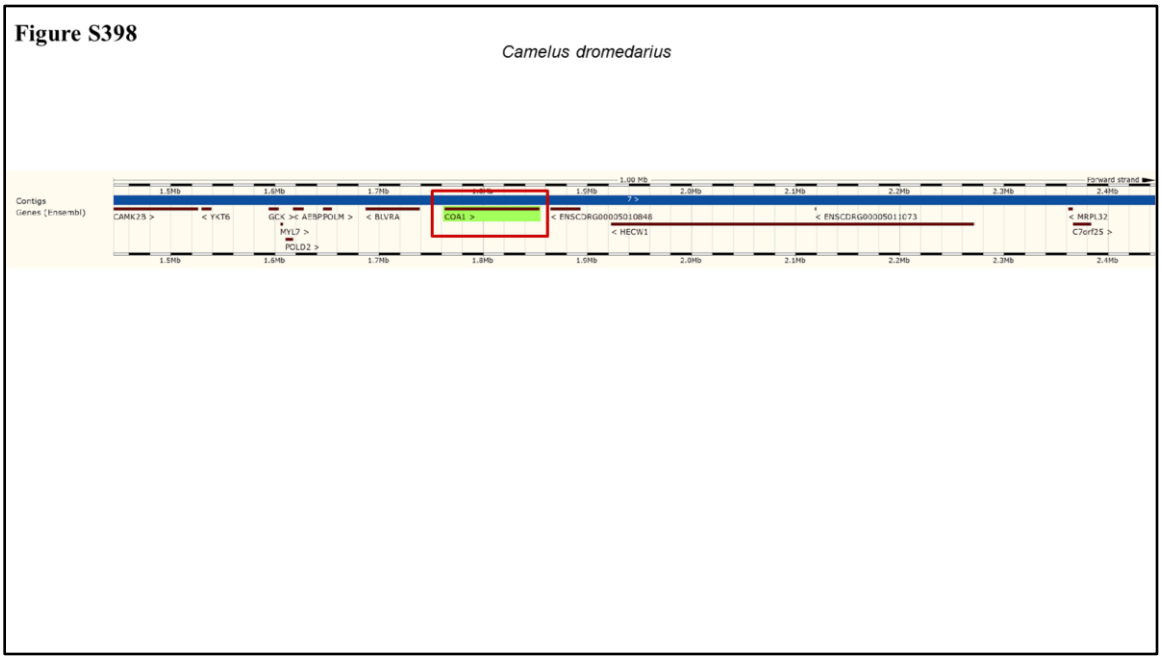

Figure S398: Gene order near *COA1* gene in the Arabian camel genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

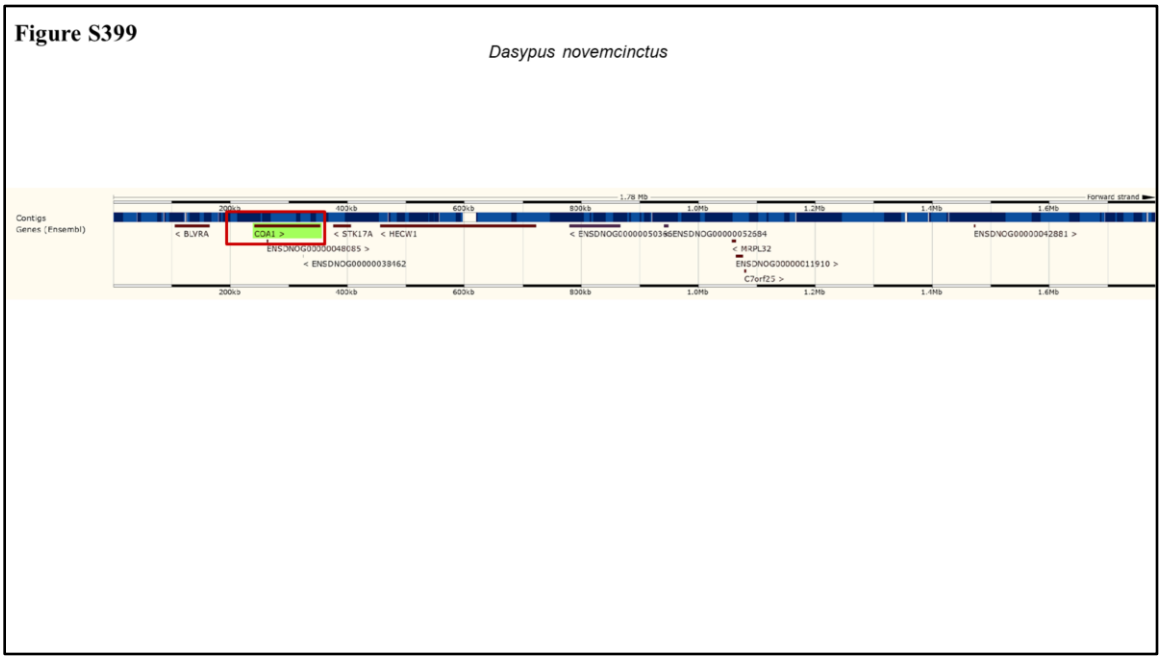

Figure S399: Gene order near *COA1* gene in the armadillo genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

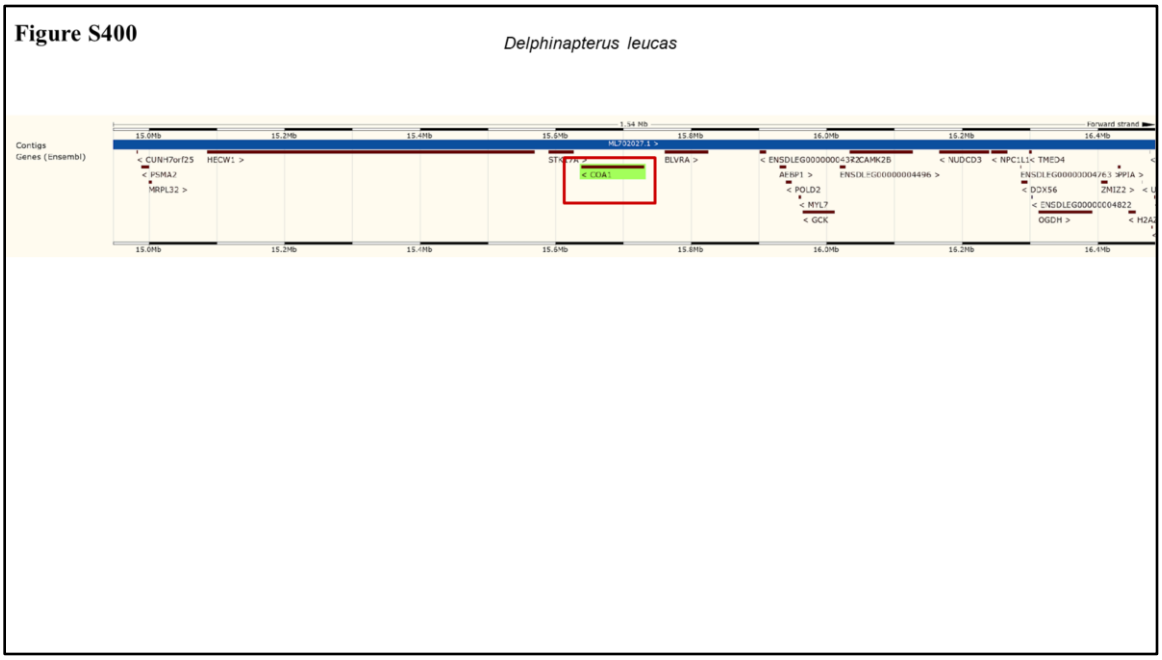

Figure S400: Gene order near *COA1* gene in the Beluga whale genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

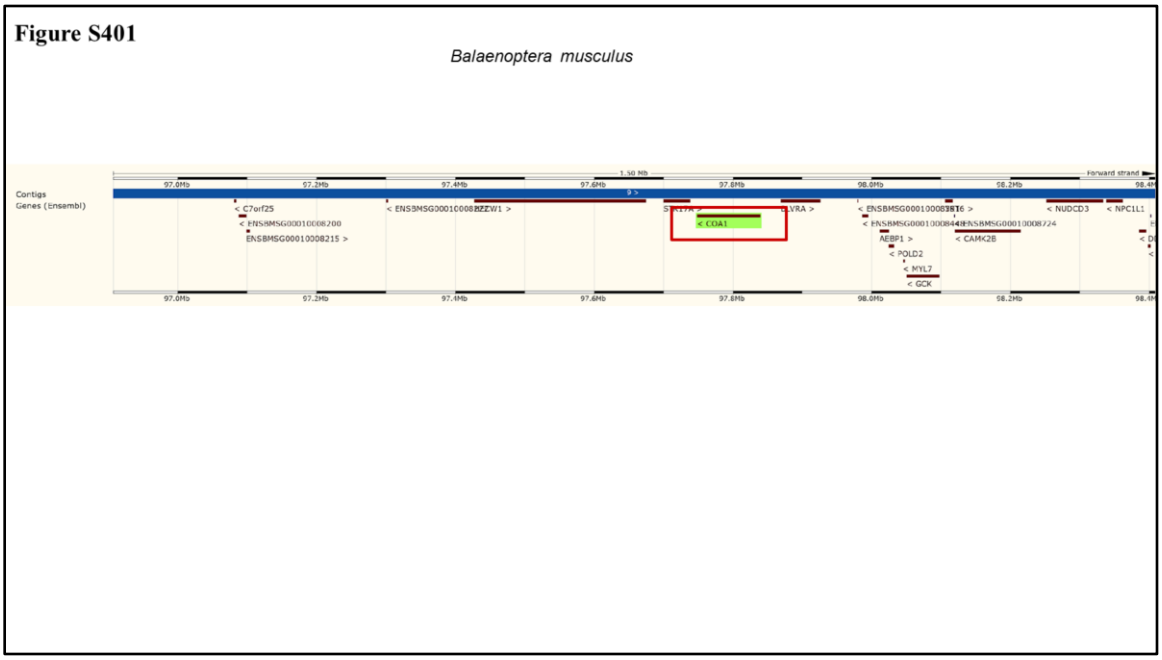

Figure S401: Gene order near *COA1* gene in the blue whale genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

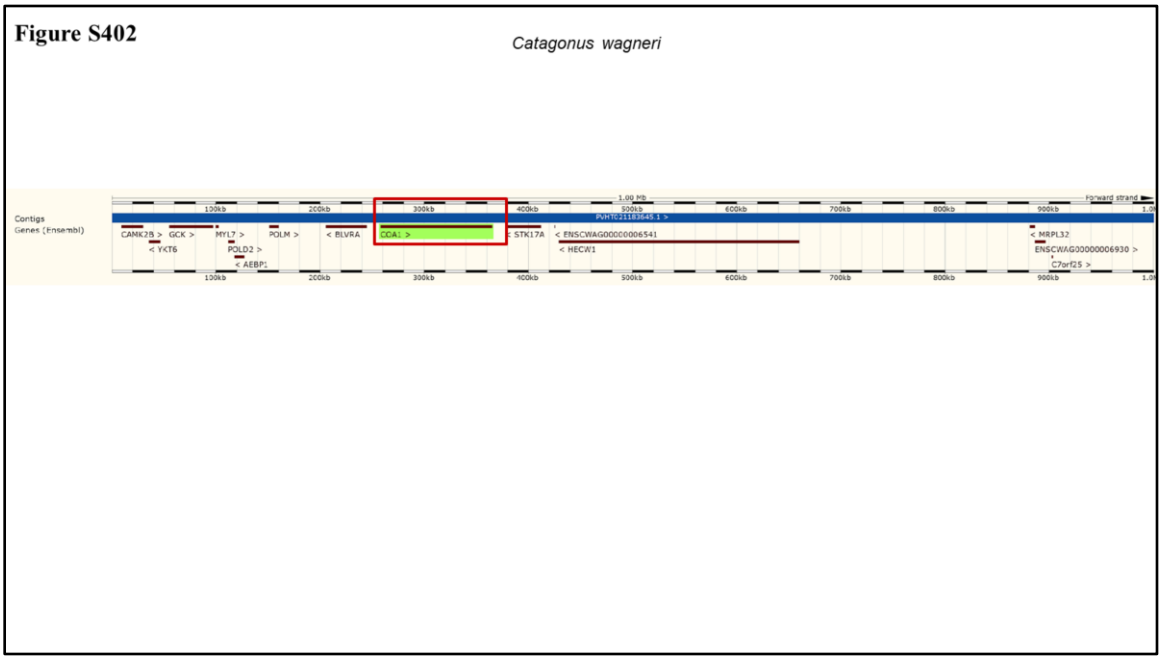

Figure S402: Gene order near *COA1* gene in the chacoan peccary genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

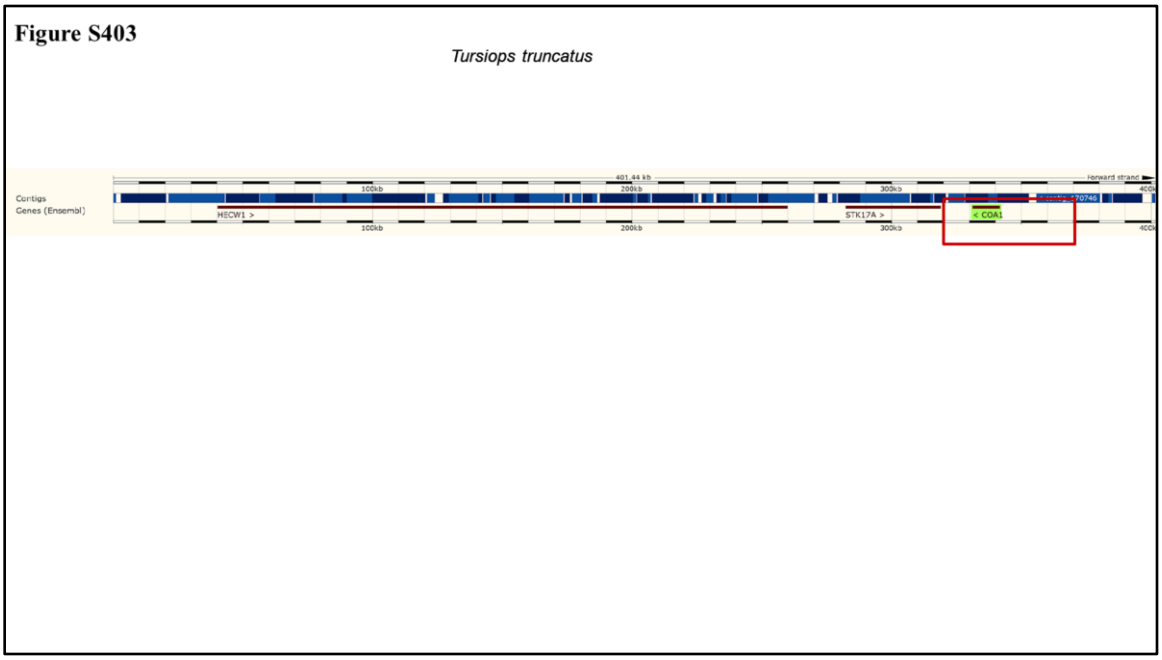

Figure S403: Gene order near *COA1* gene in the dolphin genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

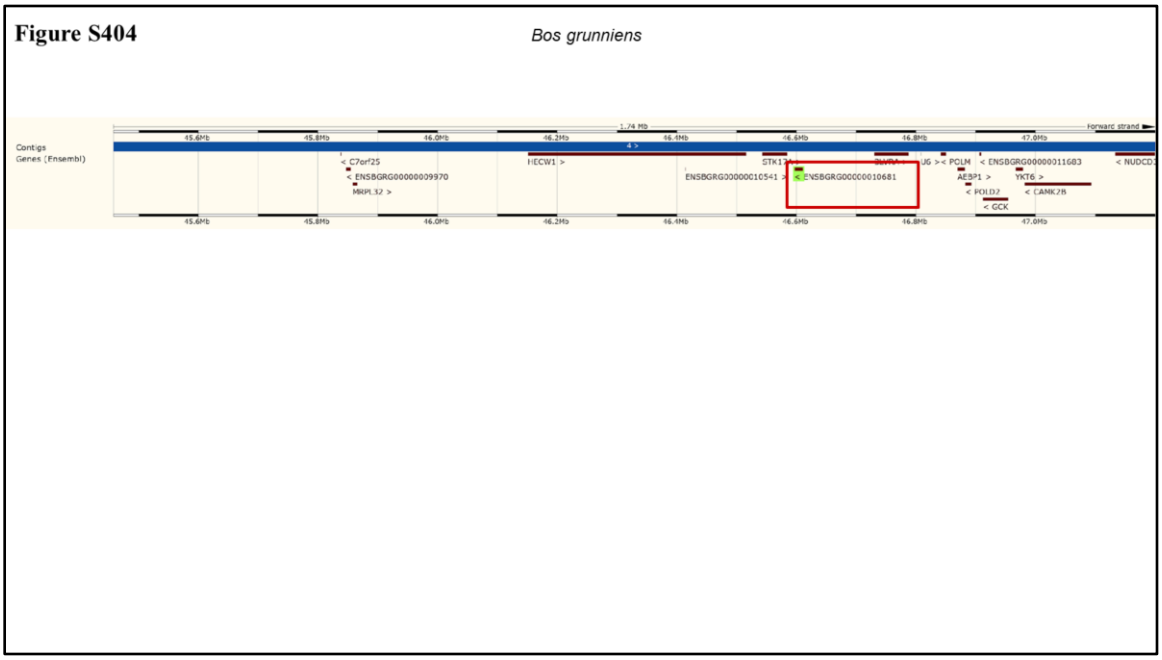

Figure S404: Gene order near *COA1* gene in the domestic yalk genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

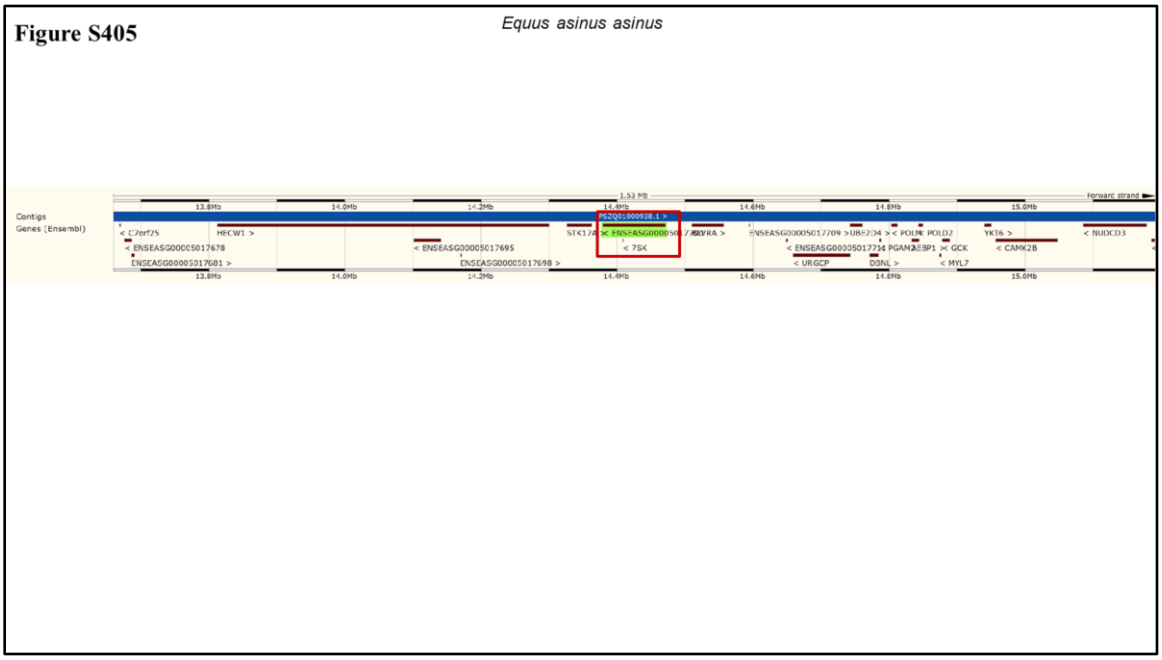

Figure S405: Gene order near *COA1* gene in the donkey genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

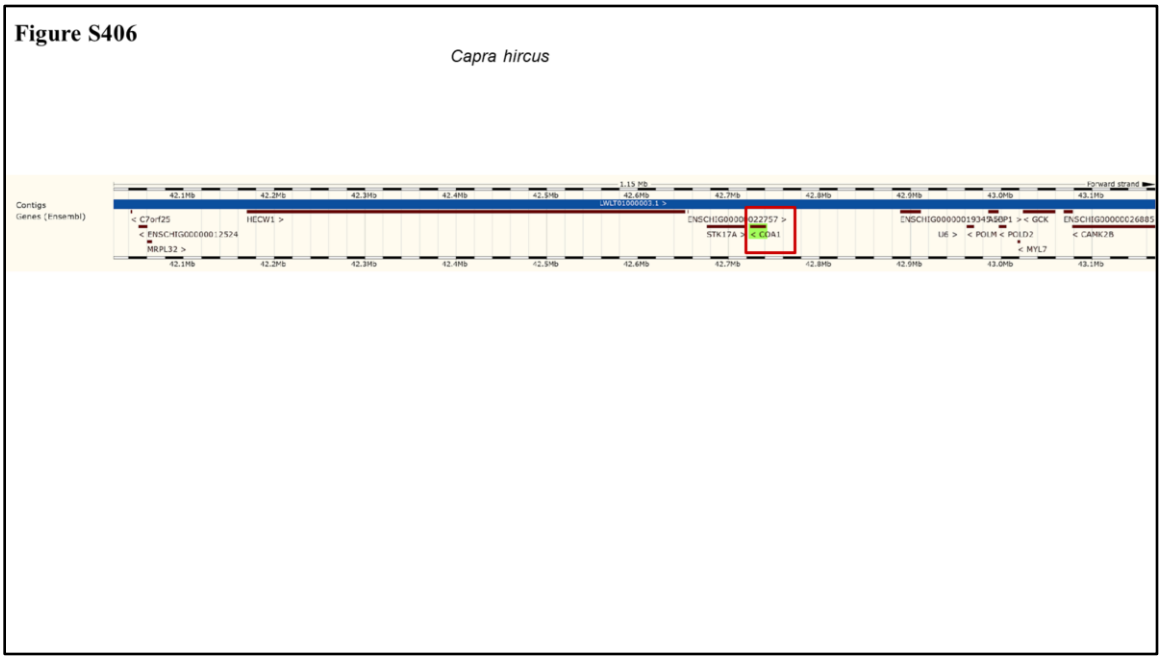

Figure S406: Gene order near *COA1* gene in the goat genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S407

Rhinolophus ferrumequinum

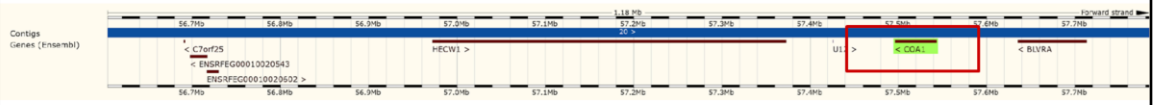

Figure S408: Gene order near *COA1* gene in the greater horseshoe bat genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

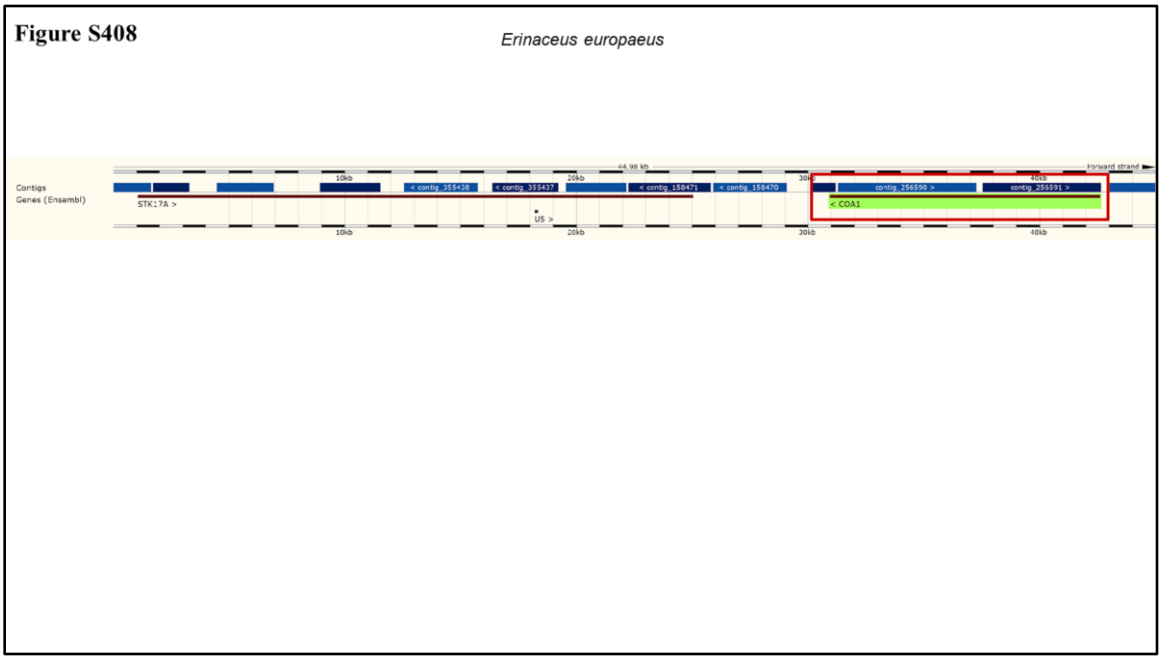

Figure S408: Gene order near *COA1* gene in the hedgehog genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

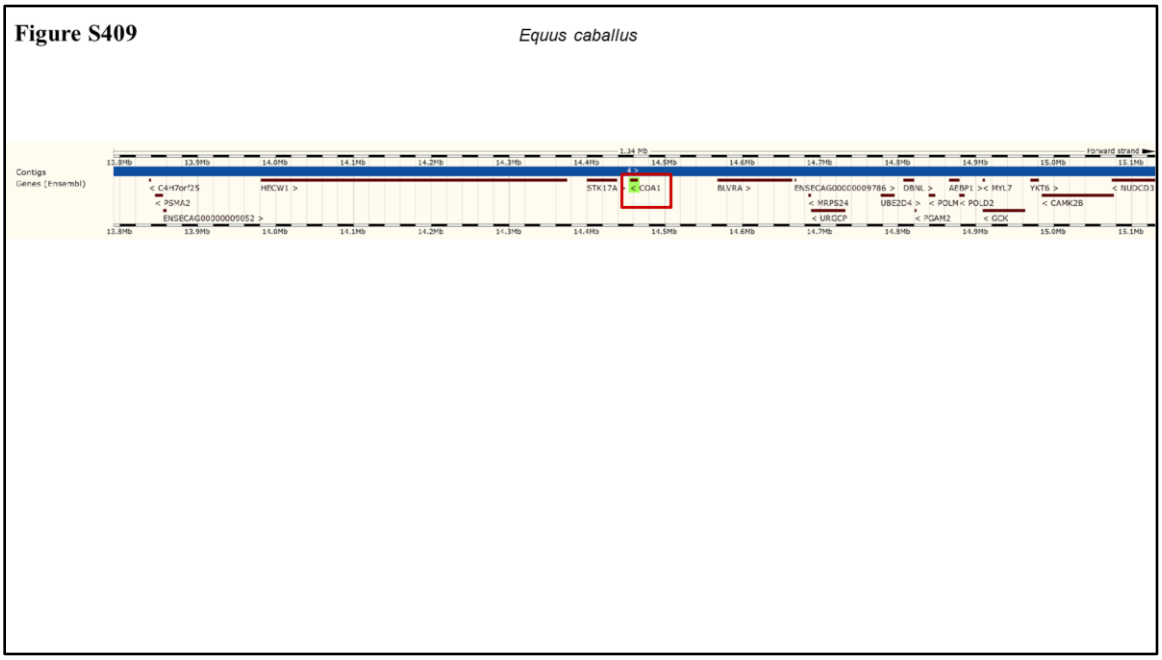

Figure S409: Gene order near *COA1* gene in the horse genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

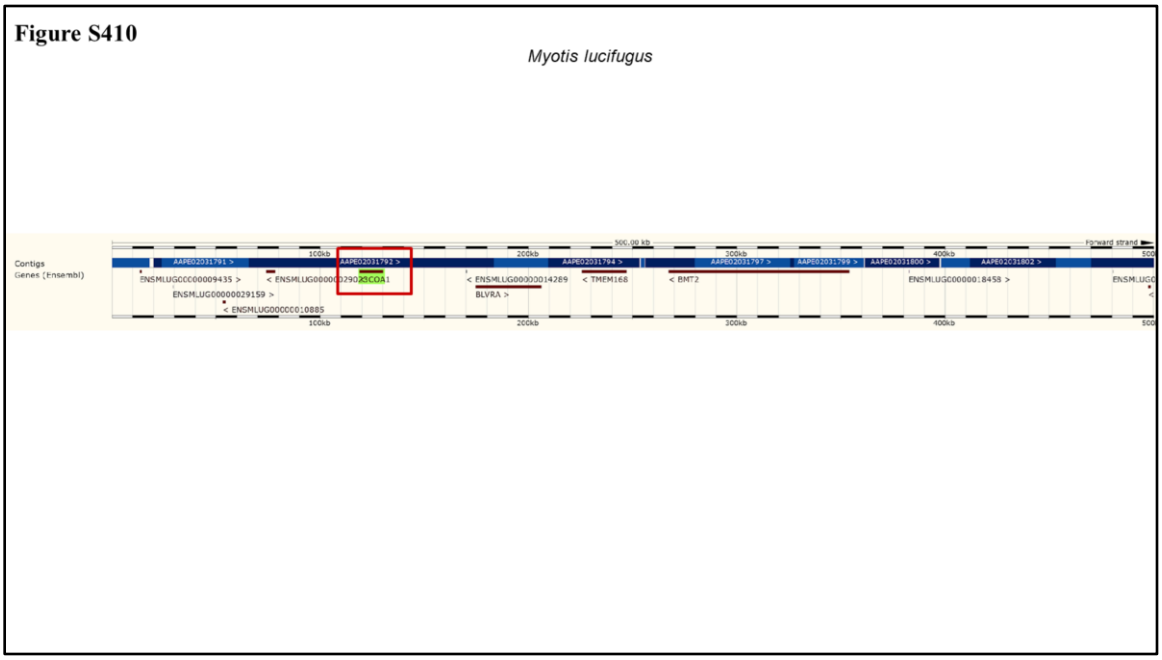

Figure S410: Gene order near *COA1* gene in the microbat genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

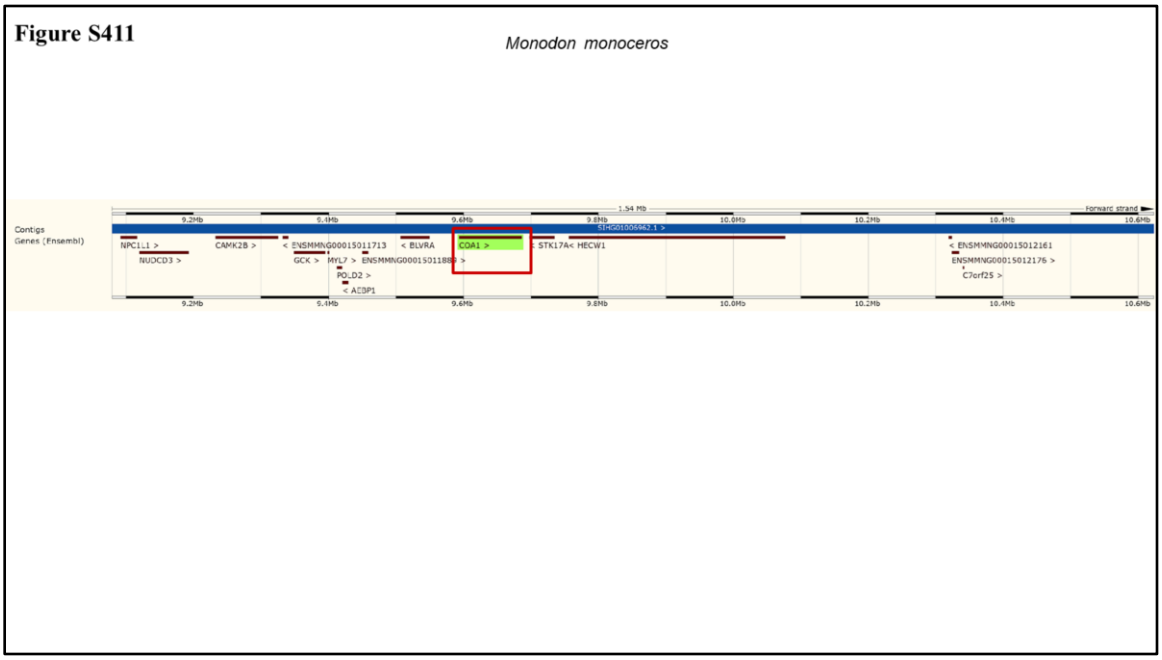

Figure S411: Gene order near *COA1* gene in the narwhal genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

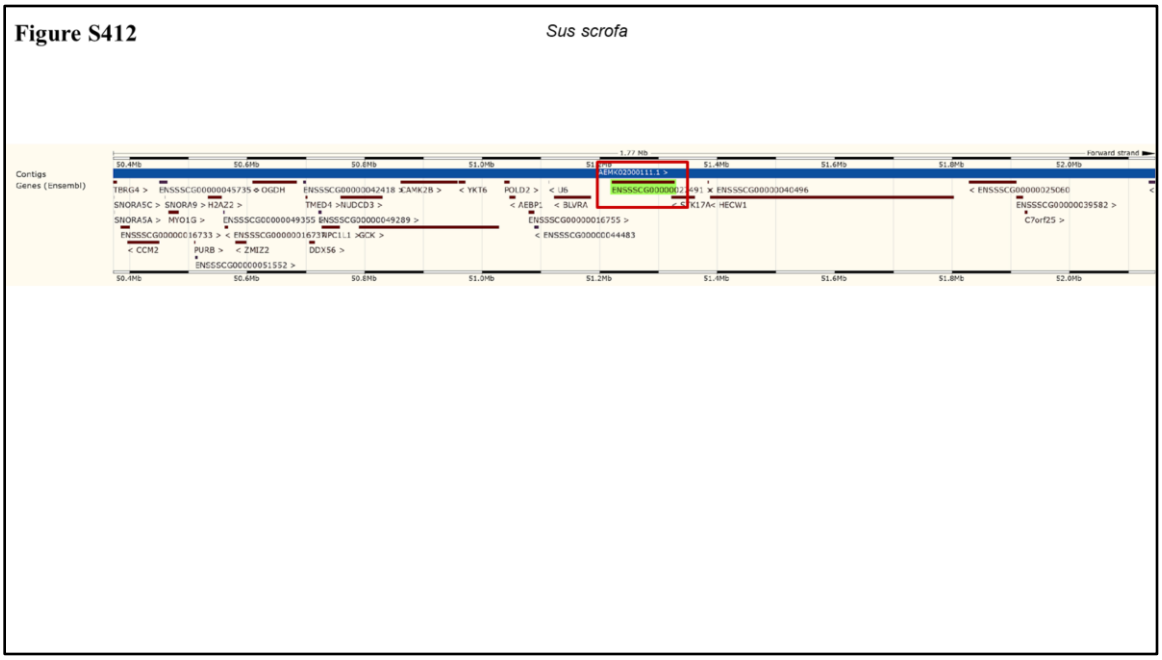

Figure S412: Gene order near *COA1* gene in the pig genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

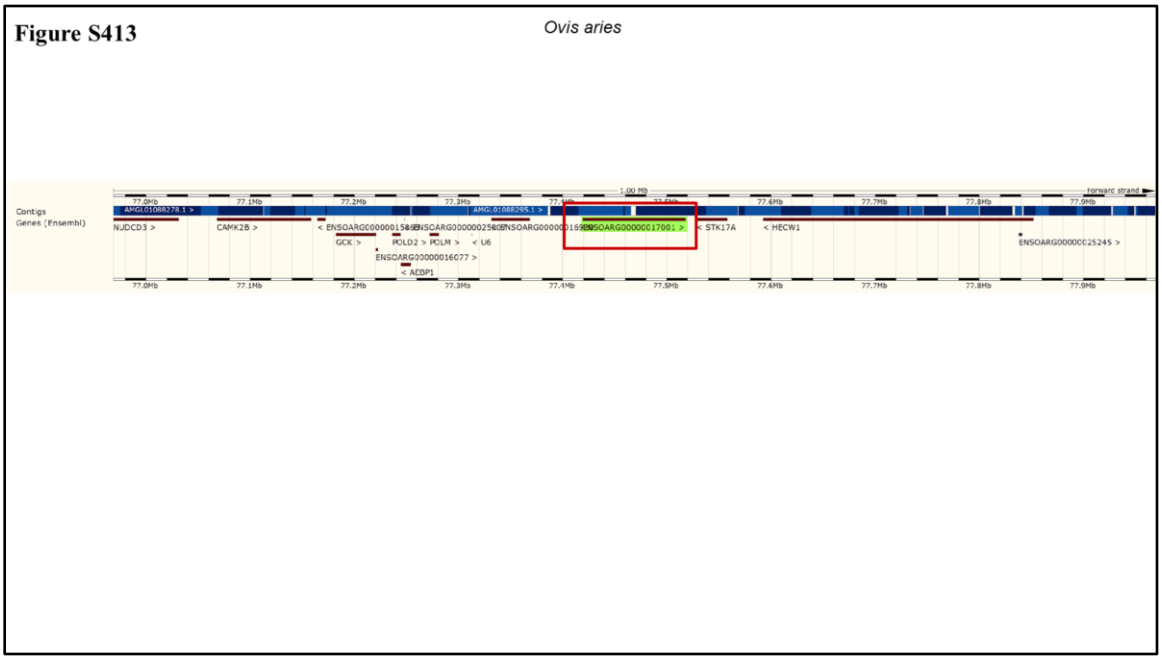

Figure S413: Gene order near *COA1* gene in the sheep genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

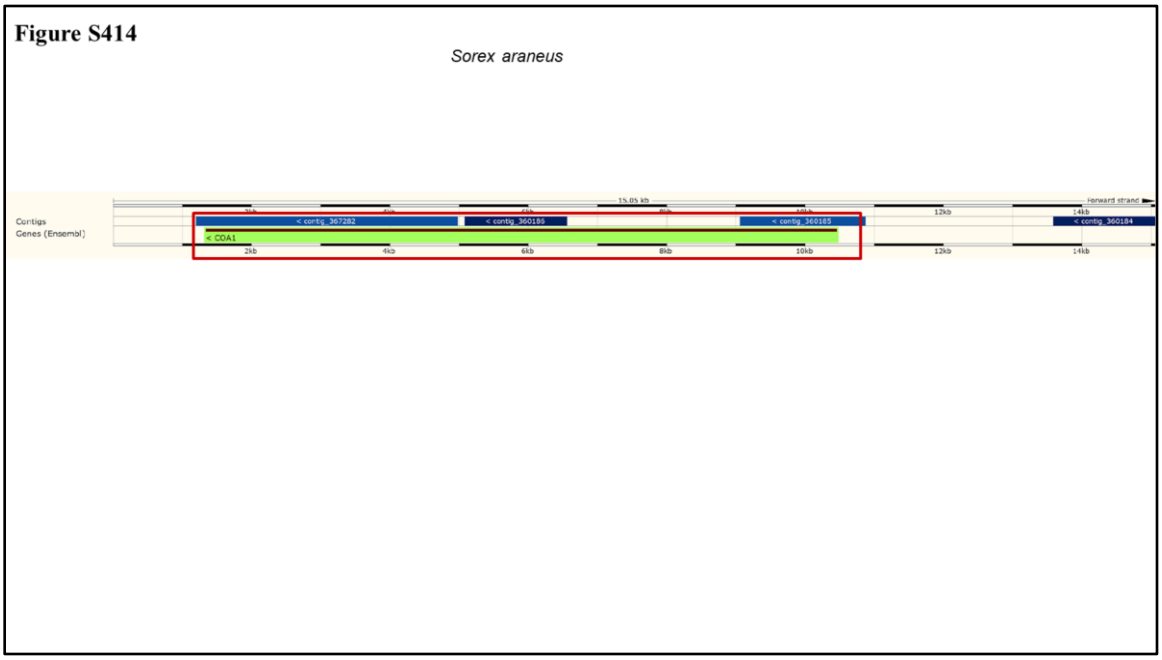

Figure S414: Gene order near *COA1* gene in the shrew genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

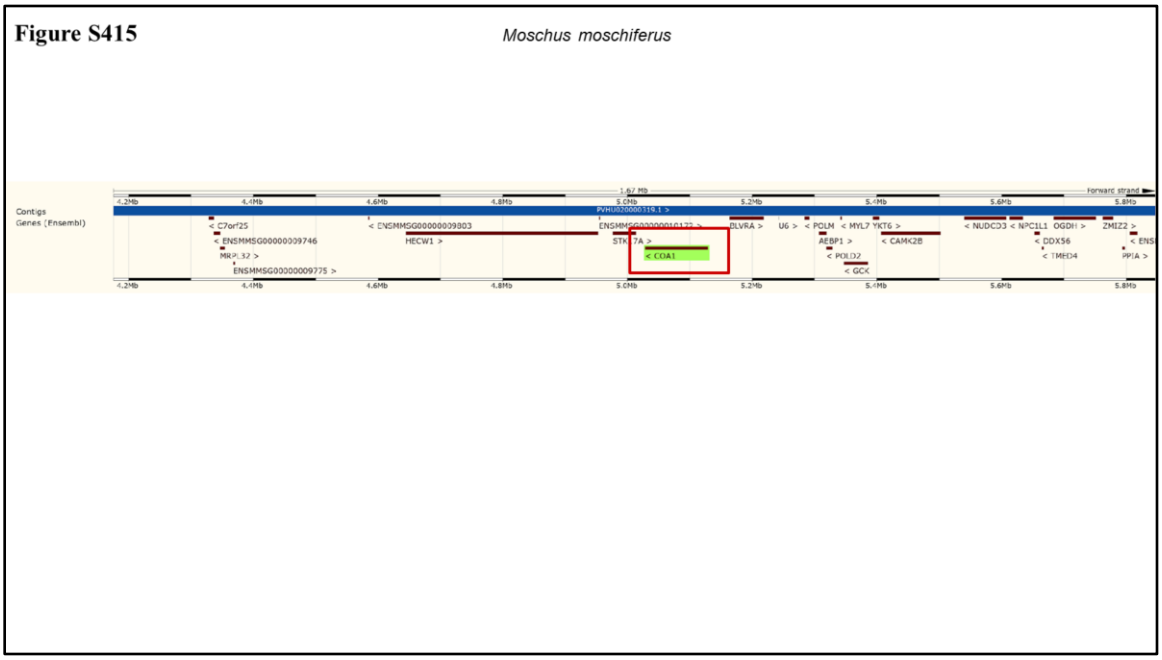

Figure S415: Gene order near *COA1* gene in the Siberian musk deer genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S416

Phocoena sinus

Figure S416: Gene order near *COA1* gene in the Vaquita genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

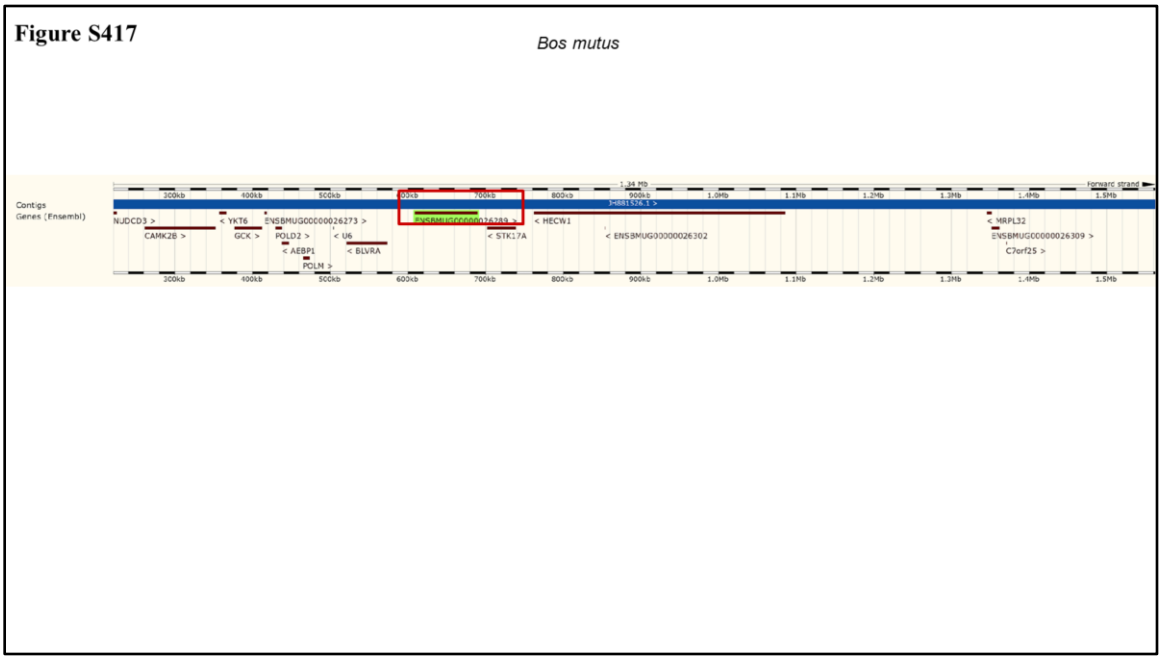

Figure S417: Gene order near *COA1* gene in the wild yak genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

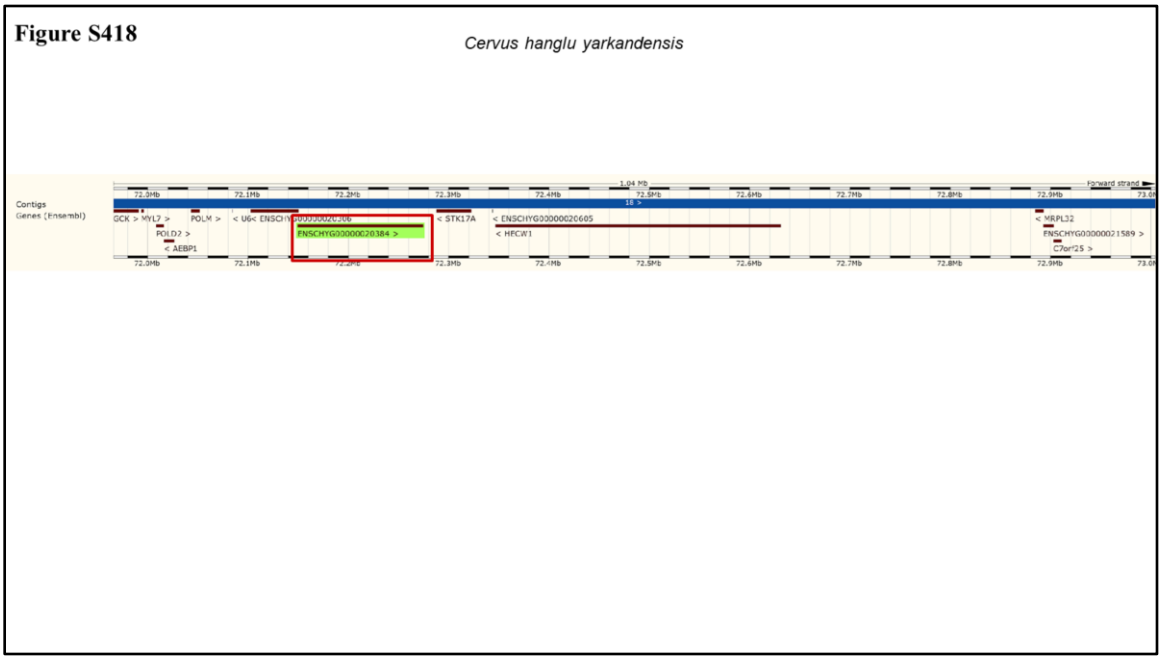

Figure S418: Gene order near *COA1* gene in the Yarkand deer genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

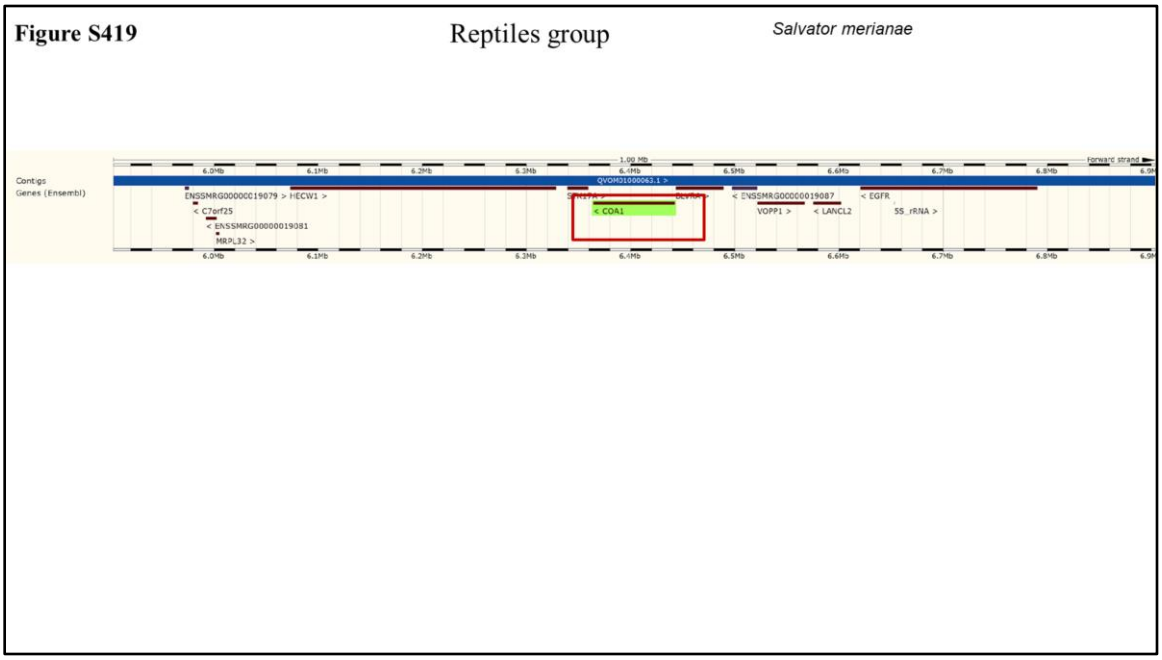

Figure S419: Gene order near *COA1* gene in the Argentine black and white tegu genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S420

Pelodiscus sinensis

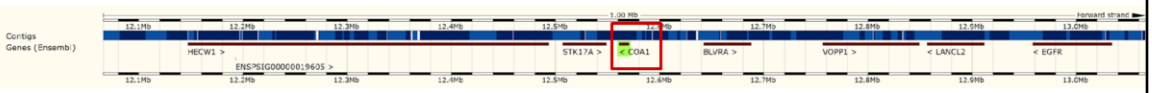

Figure S420: Gene order near *COA1* gene in the Chinese softshell turtle genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

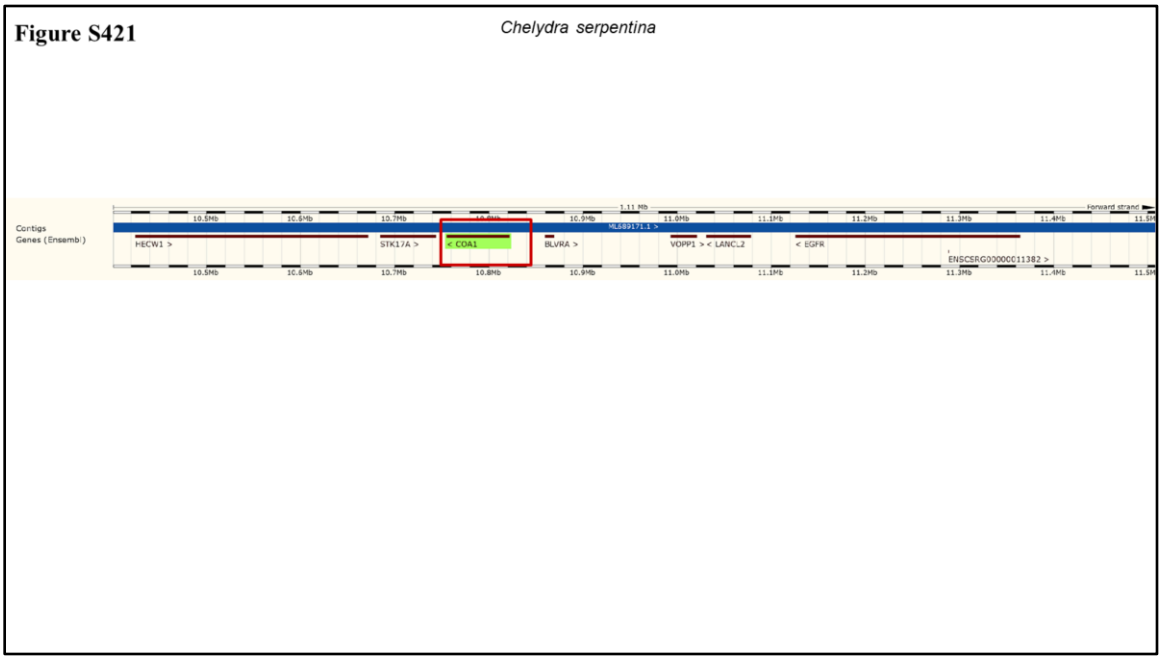

Figure S421: Gene order near *COA1* gene in the common snapping turtle genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

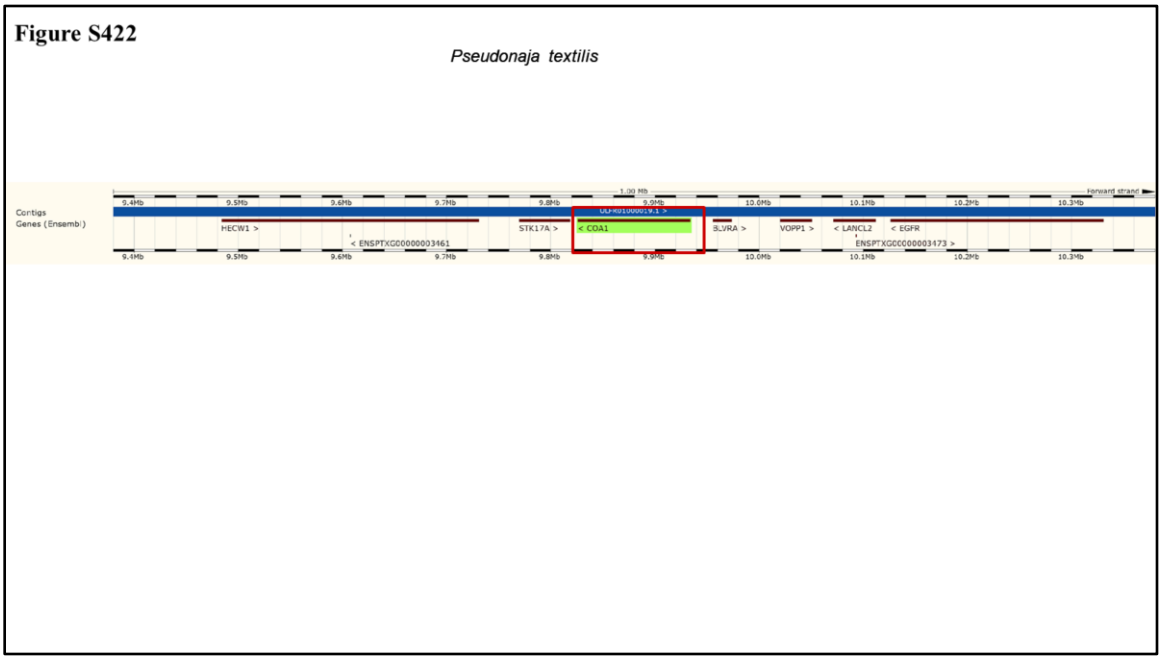

Figure S422: Gene order near *COA1* gene in the Eastern brown snake genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

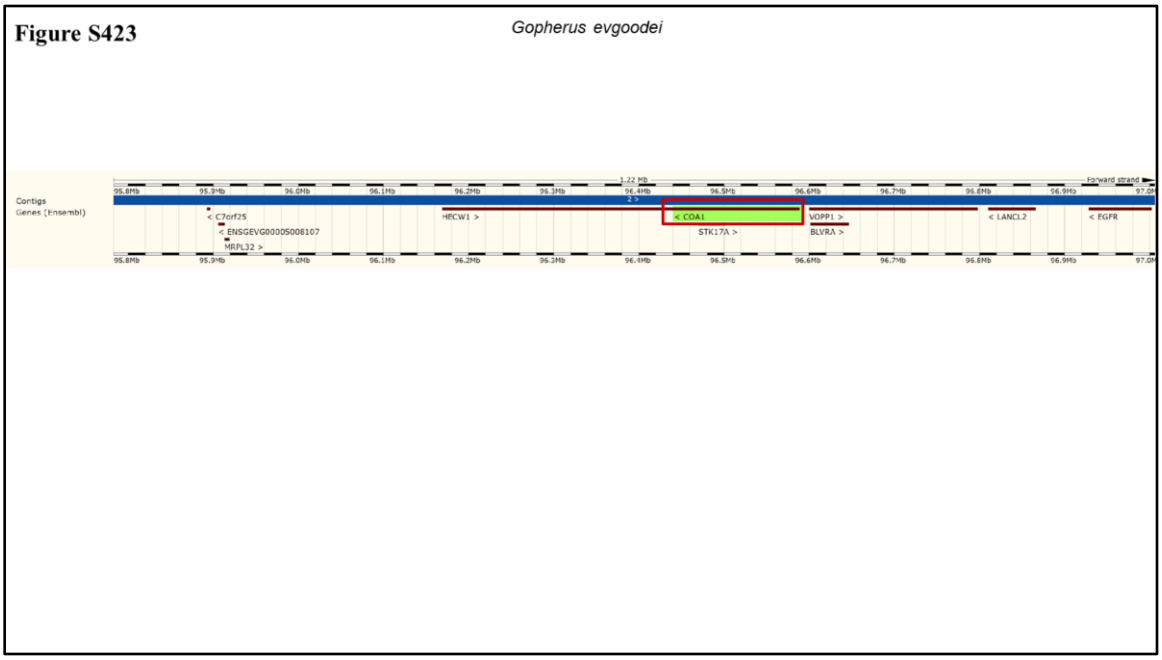

Figure S423: Gene order near *COA1* gene in the Goodes thornscrub tortoise genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

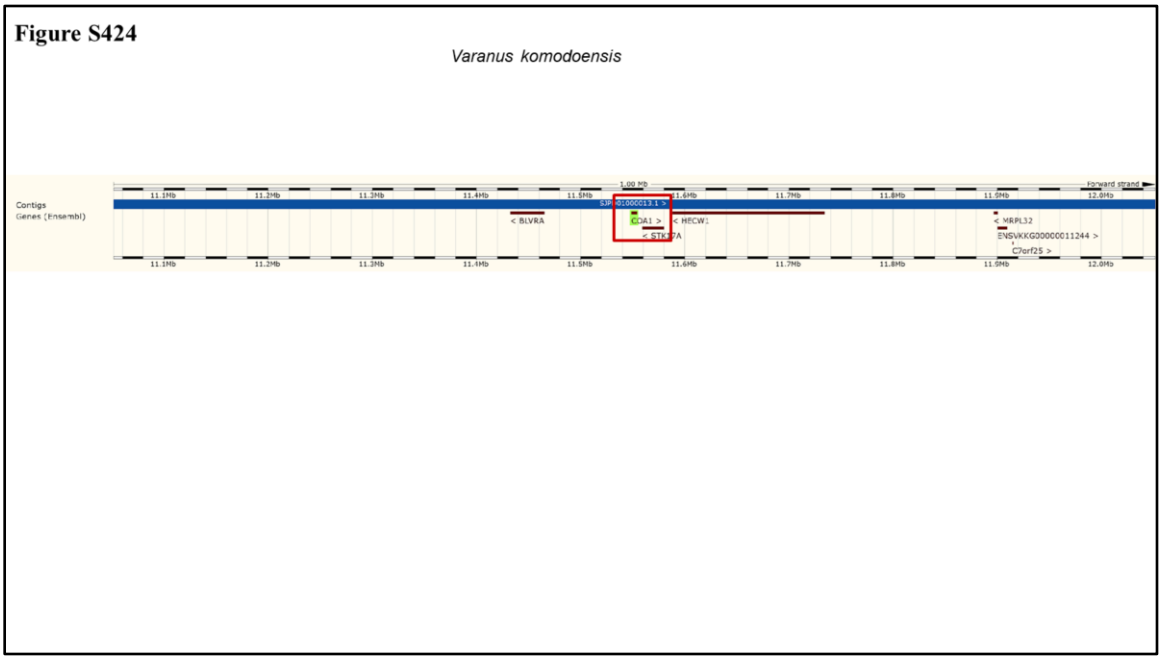

Figure S424: Gene order near *COA1* gene in the komodo dragon genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

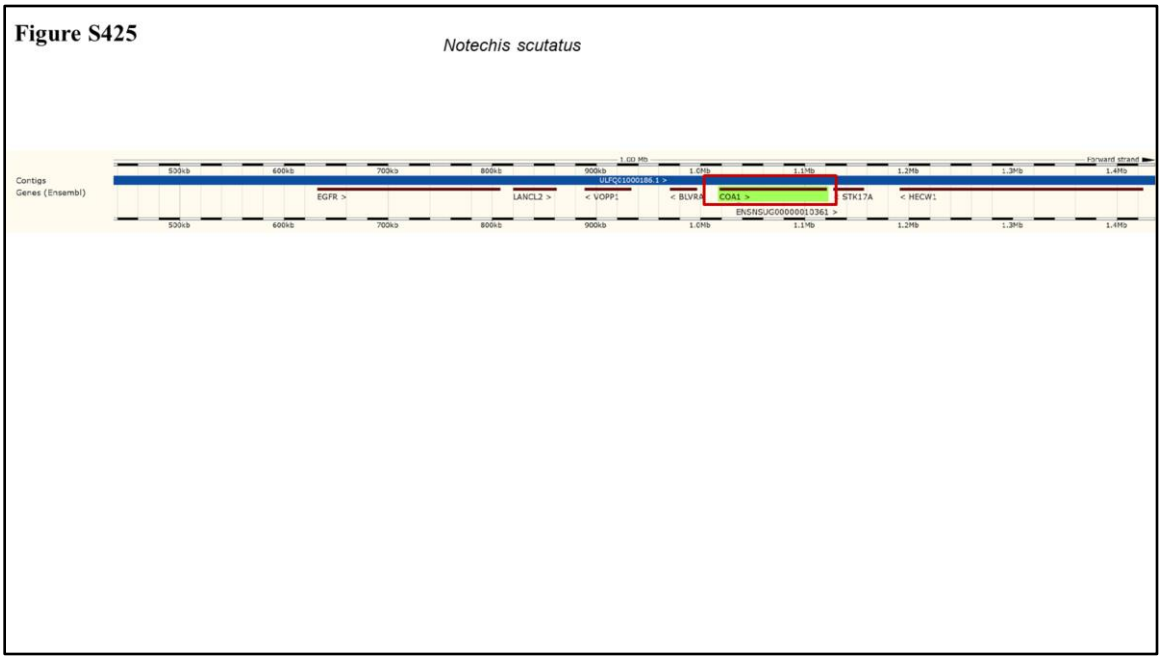

Figure S425: Gene order near *COA1* gene in the mainland tiger snake genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S426

Pelusios castaneus

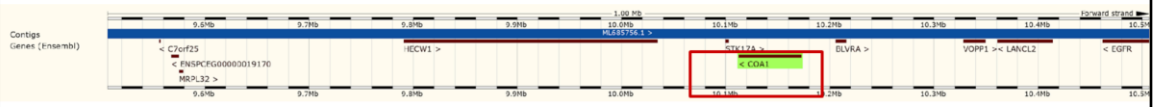

Figure S426: Gene order near *COA1* gene in the West African mud turtle genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

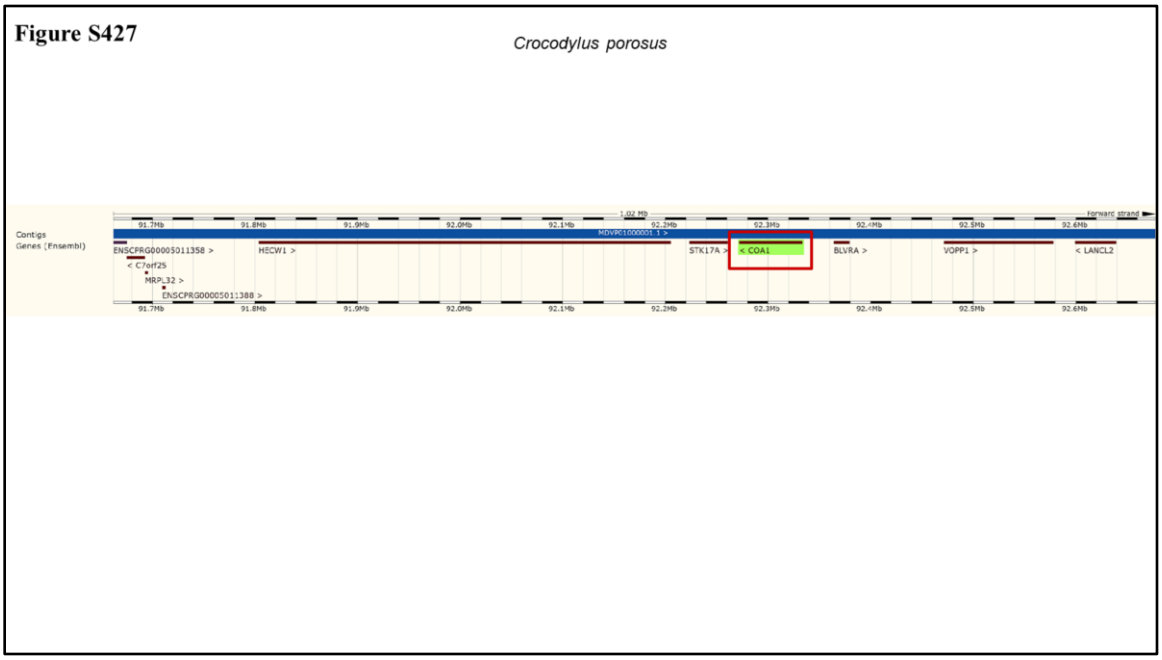

Figure S427: Gene order near *COA1* gene in the Australian saltwater crocodile genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

