

Figure S798

Mus spretus Testis, Liver and Brain

Mus_spretus.SPRET_EiJ_v1.dna_sm.toplevel.fa

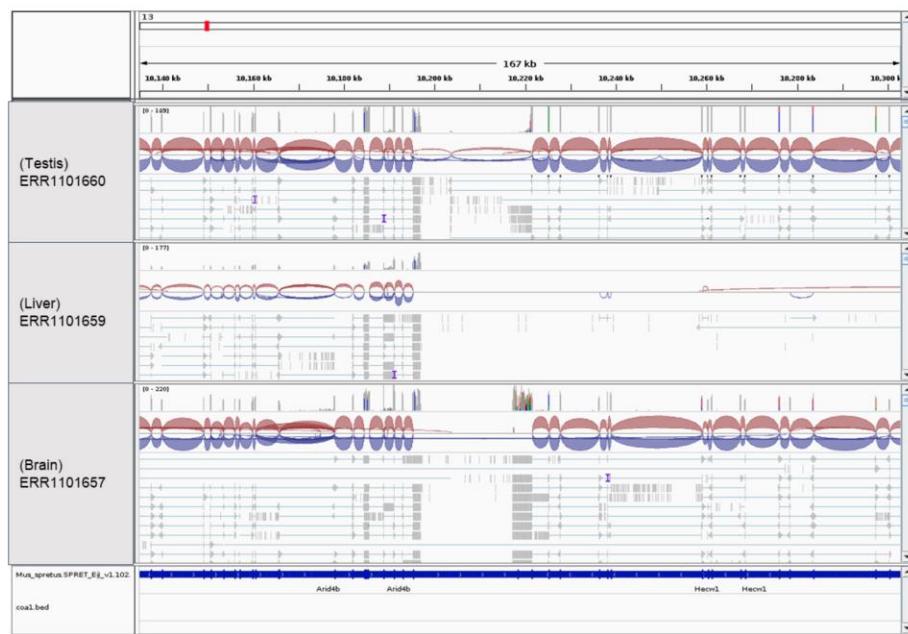


Figure S798: Screenshot of RNA-seq reads aligned each of the putative locations of *ARID4B* and *HECW1* in Algerian mouse (*Mus spretus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis (ERR1101660), liver (ERR1101659) and brain (ERR1101657) have been mapped to the *Mus_spretus.SPRET_EiJ_v1.dna_sm.toplevel.fa*. Locations of *ARID4B* and *HECW1* are depicted as *Mus_spretus.SPRET_EiJ_v1.102.gtf* record in the bottom row.

Figure S799

Mus spretus Testis, Liver and Brain

Mus_spretus.SPRET_EiJ_v1.dna_sm.toplevel.fa

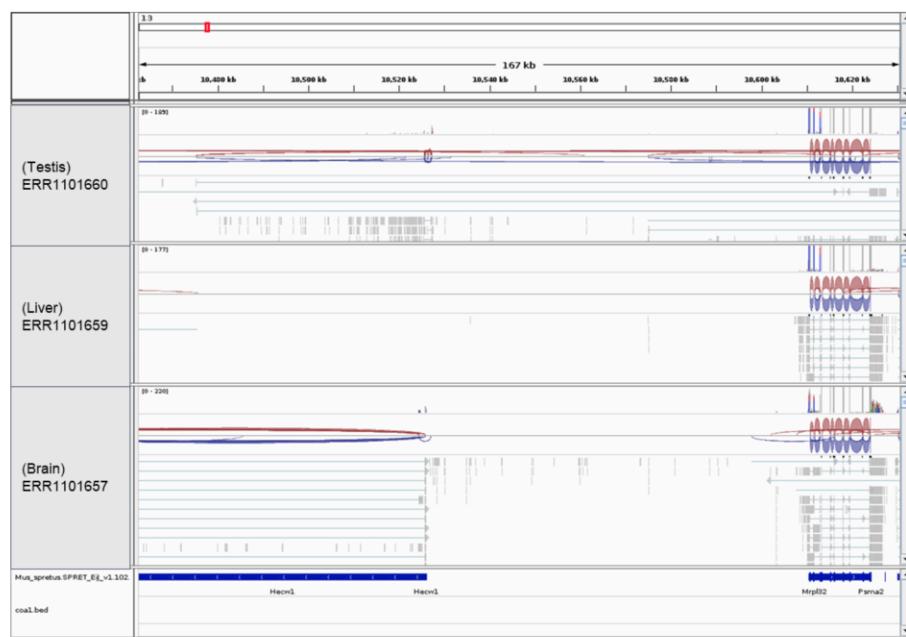


Figure S799: Screenshot of RNA-seq reads aligned each of the putative locations of *HECW1* and *MRPL32* in Algerian mouse (*Mus spretus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis (ERR1101660), liver (ERR1101659) and brain (ERR1101657) have been mapped to the *Mus_spretus.SPRET_EiJ_v1.dna_sm.toplevel.fa*. Locations of *HECW1* and *MRPL32* are depicted as *Mus_spretus.SPRET_EiJ_v1.102.gtf* record in the bottom row.

Figure S800

Mus spretus Testis, Liver and Brain

Mus_spretus.SPRET_EiJ_v1.dna_sm.toplevel.fa

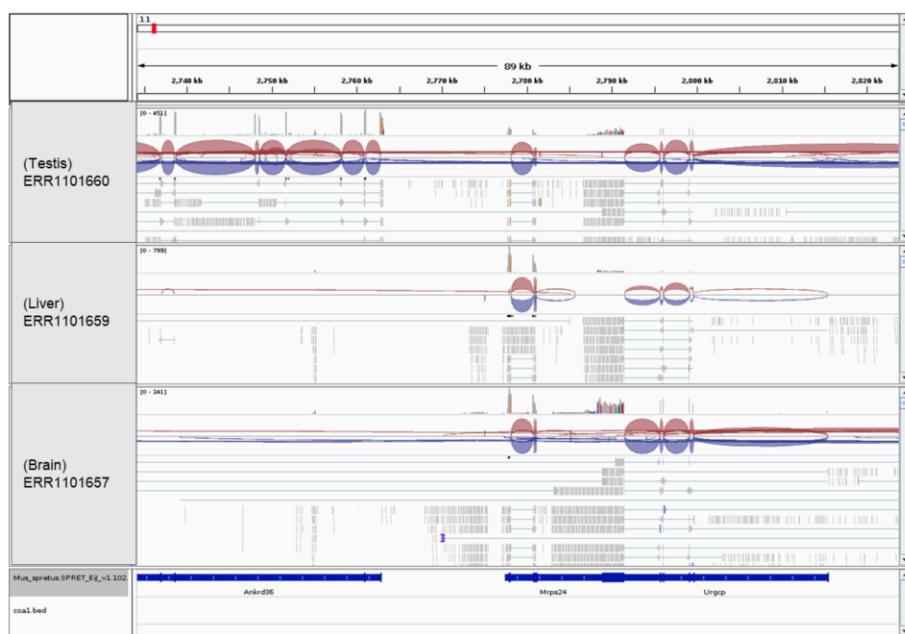


Figure S800: Screenshot of RNA-seq reads aligned each of the putative locations of *ANKRD36* and *URGCP* in Algerian mouse (*Mus spretus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis (ERR1101660), liver (ERR1101659) and brain (ERR1101657) have been mapped to the *Mus_spretus.SPRET_EiJ_v1.dna_sm.toplevel.fa*. Locations of *ANKRD36* and *URGCP* are depicted as *Mus_spretus.SPRET_EiJ_v1.102.gtf* record in the bottom row.

Figure S801

Mus spretus Testis, Liver and Brain

Mus_spretus.SPRET_EiJ_v1.dna_sm.toplevel.fa

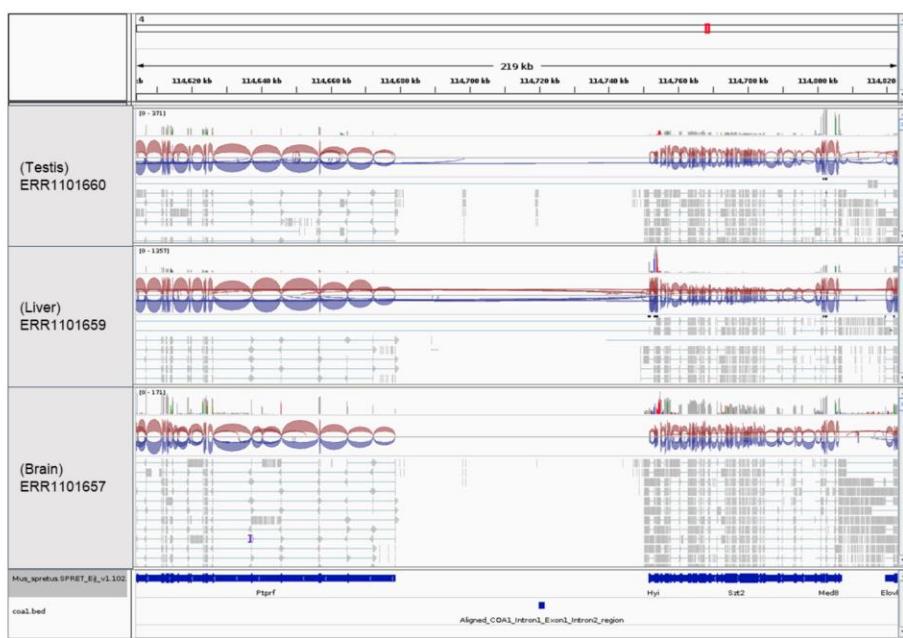


Figure S801: Screenshot of RNA-seq reads aligned each of the putative locations of truncated exon 1, intron-1 and intron-2 of *COA1* in Algerian mouse (*Mus spretus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis (ERR1101660), liver (ERR1101659) and brain (ERR1101657) have been mapped to the *Mus_spretus.SPRET_EiJ_v1.dna_sm.toplevel.fa*. Locations of truncated exon 1, intron-1 and intron-2 of *COA1* is depicted as bed record in the bottom row.

Figure S802 *Peromyscus maniculatus* Liver, Testis and Brain Peromyscus_maniculatus_bairdii.HU_Pman_2.1.dna_sm.toplevel.fa



Figure S802: Screenshot of RNA-seq reads aligned each of the putative locations of AP4E1 and NCAPH in Northern American deer mouse (*Peromyscus maniculatus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR8587280), testis (SRR8587279) and fore and mid-brain (SRR8275029) have been mapped to the Peromyscus_maniculatus_bairdii.HU_Pman_2.1.dna_sm.toplevel.fa. Locations of AP4E1 and NCAPH are depicted as Peromyscus_maniculatus_bairdii.HU_Pman_2.1.102.gtf record in the bottom row.

Figure S803 *Peromyscus maniculatus* Liver, Testis and Brain Peromyscus_maniculatus_bairdii.HU_Pman_2.1.dna_sm.toplevel.fa

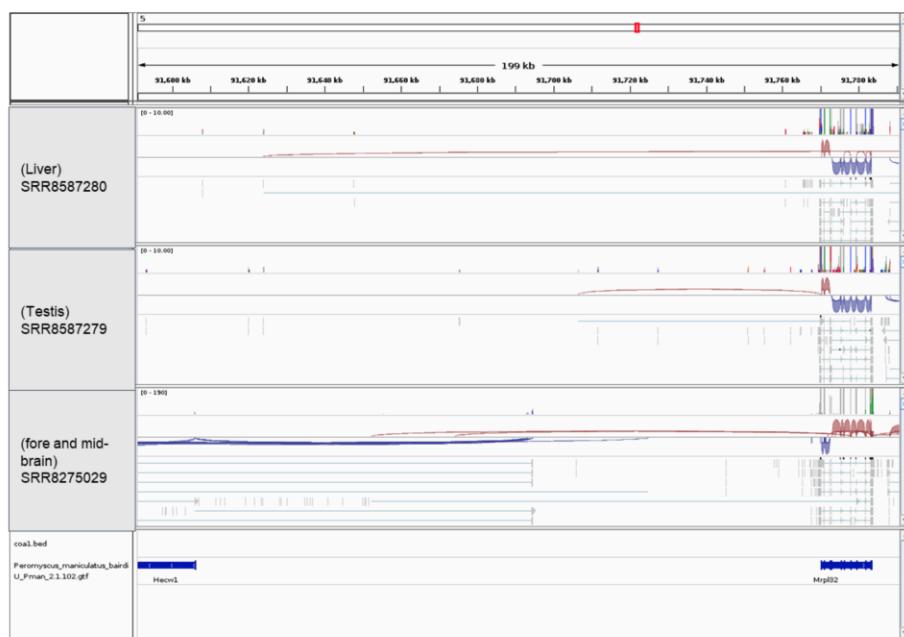


Figure S803: Screenshot of RNA-seq reads aligned each of the putative locations of HECW1 and MRPL32 in Northern American deer mouse (*Peromyscus maniculatus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis (ERR1101660), liver (ERR1101659) and brain (ERR1101657) have been mapped to the *Peromyscus_maniculatus_bairdii.HU_Pman_2.1.dna_sm.toplevel.fa*. Locations of HECW1 and MRPL32 are depicted as *Peromyscus_maniculatus_bairdii.HU_Pman_2.1.102.gtf* record in the bottom row.

Figure S804 *Peromyscus maniculatus* Liver, Testis and Brain Peromyscus_maniculatus_bairdii.HU_Pman_2.1.dna_sm.toplevel.fa

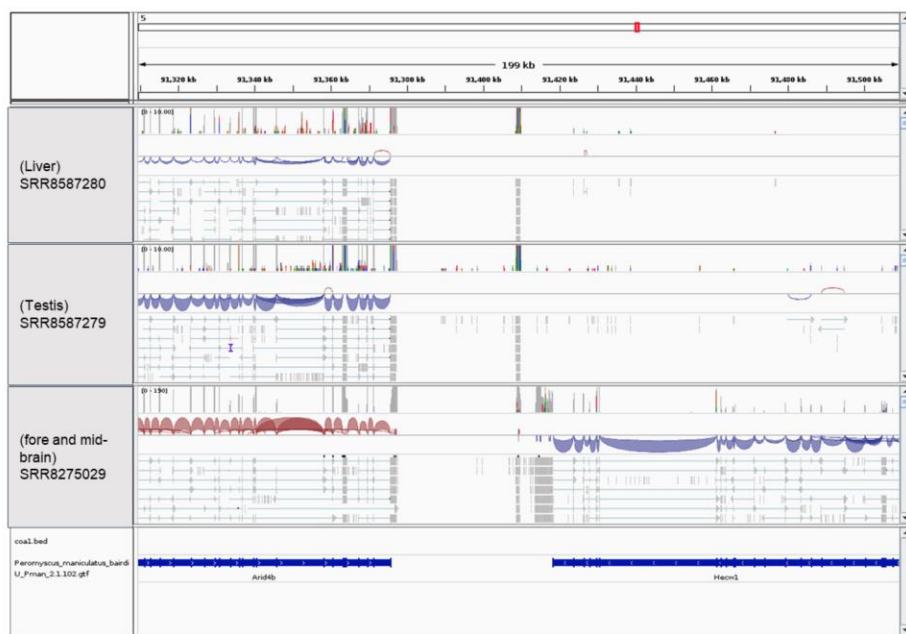


Figure S804: Screenshot of RNA-seq reads aligned each of the putative locations of ARID4B and HECW1 in Northern American deer mouse (*Peromyscus maniculatus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis (ERR1101660), liver (ERR1101659) and brain (ERR1101657) have been mapped to the *Peromyscus_maniculatus_bairdii.HU_Pman_2.1.dna_sm.toplevel.fa*. Locations of ARID4B and HECW1 are depicted as *Peromyscus_maniculatus_bairdii.HU_Pman_2.1.102.gtf* record in the bottom row.

Figure S805 *Peromyscus maniculatus* Liver, Testis and Brain Peromyscus_maniculatus_bairdii.HU_Pman_2.1.dna_sm.toplevel.fa

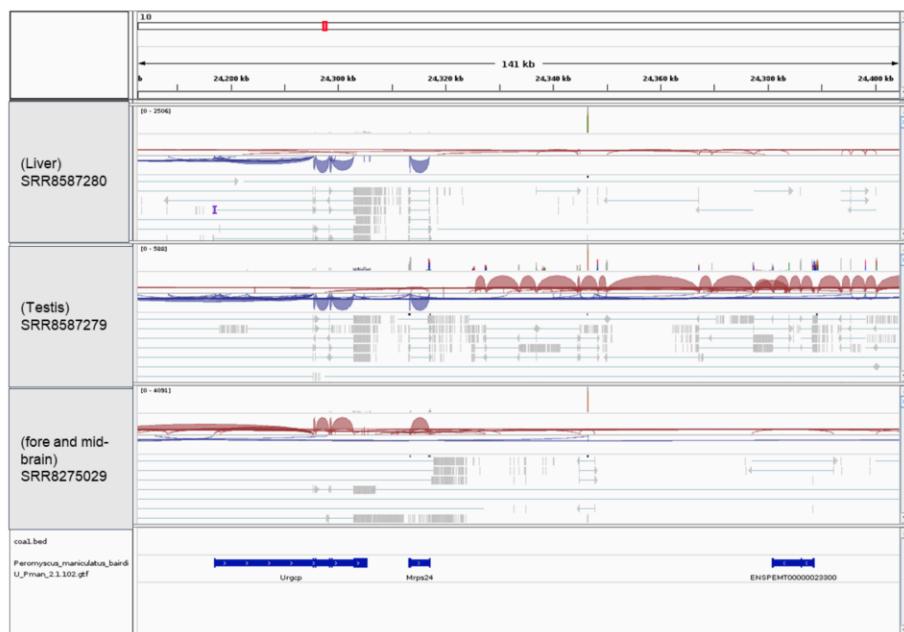


Figure S805: Screenshot of RNA-seq reads aligned each of the putative locations of URGCP and ANKRD36 in Northern American deer mouse (*Peromyscus maniculatus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis (ERR1101660), liver (ERR1101659) and brain (ERR1101657) have been mapped to the *Peromyscus_maniculatus_bairdii.HU_Pman_2.1.dna_sm.toplevel.fa*. Locations of URGCP and ANKRD36 are depicted as *Peromyscus_maniculatus_bairdii.HU_Pman_2.1.102.gtf* record in the bottom row.

Figure S806 *Peromyscus maniculatus* Liver, Testis and Brain Peromyscus_maniculatus_bairdii.HU_Pman_2.1.dna_sm.toplevel.fa

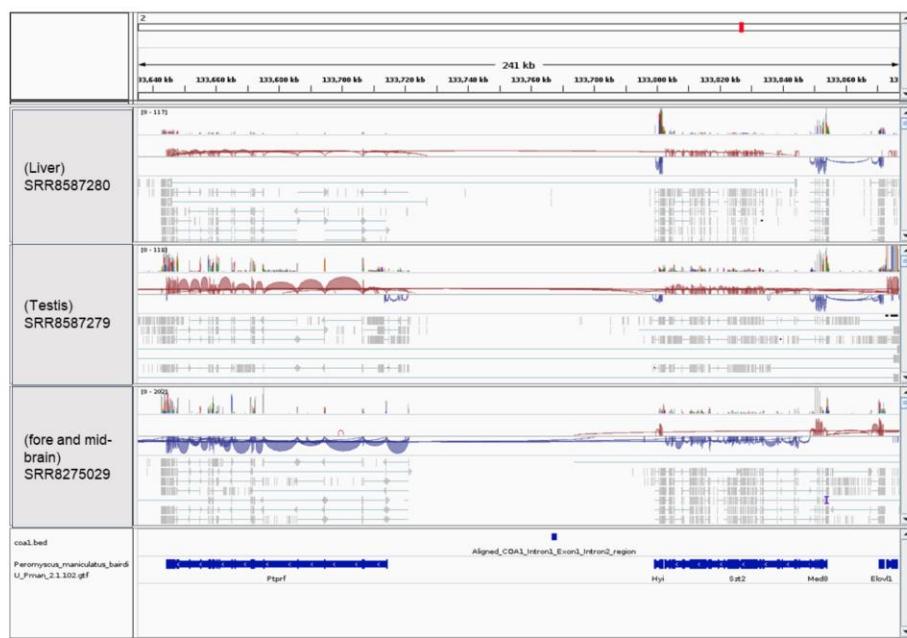


Figure S806: Screenshot of RNA-seq reads aligned each of the putative locations of truncated exon 1 and intron-1 of *COA1* gene in Northern American deer mouse (*Peromyscus maniculatus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis (ERR1101660), liver (ERR1101659) and brain (ERR1101657) have been mapped to the *Peromyscus_maniculatus_bairdii.HU_Pman_2.1.dna_sm.toplevel.fa*. Locations of truncated exon 1 and intron-1 of *COA1* gene is depicted as bed record in the bottom row.

Figure S807*Microtus ochrogaster* Brain

Microtus_ochrogaster.MicOch1.0.dna_sm.toplevel.fa

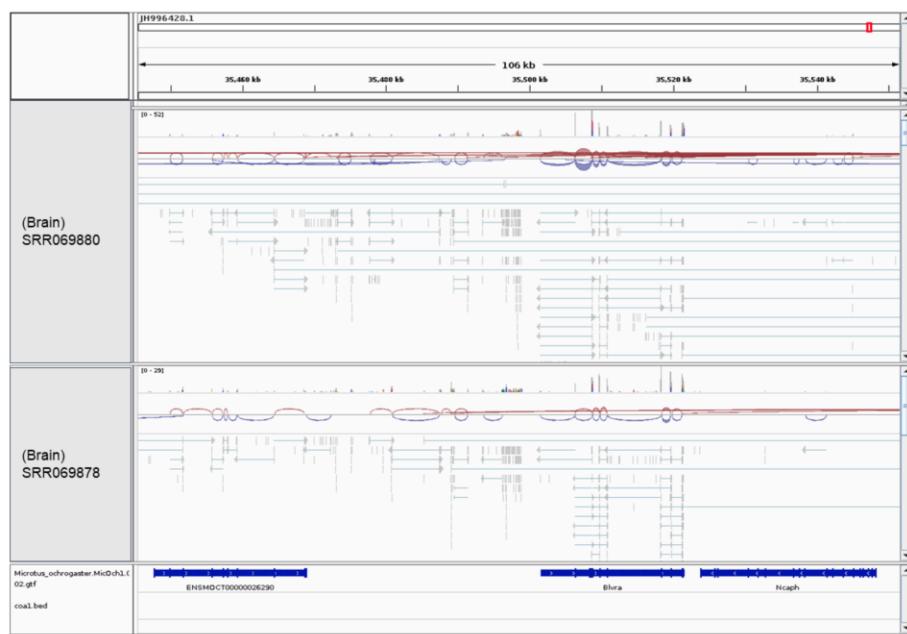


Figure S807: Screenshot of RNA-seq reads aligned each of the putative locations of *AP4E1* and *NCAPH* in Prairie vole (*Microtus ochrogaster*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (SRR069880, SRR069878) have been mapped to the *Microtus_ochrogaster.MicOch1.0.dna_sm.toplevel.fa*. Locations of *AP4E1* and *NCAPH* are depicted as *Microtus_ochrogaster.MicOch1.0.102.gtf* record in the bottom row.

Figure S808*Microtus ochrogaster* Brain

Microtus_ochrogaster.MicOch1.0.dna_sm.toplevel.fa

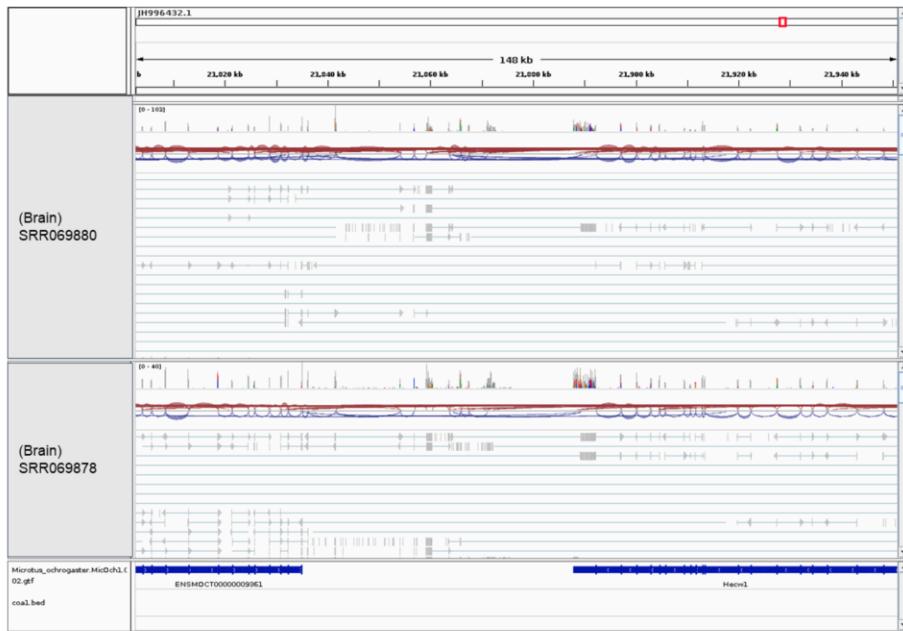


Figure S808: Screenshot of RNA-seq reads aligned each of the putative locations of *ARID4B* and *HECW1* in Prairie vole (*Microtus ochrogaster*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (SRR069880, SRR069878) have been mapped to the *Microtus_ochrogaster.MicOch1.0.dna_sm.toplevel.fa*. Locations of *ARID4B* and *HECW1* are depicted as *Microtus_ochrogaster.MicOch1.0.102.gtf* record in the bottom row.

Figure S809*Microtus ochrogaster* Brain

Microtus_ochrogaster.MicOch1.0.dna_sm.toplevel.fa

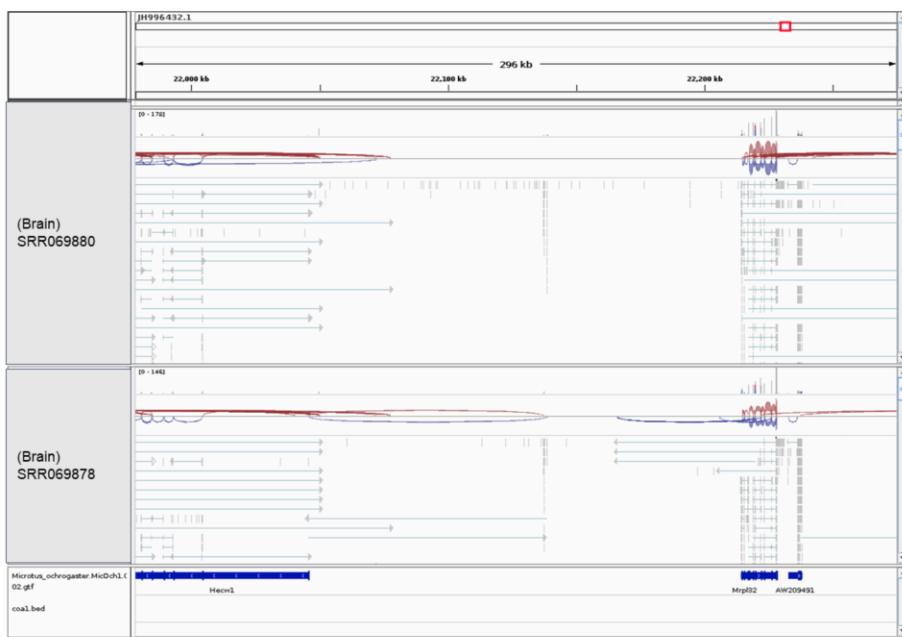


Figure S809: Screenshot of RNA-seq reads aligned each of the putative locations of *MRPL32* and *HECW1* in Prairie vole (*Microtus ochrogaster*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (SRR069880, SRR069878) have been mapped to the Microtus_ochrogaster.MicOch1.0.dna_sm.toplevel.fa. Locations of *MRPL32* and *HECW1* are depicted as Microtus_ochrogaster.MicOch1.0.102.gtf record in the bottom row.

Figure S810*Microtus ochrogaster* Brain

Microtus_ochrogaster.MicOch1.0.dna_sm.toplevel.fa

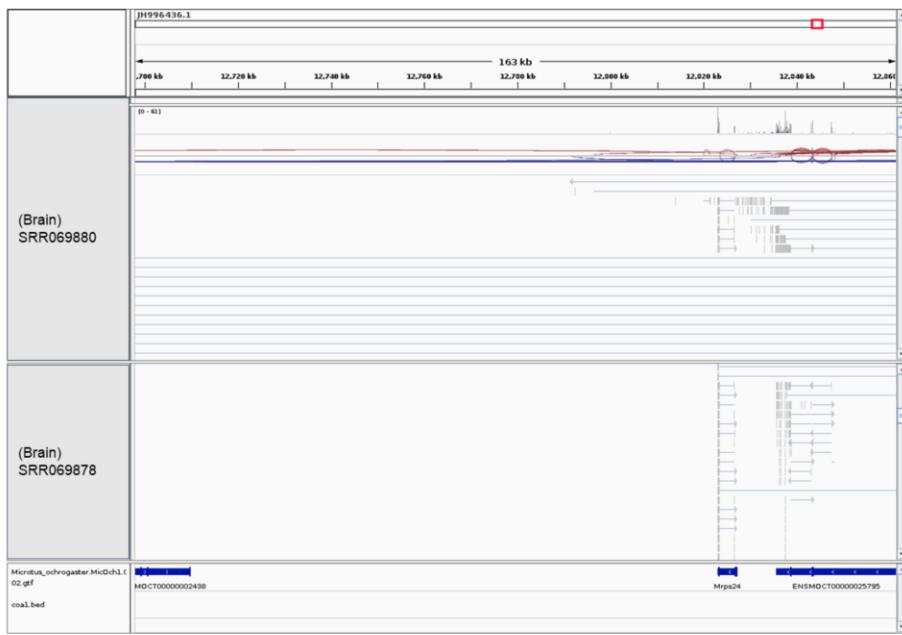


Figure S810: Screenshot of RNA-seq reads aligned each of the putative locations of *ANKRD36* and *MRPS24* in Prairie vole (*Microtus ochrogaster*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (SRR069880, SRR069878) have been mapped to the *Microtus_ochrogaster.MicOch1.0.dna_sm.toplevel.fa*. Locations of *ANKRD36* and *MRPS24* are depicted as *Microtus_ochrogaster.MicOch1.0.102.gtf* record in the bottom row.

Figure S811*Microtus ochrogaster* **Brain**

Microtus_ochrogaster.MicOch1.0.dna_sm.toplevel.fa

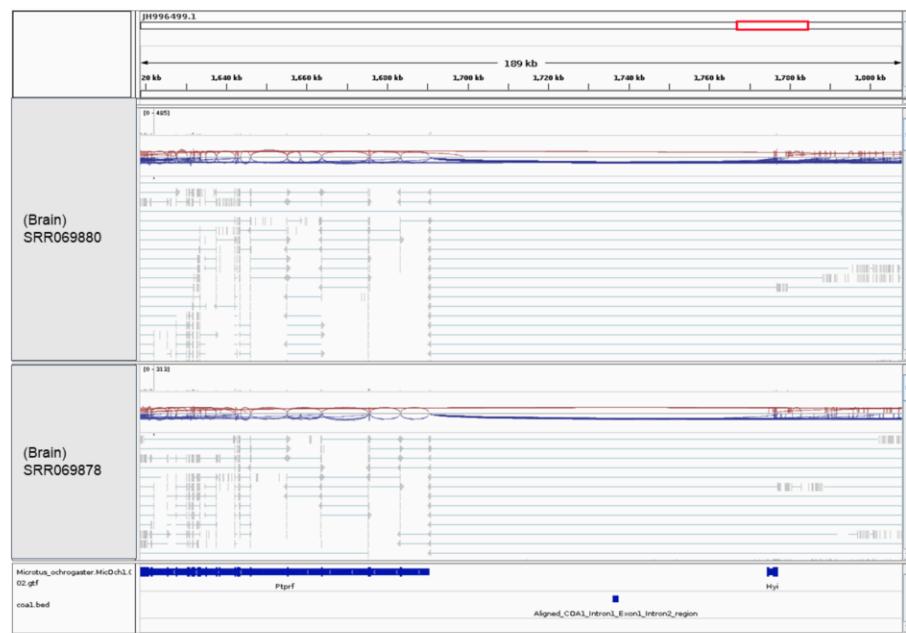


Figure S811: Screenshot of RNA-seq reads aligned each of the putative locations of truncated exon 1, intron-1 and intron-2 of *COA1* in Prairie vole (*Microtus ochrogaster*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (SRR069880, SRR069878) have been mapped to the *Microtus_ochrogaster.MicOch1.0.dna_sm.toplevel.fa*. Locations of exon 1, intron-1 and intron-2 of *COA1* is depicted as bed record in the bottom row.

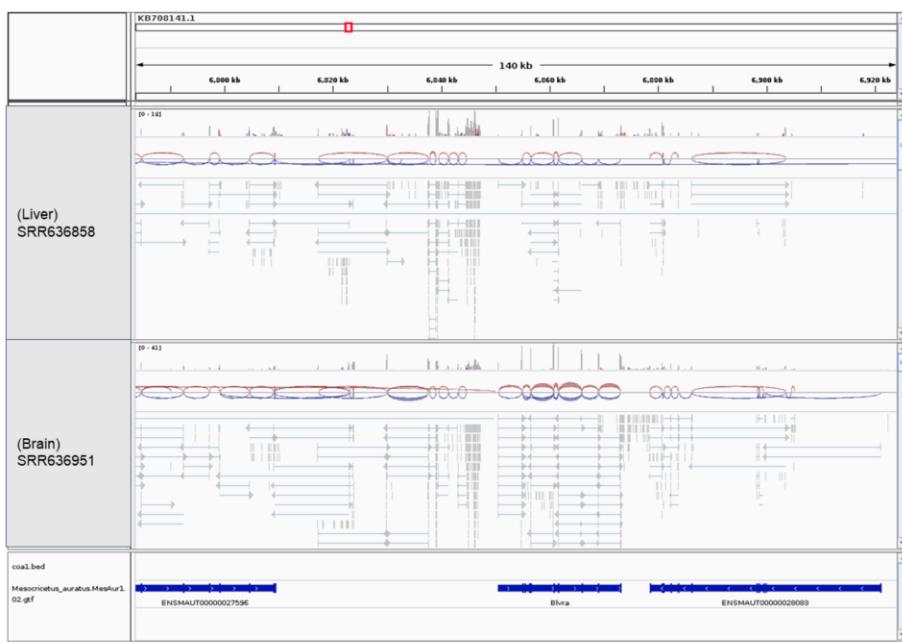
Figure S812*Mesocricetus auratus Liver and Brain* *Mesocricetus_auratus.MesAur1.0.dna_sm.toplevel.fa*

Figure S812: Screenshot of RNA-seq reads aligned each of the putative locations of *AP4E1* and *NCAPH* in golden Hamster (*Mesocricetus auratus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR636858) and brain (SRR636951) have been mapped to the *Mesocricetus_auratus.MesAur1.0.dna_sm.toplevel.fa*. Locations of *AP4E1* and *NCAPH* are depicted as *Mesocricetus_auratus.MesAur1.0.102.gtf* record in the bottom row.

Figure S813

Mesocricetus auratus Liver and Brain Mesocricetus_auratus.MesAur1.0.dna_sm.toplevel.fa

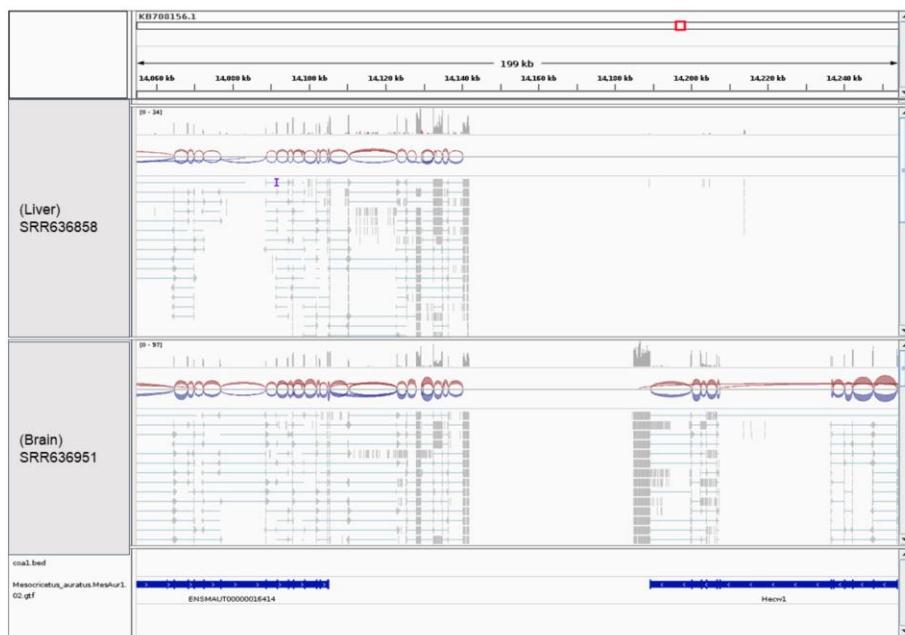


Figure S813: Screenshot of RNA-seq reads aligned each of the putative locations of *ARID4B* and *NCAPH* in golden Hamster (*Mesocricetus auratus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR636858) and brain (SRR636951) have been mapped to the *Mesocricetus_auratus.MesAur1.0.dna_sm.toplevel.fa*. Locations of *ARID4B* and *NCAPH* are depicted as *Mesocricetus_auratus.MesAur1.0.102.gtf* record in the bottom row.

Figure S814

Mesocricetus auratus Liver and Brain Mesocricetus_auratus.MesAur1.0.dna_sm.toplevel.fa

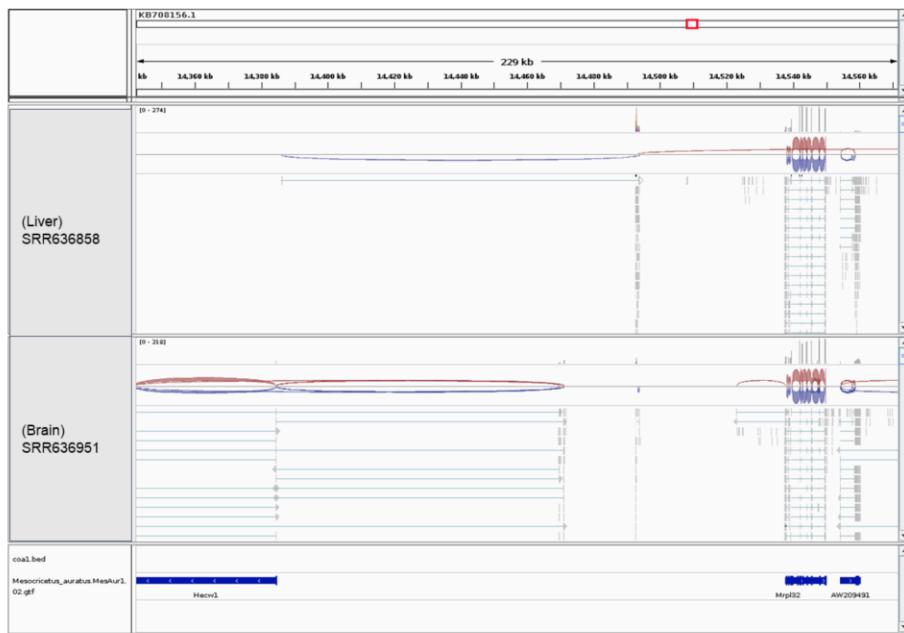


Figure S814: Screenshot of RNA-seq reads aligned each of the putative locations of *HECW1* and *MRPL32* in golden Hamster (*Mesocricetus auratus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR636858) and brain (SRR636951) have been mapped to the *Mesocricetus_auratus.MesAur1.0.dna_sm.toplevel.fa*. Locations of *HECW1* and *MRPL32* are depicted as *Mesocricetus_auratus.MesAur1.0.102.gtf* record in the bottom row.

