DISSERTATION

MOLECULAR ECOLOGY AND HIERARCHICAL MODELS ELUCIDATE CHRONIC WASTING DISEASE DYNAMICS

Submitted by

Nathan L. Galloway

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Doctoral Committee:

Advisor: Michael F. Antolin

N. Thompson Hobbs
Michael W. Miller
Kathryn P. Huyvaert

ABSTRACT

MOLECULAR ECOLOGY AND HIERARCHICAL MODELS ELUCIDATE CHRONIC WASTING DISEASE DYNAMICS

Prions present a unique evolutionary scenario because a single gene codes for both a disease agent and a functionally constrained native protein. The prion precursor gene, *Prnp*, codes for the prion precursor protein, PrP, which is constitutively expressed as a native isoform within all mammals. Upon misfolding to the disease isoform, known as prions, the same protein causes fatal neurodegenerative diseases known as transmissible spongiform encephalopathies. We review the literature and available data for the genetics of *Prnp* in order to examine its molecular evolutionary history, and the likely force of natural selection acting on it, by analyzing genetic diversity both within and between species within Class Mammalia. We accessed *Prnp* nucleotide sequences of a large number of mammalian species from GenBank. We undertook three distinct analyses of these molecular data to characterize the force of selection acting on *Prnp* through comparisons of gene sequences and allele frequencies within and between species. Our analyses include: 1.) comparisons of genetic and amino acid polymorphisms across protein domains within *Prnp*, 2.) a within and between species comparison of nucleotide diversity within Prnp to characterize natural selection acting on the gene, and 3.) observed frequencies of genetic and amino acid polymorphisms from natural populations of animals. We show that amino acid substitutions reported to correlate with prion disease risk within species do not aggregate within particular protein structural domains, but rather are disparately located throughout. Branch model estimates using Phylogenetic Analysis by Maximum Likelihood across mammals show that *Prnp* undergoes strong purifying selection at the broad scale, that purifying selection is stronger between species than it is within species but no evidence that species orally susceptible to prion disease experience unique positive selection. We do show, however, that amino acid substitutions occur at higher frequencies than synonymous substitutions within *Prnp*, in direct conflict with the expectations for purifying selection. This evidence suggests that *Prnp* is experiencing balancing selection in opposition to the purifying selection observed at the large scale; this unique selective pressure may be due to the presence of prion disease.

Ecological processes such as reproduction, habitat use, and disease epizootiology contribute to the growth or decline of wildlife populations, but many of these processes go directly unobserved. We set out to describe gene flow and disease transmission to better understand the ecological role of chronic wasting disease (CWD) in a northern Colorado population of mule deer (*Odocoileus hemionus*). CWD, a fatal prion disease, has been affecting this population for many decades. It has not caused extirpation of the deer, but may play an important limiting role in population growth and resilience. We employed genetic methods to analyze neutral genetic markers, which provide information about gene flow. Further, we examined allelic variation in the functional prion precursor gene, *Prnp*, which codes for the disease-causative prion of CWD and has alternative alleles with one (225F) that confers some resistance to prion disease within individual deer. The study in northern Colorado included sampling across four winter ranges. Genetic analysis identified four genetic lineages of deer, but lineages were distributed throughout the study area and did not correspond with winter ranges used annually with high fidelity by groups of females. Further, we show that males drive gene flow across genetic lineages. In contrast, CWD prevalence was spatially segregated: CWD-positive female deer were located in two of the winter ranges and absent from the others. This suggests that neither breeding sites nor natal dispersal are the primary means of disease spread in females across the winter ranges. Furthermore, we found, as previously reported, that an individual deer's *Prnp* genotype predicts the likelihood of a positive disease test. Even so, the frequency of the *Prnp* 225F allele was similar across winter ranges, and was notably higher than that reported in neighboring populations a decade earlier. Thus, it appears that gene flow spreads the favored allele across the study area despite different selective regimes in winter ranges. Our work shows the benefit of using population genetics to gain insight into ecological processes that go directly unobserved, such as the epizootiology of chronic wasting disease.

Chronic wasting disease is a fatal neurodegenerative prion disease that infects members of the deer family in North America and Scandinavia. We conducted a five-year mark recapture study of a northern Colorado population of mule deer (*Odocoileus hemionus*) with endemic disease, including 217 females. All study animals were also genotyped at the prion precursor gene, *Prnp*, which has alternative alleles in many species to express amino acid differences that alter prion disease dynamics. Mark-recapture analysis revealed decreased disease incidence for individuals expressing genotypes with at least one copy of the minor allele, including heterozygotes, *Prnp* 225SF (expressing both a serine and phenylalanine at amino acid position 225) , and rare homozygotes, 225FF. We found no evidence for an evolutionary trade-off of decreased survival of CWD-negative deer for this group but emphasize the difficulty in estimating dynamic rates for the rare homozygotes alone. We employed estimates of annual disease risk and survival from this study as well as recruitment estimates from the literature, to forecast the expected future minor allele frequency in the population under the observed disease risk. This forecast revealed a clear expected evolutionary increase in the *Prnp* minor allele (225F) frequency given our model and field data.

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DEDICATION

I would like to dedicate this effort to the memory of my brother.
May all the wild places, and the creatures that inhabit them,
be protected for those who find solace there.

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Chapter 1

Molecular Evolution of the Prion Precursor Gene, *Prnp*

1.1 Introduction

The genes coding for prion proteins present a unique scenario of contrasting evolutionary pressures, because disease arises from translation, expression, and mis-folding of a native protein encoded within the host's genome into a toxic and pathogenic isoform [7]. The coded proteins are constrained by native function but may also experience unique selection related to their role in prion disease. We focus our case study of this evolutionary interplay on the prion precursor gene, *Prnp*, one of five pathogenic mammalian prion proteins that have been identified that each cause a unique prion disease [7].

Prnp codes for the prion precursor protein, denoted PrP. This functional native protein, referred to as $\mathrm{PrP^C}$ in its cellular isoform, aggregates during transmissible spongiform encephalopathies (TSEs) as a result of post-translational misfolding into the diseased isoform, $\mathrm{PrP^D}$ or prions, (proteins of infectious origin). The $\mathrm{PrP^D}$ is the infectious agent for this family of fatal and transmissible diseases [7]. Prions cause disease in many mammals, including scrapie in sheep, bovine spongiform encephalopathy (BSE) in cattle, Creutzfeld Jacob Disease (CJD) and kuru in humans, and chronic wasting disease (CWD) in cervids [8].

It has been shown that genetic variation in the *Prnp* gene may have a direct effect on prion disease. Amino acid sequence plays an important role in the disease process, both in spontaneous forms and in subsequent transmission. The importance of protein sequence during transmission is a complicated interplay between the host $\mathrm{PrP^C}$ and the infectious $\mathrm{PrP^D}$. The best understood examples of this dependence are from diseases of humans and agricultural animals [9, 10]. The amino acid sequence of both the native host isoform and the disease strain directly impact the course of infection, in terms of both the likelihood of infection and time until the onset of symptoms [11]. Although disease strains may occur, transmission requires the disease protein to induce misfolding of the native host protein both between tissues as the prions disseminate throughout the body, and between individuals as an infectious disease agent.

The importance of this protein-protein interaction becomes clear in the case of the species barrier. PrP^{C} of humans, cattle and sheep exhibit differential sensitivity to conversion when exposed to CWD prions *in vitro*, providing strong evidence for a molecular barrier interfering with efficient disease transmission between certain prion strains and host proteins [12]. For example, transgenic mice expressing human prion precursor show resistance to cervid (mule deer) PrP^{Sc} [13]. Prion strain and its potential relationship to genetic polymorphism within *Prnp* is receiving increased discussion because of both host-species barriers and the initiation and spread of prion diseases in both domestic animals and wildlife [14, 15].

Understanding the evolutionary forces working on *Prnp* may shed light on the intricacies of inter-species barriers to disease transmission as well as the potential for a population to evolve resistance to endemic disease. Current literature offers conflicting conclusions regarding the force of selection which has acted on *Prnp* during its evolutionary history. Evidence has been offered for several hypotheses including balancing, purifying and positive selection [16–19]. This discrepancy may arise because *Prnp* serves two roles within a mammalian host; First, it performs a native functional role in the form of PrP^{C} [20], and secondly, it plays a vital role in an organism's susceptibility to prion disease [14, 21]. The amino acid sequence and the resulting protein structure is likely related to both of these processes.

The precursor protein is translated from a single 2.1-kb mRNA. The open reading frame (ORF) is contained within one, two or three exons depending on the organism. PrP^{C} is constitutively expressed in vertebrates, predominantly in neural and lymphatic tissues, and the mature form is a roughly 200-amino-acid polypeptide with a molecular mass of 27- to 30-kilodaltons. Post-translational modification includes cleavage of an N-terminal signal peptide and removal of a C-terminal peptide for the addition of a glychophosphotidylinositol (GPI) anchor [22]. The mature

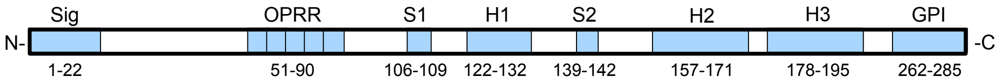


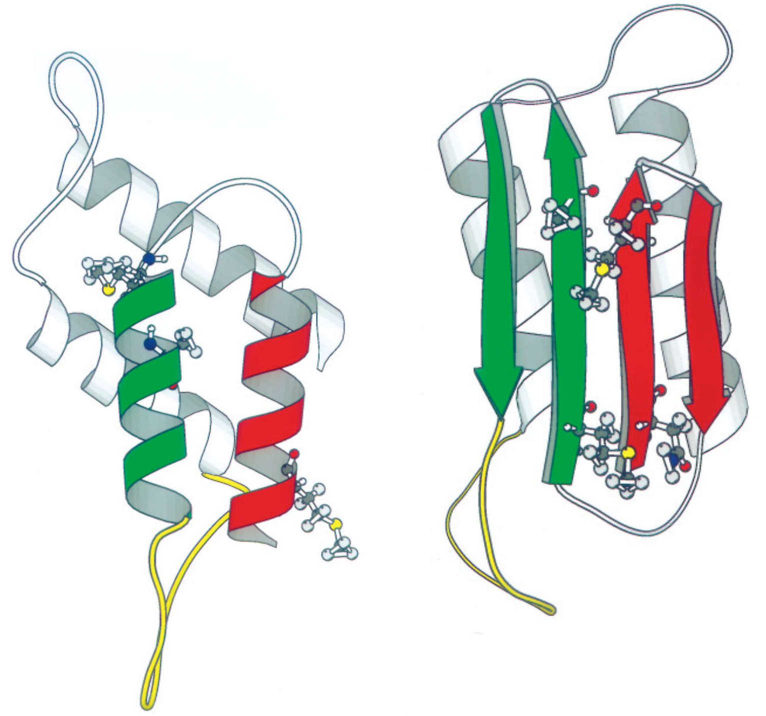
Figure 1.1: The mouse (*Mus musculus*) cellular prion precursor protein, PrP^C, with associated protein domains in blue [1] . Numbers below the domains represent the amino acid contained within each domain. From N- to C-terminal these include the signal sequence (SIG), octapeptide repeat region (OPRR), beta-pleated sheets (S#) and alpha helices (H#), and the glycophosphoinositol anchor (GPI). The N-terminal portion (from amino acid 23-100) is flexibly disordered, while the C-terminal portion is more structured.

PrP^C consists of an unstructured N-terminal region (~100 amino acids) capable of binding copper ions [23], and a C-terminal segment, (also ~100 amino acids in length). The C-terminal domain is folded into a largely α-helical conformation (three α-helices and a short antiparallel $beta$-sheet) and stabilized by a single disulphide bond linking helices 2 and 3 [24]. The pathogenic prion differs structurally from the cellular isoform with increased $beta$-sheet content [25], proteolytic resistance [26], and a tendency to form amyloid plaques [27].

In its role as a functional protein, PrP^C has been hypothesized to undergo purifying selection, with support from comparisons between species [28]. On the other hand, evidence from disease-exposed populations suggests balancing selection for rare alleles of PrP^C [17, 19] possibly because of lower conversion efficiency between heterologous forms of PrP^C and the infectious PrP^D [12].

We hypothesized that different forms of selection may act at different scales. Perhaps purifying selection for native function is most prevalent between species in broad phylogenetic comparisons, but balancing or positive selection, for instance for specific *Prnp* alleles that may code for prion disease resistance, acts within populations with endemic prion disease.

Opposing selective forces would act on the amino acid sequence of PrP, leaving a signature of differential ratios of non-synonymous (dN) vs. synonymous (dS) mutations within and between species, (dN/dS denoted omega, ω). Evolutionary theory suggests that purifying selection on a protein-coding gene results in synonymous mutations observed more often than non-synonymous mutations, assuming a random mutation process and selection against alleles with decreased function [29]. In contrast, positive selection may act on the protein in its role as a disease agent. In this case, non-synonymous mutations that confer resistance against disease may be observed more



(a) Tertiary structure model for prion precursor, the native cellular isoform.

(b) Prion tertiary structure model. The prion isoform accumulates into plaques and induces misfolding of more prion precursor in the prion disease process

Figure 1.2: Plausible Tertiary Structure of Prion Protein Isoforms. The prion precursor in 1.2a undergoes a misfolding of tertiary structure into the isoform seen in 1.2b when misfolded as prions. Colored regions correspond between the two isoforms, highlighting the change from helix to pleated sheet. Figures from [2]

often because of their effect on protein misfolding. We limit our analysis to the PrP coding sequence, which ignores the potentially important promoter region which in cattle is located more than 2kb upstream of the ORF [30] but allows for analysis of more taxa and focuses on the effect of domains within the prion precursor protein.

1.2 Methods and Results

1.2.1 Testing for Differential Association between Disease Resistance and Protein Domains

Our first formal null hypotheses state that:

- H_o1: All PrP domains show an equal ratio of non-synonymous to synonymous mutations.
- H_o2: All PrP domains show an equal rate of non-synonymous substitutions associated with prion disease.

We collected data on within-population variation of protein coding sequence from a broad search of the literature yielding 20 publications across 18 species with confirmed TSEs, including both diseased and naive populations (See Table 1.1. Sequences were aligned using the MUSCLE algorithm [31]. Domain annotations were based upon nuclear mass resonance work on *Mus musculus* PrP [1], and applied to the entire alignment. These results are included in Table 1.2. Each substitution was classified as synonymous (dS), non-synonymous (dN), or disease-associated non-synonymous (dN*).

Table 1.1: Summary of data from the literature review.

Common Name	Scientific Name	Source	GenBank Accession #
Human	*Homo sapiens*	[17, 32]	
Bison	*Bison bison*	[33]	AY769985
Domestic Cattle	*Bos taurus*	[16, 30, 34]	EU130450, AY720445-678, BN000291
Chamois	*Rupicapra rupicapra*	[35]	FJ436717
Bighorn Sheep	*Ovis canadensis*		DQ648467-73,75-77
Dall Sheep	*Ovis dalli*		DQ648474
Domestic Sheep	*Ovis aries*	[36]	
Domestic Goat	*Capra hircus*	[36–40]	AF117315-6, AF486134-8 ,AY723290-2, DQ013244, DQ345066-8, EF139167, EF139174, EF140715-6, EF192309-10, S82626, X74758, X91999
Caribou	*Rangifer tarandus*	[41]	DQ154293
Moose	*Alces americanus*	[42]	AY225484-5, DQ154298
White-tailed Deer	*Odocoileus virginianus*	[43–46]	AF156185, FJ775013,FJ775130
Mule Deer	*Odocoileus hemionus*	[6, 46]	AY22847
Elk	*Cervus canadensis*	[47, 48]	AF016227-8, EU032288-94
Red Deer	*Cervus elaphus*	[35]	AY748456, FJ436713-7
Sika Deer	*Cervus nippon hortulorum*	[49]	AY679695-6

Table 1.2: Single nucleotide polymorphisms (SNPs) across domains in 18 species with prion disease from literature review. dS, dN and dN* are synonymous, non-synonymous and disease-associated non-synonymous substitutions respectively. Domains and inter-domain spaces correspond to those in Figure 1.1. The observed omega ratio (dN/dS) differs across domains according to Fisher's Exact Test; Purifying selection exerts varying force across the gene. Similar tests reveal no difference in occurrence of dN* between domains; Disease-associated amino acid substitutions occur randomly across protein domains.

	Sig		OPRR		S1		H1		H2		S2		S3		GPI
dN*	2	2	0	1	1	5	2	0	1	1	0	0	1	3	1
dN	4	3	2	6	2	7	5	0	1	1	1	1	6	6	1
dS	5	6	14	13	2	5	1	0	0	6	2	5	4	3	1

Prion precursor domains were analyzed for differential occurrence of synonymous and non-synonymous mutations using Fisher's Exact Test. This was a simple approach to a complex question: "Do the various PrP domains show evidence of differential purifying selection (unique omega ratio, dN/dS) of mutations across domains?" We examined the observed dN/dS ratio across domains to test the first question. Stronger purifying selection would reduce the omega ratio, while weaker purifying selection would increase it. A given domain would also show a higher omega ratio if non-synonymous substitutions within that region experienced balancing selection in the face of prion disease. The second test addresses another question; do PrP domains show evidence of non-random aggregation of disease-associated non-synonymous substitutions? This would be observed through variation of the ratio between non-synonymous substitutions and non-synonymous disease-associated substitutions, dN/dN*, across domains.

Analyses reveal a non-random pattern of the omega ratio, or non-synonymous to synonymous mutations, across protein domains ($p = 0.035$; See Table 1.2). This confirms that selection is acting differentially across the various protein domains and refutes the first null hypothesis. It is, however, not particularly informative because it would be considered quite unremarkable for any protein to have variable degrees of purifying selection acting across domains of varying importance to the native molecular process.

On the other hand, the data show no association of disease-associated non-synonymous substitutions across domains ($p \rightarrow 1$; See Table 1.2). Disease-associated amino acid substitutions appear to occur randomly across protein domains, supporting the second null hypothesis. This is notable in that it might be expected for any disease-resistant amino acid changes to occur in specific key domains of the prion precursor. However, it must be remembered that within secondary and tertiary structure, amino acids from disparate domains may come into close contact and form important structural sites within $\mathrm{PrP^C}$, which would not be revealed in our analysis focused on linear domains.

