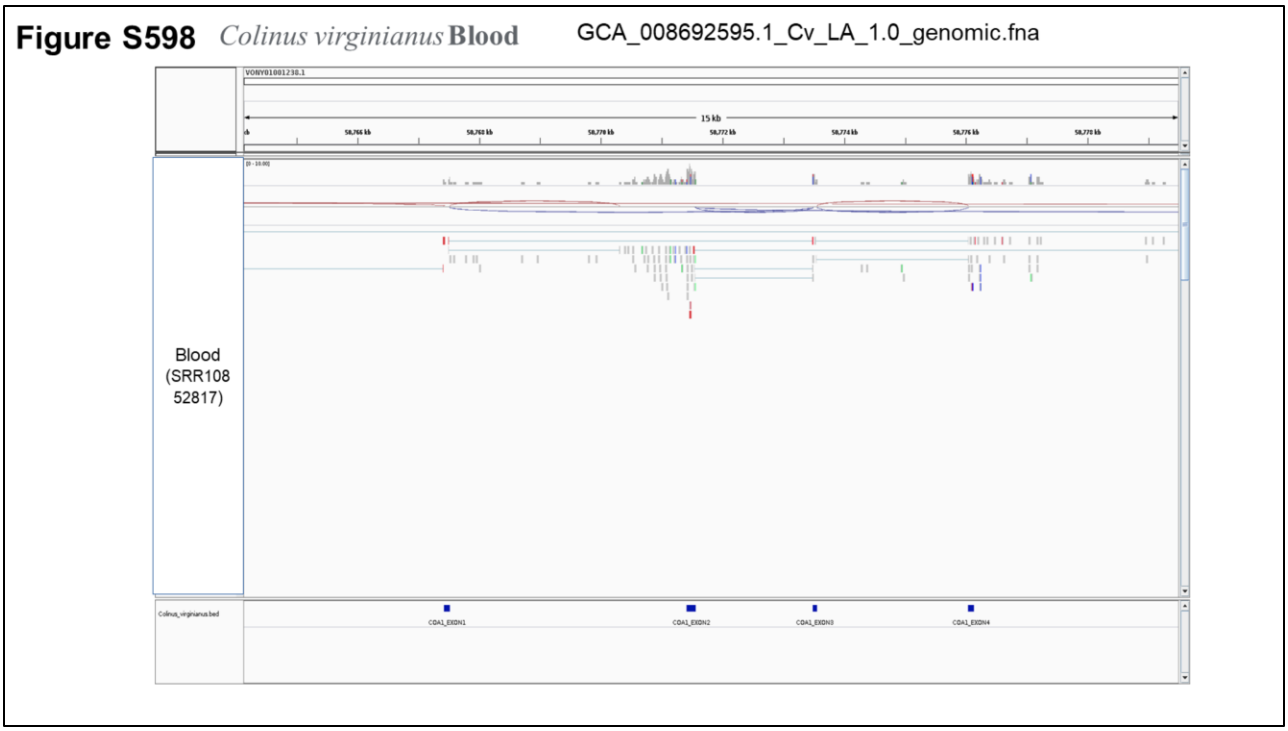

Figure S598: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in northern bobwhite (*Colinus virginianus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR10852817) have been mapped to the GCA_008692595.1_Cv_LA_1.0_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

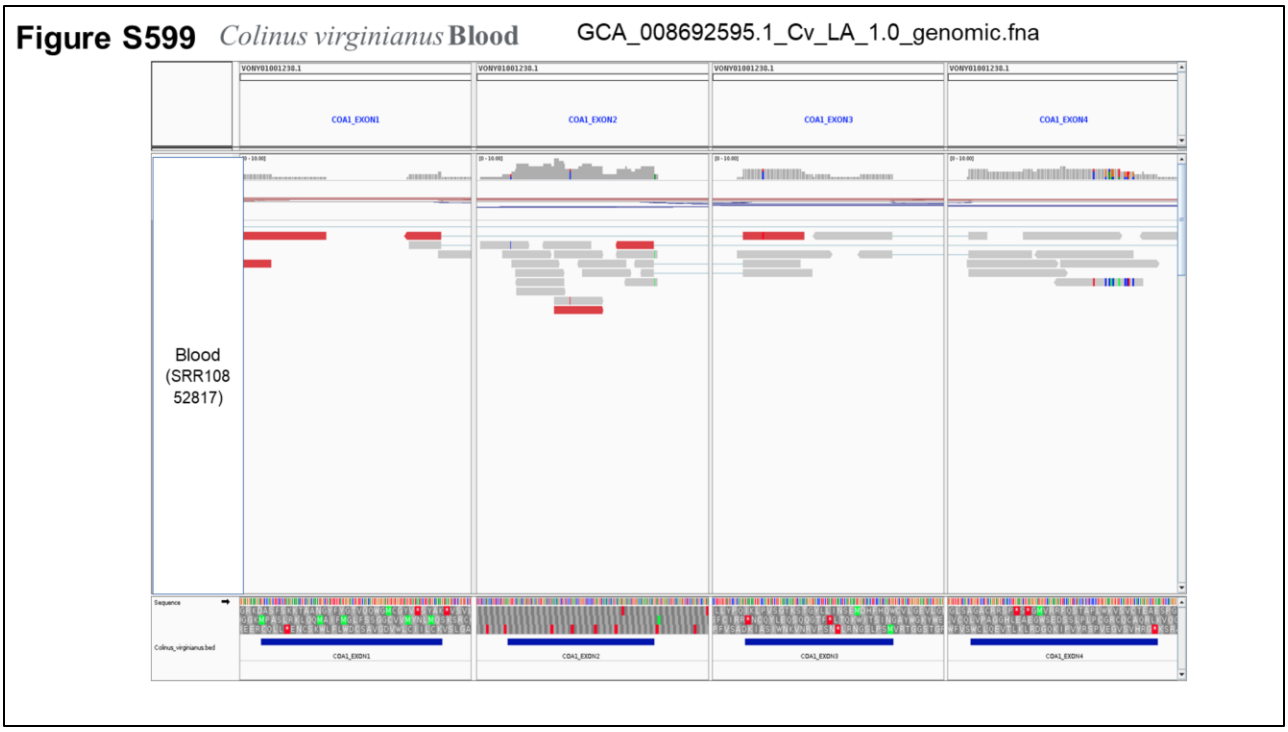

Figure S599: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S598**.

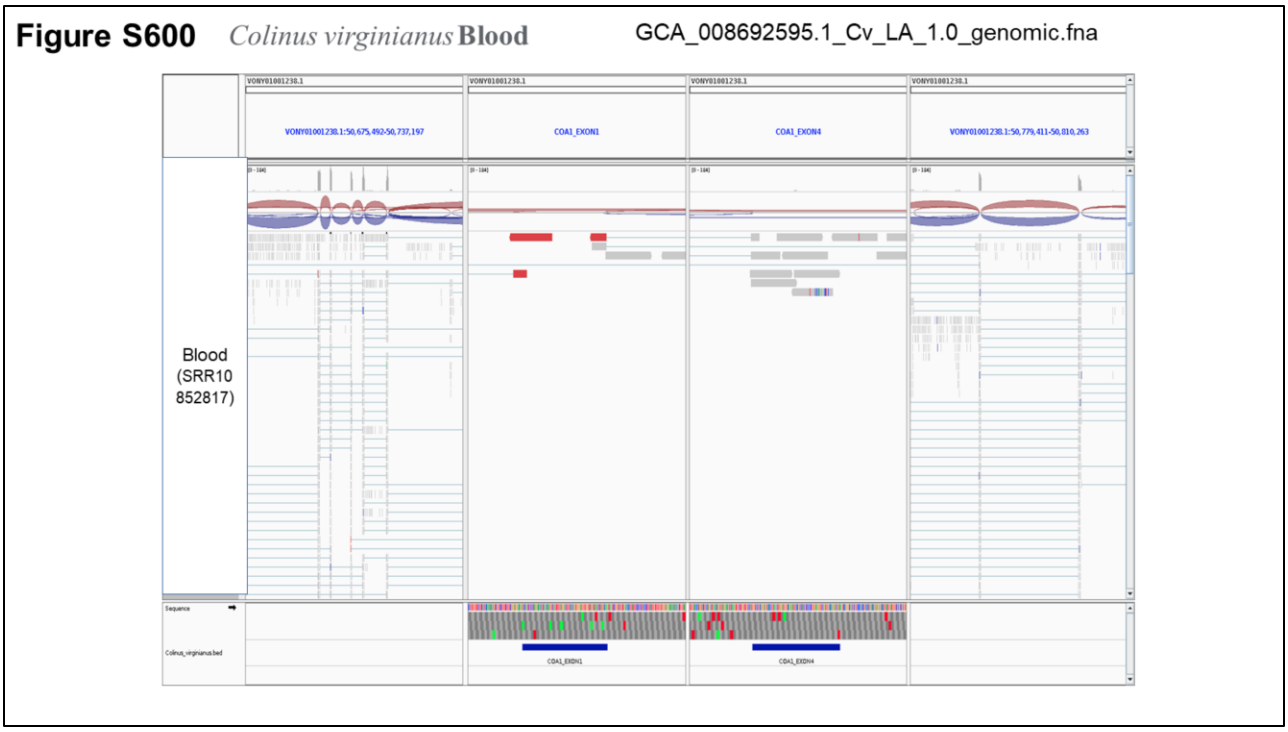

Figure S600: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in northern bobwhite (*Colinus virginianus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR10852817) have been mapped to the GCA_008692595.1_Cv_LA_1.0_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

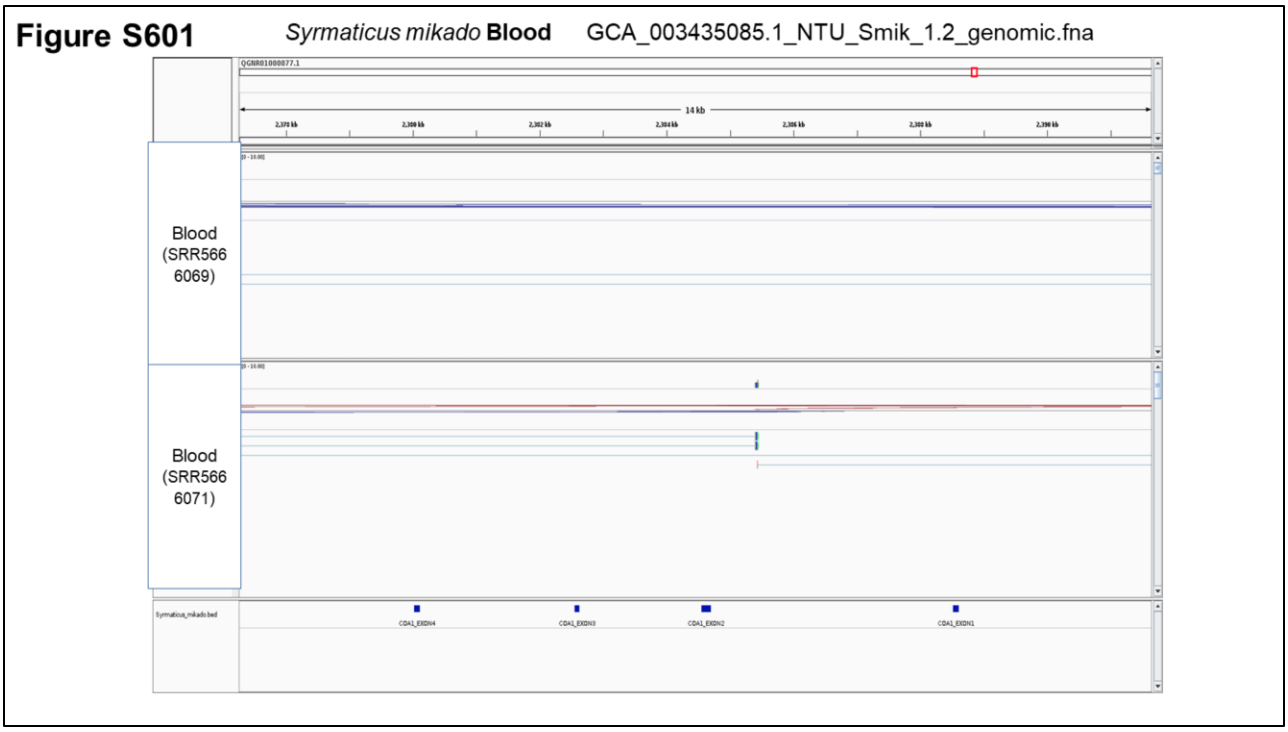

Figure S601: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Mikado pheasant (*Syrmaticus mikado*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR5666069 and SRR5666071) have been mapped to the GCA_003435085.1_NTU_Smik_1.2_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

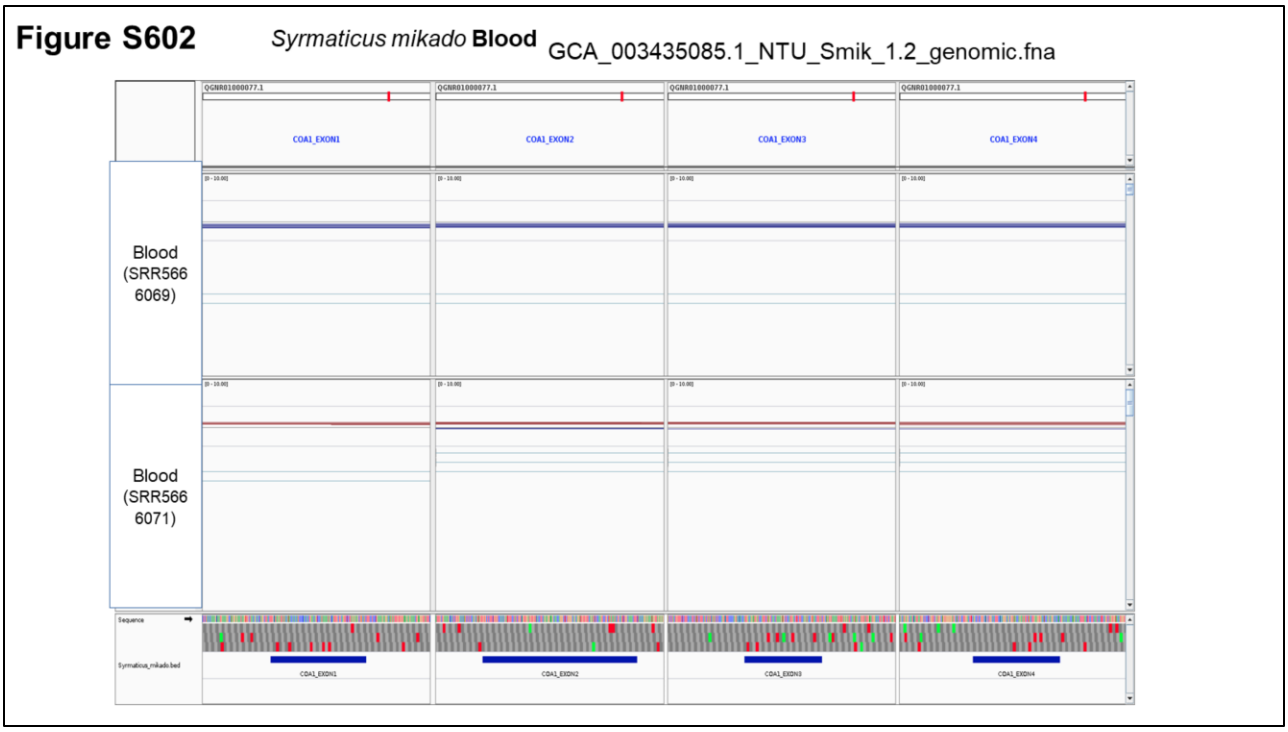

Figure S602: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S601**.

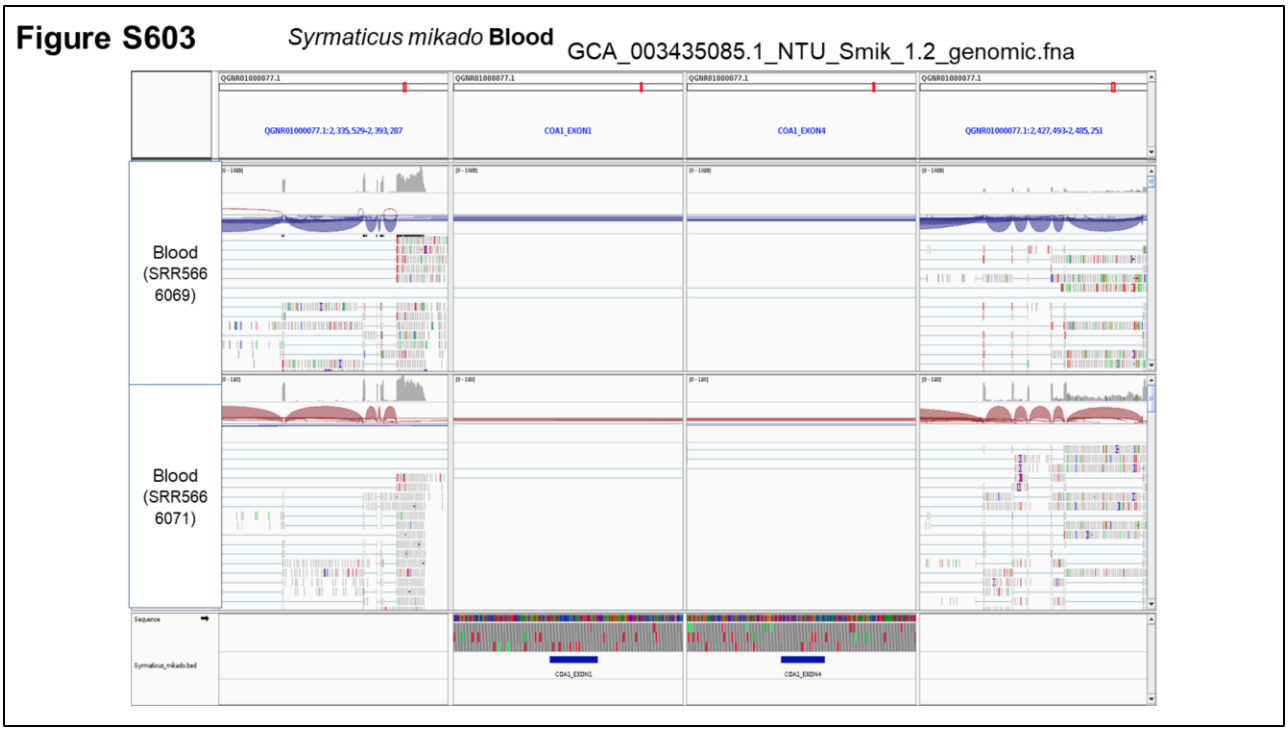

Figure S603: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in Mikado pheasant (*Syrmaticus mikado*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR5666069 and SRR5666071) have been mapped to the GCA_003435085.1_NTU_Smik_1.2_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

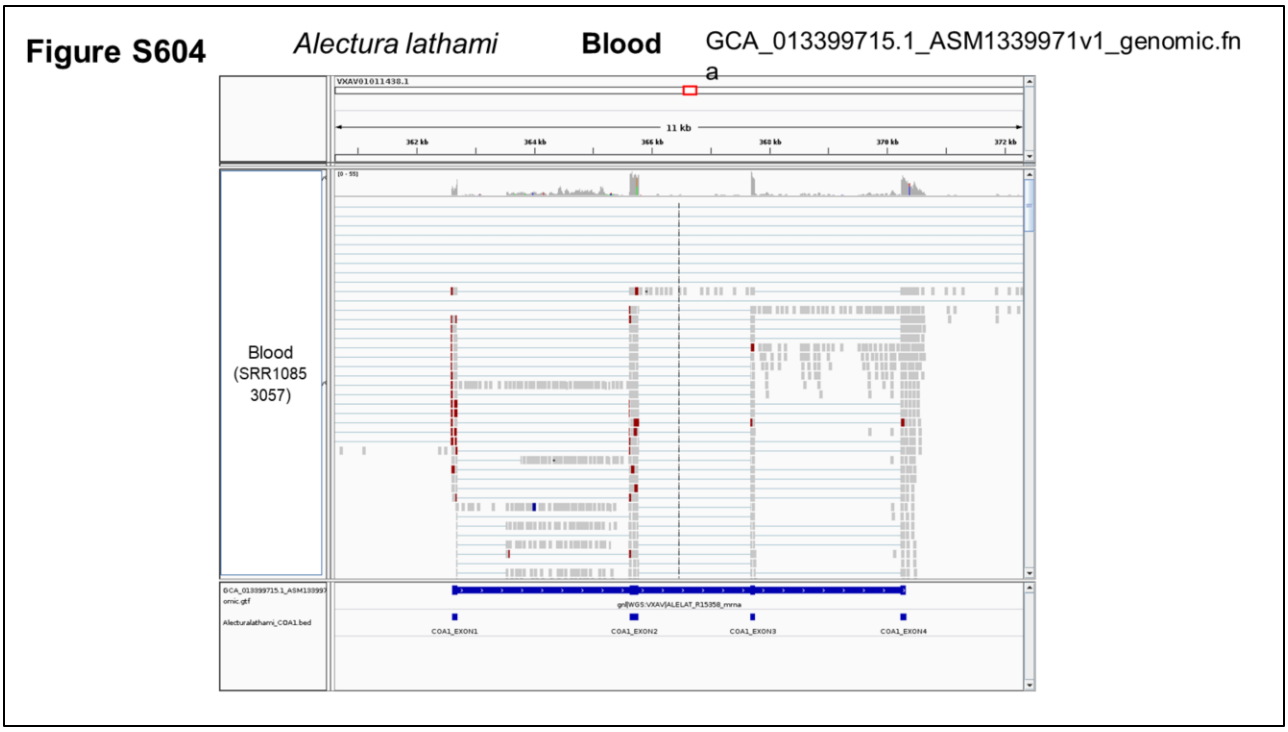

Figure S604: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Australian brush turkey (*Alectura lathami*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR10853057) have been mapped to the GCA_013399715.1_ASM1339971v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

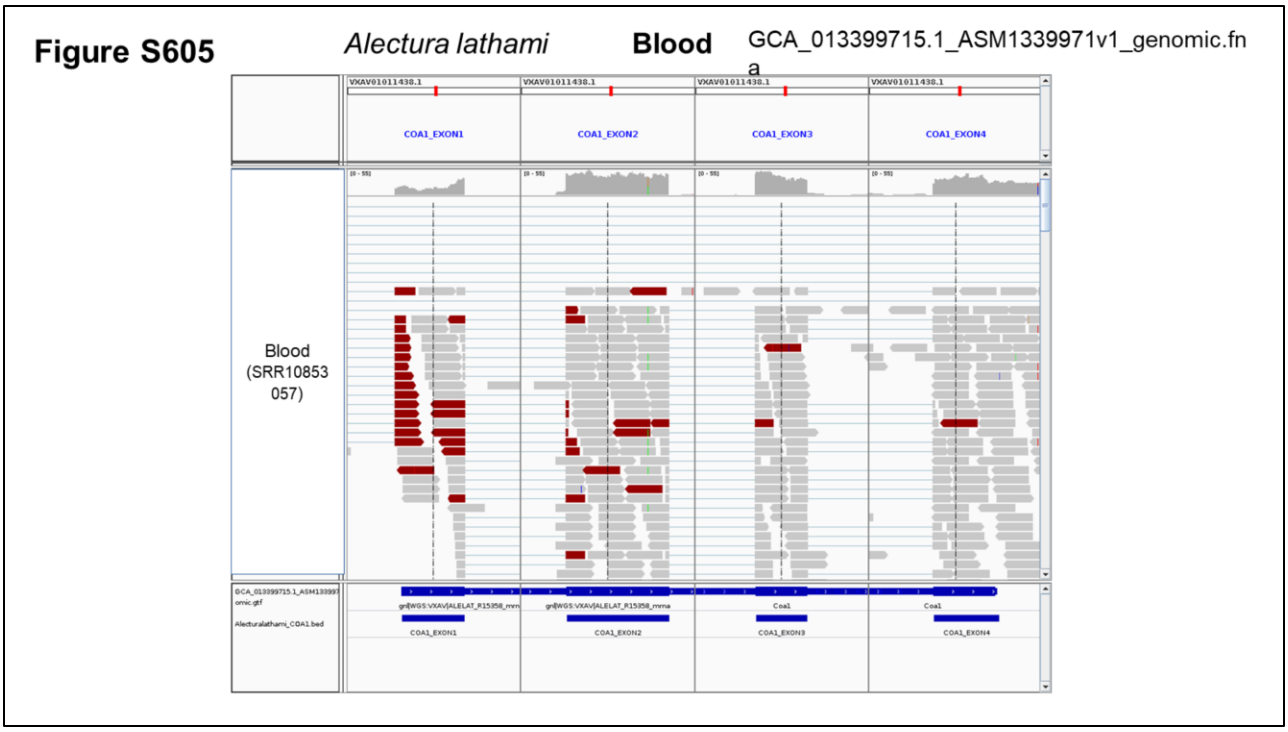

Figure S605: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S604**.

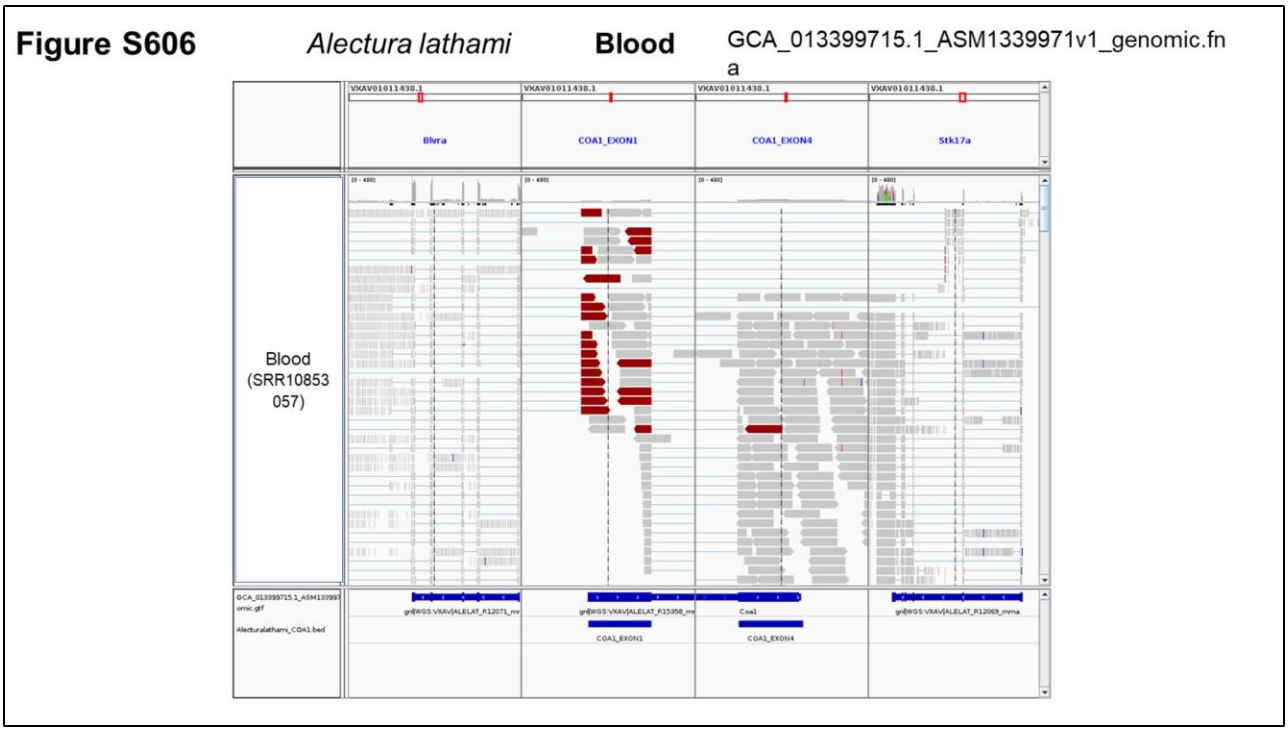

Figure S606: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in Australian brush turkey (*Alectura lathami*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR10853057) have been mapped to the GCA_013399715.1_ASM1339971v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

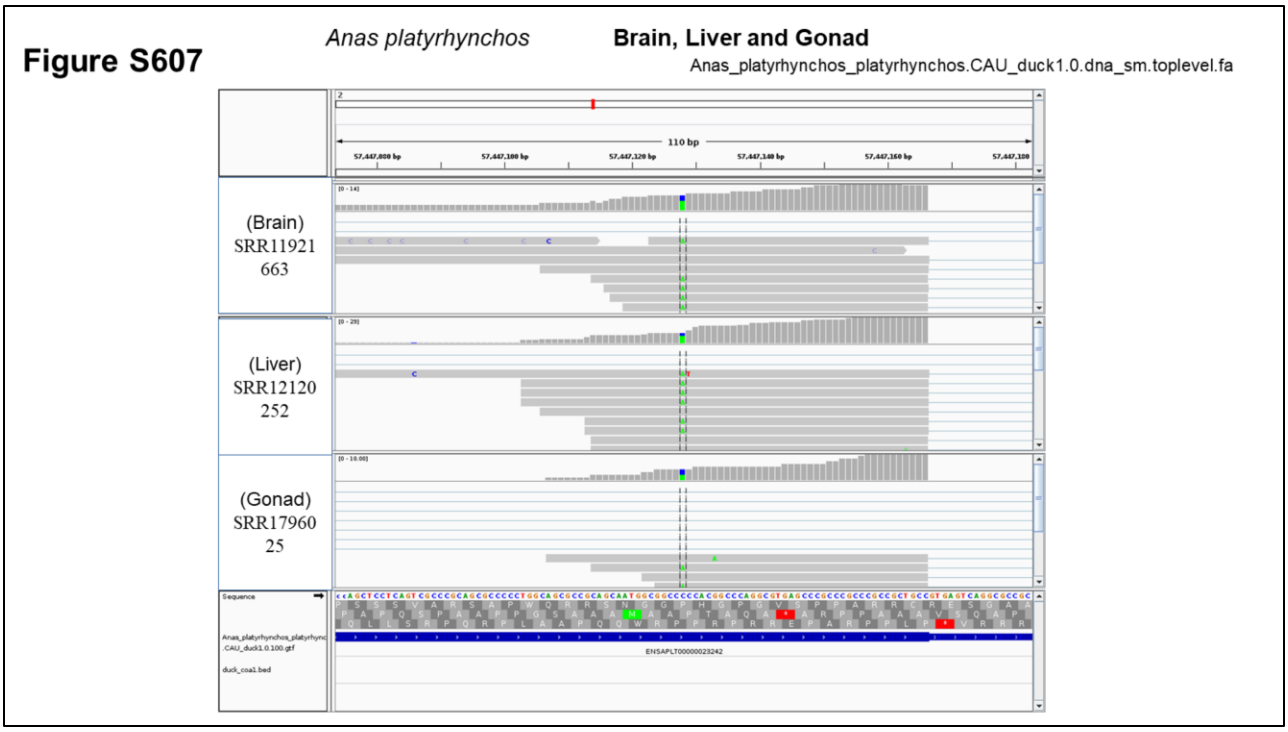

Figure S607: A premature stop codon in 1st exon of *COA1* of mallard duck (*Anas platyrhynchos*).

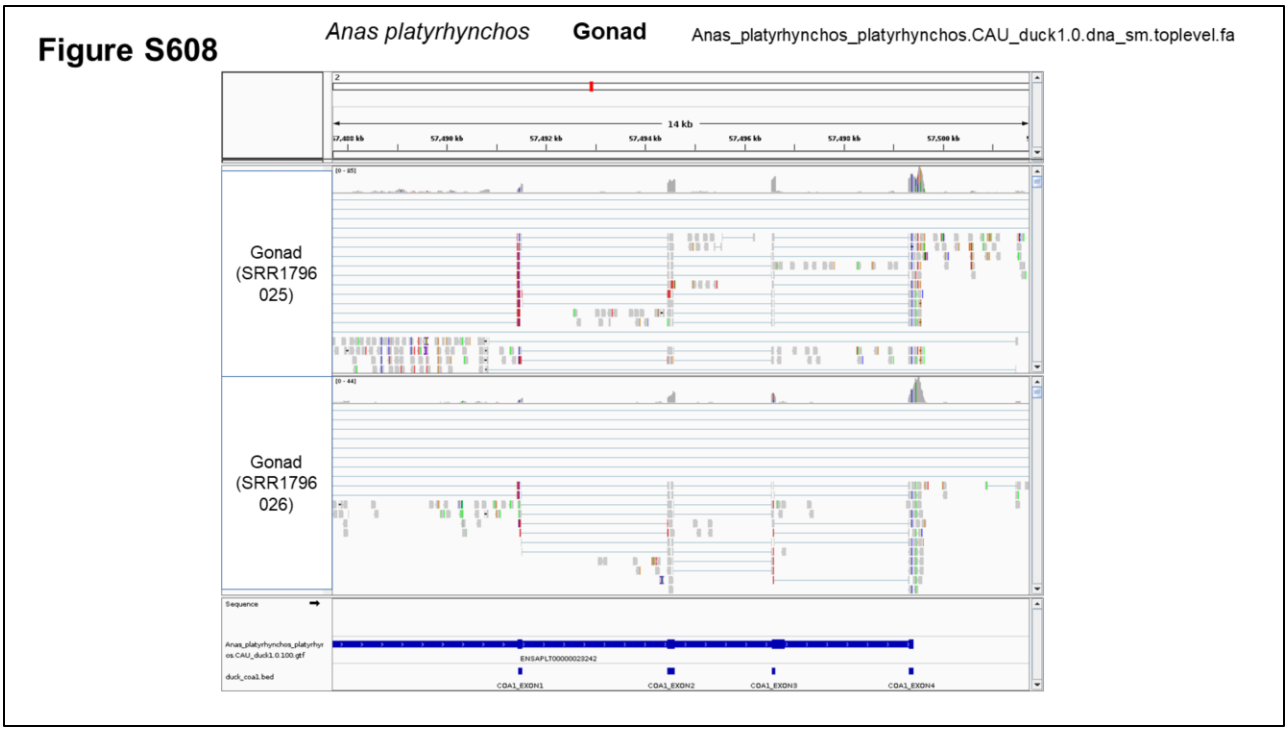

Figure S608: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in mallard duck (*Anas platyrhynchos*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from gonad (SRR1796025) and (SRR1796026) have been mapped to the Anas_platyrhynchos_platyrhynchos.CAU_duck1.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

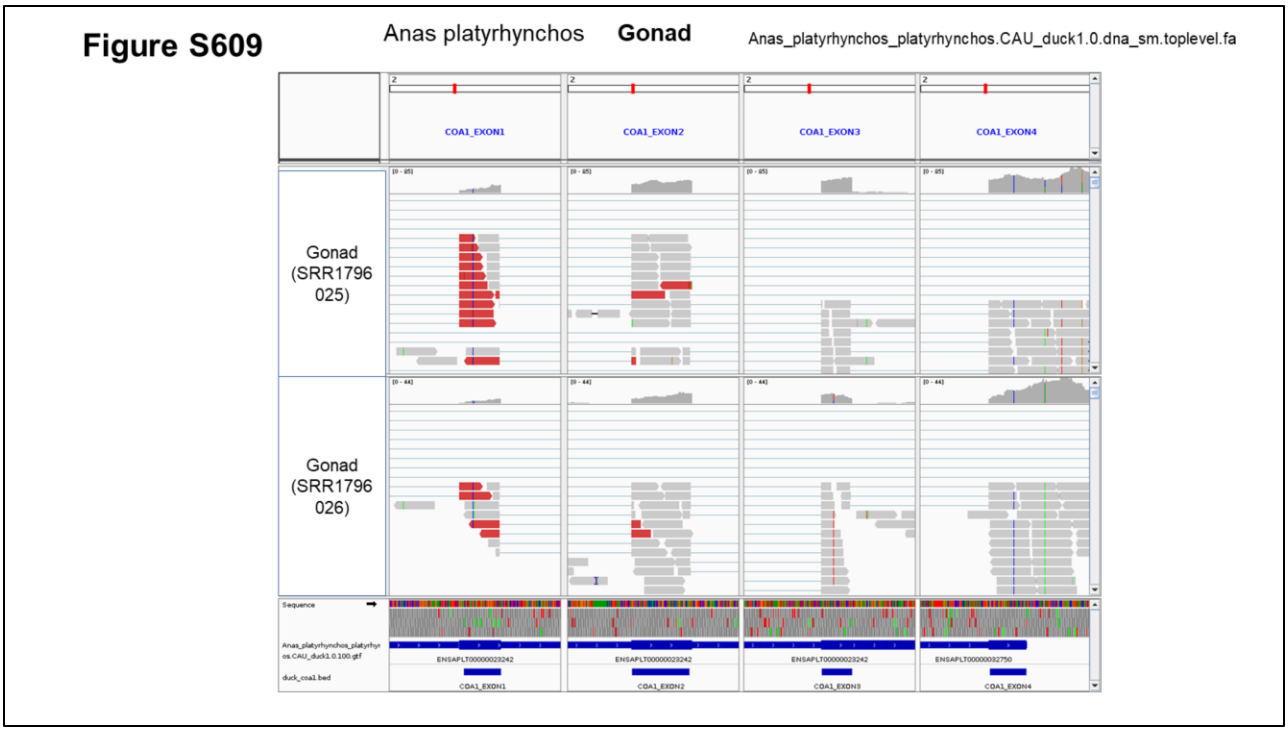

Figure S609: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S608**.

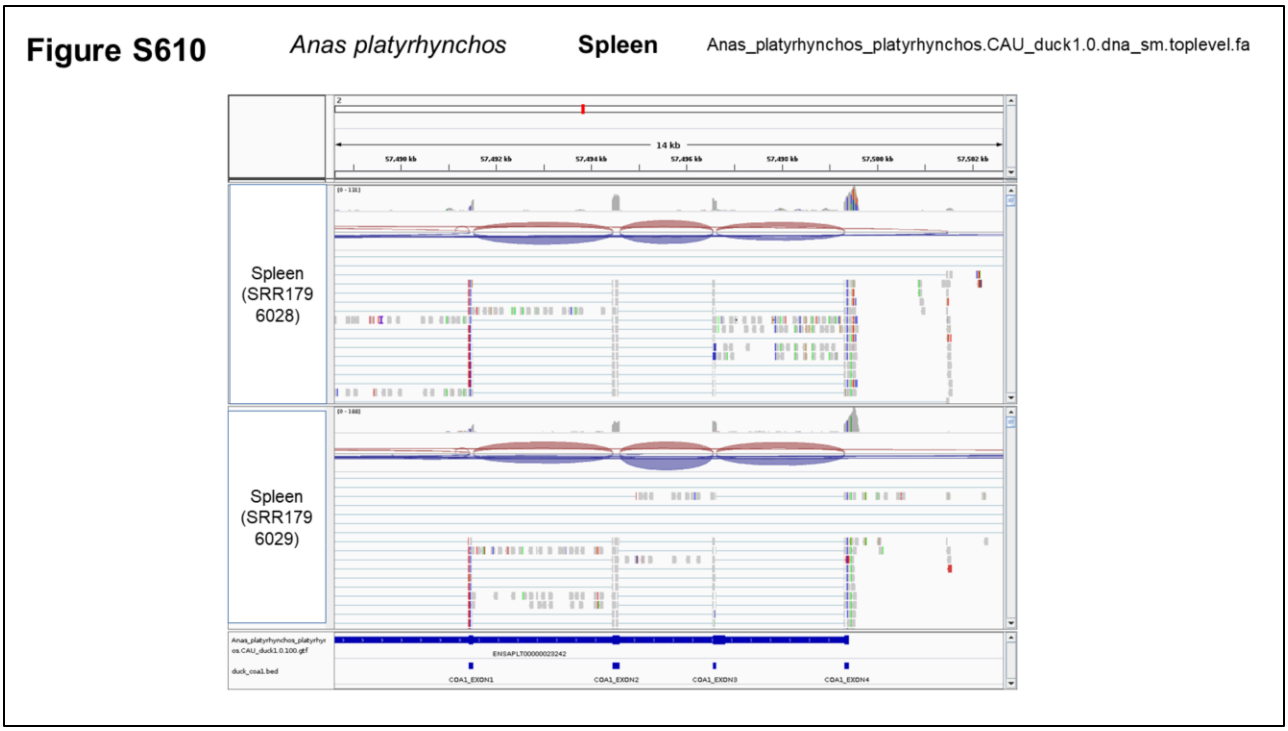

Figure S610: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in mallard duck (*Anas platyrhynchos*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR1796028) and (SRR1796029) have been mapped to the Anas_platyrhynchos_platyrhynchos.CAU_duck1.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

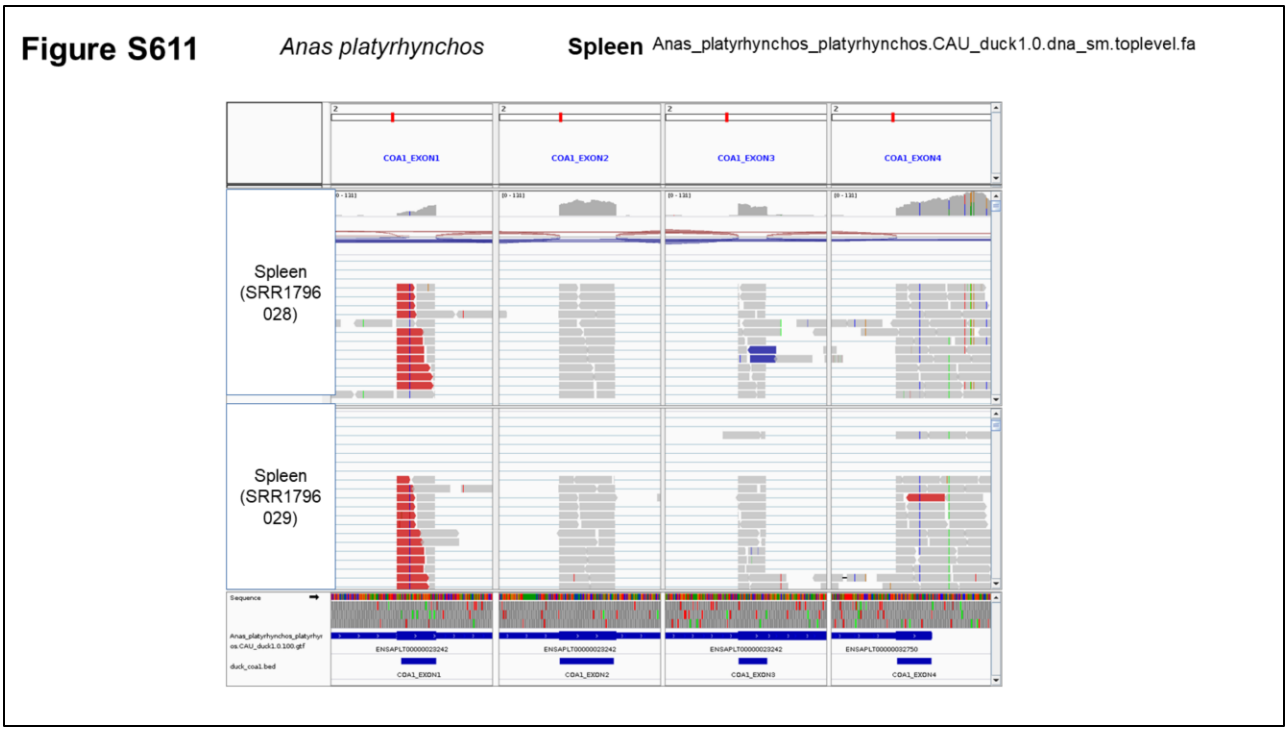

Figure S611: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S610**.

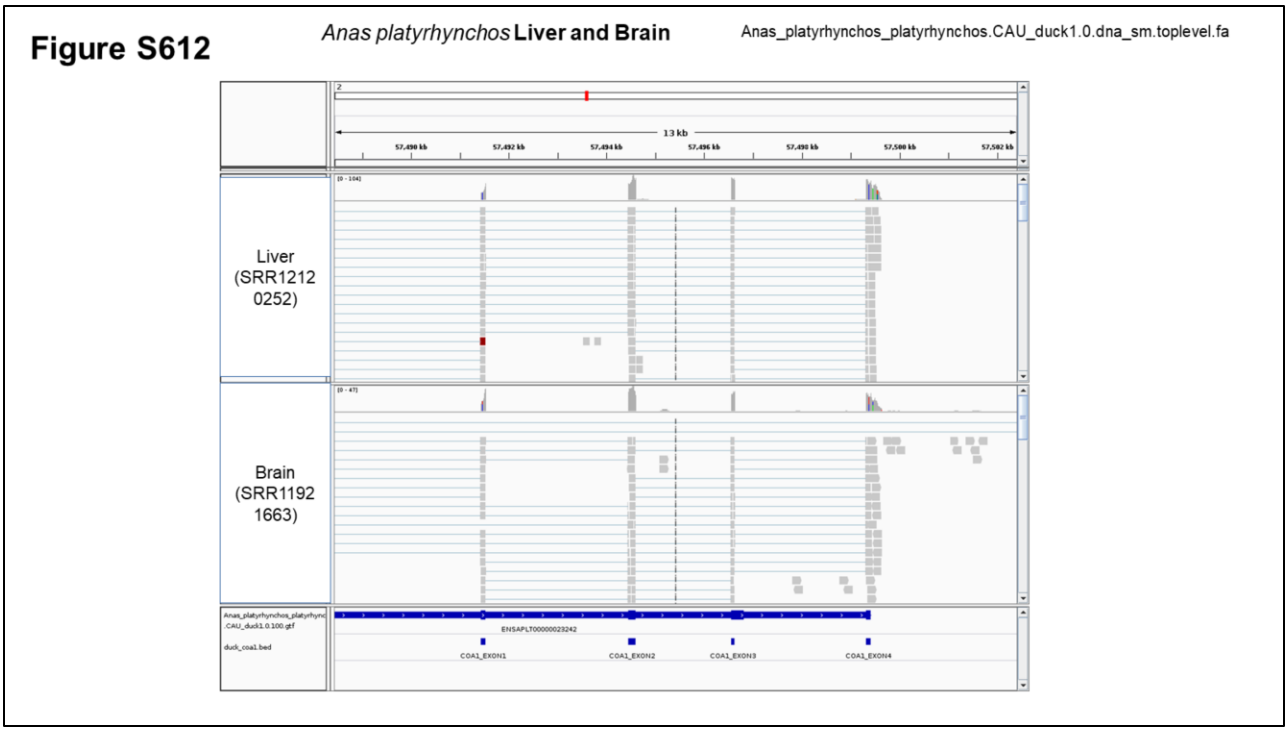

Figure S612: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in mallard duck (*Anas platyrhynchos*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR12120252) and brain (SRR11921663) have been mapped to the Anas_platyrhynchos_platyrhynchos.CAU_duck1.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

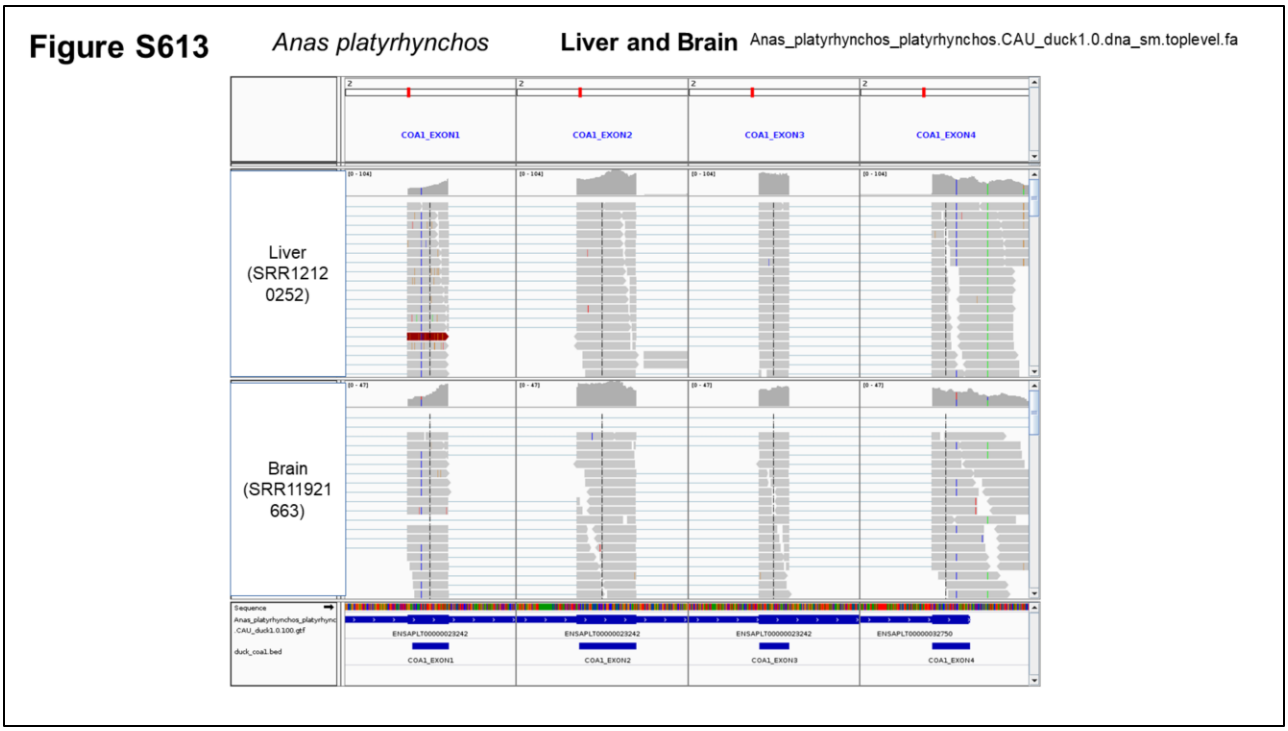

Figure S613: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S612**.

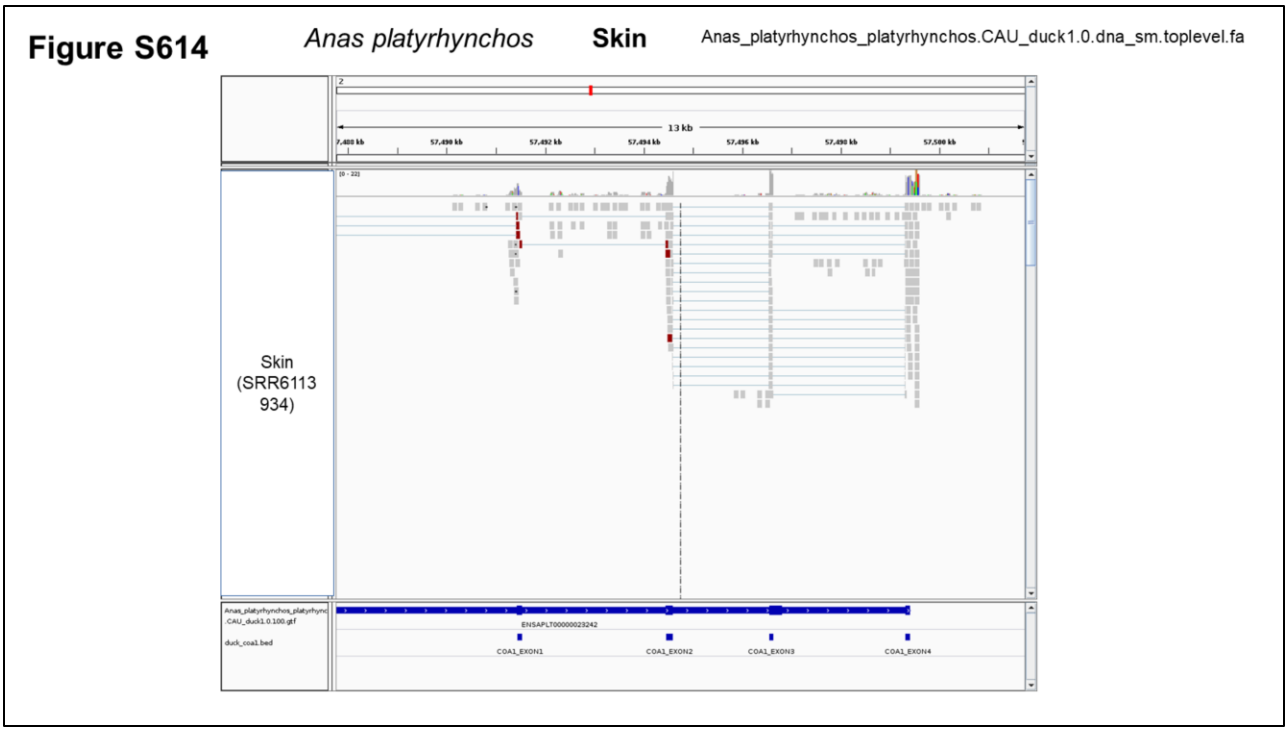

Figure S614: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in mallard duck (*Anas platyrhynchos*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from Skin (SRR6113934) have been mapped to the Anas_platyrhynchos_platyrhynchos.CAU_duck1.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

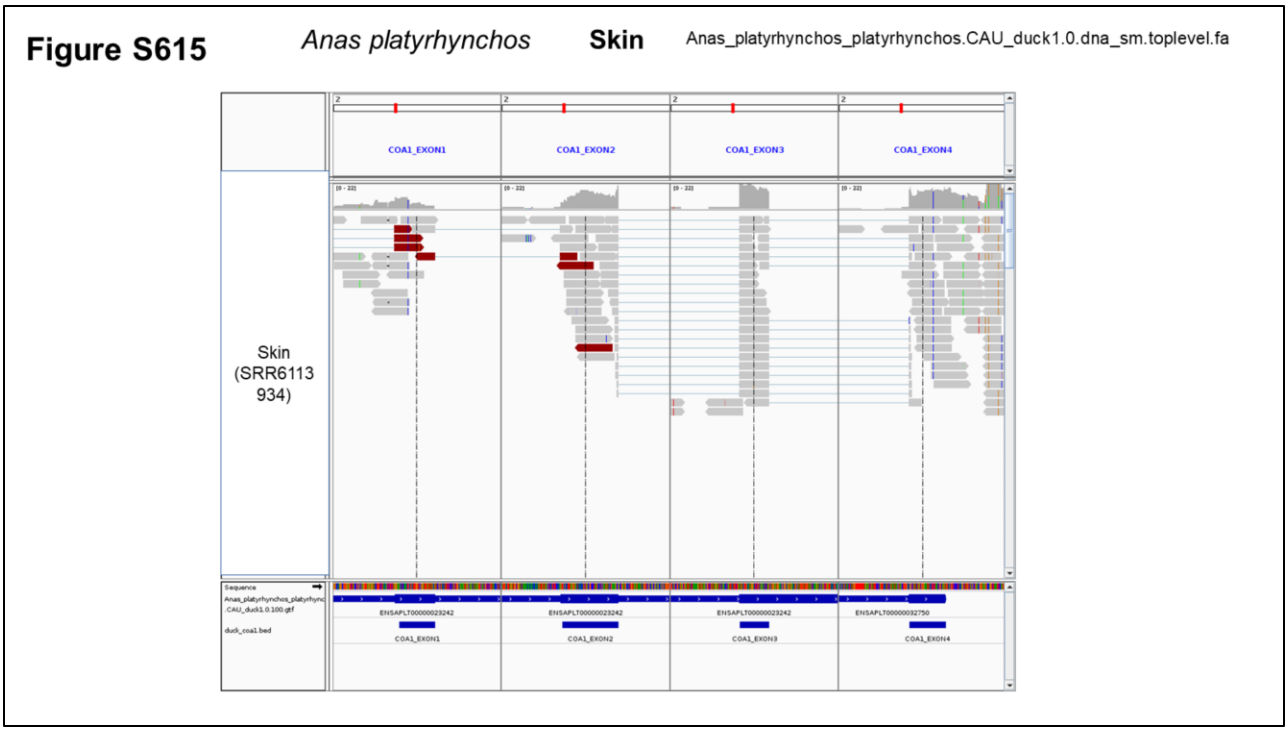

Figure S615: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S614**.

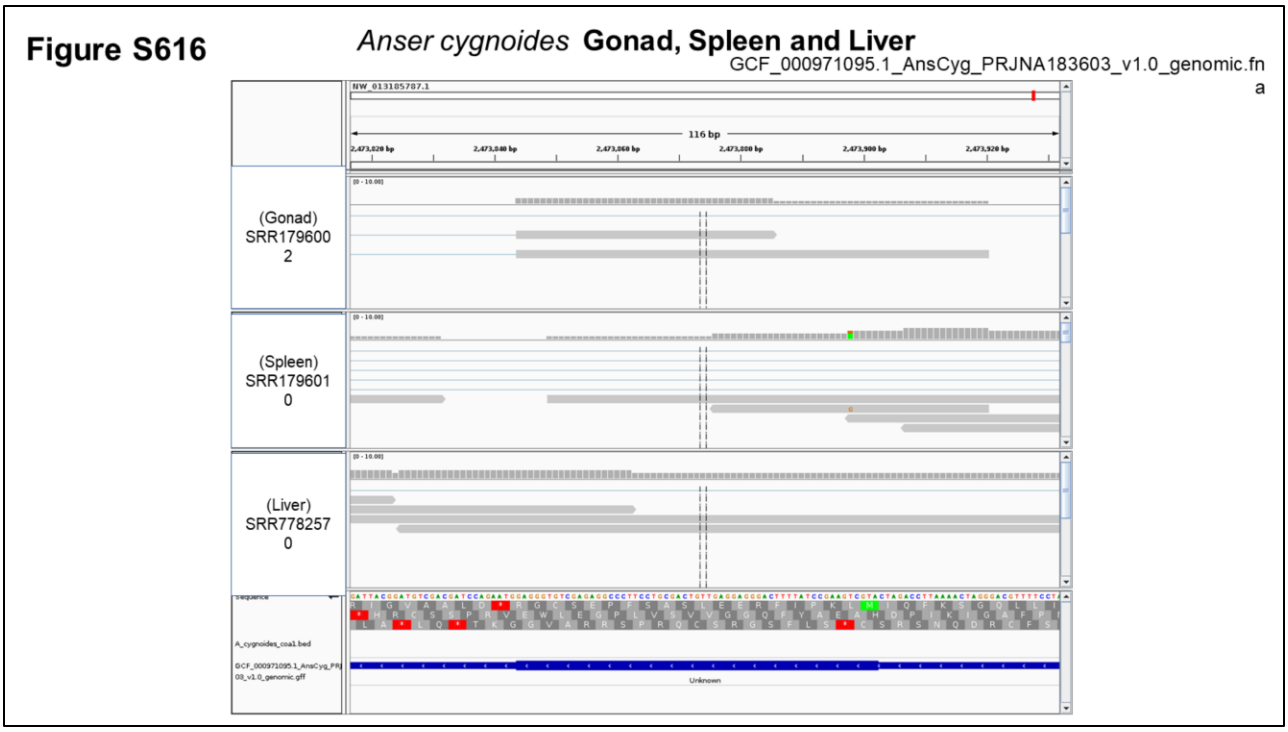

Figure S616: Less expression of first exon of 167 aa length transcript in swan goose (*Anser cygnoides*).

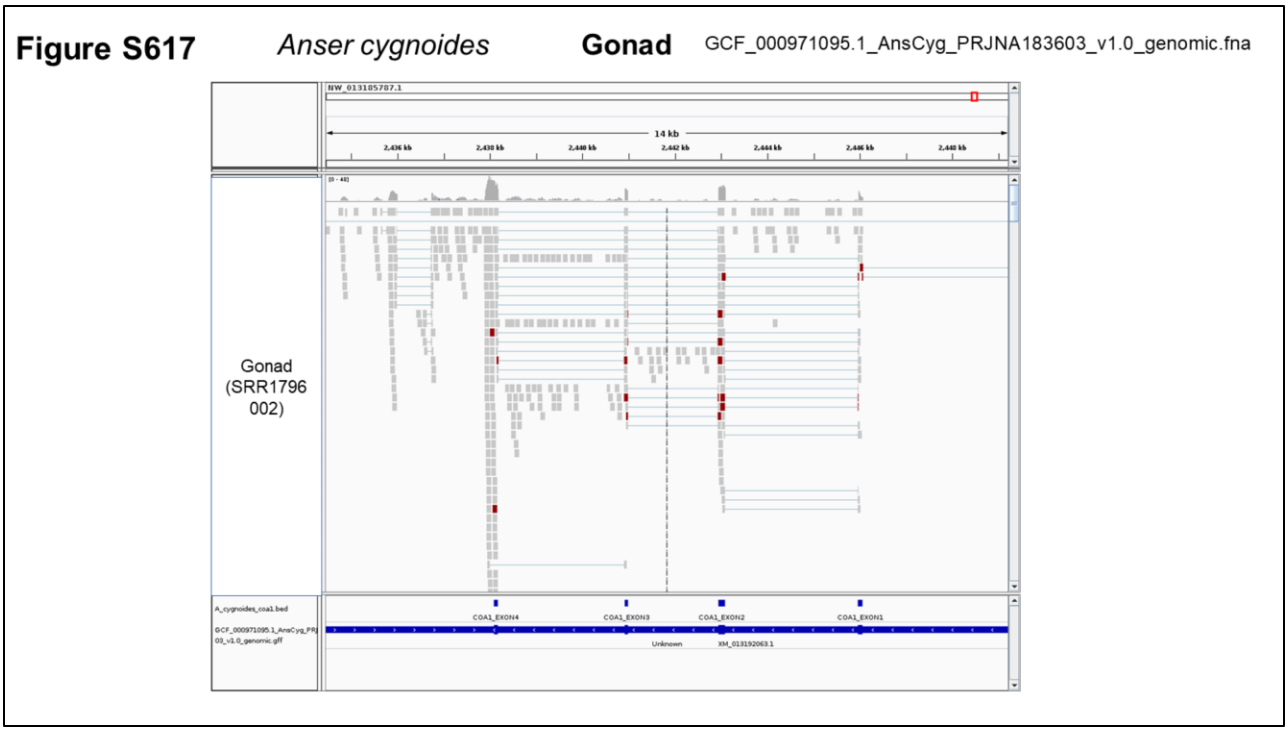

Figure S617: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in swan goose (*Anser cygnoides*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from gonad (SRR1796002) have been mapped to the GCF_000971095.1_AnsCyg_PRJNA183603_v1.0_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

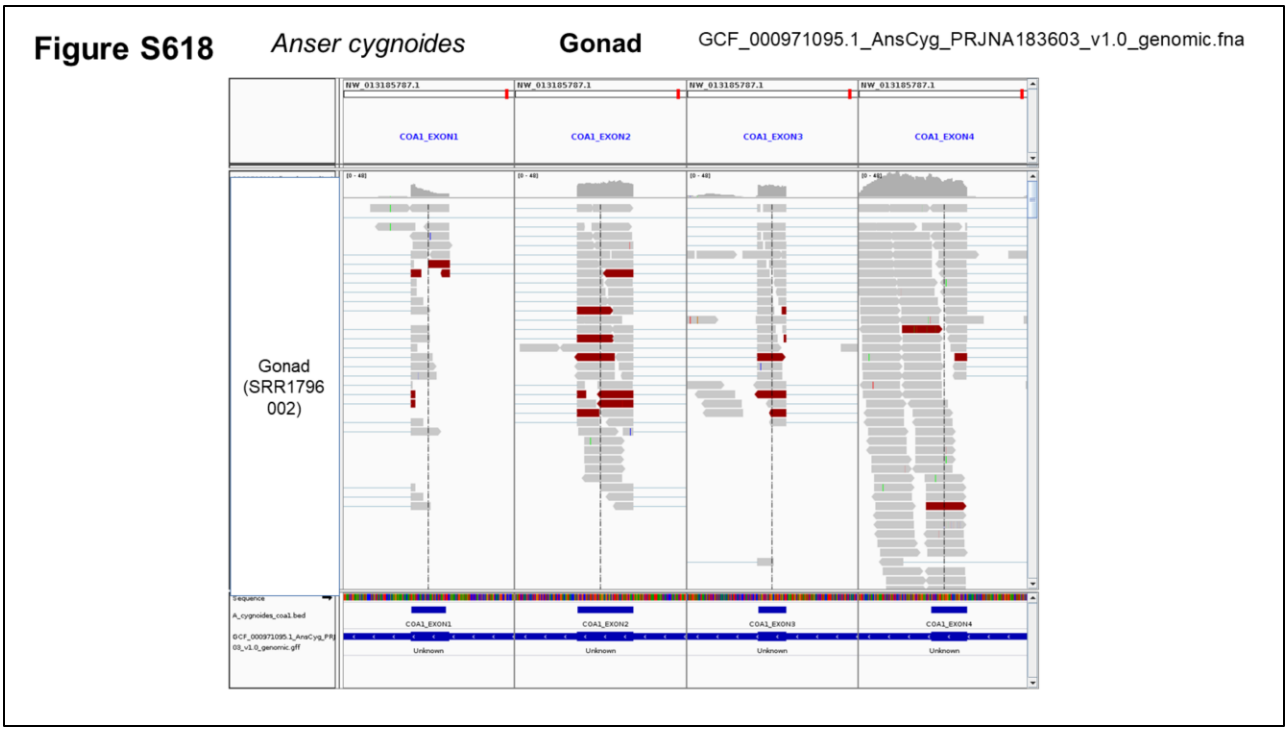

Figure S618: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S617**.

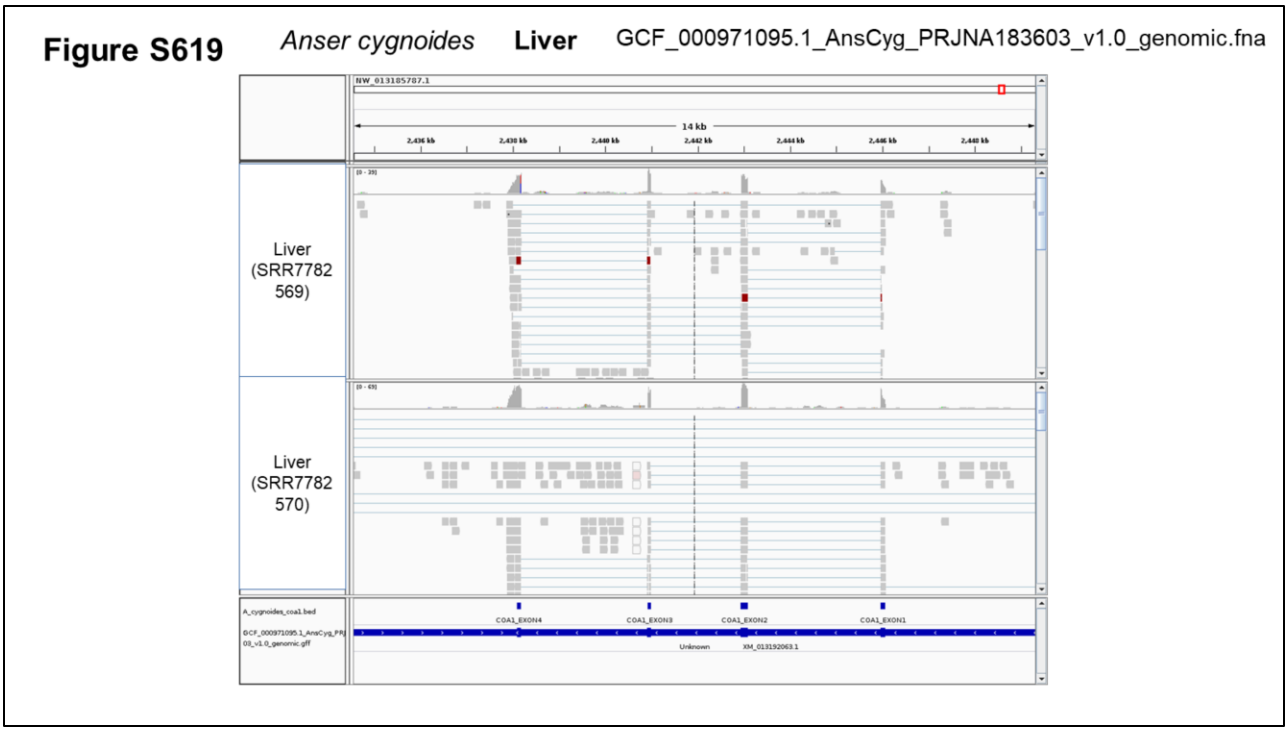

Figure S619: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in swan goose (*Anser cygnoides*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR7782569) and (SRR7782570) have been mapped to the GCF_000971095.1_AnsCyg_PRJNA183603_v1.0_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

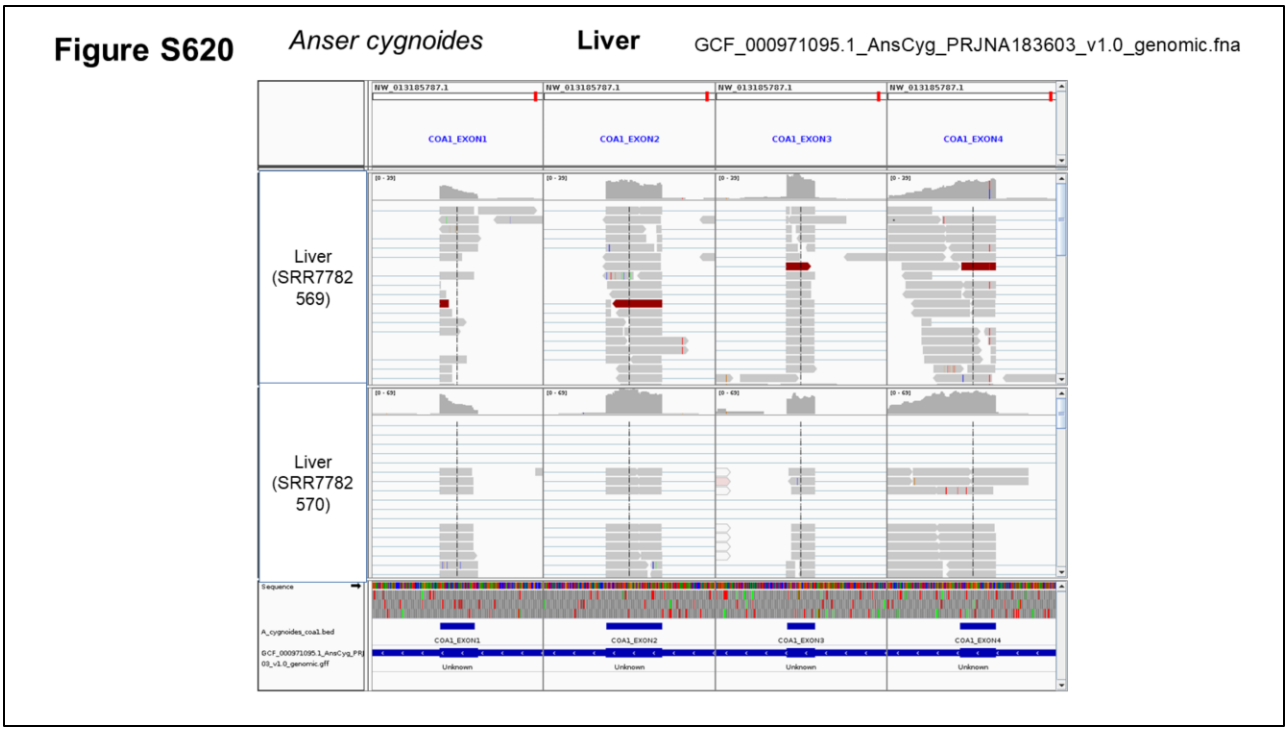

Figure S620: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S619**.

