Supplementary Material

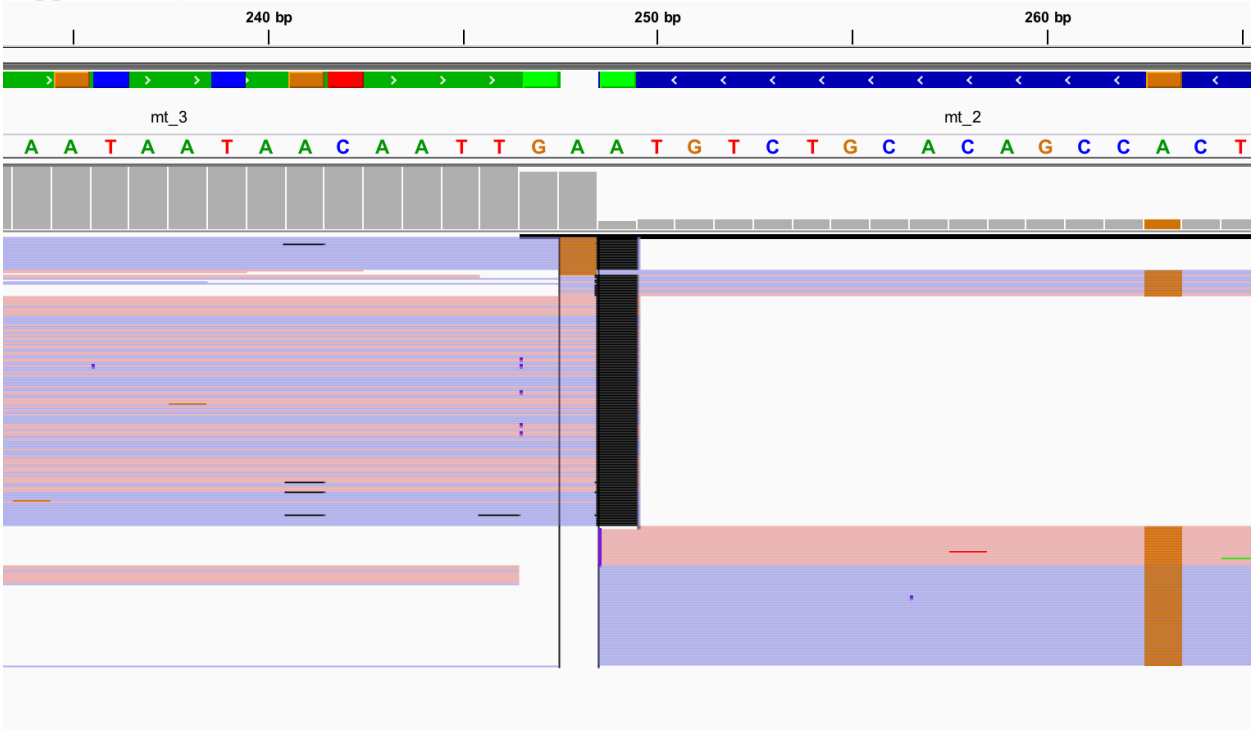
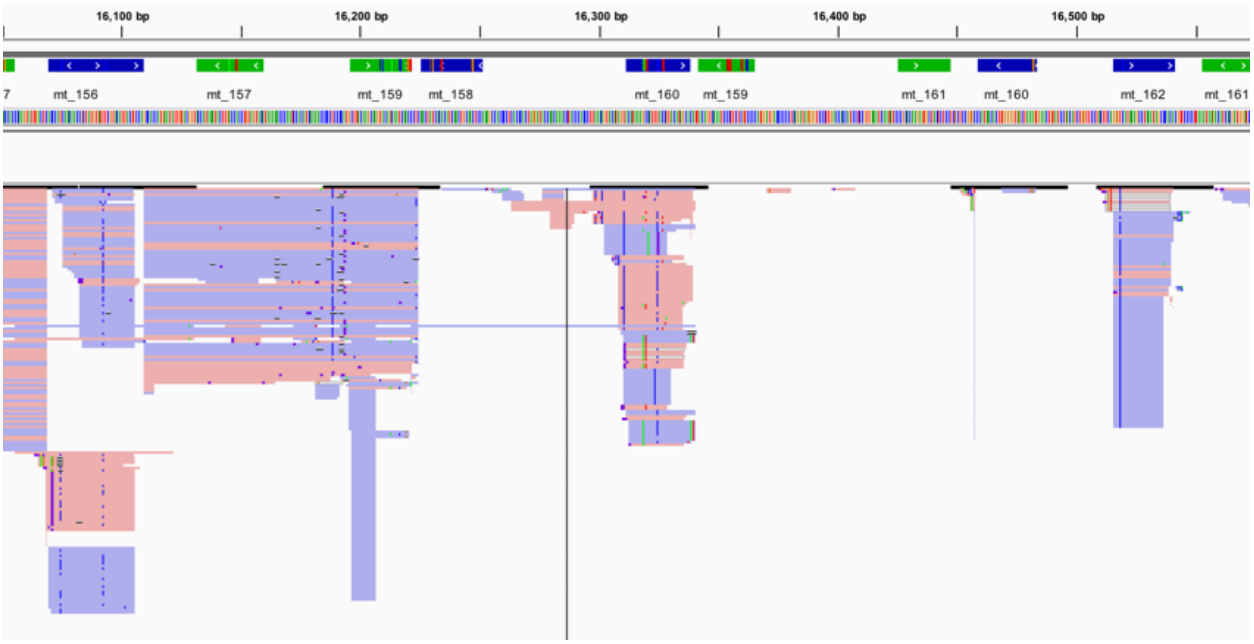