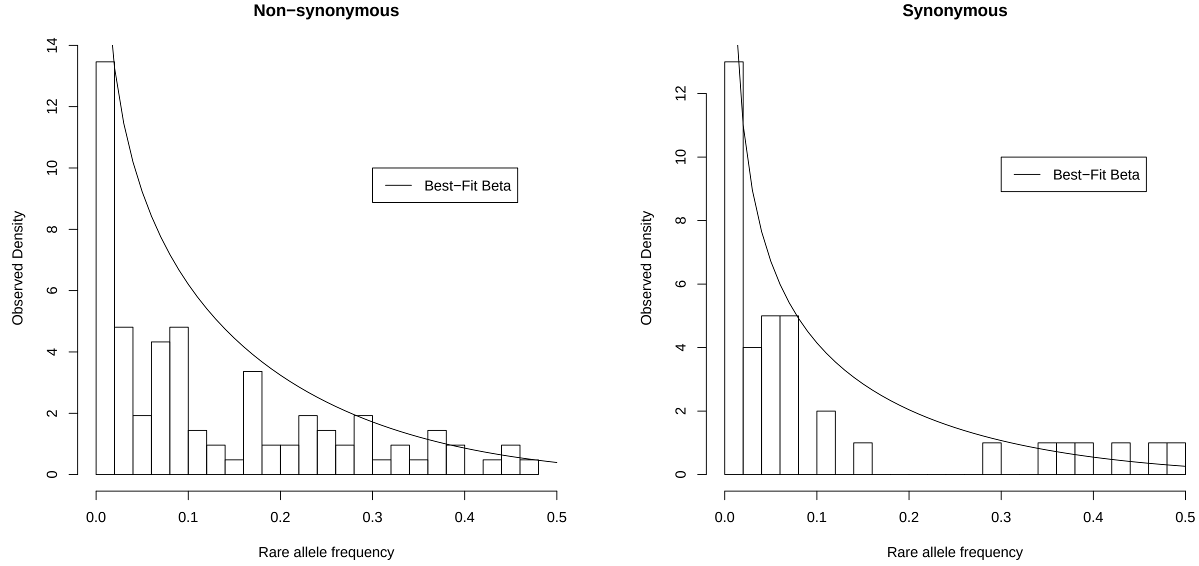
1.2.2 Testing for Differential Selection on Rare Allele Frequency Based on Substitution Type

Our next formal null hypothesis states that species susceptible to disease show an increased allele frequency for non-synonymous mutations relative to synonymous.

We also collected 21 population sets from GenBank [50], each containing the full coding sequence for a sample of individuals within a species. We combined this information with allele frequency reports from relevant publications to summarize the available information on the frequency of alternative alleles of *Prnp* within populations.

We cataloged the observed frequency of all minor alleles sorted by synonymous and non-synonymous substitutions. If synonymous and non-synonymous substitutions undergo the same evolutionary pressures, the observed frequencies of both will be drawn from the same underlying distribution. Strong purifying selection however, should reduce the frequencies of non-synonymous substitutions relative to synonymous substitutions. We employed the Kolmogorov-Smirnof Test to compare the observed distribution of allele frequencies of synonymous and non-synonymous substitutions. A visual summary of the observed frequencies of all minor alleles of *Prnp* can be seen in Figure 1.3.

Observed frequencies of all substitutions do not explicitly consider the specific codon of substitutions and instead focuses on the overall trend. The Kolmogorov-Smirnov rank sum test reveals that the cumulative distribution function of the non-synonymous substitutions is greater than that of the synonymous substitutions (See Figure 1.3; $p = 0.029$). This allows us to reject the null hy-



(a) dN: Non-Synonymous Substitutions

(b) dS: Synonymous Substitutions

Figure 1.3: Histograms summarize the data from the literature review. A best-fit beta distribution merely provides a visual summary. The Kolmogorov-Smirnov test shows that the cumulative distribution function of the non-synonymous substitutions is greater at a given value (i.e. right-skewed) compared to that of the synonymous substitutions, $p = 0.029$

pothesis that species susceptible to disease show an increased allele frequency for non-synonymous mutations relative to synonymous. In other words, frequencies of alternative *Prnp* alleles are at more intermediate frequencies that would be expected by chance, a pattern that is consistent with balancing selection despite broad-scale purifying selection.

1.2.3 Testing for Differential Selection within Prion-Disease-Positive and Naive Species

Finally, we hypthosized that species susceptible to prion disease will show a differential ratio of non-synonymous to synonymous mutations as compared to species without reported prion disease.

We gathered consensus coding sequences of the *Prnp* gene for all available species from GenBank, before May 2016. These sequences were confirmed to contain all of the same single nucleotide polymorphisms (SNPs) reported in population sets and relevant literature discussed above. These sequences represent all observed variability within populations across taxa, and include 84 species. Full sequences can be seen in Appendix A. This approach does not account for allele frequency differences between species, but allows for the inclusion of many more species. Sequences were again aligned using MUSCLE [31]. The phylogenetic tree was constructed according to accepted taxonomy and classification of mammalian species ([51–57] and see Figure 1.4). However, we made decisions regarding some sub-species to better reflect our knowledge of the prion disease component. For example, although several sub-species of elk have been proposed [58] it is unknown whether past exposure or susceptibility to prion disease differs by sub-species. So these sub-species were combined into a single operational taxonomic unit. Several species with confirmed susceptibility to prion disease [59] do not have genetic data available (*Eulemur mongoz, Eulemur fulvus, Eulemur albifrans, Oryx leucoryx, Oryx dammah,* and *Felis pardalis*) and were therefore excluded from our analysis.

We further informed our analyses by identifying species in which prion infection was reported to occur naturally, or experimentally by oral transmission. This does not include experimental intracerebral prion transmission between species which is possible by injection of prions, but these cases would not be expected to reflect the effects of natural selection in the same way being considered here. Many more species have been infected by prions via direct intra-cerebral inoculation in a laboratory setting. This unnatural route of transmission leads to a greater host range of prion diseases, but these cases would not have been under natural selection in the same way as naturally infected hosts, and are thus excluded. We labeled the foreground branches for these species as TSE-positive, and colored them red both in Figures 1.4 and 1.5.

We employed Phylogenetic Analysis by Maximum Likelihood (PAML) to test relevant hypotheses. Branch models estimate differential omega ratios across foreground branches of interest, which encompasses evolution from the branch tip to the first node. Site models estimate differential omega ratios across codons with no variation across branches. Finally, the most complex branch-site models can estimate omega ratios across combinations of both branches of interest and codon sites [60–62]. We hypothesized that convergent positive selection would not occur, as tested by the sites model in PAML. Note the lack of a shared amino acid conferring resistance in more

Figure 1.4: Unrooted phylogenetic tree used for Phylogenetic Analysis by Maximum Likelihood (PAML), includes 84 species from class Mammalia. *Species susceptible to oral transmission of prion disease are also marked with red foreground branches. PAML estimates a single $\omega = 0.106$ across the entire phylogeny. This is lower than the estimated omega ratio for the smaller phylogeny, seen in Figure 1.5.

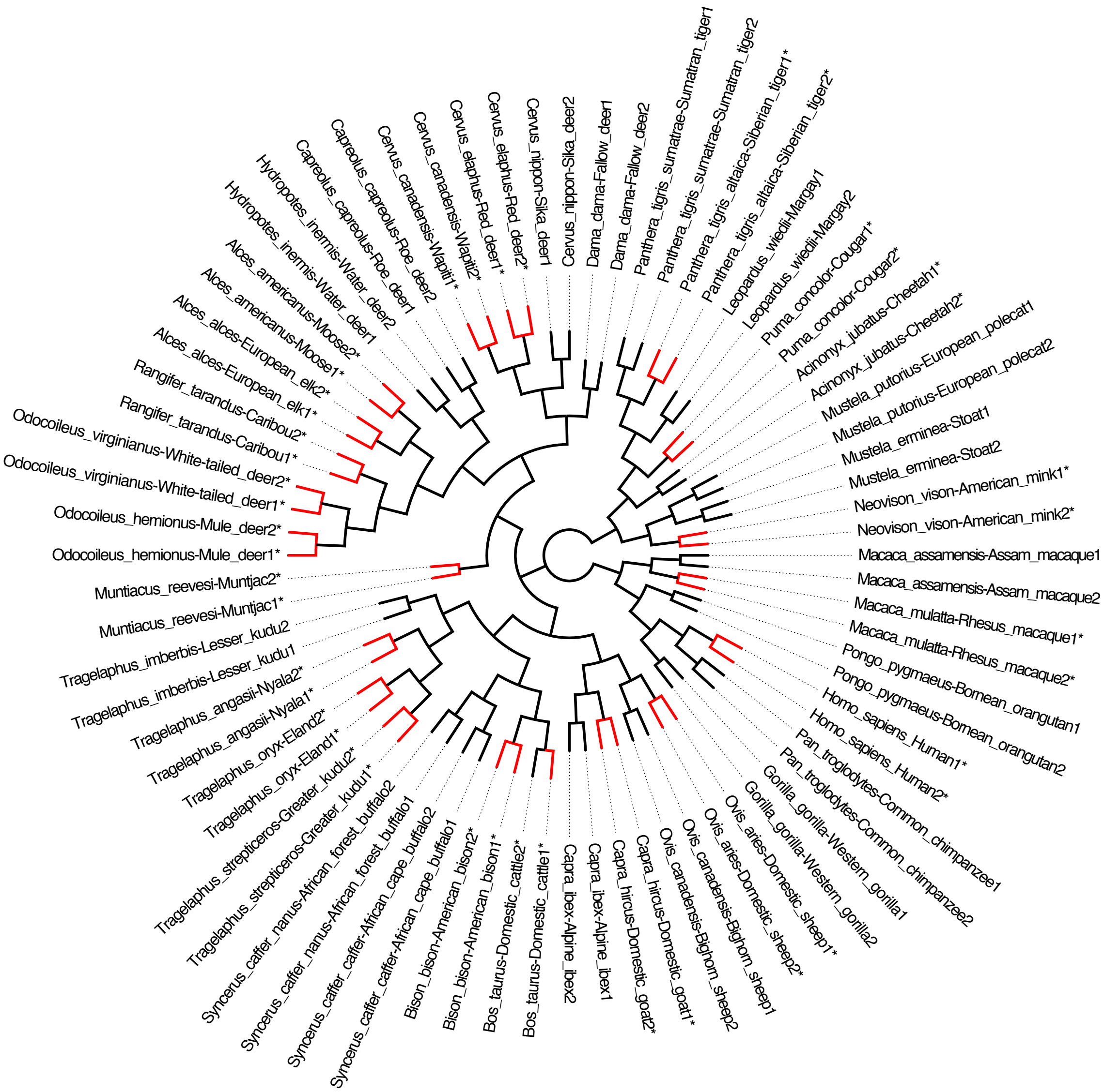


Figure 1.5: Unrooted phylogenetic tree used for Phylogenetic Analysis by Maximum Likelihood (PAML), includes 38 species from class Mammalia, each represented by two external nodes, denoted by 1 and 2. The two nodes allow for reported polymorphisms to be fully represented for species. *Species susceptible to oral transmission of prion disease are also marked with red foreground branches. In this focused within-species analysis, PAML reveals that omega within species, $\omega_{Sp} = 0.084$, differs from that between species, $\omega_B = 0.430$. There is no evidence the omega estimated within species that are susceptible to prion disease differs from that within naive species. See Table 1.3 for full model results.

than one species. PAML site models can test for evolutionary convergence, but we hypothesized that prion disease would act to drive positive selection at unique beneficial codon sites within each species in the face of disease pressure based on standing genetic variation. This branch-by-codon interaction can theoretically be tested with the branch-sites model but requires estimation of an enormous number of free parameters; each codon would be assigned to an omega value within each species. We clearly lack the power to fit such a model to detect positive selection. We employed branch models to test for differential omega ratios across the entire prion precursor coding sequence for branches of interest, namely those of species known to exhibit oral susceptibility to prion disease which we have labeled red in both Figures 1.4 and 1.5.

Broad-scale analysis of omega revealed strong purifying selection across the tree in Figure 1.4, with an estimated $\omega = 0.106$. There is no evidence that selection differs on those branches susceptible to prion disease (TSE-positive as described above and red in Figure 1.4). This further supports the qualitative observation that the prion precursor is under strong purifying selection within species.

To focus our hypothesis testing, we selected a smaller set of species for further analysis to refine our data and better focus on the potential effect of prion disease within affected species. This test also depends on the observed ratio of non-synonymous to synonymous mutations.The phylogenetic tree for this analysis can be seen in Figure 1.5. We defined this group according to several criteria: First of all, species infected with prion diseases were included. Naive sister species and clades (those never reported to suffer from prion disease) were then included to build a balanced dataset that included paired samples of prion-infected and naive species. To allow PAML to analyze polymorphisms within species, each species was split between two branches with each observed nucleotide randomly assigned to each branch. This was necessary because PAML does not consider ambiguous nucleotide codes to be observed polymorphisms but codes them as sequencing errors. PAML reads ambiguous nucleotide codes as missing data, where a Y is read ambiguously as a C or T rather than a known C/T polymorphism. PAML considers each codon site independently and does not consider interaction across codons so it is unnecessary to inform the model with true haplotypes.

By focusing our analysis down to this finer scale, we see a more nuanced result. For the null model, PAML estimates a single $\omega = 0.147$ across this tree (Figure 1.5). However, upon dividing omega within and between species (the Species Branch model), we observe that omega within species, $\omega_{Sp} = 0.430$, is increased relative to the background ratio observed between species, $\omega_B = 0.084$. Every foreground branch represents evolution within species in Figure 1.5, while comparisons across the rest of the tree test for evolution between species. Selection has had more time to remove detrimental variation from the gene pool at the larger evolutionary timescale observed between species.

Omega can be further sub-divided to distinguish species branches with and without observed oral susceptibility to prion disease (TSE-positive branches colored red in (Figure 1.5). For this model, which we refer to as the Species + TSE Branch model, PAML estimates one omega value between all species, $\omega_B = 0.084$, but now two independent within-species omega ratios, including one for TSE-positive species branches, $\omega_{TSE} = 0.457$, and another for all other foreground branches which represent within-species evolution, $\omega_{Sp} = 0.366$. Given the observed large p-value from the likelihood ratio test, there is no evidence that TSE-positive species with observed susceptibility to prion disease experience altered evolutionary pressure on *Prnp* relative to species with no observed susceptibility. See Table 1.3 for full results. If prion disease heavily altered the force of selection across the entire gene by exerting positive selection on resistant alleles, we would hypothesize relaxed purifying selection and an increased omega within TSE-positive species branches.

Table 1.3: Model comparison for branch tests across Mammalia in PAML. The Species Branch model separates within-species branches (Sp) from between-species (B), while the Prion Disease (TSE) Branch model further distinguishes those branches within TSE-positive species (susceptible to natural and orally transmitted prion disease). *Degrees of freedom (df) are shown relative to the Null Model. **P-values are shown for nested model given the general model according to the likelihood ratio test. See phylogenetic tree in Figure 1.5.

Model	lnL	κ(ts/tv)	ω(dN/dS)			df*	P-value**
Null	-3585.498	3.313	$\omega = 0.242$				
Species Branch	-3953.852	3.475	$\omega_B = 0.084$	$\omega_{Sp} = 0.430$		1	$p \vert Null \rightarrow 0$
Species + TSE Branch	-3953.740	3.475	$\omega_B = 0.084$	$\omega_{Sp} = 0.366$	$\omega_{TSE} = 0.457$	2	$p \vert Species\, Branch > 0.25$

1.3 Discussion

We analyzed the potential impact of prion disease on the evolutionary history of the prion precursor gene *Prnp*, which codes for one of the pathogenic prion proteins. Data support differential selection across protein domains, but no aggregation of allelese associated with disease resistance into specific domains. The diversity of disease-resistant amino acid substitutions does not lend itself to convergent evolution. Natural selection operates on existing genetic variation within a population, and no two species have been reported to share amino acid polymorphisms associated with resistance to prion disease. Accumulating evidence for the presence of distinct prion strains within and between species [63] suggests that those differences would be further magnified across species. Differences among prion strains in conjunction with structural differences in prion precursor proteins between species could preclude convergent evolution across branches of the mammalian phylogeny with endemic prion disease. This would be driven by the observed trend that it is the rare protein that provides the benefits that could come from resistance against disease, not the more common wild-type protein.

The prion precursor locus contains within the octapeptide repeat region an overlapping reading frame coding for a novel expressed polypeptide termed the alternative prion protein (AltPrP*; [64]*). The function of this novel polypeptide remains unknown, but it appears to be endogenously expressed in several mammals, where it localizes to the mitochondria. However, not all species possess a functional start codon. This overlapping reading frame complicates the evolutionary selective forces that may be acting on our gene of interest, *Prnp*. A synonymous mutation in one reading frame may be non-synonymous in the other. This presents a unique challenge to the analysis of *Prnp* as the AltPrP ORF may apply its own selective pressure to this genetic region which could obscure the selective effects of CWD on *Prnp*.

PAML estimates a significant relaxation of the force of purifying selection within species (corresponding to an increased omega value), relative to that observed between species. It is expected for purifying selection to relax within species relative to between species, given the extended evolutionary timescale between species. Model estimates from PAML support this hypothesis which shows that our method successfully detects changes to omega when power is sufficient.

However, PAML does not associate prion disease with positive selection in our test, which would show as a significantly increased omega value for TSE-positive species branches estimated for the phylogeny in Figure 1.5 and summarized in Table 1.3. Many things may explain this finding. First, the data suffer potential observation bias; Both endemic disease and its observation require stochastic events. The lack of disease observation in a species does not guarantee its absence while experimental susceptibility to disease does not ensure that a species has an evolutionary history of endemic prion disease.

Furthermore, we believe that balancing selection would not lead to a change in the observed omega ratio; the frequency of the beneficial minor allele would increase but may not be driven to fixation. The minor allele may experience some evolutionary fitness trade-off, perhaps only in the rare homozygote, that prevents its fixation. Such trade-offs are consistent with the observed trend that it is often the minor allele associated with a benefit against prion disease. Purifying selection for native cellular function may balance the positive selection exerted by prion disease on the minor allele which would maintain the rarity of that allele.