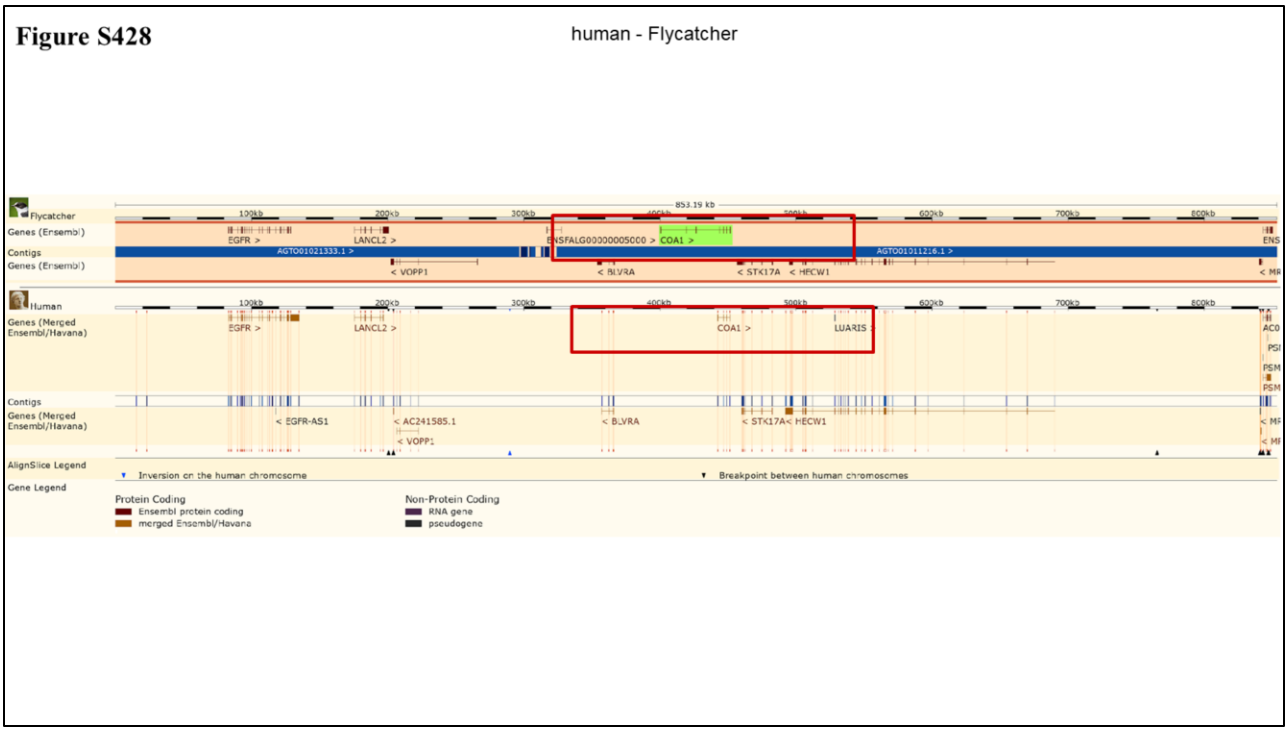

Figure S428: Gene order near *COA1* gene in the flycatcher genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

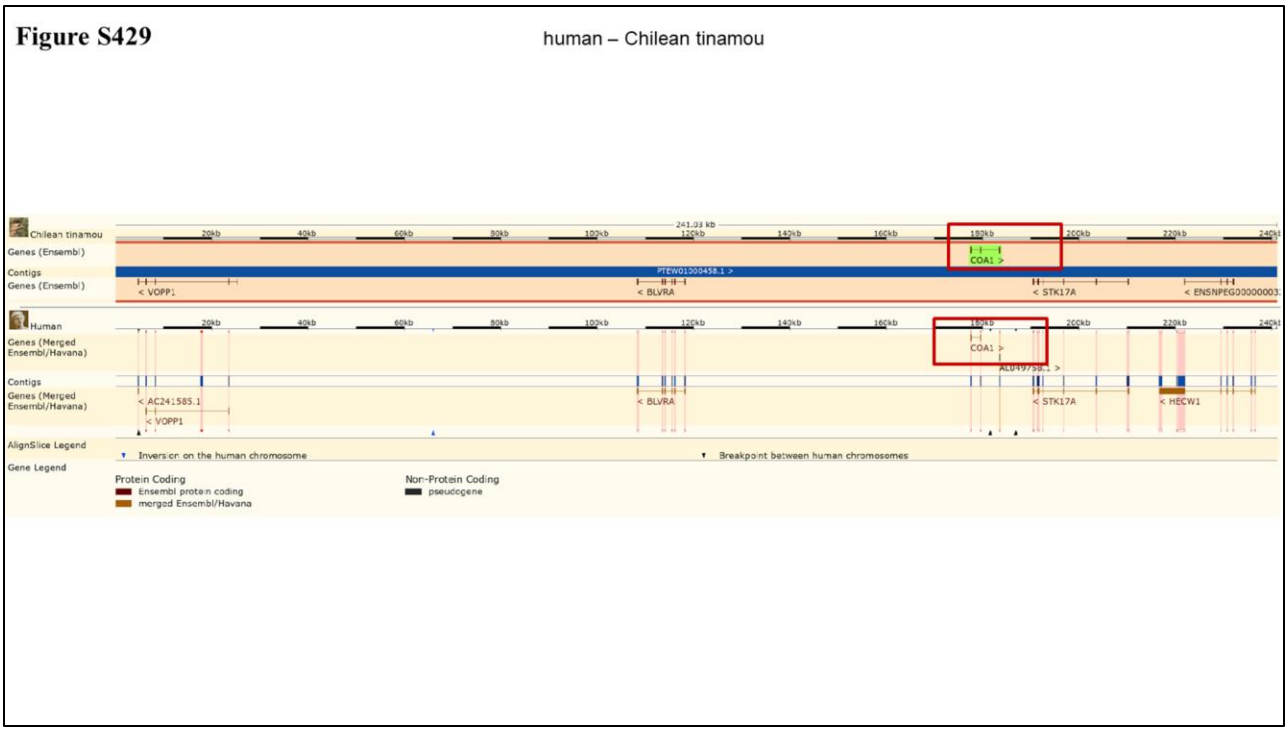

Figure S429: Gene order near *COA1* gene in the Chilean tinamou genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

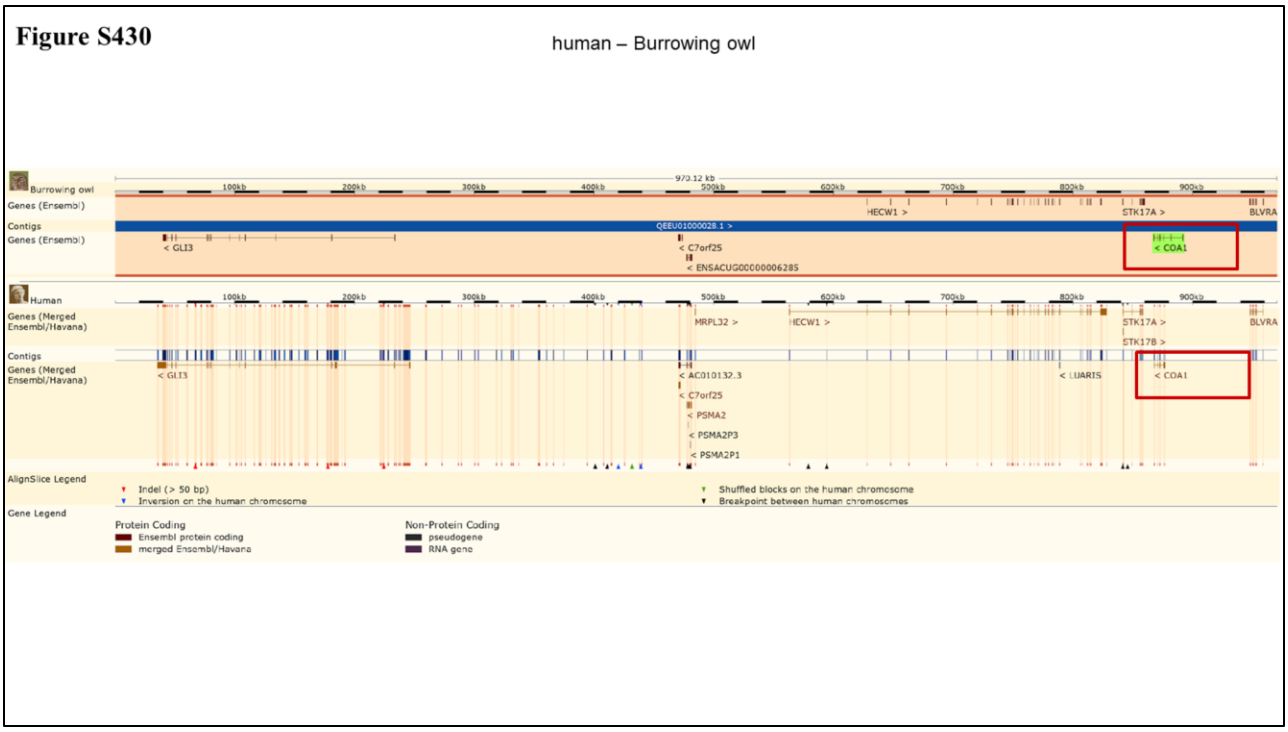

Figure S430: Gene order near *COA1* gene in the burrowing owl genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

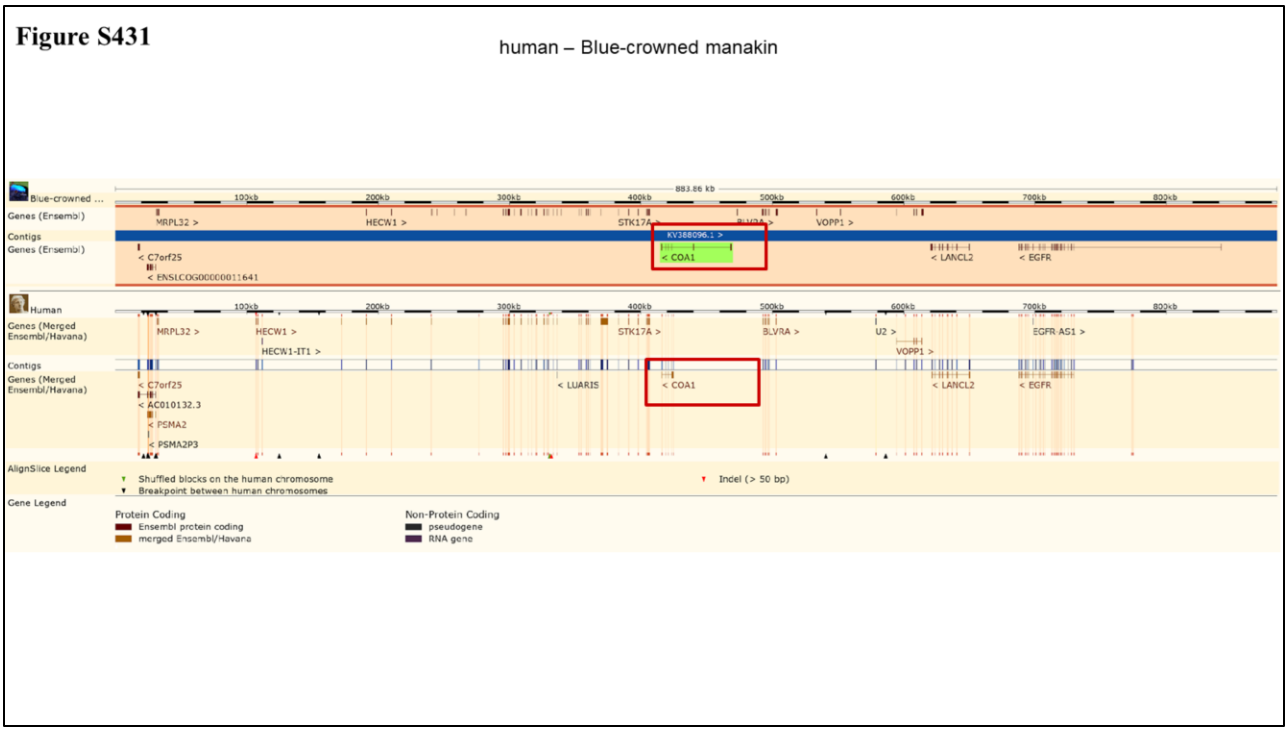

Figure S431: Gene order near *COA1* gene in the blue-crowned manakin genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

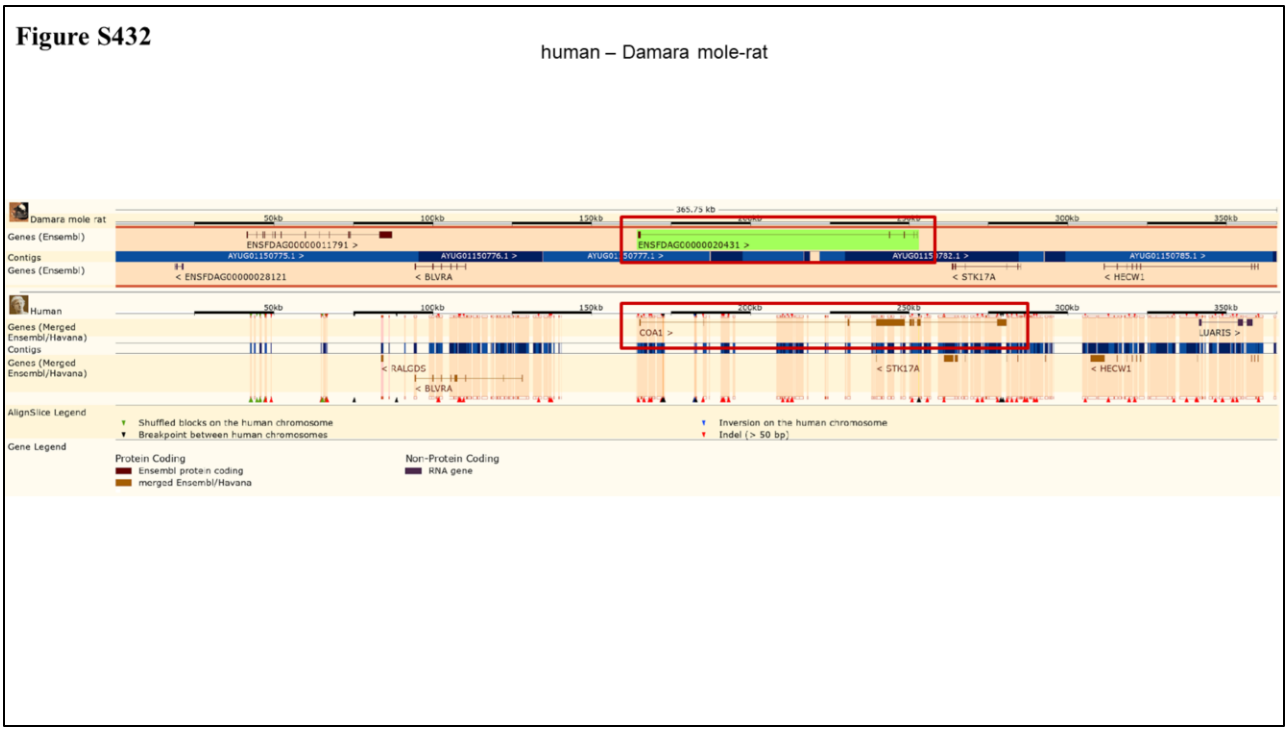

Figure S432: Gene order near *COA1* gene in the damara mole-rat genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

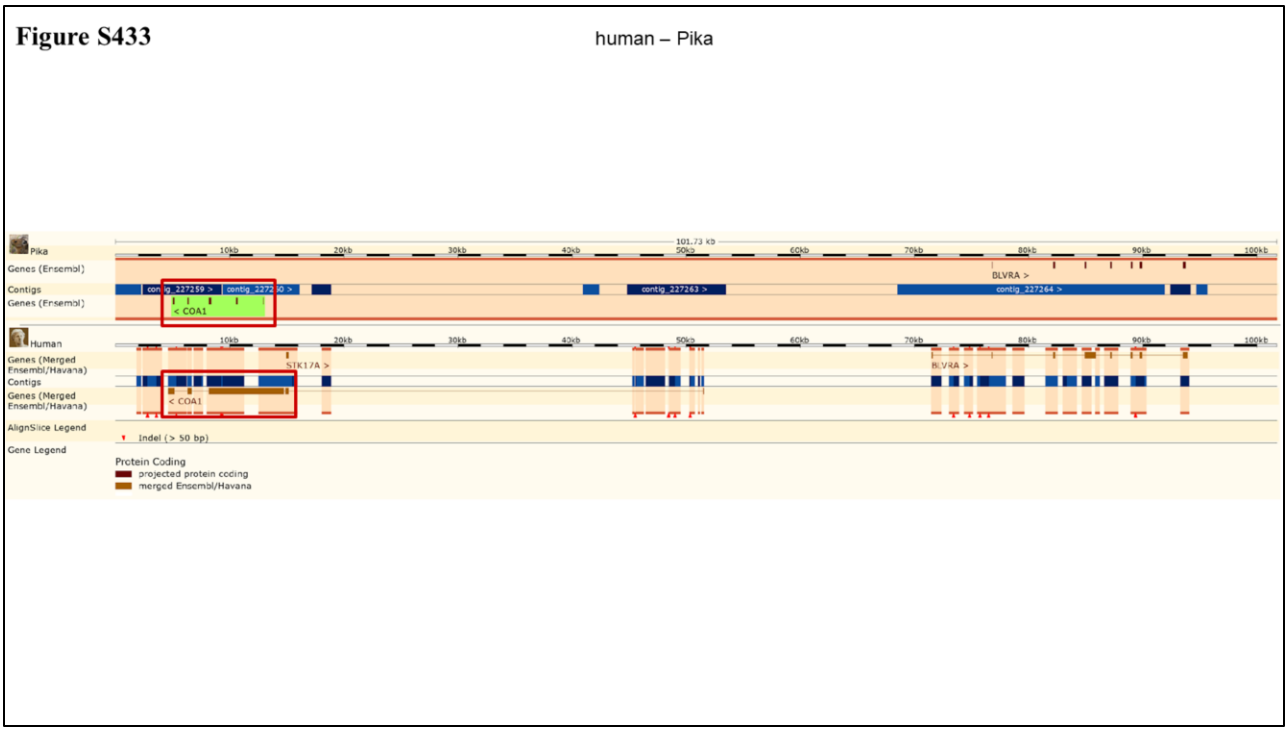

Figure S433: Gene order near *COA1* gene in the golden eagle genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

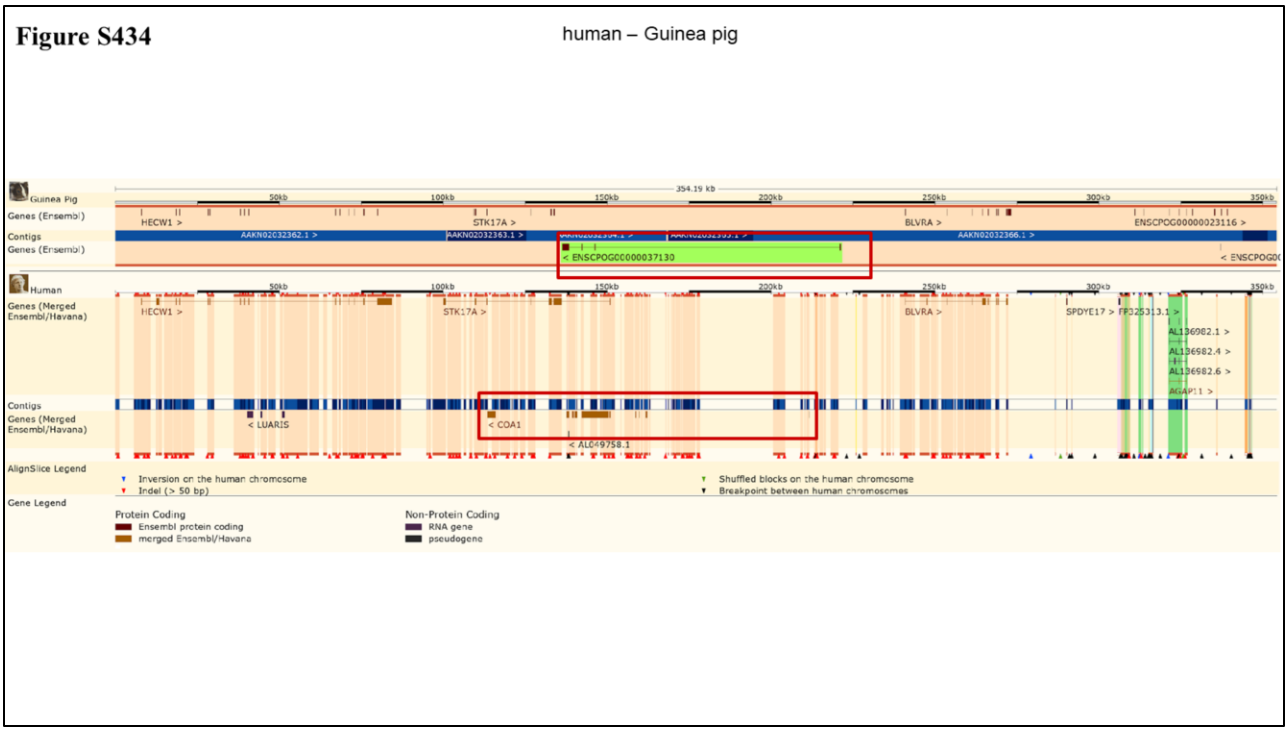

Figure S434: Gene order near *COA1* gene in the guinea pig genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

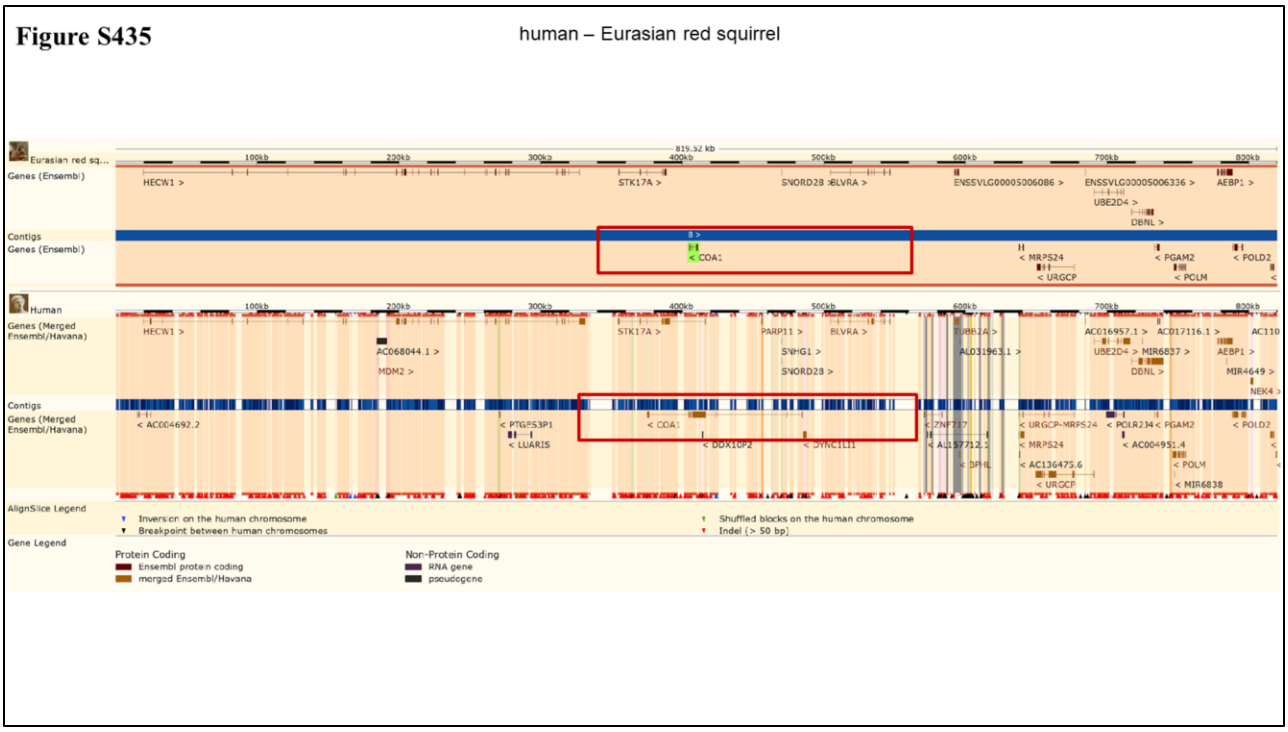

Figure S435: Gene order near *COA1* gene in the Eurasian red squirrel genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

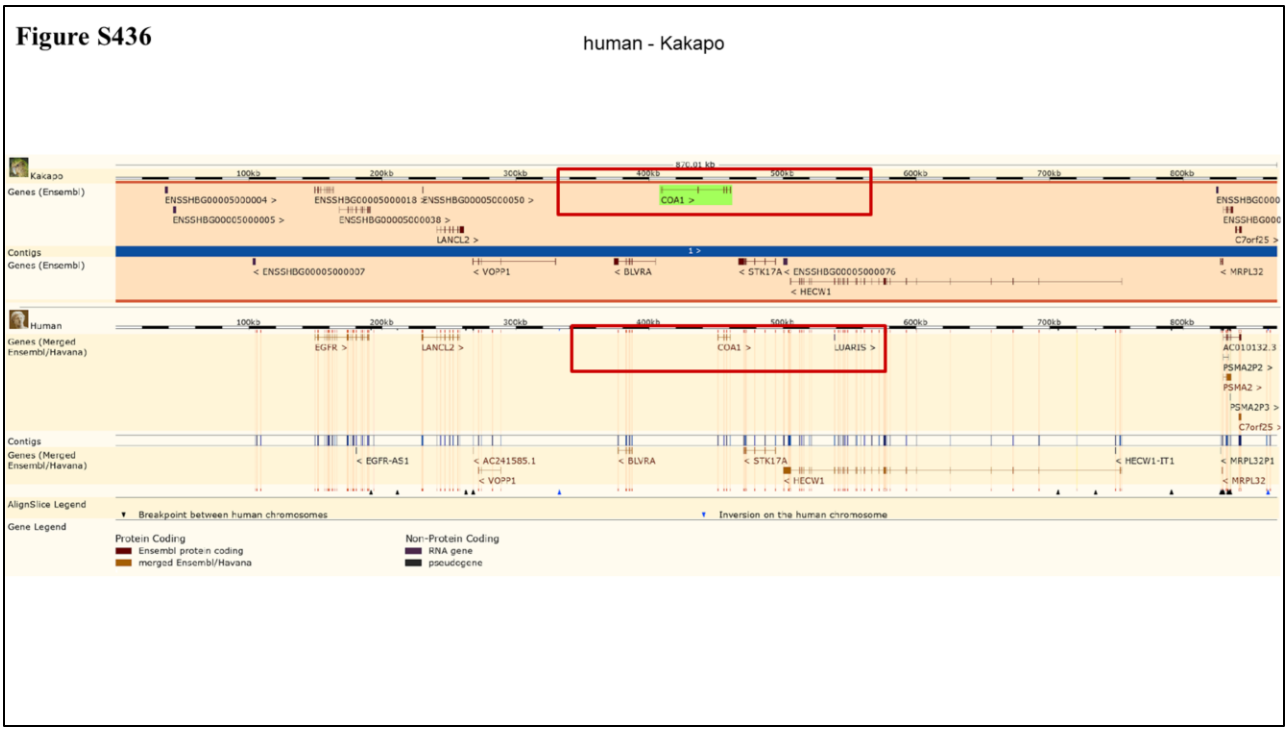

Figure S436: Gene order near *COA1* gene in the kakapo genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

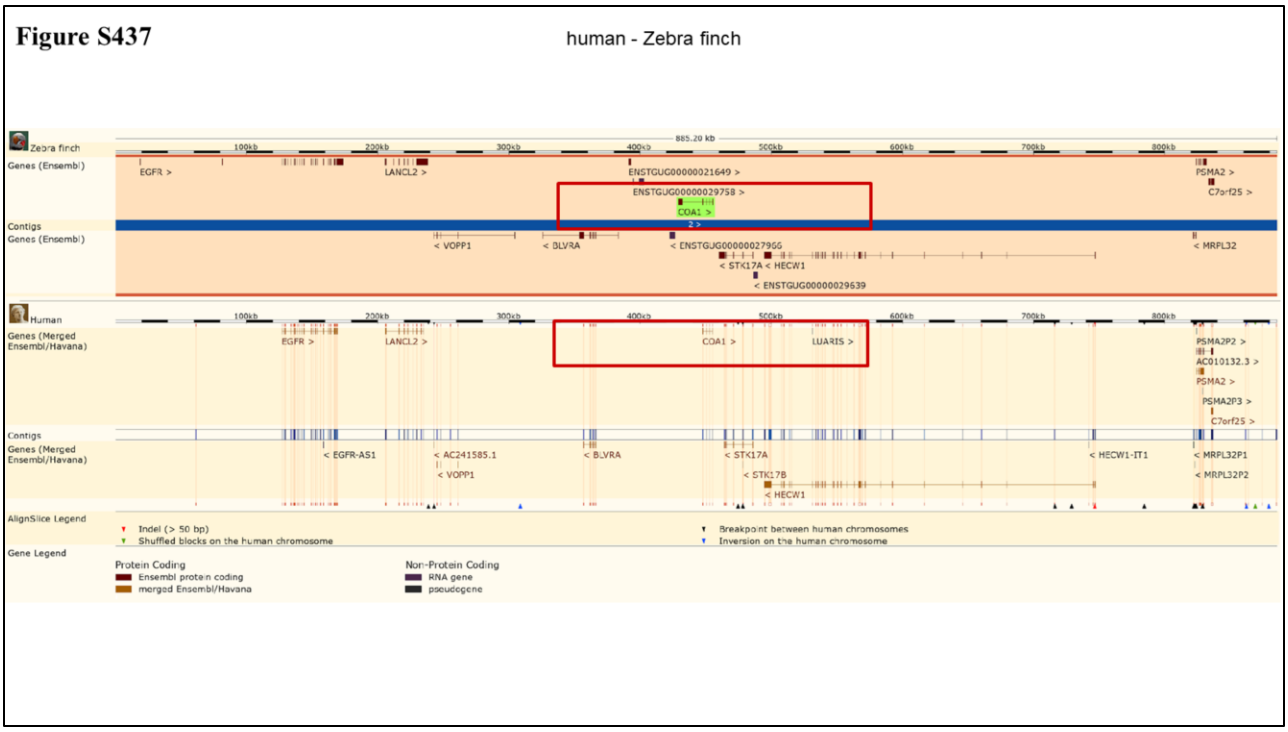

Figure S437: Gene order near *COA1* gene in the zebra finch genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

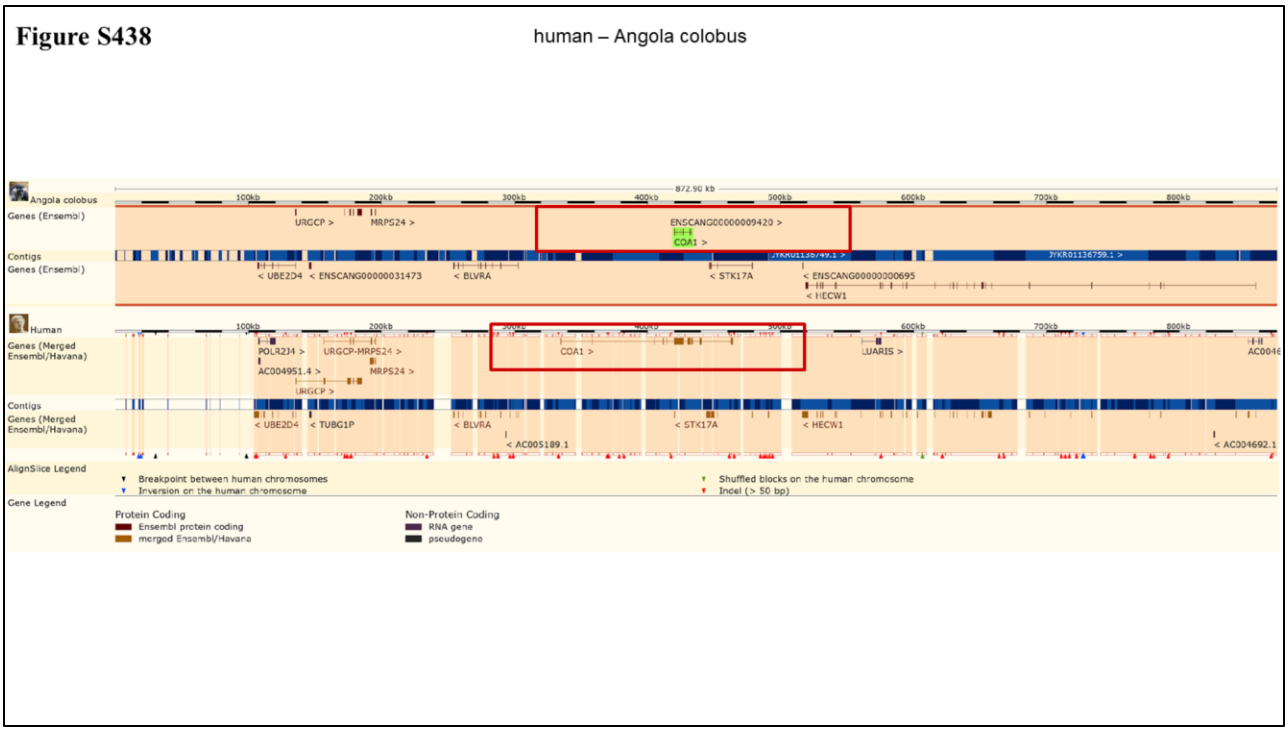

Figure S438: Gene order near *COA1* gene in the Angola colobus genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

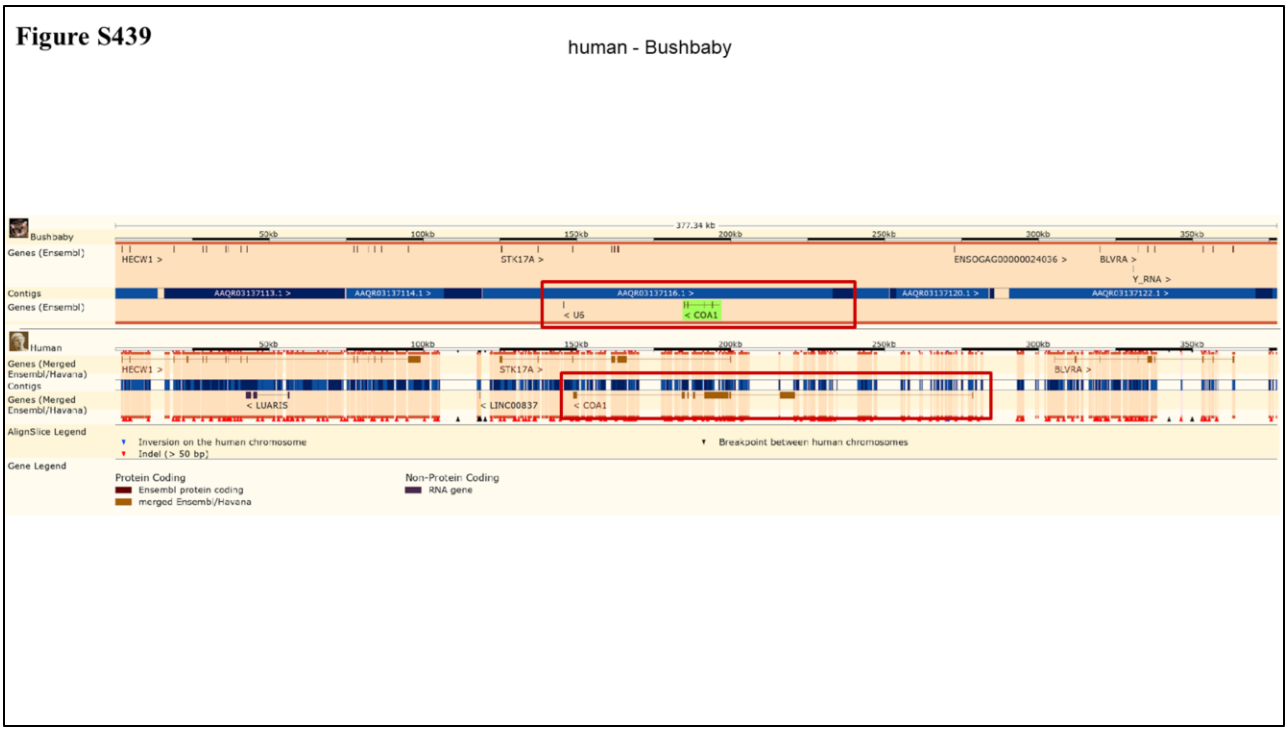

Figure S439: Gene order near *COA1* gene in the bushbaby genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

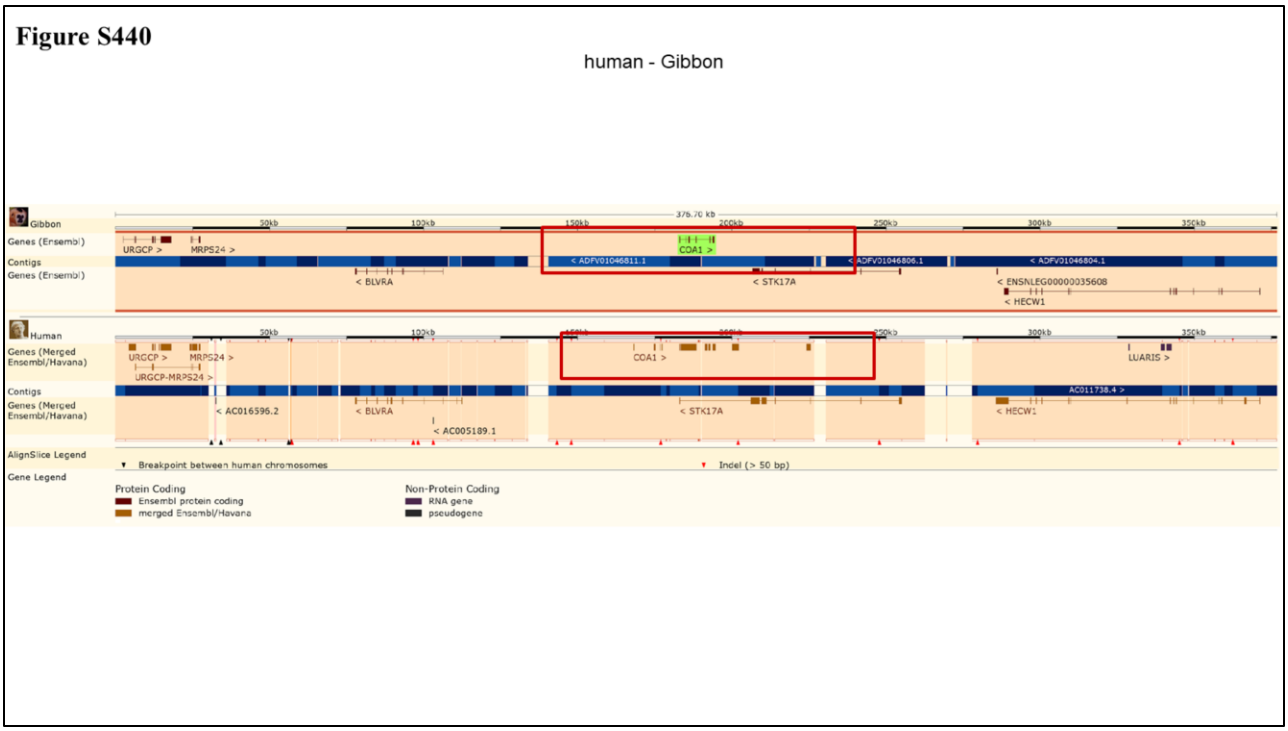

Figure S440: Gene order near *COA1* gene in the gibbon genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

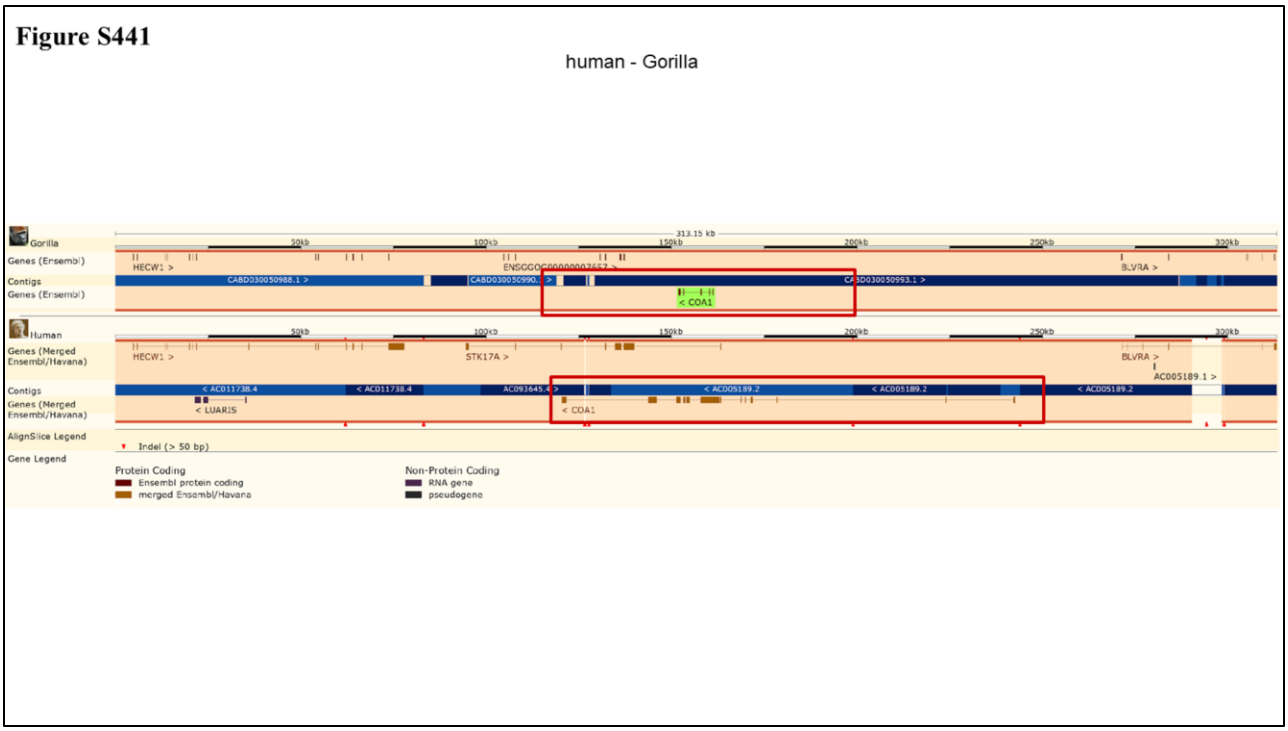

Figure S441: Gene order near *COA1* gene in the gorilla genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

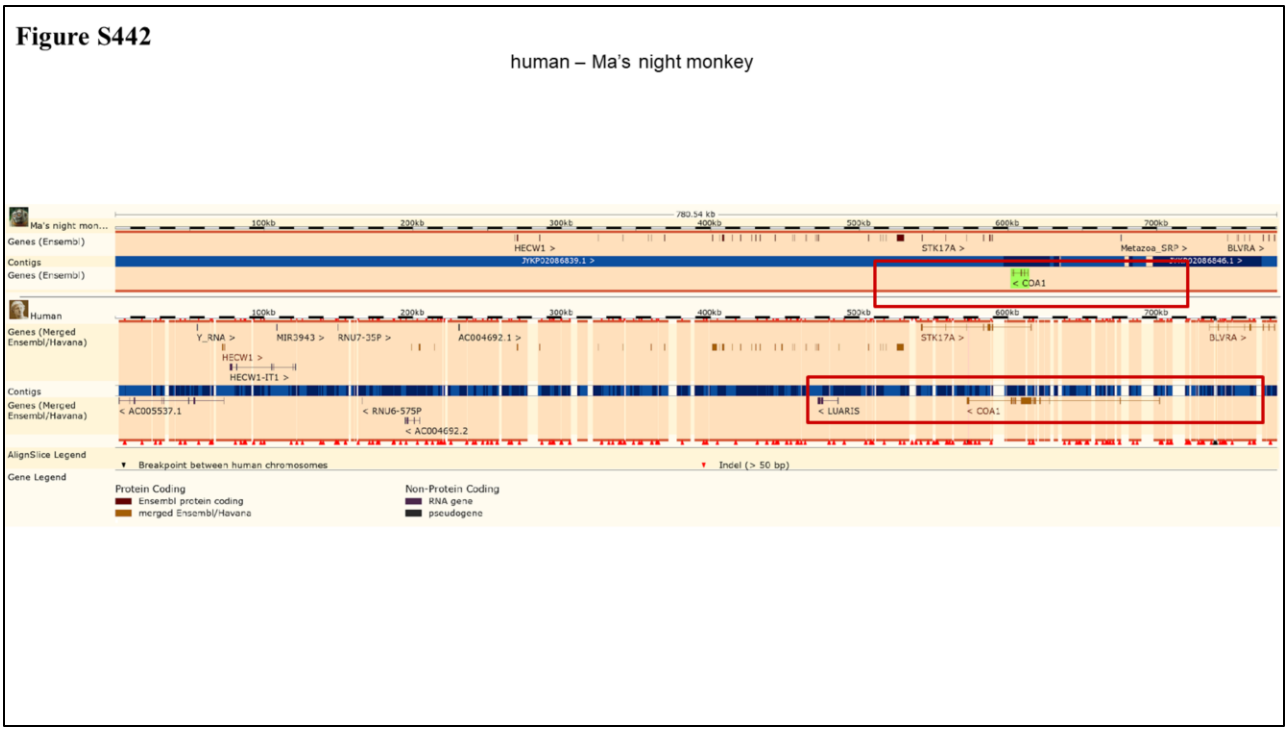

Figure S442: Gene order near *COA1* gene in the Ma's night monkey genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

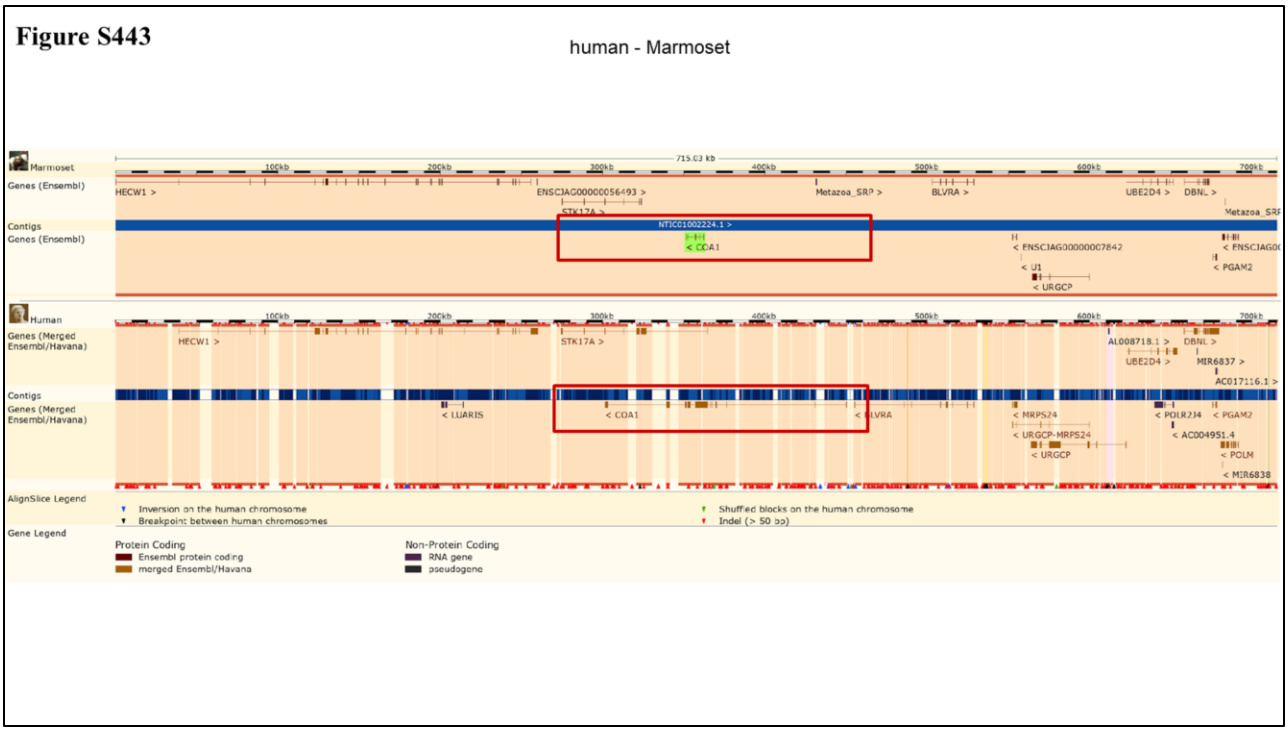

Figure S443: Gene order near *COA1* gene in the marmoset genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

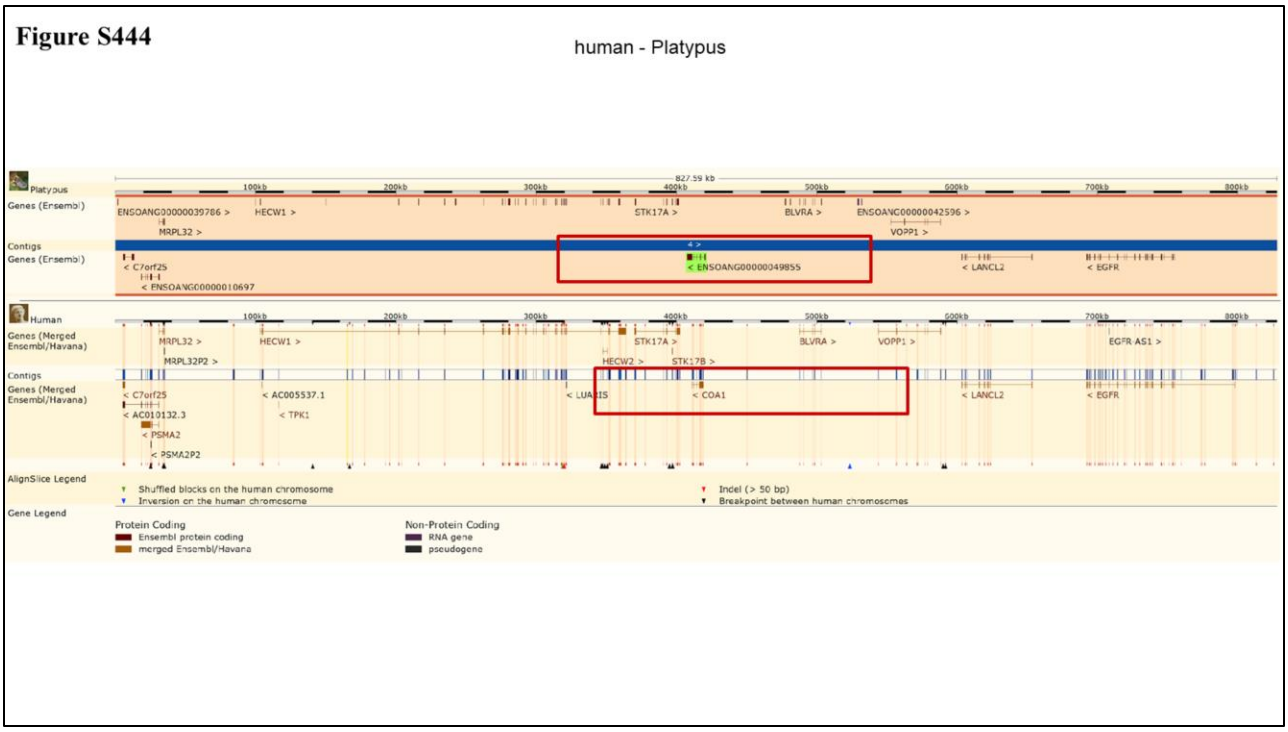

Figure S444: Gene order near *COA1* gene in the platypus genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

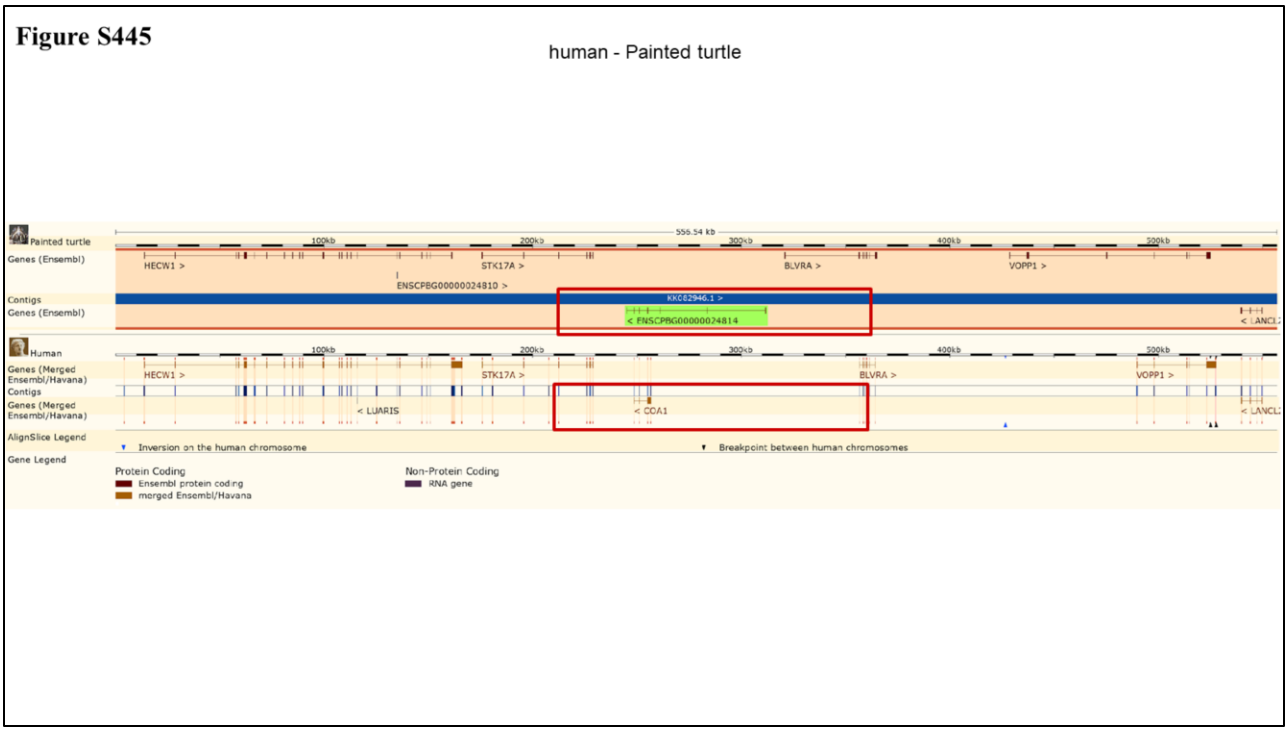

Figure S445: Gene order near *COA1* gene in the painted turtle genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

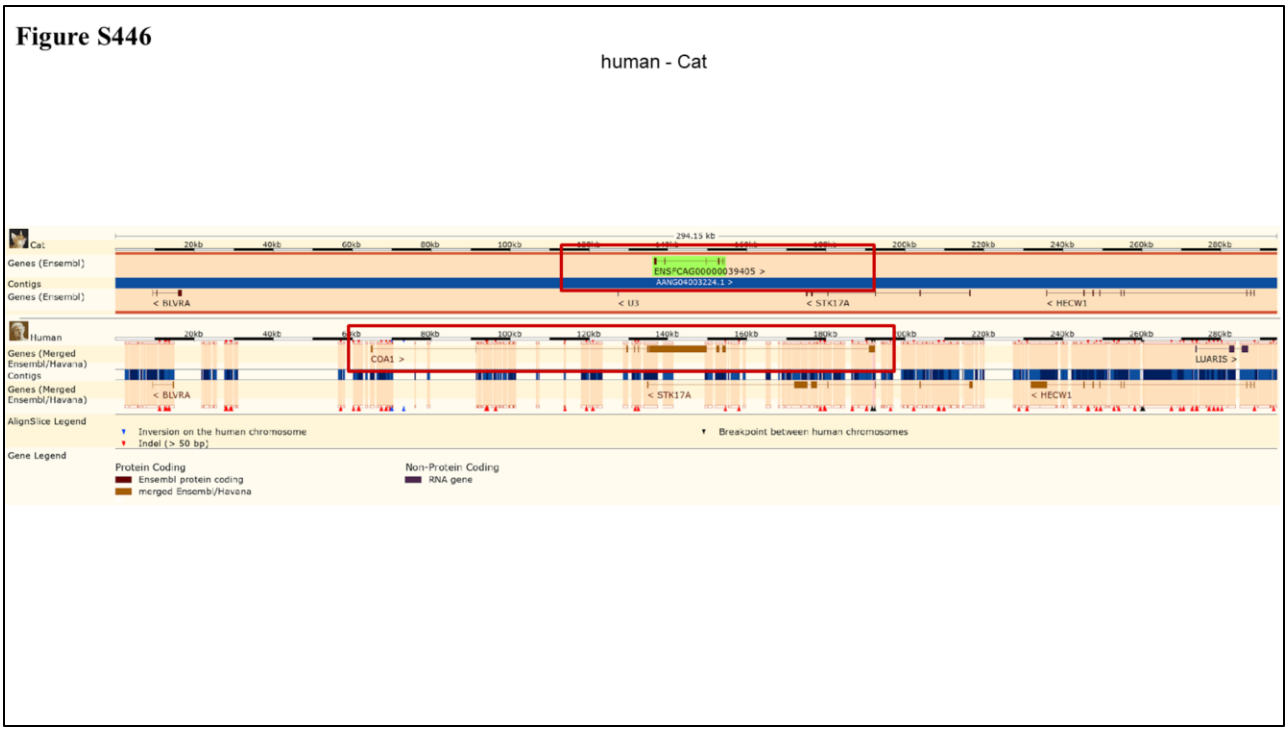

Figure S446: Gene order near *COA1* gene in the cat genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

Figure S447: Gene order near *COA1* gene in the dog genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

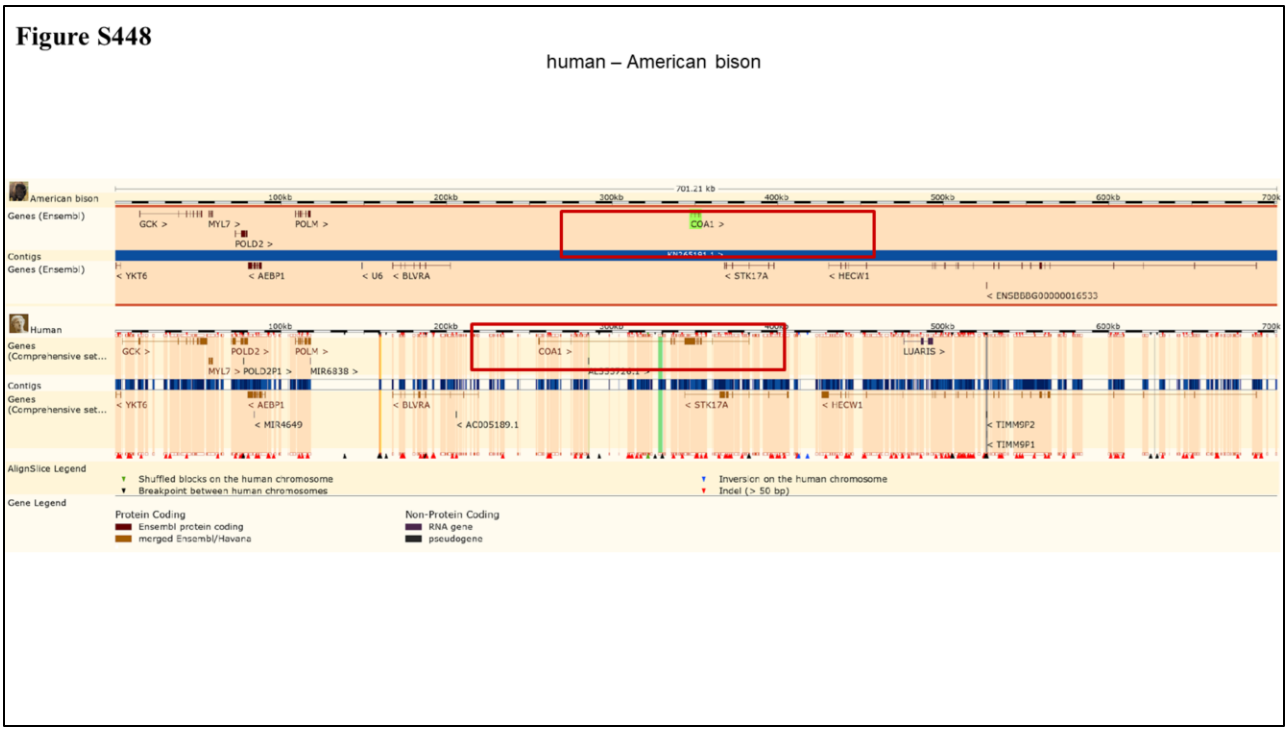

Figure S448: Gene order near *COA1* gene in the American bison genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

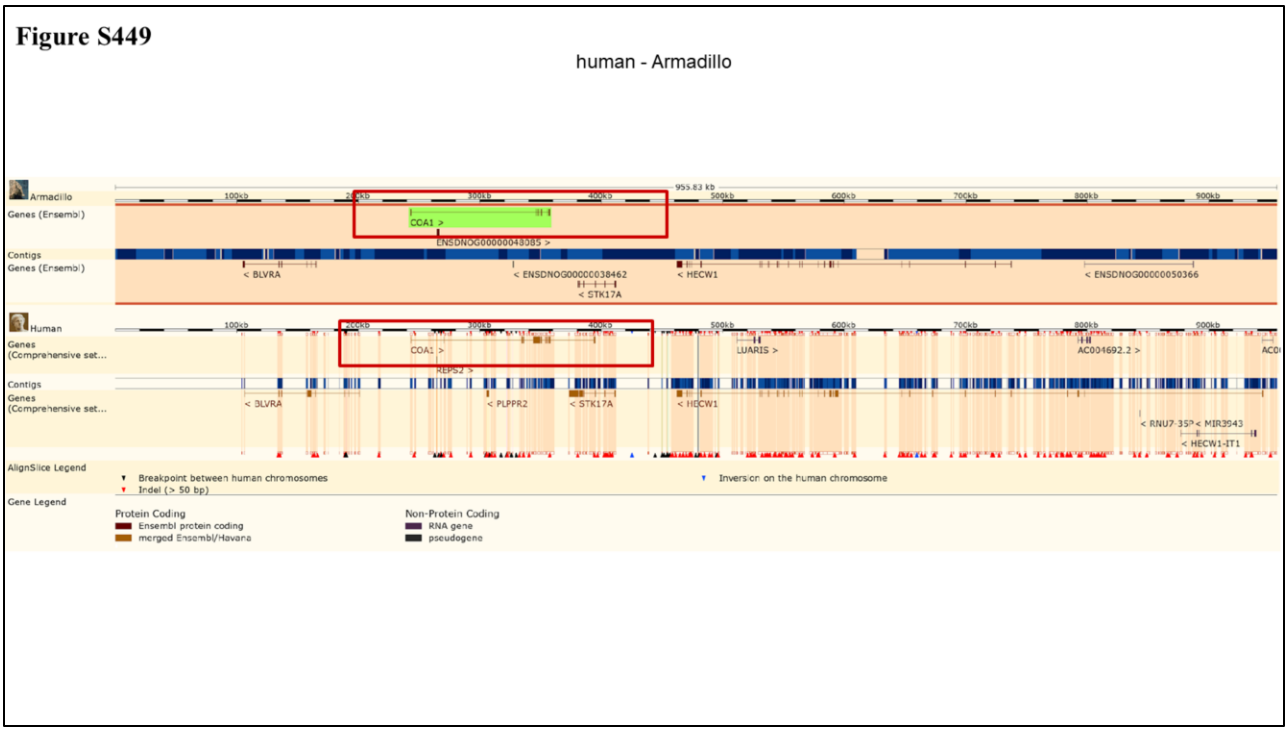

Figure S449: Gene order near *COA1* gene in the armadillo genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

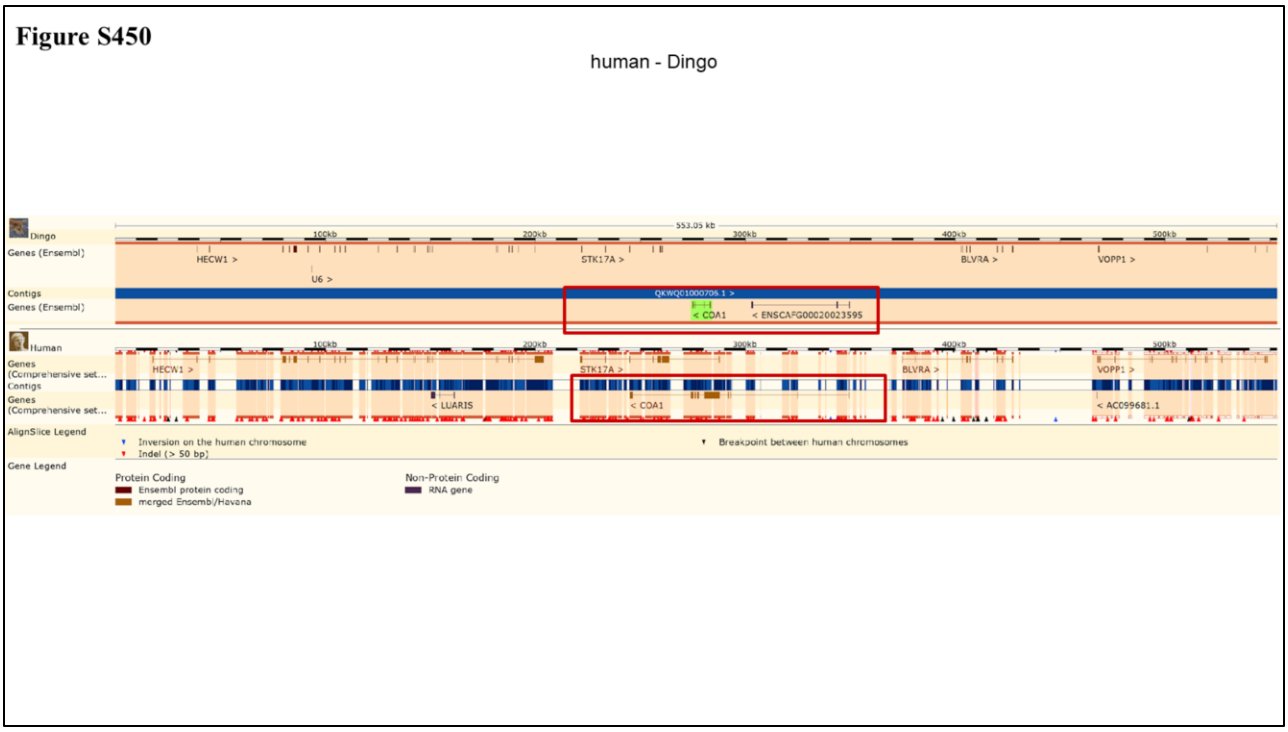

Figure S450: Gene order near *COA1* gene in the dingo genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