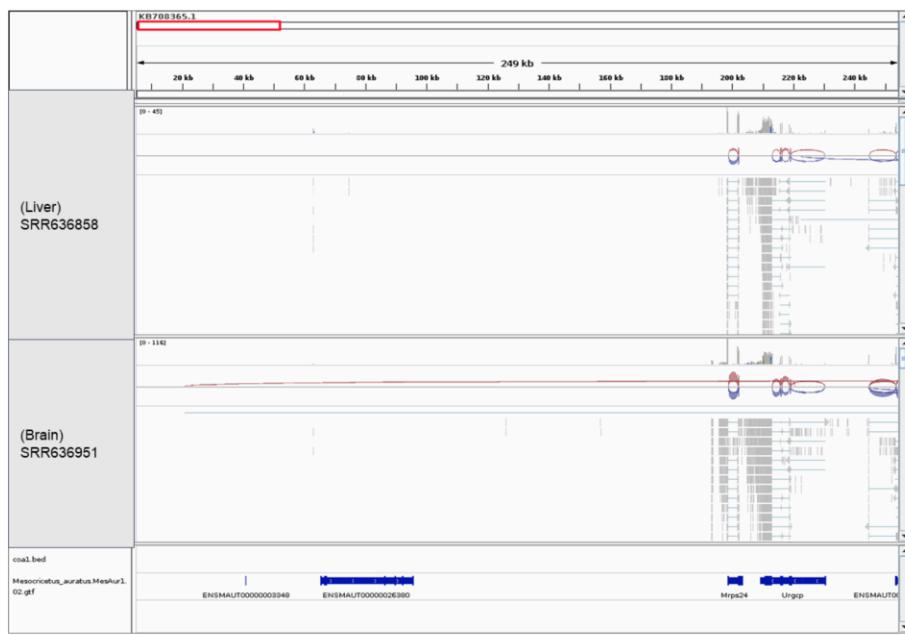
Figure S815*Mesocricetus auratus Liver and Brain Mesocricetus_auratus.MesAur1.0.dna_sm.toplevel.fa*

Figure S815: Screenshot of RNA-seq reads aligned each of the putative locations of *ANKRD36* and *MRPS24* in golden Hamster (*Mesocricetus auratus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR636858) and brain (SRR636951) have been mapped to the *Mesocricetus_auratus.MesAur1.0.dna_sm.toplevel.fa*. Locations of *ANKRD36* and *MRPS24* are depicted as *Mesocricetus_auratus.MesAur1.0.102.gtf* record in the bottom row.

Figure S816*Mesocricetus auratus Liver and Brain Mesocricetus_auratus.MesAur1.0.dna_sm.toplevel.fa*

Figure S816: Screenshot of RNA-seq reads aligned each of the putative locations of truncated exon 1, intron-1 and intron-2 of *COA1* in golden Hamster (*Mesocricetus auratus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR636858) and brain (SRR636951) have been mapped to the *Mesocricetus_auratus.MesAur1.0.dna_sm.toplevel.fa*. Locations of truncated exon 1, intron-1 and intron-2 of *COA1* is depicted as bed record in the bottom row.

Figure S817

Meriones unguiculatus Spleen and Liver Meriones_unguiculatus.MunDraft-v1.0.dna_sm.toplevel.fa

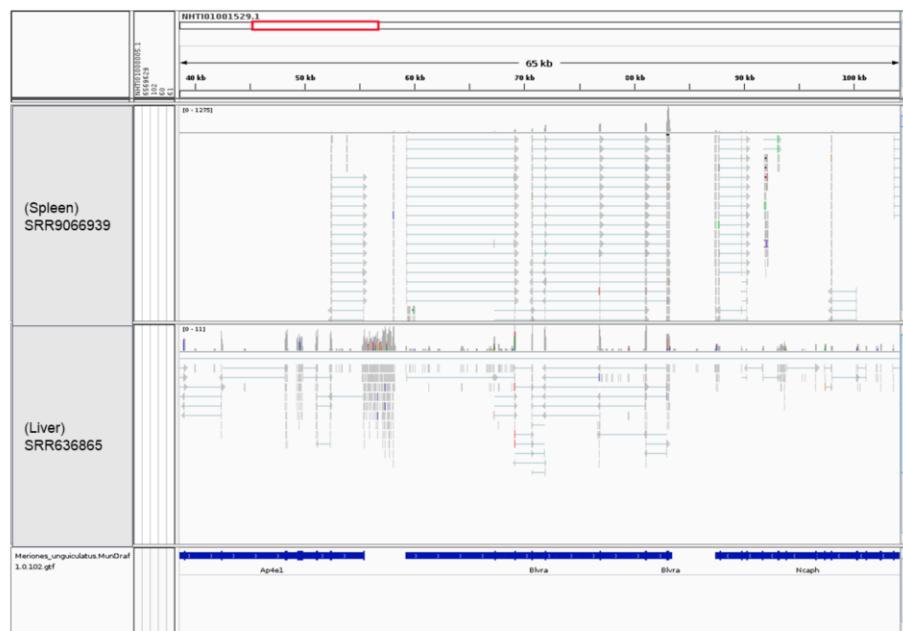


Figure S817: Screenshot of RNA-seq reads aligned each of the putative locations of *AP4E1* and *NCAPH* in Mongolian gerbil (*Meriones unguiculatus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR9066939) and liver (SRR636865) have been mapped to the *Meriones_unguiculatus.MunDraft-v1.0.dna_sm.toplevel.fa*. Locations of *AP4E1* and *NCAPH* are depicted as *Meriones_unguiculatus.MunDraft-v1.0.102.gtf* record in the bottom row.

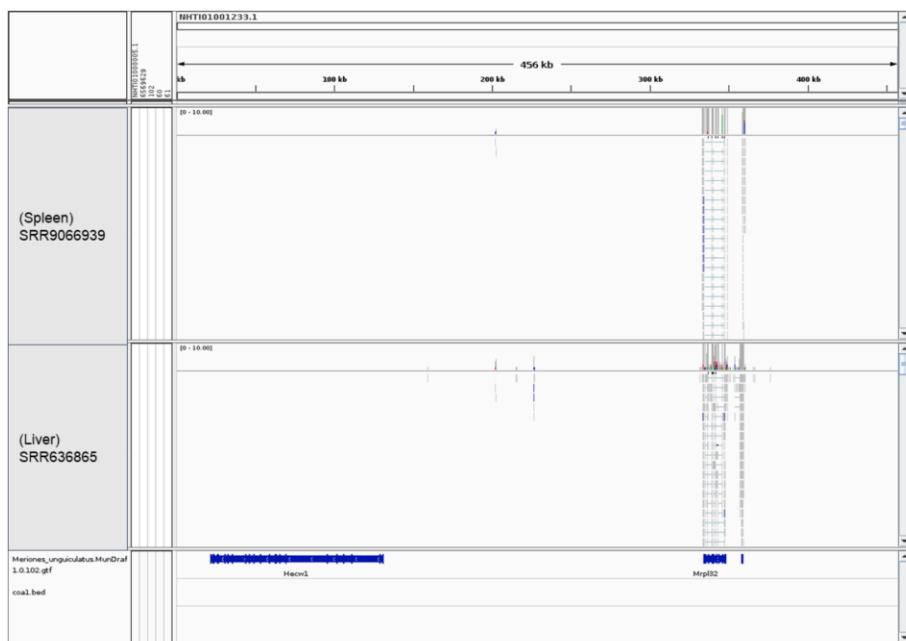
Figure S818*Meriones unguiculatus Spleen and Liver**Meriones_unguiculatus.MunDraft-v1.0.dna_sm.toplevel.fa*

Figure S818: Screenshot of RNA-seq reads aligned each of the putative locations of *HECW1* and *MRPL32* in Mongolian gerbil (*Meriones unguiculatus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR9066939) and liver (SRR636865) have been mapped to the *Meriones_unguiculatus.MunDraft-v1.0.dna_sm.toplevel.fa*. Locations of *HECW1* and *MRPL32* are depicted as *Meriones_unguiculatus.MunDraft-v1.0.102.gtf* record in the bottom row.

Figure S819

Meriones unguiculatus Spleen and LiverMeriones_unguiculatus.MunDraft-v1.0.dna_sm.toplevel.fa

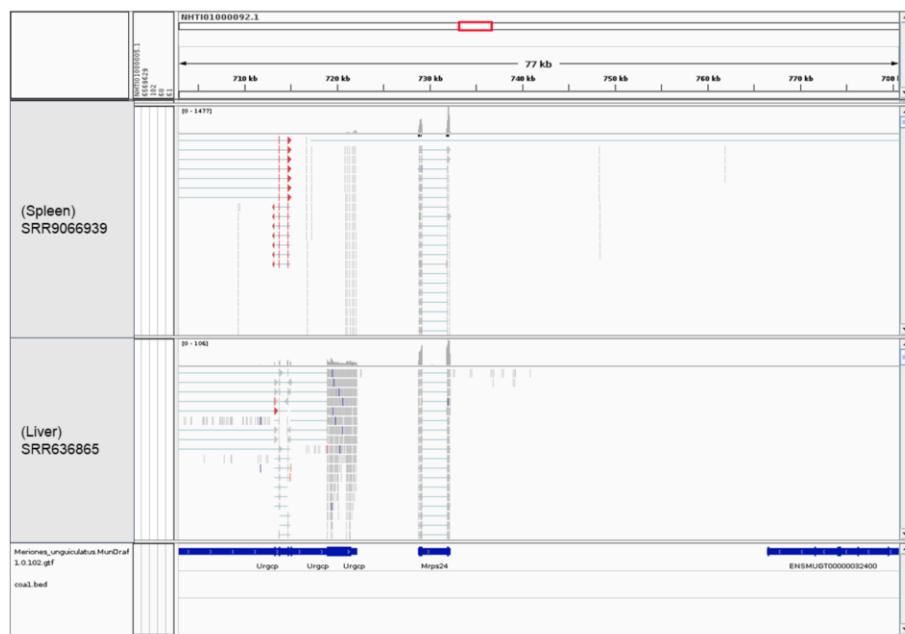


Figure S819: Screenshot of RNA-seq reads aligned each of the putative locations of *ANKRD36* and *MRPL32* in Mongolian gerbil (*Meriones unguiculatus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR9066939) and liver (SRR636865) have been mapped to the *Meriones_unguiculatus.MunDraft-v1.0.dna_sm.toplevel.fa*. Locations of *ANKRD36* and *MRPL32* are depicted as *Meriones_unguiculatus.MunDraft-v1.0.102.gtf* record in the bottom row.

Figure S820

Meriones unguiculatus Spleen and Liver Meriones_unguiculatus.MunDraft-v1.0.dna_sm.toplevel.fa



Figure S820: Screenshot of RNA-seq reads aligned each of the putative locations of truncated exon 1, intron-1 and intron-2 of *COA1* in Mongolian gerbil (*Meriones unguiculatus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR9066939) and liver (SRR636865) have been mapped to the *Meriones_unguiculatus.MunDraft-v1.0.dna_sm.toplevel.fa*. Locations of truncated exon 1, intron-1 and intron-2 of *COA1* depicted as bed record in the bottom row.

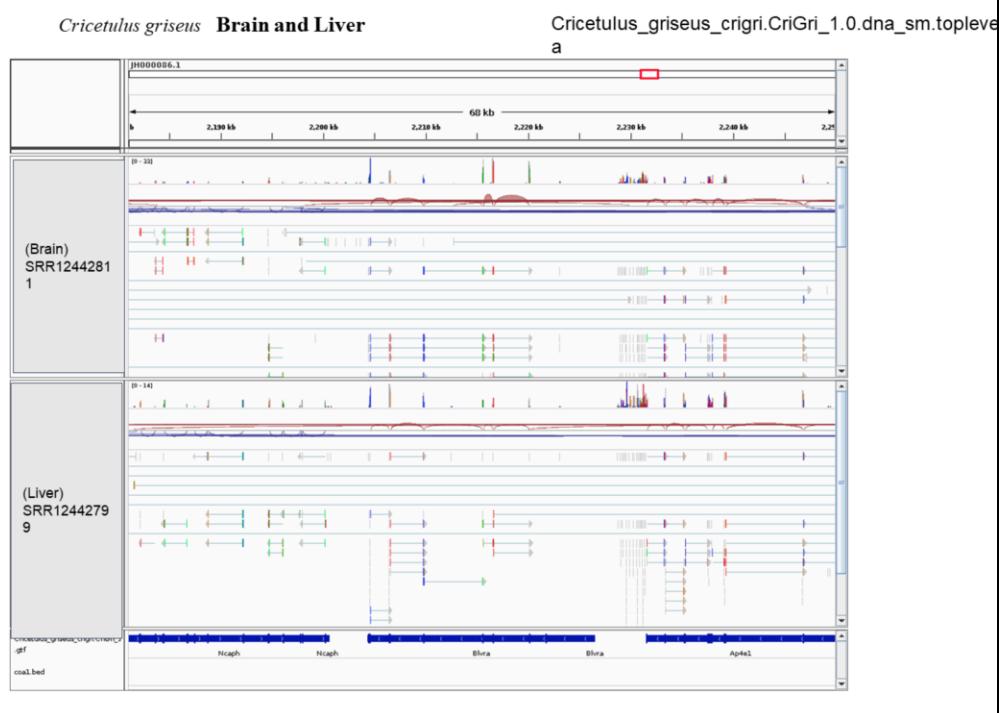
Figure S821

Figure S821: Screenshot of RNA-seq reads aligned each of the putative locations of *NCAPH*, *BLVRA* and *AP4E1* in Chinese hamster (*Cricetulus griseus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (SRR1244281) and liver (SRR12442799) have been mapped to the *Cricetulus_griseus_crigeri.CriGri_1.0.dna_sm.toplevel.fa*. Locations of *AP4E1* and *NCAPH* are depicted as *Cricetulus_griseus_crigeri.CriGri_1.0.102.gtf* record in the bottom row.

Figure S822*Cricetulus griseus Brain and Liver*

Cricetulus_griseus_crigri.CriGri_1.0.dna_sm.toplevel.fa



Figure S822: Screenshot of RNA-seq reads aligned each of the putative locations of *HECW1* and *ARID4B* in Chinese hamster (*Cricetulus griseus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (SRR12442811) and liver (SRR12442799) have been mapped to the *Cricetulus_griseus_crigri.CriGri_1.0.dna_sm.toplevel.fa*. Locations of *AP4E1* and *NCAPH* are depicted as *Cricetulus_griseus_crigri.CriGri_1.0.102.gtf* record in the bottom row.

Figure S823

Cricetulus griseus Brain and Liver

Cricetulus_griseus_crigri.CriGri_1.0.dna_sm.toplevel.fa

a

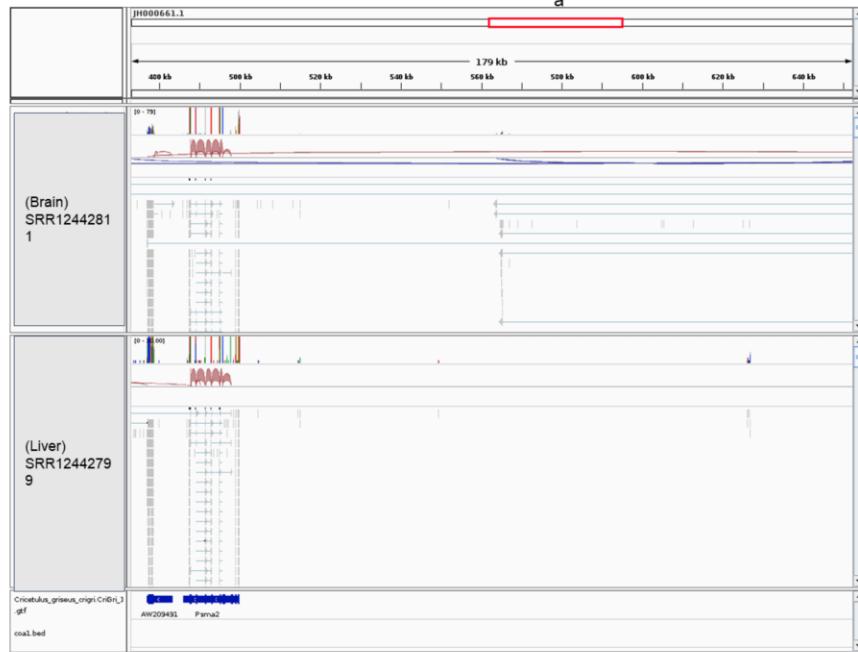


Figure S823: Screenshot of RNA-seq reads aligned each of the putative locations of *HECW1* and *PSMA2* in Chinese hamster (*Cricetulus griseus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (SRR12442811) and liver (SRR12442799) have been mapped to the *Cricetulus_griseus_crigri.CriGri_1.0.dna_sm.toplevel.fa*. Locations of *AP4E1* and *NCAPH* are depicted as *Cricetulus_griseus_crigri.CriGri_1.0.102.gtf* record in the bottom row.

Figure S824*Cricetulus griseus Brain and Liver*

Cricetulus_griseus_crigri.CriGri_1.0.dna_sm.toplevel.fa

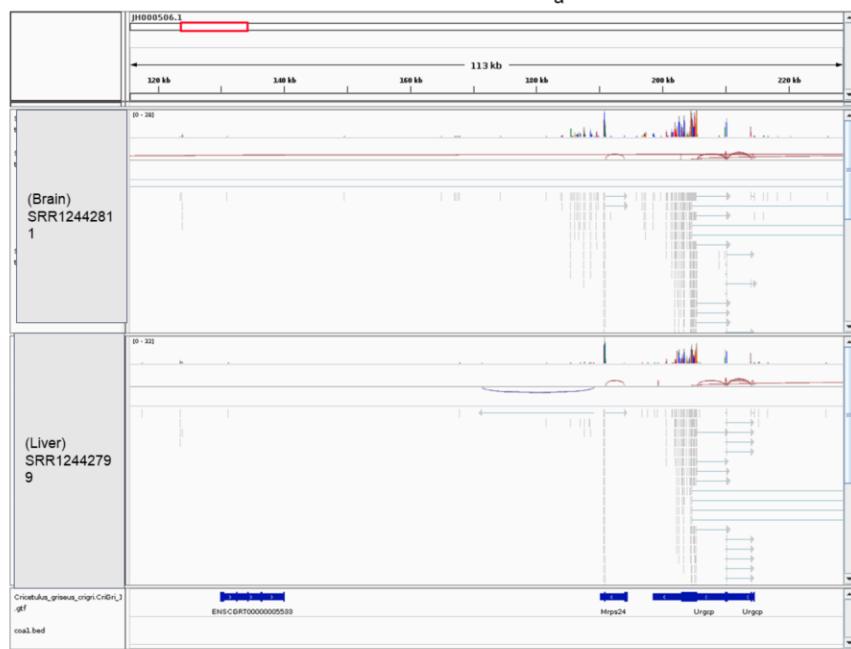


Figure S824: Screenshot of RNA-seq reads aligned each of the putative locations of *MRPS24* and *URGCP* in Chinese hamster (*Cricetulus griseus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (SRR12442811) and liver (SRR12442799) have been mapped to the *Cricetulus_griseus_crigri.CriGri_1.0.dna_sm.toplevel.fa*. Locations of *AP4E1* and *NCAPH* are depicted as *Cricetulus_griseus_crigri.CriGri_1.0.102.gtf* record in the bottom row.

Figure S825

Cricetulus griseus Brain and Liver Cricetulus_griseus_criger.CriGri_1.0.dna_sm.toplevel.fa

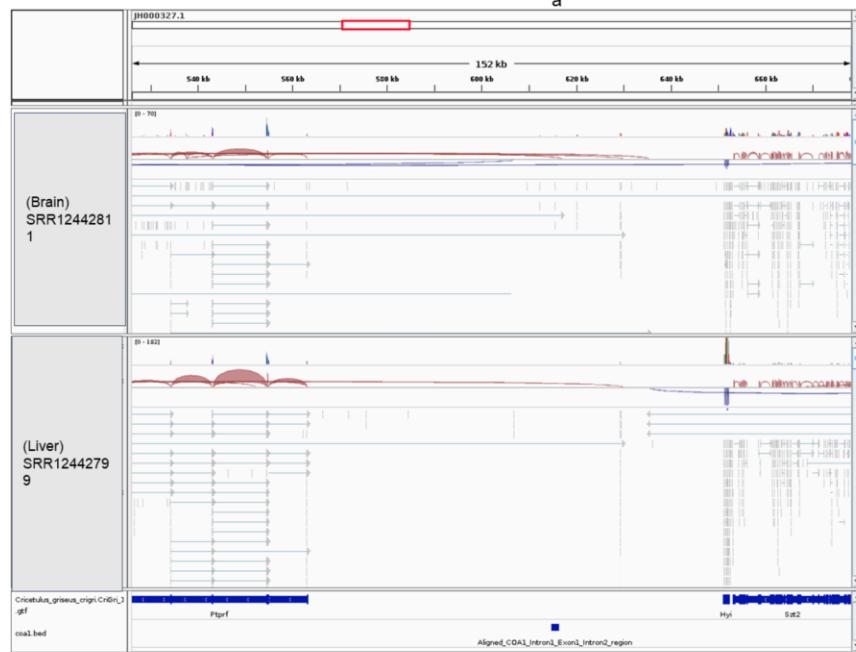


Figure S825: Screenshot of RNA-seq reads aligned each of the putative locations of truncated exon 1, intron-1 and intron-2 of *COA1* between *PTPRF* and *HYI* in Chinese hamster (*Cricetulus griseus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (SRR12442811) and liver (SRR12442799) have been mapped to the *Cricetulus_griseus_criger.CriGri_1.0.dna_sm.toplevel.fa*. Locations of *AP4E1* and *NCAPH* are depicted as *Cricetulus_griseus_criger.CriGri_1.0.102.gtf* record in the bottom row.

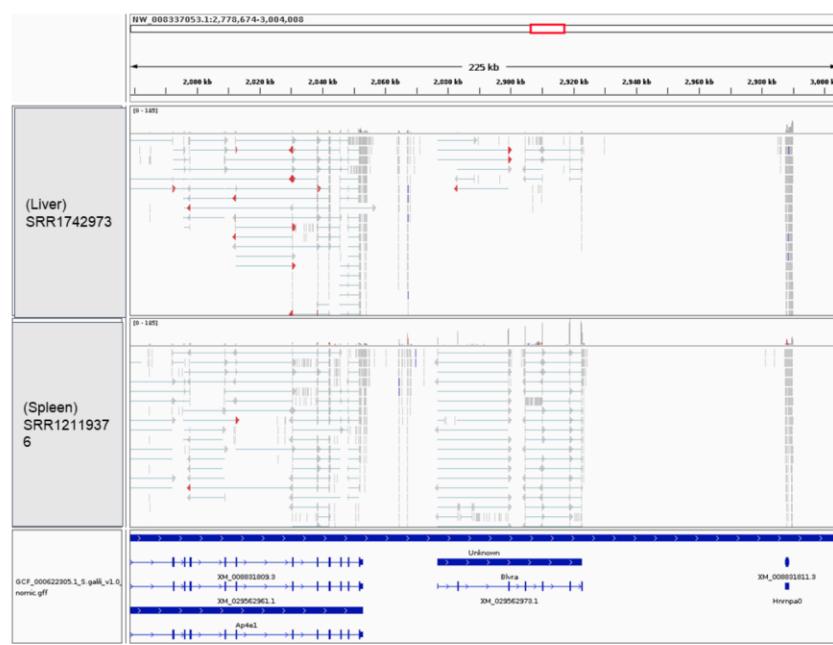
Figure S826*Nannospalax galili Liver and Spleen GCF_000622305.1_S.galili_v1.0_genomic.fna*

Figure S826: Screenshot of RNA-seq reads aligned each of the putative locations of *AP4E1* and *NCAPH* in Upper Galilee mountains blind mole-rat (*Nannospalax galili*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR1742973) and spleen (SRR12119376) have been mapped to the GCF_000622305.1_S.galili_v1.0_genomic.fna. Locations of *AP4E1* and *NCAPH* are depicted as Mesocricetus_auratus.MesAur1.0.102.gtf record in the bottom row.

Figure S827*Nannospalax galili Liver and Spleen*

GCF_000622305.1_S.galili_v1.0_genomic.fna

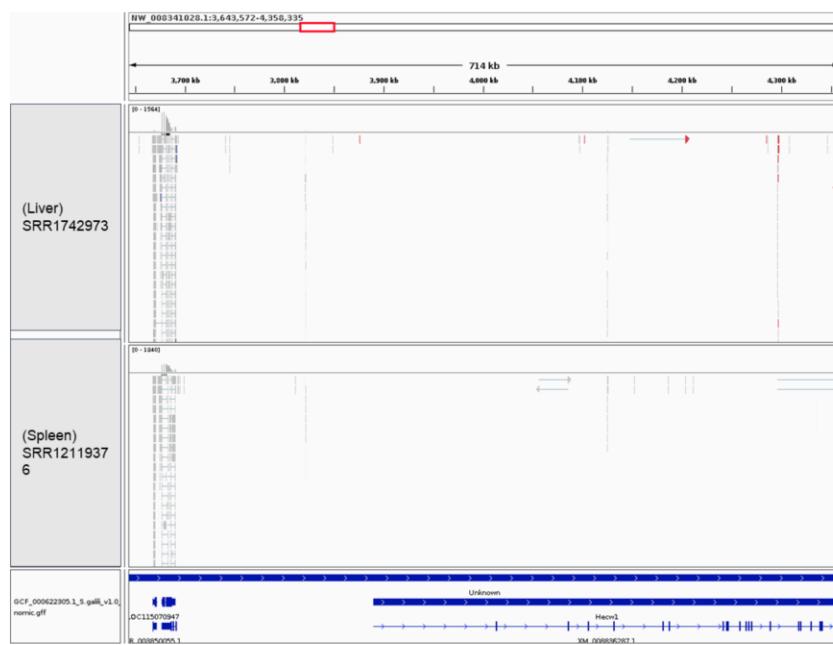


Figure S827: Screenshot of RNA-seq reads aligned each of the putative locations of *HECW1* and *ARID4B* in Upper Galilee mountains blind mole-rat (*Nannospalax galili*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR1742973) and spleen (SRR12119376) have been mapped to the GCF_000622305.1_S.galili_v1.0_genomic.fna. Locations of *HECW1* and *ARID4B* are depicted as *Mesocricetus_auratus.MesAur1.0.102.gtf* record in the bottom row.

Figure S828*Nannospalax galili Liver and Spleen*

GCF_000622305.1_S.galili_v1.0_genomic.fna

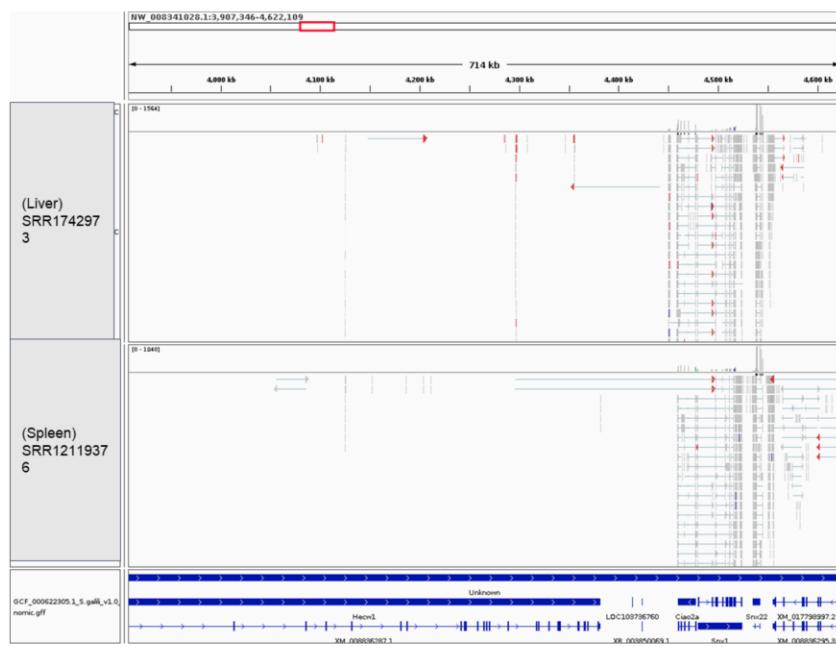


Figure S828: Screenshot of RNA-seq reads aligned each of the putative locations of *HECW1* and *MRPL32* in Upper Galilee mountains blind mole-rat (*Nannospalax galili*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR1742973) and spleen (SRR12119376) have been mapped to the GCF_000622305.1_S.galili_v1.0_genomic.fna. Locations of *HECW1* and *MRPL32* are depicted as Mesocricetus_auratus.MesAur1.0.102.gtf record in the bottom row.

Figure S829*Nannospalax galili Liver and Spleen*

GCF_000622305.1_S.galili_v1.0_genomic.fna

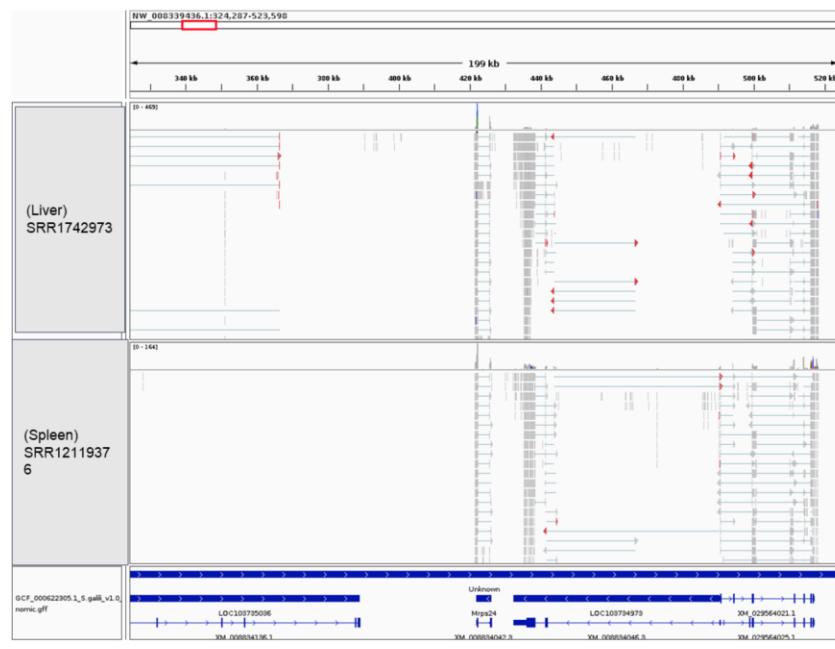


Figure S829: Screenshot of RNA-seq reads aligned each of the putative locations of *ANKRD36* and *MRPS24* in Upper Galilee mountains blind mole-rat (*Nannospalax galili*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR1742973) and spleen (SRR12119376) have been mapped to the GCF_000622305.1_S.galili_v1.0_genomic.fna. Locations of *ANKRD36* and *MRPS24* are depicted as Mesocricetus_auratus.MesAur1.0.102.gtf record in the bottom row.

Figure S830*Nannospalax galili Liver and Spleen*

GCF_000622305.1_S.galili_v1.0_genomic.fna



Figure S830: Screenshot of RNA-seq reads aligned each of the putative locations of *Ptprf* and *HYI* in Upper Galilee mountains blind mole-rat (*Nannospalax galili*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR1742973) and spleen (SRR12119376) have been mapped to the GCF_000622305.1_S.galili_v1.0_genomic.fna. Locations of *Ptprf* and *HYI* are depicted as Mesocricetus_auratus.MesAur1.0.102.gtf record in the bottom row.

Figure S831*Peromyscus leucopus Heart, Testis and Liver*

GCA_002215935.2_ASM221593v2_genomic.fna

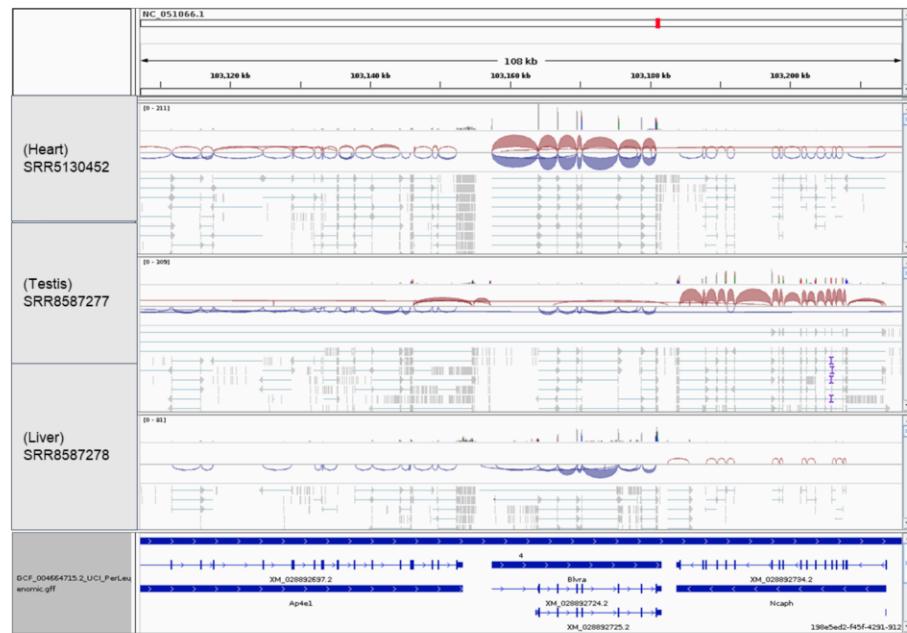


Figure S831: Screenshot of RNA-seq reads aligned each of the putative locations of *AP4E1* and *NCAPH* in White-footed mouse (*Peromyscus leucopus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart (SRR5130452), testis (SRR8587277) and liver (SRR8587278) have been mapped to the GCA_002215935.2_ASM221593v2_genomic.fna. Locations of *AP4E1* and *NCAPH* are depicted as GCF_004664715.2_UCI_PerLeu_2.1_genomic.gff record in the bottom row.

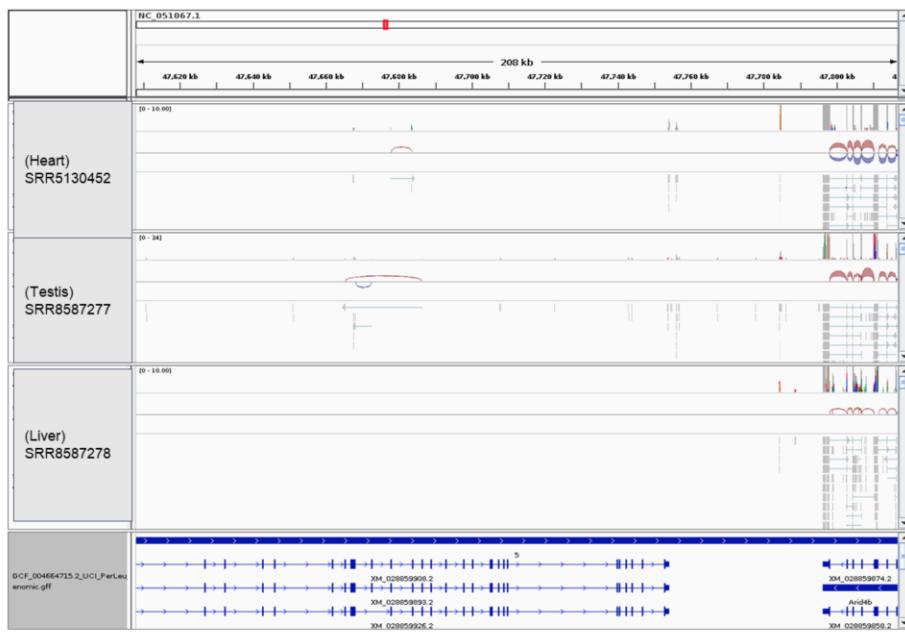
Figure S832*Peromyscus leucopus* Heart, Testis and Liver GCA_002215935.2_ASM221593v2_genomic.fna

Figure S832: Screenshot of RNA-seq reads aligned each of the putative locations of *HECW1* and *ARID4B* in White-footed mouse (*Peromyscus leucopus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart (SRR5130452), testis (SRR8587277) and liver (SRR8587278) have been mapped to the GCA_002215935.2_ASM221593v2_genomic.fna. Locations of *HECW1* and *ARID4B* are depicted as GCF_004664715.2_UCI_PerLeu_2.1_genomic.gff record in the bottom row.

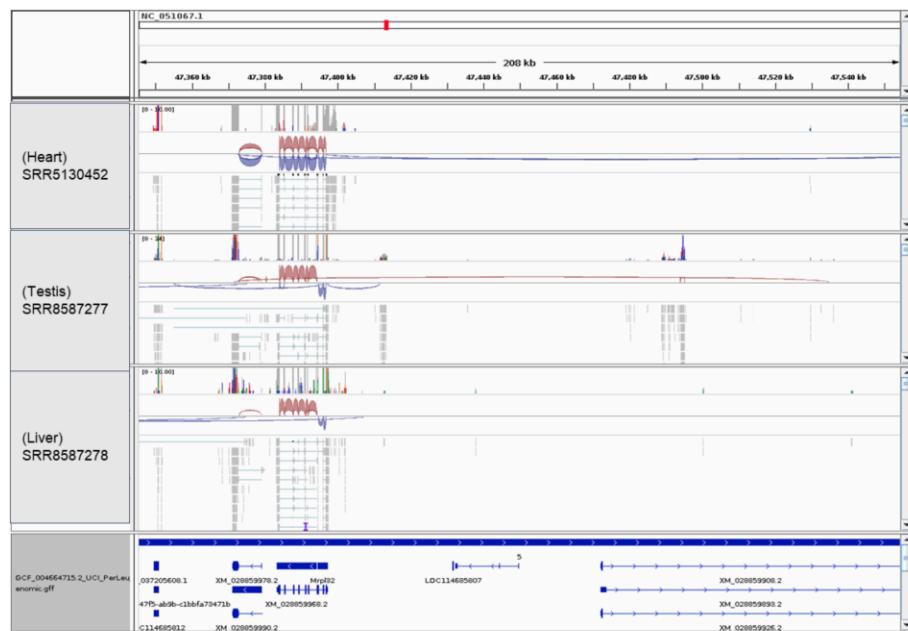
Figure S833*Peromyscus leucopus* Heart, Testis and Liver GCA_002215935.2_ASM221593v2_genomic.fna

Figure S833: Screenshot of RNA-seq reads aligned each of the putative locations of *HECW1* and *MRPL32* in White-footed mouse (*Peromyscus leucopus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart (SRR5130452), testis (SRR8587277) and liver (SRR8587278) have been mapped to the GCA_002215935.2_ASM221593v2_genomic.fna. Locations of *HECW1* and *MRPL32* are depicted as GCF_004664715.2_UCI_PerLeu_2.1_genomic.gff record in the bottom row.