The observation of an increased frequency in the distribution of non-synonymous substitutions relative to synonymous provides support for the hypothesis of balancing selection [17, 19]. This increased frequency of non-synonymous minor alleles is observed whether or not we isolate our data to species known to experience prion disease, perhaps related to the observation bias mentioned above. This increased allele frequency of non-synonymous substitutions is in contrast to the observed strong purifying selection identified by PAML that would decrease not only the number of non-synonymous mutations observed but also the frequency of those remaining within a population. We propose that some evolutionary force acts in opposition to purifying selection and suggest that this agent of natural selection is the association between rare mutant proteins and prion disease resistance.

Chapter 2

Population Genetics of Colorado Mule Deer with Endemic Chronic Wasting Disease

2.1 Introduction

Cervids play important ecological roles, serving as prey base to large predators, distributing nutrients across landscapes, and modifying vegetation communities [65]. They also serve important social roles for humans such as providing opportunities for wildlife viewing and hunting, and symbolize 'wildness' in the American West. Wildlife diseases often occur as unobserved processes but may play important roles by limiting cervid population growth and may interfere with the ecological functions performed by healthy cervid populations. We set out to better understand the ecological processes underlying population demographics and epizootiology in a northern Colorado population of mule deer (*Odocoileus hemionus*) under pressure from the recently emerged but now endemic chronic wasting disease (CWD).

To gain understanding of hidden ecological processes, we employed methods that do not observe those processes directly but instead examine the signatures that they leave behind. CWD epizootiology leaves signs of individual infection within the lymphatic and neural tissues of deer. Meanwhile, gene flow resulting from breeding may be inferred from genetic data, which allows for estimated relatedness within and divergence (or lack thereof) between breeding groups. We aim to better understand these important hidden processes by examining ecological, epidemiological, and genetic data.

We studied both neutral genetic markers and the functional gene that codes for the infectious protein that causes CWD, to different ends. Neutral genes, both those inherited maternally (e.g., mitochondrial DNA; mtDNA) and bi-parentally (e.g., microsatellites or single-sequence repeats; SSR), provide information about gene flow across the landscape.

On the other hand, the functional gene of interest in this case plays an important direct role in the development of CWD. The prion protein gene (Prnp) encodes the cellular prion precursor (PrPC) which may mis-fold by spontaneous or transmissible means to become the disease isoform ($\mathrm{PrP}^{\mathrm{CWD}}$), known as the prion [66]. Prions become toxic as they accumulate within infected individuals, cause neurodegenerative disease that is inevitably fatal, and are transmissible between individuals (prion diseases are also called transmissible spongiform encephalopathies). Non-synonymous substitutions in alternative *Prnp* alleles code for differences in the cellular prion protein amino acid sequence, which may impact disease dynamics, including transmission and disease progression, at the molecular level. Prion diseases are unique in their etiology, resulting from molecular mis-folding of cellular proteins [66], and are influenced by prion protein sequence polymorphisms in many species affected by prion diseases [14].

Our goal was to further explore the relationship between *Prnp* genetics and prion diseases generally, while also examining the gene flow of free-ranging mule deer as it relates to CWD epizootiology at the landscape level.

2.2 Materials and Methods

2.2.1 Study Area and Sampling

The Red Feather – Poudre Canyon deer herd [67] consists of an estimated ~7,500 animals across ~4,600 square kilometers and is located in northern Larimer County northwest of Fort Collins, Colorado. Study animals occupy habitat from low-elevation foothills to the east (~5,000 feet above sea level) to more mountainous terrain to the west (~11,000 ft). Land ownership includes private, United State Forest Service, the state of Colorado, the City of Fort Collins, and Larimer County. Land use includes agriculture, livestock grazing, recreational hunting, and residential development.

We captured free-ranging mule deer during the winters of 2010-2014 from a portion of the Red Feather–Poudre Canyon deer herd, by helicopter net-gun. Upon capture, rectal-anal mucosal-associated lymphoid tissue was collected as described in [68] and tested for CWD by immunohistochemistry at the Colorado State University Veterinary Diagnostic Laboratory (Fort Collins, Colorado, USA) as described in [69]. We used the term CWD-positive to refer to any animal that tested positive even once (sometimes described as CWD test-positive). Blood was drawn by jugular venipuncture for genetic analyses.

Study animals were fitted with global positioning system (GPS) or very high frequency (VHF) radio collars (Advanced Telemetry Systems, Isanti, Minnesota, USA) and released near the site of capture. We only sampled males on the last two years of the study and fitted them with blow-off GPS collars that automatically came off roughly one year after capture. We tracked animals via radio telemetry and followed them for mortality events. Upon mortality, we attempted to determine the cause of death and collected additional tissue samples for further CWD testing. We attempted to locate all animals annually during each of the four seasons which included once on each summer and winter range. Animals were re-captured annually when possible and re-tested for CWD. We attained an average annual recapture rate of 85%.

All landowners granted permission for field work, including the Colorado Division of Parks and Wildlife, the City of Fort Collins, and Laramie County, Colorado, and several private landowners. Animals handled in the field were limited to mule deer and did not involve endangered or protected species. All animals were handled in accordance with protocols approved by the Colorado State University Institutional Animal Care and Use Committee (Protocol 11-2758A). Full details on sampling and field data collection are described in [70].

Individual home range membership for each female in the study was determined (described by [70]) using methods and confirming winter ranges from previous work by [71]. Males were not assigned to winter ranges due to the paucity of available spatial data resulting from their fore-shortened time in study. Categorical migrant status was determined by testing for the distance between estimated summer and winter range centroids. We assigned individuals as non-migrants if their estimated seasonal centroids were less than 6km apart.

2.2.2 Genotyping

DNA was isolated from whole blood using DNeasy Blood and Tissue Kits (Qiagen Valencia, CA). *Prnp* was amplified and sequenced directly according to protocols from [6], to identify polymorphisms across the coding region. We genotyped our samples first for two previously characterized alleles at amino acid position 225, one coding for a serine (225S) and the other for a phenylalanine (225F). We distinguished heterozygotes (225SF) from rare homozygotes (225FF) by directly sequencing the amplified gene from each individual, rather than relying on a restriction digest analysis. By fully sequencing, we further characterized genetic differences at amino acid position 20 (D/G) and two additional synonymous substitutions at base pairs 393 and 741.

We characterized eleven microsatellite markers [72]. Modifications to these protocols included use of the Qiagen Multiplex PCR kit (Valencia, CA) with equimolar final primer concentrations of 200nM as recommended by the manufacturer. Fragments were sized on a 96–capillary, 50–cm array 3730XL DNA Analyzer (Applied BioSystems; Foster City, CA) and data analyzed in Genemapper. Mitochondrial DNA was amplified and sequenced across 691 base pairs of the control region using primers from [73].

2.2.3 Genetic Analysis

We estimated the phase of *Prnp* polymorphisms. Phase, or haplotype, refers to which nucleotides are linked to each other on the same DNA strand. We implemented the maximum likelihood algorithm of [74] in program R . We estimated the likelihood of association between alternative nucleotides at disparate sites within the gene, based on both the frequencies of the alternative nucleotides at each site and the observed unambiguous haplotypes. When uncertainty is small relative to observed unambiguous genotypes, phase estimation allows for identifying specific alleles, or haplotypes, within a gene.

Descriptive statistics of genetic divergence between populations, including F-statistics (including G'_{ST}, which allows for an unbiased direct comparison of genetic differentiation from both haploid and diploid data; [75]), heterozygosity, linkage disequilibrium, and percent missing data, were calculated using the diveRsity package in program R [76]. Statistics were calculated both for spatial clusters by winter range and also for genetic lineages as predicted by principal component ordination (PCO) clustering, as described below.

Differentiation statistics for mtDNA sequence data were calculated using package mmod in program R [77]. Confidence intervals were calculated over 1000 bootstraps for global statistics.

2.2.4 Population Structure

Program STRUCTURE [78] was used to examine whether study deer could be assigned to genetic clusters. Runs of the program extended over 100,000 iterations after a 10% burn-in. Estimates were repeated over ten chains for each value of K, the number of clusters to be estimated. Three parameter sets were tested, corresponding to “No Prior” of each deer’s geographic location, “Location Information”, and “Prior Information”, as follows: Set 1: No Prior, employed the admixture model with no prior information regarding individual winter range location, correlated allele frequencies between populations, and parameter defaults elsewhere. Set 2: Location Information, also employed the admixture model with correlated allele frequencies between populations but used inferred winter range assignment for sampling location information. Set 3: the Prior Information model, used the strongest prior in employing inferred winter range location information to assist clustering.

When possible, females were assigned to a winter range. All other individuals, including males and those females that were lost from the study, did not have location information and for these the STRUCTURE model employed the admixture model described above with no prior.

An additional clustering method, based on PCO was completed in Program R using the adegenet package [4], following [79]. PCO clustering provides a conservative test of the relative support for inferred genetic clusters. PCO modal clustering will only support genetic clusters with large differentiation compared to program STRUCTURE, thus PCO clustering is relatively conservative.

Examining mitochondrial DNA (mtDNA) variation, where mutations occur within linked haplotypes, requires a different approach. Relatedness between haplotypes can be examined by constructing minimum spanning trees which accounts for the number of mutational steps that most parsimoniously links haplotypes. We constructed consensus minimum spanning trees using program MSTgold [80]. This sored haplotypes into networks that represent the minimum number of mutational steps between all observed haplotypes within an aligned sequence, in this case the mtDNA control region. In effect, the resulting networks depict how mtDNA haplotypes are genetically related to each other. Component networks, which are simply defined as those haplotypes that are connected with each other but not connected to other component networks, were defined according to the consensus tree, with the default 50% minimum inclusion of edges (edges are the branches connecting different nodes, or haplotypes). This consensus tree structure was also confirmed in program TCS [81].

2.2.5 Disease Association Testing

We tested for non-random clustering of CWD-positive individuals across ecological categories of interest including sex, migrant status, and population units defined both by spatial winter ranges, and by genetic clusters. We used chi-squared contingency tests, and Fisher's exact tests when sample sizes were small. We considered mitochondrial haplotypes as well as clusters derived from nuclear microsatellite data when conducting these analyses.

2.3 Results

We captured 273 mule deer (223 females, 50 males) across four winter ranges (See Figure 2.1). Spatial clustering analysis of estimated winter range centroids for female deer confirmed the presence of four clusters (See [70]) which corresponded with four previously reported winter ranges [71].

Females captured on winter ranges and fitted with radio collars migrated annually from those winter ranges (~October to March) to summer ranges (~April to September) up to 60 km away.

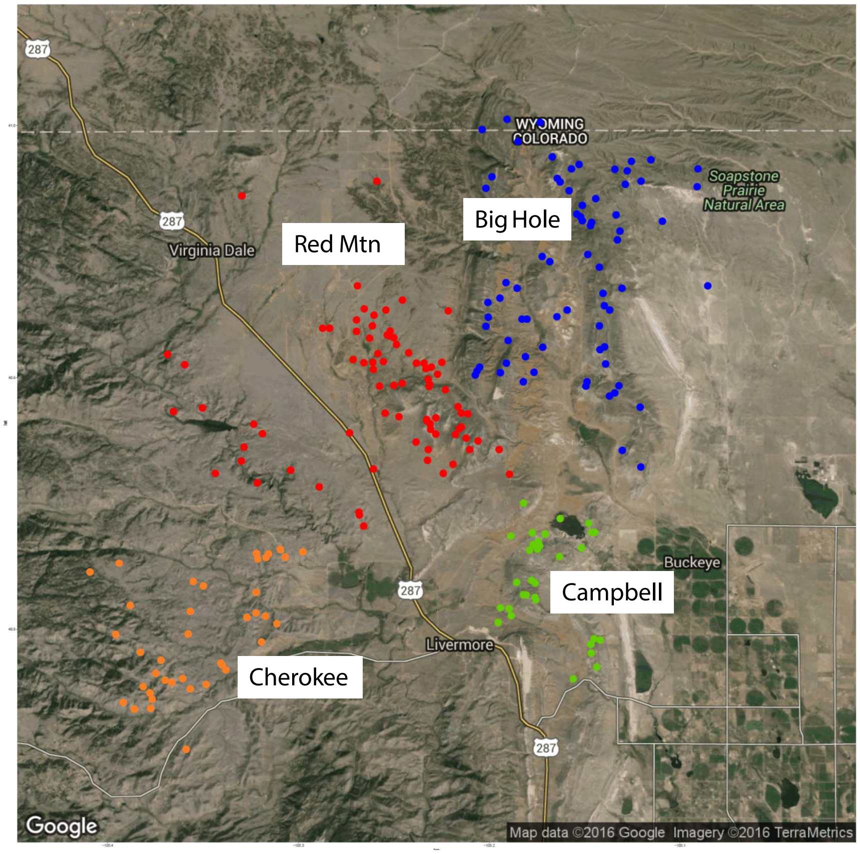


Figure 2.1: Locations of estimated winter range centroids for 223 female mule deer in a northern Colorado population show individual winter range membership across the landscape.

Across the three winter ranges at lower elevation in the east of our study area (Big Hole, Red Mountain, and Campbell Valley), all 185 females migrated. In the fourth winter range at higher elevation and in the west of our study area (Cherokee State Wildlife Area or SWA), only two of 39 females migrated. We compared these proportions to those reported previously by [71] using Fisher's exact test and showed that these proportions have shifted toward the extremes in all winter ranges (Table 2.1; all p-values < 0.05)

Table 2.1: Proportion of female mule deer within winter ranges exhibiting seasonal migration behavior differ both spatially and temporally when compared to past reports. Deer are classified as migrants if the Euclidean distance between winter and summer home range centroids is greater than 6km. The second row reports published data collected from 1996-2003 (Conner and Miller 2004). We used Fisher's Exact Test to test for differences within each winter range between the two time points and show p-values uncorrected for multiple tests. The p-value for the test between Cherokee and other winter ranges for the current work is not shown.

	Cherokee	Big Hole	Red Mtn	Campbell
Current Work	0.05 (n=39)	1.0 (80)	1.0 (73)	1.0 (32)
FET p-value	p=0.039	0.032	0.0002	0.0001
Historic Data	0.33 (9)	0.89 (18)	0.8 (41)	0.58 (19)

2.3.1 Genetic polymorphism within the prion precursor gene

By sequencing the entire prion precursor gene, we identified 618 nucleotides accounting for 206 of the 257 amino acid positions in the transcribed protein. We observed four nucleotide polymorphisms within *Prnp*, including two synonymous substitutions (both C to T at nucleotides 393 within a tyrosine codon and 741 within an isoleucine codon) and two non-synonymous substitutions at nucleotides 59 and 674. These have been previously reported [6, 46]. One results in a polymorphism at amino acid 20 - aspartate (D) or glycine (G) - designated D20G. A second occurs at amino acid 225 – a serine (S) or a phenylalanine (F) – designated S225F.

We estimated the phase of the nucleotides in relation to each other within *Prnp* in order to identify specific alleles of the gene, designated haplotypes. For instance, we determined how likely it is for a D at position 20 to be on the same DNA stand (haplotype) as an S at position 225. We limited the analysis to include only the two non-synonymous substitutions because, ultimately, we are interested in the different PrP proteins that influence the course of prion disease within a deer (Cortez and Sim 2013). Additionally, including all four nucleotide polymorphisms resulted in too many ambiguous genotypes to allow haplotypes to be estimated with confidence.

Over 99.9% of the single observed ambiguous genotype (the double heterozygote DG.SF) was estimated to represent two haplotypes, with D linked to F and with G linked with S (DF/GS; See Table 2.2). With no recombination, it was unlikely that the two minor alleles (20G and 225F) co-occurred on a single haplotype. This two-allele, two-loci problem yielded one ambiguous genotype. We observed this double heterozygote only fifteen times which allows for conclusive haplotype identification.

Table 2.2: Prion protein haplotypes based upon two nucleotide polymorphisms corresponding to amino acids D20G and S225F, observed in winter ranges for females, for all females across the entire study area regardless of winter range, and for both males and females across the entire study area. Occurrence of PrP haplotypes did not differ between winter ranges, and did not change when males were also included. PrP types are designated by amino acids at site 20 (DD, DG, or GG) and site 225 (SS, SF, FF).

Prnp haplotype corresponding to amino acids D20G and S225F	Females Only				All females across winter ranges	All females and males
	Cherokee	Red Mtn	Big Hole	Campbell		
DD.FF	1	2	1	0	5	5
DD.SF	13	15	21	11	60	71
DD.SS	19	40	30	12	101	125
DG.SF	2	3	4	2	11	15
DG.SS	3	20	13	6	42	46
GG.SS	1	1	3	0	5	5
Total	39	81	72	31	223	267

We designate the alleles of the *Prnp* gene as *Prnp* haplotypes, based upon the two non-synonymous nucleotide polymorphisms corresponding to amino acids D20G and S225F (e.g. DD.FF, DD.SF, DD.SS, DG.SF, DG.SS, and GG.SS).

Frequencies of *Prnp* haplotypes did not differ across winter ranges or between sexes (See Tables 2.3 and 2.4). *Prnp* genotypes showed no sign of deviation from Hardy-Weinberg equilibrium, either within winter ranges or genetic lineages described below, or across the entire study area.

2.3.2 Population genetic structure of mule deer populations – microsatellite variation

Microsatellite genotyping resulted in average allelic diversity of 8.2 alleles per locus across the 11 loci. Estimates for observed and expected heterozygosity can be seen in Table 2.5, while F-statistics are summarized in Tables 2.6, 2.7, and 2.8. We saw no evidence of deviations from Hardy-Weinberg equilibrium or inbreeding.

From program STRUCTURE estimates, it appears that the optimal number of genetic clusters occurs at three or four. The ΔK method from Evanno et al. (2005) shows a peak at K=3 for parameter Set 1, No Prior (See Figure 2.2). Posterior probability continues to increase, however, for K=4. PCO clustering also supports K=4 with a decrease in the Bayesian Information Criteria (BIC) greater than 2 as the model moves from K=3 to 4 (See Figure 2.3 and according to the best practices for BIC in Raftery 1995).

We suggest that the optimal number of genetic clusters is four based on the findings described above. These clusters correlate with those predicted by PCO using the same microsatellite data (χ^2 p=(2.2e)^(-16)), and deviate from that expected from the observed spatial structure of winter ranges (p = 0.0029).

However, if female winter range is used as the population prior in program STRUCTURE, the observed genetic clustering collapses and best K resolves to one (See Figure 2.2).