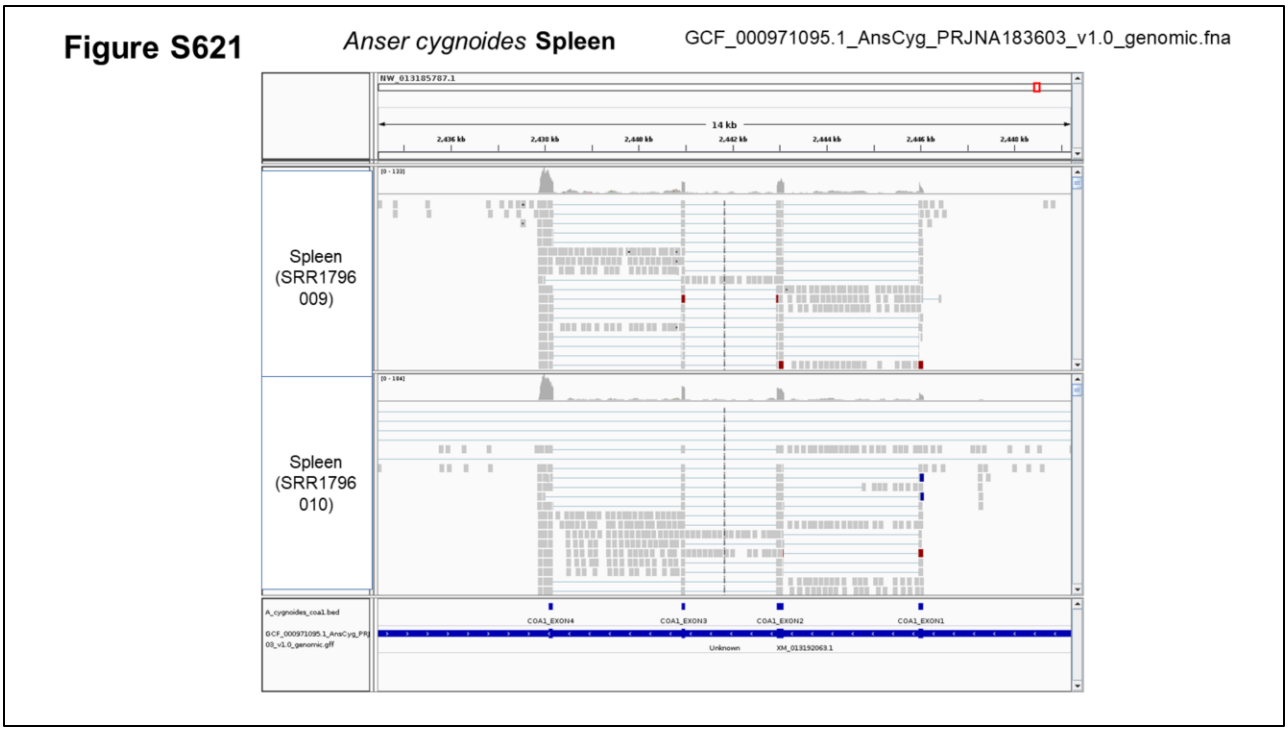

Figure S621: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in swan goose (*Anser cygnoides*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR1796009) and (SRR1796010) have been mapped to the GCF_000971095.1_AnsCyg_PRJNA183603_v1.0_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

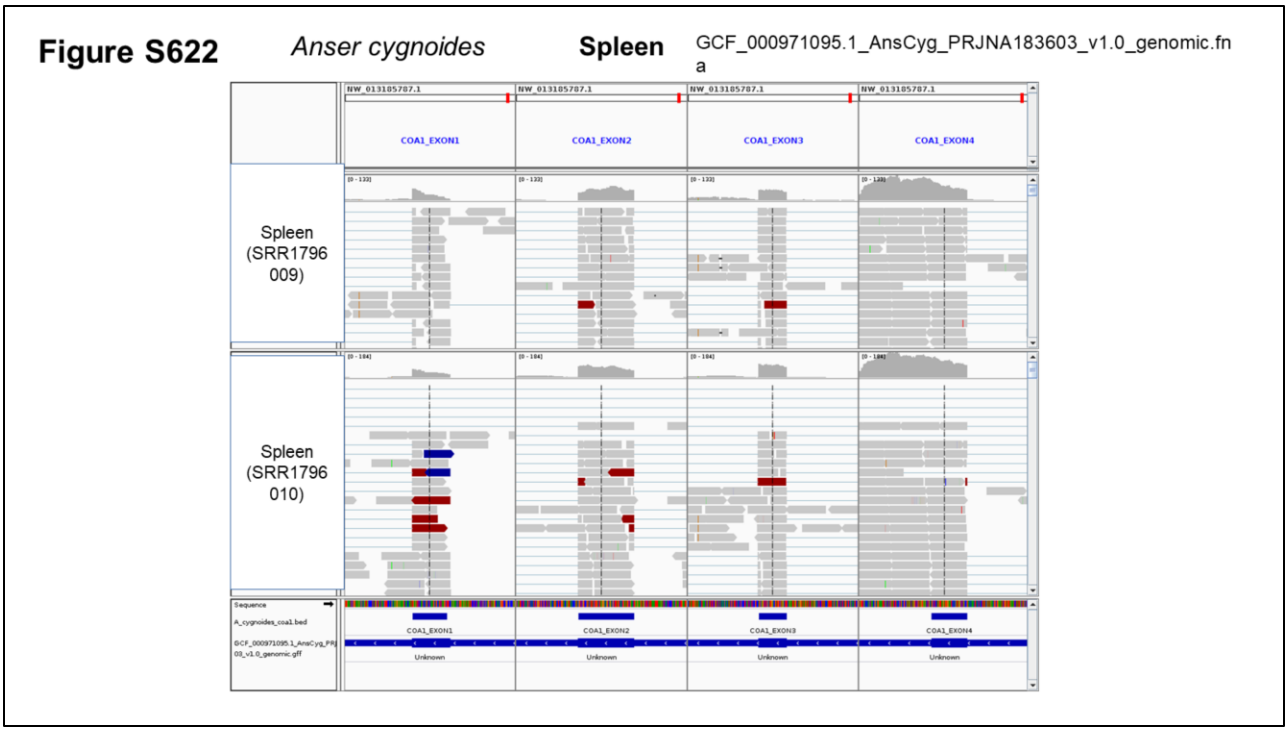

Figure S622: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S621**.

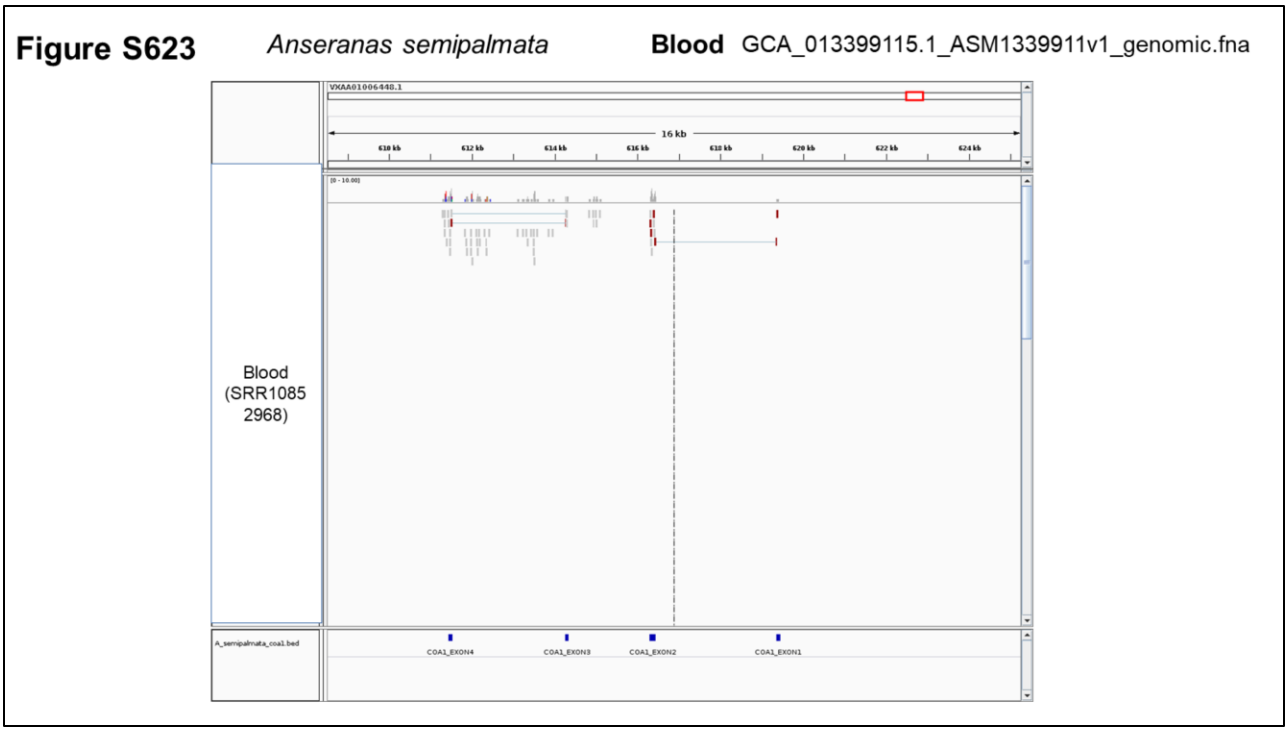

Figure S623: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in magpie goose (*Anseranas semipalmata*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR10852968) have been mapped to the GCA_013399115.1_ASM1339911v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

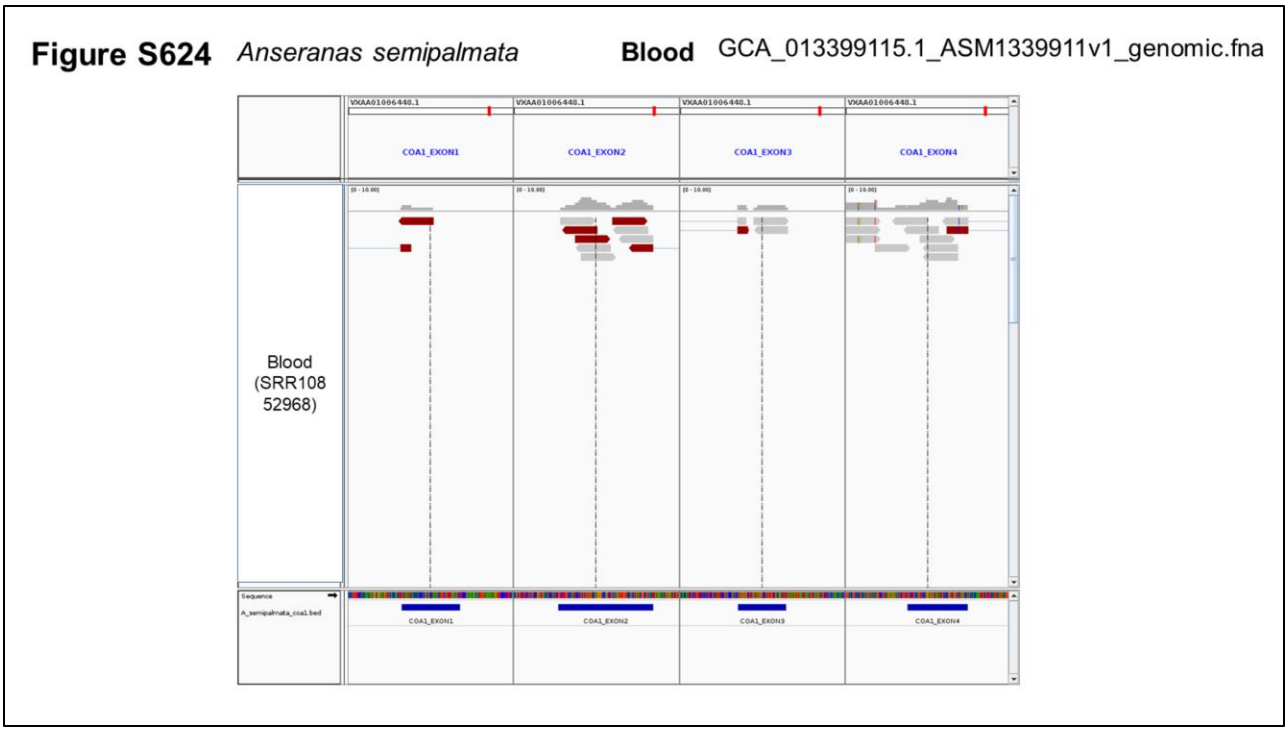

Figure S624: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S623**.

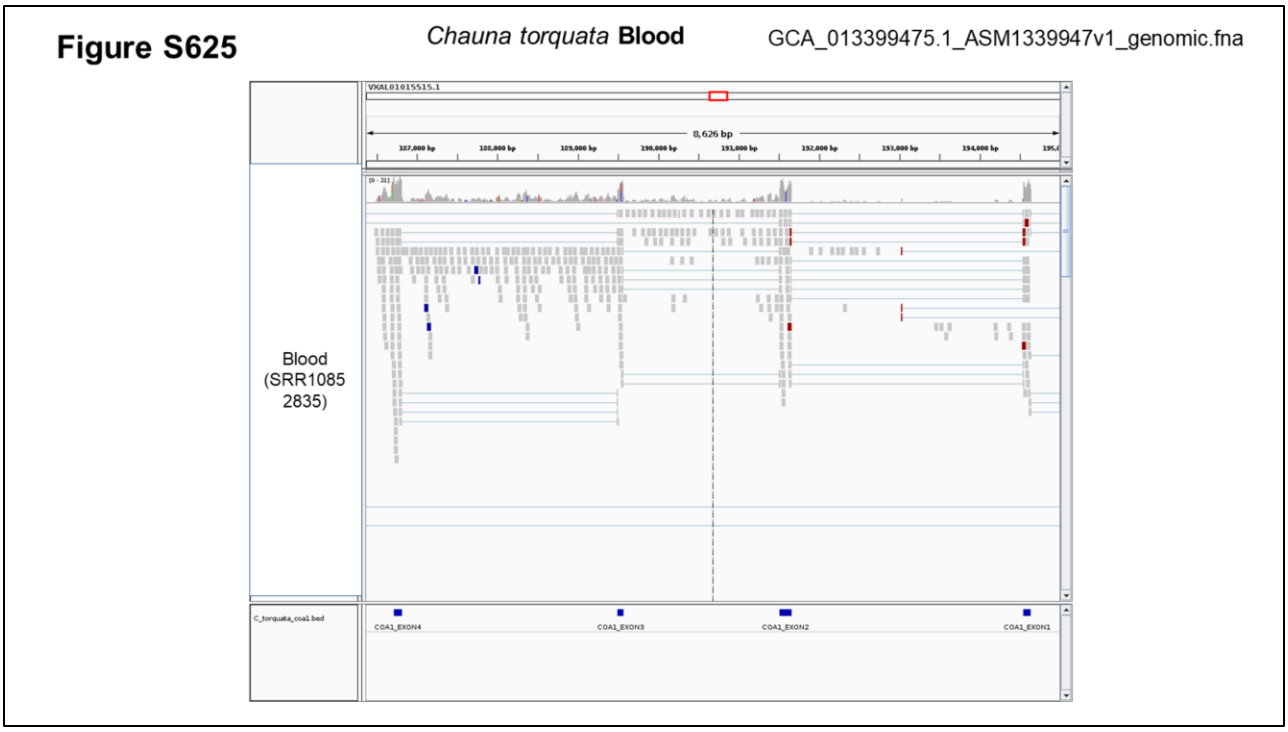

Figure S625: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in southern screamer (*Chauna torquata*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR10852835) have been mapped to the GCA_013399475.1_ASM1339947v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

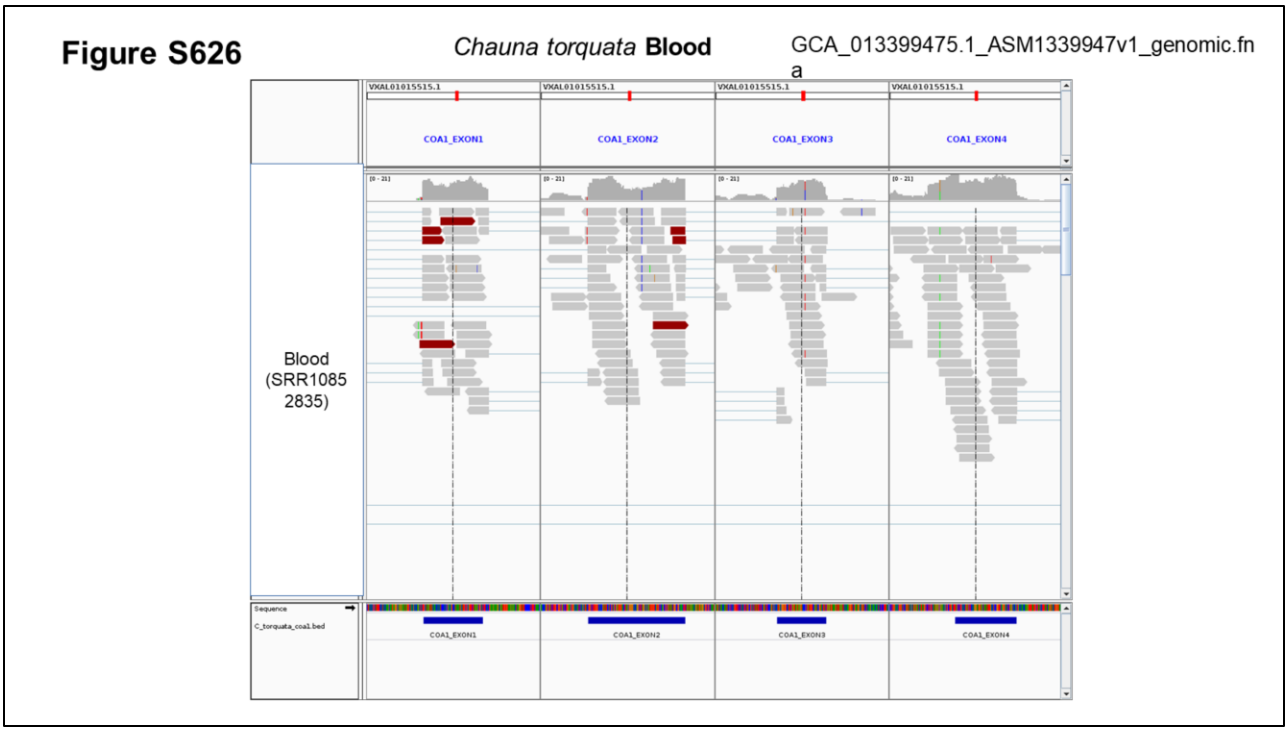

Figure S626: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S625**.

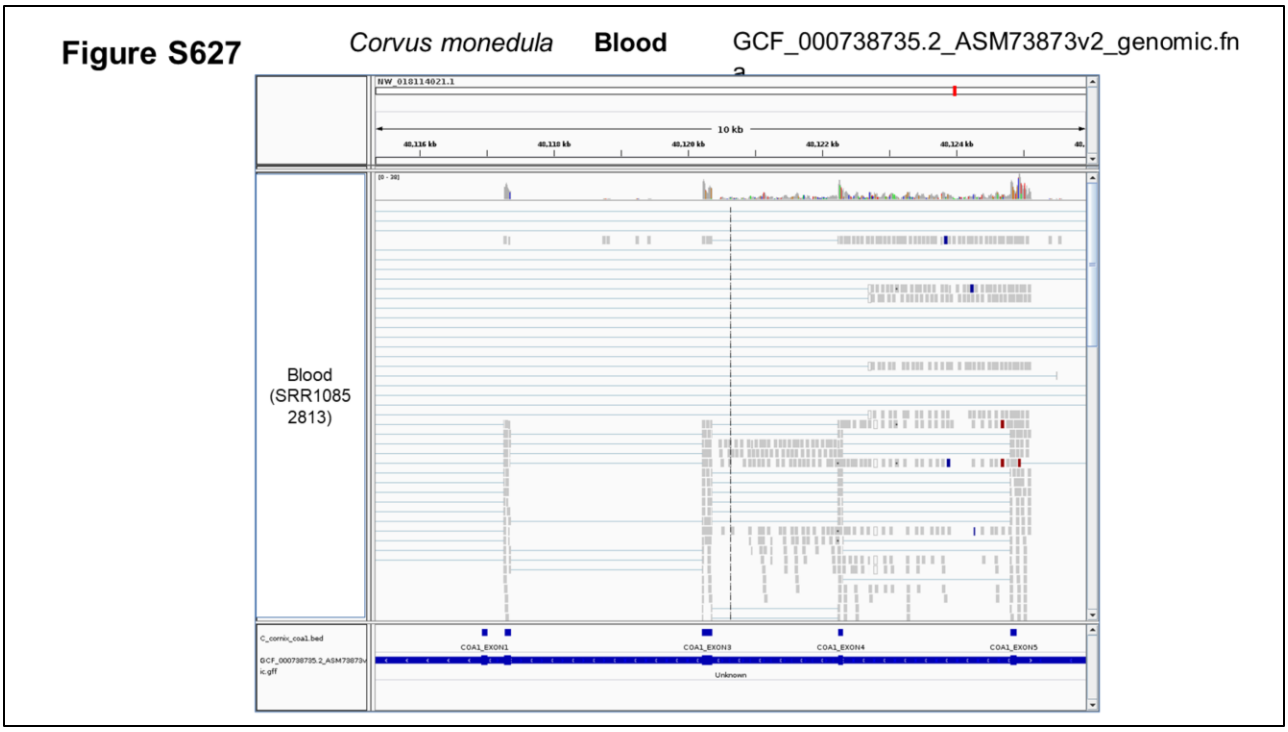

Figure S627: Screenshot of RNA-seq reads aligned to each of the putative locations of the five *COA1* exons in western Jackdaw (*Corvus monedula*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR10852813) have been mapped to the GCF_000738735.2_ASM73873v2_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

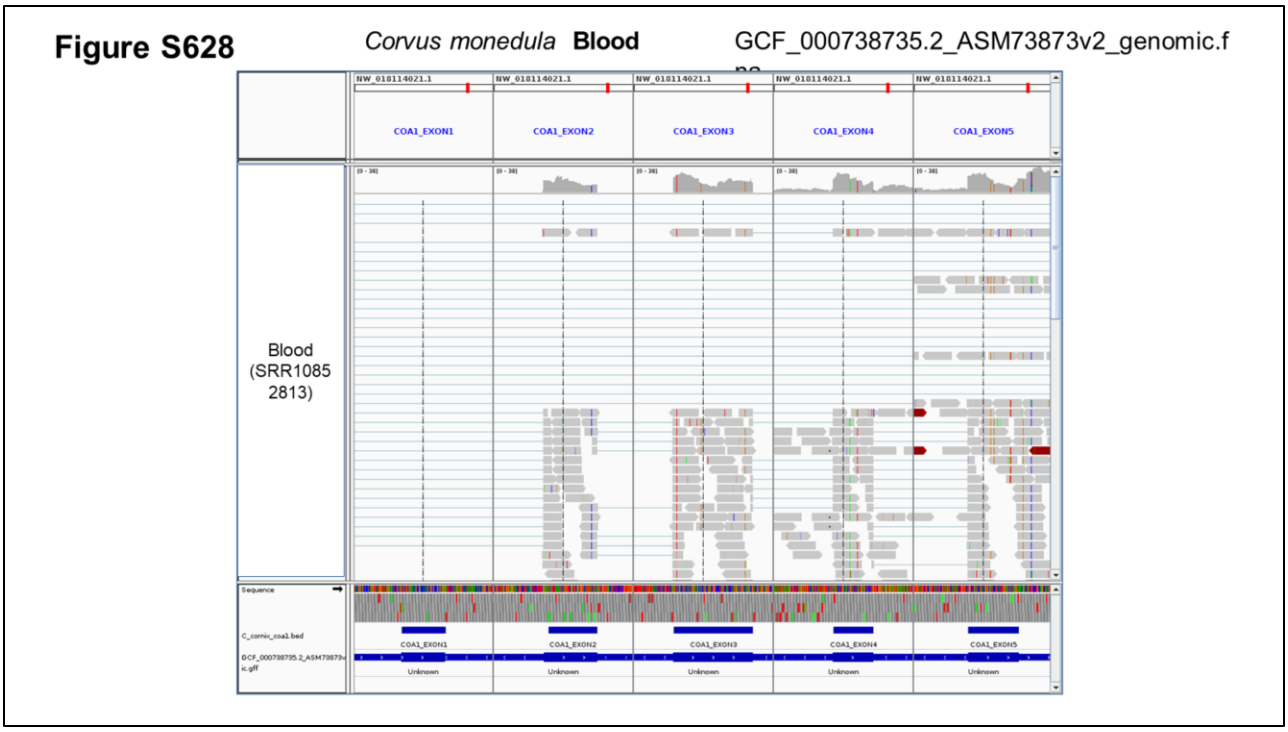

Figure S628: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S627**.

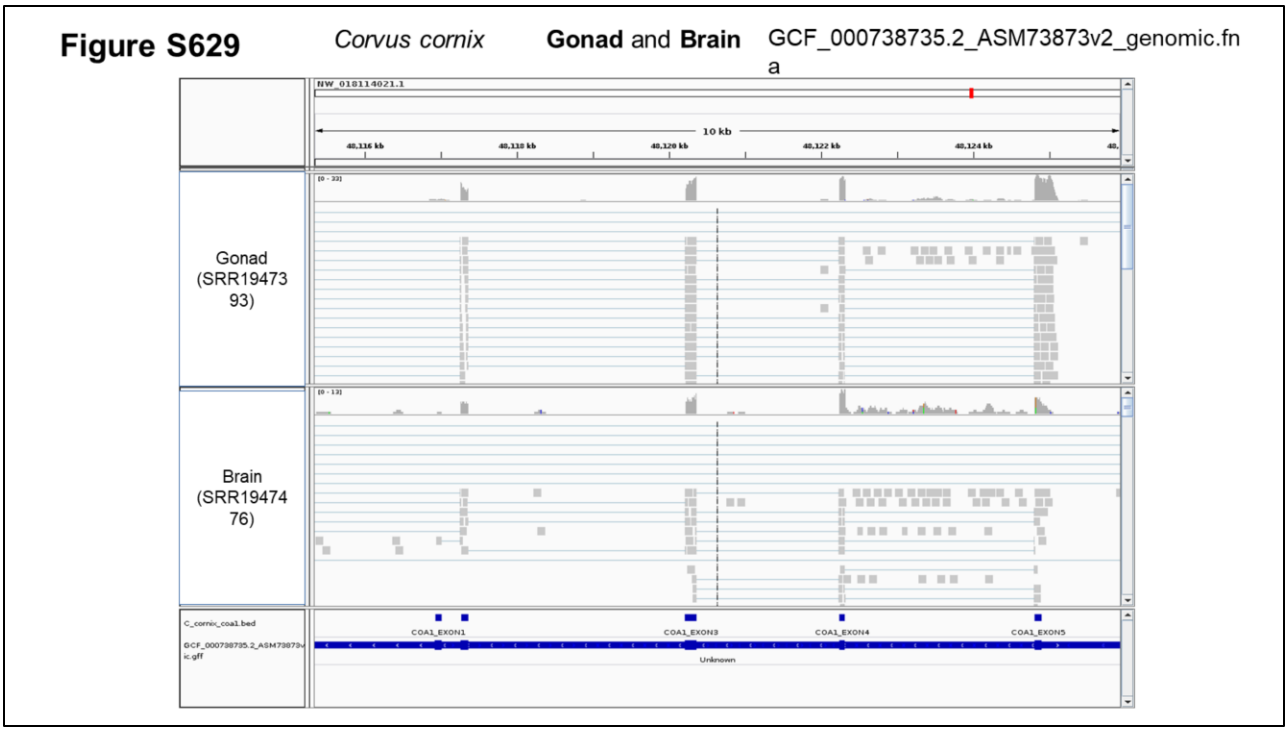

Figure S629: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in hooded crow (*Corvus cornix*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from gonad (SRR1947393) and brain (SRR1947476) have been mapped to the GCF_000738735.2_ASM73873v2_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

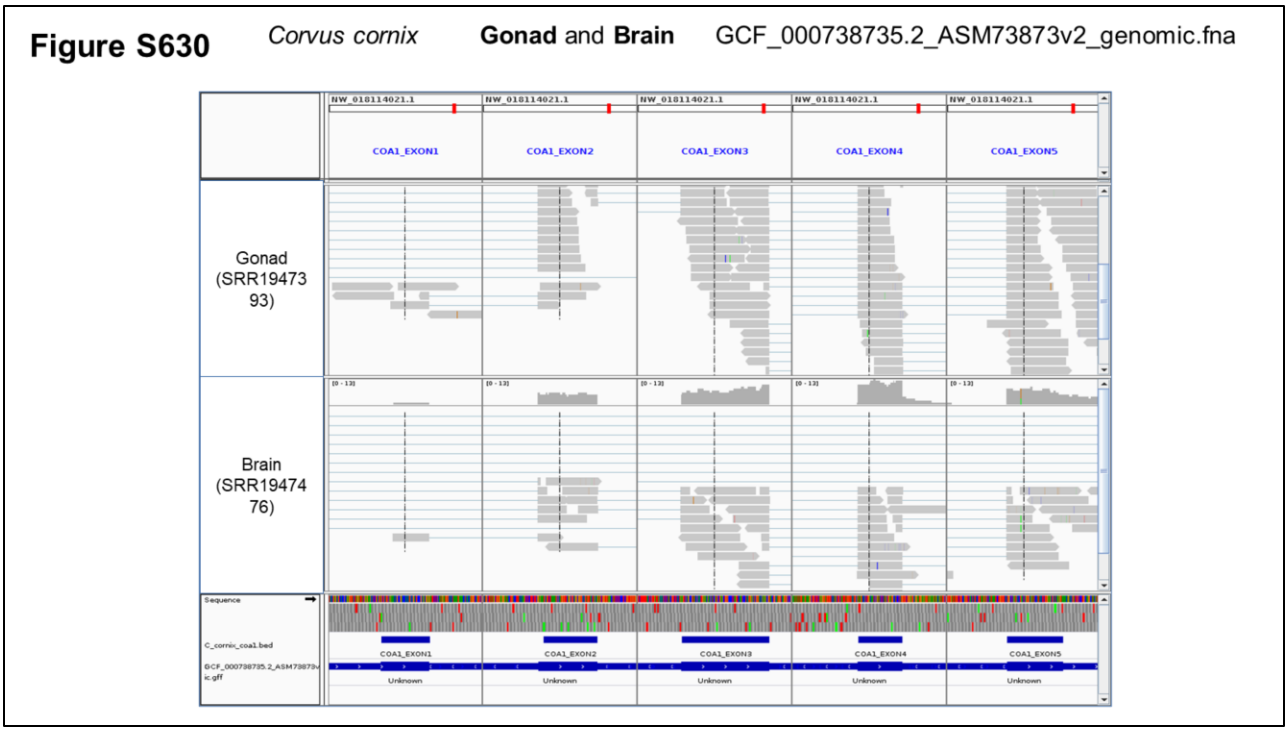

Figure S630: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S629**.

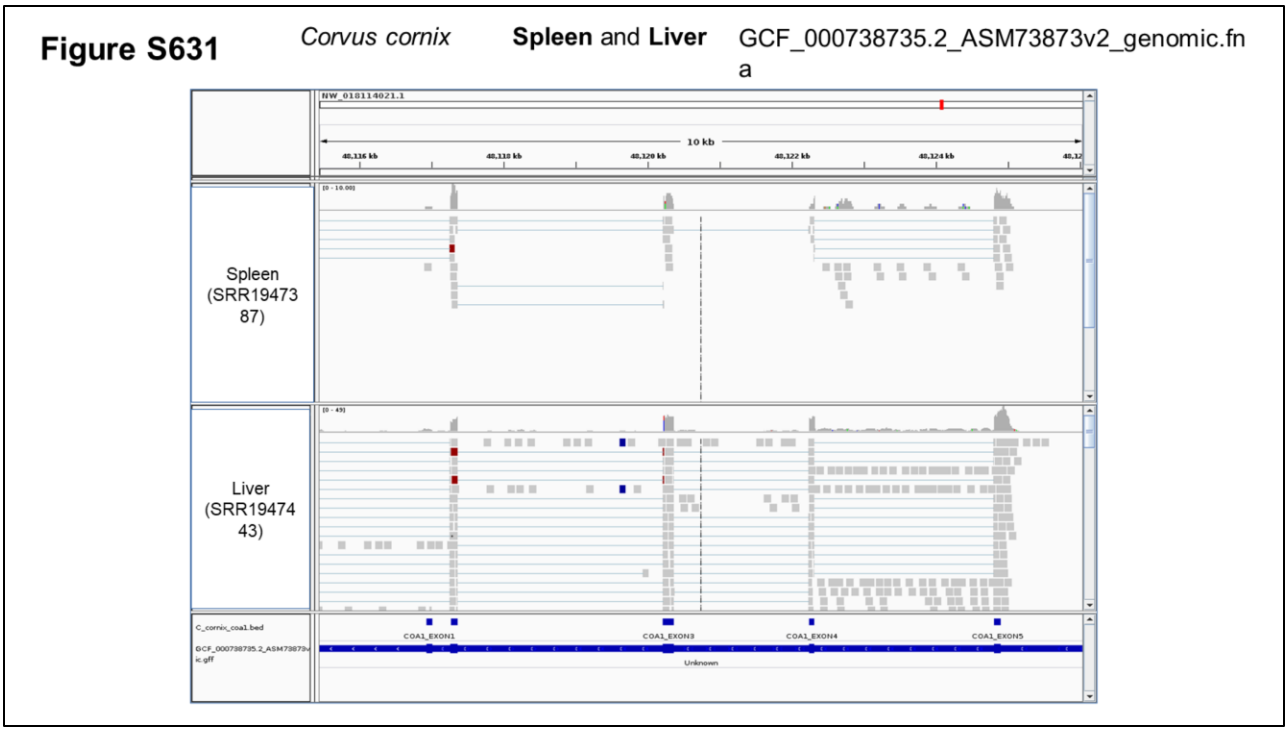

Figure S631: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in hooded crow (*Corvus cornix*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR1947387) and liver (SRR1947443) have been mapped to the GCF_000738735.2_ASM73873v2_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

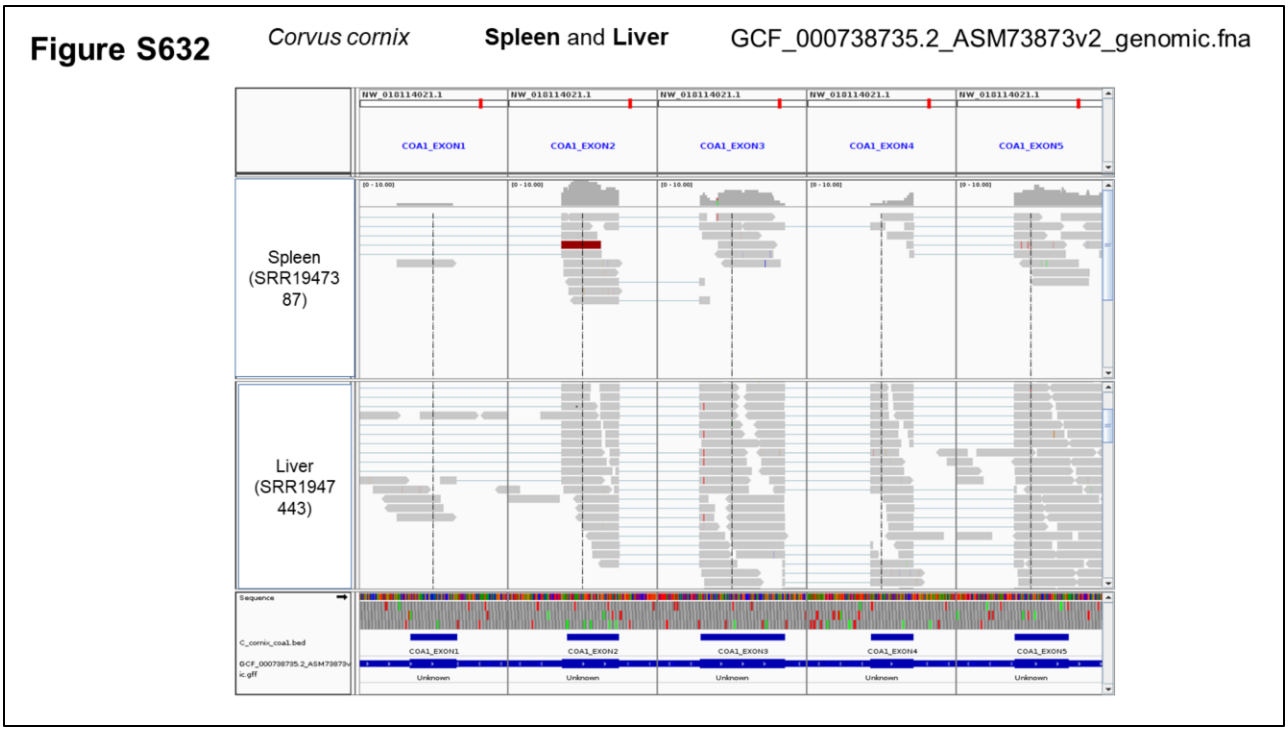

Figure S632: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S631**.

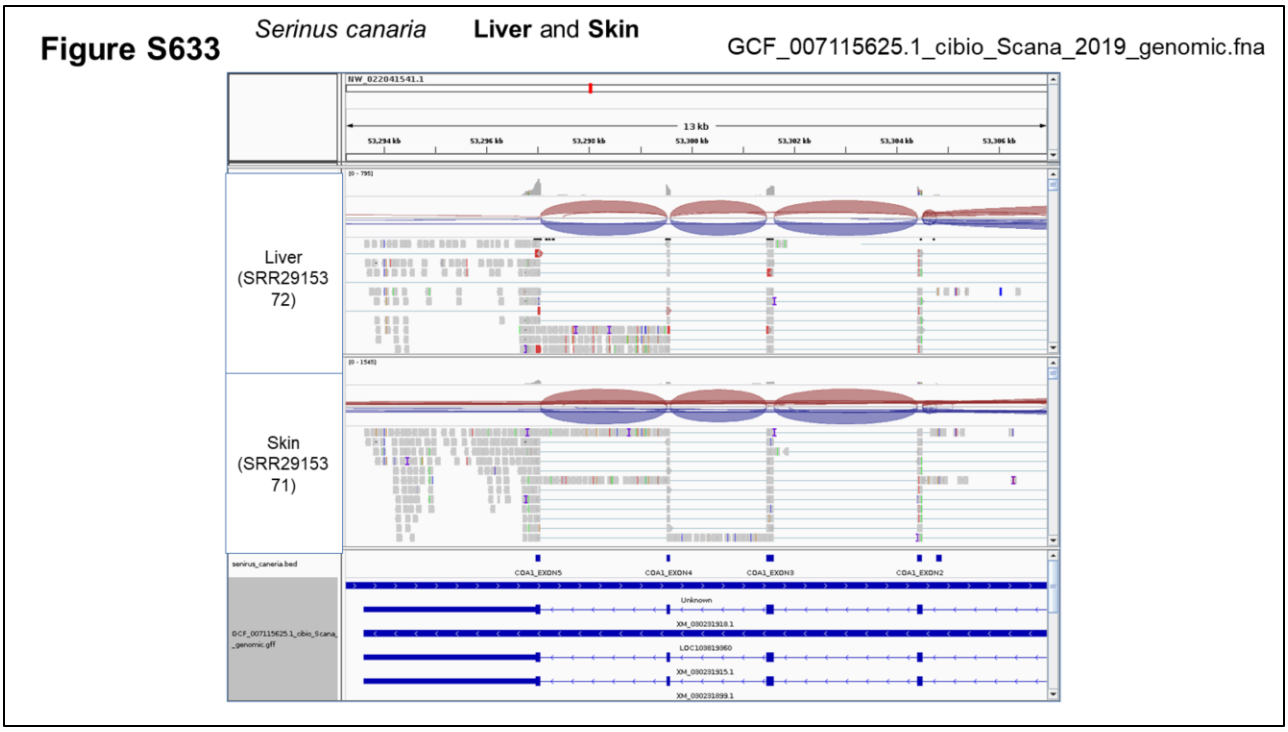

Figure S633: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in common canary (*Serinus canaria*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR152971) and skin (SRR152972) have been mapped to the GCF_007115625.1_cibio_Scana_2019_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

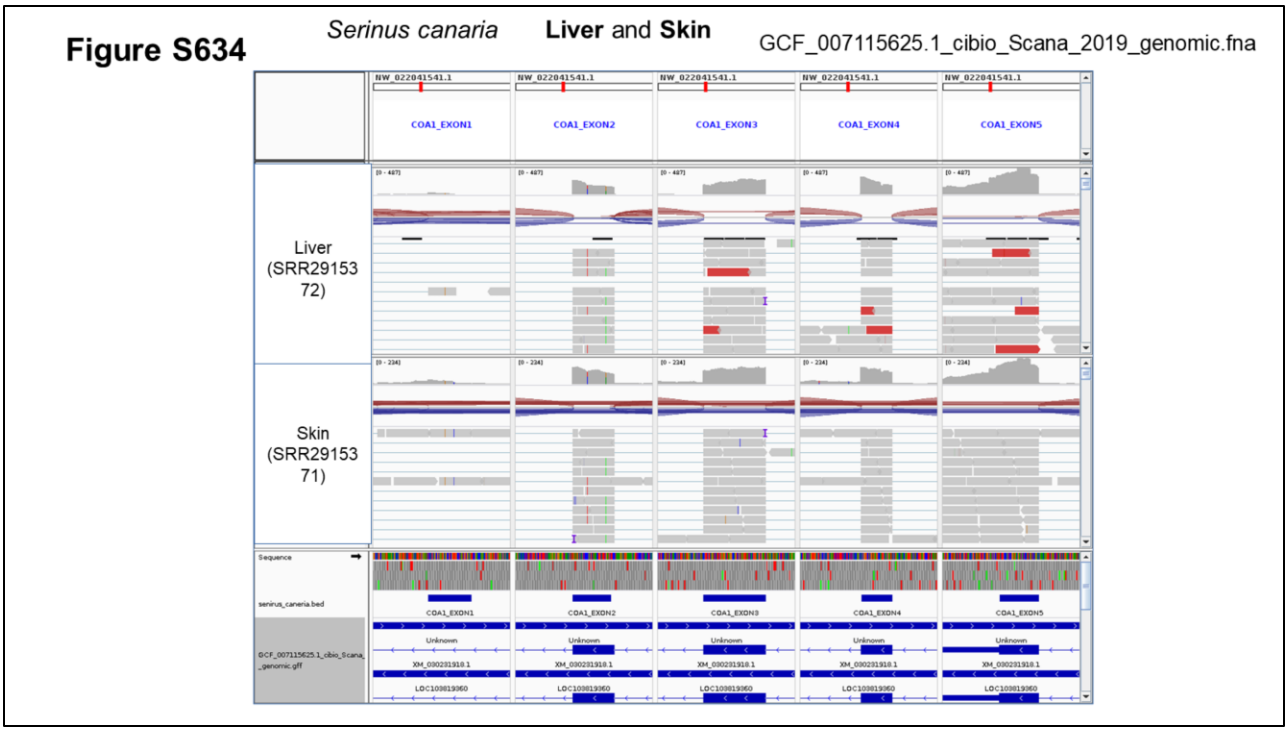

Figure S634: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S633**.

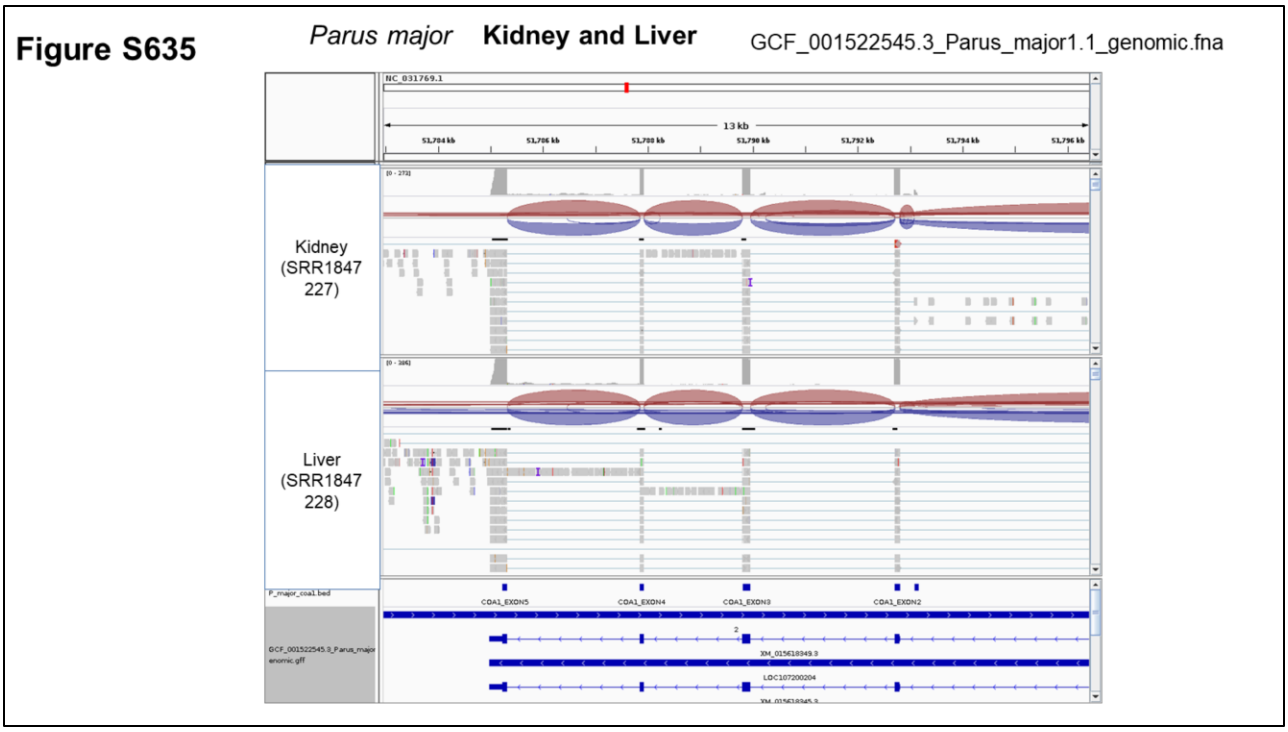

Figure S635: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in great tit (*Parus major*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from kidney (SRR1847227) and liver (SRR1847228) have been mapped to the GCF_001522545.3_Parus_major1.1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

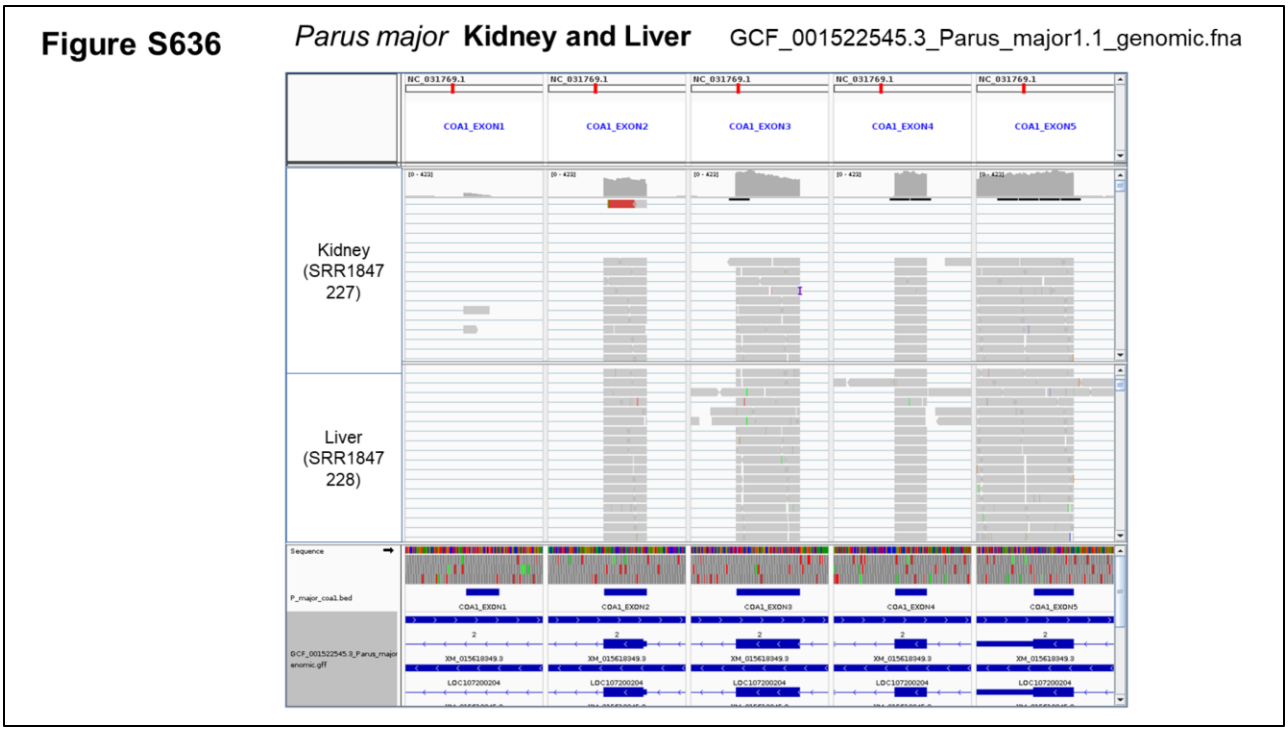

Figure S636: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S635**.

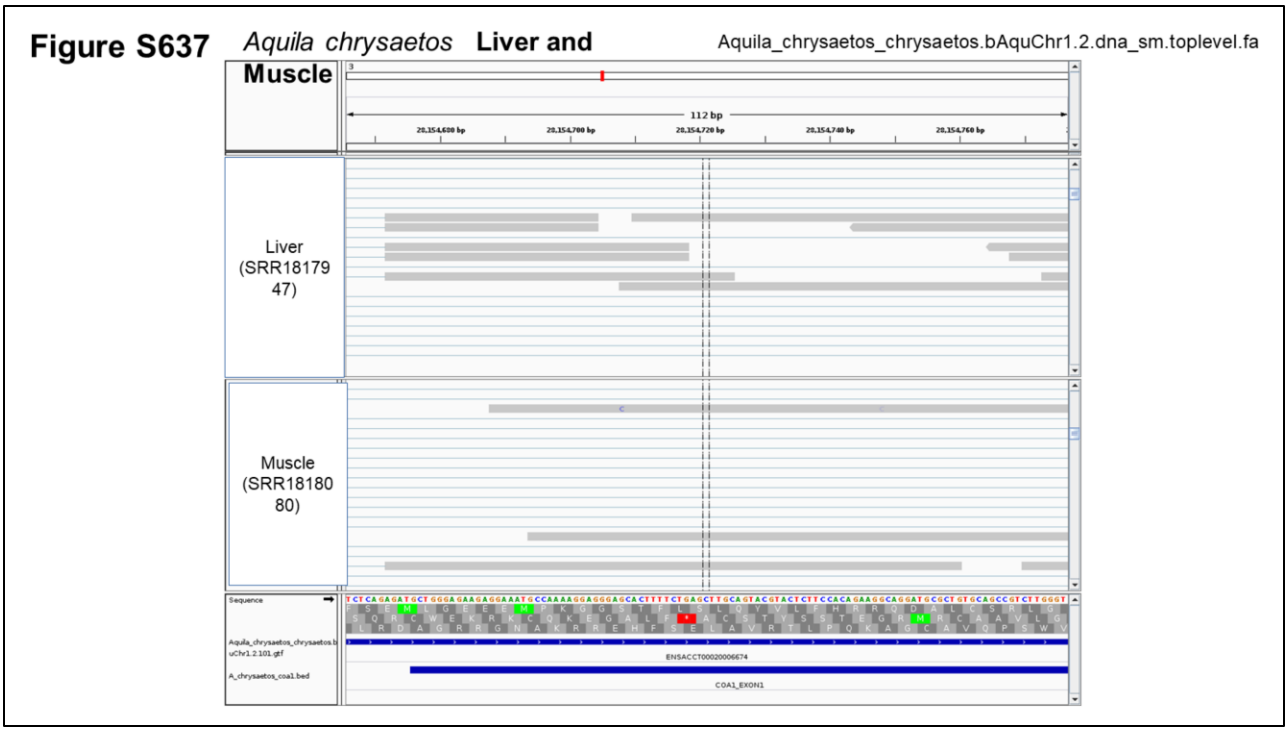

Figure S637: Less expression and in-frame stop codon in exon 1 of the six exon annotation of *COA1* of golden eagle (*Aquila chrysaetos*).

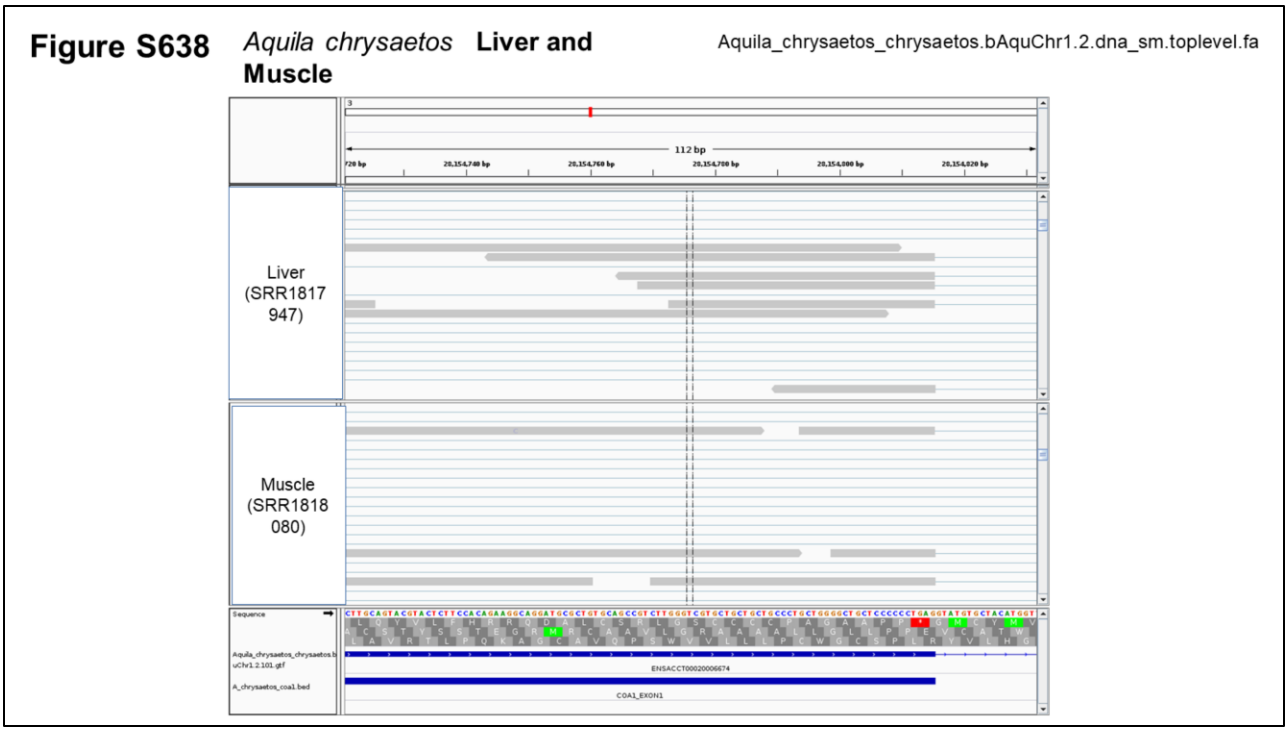

Figure S638: Continuation of **Supplementary Fig. S637** showing low expression in exon 1 of the six exon annotation of *COA1* of golden eagle (*Aquila chrysaetos*).

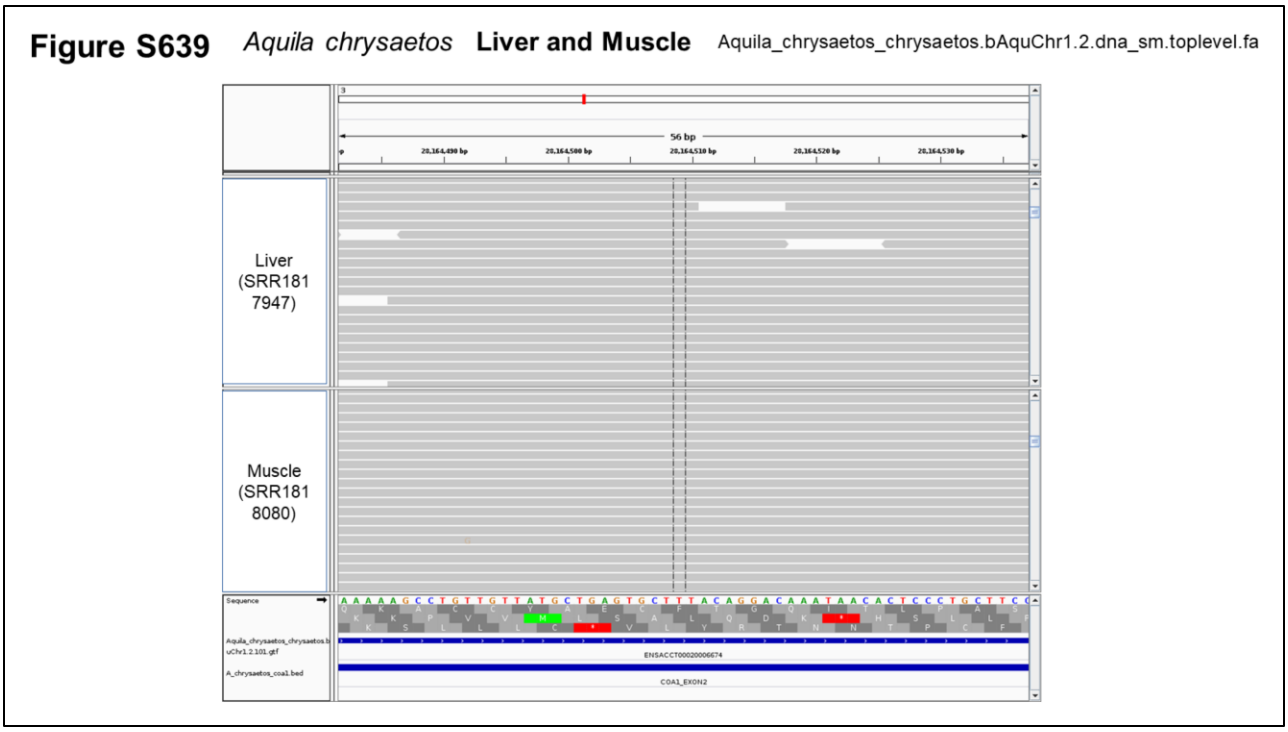

Figure S639: In-frame stop codon in exon 2 of the six exon annotation of *COA1* of golden eagle (*Aquila chrysaetos*).

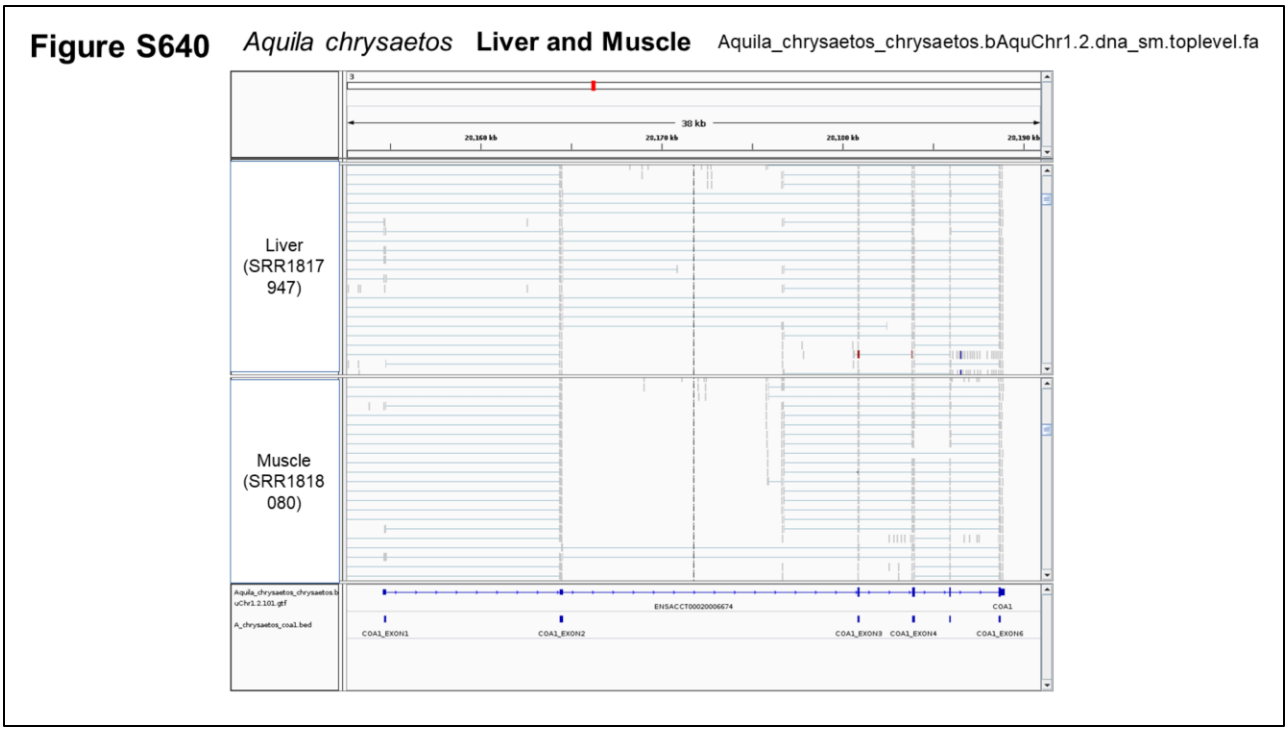

Figure S640: Screenshot of RNA-seq reads aligned to each of the putative locations of the six *COA1* exons in golden eagle (*Aquila chrysaetos*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR1817947) and muscle (SRR1818080) have been mapped to the Aquila_chrysaetos_chrysaetos.bAquChr1.2.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

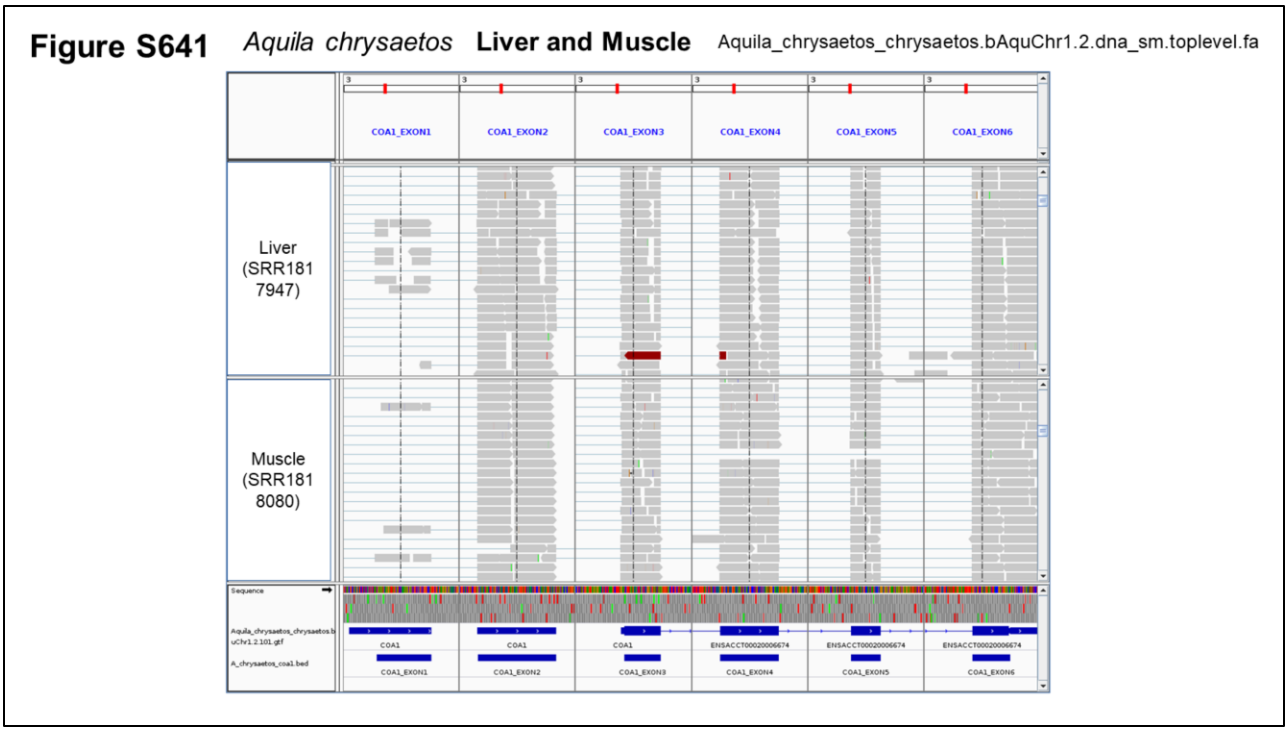

Figure S641: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S640**.

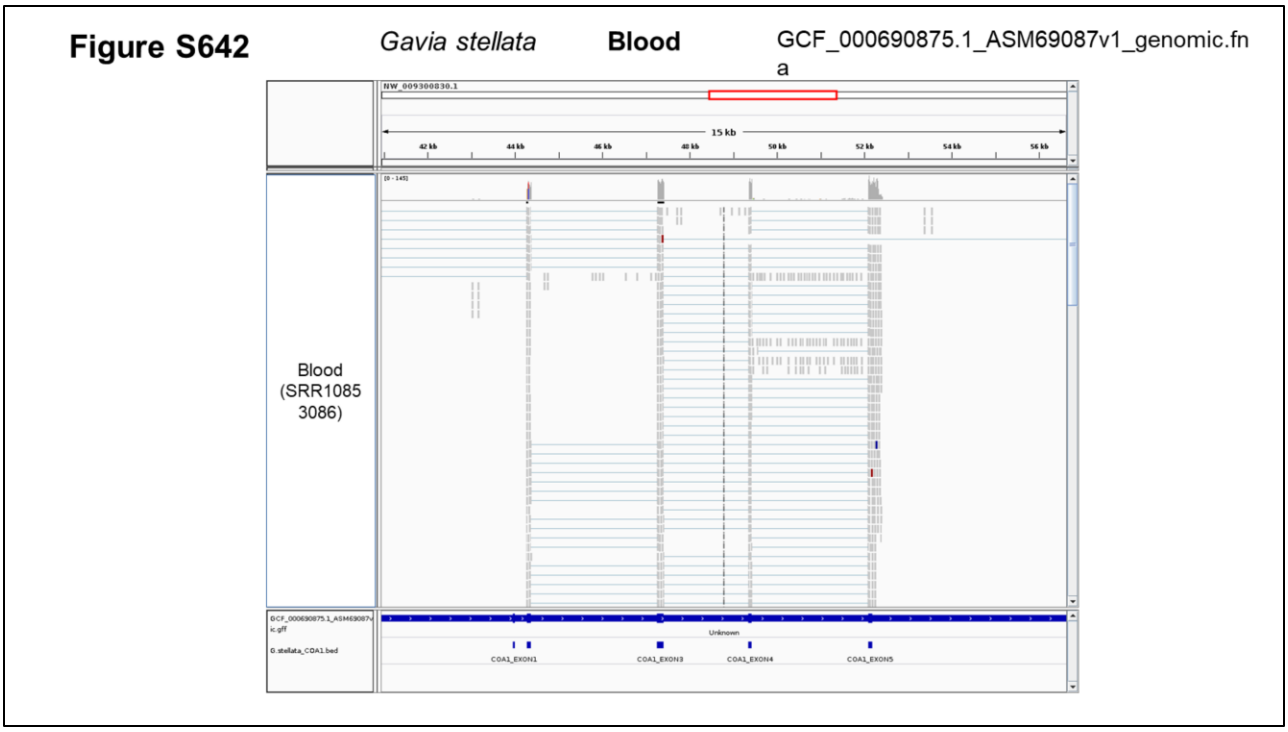

Figure S642: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in red-throated loon (*Gavia stellata*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood tissue (SRR10853086) have been mapped to the GCF_000690875.1_ASM69087v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

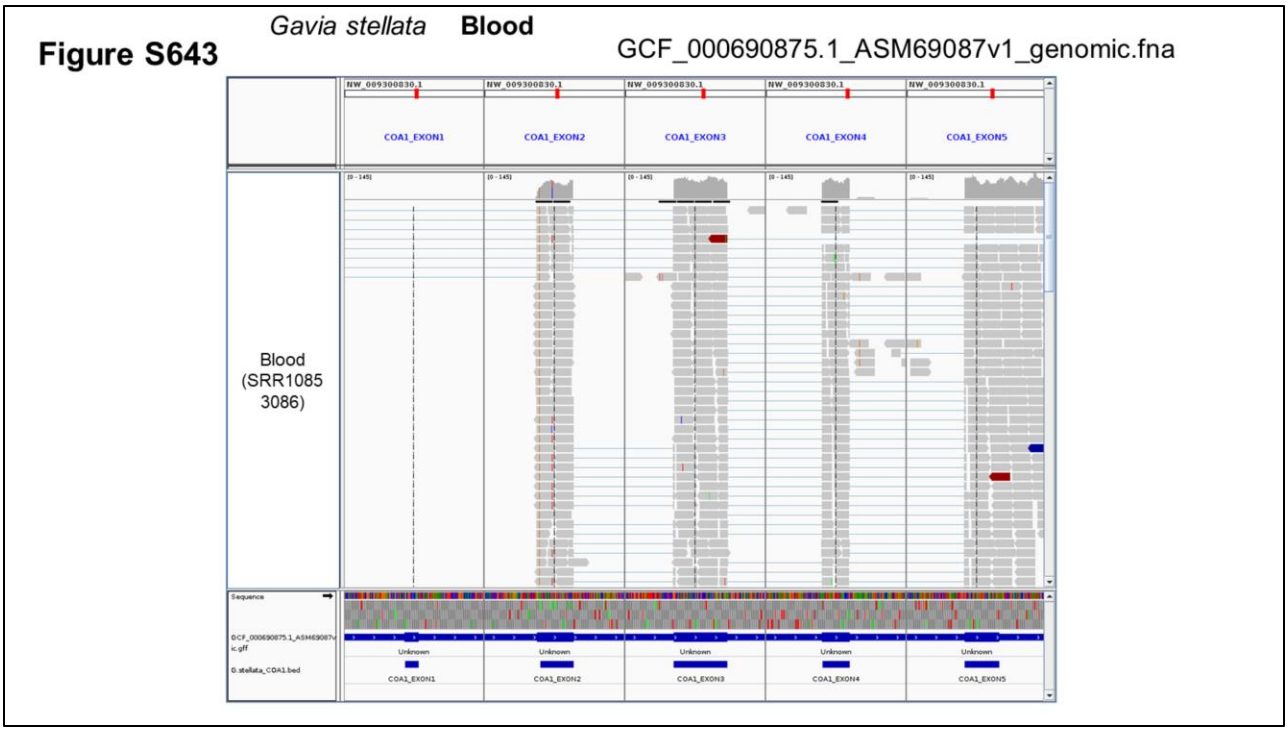

Figure S643: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S642**.

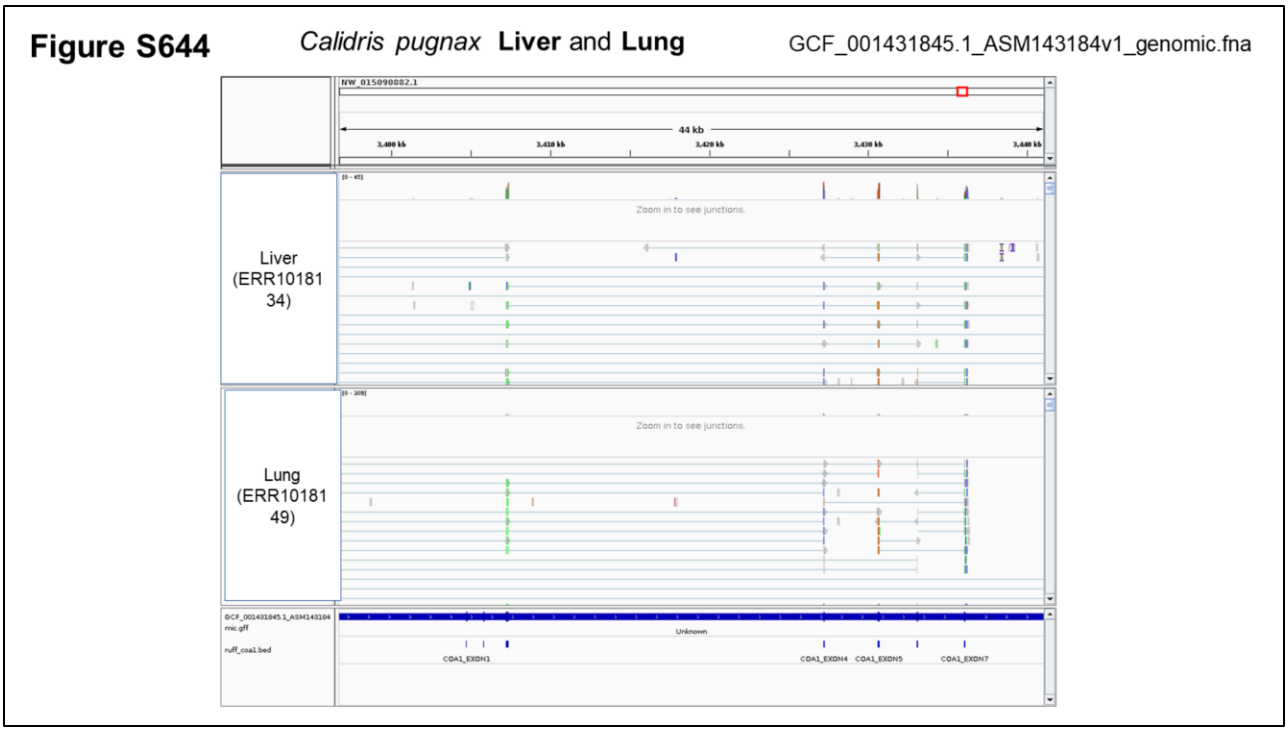

Figure S644: Screenshot of RNA-seq reads aligned to each of the putative locations of the seven annotated *COA1* exons in ruff (*Calidris pugnax*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (ERR1018134) and lung (ERR1018149) have been mapped to the GCF_001431845.1_ASM143184v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

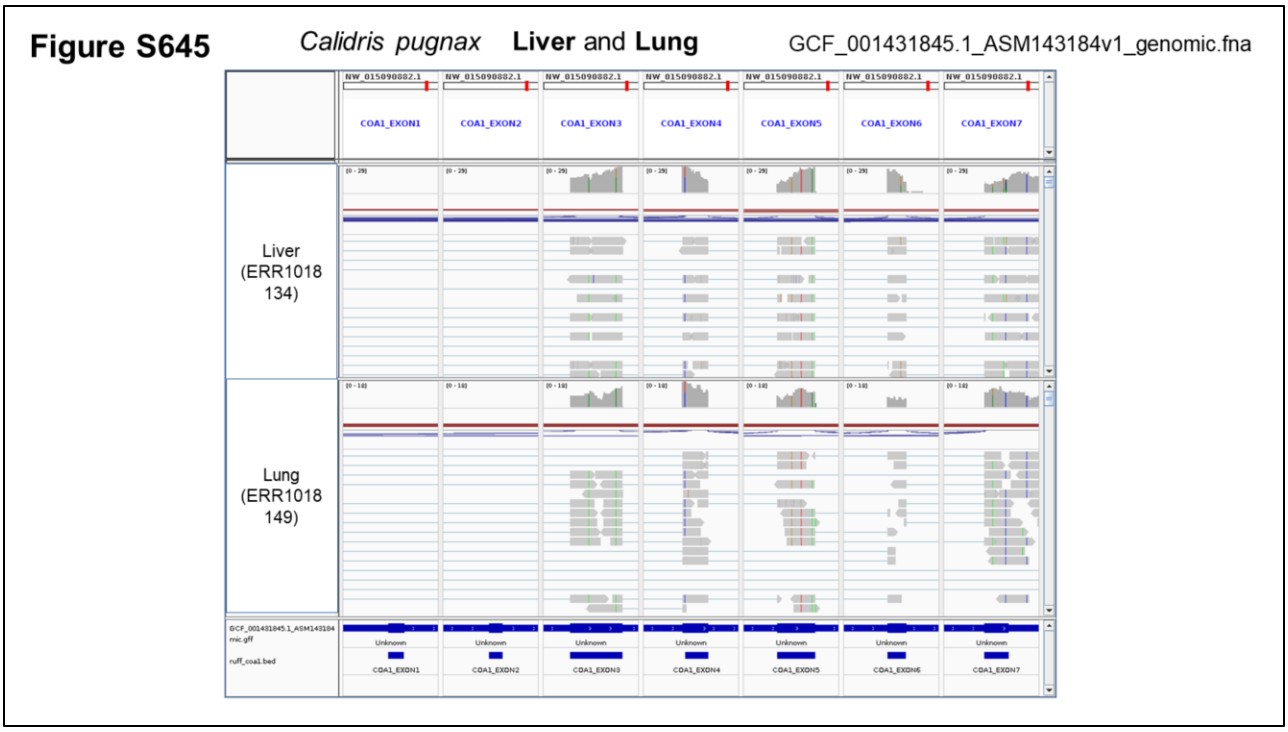

Figure S645: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S644**.