Figure S834*Peromyscus leucopus* Heart, Testis and Liver

GCA_002215935.2_ASM221593v2_genomic.fna

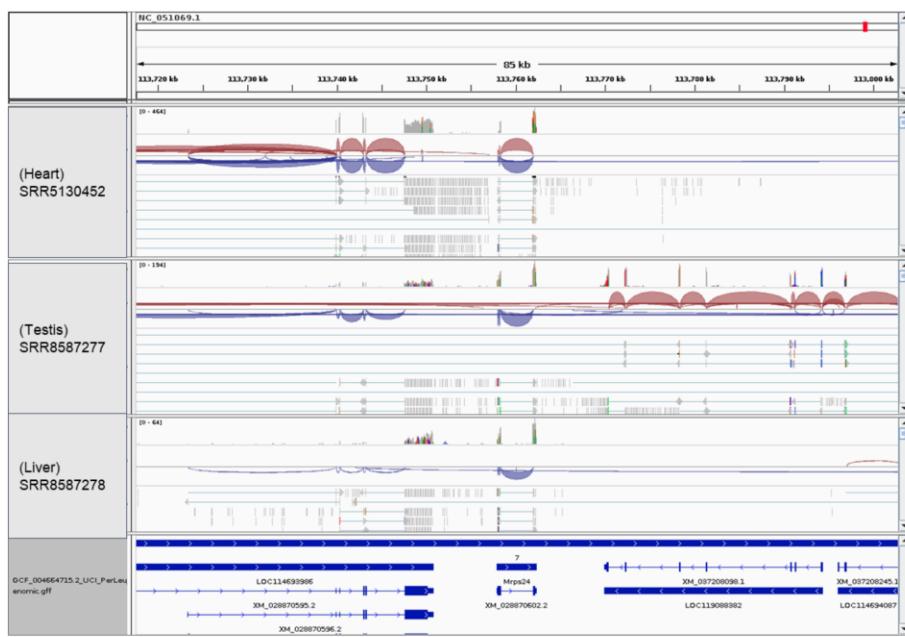


Figure S834: Screenshot of RNA-seq reads aligned each of the putative locations of *ANKRD36* and *MRPS24* in White-footed mouse (*Peromyscus leucopus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart (SRR5130452), testis (SRR8587277) and liver (SRR8587278) have been mapped to the GCA_002215935.2_ASM221593v2_genomic.fna. Locations of *ANKRD36* and *MRPS24* are depicted as GCF_004664715.2_UCI_PerLeu_2.1_genomic.gff record in the bottom row.

Figure S835 *Peromyscus leucopus* Heart, Testis and Liver

GCA_002215935.2_ASM221593v2_genomic.fna

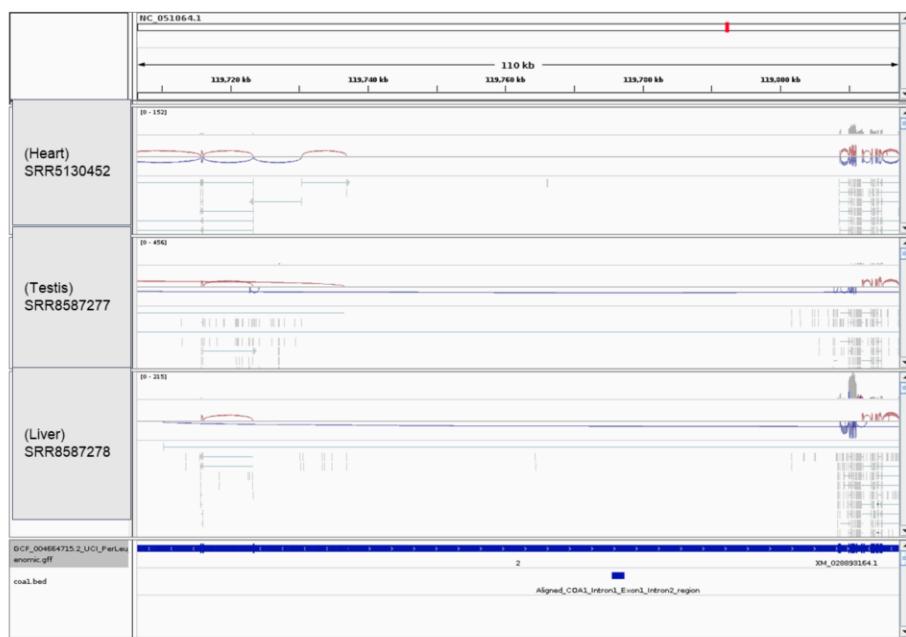


Figure S835: Screenshot of RNA-seq reads aligned each of the putative locations of truncated exon 1, intron-1 and intron-2 of *COA1* in White-footed mouse (*Peromyscus leucopus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart (SRR5130452), testis (SRR8587277) and liver (SRR8587278) have been mapped to the GCA_002215935.2_ASM221593v2_genomic.fna. Locations of truncated exon 1, intron-1 and intron-2 of *COA1* is depicted as bed record in the bottom row.

Figure S836

Psammomys obesus Duodenum, pancreatic islets and Liver

GCA_002215935.2_ASM221593v2_genomic.fna



Figure S836: Screenshot of RNA-seq reads aligned each of the putative locations of *AP4E1* and *NCAPH* in fat sand rat (*Psammomys obesus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from duodenum (SRR5092820), pancreatic islets (SRR5092819) and liver (SRR5092818) have been mapped to the GCA_002215935.2_ASM221593v2_genomic.fna. Locations of *AP4E1* and *NCAPH* are depicted as bed record in the bottom row.

Figure S837

Psammomys obesus Duodenum, pancreatic islets and Liver

GCA_002215935.2_ASM221593v2_genomic.fna

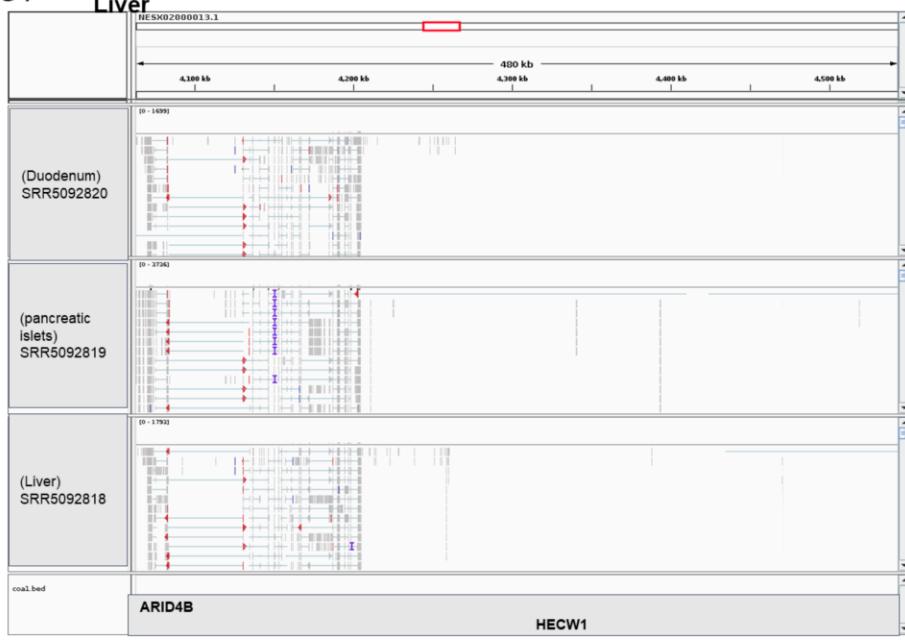


Figure S837: Screenshot of RNA-seq reads aligned each of the putative locations of *ARID4B* and *HECW1* in fat sand rat (*Psammomys obesus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from duodenum (SRR5092820), pancreatic islets (SRR5092819) and liver (SRR5092818) have been mapped to the GCA_002215935.2_ASM221593v2_genomic.fna. Locations of *ARID4B* and *HECW1* are depicted as bed record in the bottom row.

Figure S838

Psammomys obesus Duodenum, pancreatic islets and Liver

GCA_002215935.2_ASM221593v2_genomic.fna

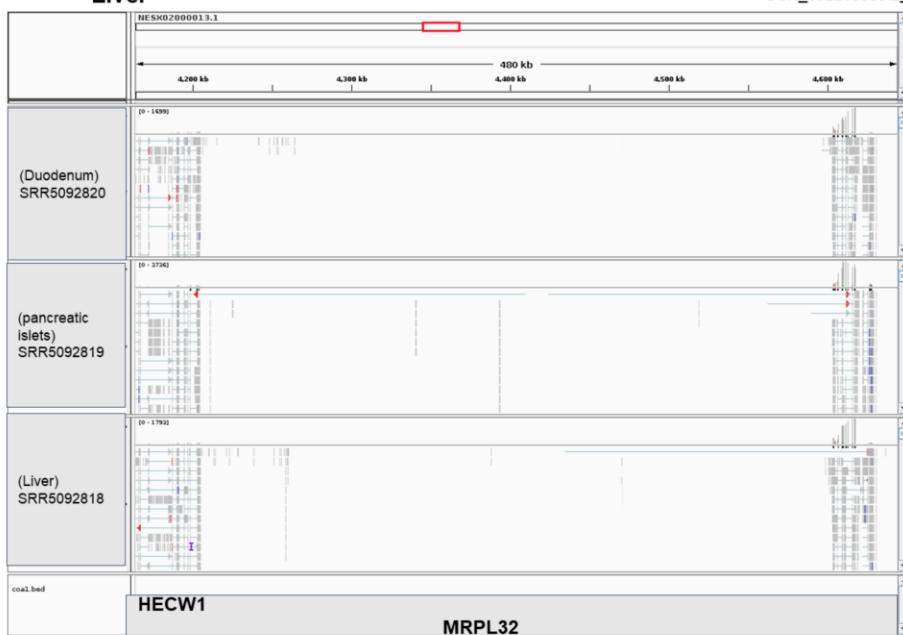


Figure S838: Screenshot of RNA-seq reads aligned each of the putative locations of *MRPL32* and *HECW1* in fat sand rat (*Psammomys obesus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from duodenum (SRR5092820), pancreatic islets (SRR5092819) and liver (SRR5092818) have been mapped to the GCA_002215935.2_ASM221593v2_genomic.fna. Locations of *MRPL32* and *HECW1* are depicted as bed record in the bottom row.

Figure S839

Psammomys obesus Duodenum, pancreatic islets and Liver

GCA_002215935.2_ASM221593v2_genomic.fna



Figure S839: Screenshot of RNA-seq reads aligned each of the putative locations of *ANKRD36* and *URGCP* in fat sand rat (*Psammomys obesus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from duodenum (SRR5092820), pancreatic islets (SRR5092819) and liver (SRR5092818) have been mapped to the GCA_002215935.2_ASM221593v2_genomic.fna. Locations of *ANKRD36* and *URGCP* are depicted as bed record in the bottom row.

Figure S840

Psammomys obesus Duodenum, pancreatic islets and Liver

GCA_002215935.2_ASM221593v2_genomic.fna

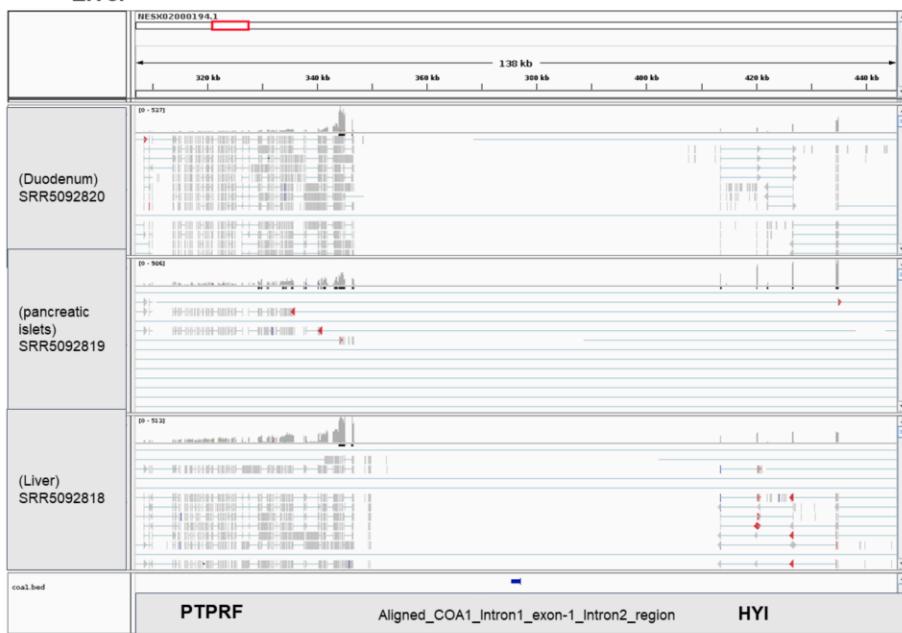


Figure S840: Screenshot of RNA-seq reads aligned each of the putative locations of truncated exon 1, intron-1 and intron-2 of *COA1* in fat sand rat (*Psammomys obesus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from duodenum (SRR5092820), pancreatic islets (SRR5092819) and liver (SRR5092818) have been mapped to the GCA_002215935.2_ASM221593v2_genomic.fna. Locations of truncated exon 1, intron-1 and intron-2 of *COA1* is depicted as bed record in the bottom row.

Figure S841*Dipodomys spectabilis* Spleen and Kidney

Dipodomys_ordii.Dord_2.0.dna_sm.toplevel.fa

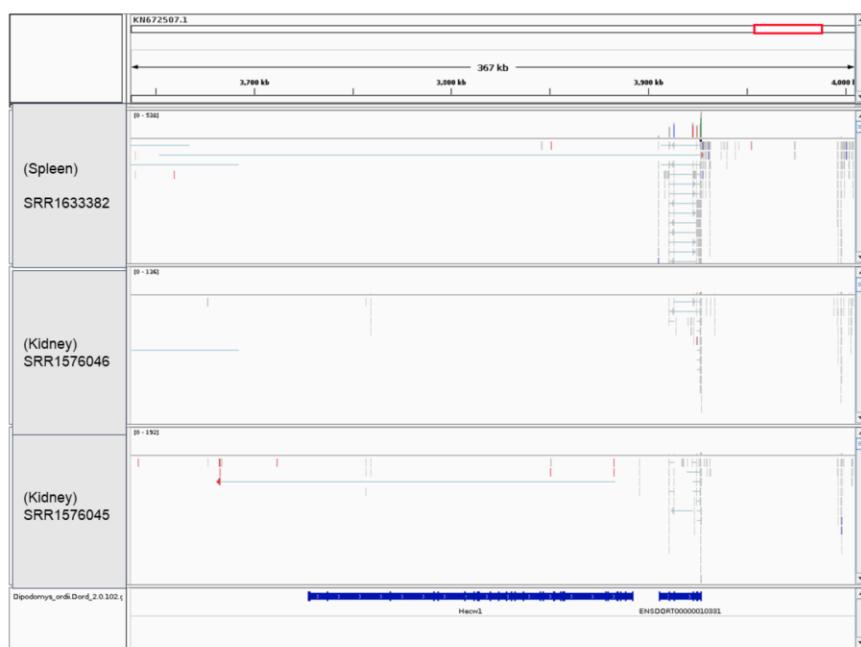


Figure S841: Screenshot of RNA-seq reads aligned each of the putative locations of *STK17A* in kangaroo rat (*Dipodomys spectabilis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR1633382) and kidney (SRR1576046 and SRR1576045) have been mapped to the Dipodomys_ordii.Dord_2.0.dna_sm.toplevel.fa. Locations of *STK17A* is depicted as Dipodomys_ordii.Dord_2.0.102.gtf record in the bottom row.

Figure S842*Dipodomys spectabilis* Spleen and Kidney

Dipodomys_ordii.Dord_2.0.dna_sm.toplevel.fa

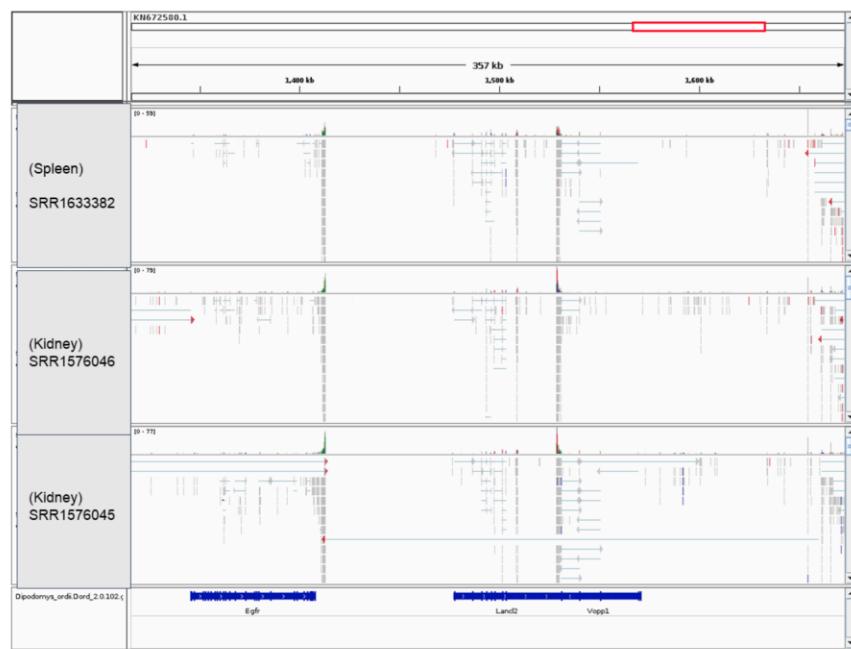


Figure S842: Screenshot of RNA-seq reads aligned each of the putative locations of *VOPP1* in kangaroo rat (*Dipodomys spectabilis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen (SRR1633382) and kidney (SRR1576046 and SRR1576045) have been mapped to the *Dipodomys_ordii.Dord_2.0.dna_sm.toplevel.fa*. Locations of *VOPP1* is depicted as *Dipodomys_ordii.Dord_2.0.102.gtf* record in the bottom row.

Figure S843*Mus musculus* -PacBio

Mus_musculus.GRCm38.dna.toplevel.fa



Figure S843: Screenshot of PacBio reads aligned to each of the putative locations of the *BLVRA* and *NCAPH* in mouse (*Mus musculus*). Gray boxes represent reads aligned to the genome. Raw read dataset which is mentioned above have been mapped to the Mus_musculus.GRCm38.dna.toplevel.fa.

Figure S844*Mus musculus* -PacBio

Mus_musculus.GRCm38.dna.toplevel.fa



Figure S844: Screenshot of PacBio reads aligned to each of the putative locations of the *BLVRA* and *AP4E1* in mouse (*Mus musculus*). Gray boxes represent reads aligned to the genome. Raw read dataset which is mentioned above have been mapped to the Mus_musculus.GRCm38.dna.toplevel.fa.

Figure S845*Mus musculus* -PacBio

Mus_musculus.GRCm38.dna.toplevel.fa



Figure S845: Screenshot of PacBio reads aligned to each of the putative locations of the *HECW1* and *ARID4B* in mouse (*Mus musculus*). Gray boxes represent reads aligned to the genome. Raw read dataset which is mentioned above have been mapped to the Mus_musculus.GRCm38.dna.toplevel.fa.

Figure S846*Mus musculus* -PacBio

Mus_musculus.GRCm38.dna.toplevel.fa

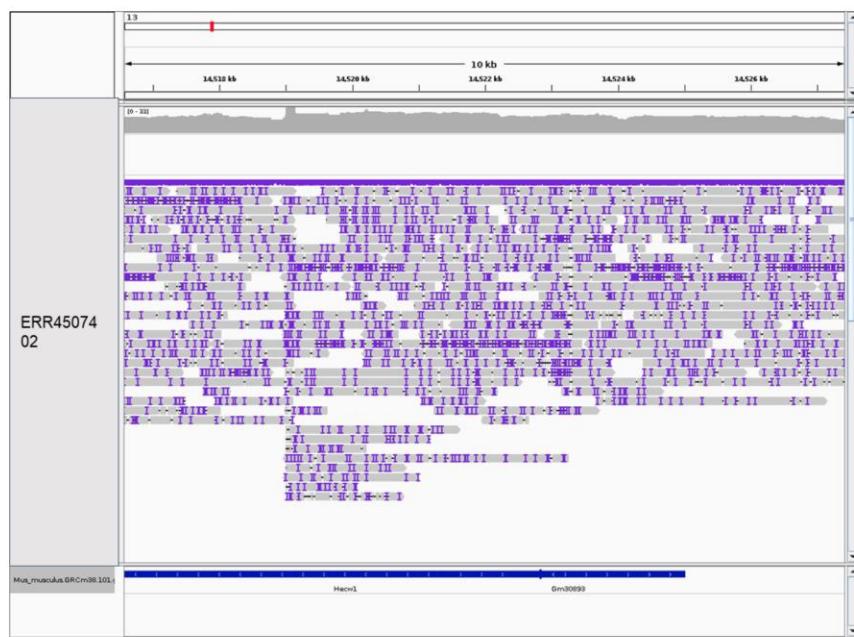


Figure S846: Screenshot of PacBio reads aligned to each of the putative locations of the *HECW1* and *MRPL32* in mouse (*Mus musculus*). Gray boxes represent reads aligned to the genome. Raw read dataset which is mentioned above have been mapped to the Mus_musculus.GRCm38.dna.toplevel.fa.

Figure S847*Mus musculus* -PacBio

Mus_musculus.GRCm38.dna.toplevel.fa



Figure S847: Screenshot of PacBio reads aligned to each of the putative locations of the *ANKRD36*, *MRPS24* and *URGCP* in mouse (*Mus musculus*). Gray boxes represent reads aligned to the genome. Raw read datasets which is mentioned above have been mapped to the *Mus_musculus.GRCm38.dna.toplevel.fa*.

Figure S848*Mus musculus* -PacBio

Mus_musculus.GRCm38.dna.toplevel.fa

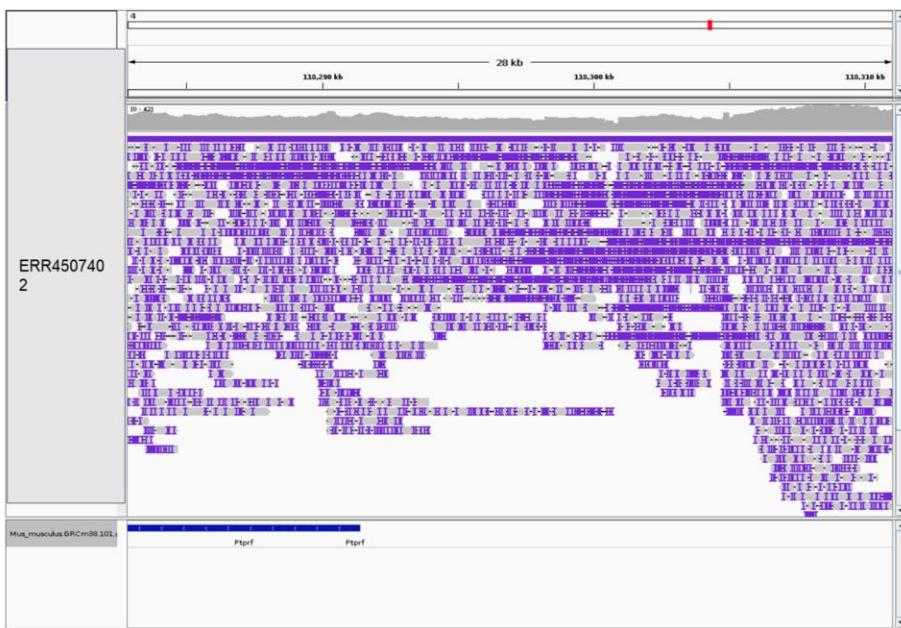


Figure S848: Screenshot of PacBio reads aligned to each of the putative locations of the *PTPRF* and *HYI* in mouse (*Mus musculus*). Gray boxes represent reads aligned to the genome. Raw read datasets which is mentioned above have been mapped to the Mus_musculus.GRCm38.dna.toplevel.fa.

Figure S849*Mus musculus* -PacBio

Mus_musculus.GRCm38.dna.toplevel.fa



Figure S849: Screenshot of PacBio reads aligned to each of the putative locations of the *PTPRF* and *HYI* in mouse (*Mus musculus*). Gray boxes represent reads aligned to the genome. Raw read datasets which is mentioned above have been mapped to the Mus_musculus.GRCm38.dna.toplevel.fa.

Figure S850*Peromyscus leucopus* -PacBio

GCF_004664715.2_UCI_PerLeu_2.1_genomic.fna



Figure S850: Screenshot of PacBio reads aligned to each of the putative locations of the *AP4E1* and *BLVRA* in white footed mouse (*Peromyscus leucopus*). Gray boxes represent reads aligned to the genome. Raw read datasets which is mentioned above have been mapped to the GCF_004664715.2_UCI_PerLeu_2.1_genomic.fna.

Figure S851*Peromyscus leucopus* -PacBio

GCF_004664715.2_UCI_PerLeu_2.1_genomic.fna

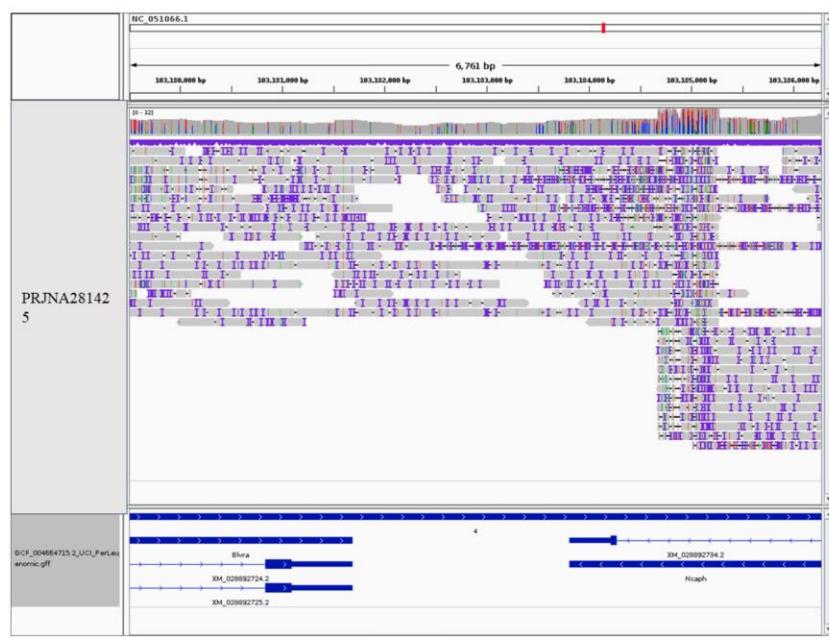


Figure S851: Screenshot of PacBio reads aligned to each of the putative locations of the *BLVRA* and *NCAPH* in white footed mouse (*Peromyscus leucopus*). Gray boxes represent reads aligned to the genome. Raw read datasets which is mentioned above have been mapped to the GCF_004664715.2_UCI_PerLeu_2.1_genomic.fna.

Figure S852

Peromyscus leucopus -PacBio

GCF_004664715.2_UCI_PerLeu_2.1_genomic.fna

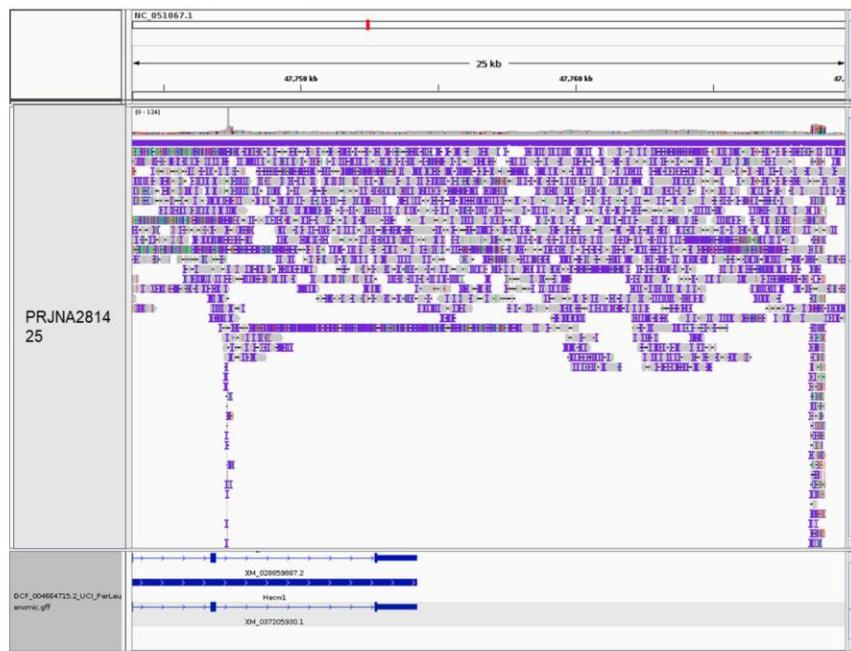


Figure S852: Screenshot of PacBio reads aligned to each of the putative locations of the *HECW1* and *ARID4B* in white footed mouse (*Peromyscus leucopus*). Gray boxes represent reads aligned to the genome. Raw read datasets which is mentioned above have been mapped to the GCF_004664715.2_UCI_PerLeu_2.1_genomic.fna.

Figure S853

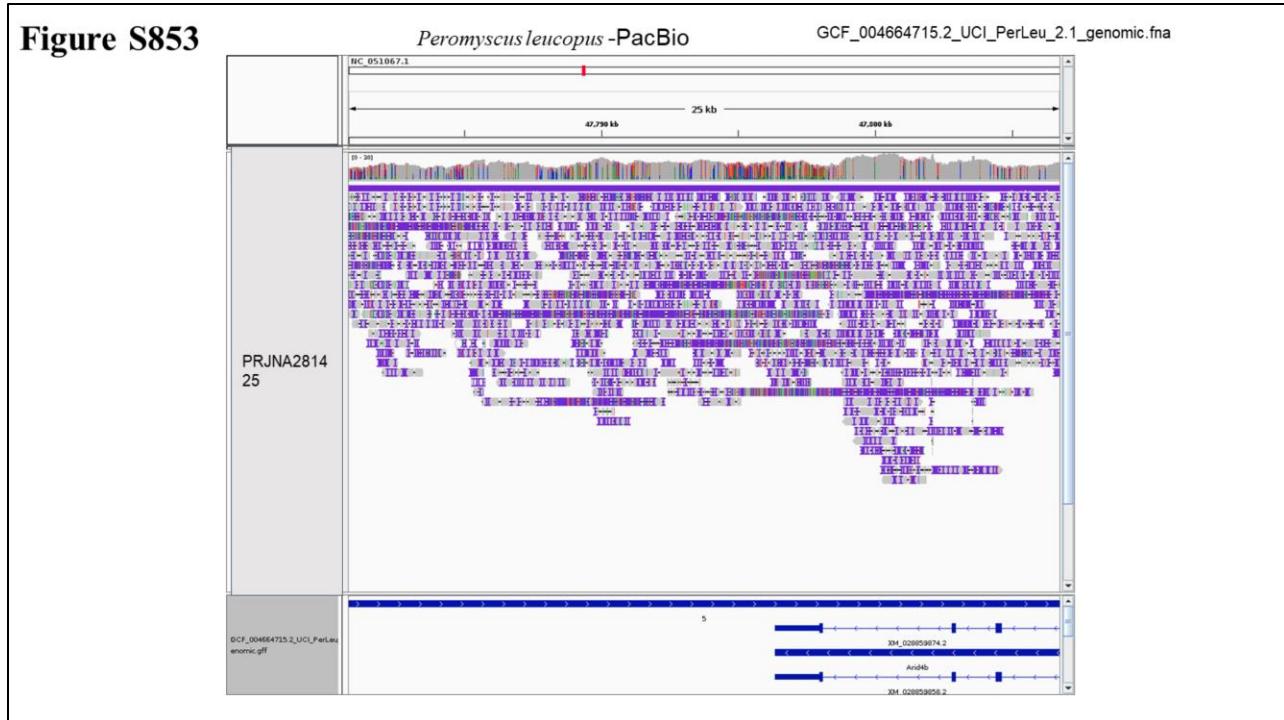


Figure S853: Screenshot of PacBio reads aligned to each of the putative locations of the *HECW1* and *ARID4B* in white footed mouse (*Peromyscus leucopus*). Gray boxes represent reads aligned to the genome. Raw read datasets which is mentioned above have been mapped to the *GCF_004664715.2_UCI_PerLeu_2.1_genomic.fna*.

Figure S854

Peromyscus leucopus -PacBio

GCF_004664715.2_UCI_PerLeu_2.1_genomic.fna



Figure S854: Screenshot of PacBio reads aligned to each of the putative locations of the *HECW1* and *MRPL32* in white footed mouse (*Peromyscus leucopus*). Gray boxes represent reads aligned to the genome. Raw read datasets which is mentioned above have been mapped to the GCF_004664715.2_UCI_PerLeu_2.1_genomic.fna.

Figure S855*Peromyscus leucopus* -PacBio

GCF_004664715.2_UCI_PerLeu_2.1_genomic.fna

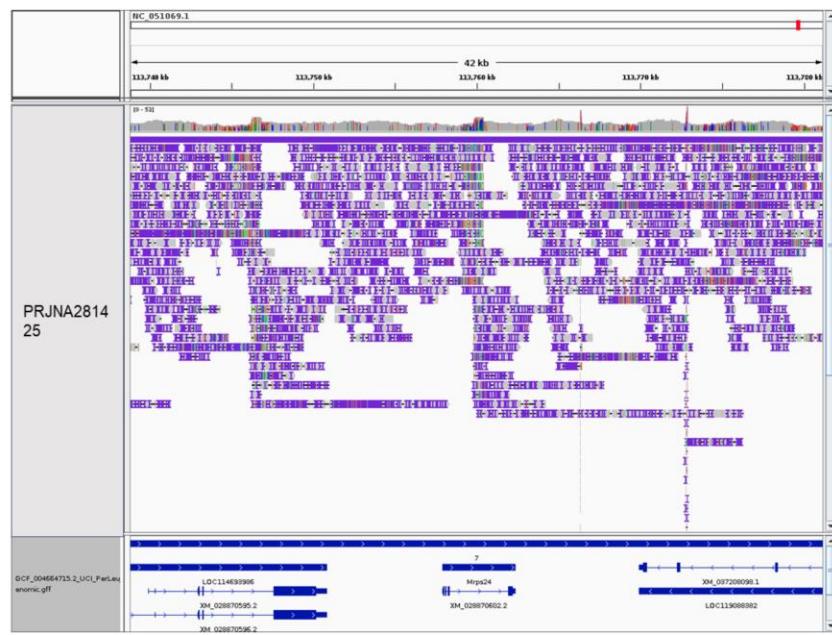


Figure S855: Screenshot of PacBio reads aligned to each of the putative locations of the *ANKRD36*, *MRPS24* and *URGCP* in white footed mouse (*Peromyscus leucopus*). Gray boxes represent reads aligned to the genome. Raw read datasets which is mentioned above have been mapped to the GCF_004664715.2_UCI_PerLeu_2.1_genomic.fna.

Figure S856*Peromyscus leucopus* -PacBio

GCF_004664715.2_UCI_PerLeu_2.1_genomic.fna

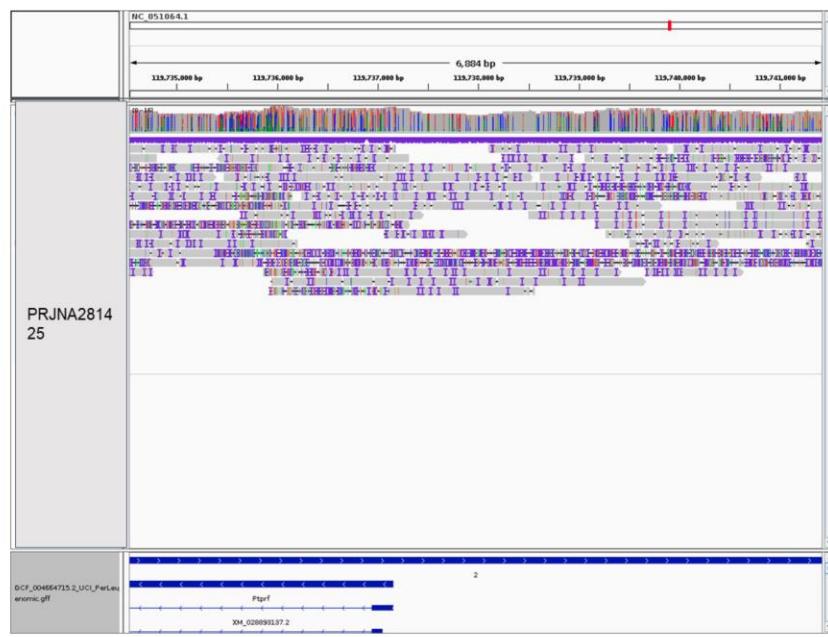


Figure S856: Screenshot of PacBio reads aligned to each of the putative locations of the *PTPRF* and *HYI* in white footed mouse (*Peromyscus leucopus*). Gray boxes represent reads aligned to the genome. Raw read datasets which is mentioned above have been mapped to the GCF_004664715.2_UCI_PerLeu_2.1_genomic.fna.

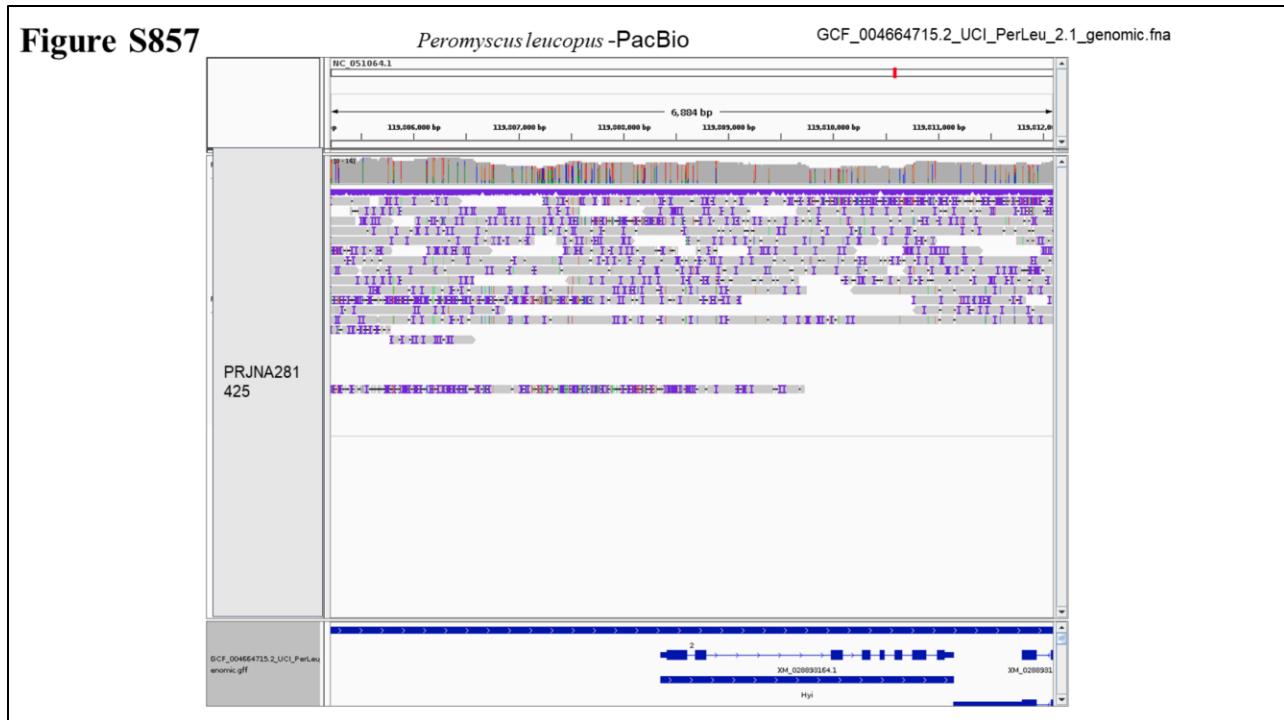
Figure S857

Figure S857: Screenshot of PacBio reads aligned to each of the putative locations of the *PTPRF* and *HYI* in white footed mouse (*Peromyscus leucopus*). Gray boxes represent reads aligned to the genome. Raw read datasets which is mentioned above have been mapped to the GCF_004664715.2_UCI_PerLeu_2.1_genomic.fna.

