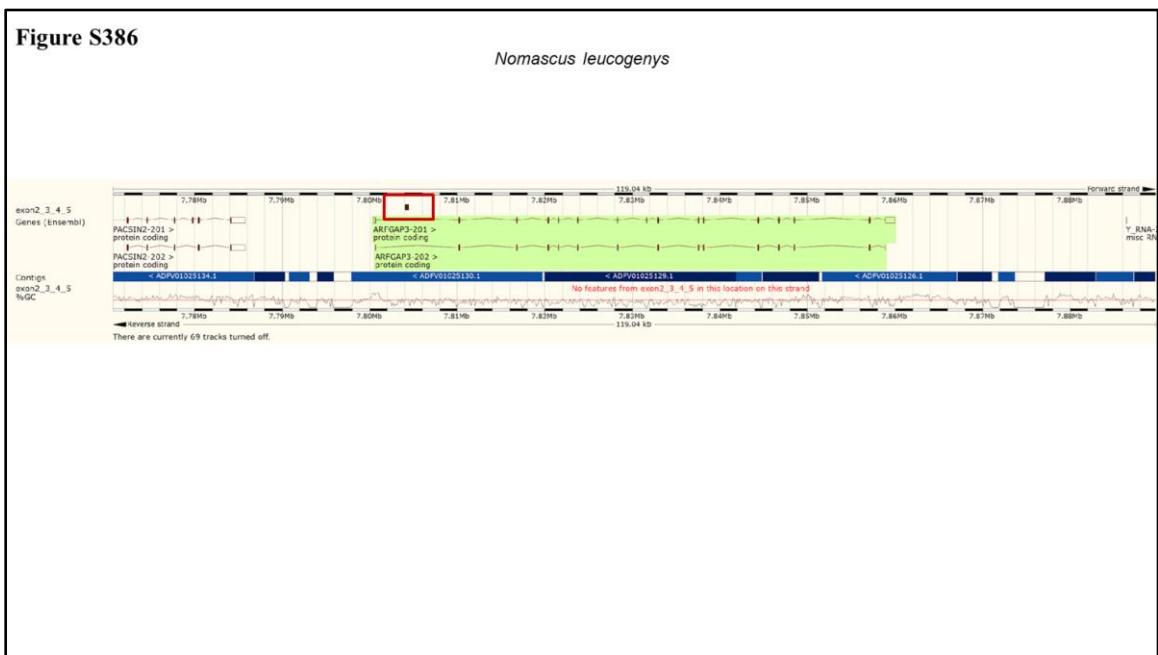


Figure S386: Gene order near *COA1* gene in the gibbon genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S387

Gorilla gorilla gorilla

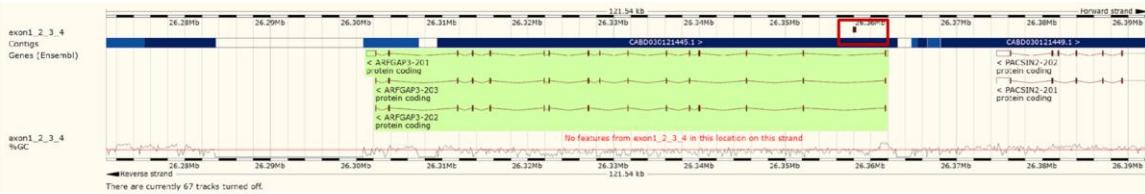


Figure S387: Gene order near *COA1* gene in the gorilla genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S388

Pan troglodytes



Figure S388: Gene order near *COA1* gene in the chimpanzee genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S389