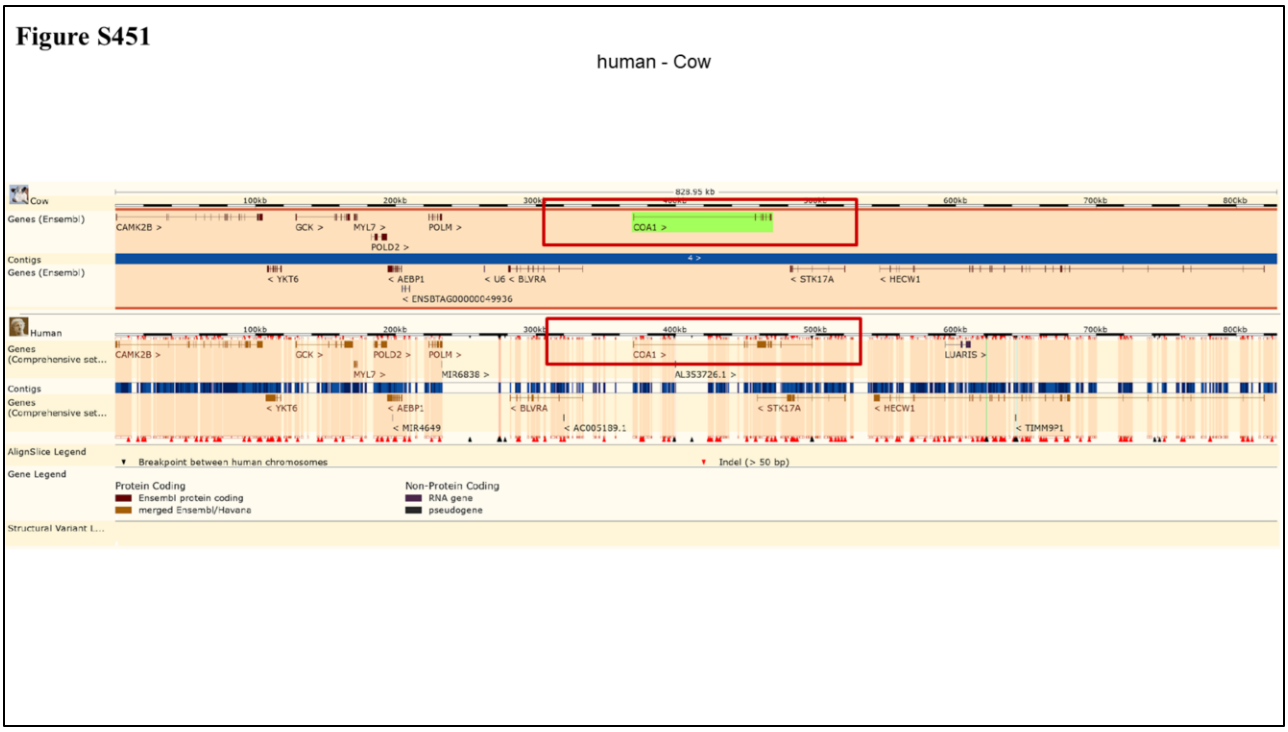

Figure S451: Gene order near *COA1* gene in the cow genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

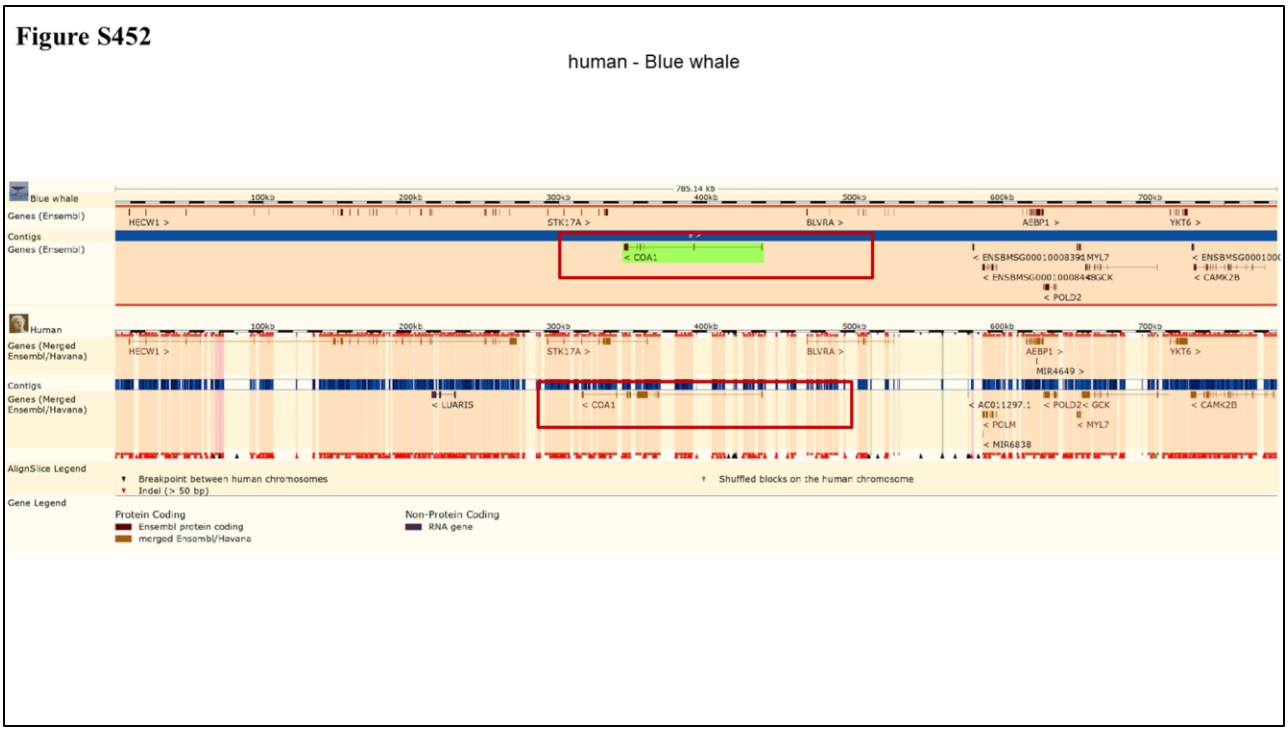

Figure S452: Gene order near *COA1* gene in the blue whale genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

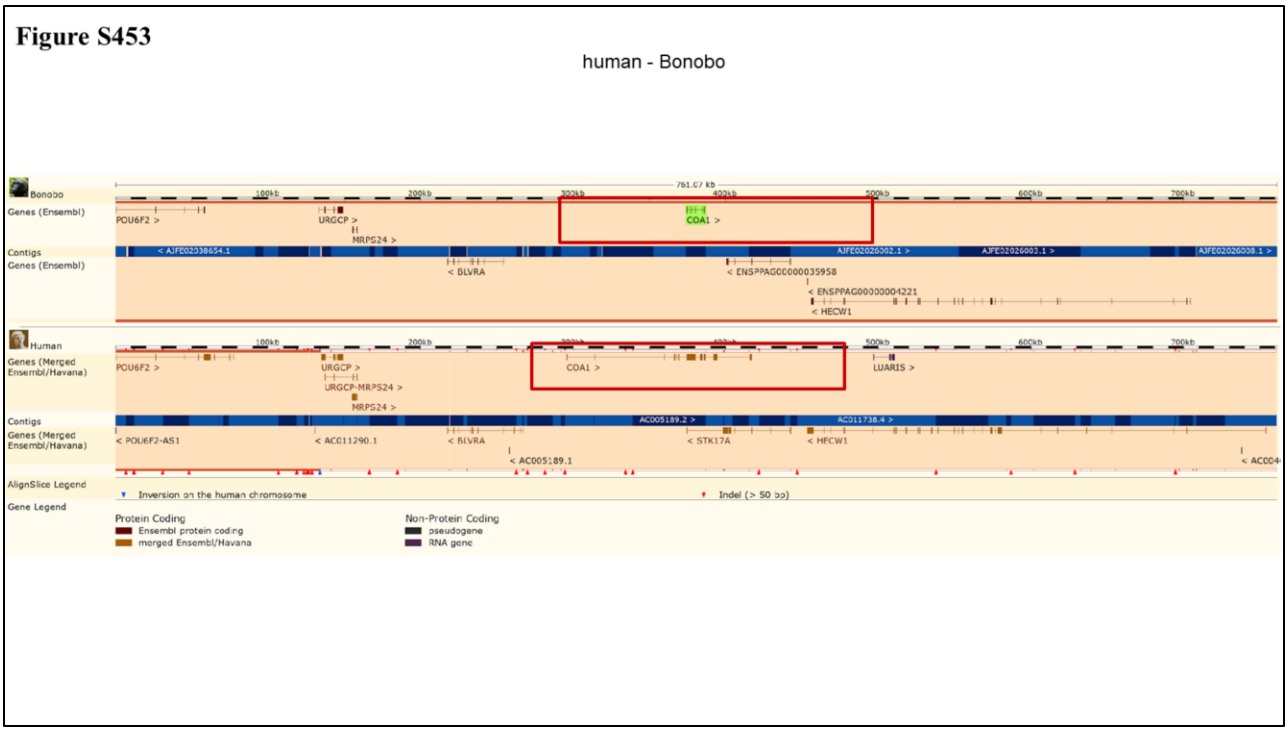

Figure S453: Gene order near *COA1* gene in the bonobo genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

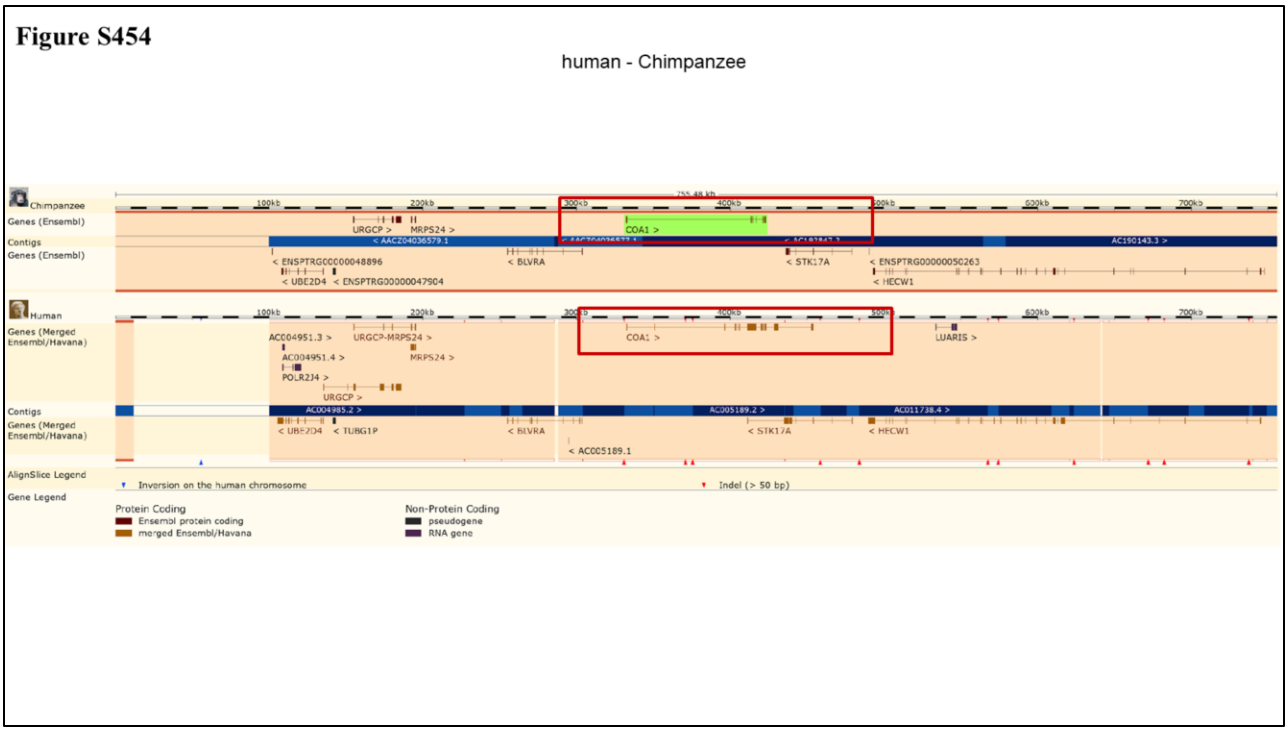

Figure S454: Gene order near *COA1* gene in the chimpanzee genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

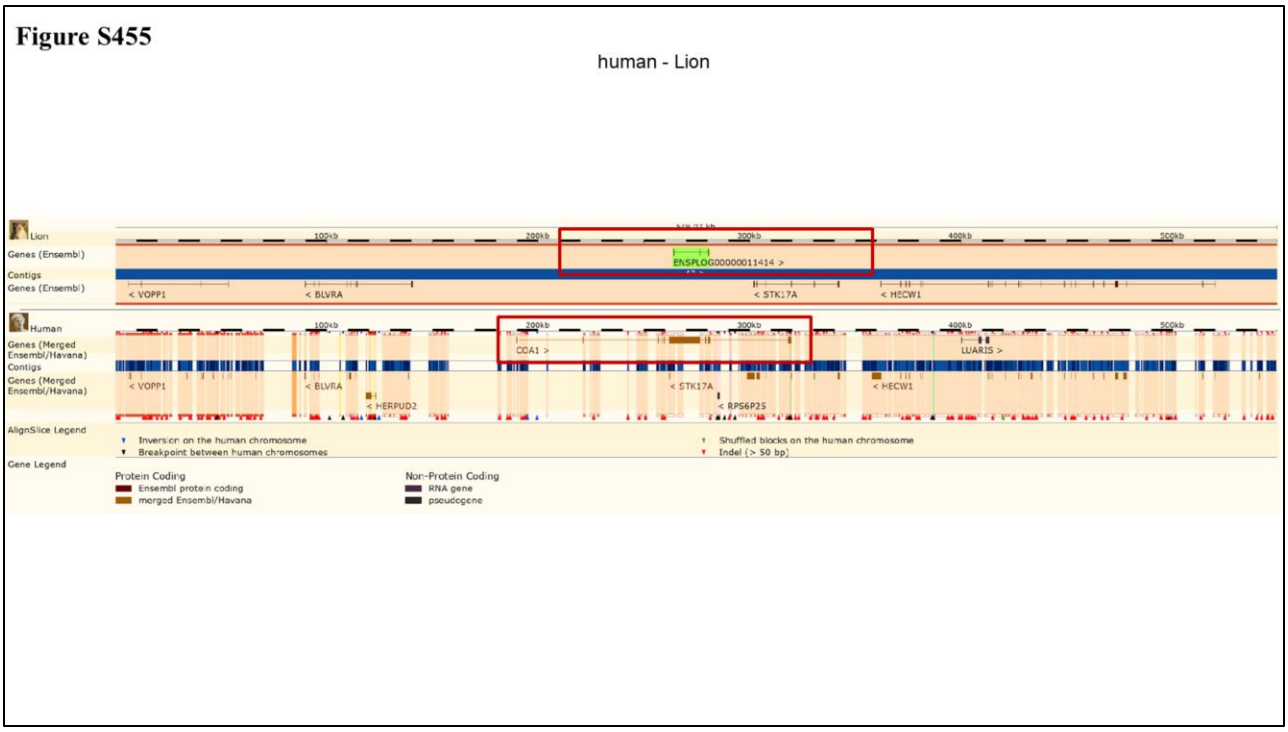

Figure S455: Gene order near *COA1* gene in the lion genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

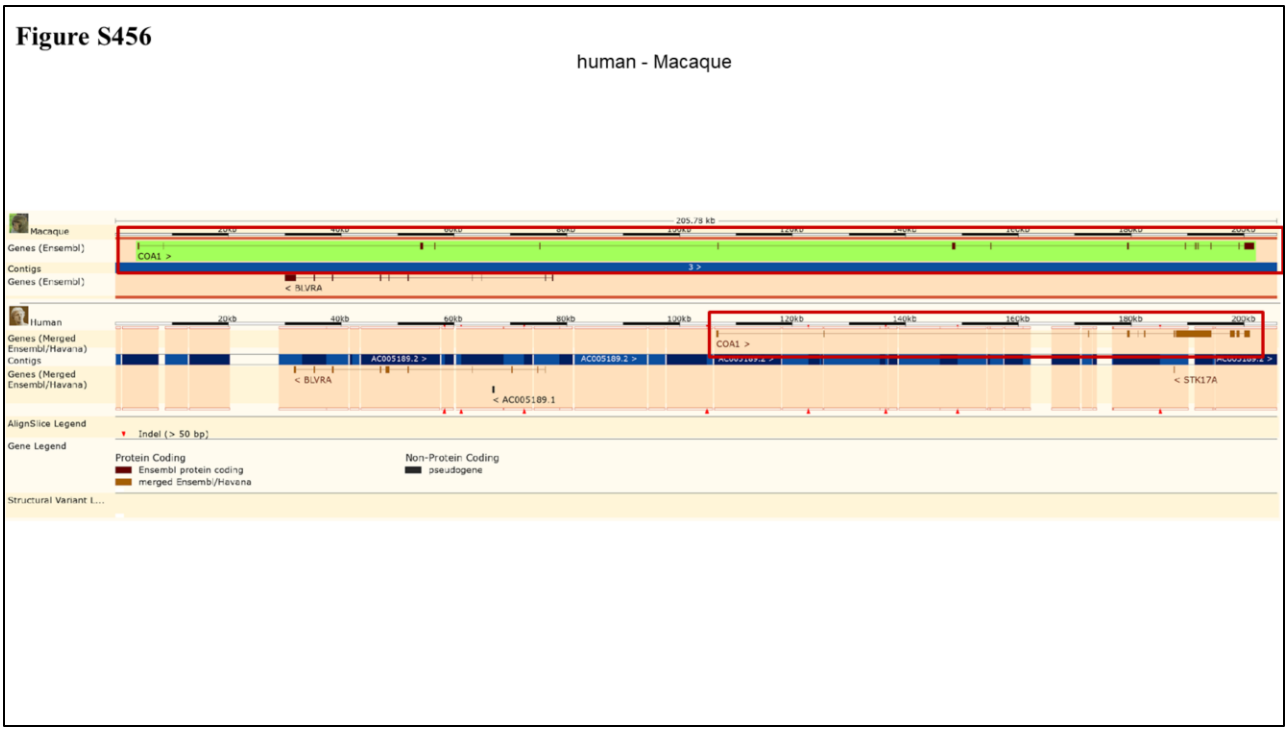

Figure S456: Gene order near *COA1* gene in the macaque genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

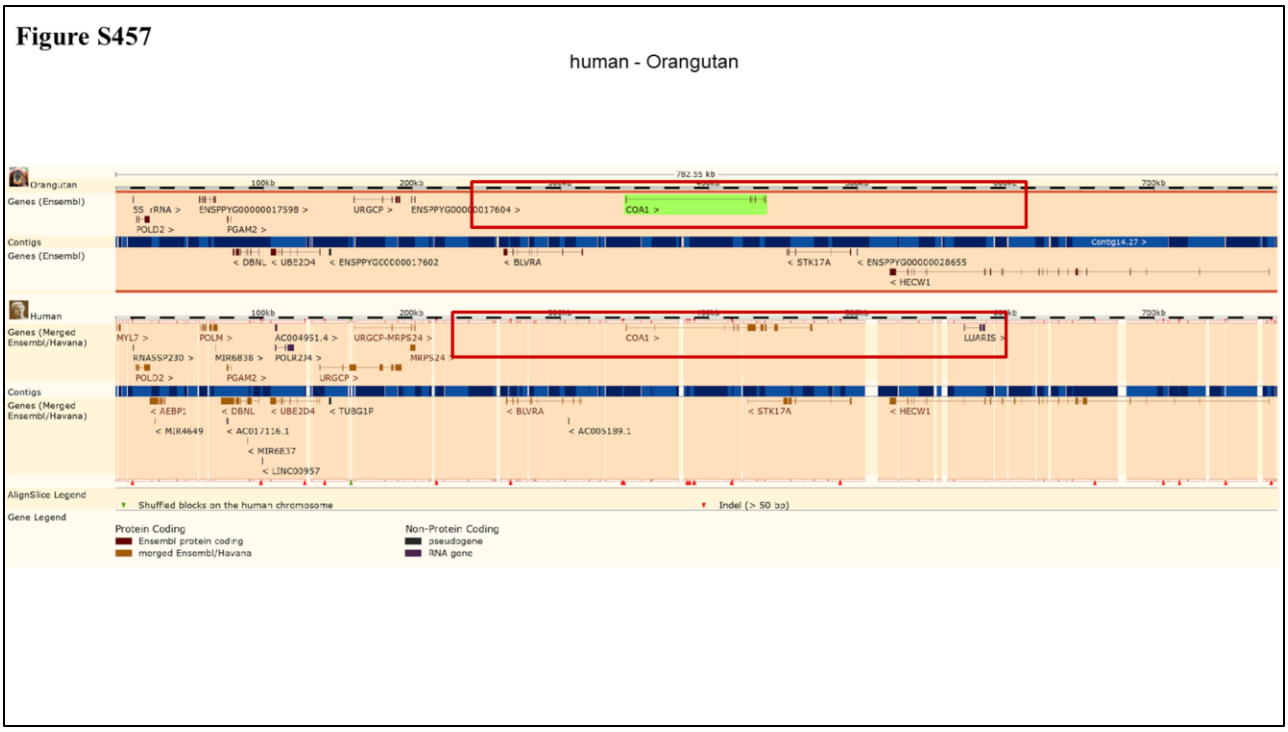

Figure S457: Gene order near *COA1* gene in the orangutan genome. The rectangular boxes connected by thin lines depict genes, with the boxes denoting exons and connecting lines being introns. Direction of transcription is denoted by the > or < symbols (signify positive and negative strand of transcription respectively) beside the gene names. chromosome bands and the genomic coordinates in kilobase (kb) are shown in the topmost row. Details of the contig and scaffold identity are provided in the blue bar located in the middle of the figure. Exact location of the *COA1* gene is depicted by a red box.

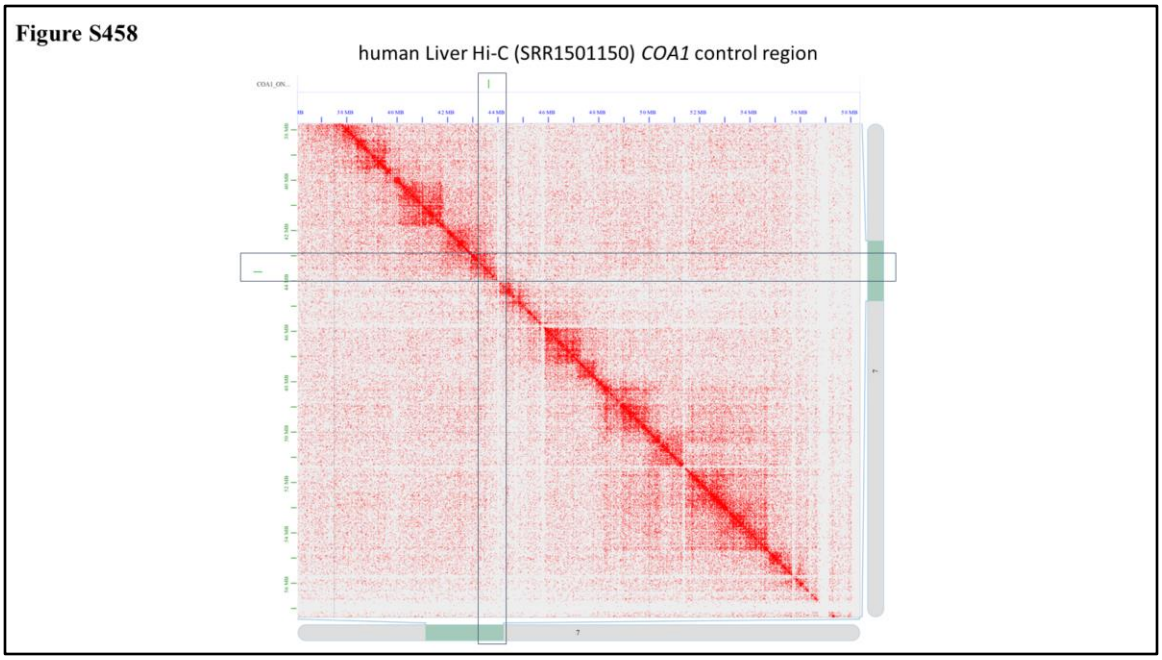

Figure S458: Hi-C figure generated using Juicebox of human liver data (SRR1501150) where red dots show the genomic loci interaction between adjacent regions and gap shows there is no interaction between the nearby region. We loaded the bed file on the top and left sides of the Hi-C plot, where the green color indicates the region of interest (*COA1*) removed the reads using bedtools subtract for control. chromosome or scaffold is mentioned on the bottom and right sides of the plot.

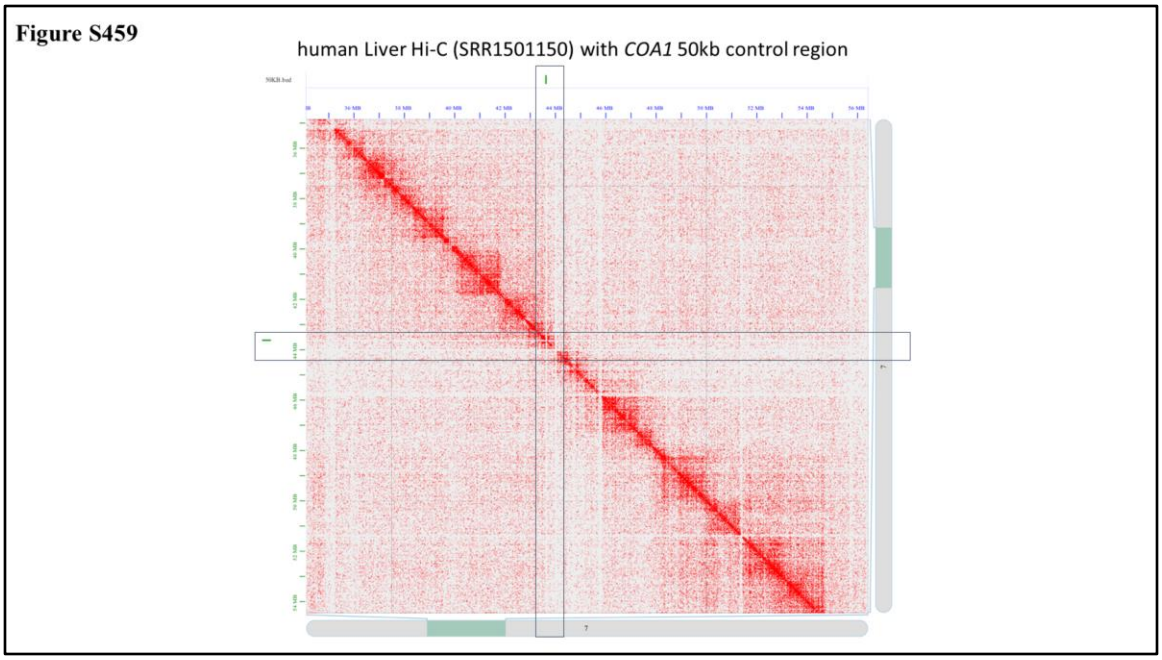

Figure S459: Hi-C figure generated using Juicebox of human liver data (SRR1501150) where red dots show the genomic loci interaction between adjacent regions and gap shows there is no interaction between the nearby region. We loaded the bed file on the top and left sides of the Hi-C plot, where the green color indicates the region of interest (with *COA1*) removed 50 kb region reads using bedtools subtract for control. chromosome or scaffold is mentioned on the bottom and right sides of the plot.

Figure S460

human Liver Hi-C (SRR1501150) with *COA1* 100kb control region

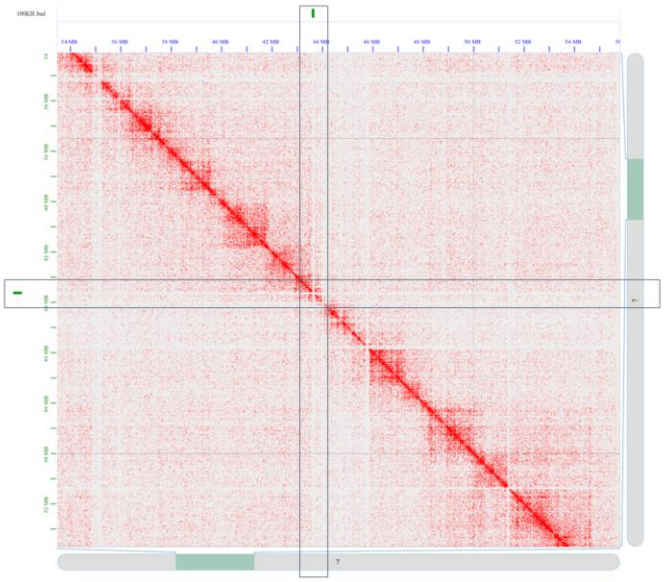

Figure S460: Hi-C figure generated using Juicebox of human liver data (SRR1501150) where red dots show the genomic loci interaction between adjacent regions and gap shows no interaction between the nearby region. We loaded the bed file on the top and left sides of the Hi-C plot, where the green color indicates the region of interest (with *COA1*) removed 100 kb region reads using bedtools subtract for control. chromosome or scaffold is mentioned on the bottom and right sides of the plot.

Figure S461

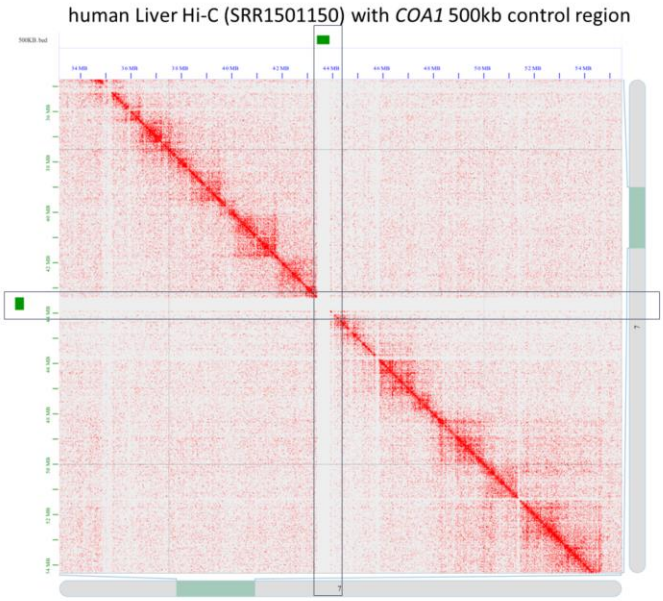

Figure S461: Hi-C figure generated using Juicebox of human liver data (SRR1501150) where red dots show the genomic loci interaction between adjacent regions and gap shows no interaction between the nearby region. We loaded the bed file on the top and left sides of the Hi-C plot, where the green color indicates the region of interest (with *COA1*) removed 500 kb region reads using bedtools subtract for control. chromosome or scaffold is mentioned on the bottom and right sides of the plot.

Figure S462

human Liver Hi-C (SRR1501150) with *COA1* 1mb control region

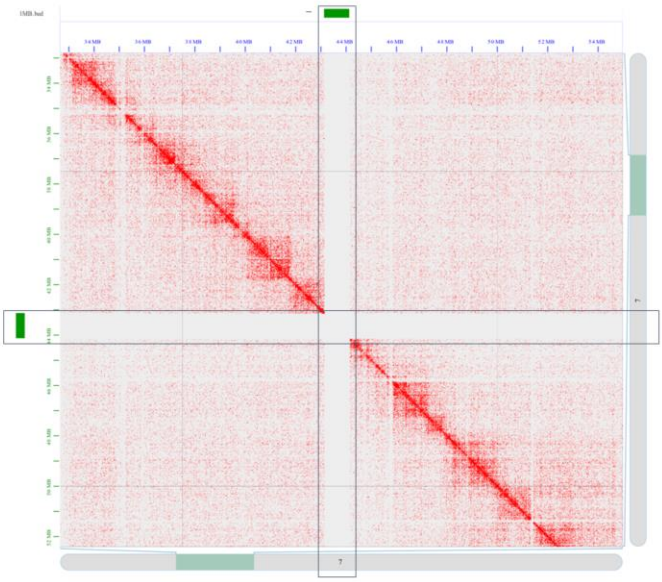

Figure S462: Hi-C figure generated using Juicebox of human liver data (SRR1501150) where red dots show the genomic loci interaction between adjacent regions and gap shows no interaction between the nearby region. We loaded the bed file on the top and left sides of the Hi-C plot, where the green color indicates the region of interest (with *COA1*) removed 100 mb region reads using bedtools subtract for control. chromosome or scaffold is mentioned on the bottom and right sides of the plot.

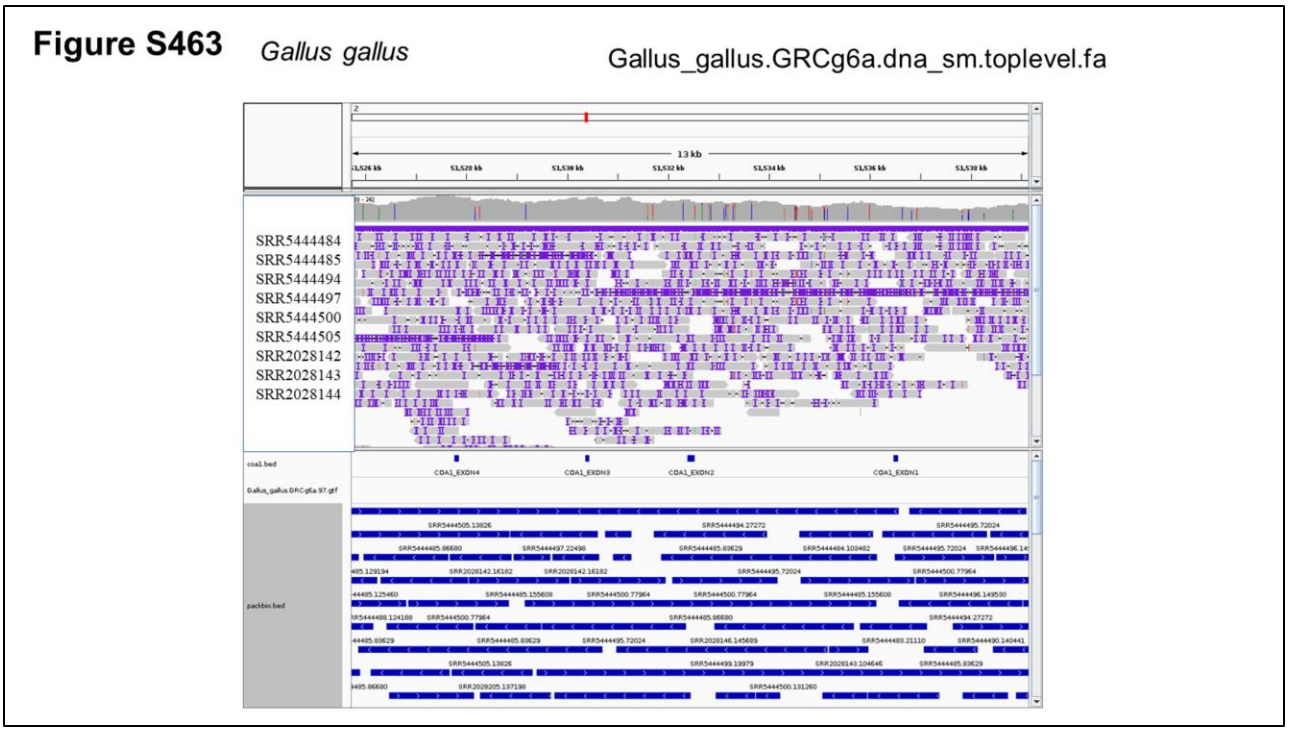

Figure S463: Screenshot of PacBio reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome. Raw read datasets which is mentioned above have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

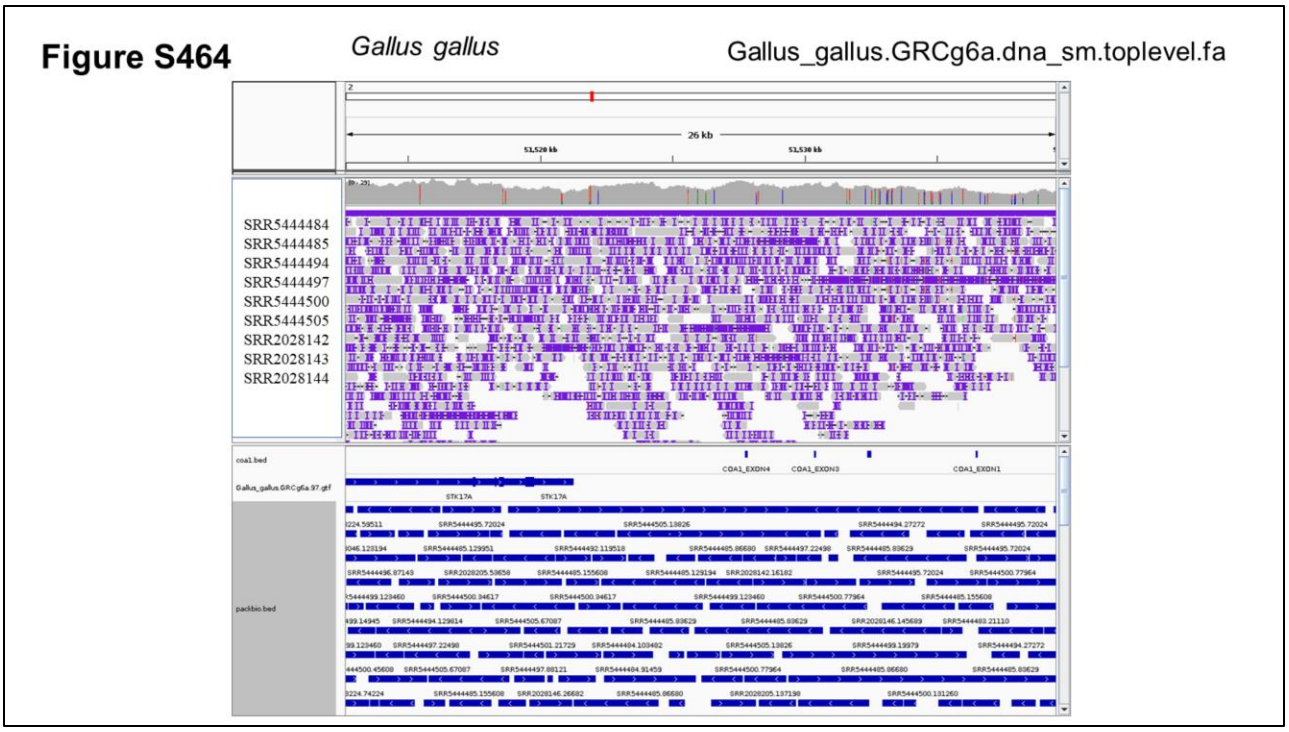

Figure S464: Screenshot of PacBio reads aligned to each of the putative locations of the four *COA1* exons and its nearby gene *STK17A* in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome. Raw read datasets which is mentioned above have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

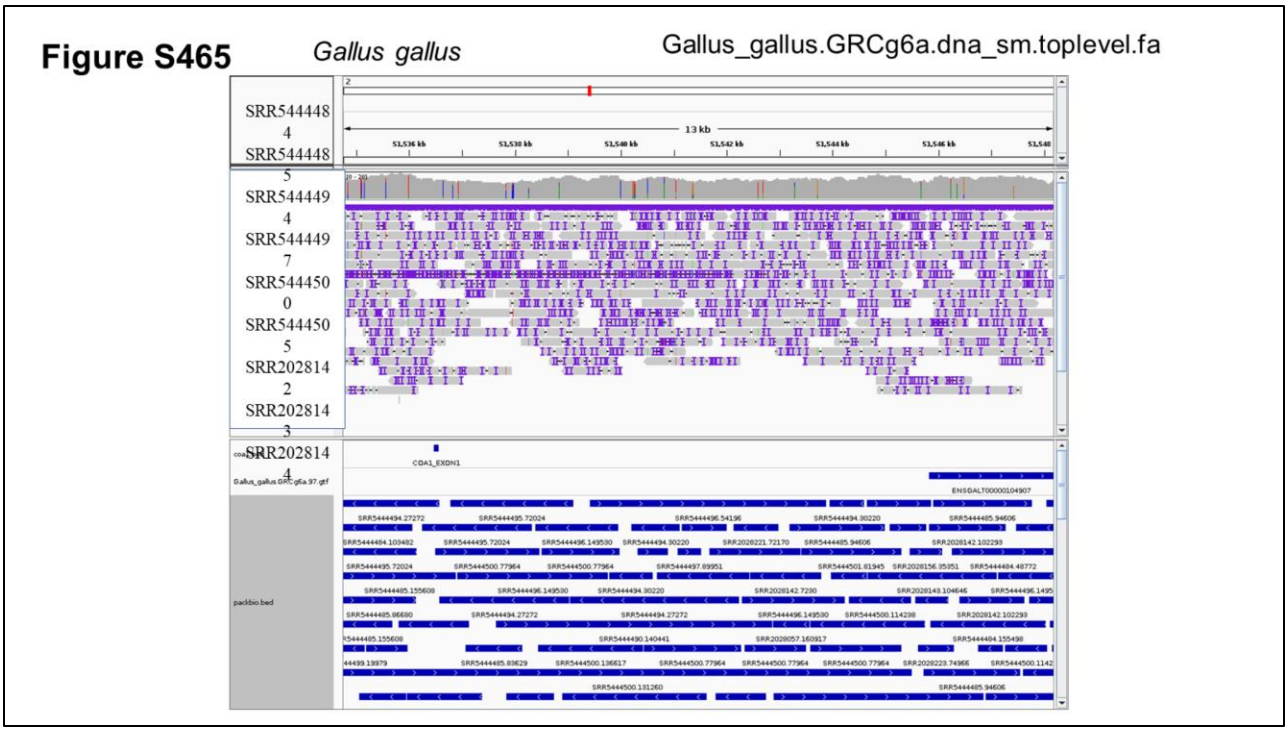

Figure S465: Screenshot of PacBio reads aligned to each of the putative locations of the four *COA1* exons and its nearby gene *BLVRA* in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome. Raw read datasets which is mentioned above have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

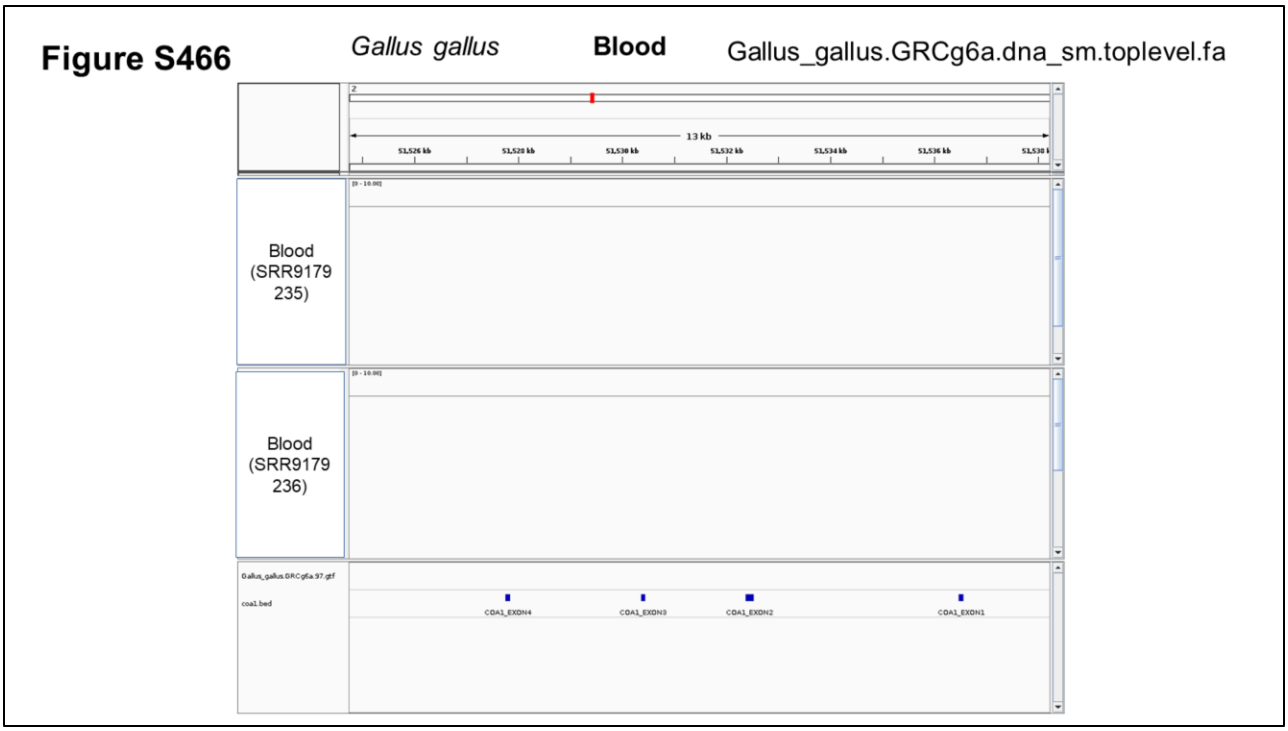

Figure S466: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR9179235) and (SRR9179236) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

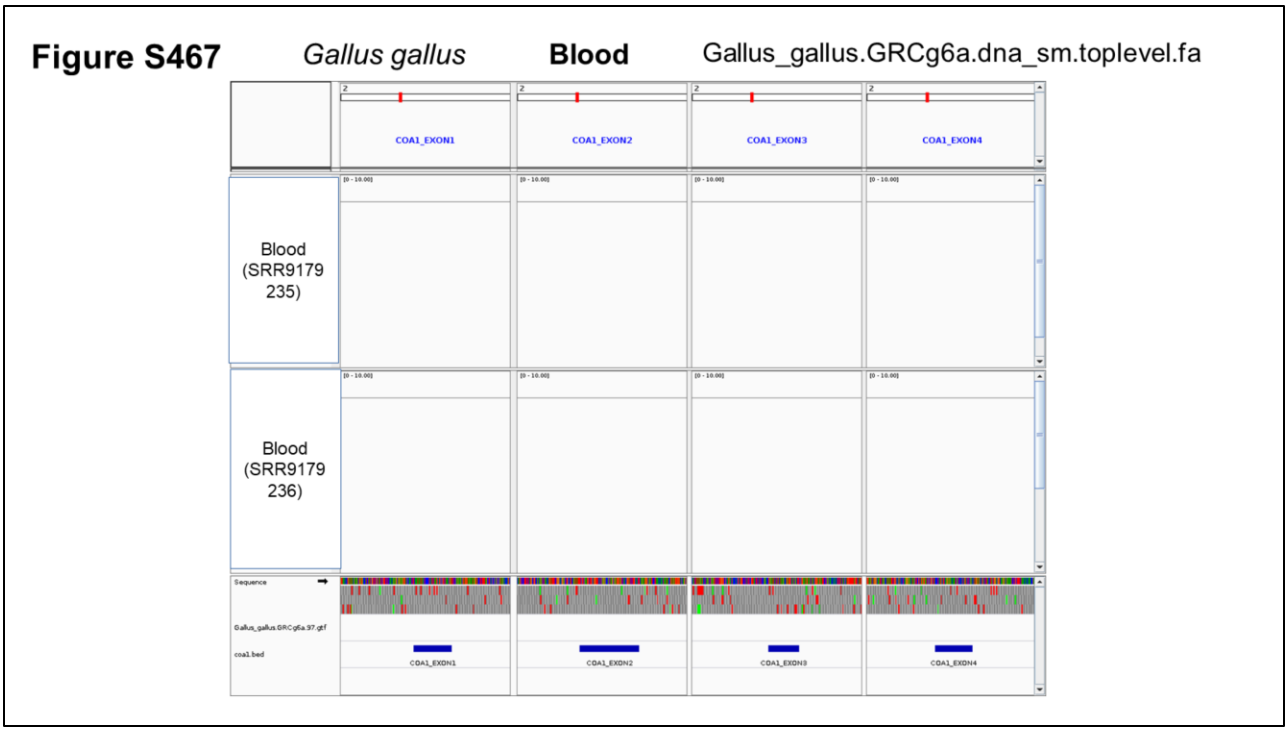

Figure S467: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S466**.

Figure S468: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR9179235) and (SRR9179236) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

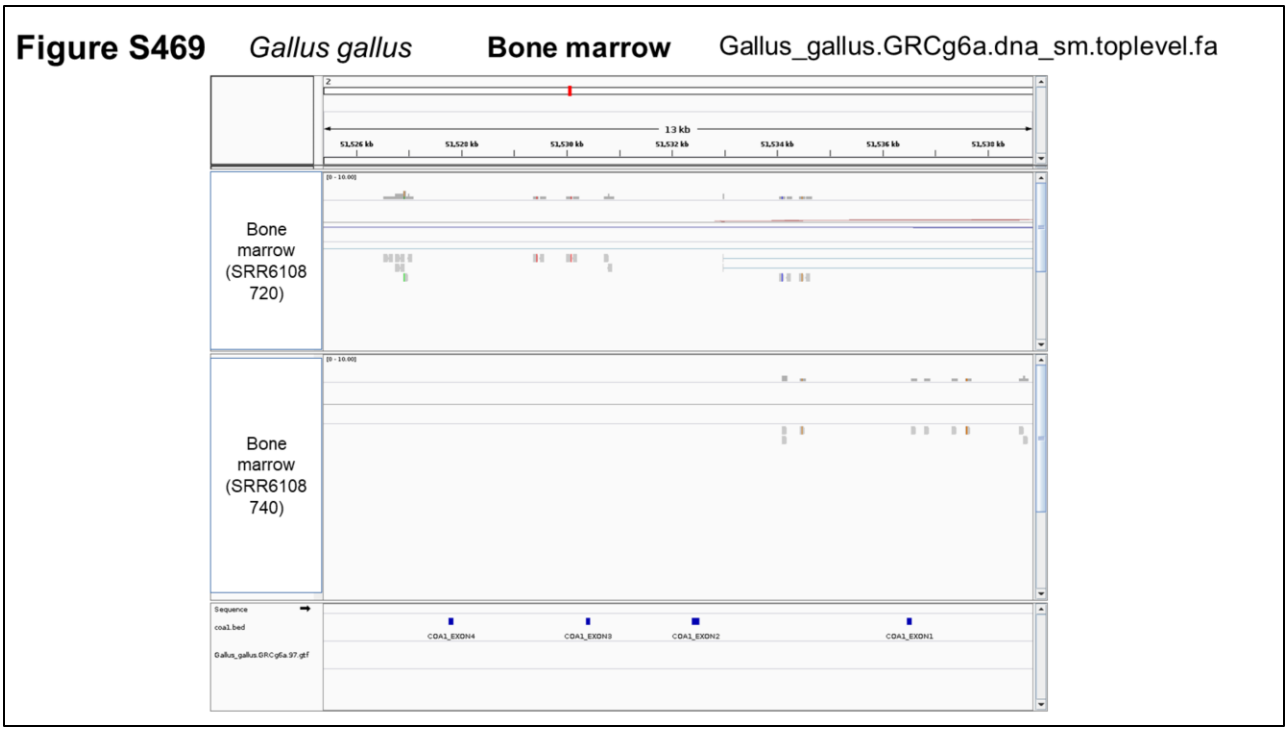

Figure S469: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from bone marrow (SRR6108720 and SRR6108740) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

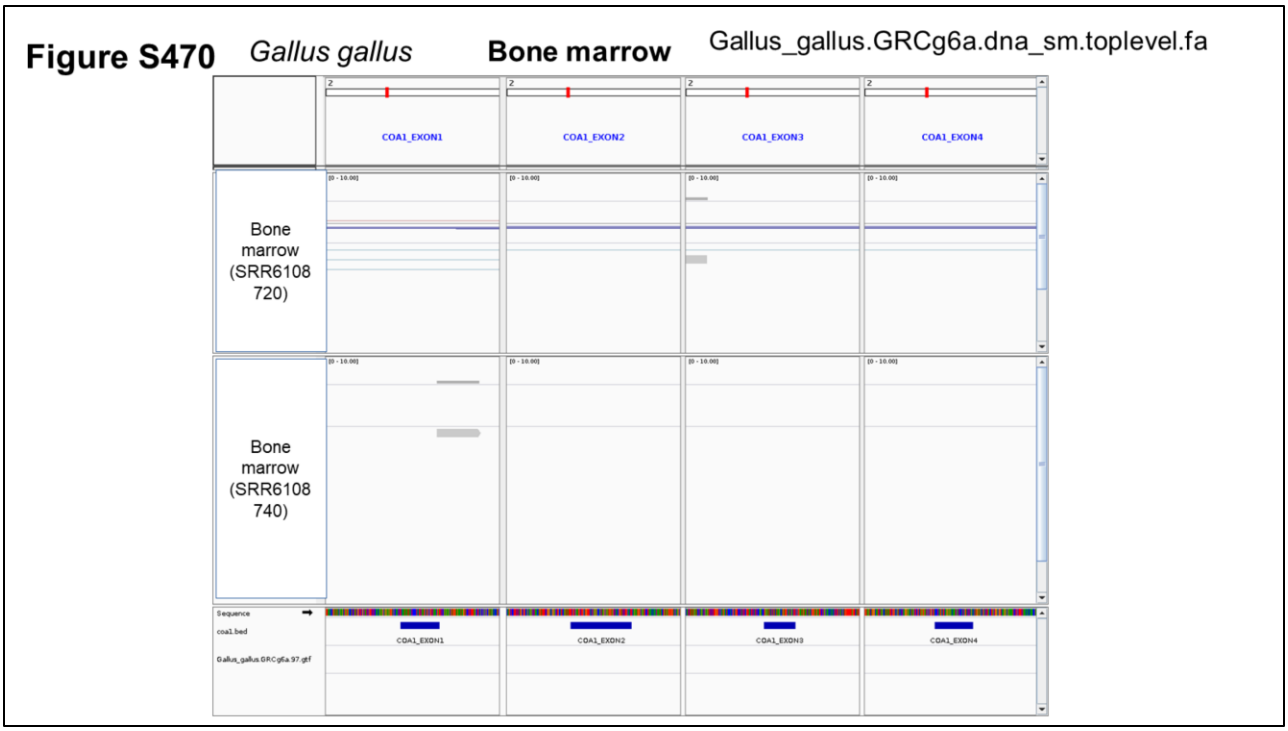

Figure S470: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S469**.

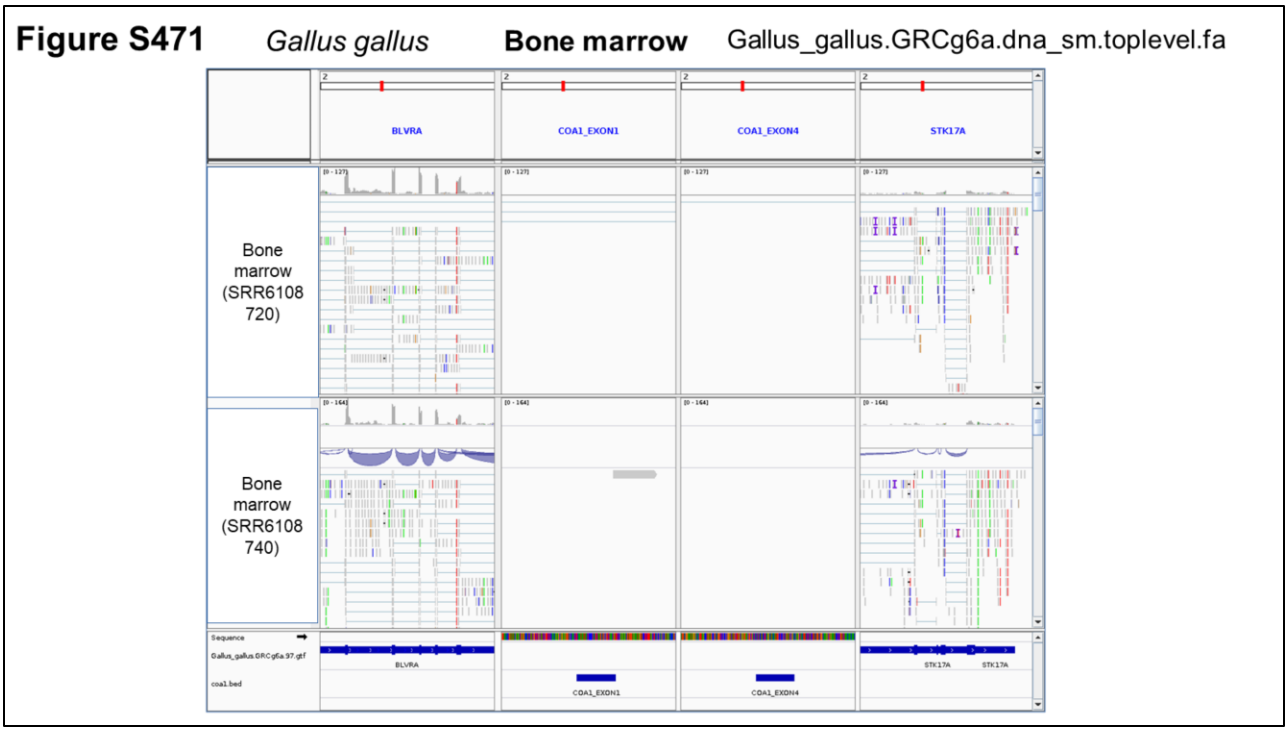

Figure S471: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from bone marrow (SRR6108720 and SRR6108740) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

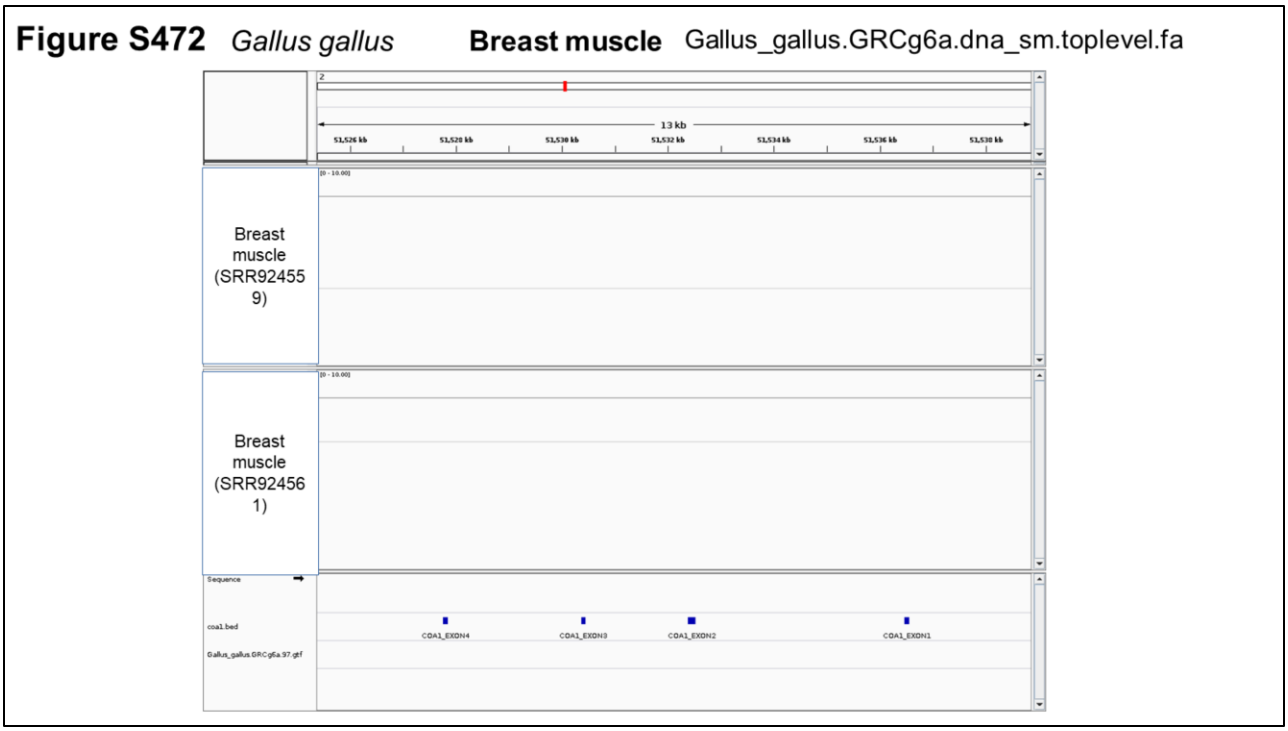

Figure S472: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from breast muscle (SRR924559 and SRR924561) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S473: A zoomed in view of each of the *COA1* exons shown **Supplementary Fig. S472**.

Figure S474: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from breast muscle (SRR924559 and SRR924561) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

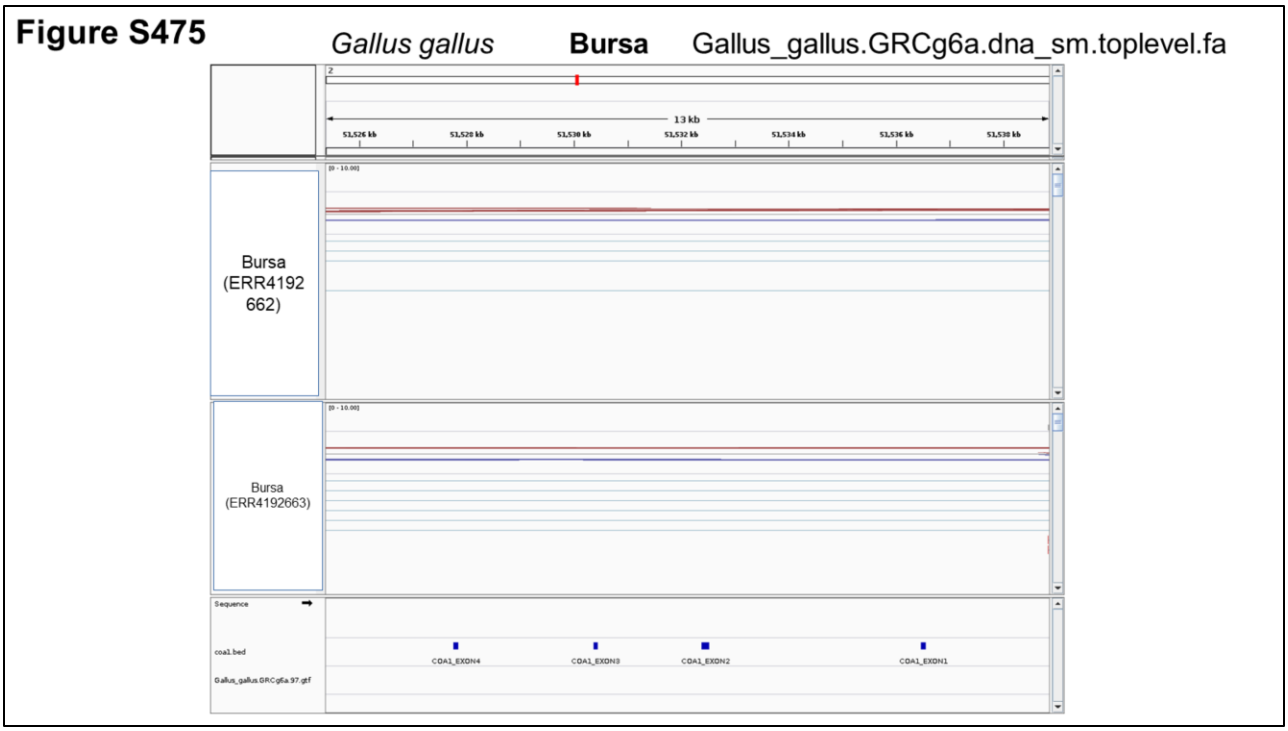

Figure S475: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from bursa (ERR4192662 and ERR4192663) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

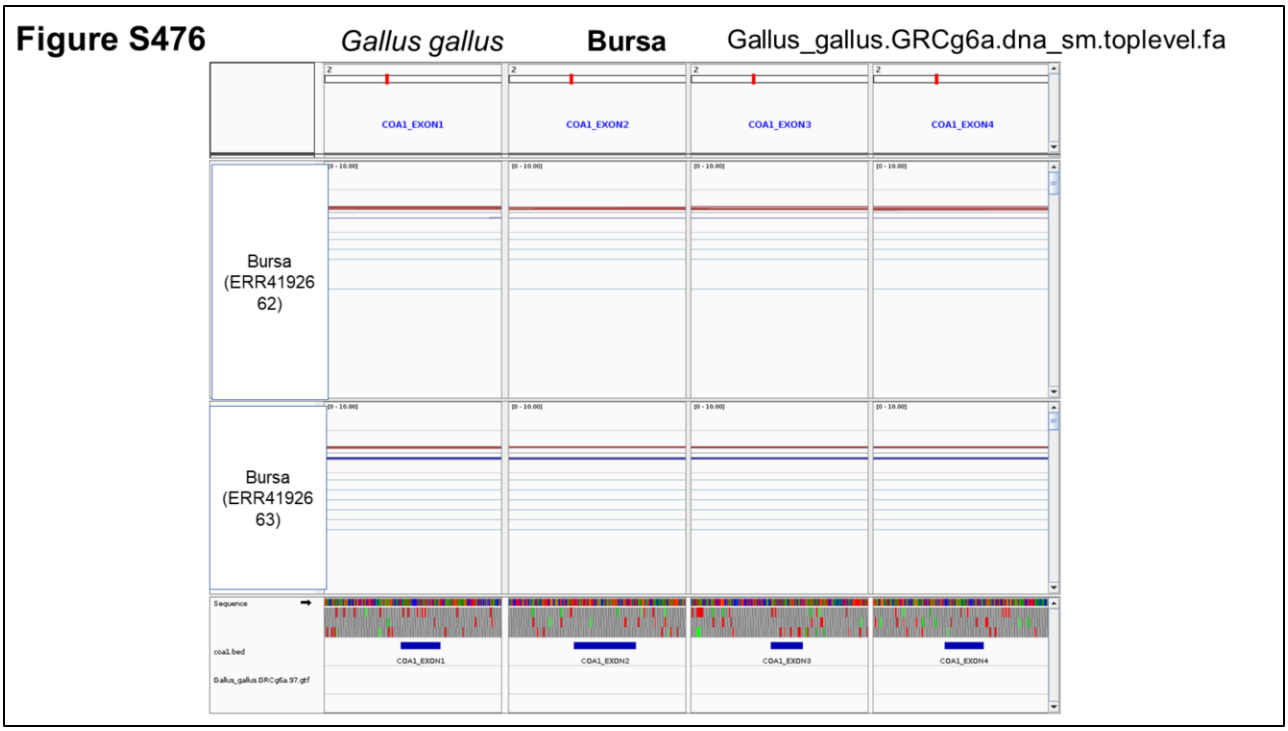

Figure S476: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S475**.