Genetic clusters inferred from PCO reveal best fit at four genetic clusters using BIC and the critical values suggested by Raftery (1995; See Figure 2.3). Discriminant analysis of principal components on these four inferred clusters also suggest a greater estimated statistical distance between the four clusters inferred from PCO than those observed on winter ranges (See Figure 2.4). These genetic lineages, or clusters, do not group spatially or by winter range (See map in Figure 2.5). The use of winter range assignment limited analyses to only those females with sufficient location data to allow assignment to one of the four winter ranges. Given that winter range does not correspond to genetic differences, we carry out all additional analyses using all study animals, including males.

Table 2.3: Chronic wasting disease is more common in male than female deer and more common in female and male deer encoding the 225SS PrP types (DD.SS and DG.SS) than expected by chance. When no number appears in parentheses, no males were observed with that PrP type.

Females (Males)	DD.FF	DD.SF	DD.SS	DG.SF	DG.SS	GG.SS
CWD-Positive	0	2	10 (4)	0	6 (1)	0
CWD-Negative	4 (1)	58 (11)	91 (16)	11(4)	37 (1)	5

Table 2.4: Neither frequencies of the minor *Prnp* S225F allele nor associated genotypes appear to differ across winter ranges for females in a population of northern Colorado mule deer. Numbers in parentheses show observed CWD-positive individuals.

Total (CWD+)	Cherokee	Big Hole	Red Mtn	Campbell	Overall
SS	23	60 (9)	47 (7)	19	149
SF	15	18 (2)	25	13	71
FF	1	2	1	0	4

Table 2.5: Summary of 11 characterized microsatellite loci in 273 mule deer of both sexes. Columns correspond to estimated allelic richness (N_A), and observed (H_O) and expected heterozygosity (H_E).

	N_A	H_O	H_E
Odh_E	6	0.4432	0.4861
Odh_K	7	0.685	0.7196
Odh_C	4	0.5348	0.524
BM848	9	0.7326	0.7763
C273	5	0.5165	0.5251
Odh_P	8	0.6374	0.6411
Odh_N	13	0.8645	0.8607
Odh_G	3	0.6447	0.629
Odh_O	11	0.5714	0.7029
RT24	12	0.7985	0.781
T40	12	0.8388	0.8534

Table 2.6: Summary pairwise F-statistics (confidence intervals; CIs) across winter range designations estimated from microsatellite data. These only include females with sufficient spatial data for winter range assignment for a population of northern Colorado mule deer and reveal there is very little genetic differentiation between winter ranges with most CIs including zero.

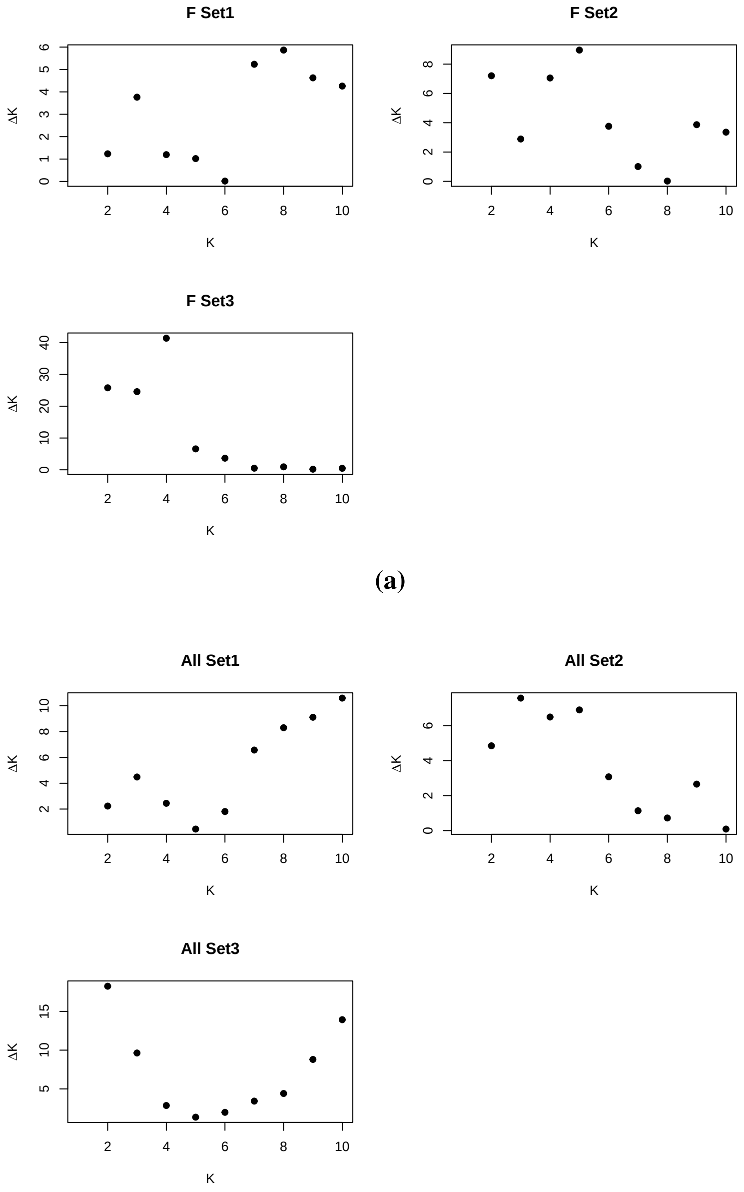
F_{ST} (95% CI)	Cherokee	Campbell	Big Hole	Red Mtn
Cherokee	NA			
Campbell	0.0109 (-0.0032, 0.0290)	NA		
Big Hole	0.0122 (0.0018, 0.0255)	0.0103 (-0.0027, 0.0262)	NA	
Red Mtn	0.0116 (0.0016, 0.0238)	0.0113 (-0.0004, 0.0261)	0.0017 (-0.0035, 0.0082)	NA

Table 2.7: Summary pairwise F-statistics (and confidence intervals; CIs) across four purported genetic lineages estimated from microsatellite data and defined by PCO clustering. These include males and females, and ignore winter range designations in a population of northern Colorado mule deer. Note that these genetic lineages do not correspond to the winter ranges in Table 2.6. These clusters show more evidence of genetic differentiation than winter range groups with larger estimated values and no CIs that include zero.

F_{ST} (95% CI)	1	2	3	4
1	NA			
2	0.0632 (0.0544, 0.0732)	NA		
3	0.0707 (0.0571, 0.0856)	0.0896 (0.0757, 0.1055)	NA	
4	0.0605 (0.0503, 0.0717)	0.0639 (0.0517, 0.0769)	0.0668 (0.0518, 0.0833)	NA

Table 2.8: Summary G'_{ST} cross four purported genetic lineages estimated from microsatellite data and defined by PCO clustering. These include males and females and ignore winter range designations and were calculated using the diffCalc package in program R. G'_{ST} corrects for haploid or diploid genetic markers and as such allows for direct comparison between maternally inherited mtDNA and bi-parentally inherited microsatellites.

G'_{ST} (95% CI)	1	2	3	4
1	NA			
2	0.1744 (0.1247, 0.1735)	NA		
3	0.1953 (0.1301, 0.2033)	0.24 (0.1701, 0.2428)	NA	
4	0.1805 (0.1259, 0.1863)	0.1835 (0.1236, 0.1925)	0.1933 (0.1247, 0.2086)	NA



(a)

(b)

Figure 2.2: Likelihood of data across varying number of clusters from program STRUCTURE. ΔK suggests that best-K occurs at three clusters with no prior while posterior probability (Ln P(D)) suggests a modest improvement at four clusters (Set 1 for All individuals). These plots also show the conflict between prior data on winter range and genetic clustering as the best fit for female deer with prior data (parameter sets 2 and 3) occurs at K=1. Genetic data is 11 SSR loci, with the upper panel including only 223 female mule deer with spatial data for winter range centroid clustering, while the lower panel includes all 273 genotyped individuals. Parameter sets include Set 1; Admixture model with no prior, Set 2; Location data model, and Set 3: Prior information model. Mean Ln(P(D)) is plotted with whiskers showing the mean estimated standard deviation from program STRUCTURE. ΔK is calculated according to the method of [3].

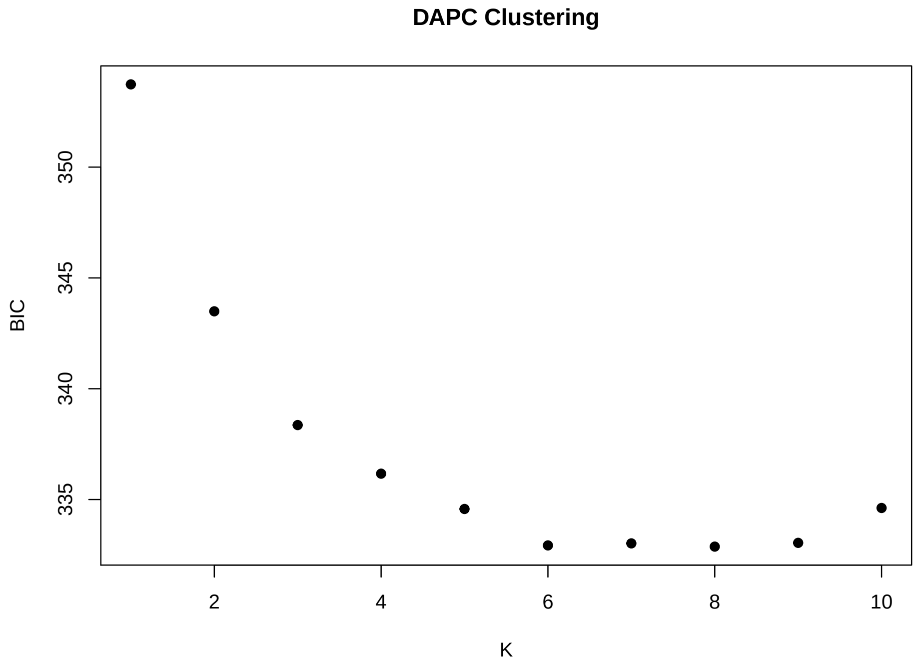
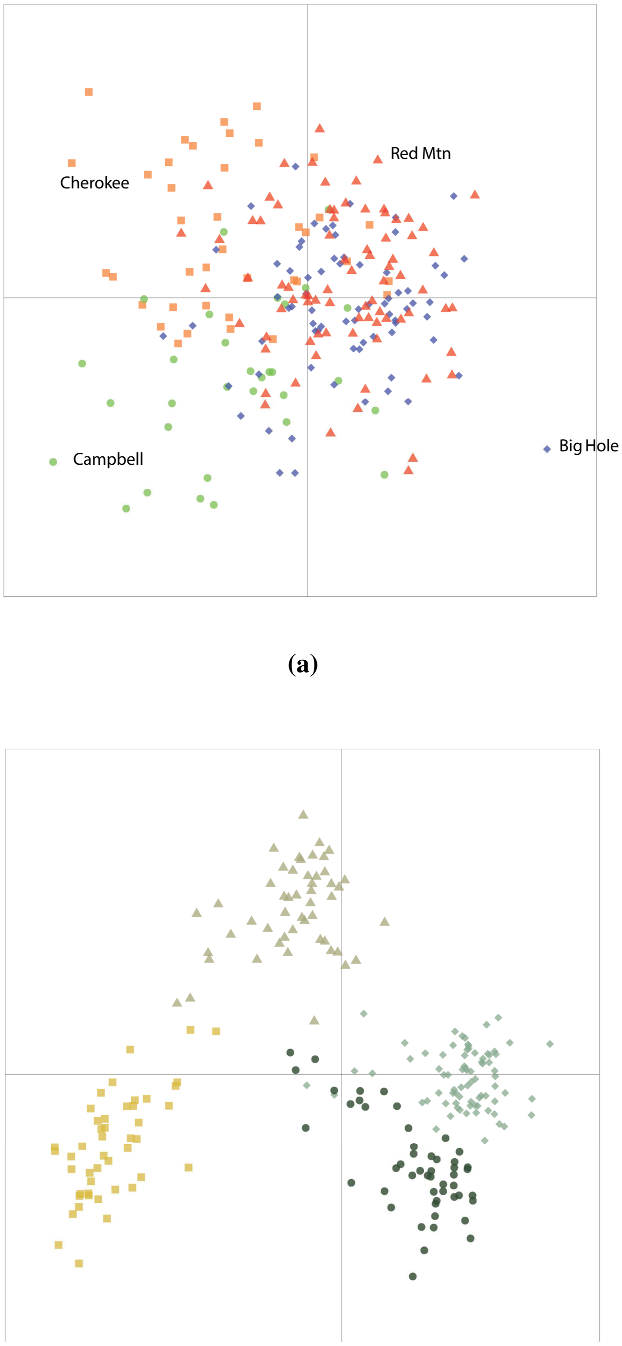


Figure 2.3: Bayesian information criteria (BIC) across cluster number K for principal component ordination clustering using adegenet [4]. Using a critical differential value of 2 as originally recommended for strong support [5] we estimate that best fit occurs at four genetic clusters. Further decreases in BIC only provide weak support for more genetic clusters.



(a)

(b)

Figure 2.4: Discriminant analysis of principal components reveals greater separation for genetic lineages inferred by PCO clustering (B) than for winter range groups (A). Data includes 11 SSR loci from 223 female mule deer in northern Colorado.

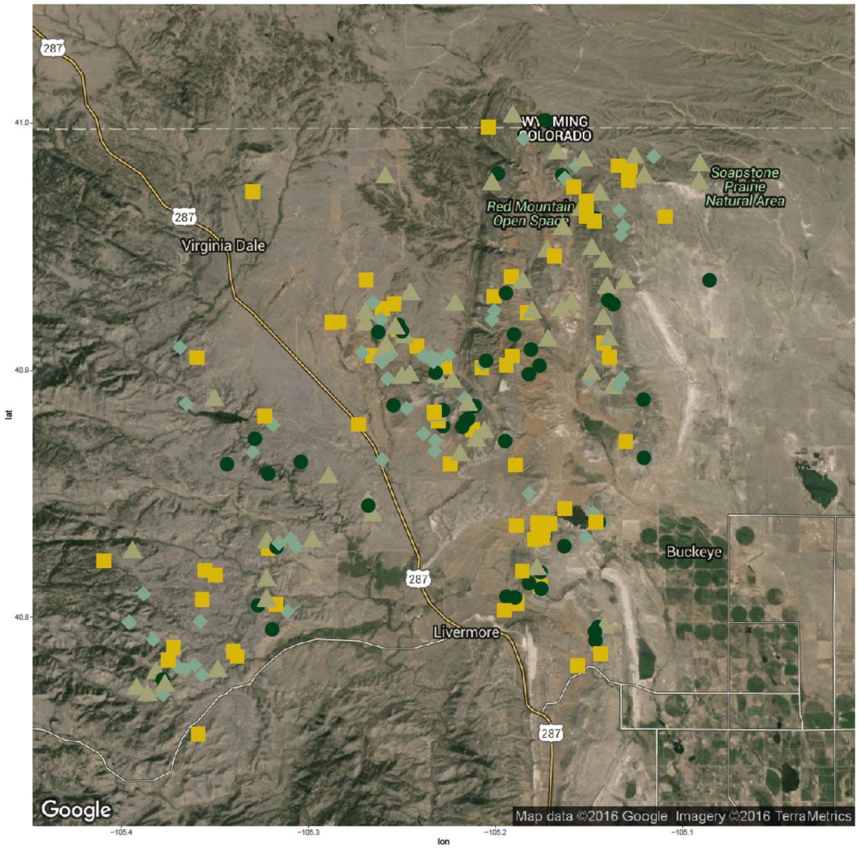


Figure 2.5: Locations of estimated winter range centroids for 223 female mule deer in a northern Colorado population, when paired with microsatellite data, show that genetic lineage assignment does not cluster spatially across the landscape. Inferred genetic lineage assignment is shown with unique symbols and colors for each of four genetic clusters. Genetic data includes 11 SSR loci and genetic lineages are predicted by principal component ordination clustering.

2.3.3 Population genetic structure of mule deer populations – maternally-inherited mtDNA

This population genetic analysis of mtDNA variation was carried out because of the maternal inheritance of mtDNA, which should reflect gene flow by related groups of females only, and thus potential pathways of prion transmission. We sequenced mtDNA in 272 deer, 222 females, because one reaction failed. Thirty-nine mtDNA haplotypes were observed, encompassing 75 single-nucleotide polymorphisms, including one single-nucleotide insertion-deletion. Four of these haplotypes were only observed in males.

The program MSTgold identified four component haplotype networks within the consensus network using the default of 50% minimum consensus (Figure 8). Four observed haplotypes are not present in the consensus network; These haplotype nodes do not connect to any others with more than the 50% minimum bootstrap support and are therefore not included in the consensus network.

We calculated global F-statistic analogs across the four winter range groups defined with spatial data from mitochondrial DNA based on average heterozygosity in package mmod. We estimated a mean G'_{ST} of -0.0068 and 95% confidence interval -0.0076 to -0.0061. Mean ϕ_{ST} was 0.0257 with a 95% CI of 0.0135 to 0.0401. These data only include 222 females with sufficient spatial data and mtDNA sequences. See Tables 2.9, 2.10, and 2.11.

Table 2.9: Global summary of mitochondrial DNA sequence data for winter range groups for 222 female deer.

H_s	H_t	G'_{ST}	D_{het}
0.23205674	0.24840275	0.11180002	0.0283806

We used the same methods across the four genetic lineages defined by PCO clustering and estimated a mean G'_{ST} of -0.0038 with 95% CI of -0.0042 to -0.0035. Mean ϕ_{ST} was -0.0607 with a 95% CI of -0.0746 to -0.047. These data include males and females and ignore winter range designations. G'_{ST} corrects for haploid vs diploid data and allows for direct comparisons of genetic differentiation between maternally inherited haploid mtDNA and bi-parentally inherited diploid microsatellites. See Tables 2.12 and 2.13.

The four genetic clusters defined from SSR data do not correlate with component network membership within the consensus minimum-spanning tree identified by MSTgold. Fisher's exact test between mitochondrial component network membership and PCO clusters shows no deviation from the null (p=0.52), revealing that all PCO clusters appear equally likely to co-occur with all mtDNA components.

2.3.4 Disease Association across *Prnp* Genotypes, Study Areas, and Genetic Lineages

Although spatial clusters defined by winter ranges failed to identify population genetic structure, cryptic genetic lineages were identified across the four winter ranges by program STRUCTURE and PCO.