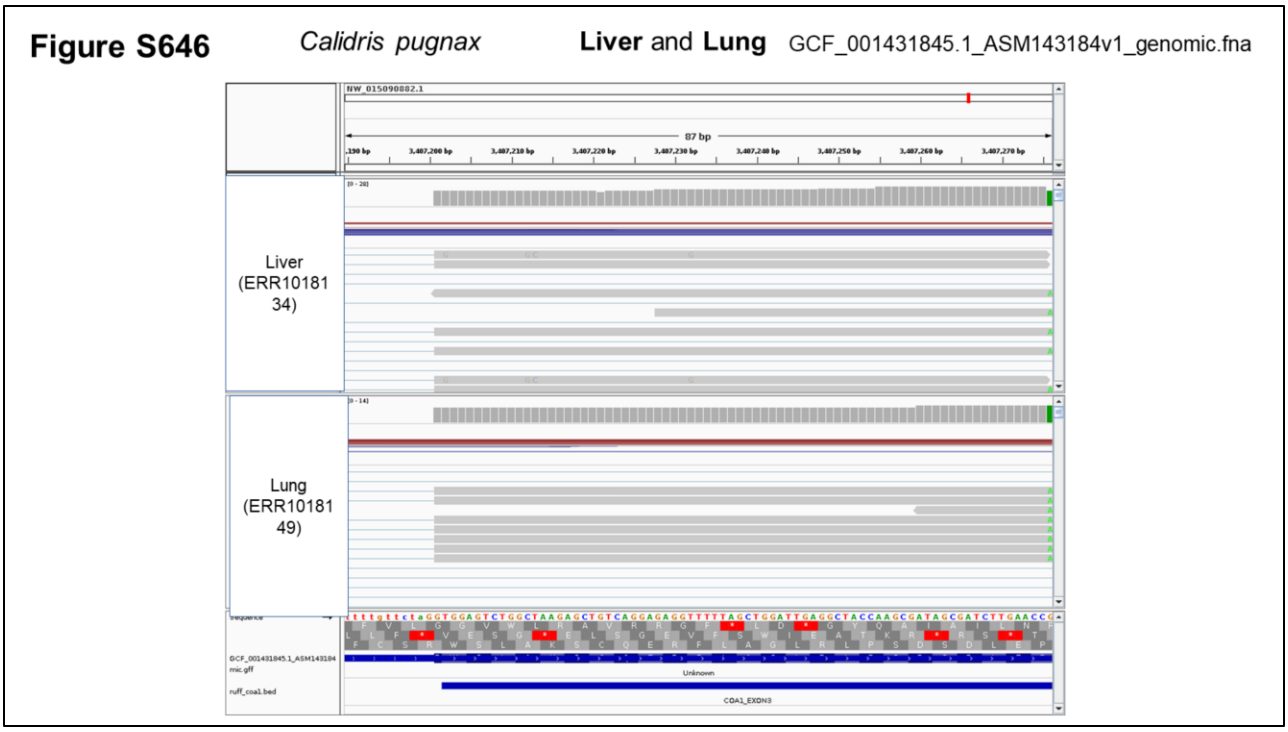

Figure S646: Exon-3 of the seven exon annotation of *COA1* in ruff (*Calidris pugnax*) did not have any start codon.

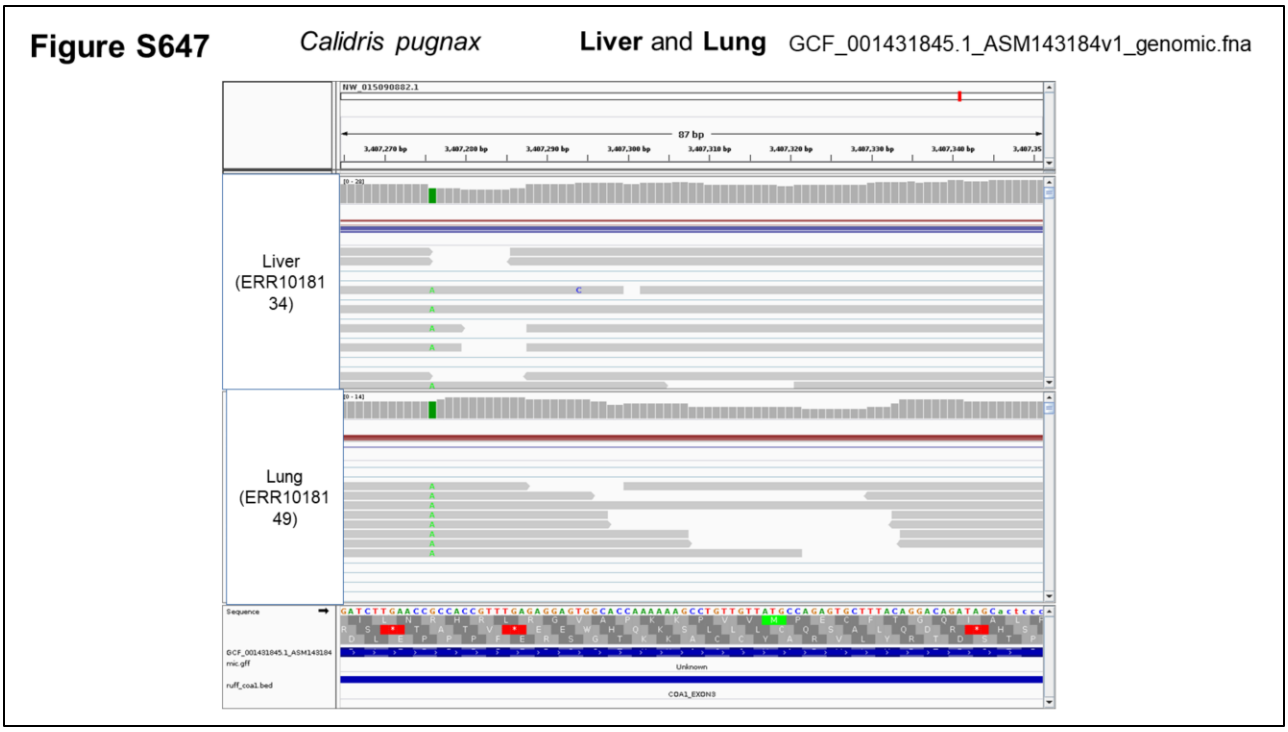

Figure S647: Continuation of **Supplementary Fig. S646**.

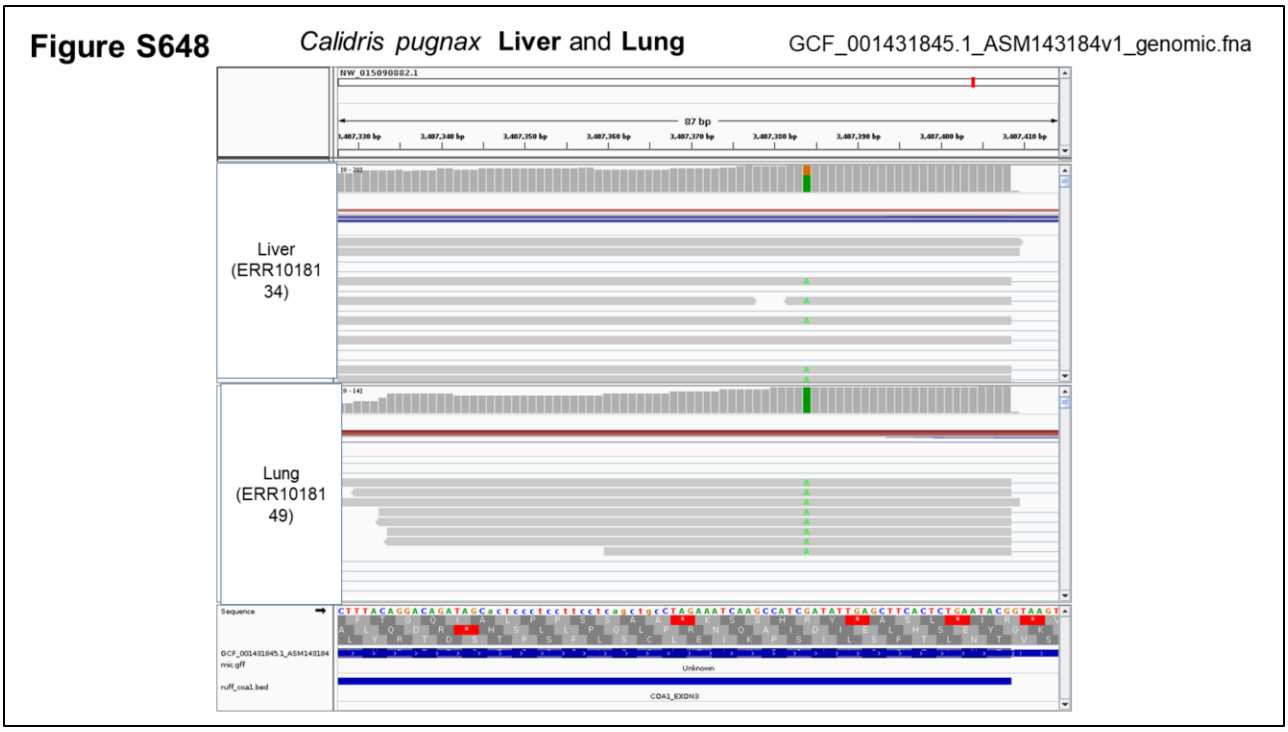

Figure S648: Continuation of **Supplementary Fig. S647**.

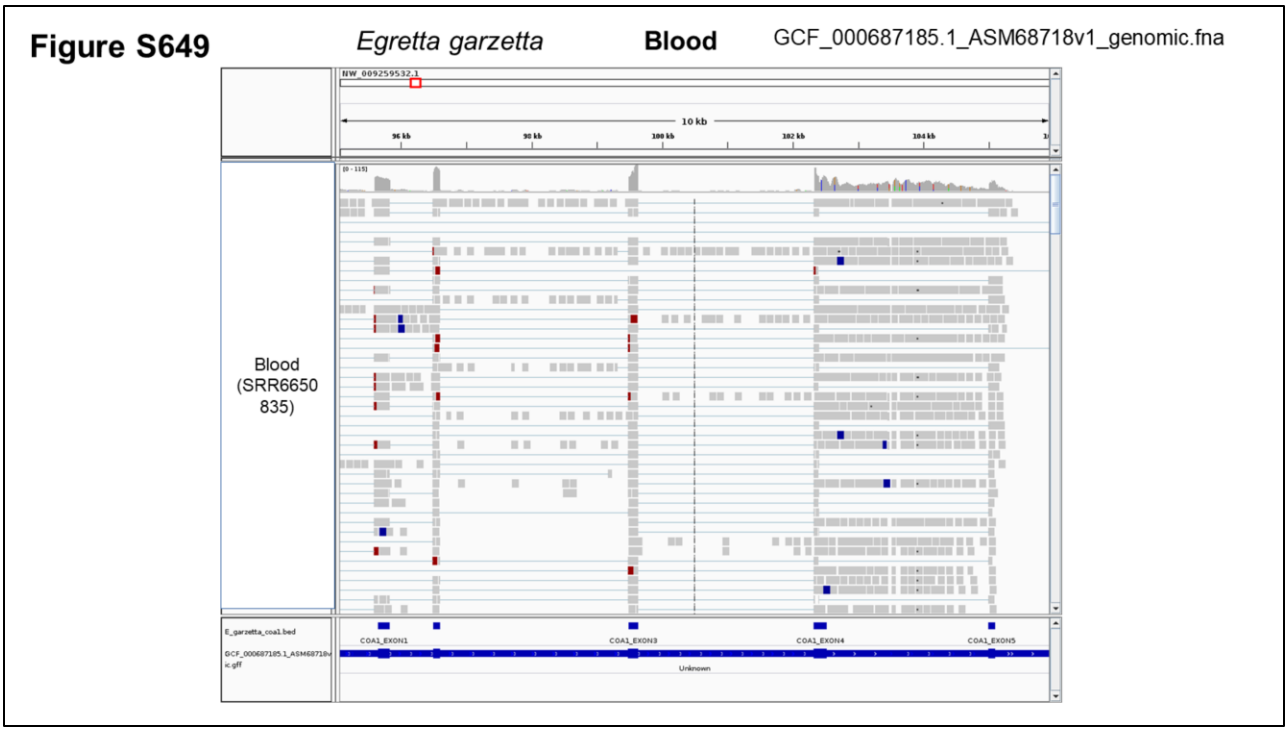

Figure S649: Screenshot of RNA-seq reads aligned to each of the putative locations of the five *COA1* exons in little egret (*Egretta garzetta*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR6650835) have been mapped to the GCF_000687185.1_ASM68718v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

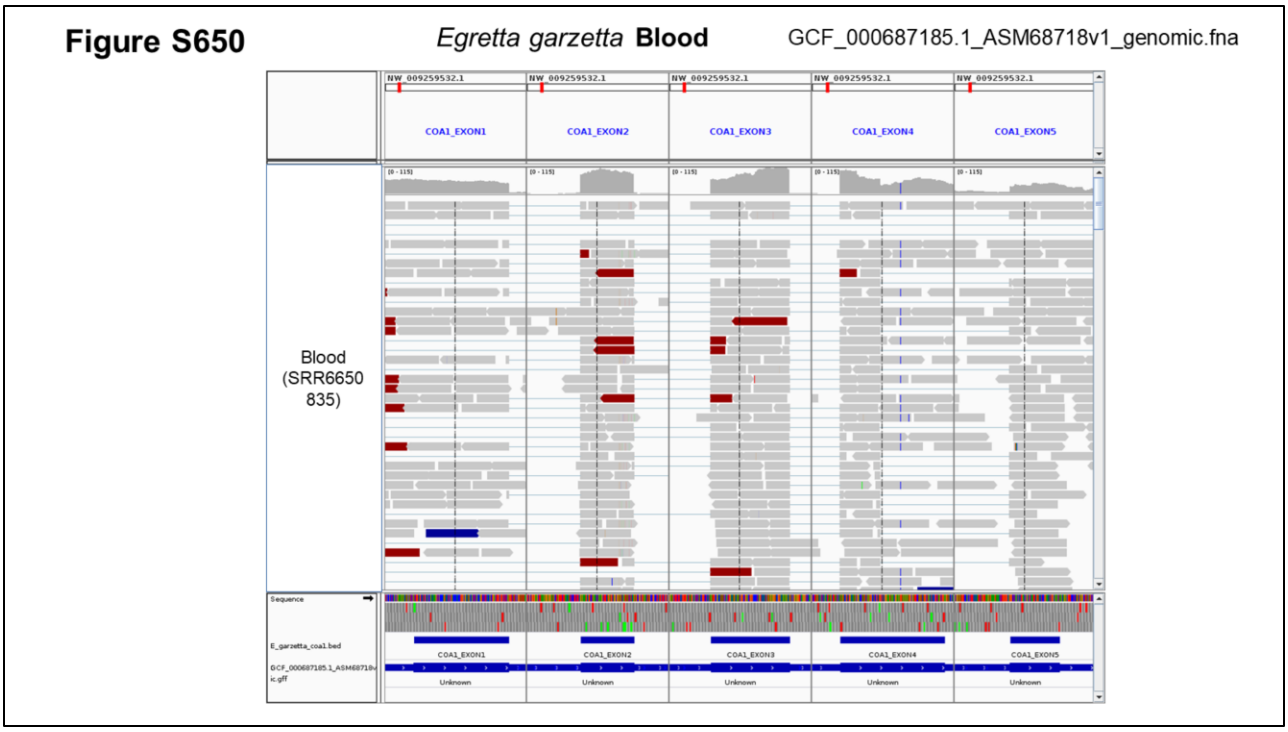

Figure S650: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S649**.

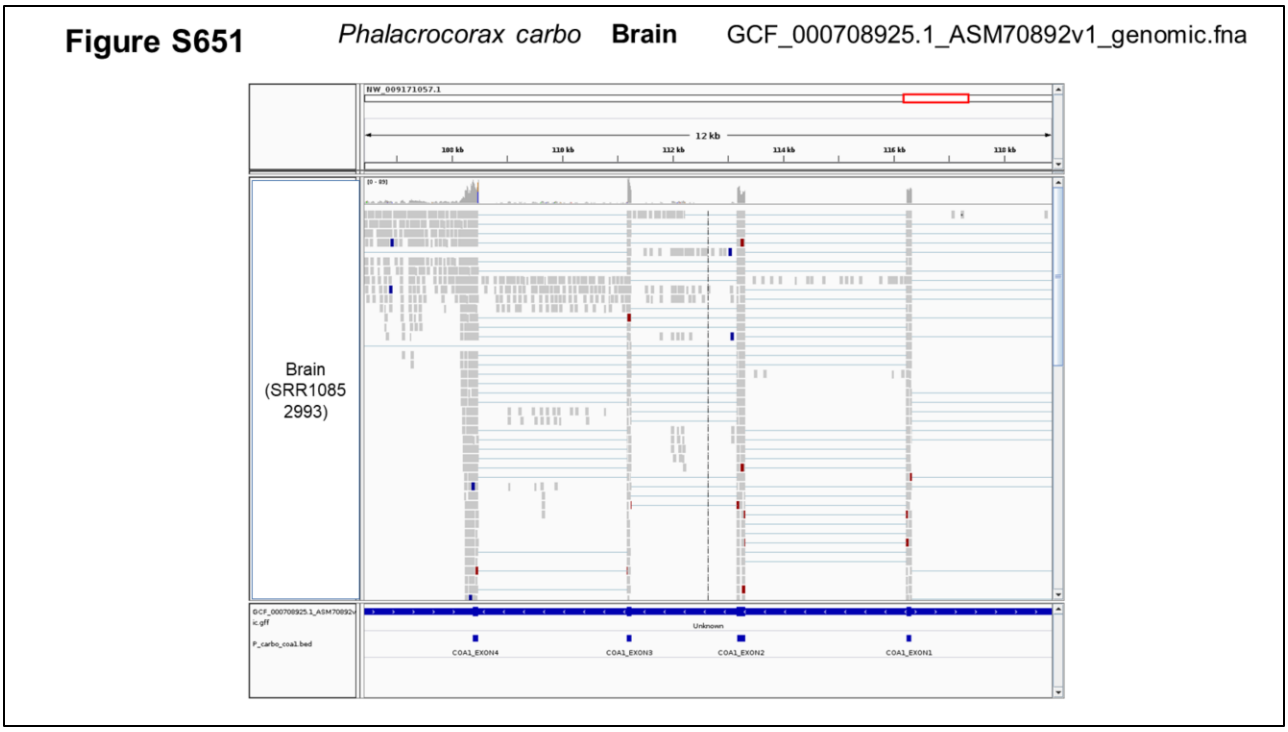

Figure S651: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in great cormorant (*Phalacrocorax carbo*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (SRR10852993) have been mapped to the GCF_000708925.1_ASM70892v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

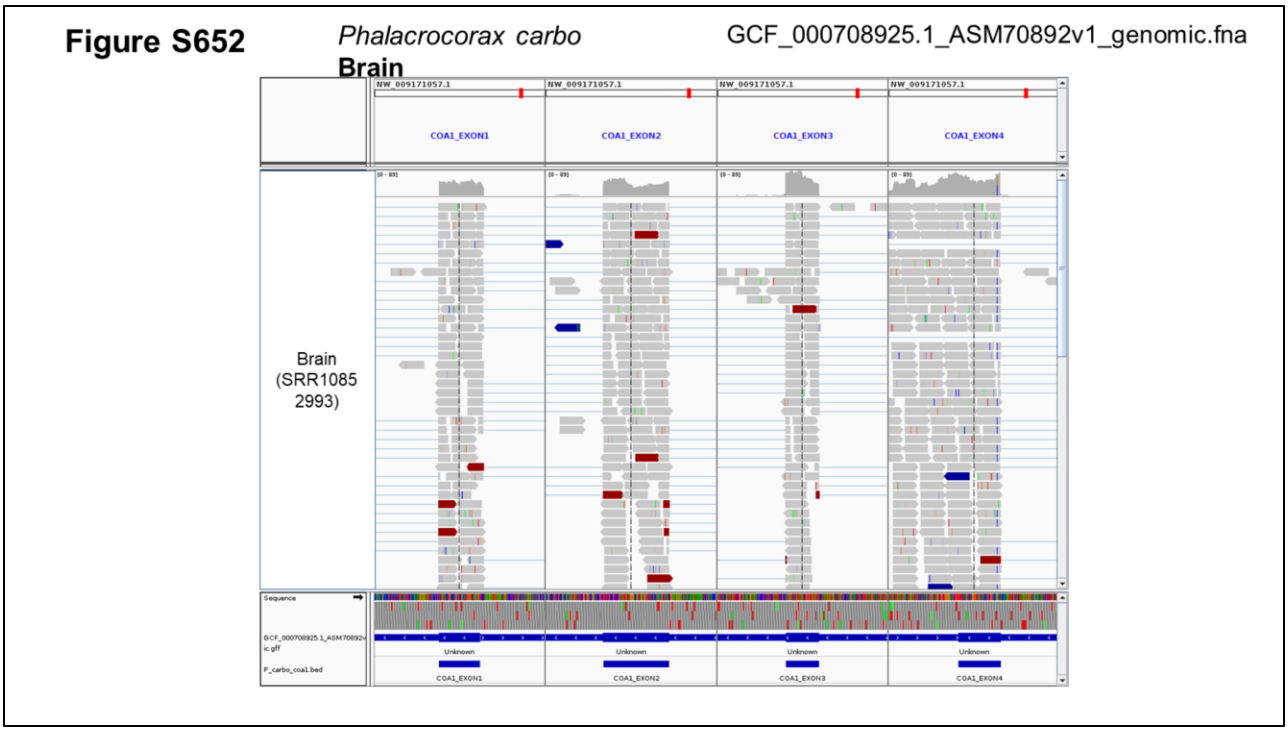

Figure S652: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S651**.

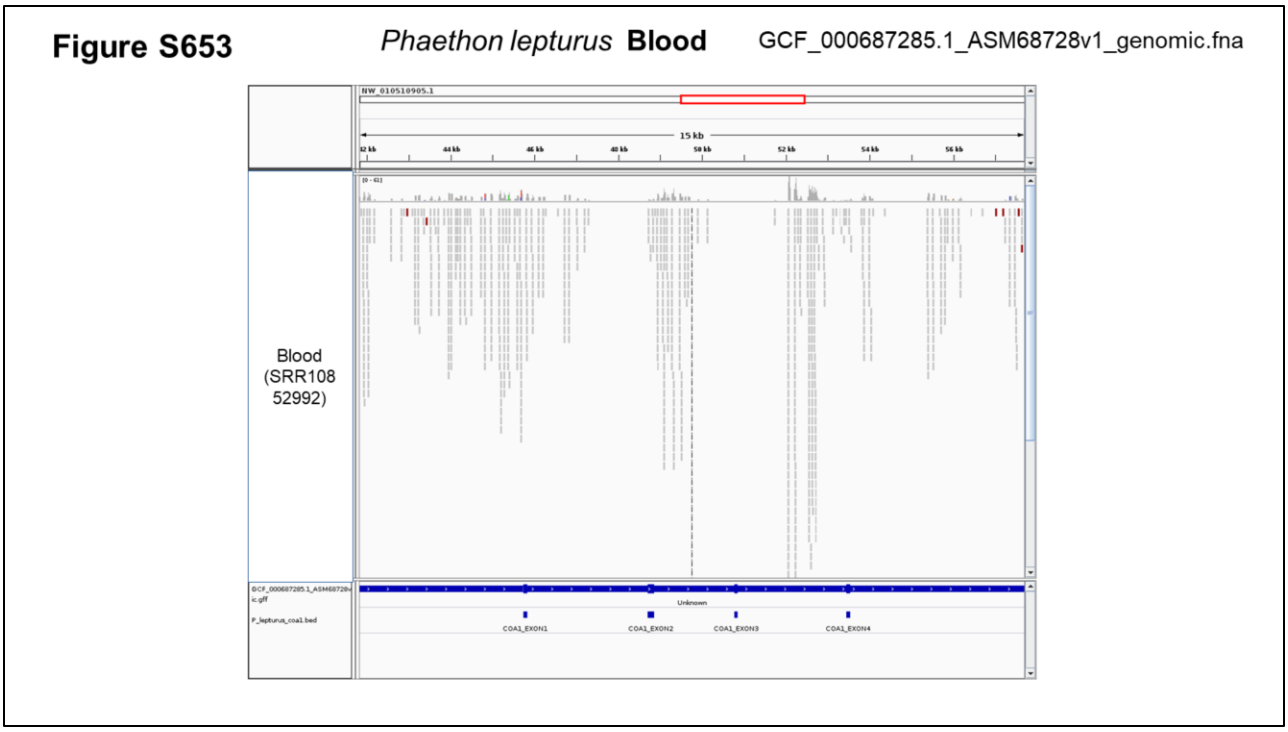

Figure S653: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in white-tailed tropicbird (*Phaethon lepturus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR10852992) have been mapped to the GCF_000687285.1_ASM68728v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

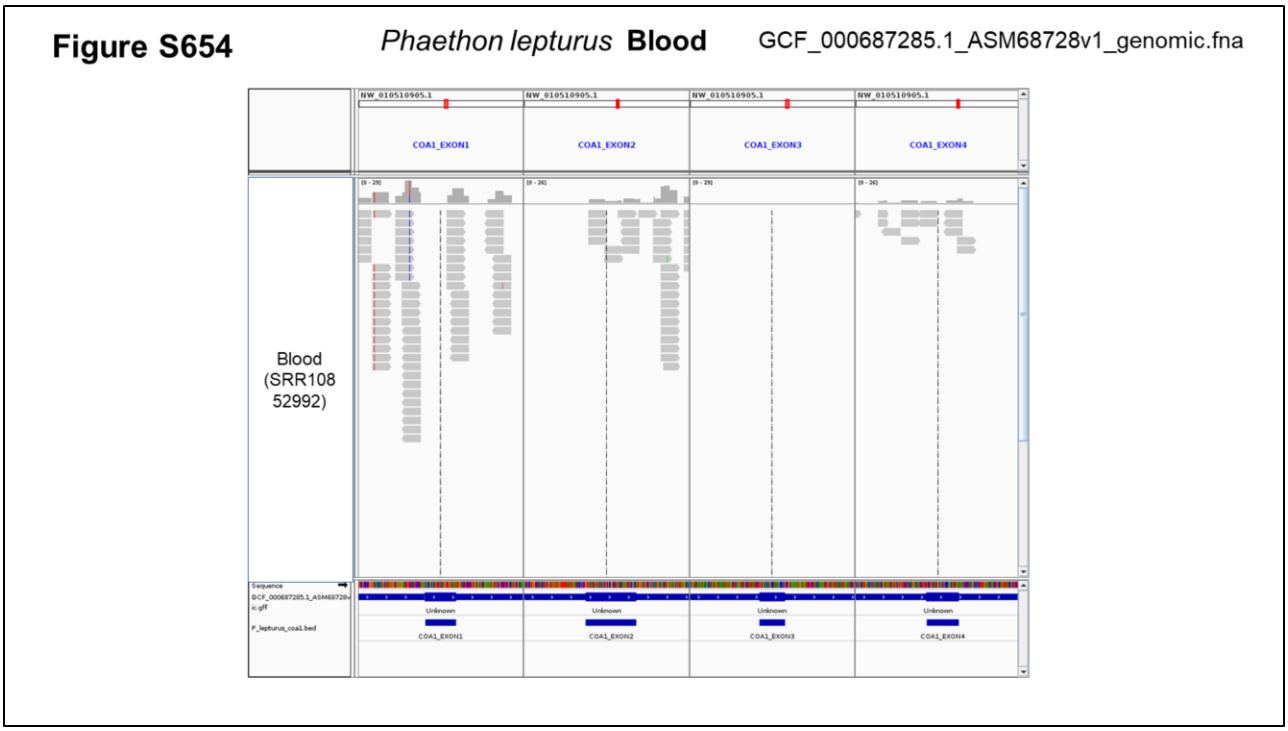

Figure S654: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S653**.

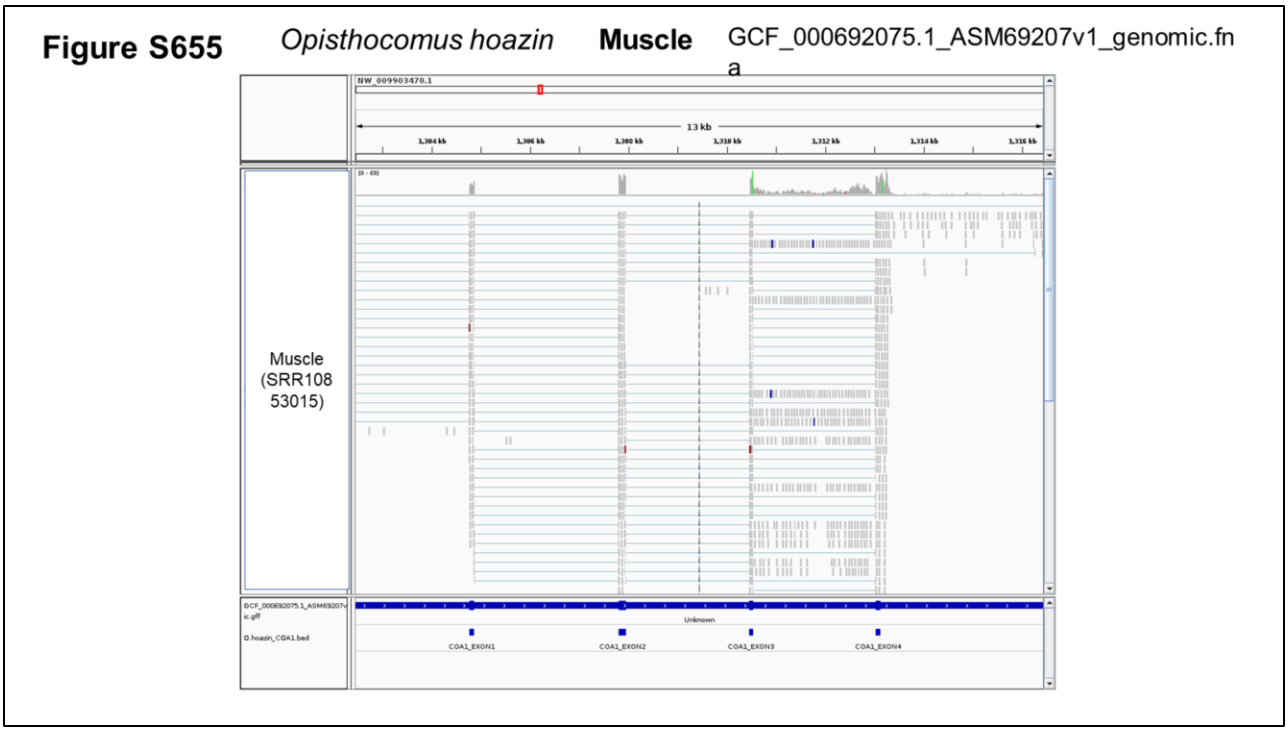

Figure S655: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in hoatzin (*Opisthocomus hoazin*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from muscle (SRR10853015) have been mapped to the GCF_000692075.1_ASM69207v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

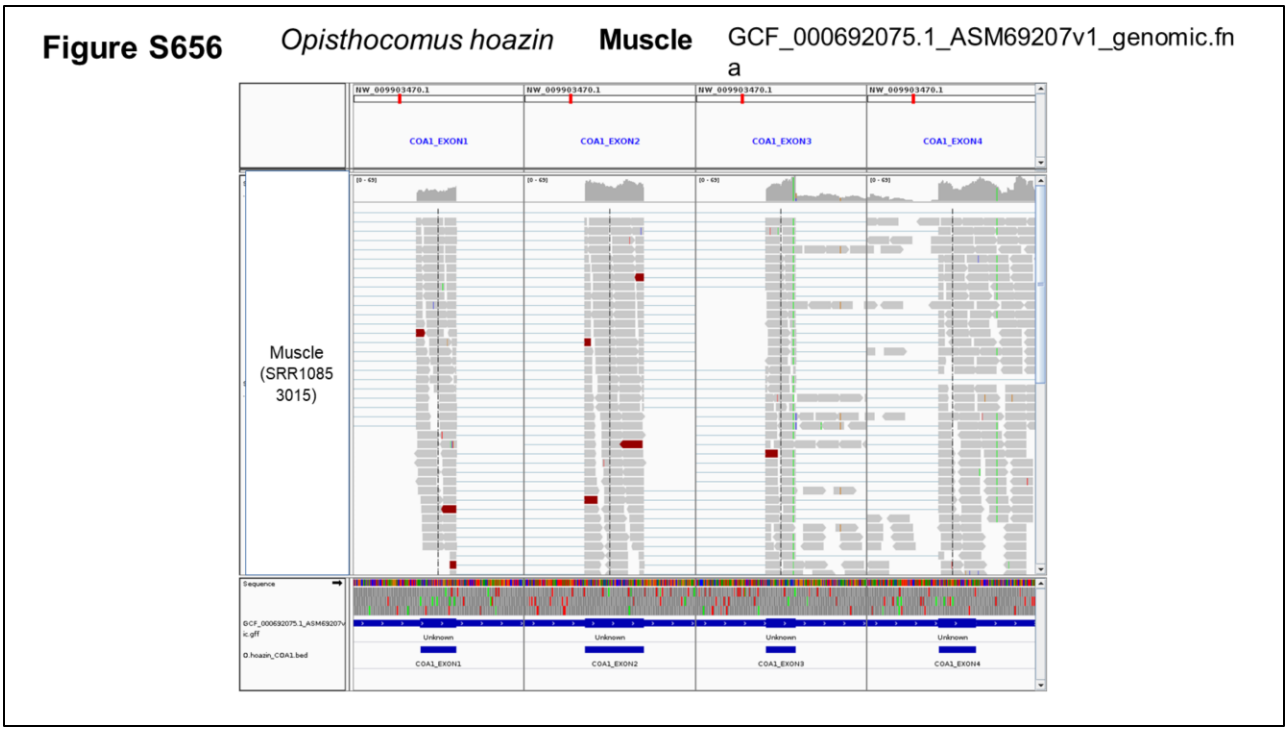

Figure S656: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S655**.

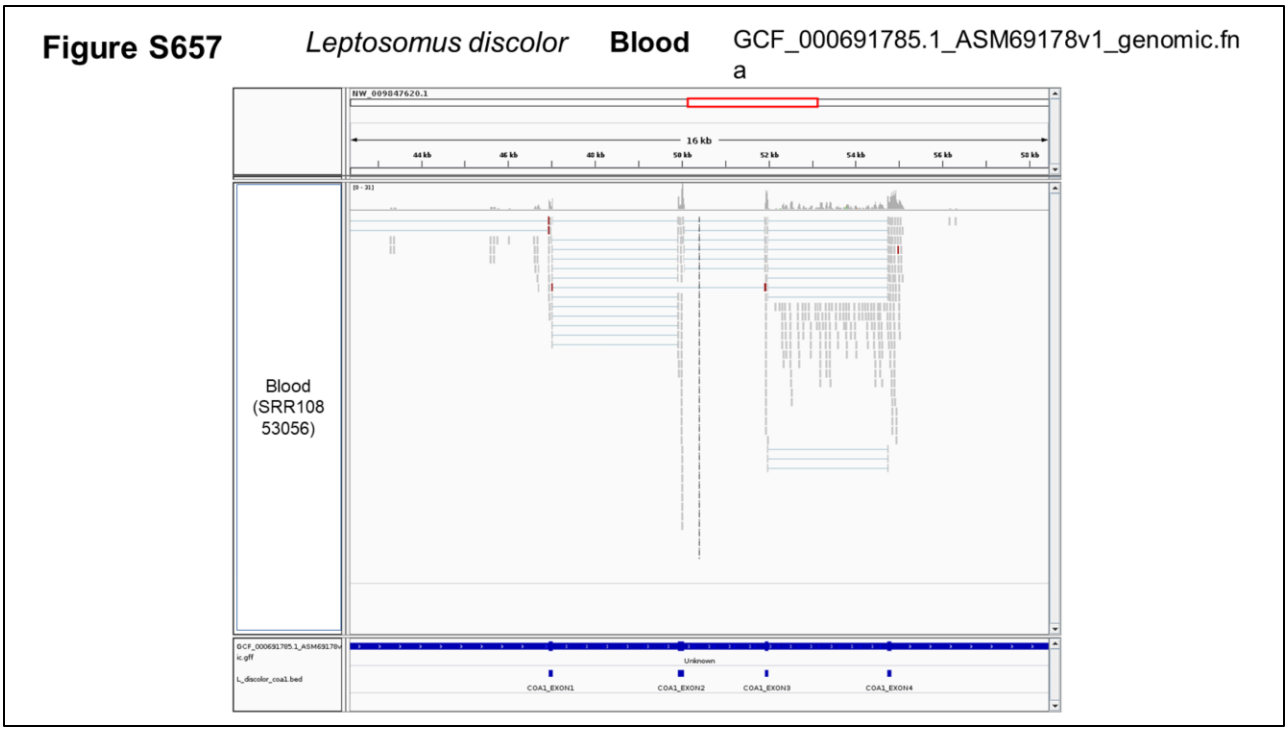

Figure S657: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in cuckoo roller (*Leptosomus discolor*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR10853056) have been mapped to the GCF_000691785.1_ASM69178v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

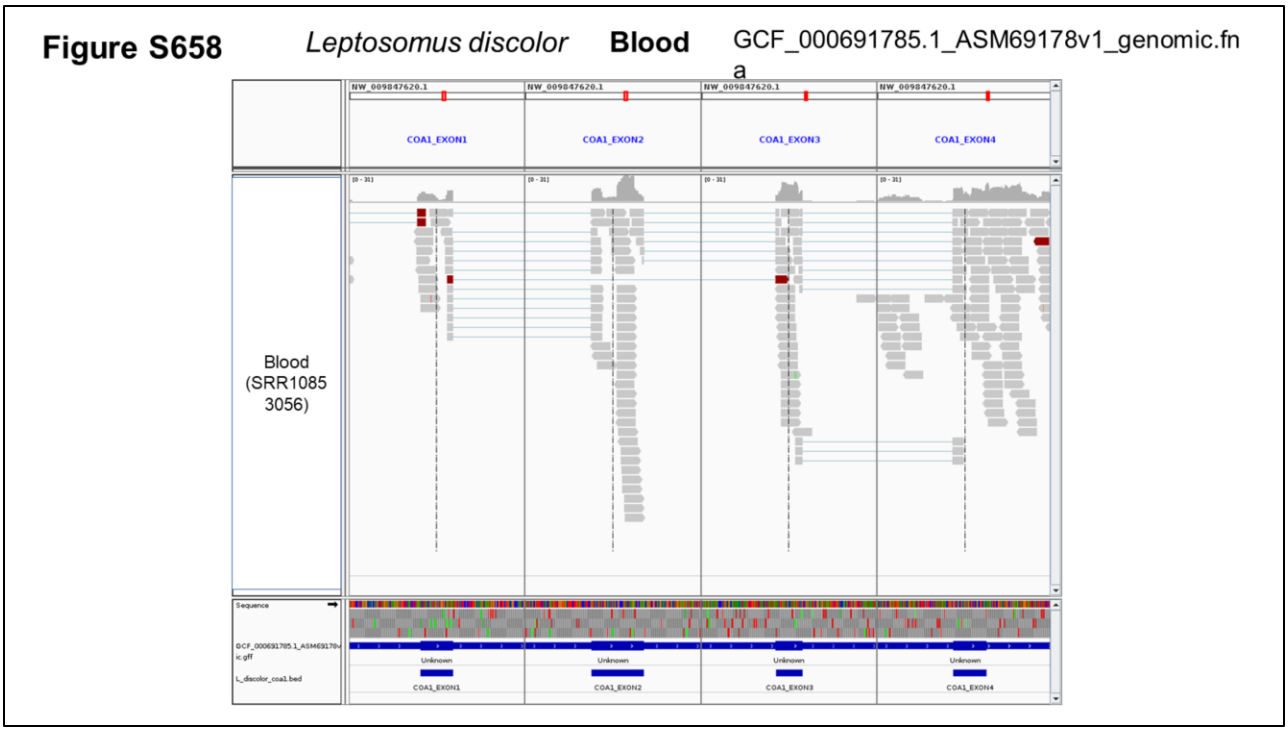

Figure S658: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S657**.

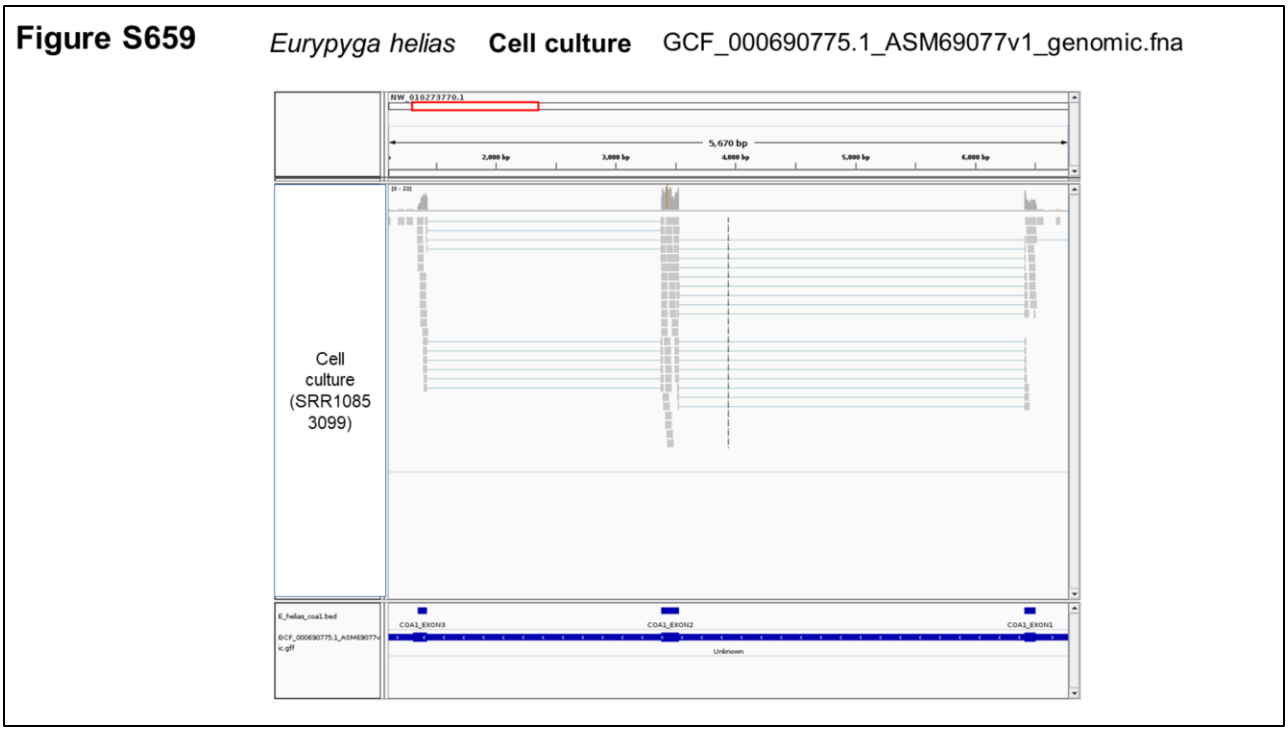

Figure S659: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* exon 1-3 in sunbittern (*Eurypyga helias*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from cell culture (SRR10853099) have been mapped to the GCF_000690775.1_ASM69077v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

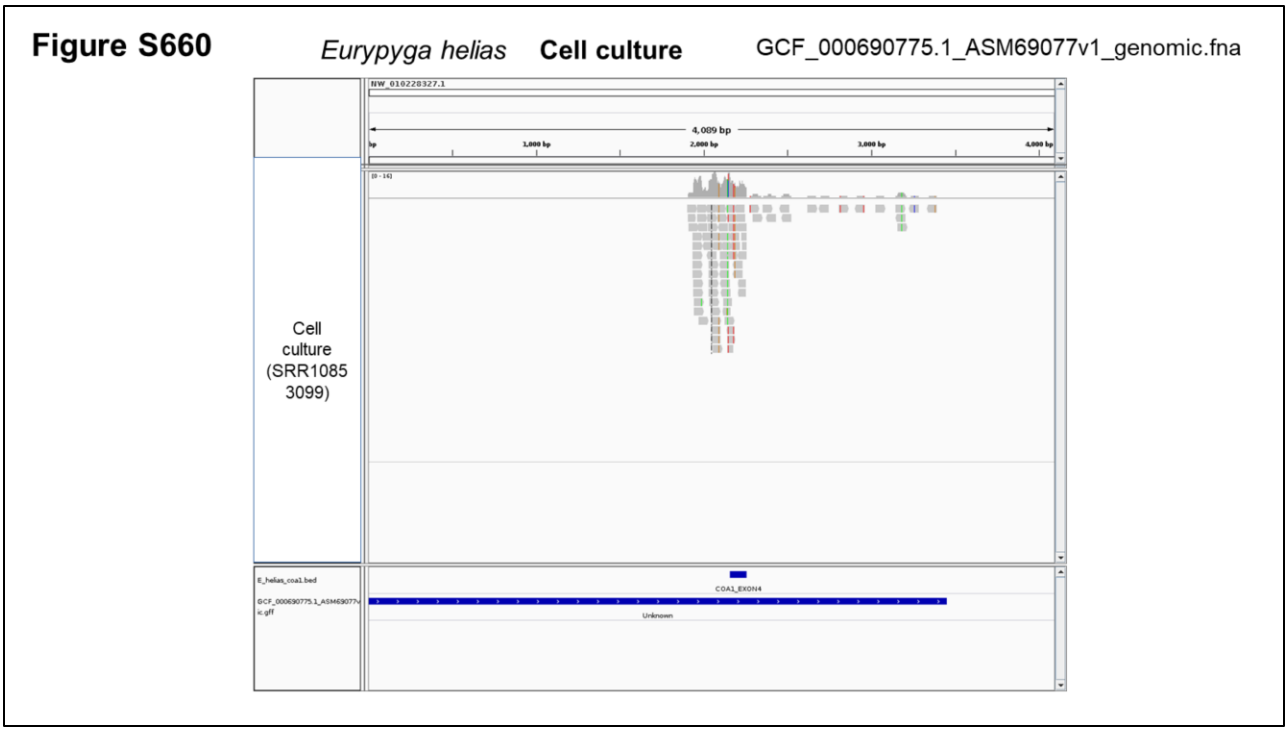

Figure S660: Screenshot of RNA-seq reads aligned to the putative locations of the *COA1* exon 4 in sunbittern (*Eurypyga helias*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from cell culture (SRR10853099) have been mapped to the GCF_000690775.1_ASM69077v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

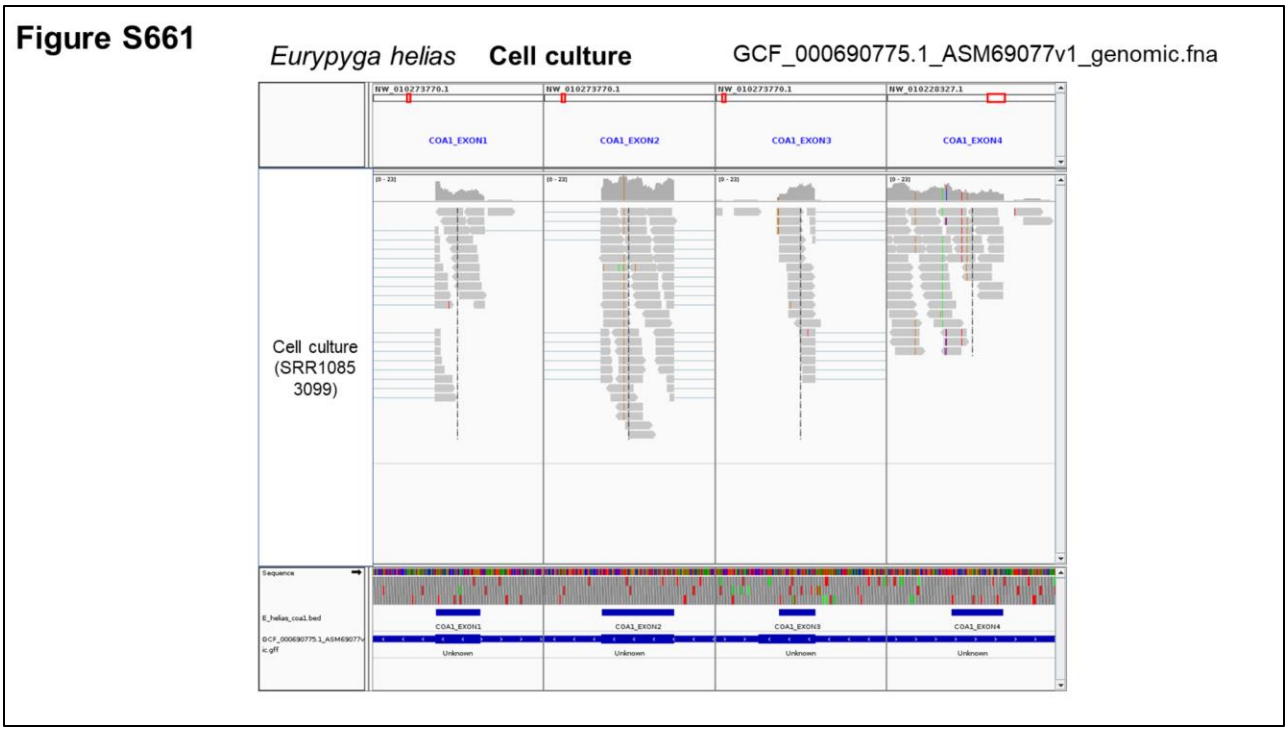

Figure S661: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S660**.

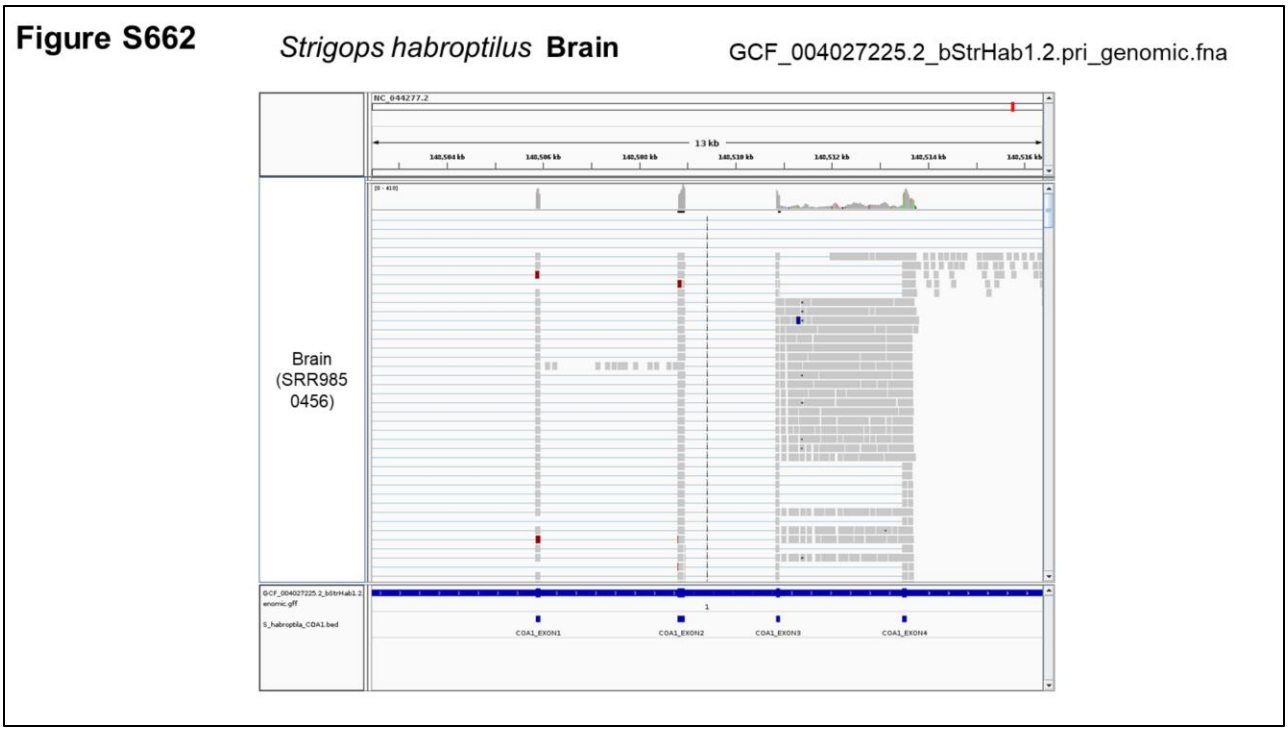

Figure S662: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in kakapo (*Strigops habroptilus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (SRR9850456) have been mapped to the GCF_004027225.2_bStrHab1.2.pri_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

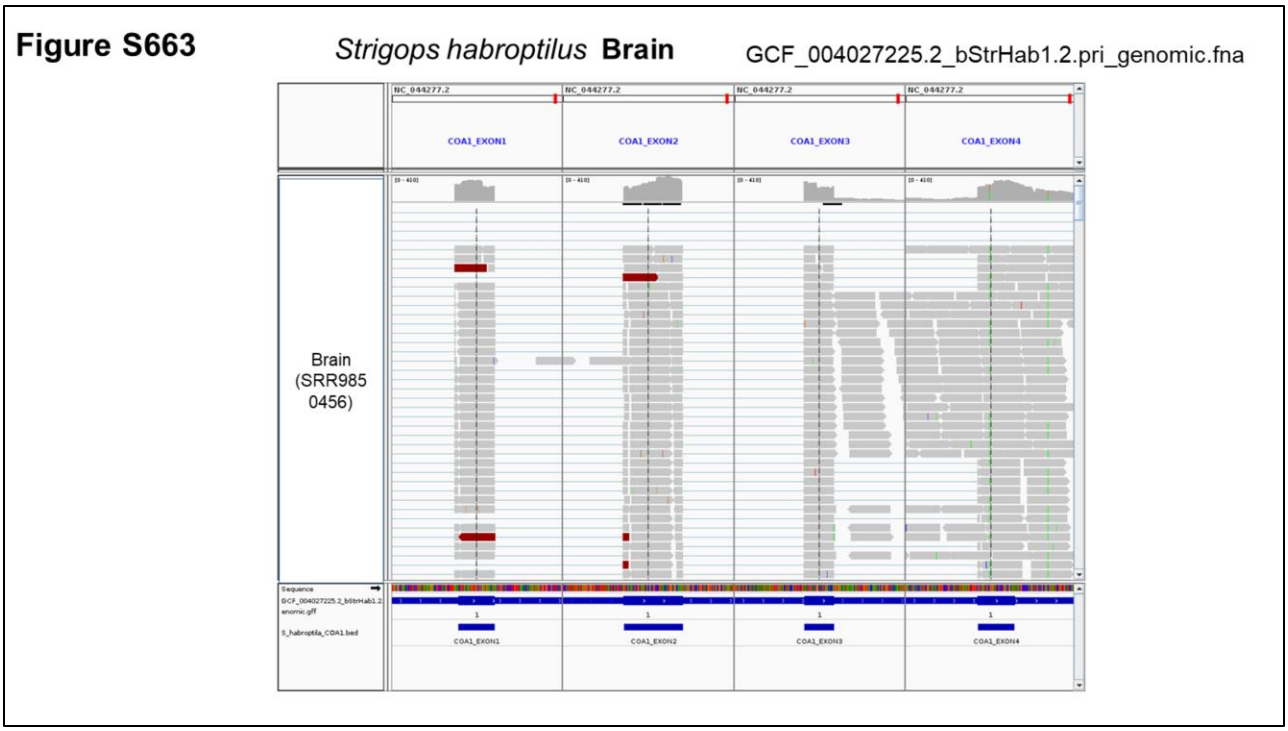

Figure S663: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S662**.

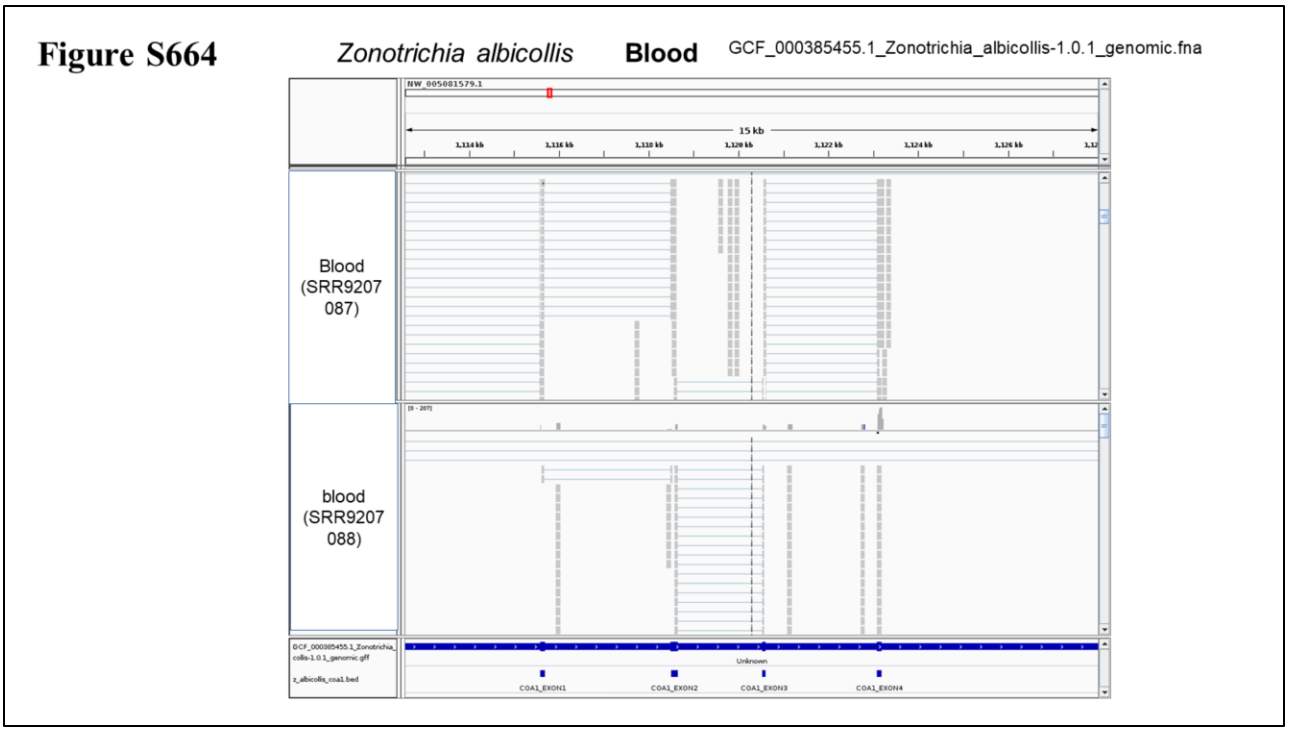

Figure S664: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in white-throated sparrow (*Zonotrichia albicollis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR9207087) and (SRR9207088) have been mapped to the GCF_000385455.1_Zonotrichia_albicollis-1.0.1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

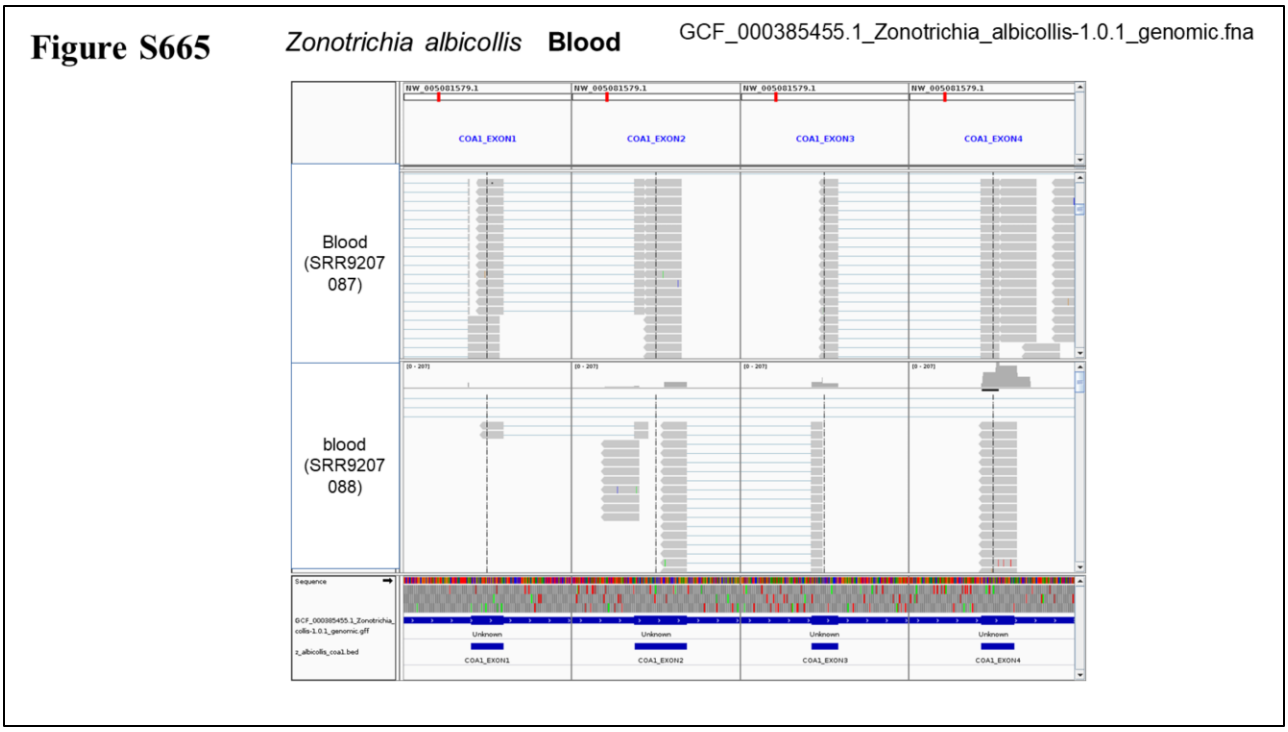

Figure S665: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S664**.

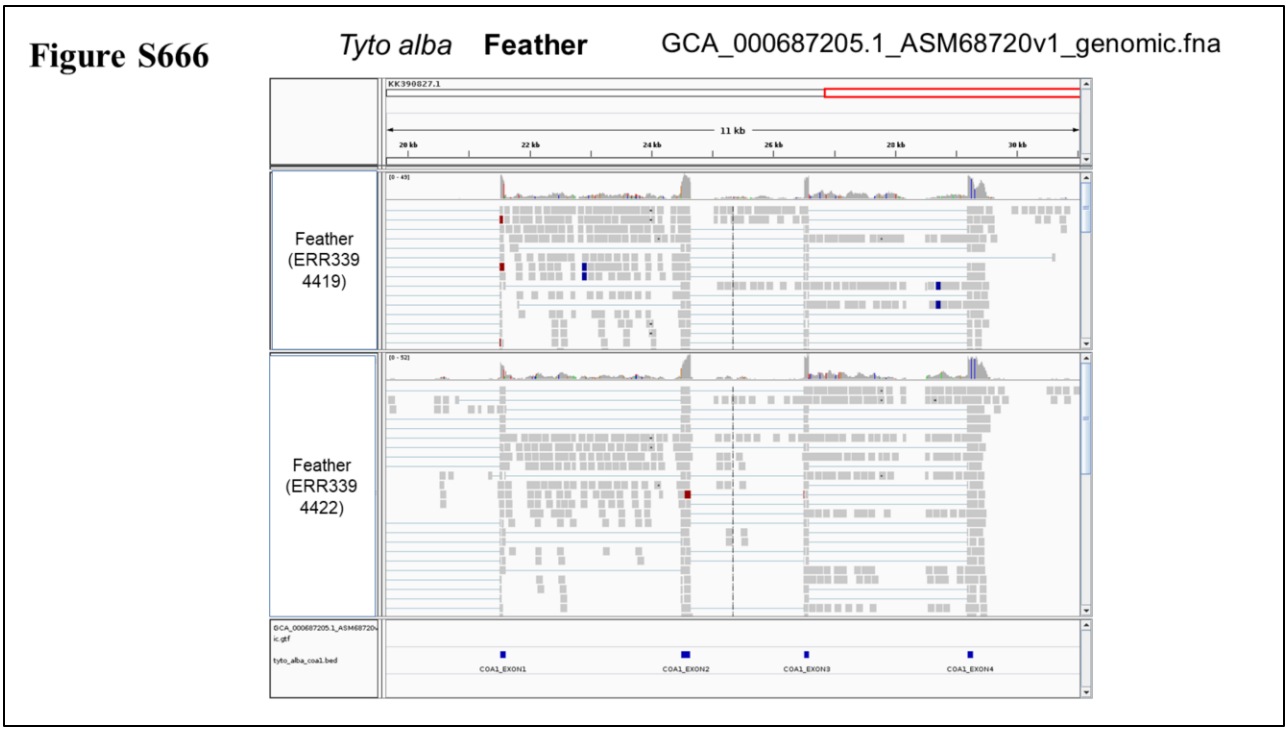

Figure S666: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in barn owl (*Tyto alba*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from feather (ERR3394419) and (ERR3394422) have been mapped to the GCA_000687205.1_ASM68720v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S667 *Tyto alba* **Feather** GCA_000687205.1_ASM68720v1_genomic.fna

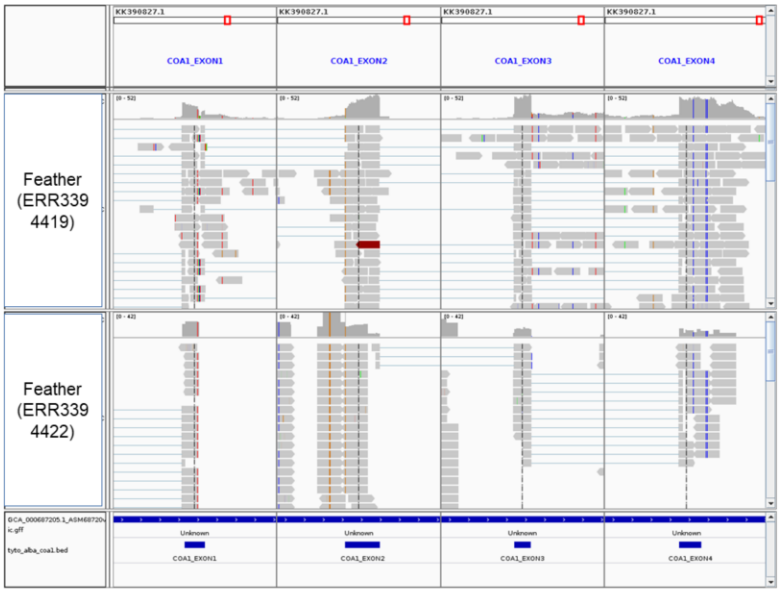

Figure S667: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S666**.

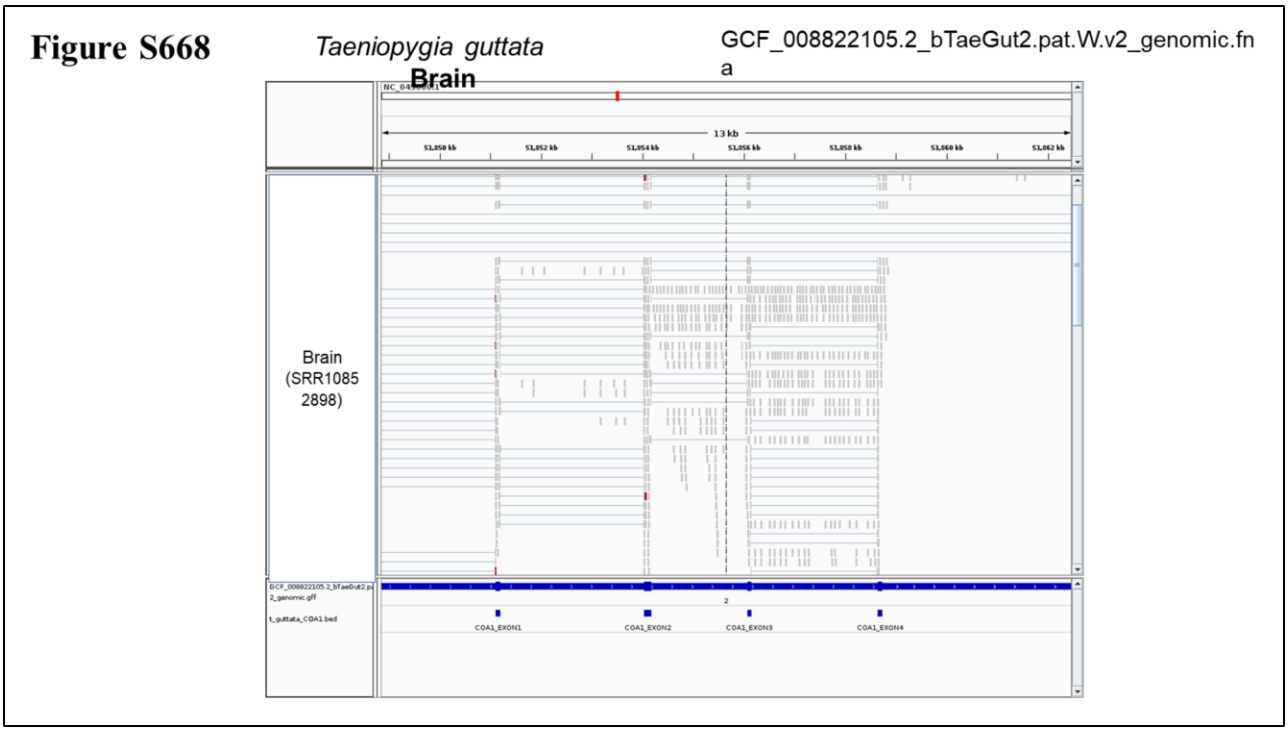

Figure S668: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in zebra finch (*Taeniopygia guttata*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (SRR10852898) have been mapped to the GCF_008822105.2_bTaeGut2.pat.W.v2_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

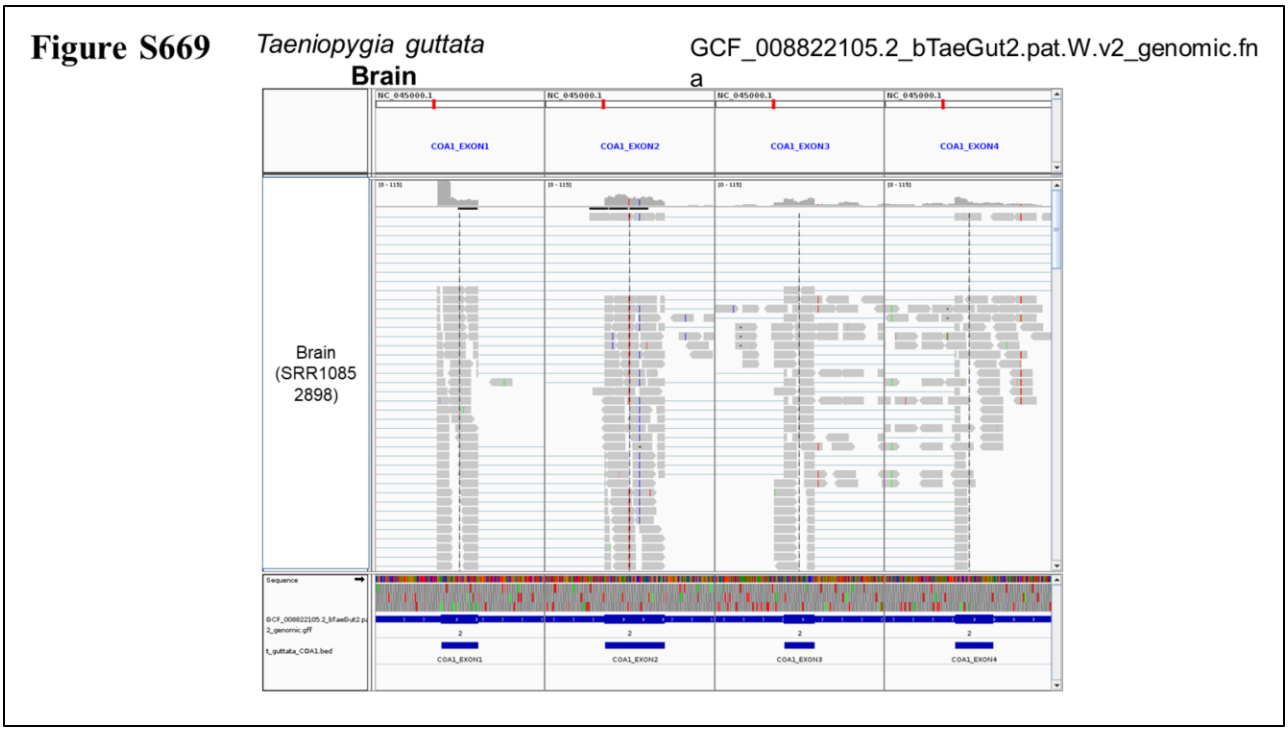

Figure S669: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S668**.