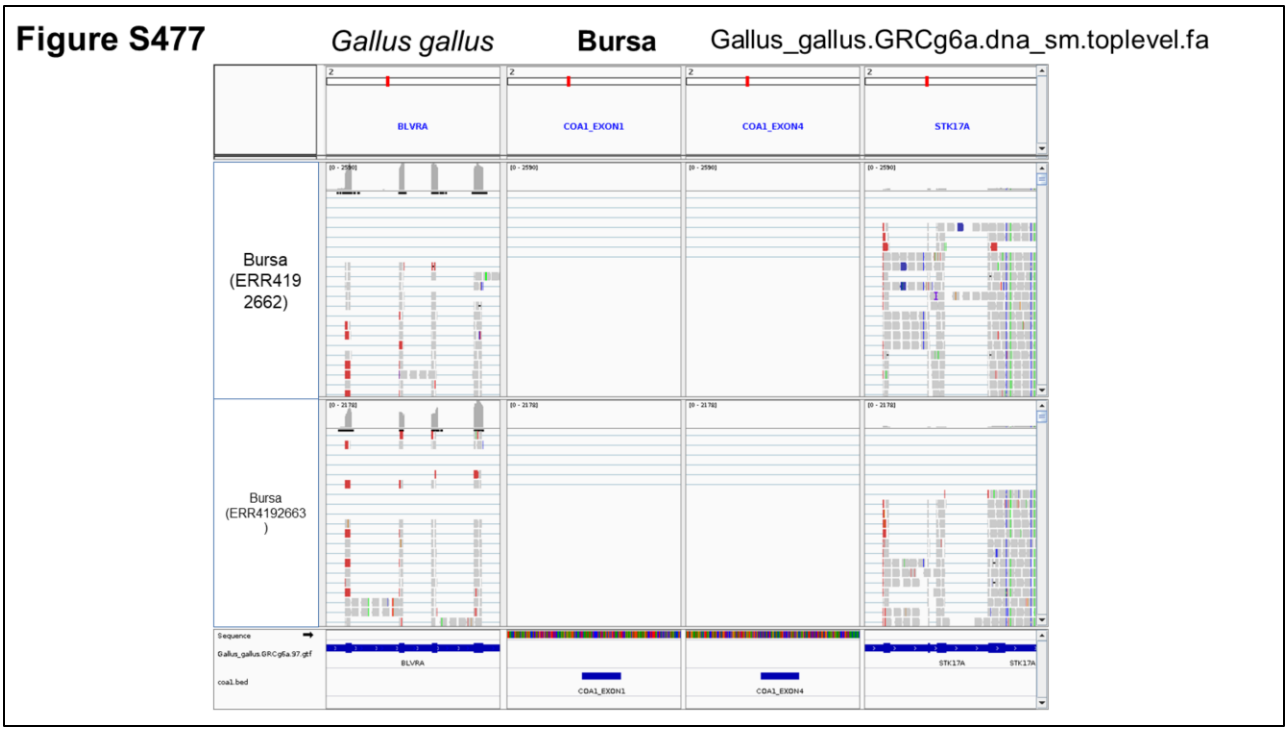

Figure. S477: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from bursa (ERR4192662 and ERR4192663) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

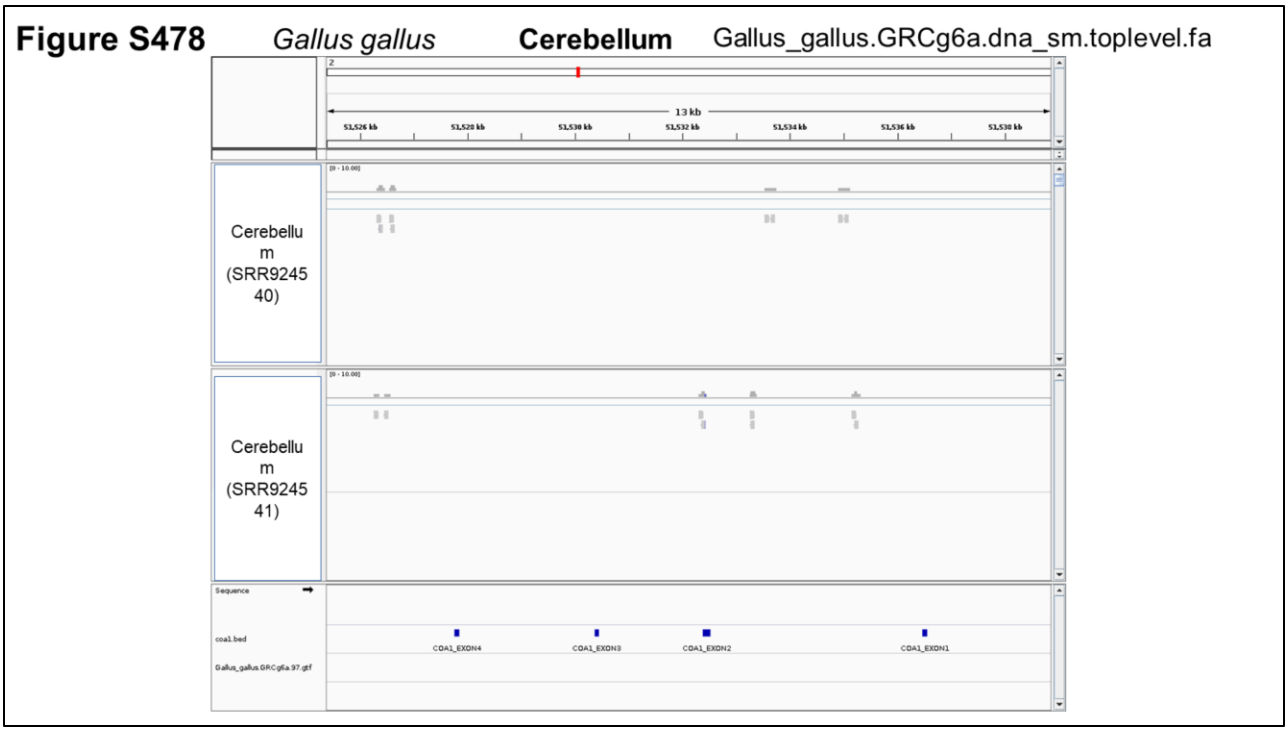

Figure S478: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from Cerebellum (SRR924540 and SRR924541) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

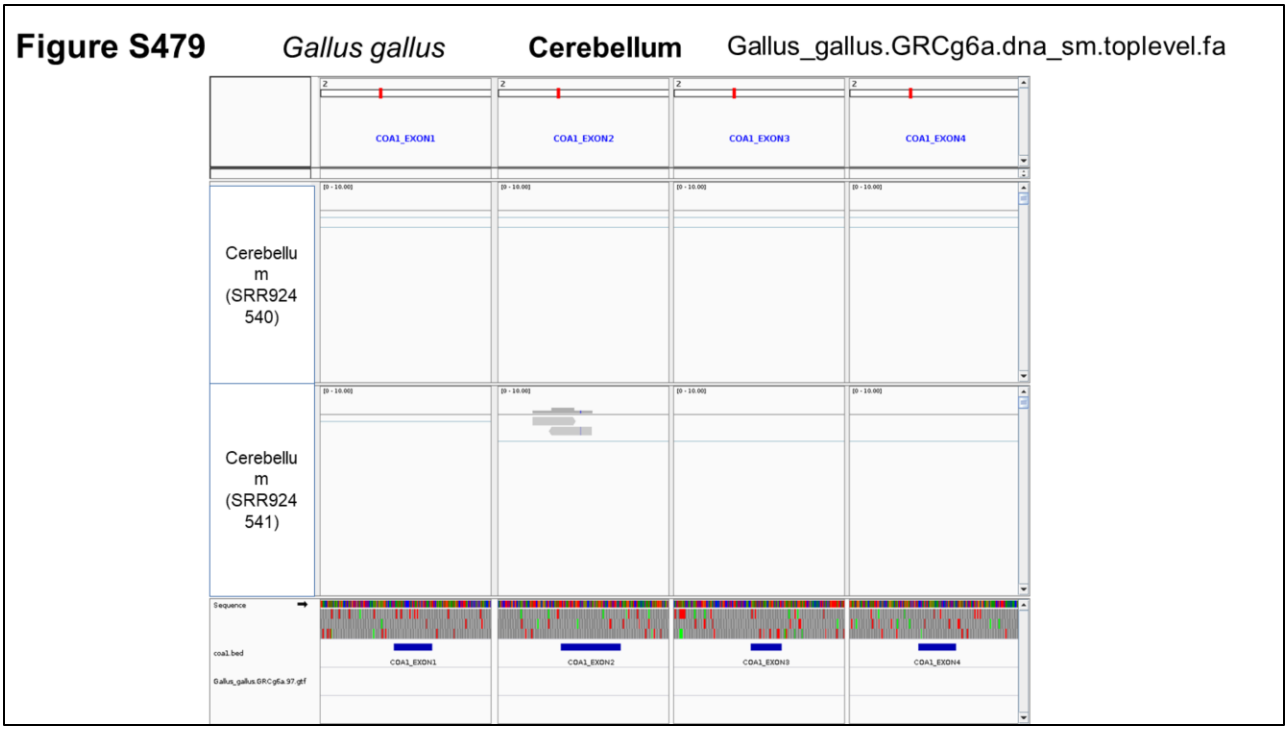

Figure S479: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S478**.

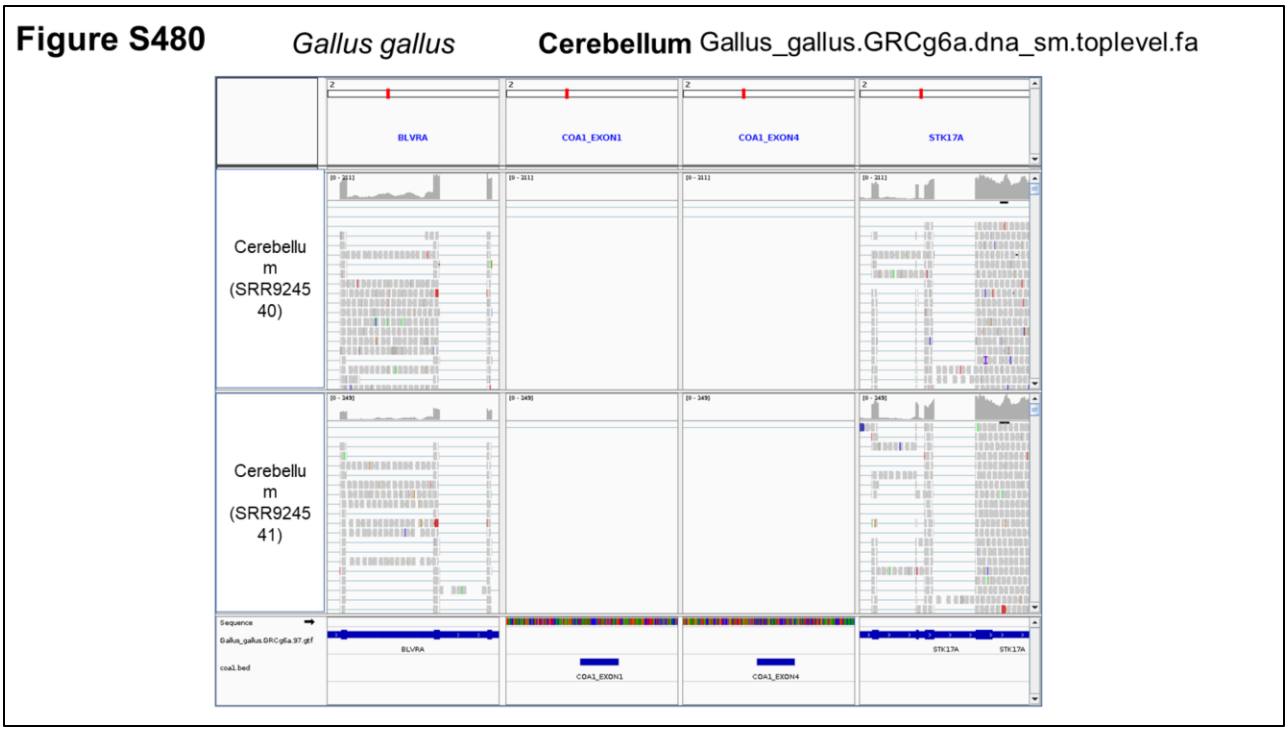

Figure S480: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from cerebellum (SRR924540 and SRR924541) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

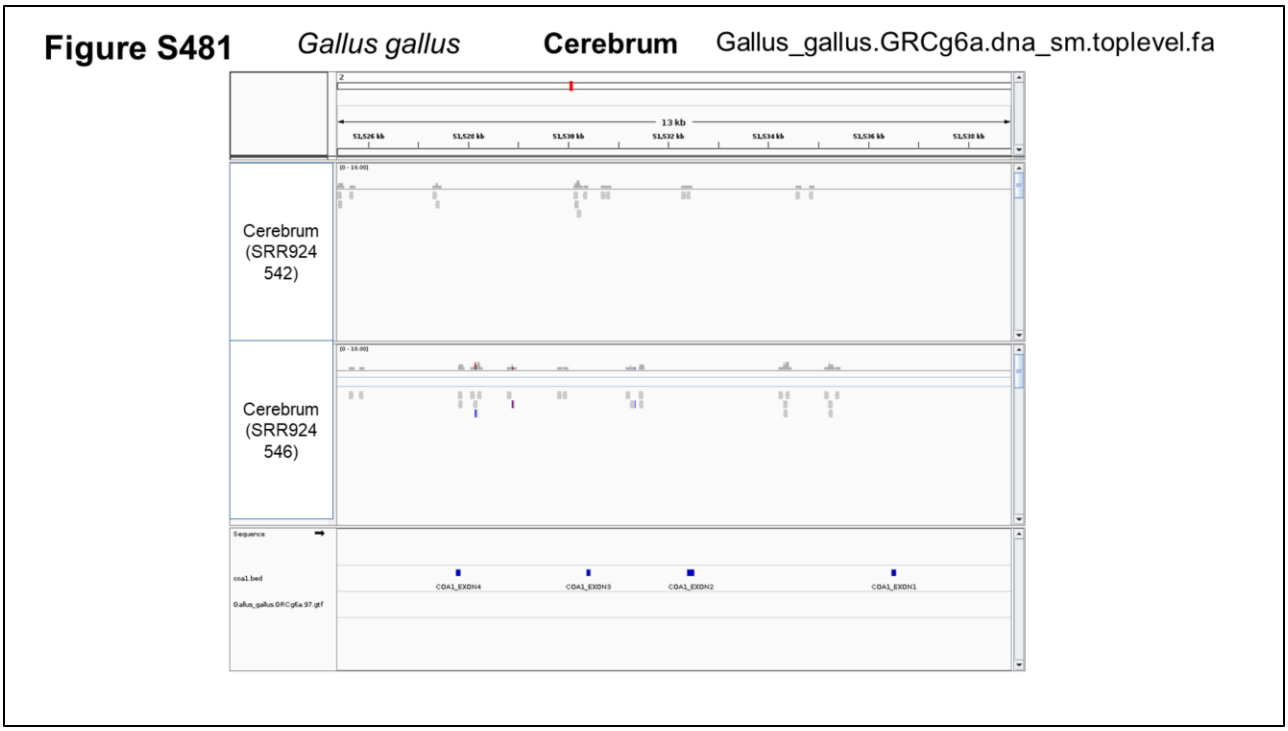

Figure S481: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from cerebrum (SRR924542 and SRR924546) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

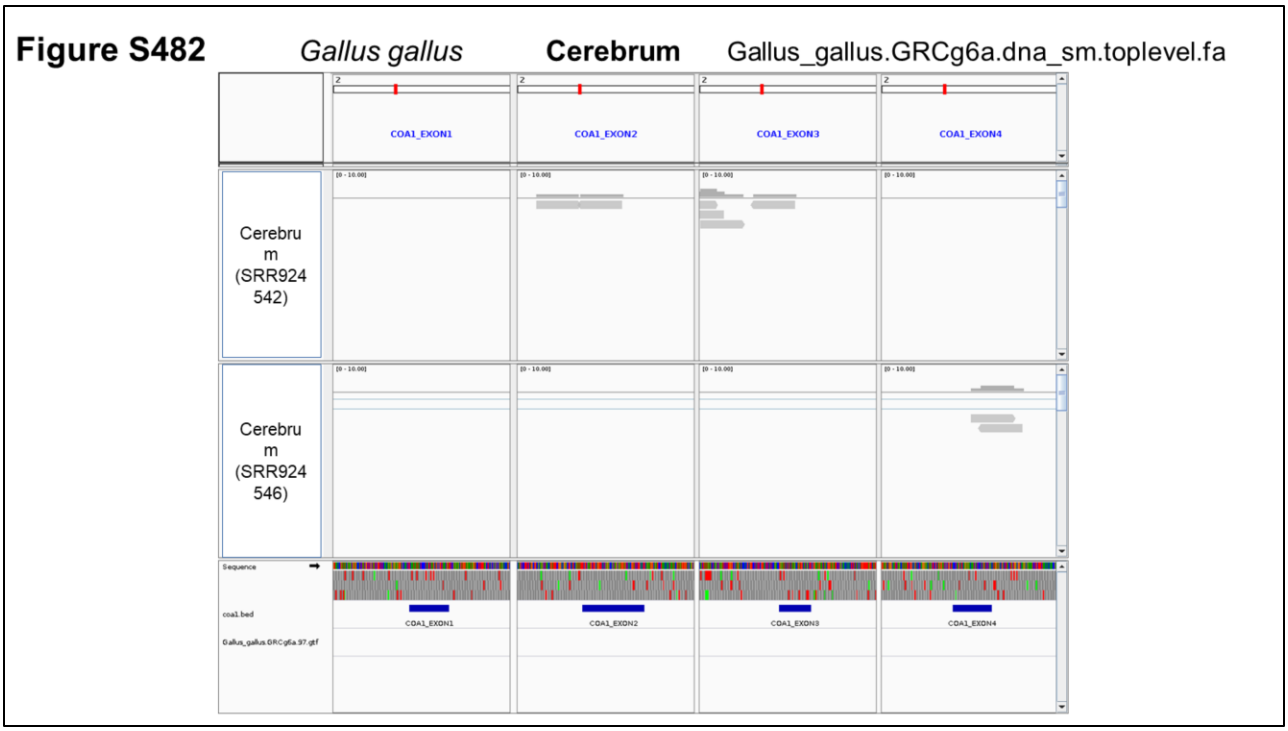

Figure S482: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S481**.

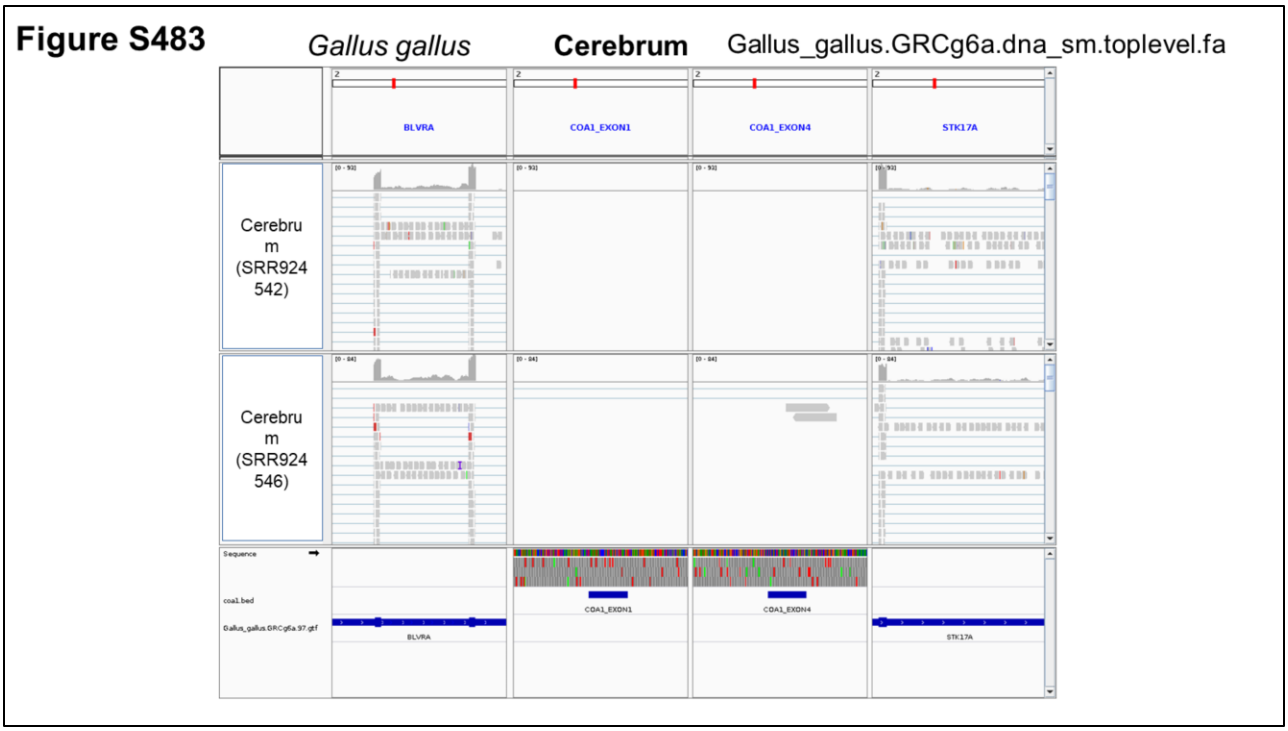

Figure S483: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from cerebrum (SRR924542 and SRR924546) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

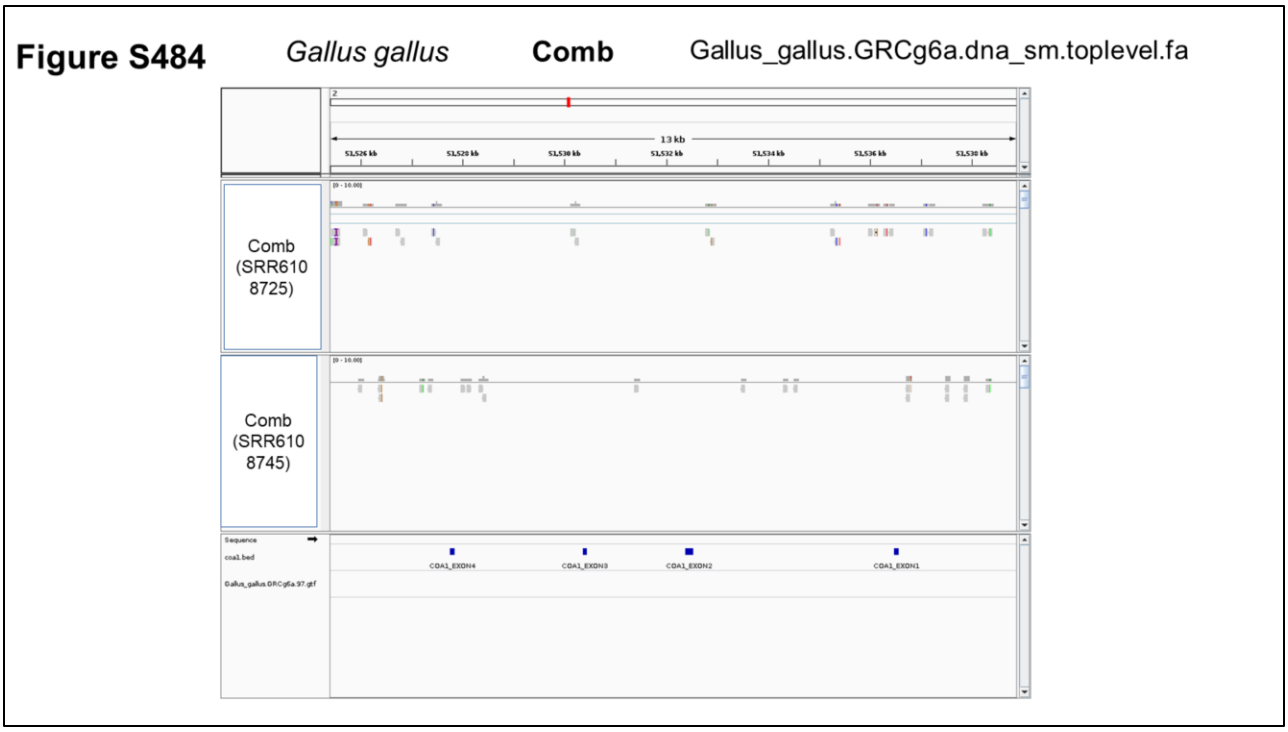

Figure S484: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from comb (SRR6108725) and (SRR6108745) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

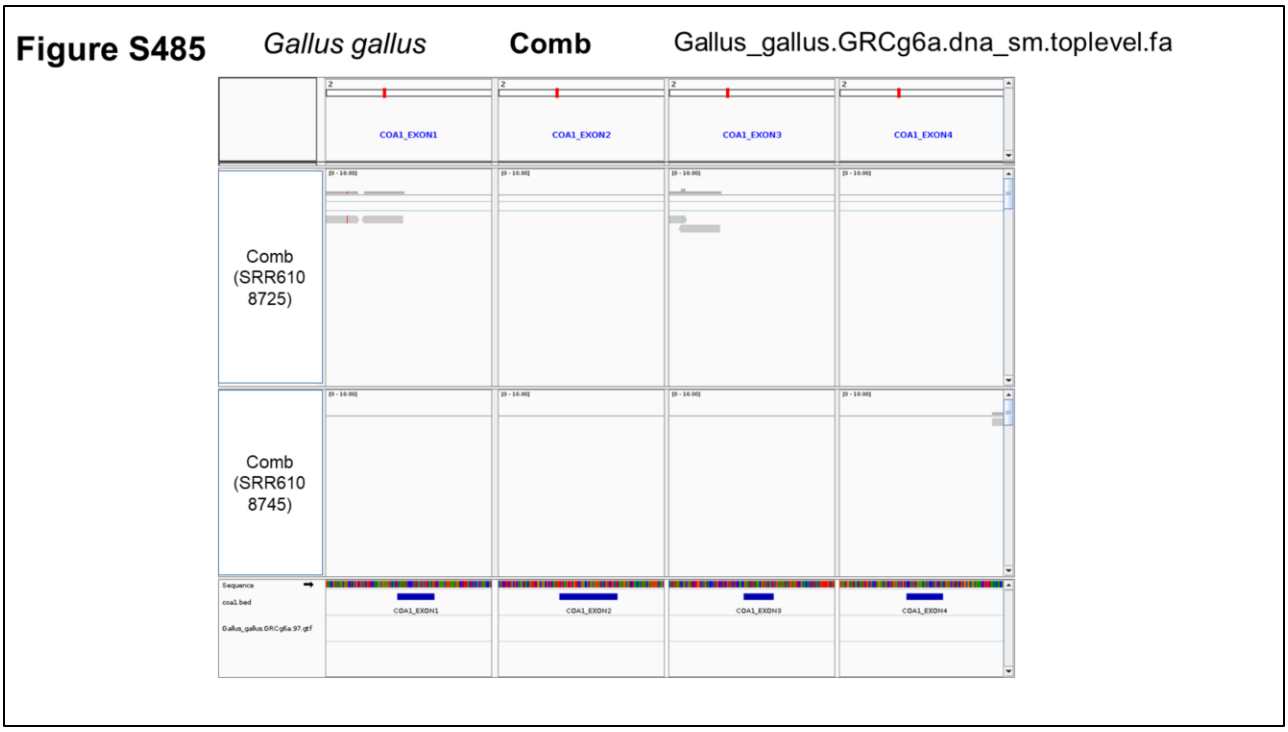

Figure S485 A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S484**.

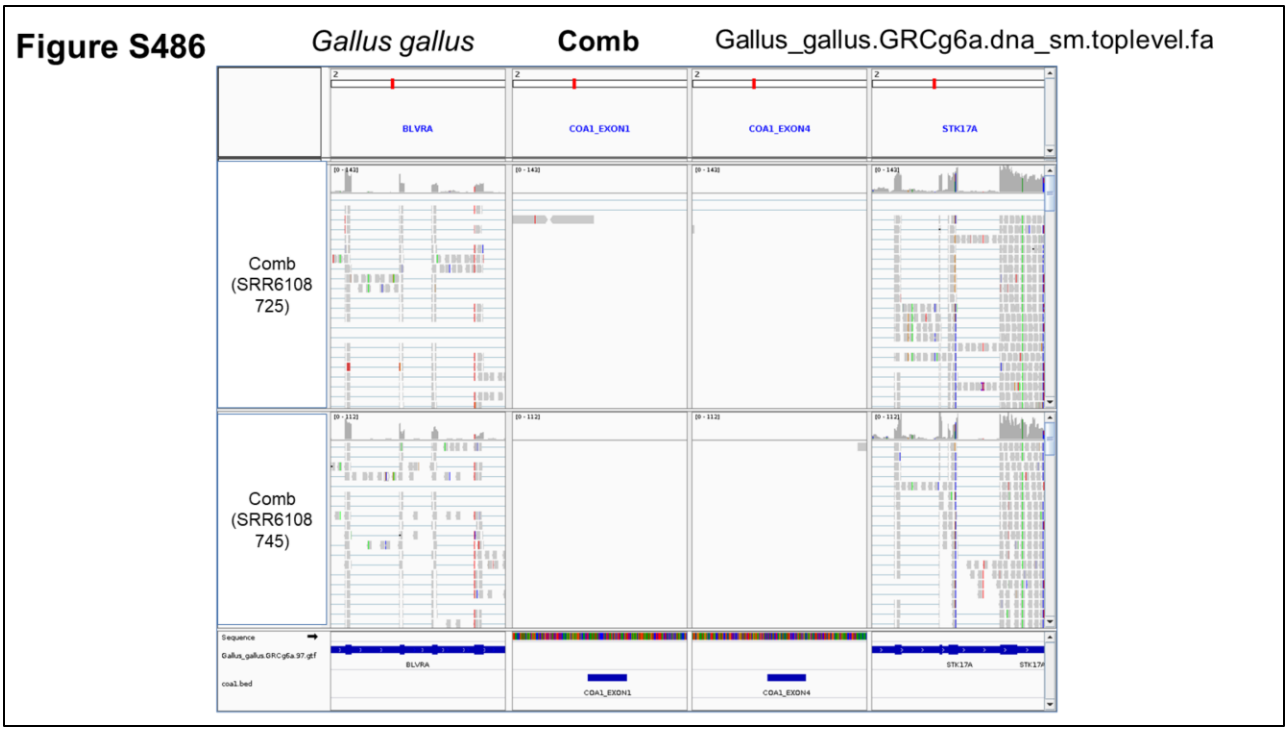

Figure S486: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from comb (SRR6108725) and (SRR6108745) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

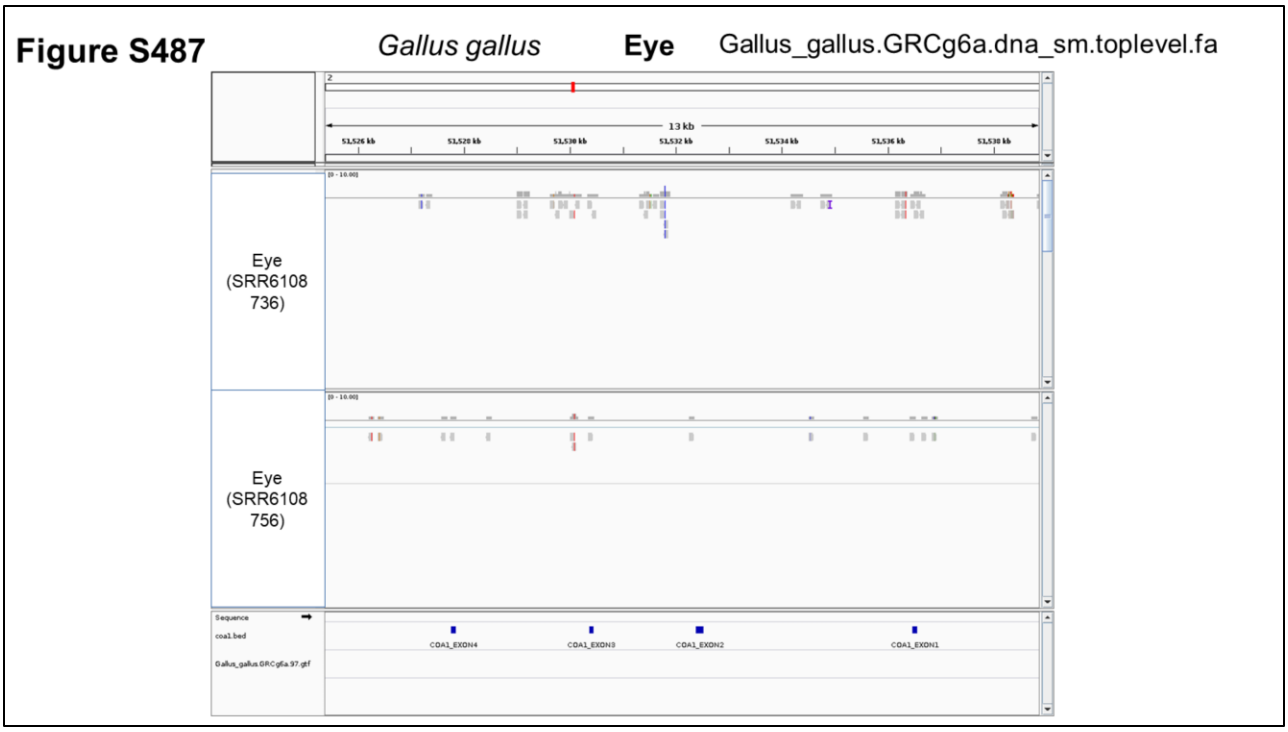

Figure S487: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from eye (SRR6108736) and (SRR6108756) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

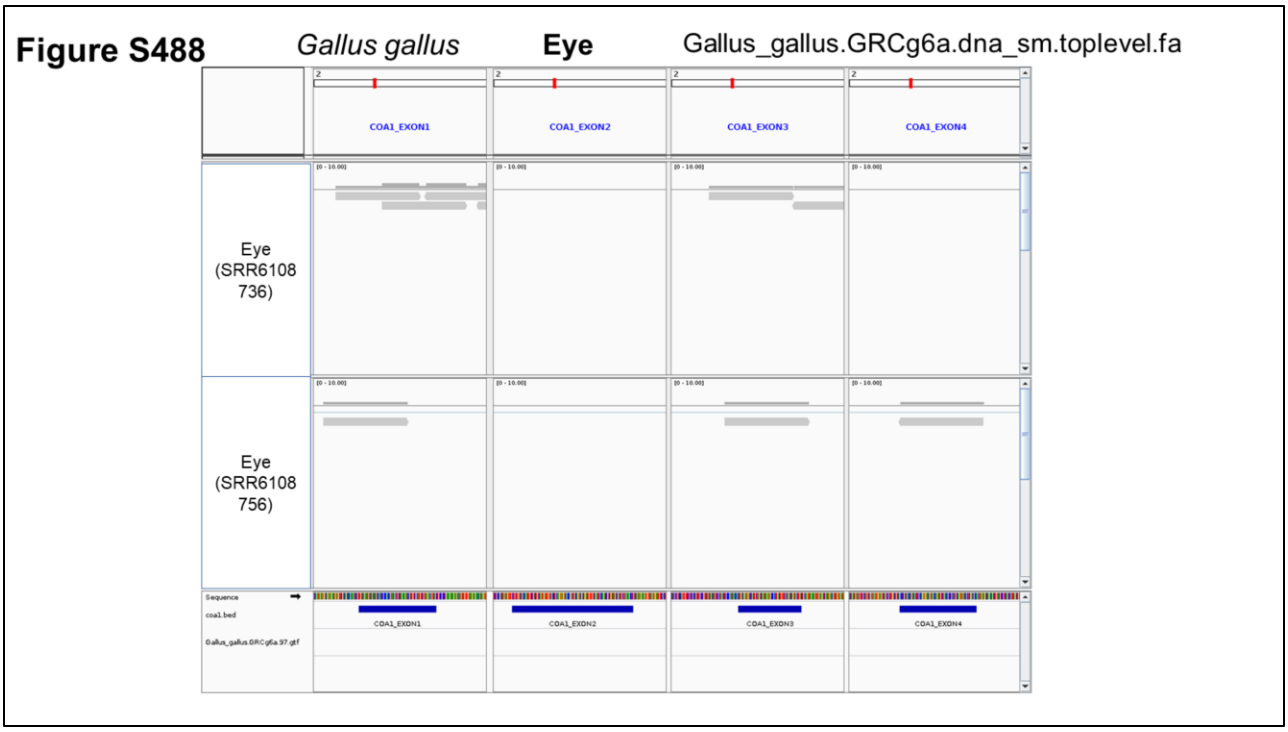

Figure S488: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S487**.

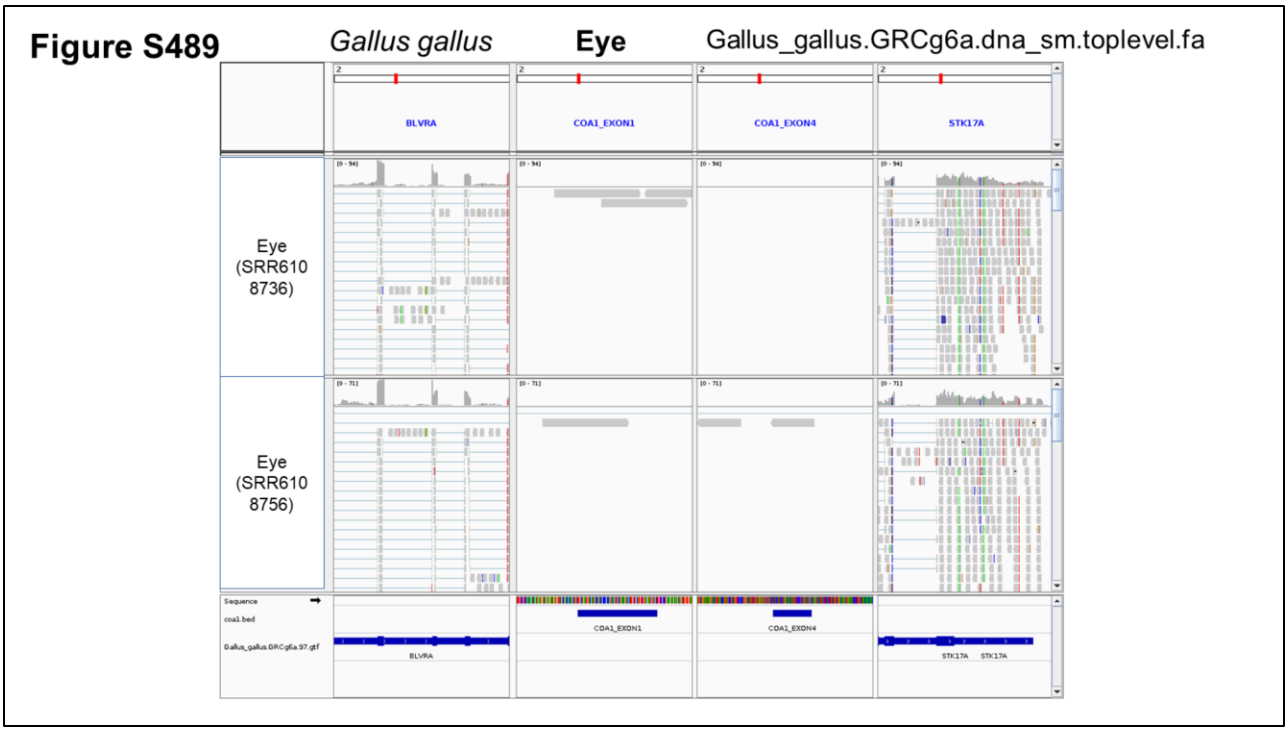

Figure S489: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from eye (SRR6108736) and (SRR6108756) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S490: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from fascia (SRR6108721) and (SRR6108741) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

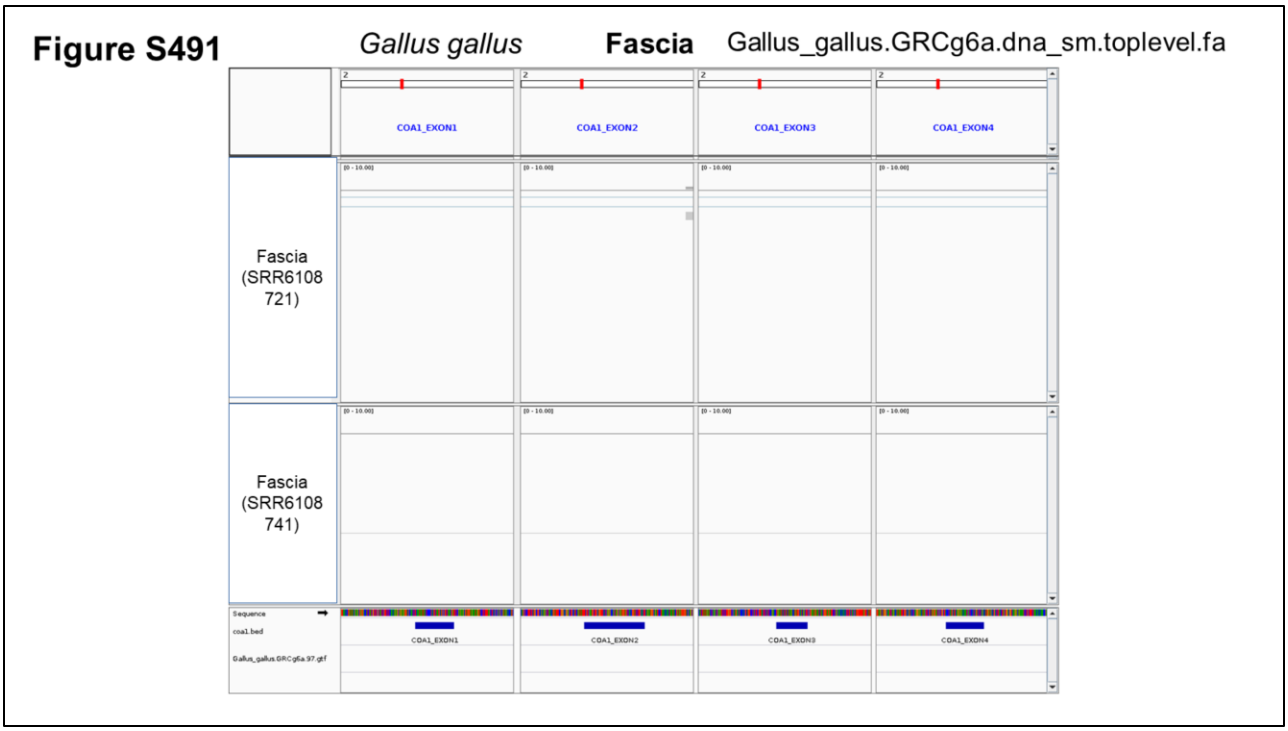

Figure S491: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S490**.

Figure S492: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from fascia (SRR6108721) and (SRR6108741) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

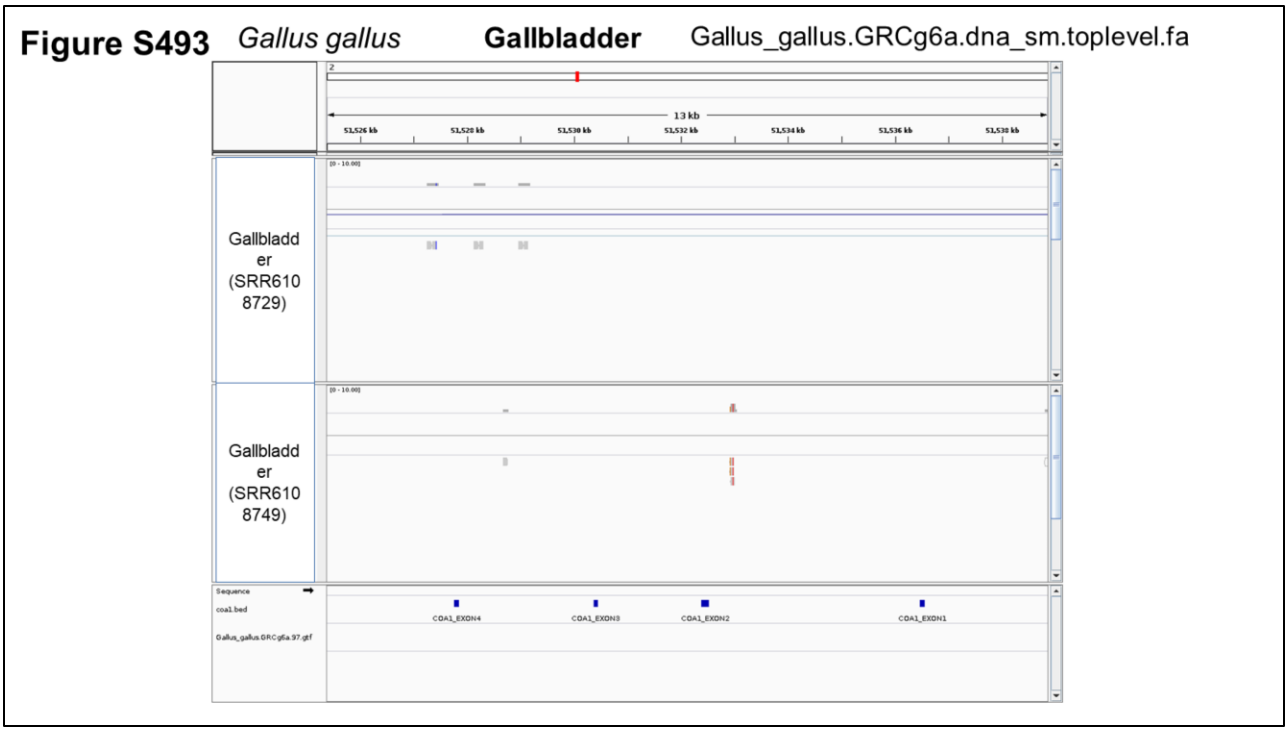

Figure S493: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from gallbladder (SRR6108729) and (SRR6108749) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

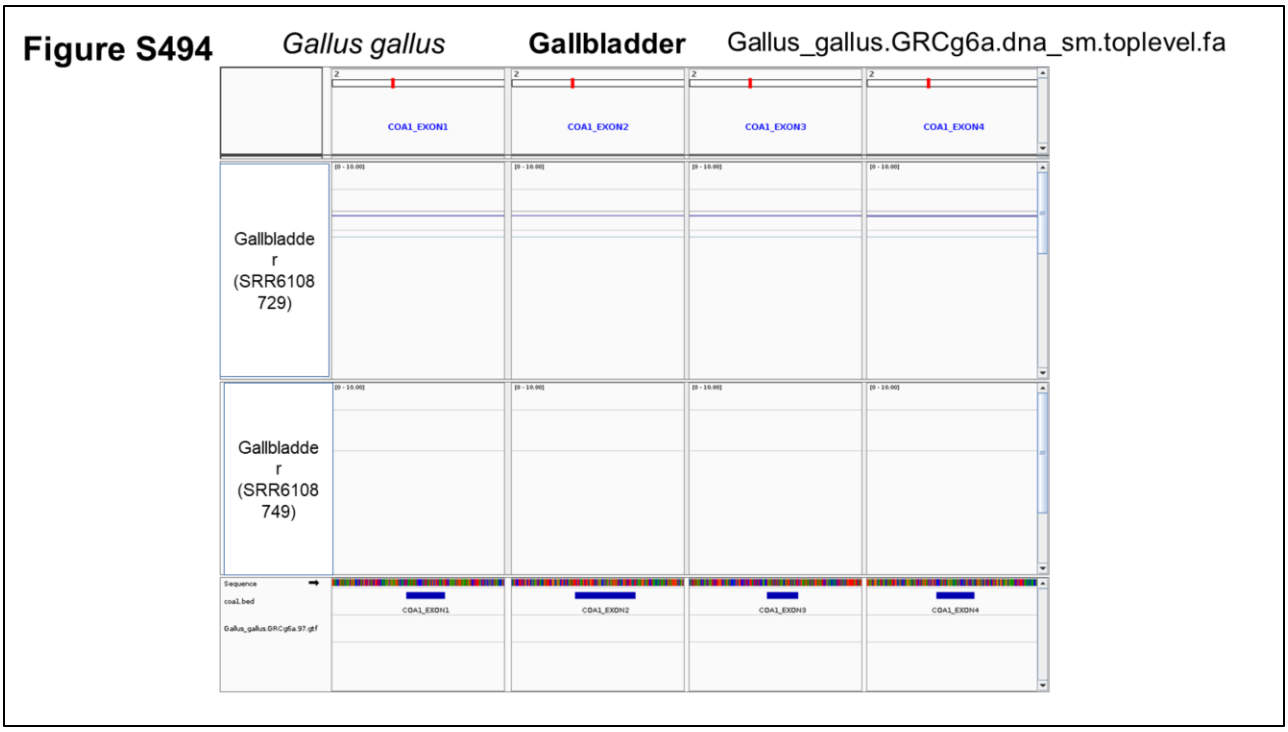

Figure S494: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S493**.

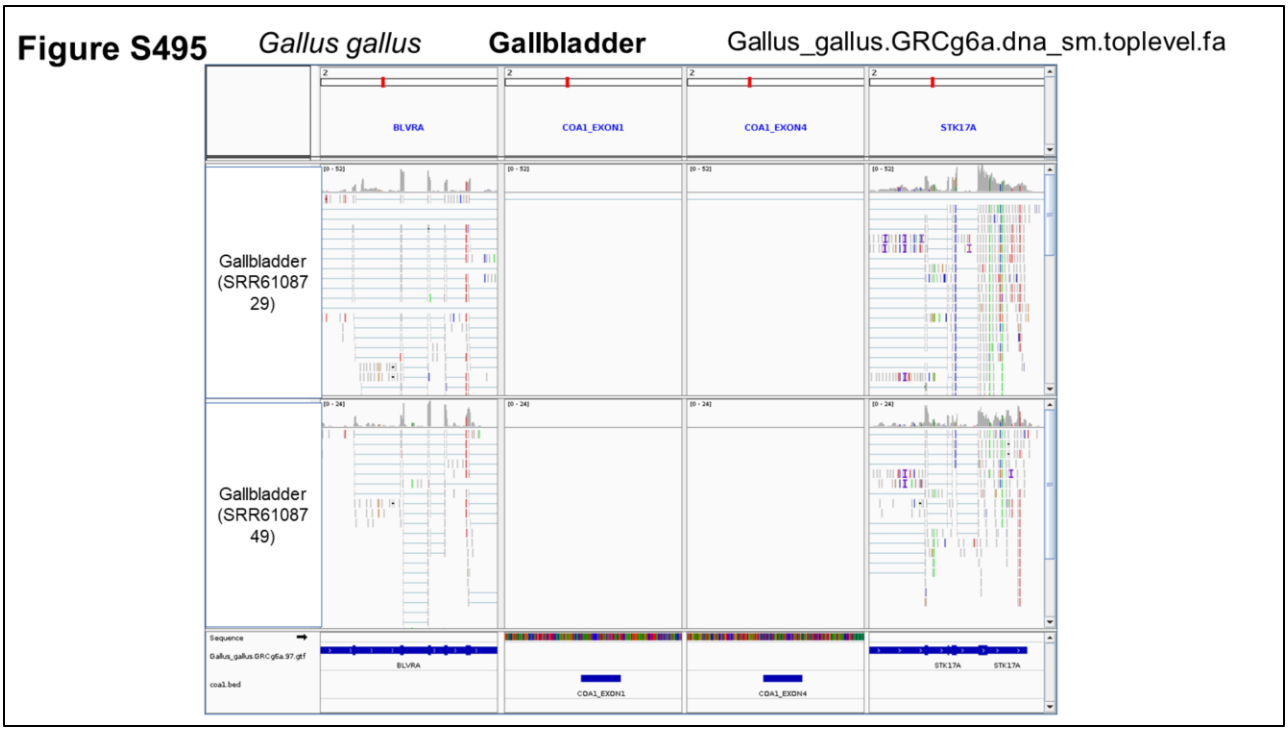

Figure S495: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from gallbladder (SRR6108729) and (SRR6108749) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

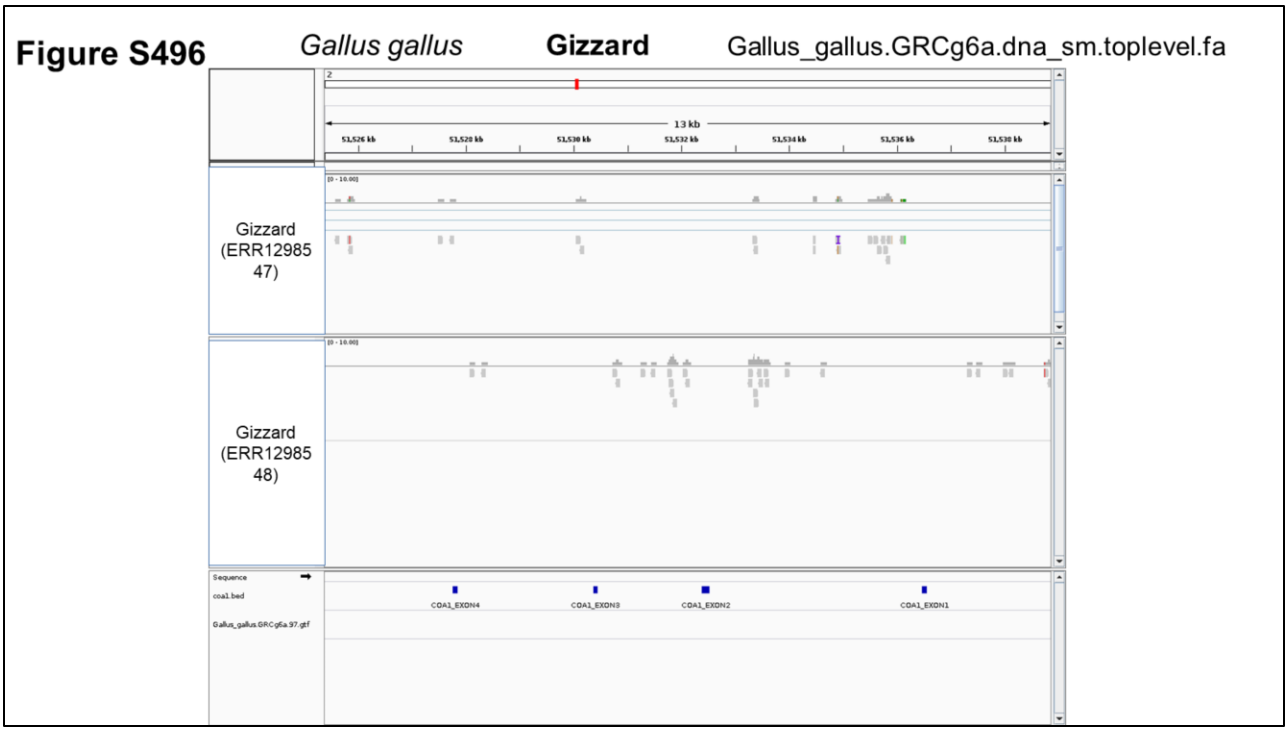

Figure S496: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from gizzard (ERR1298547) and (ERR1298548) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

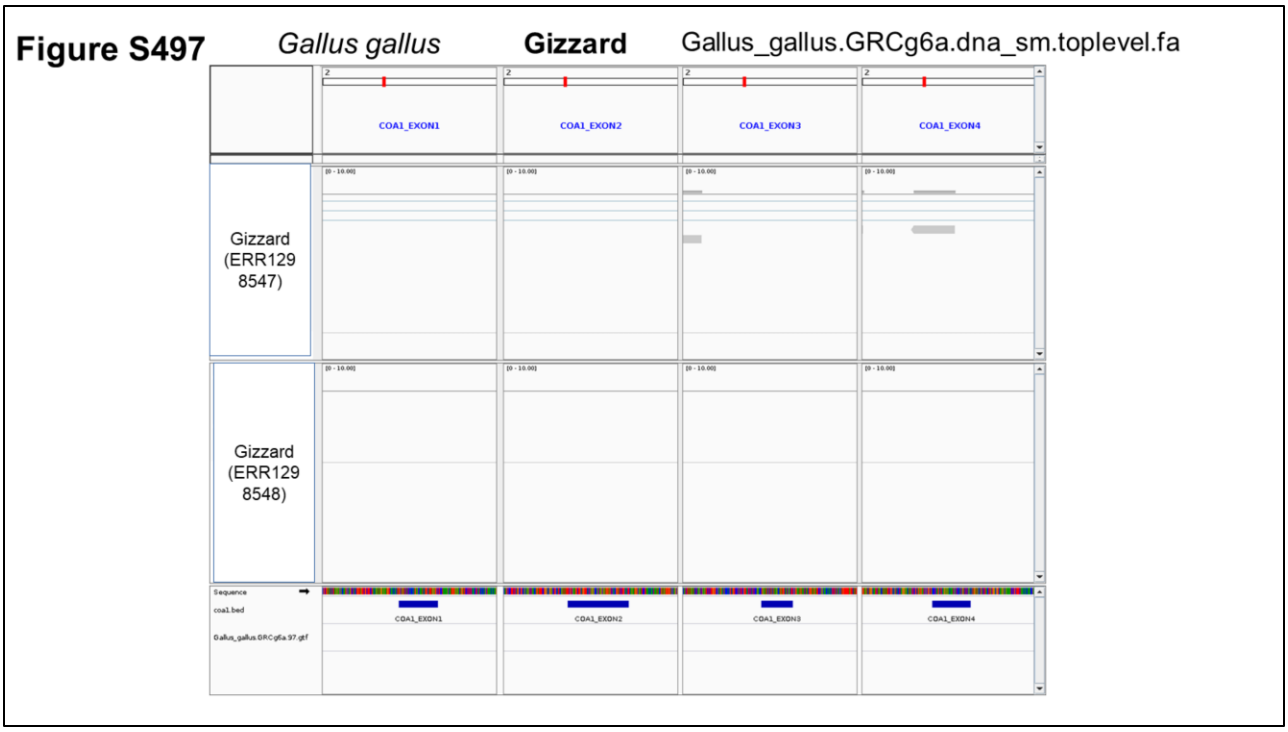

Figure S497: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S496**.

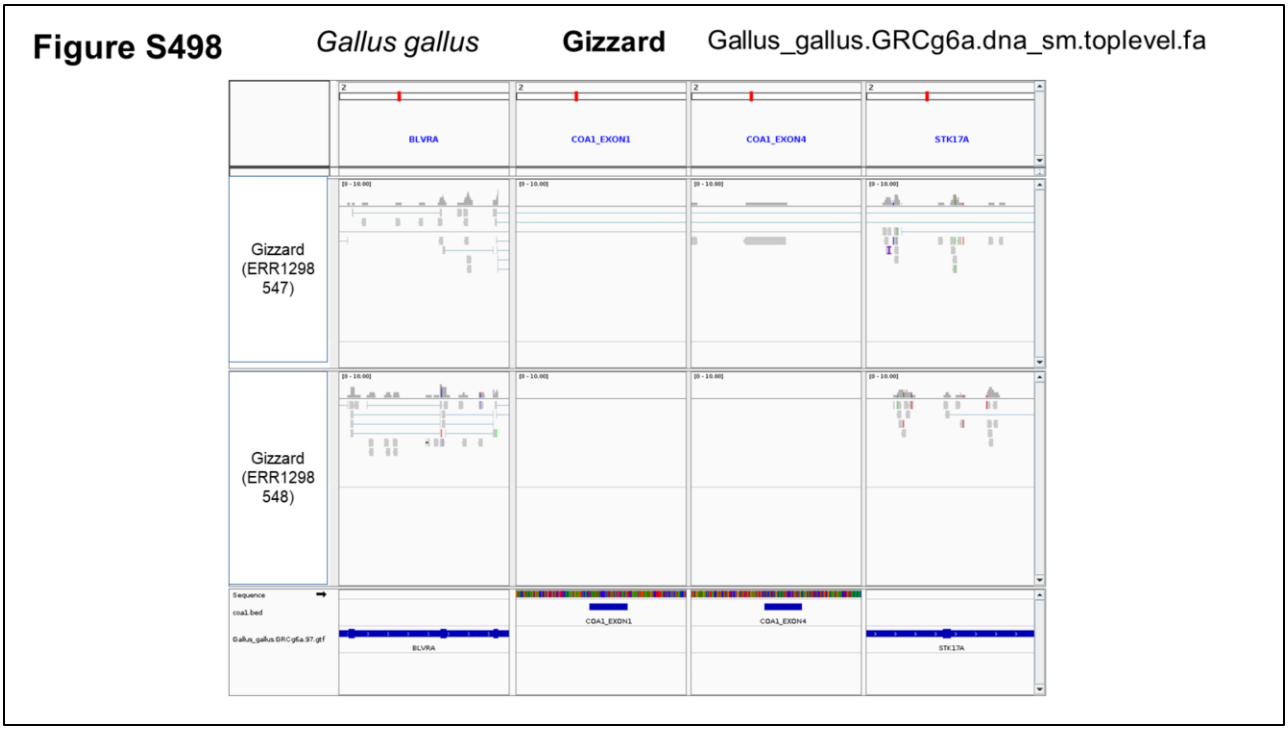

Figure S498: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from gizzard (ERR1298547) and (ERR1298548) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

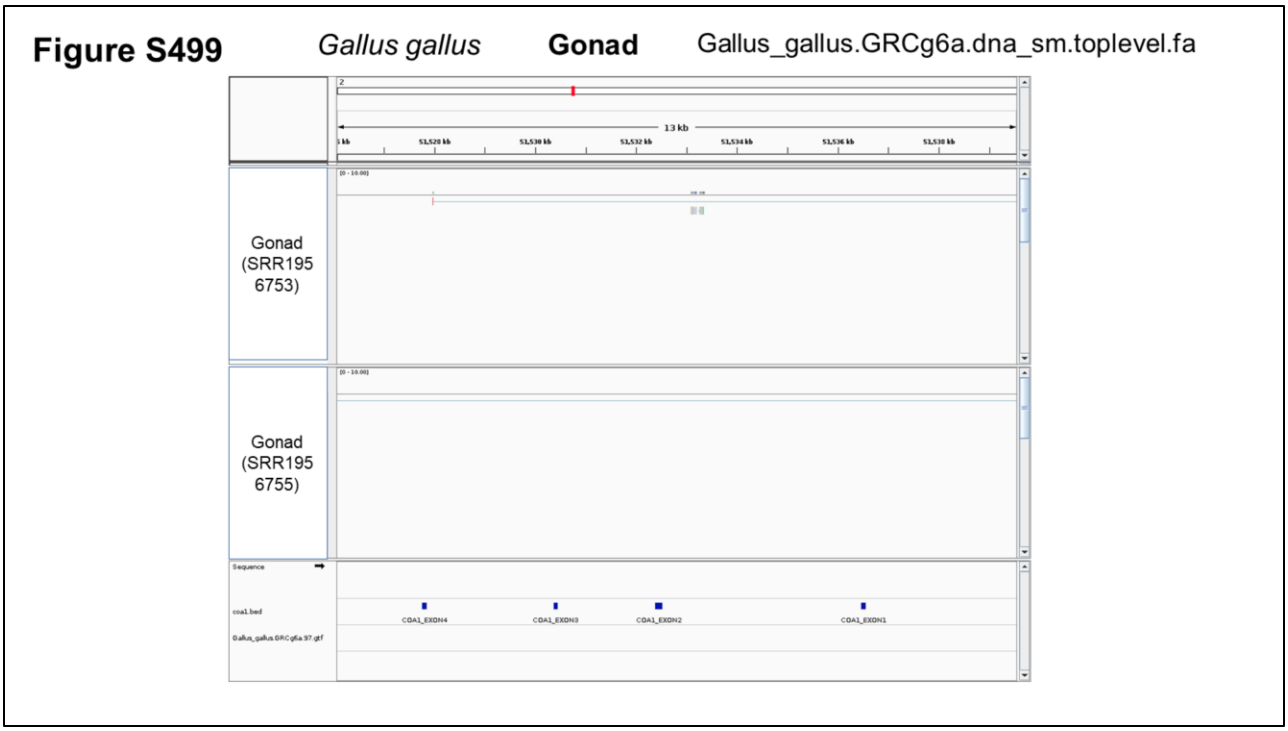

Figure S499: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from gonad (SRR1956753) and (SRR1956755) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

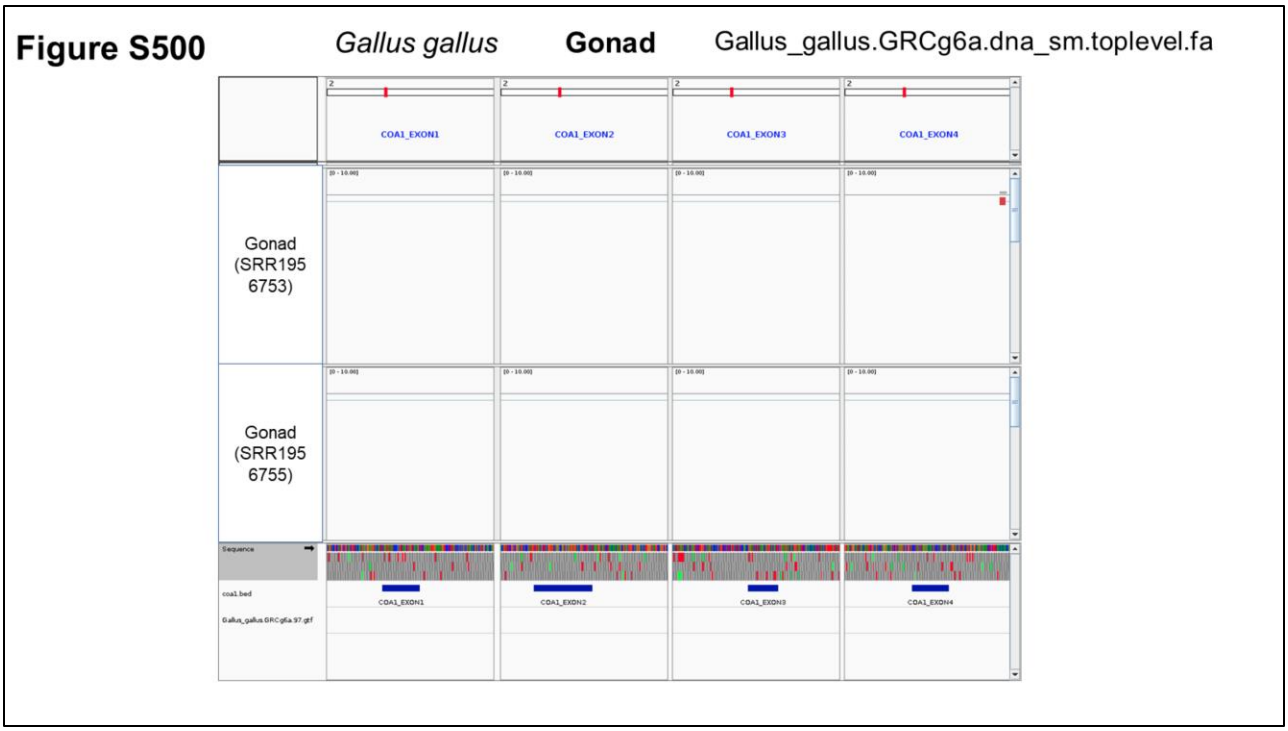

Figure S500: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S499**.