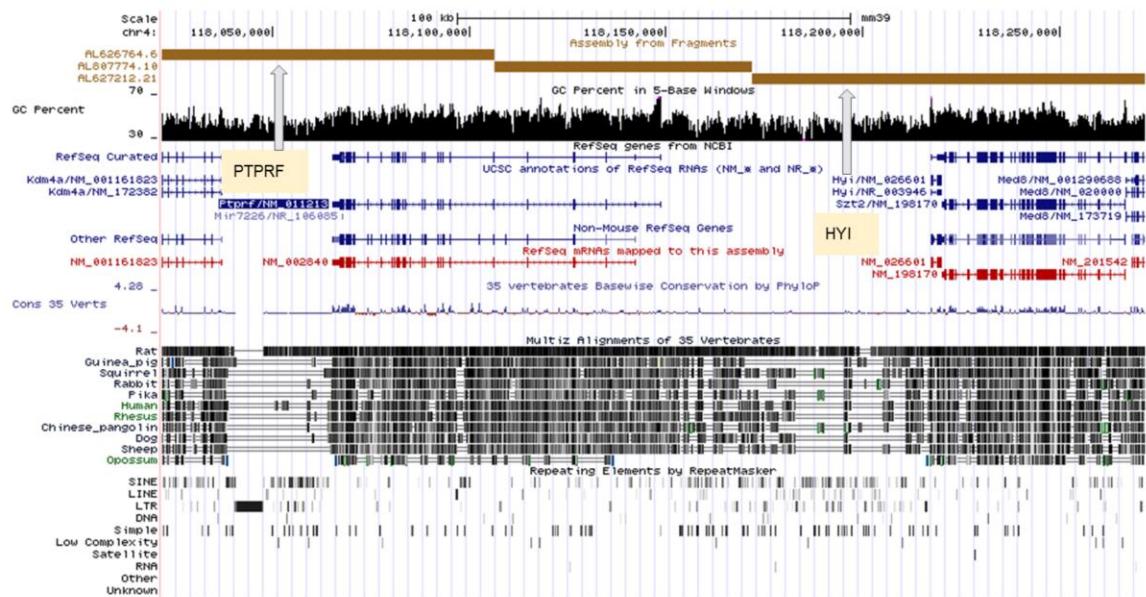
Figure S858*Mus musculus*

Figure S858: Screenshot of UCSC genome browser of the *PTPRF* and *HYI* in mouse (*Mus musculus*). Arrows are indicating the clones which used in genome assembly and covering these genes.

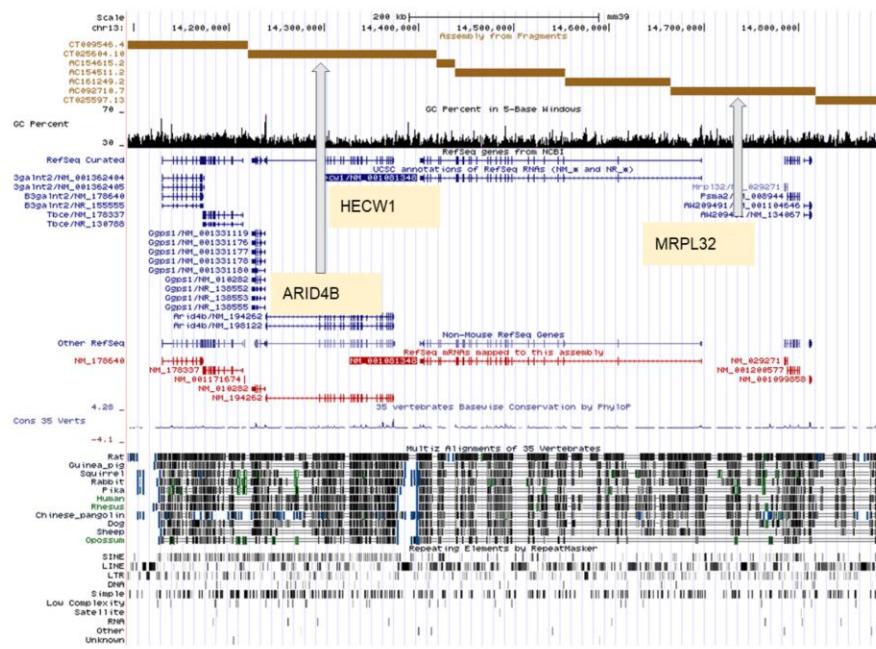
Figure S859*Mus musculus HECW1 gene*

Figure S859: Screenshot of UCSC genome browser of the *ARID4B*, *HECW1* and *MRPL32* in mouse (*Mus musculus*). Arrows are indicating the clones which used in genome assembly and covering these genes.

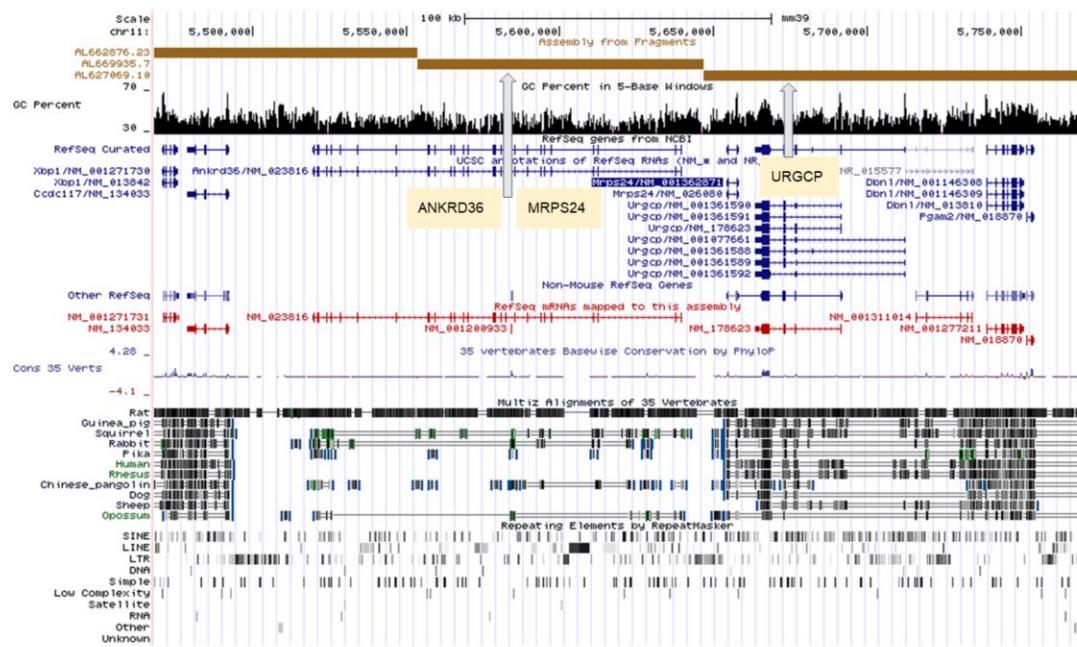
Figure S860*Mus musculus* MRPS24 gene

Figure S860: Screenshot of UCSC genome browser of the *ANKRD36*, *MRPS24* and *URGCP* in mouse (*Mus musculus*). Arrows are indicating the clones which used in genome assembly and covering these genes.

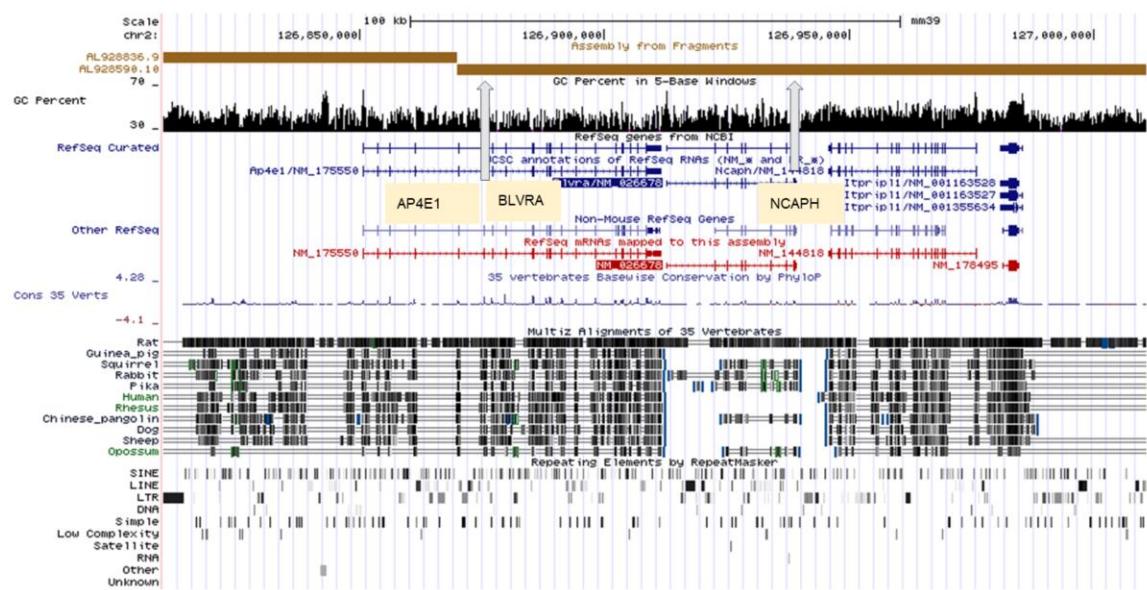
Figure S861*Mus musculus* BLVRA gene

Figure S861: Screenshot of UCSC genome browser of the *AP4E1*, *BLVRA* and *NCAPH* in mouse (*Mus musculus*). Arrows are indicating the clones which used in genome assembly and covering these genes.

Figure S862

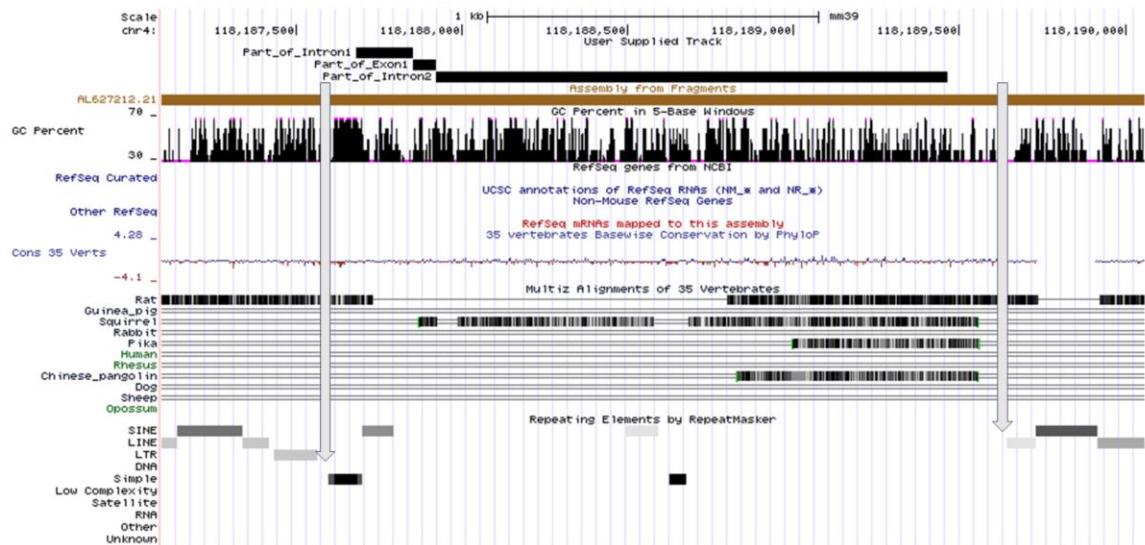


Figure S862: Screenshot of UCSC genome browser of the Intergenic region between *PTPRF* and *HYI* in mouse (*Mus musculus*), where getting the partial hits for red squirrel's exon 1, intron-1 and 2 of *COA1*. Arrows are indicating the repeats which are present at the ends of these regions.

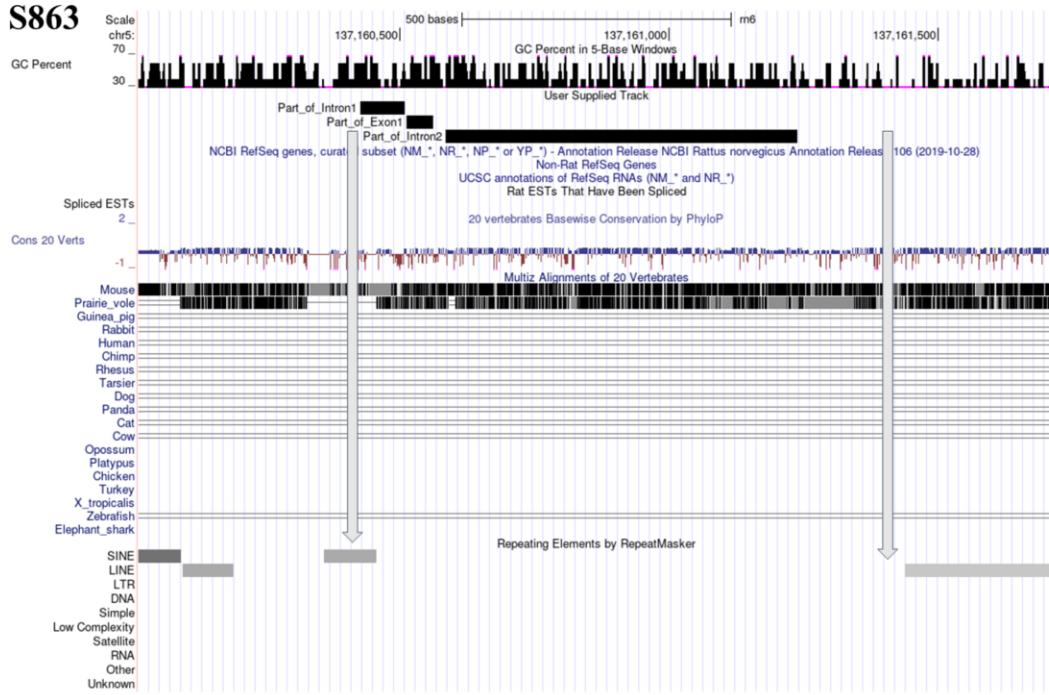
Figure S863

Figure S863: Screenshot of UCSC genome browser of the Intergenic region between *PTPRF* and *HYI* in rat (*Rattus norvegicus*), where getting the partial hits for red squirrel's exon 1, intron-1 and 2 of *COA1*. Arrows are indicating the repeats which are present at the ends of these regions.

Figure S864*Ornithorhynchus anatinus* Heart and Brain

GCF_004115215.2_mOrnAna1.pri.v4_genomic.fna

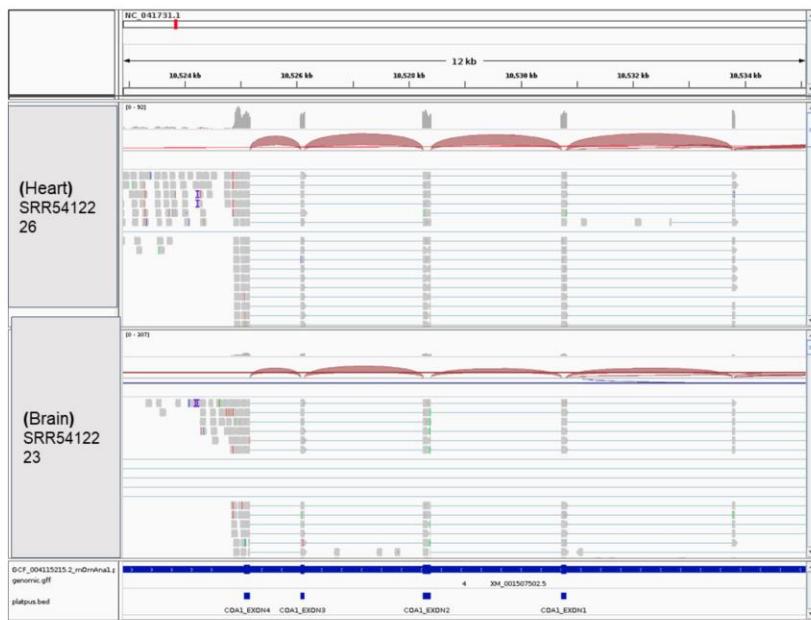


Figure S864: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in platypus (*Ornithorhynchus anatinus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart and brain (SRR541226 and SRR541223) have been mapped to the GCF_004115215.2_mOrnAna1.pri.v4_genomic.fna. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S865 *Ornithorhynchus anatinus*

Heart and Brain

GCF_004115215.2_mOrnAna1.pri.v4_genomic.fna

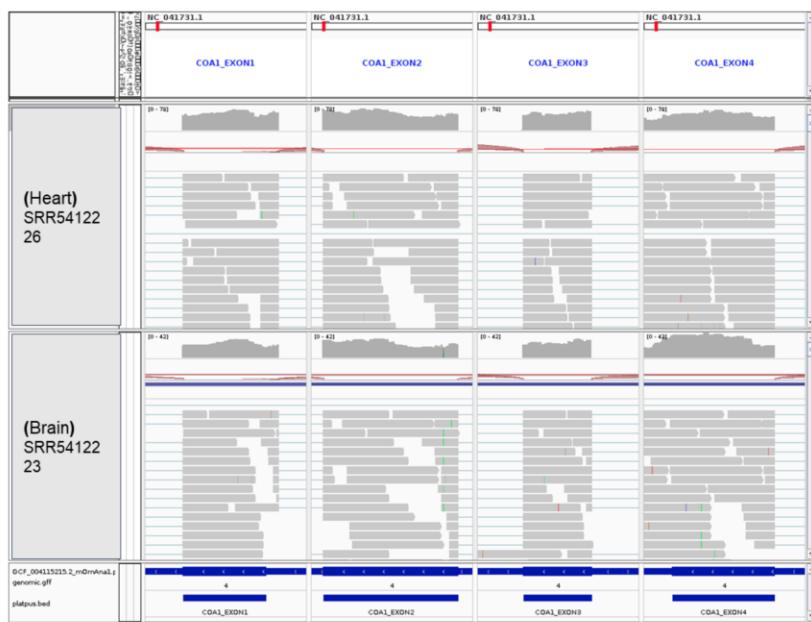


Figure S865: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S864**.

Figure S866*Ornithorhynchus anatinus* Heart and Brain

GCF_004115215.2_mOrnAna1.pri.v4_genomic.fna



Figure S866: Screenshot of RNA-seq reads aligned to *BLVRA* and *STK17A* to *COA1* exon 1 and 4 respectively in platypus (*Ornithorhynchus anatinus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart and brain (SRR5412226 and SRR5412223) have been mapped to the GCF_004115215.2_mOrnAna1.pri.v4_genomic.fna. Locations of each of the exons are depicted as bed record in the bottom row.

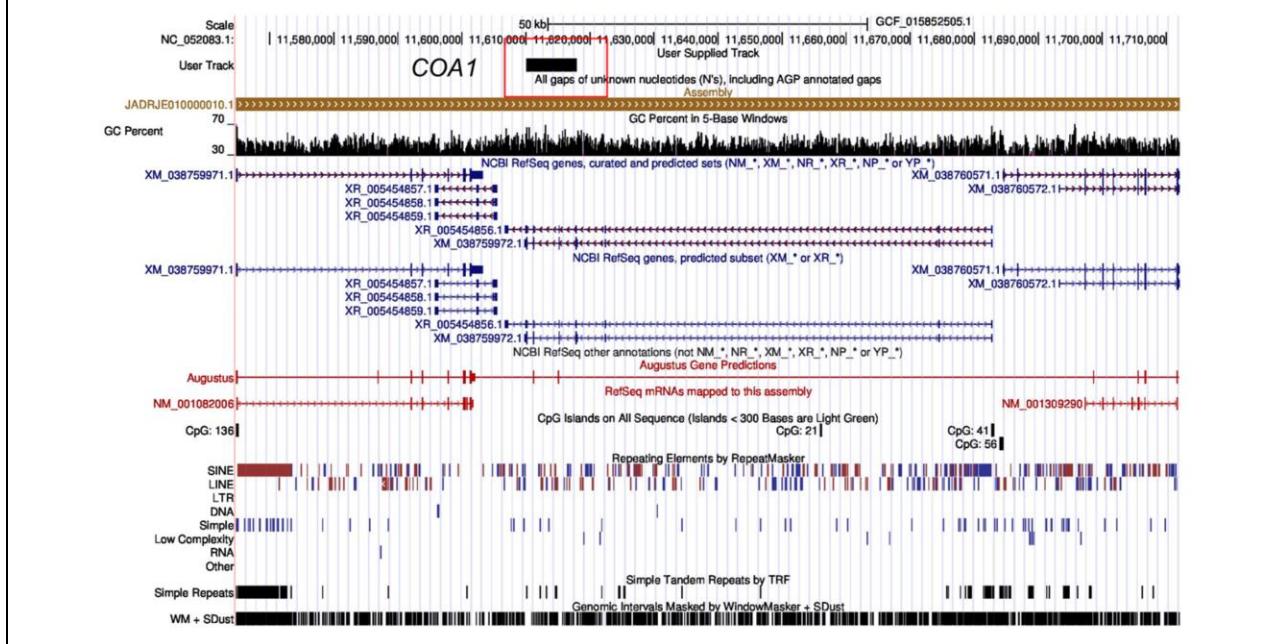
Figure S867*Tachyglossus aculeatus***Figure S867:** Screenshot of UCSC genome browser of the *COA1* in Australian echidna (*Tachyglossus aculeatus*).

Figure S868*Monodelphis domestica* Brain

GCF_000002295.2_MonDom5_genomic.fna

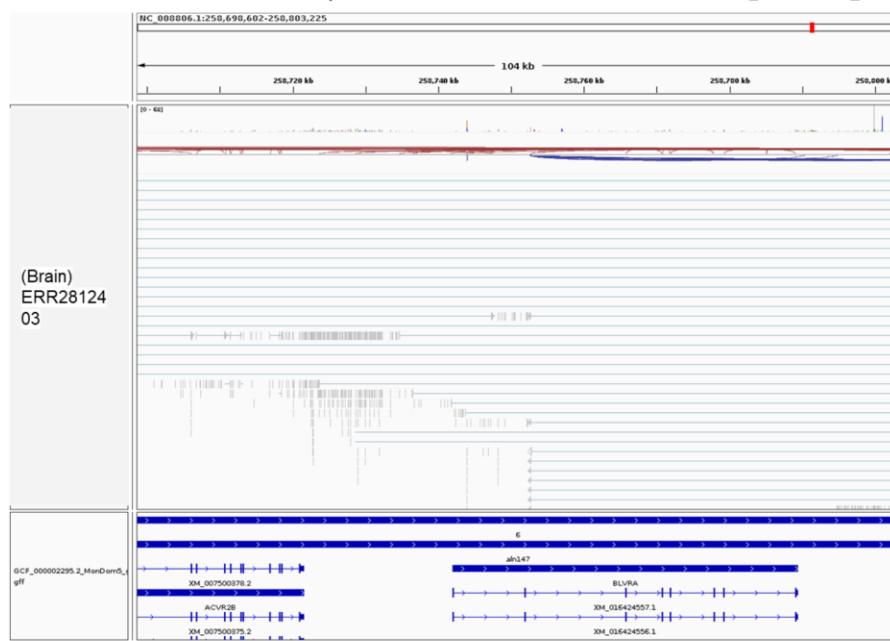


Figure S868: Screenshot of RNA-seq reads aligned each of the putative locations of *ACVR2B* and *BLVRA* in gray short-tailed opossum (*Monodelphis domestica*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (ERR2812403) have been mapped to the GCF_000002295.2_MonDom5_genomic.fna. Locations of *ACVR2B* and *BLVRA* are depicted as GCF_000002295.2_MonDom5_genomic.gff record in the bottom row.

Figure S869*Monodelphis domestica* Brain

GCF_000002295.2_MonDom5_genomic.fna

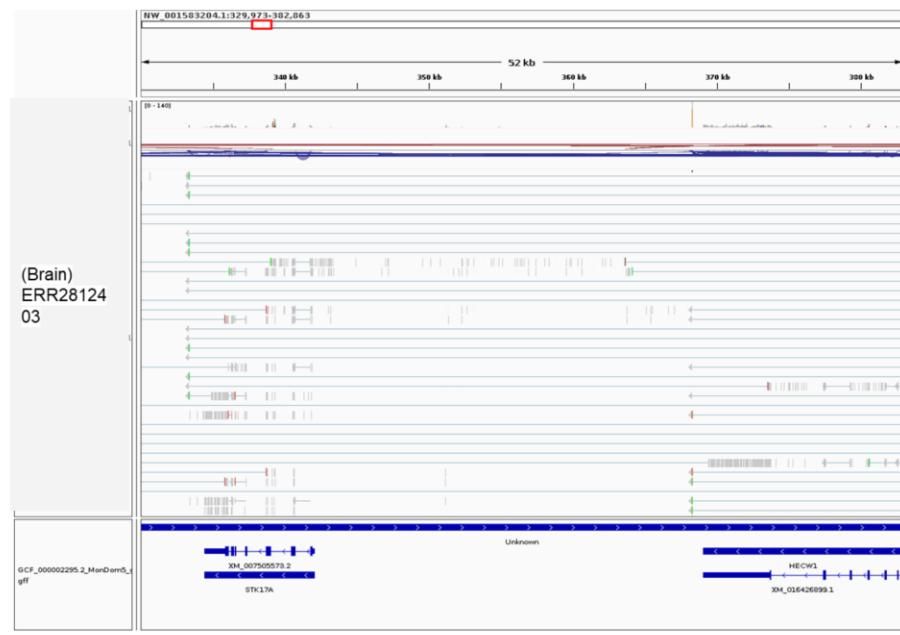


Figure S869: Screenshot of RNA-seq reads aligned each of the putative locations of *STK17A* and *HECW1* in gray short-tailed opossum (*Monodelphis domestica*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (ERR2812403) have been mapped to the GCF_000002295.2_MonDom5_genomic.fna. Locations of *STK17A* and *HECW1* are depicted as GCF_000002295.2_MonDom5_genomic.gff record in the bottom row.

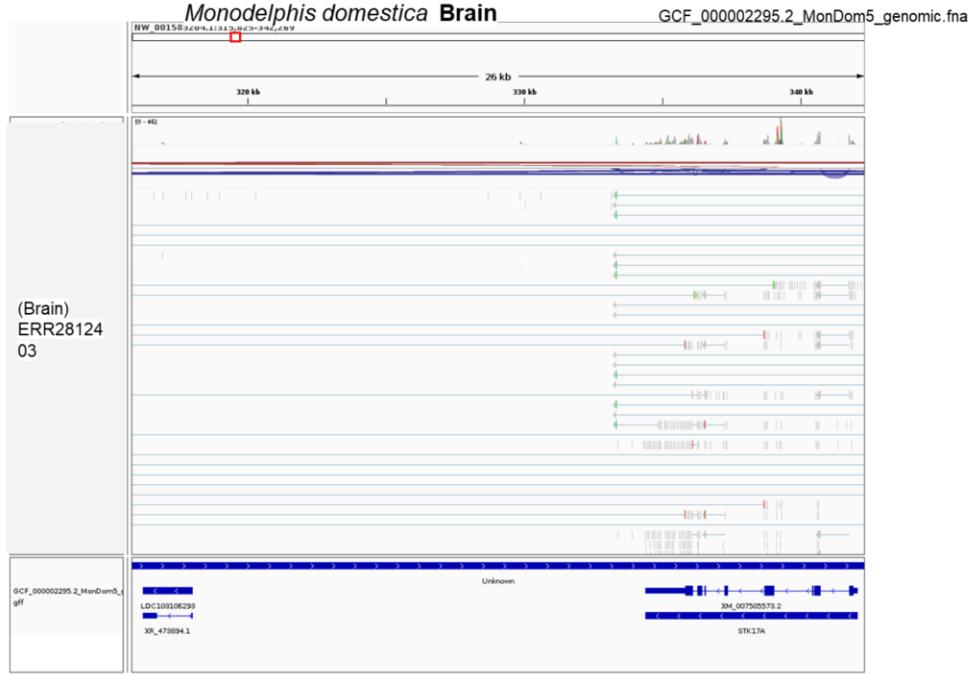
Figure S870

Figure S870: Screenshot of RNA-seq reads aligned each of the putative locations of *STK17A* and *GPR141B* in gray short-tailed opossum (*Monodelphis domestica*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from brain (ERR2812403) have been mapped to the GCF_000002295.2_MonDom5_genomic.fna. Locations of *STK17A* and *GPR141B* are depicted as GCF_000002295.2_MonDom5_genomic.gff record in the bottom row.

Figure S871*Notamacropus eugenii* Uterus

Notamacropus_eugenii.Meug_1.0.dna_sm.toplevel.fa

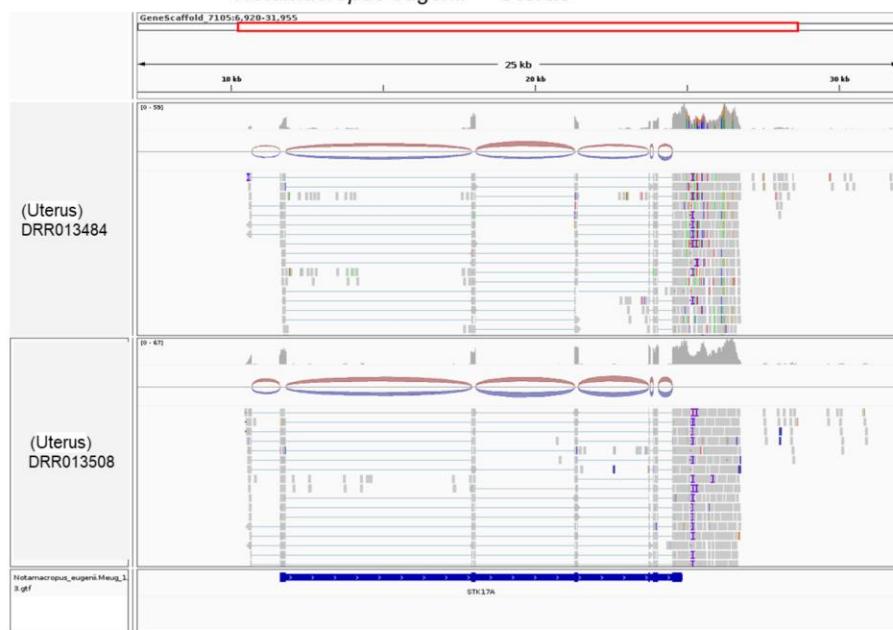


Figure S871: Screenshot of RNA-seq reads aligned each of the putative locations of *STK17A* in tammar wallaby (*Notamacropus eugenii*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from uterus (DRR013484 and DRR013508) have been mapped to the Notamacropus_eugenii.Meug_1.0.dna_sm.toplevel.fa. Locations of *STK17A* are depicted as Notamacropus_eugenii.Meug_1.0.103.gtf record in the bottom row.

Figure S872***Notamacropus eugenii* Uterus**

Notamacropus_eugenii.Meug_1.0.dna_sm.toplevel.fa

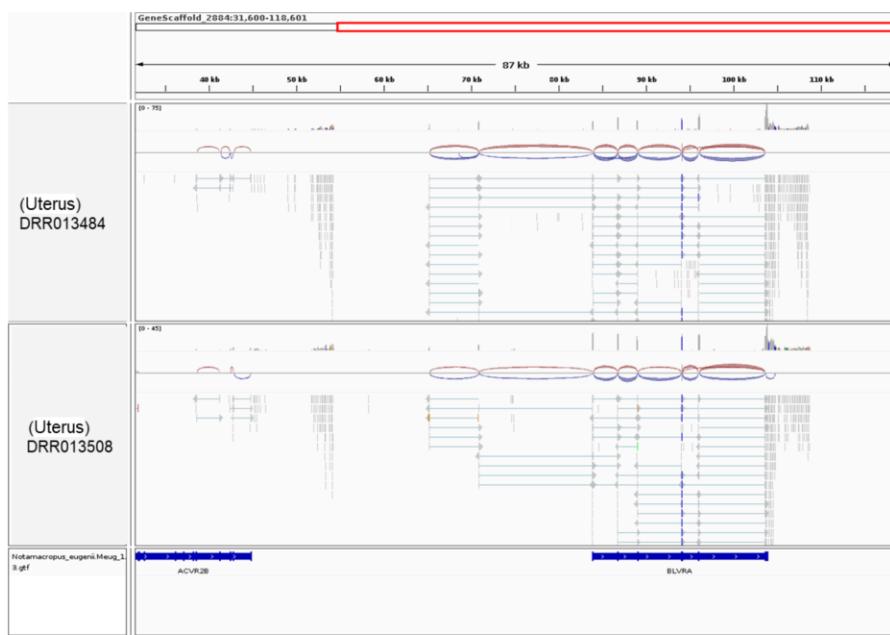


Figure S872: Screenshot of RNA-seq reads aligned each of the putative locations of *ACVR2B* and *BLVRA* in tammar wallaby (*Notamacropus eugenii*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from uterus (DRR013484 and DRR013508) have been mapped to the *Notamacropus_eugenii.Meug_1.0.dna_sm.toplevel.fa*. Locations of *ACVR2B* and *BLVRA* are depicted as *Notamacropus_eugenii.Meug_1.0.103.gtf* record in the bottom row.

Figure S873*Phascolarctos cinereus Liver and PBMC*

GCF_002099425.1_phacIn_unsw_v4.1_genomic.fna



Figure S873: Screenshot of RNA-seq reads aligned each of the putative locations of *HECW1* and *STK17A* in koala (*Phascolarctos cinereus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR8708137) and PBMC (SRR10337975) have been mapped to the GCF_002099425.1_phacIn_unsw_v4.1_genomic.fna. Locations of *HECW1* and *STK17A* are depicted as GCF_002099425.1_phacIn_unsw_v4.1_genomic.gff record in the bottom row.

Figure S874*Phascolarctos cinereus Liver and PBMC*

GCF_002099425.1_phacIn_unsw_v4.1_genomic.fna

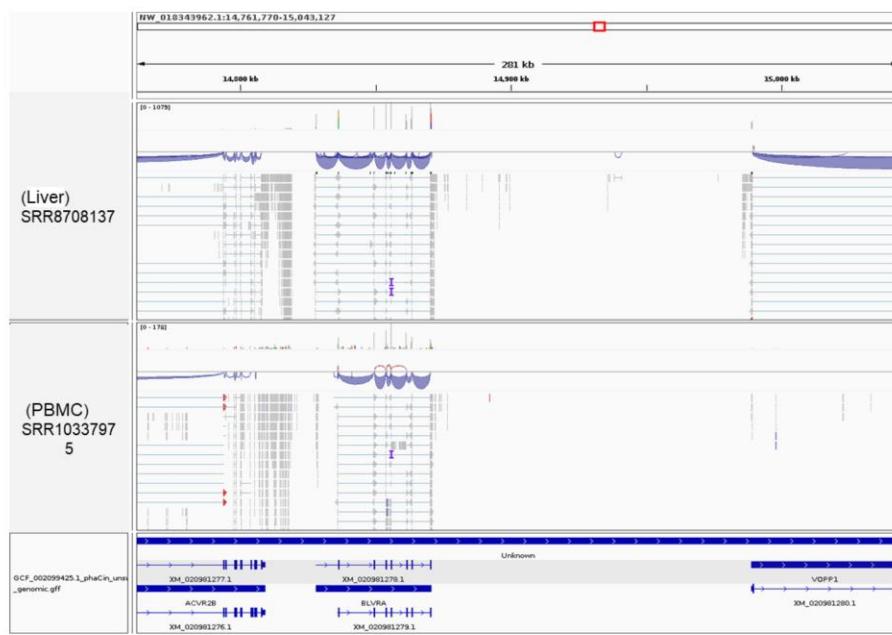


Figure S874: Screenshot of RNA-seq reads aligned each of the putative locations of *ACVR2B* and *VOPP1* in koala (*Phascolarctos cinereus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR8708137) and PBMC (SRR10337975) have been mapped to the GCF_002099425.1_phacIn_unsw_v4.1_genomic.fna. Locations of *ACVR2B* and *VOPP1* are depicted as GCF_002099425.1_phacIn_unsw_v4.1_genomic.gff record in the bottom row.

Figure S875*Phascolarctos cinereus Liver and PBMC*

GCF_002099425.1_phacIn_unsw_v4.1_genomic.fna

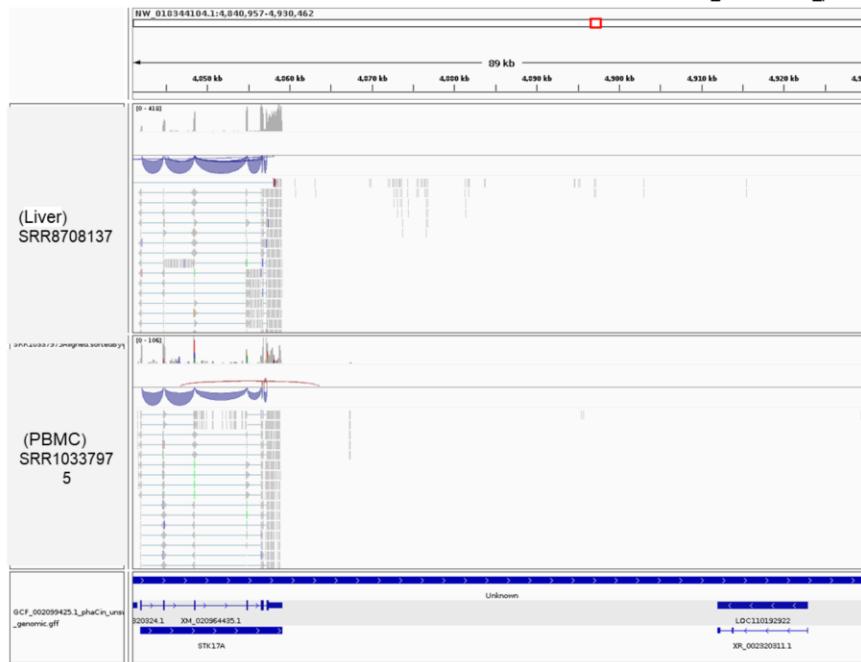


Figure S875: Screenshot of RNA-seq reads aligned each of the putative locations of *STK17A* and *GPR141B* in koala (*Phascolarctos cinereus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR8708137) and PBMC (SRR1033797) have been mapped to the GCF_002099425.1_phacIn_unsw_v4.1_genomic.fna. Locations of *STK17A* and *GPR141B* are depicted as GCF_002099425.1_phacIn_unsw_v4.1_genomic.gff record in the bottom row.