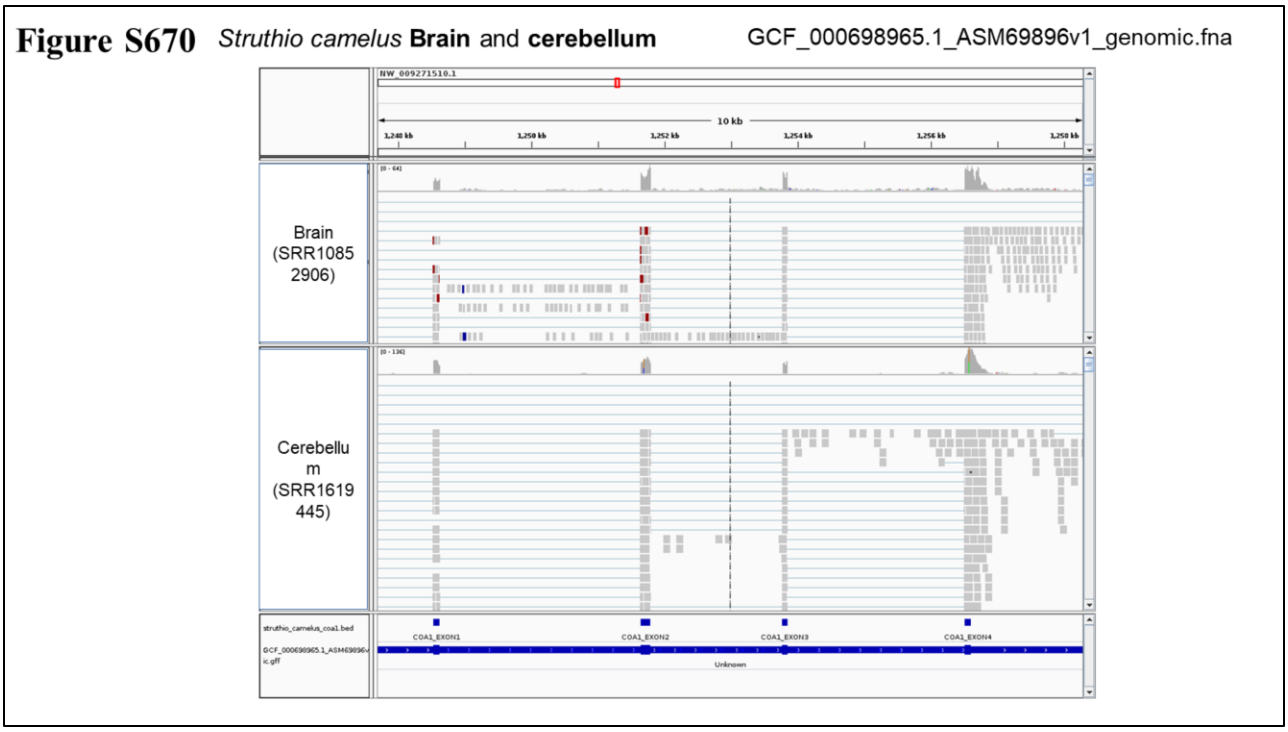

Figure S670: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in ostrich (*Struthio camelus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (SRR10852906) and cerebellum (SRR1619445) have been mapped to the GCF_000698965.1_ASM69896v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

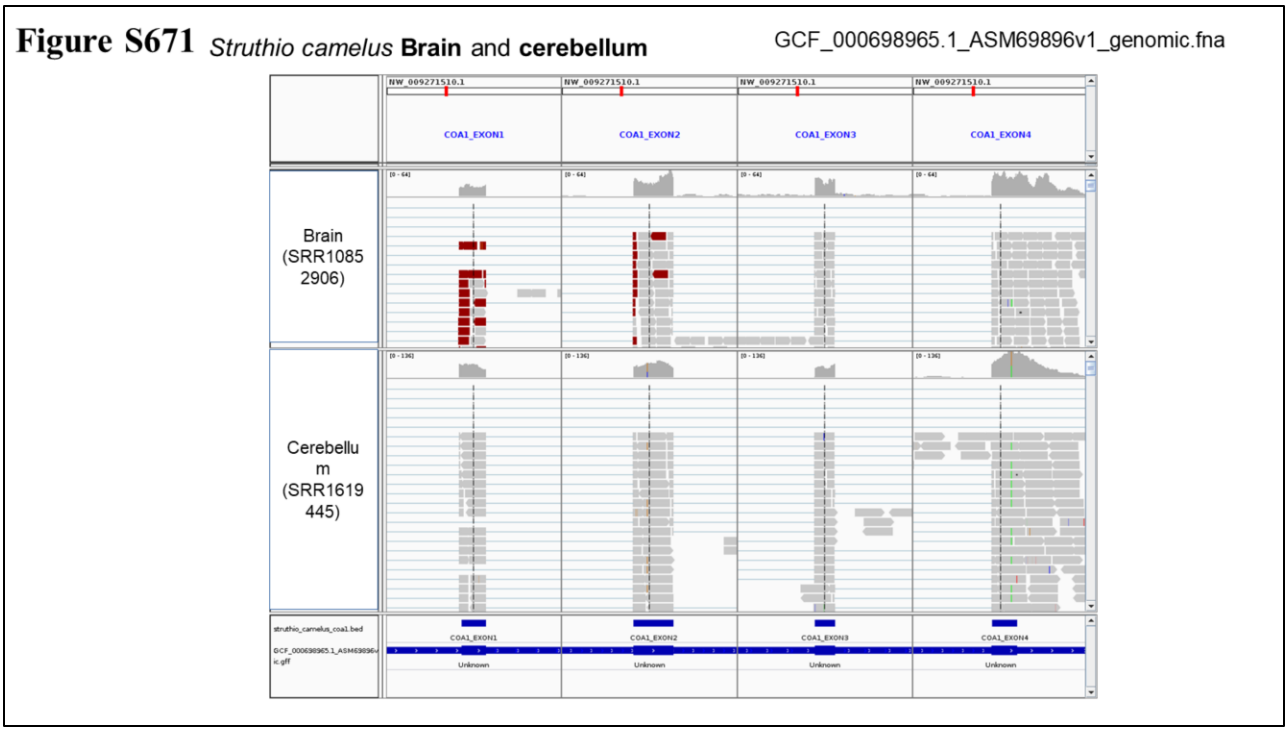

Figure S671: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S670**.

Figure S672 *Pygoscelis adeliae* **Cloacal swab and Muscle** GCF_000699105.1_ASM69910v1_genomic.fna

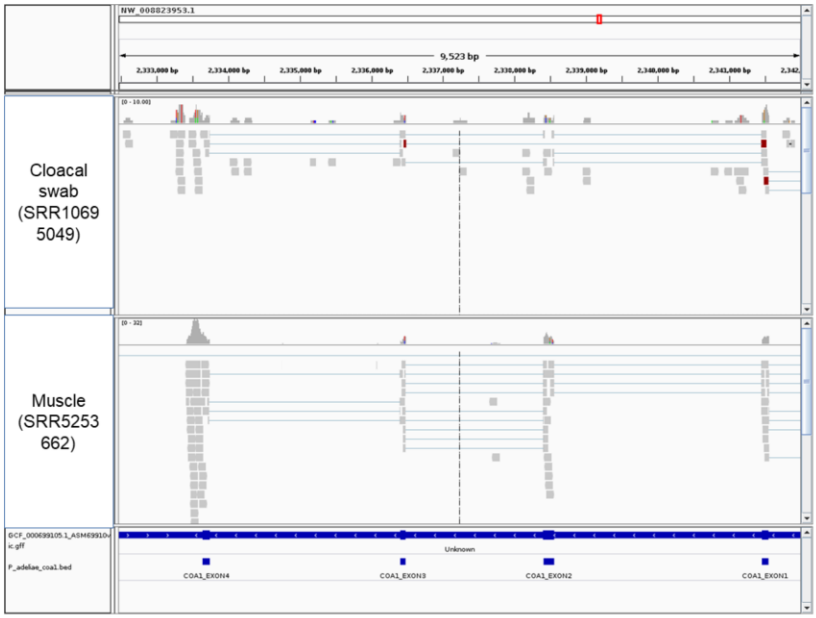

Figure S672: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Adélie penguin (*Pygoscelis adeliae*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from cloacal swab (SRR10695049) and muscle (SRR5253662) have been mapped to the GCF_000699105.1_ASM69910v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

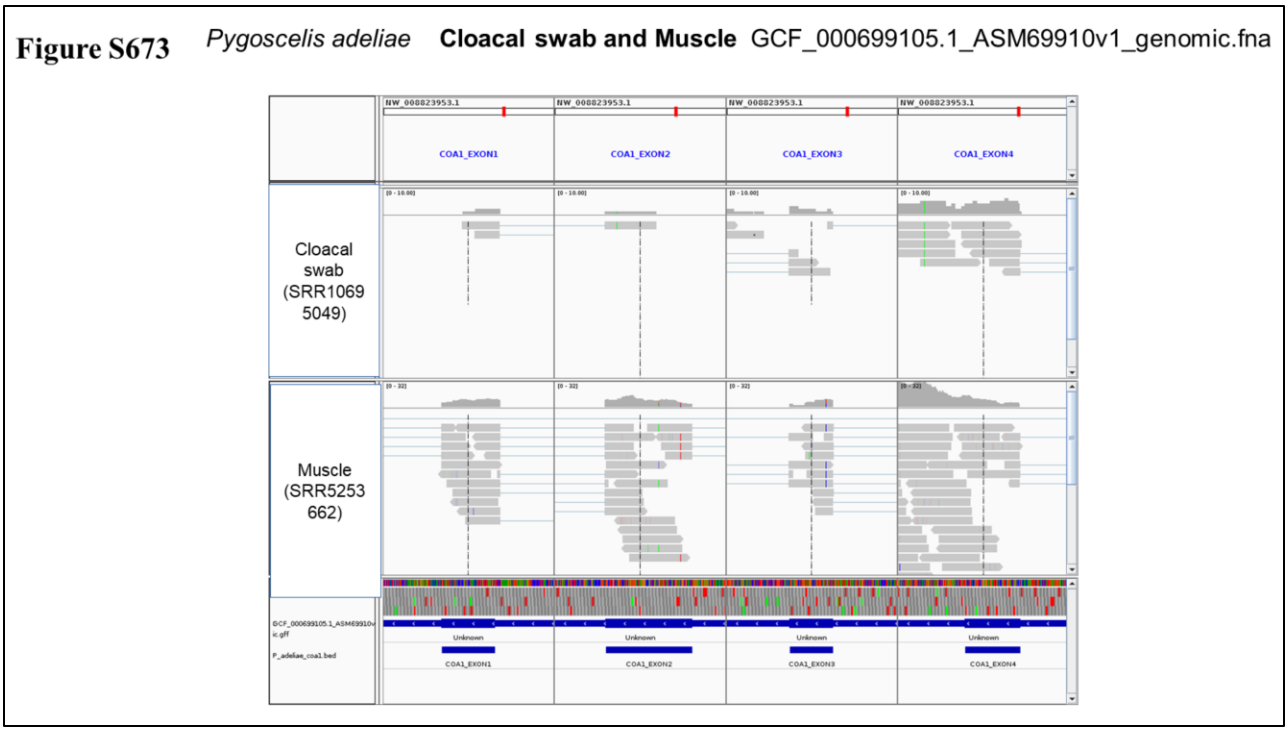

Figure S673: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S672**.

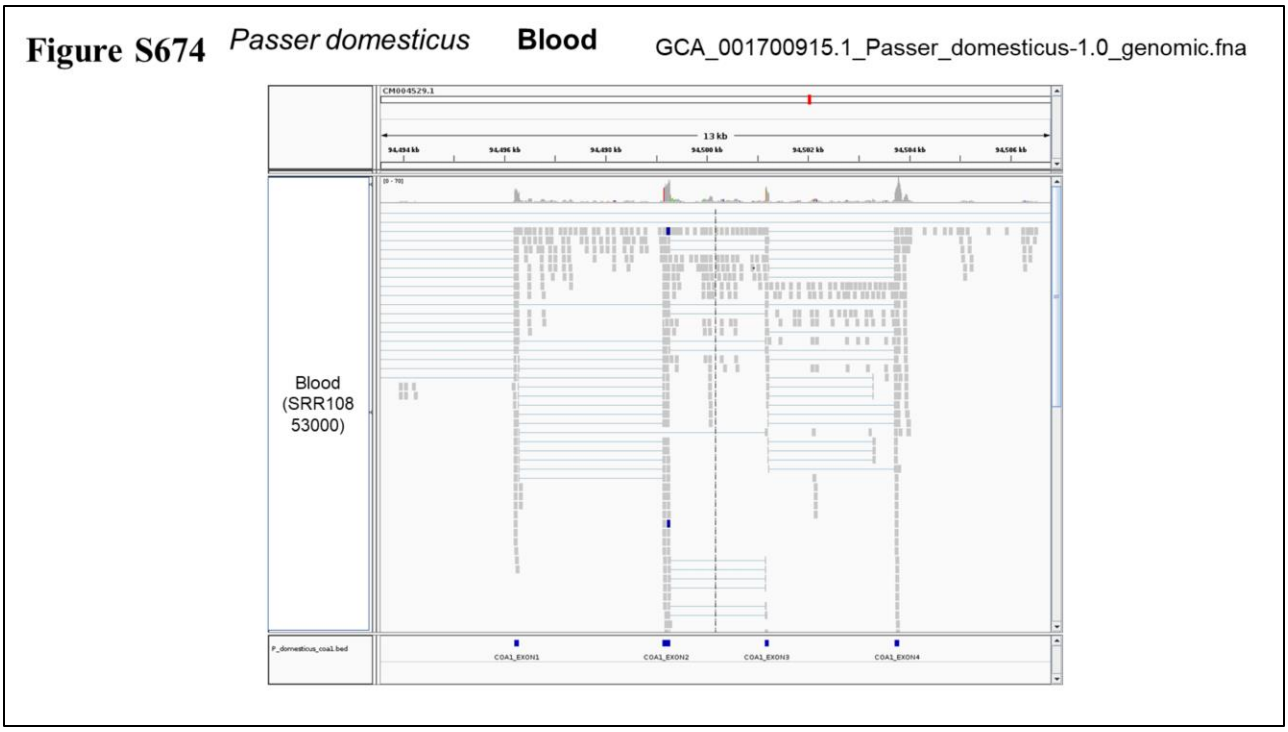

Figure S674: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in house sparrow (*Passer domesticus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR10853000) have been mapped to the GCA_001700915.1_Passer_domesticus-1.0_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

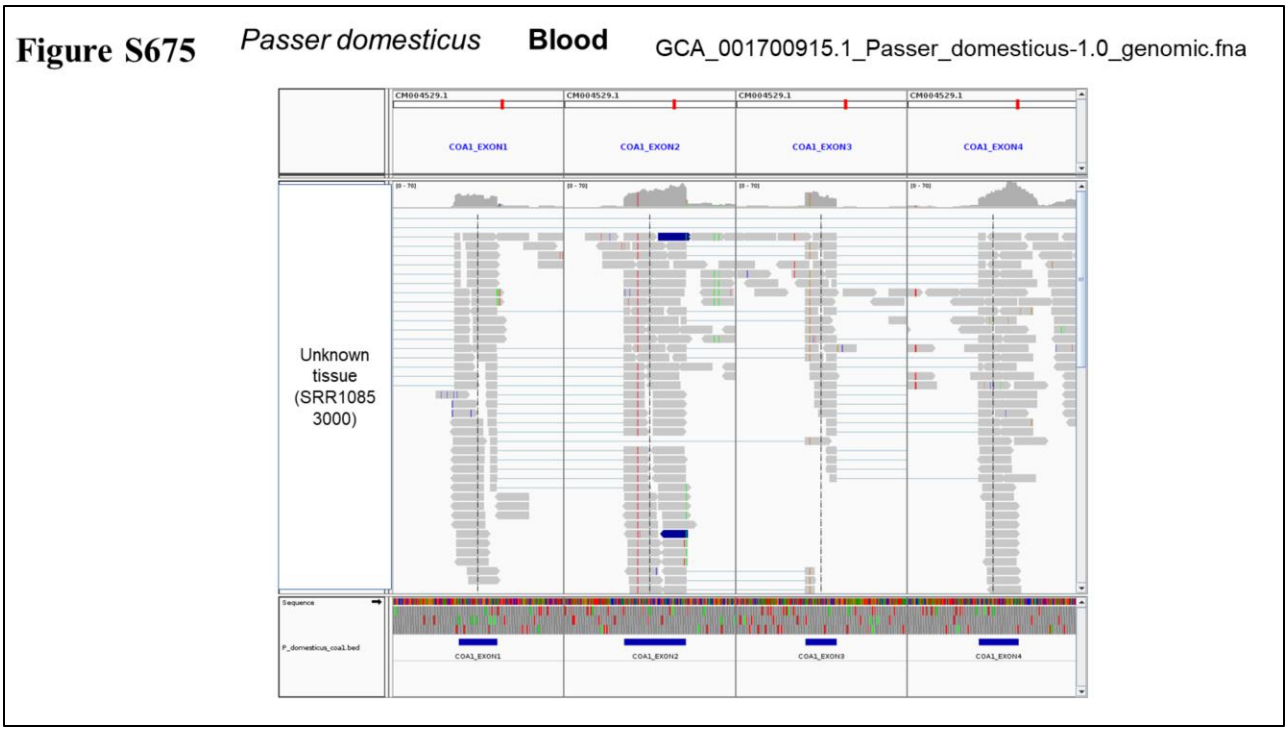

Figure S675: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S674**.

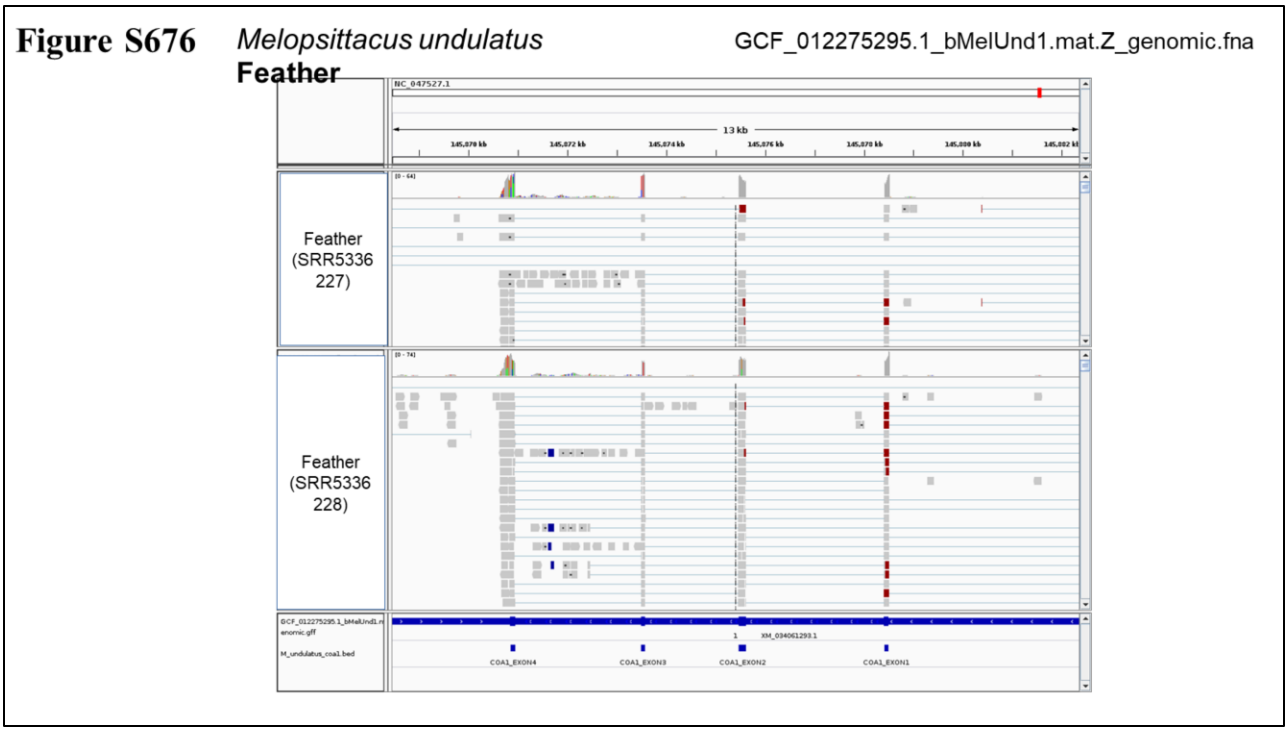

Figure S676: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in budgerigar (*Melopsittacus undulatus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from feather (SRR5336227) and (SRR5336228) have been mapped to the GCF_012275295.1_bMelUnd1.mat.Z_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

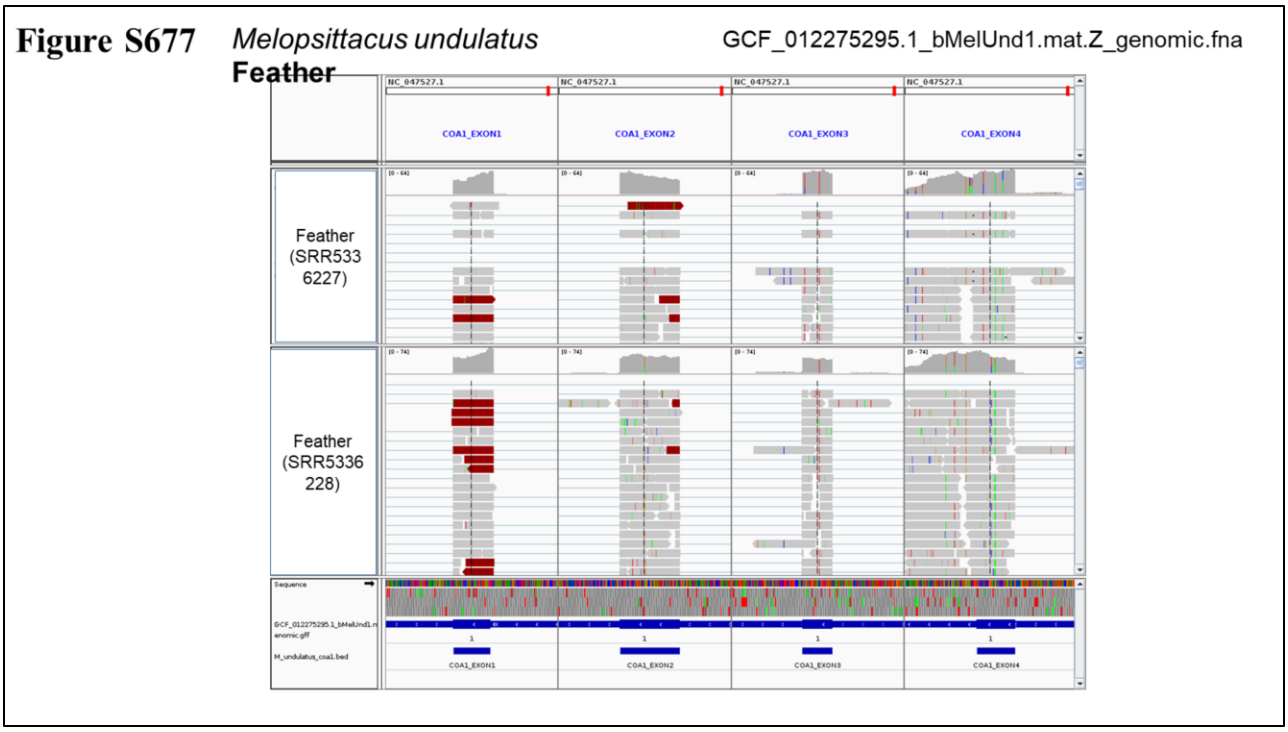

Figure S677: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S676**.

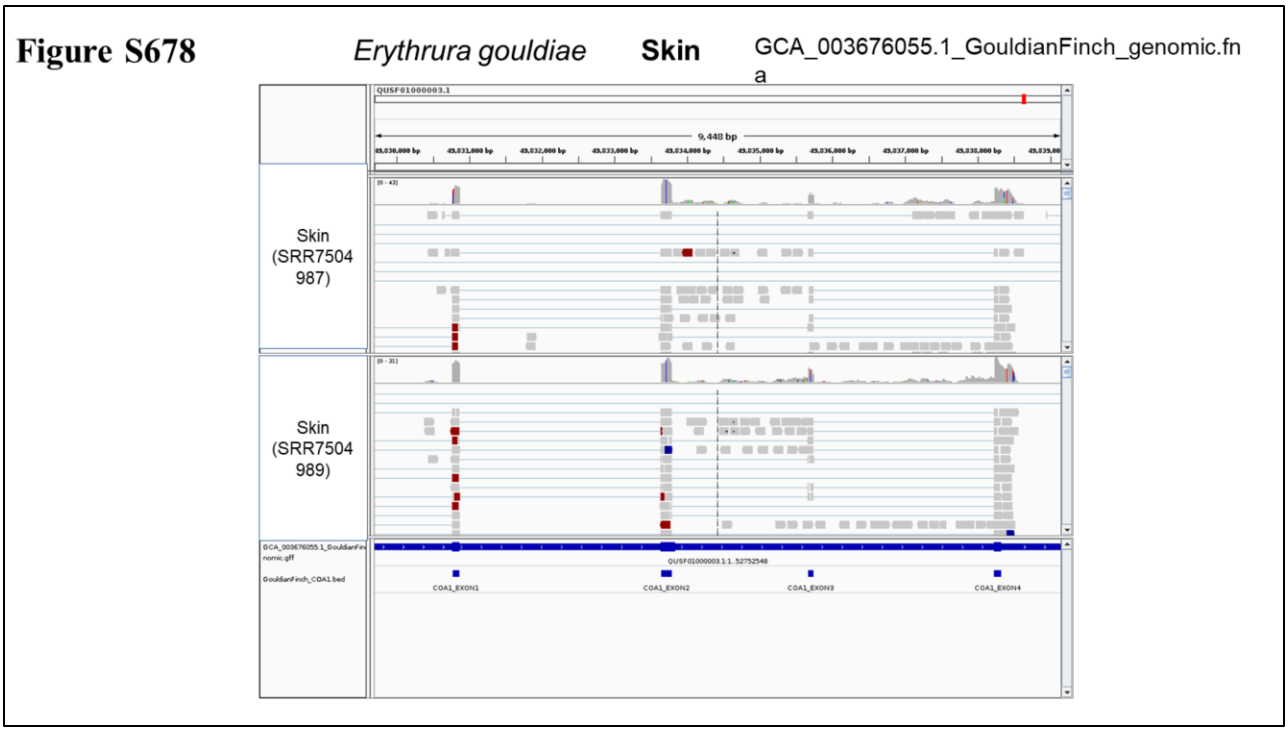

Figure S678: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in gouldian finch (*Erythrura gouldiae*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from skin (SRR7504987) and (SRR7504989) have been mapped to the GCA_003676055.1_GouldianFinch_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

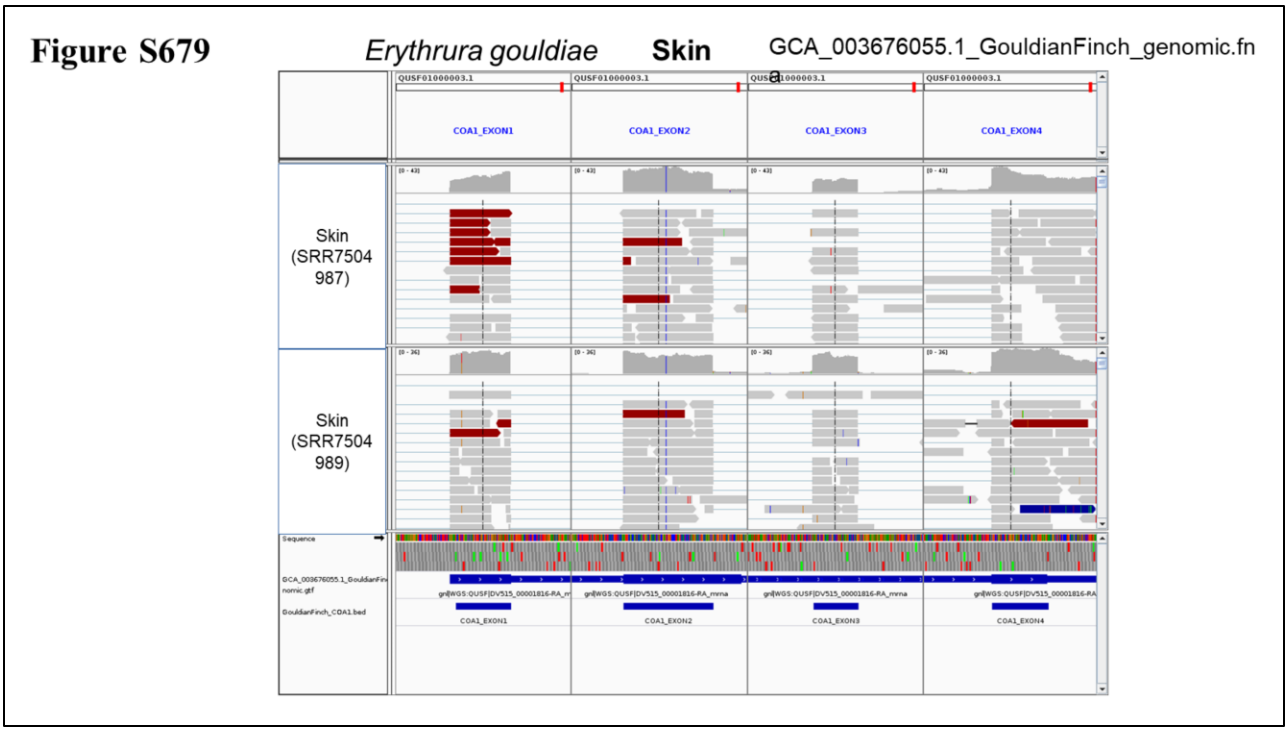

Figure S679: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S678**.

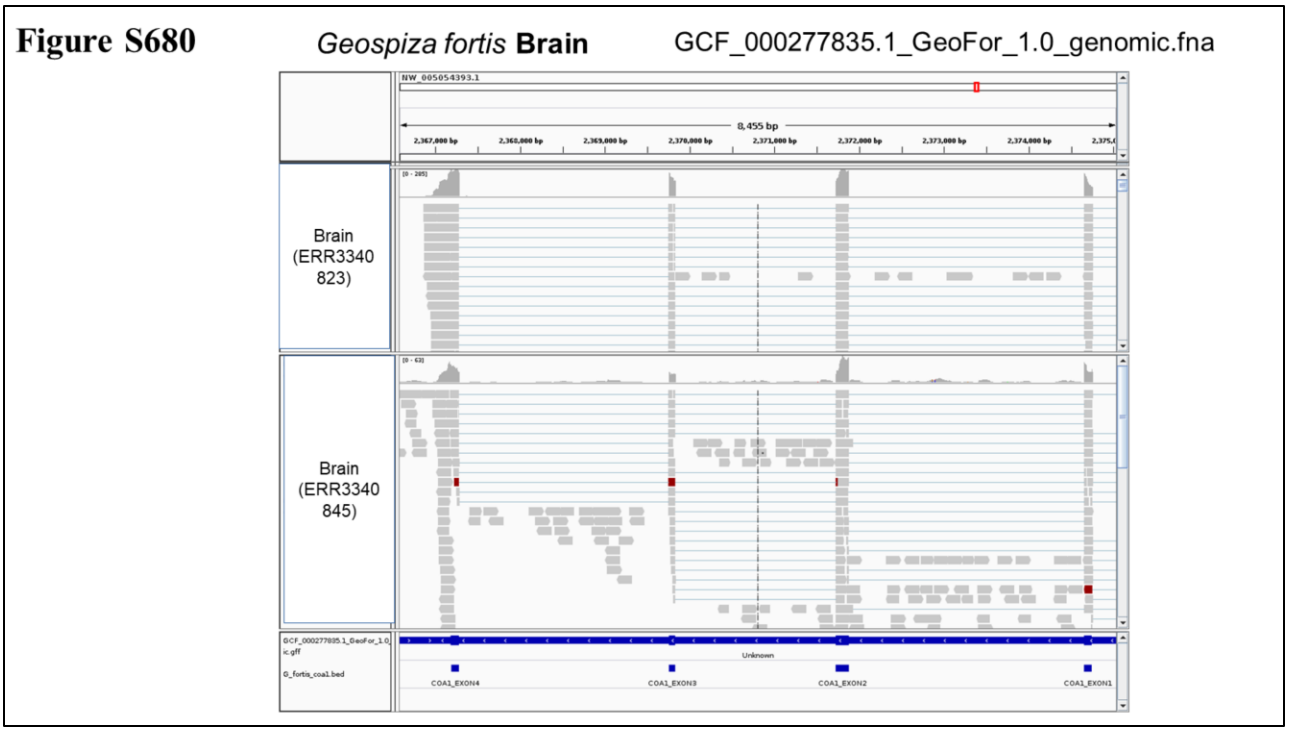

Figure S680: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in medium ground finch (*Geospiza fortis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (ERR3340823) and (ERR3340845) have been mapped to the GCF_000277835.1_GeoFor_1.0_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

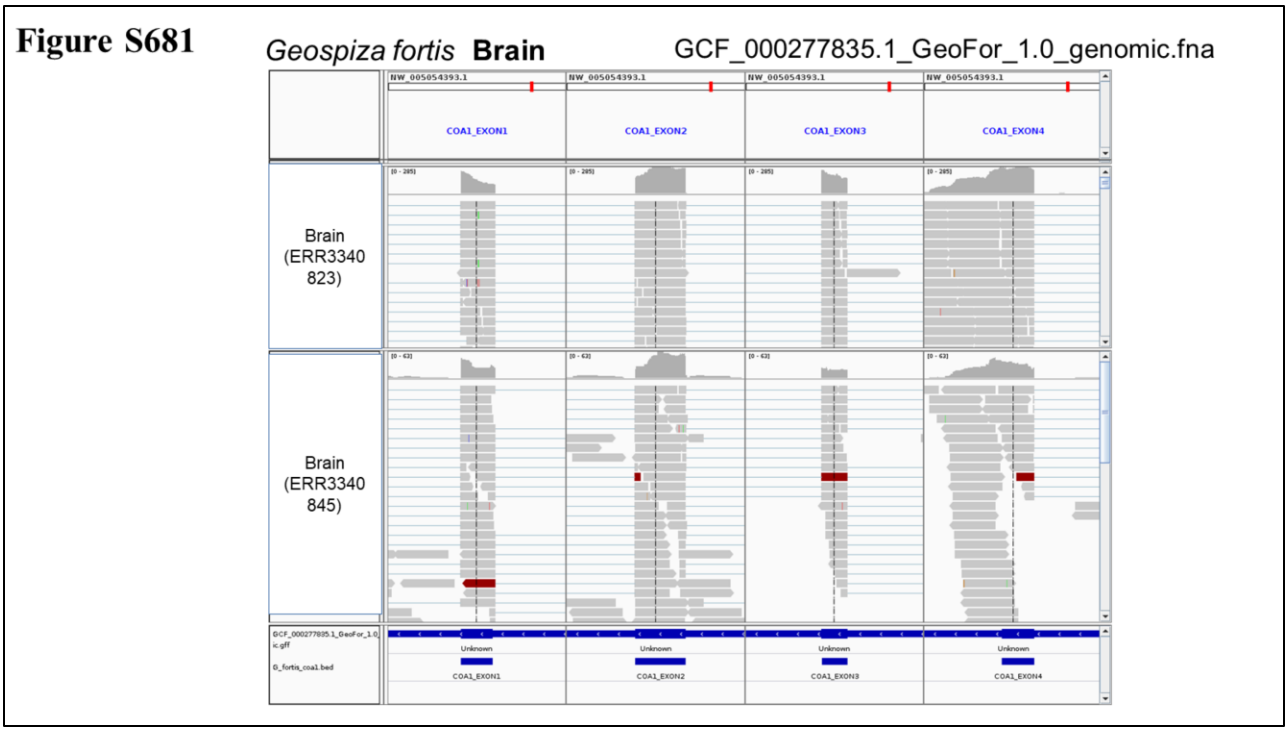

Figure S681: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S680**.

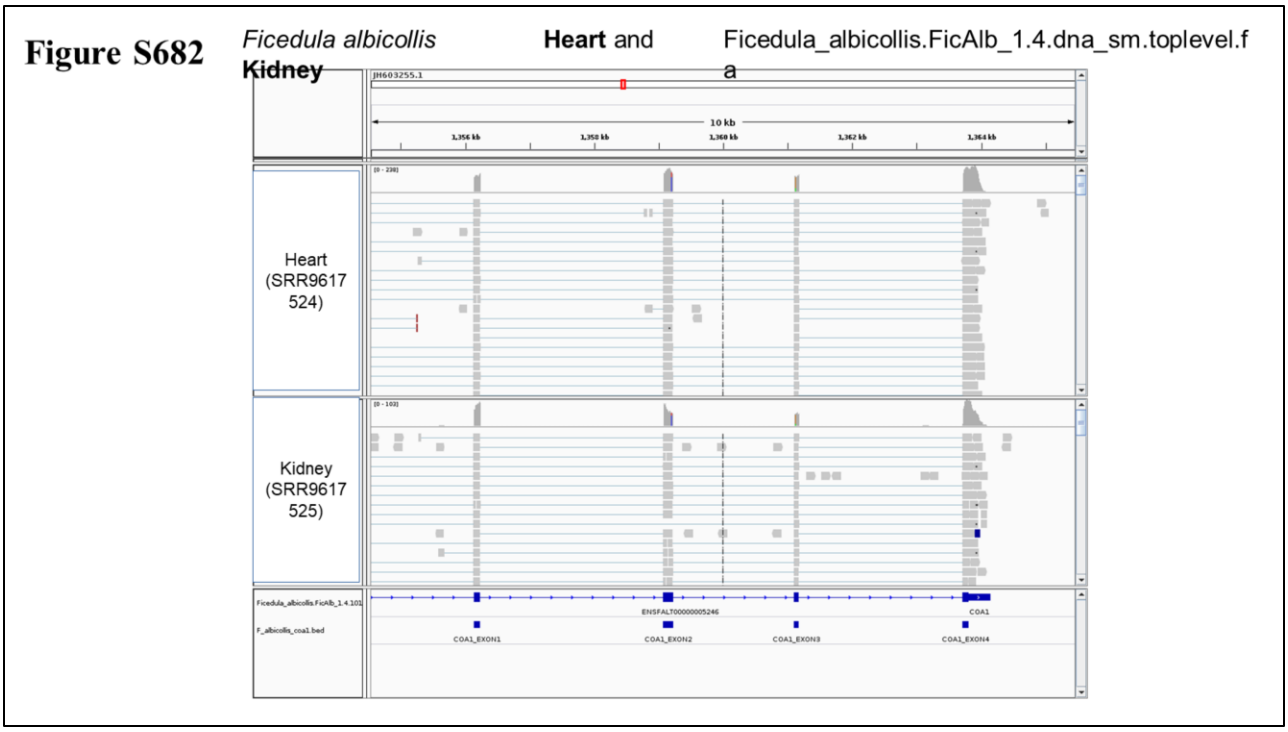

Figure S682: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in collared flycatcher (*Ficedula albicollis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart (SRR9617524) and kidney (SRR9617525) have been mapped to the Ficedula_albicollis.FicAlb_1.4.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

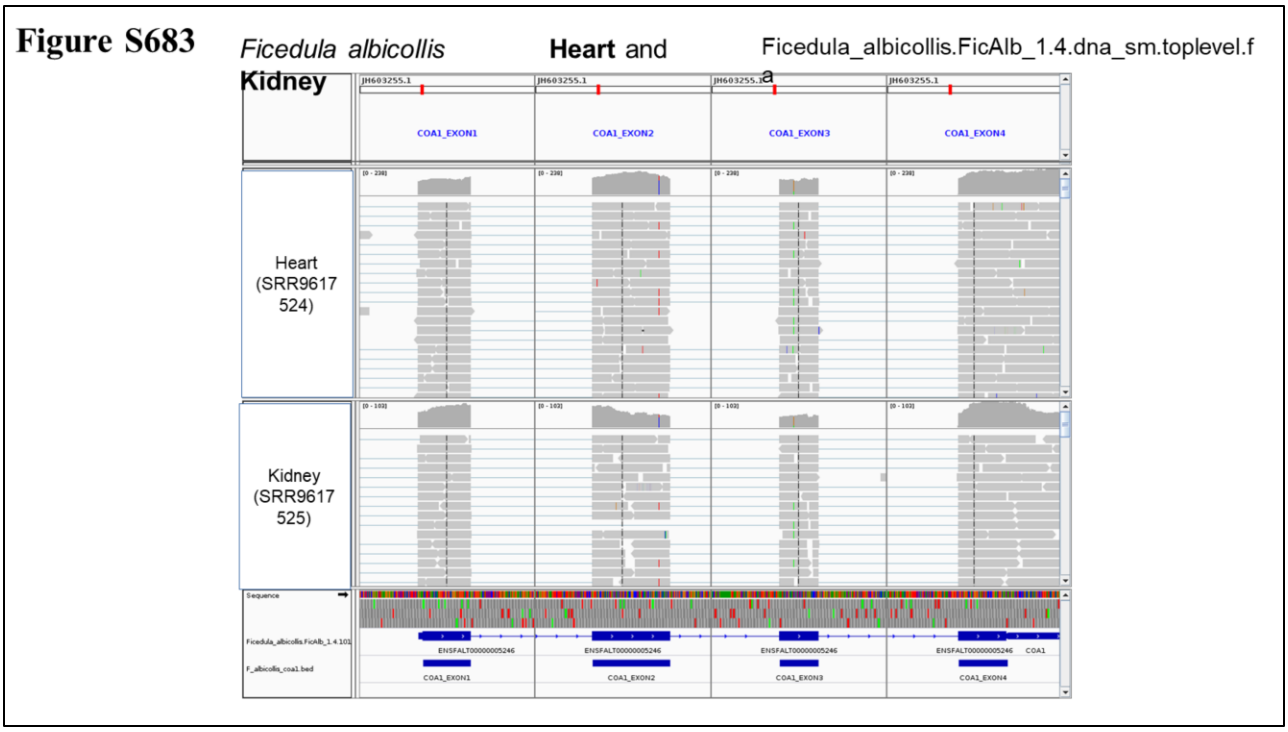

Figure S683: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S682**.

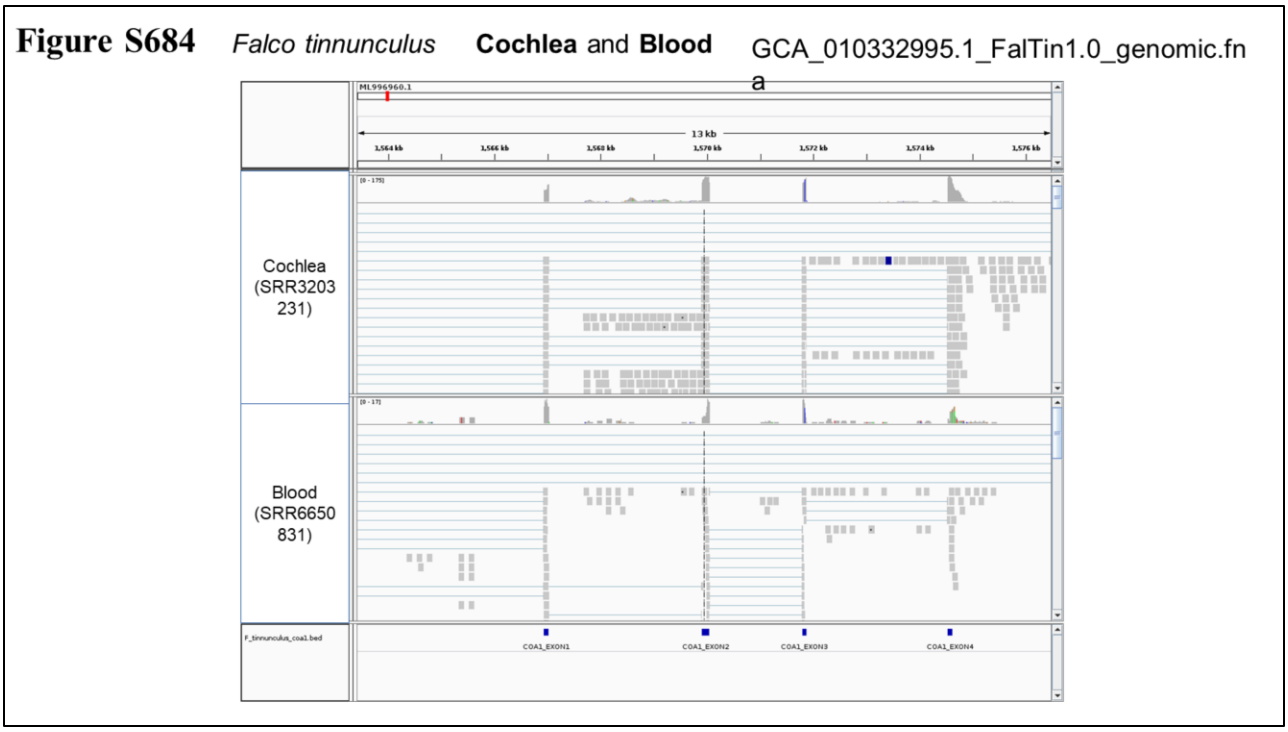

Figure S684: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in common kestrel (*Falco tinnunculus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from cochlea (SRR3203231) and blood (SRR6650831) have been mapped to the GCA_010332995.1_FalTin1.0_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

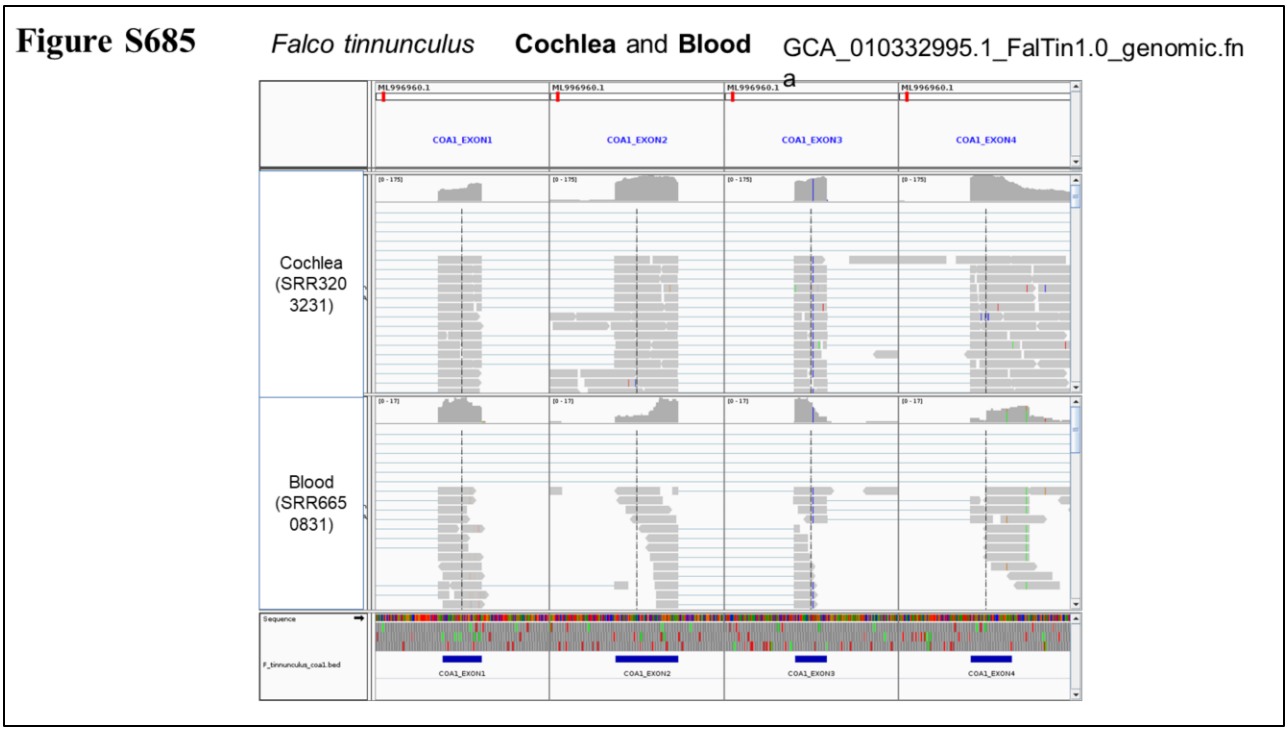

Figure S685: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S684**.

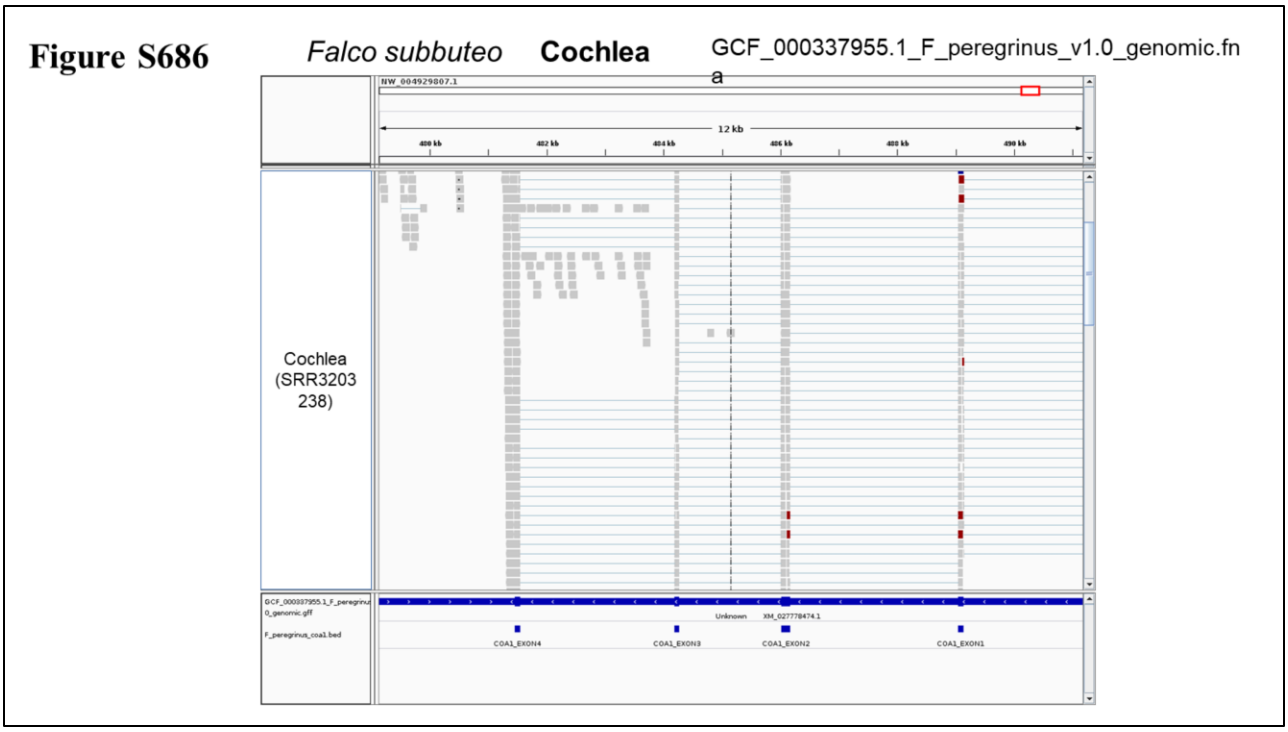

Figure S686: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Eurasian hobby (*Falco subbuteo*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from cochlea (SRR3203238) have been mapped to the GCF_000337955.1_F_peregrinus_v1.0_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

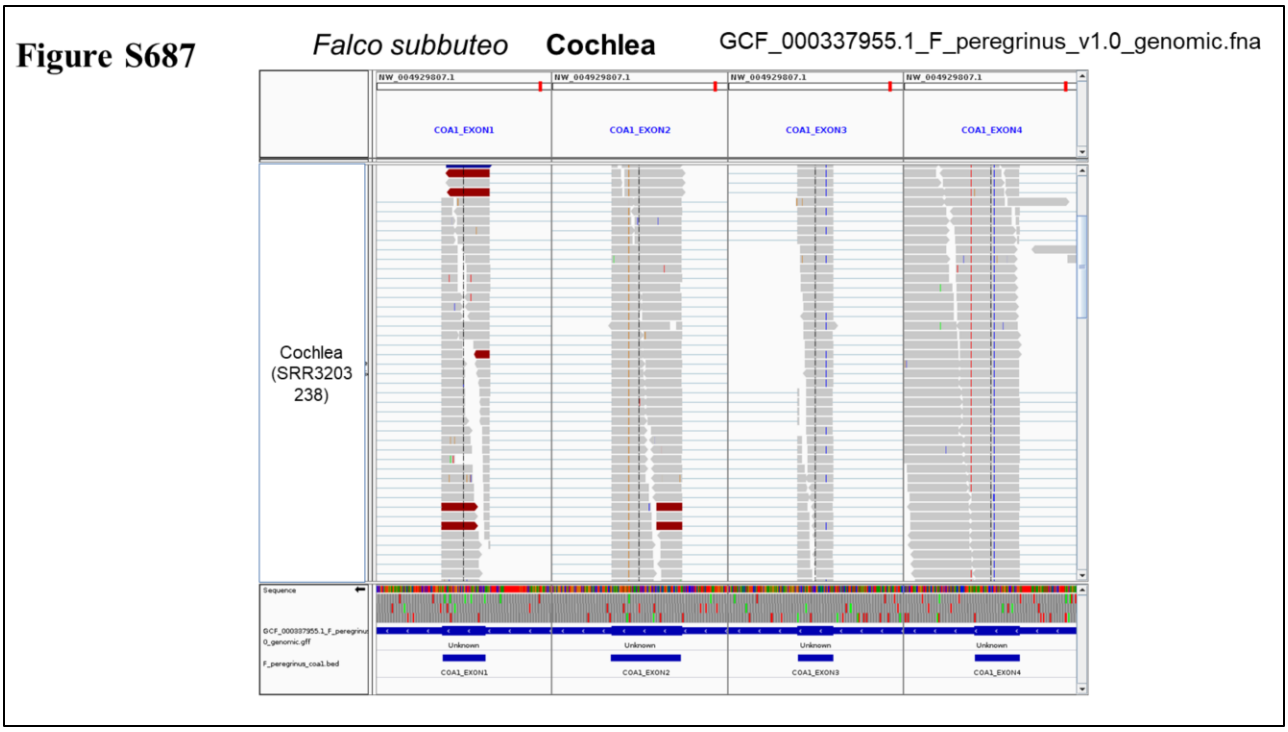

Figure S687: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S686**.

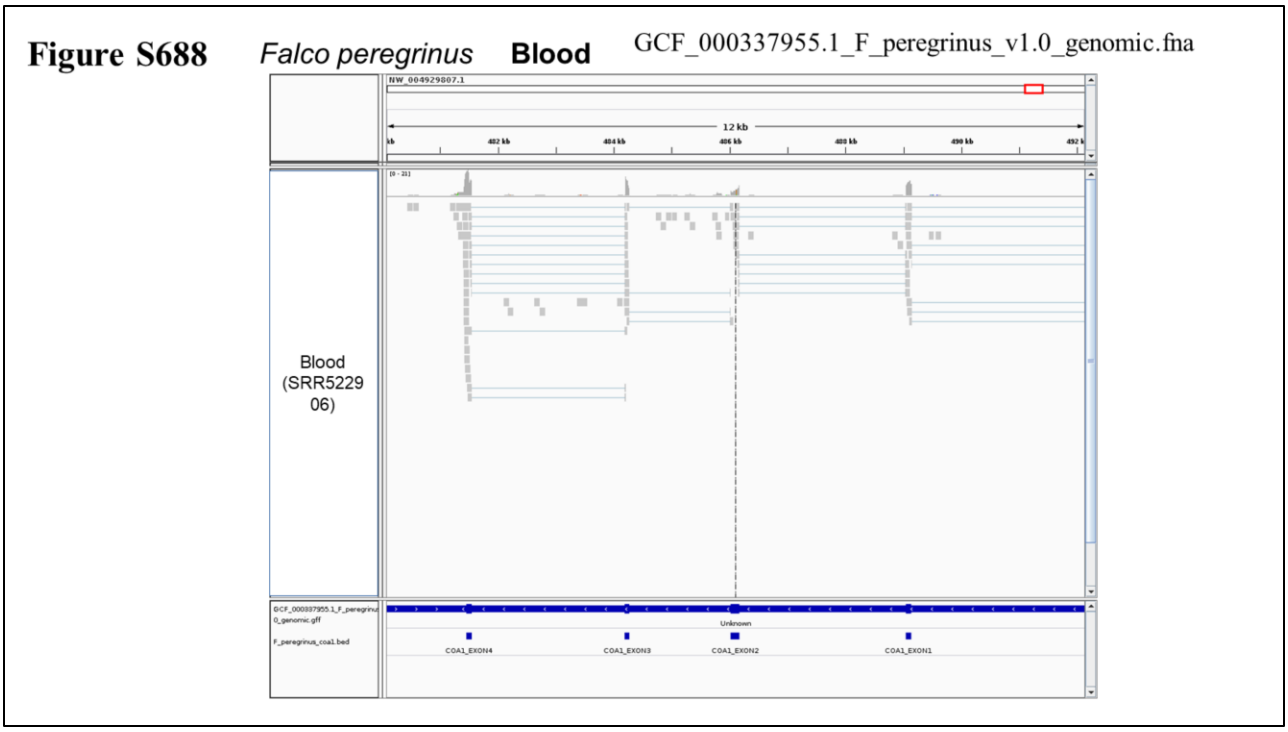

Figure S688: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in peregrine falcon (*Falco peregrinus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR522906) have been mapped to the GCF_000337955.1_F_peregrinus_v1.0_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

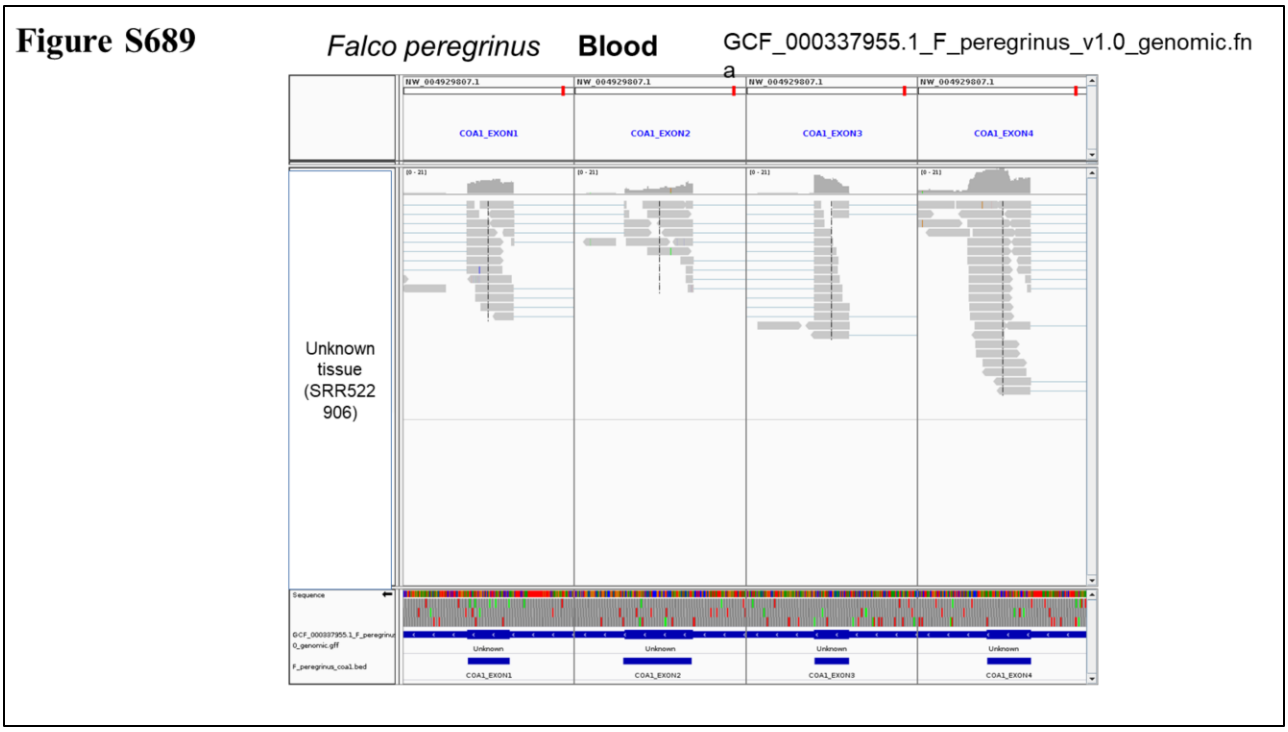

Figure S689: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S688**.

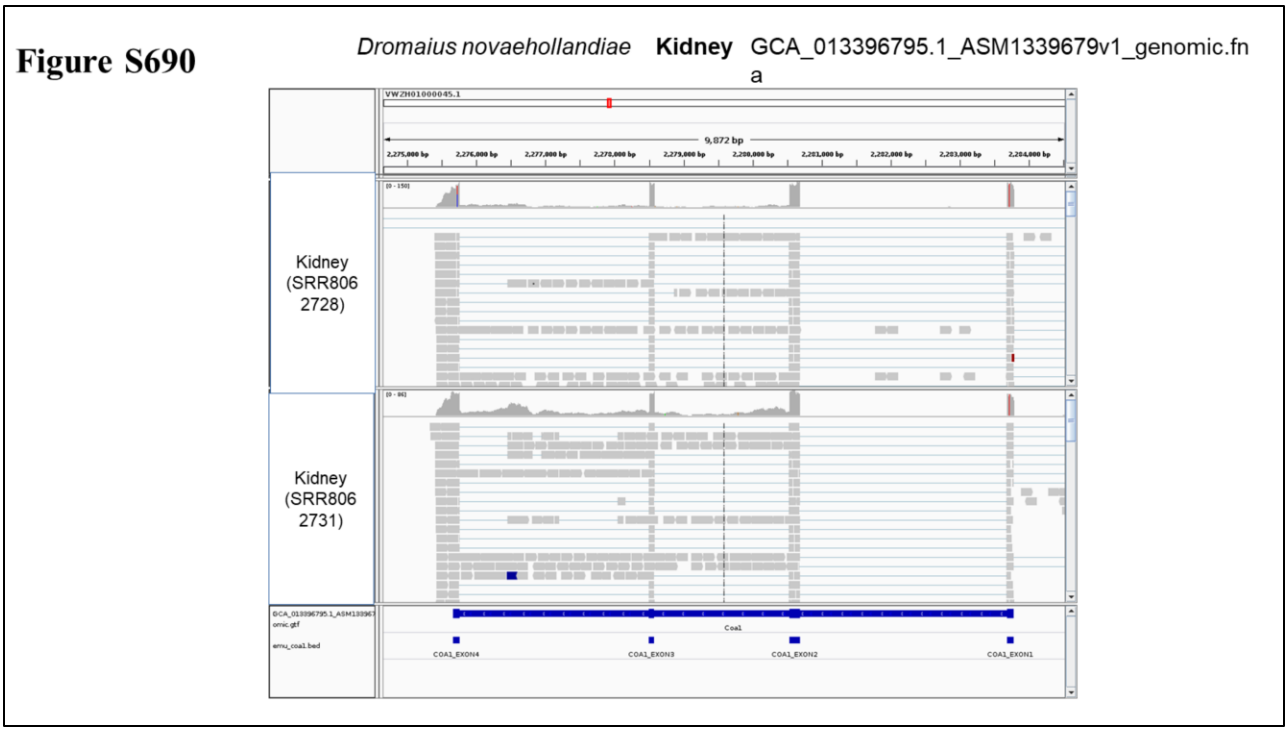

Figure S690: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in emu (*Dromaius novaehollandiae*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from kidney (SRR8062728) and (SRR8062731) have been mapped to the GCA_013396795.1_ASM1339679v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

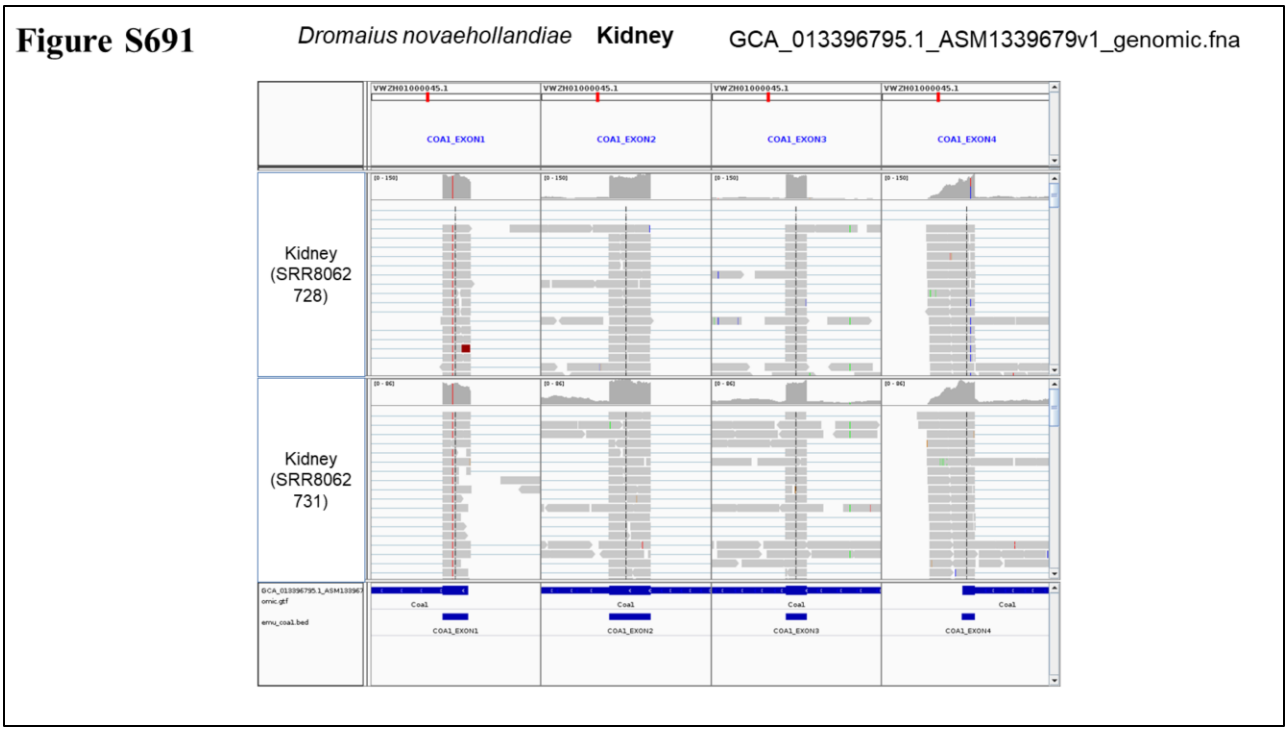

Figure S691: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S690**.

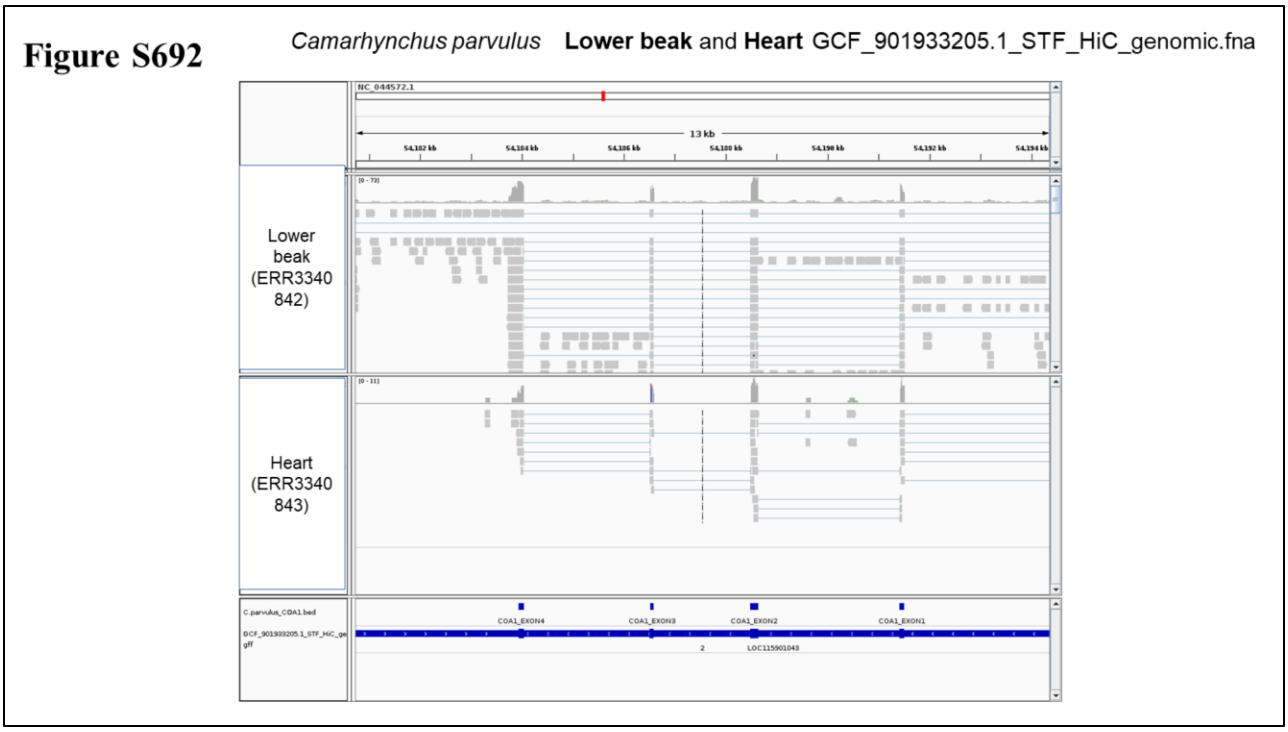

Figure S692: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in small tree finch (*Camarhynchus parvulus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from lower beak (ERR3340842) and heart (ERR3340843) have been mapped to the GCF_901933205.1_STF_HiC_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

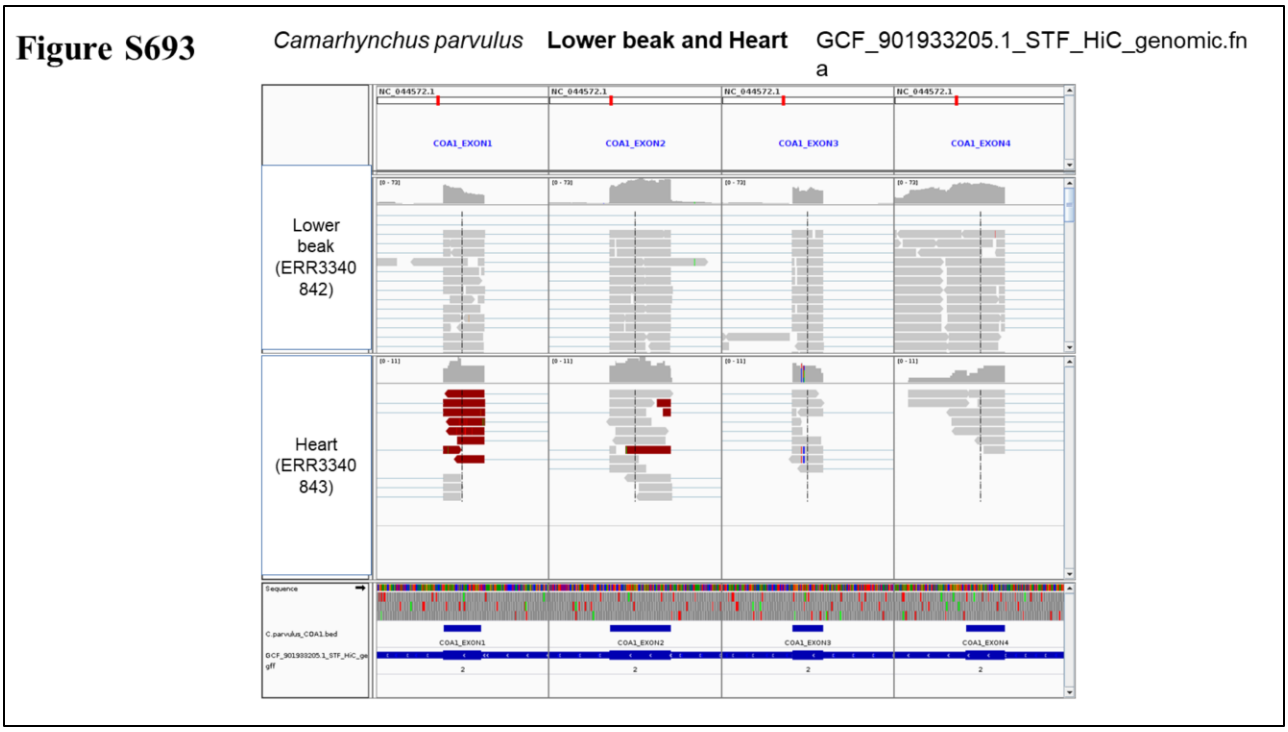

Figure S693: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S692**.