Figure S1. Screen shot from IGV of the alignment difficulties in the mt_2 and mt_3 amplicon overlap with a 249del present.

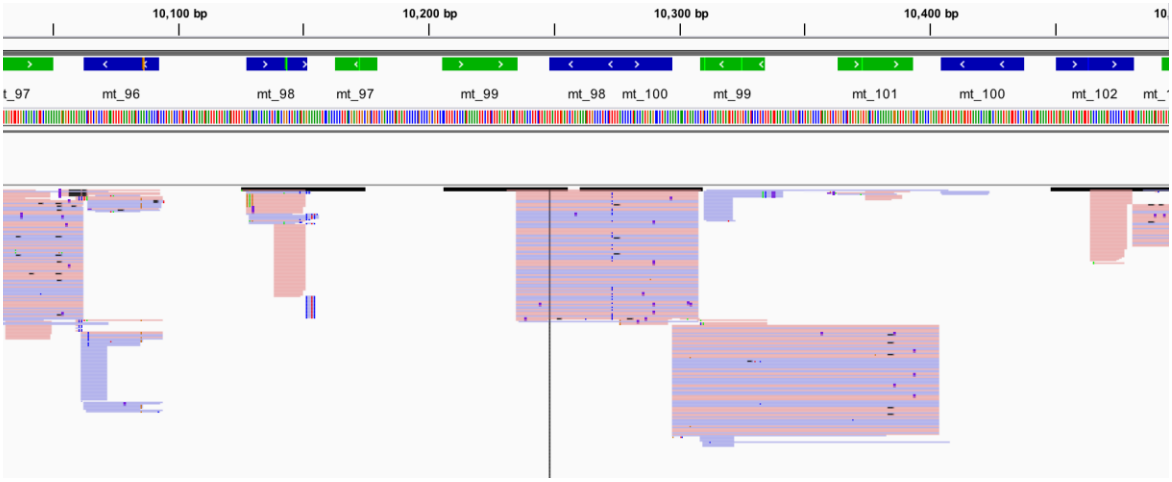
(A)



(B)


16,100 bp
16,200 bp
16,300 bp
16,400 bp
16,500 bp
mt_156
mt_157
mt_159
mt_158
mt_160
mt_159
mt_161
mt_160
mt_162

(C)


10,100 bp
10,200 bp
10,300 bp
10,400 bp
t_97
mt_96
mt_98
mt_97
mt_99
mt_98
mt_100
mt_99
mt_101
mt_100
mt_102

(D)