Figure S876**Sarcophilus harrisii Lung Spleen**

GCF_902635505.1_mSarHar1.11_genomic.fna

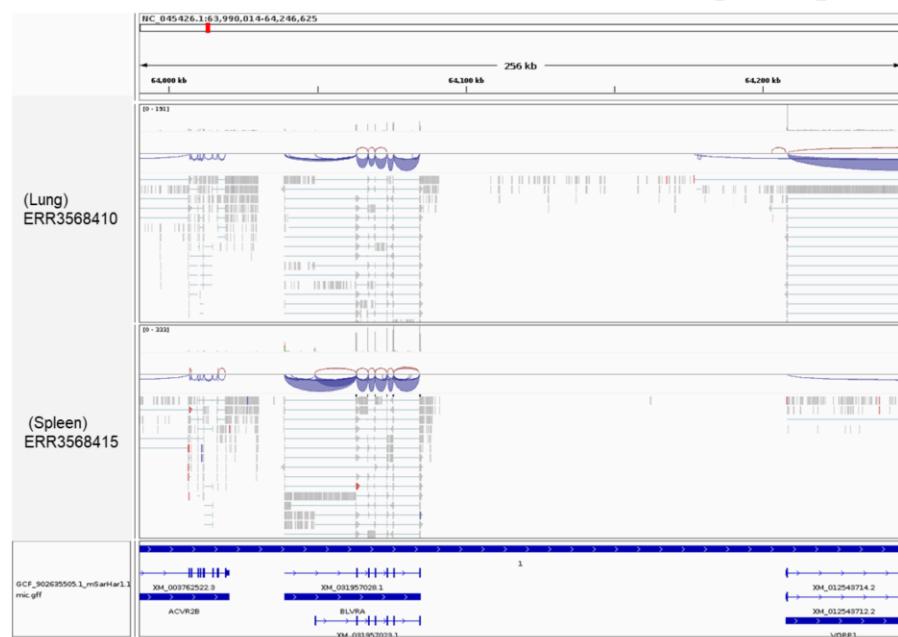


Figure S876: Screenshot of RNA-seq reads aligned each of the putative locations of ACVR2B and VOPP1 in Tasmanian devil (*Sarcophilus harrisii*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from lung (ERR3568410) and spleen (ERR3568415) have been mapped to the GCF_902635505.1_mSarHar1.11_genomic.fna. Locations of ACVR2B and VOPP1 are depicted as GCF_902635505.1_mSarHar1.11_genomic.gff record in the bottom row.

Figure S877*Sarcophilus harrisii* Lung Spleen

GCF_902635505.1_mSarHar1.11_genomic.fna

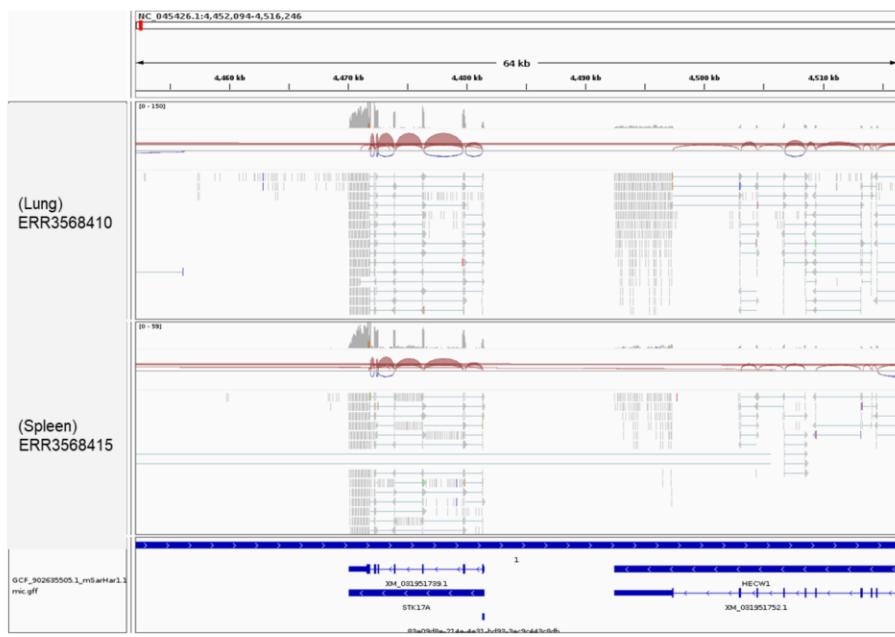


Figure S877: Screenshot of RNA-seq reads aligned each of the putative locations of *STK17A* and *HECW1* in Tasmanian devil (*Sarcophilus harrisii*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from lung (ERR3568410) and spleen (ERR3568415) have been mapped to the GCF_902635505.1_mSarHar1.11_genomic.fna. Locations of *STK17A* and *HECW1* are depicted as GCF_902635505.1_mSarHar1.11_genomic.gff record in the bottom row.

Figure S878*Sarcophilus harrisii* Lung Spleen

GCF_902635505.1_mSarHar1.11_genomic.fna

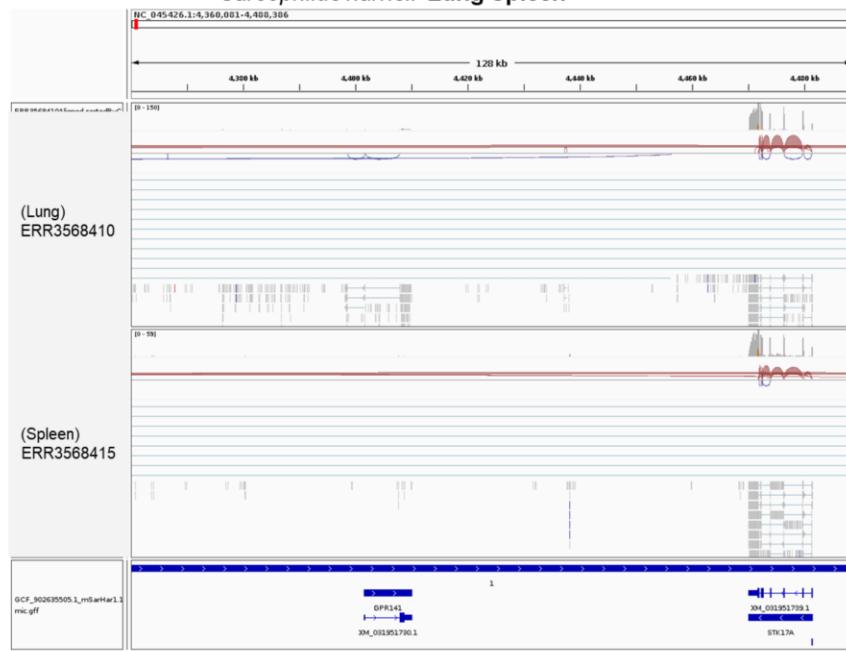


Figure S878: Screenshot of RNA-seq reads aligned each of the putative locations of *STK17A* and *GPR141B* in Tasmanian devil (*Sarcophilus harrisii*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from lung (ERR3568410) and spleen (ERR3568415) have been mapped to the GCF_902635505.1_mSarHar1.11_genomic.fna. Locations of *STK17A* and *GPR141B* are depicted as GCF_902635505.1_mSarHar1.11_genomic.gff record in the bottom row.

Figure S879*Trichosurus vulpecula Liver*

GCF_011100635.1_mTriVul1.pri_genomic.fna



Figure S879: Screenshot of RNA-seq reads aligned each of the putative locations of *ACVR2B* and *BLVRA* in common brushtail (*Trichosurus vulpecula*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR11483672 and SRR11483674) have been mapped to the GCF_011100635.1_mTriVul1.pri_genomic.fna. Locations of *ACVR2B* and *BLVRA* are depicted as GCF_011100635.1_mTriVul1.pri_genomic.gff record in the bottom row.

Figure S880*Trichosurus vulpecula Liver*

GCF_011100635.1_mTriVul1.pri_genomic.fna

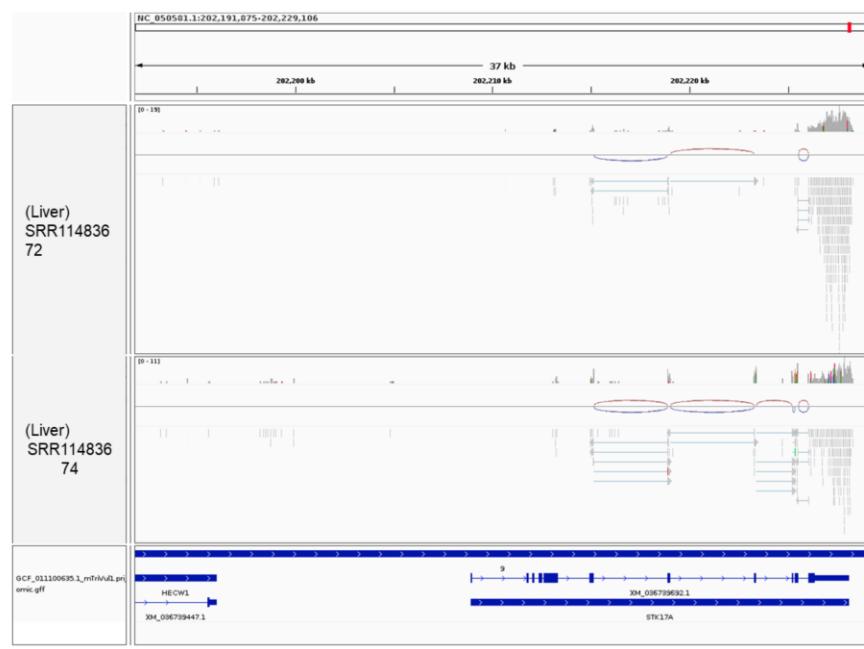


Figure S880: Screenshot of RNA-seq reads aligned each of the putative locations of *HECW1* and *STK17A* in common brushtail (*Trichosurus vulpecula*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR11483672 and SRR11483674) have been mapped to the GCF_011100635.1_mTriVul1.pri_genomic.fna. Locations of *HECW1* and *STK17A* are depicted as GCF_011100635.1_mTriVul1.pri_genomic.gff record in the bottom row.

Figure S881*Trichosurus vulpecula Liver*

GCF_011100635.1_mTriVul1.pri_genomic.fna

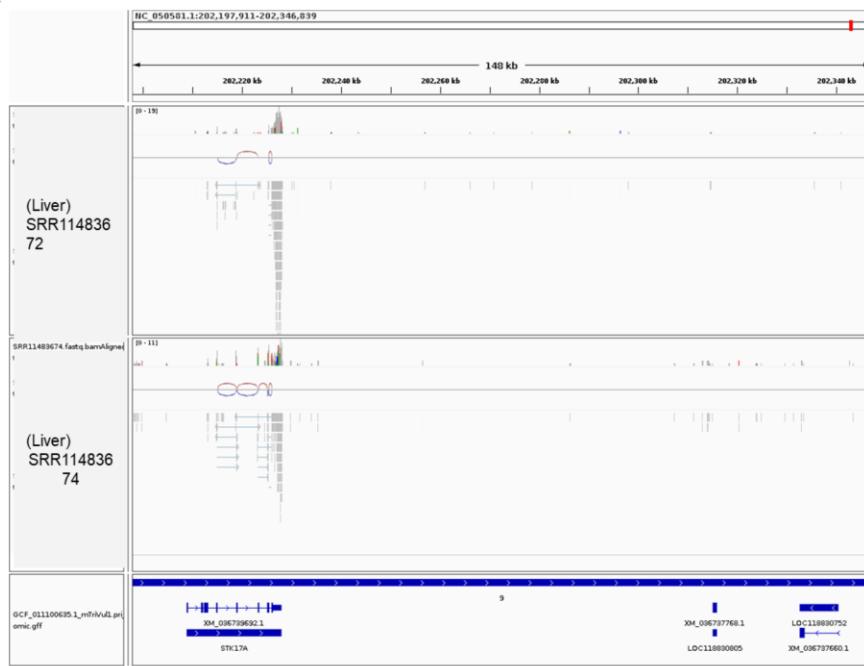


Figure S881: Screenshot of RNA-seq reads aligned each of the putative locations of *STK17A* and *GPR141B* in common brushtail (*Trichosurus vulpecula*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR11483672 and SRR11483674) have been mapped to the GCF_011100635.1_mTriVul1.pri_genomic.fna. Locations of *STK17A* and *GPR141B* are depicted as GCF_011100635.1_mTriVul1.pri_genomic.gff record in the bottom row.

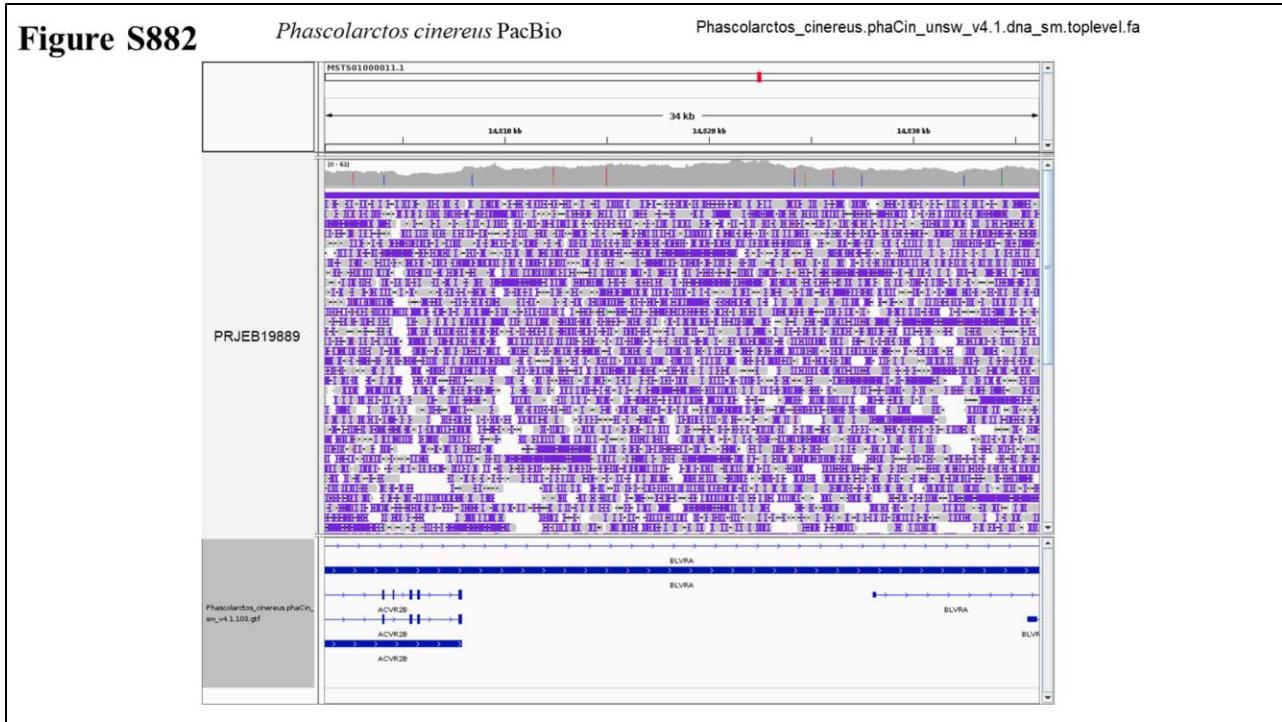
Figure S882*Phascolarctos cinereus* PacBio

Figure S882: Screenshot of PacBio reads aligned to each of the putative locations of the *ACVR2B* and *BLVRA* in koala (*Phascolarctos cinereus*). Gray boxes represent reads aligned to the genome. Raw read datasets which is mentioned above have been mapped to the *Phascolarctos_cinereus.phaCin_unsw_v4.1.dna_sm.toplevel.fa*.

Figure S883*Phascolarctos cinereus* PacBio

Phascolarctos_cinereus.phaCin_unsw_v4.1.dna_sm.toplevel.fa

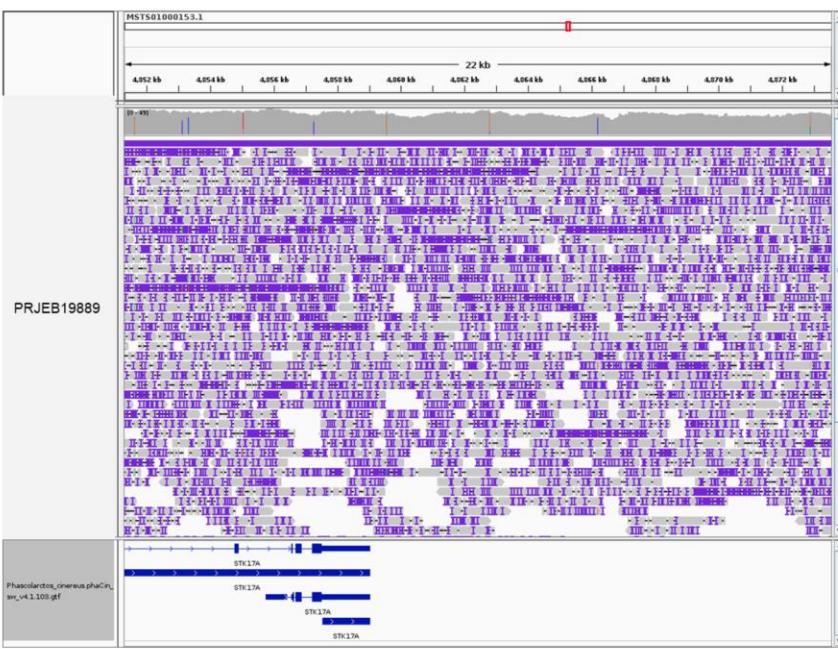


Figure S883: Screenshot of PacBio reads aligned to each of the putative locations of the *STK17A* and *GPR141B* in koala (*Phascolarctos cinereus*). Gray boxes represent reads aligned to the genome. Raw read datasets which is mentioned above have been mapped to the *Phascolarctos_cinereus.phaCin_unsw_v4.1.dna_sm.toplevel.fa*

Figure S884*Phascolarctos cinereus* PacBio

Phascolarctos_cinereus.phaCin_unsw_v4.1.dna_sm.toplevel.fa

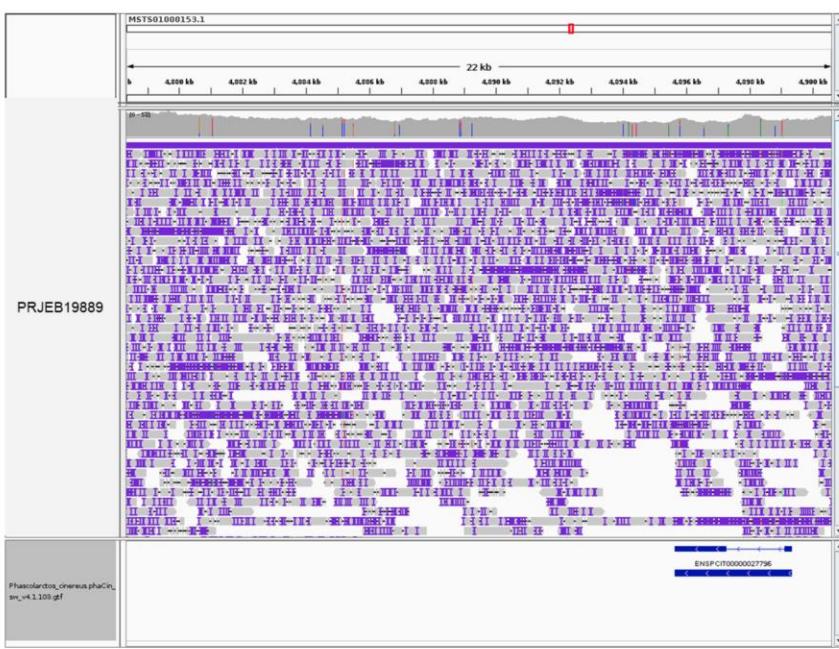


Figure S884: Screenshot of PacBio reads aligned to each of the putative locations of the *STK17A* and *GPR141B* in koala (*Phascolarctos cinereus*). Gray boxes represent reads aligned to the genome. Raw read datasets which is mentioned above have been mapped to the Phascolarctos_cinereus.phaCin_unsw_v4.1.dna_sm.toplevel.fa

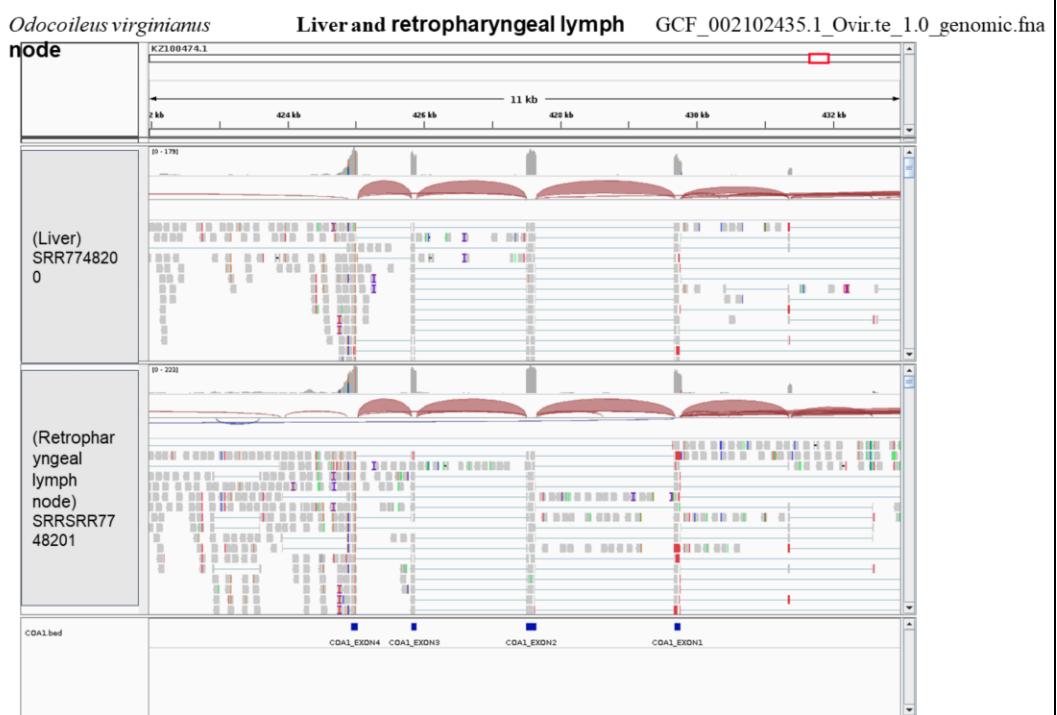
Figure S885

Figure S885: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* in white-tailed deer (*Odocoileus virginianus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver and retropharyngeal lymph node (SRR7748200 and SRR7748201) have been mapped to the GCF_002102435.1_Ovir.te_1.0_genomic.fna. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S886 *Odocoileus virginianus*

Liver and retropharyngeal lymph node GCF_002102435.1_Ovir.te_1.0_genomic.fna



Figure S886: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S885**.

Figure S887*Cervus elaphus*

Blood

GCA_002197005.1_CerEla1.0_genomic.fna

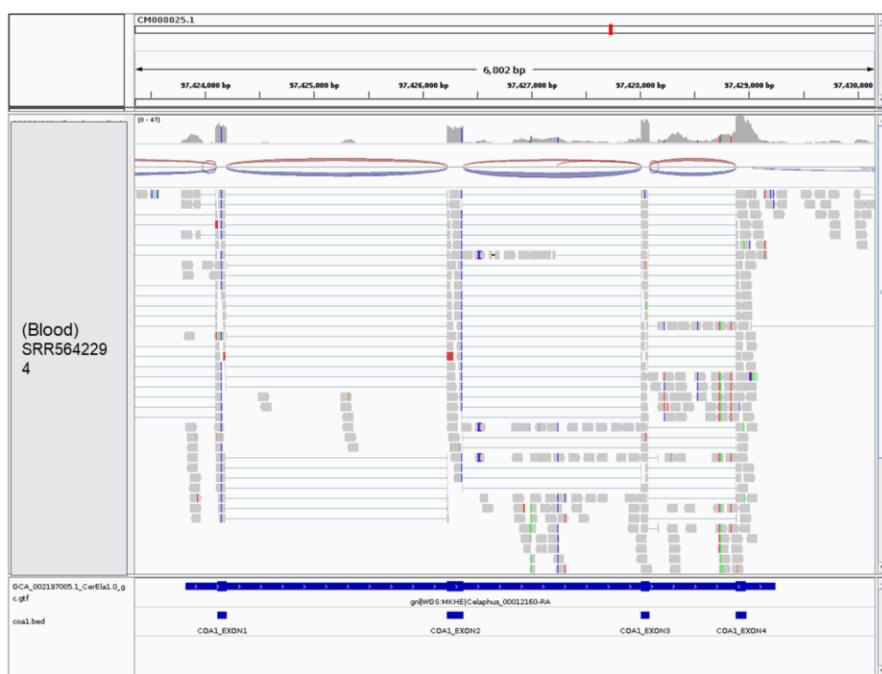


Figure S887: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* in red deer (*Cervus elaphus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR564229) have been mapped to the GCA_002197005.1_CerEla1.0_genomic.fna. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S888*Cervus elaphus* Blood

GCA_002197005.1_CerEla1.0_genomic.fna

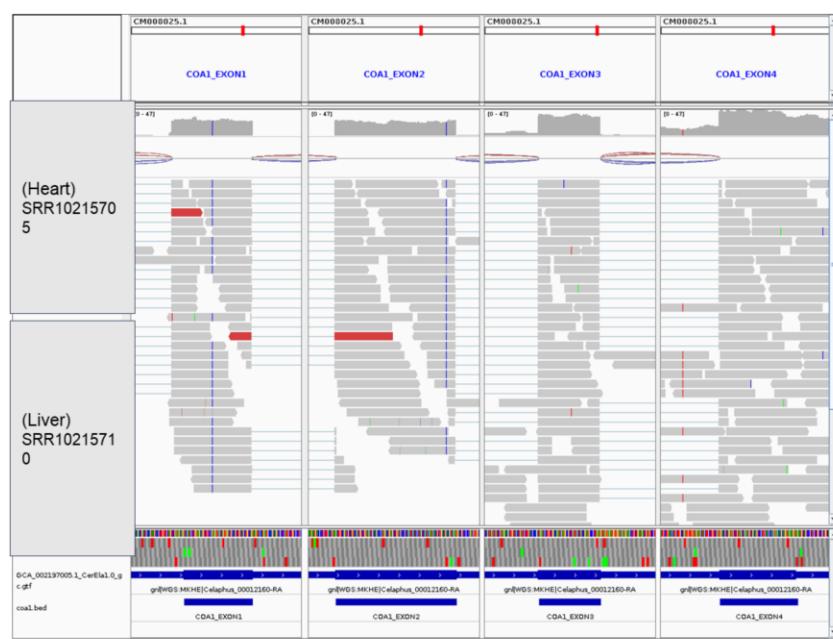
**Figure S888:** A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S887**.

Figure S889*Microcebus murinus Kidney and Lung*

Microcebus_murinus.Mmur_3.0.dna_sm.toplevel.fa



Figure S889: Screenshot of RNA-seq reads aligned to each of the putative locations of the five *COA1* exons in Gray mouse lemur (*Microcebus murinus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from kidney and lung (SRR1758996 and SRR1758998) have been mapped to the *Microcebus murinus.Mmur_3.0.dna_sm.toplevel.fa*. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S890*Microcebus murinus Lung and Kidney*

Microcebus_murinus.Mmur_3.0.dna_sm.toplevel.fa

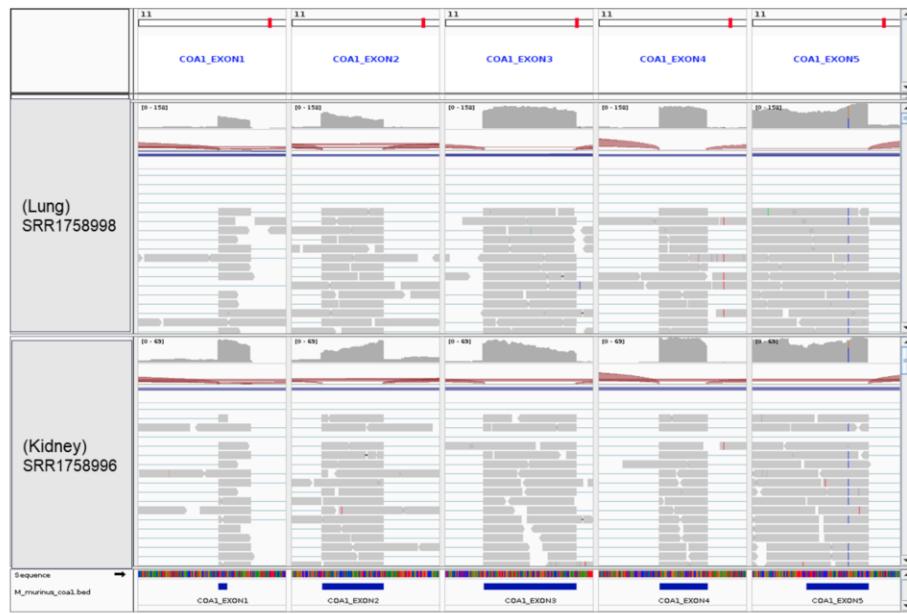
**Figure S890:** A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S889**.

Figure S891*Otolemur garnettii Liver*

GCF_000181295.1_OtoGar3_genomic.fna

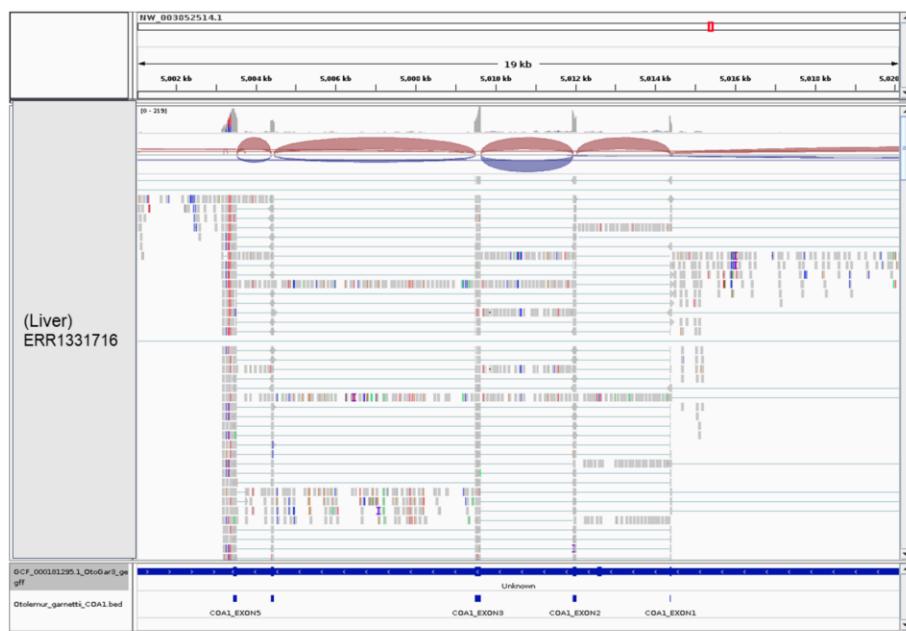


Figure S891: Screenshot of RNA-seq reads aligned to each of the putative locations of the five *COA1* exons in Northern greater galago (*Otolemur garnettii*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (ERR1331716) have been mapped to the GCF_000181295.1_OtoGar3_genomic.fna. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S892*Propithecus coquereli*

Propithecus_coquereli.Pcoq_1.0.dna_sm.toplevel.fa

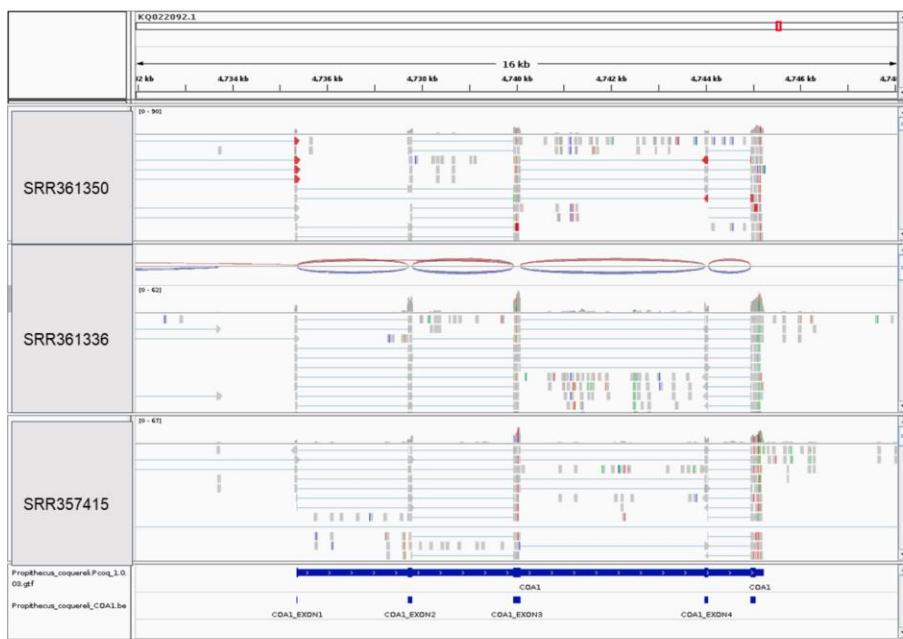


Figure S892: Screenshot of RNA-seq reads aligned to each of the putative locations of the five *COA1* exons in Coquerel's sifaka (*Propithecus coquereli*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from unknown tissue (SRR361350, SRR361336 and SRR357415) have been mapped to the *Propithecus_coquereli.Pcoq_1.0.dna_sm.toplevel.fa*. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S893 *Aotus nancymaae* Liver, Heart and Kidney -Functional copy GCF_000952055.2_Anan_2.0_genomic.fna

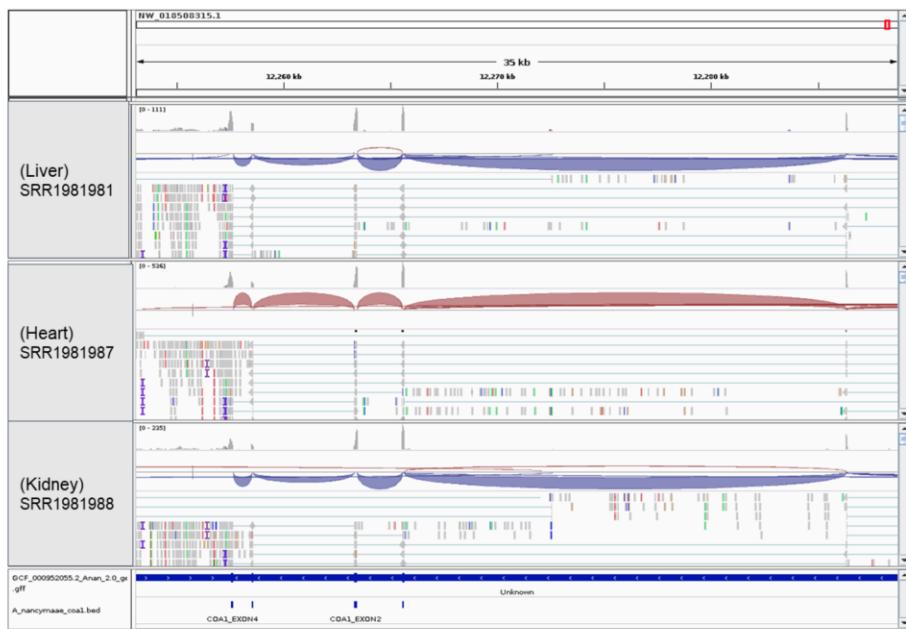


Figure S893: Screenshot of RNA-seq reads aligned to each of the putative locations of the five *COA1* exons in Nancy Ma's night monkey (*Aotus nancymaae*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver, heart and kidney (SRR1981981, SRR1981987 and SRR1981988) have been mapped to the GCF_000952055.2_Anan_2.0_genomic.fna. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S894 *Aotus nancymaae* Liver, Heart, Kidney -Duplicated copy2 GCF_000952055.2_Anan_2.0_genomic.fna



Figure S894: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* duplicated exons in Nancy Ma's night monkey (*Aotus nancymaae*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments in *ARFGAP3* gene region. Datasets from liver, heart and kidney (SRR1981981, SRR1981987 and SRR1981988) have been mapped to the GCF_000952055.2_Anan_2.0_genomic.fna. Locations of each of the duplicated exons are depicted as bed record in the bottom row.

Figure S895

Aotus nancymaae Liver, Heart, Kidney -Duplicated copy2 GCF_000952055.2_Anan_2.0_genomic.fna

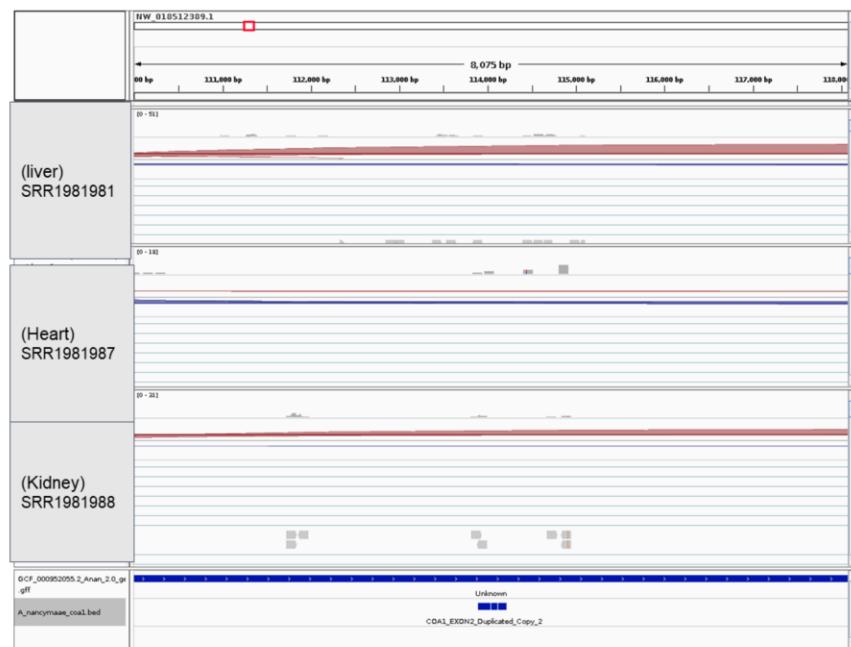


Figure S895: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* duplicated exons in Nancy Ma's night monkey (*Aotus nancymaae*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments in *ARFGAP3* gene region. Datasets from liver, heart and kidney (SRR1981981, SRR1981987 and SRR1981988) have been mapped to the GCF_000952055.2_Anan_2.0_genomic.fna. Locations of each of the duplicated exons are depicted as bed record in the bottom row.