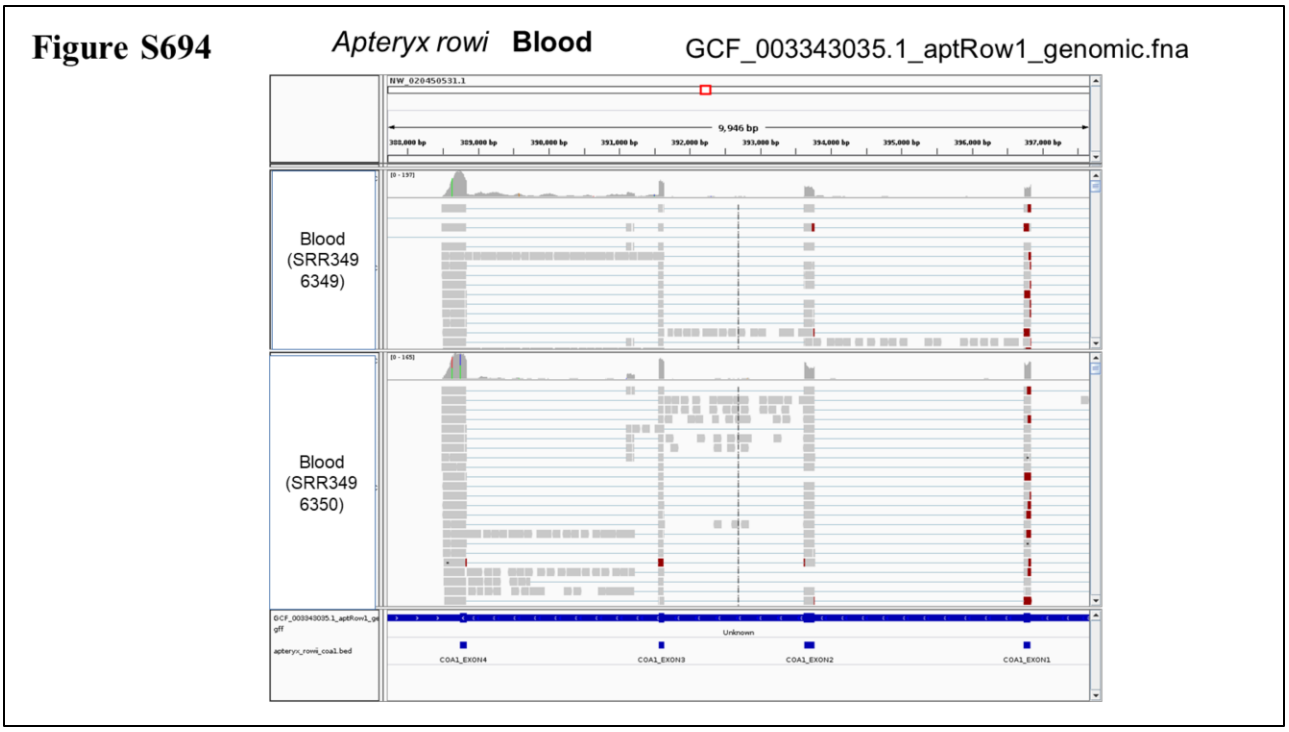

Figure S694: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in okarito kiwi (*Apteryx rowi*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR3496349) and (SRR3496350) have been mapped to the GCF_003343035.1_aptRow1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

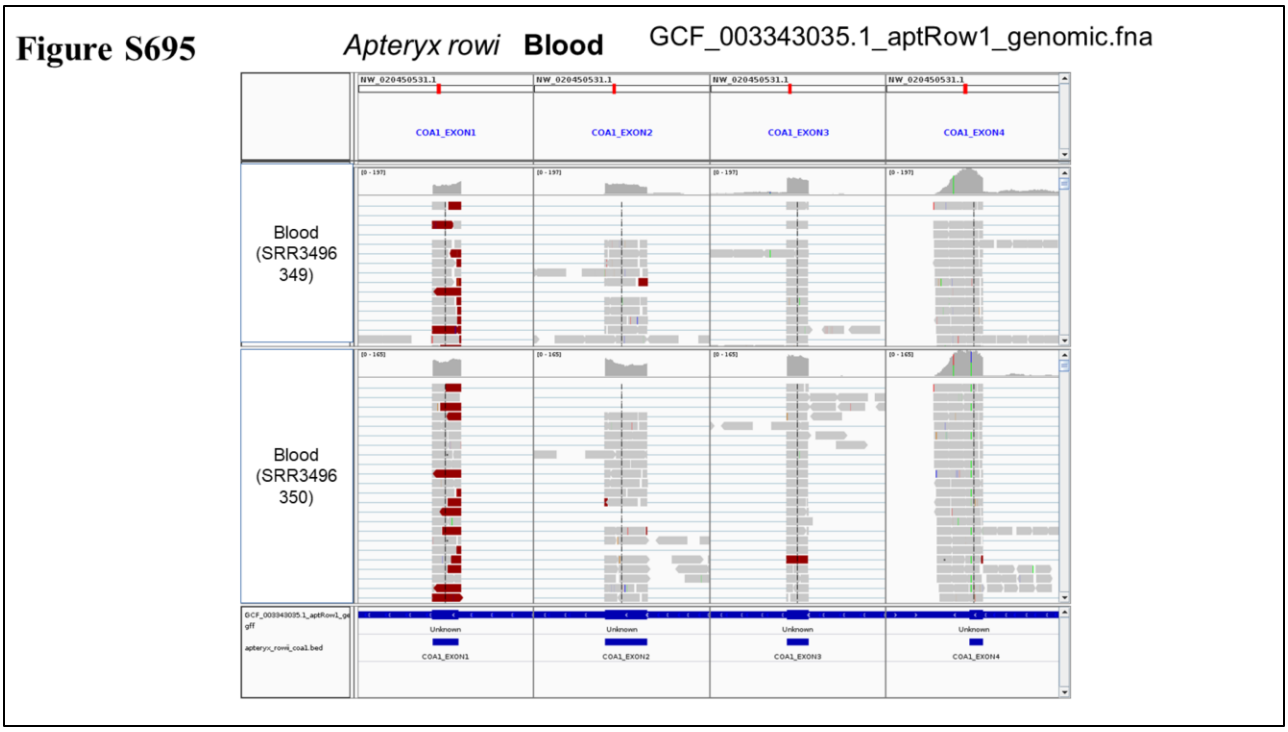

Figure S695: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S694**.

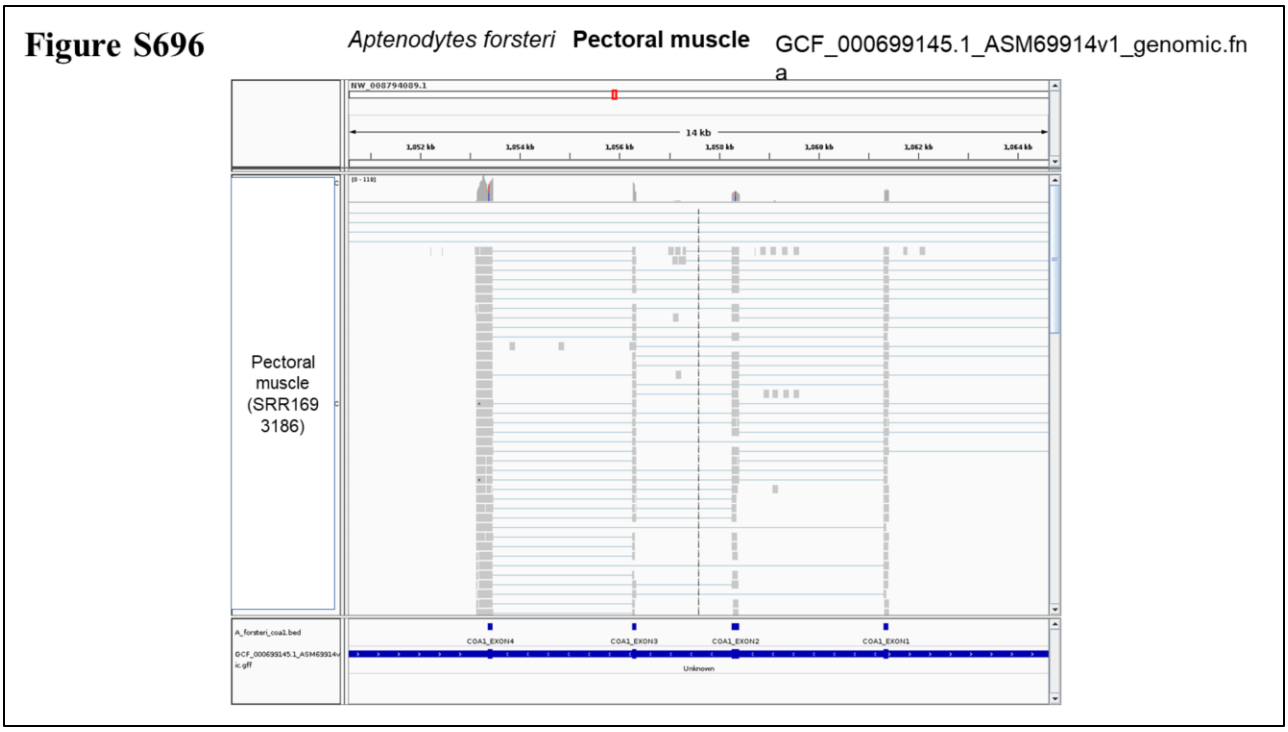

Figure S696: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in emperor penguin (*Aptenodytes forsteri*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from pectoral muscle (SRR1693186) have been mapped to the GCF_000699145.1_ASM69914v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

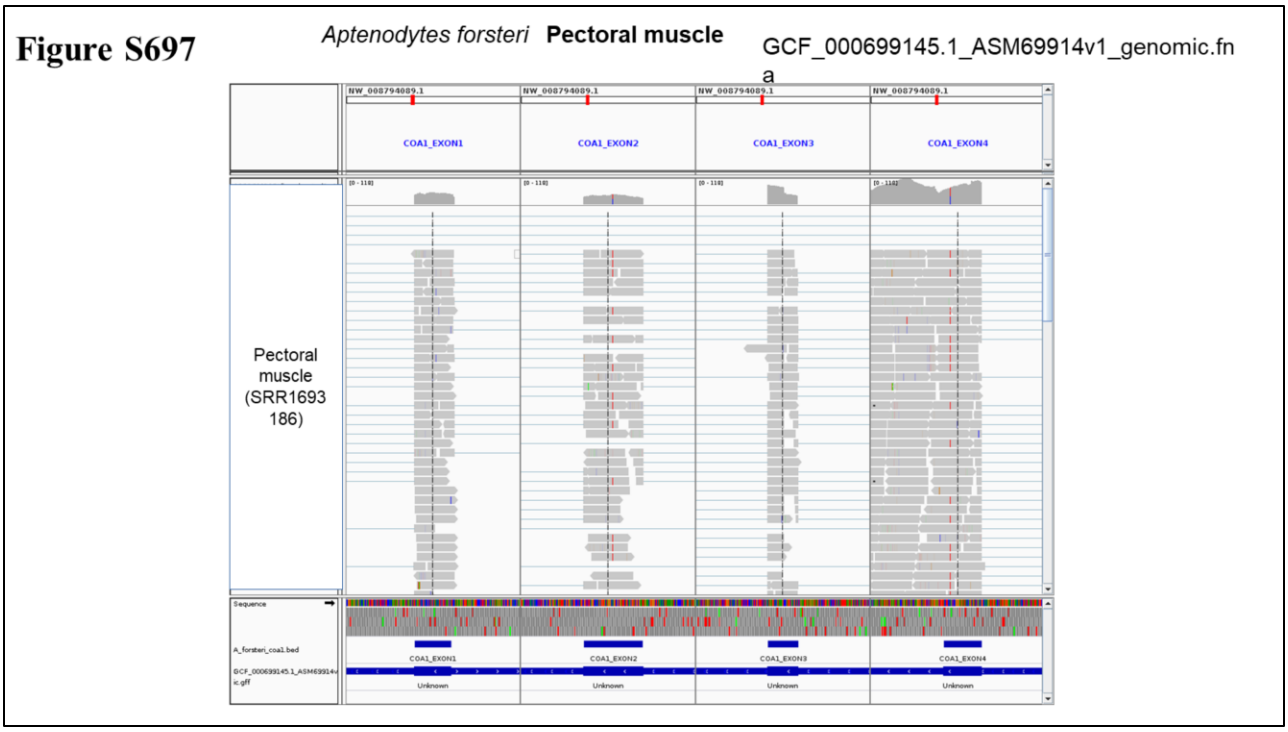

Figure S697: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S696**.

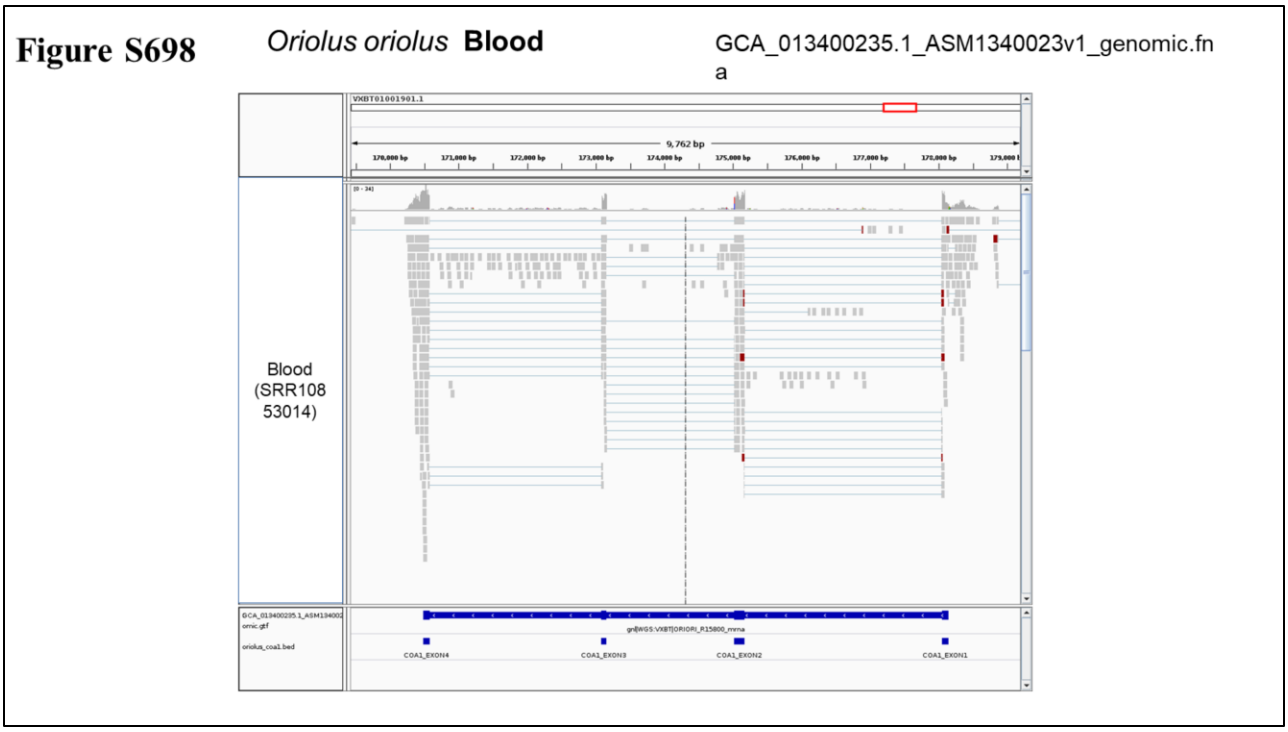

Figure S698: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Eurasian golden oriole (*Oriolus oriolus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR10853014) have been mapped to the GCA_013400235.1_ASM1340023v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

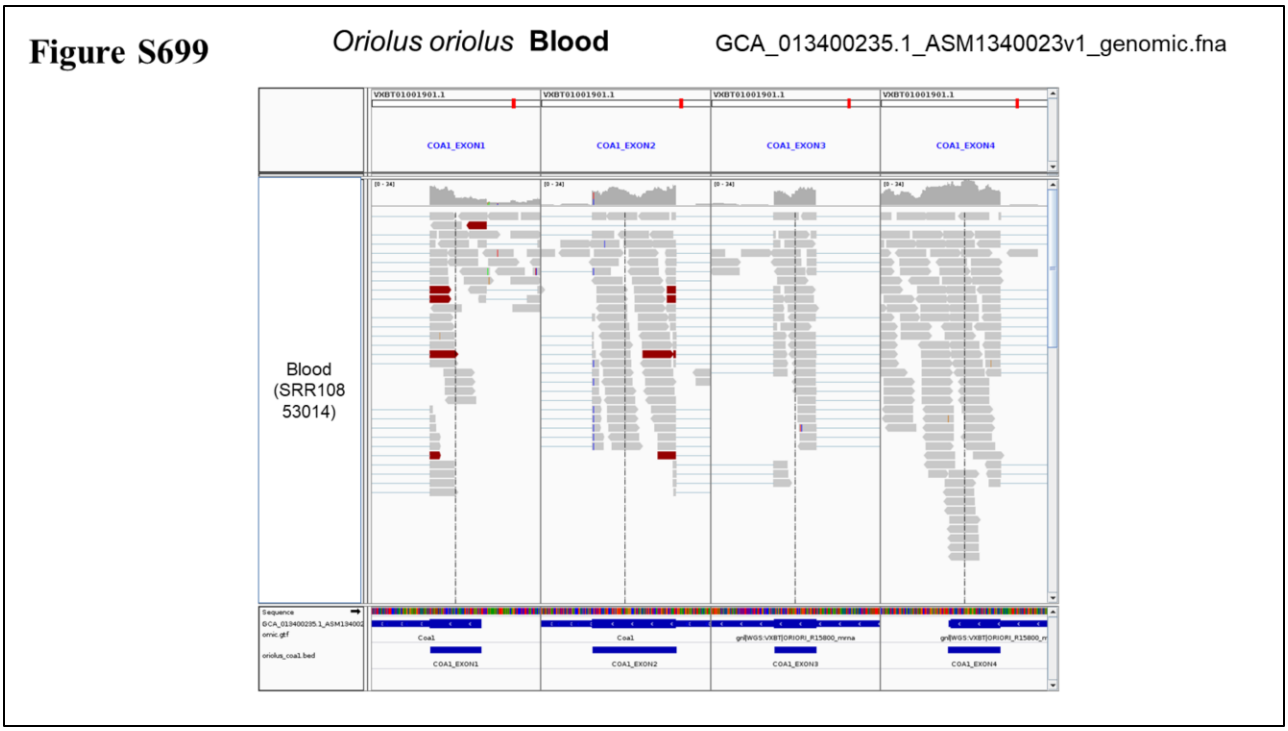

Figure S699: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S688**.

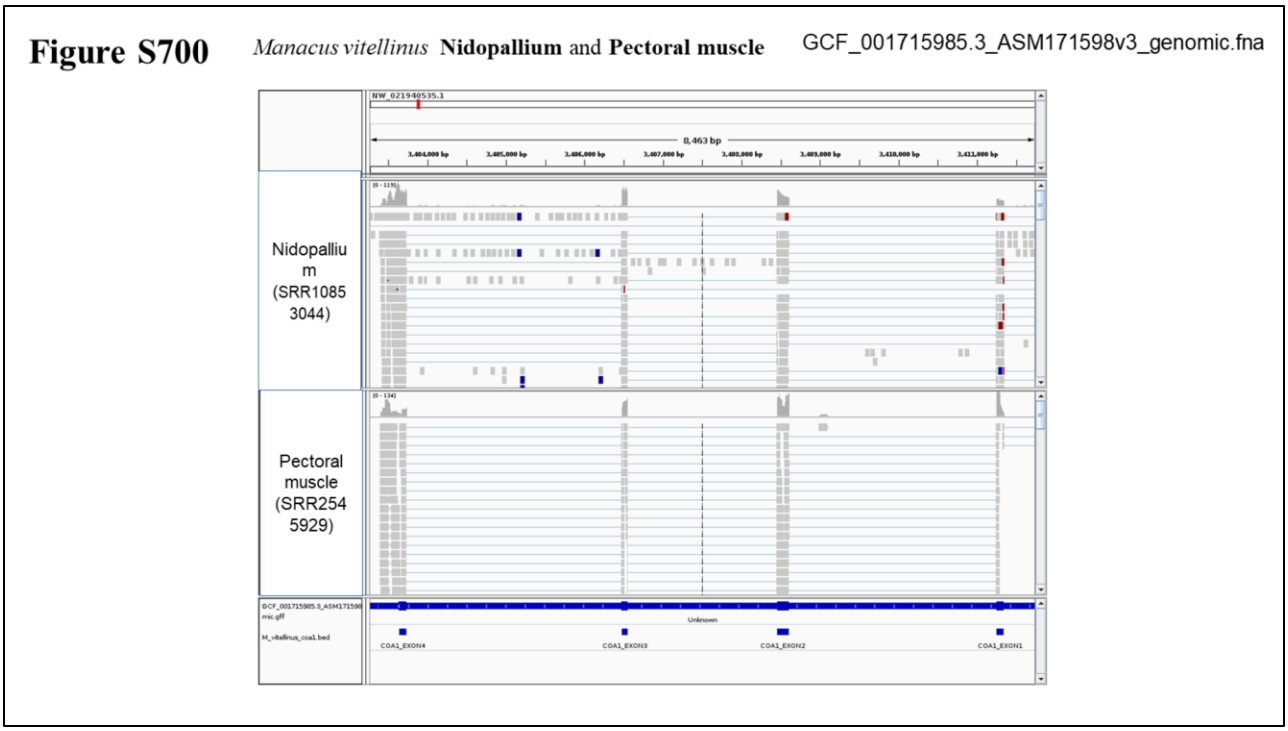

Figure S700: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in golden-collared manakin (*Manacus vitellinus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from nidopallium (SRR10853044) and pectoral muscle (SRR2545929) have been mapped to the GCF_001715985.3_ASM171598v3_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

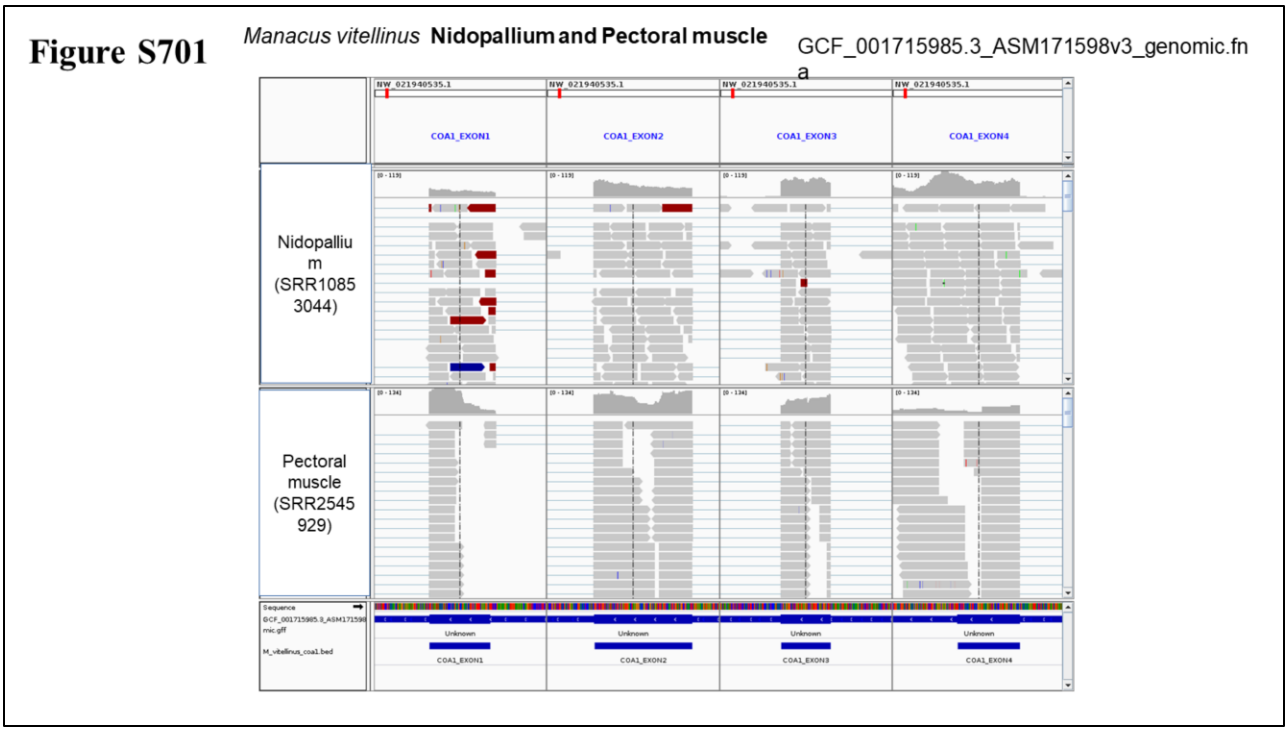

Figure S701: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S700**.

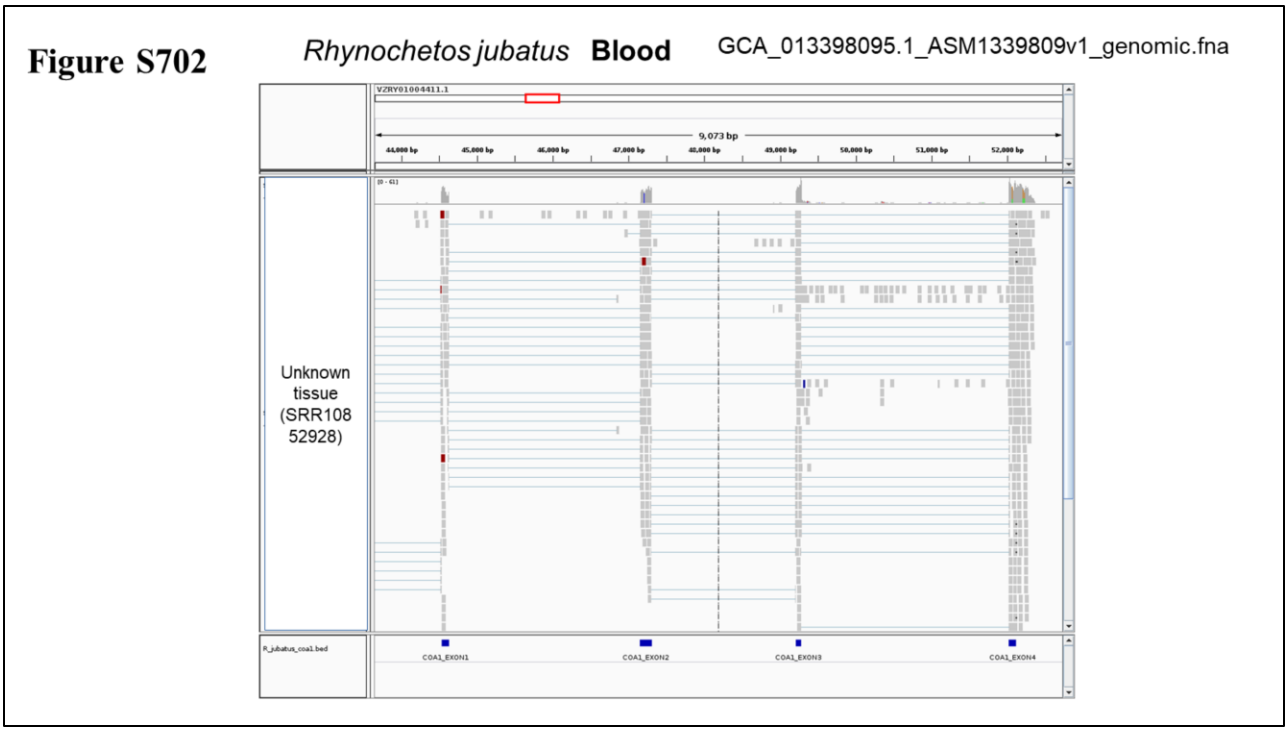

Figure S702: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Kagu (*Rhynochetos jubatus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR10852928) have been mapped to the GCA_013398095.1_ASM1339809v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

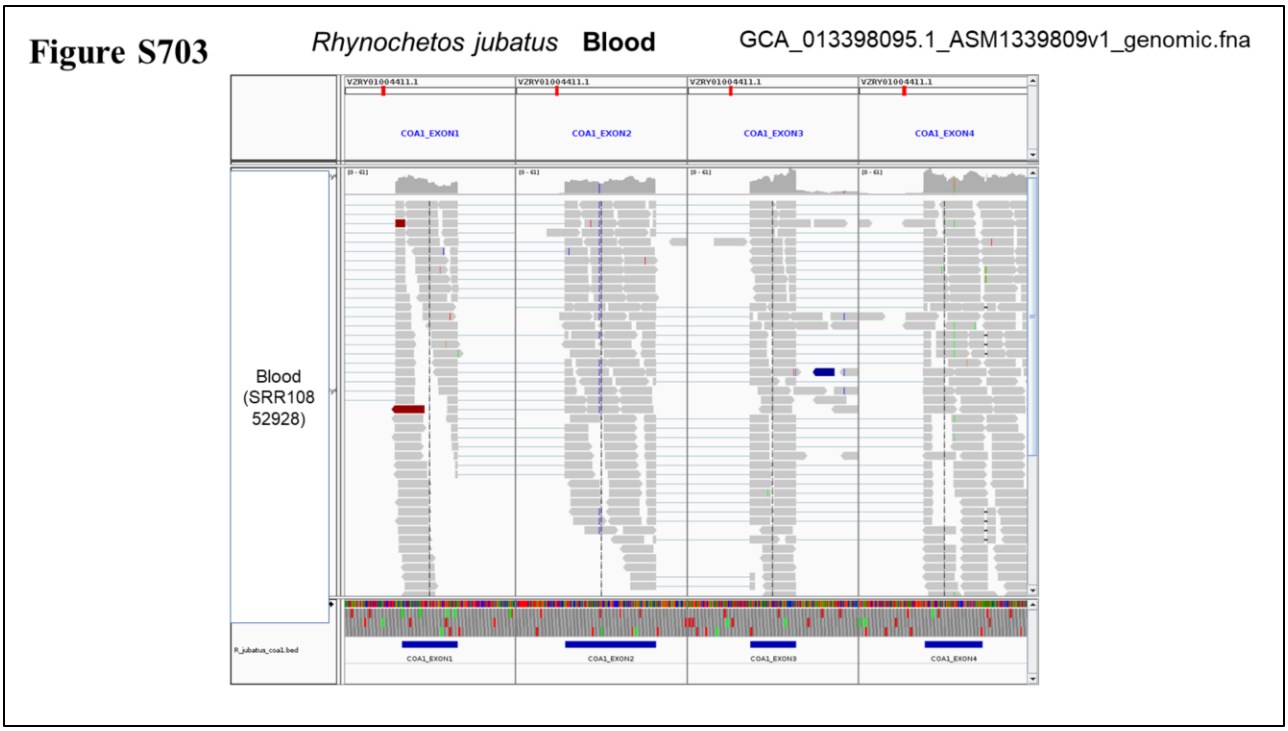

Figure S703: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S702**.

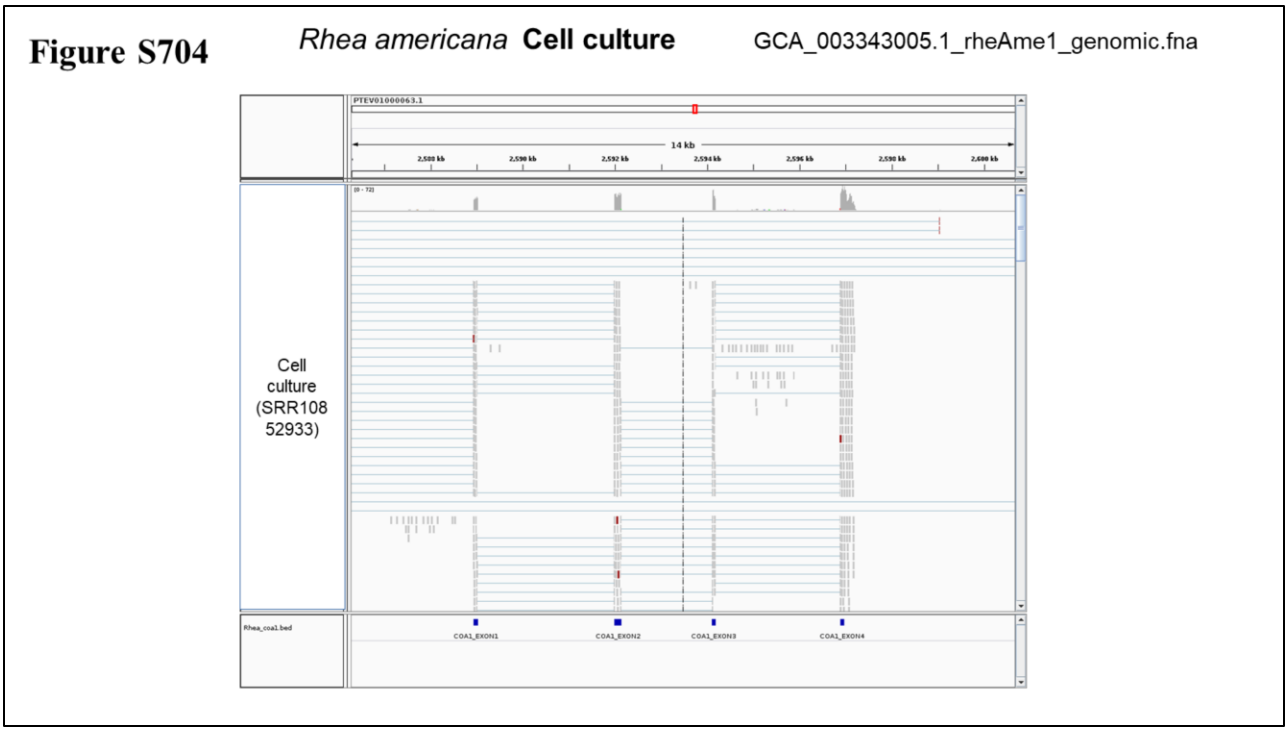

Figure S704: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in greater rhea (*Rhea americana*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from cell culture (SRR10582933) have been mapped to the GCA_003343005.1_rheAme1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

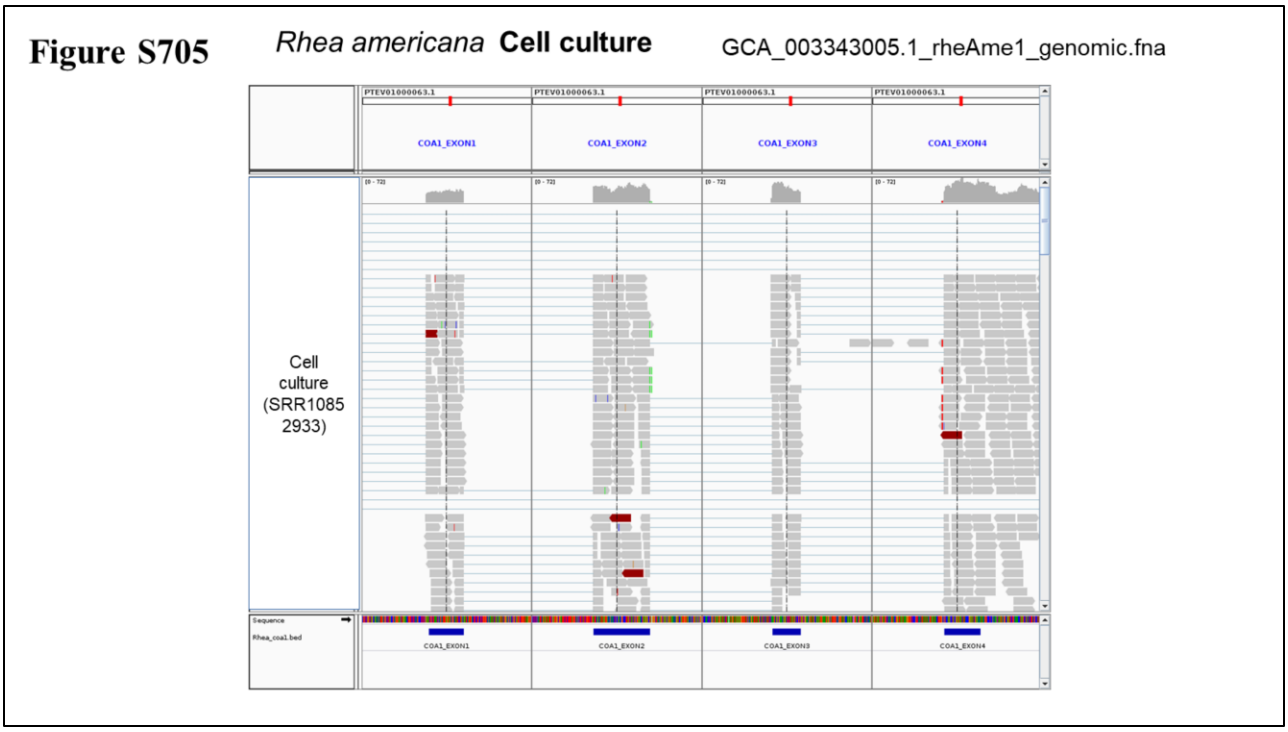

Figure S705: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S704**.

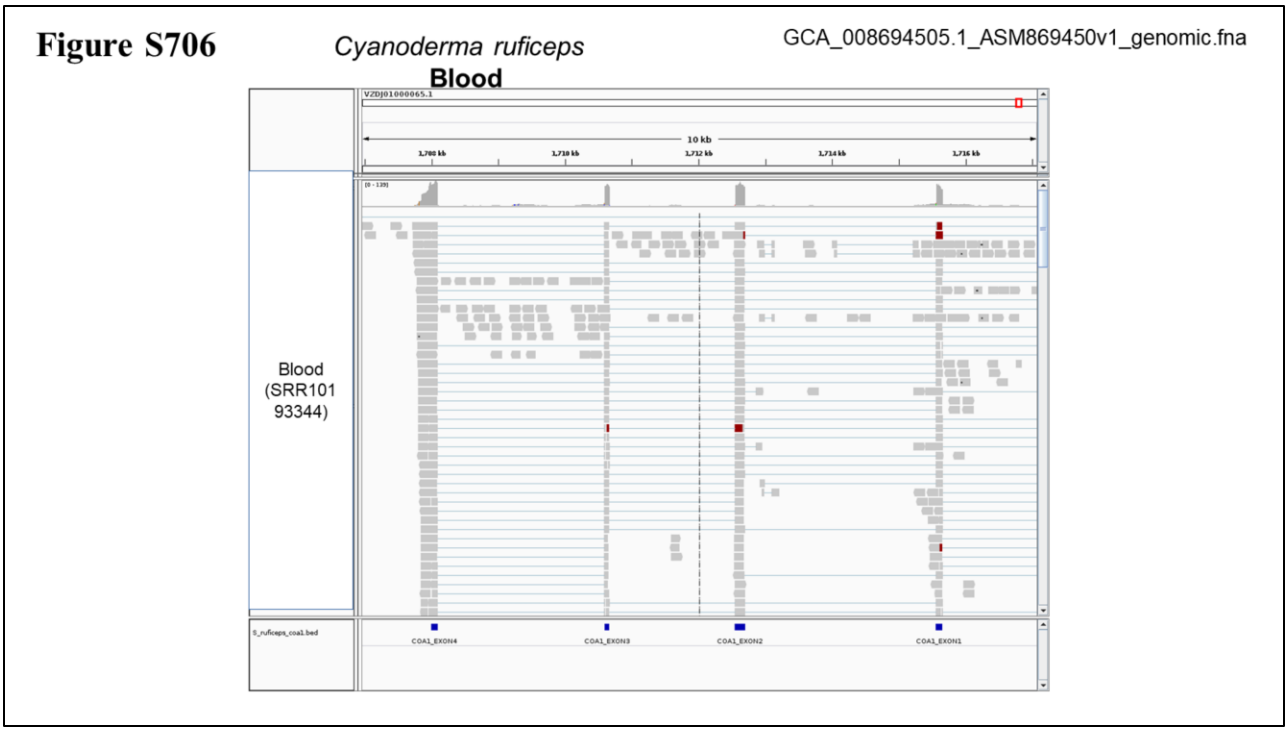

Figure S706: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in rufous-capped babbler (*Cyanoderma ruficeps*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR10193344) have been mapped to the GCA_008694505.1_ASM869450v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

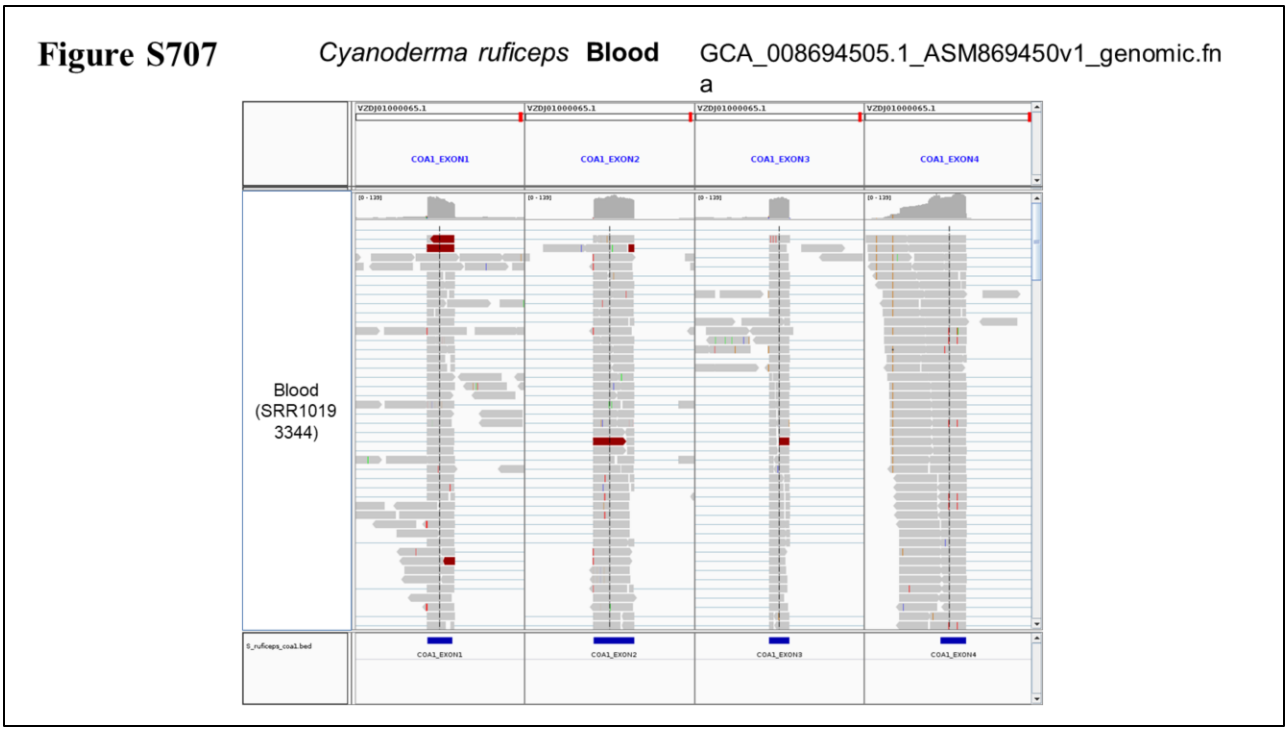

Figure S707: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S706**.

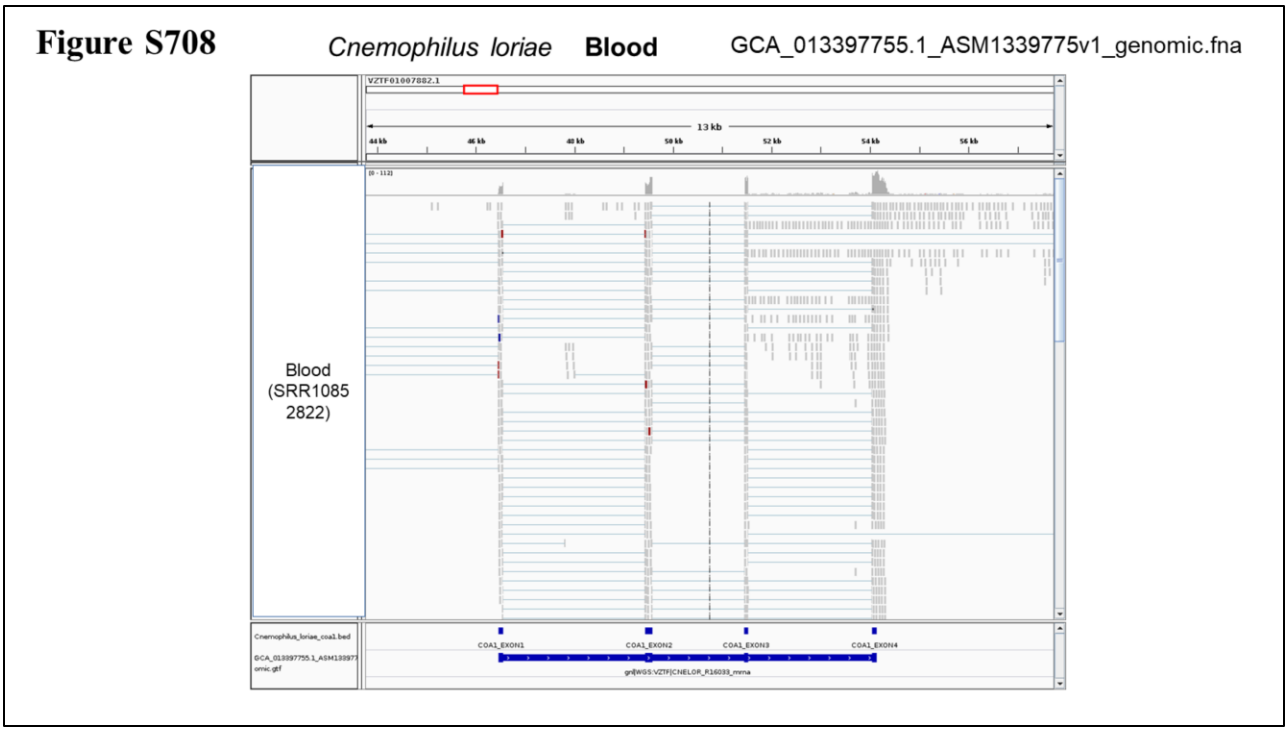

Figure S708: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Loria's satinbird (*Cnemophilus loriae*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR10852822) have been mapped to the GCA_013397755.1_ASM1339775v1_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

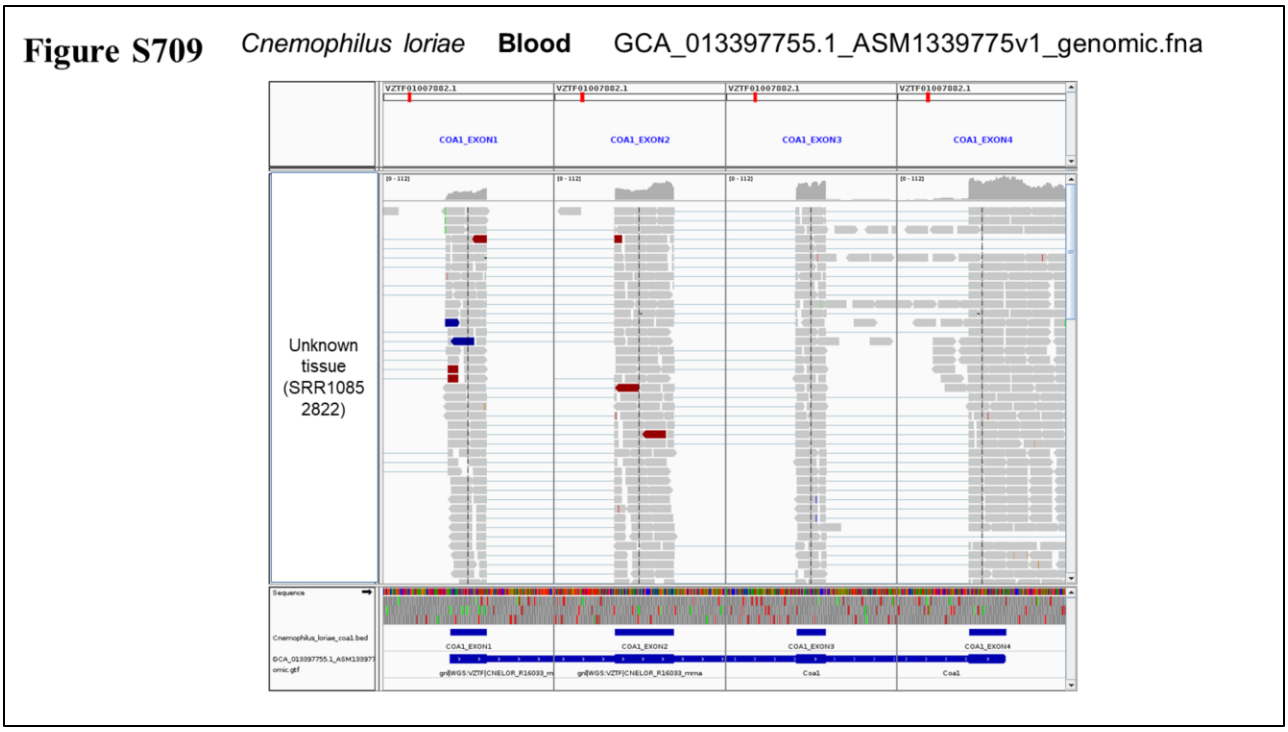

Figure S709: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S708**.

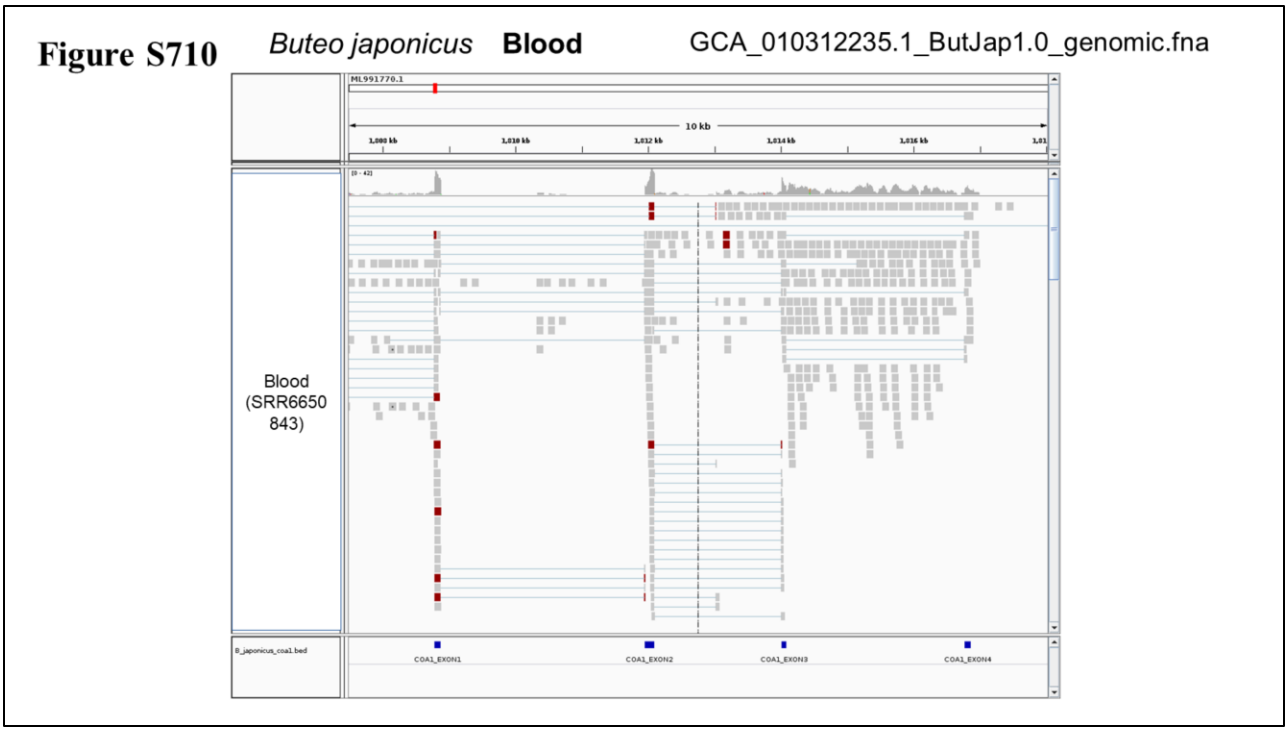

Figure S710: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in eastern buzzard (*Buteo japonicus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR6650843) have been mapped to the GCA_010312235.1_ButJap1.0_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

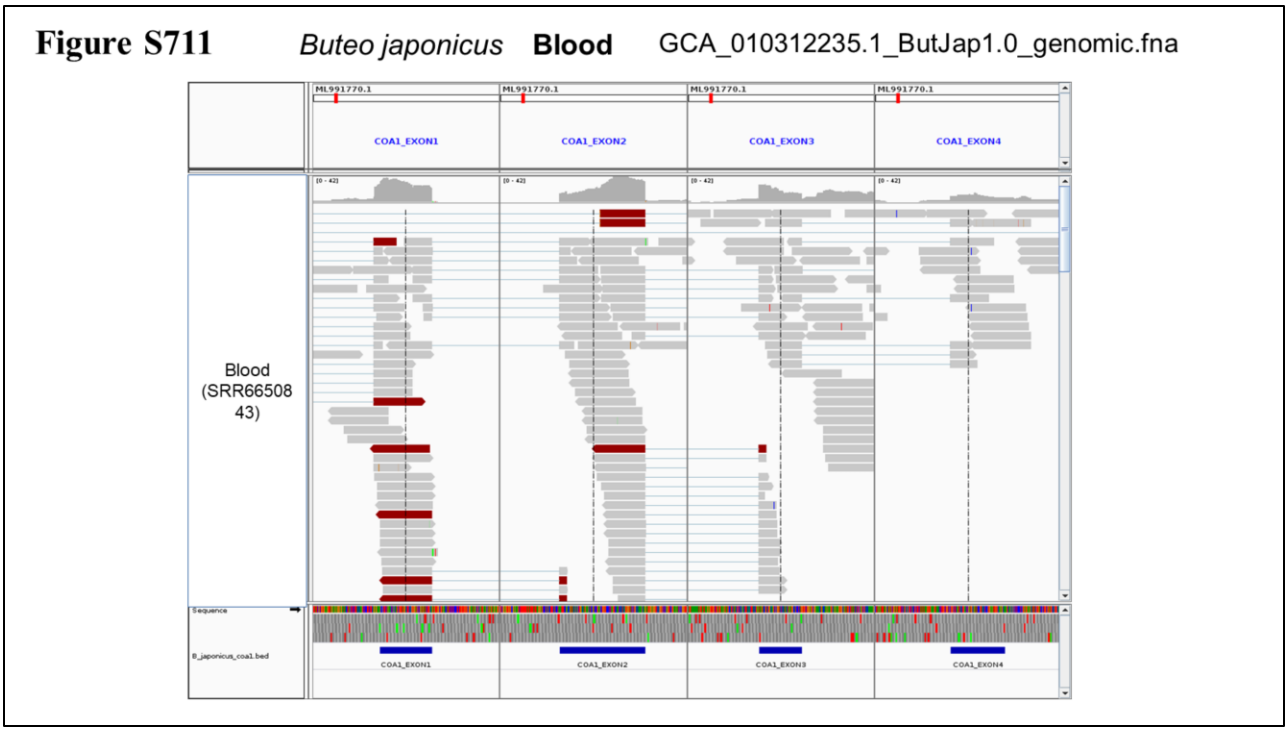

Figure S711: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S710**.

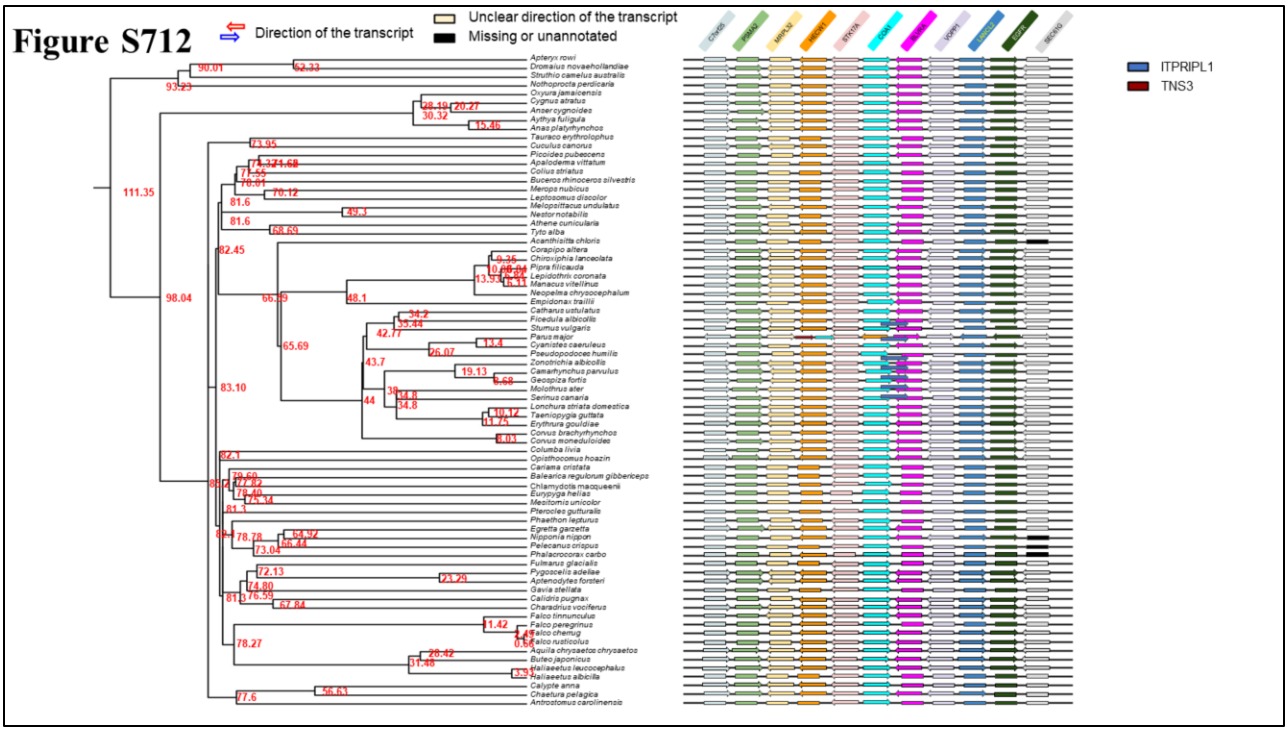

Figure S712: The birds synteny with the time calibrated phylogenetic tree from TimeTree website. The insertion of *TNS3* and rearrangement of *COA1* position occurred in *Parus major* as depicted in figure. The direction of gene transcription is depicted using red and blue arrows relative to the *COA1* gene for consistency across species. Gray boxes represent the genes which are located on short scaffolds and their orientation could not be verified.

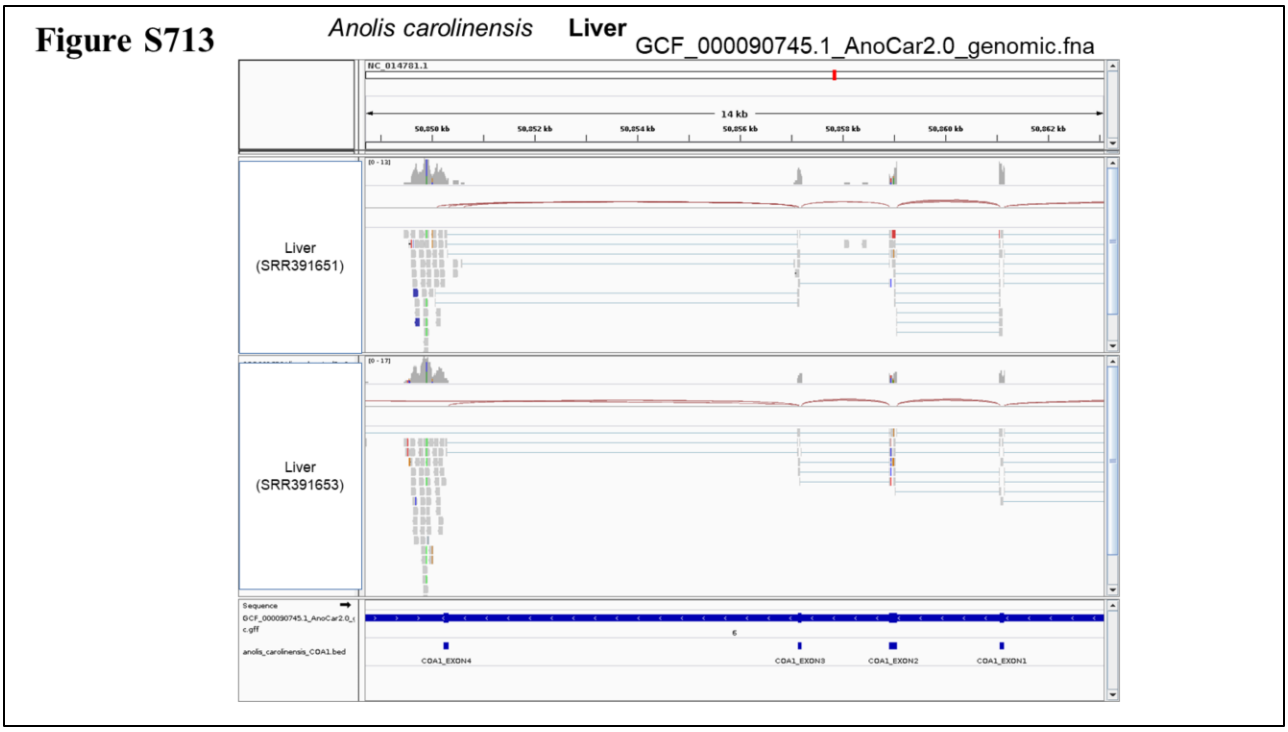

Figure S713: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in green anole (*Anolis carolinensis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR391651) and (SRR391653) have been mapped to the GCF_000090745.1_AnoCar2.0_genomic.fna genome. Locations of each of the exons are depicted as bed record in the bottom row.

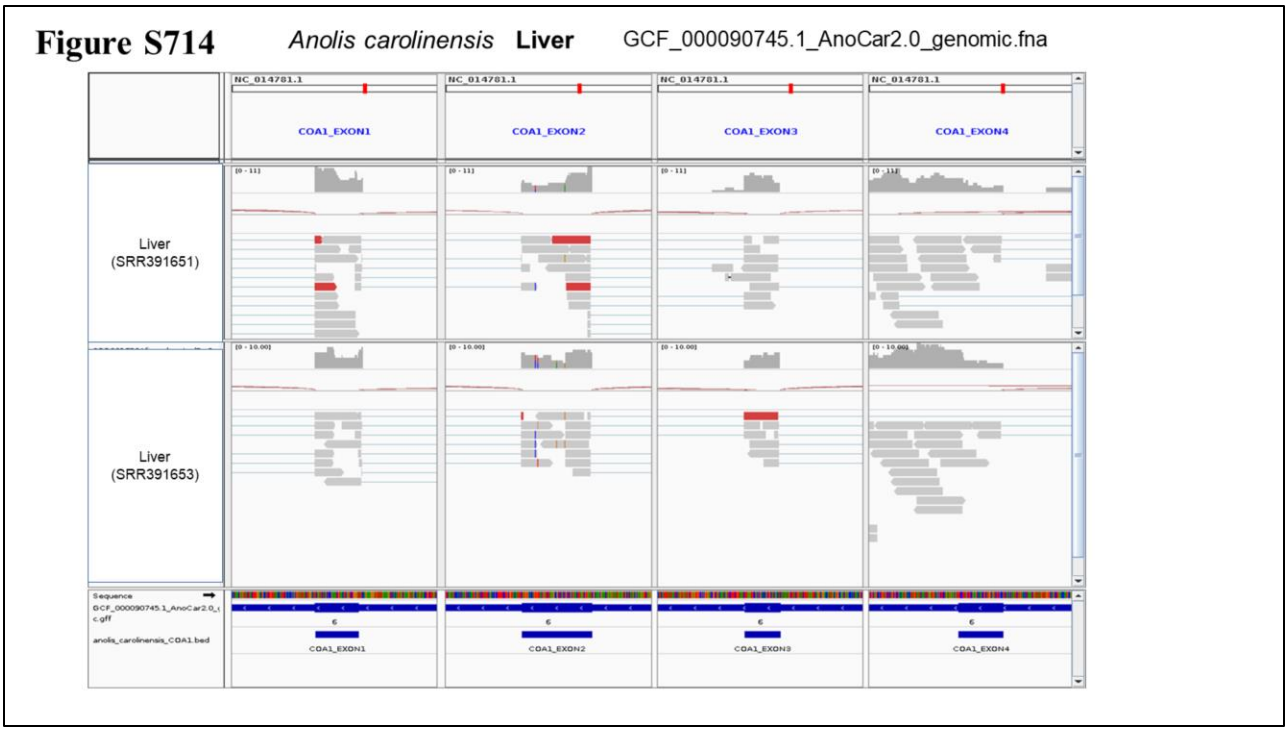

Figure S714: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S484**.

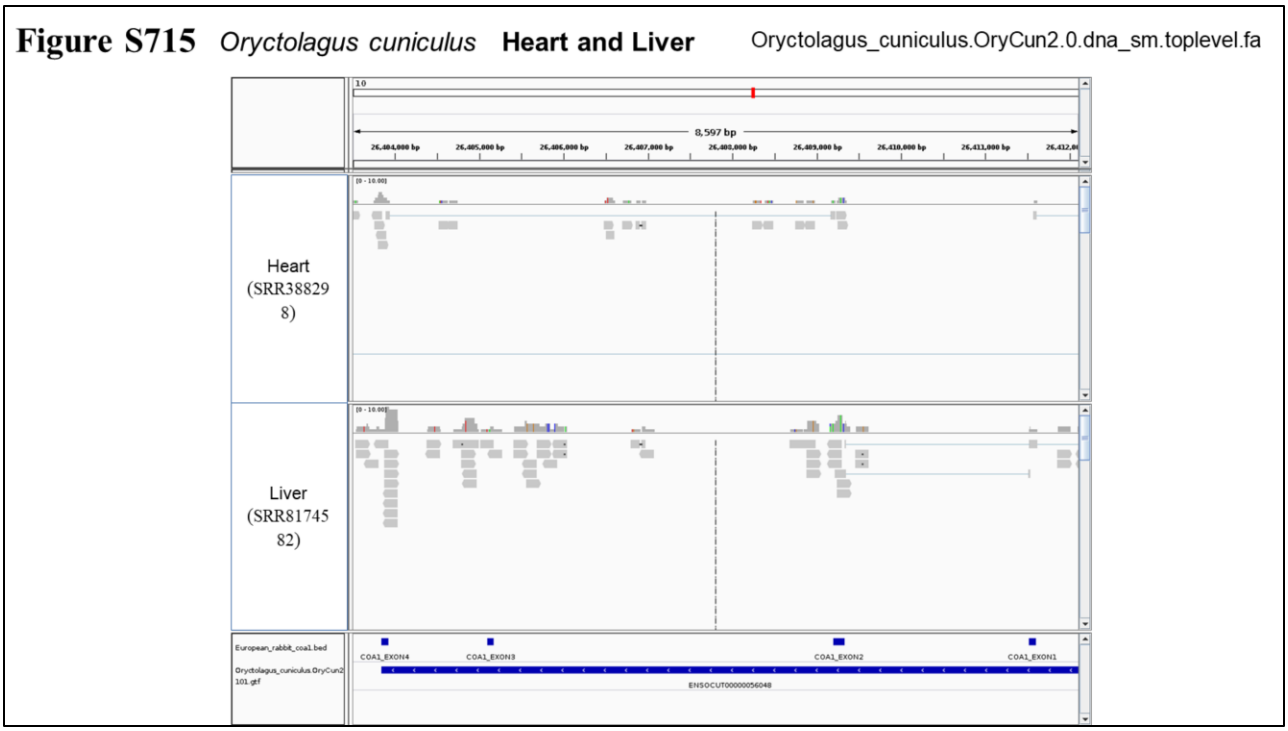

Figure S715: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in European rabbit (*Oryctolagus cuniculus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart (SRR388298) and liver (SRR8174582) have been mapped to the Oryctolagus_cuniculus.OryCun2.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

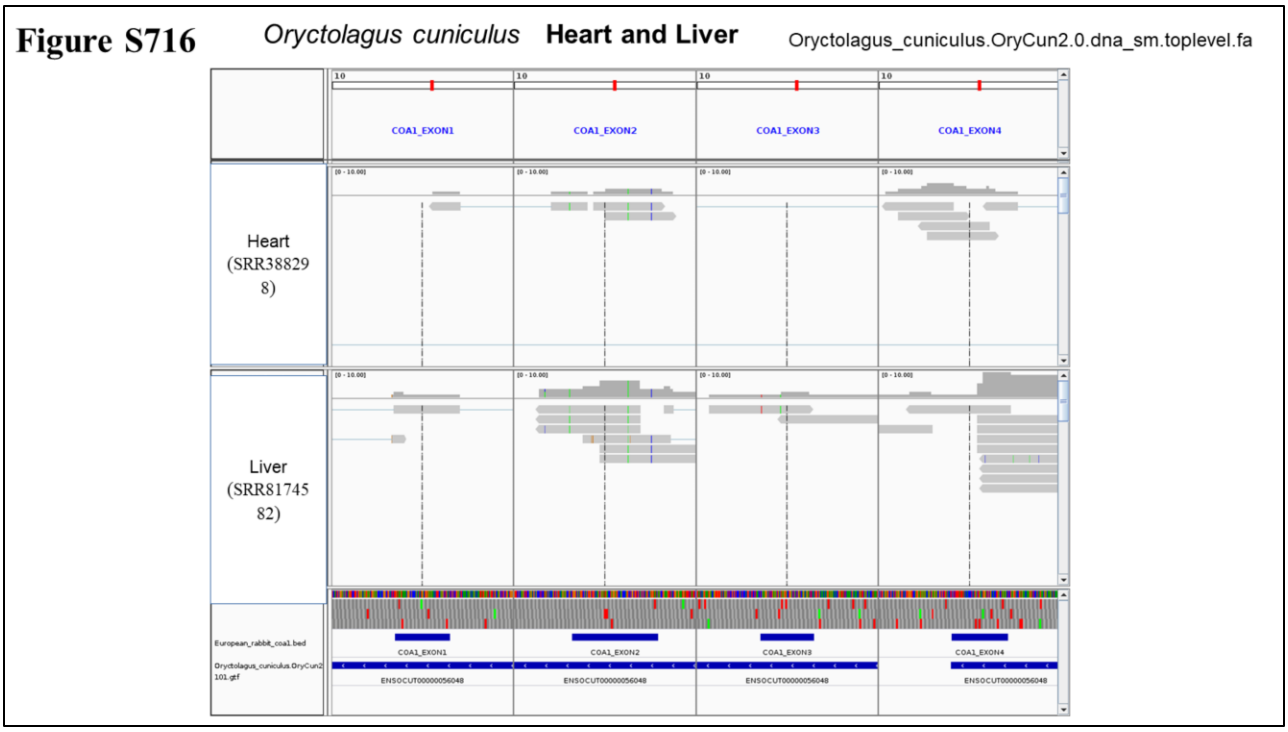

Figure S716: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S715**.