Pan paniscus

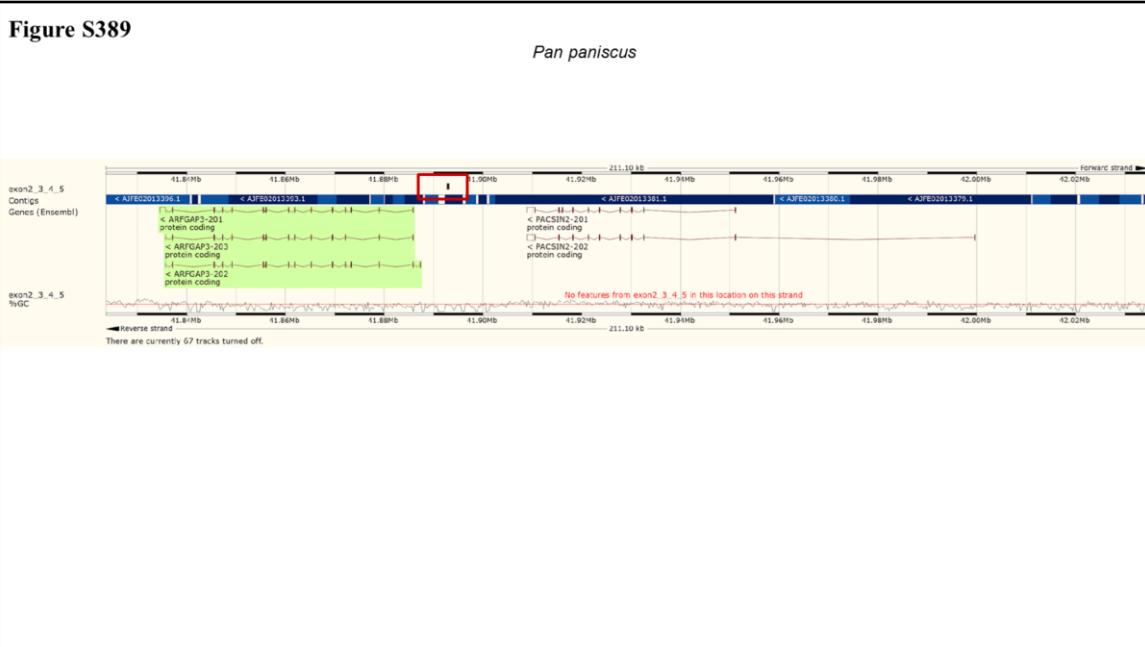


Figure S389: Gene order near *COA1* gene in the bonobo genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

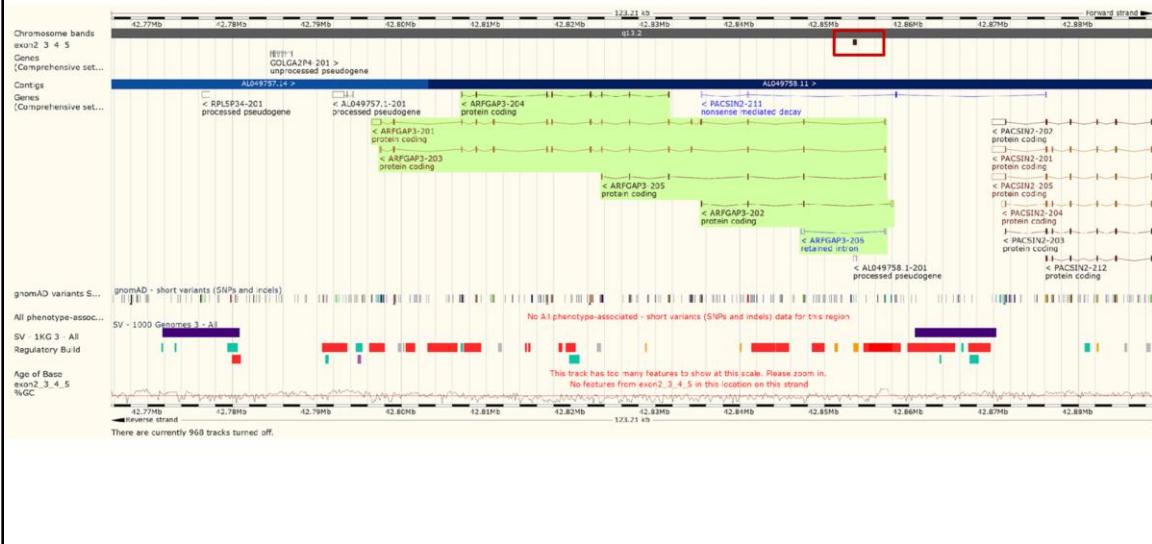
Figure S390*Homo sapiens*

Figure S390: Gene order near *COA1* gene in the *human* genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. Chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S391

Pongo abelii



Figure S391: Gene order near *COA1* gene in the orangutan genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S392