Figure S896 *Callithrix jacchus* Lung,Liver and Kidney -Functional copy Callithrix_jacchus.ASM275486v1.dna_sm.toplevel.fa

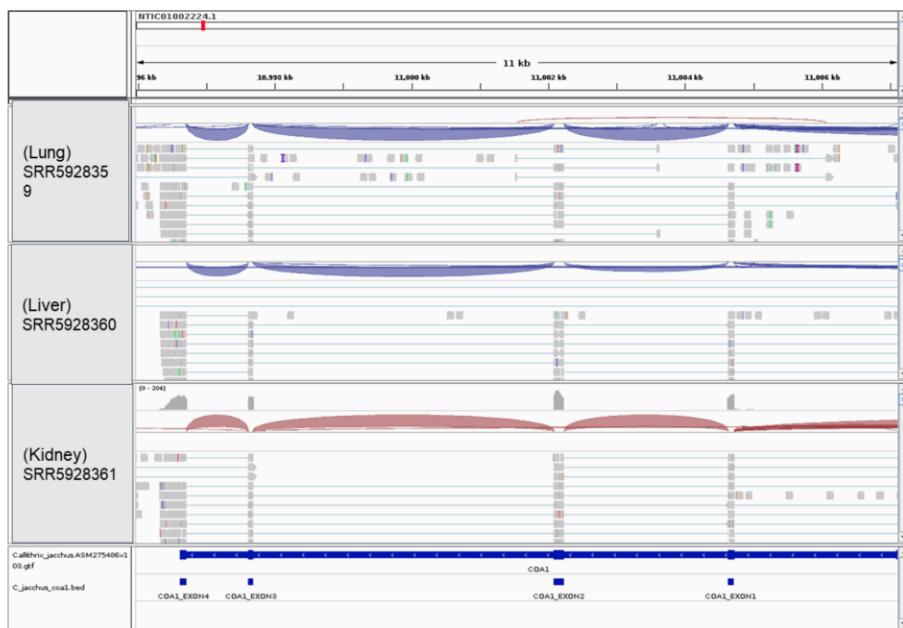


Figure S896: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Common marmoset (*Callithrix jacchus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from lung, liver and kidney (SRR5928359, SRR5928360 and SRR5928361) have been mapped to the *Callithrix_jacchus.ASM275486v1.dna_sm.toplevel.fa*. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S897 *Callithrix jacchus* Lung,Liver and Kidney -Duplicated copy Callithrix_jacchus.ASM275486v1.dna_sm.toplevel.fa

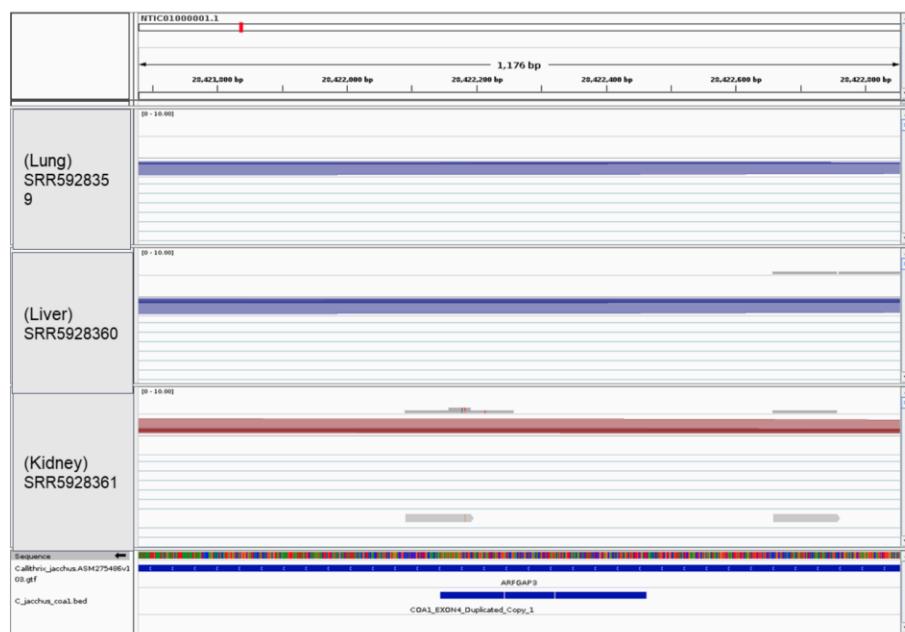


Figure S897: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Common marmoset (*Callithrix jacchus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments in *ARFGAP3* gene region. Datasets from lung, liver and kidney (SRR5928359, SRR5928360 and SRR5928361) have been mapped to the *Callithrix_jacchus.ASM275486v1.dna_sm.toplevel.fa*. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S898*Cebus imitator* Blood -Functional copy

Cebus_capucinus.Cebus_imitator-1.0.dna_sm.toplevel.fa



Figure S898: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Panamanian White-faced Capuchin (*Cebus imitator*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR3412937) have been mapped to the Cebus_capucinus.Cebus_imitator-1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S899*Cebus imitator* Blood -Duplicated copy 1

Cebus_capucinus.Cebus_imitator-1.0.dna_sm.toplevel.fa

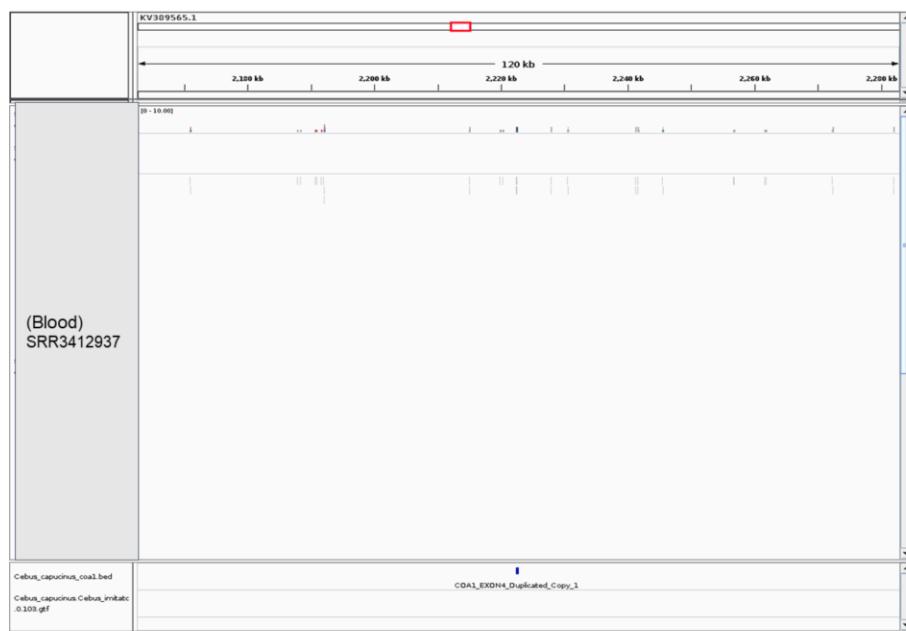


Figure S899: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* duplicated exons in Panamanian White-faced Capuchin (*Cebus imitator*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments in this located region. Datasets from blood (SRR3412937) have been mapped to the Cebus_capucinus.Cebus_imitator-1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S900**Cebus imitator Blood -Duplicated copy 2**

Cebus_capucinus.Cebus_imitator-1.0.dna_sm.toplevel.fa

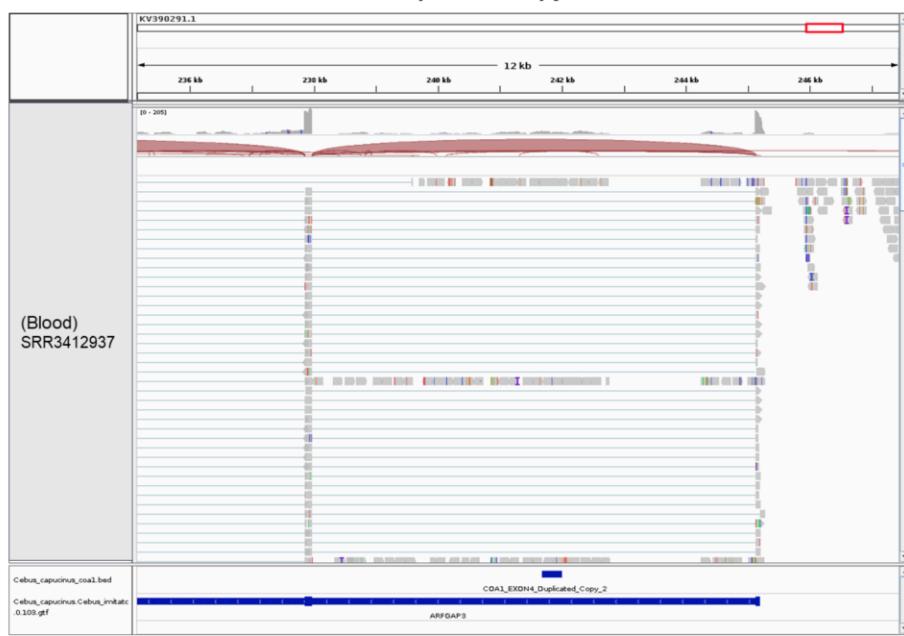


Figure S900: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Panamanian White-faced Capuchin (*Cebus imitator*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments in ARFGAP3 gene region. Datasets from blood (SRR3412937) have been mapped to the Cebus_capucinus.Cebus_imitator-1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S901

Saimiri_boliviensis_boliviensis.Ovary and Heart

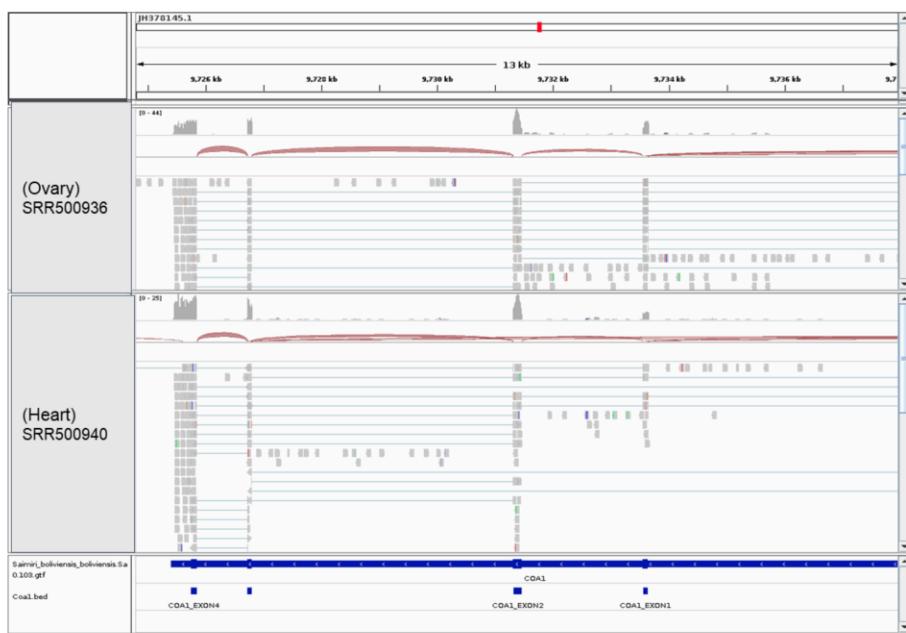


Figure S901: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Black-capped squirrel monkey (*Saimiri boliviensis boliviensis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from ovary and heart (SRR500936, SRR500940) have been mapped to the Saimiri_boliviensis_boliviensis.SaiBol1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S902

Saimiri_boliviensis_boliviensis.SaiBol1.0.dna_sm.toplevel.fa
Saimiri boliviensis boliviensis Ovary and Heart exon-wise-4

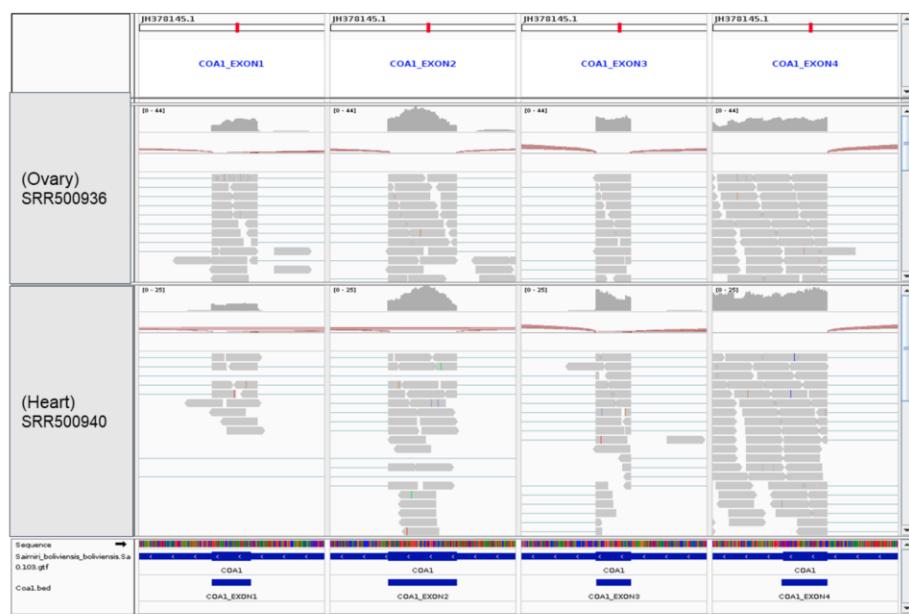


Figure S902: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S901**.

Figure S903**Saimiri boliviensis boliviensis Ovary and Heart -Duplicated copy1**

Saimiri_boliviensis_boliviensis.SaiBol1.0.dna_sm.toplevel.fa

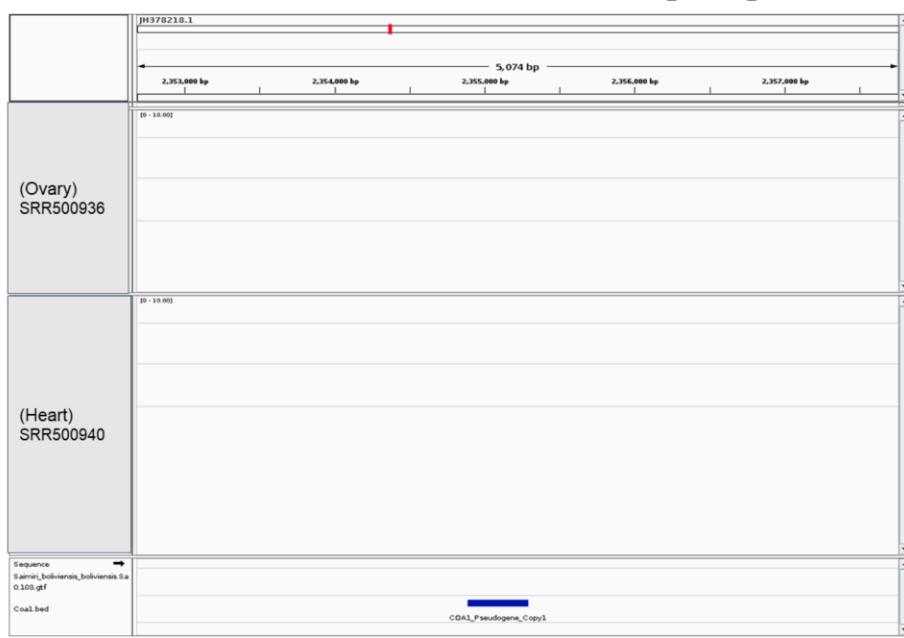


Figure S903: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* duplicated exons in Black-capped squirrel monkey (*Saimiri boliviensis boliviensis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments in this region. Datasets from ovary and heart (SRR500936 and SRR500940) have been mapped to the Saimiri_boliviensis_boliviensis.SaiBol1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S904**Saimiri boliviensis boliviensis Ovary and Heart -Duplicated copy2**

Saimiri_boliviensis_boliviensis.SaiBol1.0.dna_sm.toplevel.fa



Figure S904: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* duplicated exons in Black-capped squirrel monkey (*Saimiri boliviensis boliviensis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments in *ARFGAP3* gene region. Datasets from ovary and heart (SRR500936 and SRR500940) have been mapped to the Saimiri_boliviensis_boliviensis.SaiBol1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S905*Cercocebus atys Liver Functional copy*

Cercocebus_atys.Caty_1.0.dna_sm.toplevel.fa

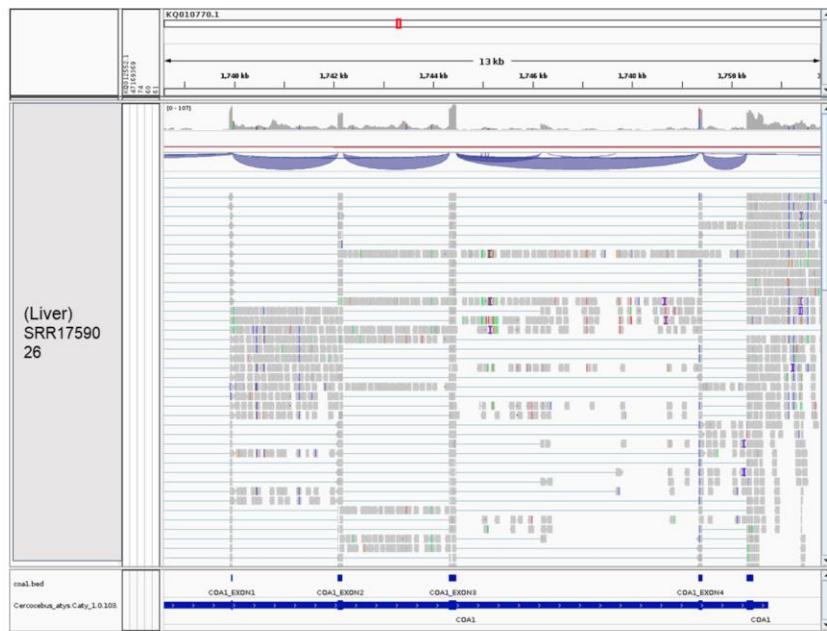


Figure S905: Screenshot of RNA-seq reads aligned to each of the putative locations of the five *COA1* exons in Sooty mangabey (*Cercocebus atys*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (SRR1759026) have been mapped to the *Cercocebus_atys.Caty_1.0.dna_sm.toplevel.fa*. Locations of each of the exons are depicted as coal.bed record in the bottom row.

Figure S906

Cercocetus atys Liver -Duplicated copy Cercocetus_atys.Caty_1.0.dna_sm.toplevel.fa

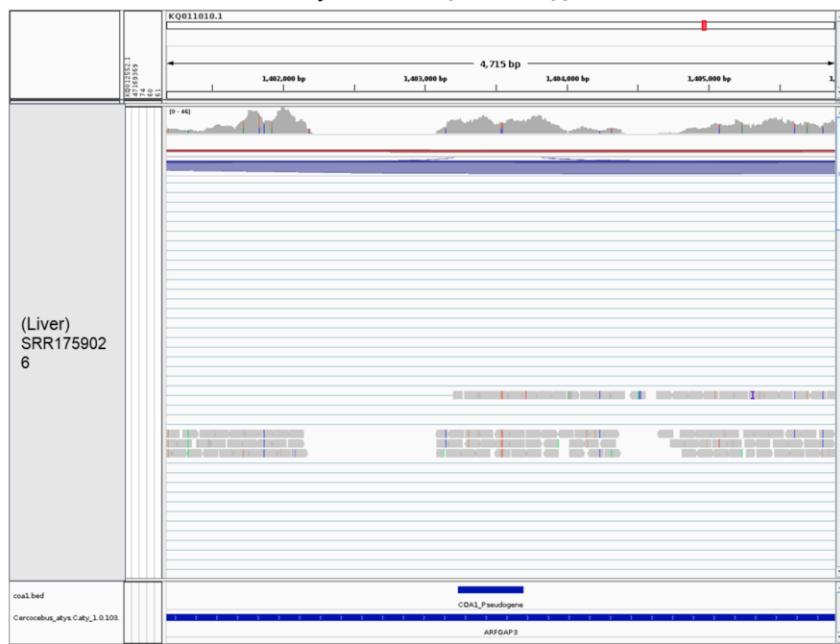


Figure S906: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* duplicated exons in Sooty mangabey (*Cercocetus atys*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments in *ARFGAP3* gene region. Datasets from liver (SRR1759026) have been mapped to the *Cercocetus_atys.Caty_1.0.dna_sm.toplevel.fa*. Locations of each of the exons are depicted as coal.bed record in the bottom row.

Figure S907**Papio anubis Kidney and Heart Functional copy**

Papio_anubis.Panu_3.0.dna_sm.toplevel.fa



Figure S907: Screenshot of RNA-seq reads aligned to each of the putative locations of the five *COA1* exons in Olive baboon (*Papio anubis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from kidney and heart (SRR1758907, SRR1758906) have been mapped to the Papio_anubis.Panu_3.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as coa1.bed record in the bottom row.

Figure S908**Papio anubis Kidney and Heart Duplicated copy**

Papio_anubis.Panu_3.0.dna_sm.toplevel.fa

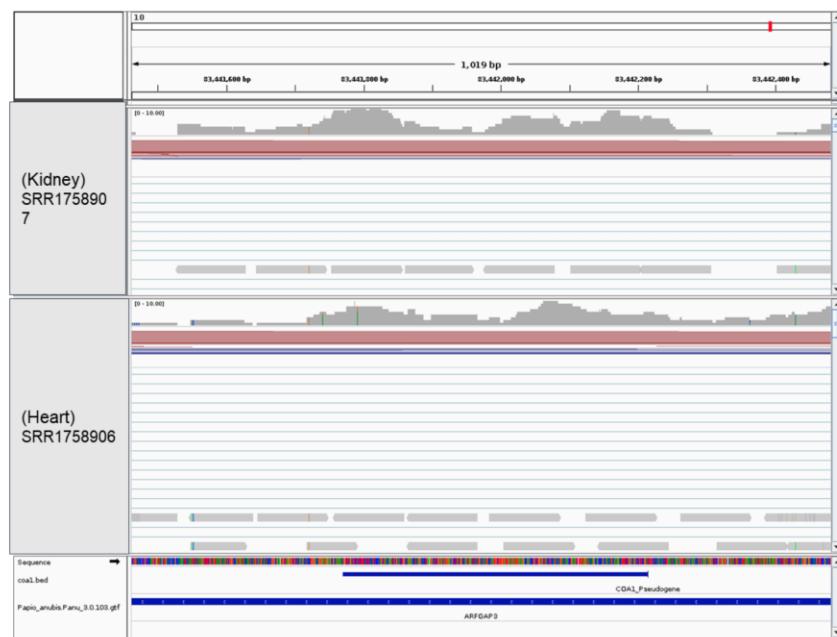


Figure S908: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* duplicated exons in Olive baboon (*Papio anubis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments in *ARFGAP3* gene region. Datasets from kidney and heart (SRR1758907, SRR1758906) have been mapped to the *Papio_anubis.Panu_3.0.dna_sm.toplevel.fa*. Locations of each of the exons are depicted as coal.bed record in the bottom row.

Figure S909

Macaca_fascicularis.Blood and Liver -Functional copy

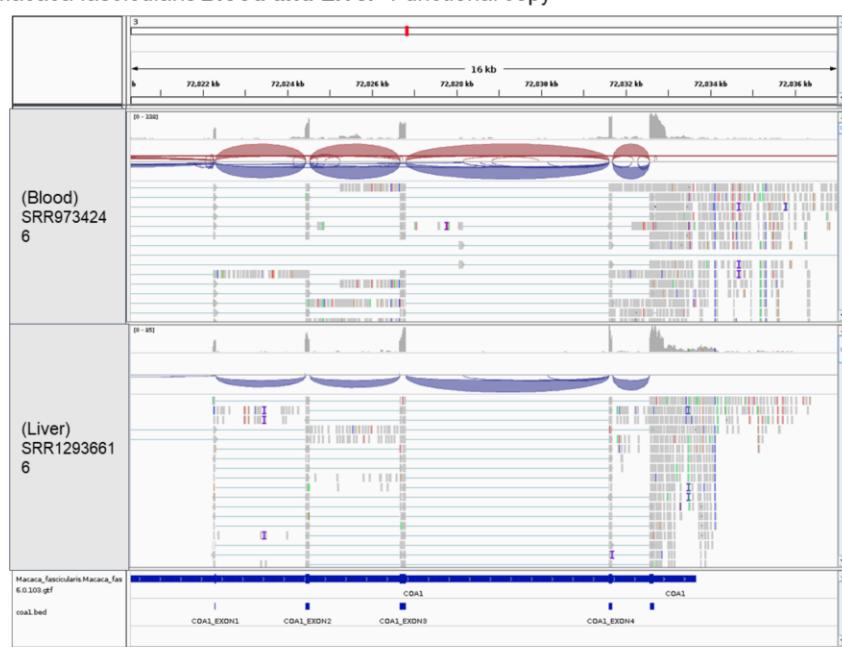


Figure S909: Screenshot of RNA-seq reads aligned to each of the putative locations of the five *COA1* exons in Crab-eating macaque (*Macaca fascicularis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood and liver (SRR9734246, SRR12936616) have been mapped to the *Macaca_fascicularis.Macaca_fascicularis_6.0.dna_sm.toplevel.fa*. Locations of each of the exons are depicted as *coal.bed* record in the bottom row.

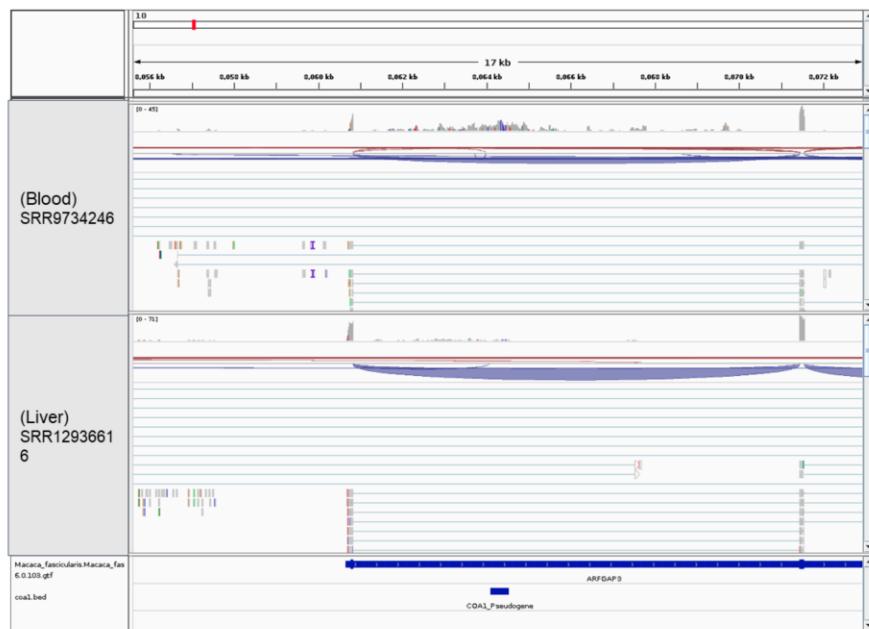
Figure S910Macaca fascicularis Blood and Liver -Functional copy^{Macaca_fascicularis.Macaca_fascicularis_6.0.dna_sm.toplevel.fa}

Figure S910: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* duplicated exons in Crab-eating macaque (*Macaca fascicularis*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments in *ARFGAP3* gene region. Datasets from blood and liver (SRR9734246, SRR1293661) have been mapped to the *Macaca_fascicularis.Macaca_fascicularis_6.0.dna_sm.toplevel.fa*. Locations of each of the exons are depicted as *coa1.bed* record in the bottom row.

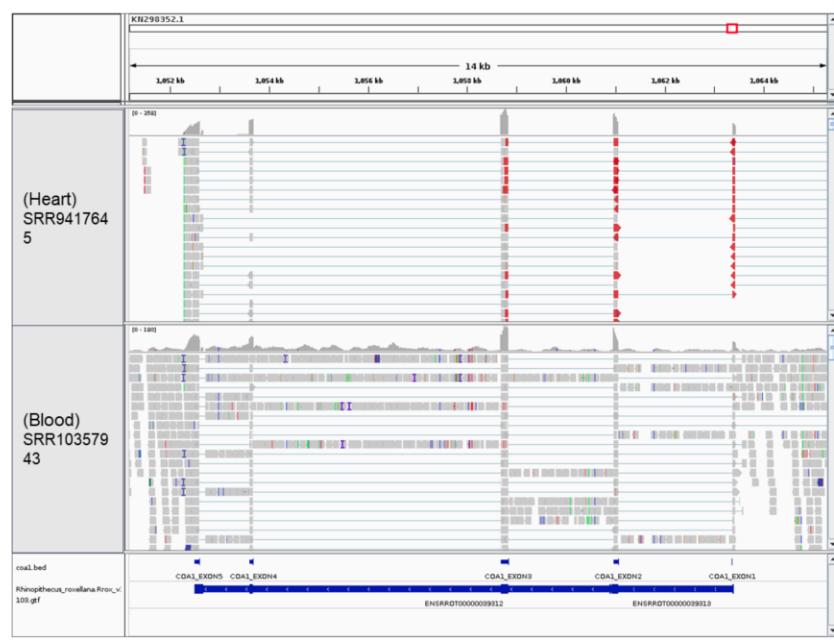
Figure S911**Rhinopithecus roxellana Heart and Blood Functional copy**

Figure S911: Screenshot of RNA-seq reads aligned to each of the putative locations of the five *COA1* exons in Golden snub-nosed monkey (*Rhinopithecus roxellana*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart and blood (SRR9417645, SRR10357943) have been mapped to the *Rhinopithecus_roxellana.Rrox_v1.dna_sm.toplevel.fa*. Locations of each of the exons are depicted as coa1.bed record in the bottom row.

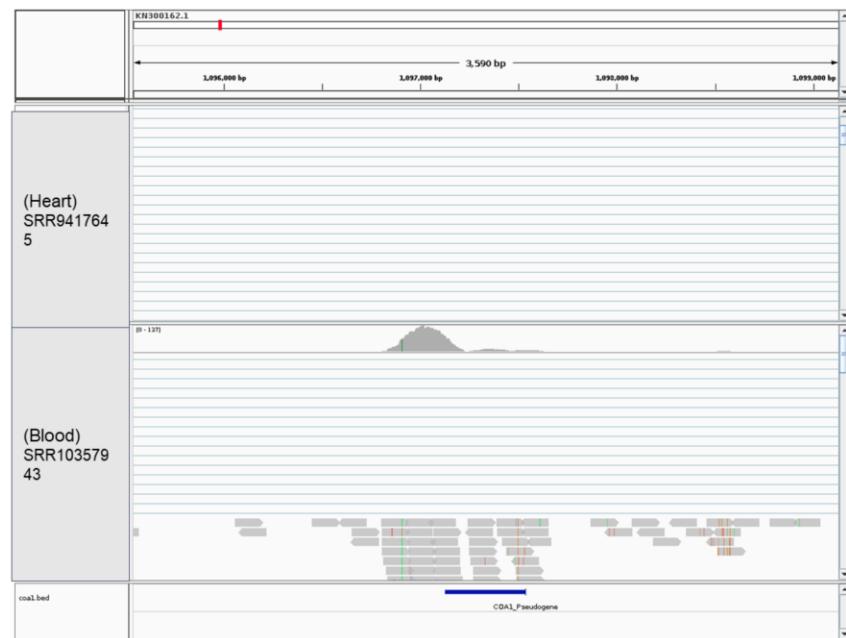
Figure S912*Rhinopithecus roxellana Heart and Blood Duplicated copy*^{Rhinopithecus_roxellana.Rrox_v1.dna_sm.toplevel.fa}

Figure S912: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* duplicated exons in Golden snub-nosed monkey (*Rhinopithecus roxellana*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments in *ARFGAP3* gene region. Datasets from heart and blood (SRR9417645, SRR10357943) have been mapped to the *Rhinopithecus_roxellana.Rrox_v1.dna_sm.toplevel.fa*. Locations of each of the exons are depicted as coal.bed record in the bottom row.

Figure S913*Homo sapiens Liver -Functional copy*

GCF_000001405.39_GRCh38.p13_genomic.fna



Figure S913: Screenshot of RNA-seq reads aligned to each of the putative locations of the five *COA1* exons in human (*Homo sapiens*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver (ERR1138635, ERR1138636) have been mapped to the GCF_000001405.39_GRCh38.p13_genomic.fna. Locations of each of the exons are depicted as.bed record in the bottom row.

Figure S914*Homo sapiens Liver exon-wise-5*

GCF_000001405.39_GRCh38.p13_genomic.fna

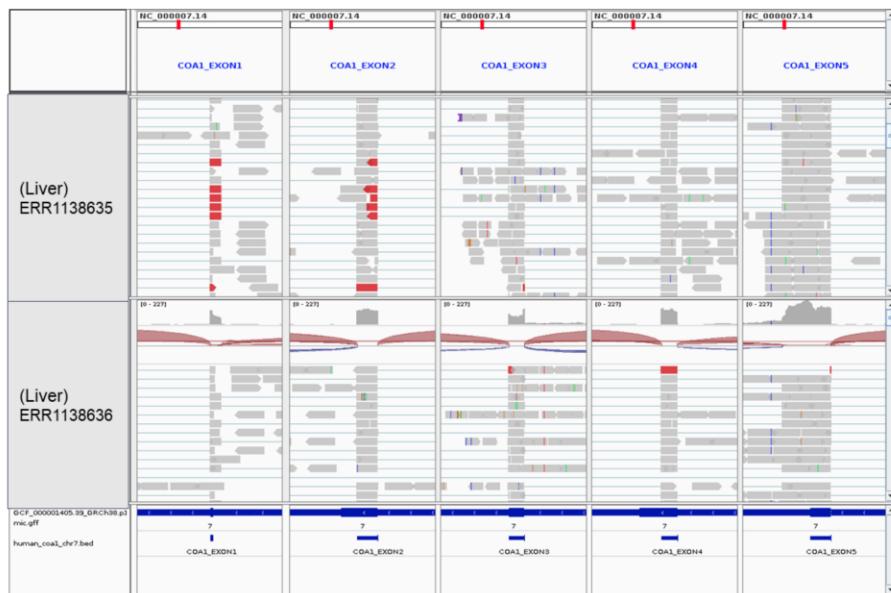
**Figure S914:** A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S913**.

Figure S915*Homo sapiens Liver -Duplicated copy*

GCF_000001405.39_GRCh38.p13_genomic.fna

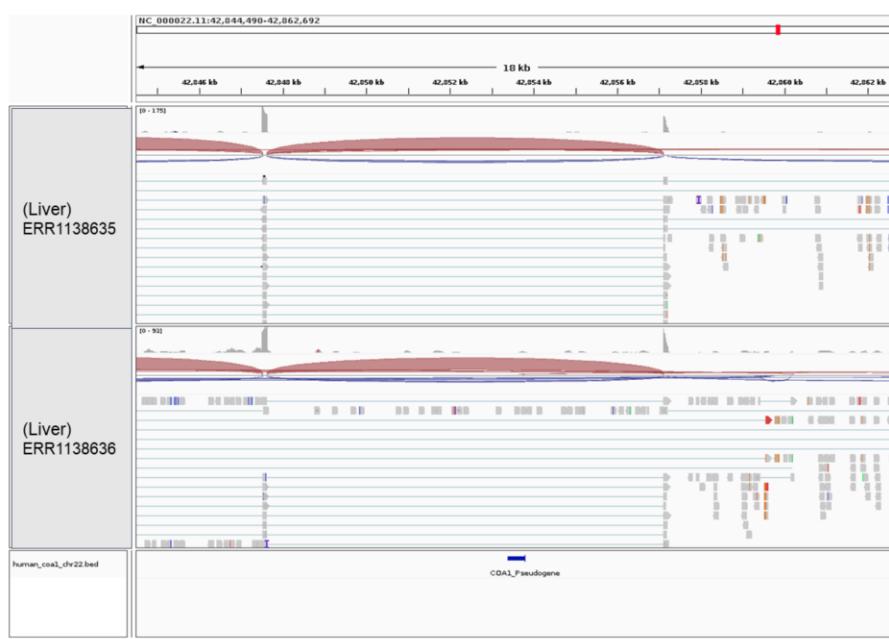


Figure S915: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* duplicated exons in human (*Homo sapiens*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments in *ARFGAP3* gene region. Datasets from liver (ERR1138635, ERR1138636) have been mapped to the GCF_000001405.39_GRCh38.p13_genomic.fna. Locations of each of the exons are depicted as.bed record in the bottom row.

Figure S916*Homo sapiens Testis Functional copy*

GCF_000001405.39_GRCh38.p13_genomic.fna

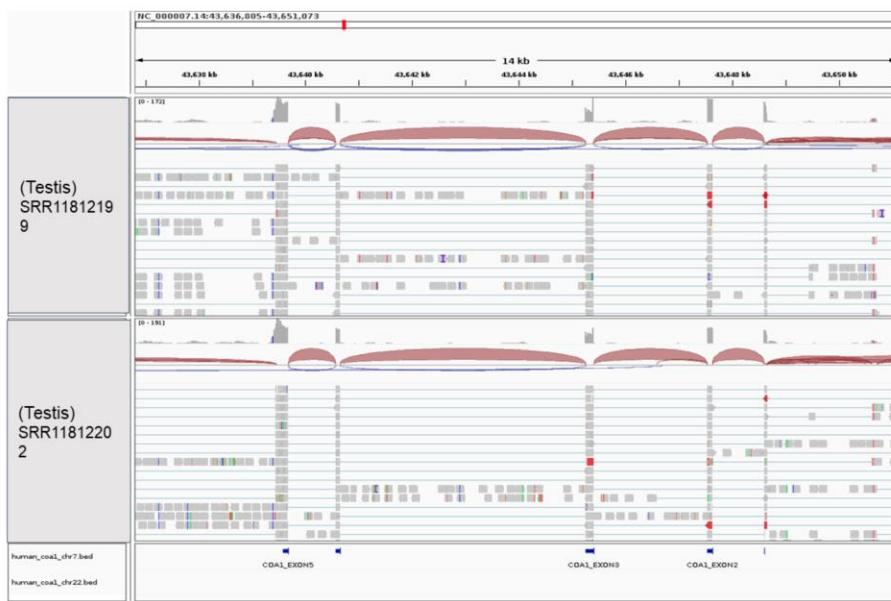


Figure S916: Screenshot of RNA-seq reads aligned to each of the putative locations of the five *COA1* exons in human (*Homo sapiens*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis (SRR11812199, SRR11812202) have been mapped to the GCF_000001405.39_GRCh38.p13_genomic.fna. Locations of each of the exons are depicted as.bed record in the bottom row.

Figure S917**Homo sapiens Testis exon-wise-**

GCF_000001405.39_GRCh38.p13_genomic.fna

5

NC_000007.14:43,640,412-43,647,397-43,645,130-43,640,417-43,639,444-43,644

COA1_EXON1 COA1_EXON2 COA1_EXON3 COA1_EXON4 COA1_EXONS

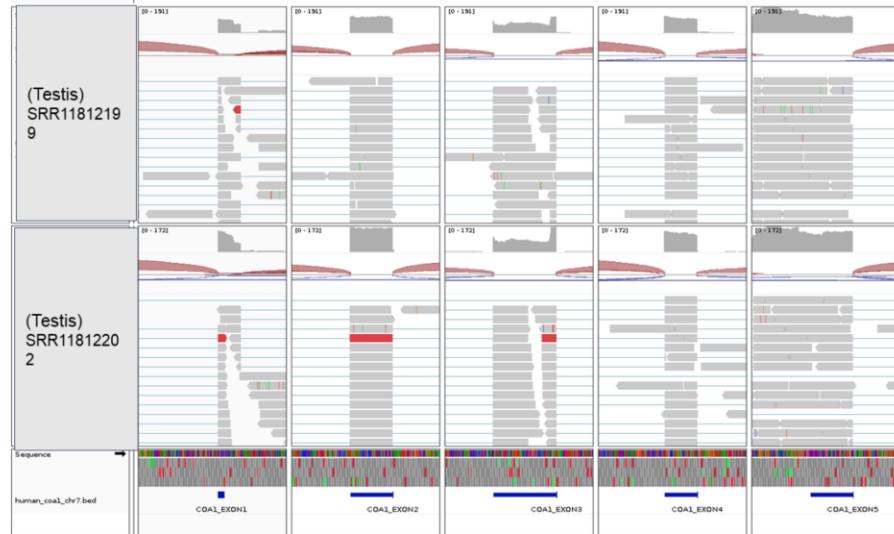
**Figure S917:** A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S916**.