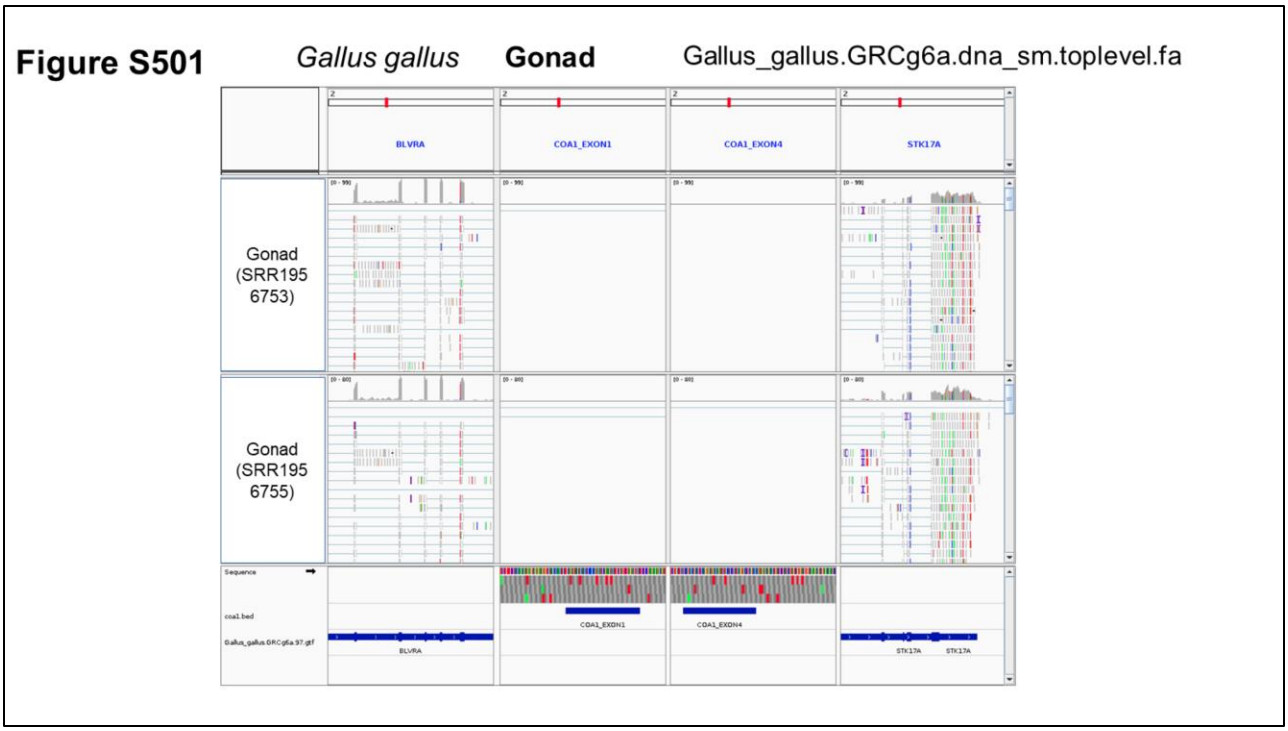

Figure S501: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from gonad (SRR1956753) and (SRR1956755) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

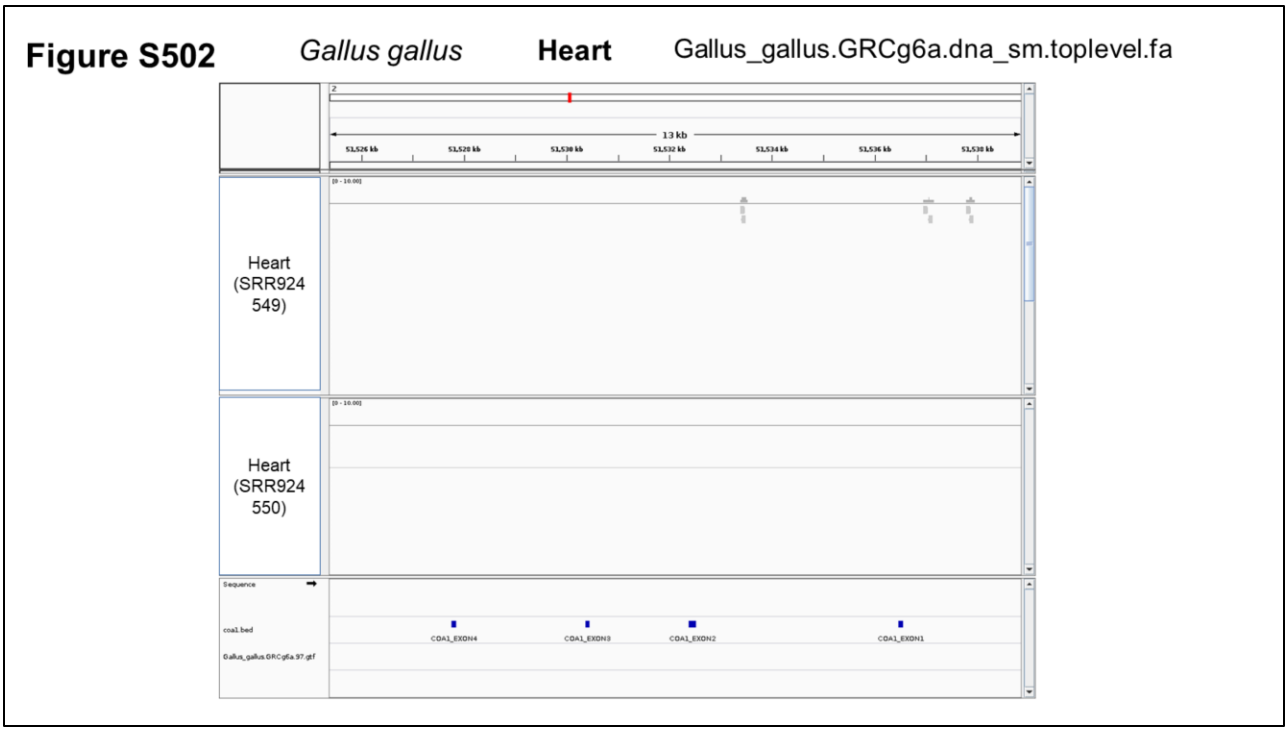

Figure S502: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart (SRR924549) and (SRR924550) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

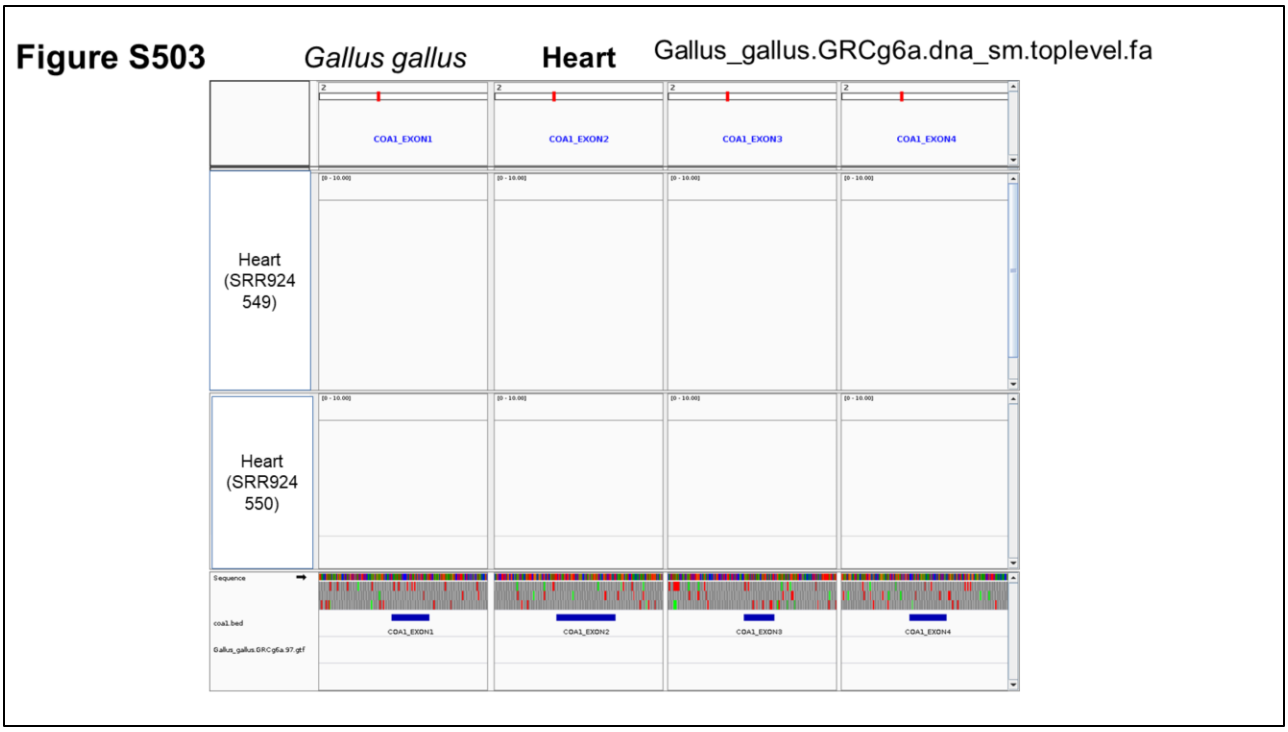

Figure S503: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S502**.

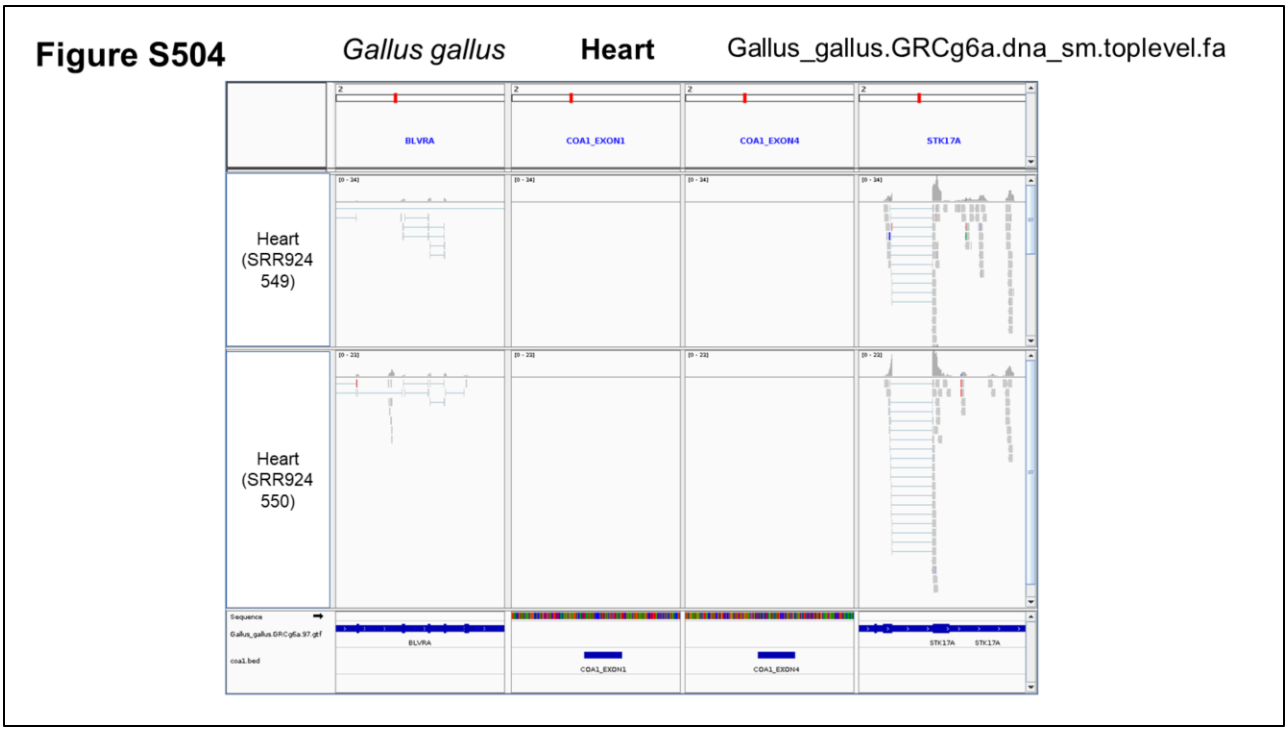

Figure S504: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart (SRR924549) and (SRR924550) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

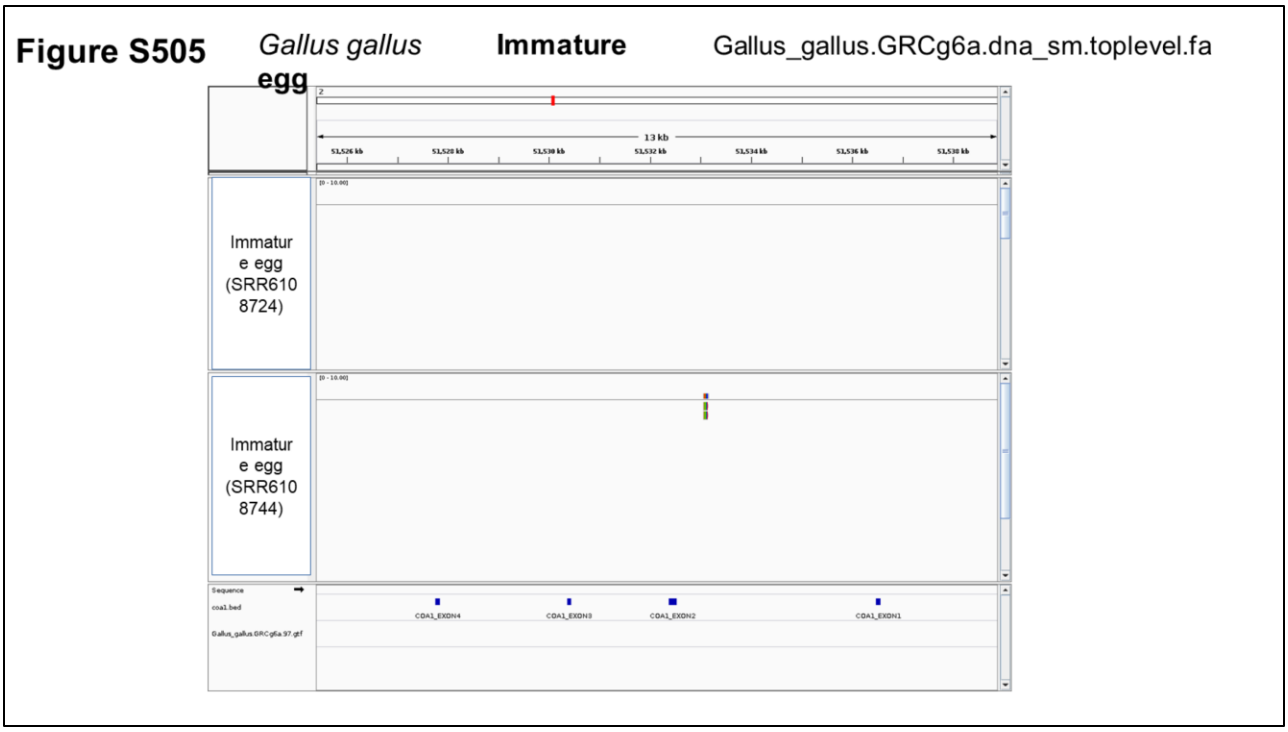

Figure S505: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from immature egg (SRR5108724) and (SRR5108744) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

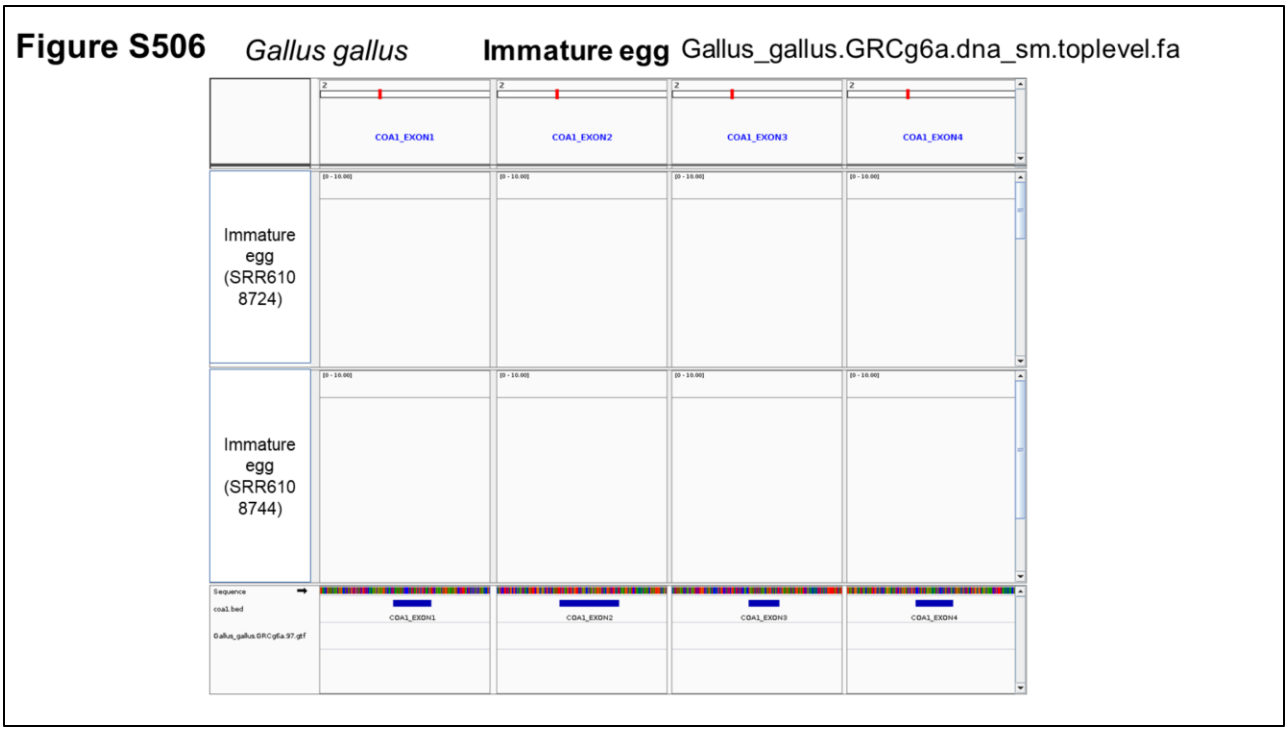

Figure S506: A zoomed in view of each of the *COA1* exons shown in shown in **Supplementary Fig. S505**.

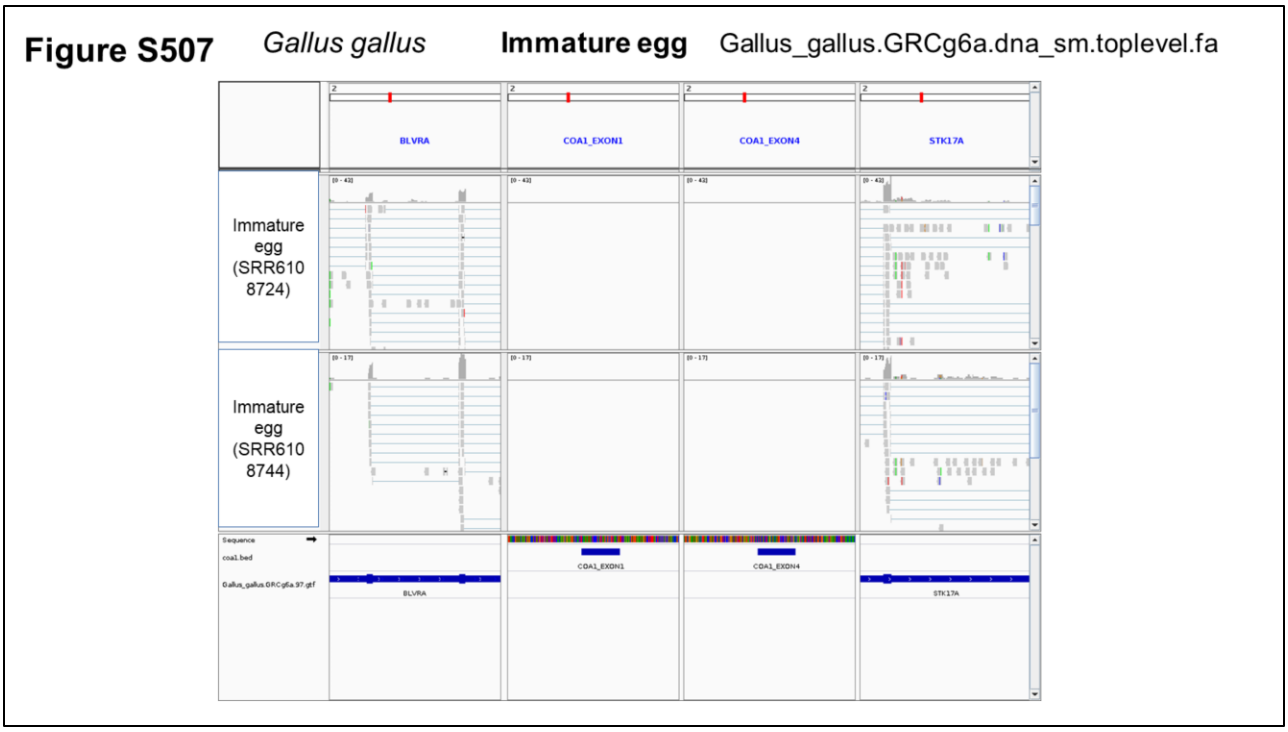

Figure S507: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from immature egg (SRR5108724) and (SRR5108744) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

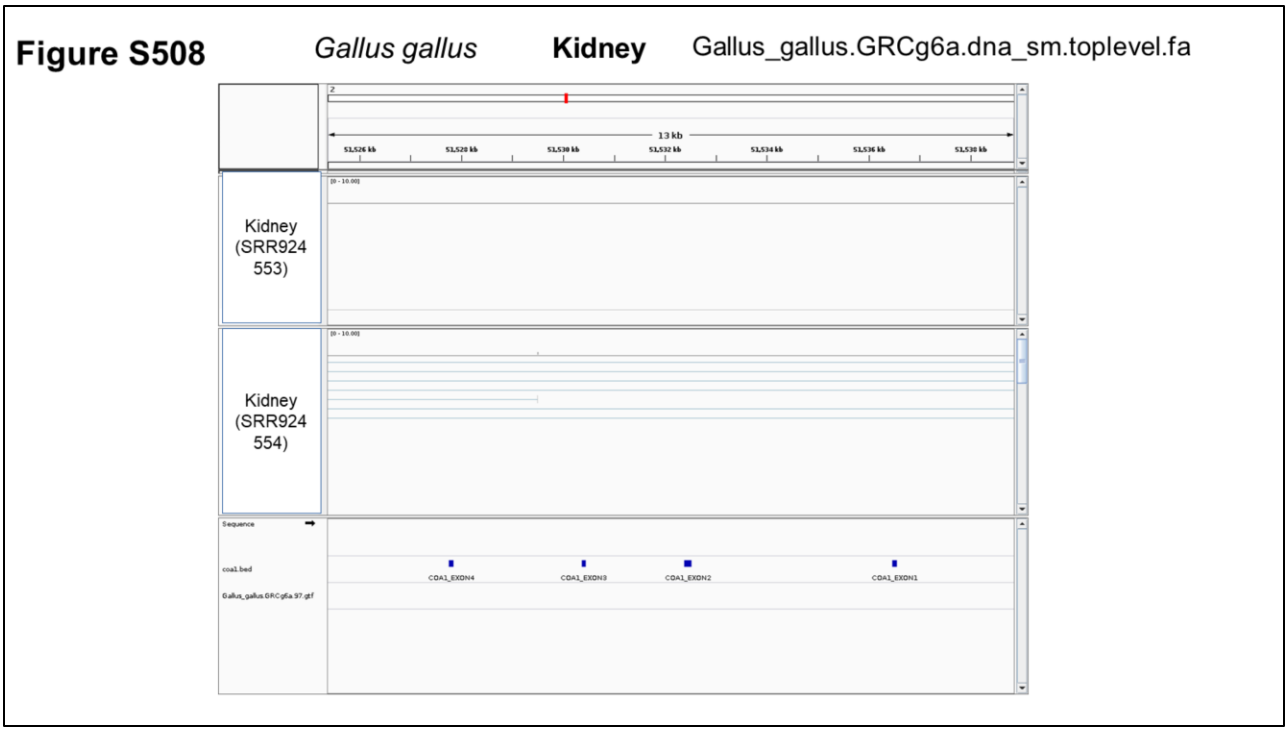

Figure S508: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from kidney (SRR924553) and (SRR924554) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

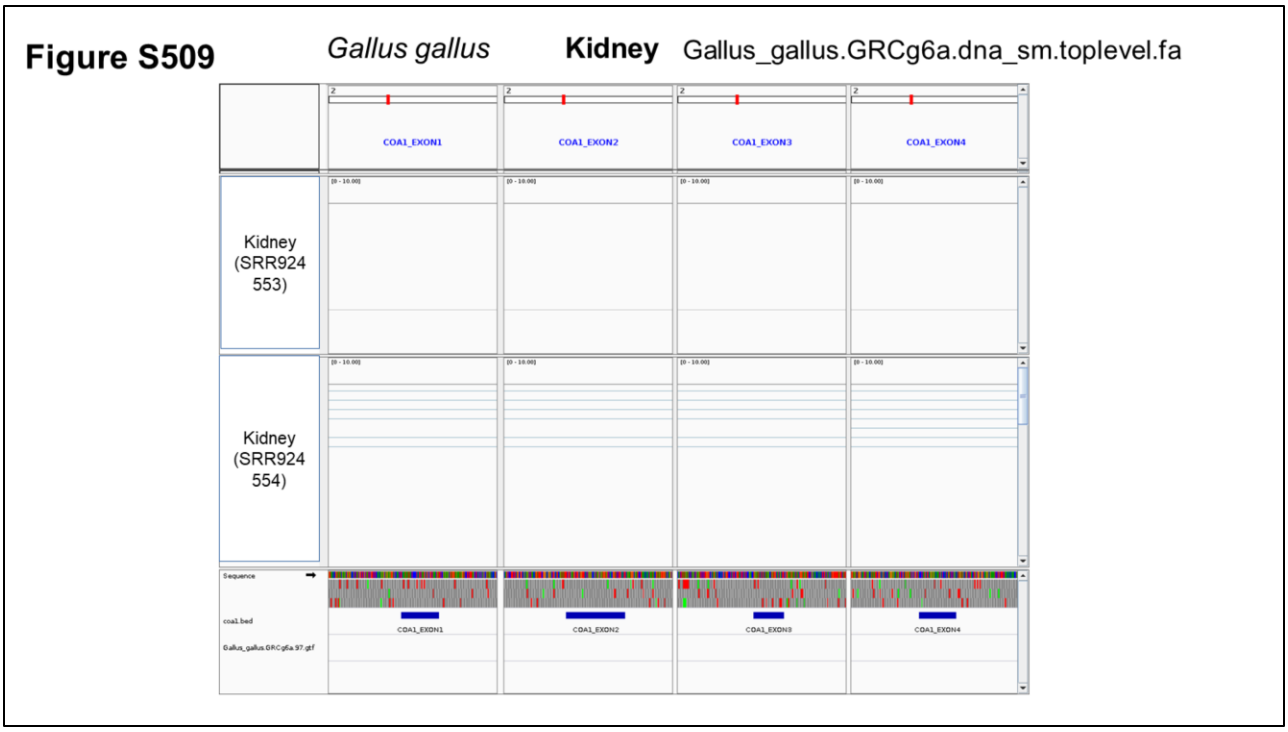

Figure S509: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S508**.

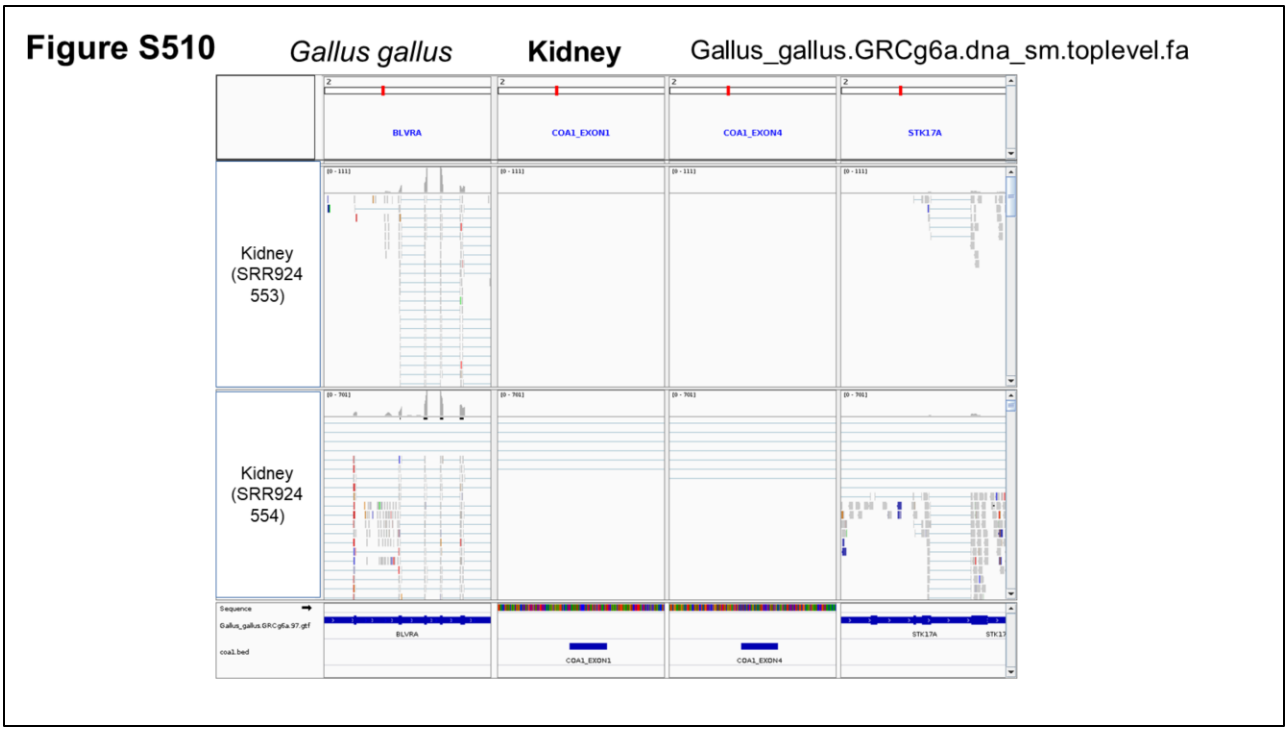

Figure S510: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from kidney (SRR924553) and (SRR924554) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

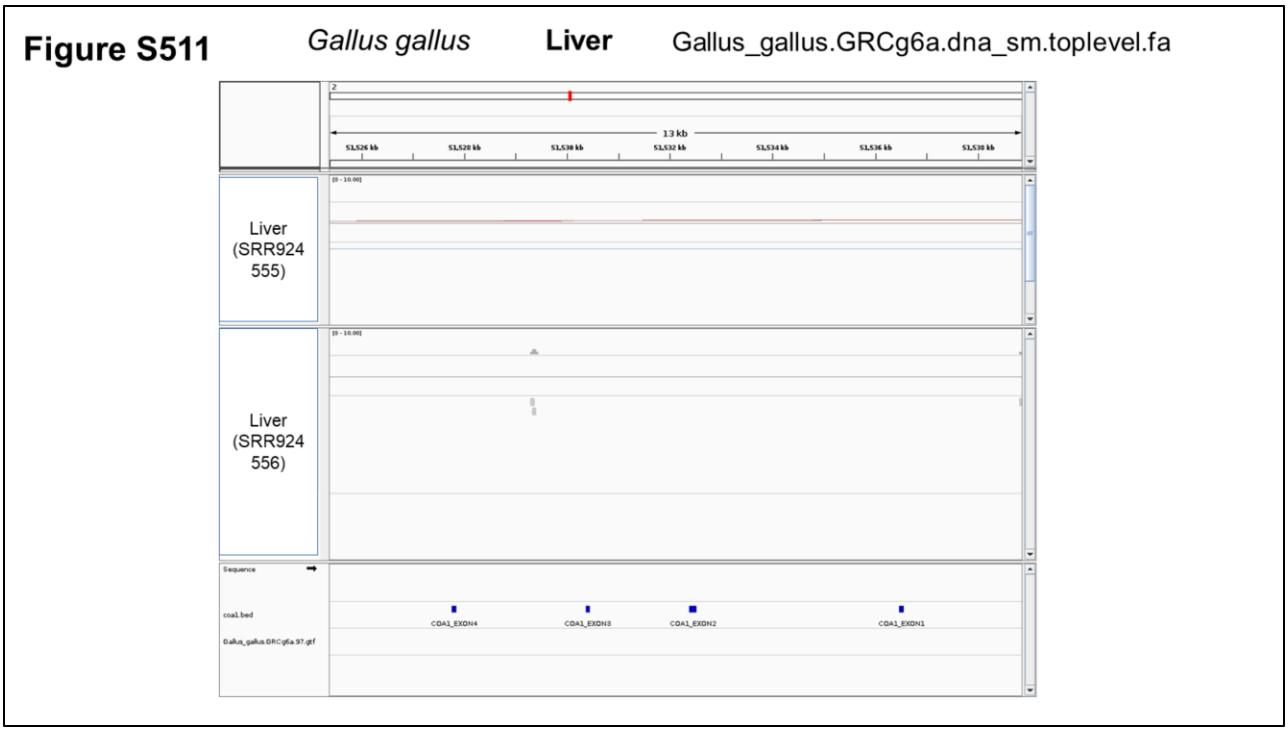

Figure S511: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR924555) and (SRR924556) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

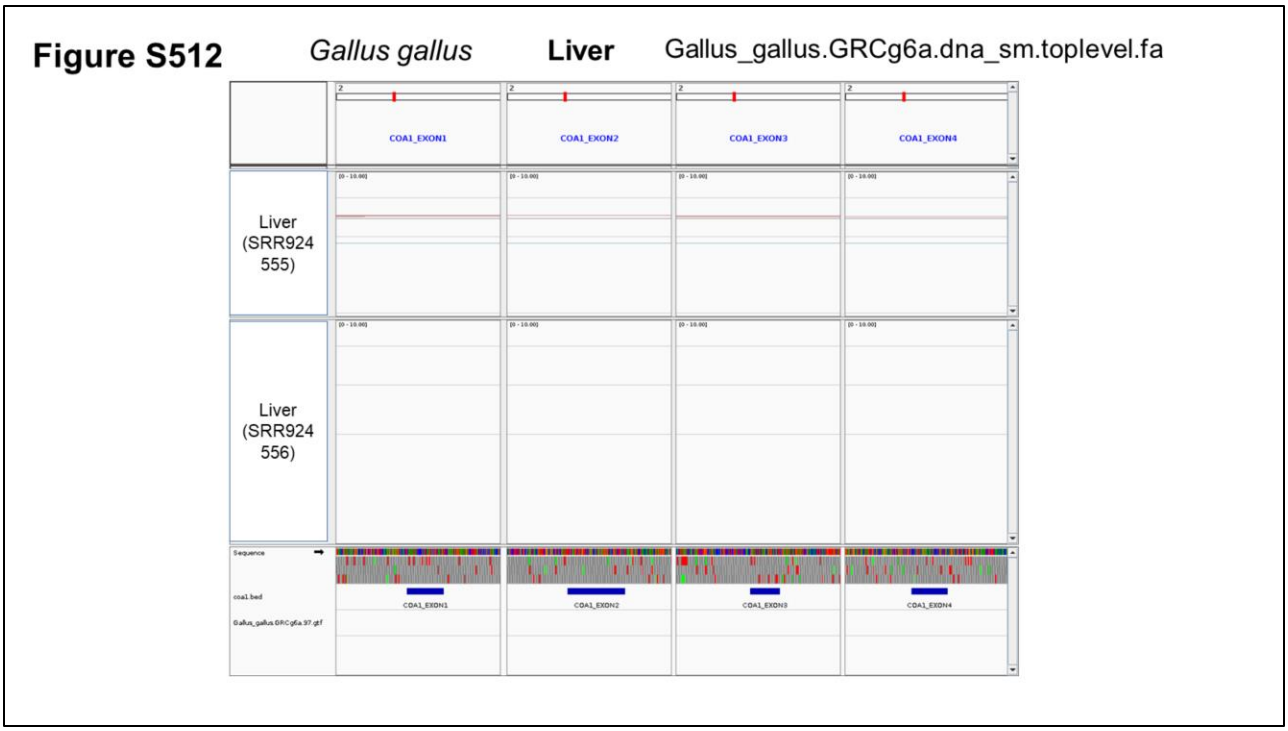

Figure S512: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S511**.

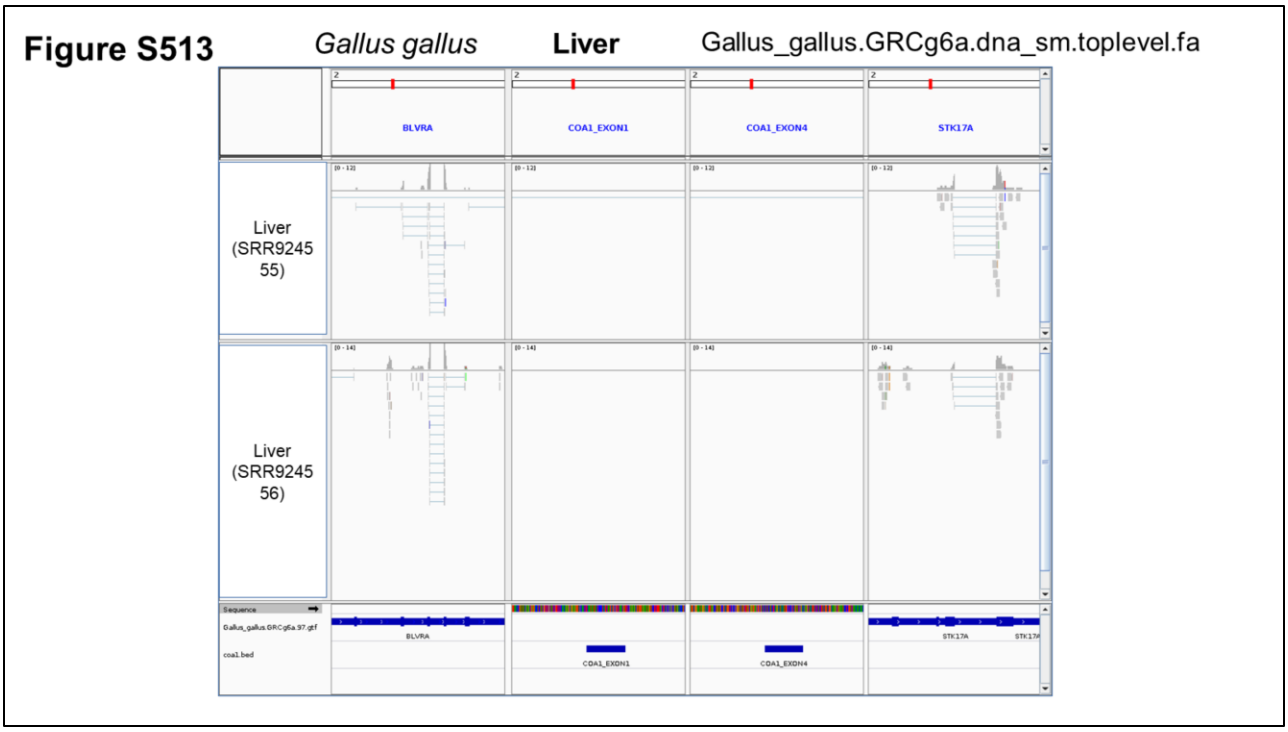

Figure S513: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR924555) and (SRR924556) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

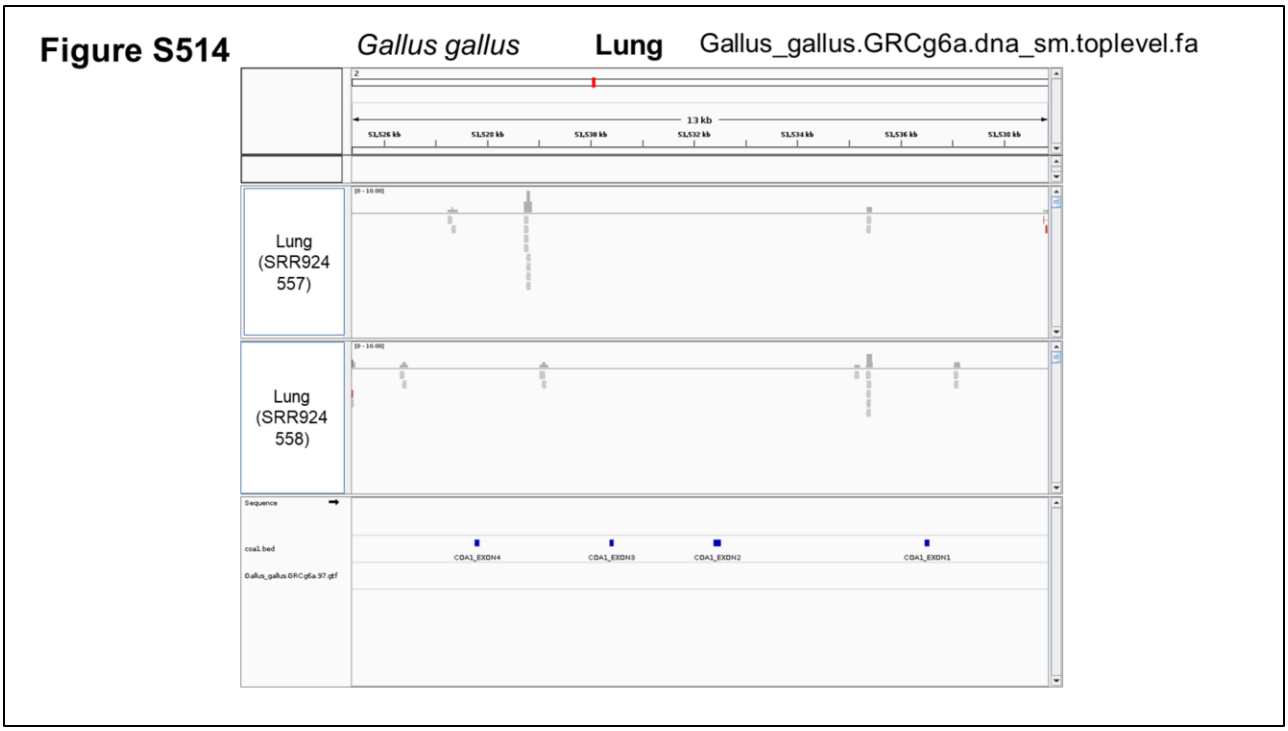

Figure S514: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from lung (SRR924557) and (SRR924558) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

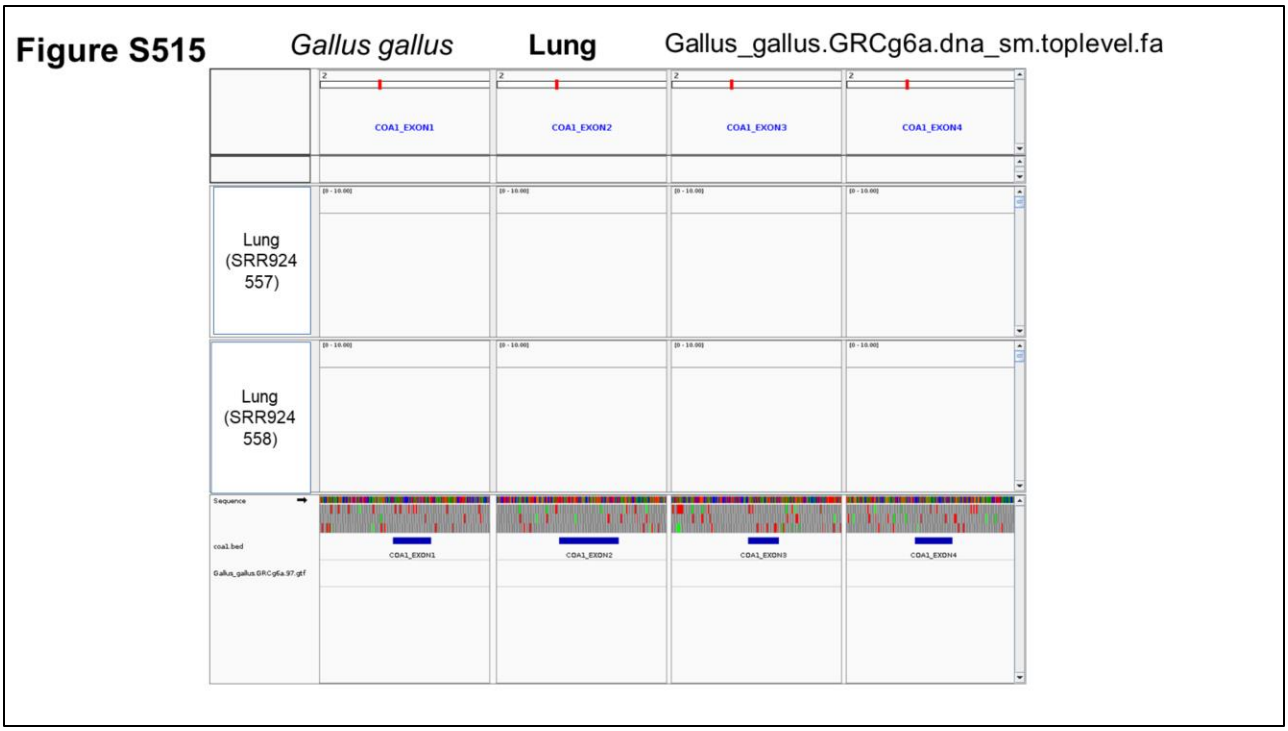

Figure S515: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S514**.

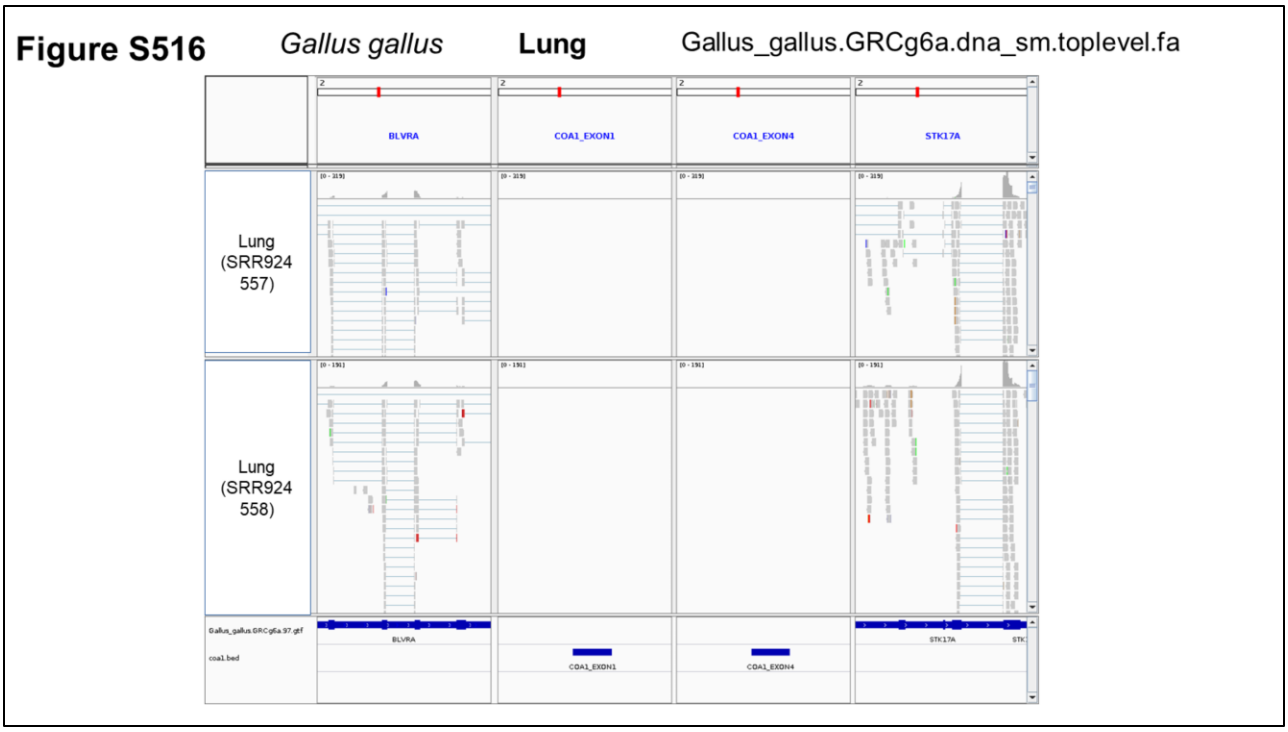

Figure S516: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from lung (SRR924557) and (SRR924558) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

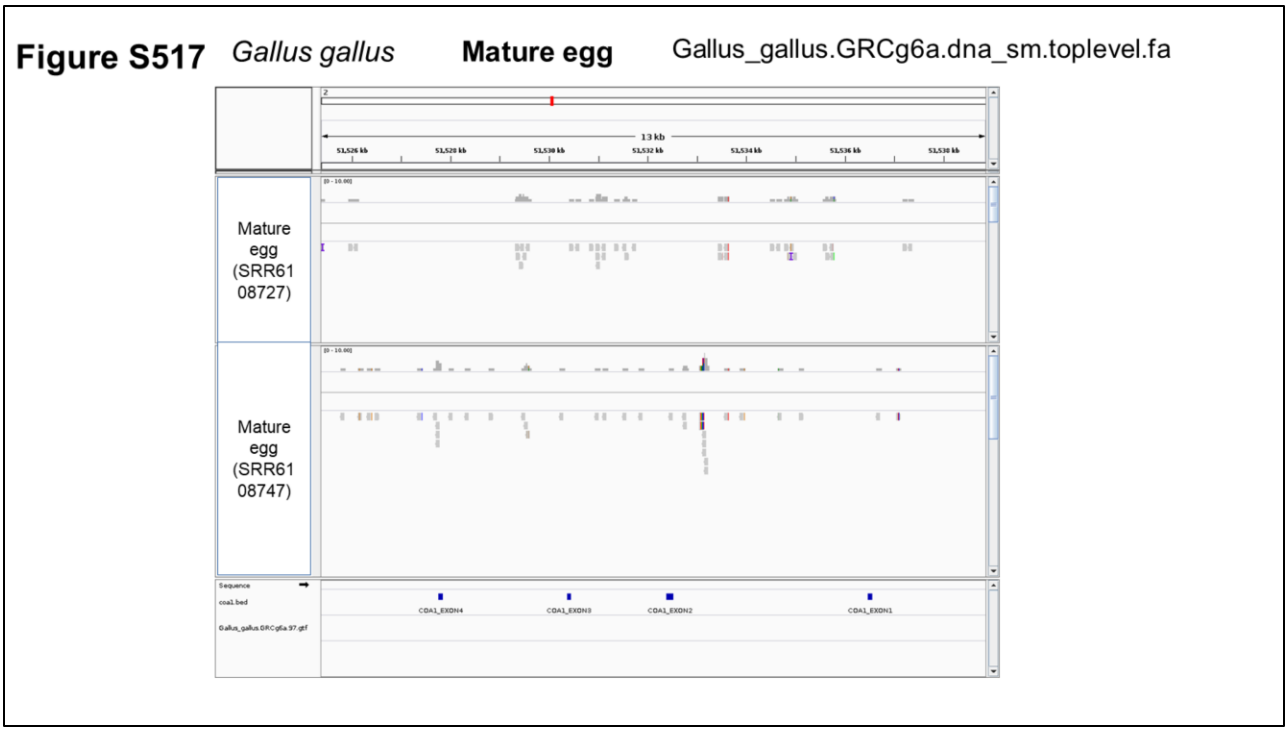

Figure S517: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from mature egg (SRR6108727) and (SRR6108747) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

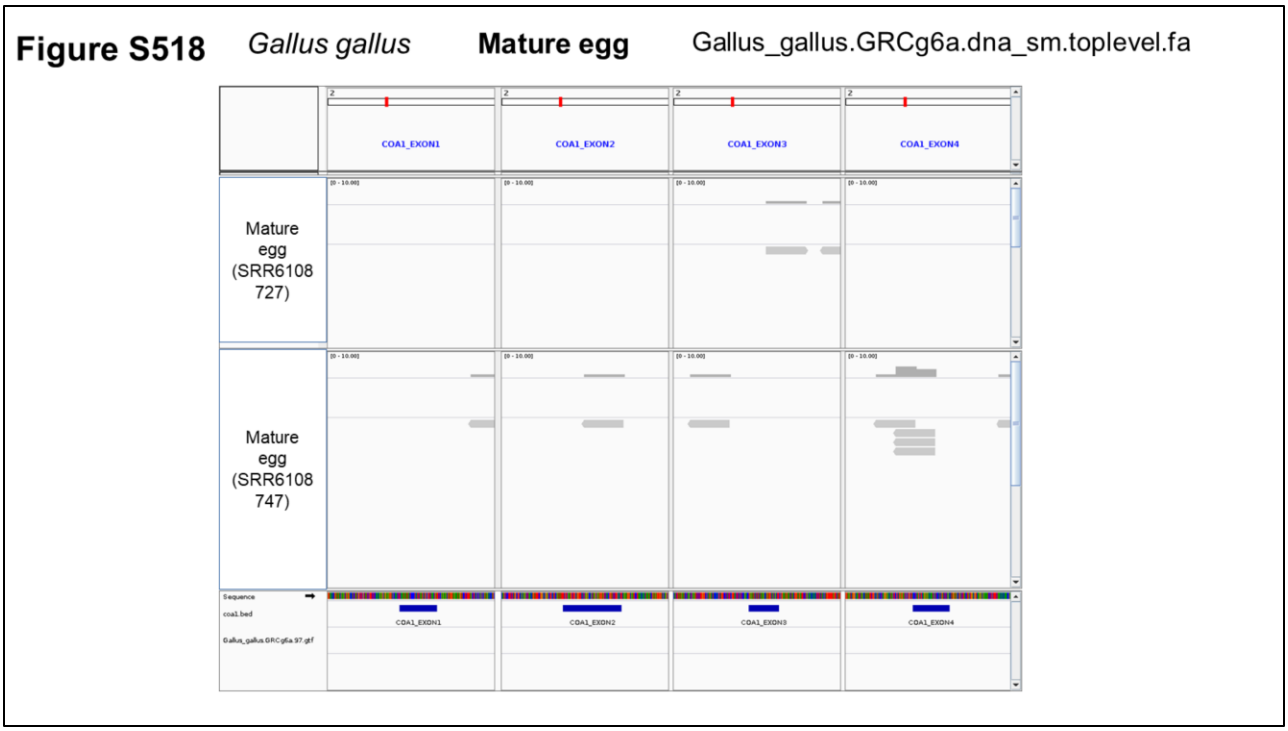

Figure S518: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S517**.

Figure S519: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from mature egg (SRR6108727) and (SRR6108747) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

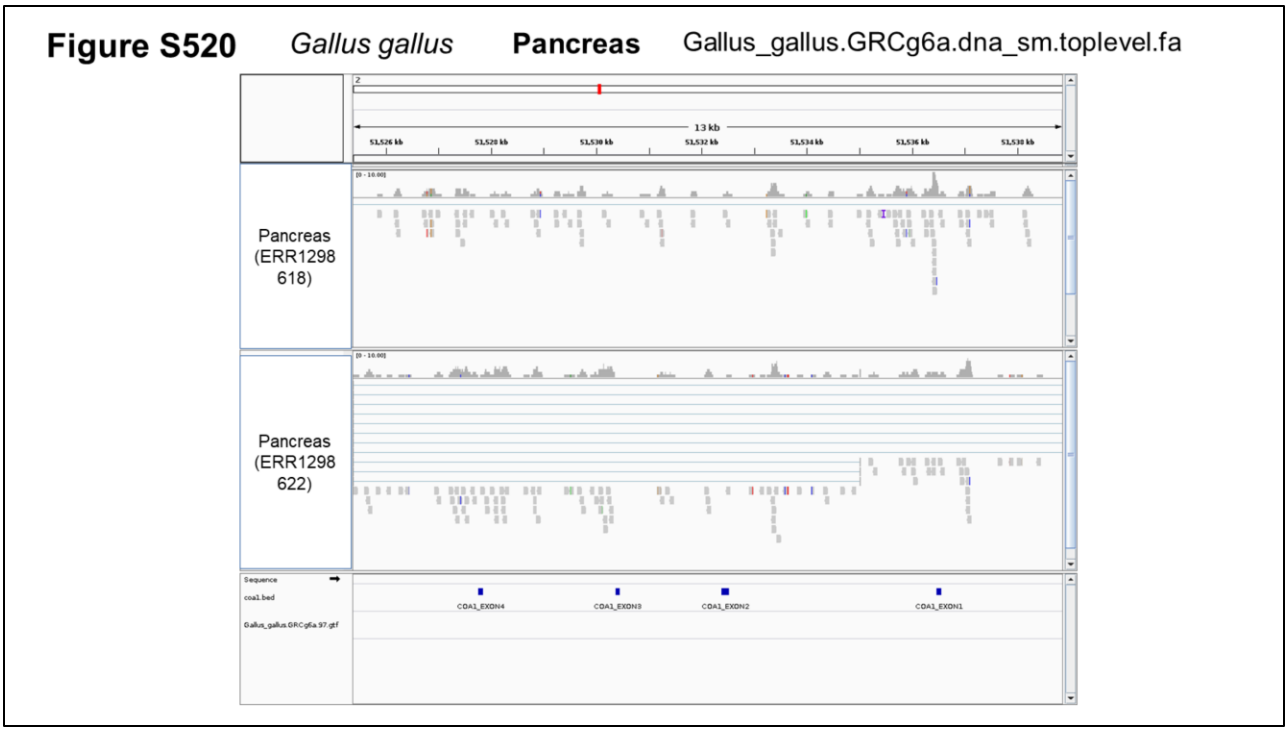

Figure S520: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from pancreas (ERR1298618) and (ERR1298622) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

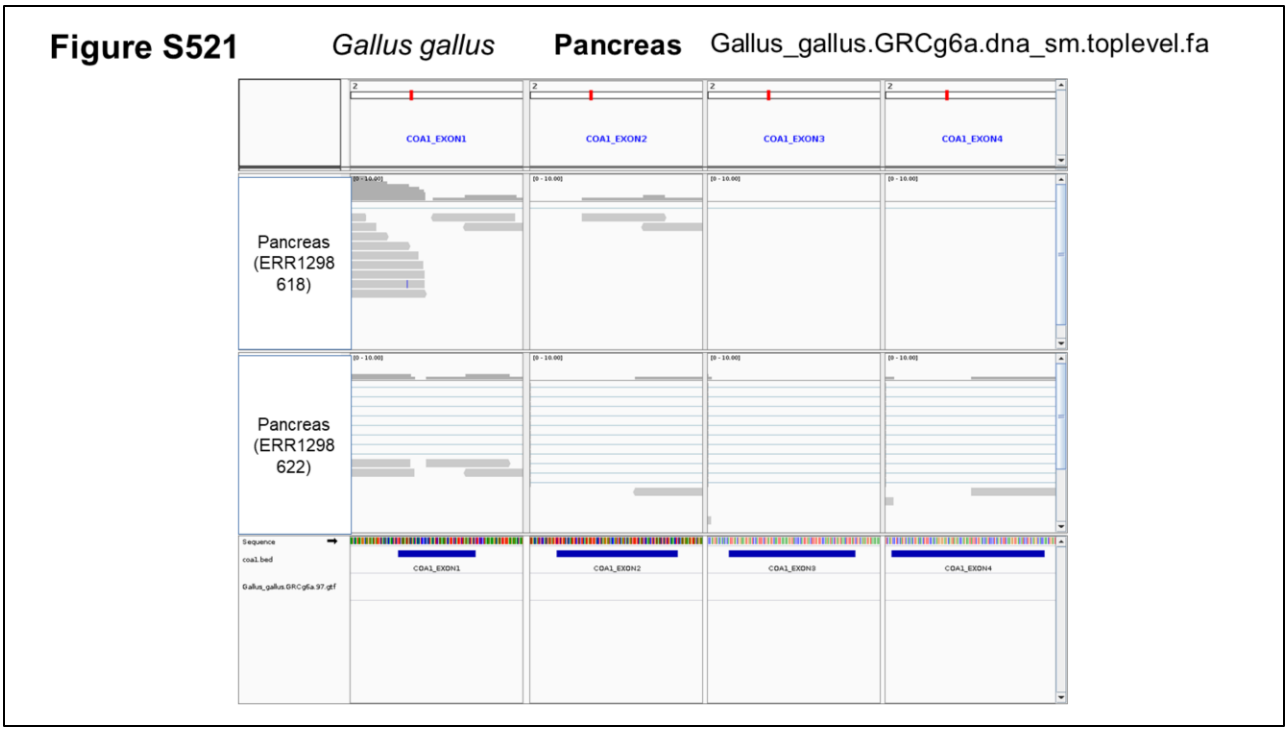

Figure S521: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S520**.