CWD-positive female mule deer were found only in the Red Mountain and Big Hole areas of our study (See Table 2.14 or [70]). However, CWD infection does not correlate with PCO genetic clusters (Fisher's Exact Test p=0.62) or mtDNA haplotypes (Fisher's Exact Test p=0.26), or mtDNA component networks (Fisher's Exact Test p=0.73). Members of all genetic lineages appear equally likely of testing positive for CWD.

We were unable to test for CWD association with seasonal migratory behavior because all observed females in winter ranges with higher CWD prevalence were seasonal migrants and disease was too rare in the one winter range with heterogeneous seasonal migration behavior to provide sufficient power.

Migratory behavior was not associated with genetic lineages as defined by microsatellite data (Fisher's Exact Test p=0.92), but it was strongly linked to component network membership of mitochondrial haplotypes ($p<10^{-5}$).

Table 2.10: Summary pairwise G'$_{ST}$ across four observed winter range groups estimated from mitochondrial DNA. These include 222 female mule deer with sufficient spatial data for winter range designations and mitochondrial DNA sequences.

G'$_{ST}$	Cherokee	Campbell	Big Hole	Red Mtn
Cherokee	NA			
Campbell	0.15797	NA		
Big Hole	0.16937	0.0154	NA	
Red Mtn	0.23997	0.03197	0.02323	NA

Table 2.11: Summary G'$_{ST}$ across four observed winter range groups estimated from 11 microsatellites. These include 222 female mule deer with sufficient spatial data for winter range designations and mtDNA sequences.

G'$_{ST}$	Cherokee	Campbell	Big Hole	Red Mtn
Cherokee	NA			
Campbell	0.0371 (-0.0117 , 0.0791)	NA		
Big Hole	0.0381, (0.0010, 0.0707)	0.0314, (-0.0122, 0.0737)	NA	
Red Mtn	0.0381, (0.0008, 0.0672)	0.0365, (-0.0029, 0.0795)	0.0053, (-0.0113, 0.0233)	NA

Table 2.12: Global summary of mtDNA sequence data for four genetic lineages defined by PCO clustering for 272 male and female deer.

H_s	H_t	G'$_{ST}$	D_{het}
0.246	0.248	0.010	0.003

Table 2.13: Summary G'$_{ST}$ estimated from mitochondrial DNA across four purported genetic lineages as defined by PCO of microsatellite data. These include males and females and ignore winter range designations.

G'$_{ST}$	1	2	3	4
1	NA			
2	0.0075	NA		
3	0.0212	0.0002	NA	
4	0.0188	0.0032	0.0117	NA

Disease did not associate with either mtDNA haplotype, component membership on the mtDNA minimum spanning tree or the PCO-predicted genetic clusters. Only females were used for these analyses to avoid the bias of males with higher disease prevalence.

Individuals heterozygous for *Prnp* S225F were less likely to test positive at any point for CWD (Fisher's Exact Test p=0.038). Only four *Prnp* 225FF homozygous females were observed and none tested positive for CWD during our study. Neither time in study nor age appeared biased across *Prnp* S225F genotypes when compared by box plot. There was no observed deviation from the null relative to disease test status at the D20G site. D20G and S225F showed strong genetic linkage with no observed recombinants so we did not have the statistical power necessary to test these independently.

*Prnp*225F allele frequency shows no evidence of differing across winter ranges or genetic clusters (Chi-squared p>0.3; See Figure 2.6). Overall *Prnp* 225F allele frequency for all sequenced animals was 0.180 (95% asymptotic CI: 0.147-0.212). This is greater than previously reported in neighboring areas by [6]. See Figure 2.7 for a visual summary of the frequency of the two minor *Prnp* genotypes at codon 225 compared to reports from [6].

2.4 Discussion

We noted a distinct difference in the proportion of seasonal migrants across winter ranges as well as from historical data in the same area (See Table 2.1 and [71]). From 185 females in three winter ranges with highest disease pressure, including Big Hole, Red Mountain, and Campbell Valley, all female deer migrated. On the other hand, in Cherokee SWA which showed much less local disease, almost all females (37 of 39) did not migrate. Although there are some distinct ecological differences between these winter ranges related to elevation differences and associated vegetation communities, we believe this difference may also be related to heterogeneous CWD pressure.

Migration behavior within winter ranges has shifted towards the extremes compared to historical data from [71], becoming more common in winter ranges with high disease pressure and more

Table 2.14: Chronic wasting disease (CWD) infection was detected in female mule deer captured on winter ranges in the Red Mountain and Big Hole areas of the study. CWD-positive refers to study animals that tested positive at any time in the study. Confidence intervals were calculated using the Bayesian beta-binomial with uniform prior in package ‘binom’ in program R.

Females	Cherokee	Red Mtn	Big Hole	Campbell
CWD-Positive	0	11	7	0
Total	39	69	66	33
P(CWD+); 95% BCI	0; 0-0.048	0.14; 0.07-0.22	0.10; 0.04-0.17	0; 0-0.06

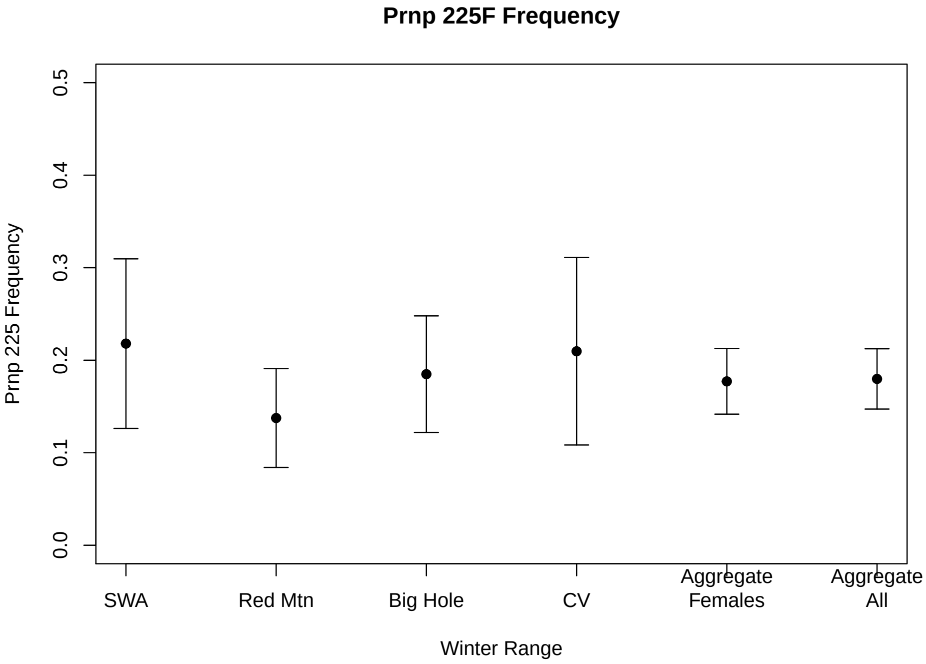


Figure 2.6: Observed frequency of the *Prnp* S225F minor allele does not differ across winter ranges for Colorado mule deer.

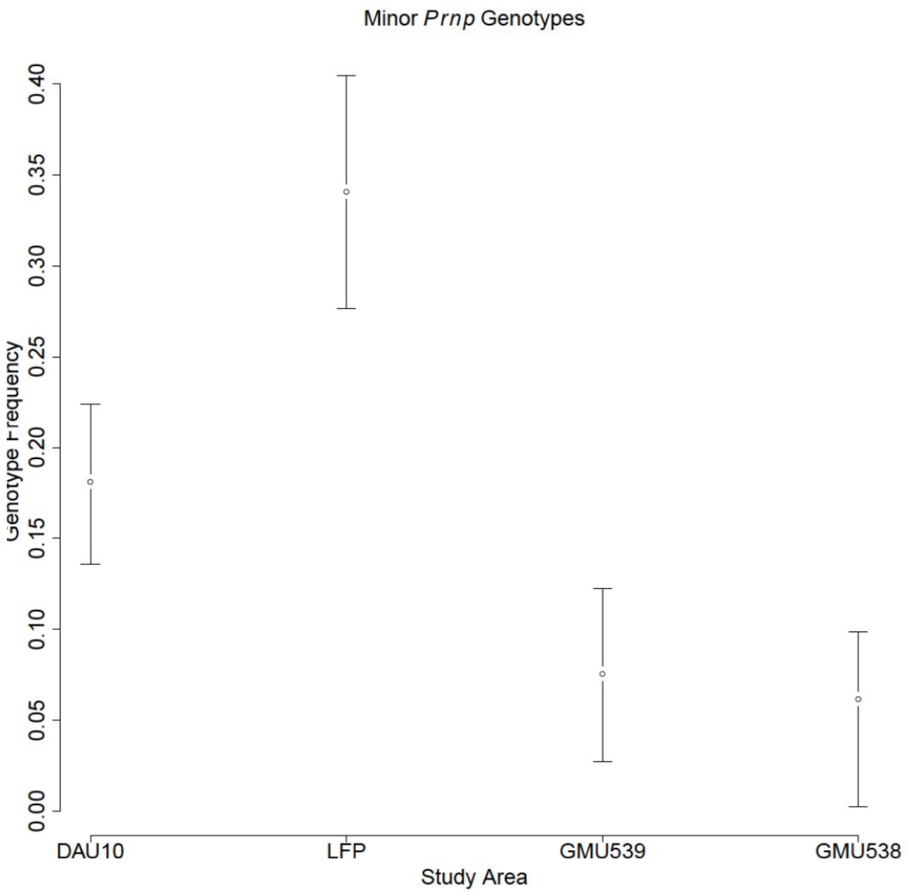


Figure 2.7: Estimated frequency of both minor *Prnp* genotypes at codon 225 in mule deer, including 225SF and 225FF, suggests an increase of the minor allele associated with decreased risk of CWD within our study area (Larimer Foothills Project; LFP) relative to neighboring areas reported in [6]. Minor genotypes are combined to allow comparison with previous reports. Data from [6] is reported according to wildlife management units. Data analysis unit (DAU) 10 is in Colorado to the south of the LFP, while game management units (GMU) 539 and 538 are in Wyoming, to the north of the LFP. No historical data from our study area were available.

rare in nearby winter ranges with lower local disease. We propose that CWD has acted historically as a selective agent against differing seasonal migration behaviors in different winter range population units depending on the history of CWD in that area.

We tested for individual disease status correlating with *Prnp* genotype. There was no evidence that *Prnp* D20G differed by CWD status, but S225F was strongly associated. This was despite the fact that CWD was spatially segregated with the highest observed prevalence in the Big Hole and Red Mountain winter ranges, with a moderate level in Campbell Valley and only a single test-positive male observed in Cherokee SWA. Any correlation between *Prnp* S225F and CWD status across the entire study area would only be stronger within the areas with high disease levels.

Our primary hypothesis regarding population genetic structure was a natural one: genetic clusters will correlate with winter range use by females. Females exhibited high fidelity to winter ranges as adults. We expected gene flow driven by both male movements during the breeding season and natal dispersal of either sex to not fully counteract the underlying genetic structure resulting from resident females. We initially tested for genetic clusters in program STRUCTURE using only females and winter range assignment as defined by [70] as population priors. It became immediately clear that likelihood quickly decreased as the number of clusters (K) increased above one.

However, testing for genetic clusters with the same female genetic data and no population prior yielded a drastically different result. Likelihood improved with increasing K up to four or five, depending on the optimization method. We conclude that genetic lineages do not correspond with winter range.

This conclusion allowed us to include males in our genetic data set, for which we were unable to clearly define winter range due to foreshortened data. The complete data showed similar results as the female-only, with best-K appearing at four or five clusters.

Our secondary hypotheses then focused on congruence between the newly defined cryptic genetic structure and other potentially correlated ecological traits, including migrant status, CWD status and *Prnp* genetics. There was no evidence to support deviation from the null (random association between genetic lineage assignment and an ecological trait) for any of these variables. Membership in genetic lineages as defined by SSR data does not predict migrant status, CWD test results, or *Prnp* 225 genotype.

Note that some lack of congruence may be a direct result of the scale and methods of sampling. Our sampling scheme attempted to disperse samples across all observed groups of deer; capture crews were advised to aim to capture new deer in unmarked groups over groups with multiple collars already present. We chose this approach in order to get a more representative sample at the winter range scale without too much sampling within social groups that may have locally variant levels of CWD. As a result, we did not obtain a lot of genetic samples from very closely related individuals. At that smaller scale within small social groups of females, genetic relatedness may well be correlated with CWD levels due to the sharing of both the environmental prion pool and individual contacts within social groups. At a larger scale, one may also expect better congruence between genetic clusters and spatial distribution (As in Latch et al. 2008). In our study, however, the scale of sampling did not illuminate these processes.

Prnp genotyping revealed that S225F genotype corresponded strongly with CWD test status for individuals but neither *Prnp* alleles nor genotypes differed between genetic lineages or winter ranges. This provides a key piece of information: the same processes that have driven gene flow between genetic lineages (natal dispersal and male movements between female social groups during the breeding season) have not homogenized disease across these same groups. It can be inferred that the processes primarily driving disease transmission are separate from those causing gene flow. This opposes the hypothesis of male-mediated disease spread across the landscape (as suggested in Conner and Miller 2004) and notable given the higher prevalence of disease in males. This suggests that environmental transmission or female:female contact transmits more disease in this system.

There is no evidence that migrants cluster within genetic lineages as defined by microsatellite data. Rather, this behavior, presumably a learned social behavior, occurs in females in all observed genetic lineages roughly equally.

On the other hand, seasonal migration behavior did correlate with mtDNA haplotype (p=7.5e-12 for mtDNA haplotypes and 9.6e-6 for mtDNA component network membership). This supports the hypothesis of seasonal migration behavior being learned within matrilineal social groups.

We lack the ability to test for correlation of migrant behavior and CWD status at the individual level to further test this hypothesis because no winter range population units were observed with a mixture of migration behaviors and a sufficient sample of CWD-positive individuals.

This hypothesis incorporates two opposing drivers. In winter range population units with high disease pressure, seasonal migrants may experience less exposure to the environmental prion pool and therefore less disease risk than resident deer. Alternatively, season migrants from winter ranges with less disease pressure are more likely to encounter prions on their summer range that were transported from nearby winter ranges with high disease prevalence. This risk has previously been hypothesized by [71] and [70], but we point out the potential evolutionary response as the population frequency of seasonal migration behavior shifts.

We continued to test for congruence between genetic lineages as defined by SSR data and relatedness as defined by mtDNA. The consensus minimum spanning tree was employed as a summary of these data and we found no evidence that genetic lineages inferred from bi-parentally inherited SSR corresponded with relatedness from matrilineal DNA as summarized by component network membership on the mtDNA minimum spanning tree. Component network membership was examined as a way to summarize the tree and these categorical data corresponded in no way with categorical assignment of genetic cluster membership from program STRUCTURE or PCO with four genetic clusters (k=4).

The principal component ordination modal clustering (PCO-MC; As per [79]) provides no evidence that the observed genetic clusters were significant. This is a very conservative test for genetic clustering, and as such we do not dismiss the potential importance of the predicted genetic clusters, but this result emphasizes the high degree of gene flow between genetic clusters, which prevents further divergence.

The study population experienced management actions designed to reduce the population size roughly one decade before our work [82] which may have had consequences for relationships between genetic lineages. It is possible that a large population reduction and subsequent growth may open areas of habitat and promote a high degree of dispersal and re-homing across the landscape which would reduce concurrence between genetic clusters and spatial range.

The presence of disease hotspots across the landscape that do not correlate with unique genetic clusters suggests that male-to-female prion transfer is not the primary mechanism of disease spread. Rather, the majority of prion transfer for the female population likely originates with other females.

2.4.1 Cryptic genetic structure

CWD correlates with *Prnp* genotype at the individual level but CWD prevalence does not correlate with *Prnp* allele frequency across winter ranges. High gene flow across winter ranges tends to homogenize genotypes despite potential differences in the selective pressure of disease on *Prnp*.

Managers reduced the deer population in the study area approximately a decade before our work started. This removal may have increased subsequent gene flow as animals re-distributed across the landscape (As hypothesized by [83]).

We used the best available data for disease status, but acknowledge the possibility of disease test bias across *Prnp* 225 genotypes [84].

Our work provides support from field observations to the hypothesis for molecular evolution of *Prnp* in response to chronic wasting disease. We observed differential association of CWD-positive animals with the minor allele coding for phenylalanine at codon 225, and also report an increased frequency of this allele in our population relative to past reports in neighboring areas [6]. We caution against an over-reliance on the potential for molecular evolution to mitigate the harmful effects of CWD, however. We observed two CWD-positive females carrying a single copy of the minor allele, 225F. We also report that, despite long-term endemic disease in this area, allele frequencies have only shown a moderate shift and populations may still suffer the negative effects of disease (As reported by [70]).

Chapter 3

Field Observations and Bayesian Models Forecast Evolutionary Response to Chronic Wasting Disease in Colorado Mule Deer

3.1 Introduction

We ask whether populations with prion disease will evolve their way out of trouble, through a disease resistance mechanism driven by genetic variation, or rather, will the evolution of the afflicted host populations simply lag behind, either under the steady pressure of prion disease or as evolution of the prion itself outpaces them?

Molecular evolution in free-ranging wildlife is often discussed but difficult to observe directly. The combined effects of stochasticity of the natural environment with genetic diversity easily confounds an observable evolutionary response to a single agent of selection. Pathogen-mediated selection in wildlife is one area where the relationship between host genetics and the selective agent may be strong enough to allow for clear inference [85]. However, there are very few examples that have shown not merely a correlation between a genetic trait and variable fitness, but rather clearly illustrated the response to that selection in a population [86].

Prion diseases, (also called transmissible spongiform encephalopathies or TSEs), arise through a unique mechanism. Native proteins undergo a mis-folding, spontaneously or transmissed from the mis-folded isomer, referred to as a protein of infectious origin, or prion, pronounced pree-on. The prion in itself is free of a nucleotide genome, and its amino acid sequence is determined by the host. The prion precursor gene, *Prnp*, encodes a functional native protein, PrP, which in its cellular isoform, PrP^{C}, serves a role perhaps related to cation transport [20]. This same protein, however, may misfold into the disease isoform, PrPD, aggregate, and cause fatal neurodegenerative disease.

Our study system focuses on the prion protein of North American cervids infected with chronic wasting disease [7].