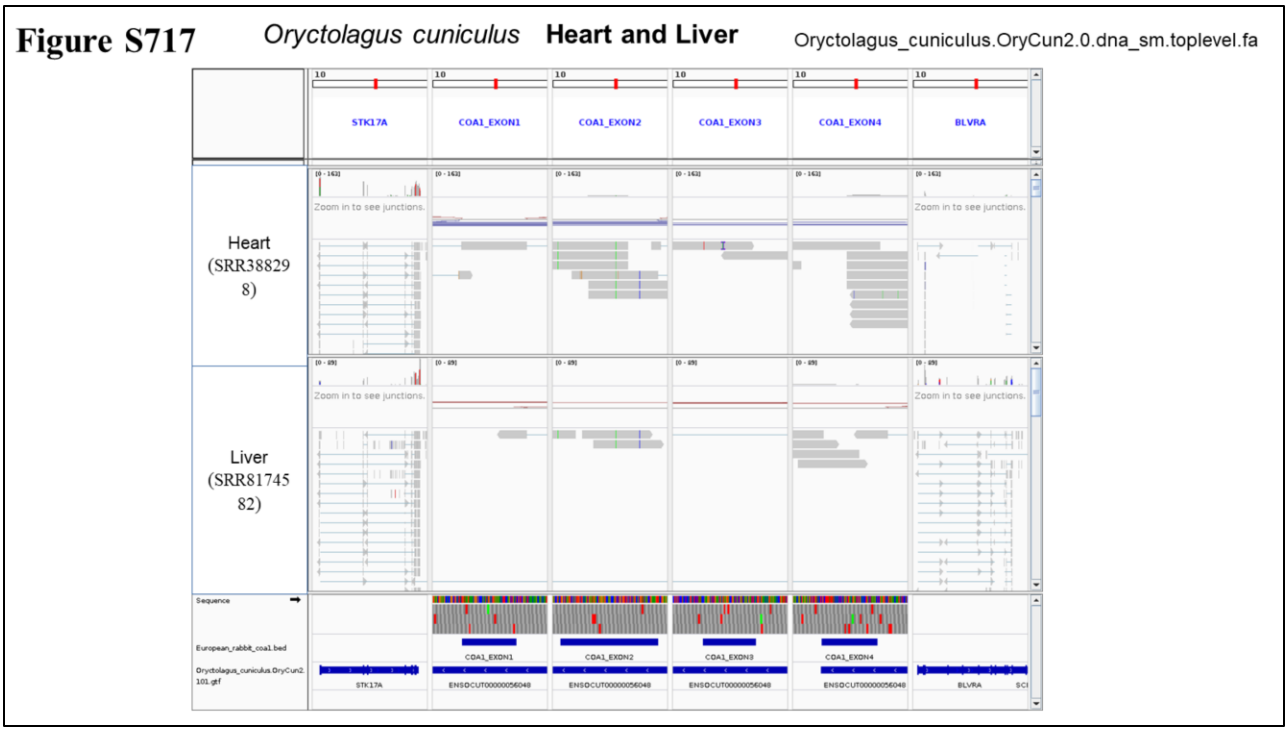

Figure S717: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in European rabbit (*Oryctolagus cuniculus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart (SRR388298) and liver (SRR8174582) have been mapped to the Oryctolagus_cuniculus.OryCun2.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S718: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Royle's pika (*Ochotona roylei*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR5428001 and SRR5427990) have been mapped to the GCF_014633375.1_OchPri4.0_genomic.fna. Locations of each of the exons are depicted as bed record in the bottom row.

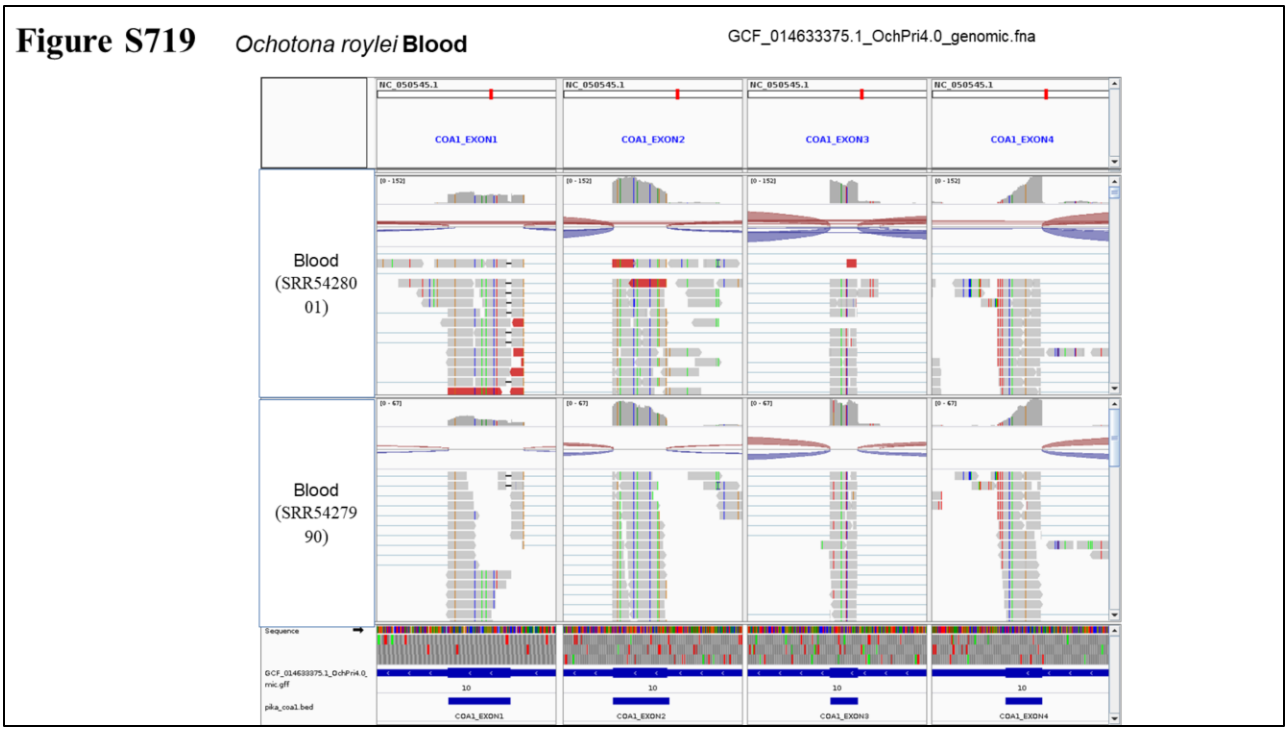

Figure S719: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exonwise in Royle's pika (*Ochotona roylei*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR5428001 and SRR5427990) have been mapped to the GCF_014633375.1_OchPri4.0_genomic.fna. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S720 (*Heterocephalus glaber*) Ovary and Spleen Heterocephalus_glaber_male.HetGla_1.0.dna_sm.toplevel.fa

Figure S720: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in naked mole-rat (*Heterocephalus glaber*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from ovary and spleen (SRR2124230 and SRR9291386) respectively have been mapped to the Heterocephalus_glaber_male.HetGla_1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S721 (*Heterocephalus glaber*) Ovary and Spleen Heterocephalus_glaber_male.HetGla_1.0.dna_sm.toplevel.fa

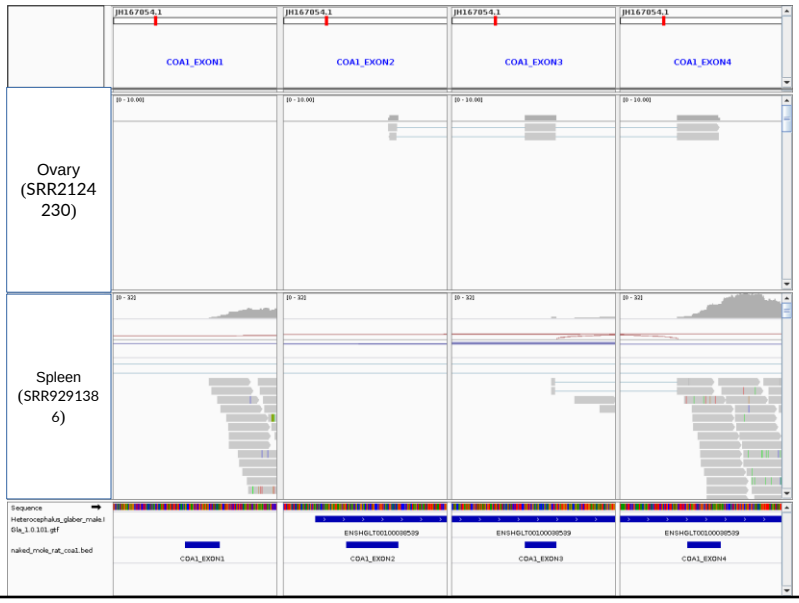

Figure S721: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S720**.

Figure S722 (*Heterocephalus glaber*) Ovary and Spleen Heterocephalus_glaber_male.HetGla_1.0.dna_sm.toplevel.fa

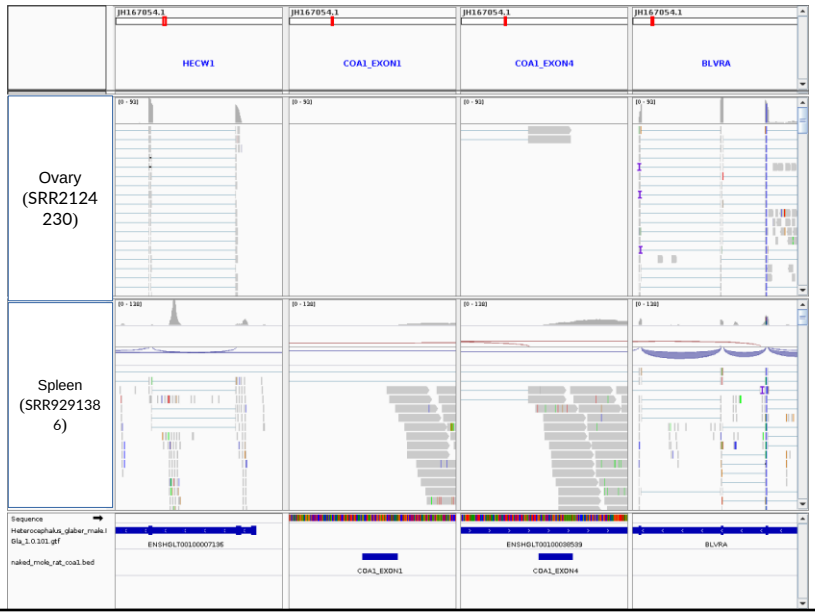

Figure S722: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exons in naked mole-rat (*Heterocephalus glaber*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from ovary and spleen (SRR2124230 and SRR9291386) respectively have been mapped to the Heterocephalus_glaber_male.HetGla_1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

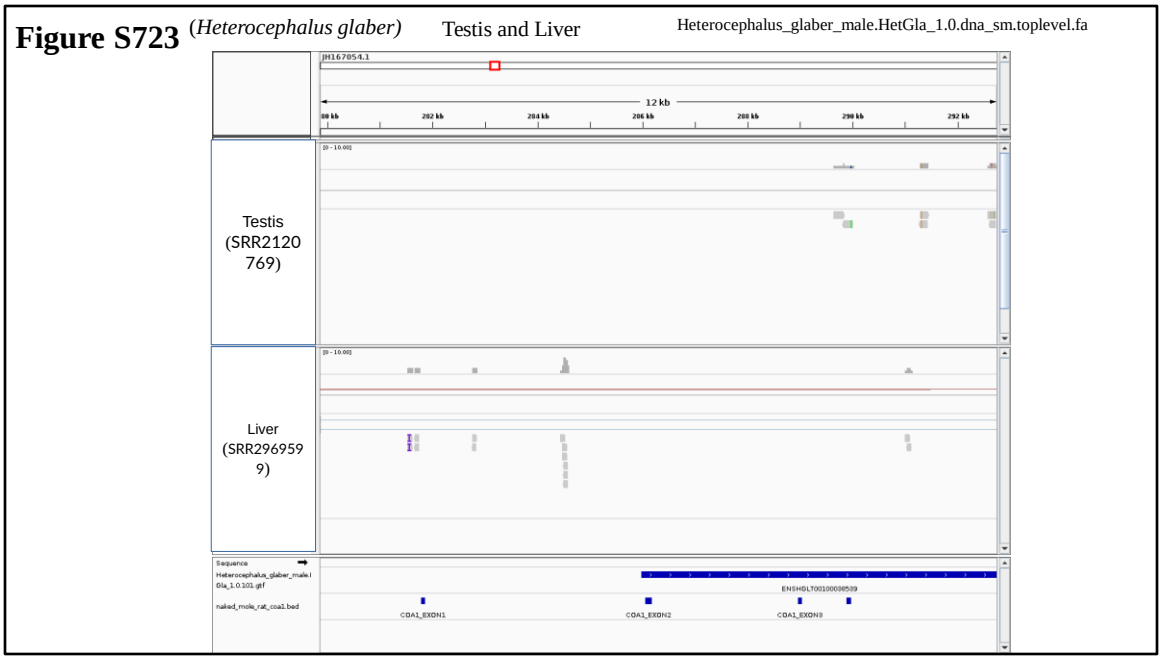

Figure S723: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in naked mole-rat (*Heterocephalus glaber*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis and liver (SRR2120769 and SRR2969599) respectively have been mapped to the Heterocephalus_glaber_male.HetGla_1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S724 (*Heterocephalus glaber*) Testis and Liver Heterocephalus_glaber_male.HetGla_1.0.dna_sm.toplevel.fa

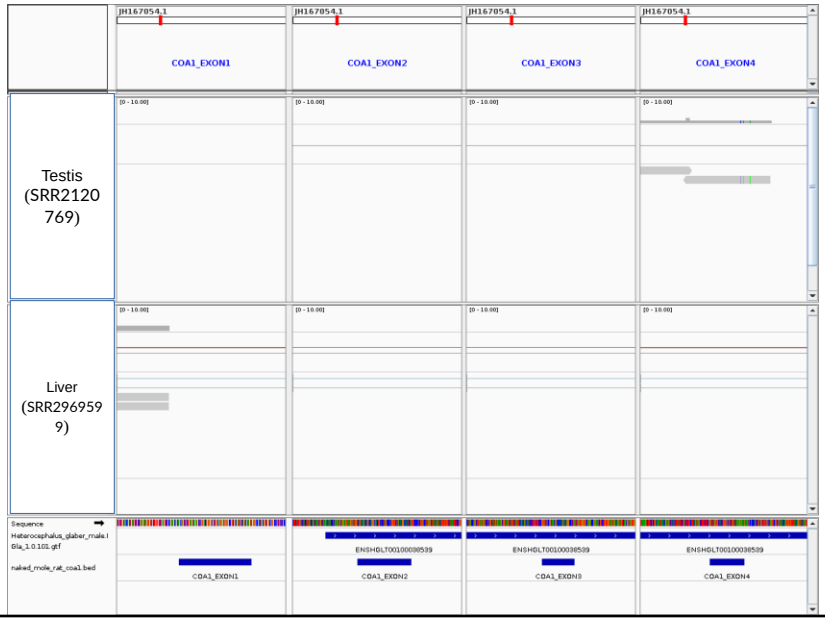

Figure S724: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S723**.

Figure S725 (*Heterocephalus glaber*) Testis and Liver Heterocephalus_glaber_male.HetGla_1.0.dna_sm.toplevel.fa

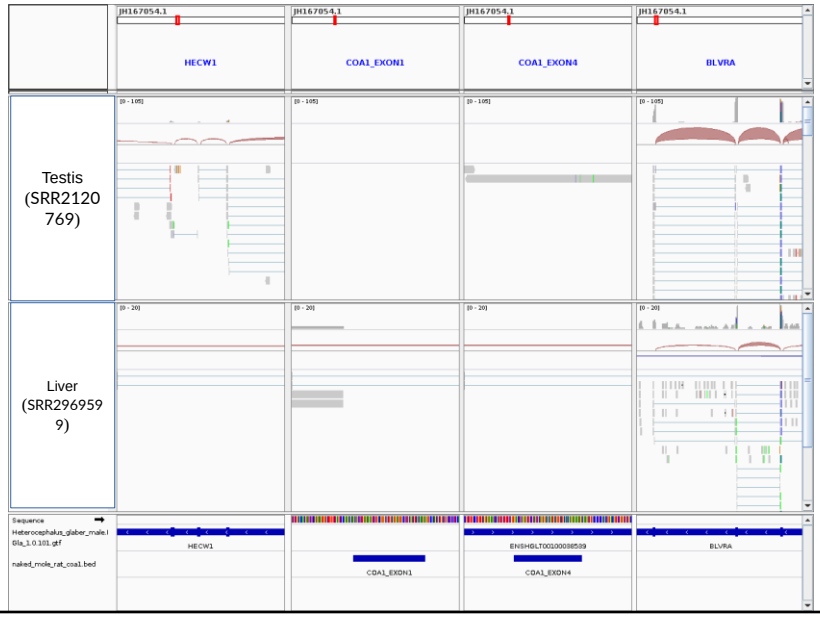

Figure S725: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exons in naked mole-rat (*Heterocephalus glaber*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis and liver (SRR2120769 and SRR2969599) respectively have been mapped to the Heterocephalus_glaber_male.HetGla_1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S726 (*Heterocephalus glaber*) Root ganglion and Spinal cord Heterocephalus_glaber_male.HetGla_1.0.dna_sm.toplevel.fa

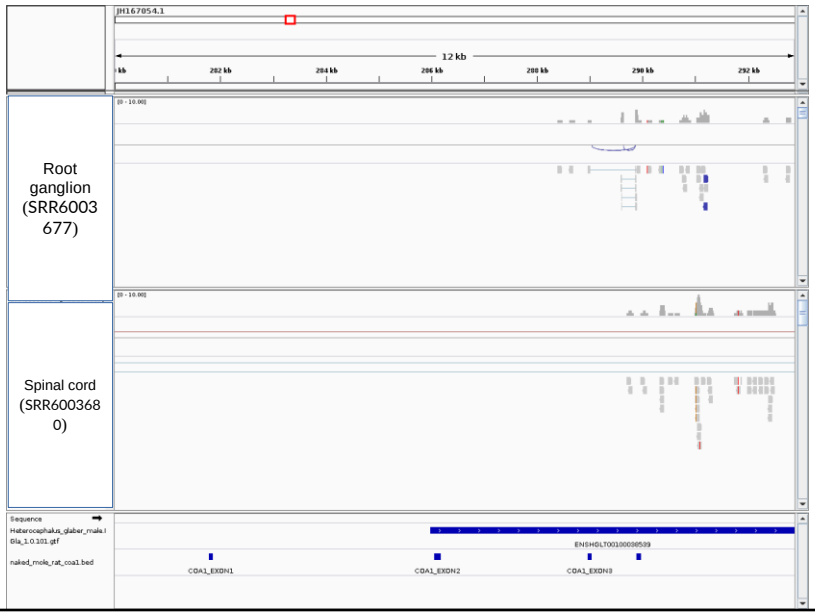

Figure S726: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in naked mole-rat (*Heterocephalus glaber*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from root ganglion and spinal cord (SRR6003677 and SRR6003680) respectively have been mapped to the Heterocephalus_glaber_male.HetGla_1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S727 (*Heterocephalus glaber*) Root ganglion and Spinal cord Heterocephalus_glaber_male.HetGla_1.0.dna_sm.toplevel.fa

Figure S727: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S726**.

Figure S728 (*Heterocephalus glaber*) Root ganglion and Spinal cord Heterocephalus_glaber_male.HetGla_1.0.dna_sm.toplevel.fa

Figure S728: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exons in naked mole-rat (*Heterocephalus glaber*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from root ganglion and spinal cord (SRR6003677 and SRR6003680) respectively have been mapped to the Heterocephalus_glaber_male.HetGla_1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

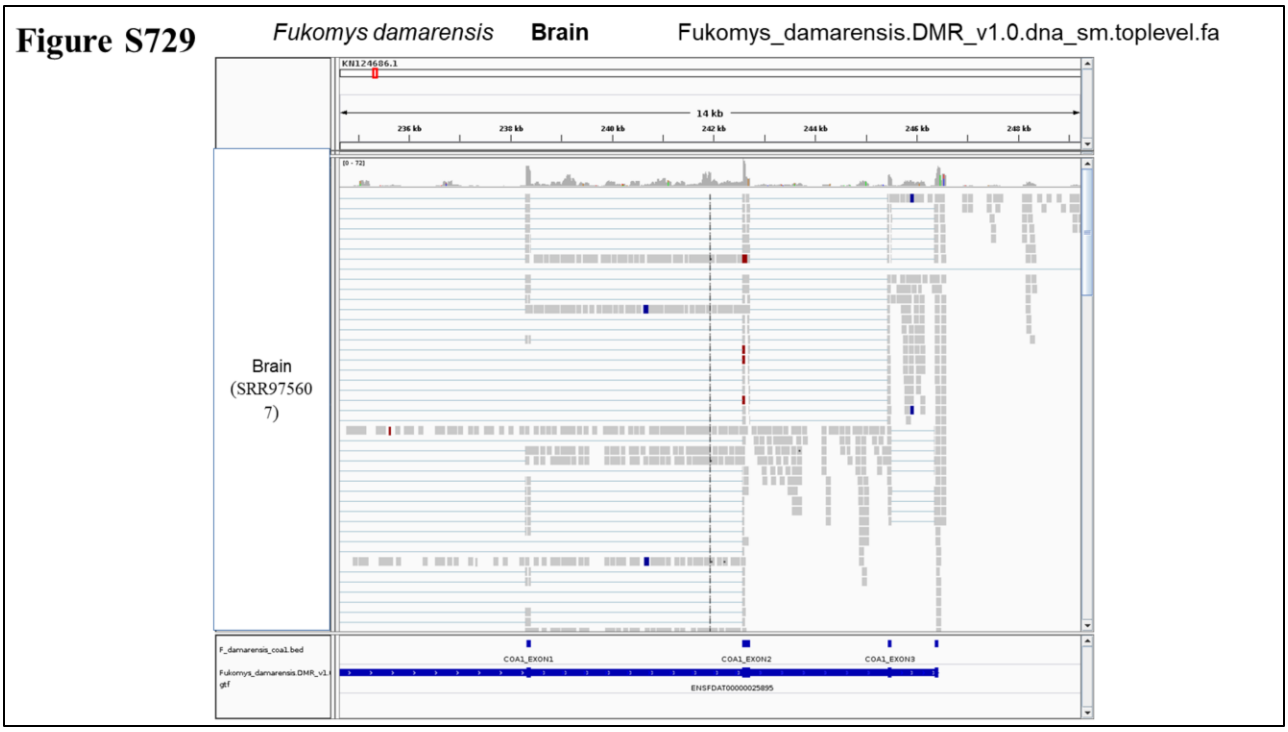

Figure S729: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in damara mole-rat (*Fukomys damarensis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (SRR975607) have been mapped to the Fukomys_damarensis.DMR_v1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

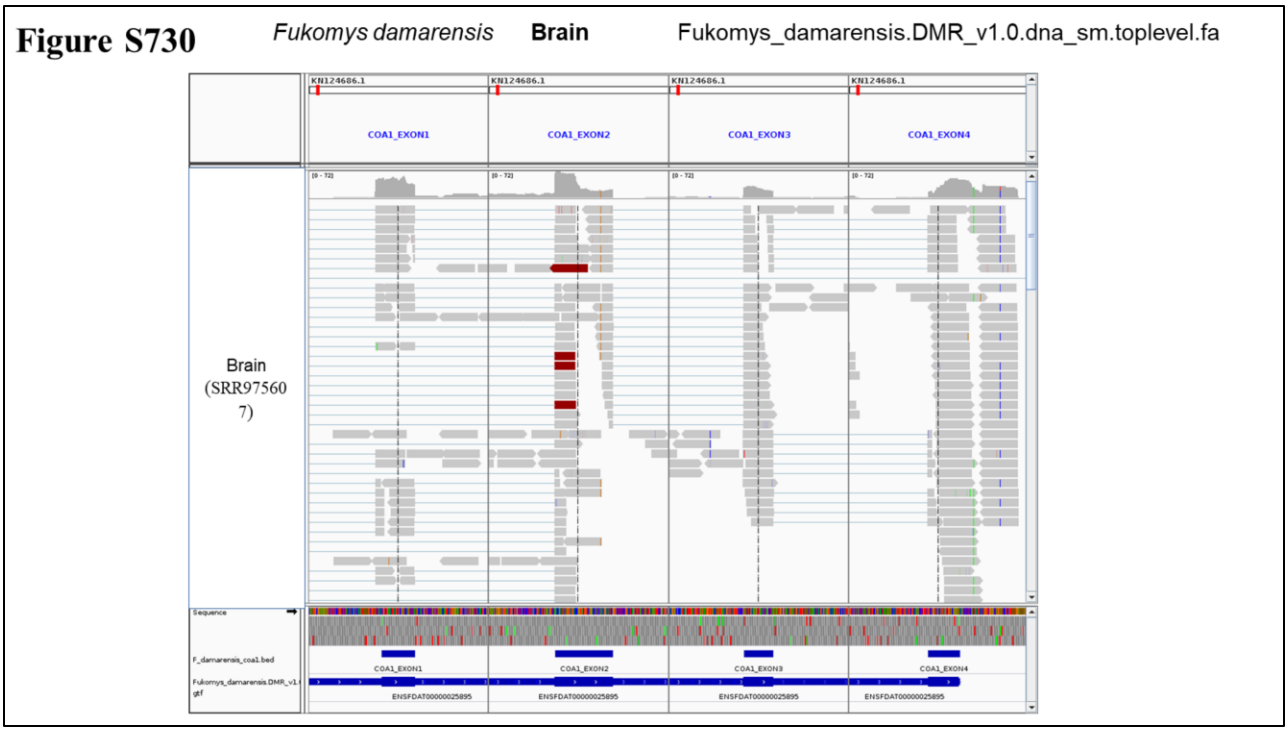

Figure S730: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S729**.

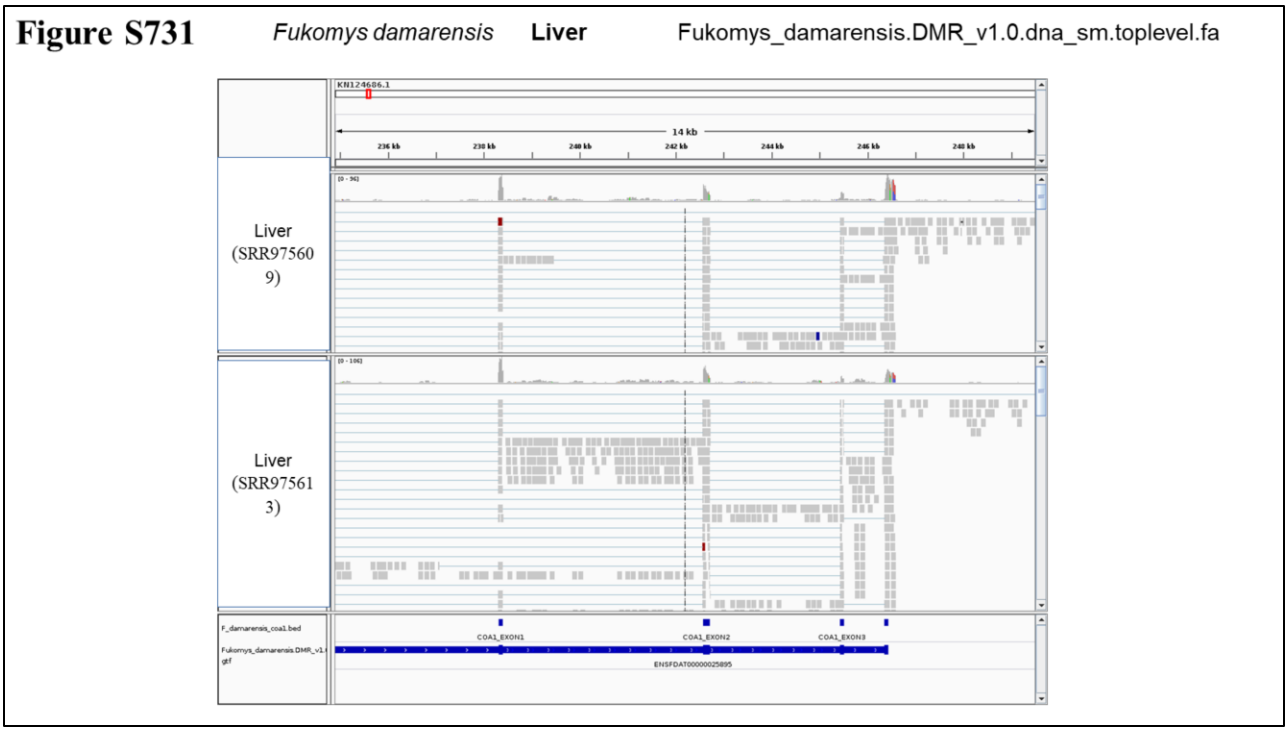

Figure S731: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in damara mole-rat (*Fukomys damarensis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR975609 and SRR975613)have been mapped to the Fukomys_damarensis.DMR_v1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

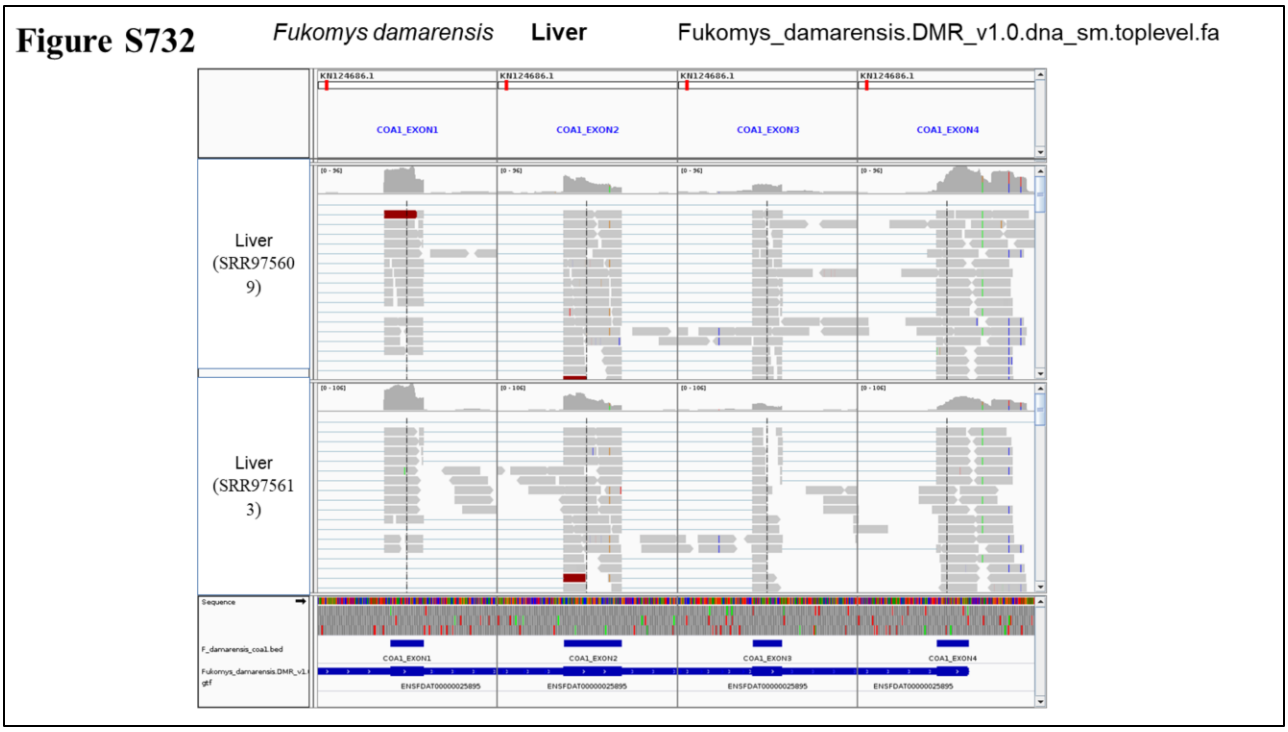

Figure S732: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S731**.

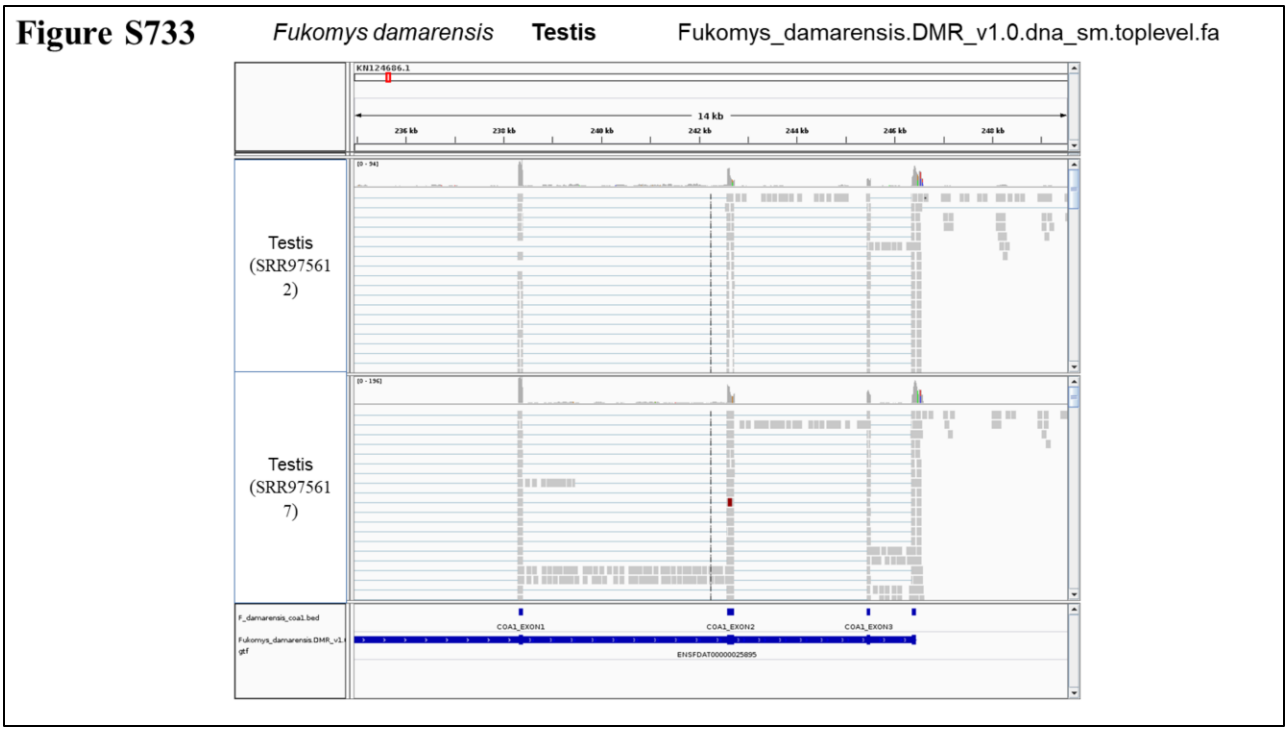

Figure S733: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in damara mole-rat (*Fukomys damarensis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis (SRR975612 and SRR975617) have been mapped to the Fukomys_damarensis.DMR_v1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S734

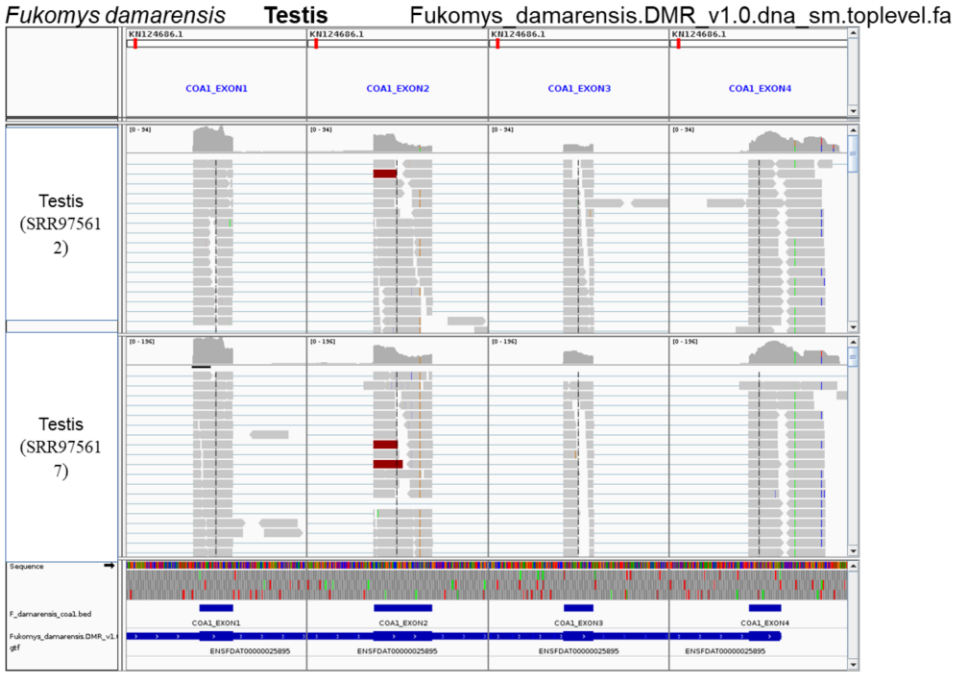

Figure S734: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S733**.

Figure S735: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Brazilian guinea pig (*Cavia aperea*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (ERR266353 and ERR162222)have been mapped to the Cavia_aperea.CavAp1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

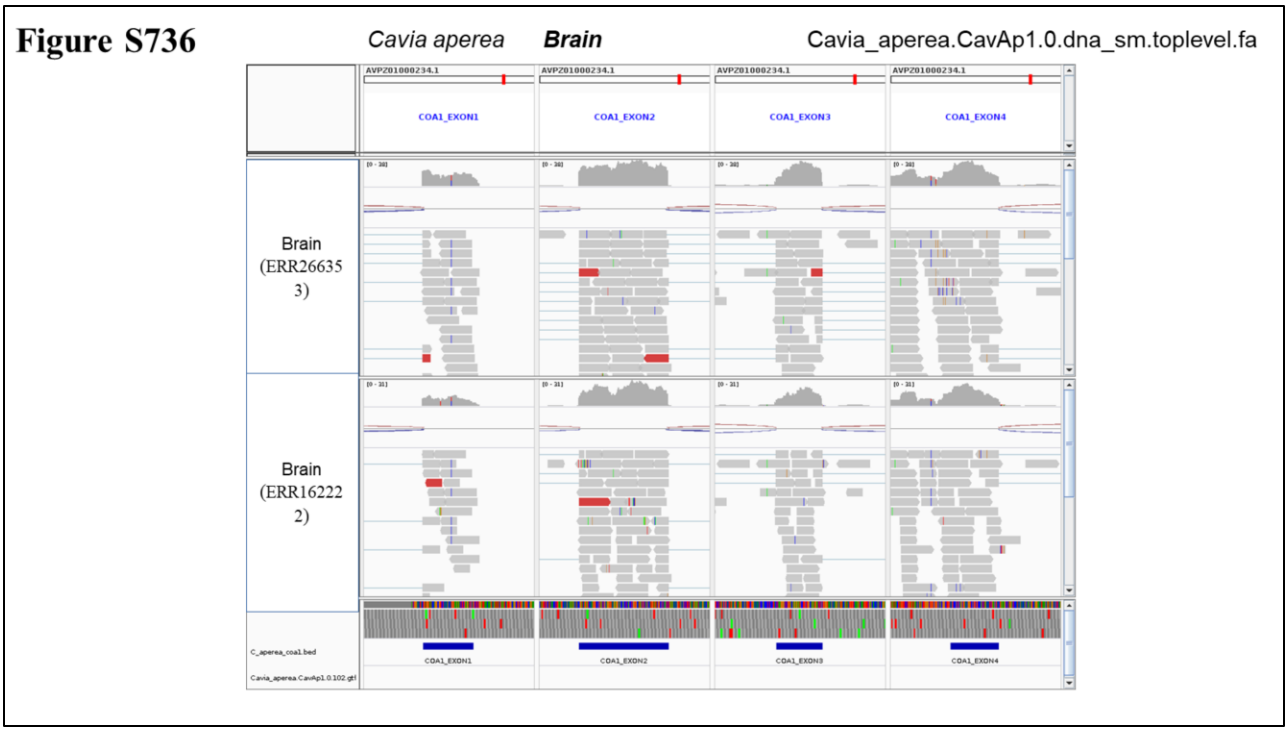

Figure S736: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S735**.

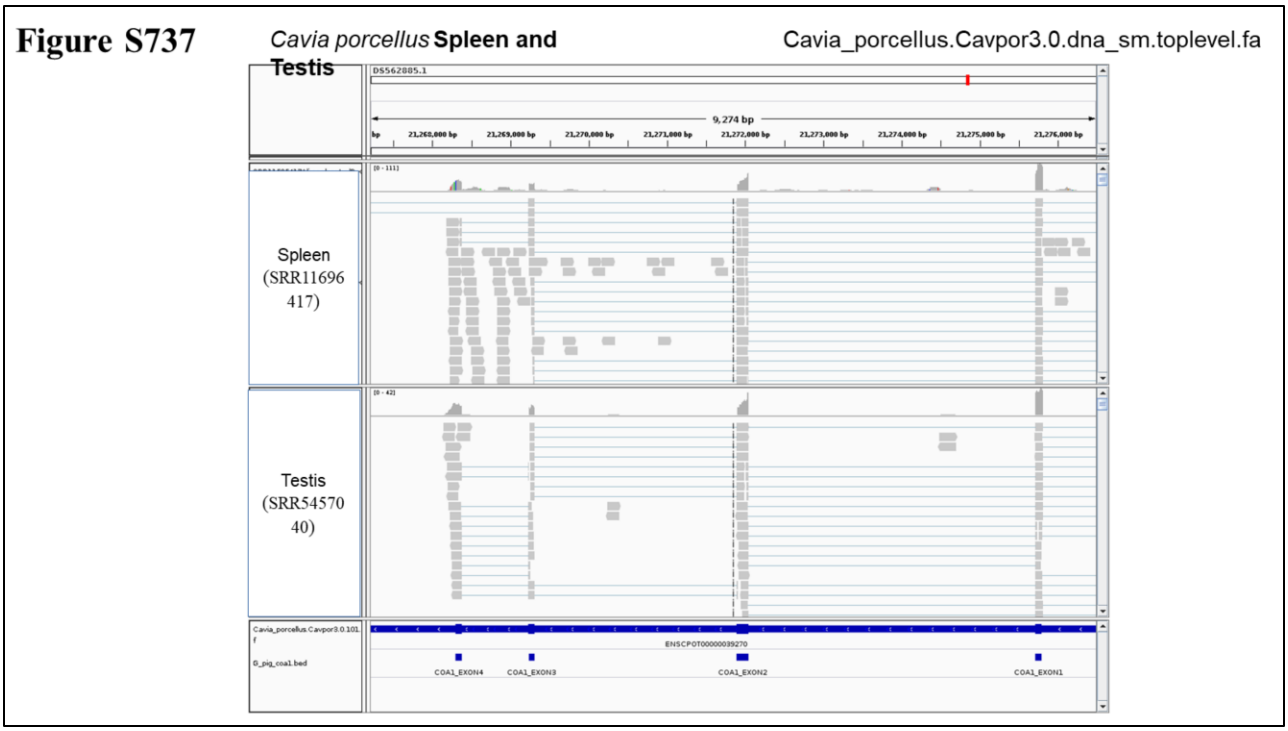

Figure S737: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in domestic guinea pig (*Cavia porcellus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR11696417) and testis (SRR5457040) have been mapped to the Cavia_porcellus.Cavpor3.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

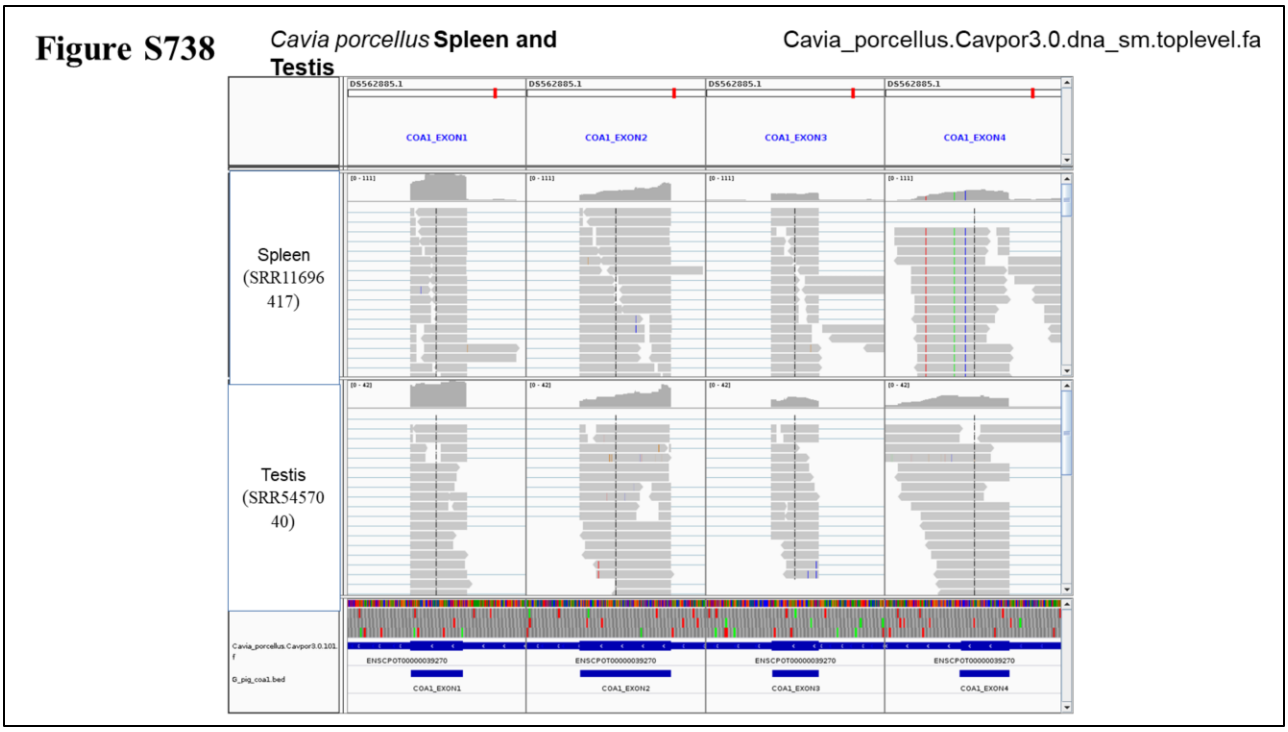

Figure S738: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S737**.

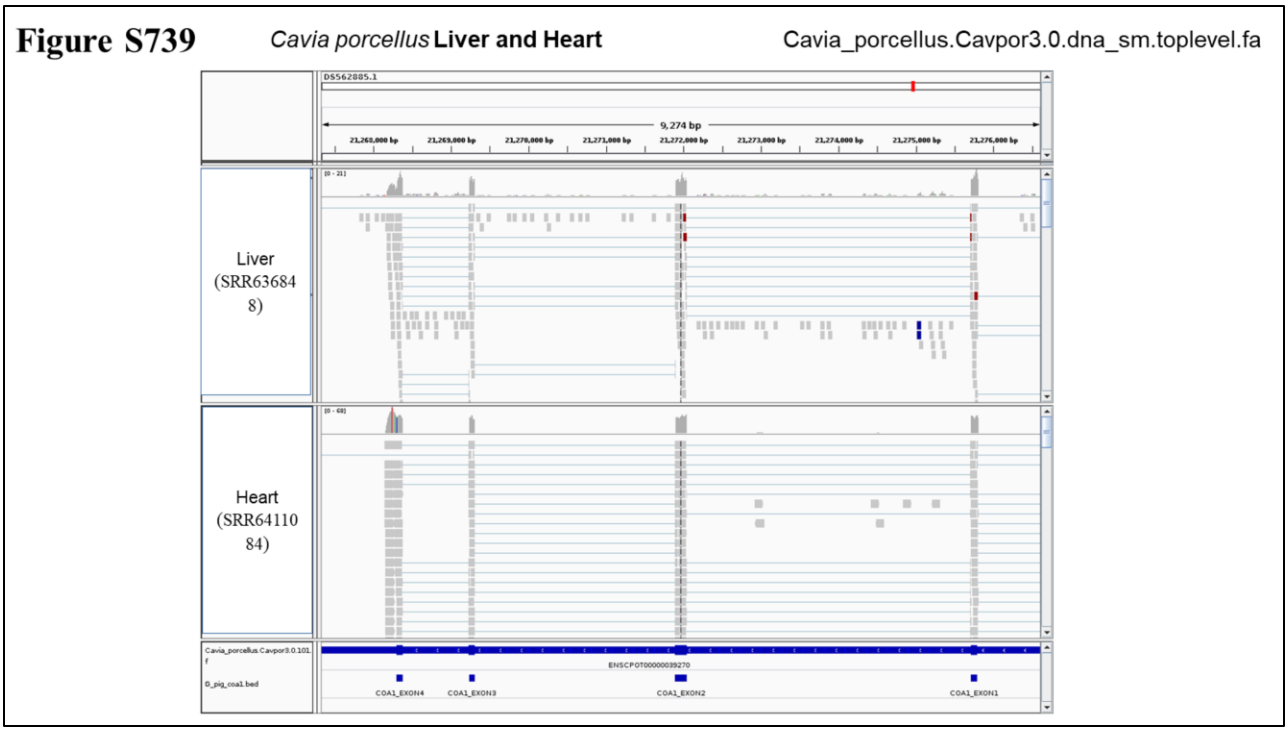

Figure S739: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in domestic guinea pig (*Cavia porcellus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR636848) and heart (SRR6411084) have been mapped to the Cavia_porcellus.Cavpor3.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

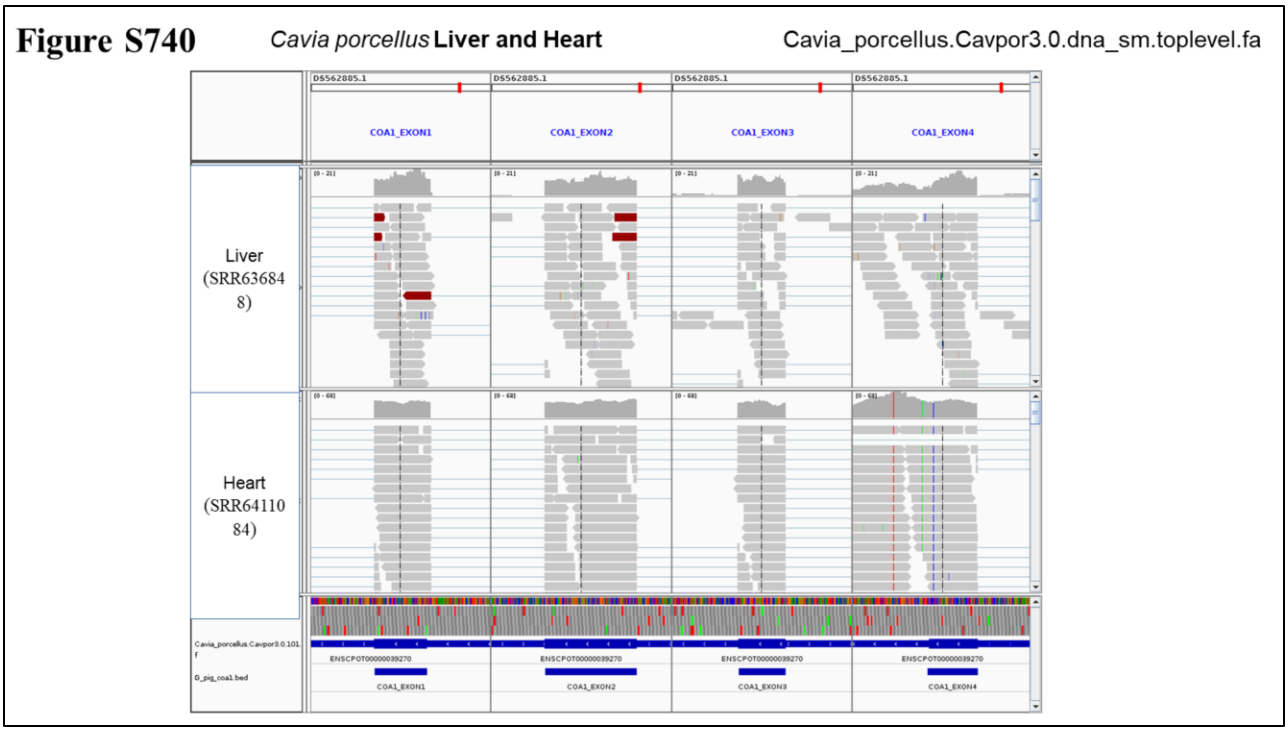

Figure S740: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S739**.

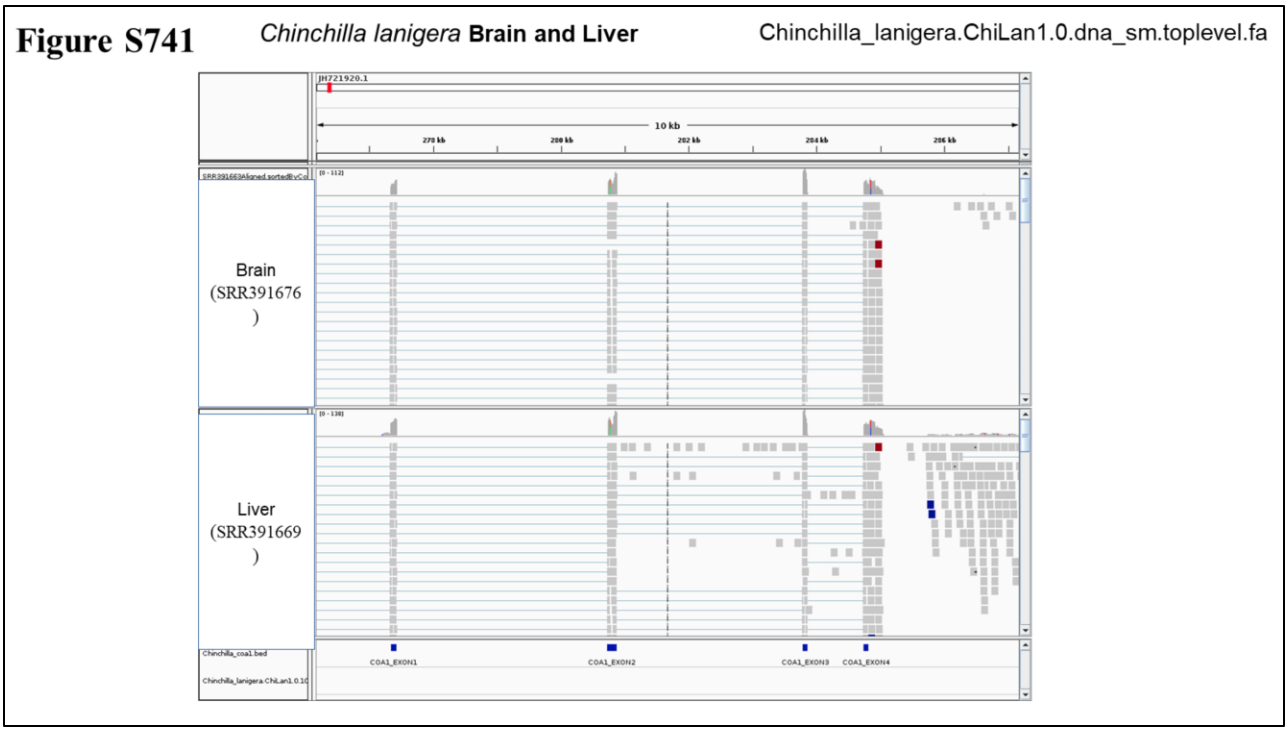

Figure S741: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in long tailed chinchilla (*Chinchilla lanigera*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (SRR391676) and liver (SRR391669) have been mapped to the Chinchilla_lanigera.ChiLan1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

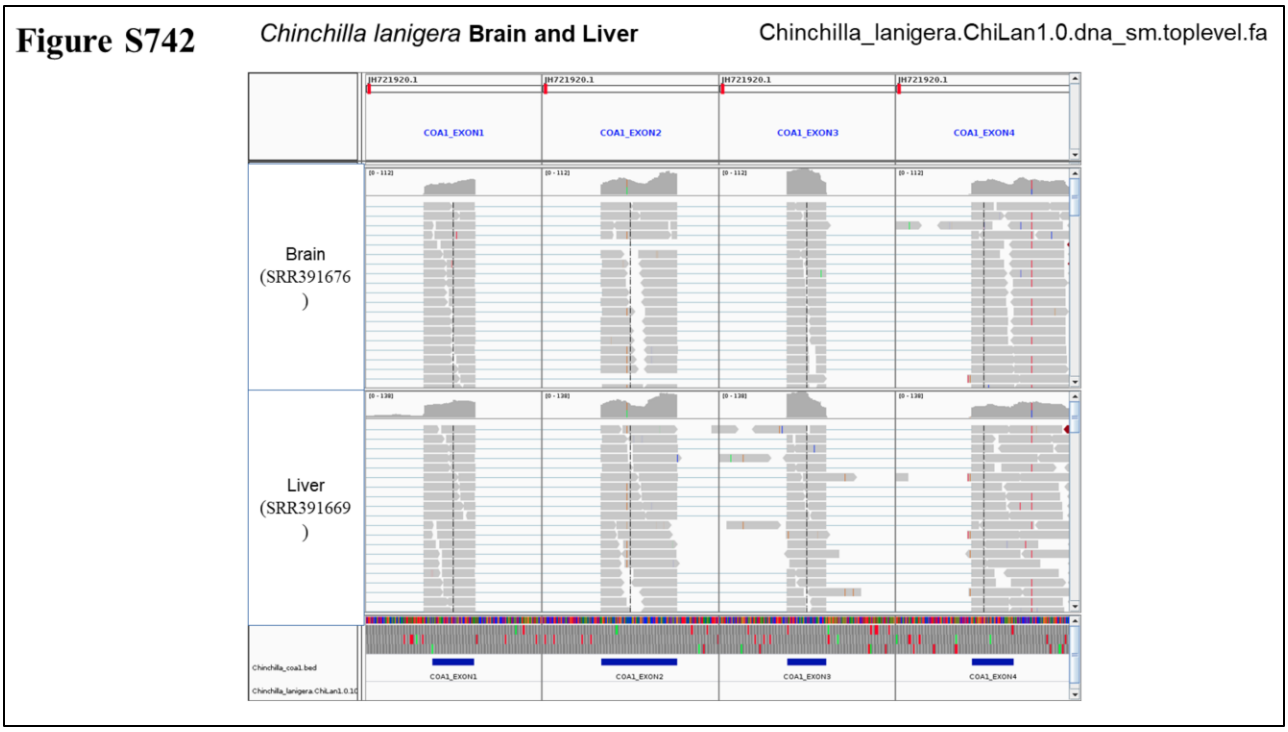

Figure S742: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S741**.

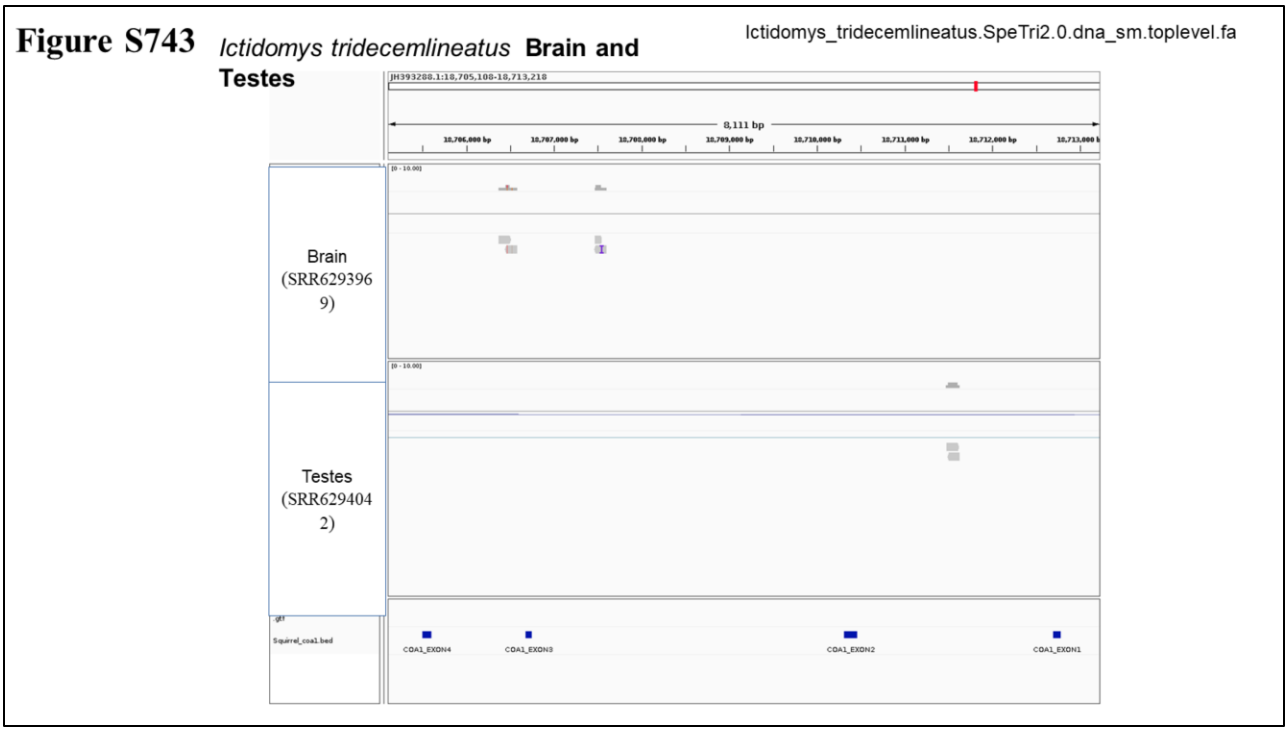

Figure S743: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in thirteen-lined ground squirrel (*Ictidomys tridecemlineatus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain and testes (SRR6293969 and SRR6294042) have been mapped to the Ictidomys_tridecemlineatus.SpeTri2.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

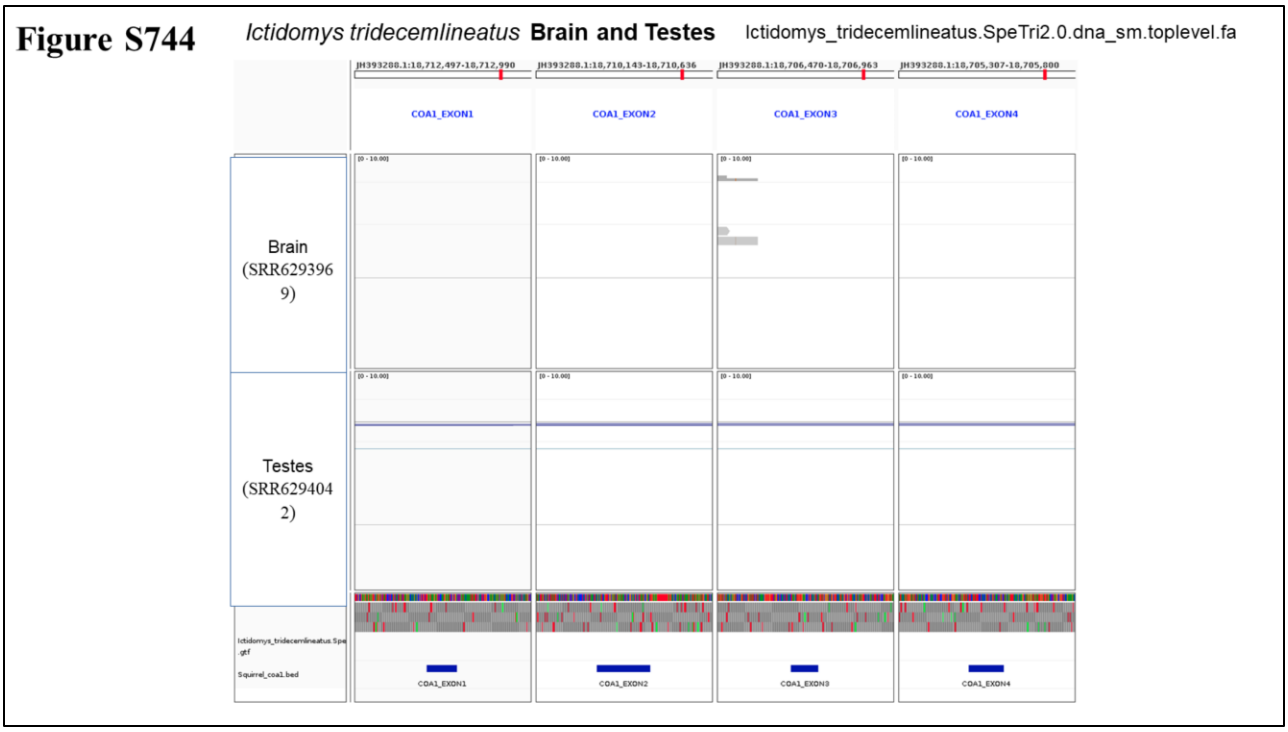

Figure S744: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S743**.

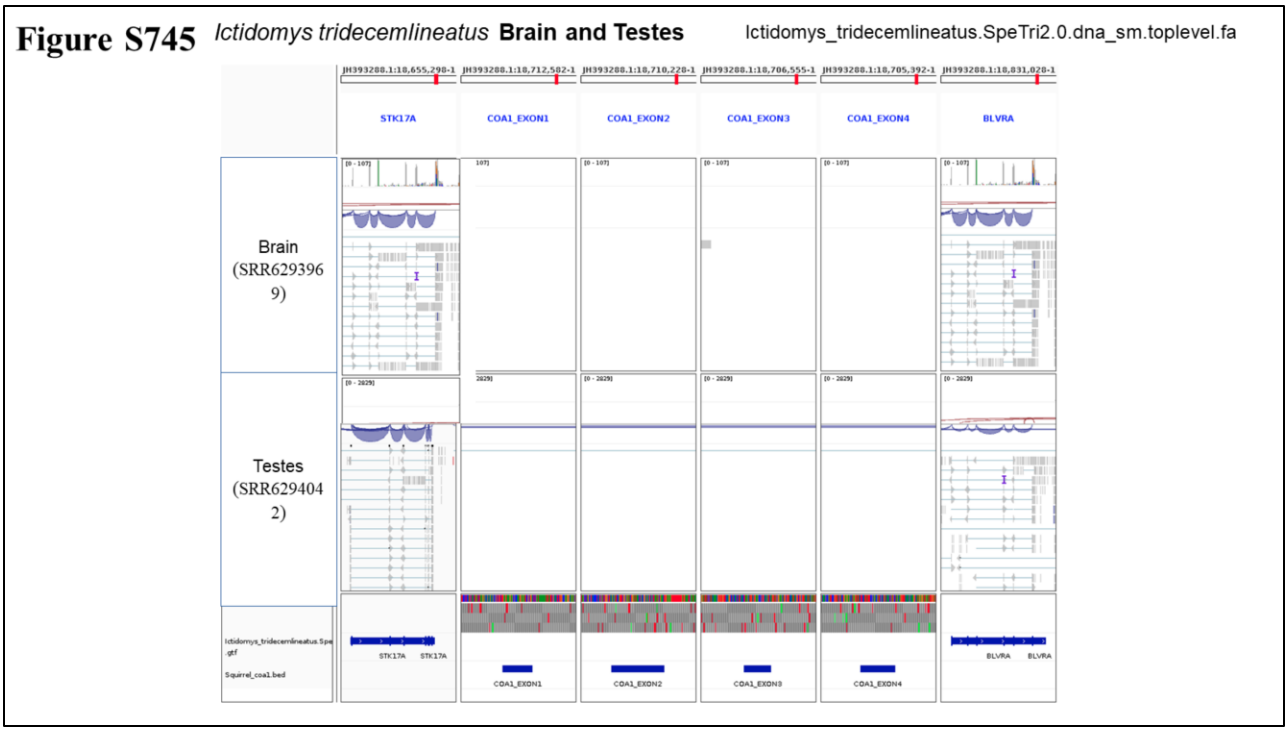

Figure S745: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in thirteen-lined ground squirrel (*Ictidomys tridecemlineatus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain and testes (SRR6293969 and SRR6294042) have been mapped to the Ictidomys_tridecemlineatus.SpeTri2.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

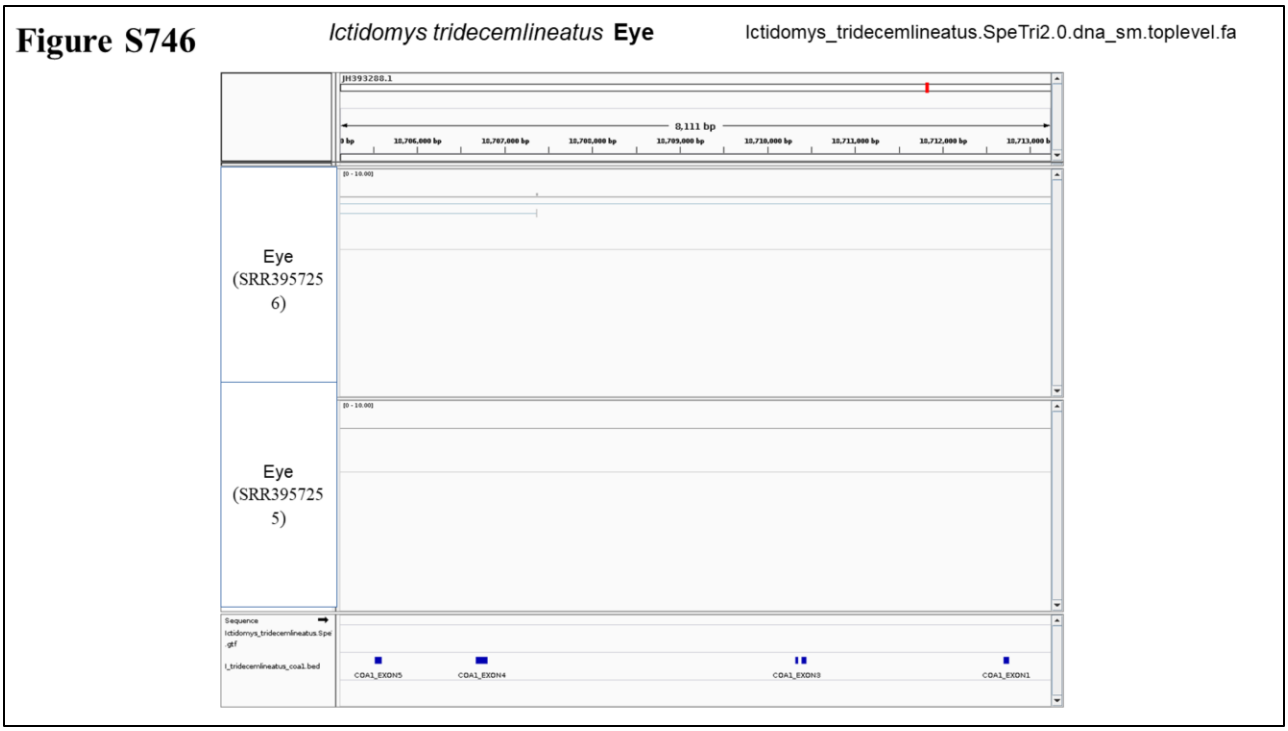

Figure S746: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in thirteen-lined ground squirrel(*Ictidomys tridecemlineatus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from eye (SRR3957255 and SRR3957256) have been mapped to the Ictidomys_tridecemlineatus.SpeTri2.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

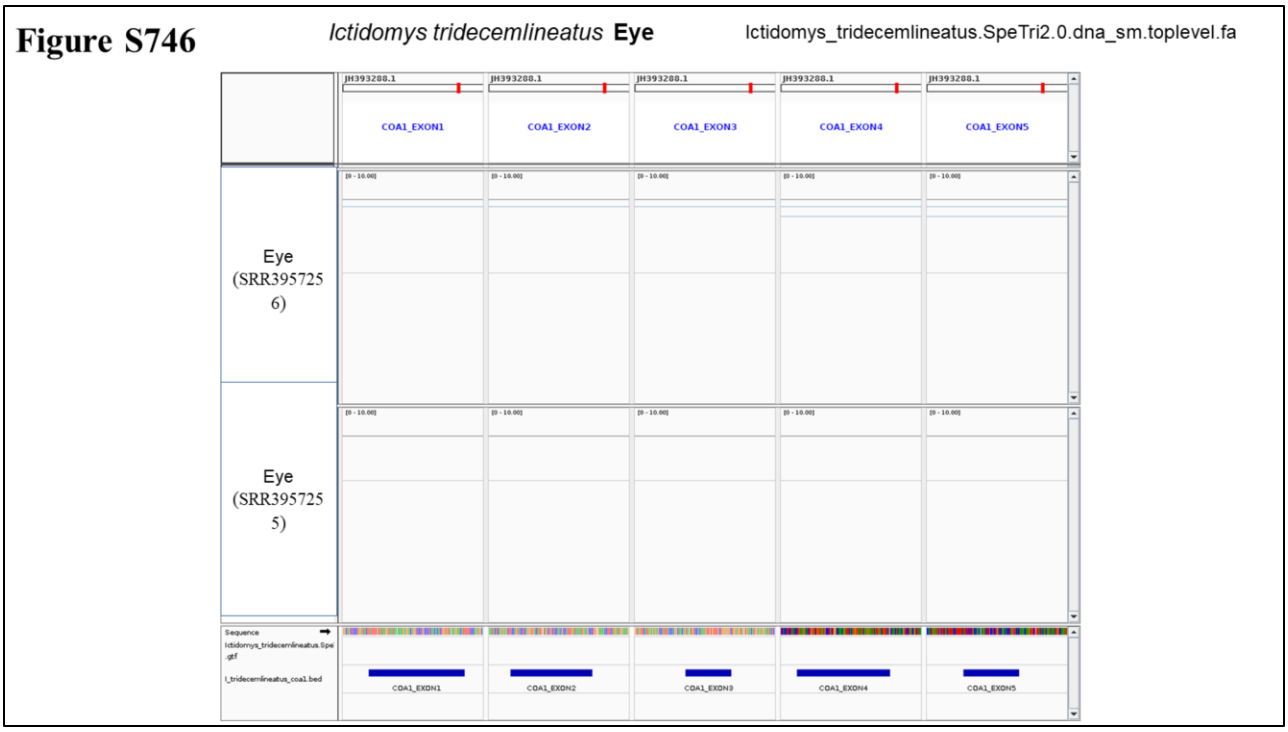

Figure S747: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S745**.