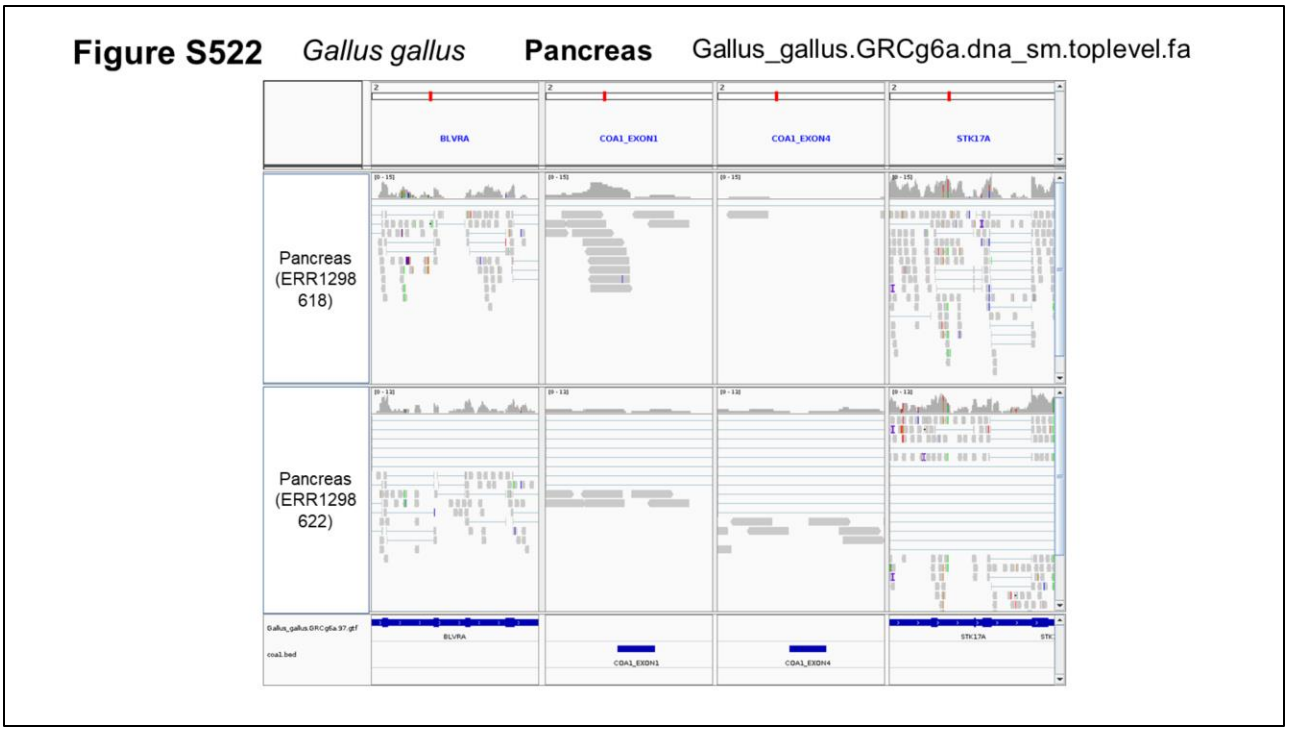

Figure S522: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from pancreas (ERR1298618) and (ERR1298622) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

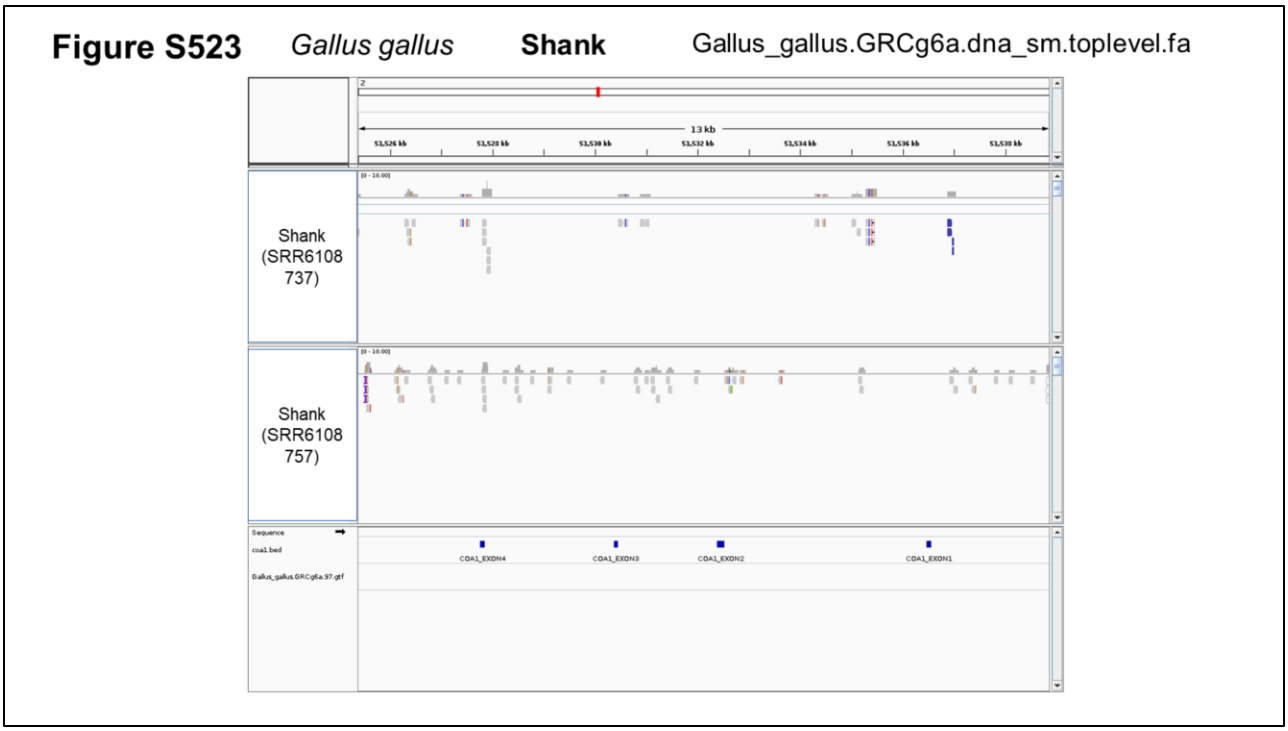

Figure S523: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from shank (SRR6108737) and (SRR6108757) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

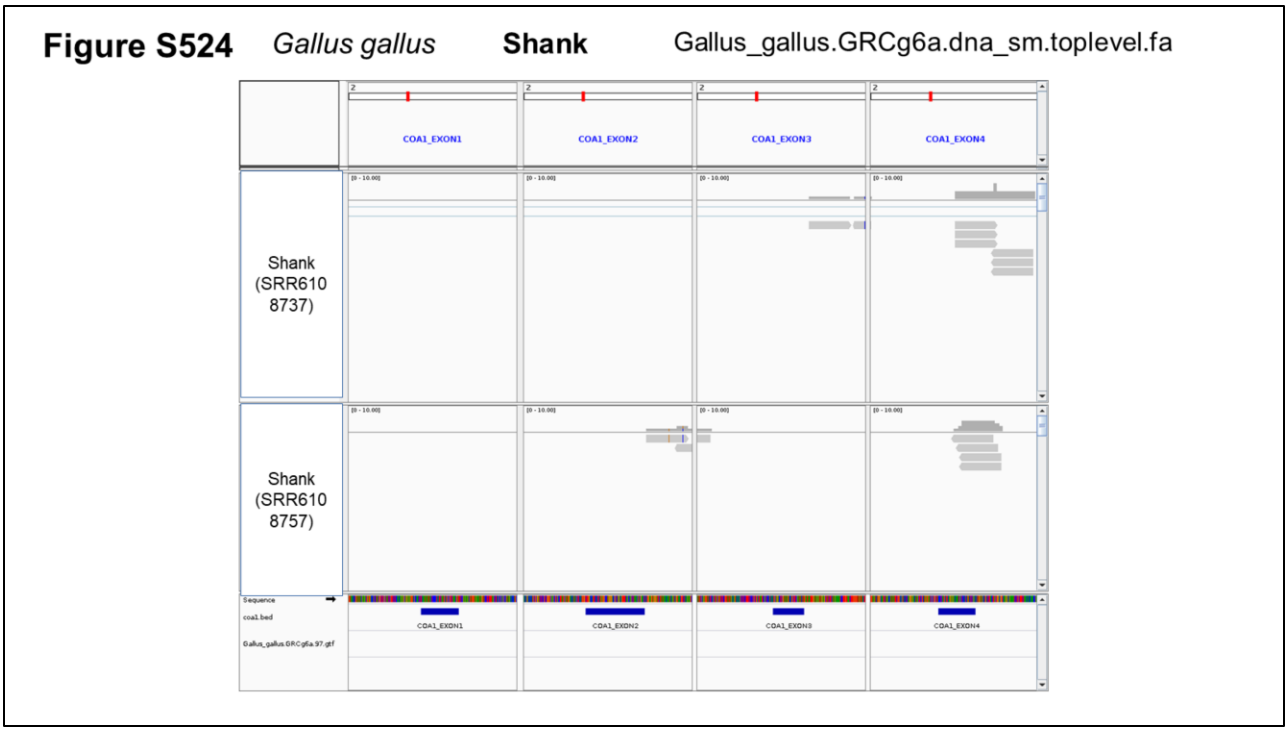

Figure S524: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S523**

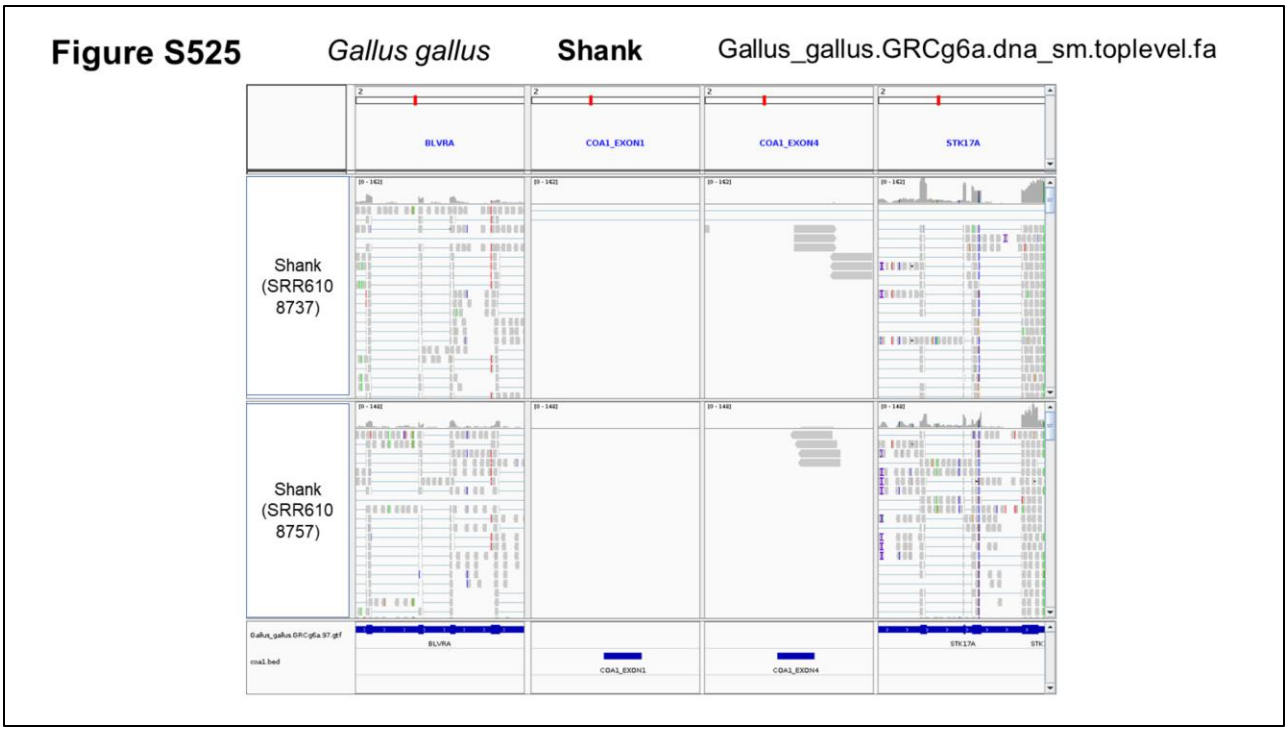

Figure S525: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from shank (SRR6108737) and (SRR6108757) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

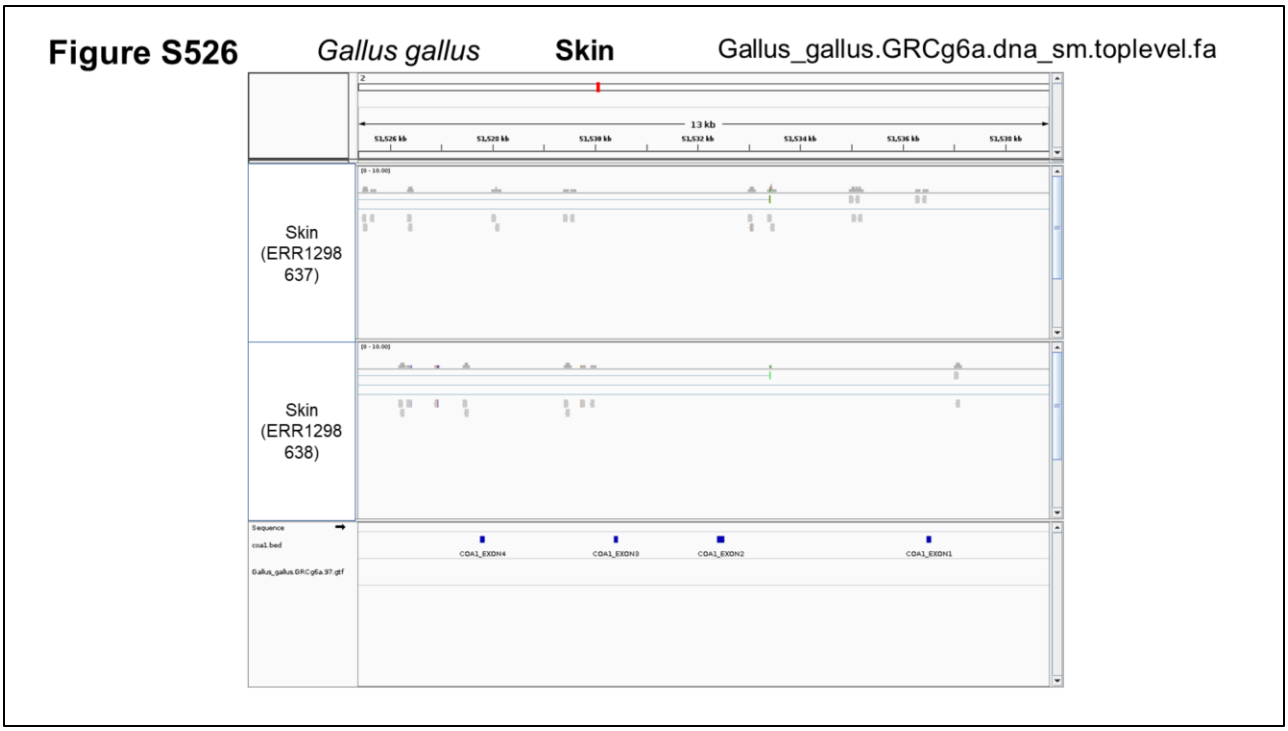

Figure S526: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from skin (ERR1298637) and (ERR1298638) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S527: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S526**.

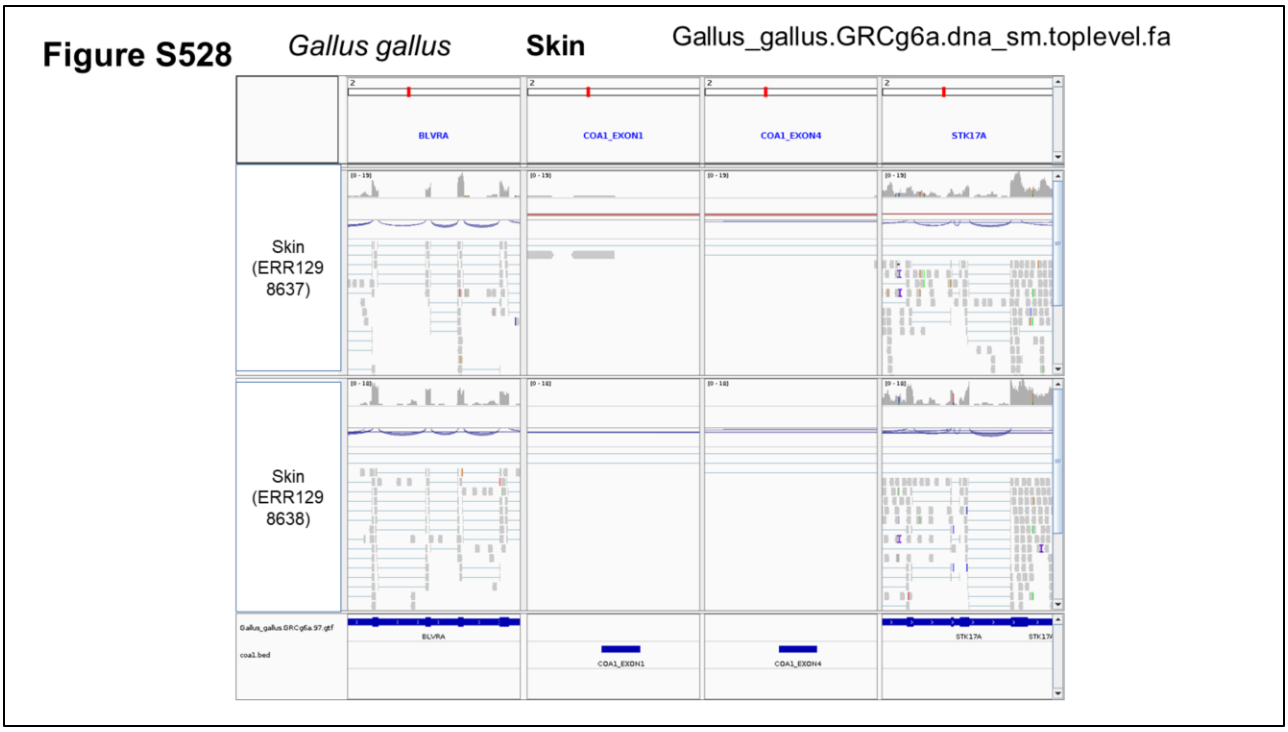

Figure S528: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from skin (ERR1298637) and (ERR1298638) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

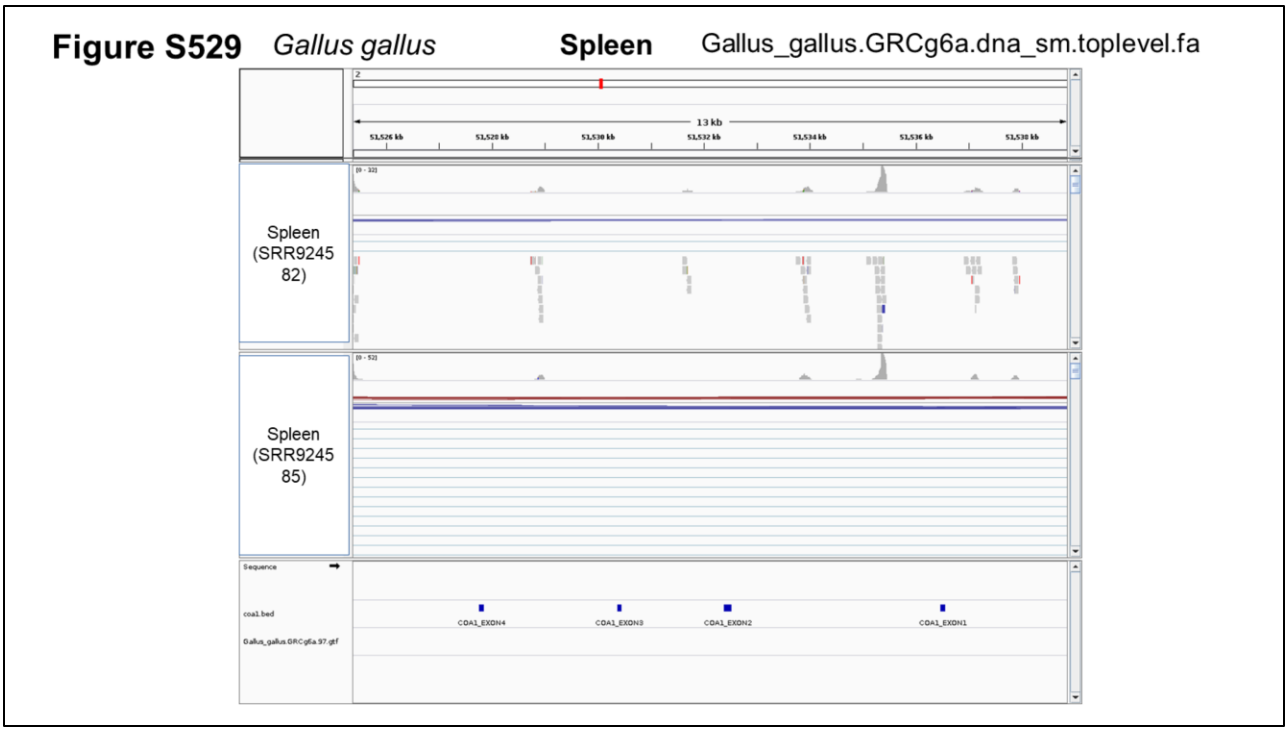

Figure S529: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR924582) and (SRR924585) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

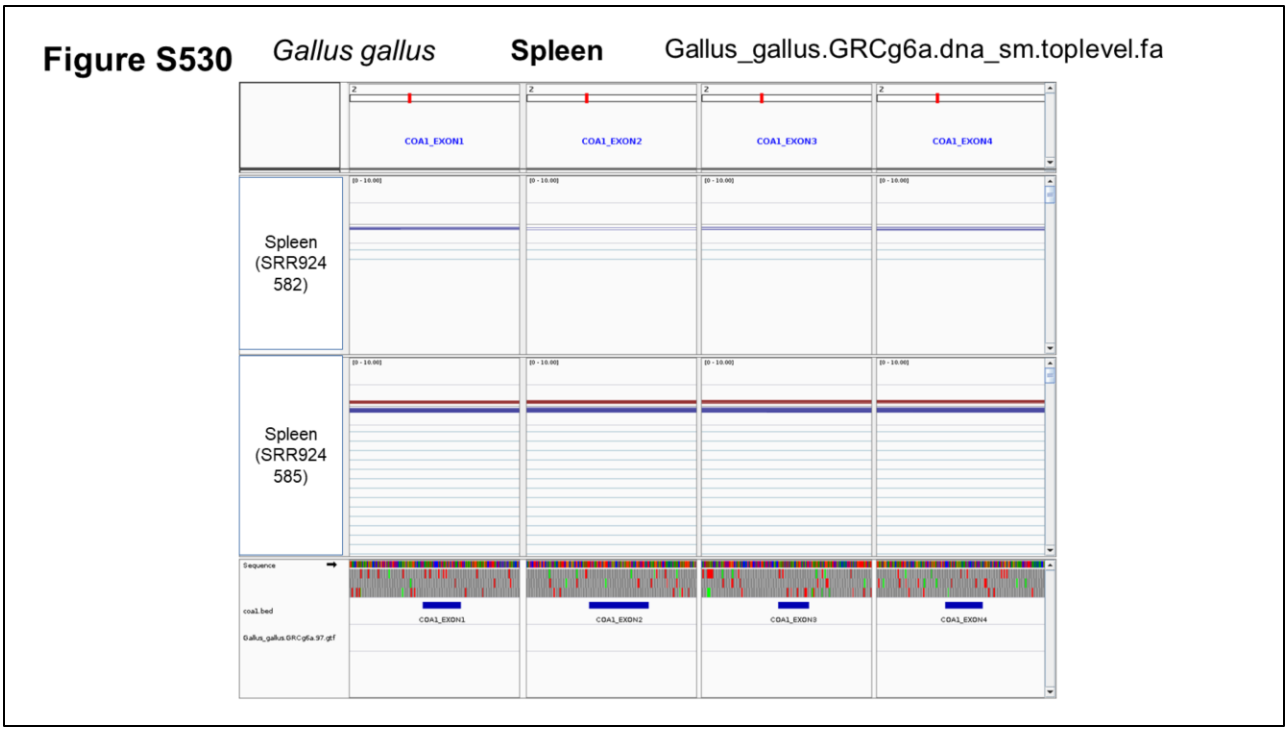

Figure S530: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S529**.

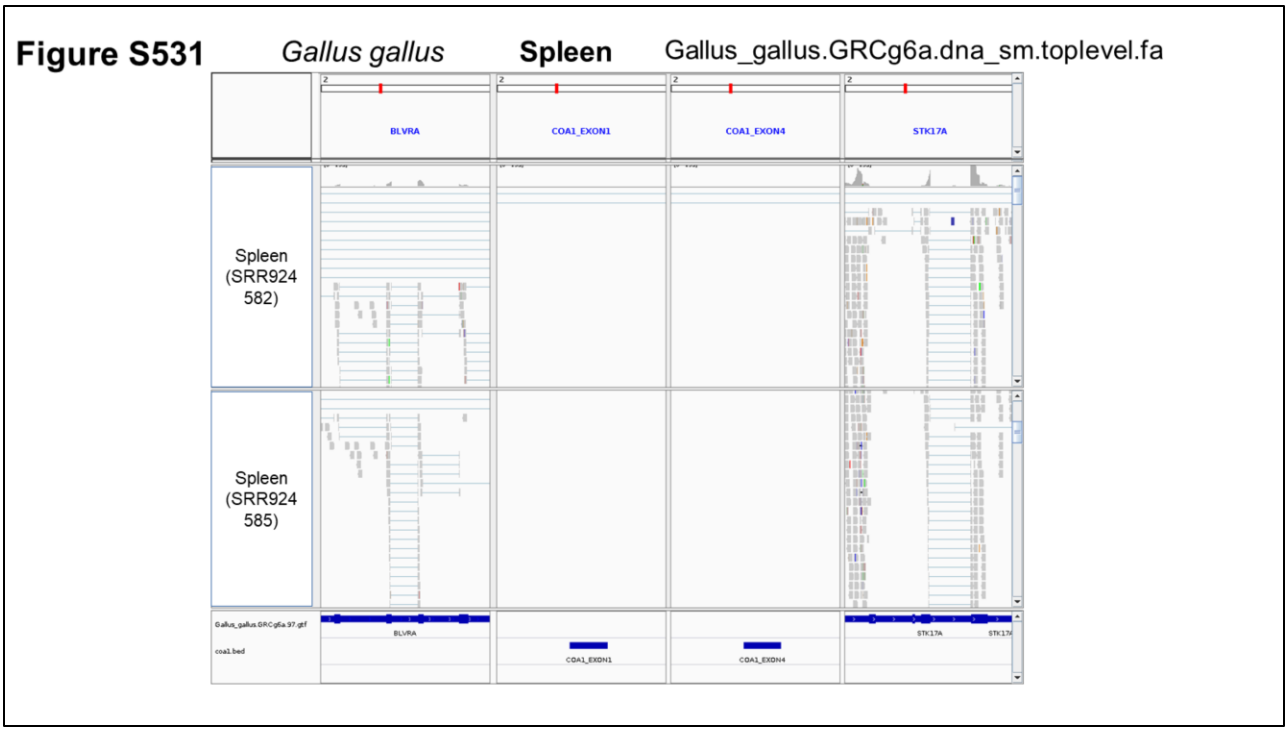

Figure S531: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR924582) and (SRR924585) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

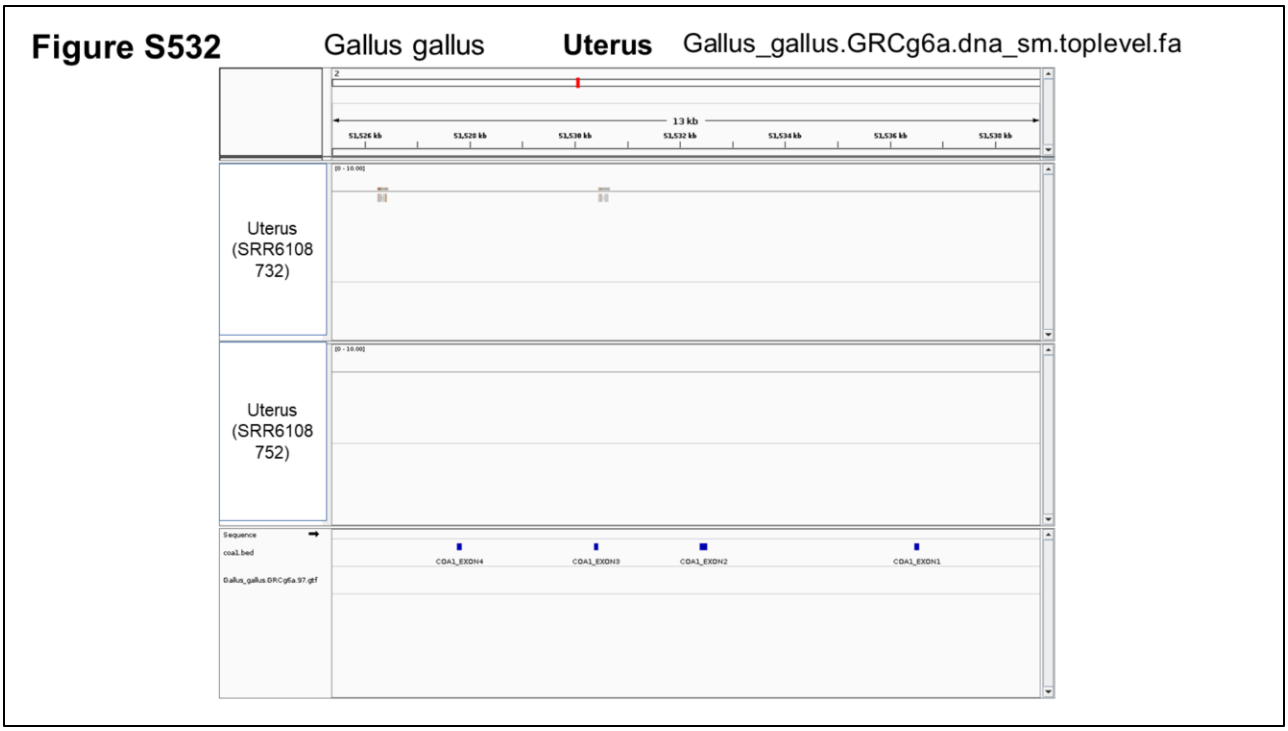

Figure S532: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from uterus (SRR6108732) and (SRR6108752) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

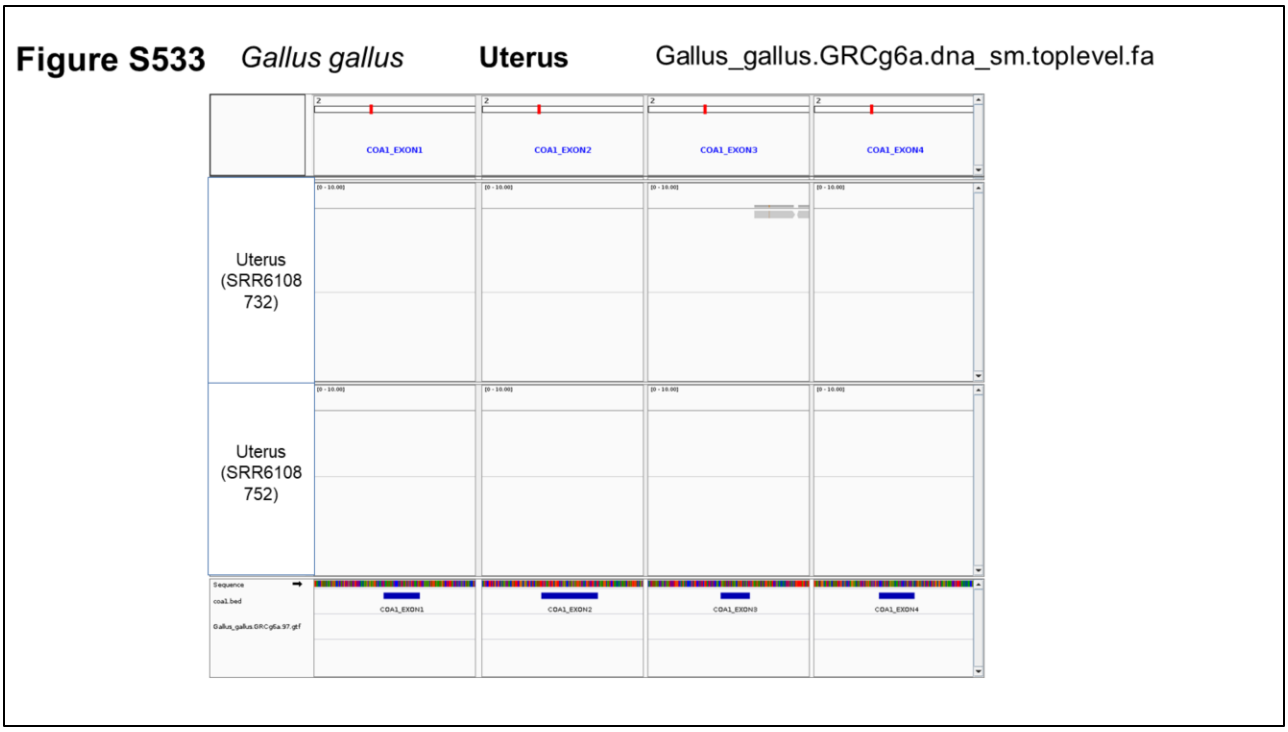

Figure S533: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S532**.

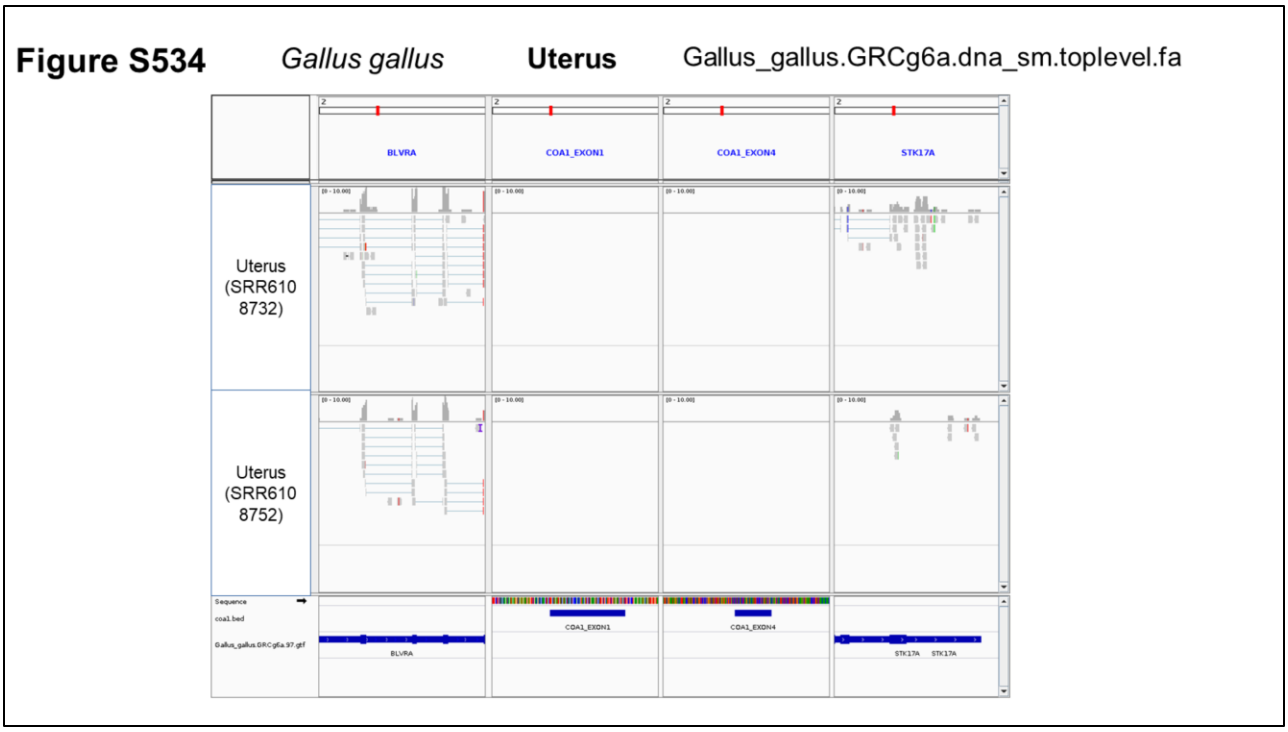

Figure S534: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in chicken (*Gallus gallus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from uterus (SRR6108732) and (SRR6108752) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

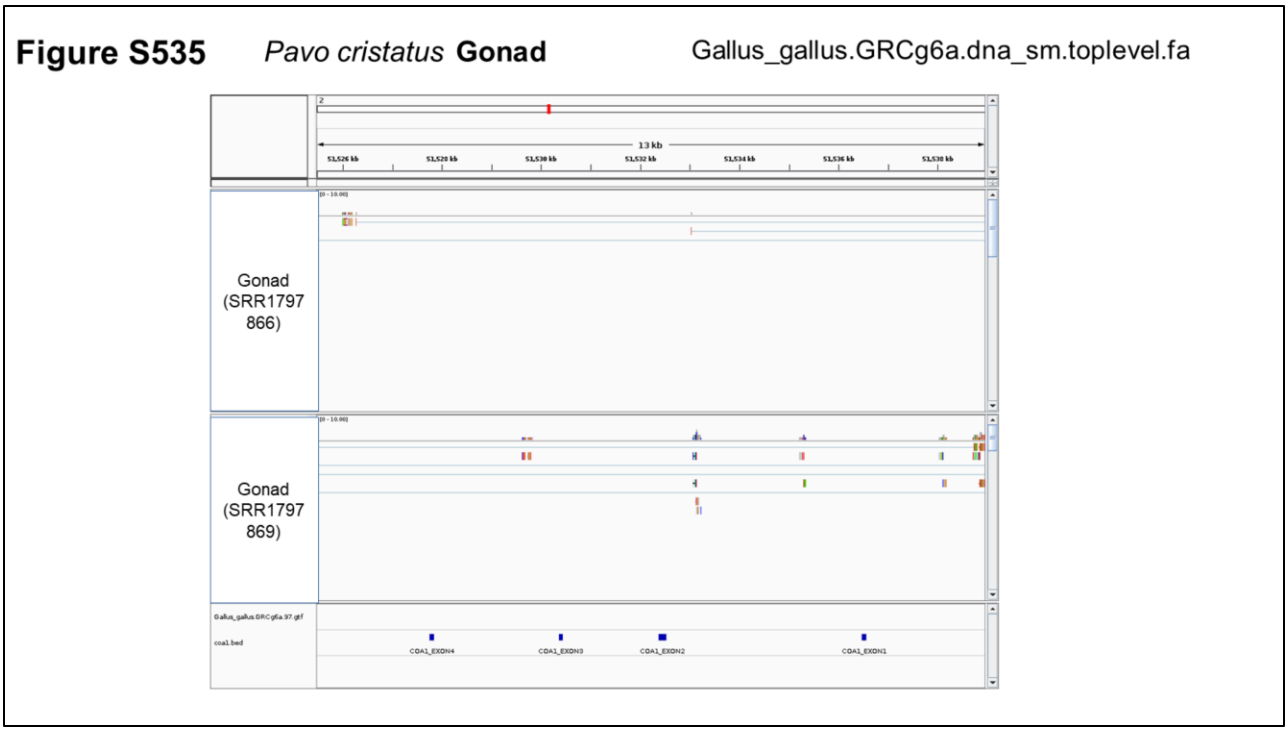

Figure S535: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Peacock (*Pavo cristatus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from gonad (SRR1797866) and (SRR1797869) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

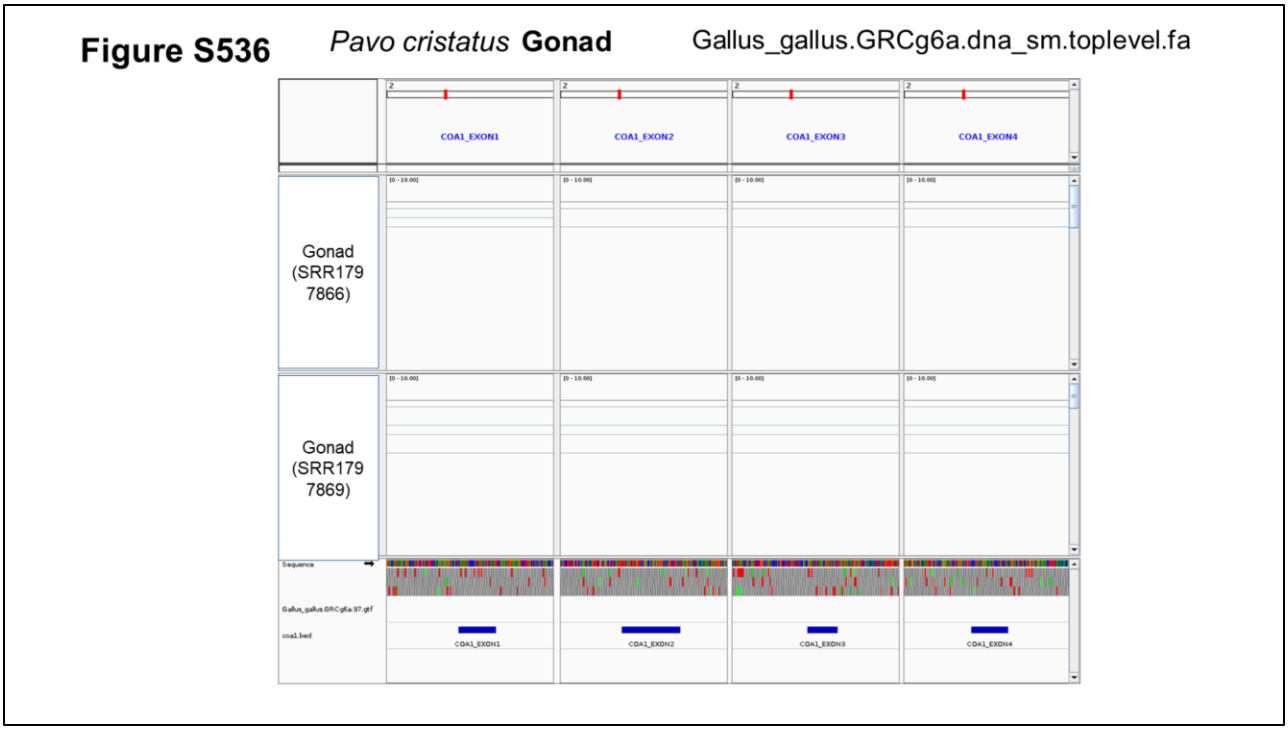

Figure S536: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S535**.

Figure S537: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in Peacock (*Pavo cristatus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from gonad (SRR1797866) and (SRR1797869) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

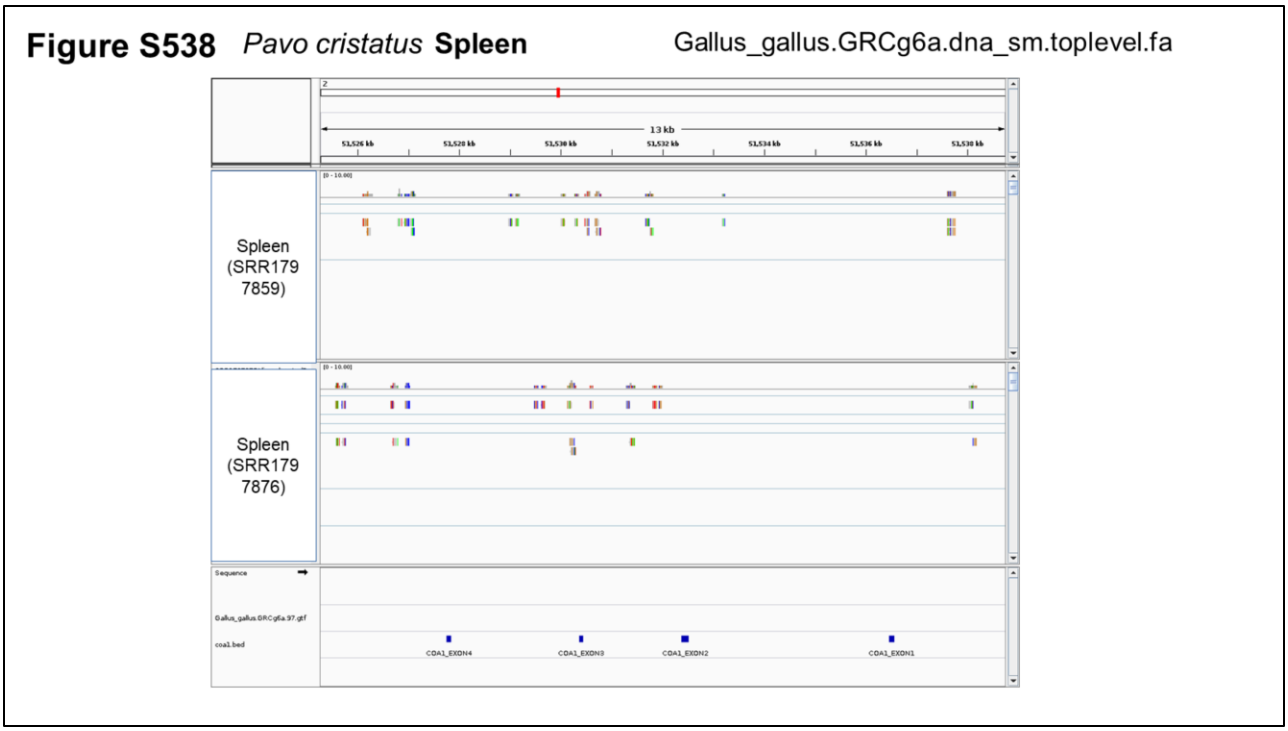

Figure S538: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Peacock (*Pavo cristatus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR1797859) and (SRR1797876) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

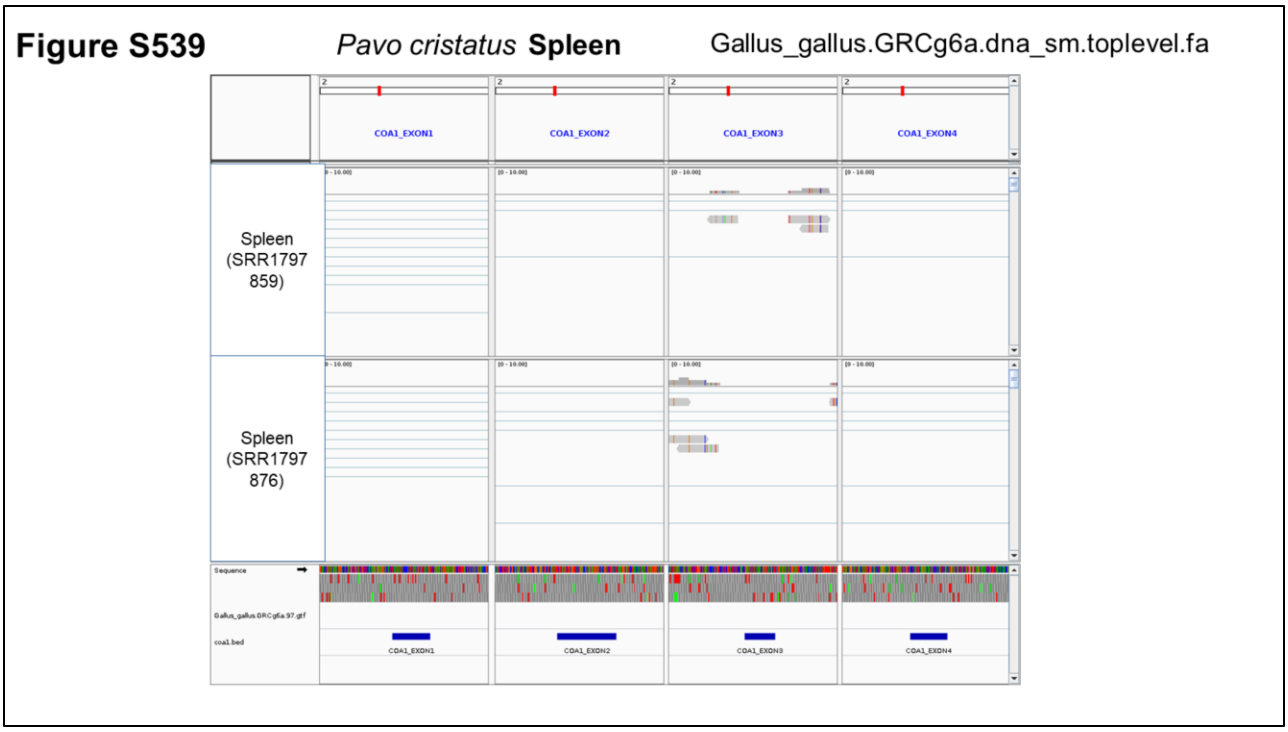

Figure S539: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S538**.

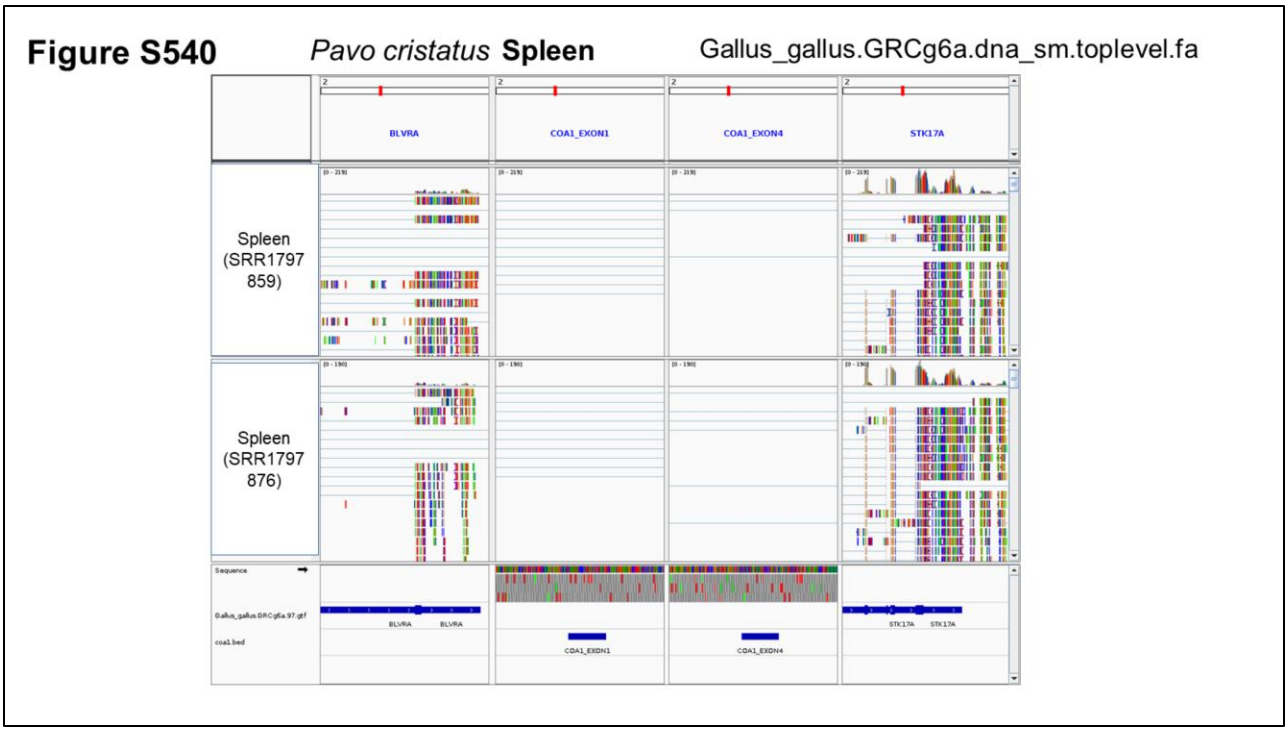

Figure S540: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in Peacock (*Pavo cristatus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR1797859) and (SRR1797876) have been mapped to the Gallus_gallus.GRCg6a.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

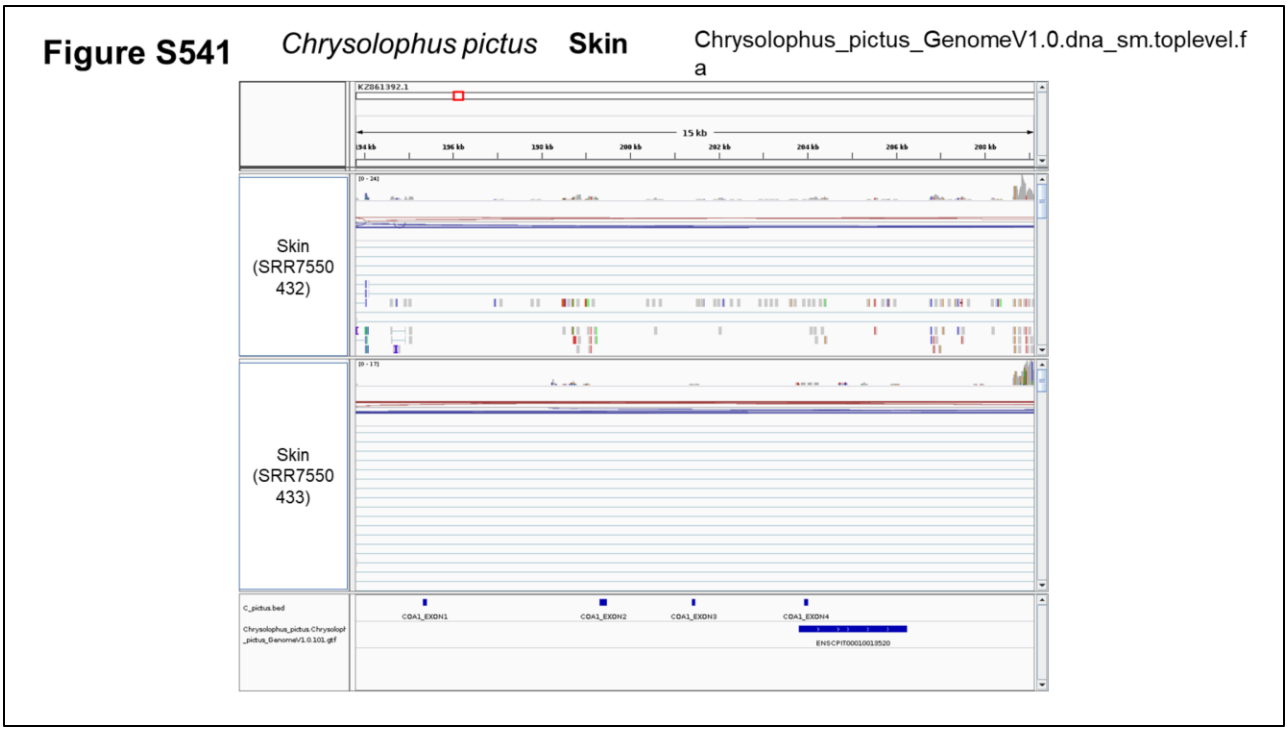

Figure S541: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in golden pheasant (*Chrysolophus pictus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from skin (SRR7550432) and (SRR7550433) have been mapped to the Chrysolophus_pictus_GenomeV1.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

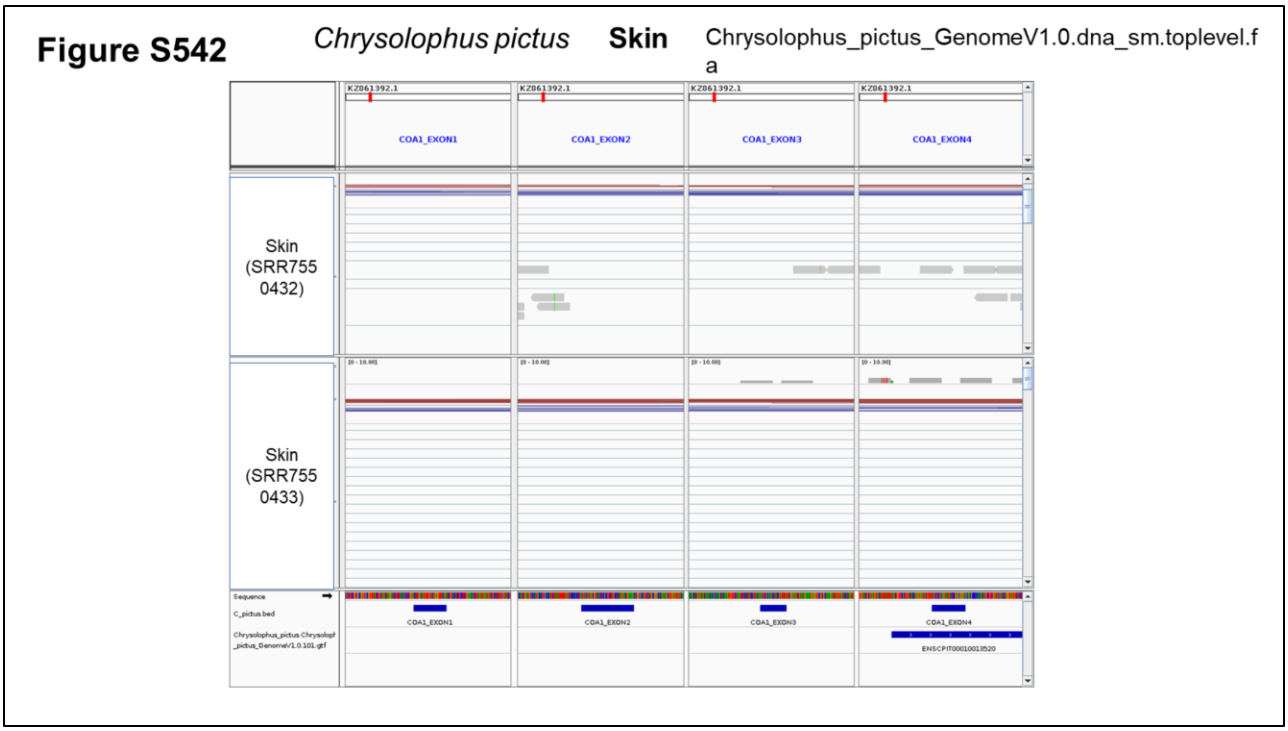

Figure S542: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S541**.

Figure S543: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in golden pheasant (*Chrysolophus pictus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from skin (SRR7550432) and (SRR7550433) have been mapped to the Chrysolophus_pictus_GenomeV1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

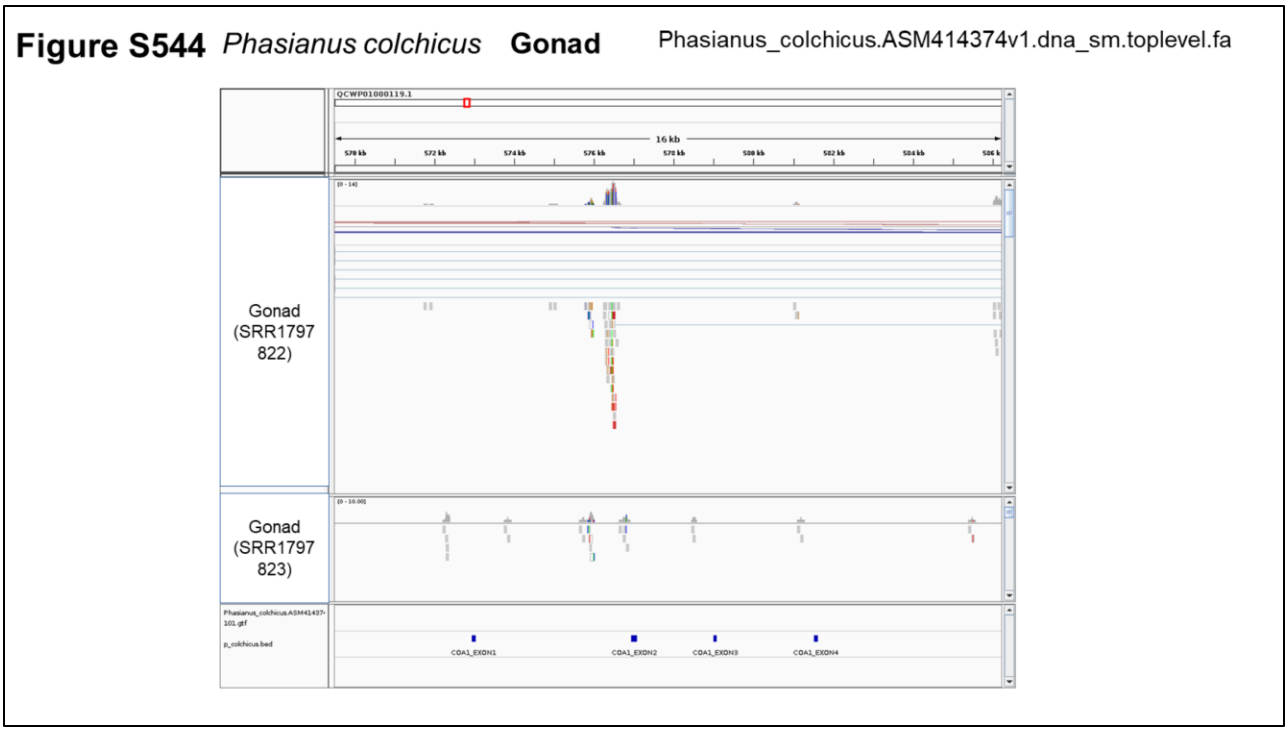

Figure S554: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in common pheasant (*Phasianus colchicus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from gonad (SRR1797822) and (SRR1797823) have been mapped to the Phasianus_colchicus.ASM414374v1.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

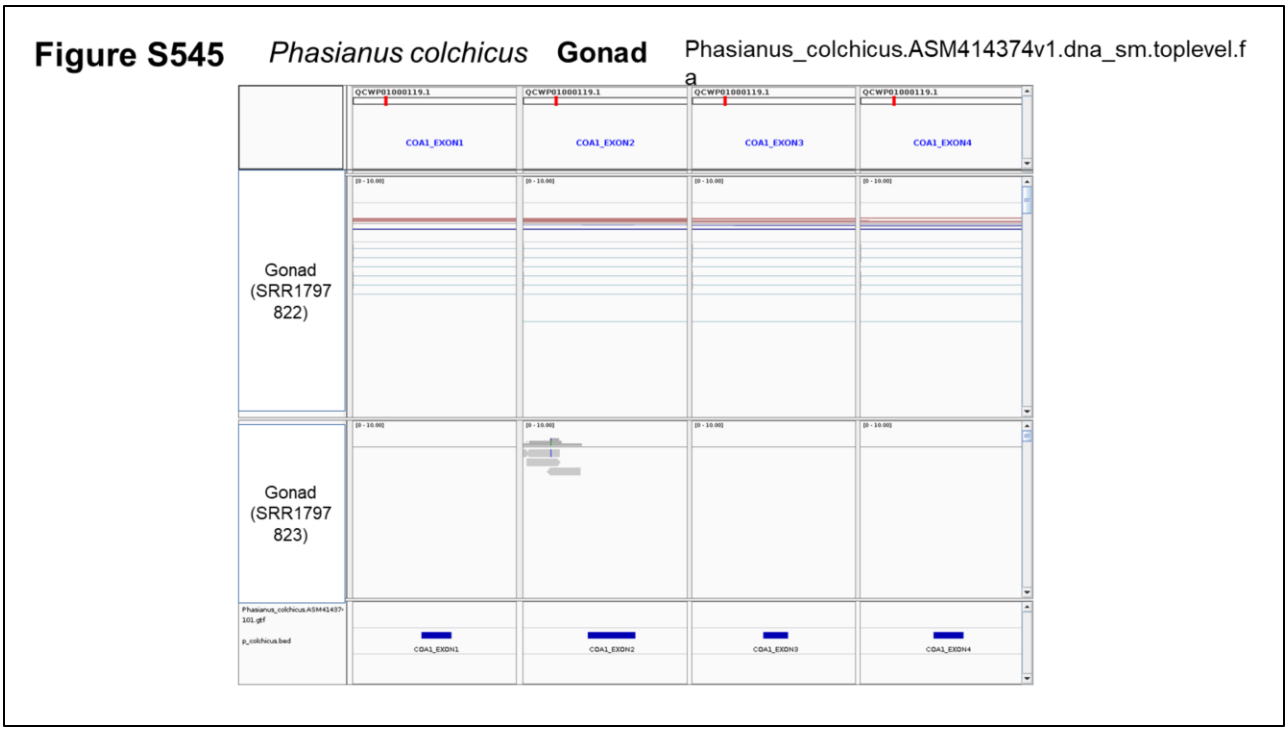

Figure S545: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S544**.

Figure S546: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in common pheasant (*Phasianus colchicus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from gonad (SRR1797822) and (SRR1797823) have been mapped to the Phasianus_colchicus.ASM414374v1.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

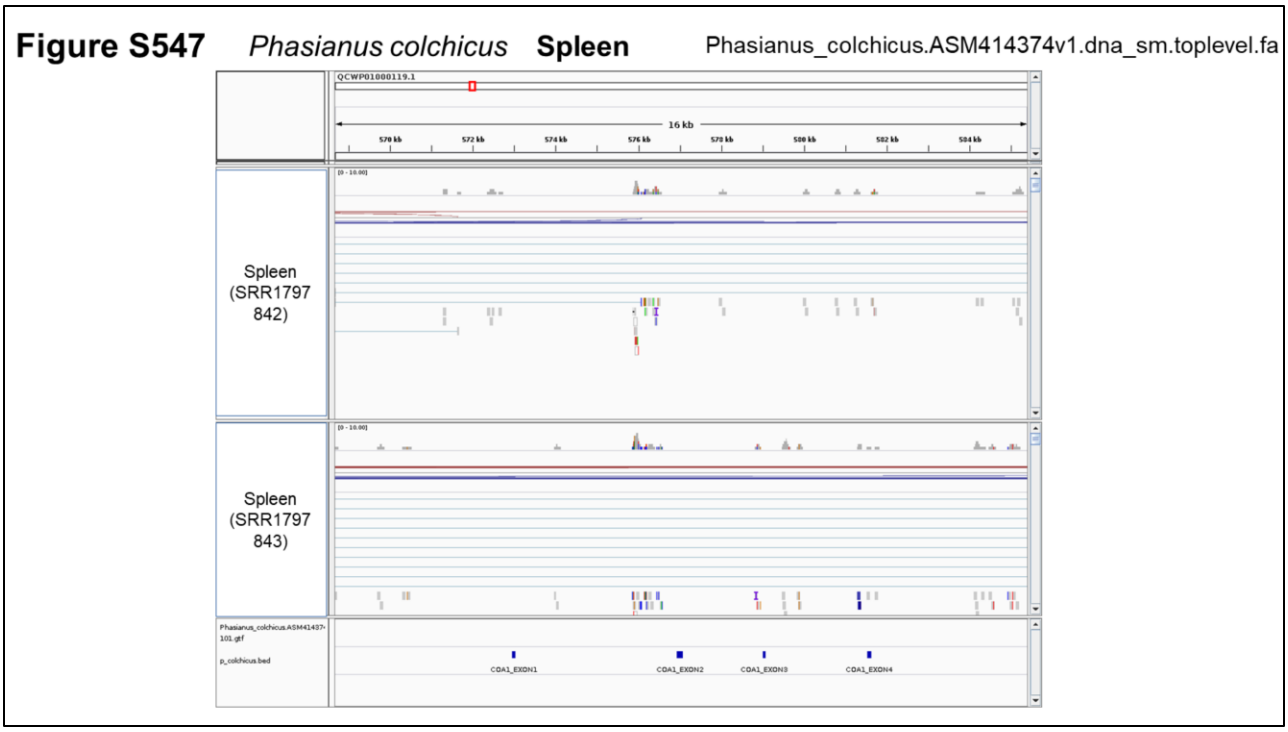

Figure S547: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in common pheasant (*Phasianus colchicus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR1797842) and (SRR1797843) have been mapped to the Phasianus_colchicus.ASM414374v1.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

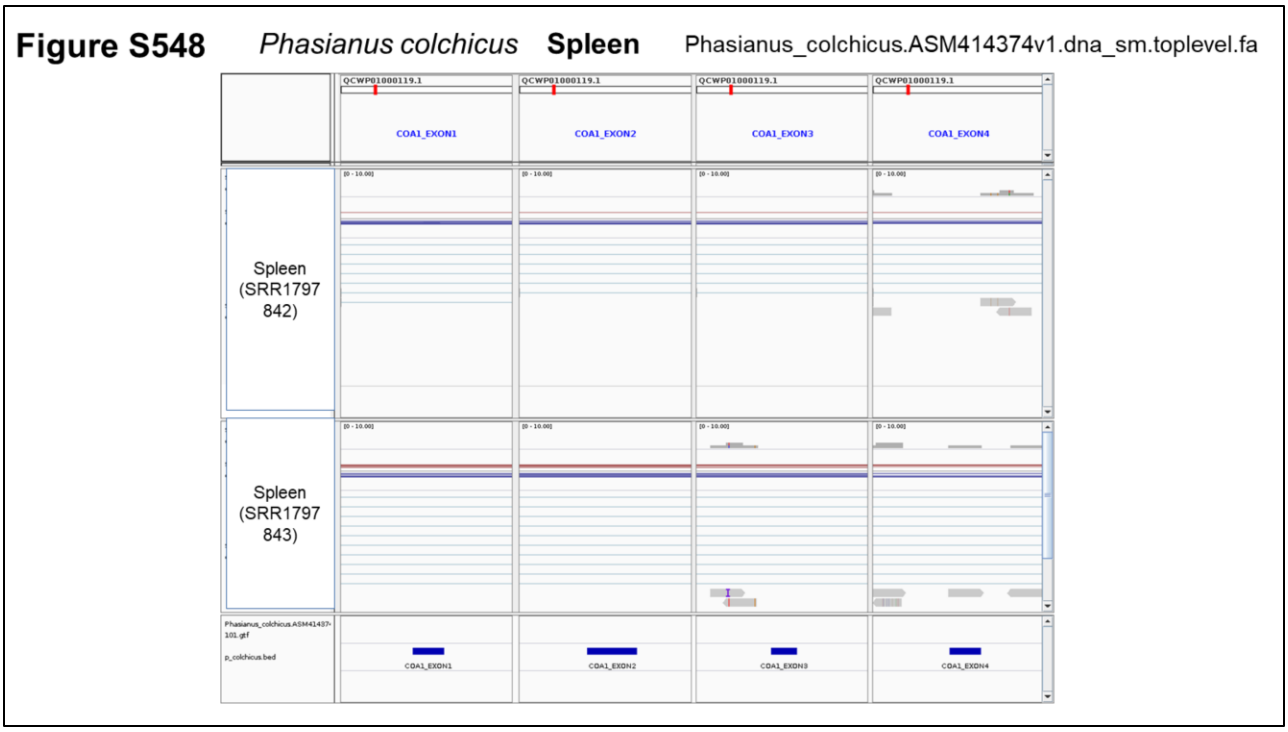

Figure S548: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S547**.