Chronic wasting disease (CWD) is a fatal neurodegenerative prion disease that is known to infect white-tail deer (*Odocoileus virginianus*), mule deer (*Odocoileus hemionus*), Rocky Mountain elk (*Cervus elaphus nelsoni*), and occasionally moose (*Alces alces*), in North America [87]. Non-synonymous changes in the prion precursor gene (*Prnp*) that result in changes to PrP amino acids play an important role in prion disease dynamics across many species, perhaps best characterized in humans [9] and agricultural animals [8, 10].

[85], [88] and others have suggested that variation in *Prnp* may provide a mechanism for host populations to respond to CWD, and potentially mediate the impact of disease on populations, but there is much that is still unknown about the relationship between *Prnp* and disease, including much about around the dynamics of evolution. We focus on cervid *Prnp* and CWD [15], with a mule deer study system located in northern Colorado.

Mule deer in western North America have been reported with two unique *Prnp* polymorphisms, at codons 20 and 225, with one study associating CWD status with codon 225, [6]. Another study showed an association in mule deer with codon 20, [46], and also reported *Prnp* polymorphisms in white-tailed deer, with an association between the polymorphism at codon 96 and CWD. White-tailed deer in mid-western populations exhibit the same rare amino acid at codon 96, which both decreases disease risk and prolongs survival after infection [85]. Captive elk coding for a rare polymorphism at codon 132 infected with CWD prions experienced delayed disease onset and death [47]. Field observations from wild populations also show an increase in the rare allele frequency in elk populations with a history of endemic disease [86].

My goal was to quantify and explore the potential impact of variable CWD response linked to genetic markers. Given observed vital rates, how should we expect infected populations to respond in nature?

I first set out to incorporate Mendelian genetics. The genotype known to confer tolerance is a diploid heterozygote SF. This population does not simply create offspring of the same genotype.

Even if breeding is restricted to the heterozygotes, 25% of the offspring from a double heterozygote cross would be expected to be homozygous SS and therefore susceptible. The inclusion of Mendalian genetics accounts for realistic breeding between the three genotypes.

I also aim to clarify the implications of the assumptions regarding the rare homozygous genotype, SS. Assuming complete dominance for the S allele implies that disease tolerance and associated fitness is equal for of the rare homozygote, FF, and the heterozygote, SF. Support for this assumptions is missing from the literature of natural systems because the rare genotype is too rare to allow inference. As as result, it is unclear if selection favors a rare allele, i.e., positive or directional selection, or a single rare genotype, i.e., balancing selection.

I have designed a model that nests the processes of random mating and segregation of alleles across a single-locus diploid genotype within a classic state-space Lefkovitch matrix, incorporating age structure and uninfected and infected disease states. This model can incorporate non-linearities across the full range of potential allele frequencies.

I present evidence that mule deer with different *Prnp* genotypes experience differential disease risk and consequently differential survival in a population with endemic CWD. Our goal was to quantitatively estimate the rate of *Prnp* evolution in a population infected with endemic chronic wasting disease.

3.2 Methods

3.2.1 Field Estimates of Incidence

Field data were collected from a northern Colorado population of mule deer located in Larimer County, from the population that Colorado Parks and Wildlife (CPW) designates the Poudre River-Red Feather Lakes herd [67]. Female mule deer were captured and recaptured annually by helicopter net-gun [70], and tested for CWD by immunohistochemistry of the recto-anal mucosal tissue [68]). Captured deer were fit with radio or global positioning satellite collars which allowed us to attempt to locate them four times each year to detect and follow up on mortality for additional

CWD tests. Using DNA from blood collected by venipuncture during capture, the prion precursor gene (*Prnp*) was Sanger sequenced for codon 225 genotype using PCR primers from [6].

Mark-recapture data were then fit to a Bayesian hierarchical model to estimate annual survival and disease incidence, as described in [70] with some modifications.

Parameter estimates are informed from the literature where needed. Other demographic parameters are estimated from field data from a northern Colorado population of mule deer, *Odocoileus hemionus*, including survival and annual disease risk. Our forecast model combines prior information (See Table 3.2) and field data to predict *Prnp* minor allele frequency changes over time.

Disease status and survival of CWD-infected and un-infected deer were determined from mark-recapture data. For disease status, we constructed a matrix, $\boldsymbol{Z}$, where $\boldsymbol{Z} = z_{i,t}$ for deer i for $i = 1 \dots m$ at time t, corresponding to annual tests $t = 1 \dots T$. A total of m individuals were in the study for a variable number years, up to five. $z_{i,t} = 1$ when individual i was infected in the t^{th} year; otherwise $z_{i,t} = 0$.

All initial tests, $z_{i,1}$, were a function of disease prevalence, ψ_0.

$$[z_{i,1}|y_{i,1}, \psi_0] = \begin{cases} 1, & y_{i_1} \geq 1 \\ \text{Bernoulli}(\psi_0), & y_{i,1} = 0 \end{cases}$$

After the initial test, infection status at the current time t was conditioned on the infection status at the previous time $t-1$ where

$$[z_{i,t}|z_{i,t-1}, \psi_i] = \begin{cases} 1, & z_{i,t-1} = 1 \\ \text{Bernoulli}(\psi_i), & z_{i,t-1} = 0 \end{cases}$$

Once individuals were infected they remained so in all following tests. Each uninfected individual became infected with probability ψ_i. Incidence was modeled as time-invariant but was allowed to vary among individuals as a function of covariates x_i where $logit(\psi_i) = \epsilon_0 + \epsilon_k x_i$ and ϵ_k is the logistic model coefficient for the *Prnp* genotype of interest. We sampled insufficient rare homozygotes, 225FF, to estimate disease risk independently so they were grouped with heterozygotes, 225SF, and collectively referred to as 225F*. This is the principle change of the model from that published by [70] which focused on variable infection risk across winter ranges.

Disease status of deer depended on immuno-histochemical staining of the mis-folded prion proteins in lymphatic follicles in recto-anal mucosal tissues collected from each deer during each capture [68]. In each test, a variable number of lymphoid follicles were observed and the presence of infection was tested for in each follicle as described in [69]. We defined Y as an observation matrix, where $y_{i,t}$ represents the observed number of follicles tested positive for disease within an individual deer. We defined the corresponding matrix, J, where $j_{i,t}$ is the total number of follicles observed within a test. We do not believe false positive test results occur. Therefore, when $z_{i,t} = 0$ then $y_{i,t} = 0$. However, false negatives can occur if we fail to observe a positive follicle from an infected individual, meaning when $z_{i,t} = 1$, then $y_{i,t} \geq 0$. The probability that a single follicle within an infected individual was positive is π, and

$$y_{i,t}|\pi, J_{i,t}, z_{i,t}] = \begin{cases} 0, & z_{i,t} = 0 \\ \text{Binomial}(J_{i,t}, \pi), & z_{i,t} = 1 \end{cases}$$

We specified diffuse Beta$(1, 1)$ prior distributions for ψ_0 and π and N$(0, 5)$ distributions for elements of ϵ.

Survival probability was estimated from capture-recapture data using a hazard model. We measured survival over monthly intervals and defined t as a vector of final time intervals after initial capture that individuals were observed. We were unable to observe the time of death for every deer, since deer died unnaturally due to hunter harvest or capture-related cause, telemetry devices failed, or animals survived the extent of study. These animals were right censored. We needed to account for the disease status of each individual and that it could change over time, with newly infected animals converting sometime between annual CWD tests. We used interval censoring and assumed that disease conversion happened continually over the entire year. This would mean that the average date of conversion would be at the halfway point between the captures as an uninfected and as a newly infected individual, with $\phi_S^{(\frac{1}{2})}\phi_I^{(\frac{1}{2})}\psi$ reflecting half of the year surviving as uninfected and half of the year as an infected individual.

Interval censoring could overestimate CWD mortality rate. But, potential bias was reduced by recapturing 85% of deer on average each year, which improved our ability to detect newly exposed animals. Some deer were infected prior to initial capture and including these data could lead to overestimates of CWD mortality rate. In preliminary analyses, incorporating these individuals did not affect results and we chose to include these deer in final model runs.

Separate Cox proportional hazard functions were used for CWD infected and uninfected deer. For uninfected deer, $h(t_i) = \lambda_1 \alpha_1 t_1^{(\alpha_1 - 1)} exp(\beta x_i)$ and for infected deer $h(t_i) = \lambda_2 \alpha_2 t_2^{(\alpha_2 - 1)}$ where t_i is the final time interval that the i^{th} individual was observed, λ is the hazard rate, α represents increases in hazards over time , and β are Cox proportional hazard coefficients for *Prnp* genotype. We used the variable w_i to indicate infected and uninfected deer, such that

$$[t_i|\alpha, \beta, \lambda, w_i] = \begin{cases} \text{Weibull}(\lambda_2 \alpha_2), & w_i = 0 \\ \text{Weibull}(\lambda_1 \alpha_1, |\beta), & w_i = 1 \end{cases}$$

We specified $N(0, 1000)$ prior distributions for elements of $log(\alpha_2), log(\lambda)$, and β while α_1 was set equal to one as we were uninterested in the senescence of uninfected individuals.

We were unable to estimate survival of infected deer with at least one copy of the minor allele, 225F*, (as no infected 225F* females were observed) so we assume that it matches infected 225SS deer. This assumption will likely lead to under-estimates of the rate of evolutionary change in the 225F allele, because this minor allele may also delay death after disease onset, as has been reported with the minor allele in captive elk [47].

3.2.2 Forecasting Evolution

We hoped to estimate the finite rate of evolution in a natural population under prion disease selective pressure, and approximated this through a combination of parameter estimates from field observations and the literature.

We developed a state-space model of disease that incorporates random mating among the three *Prnp* genotypes. We employed a female-only model and assume that male genotype frequencies mirror those observed in females (Galloway et al. 2018). This allowed the inclusion of Mendelian breeding within a classic state-space Lefkovitch matrix, incorporating a simple age structure and disease states (uninfected and infected).

The forecast model occurs in discrete annual time that corresponds with the birth pulse and larger winter mortality seen in deer, $\boldsymbol{\mu}_{(t+1)} = \boldsymbol{M}\boldsymbol{n}_{(t)}$, where $\boldsymbol{\mu}_{(t+1)}$ represents the mean expected of the number of individuals within each state (across genotypes, ages, and disease status) and $\boldsymbol{M}$ is the projection matrix. The latent number of individuals is then a function of the expected mean across all years as follows:

$\boldsymbol{n}_{(t)} \sim \text{Poisson}(\boldsymbol{\mu}_{(t)})$

We will notate vectors using lower case bold. Matrices will be notated in upper case bold. All sources of mortality were combined, unlike the separation in some models of winter die-off, hunter harvest, and culling [89,90]. Annual juvenile survival was assumed to be equal to uninfected adult survival where $\phi_S = exp(-\lambda_1 * (12))$. Annual survival of infected adults was calculated from the three-year average of monthly survival probability for infected animals $\phi_I = exp(-\lambda_2 * (36^{\alpha_2}))^{\frac{1}{3}}$.

Model states include uninfected juveniles and both uninfected and infected adults across all three genotypes. We assume no juveniles were yet infected with CWD.

The transition matrix $\boldsymbol{M}$ is fully described in Appendix D. The key detail is in the birth process. By assuming random mating and segregation of zygotes, the expected number of juveniles born with each genotype, (e.g., $\mu_{(t),1}$), can be calculated from genotype frequencies, calculated from the number of breeding adults of each genotype in the previous generation, $\boldsymbol{n}_{(t-1),4:6}$, and recruitment (r).

All sources of mortality were combined, unlike the separation in some models of winter die-off, hunter harvest and culling ([85,89,90]). We have added the complexity of Mendelian random mating and segregation.

We used fixed incidence rates within genotypes. Long-term dynamics are likely influenced by the number of infected individuals, either directly or through an environmental prion pool, but we make this simplifying assumption and believe that it may be a reasonable approximation in the short-term.

Model states include juvenile and adult, uninfected and infected, across all three genotypes (See Table 3.1.)

Table 3.1: The population vector, $\boldsymbol{n}_{(t)}$, includes nine states across two ages, three *Prnp* genotypes, and two disease conditions

State Class	Definition
n_1	Uninfected Juvenile SS
n_2	Uninfected Juvenile SF
n_3	Uninfected Juvenile FF
n_4	Uninfected Adult SS
n_5	Uninfected Adult SF
n_6	Uninfected Adult FF
n_7	Infected Adult SS
n_8	Infected Adult SF
n_9	Infected Adult FF

We predicted the initial 225F allele frequency (designated q) from observed allele counts using the beta-binomial conjugate relationship such that $p \sim \text{Beta}(1 + y, 1 + (2 * m) - y)$ where y is the observed count of 225F alleles and m is the sample size. We observed no deviation from Hardy-Weinberg equilibrium in our data so we calculated expected genotype frequencies using that as predicted. Using standard convention, the frequency of more common allele, 225S, is designated $p = 1 - q$.

Other parameters were derived from prior information (See Table 3.2). Total abundance was predicted from a poisson prior with the estimated population mean from CPW for the year 2016 [91]. The proportion of the population that was female was also taken from CPW's mean estimate of 0.77 with a standard deviation of 0.01 added for a beta prior with shape parameters 22.04 and 6.67. Initial female abundance was then calculated as the product of total abundance and the proportion female. The initial proportion that was juvenile was defined using recruitment predictions from [70], with an estimated fit to a beta distribution for shape parameters 109.94 and 410.68. We used ψ_0 as described above for the initial CWD prevalence, uncorrected for genotype.

The initial predicted mean for each class was then calculated as the conditional probability product from the appropriate preceding parameters, for example juvenile 225SS $\boldsymbol{\mu}_{(0),1} = p_{juv} * p_{fem} * abundance * p^2$, while CWD-infected 225SF $\boldsymbol{\mu}_{(0),8} = (1 - p_{juv}) * p_{fem} * abundance * 2p(1-p) * \psi_0$. This initial condition over-estimates the initial number of both 225SF and 225FF individuals infected with CWD, but this effect is quickly lost as the genotype-specific incidence drives new infections.

The full transition matrix $\boldsymbol{M}$ is shown in Appendix D. The key detail is in the birth process. By assuming random segregation and mating of zygotes, the expected number of juveniles born with each genotype, eg. μ_1, can be calculated based on the number of breeding adults, $\sum\limits_{i=4}^{6} n_i$, genotype frequencies, SS, SF and FF, and recruitment r independently for the uninfected and infected components of the population. Here, recruitment includes both birth and fawn survival to the next winter census.

$$\mu_1 = \left(\sum_{i=4}^{6} n_i\right) r \left(SS^2 + SS * SF + \frac{1}{4}SF^2\right)$$

$$\mu_2 = \left(\sum_{i=4}^{6} n_i\right) r \left(SS * SF + 2SS * FF + \frac{1}{2}SF^2 + SF * FF\right)$$

$$\mu_3 = \left(\sum_{i=4}^{6} n_i\right) r \left(\frac{1}{4}SF^2 + SF * FF + FF^2\right)$$

We factored out genotype frequencies of zygotes and realized that $\left(\sum\limits_{i=4}^{6} n_i\right) * SS = n_4$ which was then modified for the transition matrix, where infected and uninfected components of the population breed independently. This allowed for differential reproductive success for diseased dams, which we explored but did not include in the final model because it became clear that the majority of evolutionary pressure resulted from disease impacts on survival.

Table 3.2: Parameter estimates drawn from the literature for the forecast model.

Parameter	Prior Distribution	Mean	Variance	Source
Total Initial Abundance	Poisson	14070	-	[91]
Proportion Female, p_{fem}	Beta	0.77	0.006	[91]
Recruitment, r and Proportion Juvenile, p_{juv}	Beta	0.27	0.00065	[70]

3.3 Results

3.3.1 Incidence Estimates

Data fit to the model revealed a strong divergence between the most common homozygote, *Prnp* 225SS, and the group with at least one copy of the minor allele, 225F*, which included both the heterozygous 225SF and the rare homozygote 225FF. Annual disease risk for the rare genotypes was predicted to be one third of that for the common homozygote. (See Table 3.3 and Figure 3.1)

Survival data reveal a large decrease in annual survival once a female mule deer becomes infected with CWD (See Figure 3.2). We also examined the possibility that *Prnp* genotype may exert an influence directly on survival of uninfected individuals, perhaps as an evolutionary trade-off that would explain the low observed allele frequency. Our data show no decline in survival for uninfected 225F* individuals so that effect was not included in the model.

3.3.2 Forecasting Evolution

Model predictions include a slight but consistent increase in the frequency of the *Prnp* minor allele, 225F (See Table 3.4). Our quantity of interest, however, is the change in allele frequency as

Table 3.3: Summary statistics of predicted parameters from model fit. *Prnp* genotype alters disease risk for female mule deer in northern Colorado at risk of chronic wasting disease.