Tupaia belangeri

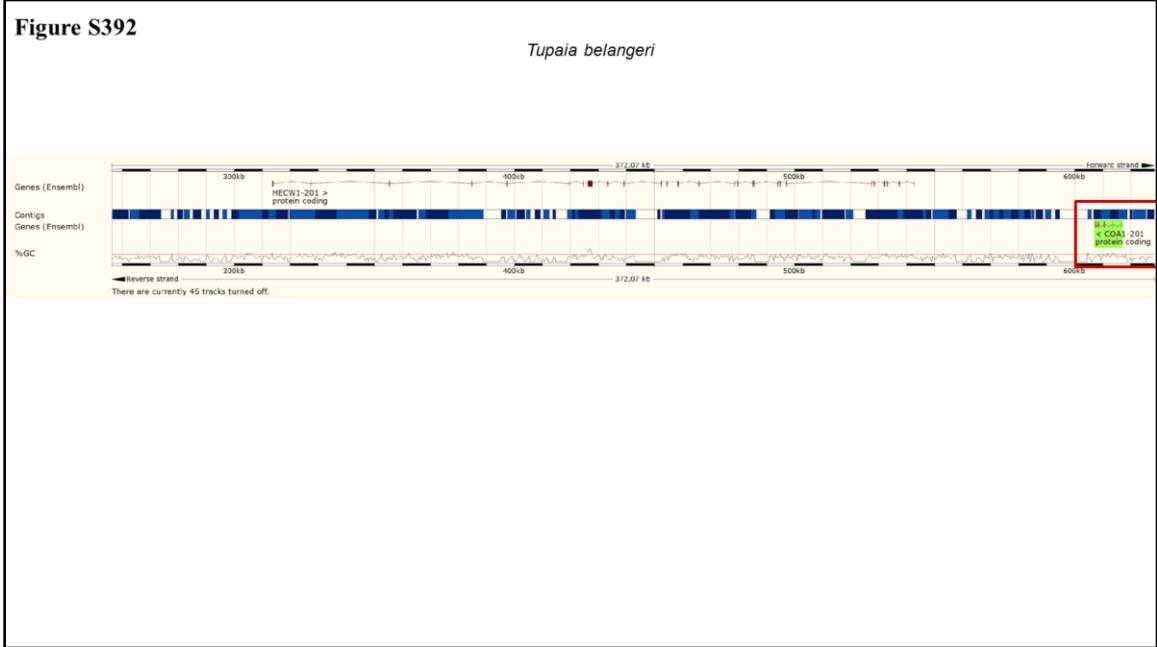


Figure S392: Gene order near *COA1* gene in the tree shrew genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the $>$ or $<$ symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosomal bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S393

Ursus thibetanus thibetanus

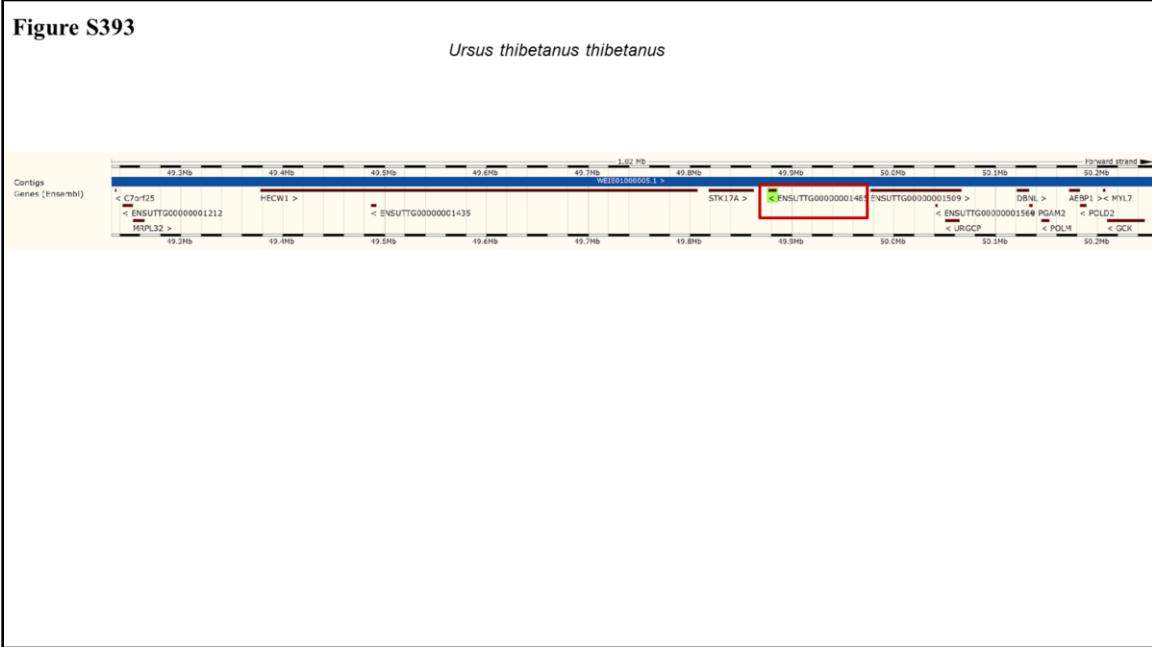


Figure S393: Gene order near *COA1* gene in the American black bear genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S394