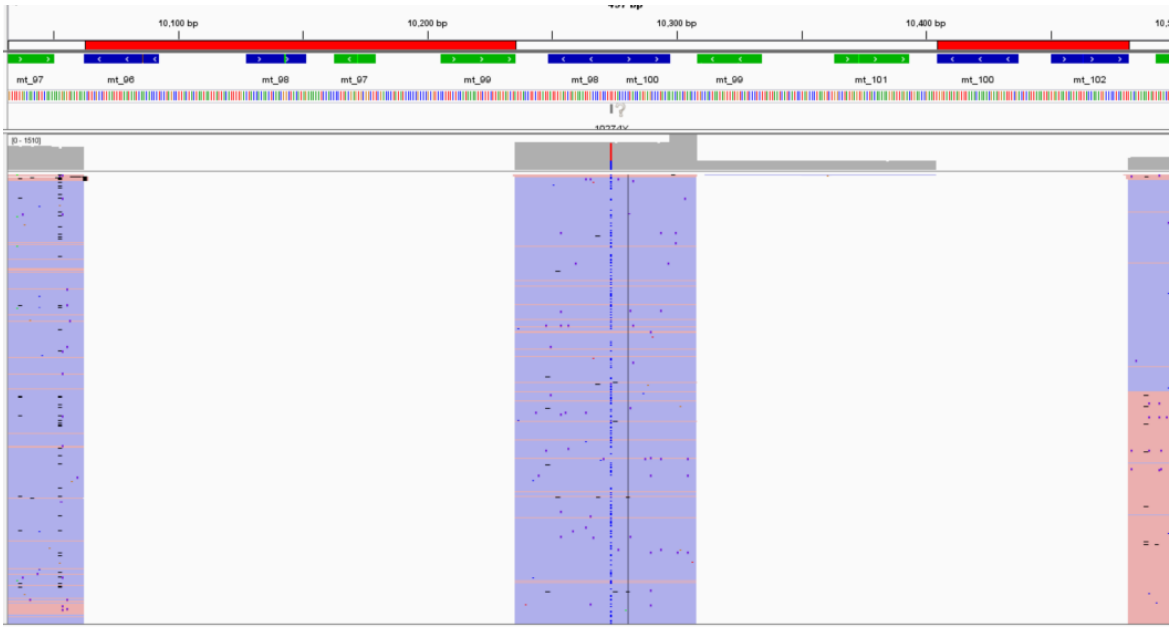
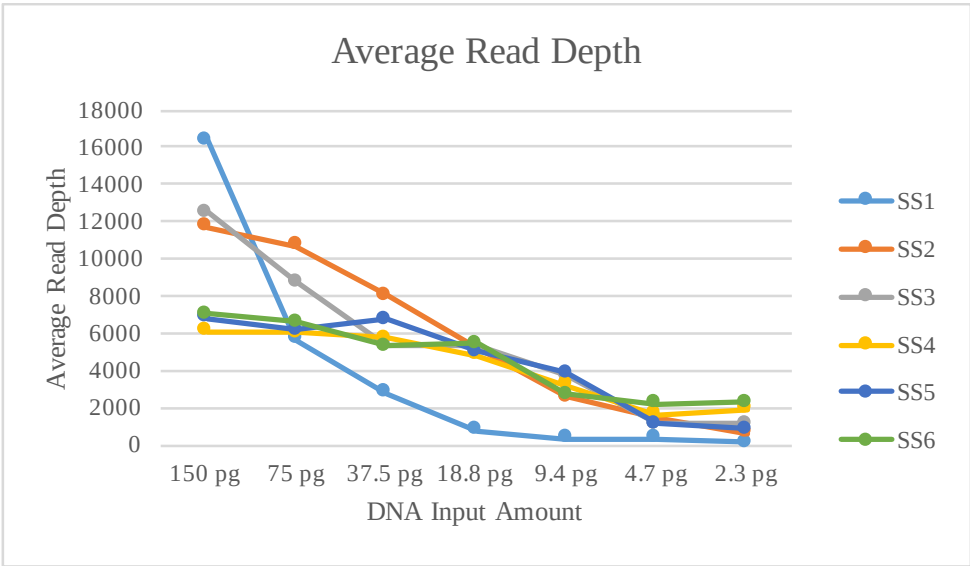


Figure S2. Screen shot from IGV of the reads from a negative control. A and B show the same region of the mtGenome prior to **(A)** and after **(B)** the latest Converge update. C and D show the same region of the mtGenome prior to **(C)** and after **(D)** the latest Converge update. The number of short reads is visibly less in B and D.

(A)



(B)

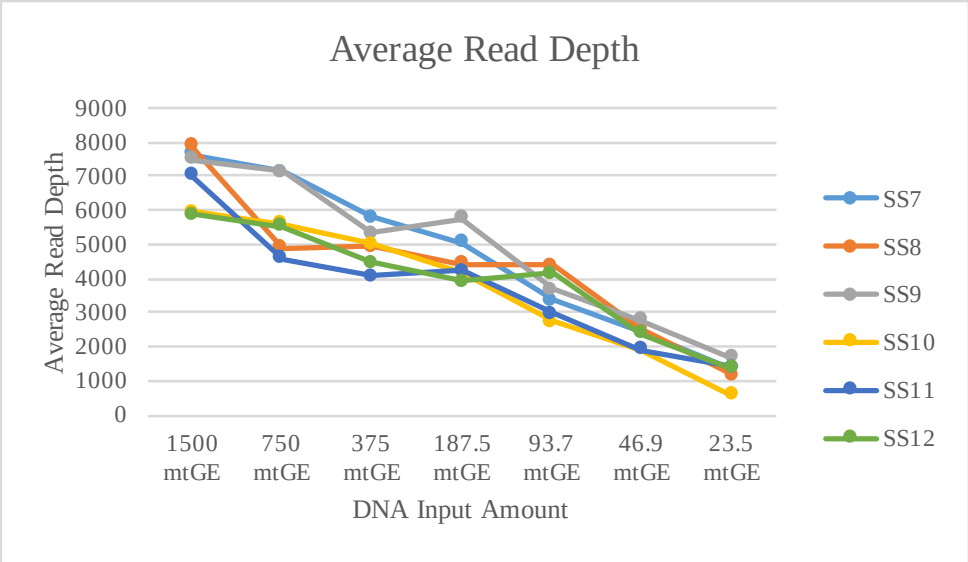


Figure S3. (A) Average read depth across the mtGenome for the six nuclear DNA quantitated dilution series samples. **(B)** Average read depth across the mtGenome for the six mtDNA quantitated dilution series samples.