		Mean	Median	Std Dev	0.025%	0.975%
Initial Disease Prevalence	ψ_0	0.048	0.046	0.015	0.021	0.077
Annual Disease Risk of 225SS	ψ_{SS}	0.051	0.049	0.015	0.022	0.080
Annual Disease Risk of 225F*	ψ_F	0.017	0.013	0.013	0.000	0.043
Annual Survival of Uninfected Adults	ϕ_S	0.825	0.826	0.018	0.789	0.861
Annual Survival of Infected Adults	ϕ_I	0.418	0.420	0.132	0.158	0.665
Follicle Infection Probability	π	0.554	0.555	0.027	0.502	0.606
Disease Risk Intercept	ϵ_0	-2.972	-2.957	0.326	-3.618	-2.338
Disease Risk *Prnp* 225F* Coeffient	ϵ_k	-1.476	-1.352	1.019	-3.517	0.360
	α_2	1.939	1.904	0.458	1.121	2.882
	λ_1	0.016	0.016	0.002	0.012	0.020
	λ_2	0.006	0.003	0.008	0.000	0.021
	β	0.611	0.614	0.225	0.1644	1.046

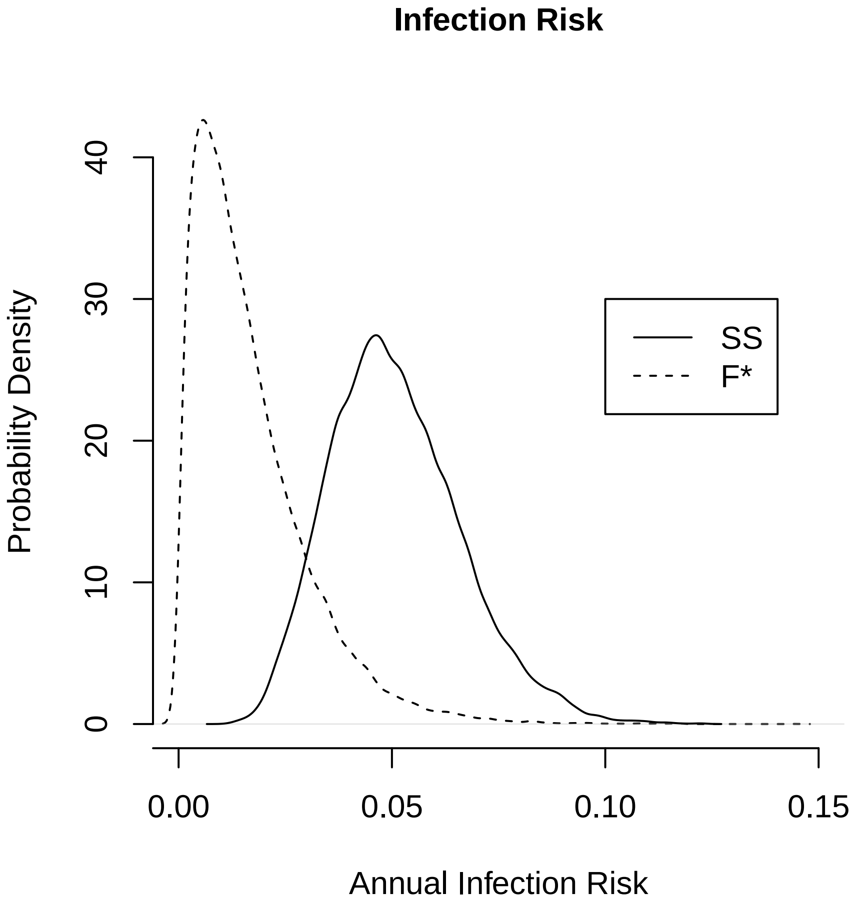


Figure 3.1: Chronic wasting disease presents less risk to female mule deer in northern Colorado at risk of disease that carry at least one copy of the *Prnp* 225F allele.

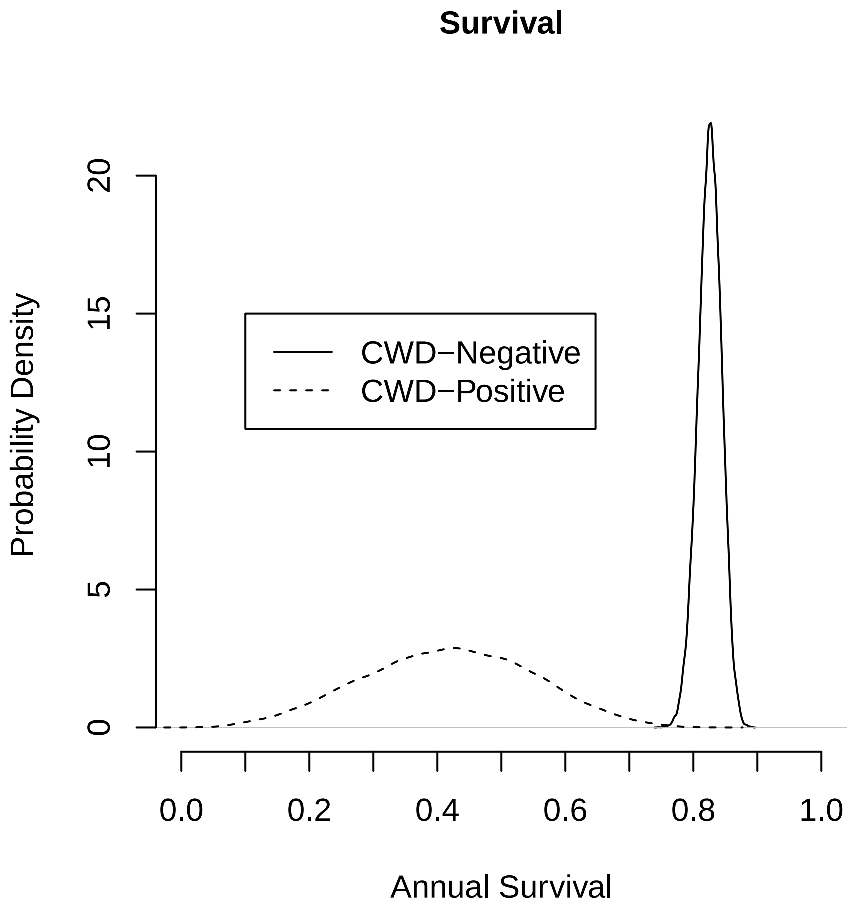


Figure 3.2: CWD-positive female mule deer suffer additional mortality risk in a free-ranging population in northern Colorado.

Table 3.4: Model forecast allows for prediction of the *Prnp* 225F rare allele frequency over time. The first column refers to annual time steps including forecast initialization and each row represents the derived allele frequency.

	Mean	Median	Std Dev	0.025%	0.975%
0	0.179	0.179	0.018	0.143	0.215
1	0.184	0.183	0.019	0.146	0.220
2	0.189	0.188	0.020	0.150	0.227
3	0.195	0.195	0.021	0.154	0.235
4	0.202	0.201	0.022	0.159	0.244
5	0.209	0.208	0.023	0.165	0.256
6	0.216	0.216	0.025	0.169	0.265
7	0.224	0.223	0.026	0.173	0.275
8	0.232	0.231	0.028	0.178	0.286
9	0.240	0.239	0.029	0.182	0.296
10	0.248	0.247	0.031	0.188	0.308

Table 3.5: Model forecast predicts an increase in the frequency of the minor *Prnp* allele, 225F. The first column refers to annual time steps after forecast initialization and each row represents the derived change in allele frequency from the initial condition.

	Mean	Median	Std Dev	0.025%	0.975%
1	0.005	0.005	0.003	-0.001	0.010
2	0.010	0.010	0.005	0.001	0.019
3	0.016	0.016	0.007	0.003	0.029
4	0.023	0.022	0.008	0.007	0.040
5	0.030	0.029	0.011	0.010	0.051
6	0.037	0.037	0.013	0.013	0.063
7	0.045	0.044	0.015	0.017	0.074
8	0.053	0.052	0.017	0.021	0.087
9	0.061	0.060	0.019	0.025	0.099
10	0.069	0.068	0.021	0.029	0.112

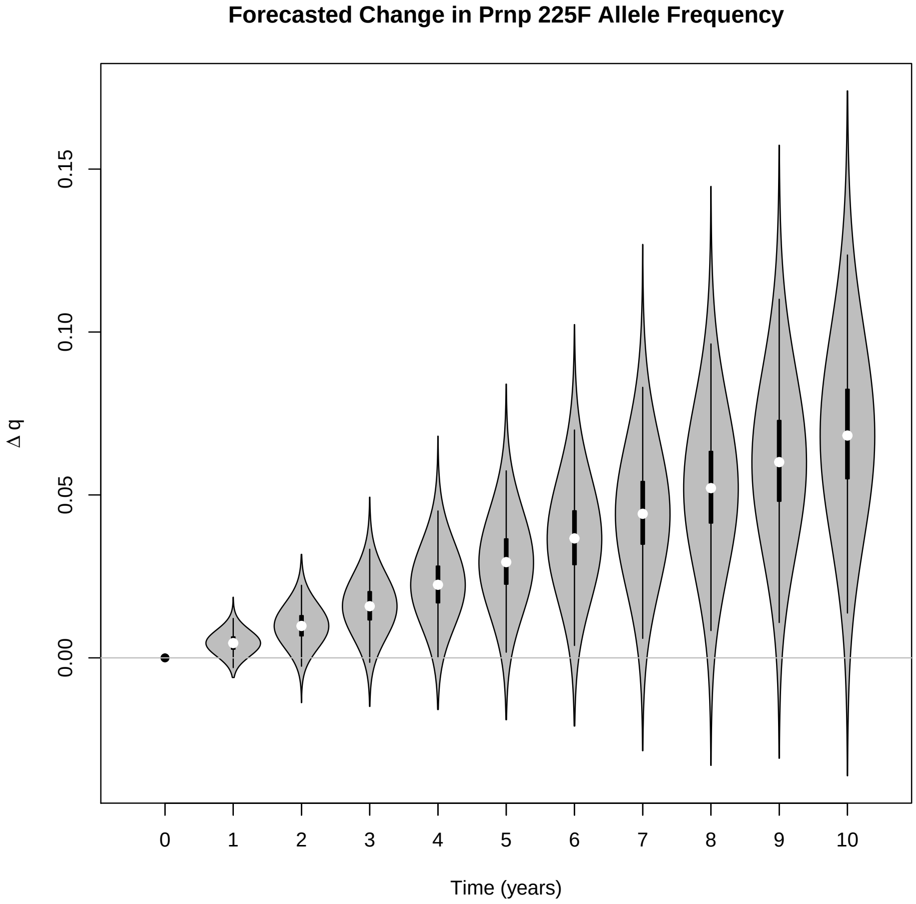


Figure 3.3: Model forecast predicts evolution; The 225F minor allele frequency, q, increases under observed rates of disease risk. Full posterior distributions are plotted in kernal density plots with the mean estimate in white and the first and third quantiles in black box plots with whiskers that roughly correspond to 95% credible intervals. The grey horizontal line corresponds to no change, or $\Delta q = 0$.

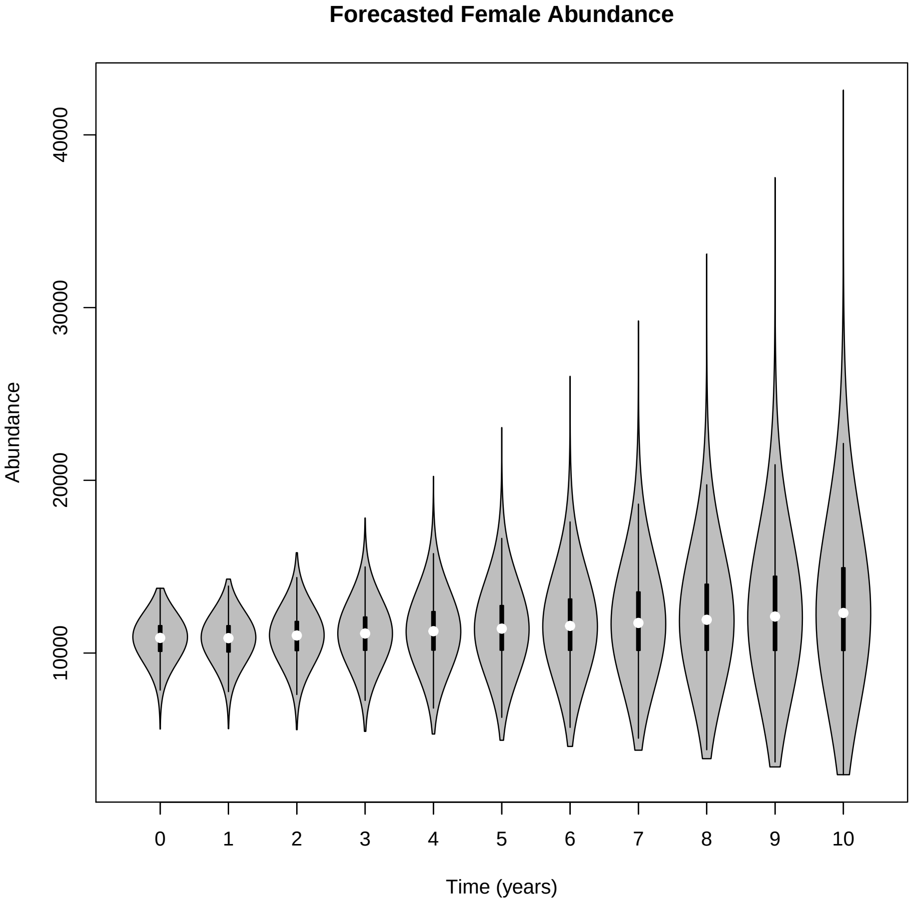


Figure 3.4: Model forecast predicts little change to female population abundance under observed rates of disease risk. Full posterior distributions are plotted in kernal density plots with the mean estimate in white and the first and third quantiles in black box plots with whiskers that roughly correspond to 95% credible intervals.

opposed to the allele frequency itself. For that reason, we also derived Δq defined as the difference between the predicted 225F allele frequency in each year and the frequency in the initial population. We forecast that quantity for ten years with results in Table 3.5 and plotted in Figure 3.3. We also have forecast total female population abundance in Figure 3.4 which reflects the cumulative impact of disease on the population growth rate given potential for *Prnp* evolution.

3.4 Discussion

Chronic wasting disease continues to spread into new areas and species, while its effects are only poorly understood in the areas that have sustained endemic disase for many decades.

Data showed a clear disease risk differential for the most common *Prnp* genotype, 225SS, for the study population of female mule deer, corraborating previous reports [6, 46]. Our methods, however, also allowed for quantitative prediction of the annual risk of disease incidence. *Prnp* 225SS mule deer experienced three times the annual risk of disease relative to heterozygous individuals, 225SF, when grouped with the rare homozygotes. Regrettably, we were unable to make independent inference on rare homozygotes due to their sparcity within the sample.

Matrix projections predicted the impact that this disease risk differential will exert on the minor *Prnp* allele frequency in this population. Model fit predicted a clear positive trend in 225F allele frequency, with roughly a 6% annual increase. (See Table 3.5). The annual predicted change in allele frequency changes slightly over time, resulting from two areas of divergence. First, we used ψ_0 for the initial prevalence regardless of genotype. This does not perfectly agree with the variable annual risk observed across genotypes and employed in our projection matrix.

Given this projection, why did we observe an estimated minor allele frequency (225F) of only 0.18? CWD has been endemic in this mule deer population for at least three decades [71], which would lead to the expectation that past selection should have driven this up higher. We see several possible explanations for this discrepancy.

One possibility is that there may be an evolutionary trade-off for the minor *Prnp* alleles. We did not observe it, but our power was severely limited. The observed minor allele frequency corresponds to few expected rare 225FF homozygotes (At a minor allele frequency of 0.2 only 4 in 100 individuals are expected to be rare homozygotes). This is consistent with all other reported minor alleles that confer some benefit against CWD [15]. Given the strong purifying selection consistently reported for this functional gene ([16] and see Chapter 1) we see it as quite likely that similar purifying selection may simultaneously act against these rare homozygotes. This oppositional selection would create a unique system of balancing selection (Previously discussed in [86]). In this system, in the presence of a high force of infection the rare *Prnp* allele would confer some advantage and increase in frequency. Balancing selection would push back through an evolutionary trade-off against rare homozygotes. As disease dynamics waxed and waned the equilibrium point for this system would shift over time, depending also on the fitness cost associated with the rare homozygotes.

Many wildlife managers would love to put their hope in the process of evolution through natural selection for variable response to disease [88], but there is very little evidence that suggests that cervids can truly escape the risk of CWD through evolution. Evidence of disease tolerance arise from a variety of sources: cross-sectional studies in nature [85], laboratory or captive animal studies [47], and a few longitudinal studies in nature [92]. It is clear that some variations of the prion protein offer some protection to individuals at risk of disease. This is manifest in lower observed prevalence in nature, extended survival time after infectious dosing in captivity, as well as molecular studies of protein tendency to misfold into prions. However, these studies are unable to address the natural population-level effects of such benefits in free-ranging wildlife. We stress the potential that an evolutionary trade-off may mitigate the benefit of these rare alleles. Also, there is the independent risk of prion strain evolution leading to an evolutionary arms race with host evolution.

3.4.1 Caveats

The model employs time-invariant incidence to examine the effect of a selection differential across genotypes, with the consideration of random Mendelian breeding. The modeled disease incidence lacks an explicit model of infection dynamics, including alternative transmission pathways via direct contact or from an infectious environmental reservoir. These could perhaps be driven by the abundance of infected individuals, density of uninfected hosts, or the environmental prion load.

Environmental transmission is more likely to represent the true nature of chronic wasting disease ([93, 94]) but unfortunately very little is known about this mechanism. The total environmental pool as well as deposition and loss rate have not yet been quantified so we did not incorporate this into our model. The environmental pool is one important long-term source of system dynamics but is likely to change very slowly given the persistence of prions. This suggests that our simplifying assumption of fixed incidence over time may not stray too far from reality at least for short-term forecasting as we have done.

We also do not account for the possibility that the minor allele may also extend survival of infected animals which could allow for additional environmental prion deposition (See [95]). Nor do we address the possibility of prion strain adaptation [96]. This is one omission that holds the potential to completely upend expectations, as seen with atypical scrapie [97].

Some readers may note the slight dissonance between the predicted prevalence from the observed annual disease risk and the initial prevalence across genotypes (See Figure 6 in [70]). This effect is minor, and beyond the first several years of the forecast, annual disease risk is driving the rate of CWD-positive mortality across genotypes, but it may decrease the rate of evolutionary increase of 225F allele frequency at first.

3.4.2 Incidence and Genotype

Our data support the hypothesis that the *Prnp* gene may mediate individual risk to chronic wasting disease. We have quantified and predicted annual risk for female mule deer in a northern Colorado population. We chose to not focus on spatial differences in CWD risk across winter ranges in order to instead estimate the average effect this selective advantage may exert across the entire population.

We were forced to make a simplifying assumption in order to fit our risk model to field data on incidence across genotypes; We assumed that the 225F allele behaves in a dominant manner to the major 225S allele. We carry this assumption through both the model specifications for disease risk and forecast. This assumption is often how researchs deal with the small number of rare homozygotes within a sample and is largely untested. However, it is unclear if the rare homozygote 225FF experiences differential disease risk relative to the heterozygote. Furthermore, and perhaps more concerning, is the possibility that the 225FF animals suffer some evolutionary trade-off, perhaps through decreased survival while uninfected individuals. The impact that these differences have on the dynamics of the system increase as the rare allele increases in frequency. At the observed levels, rare homozygotes present an extremely small number of animals to the forces of natural selection.

3.4.3 Forecasting Evolution

The constant incidence model allows us to forecast short-term *Prnp* evolution given the observed variable disease risk between genotypes and the steep decline in survival for infected individuals.