Figure S918*Homo sapiens Testis Duplicated copy*

GCF_000001405.39_GRCh38.p13_genomic.fna

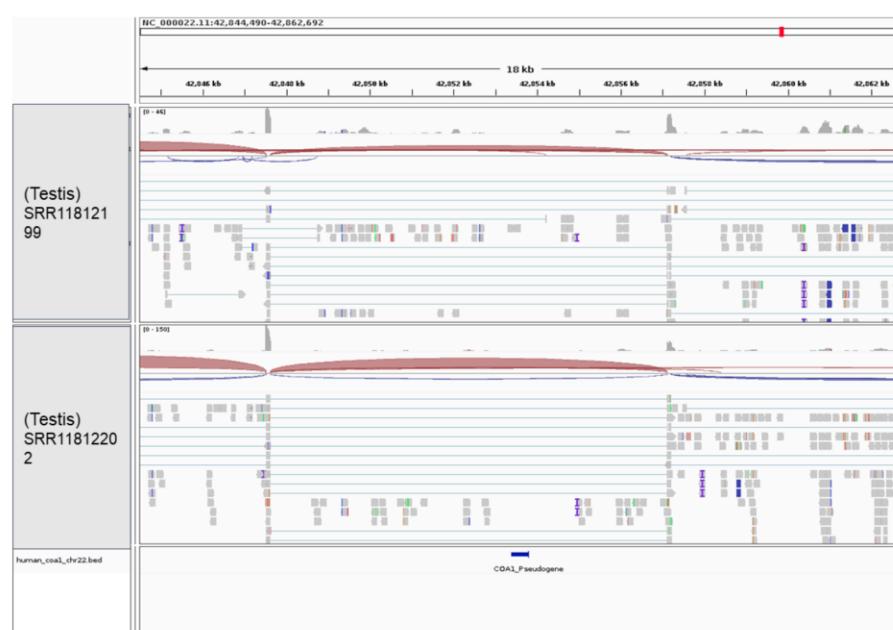


Figure S918: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* duplicated exons in human (*Homo sapiens*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments in *ARFGAP3* gene region. Datasets from testis (SRR11812199, SRR11812202) have been mapped to the GCF_000001405.39_GRCh38.p13_genomic.fna. Locations of each of the exons are depicted as.bed record in the bottom row.

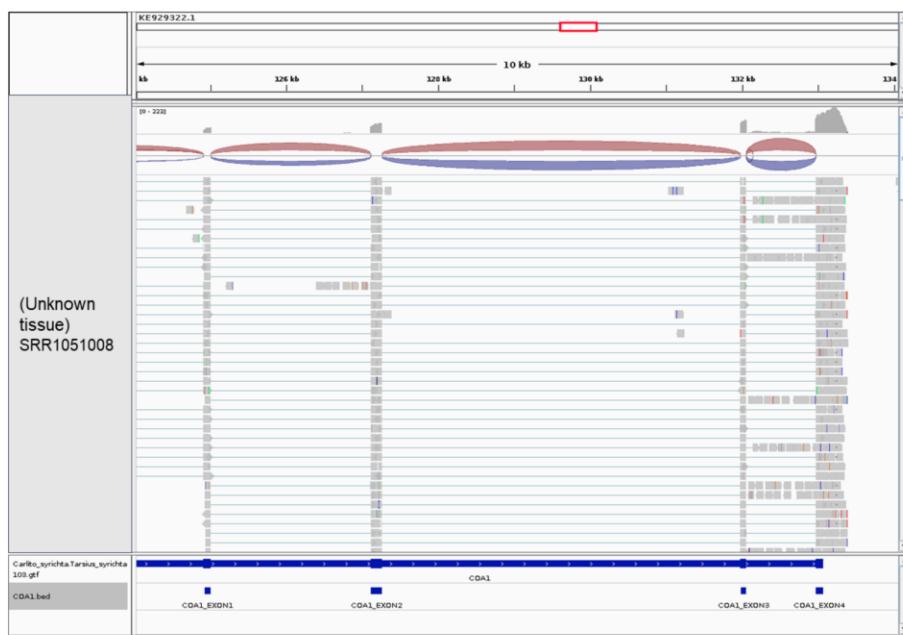
Figure S919***Carlito syrichta Unknown tissue***

Figure S919: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Philippine tarsier (*Carlito syrichta*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from Unknown tissue (SRR1051008) have been mapped to its own genome. Locations of each of the exons are depicted as bed record in the bottom row.

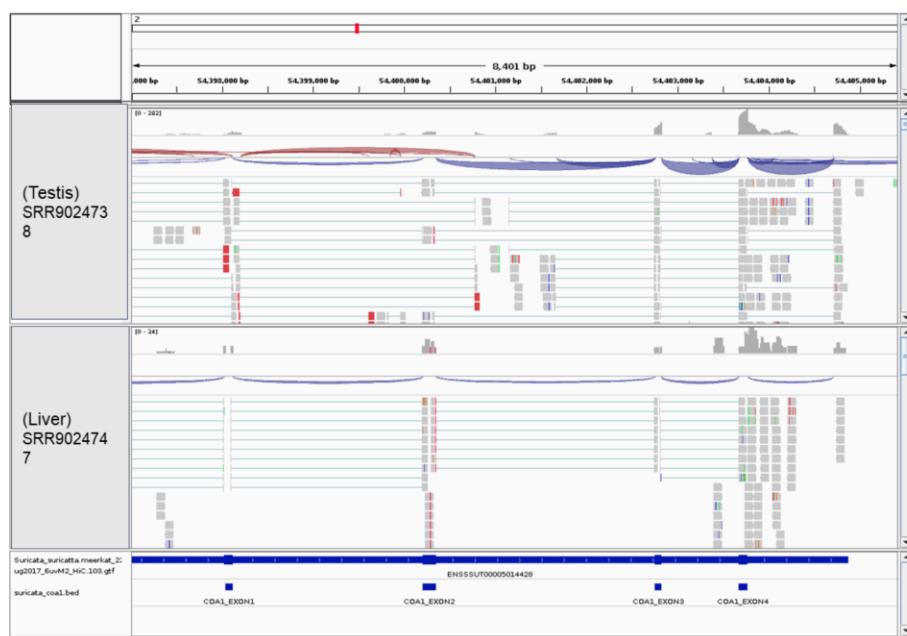
Figure S920Suricata_suricatta.meerkat_22Aug2017_6uvM2_HiC.dna_sm.toplevel.fa
Suricata suricatta Testis and Liver -Functional copy

Figure 920: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in meerkat (*Suricata suricatta*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis and liver (SRR9024738 and SRR9024747) have been mapped to the Suricata_suricatta.meerkat_22Aug2017_6uvM2_HiC.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

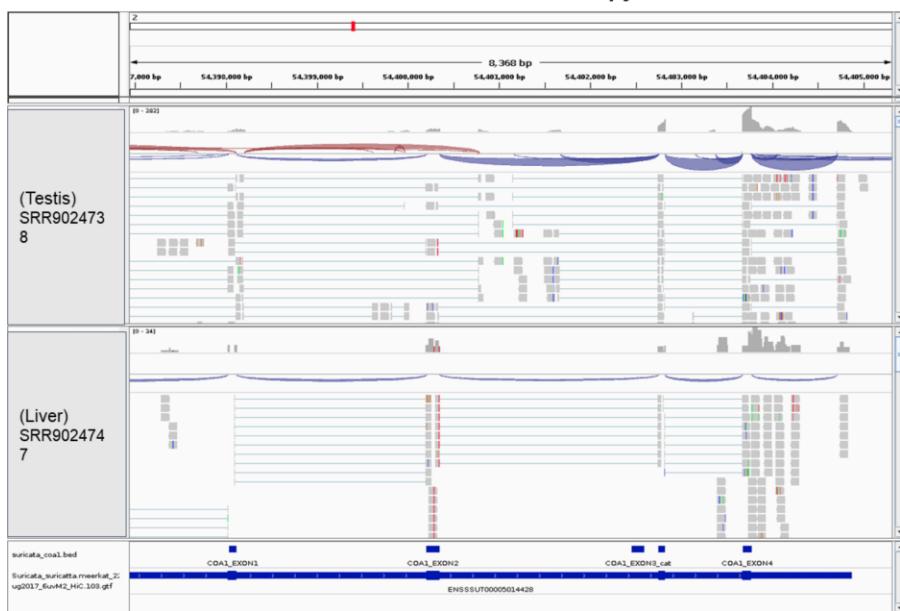
Figure S921Suricata_suricatta.meerkat_22Aug2017_6uvM2_HiC.dna_sm.toplevel.fa
Suricata suricatta Testis and Liver -Functional copy

Figure S921: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons with exon 3 cat in meerkat (*Suricata suricatta*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from testis and liver (SRR9024738 and SRR9024747) have been mapped to the Suricata_suricatta.meerkat_22Aug2017_6uvM2_HiC.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

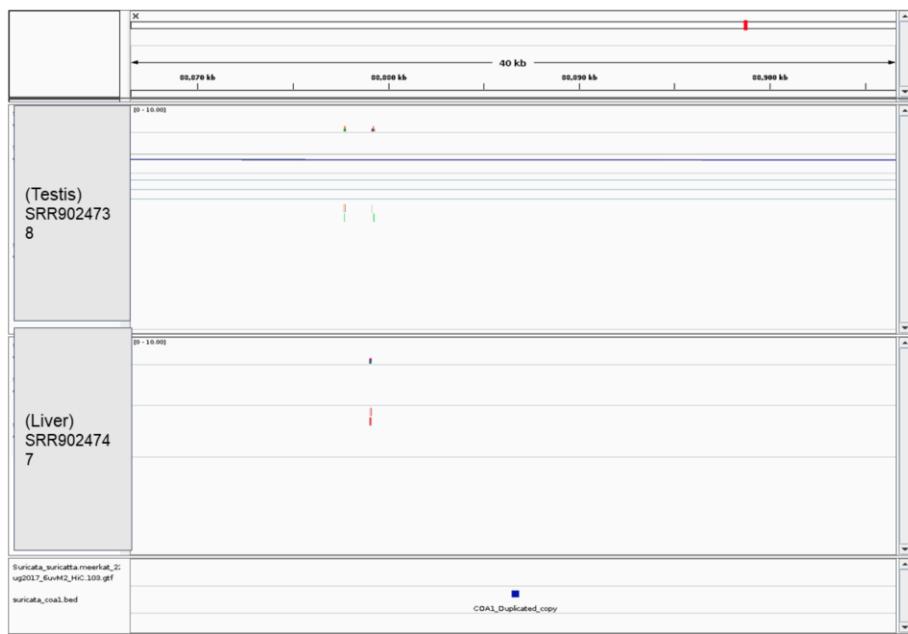
Figure S922***Suricata suricatta* Testis and Liver -Duplicated copy**

Figure S922: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* duplicated copy in meerkat (*Suricata suricatta*). Datasets from testis and liver (SRR9024738 and SRR9024747) have been mapped to the Suricata_suricatta.meerkat_22Aug2017_6uvM2_HiC.dna_sm.toplevel.fa. Locations of the *COA1* gene duplicated copy is depicted as bed record in the bottom row.

Figure S923***Canis lupus familiaris* Spleen and Skeletal Muscle -Functional copy**

Canis_lupus_familiaris.CanFam3.1.dna_sm.toplevel.fa

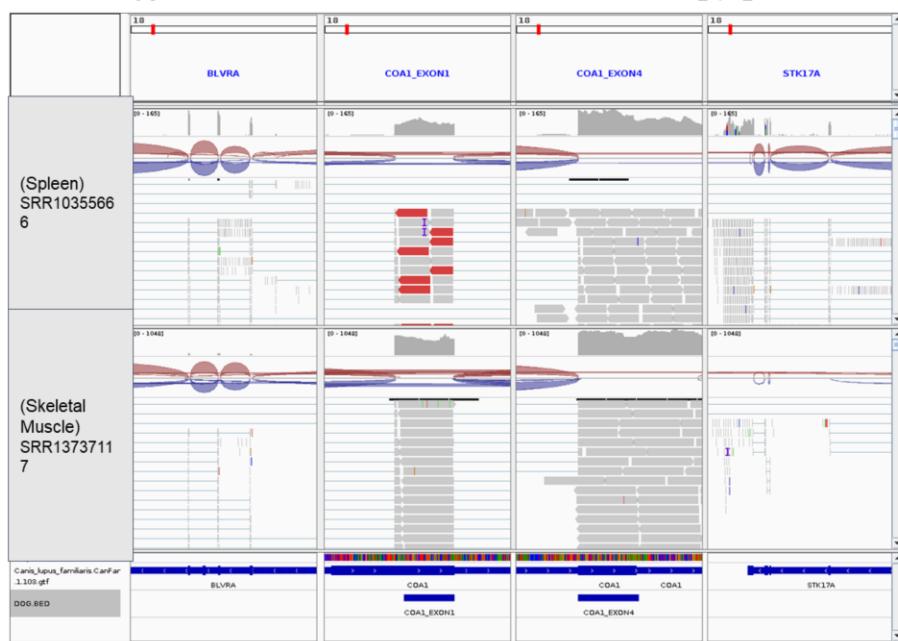


Figure S923: Screenshot of RNA-seq reads aligned to each of the putative locations of *COA1* gene and the flanking genes *BLVRA* and *STK17A* in dog (*Canis lupus familiaris*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen and skeletal muscle (SRR10355666 and SRR13737117) have been mapped to the Canis_lupus_familiaris.CanFam3.1.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S924**Canis lupus familiaris Spleen and Skeletal Muscle -Functional**

Canis_lupus_familiaris.CanFam3.1.dna_sm.toplevel.fa

COPY

6,563-6,577,525

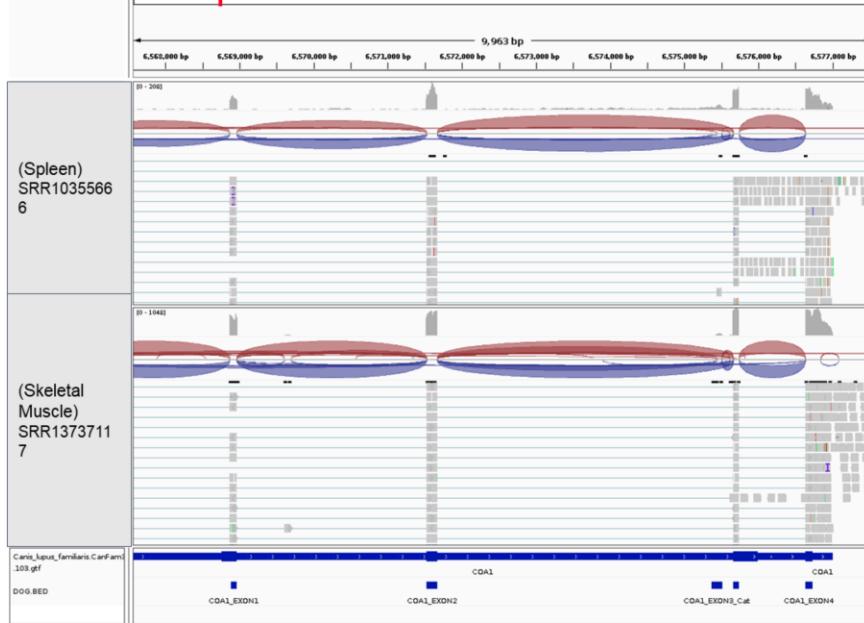


Figure S924: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in dog (*Canis lupus familiaris*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from spleen and skeletal muscle (SRR1035566 and SRR1373711) have been mapped to the Canis_lupus_familiaris.CanFam3.1.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S925

Canis lupus familiaris Spleen and Skeletal Muscle Canis_lupus_familiaris.CanFam3.1.dna_sm.toplevel.fa

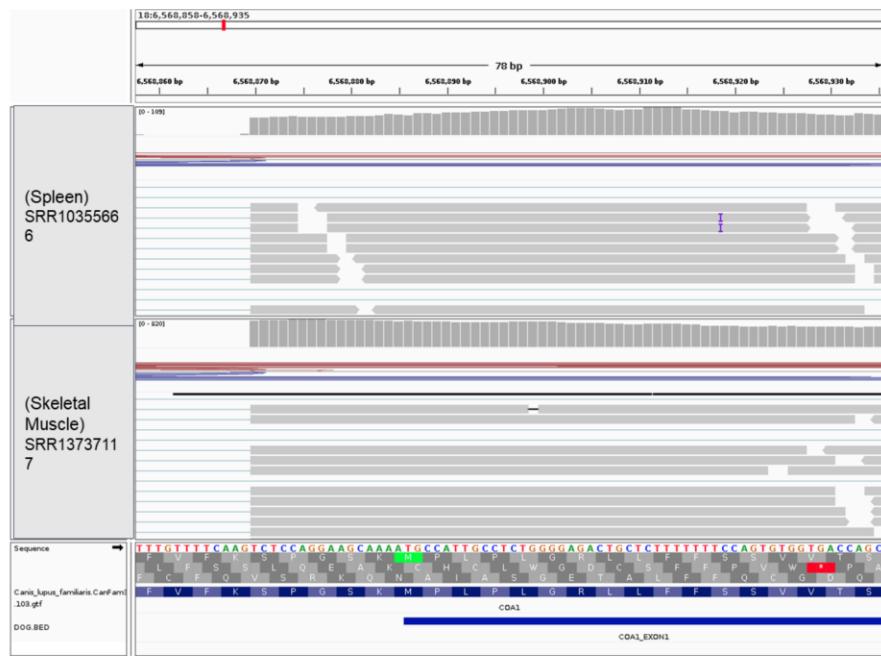


Figure S925: Zoomed view of exon 1 shown in **Supplementary Fig. S924**.

Figure S926

Canis lupus familiaris Spleen and Skeletal Muscle Canis_lupus_familiaris.CanFam3.1.dna_sm.toplevel.fa

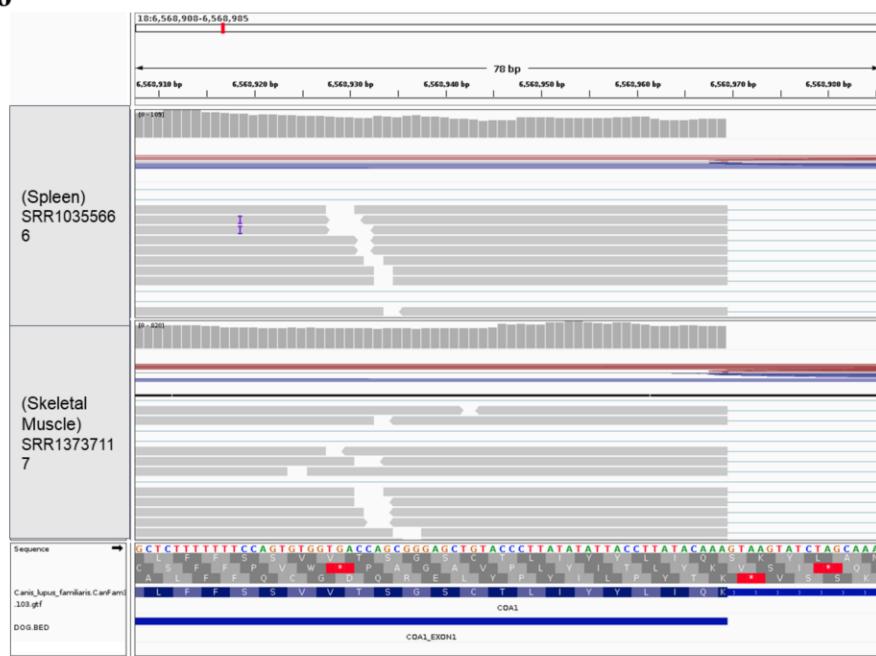


Figure S926: Zoomed view of exon 1 shown in Supplementary Fig. S924.

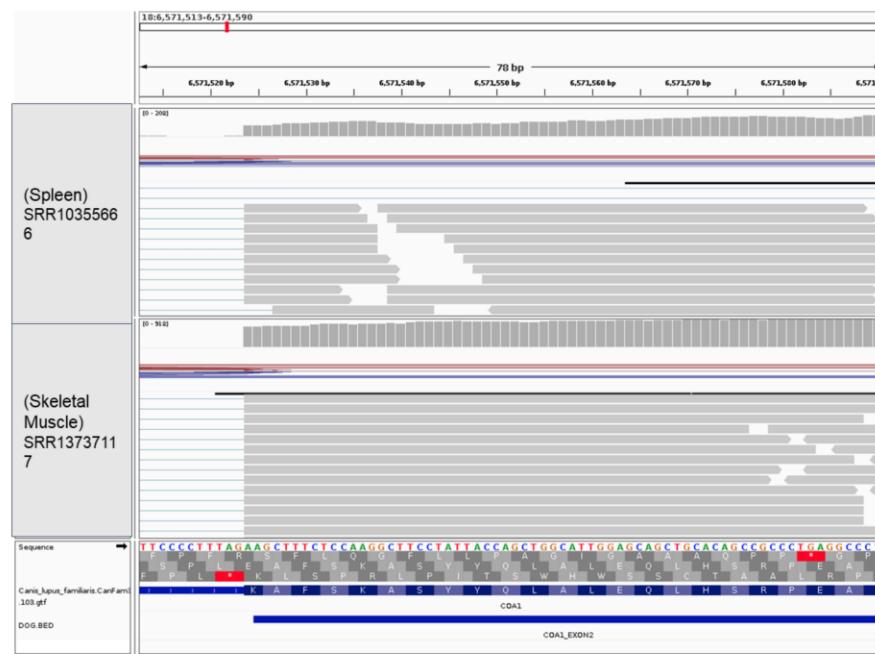
Figure S927***Canis lupus familiaris* Spleen and Skeletal Muscle Canis_lupus_familiaris.CanFam3.1.dna_sm.toplevel.fa****Figure S927:** Zoomed view of exon 2 shown in **Supplementary Fig. S924**.

Figure S928

*Canis lupus familiaris Spleen and Skeletal Muscle*Canis_lupus_familiaris.CanFam3.1.dna_sm.toplevel.fa

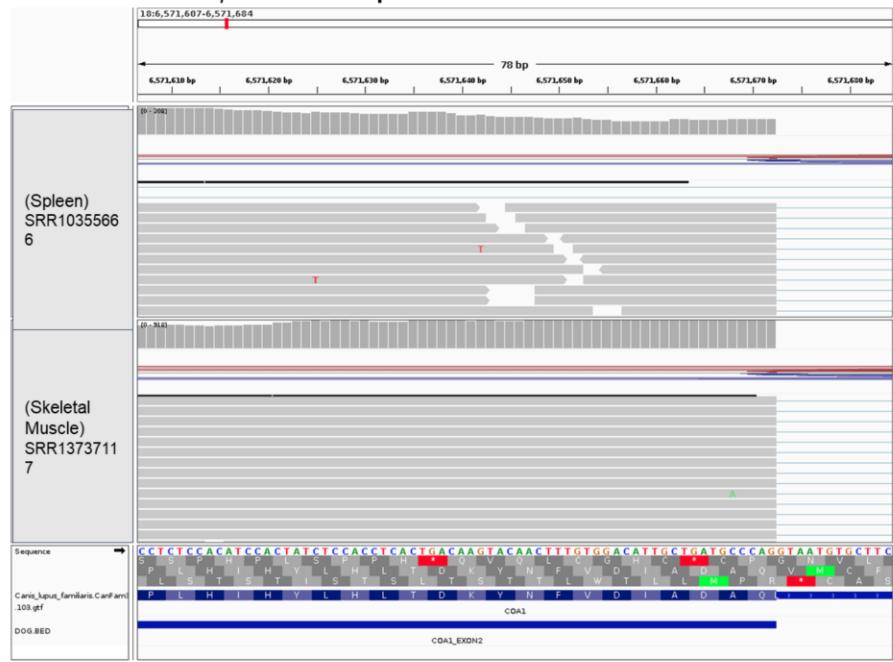


Figure S928: Zoomed view of exon 2 shown in **Supplementary Fig. S924**.

Figure S929

Canis lupus familiaris Spleen and Skeletal Muscle Canis_lupus_familiaris.CanFam3.1.dna_sm.toplevel.fa

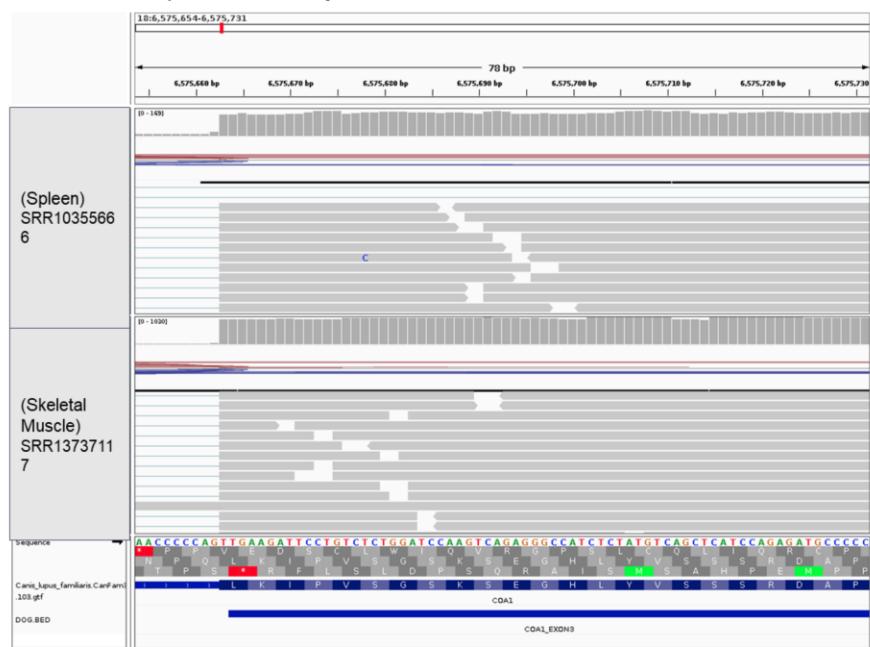


Figure S929: Zoomed view of exon 3 shown in **Supplementary Fig. S924**.

Figure S930

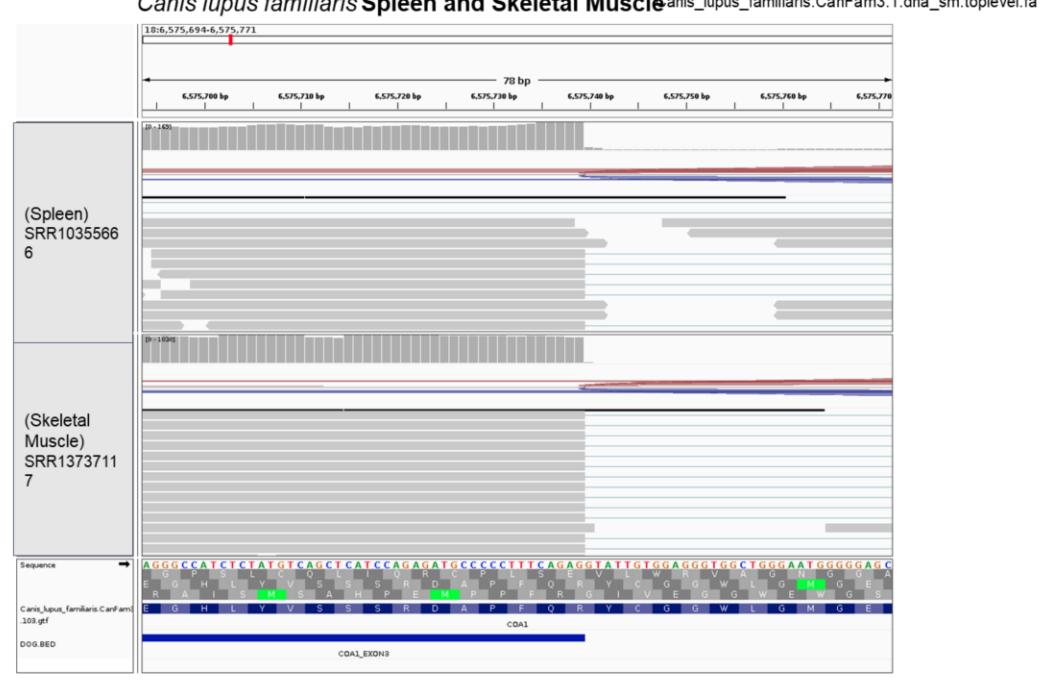


Figure S930: Zoomed view of exon 3 shown in **Supplementary Fig. S924**.

Figure S931

Canis lupus familiaris Spleen and Skeletal Muscle Canis_lupus_familiaris.CanFam3.1.dna_sm.toplevel.fa

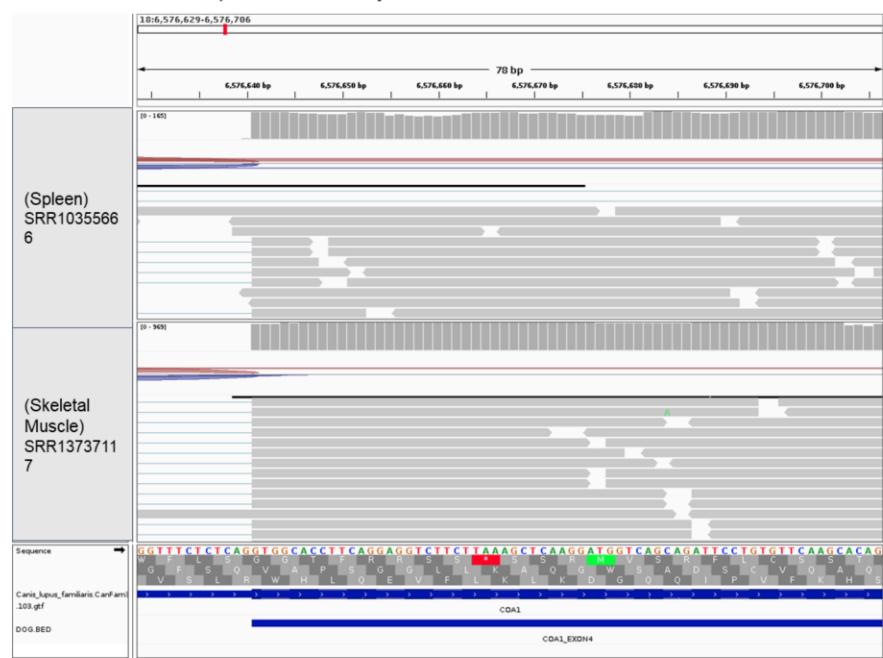


Figure S931: Zoomed view of exon 4 shown in **Supplementary Fig. S924**.

Figure S932

Canis lupus familiaris Spleen and Skeletal Muscle Canis_lupus_familiaris.CanFam3.1.dna_sm.toplevel.fa

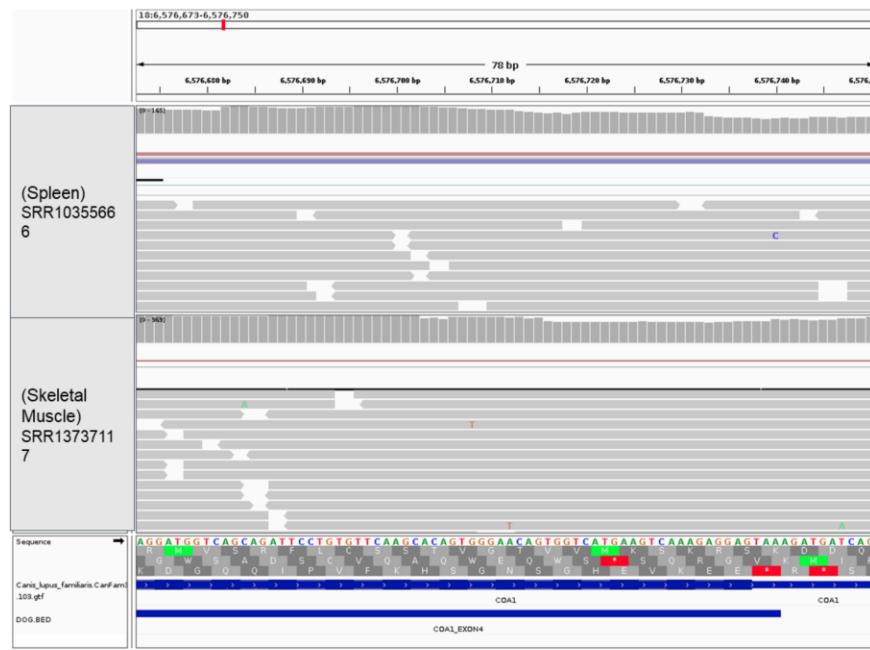


Figure S932: Zoomed view of exon 4 shown in **Supplementary Fig. S924**.

Figure S933

Canis lupus familiaris Spleen and Skeletal Muscle -Functional copy

Canis_lupus_familiaris.CanFam3.1.dna_sm.toplevel.fa



Figure S933: A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S924**.

Figure S934*Canis lupus familiaris* Spleen and Skeletal Muscle -Duplicated Copy

Canis_lupus_familiaris.CanFam3.1.dna_sm.toplevel.fa

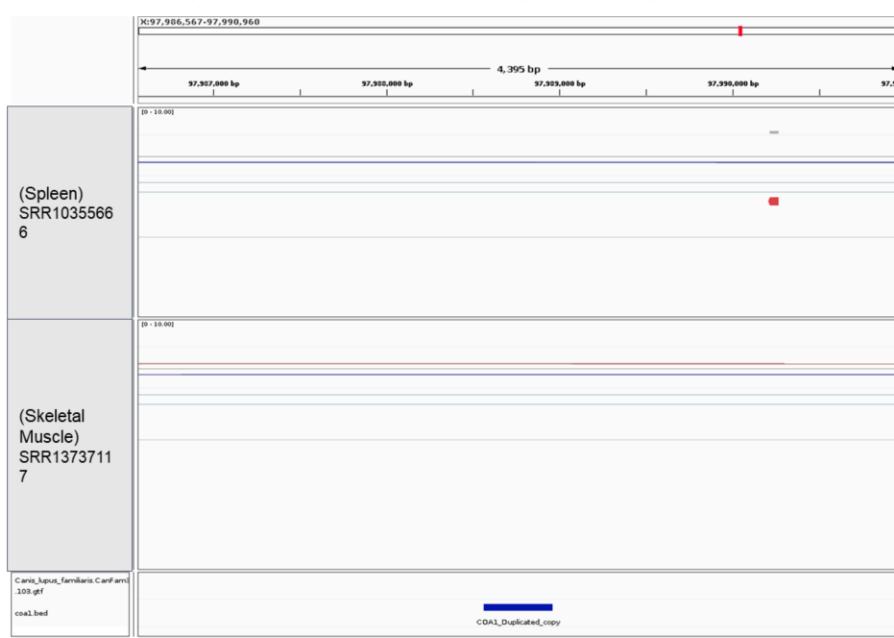


Figure S934: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* duplicated copy in dog (*Canis lupus familiaris*). Datasets from spleen and skeletal muscle (SRR10355666 and SRR3218716) have been mapped to the *Canis_lupus_familiaris.CanFam3.1.dna_sm.toplevel.fa*. Locations of the *COA1* gene duplicated copy is depicted as bed record in the bottom row.

Figure S935 *Mustela putorius furo* Heart and Kidney -Functional copy *Mustela_putorius_furo.MusPutFur1.0.dna_sm.toplevel.fa*

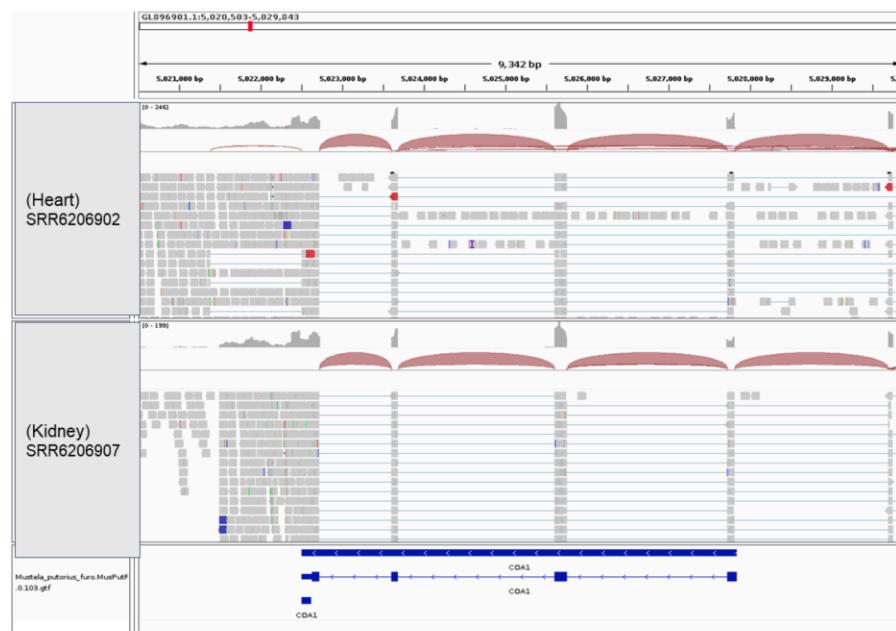


Figure S935: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Ferret (*Mustela putorius furo*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart and kidney (SRR6206902 and SRR6206907) have been mapped to the *Mustela_putorius_furo.MusPutFur1.0.dna_sm.toplevel.fa*. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S936 *Mustela putorius furo* Heart and Kidney -Duplicated copy Mustela_putorius_furo.MusPutFur1.0.dna_sm.toplevel.fa

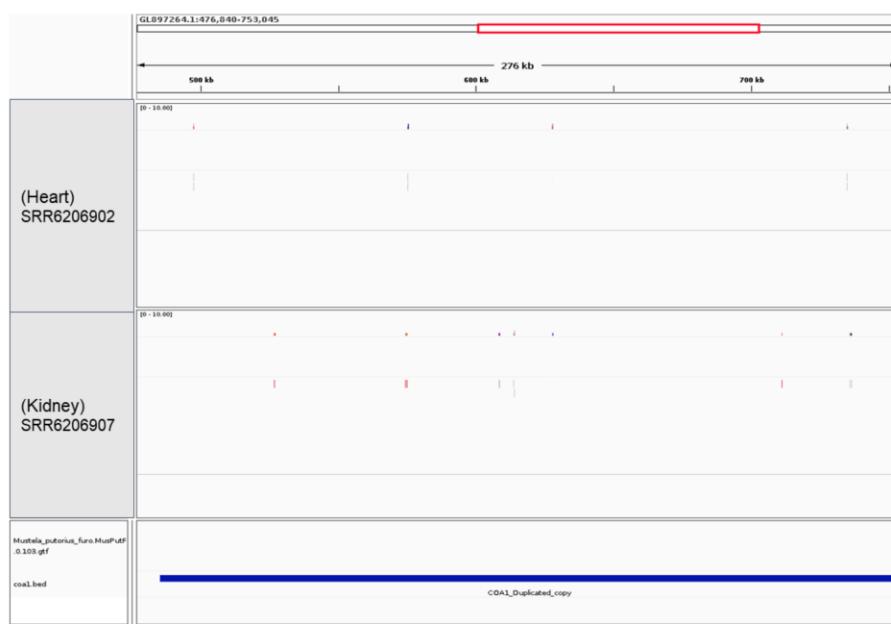


Figure S936: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* duplicated copy in ferret (*Mustela putorius furo*). Datasets from heart and kidney (SRR6206902 and SRR6206907) have been mapped to the *Mustela_putorius_furo.MusPutFur1.0.dna_sm.toplevel.fa*. Locations of the *COA1* gene duplicated copy is depicted as bed record in the bottom row.

Figure S937*Ailuropoda melanoleuca Heart and liver -Functional copy*

Ailuropoda_melanoleuca_ASM200744v2.dna_sm.toplevel.fa



Figure S937: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Giant panda (*Ailuropoda melanoleuca*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from heart and liver (SRR10215705 and SRR10215710) have been mapped to the *Ailuropoda_melanoleuca_ASM200744v2.dna_sm.toplevel.fa*. Locations of each of the exons are depicted as bed record in the bottom row.