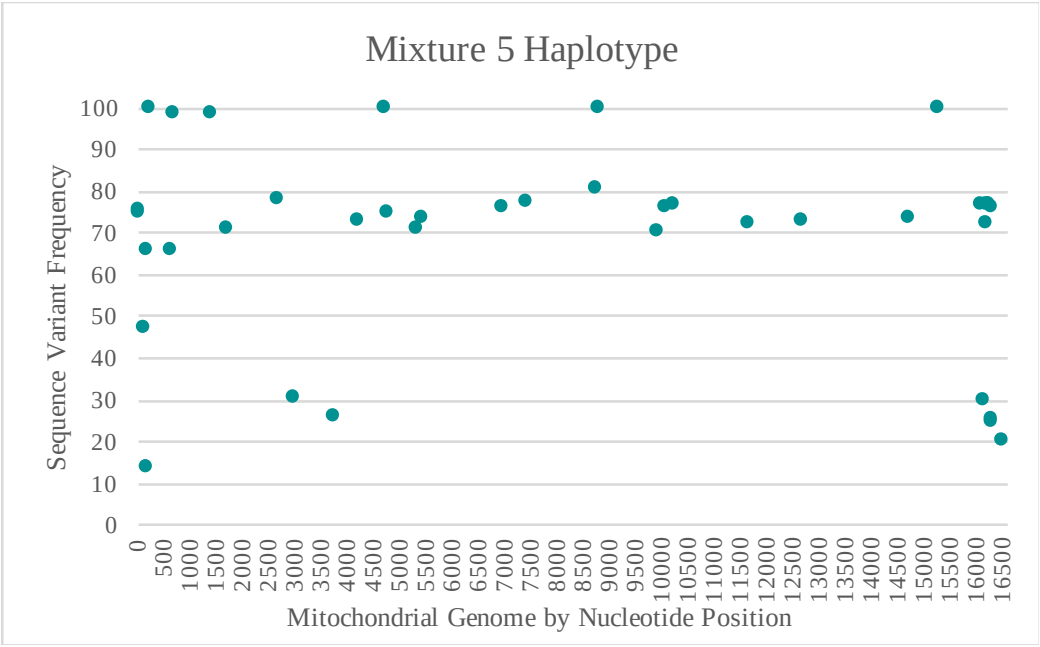


Figure S4. The sequence variant frequencies for one of the 2:1 mixtures included in Sequencing Run 31were plotted against the nucleotide position of that sequence variant to illustrate the quantitative contribution of each contributor to the total read depth of the mixed haplotype. The sequence variants present in both contributors, the major contributor, and the minor contributor cluster together with the personal point heteroplasmy present in each contributor falling out of these clusters.