Canis lupus dingo

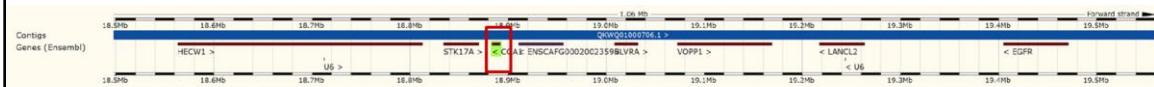


Figure S394: Gene order near *COA1* gene in the dingo genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

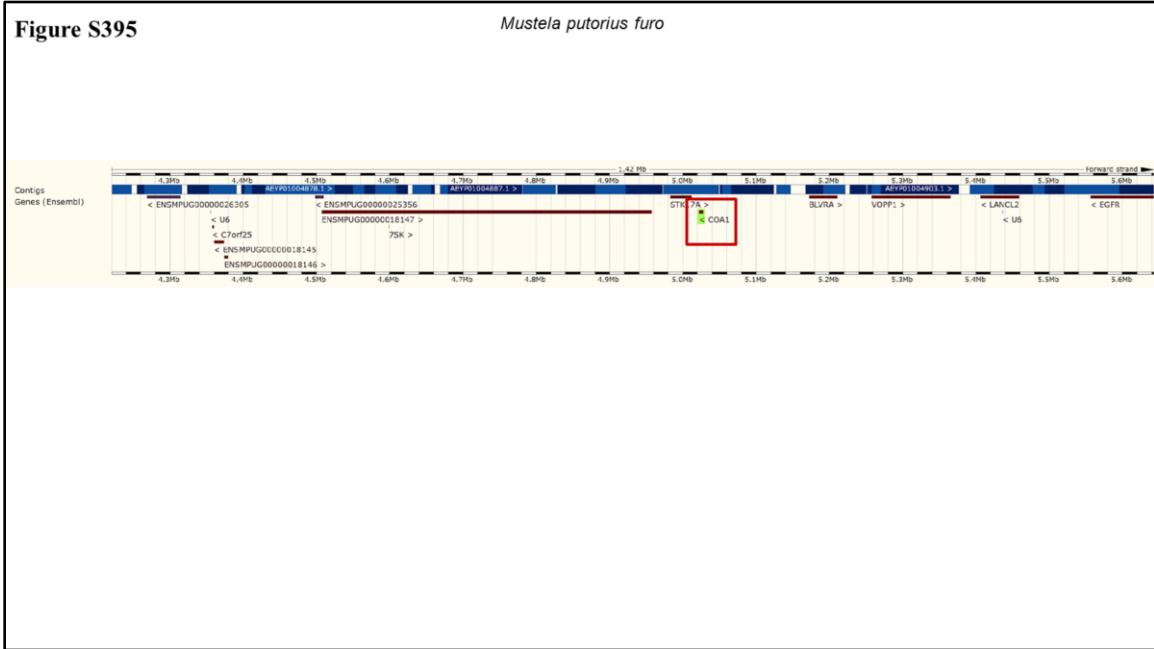
Figure S395*Mustela putorius furo*

Figure S395: Gene order near *COA1* gene in the ferret genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