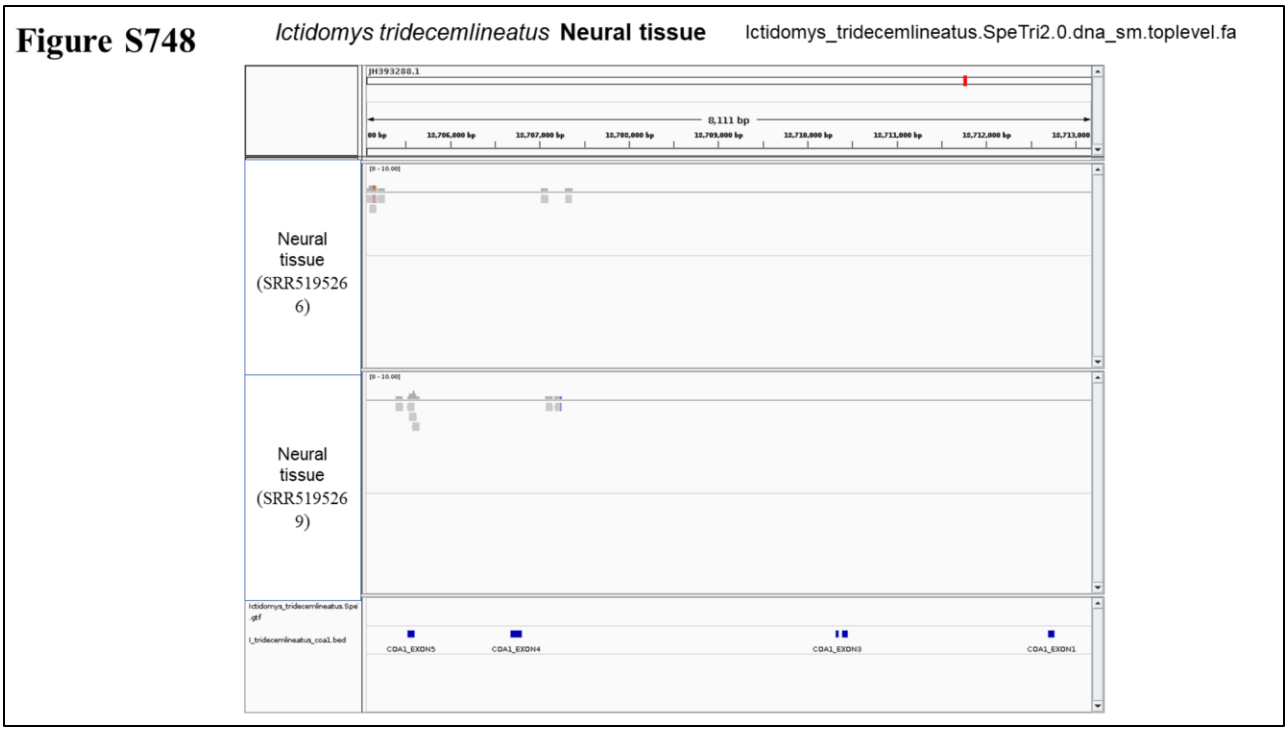

Figure S748: Screenshot of RNA-seq reads aligned to each of the putative locations of the five *COA1* exons in thirteen-lined ground squirrel (*Ictidomys tridecemlineatus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from neural tissue (SRR5195266 and SRR5195269) have been mapped to the Ictidomys_tridecemlineatus.SpeTri2.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

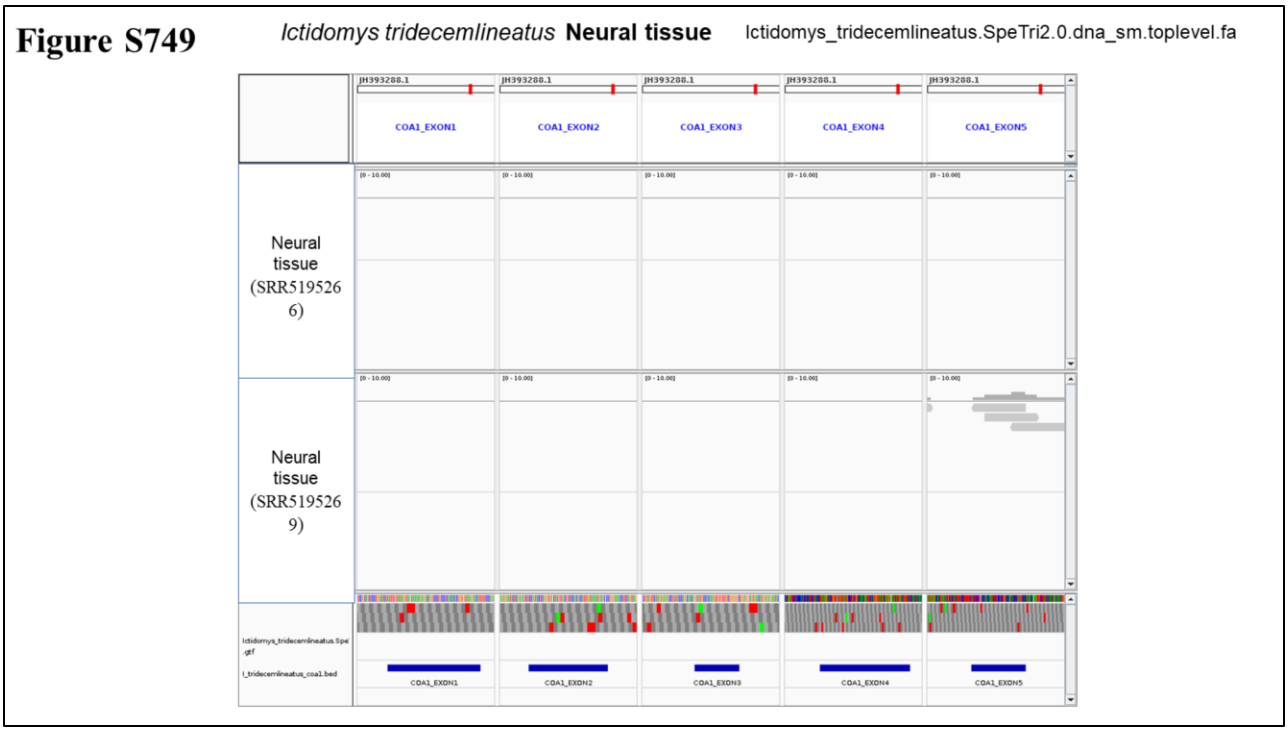

Figure S749: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S748**.

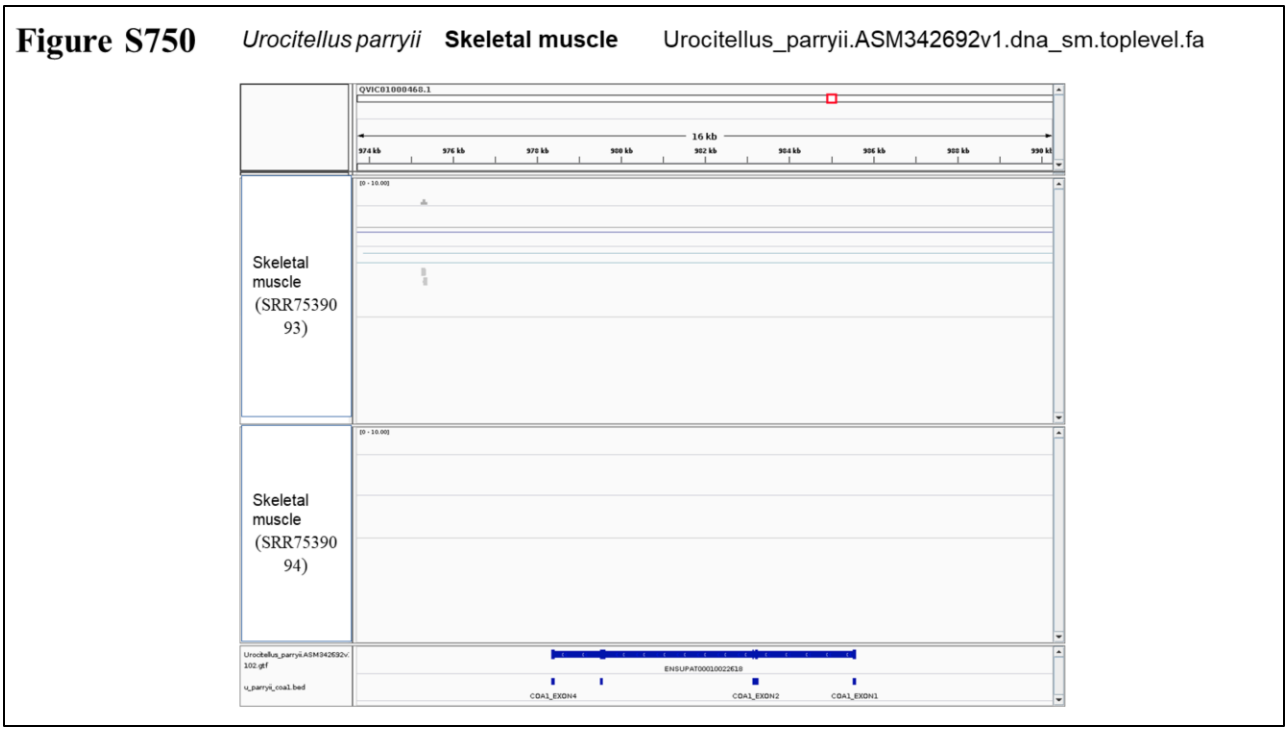

Figure S750: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Arctic ground squirrel (*Urocitellus parryii*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from skeletal muscle (SRR7539093 and SRR7539094) have been mapped to the Urocitellus_parryii.ASM342692v1.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S751 *Urocitellus parryii* **Skeletal muscle** Urocitellus_parryii.ASM342692v1.dna_sm.toplevel.fa

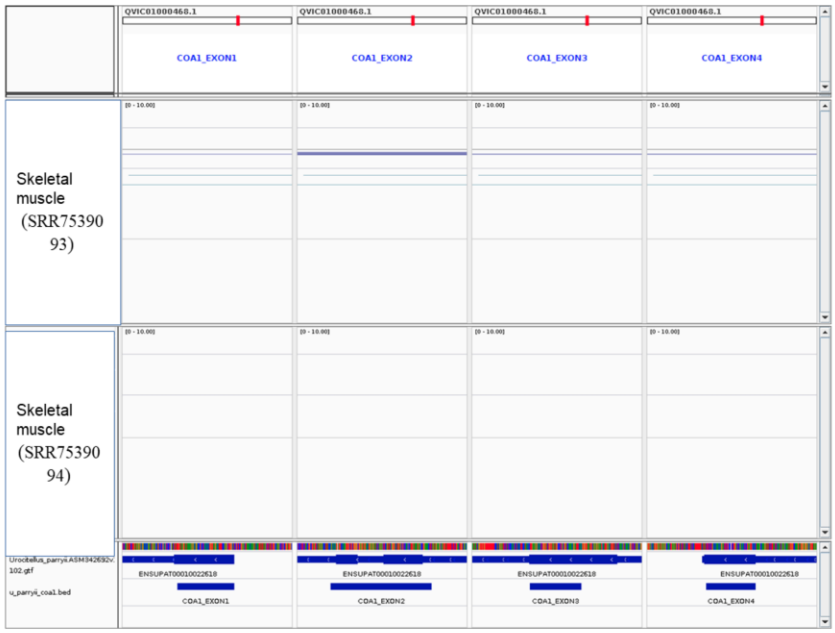

Figure S751: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S750**.

Figure S752 *Urocitellus parryii* **Skeletal muscle** Urocitellus_parryii.ASM342692v1.dna_sm.toplevel.fa

Figure S752: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exon-wise with nearby gene region in Arctic ground squirrel (*Urocitellus parryii*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from skeletal muscle (SRR7539093 and SRR7539094) have been mapped to the Urocitellus_parryii.ASM342692v1.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S753 *Urocitellus parryii* **Skeletal muscle** Urocitellus_parryii.ASM342692v1.dna_sm.toplevel.fa

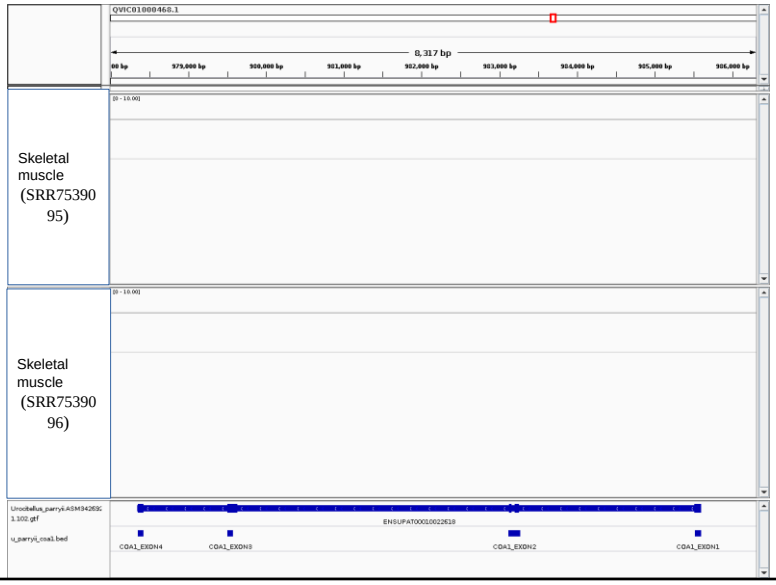

Figure S753: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Arctic ground squirrel (*Urocitellus parryii*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from skeletal muscle (SRR7539095 and SRR7539096) have been mapped to the Urocitellus_parryii.ASM342692v1.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S754 *Urocitellus parryii* **Skeletal muscle** Urocitellus_parryii.ASM342692v1.dna_sm.toplevel.fa

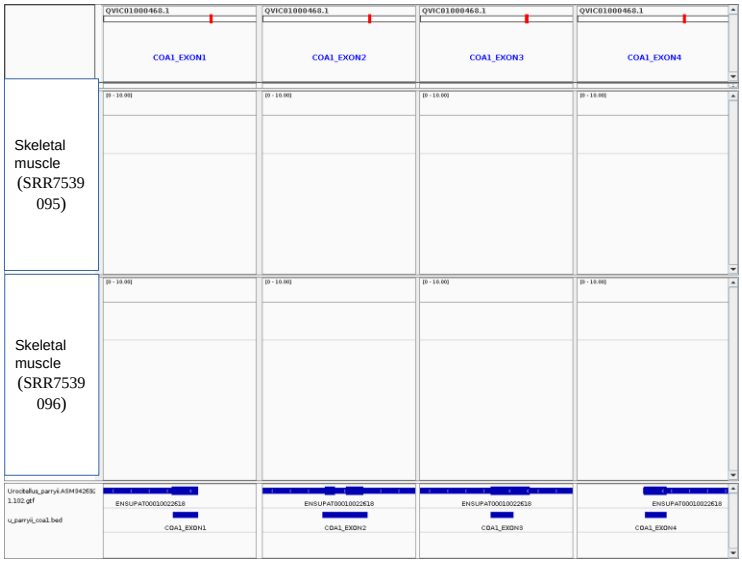

Figure S754: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S753**.

Figure S755 *Urocitellus parryii* **Skeletal muscle** Urocitellus_parryii.ASM342692v1.dna_sm.toplevel.fa

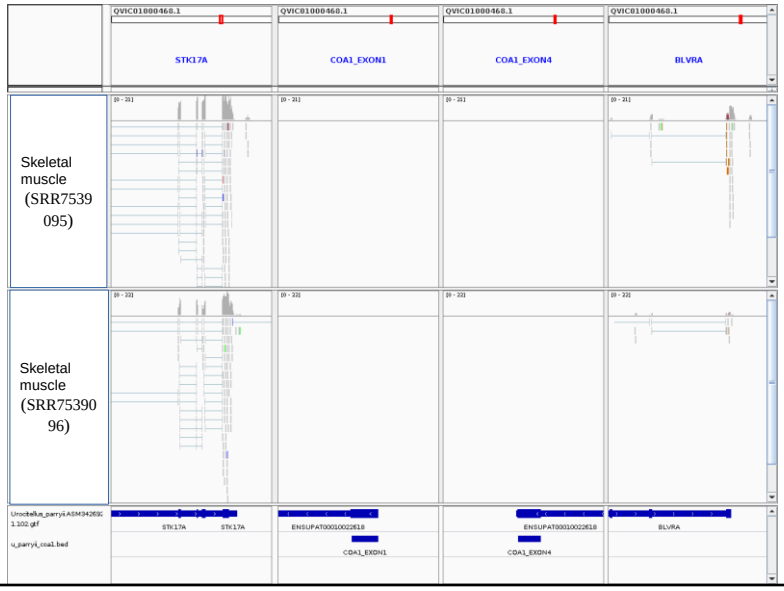

Figure S755: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons with nearby gene region in Arctic ground squirrel (*Urocitellus parryii*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from skeletal muscle (SRR7539095 and SRR7539096) have been mapped to the Urocitellus_parryii.ASM342692v1.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

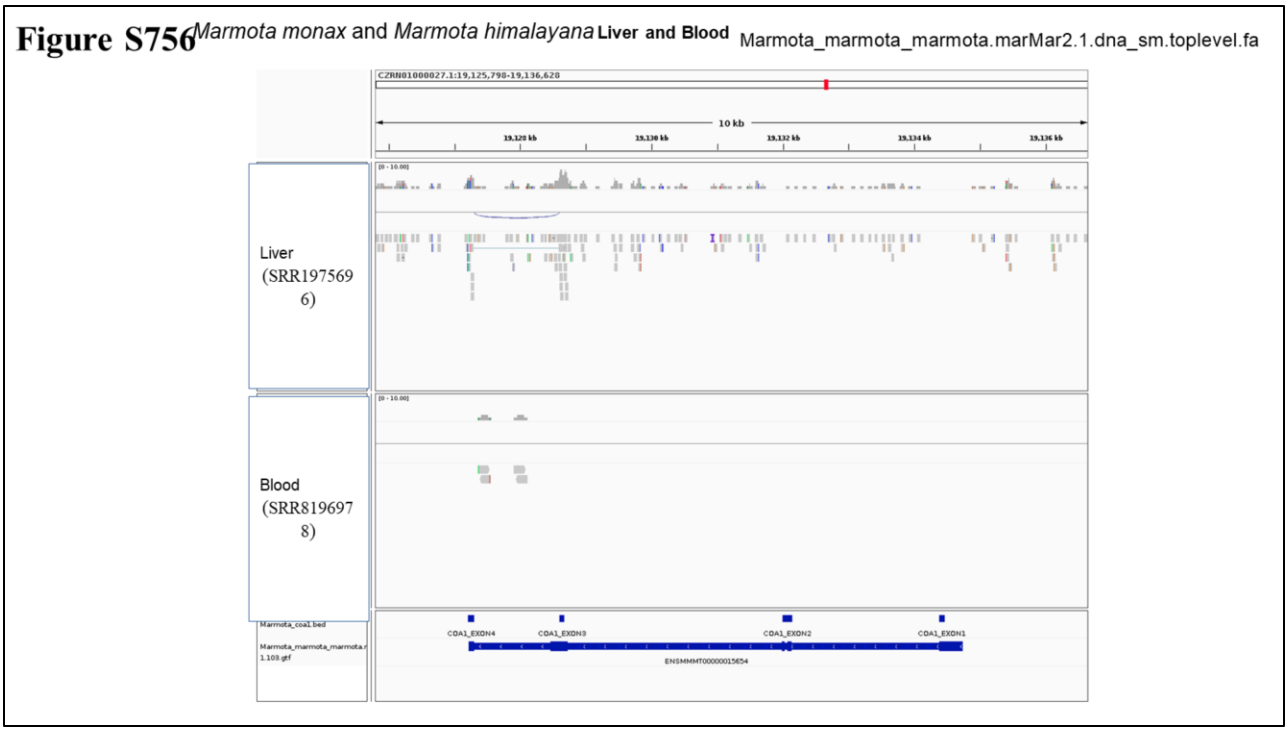

Figure S756: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in groundhog (*Marmota monax*) and Himalayan marmot(*Marmota himalayana*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver and blood (SRR1975696 and SRR8196978) have been mapped to the Marmota_marmota_marmota.marMar2.1.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

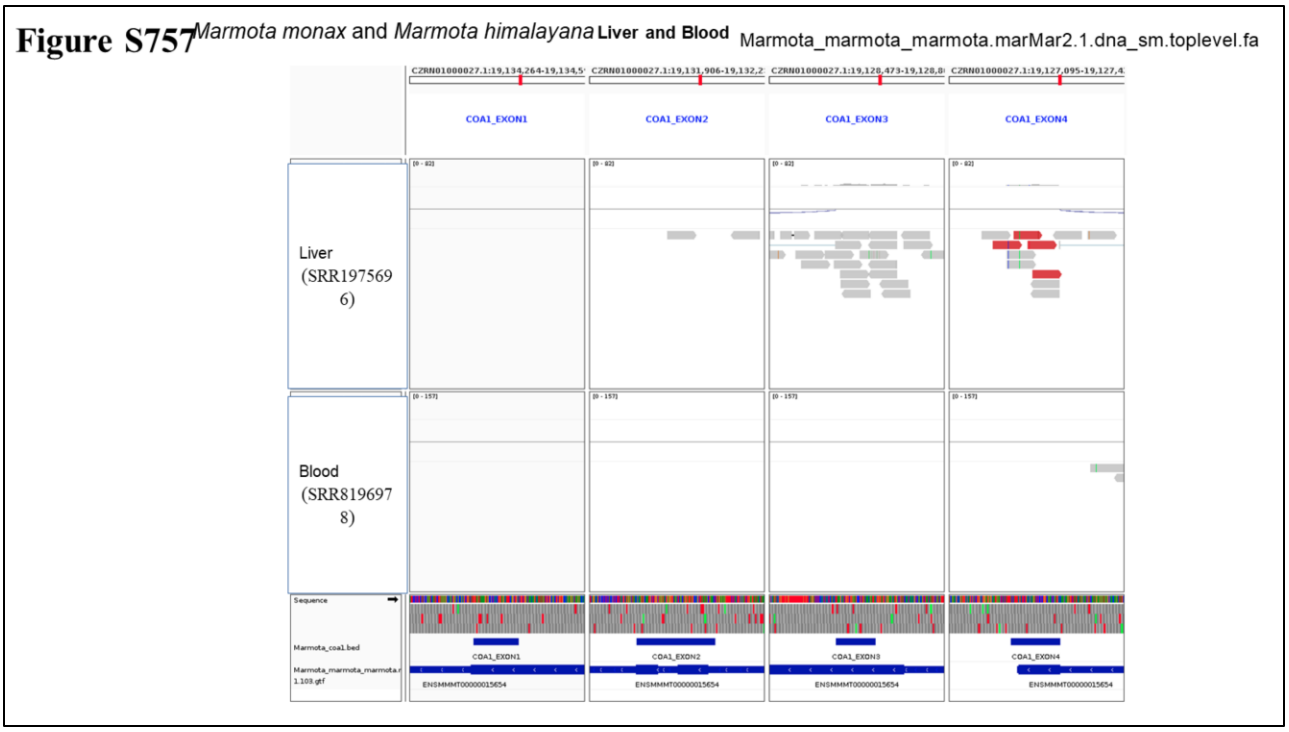

Figure S757: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S756**.

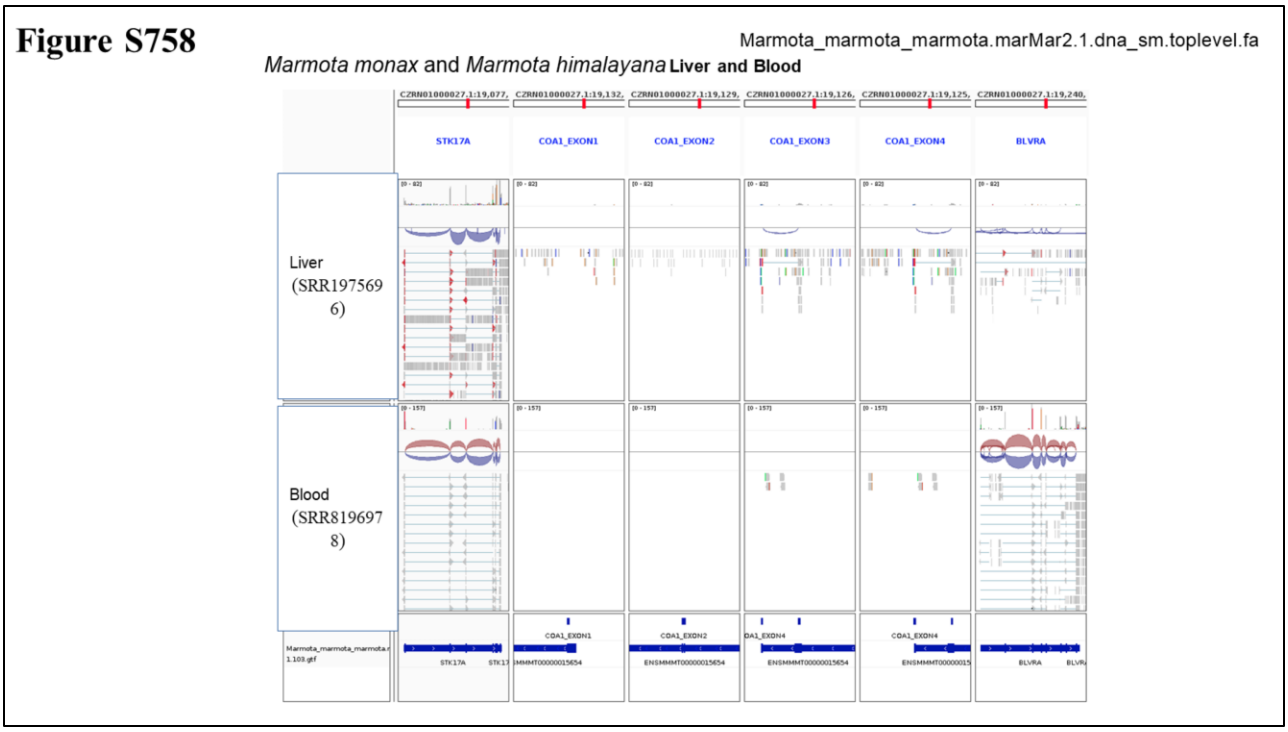

Figure S758: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in groundhog (*Marmota monax*) and Himalayan marmot(*Marmota himalayana*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver and blood (SRR1975696 and SRR8196978) have been mapped to the Marmota_marmota_marmota.marMar2.1.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

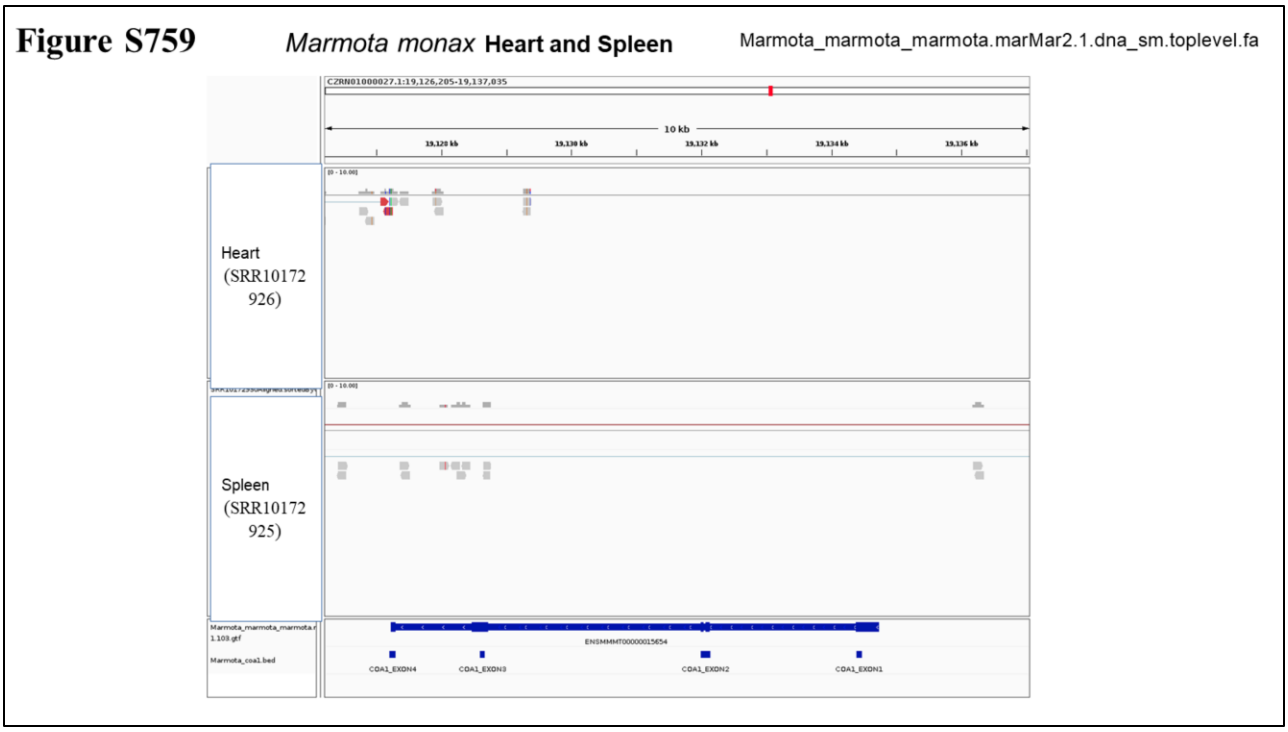

Figure S759: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in groundhog (*Marmota monax*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart and spleen (SRR10172926 and SRR10172925) have been mapped to the Marmota_marmota_marmota.marMar2.1.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

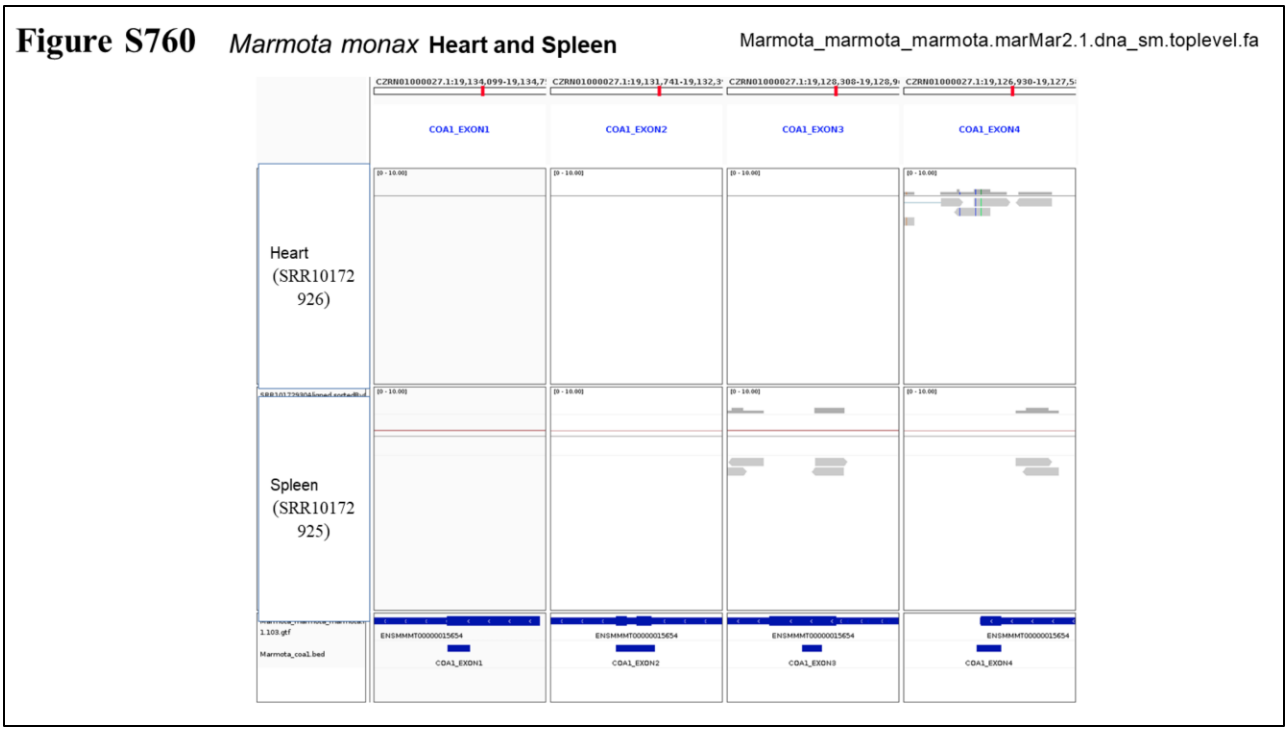

Figure S760: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S759**.

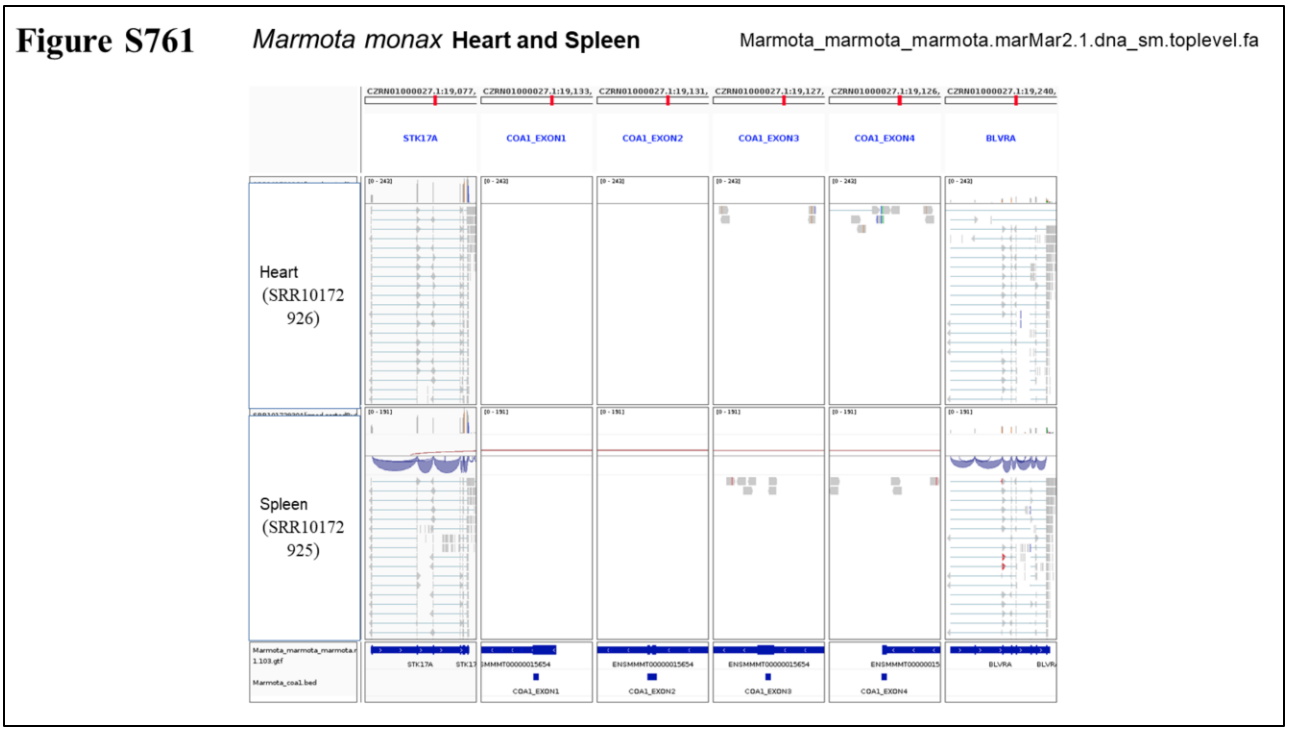

Figure S761: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in groundhog (*Marmota monax*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart and spleen (SRR10172926 and SRR10172925) have been mapped to the Marmota_marmota_marmota.marMar2.1.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

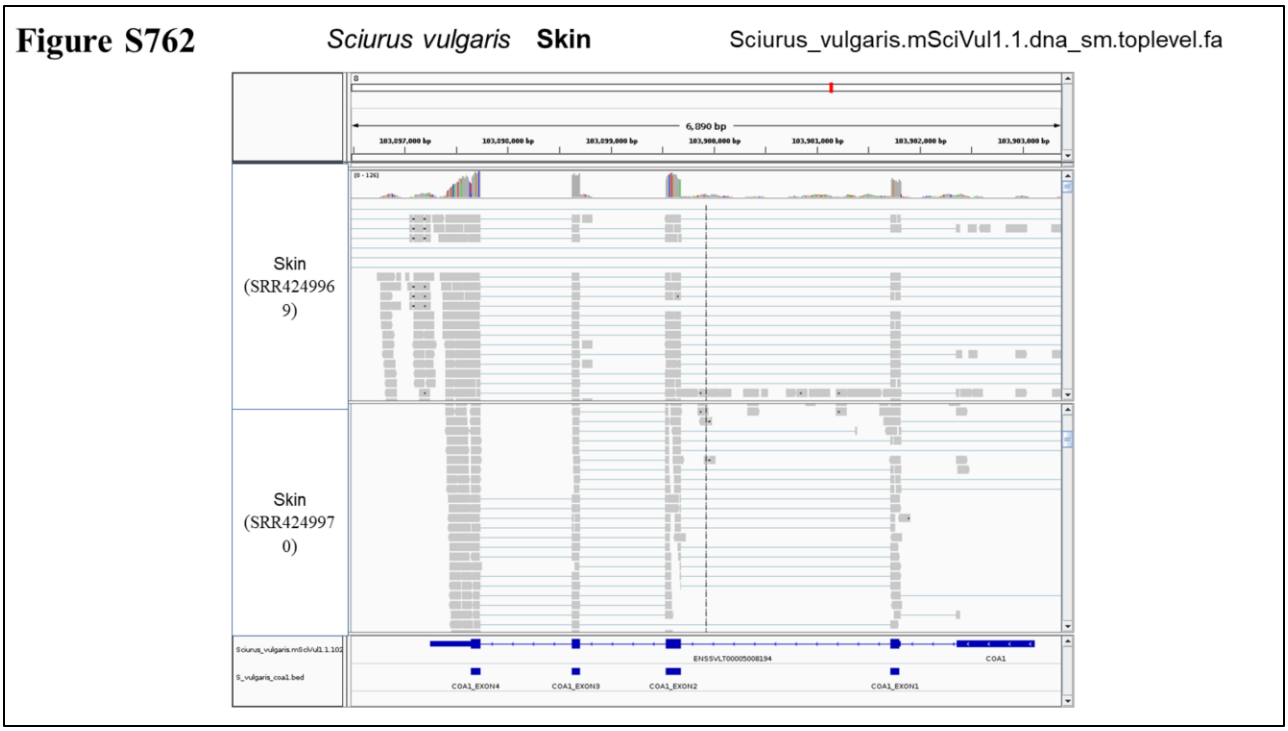

Figure S762: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Eurasian red squirrel (*Sciurus vulgaris*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from skin (SRR4249969 and SRR4249970) have been mapped to the Sciurus_vulgaris.mSciVul1.1.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

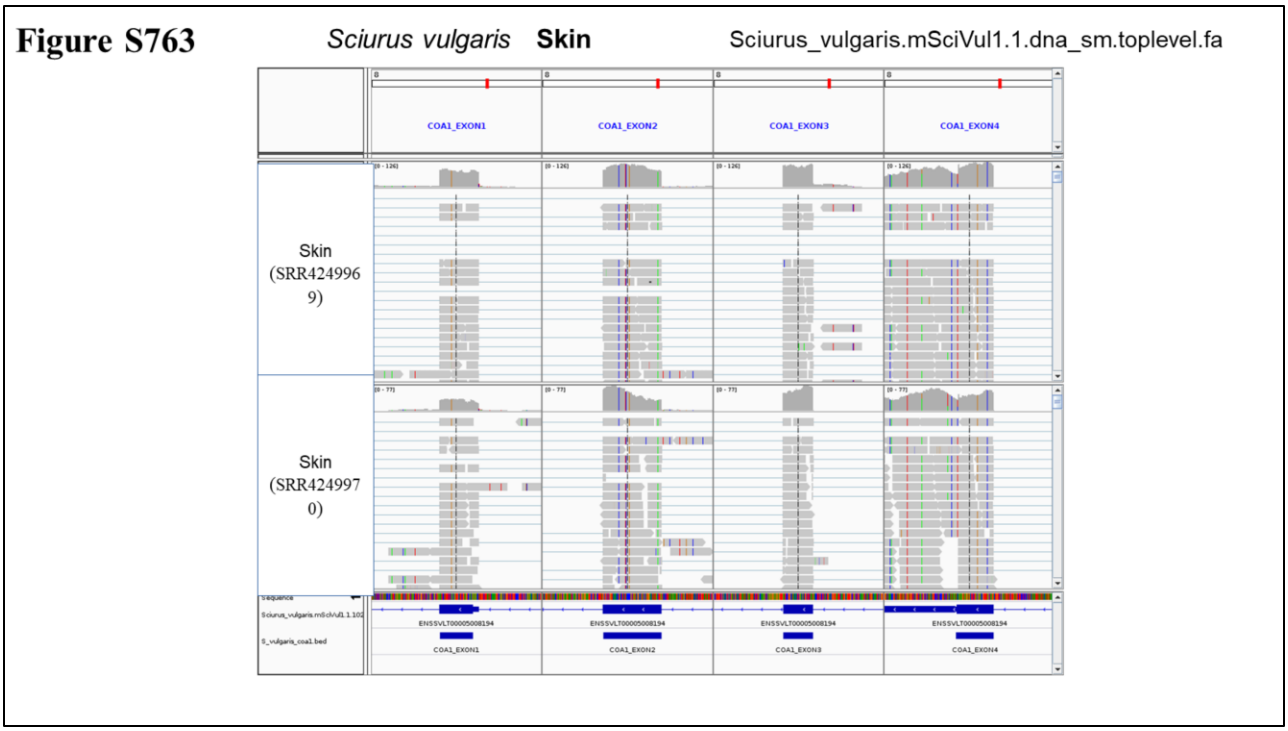

Figure S763: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S762**.

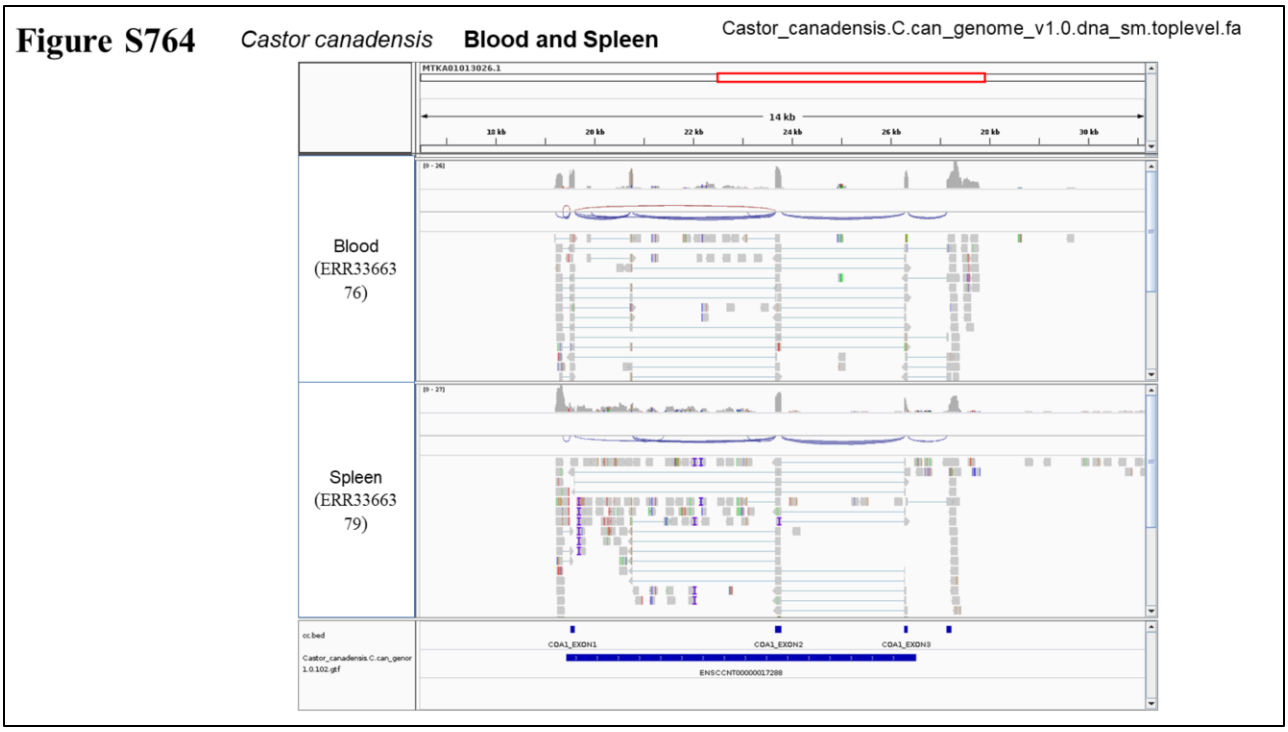

Figure S764: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in American beaver (*Castor canadensis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (ERR3366376) and spleen (ERR3366379) have been mapped to the Castor_canadensis.C.can_genome_v1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

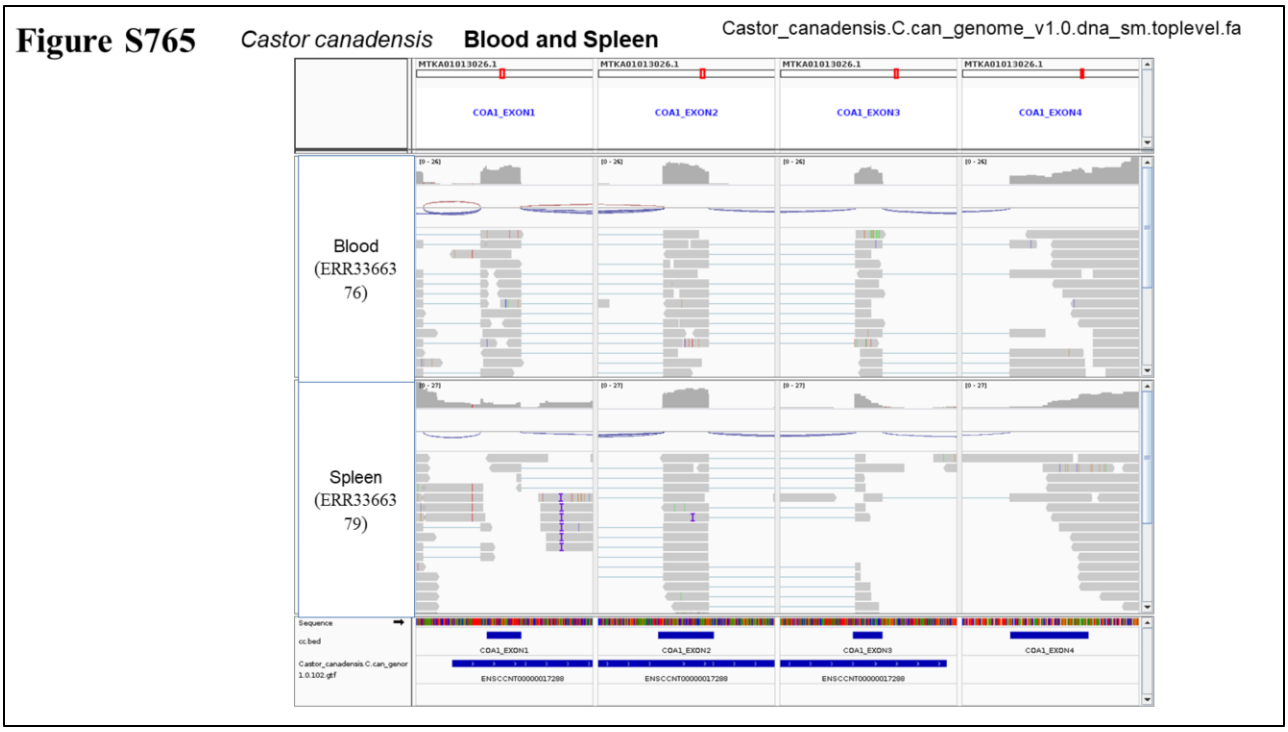

Figure S765: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S764**.

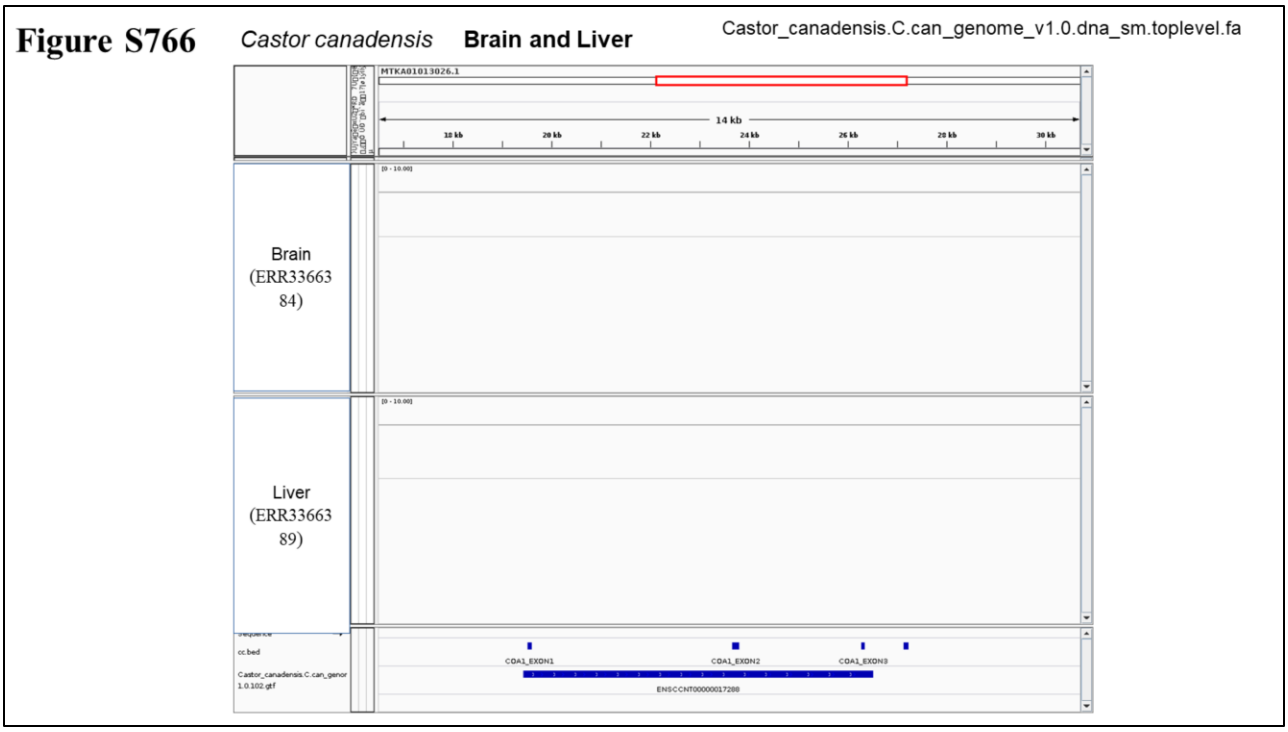

Figure S766: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in American beaver (*Castor canadensis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (ERR3366384) and liver (ERR3366389) have been mapped to the Castor_canadensis.C.can_genome_v1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

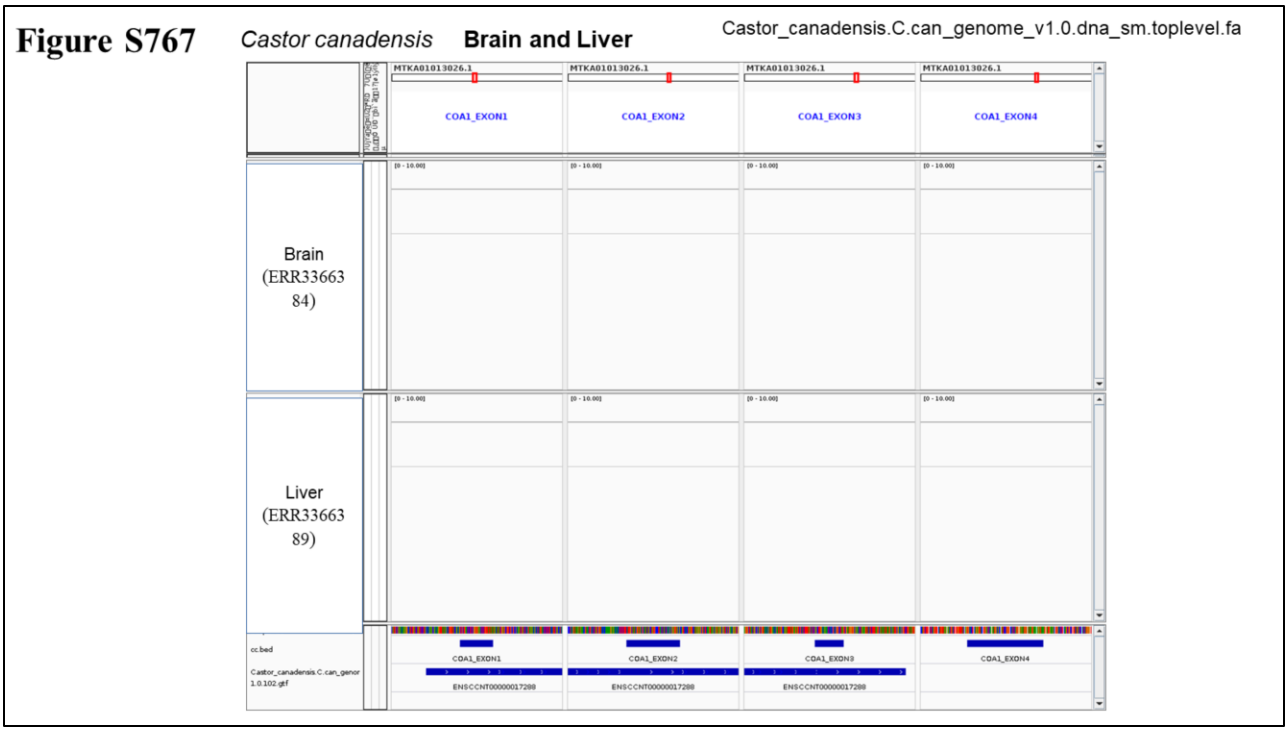

Figure S767: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S765**.

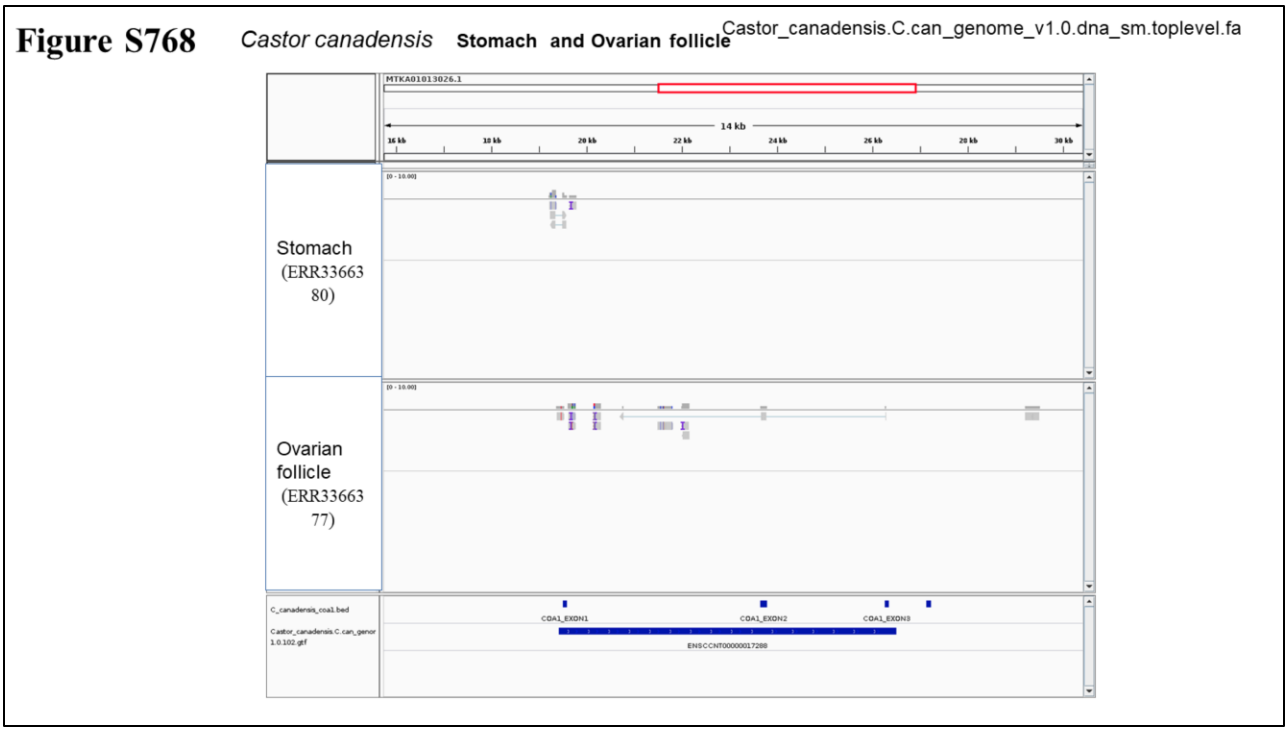

Figure S768: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in American beaver (*Castor canadensis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from stomach (ERR3366380) and ovarian follicle (ERR3366377) have been mapped to the Castor_canadensis.C.can_genome_v1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

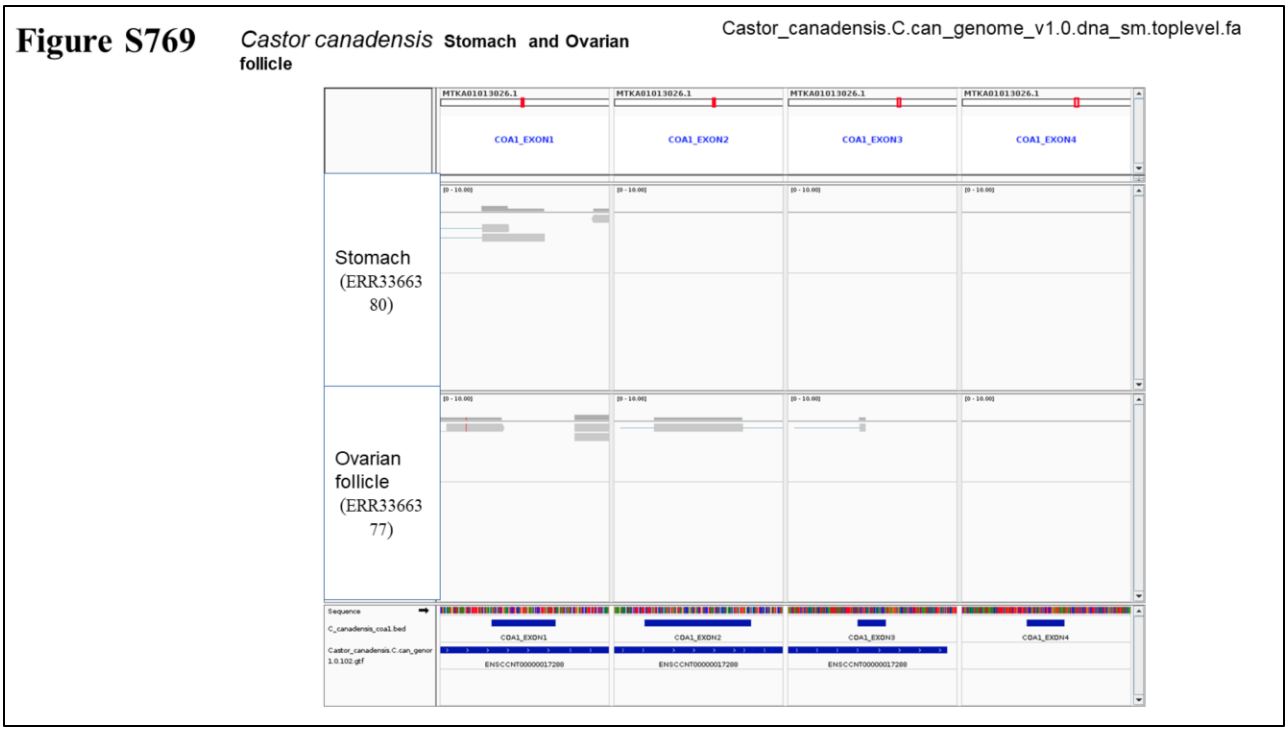

Figure S769: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S768**.

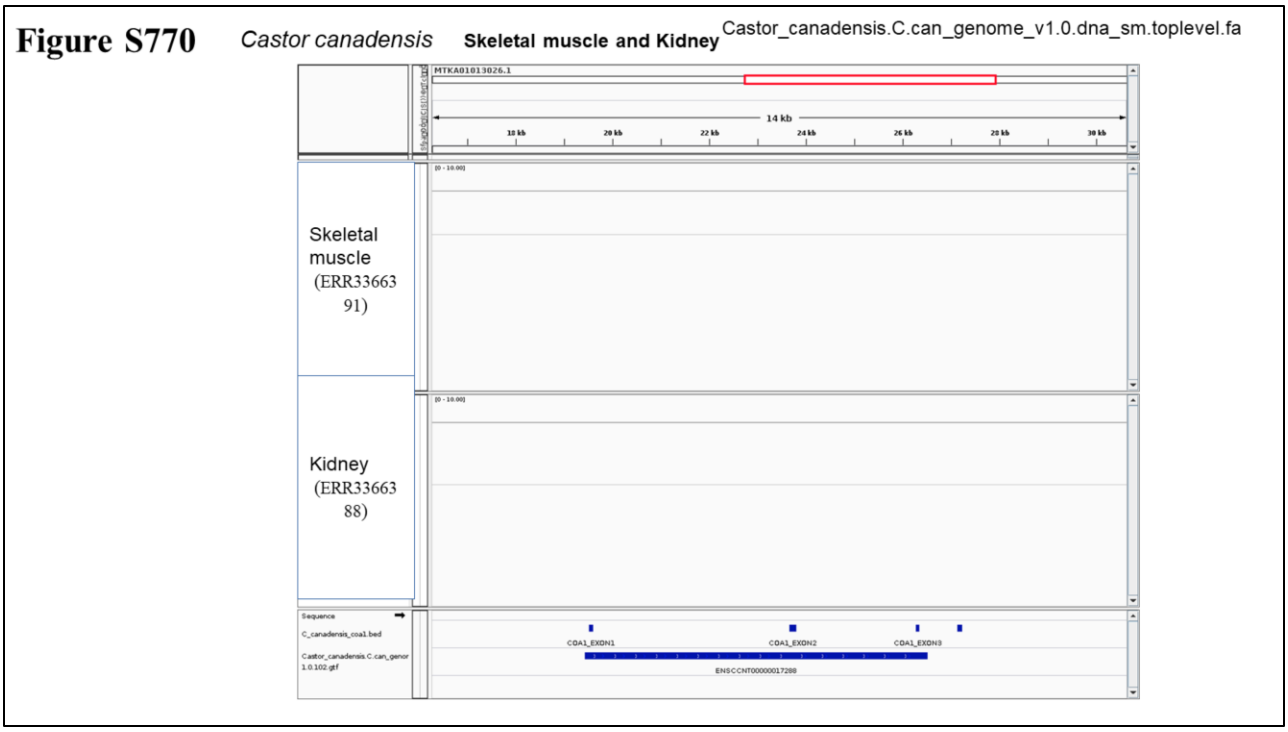

Figure S770: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in American beaver (*Castor canadensis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from skeletal muscle (ERR3366391) and kidney (ERR3366388) have been mapped to the Castor_canadensis.C.can_genome_v1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

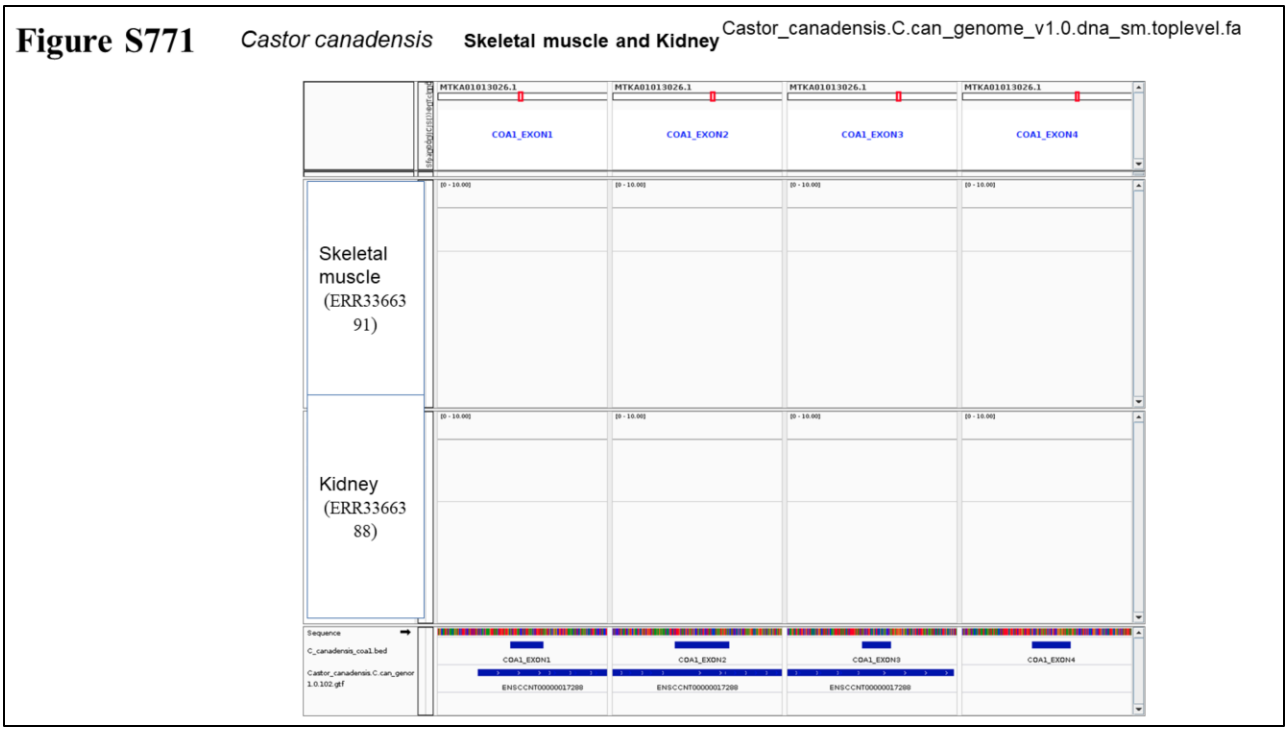

Figure S771: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S770**.

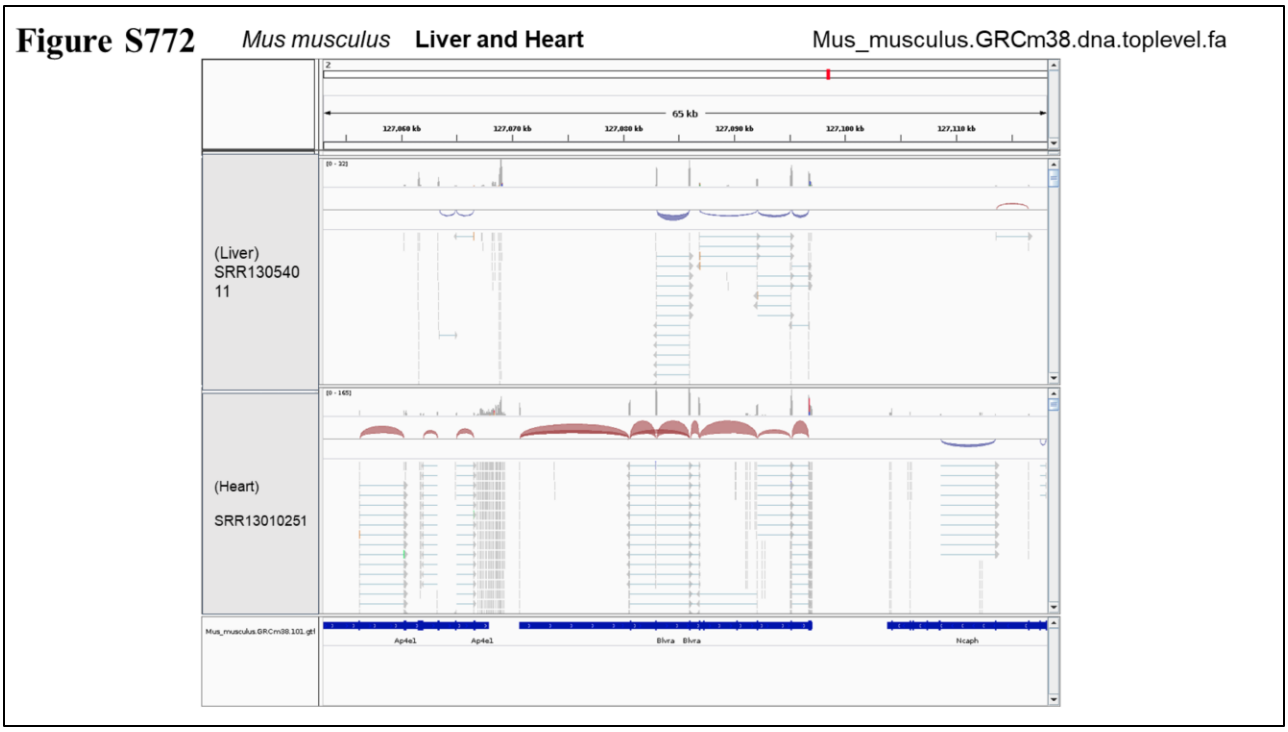

Figure S772: Screenshot of RNA-seq reads aligned each of the putative locations of *AP4E1* and *NCAPH* in mouse (*Mus musculus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR13054011) and heart (SRR13010251) have been mapped to the Mus_musculus.GRCm38.dna.toplevel.fa genome. Locations of *AP4E1* and *NCAPH* are depicted as Mus_musculus.GRCm38.101.gtf record in the bottom row.

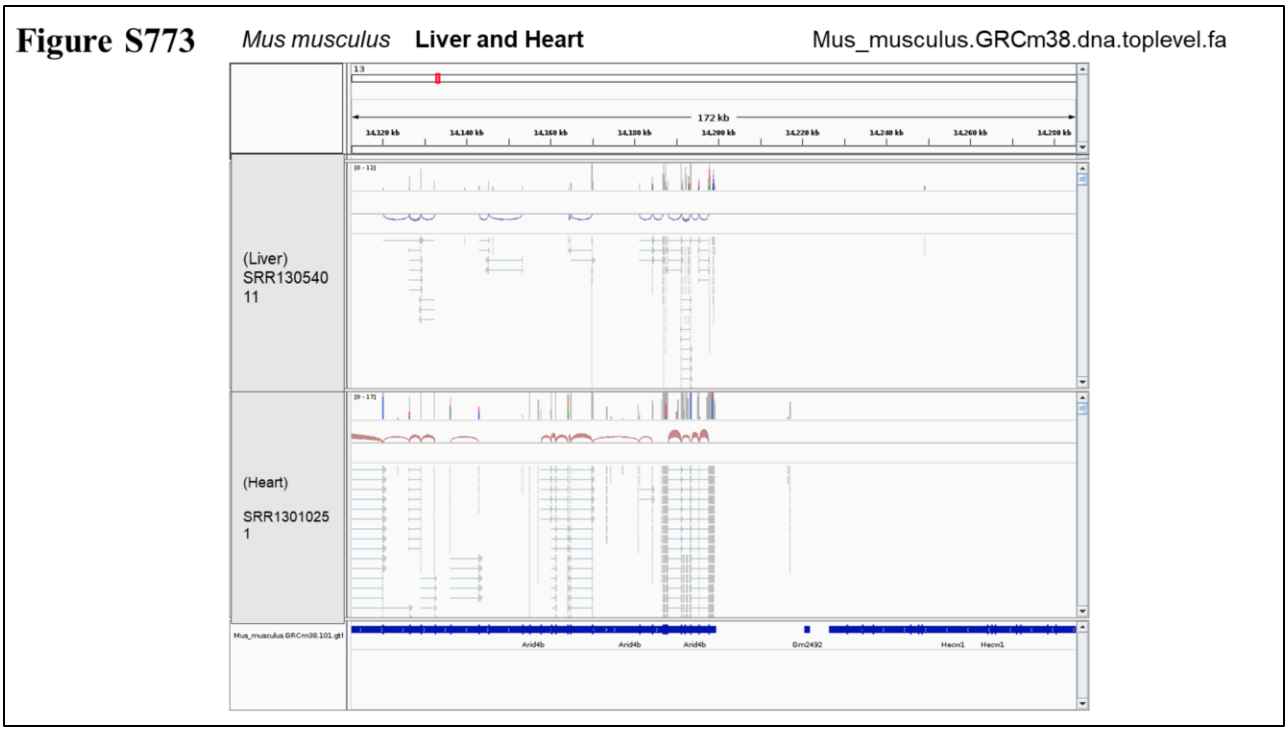

Figure S773: Screenshot of RNA-seq reads aligned each of the putative locations of *HECW1* and *ARID4B* in mouse (*Mus musculus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR13054011) and heart (SRR13010251) have been mapped to the Mus_musculus.GRCm38.dna.toplevel.fa genome. Locations of *HECW1* and *ARID4B* are depicted as Mus_musculus.GRCm38.101.gtf record in the bottom row.