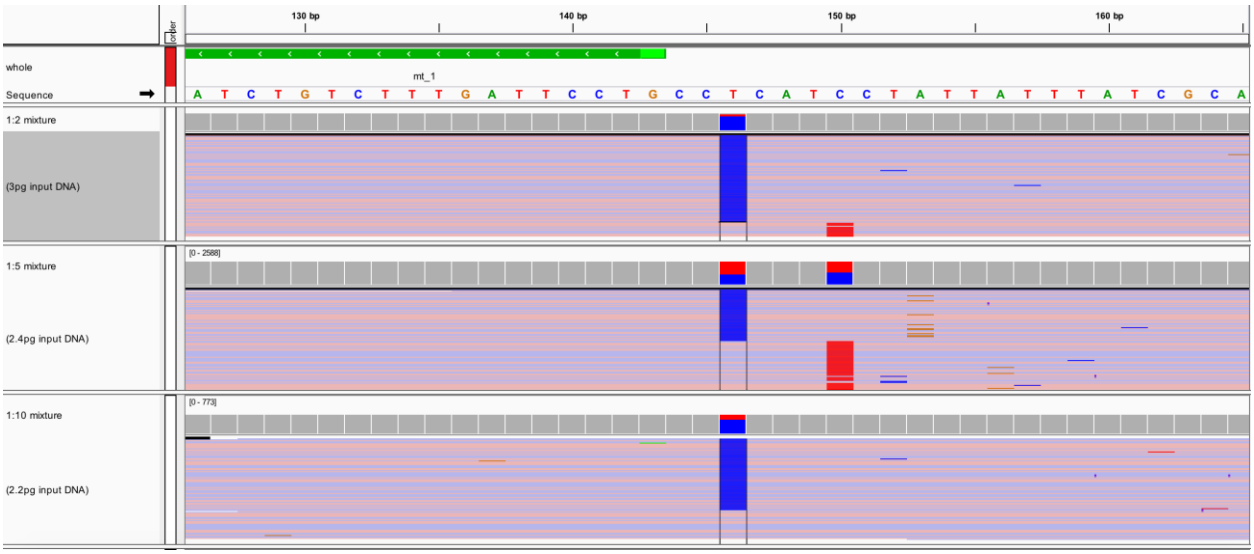
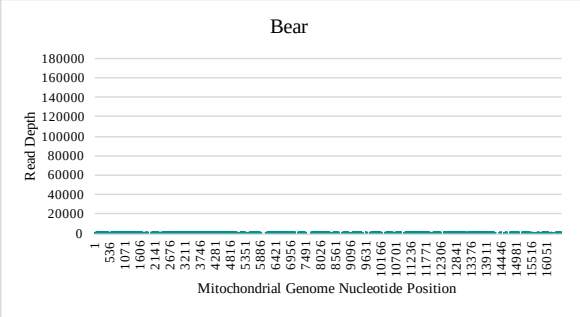
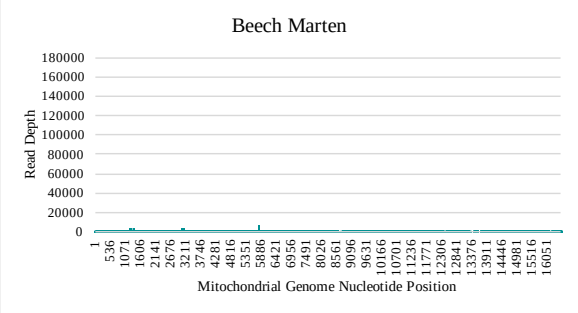
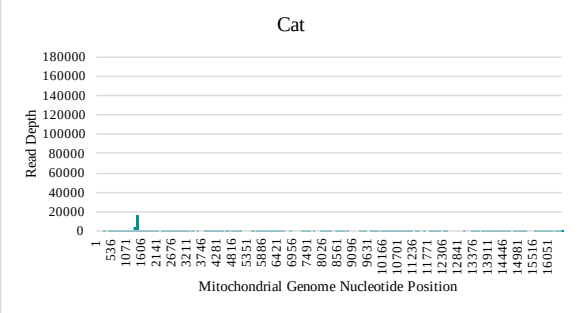
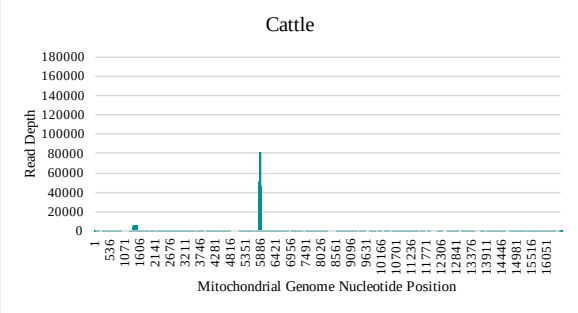


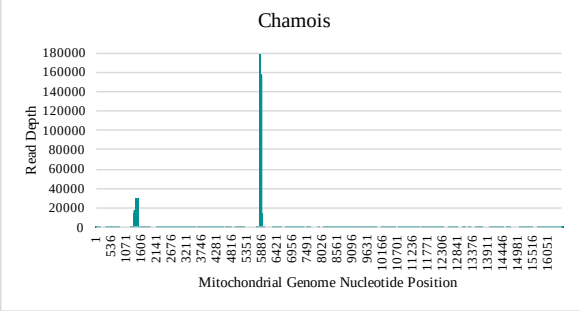
Figure S5. Screen shot from IGV illustrating the stochastic effects (i.e., variable sequence variant frequencies and drop-out) that can take place when amplifying lower amounts of input DNA, increasing the difficulty of deconvolution from these mixtures in mixture series 1 (Sequencing Run 29).