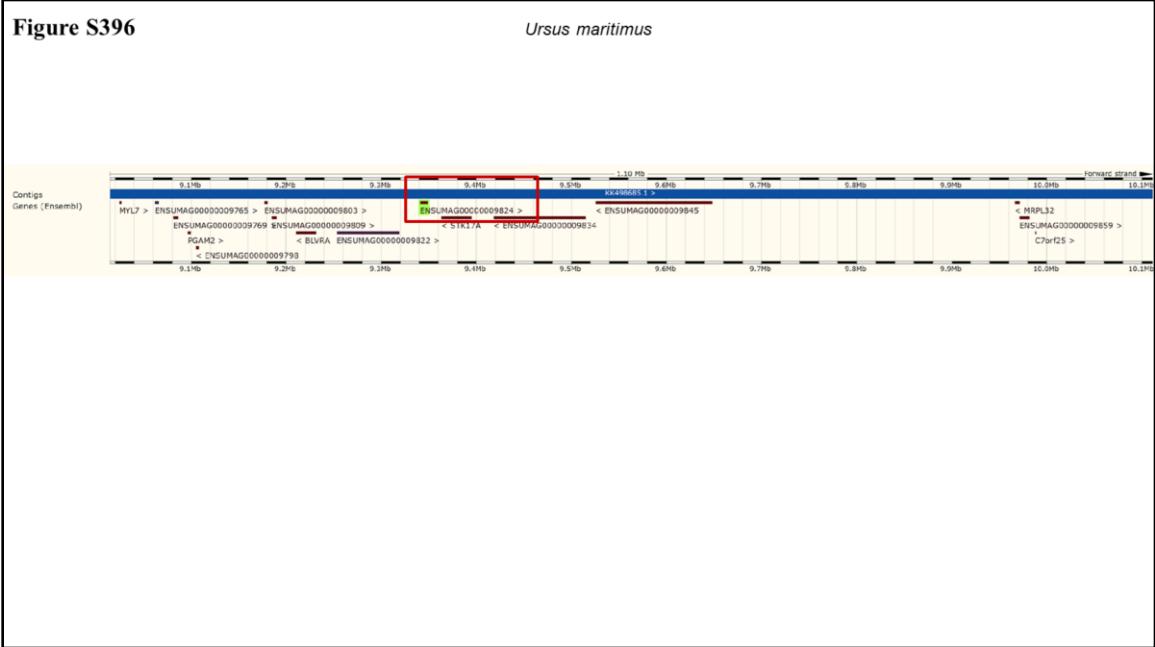
Figure S396*Ursus maritimus*

Figure S396: Gene order near *COA1* gene in the polar bear genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S397

Vulpes vulpes

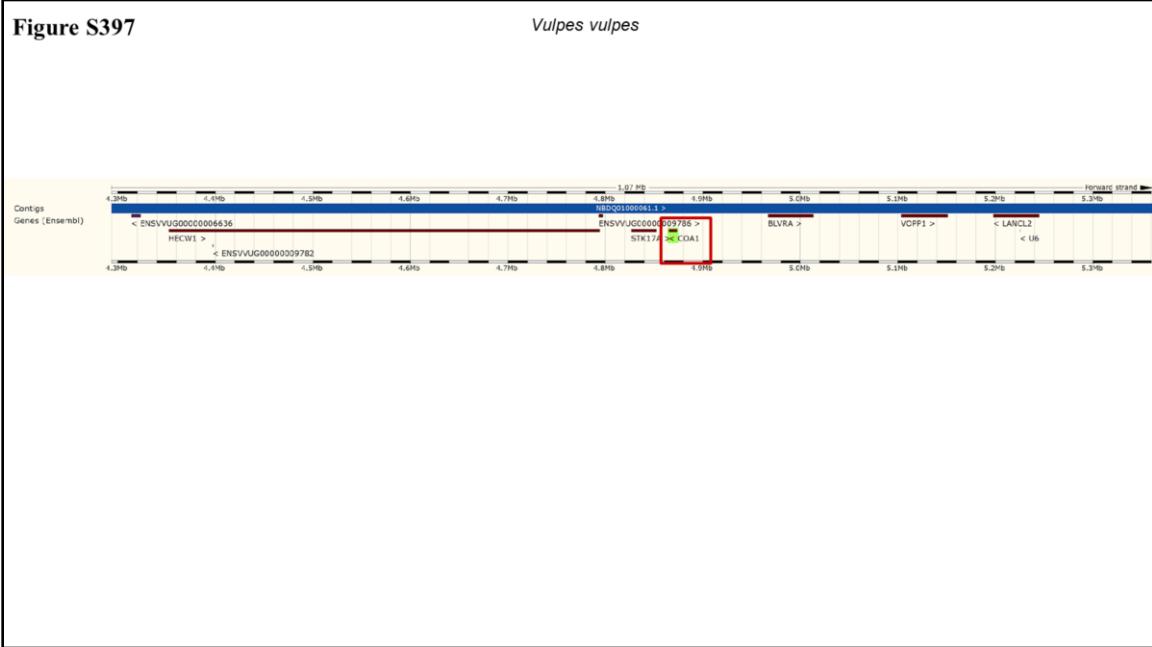


Figure S397: Gene order near *COA1* gene in the red fox genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.