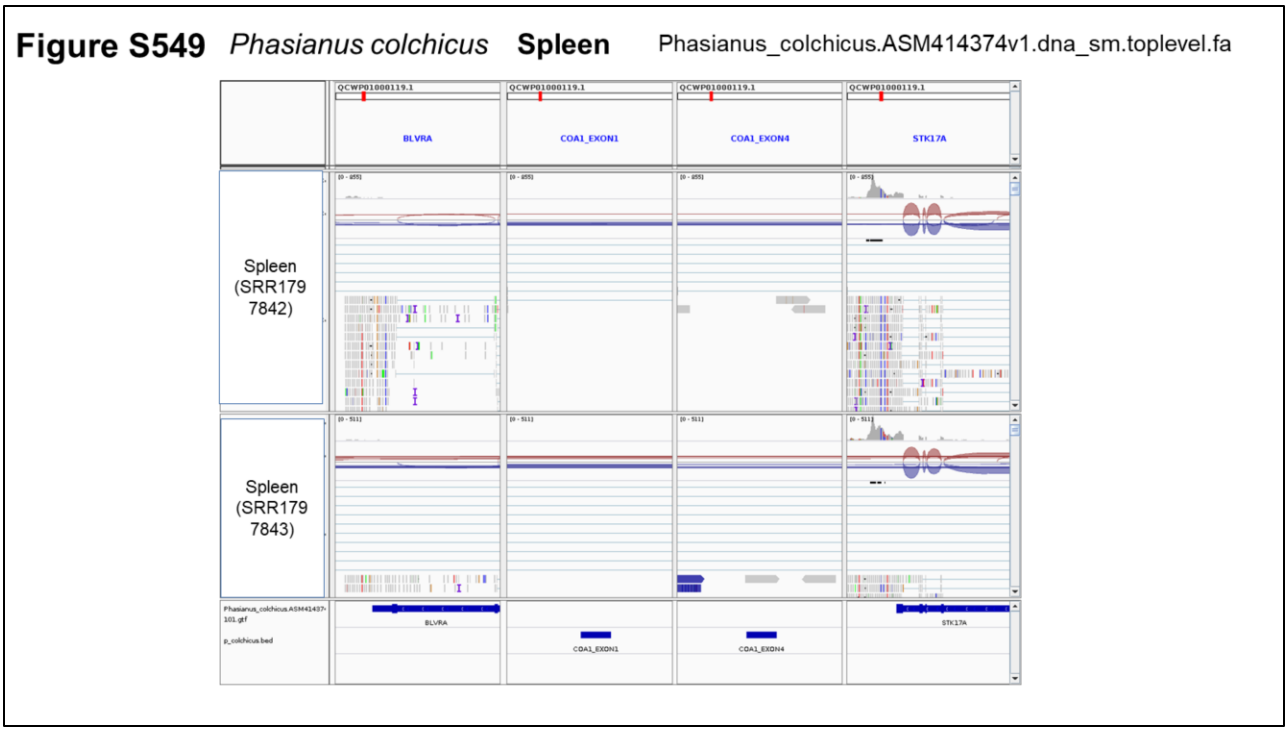

Figure S549: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in common pheasant (*Phasianus colchicus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR1797842) and (SRR1797843) have been mapped to the Phasianus_colchicus.ASM414374v1.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

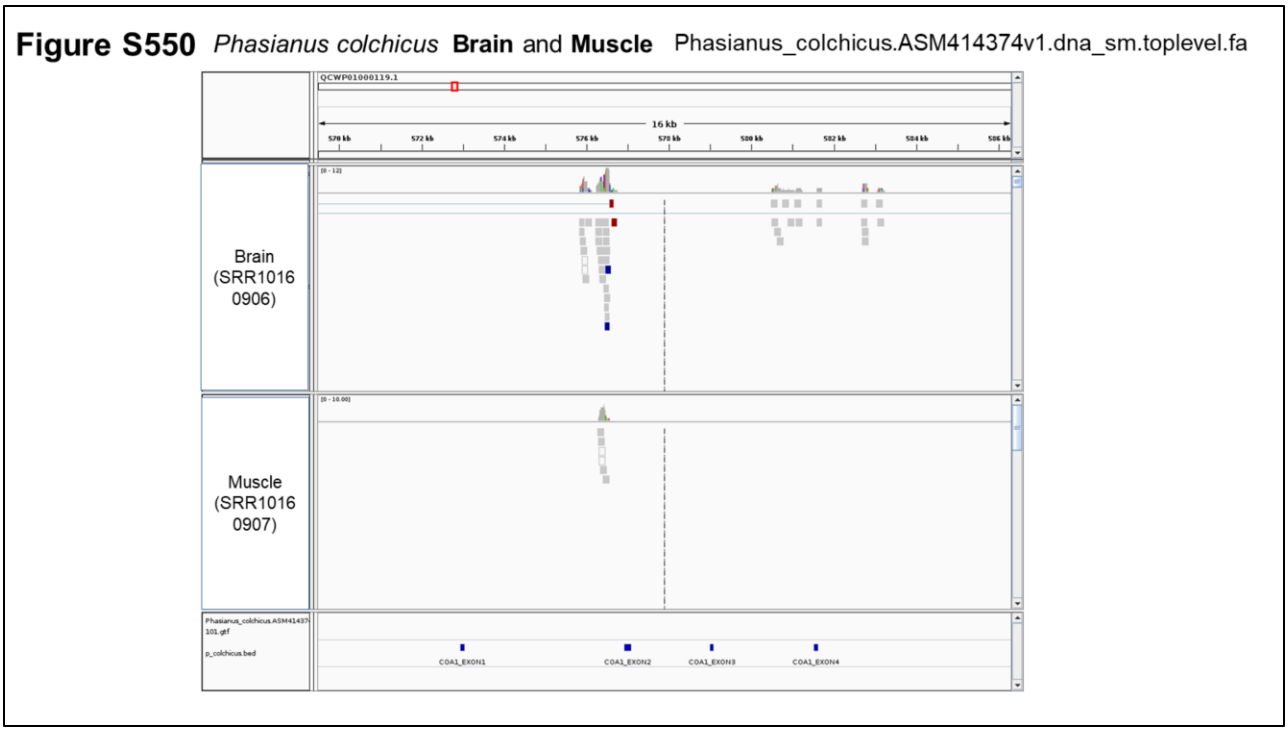

Figure S550: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in common pheasant (*Phasianus colchicus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from Brain (SRR10160906) and Muscle (SRR10160907) have been mapped to the Phasianus_colchicus.ASM414374v1.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

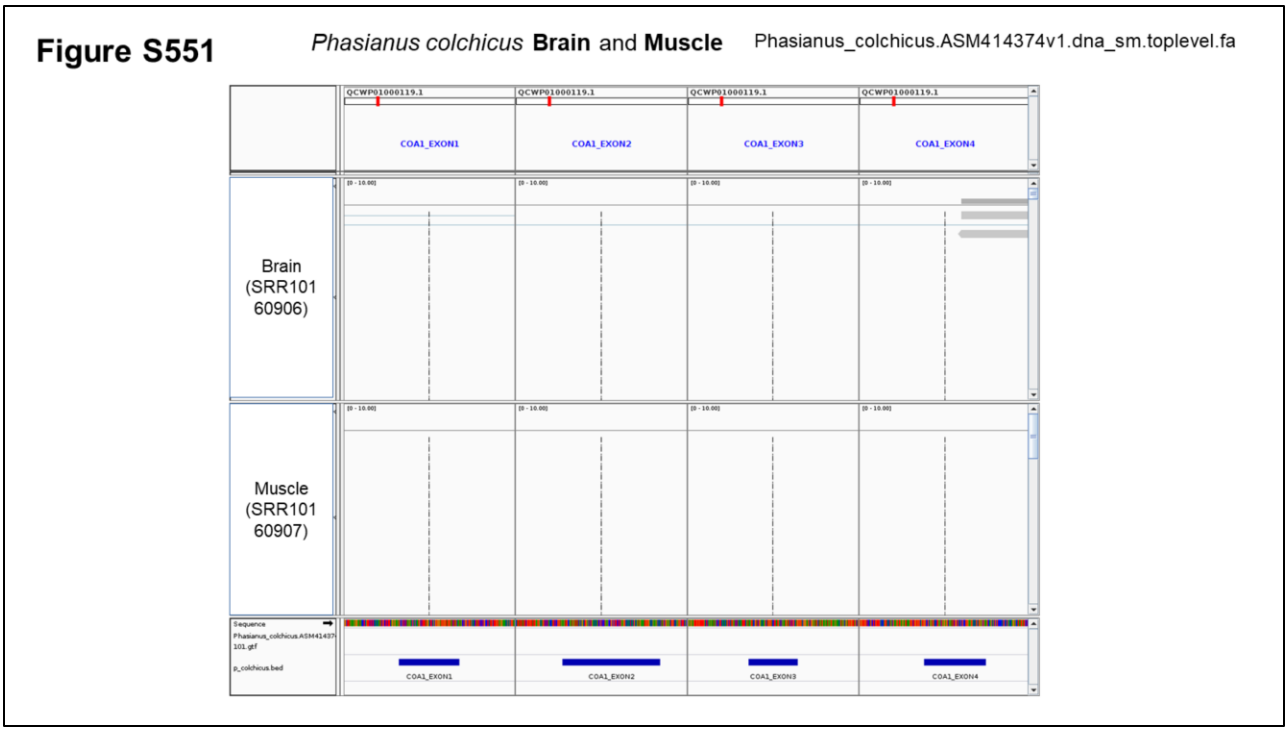

Figure S551: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S550**.

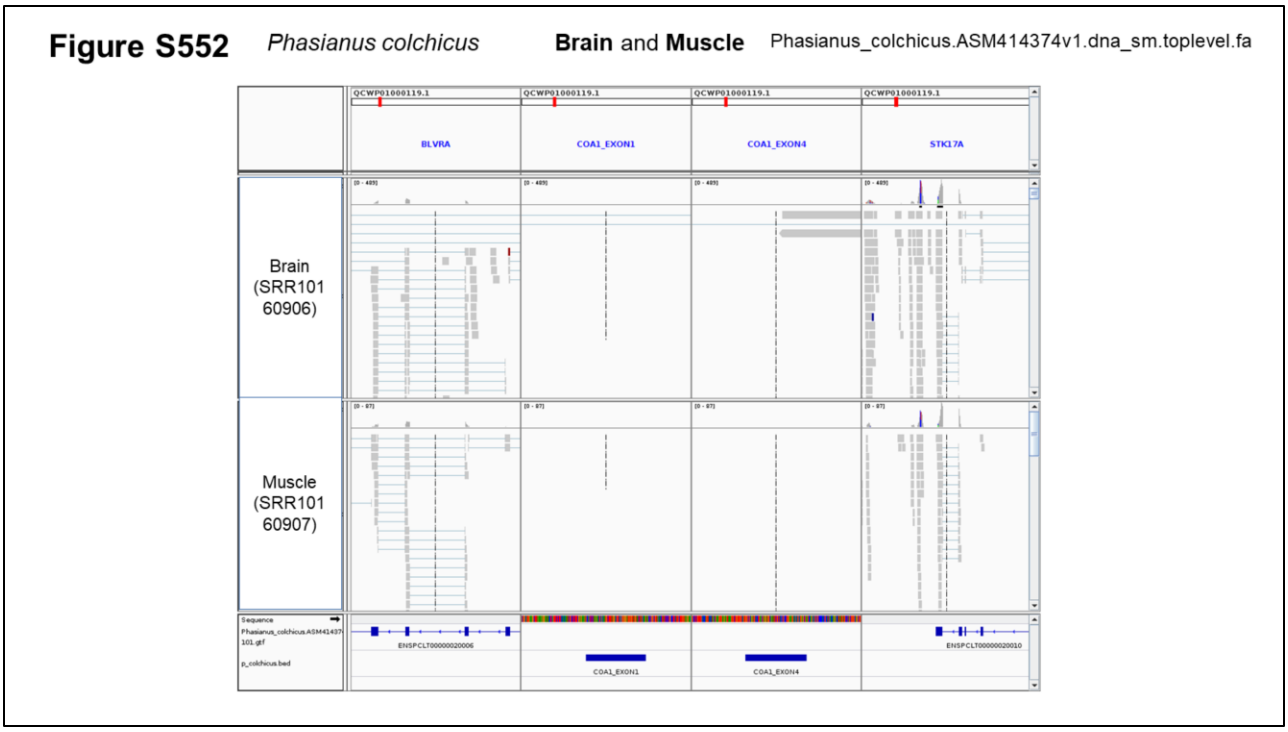

Figure S552: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in common pheasant (*Phasianus colchicus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (SRR10160906) and muscle (SRR10160907) have been mapped to the Phasianus_colchicus.ASM414374v1.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

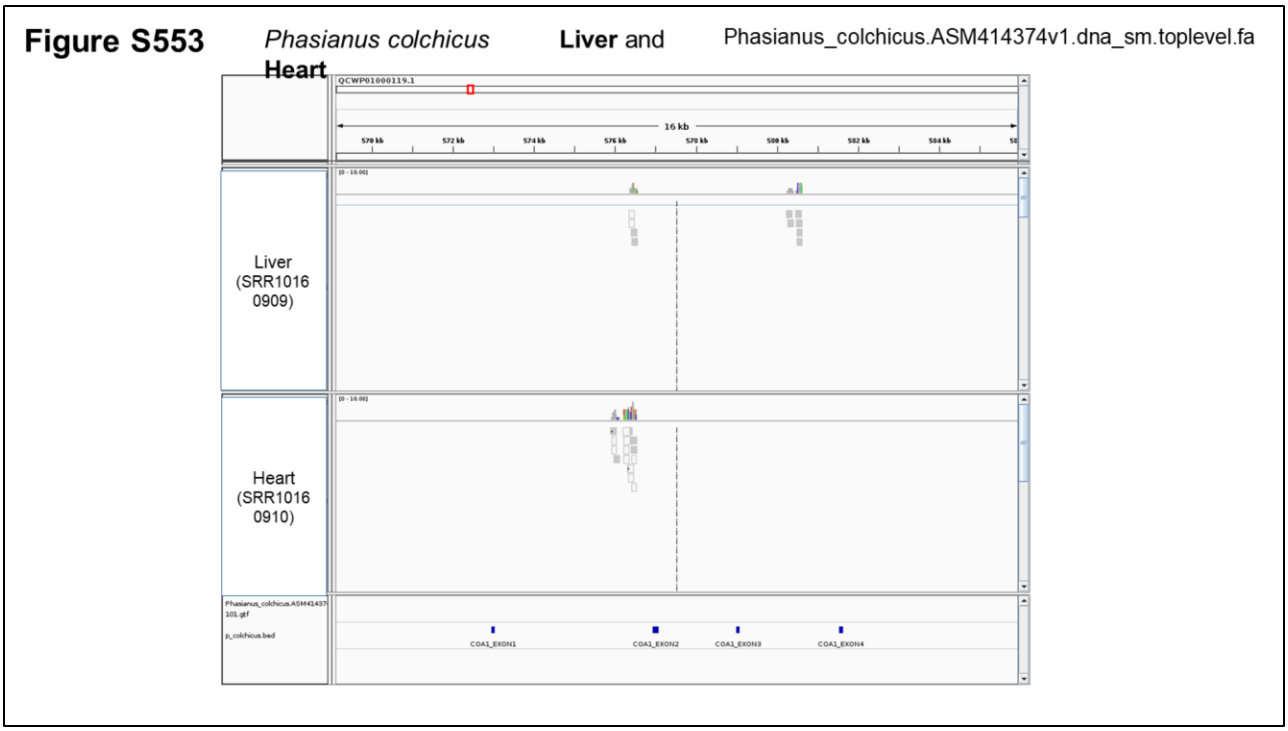

Figure S553: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in common pheasant (*Phasianus colchicus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR10160909) and heart (SRR10160910) have been mapped to the Phasianus_colchicus.ASM414374v1.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

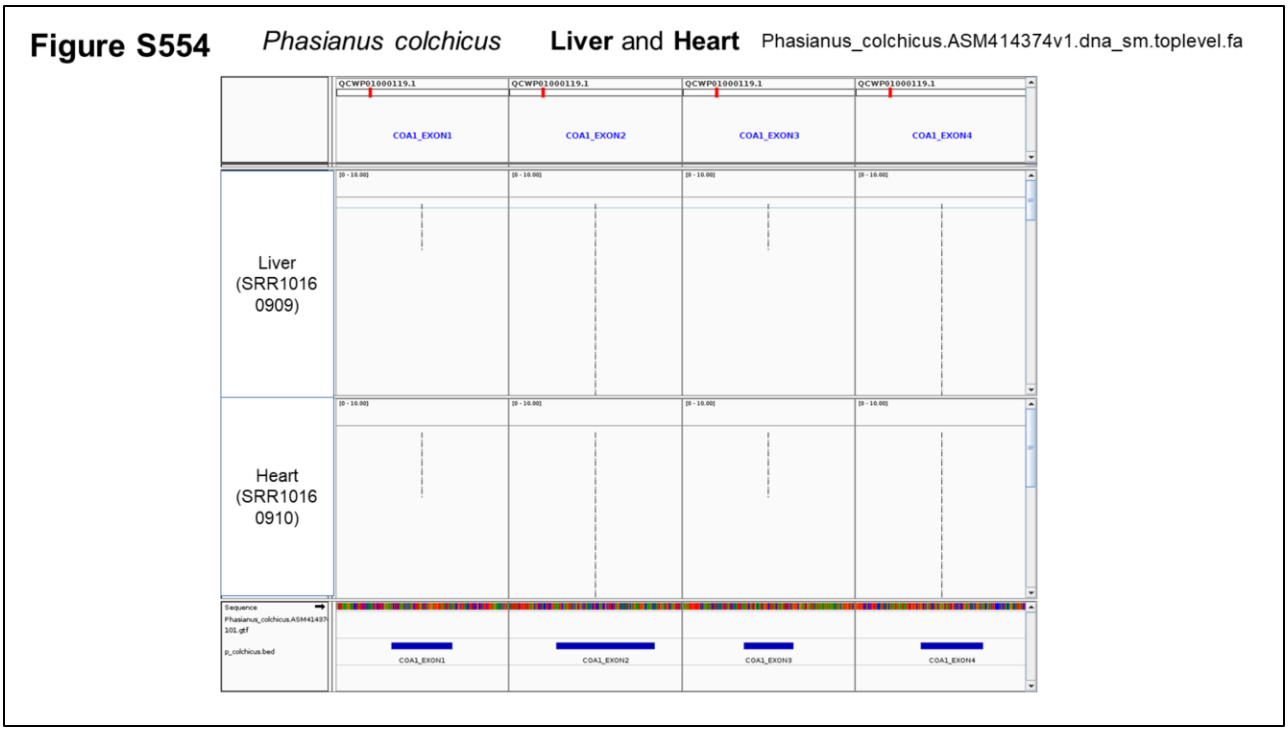

Figure S554: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S553**.

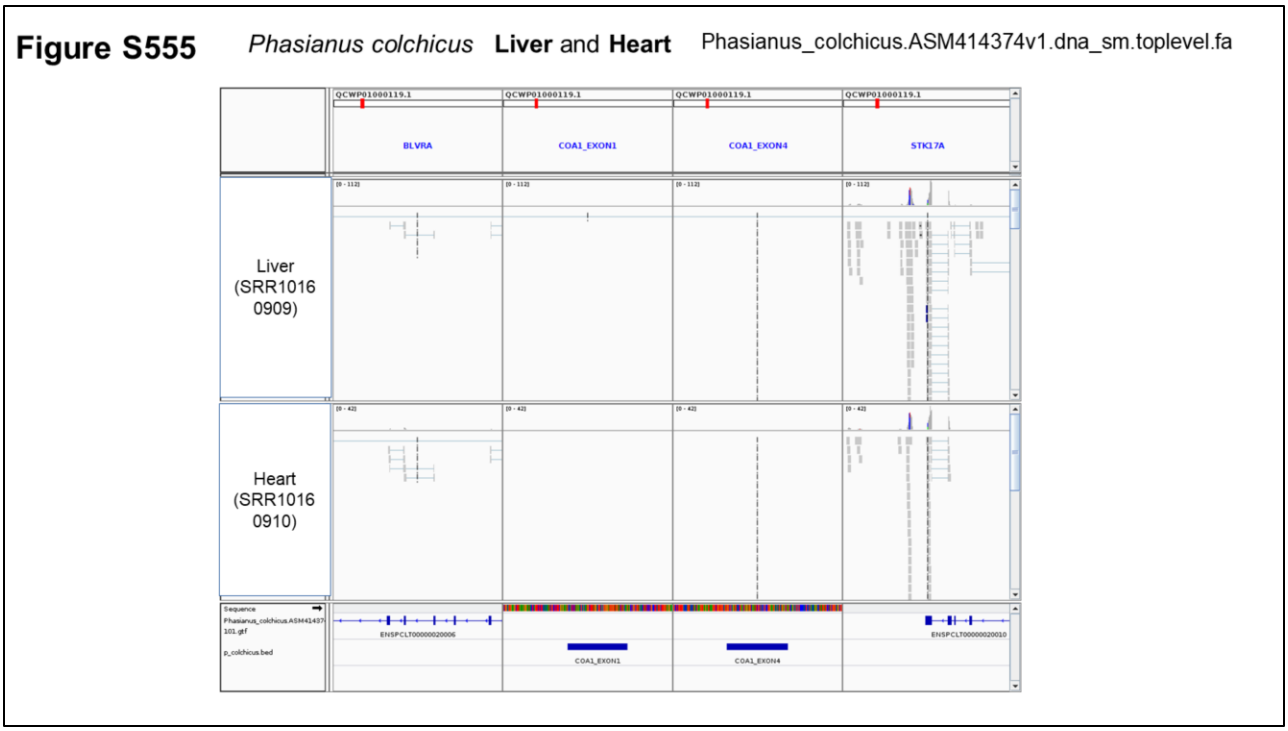

Figure S555: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in common pheasant (*Phasianus colchicus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR10160909) and heart (SRR10160910) have been mapped to the Phasianus_colchicus.ASM414374v1.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

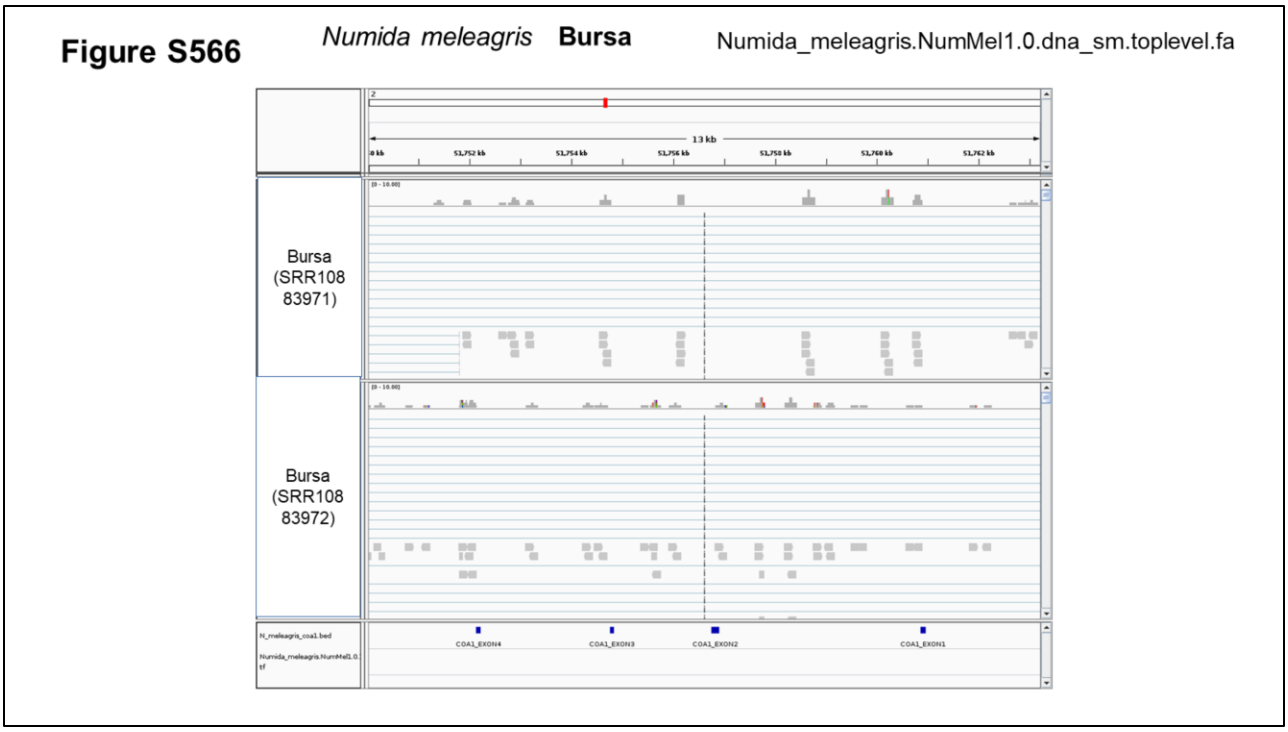

Figure S556: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in helmeted guineafowl (*Numida meleagris*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from bursa (SRR10883971) and (SRR10883972) have been mapped to the Numida_meleagris.NumMel1.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

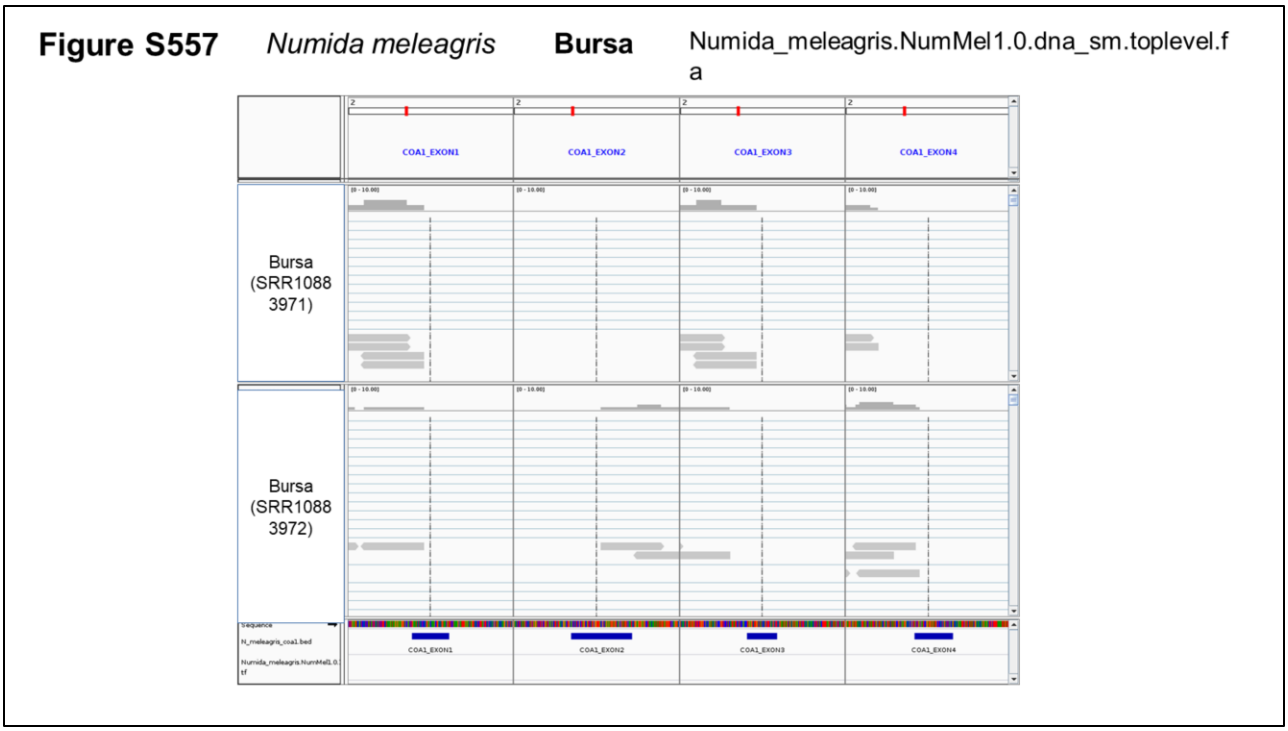

Figure S557: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S556**.

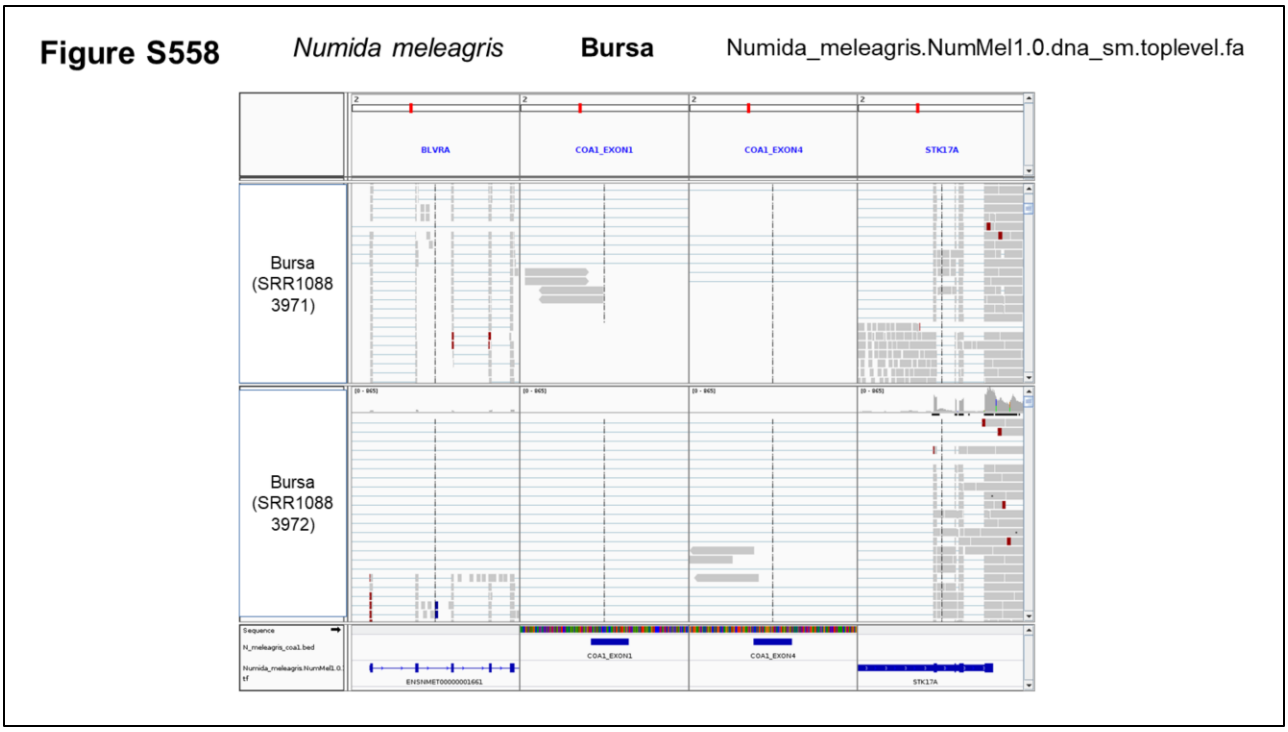

Figure S558: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in helmeted guineafowl (*Numida meleagris*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from bursa (SRR10883971) and (SRR10883972) have been mapped to the Numida_meleagris.NumMel1.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

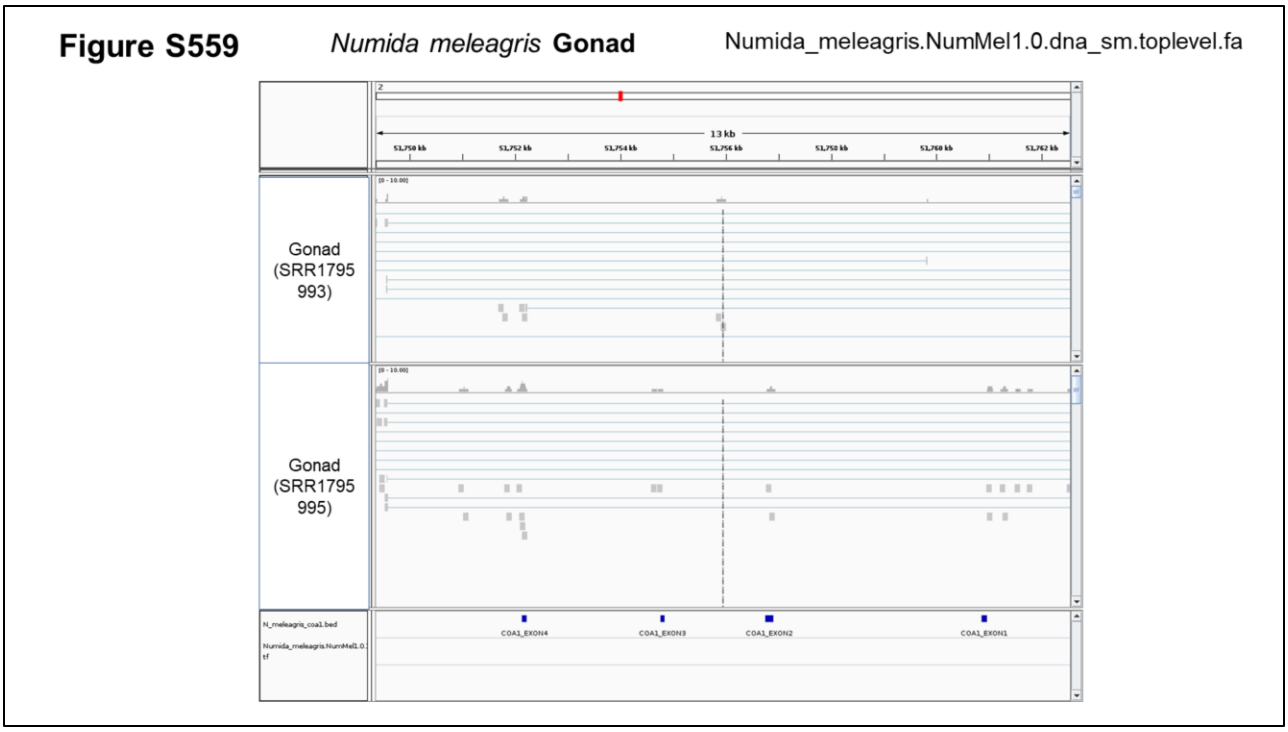

Figure S559: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in helmeted guineafowl (*Numida meleagris*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from gonad (SRR1795993) and (SRR1795995) have been mapped to the Numida_meleagris.NumMel1.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

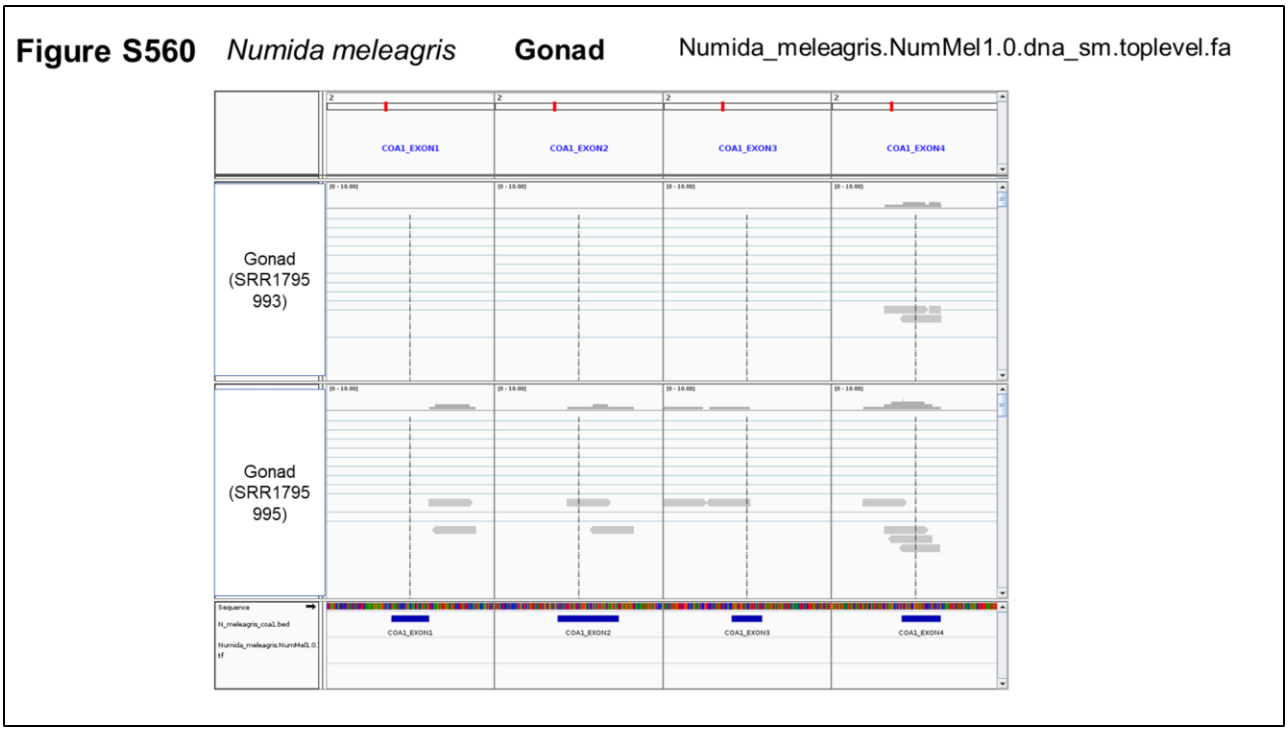

Figure S560: A zoomed in view of each of the *COA1* exons **Supplementary Fig. S559**.

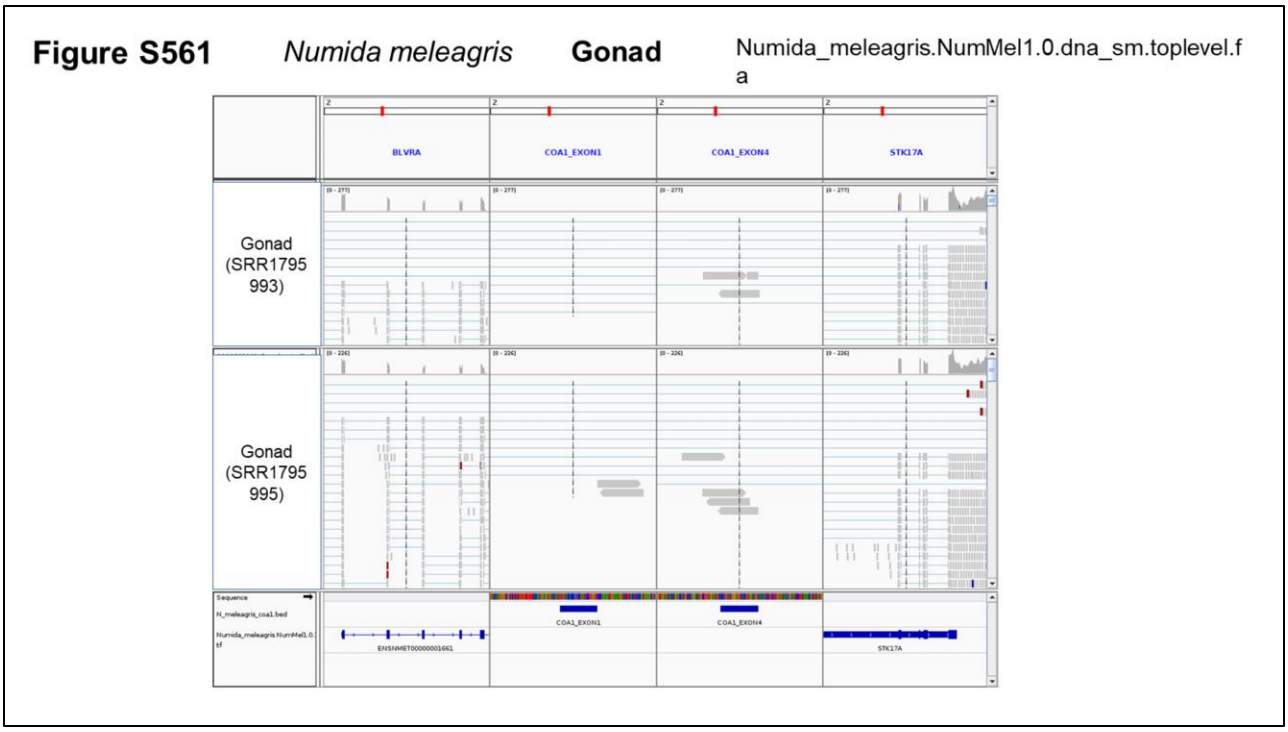

Figure S561: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in helmeted guineafowl (*Numida meleagris*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from gonad (SRR1795993) and (SRR1795995) have been mapped to the Numida_meleagris.NumMel1.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

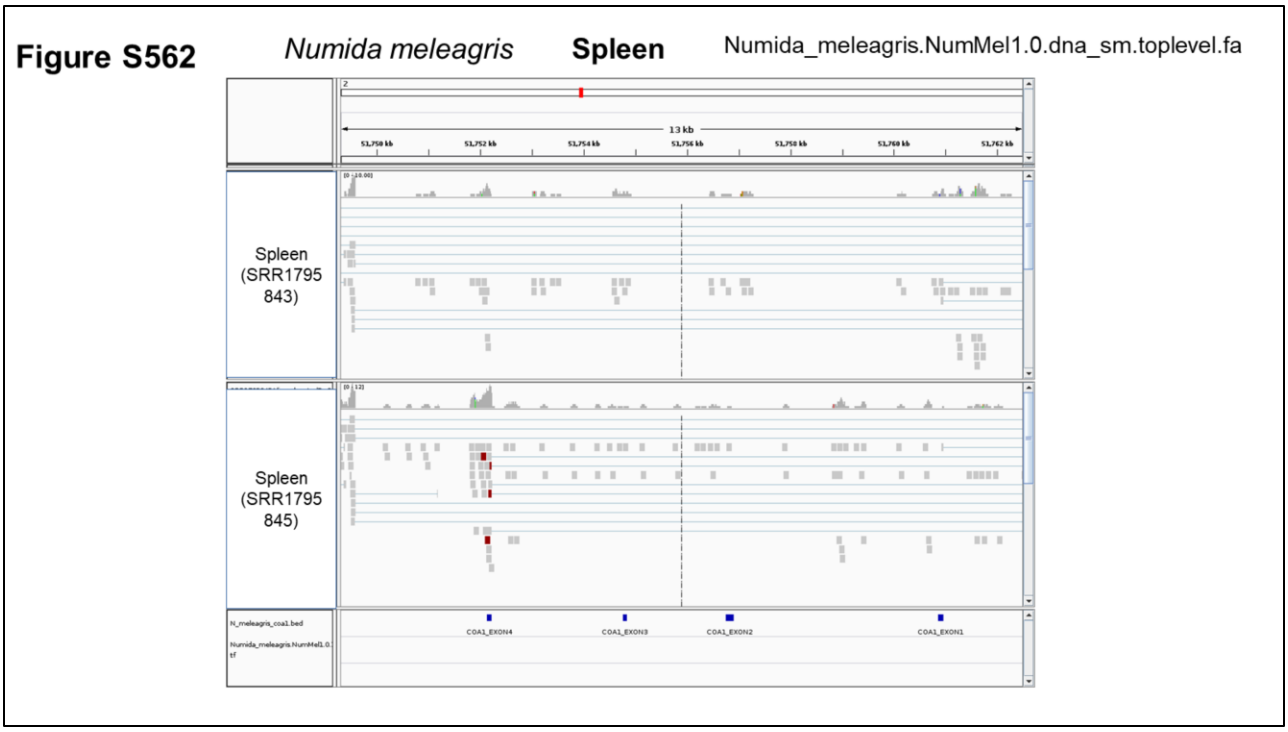

Figure S562: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in helmeted guineafowl (*Numida meleagris*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR1795843) and (SRR1795845) have been mapped to the Numida_meleagris.NumMel1.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

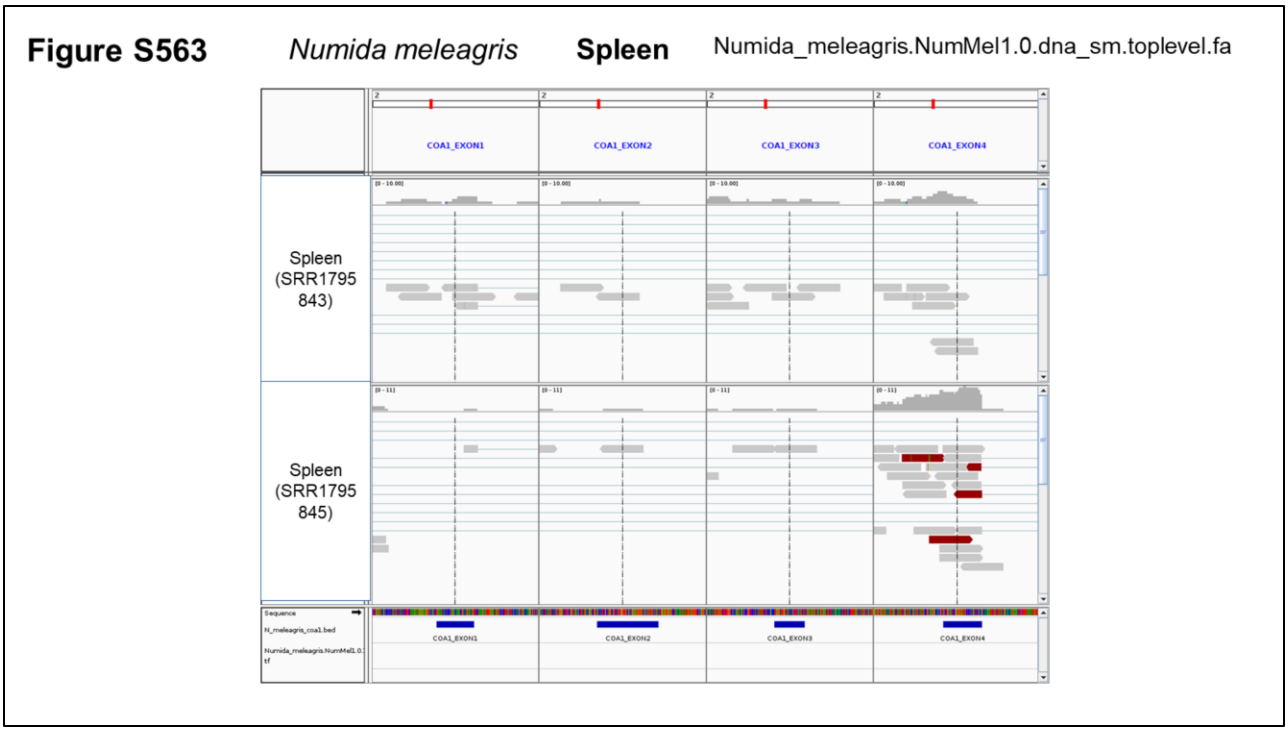

Figure S563: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S562**.

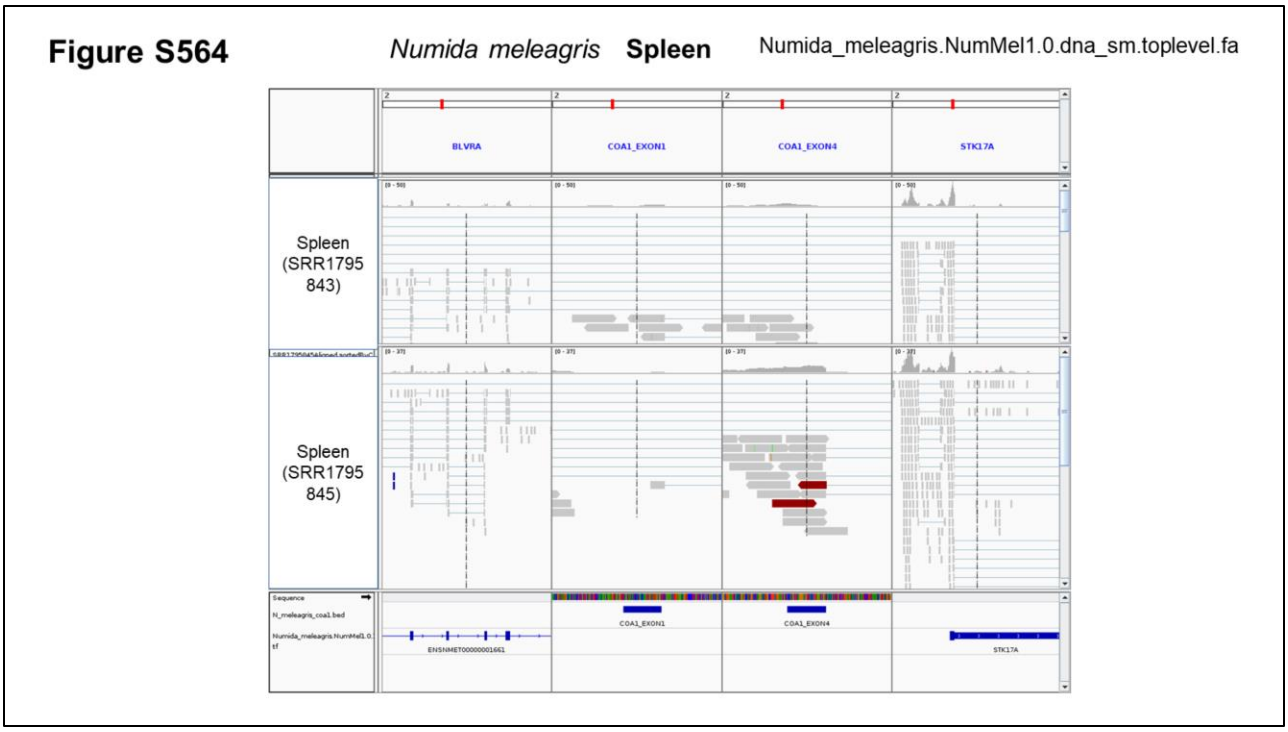

Figure S564: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in helmeted guineafowl (*Numida meleagris*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR1795843) and (SRR1795845) have been mapped to the Numida_meleagris.NumMel1.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

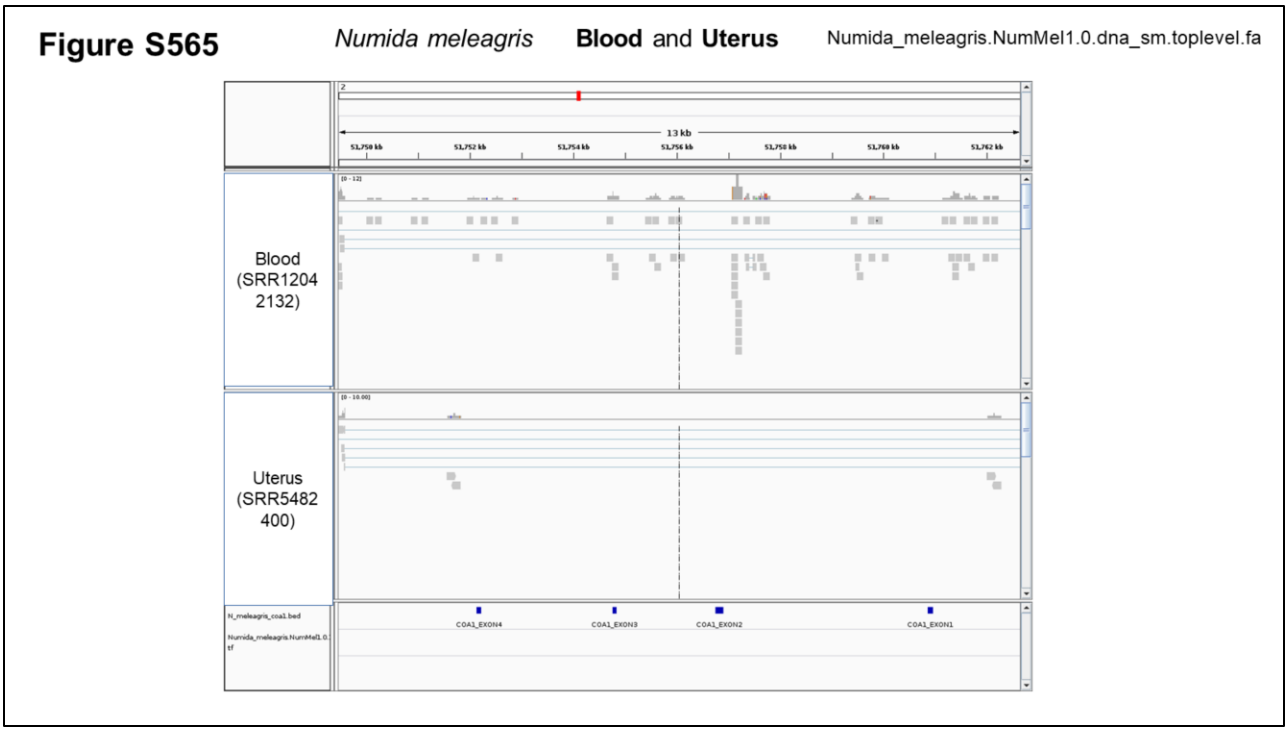

Figure S565: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in helmeted guineafowl (*Numida meleagris*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR12042132) and uterus (SRR5482400) have been mapped to the Numida_meleagris.NumMel1.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

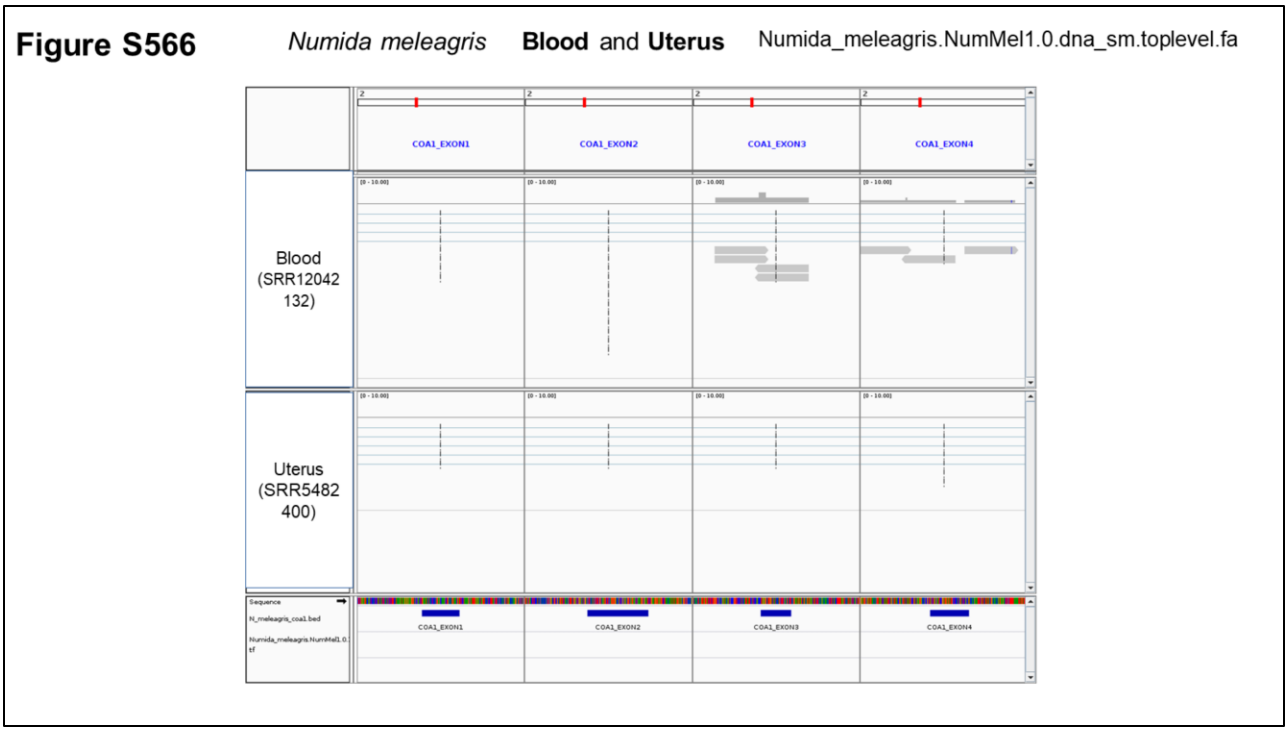

Figure S566: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S565**.

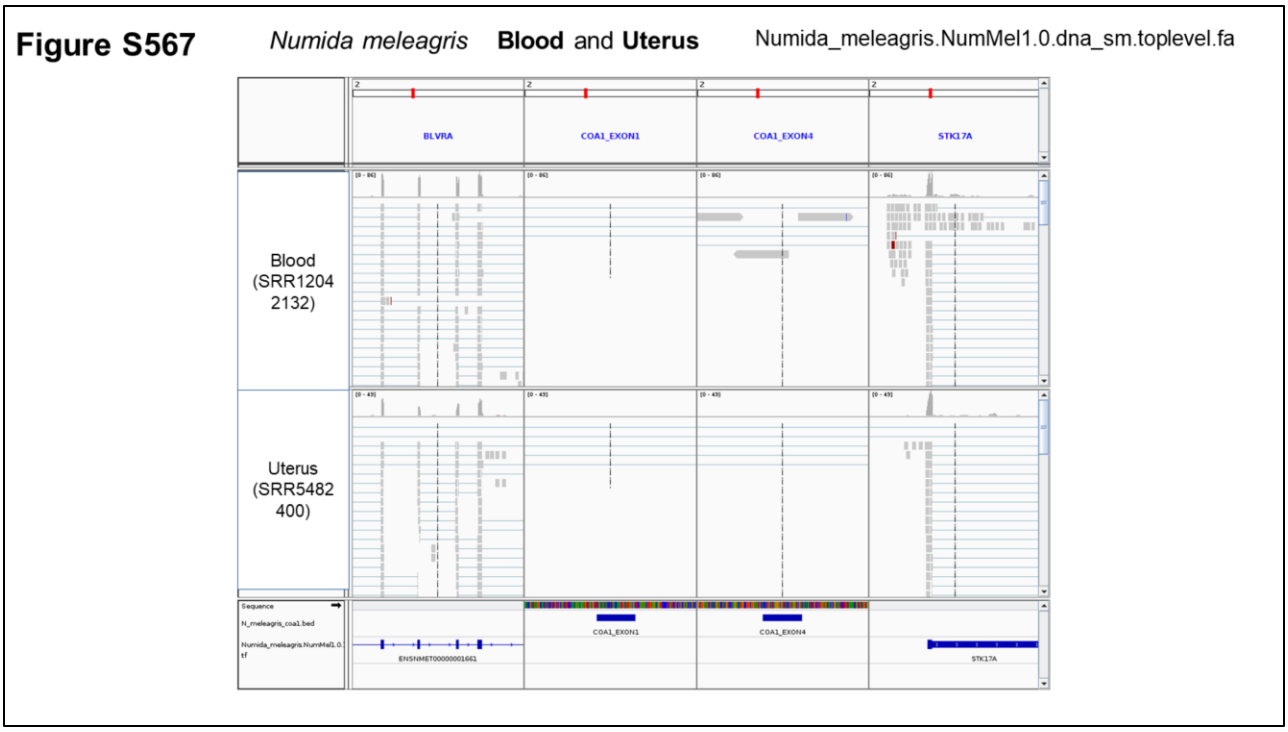

Figure S567: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in helmeted guineafowl (*Numida meleagris*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR12042132) and uterus (SRR5482400) have been mapped to the Numida_meleagris.NumMel1.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S568: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in turkey (*Meleagris gallopavo*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from breast muscle (SRR478416) and (SRR478417) have been mapped to the Meleagris_gallopavo.Turkey_2.01.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S569: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S568**.

Figure S570: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in turkey (*Meleagris gallopavo*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from breast muscle (SRR478416) and (SRR478417) have been mapped to the Meleagris_gallopavo.Turkey_2.01.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

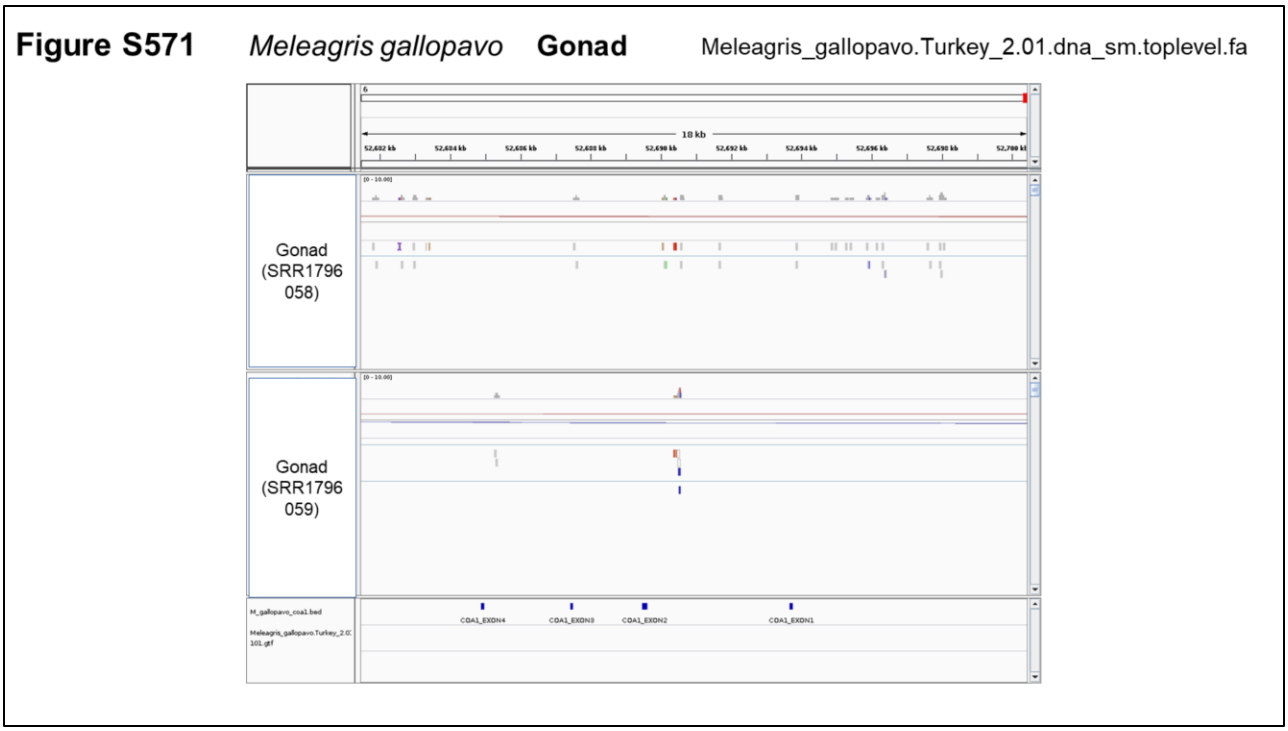

Figure S571: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in turkey (*Meleagris gallopavo*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from gonad (SRR1796058) and (SRR1796059) have been mapped to the Meleagris_gallopavo.Turkey_2.01.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

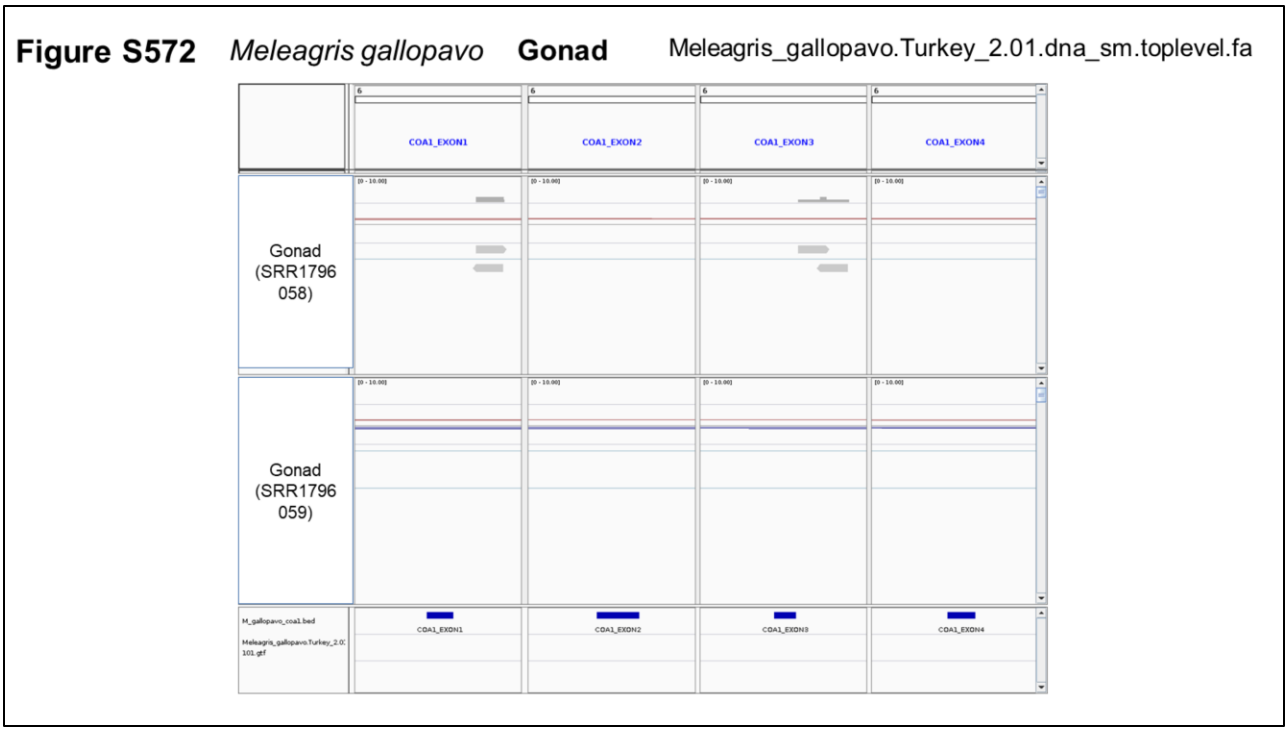

Figure S572: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S571**.