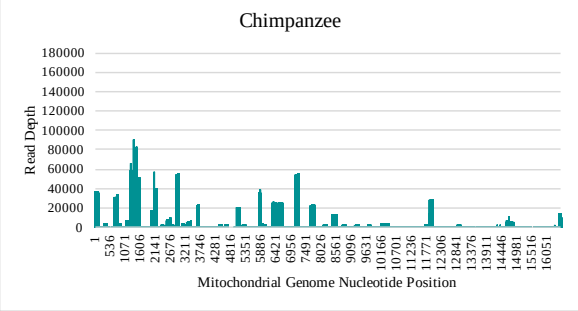

Bear
Read Depth
Mitochondrial Genome Nucleotide Position

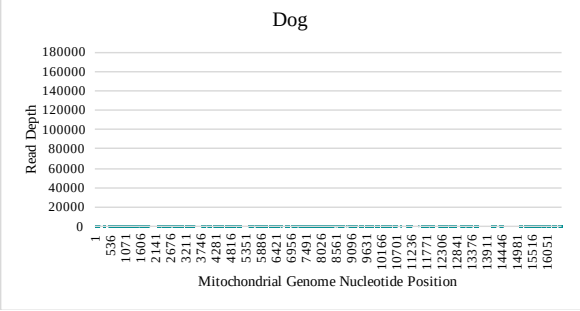

Beech Marten
Read Depth
Mitochondrial Genome Nucleotide Position

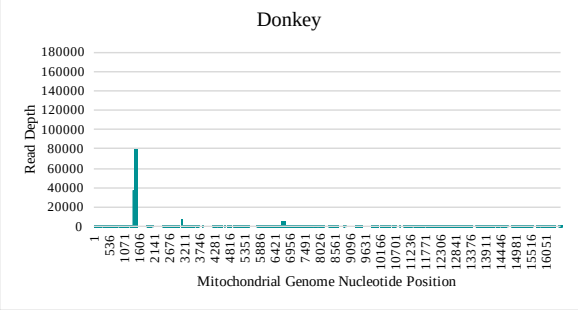

Cat
Read Depth
Mitochondrial Genome Nucleotide Position

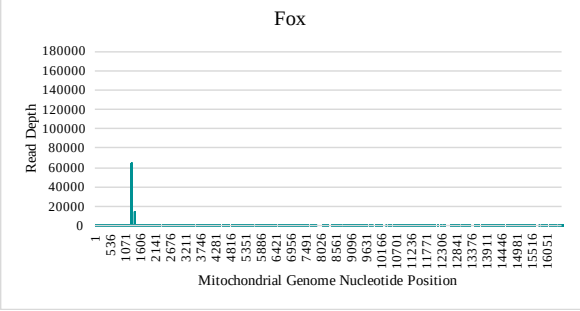

Cattle
Read Depth
Mitochondrial Genome Nucleotide Position

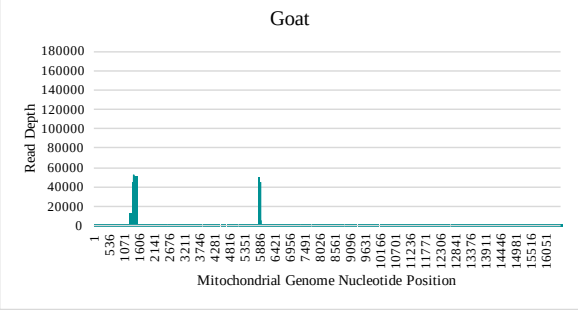

Chamois
Read Depth
Mitochondrial Genome Nucleotide Position

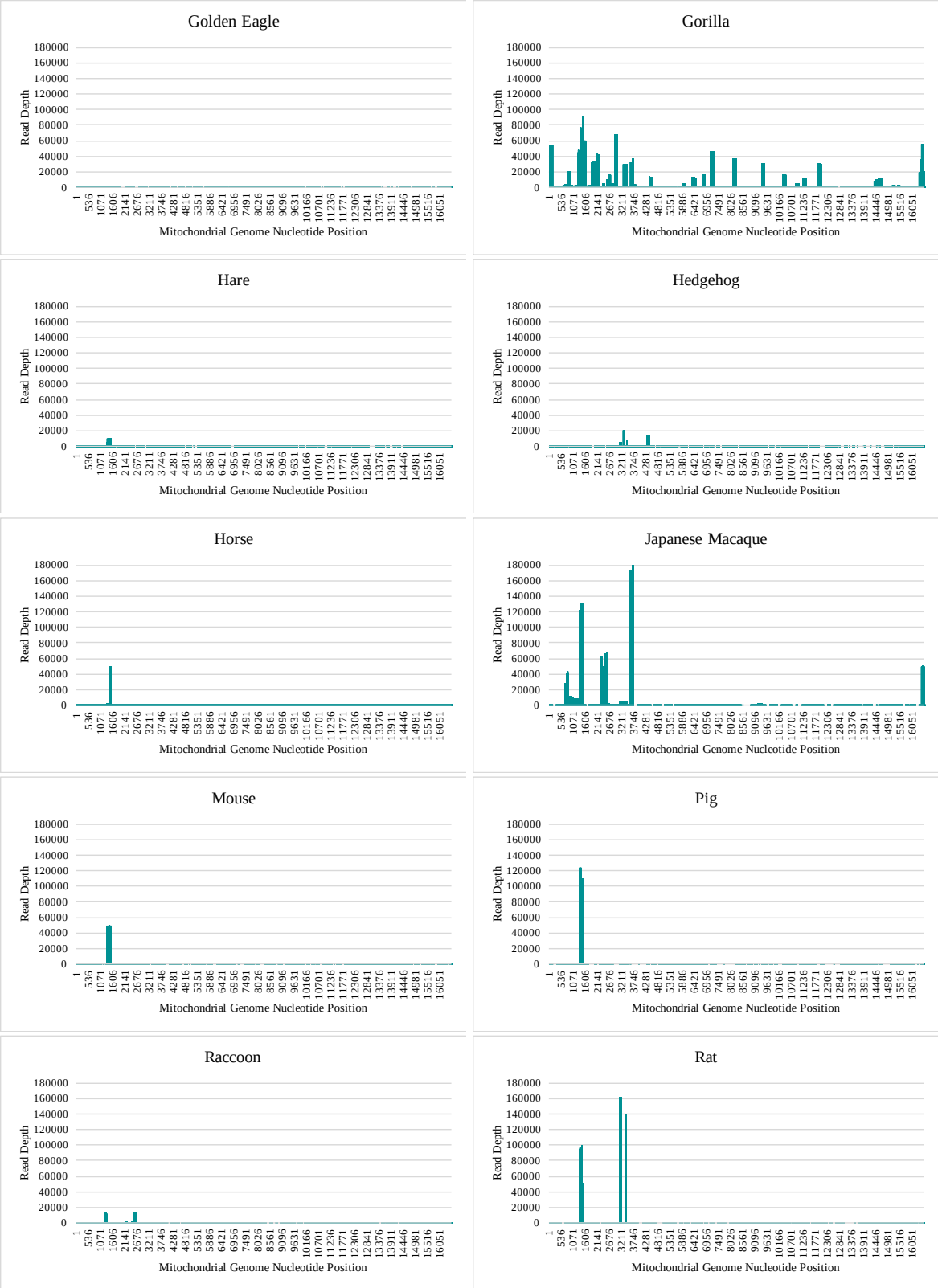

Chimpanzee
Read Depth