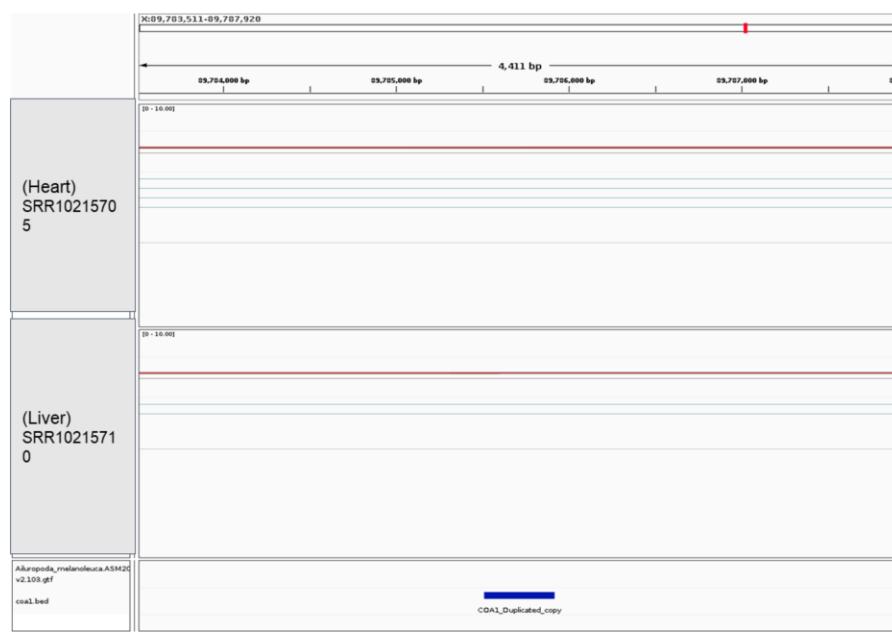
Figure S938*Ailuropoda melanoleuca* Heart and liver -Duplicated copy

Figure S938: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* duplicated copy in Giant panda (*Ailuropoda melanoleuca*). Datasets from heart and liver (SRR10215705 and SRR10215710) have been mapped to the *Ailuropoda melanoleuca*.ASM200744v2.dna_sm.toplevel.fa. Locations of the *COA1* gene duplicated copy is depicted as bed record in the bottom row.

Figure S939

Ursus_americanus_ASM334442v1.dna_sm.toplevel.fa

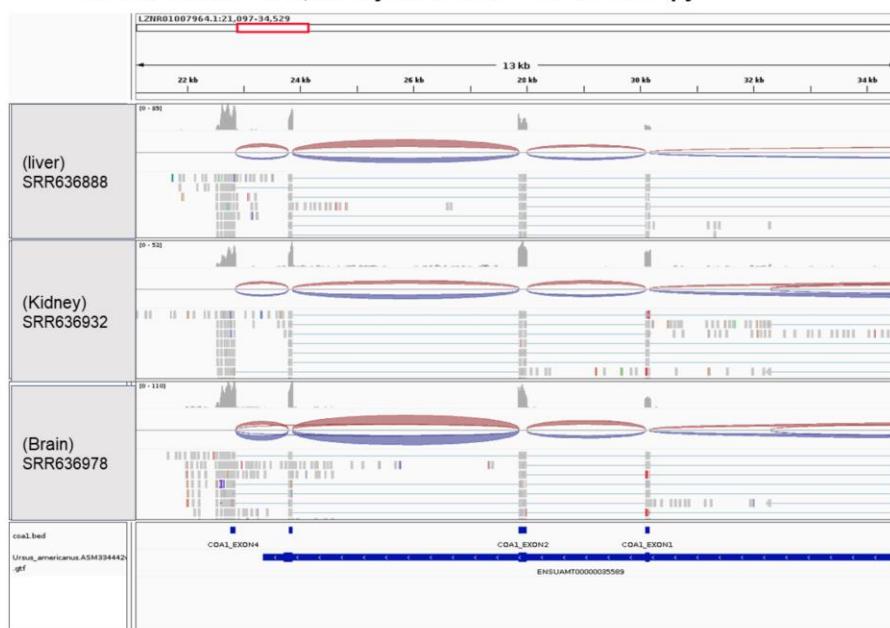
Ursus americanus Liver,Kidney and Brain Functional copy

Figure S939: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in American black bear (*Ursus americanus*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from liver, kidney and brain (SRR636888, SRR636932 and SRR636978) have been mapped to the Ursus_americanus_ASM334442v1.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S940

Ursus_americanus_ASM334442v1.dna_sm.toplevel.fa

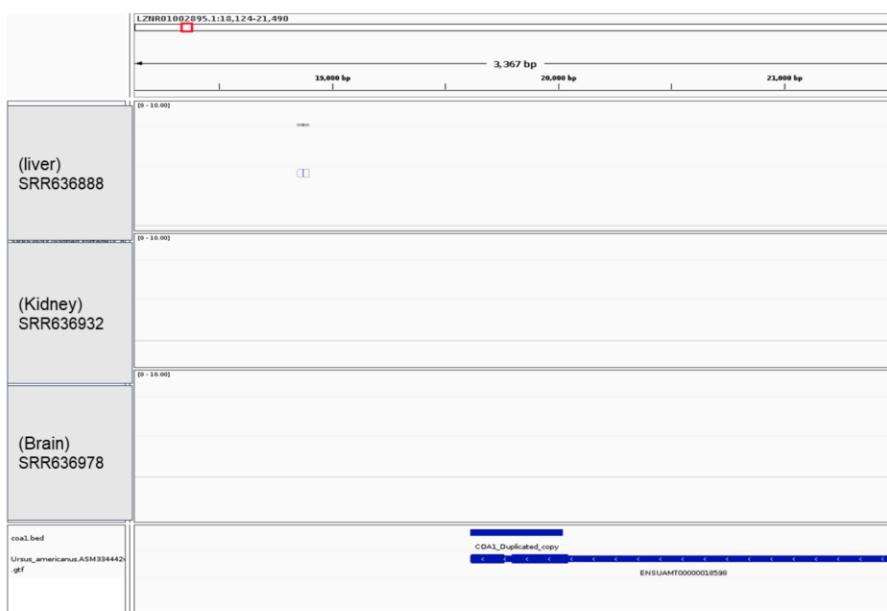
Ursus americanus Liver,Kidney and Brain -Duplicated copy

Figure S940: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* duplicated copy in American black bear(*Ursus americanus*). Datasets from liver, kidney and brain (SRR636888, SRR636932 and SRR636978) have been mapped to the Ursus_americanus_ASM334442v1.dna_sm.toplevel.fa. Locations of of the *COA1* gene duplicated copy is depicted as bed record in the bottom row.

Figure S941

Leptonychotes weddellii Lung and Muscle

GCF_000349705.1_LepWed1.0_genomic.fna

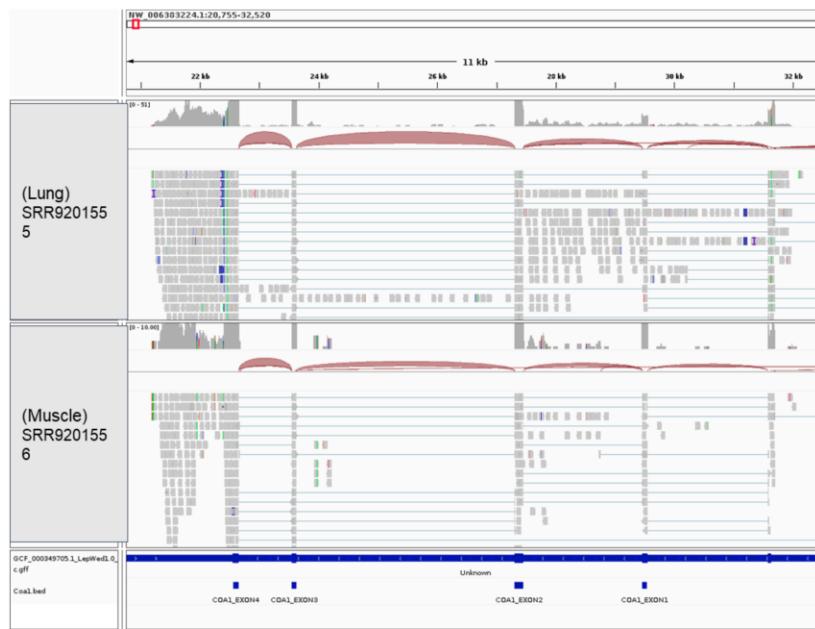


Figure S941: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Weddell seal (*Leptonychotes weddellii*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from lung and muscle (SRR9201555 and SRR9201556) have been mapped to the GCF_000349705.1_LepWed1.0_genomic.fna. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S942*Leptonychotes weddellii* Lung and Muscle

GCF_000349705.1_LepWed1.0_genomic.fna

**Figure S942:** A zoomed in view of each of the *COA1* exons shown in **Supplementary Fig. S941**.

Figure S943**Leptonychotes weddellii Lung and Muscle GCF_000349705.1_LepWed1.0_genomic.fna**

Figure S943: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* duplicated copy in Weddell seal (*Leptonychotes weddellii*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from lung and muscle (SRR9201555 and SRR9201556) have been mapped to the GCF_000349705.1_LepWed1.0_genomic.fna. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S944 *Panthera tigris altaica* Blood -Functional copy Panthera_tigris_altaica.PanTig1.0.dna_sm.toplevel.fa



Figure S944: Screenshot of RNA-seq reads aligned to each of the putative locations of the three *COA1* exons in Siberian Tiger (*Panthera tigris altaica*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR924676) have been mapped to the *Panthera_tigris_altaica.PanTig1.0.dna_sm.toplevel.fa*. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S945 *Panthera tigris altaica* Blood -Functional copy Panthera_tigris_altaica.PanTig1.0.dna_sm.toplevel.fa

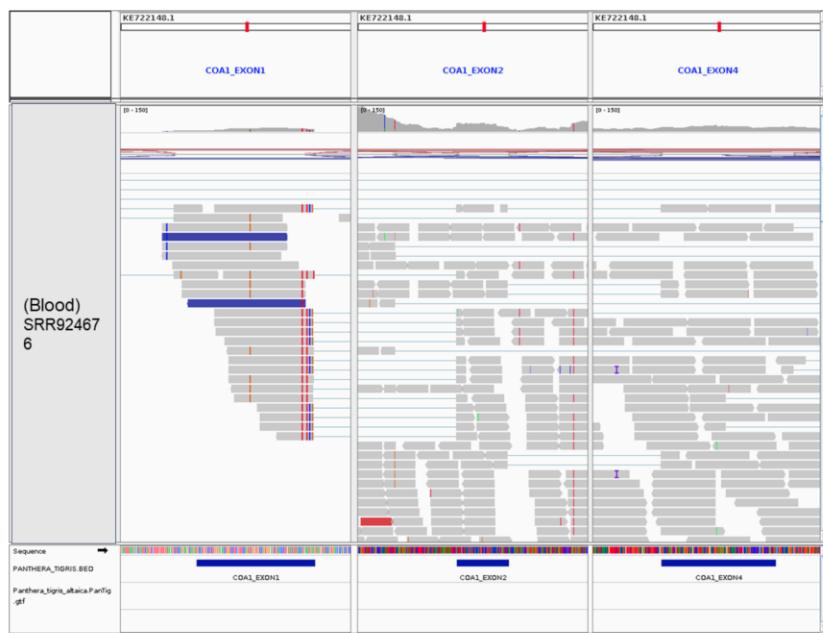


Figure S945: Zoomed view of all three exons 1, 2, and 4 containing cds of *COA1* shown in **Supplementary Fig. S944**.

Figure S946

Panthera tigris altaica Pooled samples and Blood -Duplicated copy

Panthera_tigris_altaica.PanTig1.0.dna_sm.toplevel.fa

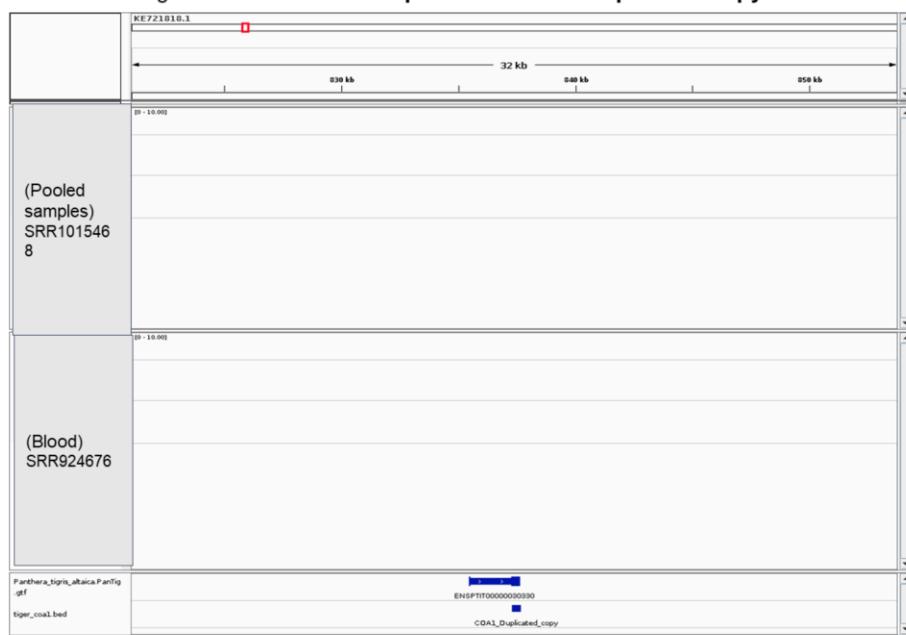


Figure S946: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* duplicated copy in Siberian Tiger (*Panthera tigris altaica*). Datasets from Pooled samples and blood (SRR1015468 and SRR924676) have been mapped to the Panthera_tigris_altaica.PanTig1.0.dna_sm.toplevel.fa. Locations of the *COA1* duplicated copy is depicted as bed record in the bottom row.

Figure S947*Panthera leo persica* Blood -Functional copy

Panthera_leo.PanLeo1.0.dna_sm.toplevel.fa

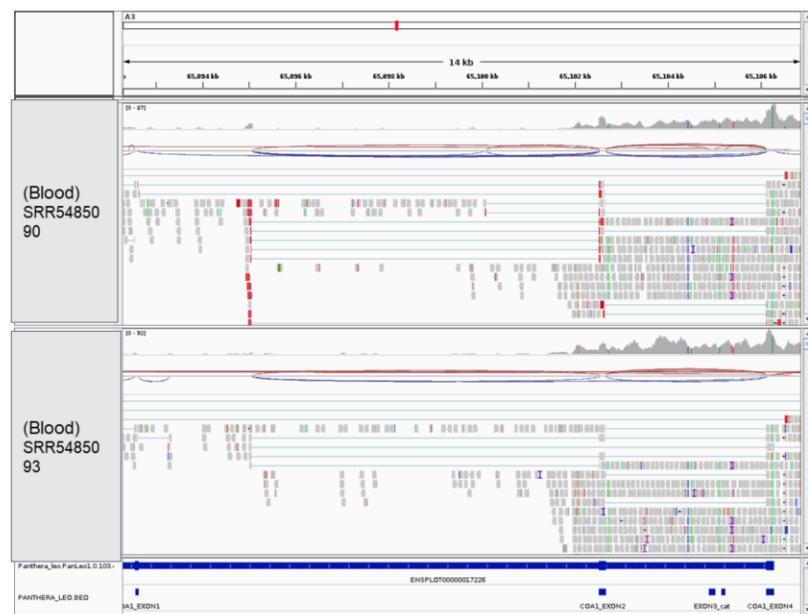


Figure S947: Screenshot of RNA-seq reads aligned to each of the putative locations of the four *COA1* exons in Asiatic lion (*Panthera leo persica*). Gray boxes represent reads aligned to the genome and thin lines connecting these boxes represent the spliced read alignments. Datasets from blood (SRR5485090 and SRR5485093) have been mapped to the Panthera_leo.PanLeo1.0.dna_sm.toplevel.fa. Locations of each of the exons are depicted as bed record in the bottom row.

Figure S948*Panthera leo persica* Blood -Functional copy

Panthera_leo.PanLeo1.0.dna_sm.toplevel.fa

**Figure S948:** Zoomed view of all CDS containing three exons.

Figure S949*Panthera leo persica* Blood -Duplicated copy

Panthera_leo.PanLeo1.0.dna_sm.toplevel.fa

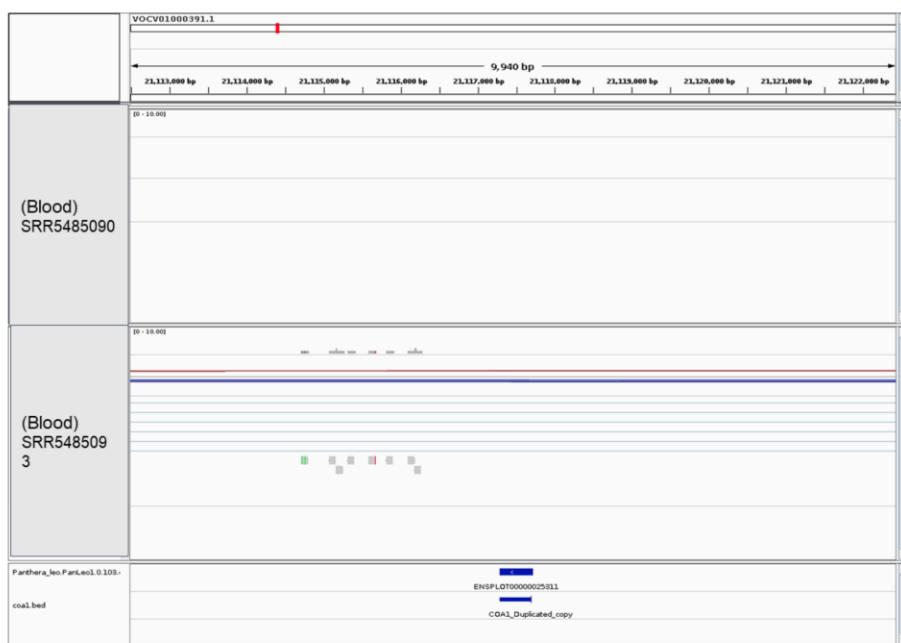


Figure S949: Screenshot of RNA-seq reads aligned to each of the putative locations of the *COA1* duplicated copy in Asiatic lion (*Panthera leo persica*). Datasets from blood (SRR5485090 and SRR5485093) have been mapped to the Panthera_leo.PanLeo1.0.dna_sm.toplevel.fa. Locations of the *COA1* gene duplicated copy is depicted as bed record in the bottom row.

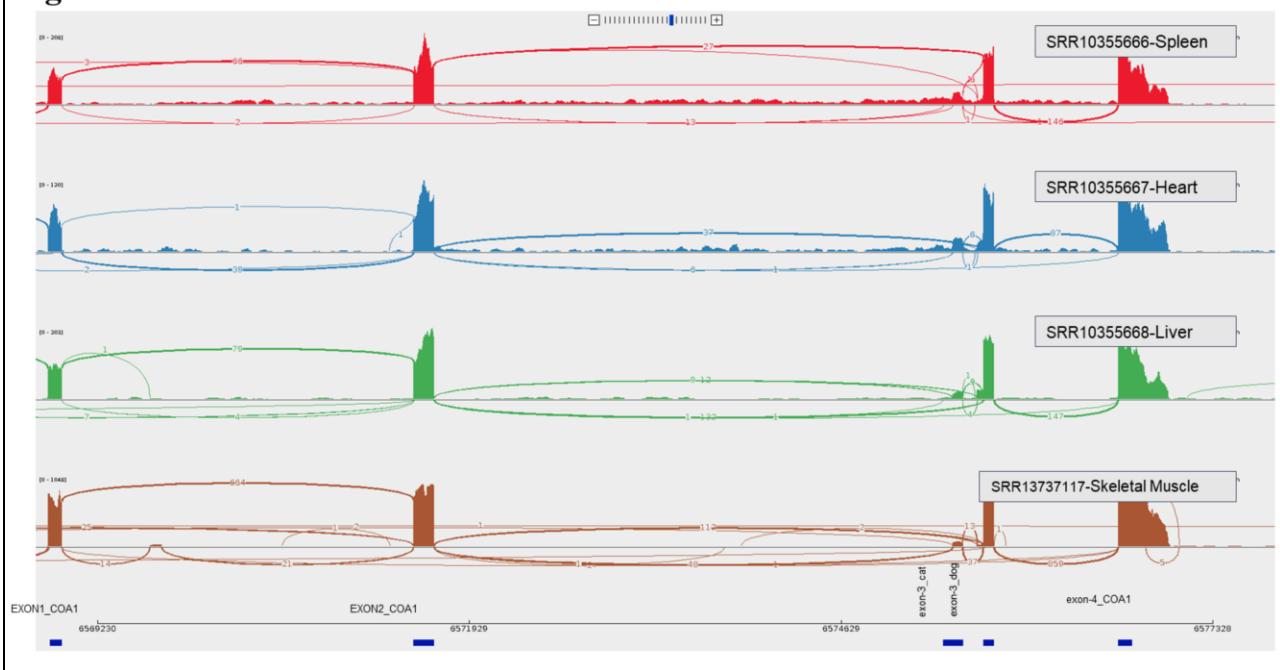
Figure S950*Canis lupus familiaris*

Figure S950: Screenshot of Sashimi plot of *COA1* exon 1, 2, exon-3 cat, exon-3 dog, and exon 4 in dog (*Canis lupus familiaris*). Red, blue, green and brown lines are different tissues and circles represent the spliced reads in different exons with coverage.

Figure S951

Panthera tigris

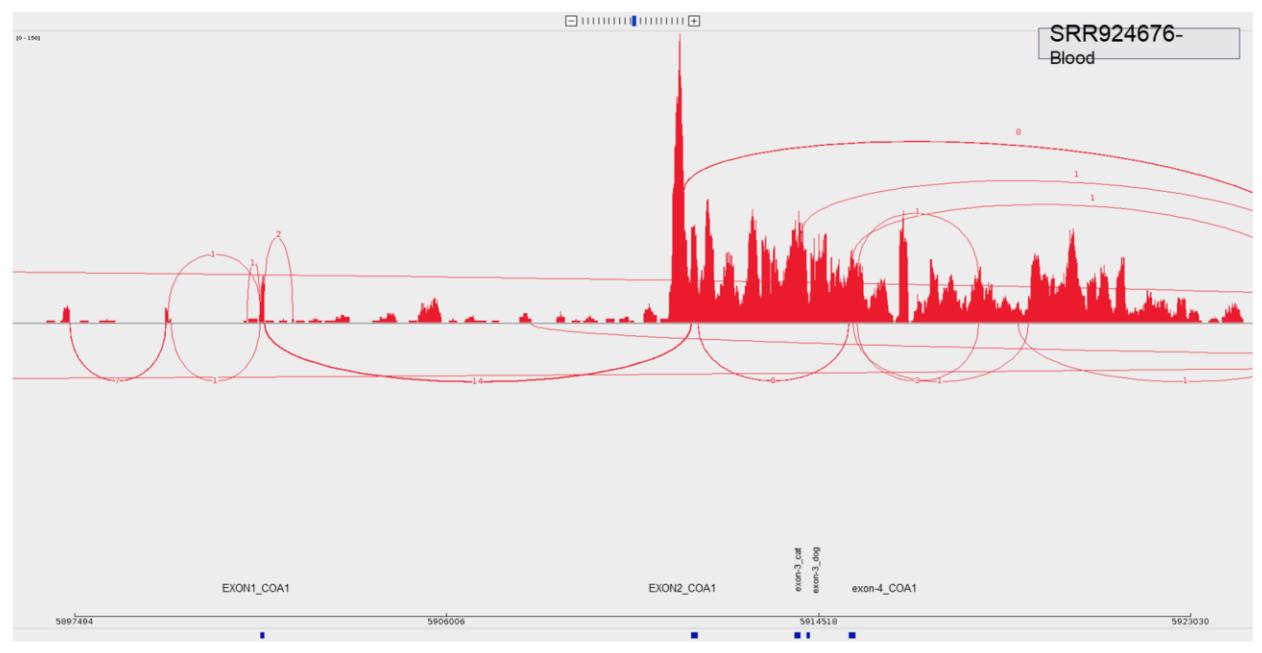


Figure S954: Screenshot of Sashimi plot of *COA1* exon 1, 2, exon-3 cat, exon-3 dog, and exon 4 in *Panthera tigris*. Red circles represent the spliced reads in different exons with coverage.

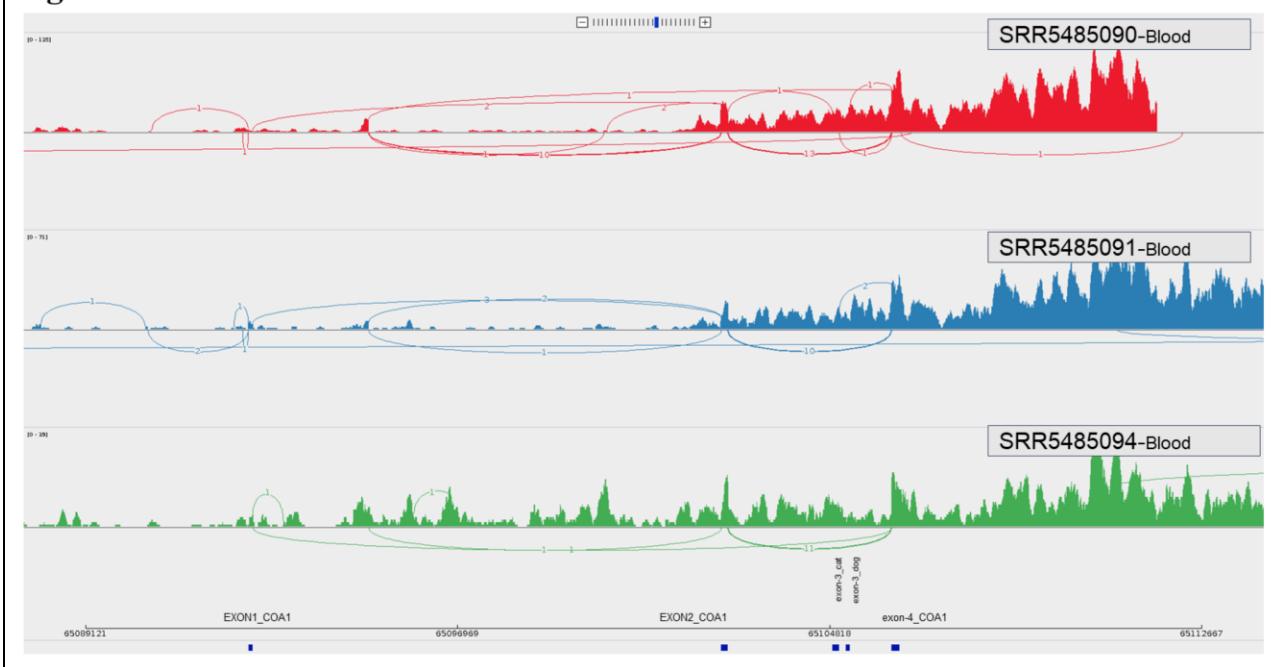
Figure S952*Panthera leo*

Figure S952: Screenshot of Sashimi plot of *COA1* exon 1, 2, exon-3 cat, exon-3 dog, and exon 4 in *Panthera leo*. Red, blue and green lines are different tissues and circles represent the spliced reads in different exons with coverage.

Figure S953

Felis catus

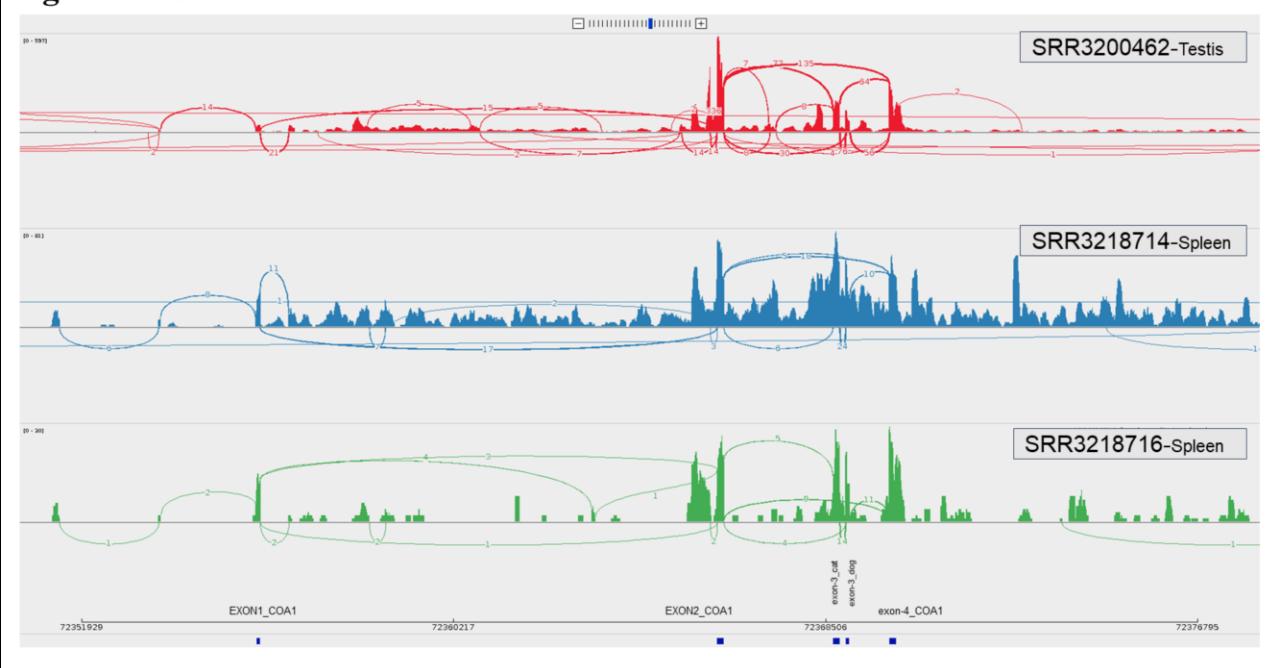


Figure S953: Screenshot of Sashimi plot of *COA1* exon 1, 2, exon-3 cat, exon-3 dog, and exon 4 in cat (*Felis catus*). Red, blue and green lines are different tissues and circles represent the spliced reads in different exons with coverage.

Figure S954

Puma concolor

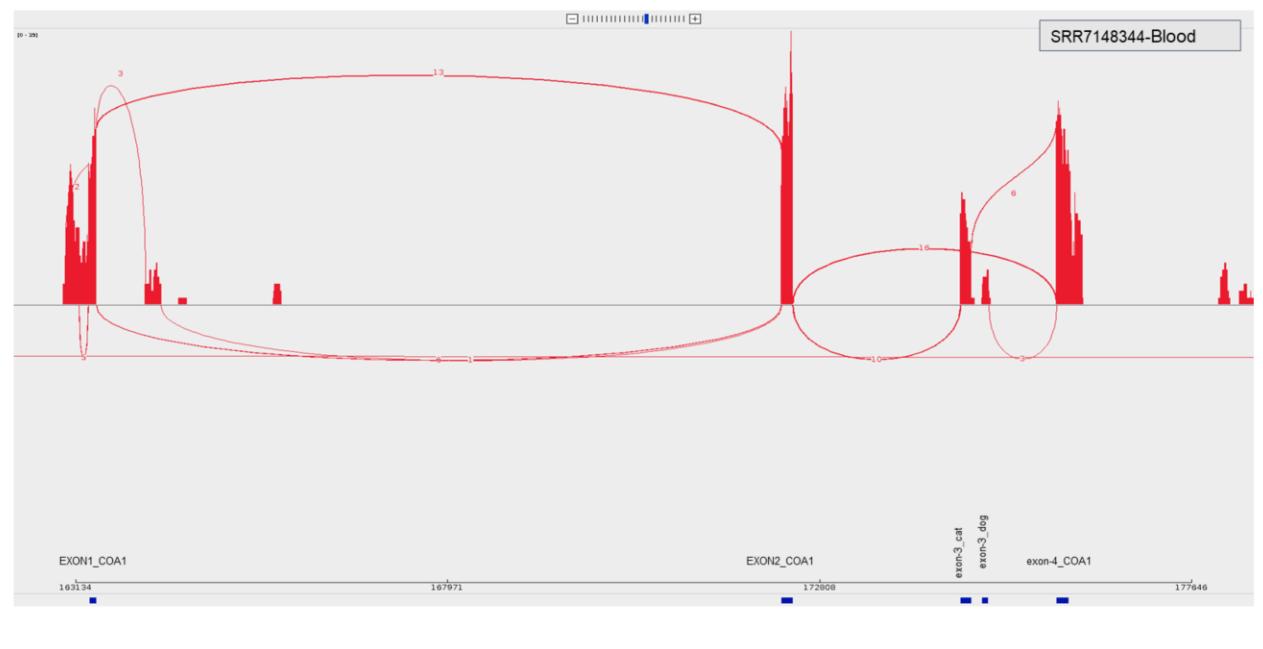


Figure S954: Screenshot of Sashimi plot of *COA1* exon 1, 2, exon-3 cat, exon-3 dog, and exon 4 in *Puma concolor*. Red circles represent the spliced reads in different exons with coverage.

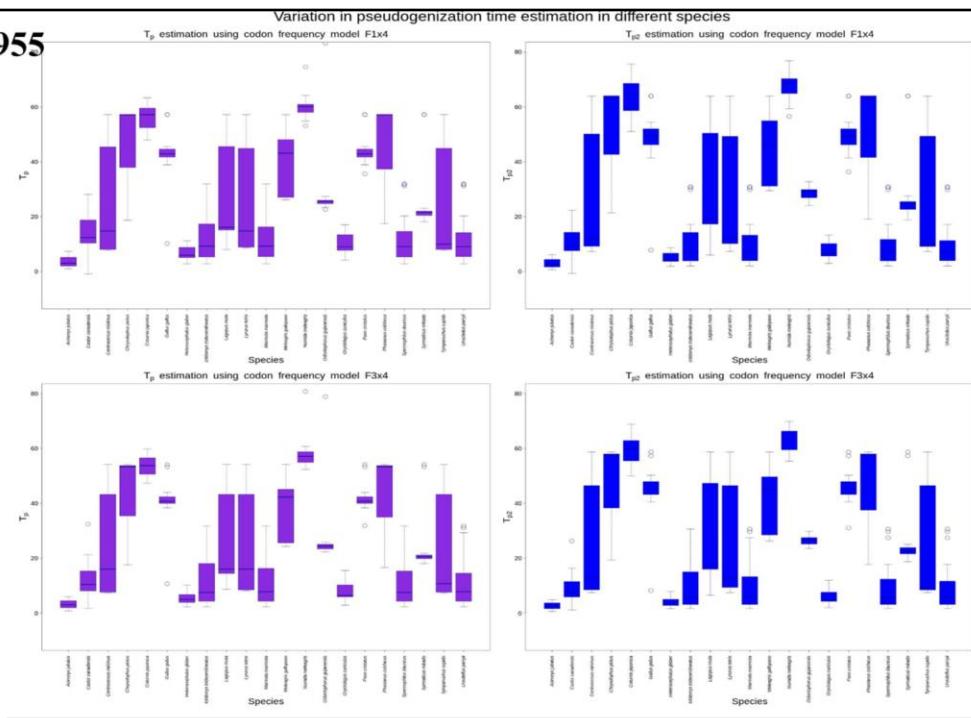
Figure S955

Figure S955: Gene loss timing is estimated using different labellings like pseudogene, mixed and functional. Other than these, we used a combination of background species. All the results were obtained from various combinations plotted in a boxplot. The y-axis represents $tp(1ds)$ $tp2(2ds)$, and the x-axis contains species names in the boxplot. Based on codon frequency models, different plots are mentioned.

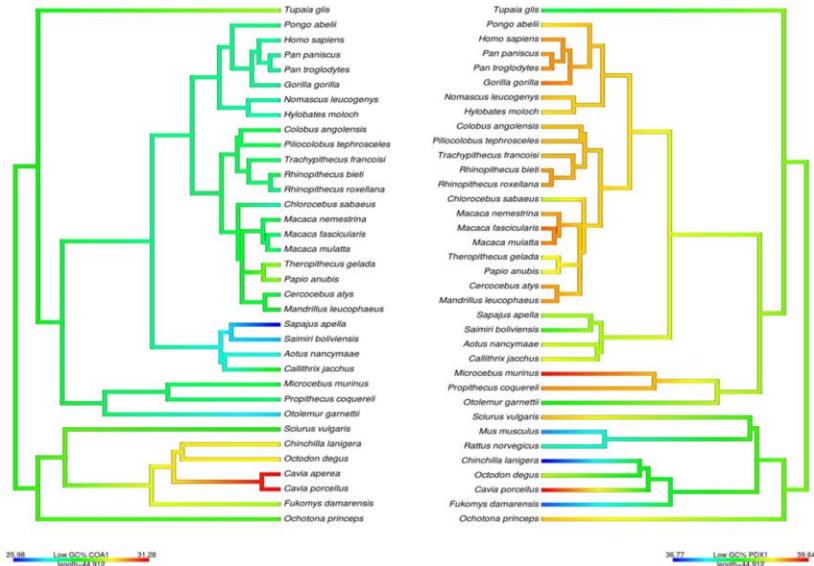
Figure S956Comparison GC% of *COA1* and *PDX1* gene in primates and rodent group
1.Low GC%

Figure S956: The color represents the GC% of *COA1* and *PDX1* gene using in different species of primates and rodents. The figure showed the possible lowest GC% based synonymous codon using CodSeqGen tools.

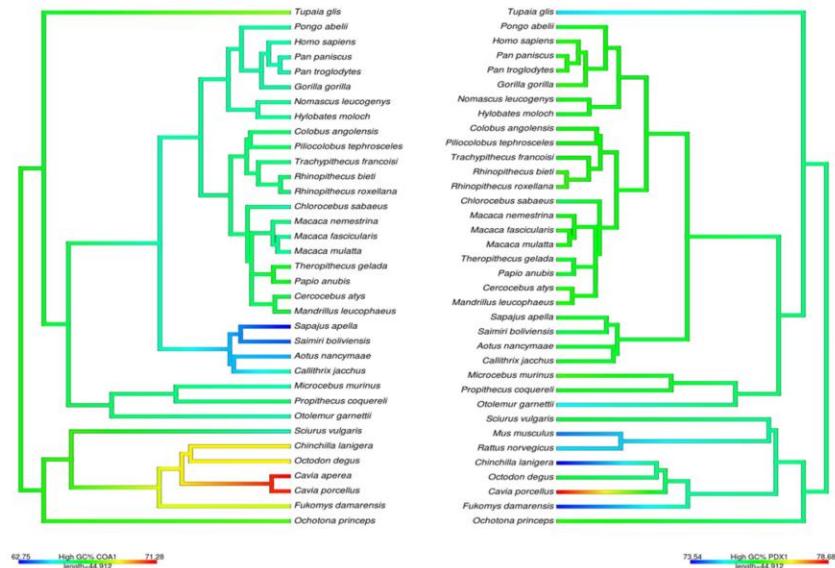
Figure S957Comparison GC% of *COA1* and *PDX1* gene in primates and rodents
2.High GC%

Figure S957: The color represents the GC% of *COA1* and *PDX1* gene using in different species of primates and rodents. The figure showed the possible highest GC% based synonymous codon using CodSeqGen tools.