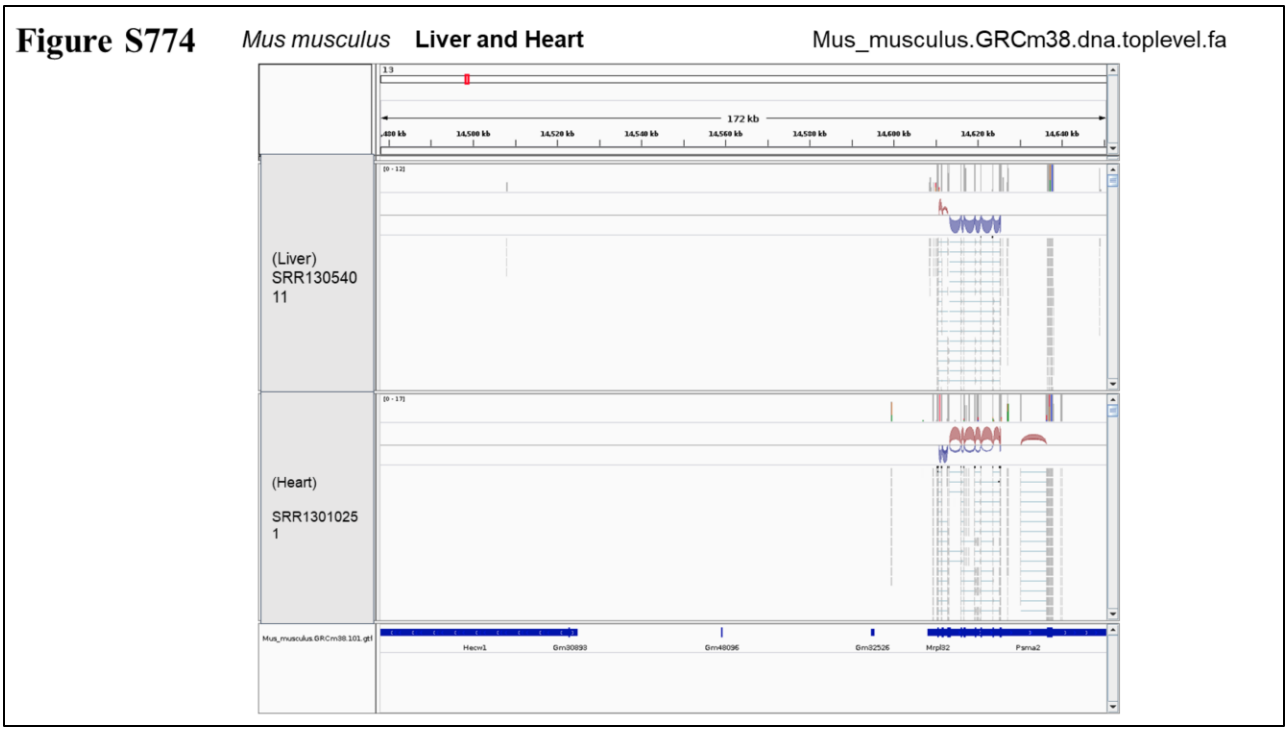

Figure S774: Screenshot of RNA-seq reads aligned each of the putative locations of *HECW1* and *PSMA2* in mouse (*Mus musculus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR13054011) and heart (SRR13010251) have been mapped to the Mus_musculus.GRCm38.dna.toplevel.fa genome. Locations of *HECW1* and *PSMA2* are depicted as Mus_musculus.GRCm38.101.gtf record in the bottom row.

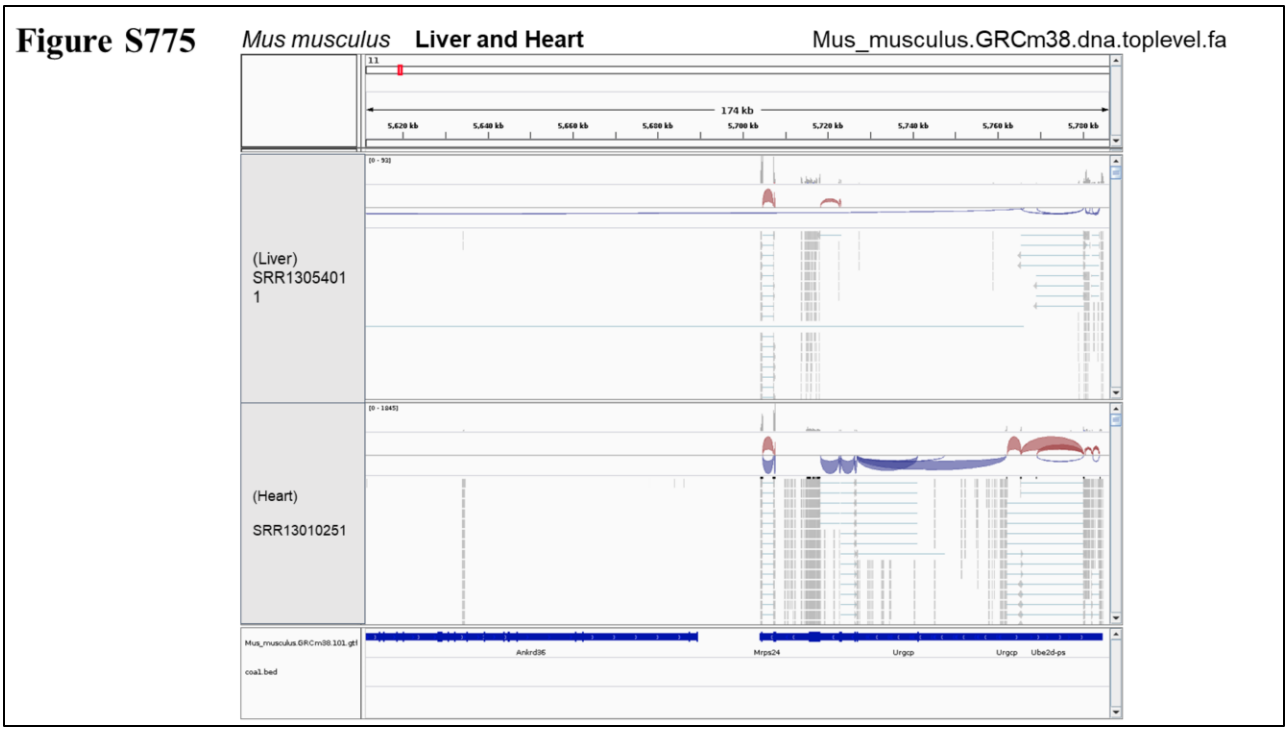

Figure S775: Screenshot of RNA-seq reads aligned each of the putative locations of *ANKRD36* and *URGCP* in mouse (*Mus musculus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR13054011) and heart (SRR13010251) have been mapped to the Mus_musculus.GRCm38.dna.toplevel.fa genome. Locations of *ANKRD36* and *URGCP* are depicted as Mus_musculus.GRCm38.101.gtf record in the bottom row.

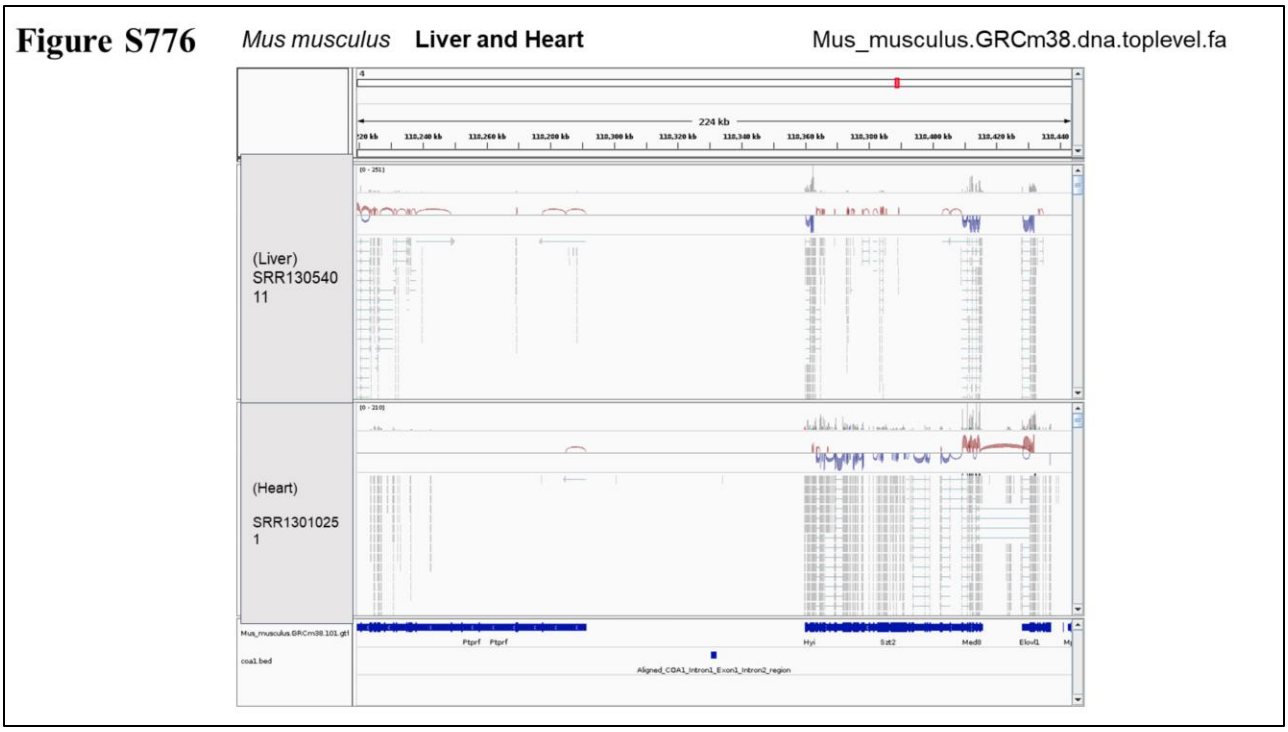

Figure S776: Screenshot of RNA-seq reads aligned each of the putative locations of truncated exon 1, intron-1 and intron-2 of *COA1* in mouse (*Mus musculus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR13054011) and heart (SRR13010251) have been mapped to the Mus_musculus.GRCm38.dna.toplevel.fa genome. Locations of truncated exon 1, intron-1 and intron-2 of *COA1* is depicted as bed record in the bottom row.

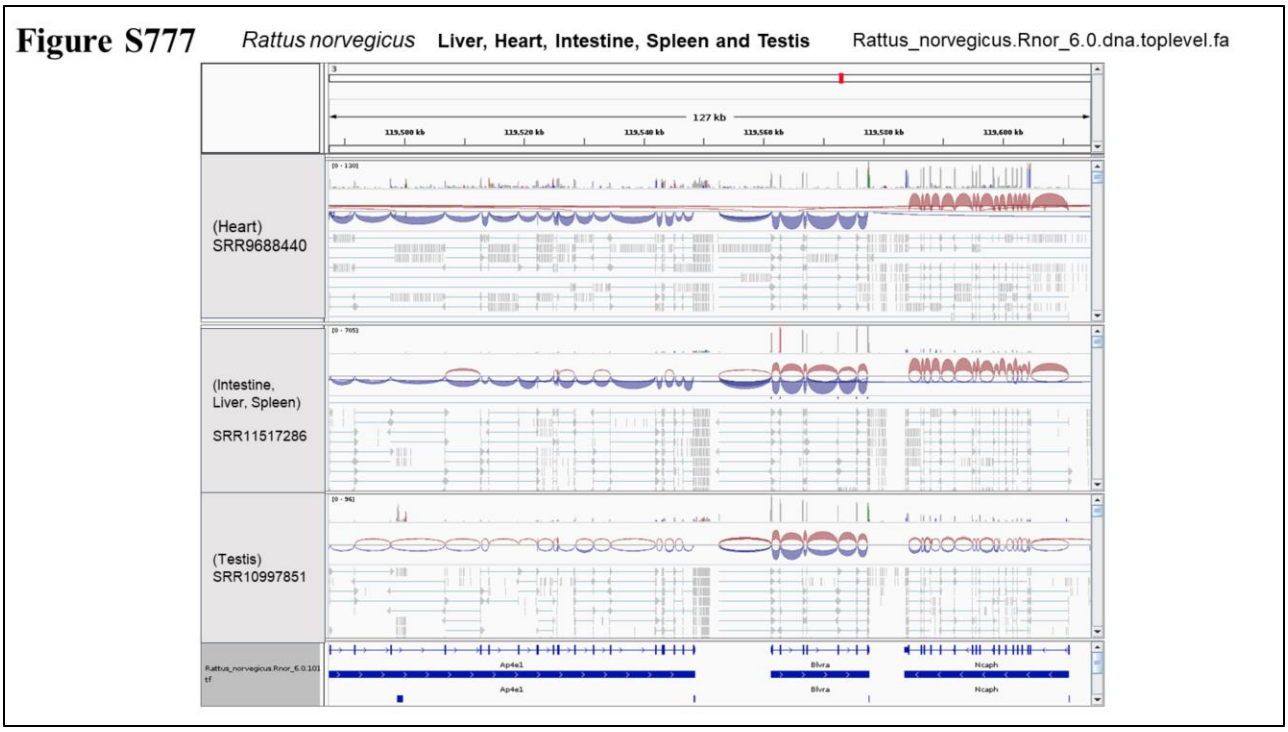

Figure S777: Screenshot of RNA-seq reads aligned each of the putative locations of *AP4E1* and *NCAPH* in rat (*Rattus norvegicus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver, spleen and intestine (SRR11517286) and heart (SRR9688440) and testis (SRR10997851) have been mapped to the Rattus_norvegicus.Rnor_6.0.dna.toplevel.fa genome. Locations of *AP4E1* and *NCAPH* are depicted as Rattus_norvegicus.Rnor_6.0.101.gtf record in the bottom row.

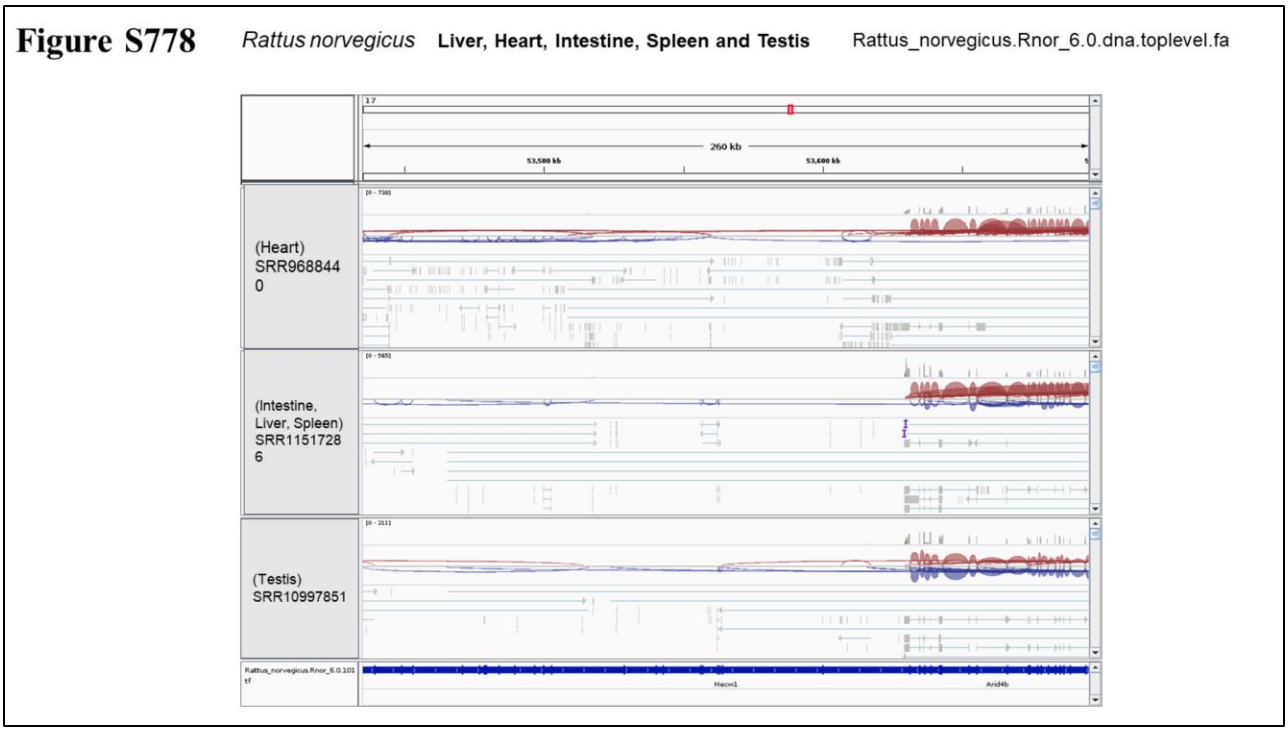

Figure S778: Screenshot of RNA-seq reads aligned each of the putative locations of *HECW1* and *ARID4B* in rat (*Rattus norvegicus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver, spleen and intestine (SRR11517286) and heart (SRR9688440) and testis (SRR10997851) have been mapped to the Rattus_norvegicus.Rnor_6.0.dna.toplevel.fa genome. Locations of *HECW1* and *ARID4B* are depicted as Rattus_norvegicus.Rnor_6.0.101.gtf record in the bottom row.

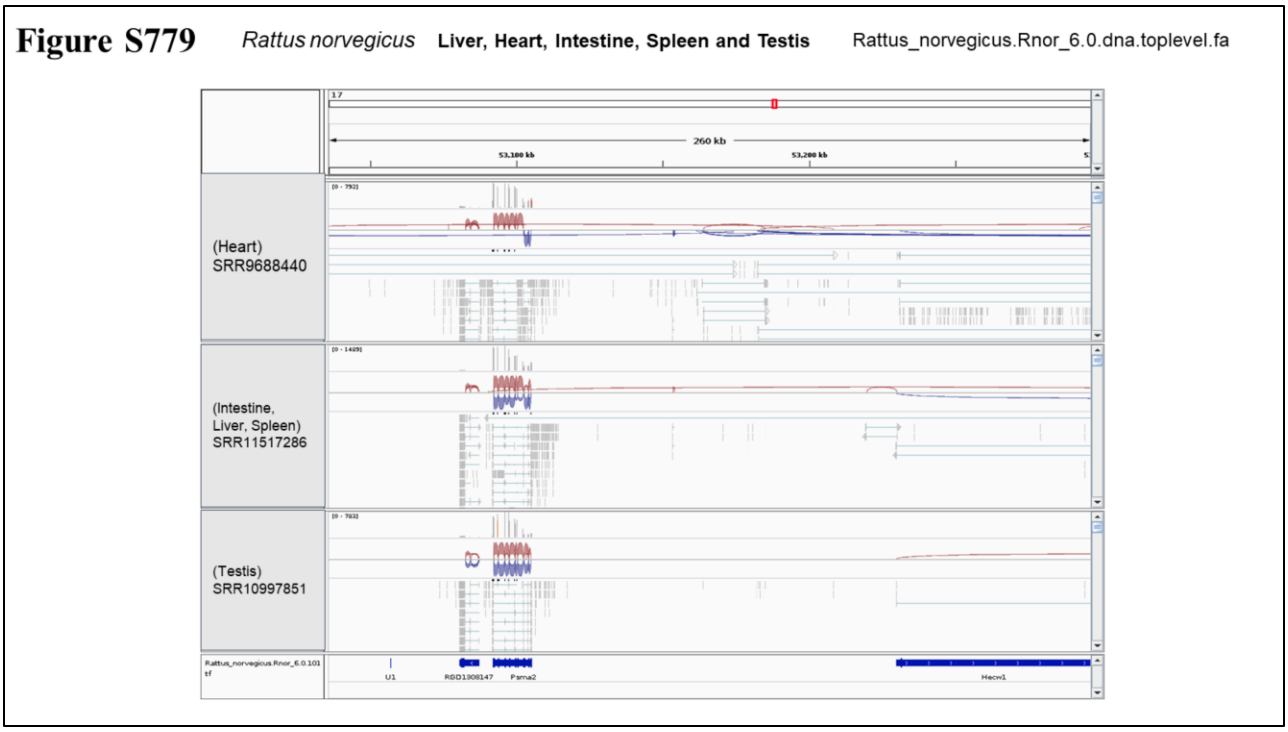

Figure S779: Screenshot of RNA-seq reads aligned each of the putative locations of *PSMA2* and *HECW1* in rat (*Rattus norvegicus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver, spleen and intestine (SRR11517286) and heart (SRR9688440) and testis (SRR10997851) have been mapped to the Rattus_norvegicus.Rnor_6.0.dna.toplevel.fa genome. Locations of *PSMA2* and *HECW1* are depicted as Rattus_norvegicus.Rnor_6.0.101.gtf record in the bottom row.

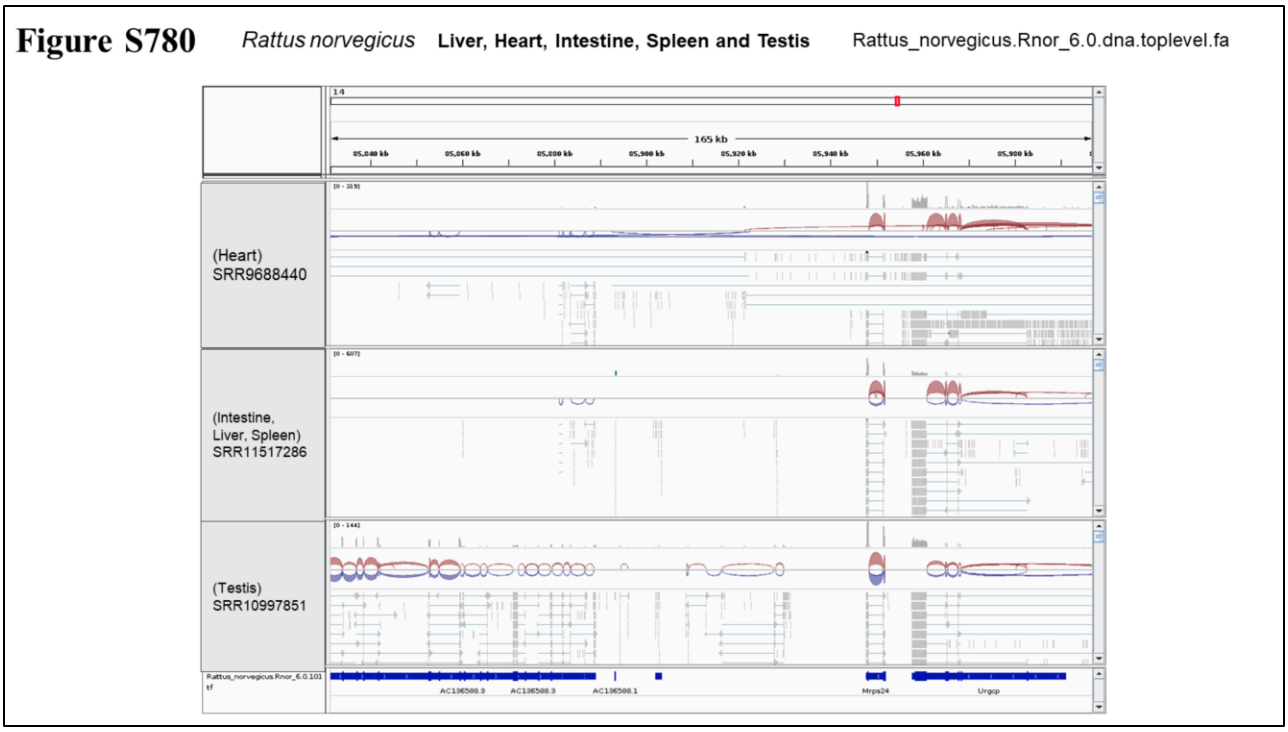

Figure S780: Screenshot of RNA-seq reads aligned each of the putative locations of *ANKRD26* and *URGCP* in rat (*Rattus norvegicus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver, spleen and intestine (SRR11517286) and heart (SRR9688440) and testis (SRR10997851) have been mapped to the Rattus_norvegicus.Rnor_6.0.dna.toplevel.fa genome. Locations of *ANKRD26* and *URGCP* are depicted as Rattus_norvegicus.Rnor_6.0.101.gtf record in the bottom row.

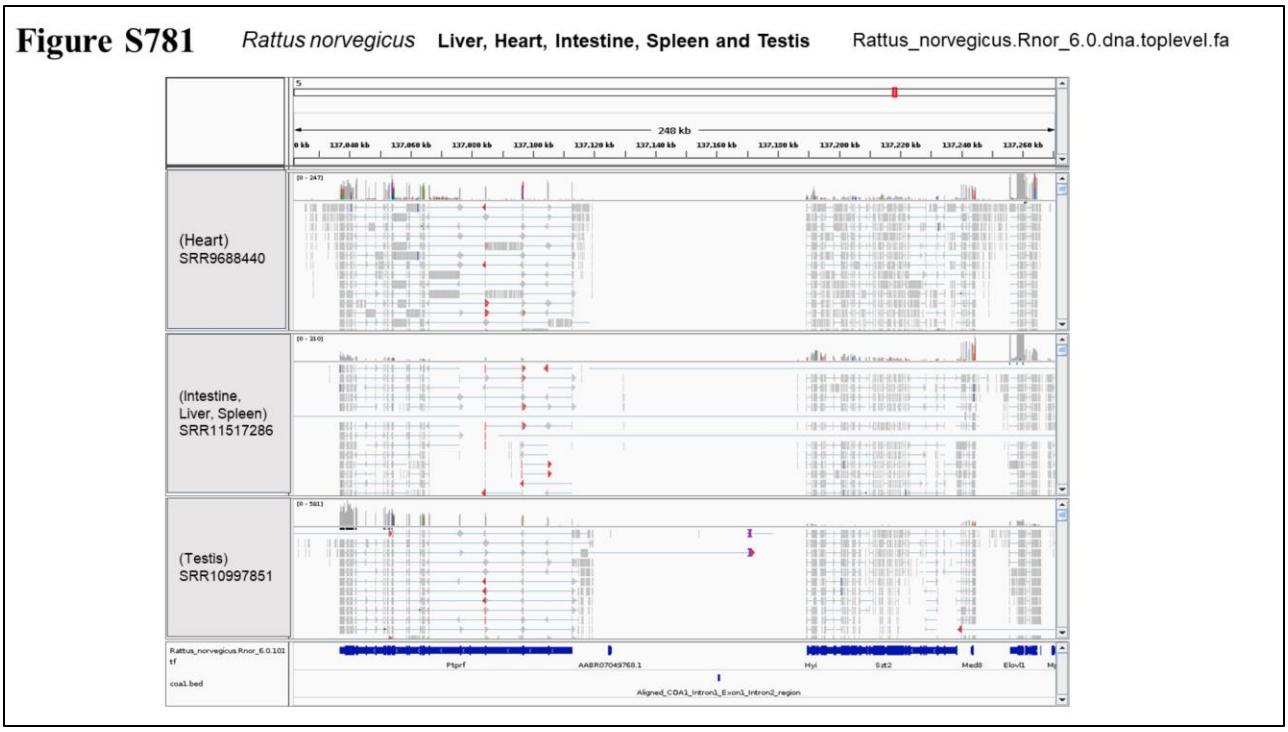

Figure S781: Screenshot of RNA-seq reads aligned each of the putative locations of truncated exon 1, intron-1 and intron-2 in rat (*Rattus norvegicus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver, spleen and intestine (SRR11517286) and heart (SRR9688440) and testis (SRR10997851) have been mapped to the Rattus_norvegicus.Rnor_6.0.dna.toplevel.fa genome. Locations of truncated exon 1, intron-1 and intron-2 is depicted as bed record in the bottom row.

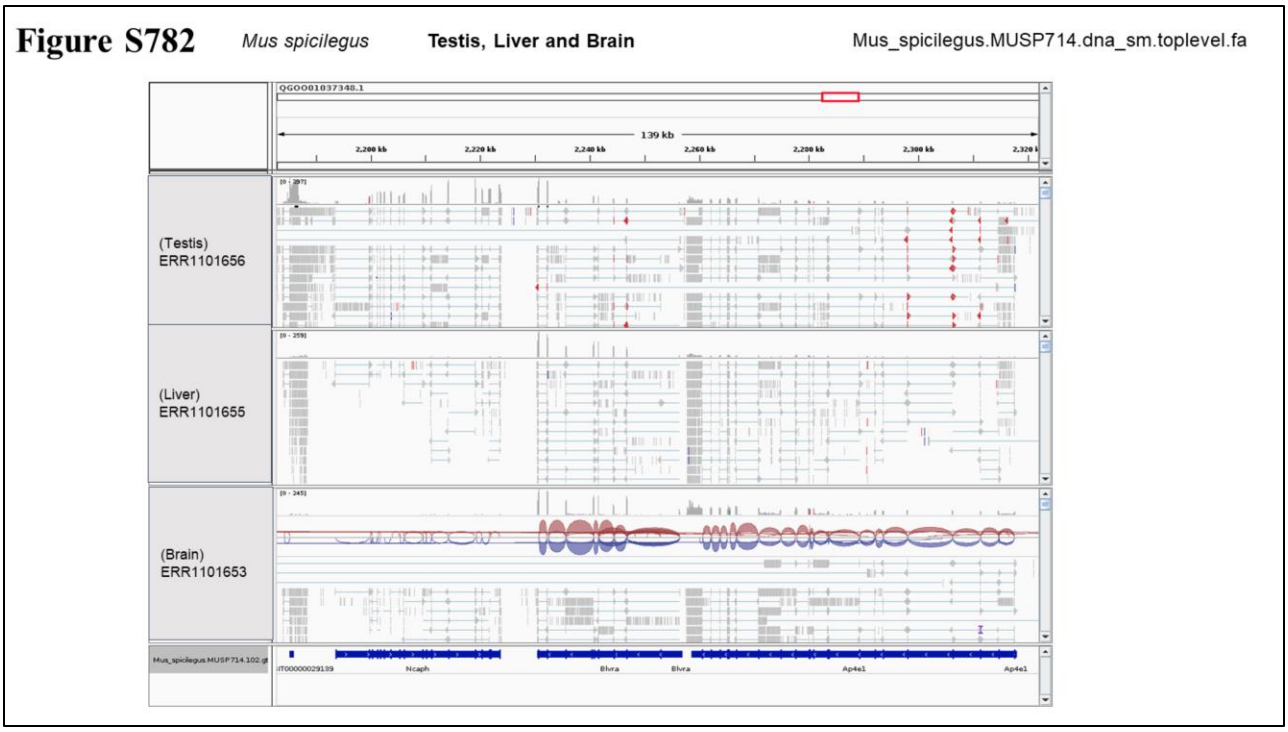

Figure S782: Screenshot of RNA-seq reads aligned each of the putative locations of *AP4E1* and *NCAPH* in Steppe mouse (*Mus spicilegus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis (ERR1101656), liver (ERR1101655) and brain (ERR1101653) have been mapped to the Mus_spicilegus.MUSP714.dna_sm.toplevel.fa genome. Locations of *AP4E1* and *NCAPH* are depicted as Mus_spicilegus.MUSP714.102.gtf record in the bottom row.

Figure S783: Screenshot of RNA-seq reads aligned each of the putative locations of *HECW1* and *ARID4B* in Steppe mouse (*Mus spicilegus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis (ERR1101656), liver (ERR1101655) and brain (ERR1101653) have been mapped to the Mus_spicilegus.MUSP714.dna_sm.toplevel.fa genome. Locations of *HECW1* and *ARID4B* are depicted as Mus_spicilegus.MUSP714.102.gtf record in the bottom row.

Figure S784: Screenshot of RNA-seq reads aligned each of the putative locations of *MRPL32* and *PSMA2* in Steppe mouse (*Mus spicilegus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis (ERR1101656), liver (ERR1101655) and brain (ERR1101653) have been mapped to the Mus_spicilegus.MUSP714.dna_sm.toplevel.fa genome. Locations of *MRPL32* and *PSMA2* are depicted as Mus_spicilegus.MUSP714.102.gtf record in the bottom row.

Figure S785: Screenshot of RNA-seq reads aligned each of the putative locations of *ANKRD36* and *URGCP* in Steppe mouse (*Mus spicilegus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis (ERR1101656), liver (ERR1101655) and brain (ERR1101653) have been mapped to the Mus_spicilegus.MUSP714.dna_sm.toplevel.fa genome. Locations of *ANKRD36* and *URGCP* are depicted as Mus_spicilegus.MUSP714.102.gtf record in the bottom row.

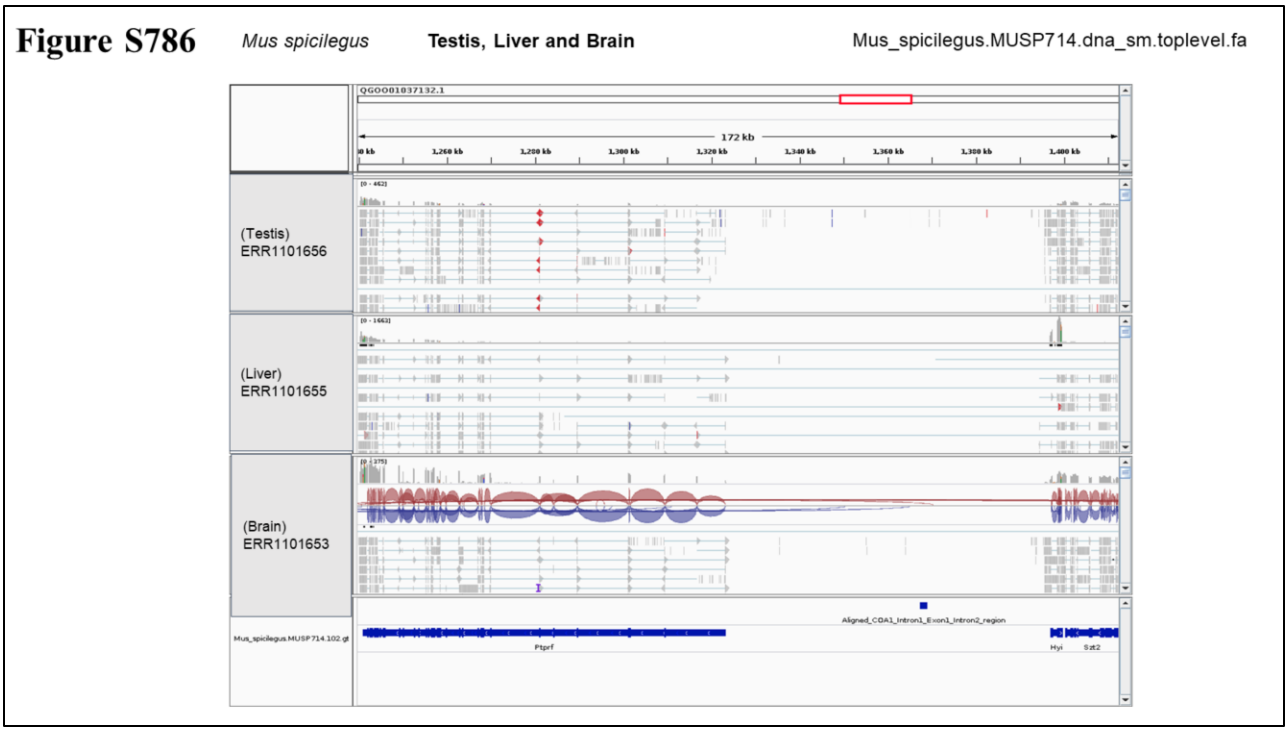

Figure S786: Screenshot of RNA-seq reads aligned each of the putative locations of truncated exon1, intron-1 and intron-2 of *COA1* in Steppe mouse (*Mus spicilegus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis (ERR1101656), liver (ERR1101655) and brain (ERR1101653) have been mapped to the Mus_spicilegus.MUSP714.dna_sm.toplevel.fa genome. Locations of truncated exon 1, intron-1 and intron-2 of *COA1* is depicted as bed record in the bottom row.

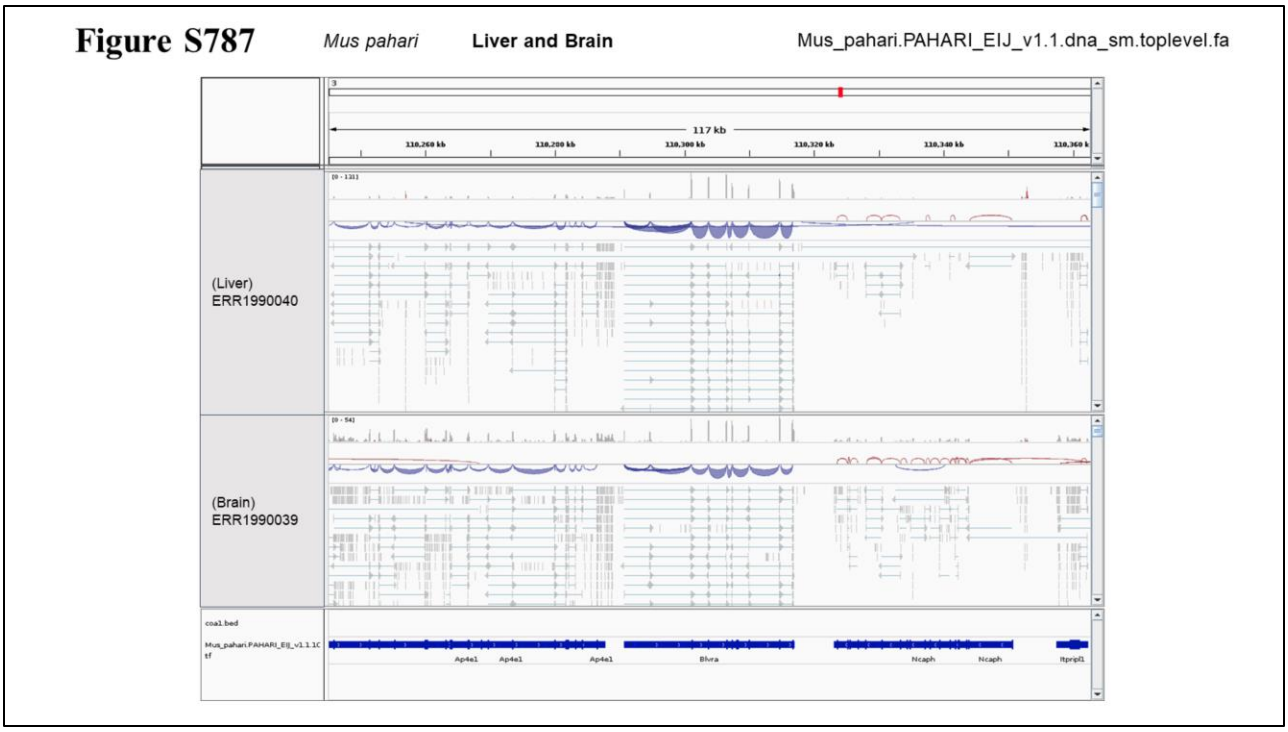

Figure S787: Screenshot of RNA-seq reads aligned each of the putative locations of *AP4E1* and *NCAPH* in Shrew mouse (*Mus pahari*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (ERR1990040) and brain (ERR1990039) have been mapped to the Mus_pahari.PAHARI_EIJ_v1.1.dna_sm.toplevel.fa genome. Locations of *AP4E1* and *NCAPH* are depicted as Mus_pahari.PAHARI_EIJ_v1.1.102.gtf record in the bottom row.

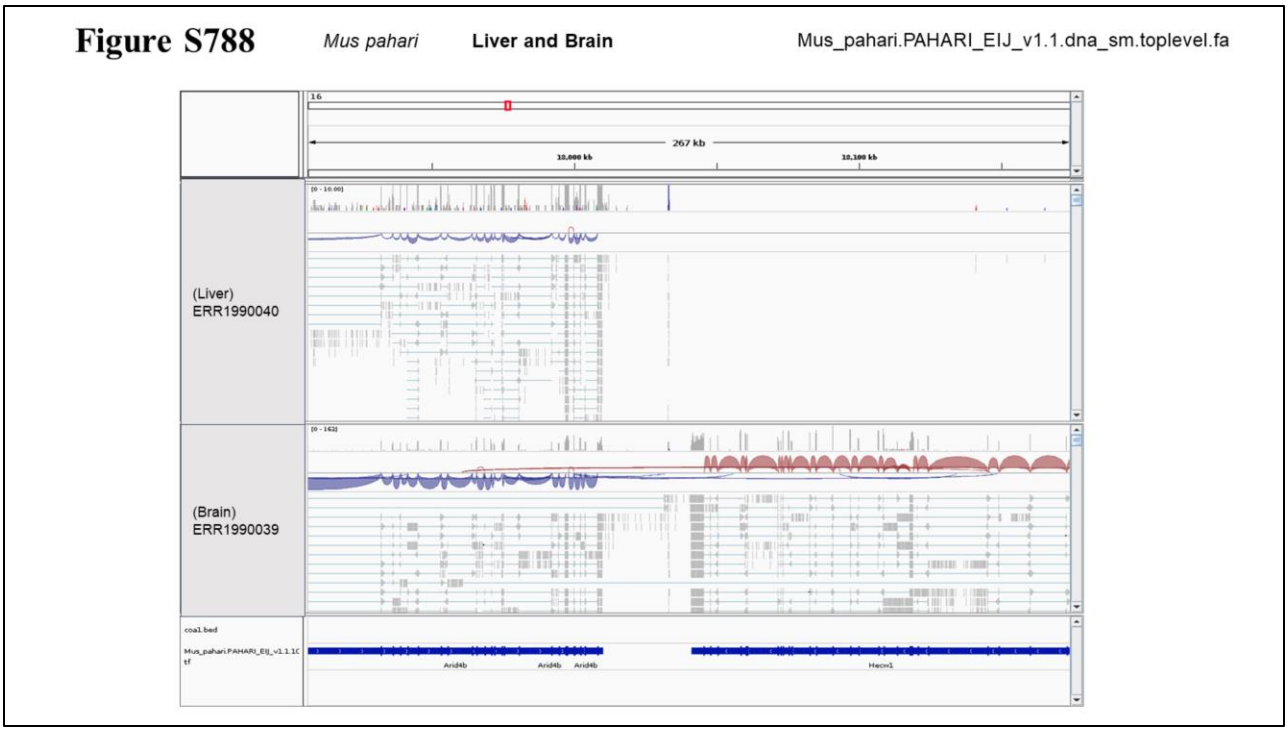

Figure S788: Screenshot of RNA-seq reads aligned each of the putative locations of *ARID4B* and *HECW1* in shrew mouse (*Mus pahari*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (ERR1990040) and brain (ERR1990039) have been mapped to the Mus_pahari.PAHARI_EIJ_v1.1.dna_sm.toplevel.fa genome. Locations of *ARID4B* and *HECW1* are depicted as Mus_pahari.PAHARI_EIJ_v1.1.102.gtf record in the bottom row.

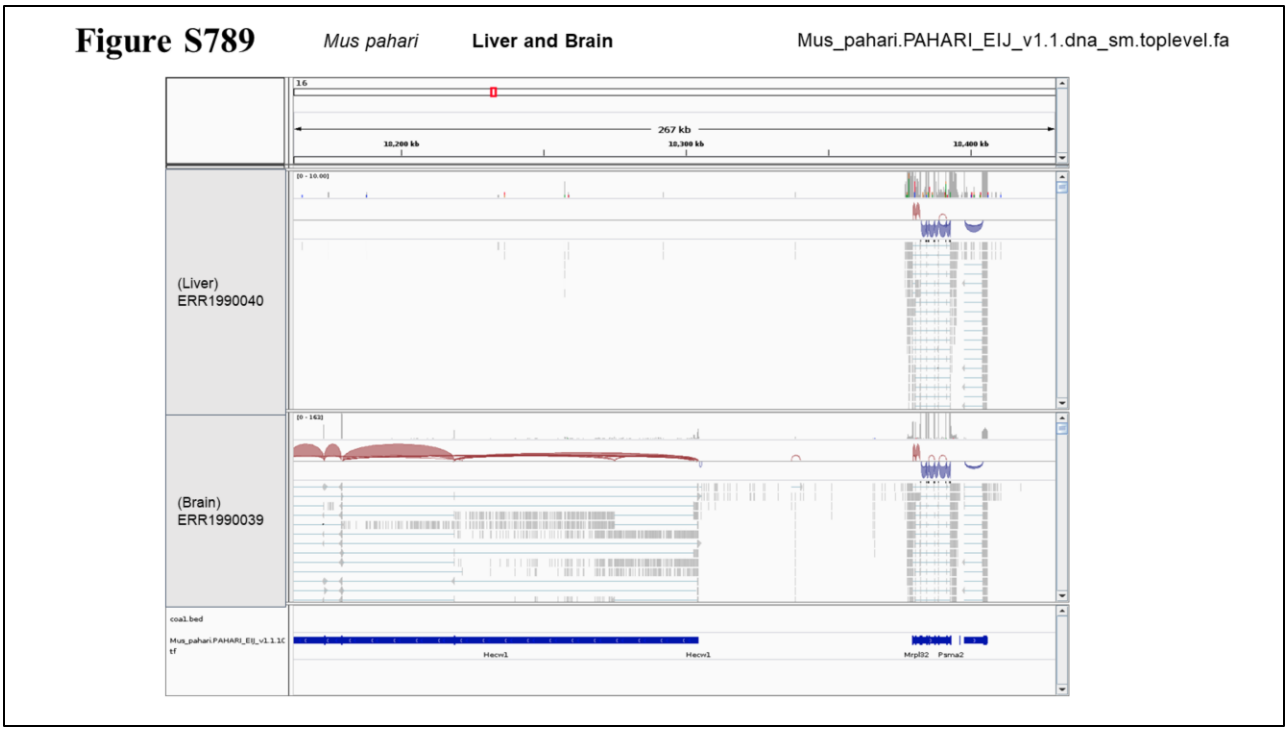

Figure S789: Screenshot of RNA-seq reads aligned each of the putative locations of *PSMA2* and *HECW1* in shrew mouse (*Mus pahari*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (ERR1990040) and brain (ERR1990039) have been mapped to the Mus_pahari.PAHARI_EIJ_v1.1.dna_sm.toplevel.fa genome. Locations of *PSMA2* and *HECW1* are depicted as Mus_pahari.PAHARI_EIJ_v1.1.102.gtf record in the bottom row.

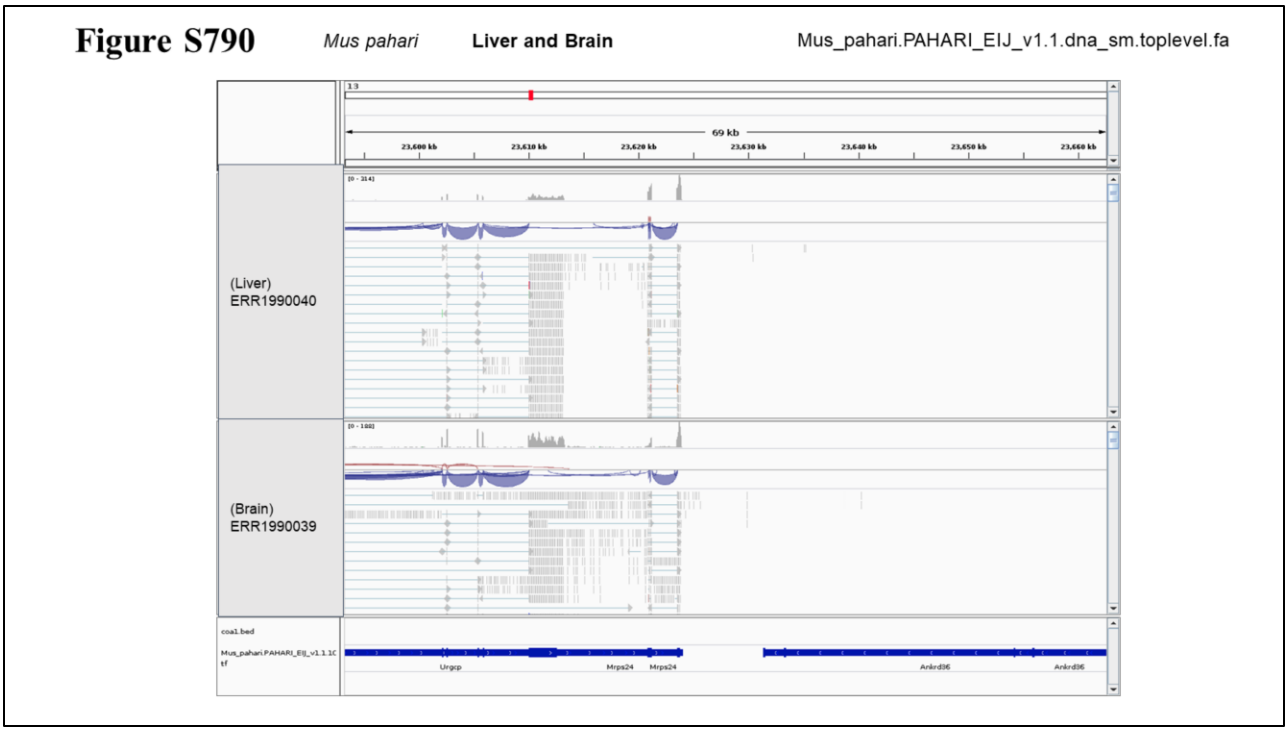

Figure S790: Screenshot of RNA-seq reads aligned each of the putative locations of *URGCP* and *ANKRD36* in shrew mouse (*Mus pahari*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (ERR1990040) and brain (ERR1990039) have been mapped to the Mus_pahari.PAHARI_EIJ_v1.1.dna_sm.toplevel.fa genome. Locations of *URGCP* and *ANKRD36* are depicted as Mus_pahari.PAHARI_EIJ_v1.1.102.gtf record in the bottom row.

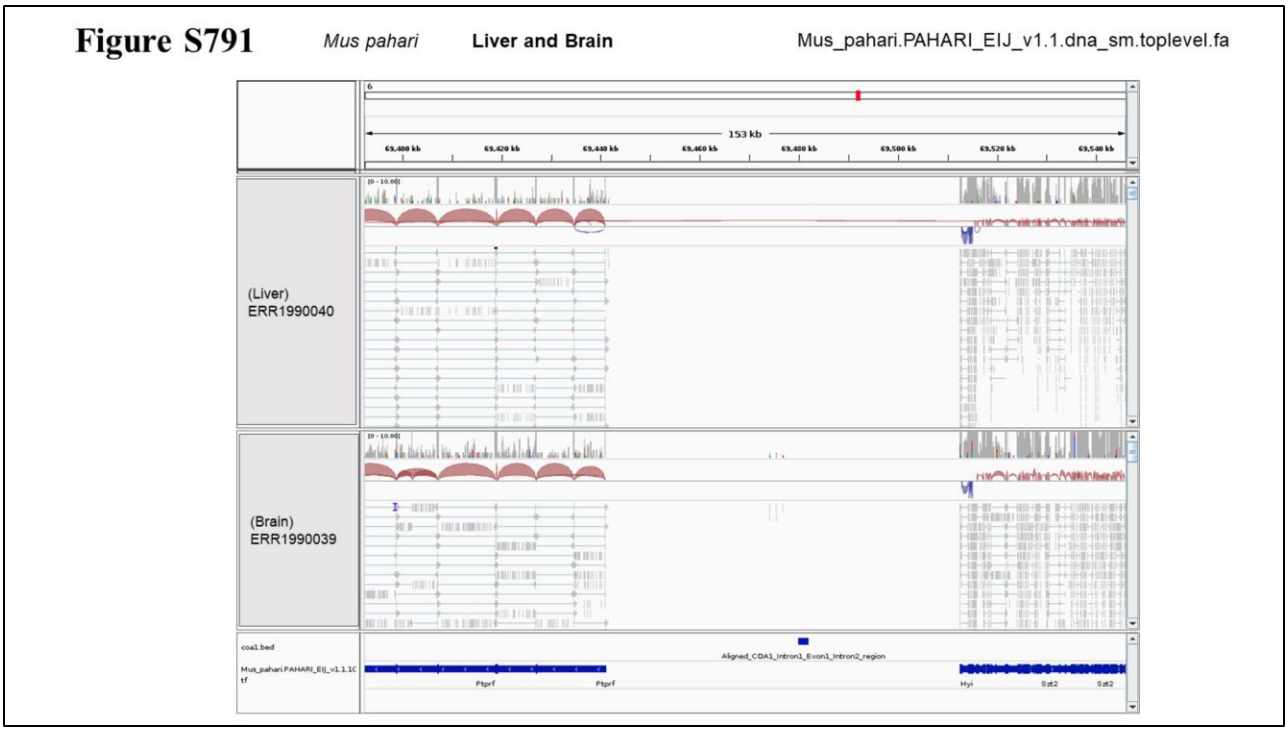

Figure S791: Screenshot of RNA-seq reads aligned each of the putative locations of truncated exon-1, intron-1 and intron-2 of *COA1* in shrew mouse (*Mus pahari*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (ERR1990040) and brain (ERR1990039) have been mapped to the Mus_pahari.PAHARI_EIJ_v1.1.dna_sm.toplevel.fa genome. Locations of truncated exon 1, intron-1 and intron-2 of *COA1* is depicted as bed record in the bottom row.

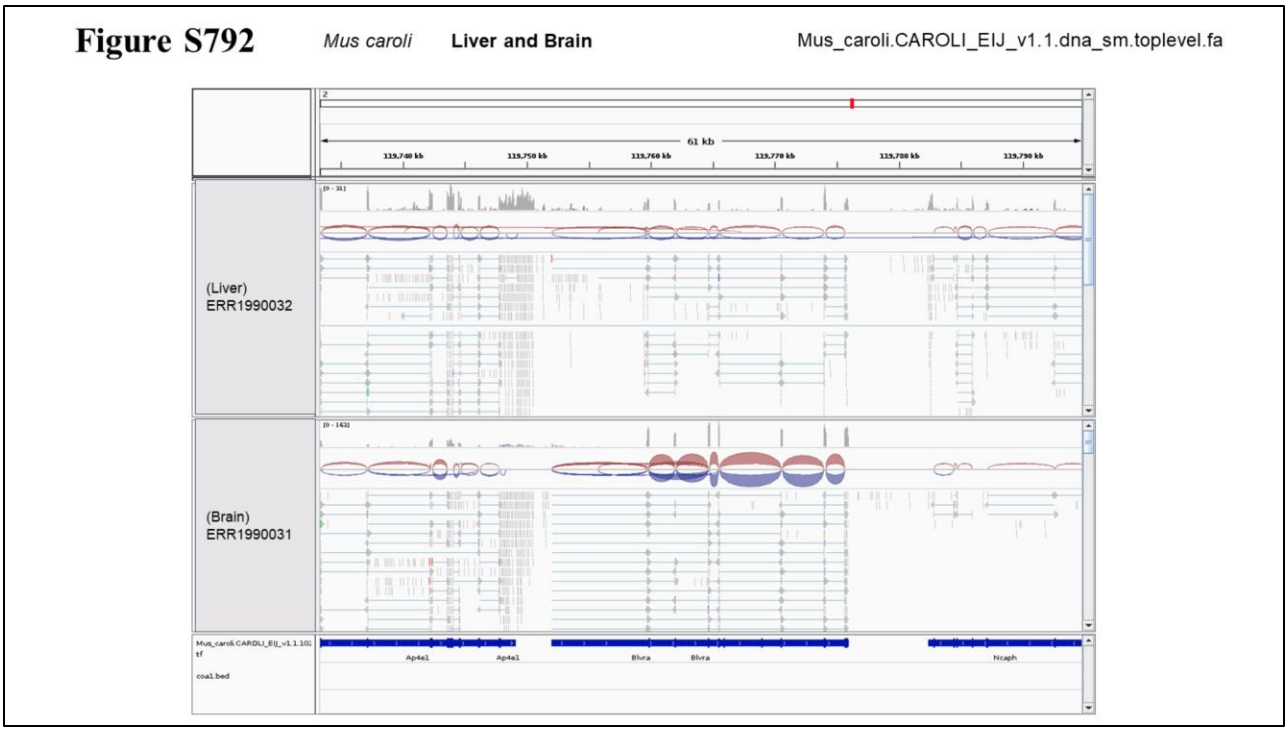

Figure S792: Screenshot of RNA-seq reads aligned each of the putative locations of *AP4E1* and *NCAPH* in Ryukyu mouse (*Mus caroli*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (ERR1990032) and brain (ERR1990031) have been mapped to the Mus_caroli.CAROLI_EIJ_v1.1.dna_sm.toplevel.fa genome. Locations of *AP4E1* and *NCAPH* are depicted as Mus_caroli.CAROLI_EIJ_v1.1.102.gtf record in the bottom row.

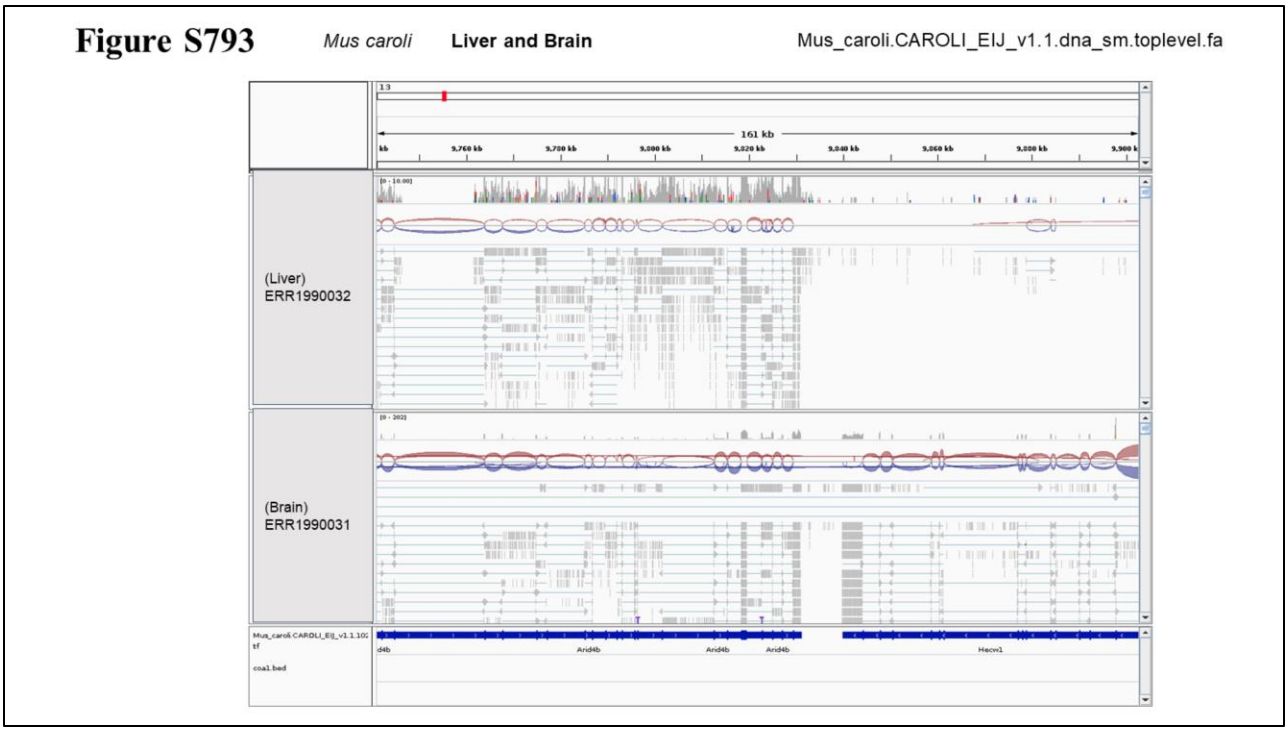

Figure S793: Screenshot of RNA-seq reads aligned each of the putative locations of *ARIDB* and *HECW1* in Ryukyu mouse (*Mus caroli*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (ERR1990032) and brain (ERR1990031) have been mapped to the Mus_caroli.CAROLI_EIJ_v1.1.dna_sm.toplevel.fa genome. Locations of *ARID4B* and *HECW1* are depicted as Mus_caroli.CAROLI_EIJ_v1.1.102.gtf record in the bottom row.

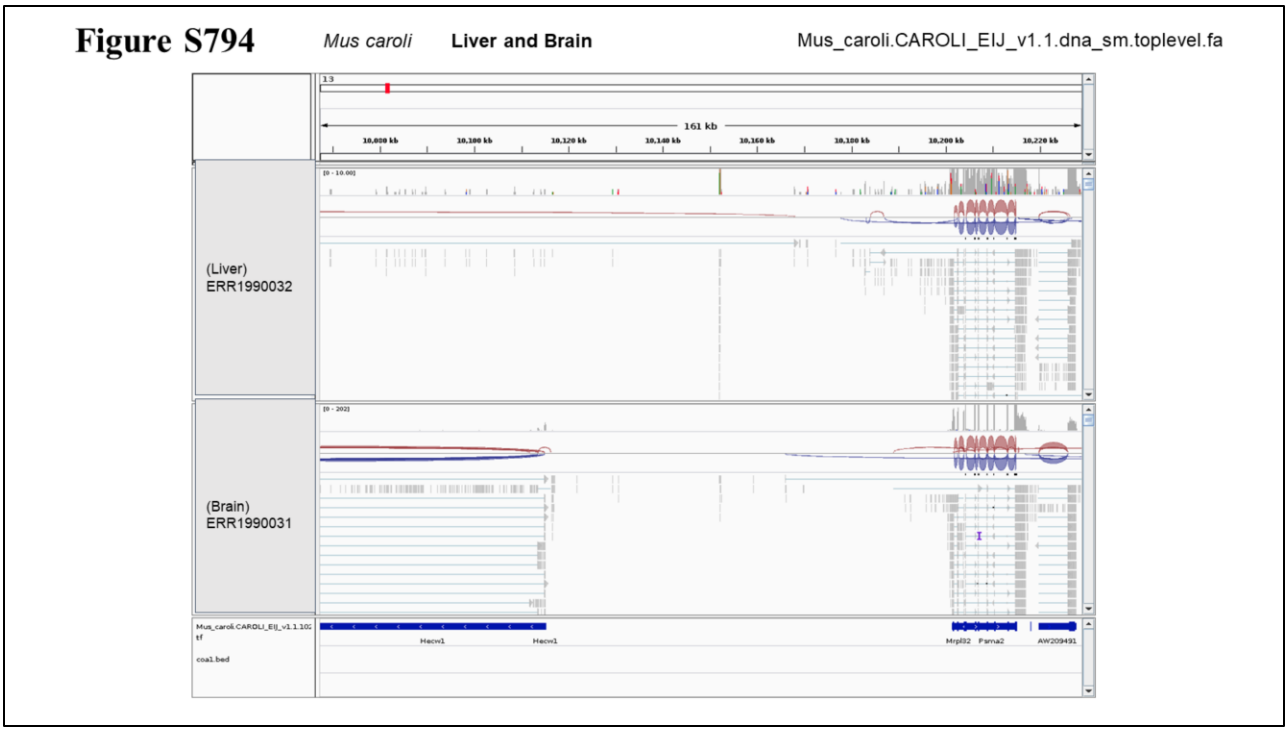

Figure S794: Screenshot of RNA-seq reads aligned each of the putative locations of *HECW1* and *MRPL32* in Ryukyu mouse (*Mus caroli*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (ERR1990040) and brain (ERR1990039) have been mapped to the Mus_caroli.CAROLI_EIJ_v1.1.dna_sm.toplevel.fa genome. Locations of *HECW1* and *MRPL32* are depicted as Mus_caroli.CAROLI_EIJ_v1.1.102.gtf record in the bottom row.

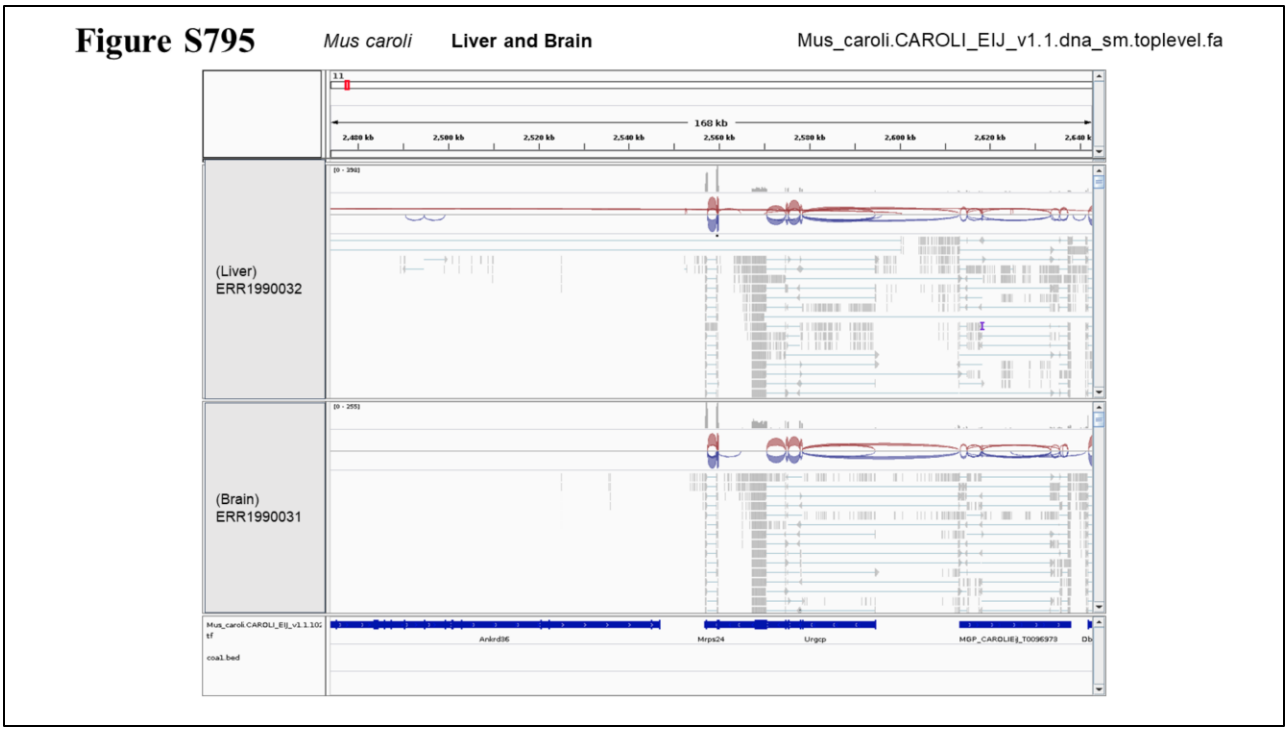

Figure S795: Screenshot of RNA-seq reads aligned each of the putative locations of *ANKRD36* and *URGCP* in Ryukyu mouse (*Mus caroli*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (ERR1990040) and brain (ERR1990039) have been mapped to the Mus_caroli.CAROLI_EIJ_v1.1.dna_sm.toplevel.fa genome. Locations of *ANKRD36* and *URGCP* are depicted as Mus_caroli.CAROLI_EIJ_v1.1.102.gtf record in the bottom row.

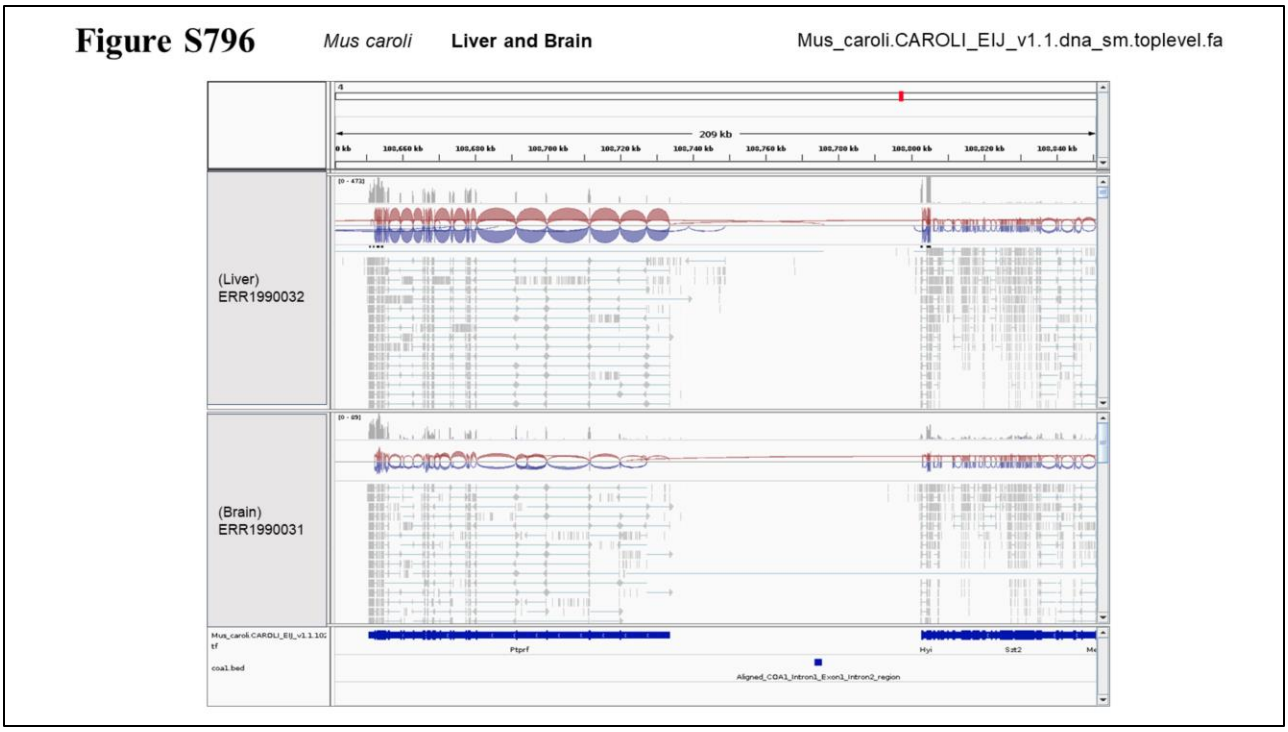

Figure S796: Screenshot of RNA-seq reads aligned each of the putative locations of truncated exon 1, intron-1 and intron-2 of *COA1* in Ryukyu mouse (*Mus caroli*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (ERR1990040) and brain (ERR1990039) have been mapped to the Mus_caroli.CAROLI_EIJ_v1.1.dna_sm.toplevel.fa genome. Locations of truncated exon 1, intron-1 and intron-2 of *COA1* is depicted as bed record in the bottom row.

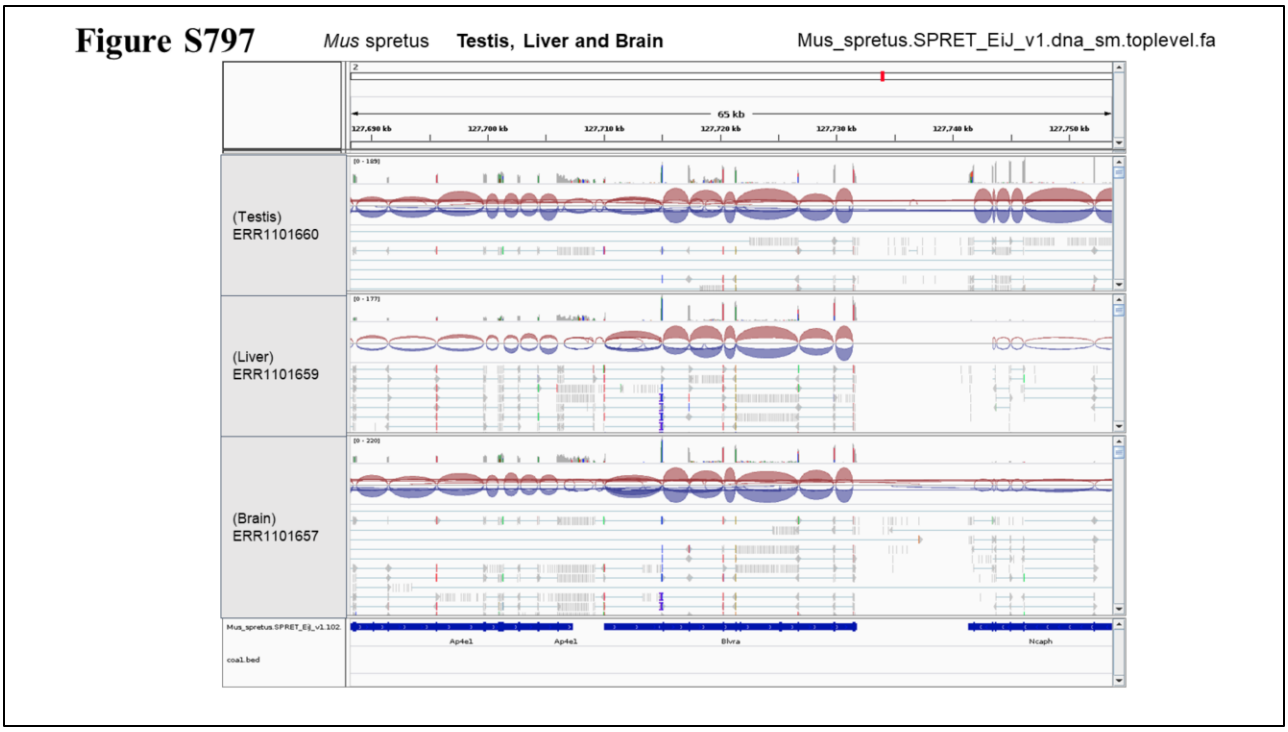

Figure S797: Screenshot of RNA-seq reads aligned each of the putative locations of *AP4E1* and *NCAPH* in Algerian mouse (*Mus spretus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis (ERR1101660), liver (ERR1101659) and brain (ERR1101657) have been mapped to the Mus_spretus.SPRET_EiJ_v1.dna_sm.toplevel.fa. Locations of *AP4E1* and *NCAPH* are depicted as Mus_spretus.SPRET_EiJ_v1.102.gtf record in the bottom row.