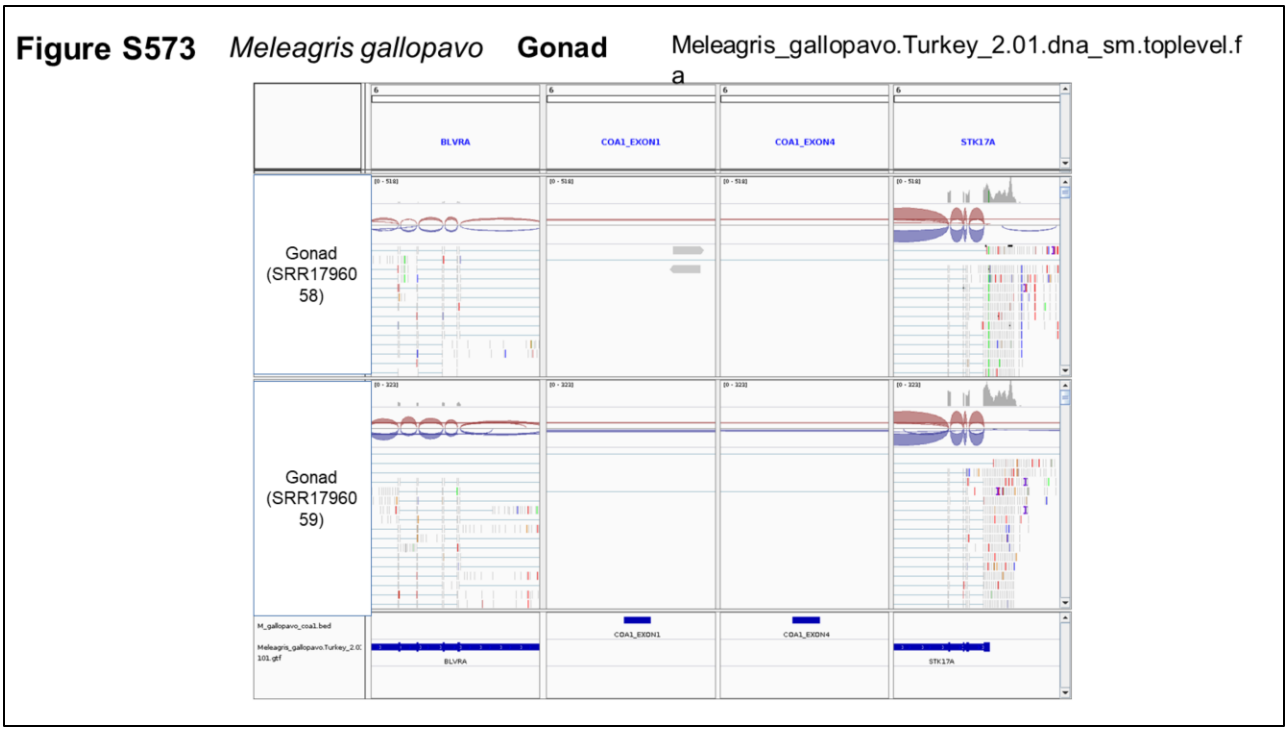

Figure S573: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in turkey (*Meleagris gallopavo*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from gonad (SRR1796058) and (SRR1796059) have been mapped to the Meleagris_gallopavo.Turkey_2.01.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

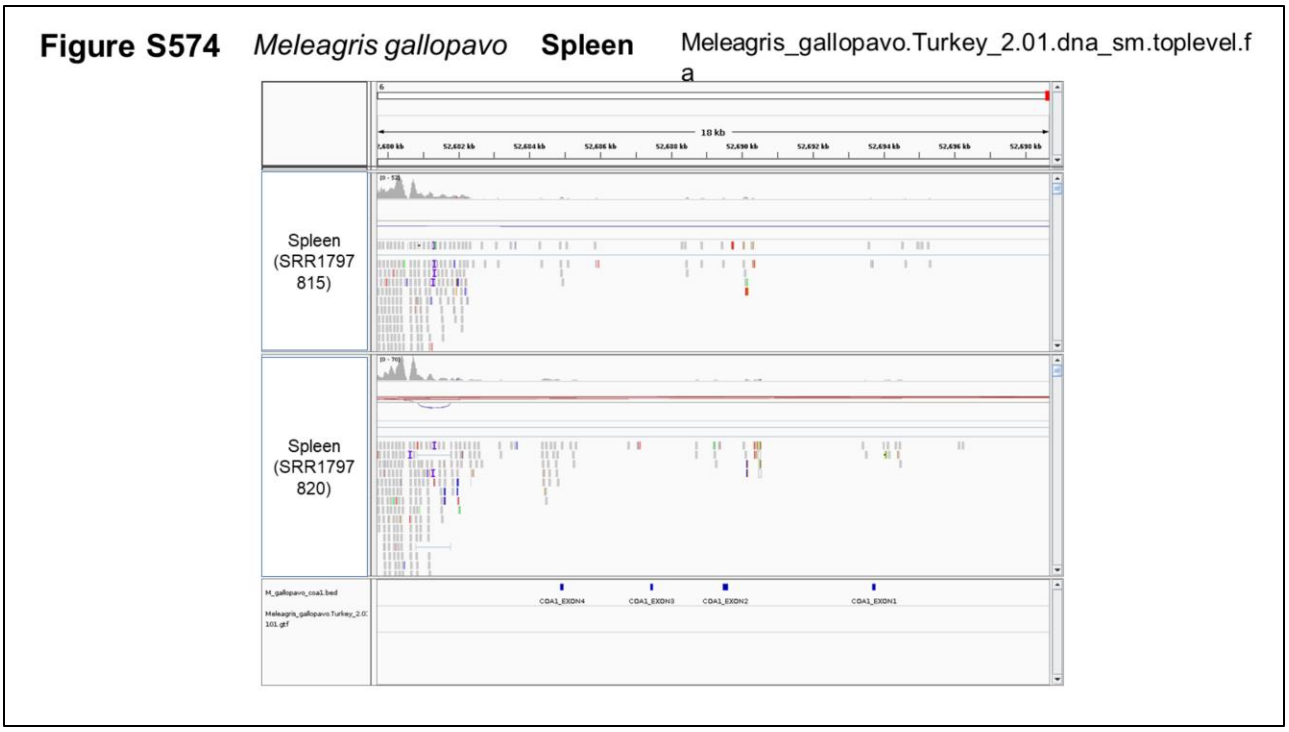

Figure S574: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in turkey (*Meleagris gallopavo*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR1797815) and (SRR1797820) have been mapped to the Meleagris_gallopavo.Turkey_2.01.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

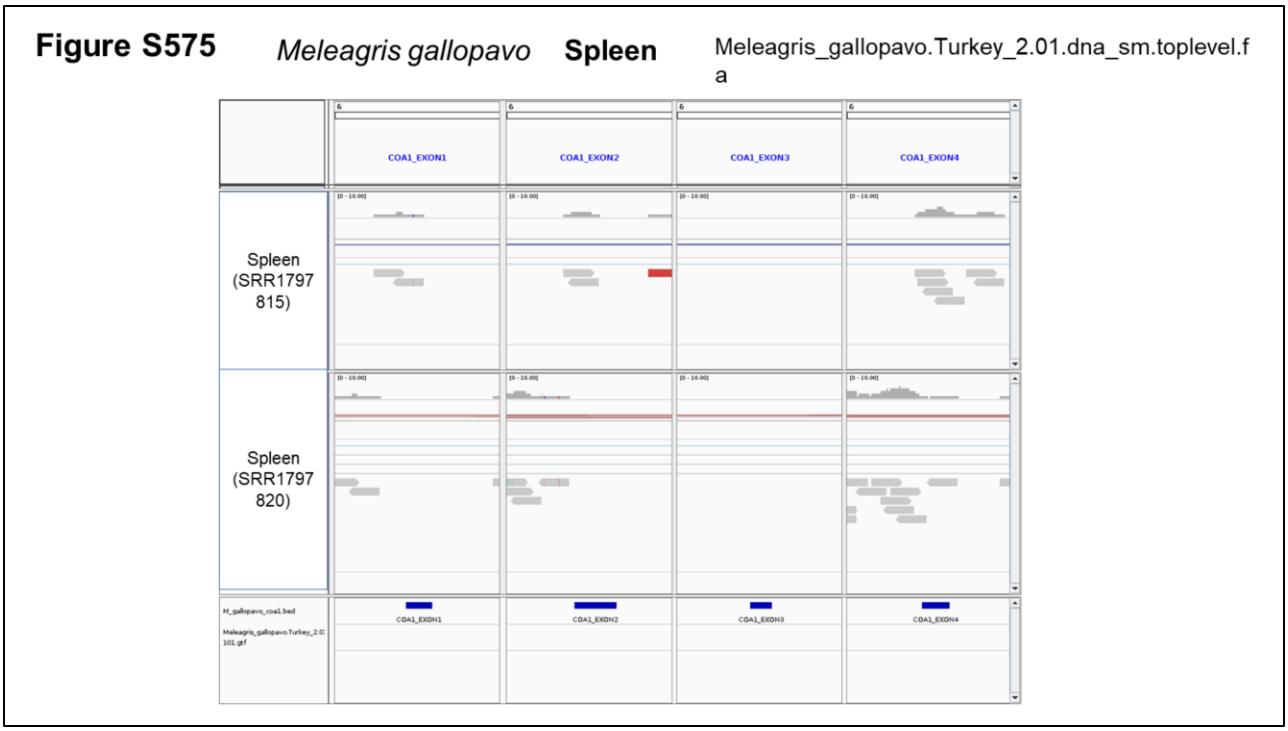

Figure S575: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S574**.

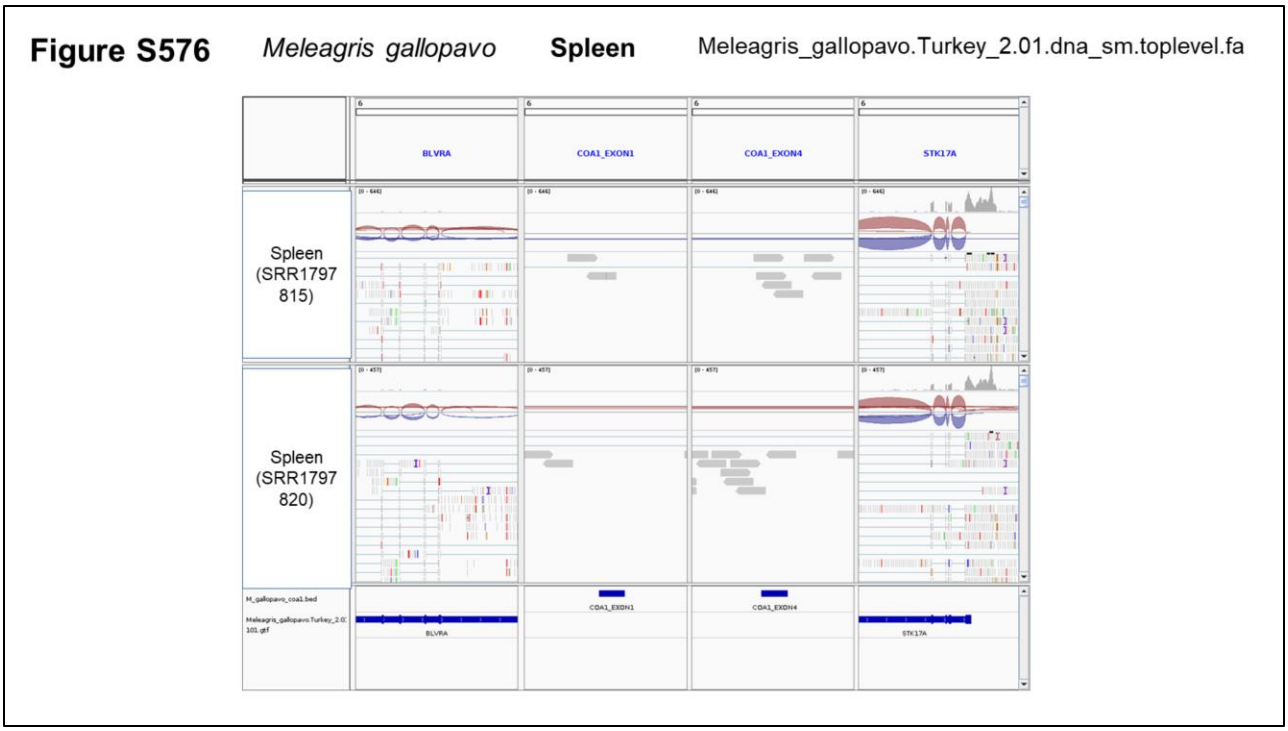

Figure S576: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in turkey (*Meleagris gallopavo*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR1797815) and (SRR1797820) have been mapped to the Meleagris_gallopavo.Turkey_2.01.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

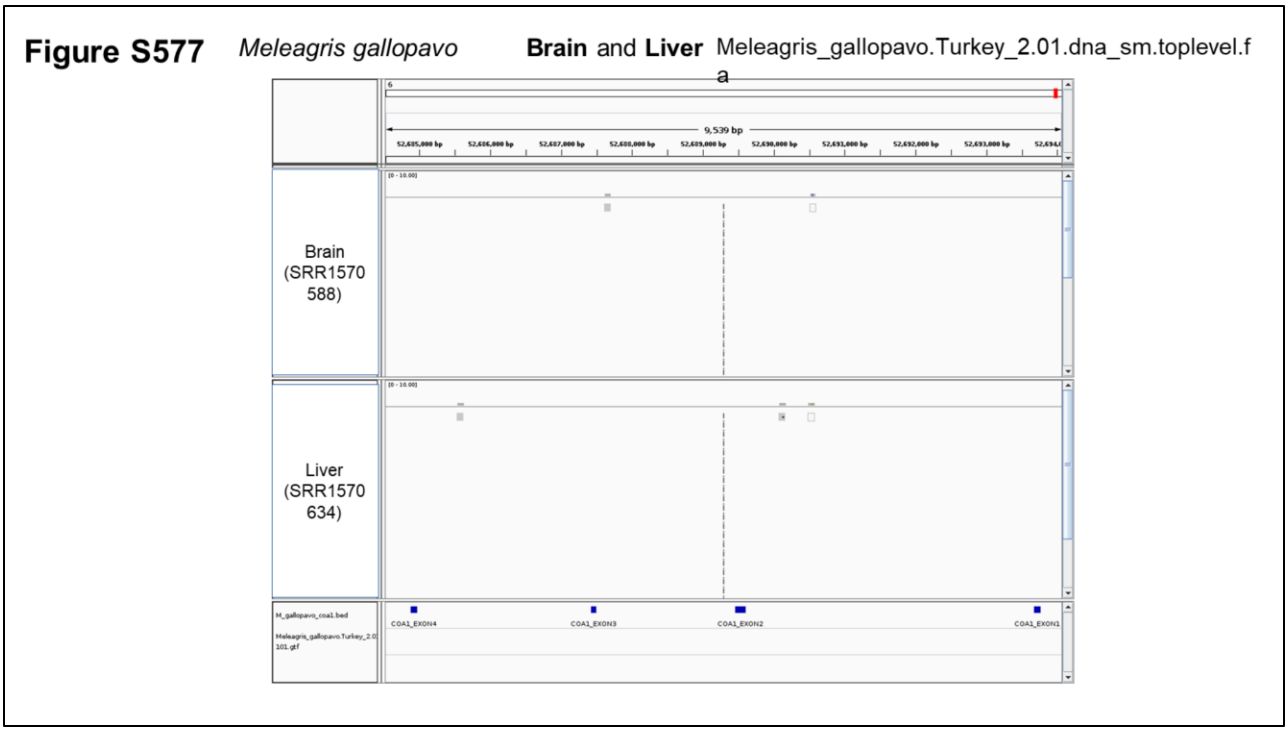

Figure S577: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in turkey (*Meleagris gallopavo*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from Brain (SRR1570588) and liver (SRR1570634) have been mapped to the Meleagris_gallopavo.Turkey_2.01.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

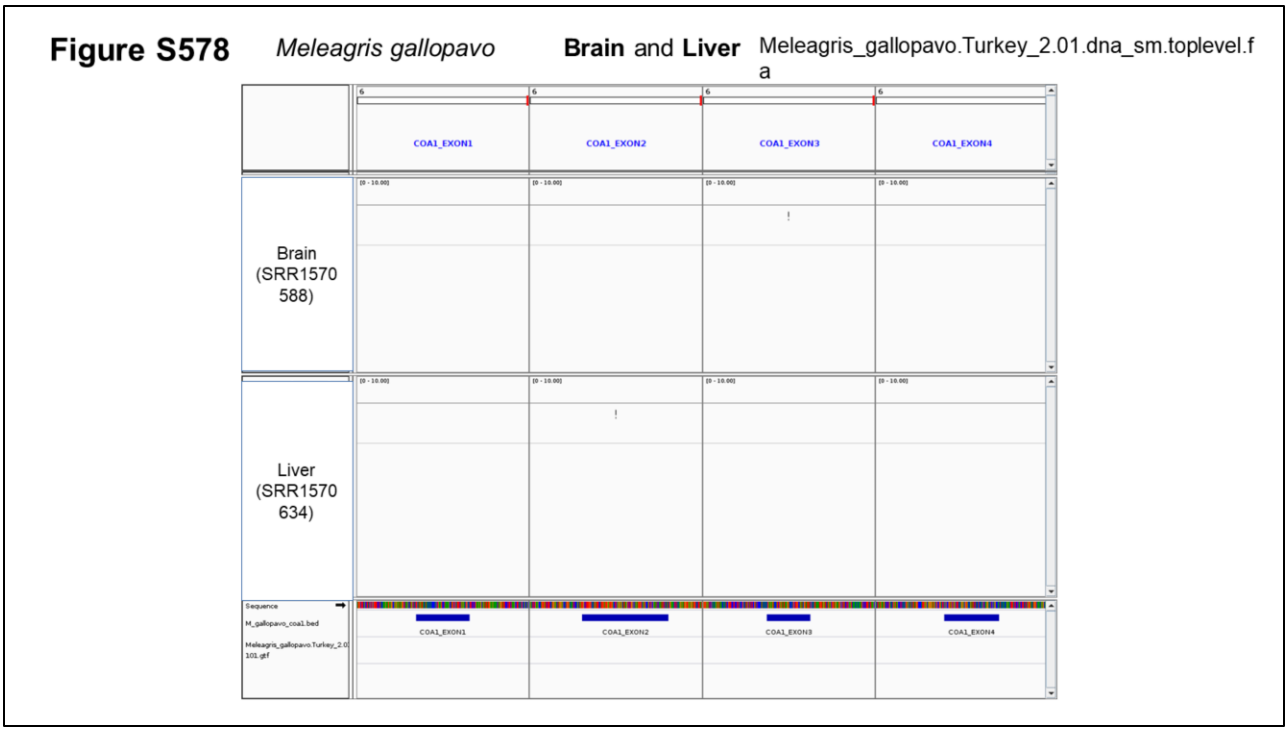

Figure S578: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S577**.

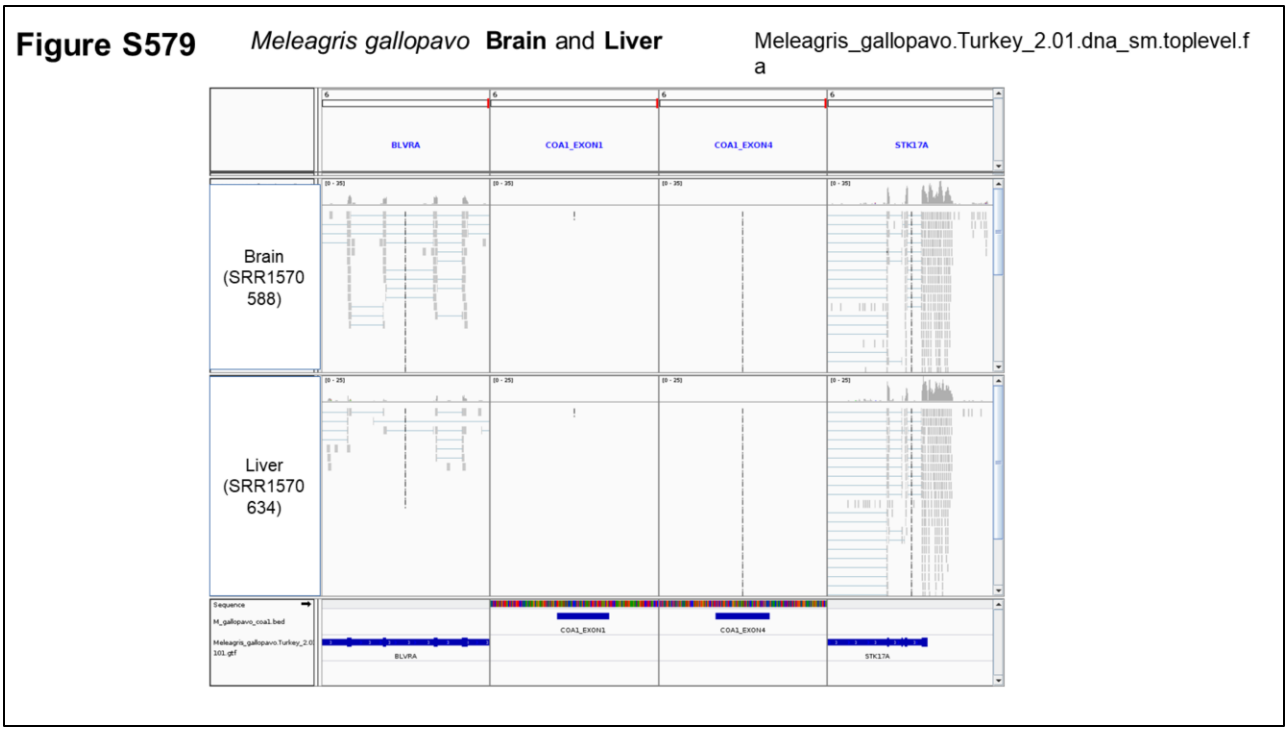

Figure S579: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in turkey (*Meleagris gallopavo*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from Brain (SRR1570588) and liver (SRR1570634) have been mapped to the Meleagris_gallopavo.Turkey_2.01.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S580: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in turkey (*Meleagris gallopavo*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart (SRR1570480) and bursa (SRR1570548) have been mapped to the Meleagris_gallopavo.Turkey_2.01.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

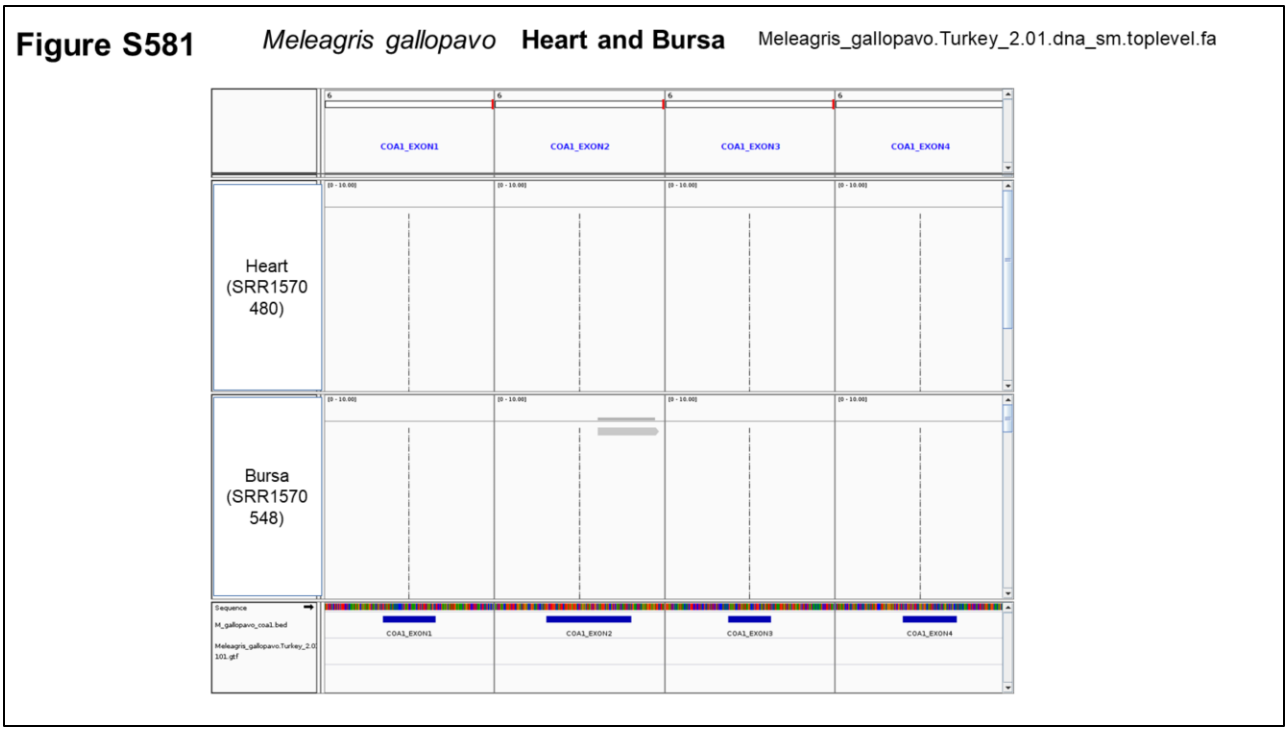

Figure S581: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S580**.

Figure S582: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in turkey (*Meleagris gallopavo*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart (SRR1570480) and bursa (SRR1570548) have been mapped to the Meleagris_gallopavo.Turkey_2.01.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

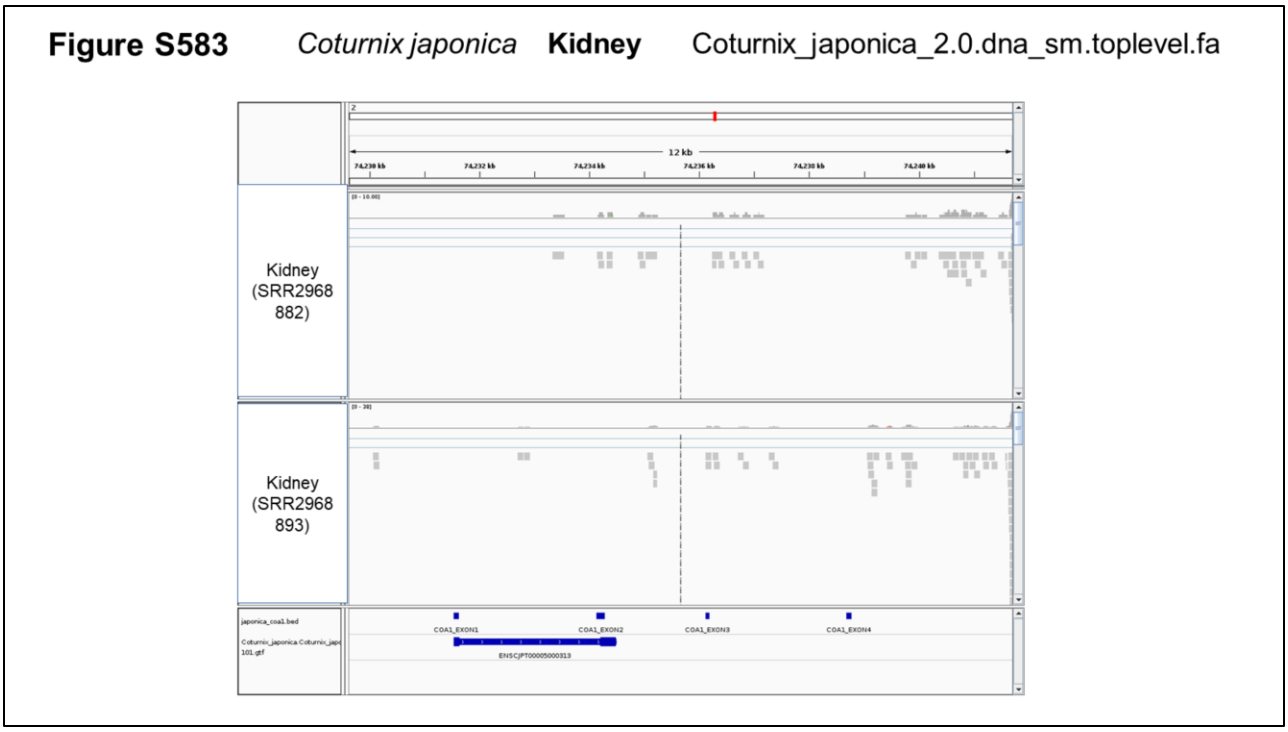

Figure S583: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Japanese quail (*Coturnix japonica*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from kidney (SRR1570480) and (SRR1570548) have been mapped to the Coturnix_japonica_2.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

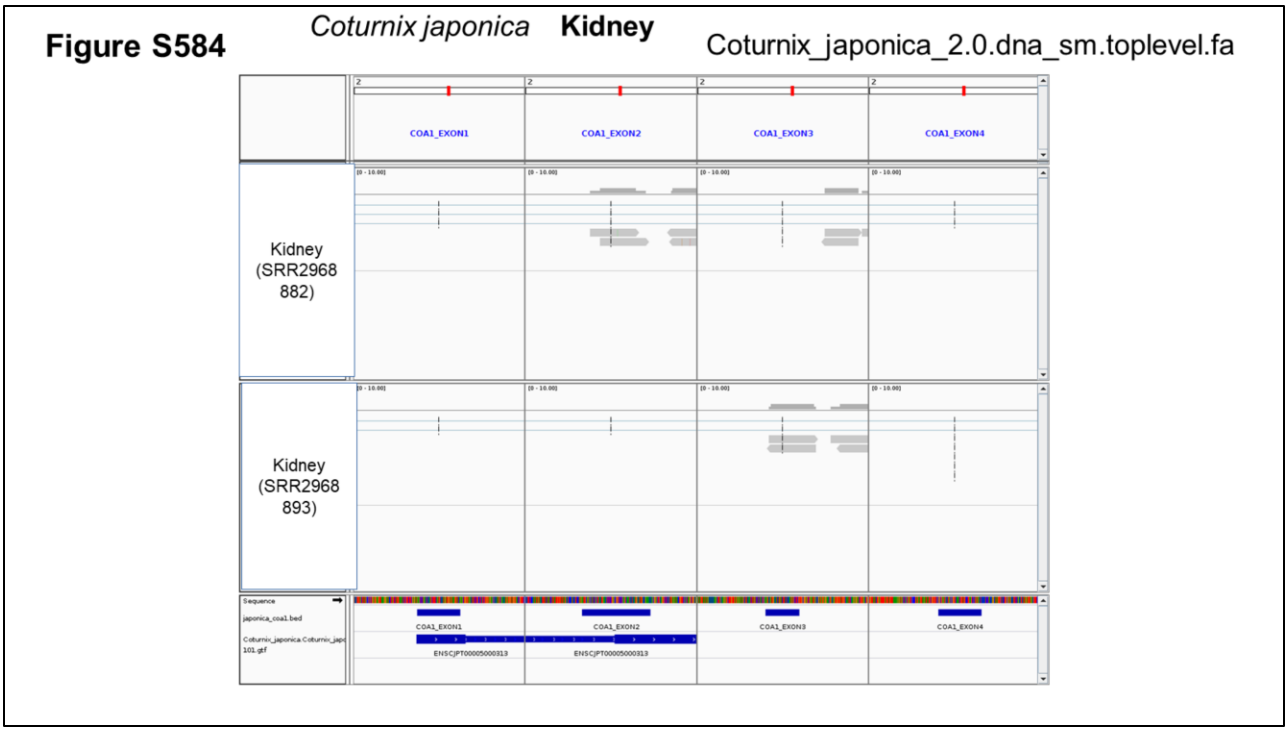

Figure S584: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S583**.

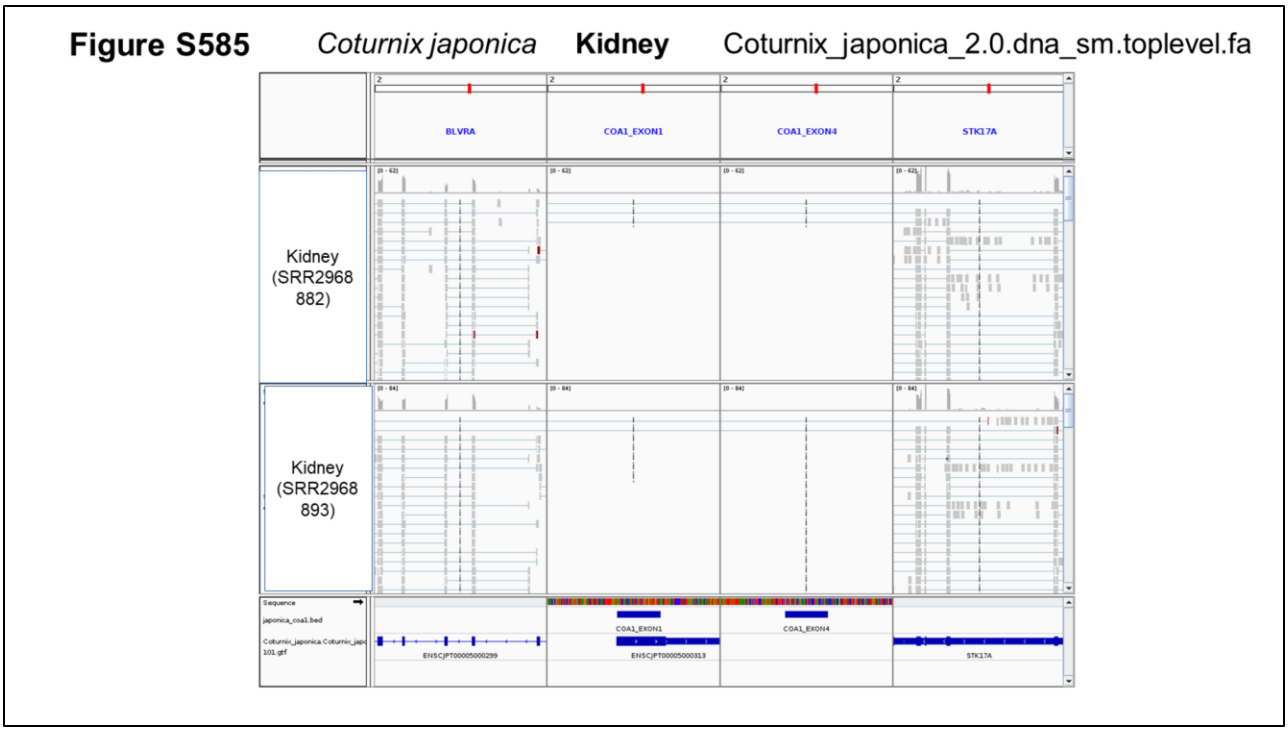

Figure S585: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in Japanese quail (*Coturnix japonica*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from kidney (SRR1570480) and (SRR1570548) have been mapped to the Coturnix_japonica_2.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

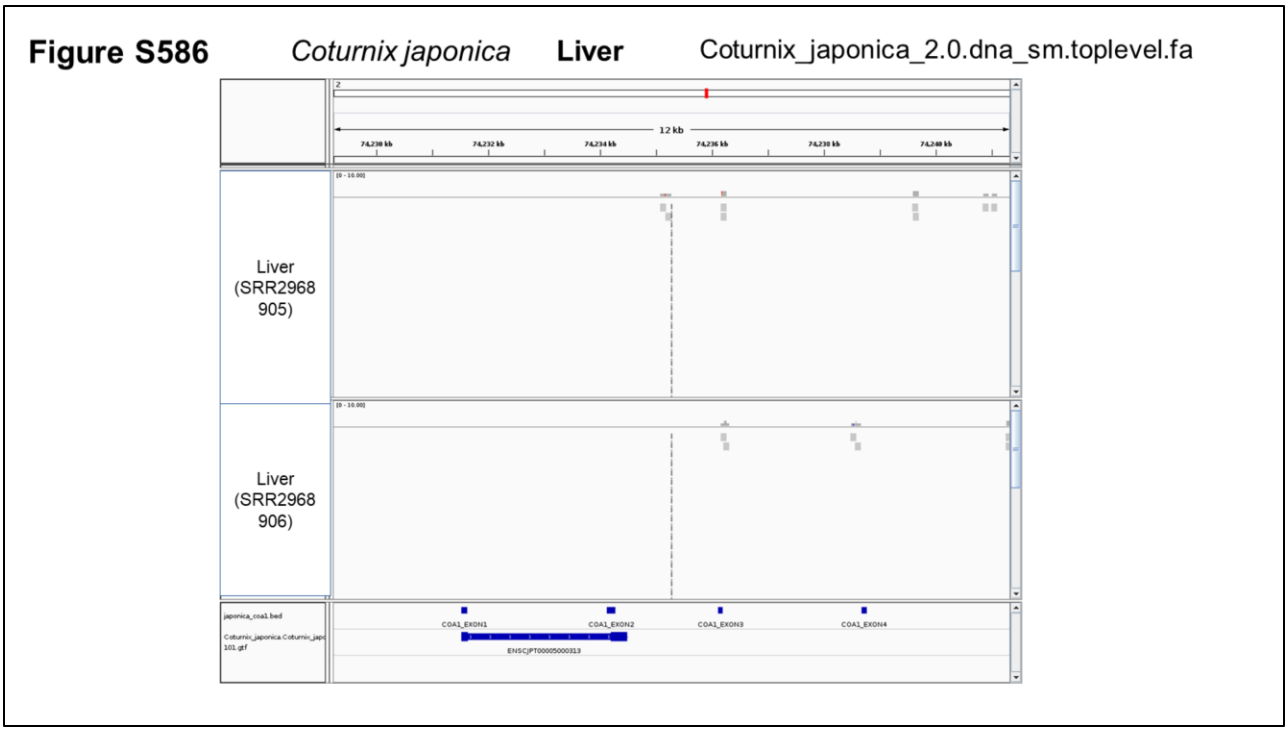

Figure S586: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Japanese quail (*Coturnix japonica*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR2968905) and (SRR2968906) have been mapped to the Coturnix_japonica_2.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

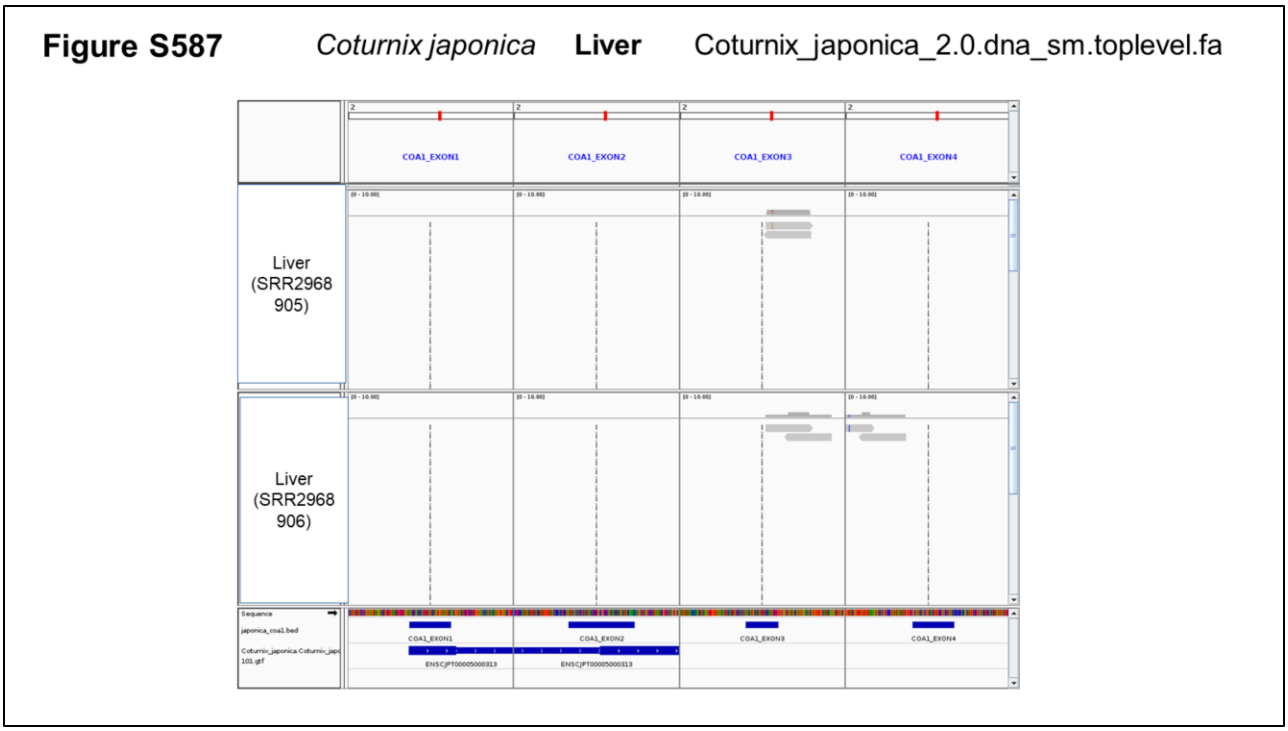

Figure S587: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S586**.

Figure S588 *Coturnix japonica* **Liver** Coturnix_japonica_2.0.dna_sm.toplevel.fa

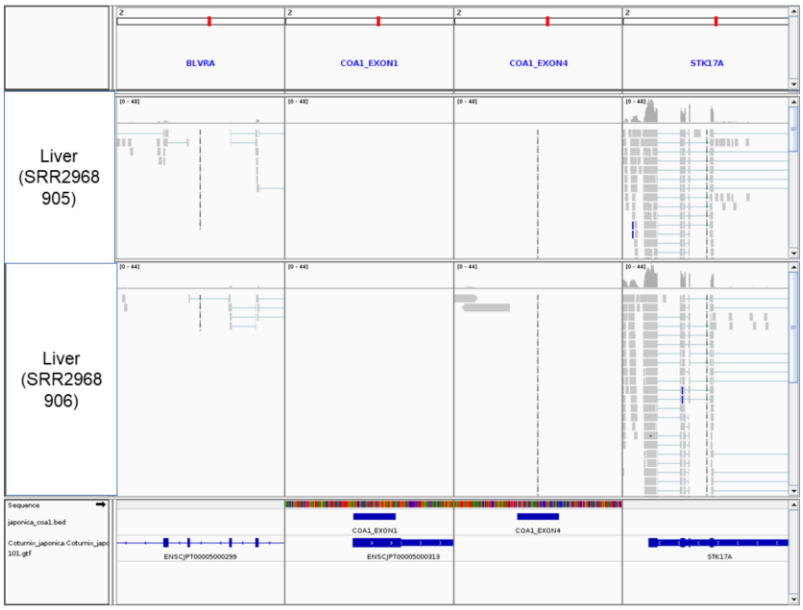

Figure S588: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in Japanese quail (*Coturnix japonica*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR2968905) and (SRR2968906) have been mapped to the Coturnix_japonica_2.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

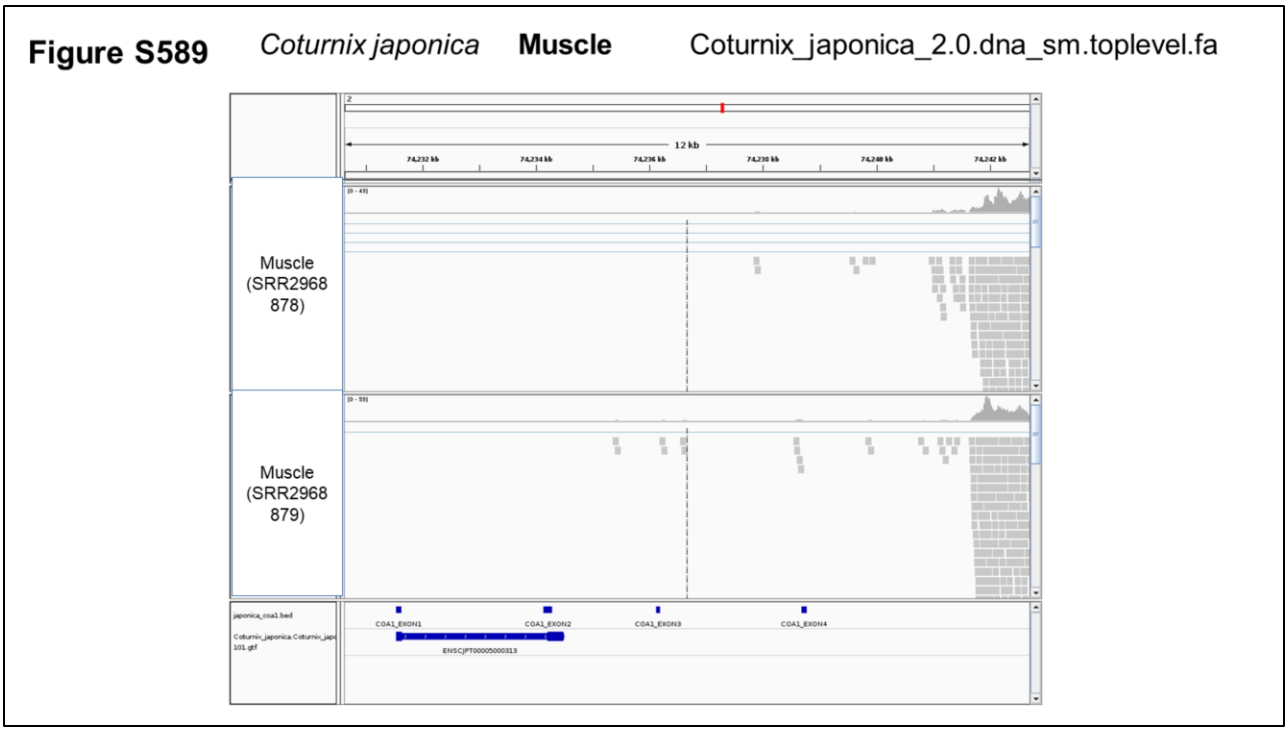

Figure S589: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Japanese quail (*Coturnix japonica*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from muscle (SRR2968878) and (SRR2968879) have been mapped to the Coturnix_japonica_2.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S590 *Coturnix japonica* **Muscle** Coturnix_japonica_2.0.dna_sm.toplevel.fa

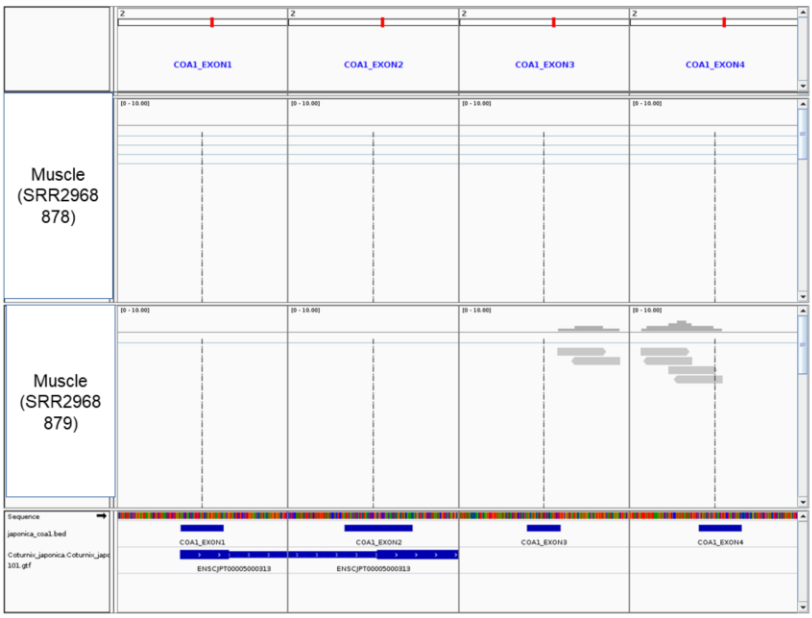

Figure S590: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S589**.

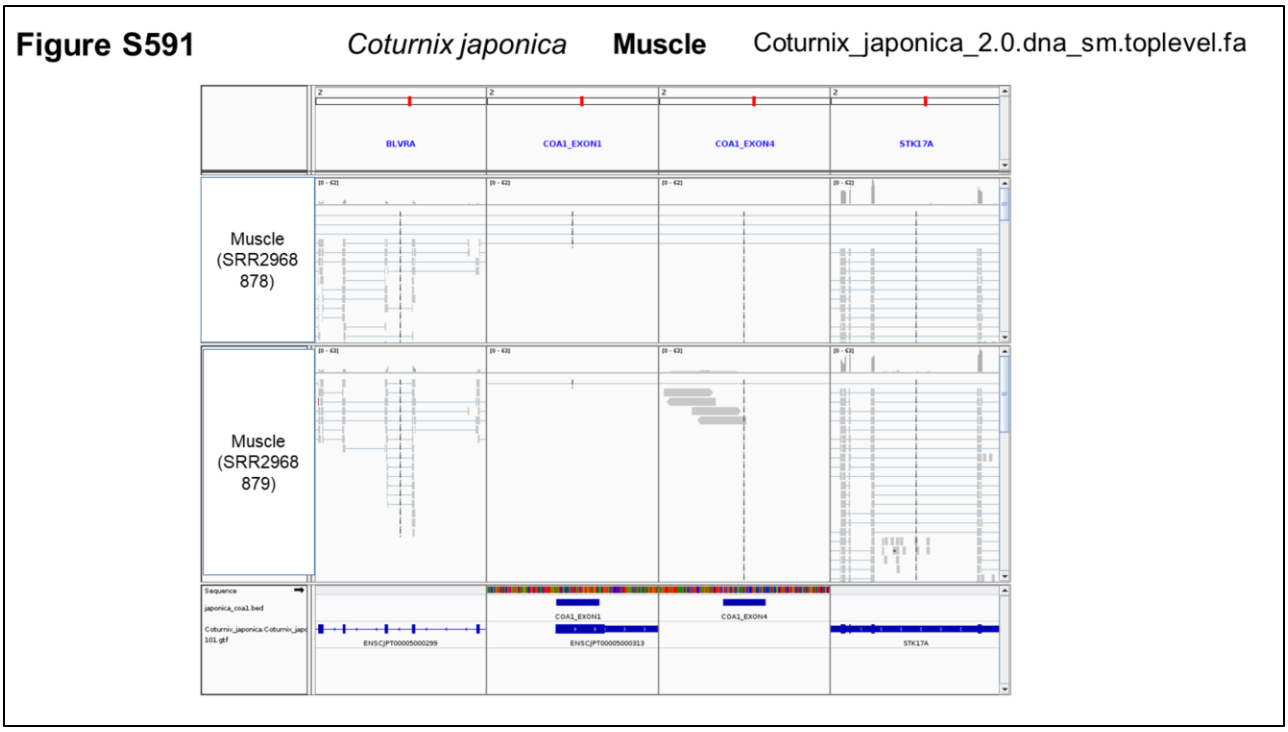

Figure S591: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in Japanese quail (*Coturnix japonica*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from muscle (SRR2968878) and (SRR2968879) have been mapped to the Coturnix_japonica_2.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S592 *Coturnix japonica* **Lung** Coturnix_japonica_2.0.dna_sm.toplevel.fa

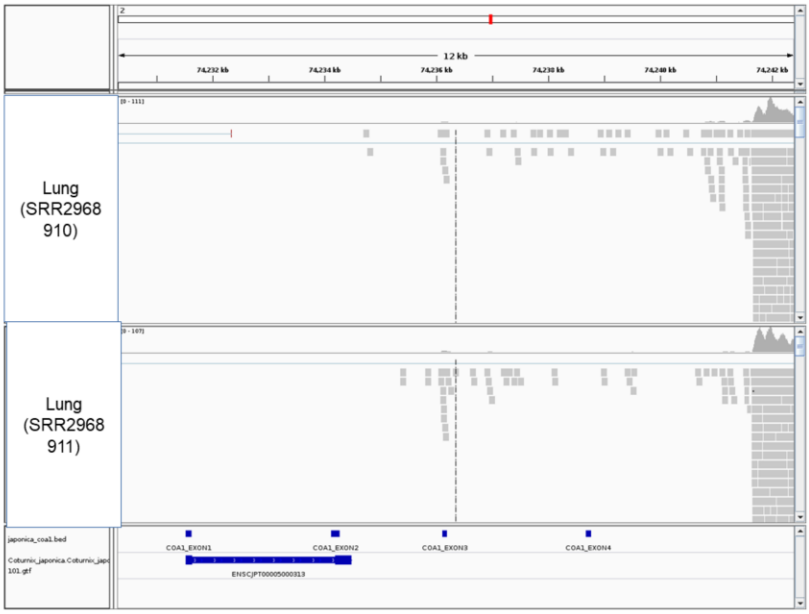

Figure S592: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Japanese quail (*Coturnix japonica*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from lung (SRR2968910) and (SRR2968911) have been mapped to the Coturnix_japonica_2.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

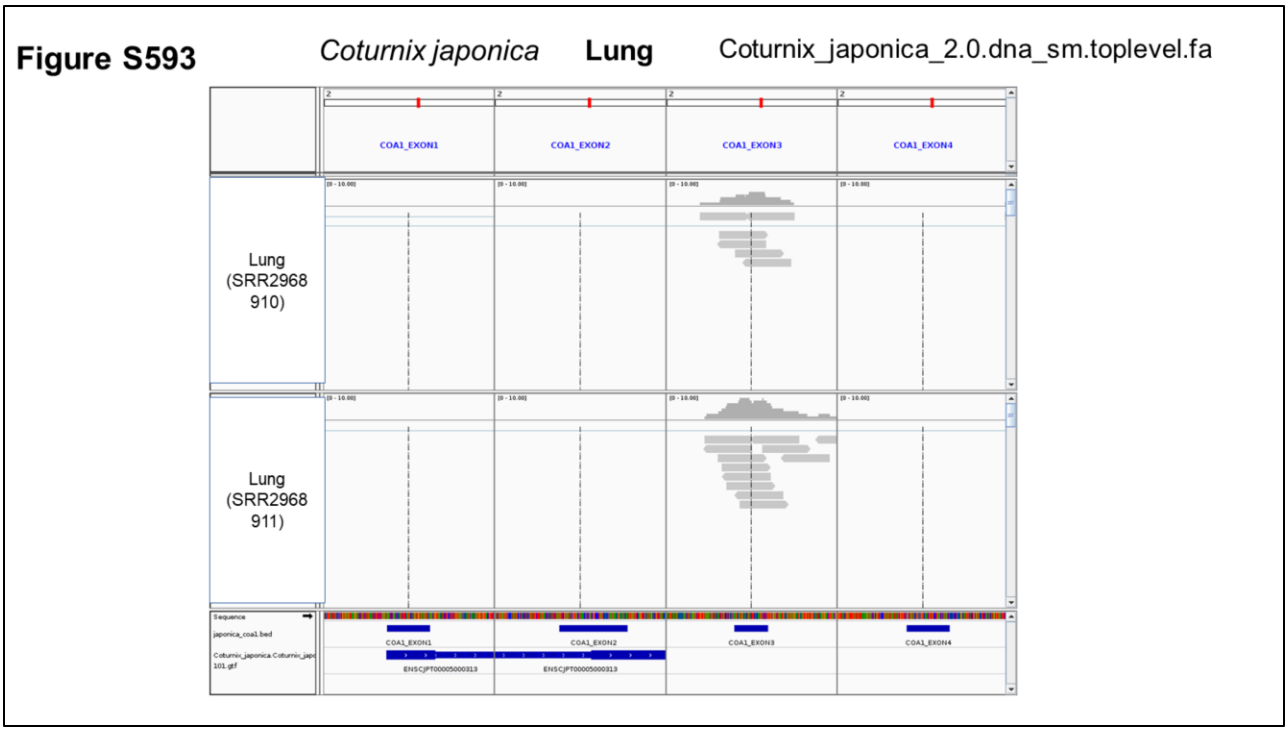

Figure S593: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S592**.

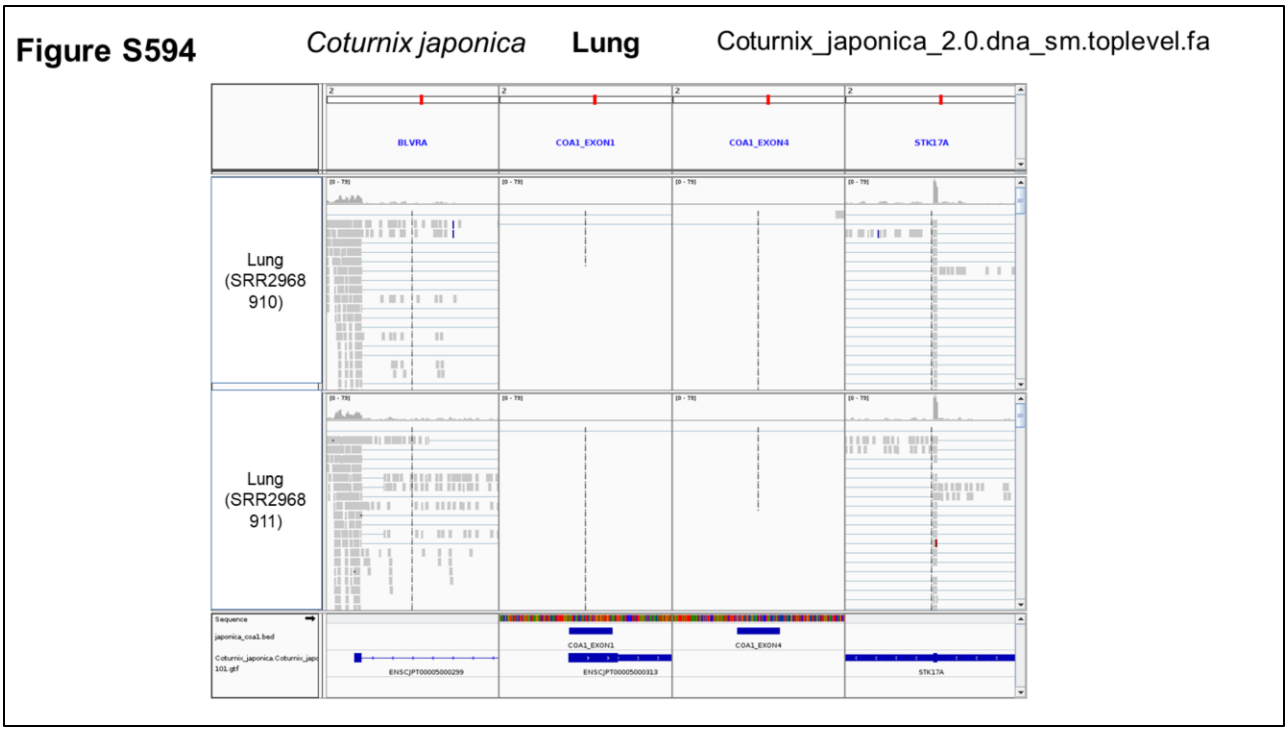

Figure S594: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in Japanese quail (*Coturnix japonica*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from lung (SRR2968910) and (SRR2968911) have been mapped to the Coturnix_japonica_2.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

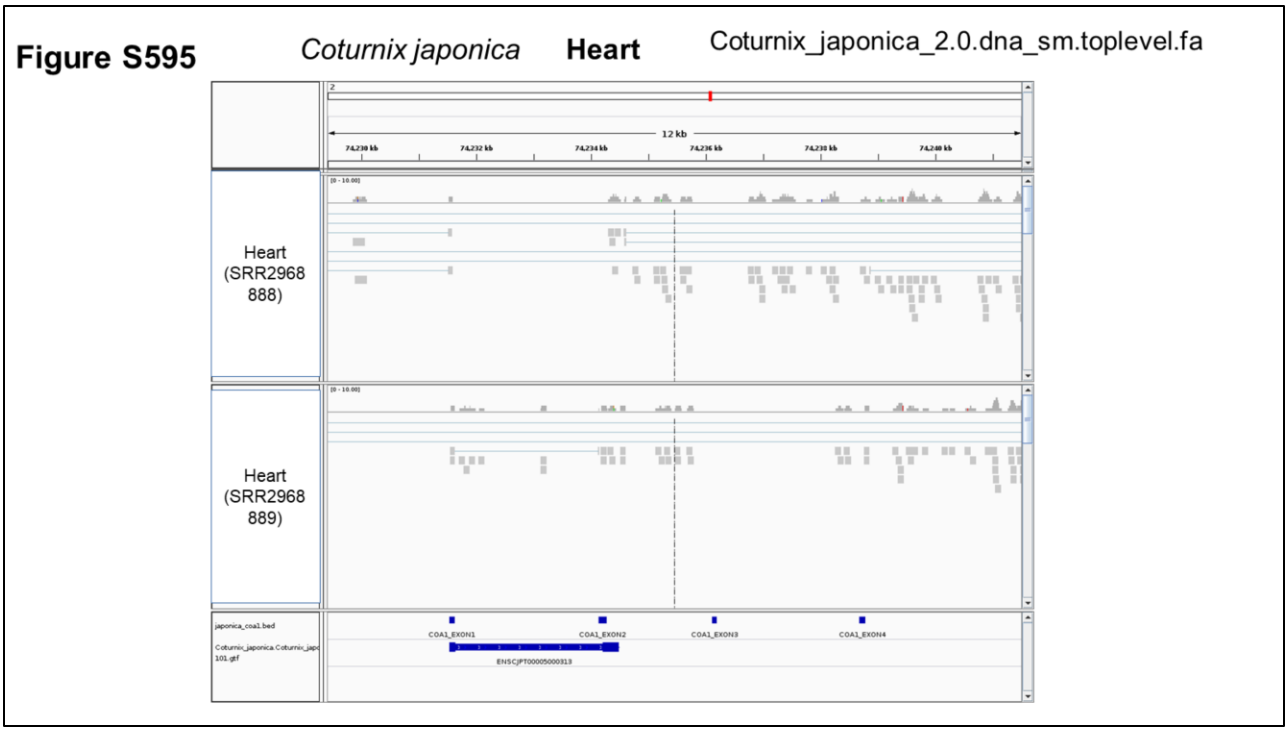

Figure S595: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Japanese quail (*Coturnix japonica*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart (SRR2968888) and (SRR2968889) have been mapped to the Coturnix_japonica_2.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.

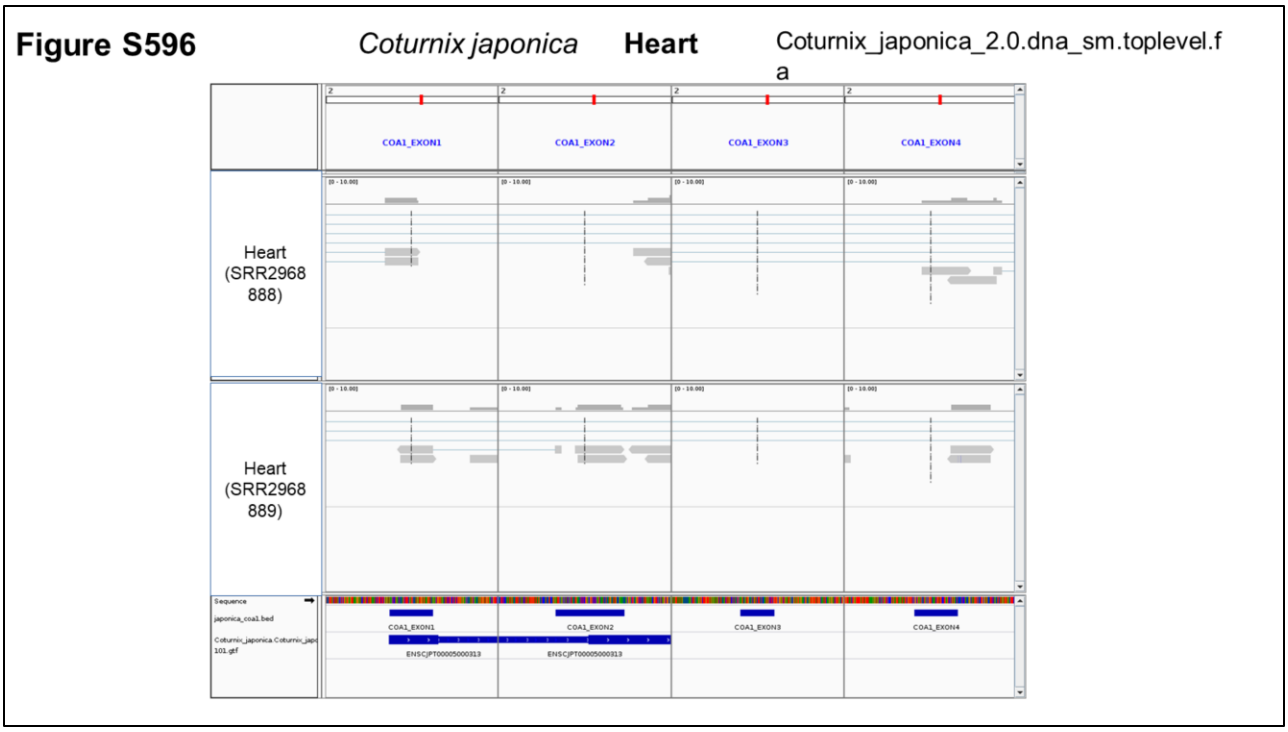

Figure S596: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S595**.

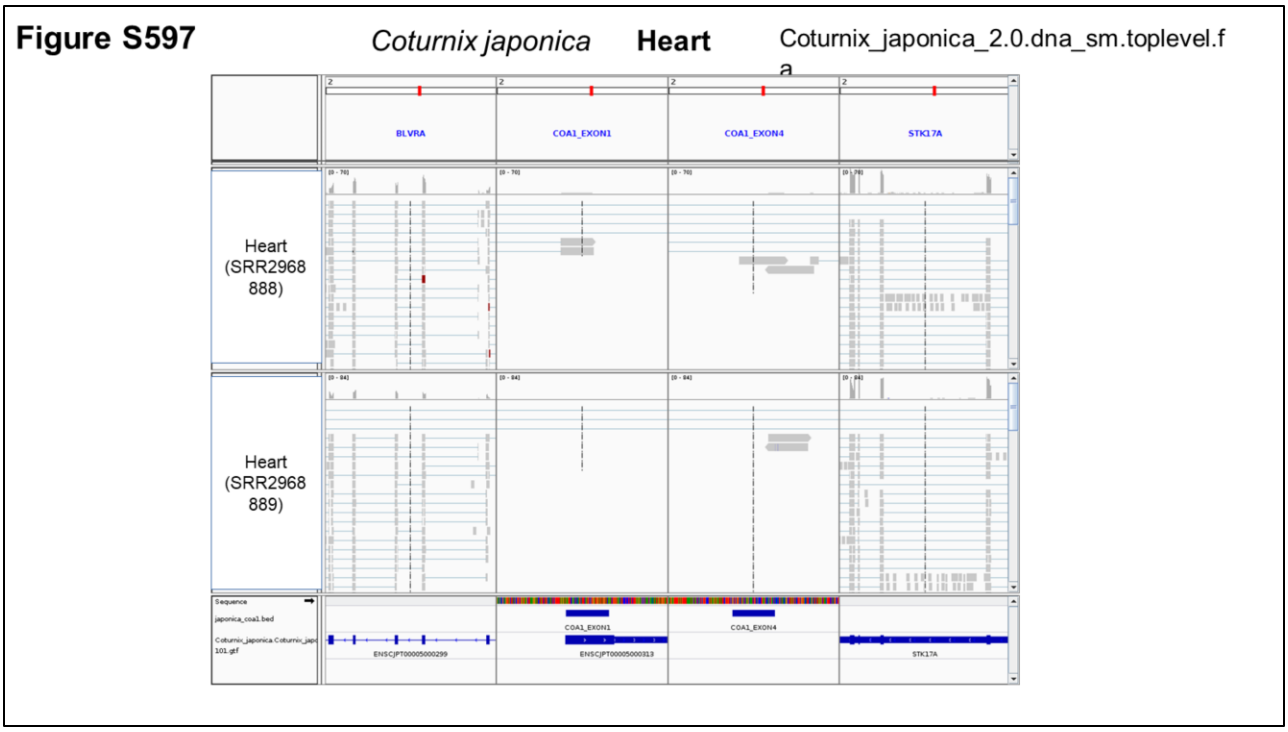

Figure S597: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in Japanese quail (*Coturnix japonica*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart (SRR2968888) and (SRR2968889) have been mapped to the Coturnix_japonica_2.0.dna_sm.toplevel.fa genome. Locations of each of the exons are depicted as bed record in the bottom row.