Mitochondrial Genome Nucleotide Position

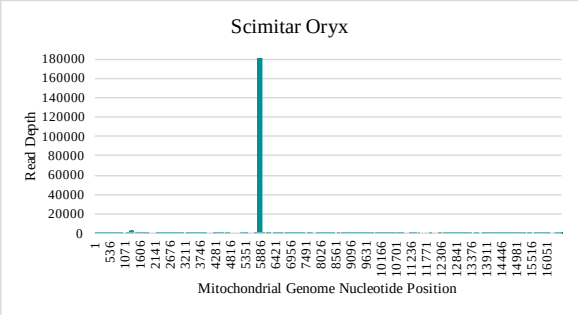

Dog
Read Depth
Mitochondrial Genome Nucleotide Position

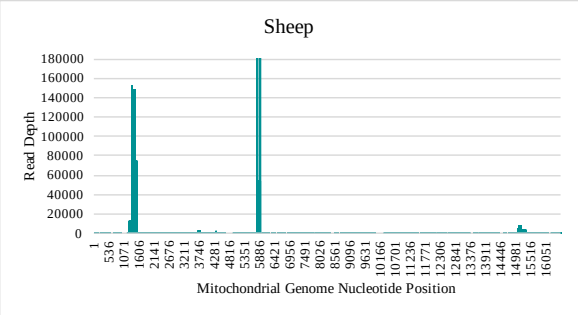

Donkey
Read Depth
Mitochondrial Genome Nucleotide Position

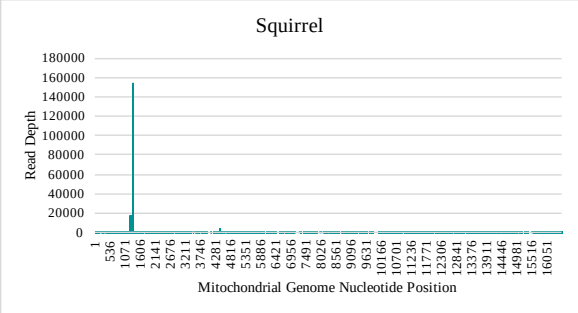

Fox
Read Depth
Mitochondrial Genome Nucleotide Position

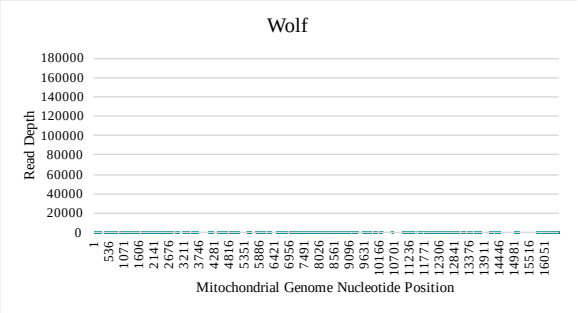

Goat
Read Depth
Mitochondrial Genome Nucleotide Position

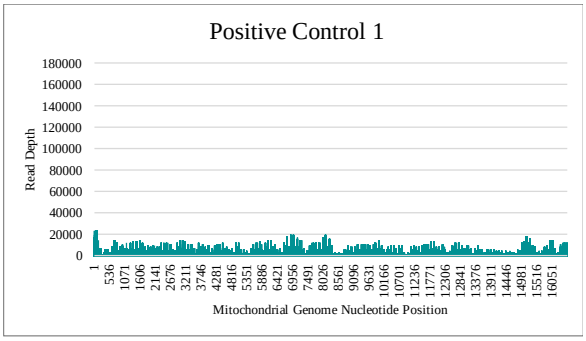

Golden Eagle
Gorilla
Hare
Hedgehog
Horse
Japanese Macaque
Mouse
Pig
Raccoon
Rat
Read Depth
Mitochondrial Genome Nucleotide Position

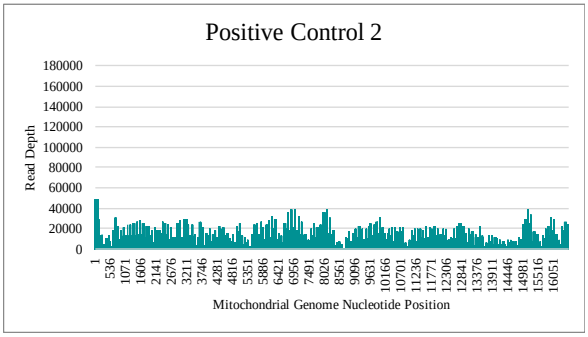

Scimitar Oryx
Read Depth
Mitochondrial Genome Nucleotide Position

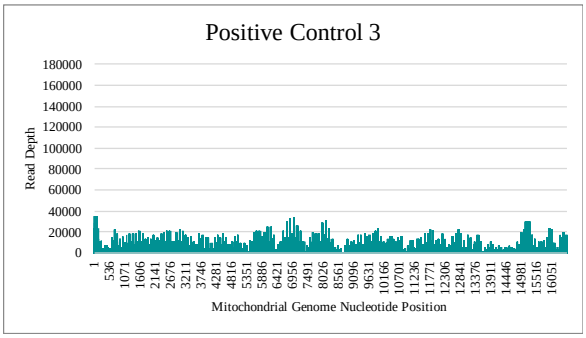

Sheep
Read Depth
Mitochondrial Genome Nucleotide Position

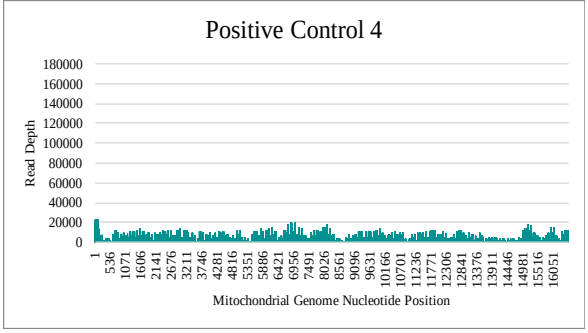

Squirrel
Read Depth
Mitochondrial Genome Nucleotide Position


Wolf
Read Depth
Mitochondrial Genome Nucleotide Position


Positive Control 1
Read Depth
Mitochondrial Genome Nucleotide Position


Positive Control 2
Read Depth
Mitochondrial Genome Nucleotide Position


Positive Control 3
Read Depth
Mitochondrial Genome Nucleotide Position


Positive Control 4
Read Depth
Mitochondrial Genome Nucleotide Position

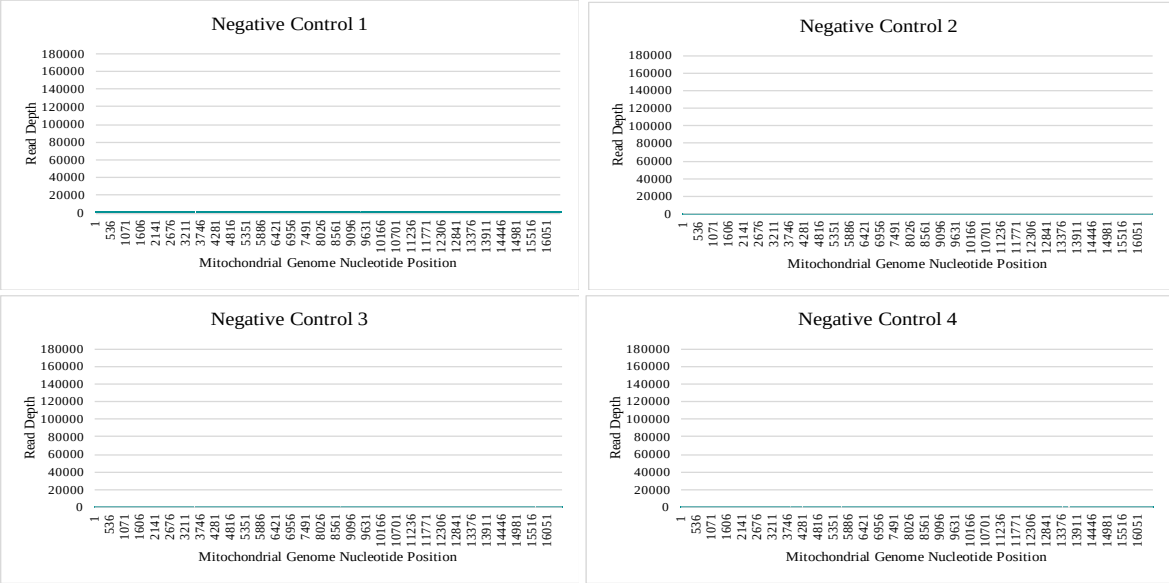


Figure S6. Read depth for each nucleotide position across the rCRS reference genome for each of the 24 vertebrate DNAs, four positive controls, and four negative controls included in the species specificity run. The X- and Y-axis for each chart has been scaled the same to allow for comparisons.