The poisson process model accounts for the effect of genetic drift when one allele is rare and strictly defines allelic extinction. Other interesting modifications would include adding sex classes and even separating high- and low-success males. In the natural breeding structure of deer, it would be expected that a few males contribute disproportionately to the zygote pool, which reduces the effective population size relative to the census.

It is also important to note that this model does not include the possibility of reduced reproduction by CWD-infected individuals. This may be an important population-level effect, but we were unable to observe it directly. Reduced fertility for infected dams should further decrease fitness for the infected segment of the population and thereby increase the rate of evolution as observed by [98]. We also fit a secondary model to explore the effect that differential recruitment may play on the rate of evolutionary change, using reduced recruitment for infected dams and examined its relative impact. We chose to not include the reduced recruitment for infected dams as it appeared that the effect of CWD on recruitment is minor relative to its effects on dam survival.

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Appendix A

Mammalia *Prnp* Alignment

Complete Sequences Used for PAML Analysis

84 1053

Macropus_eugenii_Tammar_wallaby

```
  1 AUGGCAAAAA UCCAGUUGGG AUACUGGAUC UUGGCUCUCU UCAUUGUGAC
 51 CUGGAGUGAA CUAGGCCUCU GUAAGAAGCC AAAGACAAGA CCC---GGAG
101 GGGGAUGGAA CAGCGGAGGA AGCAACCGC- --------UA CCCAGGCCAG
151 CCUGGUAGCC CUGGAGGCAA CCGAUACCCU ---------- ----------
201 ---------- ---------- ---------- ---------- ----------
251 ---------- ---------- ---------- ---------- ----------
301 ---------- --------GG CUGGGGG--- CACCCUCAG- --GGAGGUGG
351 CACCAAUUGG GGUCAG---C CCCAUCCUGG AGGUUCCAGU UGGGGU---C
401 AGCCCCAUGC CGGGGGUUCC AACUGG---- --------GG U---CAGCCU
451 CAUGGUGGAU CU------AA CUGGGGUCAG GGC------- --------GG
501 UGGCAGCUAC GGC---AAAU GG---AAACC AGAUAAACCC ---AAAACCA
551 ACCUAAAACA UGUAGCUGGG GCUGCUGCUG CUGGGGCAGU UGUGGGAGGG
601 CUUGGUGGCU ACAUGCUGGG GAGUGCCAUG AGCAGGCCUG UCAUGCACUU
651 UGGCAAUGAA UAUGARGACC GCUACUAUCG UGAAAACCAG UACCGCUACC
701 CCAACCAA-- -GUUAUGUAC CGGCCCAUUG ACCAGUACGG CAGCCAGAAC
751 AGUUUUGUUC AUGAUUGCGU CAAUAUCACC GUGAAGCAAC ACACCACC--
801 -ACCACCACC ACCAAA---- ---------- ---------- ---GGGGAGA
851 ACUUCACAGA AACUGACAUC AAGAUCAUGG AGCGUGUGGU CGAGCAGAUG
901 UGCAUCACAC AGUACCAGAA UGAGUACCAG ------GCUG CU------CA
951 GCGCUACUAC AACAUGGCUU UCUUCUCUGC CCCACCAGUG ACC---CUCC
```

```
1001 UCUUACUCAG UUUCCUUAUU UUCCUGAUCG UGAGC----- ----------
1051 ---
```

Monodelphis_domestica_Gray_short–tailed_opossum

```
   1 AUGGGGAAAA UCCACUUGGG AUACUGGUUC UUGGCUCUUU UUAUUAUGAC
  51 CUGGAGUGAU CUGACUCUCU GUAAGAAACC GAAGCCAAGA CCU---GGAG
 101 GGGGAUGGAA CAGUGGAGGC ---AACCGC- --------UA UCCUGGCCAG
 151 ---------U CUGGAGGCUG GGGACAUCCU CAGGGA---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGU------ ---------- ---------- ----------
 301 ---------- --GGCACCAA UUGGGGU--- CAACCCCAU- --GCUGGGGG
 351 UUCCAAUUGG GGUCAG---C CACGUCCUGG GGGUUCCAAU UGGGGC---C
 401 AGCCCCAUCC AGGGGGUUCC AACUGG---- --------GG A---CAGCCC
 451 CAUCCAGGGG GU---UCCAA CUGGGGUCAA GCC------- --------GG
 501 UAGCAGCUAC AACCAGAAGU GG---AAACC AGAUAAACCC ---AAAACCA
 551 ACAUGAAACA UGUGGCUGGG GCUGCUGCUG CUGGGGCAGU UGUAGGAGGG
 601 CUUGGUGGAU ACAUGCUGGG GAGUGCCAUG AGCAGGCCCA UCAUGCACUU
 651 UGGCAGCGAC UACGAAGACC GUUACUAUCG UGAAAACCAA UAUCGCUAUC
 701 CCAACCAA-- -GUCAUGUAU CGGCCCAUUG AUCAGUACAA CAACCAGAAC
 751 AAUUUUGUGC AUGACUGUGU CAACAUAACG GUGAAGCAAC ACACCACC--
 801 -ACCACCACU ACCAAA---- ---------- ---------- ---GGGGAGA
 851 ACUUCACUGA AACGGAUAUC AAGAUCAUGG AGCGAGUGGU GGAACAGAUG
 901 UGCAUCACGC AGUACCAGAA CGAGUACCGC AGU---GCUU AC--------
 951 ---------- AGCGUGGCGU UCUUCUCUGC CCCACCUGUG ACC---CUCC
1001 UCCUCCUCAG UUUCCUUAUU UUCCUGAUUA UCCCAGAUGC CCAUUCCGUG
1051 GAA
```

Dasypus_novemcinctus_Nine–banded_armadillo

```
   1 ATGGTGAGAA GCCGCGTAGG CTTCTGGCTC TTGCTGCTCT TTGTGGCCAC
  51 ATGGAGTGAG CTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCC---GGAG
 101 GAGGGTGGAA CACGGGGGGG ---AGCCGG- --------TA CCCGGGCCAG
 151 ---GGCAGCC CTGGGGGCAA CCGCTACCCG CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- ---------- ---------- ---------- ----------
 301 ---------- --GGCGGCGG CTGGGGT--- CAGCCCCAC- --GGGGGCGG
 351 C------TGG GGTCAG---C CCCAC---GG CGGCGGC--- TGGGGC---C
 401 AGCCTCAC-- -GGCGGCGGC ---TGG---- --------GG C---CAGCCC
 451 CACGGCGGCG GC-------- -TGGGGCCAA ---------- --------GG
 501 CGGCGCCCAC GGT---CAGT GGAACAAGCC GAGTAAACCG ---AAGACCA
 551 ACATGAAGCA CGTGGCGGGC GCGGCGGCGG CCGGGGCGGT GGTGGGCGGC
 601 CTCGGCGGCT ACCTGGTCGG GAGCGCCATG AGCAGGCCCC TCATCCACTT
 651 CGGCAACGAC TACGAGGACC GCTACTACCG CGAGAACATG TACCGCTACC
 701 CCAACCAG-- -GTGTACTAC CGGCCCGTGG AGCAGTACAG CAGCGAGAAG
 751 AACTTCGTGC ACGACTGCGT CAACATCACC ATCAAGGAGC ACACCGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGCGAGA
 851 ACTTCACCGA GACCGACGTG CGCATGATGG AGCGCGTGGT CGAGCAGATG
 901 TGCATCACCC AGTACCAGCG GGAGGCCCAG GCC---GCCT AC------CA
 951 GCGCGGCGCC GGCGCCCAGC TCTTCTGTGC CTCCCCGCTG GGC------C
1001 TCCTGCTCGC CCTCCTCCTC TTCCTGGTGG TCGGG----- ----------
1051 ---
```

Loxodonta_africana_African_bush_elephant

```
   1 ATGGTGAAAA GCAGCTTGGG CTGCTGGATC CTGGTTCTCT TCGTGGCCAC
  51 ATGGAGTGAC ATGGGCCTCT GCAAGAAG-- -CGACCAAAG CCT---GGAG
 101 GAGGATGGAA CACTGGGGGA ---AGCCGA- --------TA CCCGGGGCAG
 151 ---GGGAGTC CTGGAGGCAA CCGCTACCCA CCTCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGT------ ---------- ---------- ----------
 301 ---------- --GGTGGTGG CTGGGGT--- CAGCCTCAC- --GGTGGCGG
 351 C------TGG GGACAG---C CCCATGGTGG TGGCGGC--- TGGGGT---C
 401 AGCCCCAC-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCC
 451 CATGGTGGTG GT------GG CTGGGGTCAA ---------- --------GG
 501 TAGCTCCCAT AGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACTTGAAGCA TGTGGCAGGG GCTGCTGCAG CTGGGGCAGT AGTGGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGCGCCATG AGCAGGCCTC TCATACATTT
 651 TGGTAACGAC TATGAGGACC GTTACTACCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCCGTGA ATGAGTACAG CAACGAGAAC
 751 AACTTCGTGC ACGACTGCGT CAACATTACA GTCAAGCAGC ACACGACC--
 801 -ACCACCATC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACTGA GACCGATACC AAGATAATGG AGCGCATGGT CGAGCAGATG
 901 TGCGTAACCC AGTACCGCAA AGAATTCCAG GCT------T AC------CA
 951 GAGAGGGTCG AGCATGGTCC TCTTCTCCTC CCCGCCTGTG ATC------C
1001 TCCTCCTCTC TTTCCTCATT TTCCTGATAG TGGGA----- ----------
1051 ---
```

Saimiri_sciureus_Squirrel_monkey

```
   1 ------ATGG CGAACCTTGG CTGCTGGATG CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC CTGGGCCTCT GCAAGAAG-- -CGCCCGAAA CCT------G
 101 GAGGATGGAA TACTGGGGGS ---AGCCGA- --------TA CCCAGGCCAG
 151 ---GGCAGCC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGT------ ---------- ---------- -GGTGGCTGG
 301 GGGCAGCCTC ATGGTGGTGG CTGGGGG--- CAACCCCAT- --GGTGGCGG
 351 C------TGG GGACAG---C CCCAT---GG TGGCGGC--- TGGGGA---C
```

```
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCT
 451 CATGGTGGCG GC-------- -TGGGGTCAA GGA------- --------GG
 501 TGGCACCCAC AAT---CAAT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA CATGGCTGGT GCTGCAGCGG CTGGGGCAGT GGTGGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCCC TCATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAGCCAA-- -GTATACTAC AGGCCCGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACGTCACG ATCAAGCAGC ACACAGTC--
 801 -ACCACCACC ACCAAA---- ---------- ---------- ---GGGGAGA
 851 ACTTCACTGA GACCGACGTK AAGATGATGG AGCGCGTGGT TGAGCAGATG
 901 TGTATCACTC AGTACGAGAA GGAATCCCAG GCC---TATT AC------CA
 951 GAGAGGATCG AGCATGGTCC TCTTCTCCTC CCCACCTGTG ATC------C
1001 TCCTGATCTC TTTCCTCATC TTCCTGATAG TGGGA----- ----------
1051 ---
```

Macaca_assamensis_Assam_macaque

```
   1 ------ATGG CGAACCTTGG CTGCTGGATG CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC CTGGGCCTCT GCAAGAAG-- -CGCCCAAAG CCT------G
 101 GAGGATGGAA CACTGGAGGC ---AGCCGA- --------TA CCCGGGGCAG
 151 ---GGCAGCC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGT------ ---------- ---------- ----------
 301 ---------- --GGTGGTGG CTGGGGG--- CAGCCTCAT- --GGTGGTGG
 351 C------TGG GGGCAA---C CCCAT---GG TGGCGGC--- TGGGGA---C
 401 AGCCTCAT-- -GGTGGCGGC ---TGG---- --------GG A---CAGCCT
 451 CATGGTGGTG GC-------- -TGGGGTCAA GGA------- --------GG
 501 TGGCACCCAC AAT---CAGT GGCACAAGCC CAGTAAGCCA ---AAAACCA
 551 GCATGAAGCA CATGGCTGGT GCTGCAGCAG CTGGGGCAGT GGTGGGGGGC
```

```
 601 CTTGGCGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCCC TCATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCTGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAATATCACA ATTAAGCAGC ACACAGTC--
 801 -ACCACCACC ACCAAA---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA GACCGACGTT AAGATGATGG AGCGCGTGGT TGAGCAGATG
 901 TGTATCACCC AGTACGAGAA GGAATCACAG GCC---TATT AT------CA
 951 GAGAGGATCG AGCATGGTCC TGTTCTCCTC CCCGCCTGTG ATC------C
1001 TCCTGATTTC TTTCCTCATC TTCCTGATAG TGGGA----- ----------
1051 ---
```

Macaca_mulatta_Rhesus_macaque

```
   1 ------AUGG CGAACCUUGG CUGCUGGAUG CUGGUUCUCU UUGUGGCCAC
  51 AUGGAGUGAC CUGGGCCUCU GCAAGAAG-- -CGCCCAAAG CCU------G
 101 GAGGAUGGAA CACUGGAGGC ---AGCCGA- --------UA CCCGGGGCAG
 151 ---GGCAGCC CUGGAGGCAA CCGCUACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGU------ ---------- ---------- ----------
 301 ---------- --GGUGGUGG CUGGGGG--- CAGCCUCAU- --GGUGGUGG
 351 C------UGG GGGCAA---C CCCAU---GG UGGCGGC--- UGGGGA---C
 401 AGCCUCAU-- -GGUGGCGGC ---UGG---- --------GG A---CAGCCU
 451 CAUGGUGGUG GC-------- -UGGGGUCAA GGA------- --------GG
 501 UGGCACCCAC AAU---CAGU GGCACAAGCC CAGUAAGCCA ---AAAACCA
 551 GCAUGAAGCA CAUGGCUGGU GCUGCAGCAG CUGGGGCAGU GGUGGGGGGC
 601 CUUGGCGGCU ACAUGCUGGG AAGUGCCAUG AGCAGGCCCC UCAUACAUUU
 651 UGGCAAUGAC UAUGAGGACC GUUACUAUCG UGAAAACAUG UACCGUUACC
 701 CCAACCAA-- -GUGUACUAC AGGCCUGUGG AUCAGUACAG CAACCAGAAC
 751 AACUUUGUGC ACGACUGCGU CAAUAUCACG AUUAAGCAGC ACACAGUC--
```

```
 801 -ACCACCACC ACCAAA---- ---------- ---------- ---GGGGAGA
 851 ACUUCACCGA GACCGACGUU AAGAUGAUGG AGCGCGUGGU UGAGCAGAUG
 901 UGUAUCACCC AGUACGAGAA GGAAUCACAG GCC---UAUU AU------CA
 951 GAGAGGAUCG AGCAUGGUCC UCUUCUCCUC CCCGCCUGUG AUC------C
1001 UCCUGAUUUC UUUCCUCAUC UUCCUGAUAG UGGGA----- ----------
1051 ---
```

Pongo_pygmaeus_Bornean_orangutan

```
   1 ------AUGG CGAACCUUGG CUGCUGGAUG CUGGUUCUCU UUGUGGCCAC
  51 AUGGAGUAAC CUGGGCCUCU GCAAGAAG-- -CGCCCAAAG CCU------G
 101 GAGGAUGGAA CACUGGGGGC ---AGCCGA- --------UA CCCGGGGCAG
 151 ---GGCAGCC CUGGAGGCAA CCGCUACCCA CCUCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGUGGUGG CUGGGGG--- CAGCCUCAU- --GGUGGUGG
 351 C------UGG GGGCAG---C CUCAU---GG UGGUGGC--- UGGGGG---C
 401 AGCCCCAU-- -GGUGGUGGC ---UGG---- --------GG G---CAGCCU
 451 CAUGGUGGUG GC-------- -UGGGGUCAA GGA------- --------GG
 501 UGGUACCCAC AGU---CAGU GGAACAAGCC CAGUAAGCCA ---AAAACCA
 551 ACAUGAAGCA CAUGGCUGGU GCUGCAGCAG CUGGGGCAGU GGUGGGGGGC
 601 CUUGGUGGCU ACAUGCUGGG AAGUGCCAUG AGCAGGCCCA UCAUACAUUU
 651 UGGCAAUGAC UAUGAGGACC GUUACUAUCG UGAAAACAUG UACCGUUACC
 701 CCAACCAA-- -GUGUACUAC AGGCCCGUGG AUCAGUACAG CAACCAGAAC
 751 AACUUUGUGC ACGACUGCGU CAAUAUCACA AUCAAGCAGC ACACAGUC--
 801 -ACCACAACC ACCAAA---- ---------- ---------- ---GGGGAGA
 851 ACUUCACCGA GACCGACGUU AAGAUGAUGG AGCGUGUGGU UGAGCAGAUG
 901 UGUAUCACGC AGUACGAGAG GGAAUCUCAG GCC---UAUU AC------CA
 951 GAGAGGAUCG AGCAUGGUCC UCUUCUCCUC CCCACCUGUG AUC------C
```

```
1001 UUCCUGAUCUC UUUCCUCAUC UUCCUAAUAG UGGGA----- ----------
1051 ---
```

Homo_sapiens_Human

```
   1 ------AUGG CGAACCUUGG CURCUGGAUG CUGGUUCUCU UUGUGGCCAC
  51 AUGGAGUGAC CUGGGCCUCU GCAAGAAG-- -CGCCCGAAG CCU------G
 101 GAGGAUGGAA CACUGGGGGC ---AGCCGA- --------UA CCCGGGGCAG
 151 ---GGCAGCC CUGGAGGCAA CCGCUACCCA CCUCAGGGCG GUGGUGGCUG
 201 GGGGCAGCCU CAUGGUGGUG GCUGGGGGCA GCCUCAUGGU GGUGGCUGGG
 251 GGCAGCCCCA UGGU------ ---------- ---------- -GGUGGCUGG
 301 GGGCAGCCUC AUGGUGGUGG CUGGGGR--- CAGCCUCAU- --GGUGGUGG
 351 C------UGG GGGCAG---C CUCAU---GG UGGUGGC--- UGGGGG---C
 401 AGCCCCAU-- -GGUGGUGGC ---UGG---- --------GG A---CAGCCU
 451 CAUGGUGGUG GC-------- -UGGGGUCAA GGA------- --------GG
 501 UGGCACCCAC AGU---CAGY GGAACAAGCC GAGUAAGCCA ---AAAACCA
 551 ACAUGAAGCA CAUGGCUGGU GCWGCAGCRG CUGGGGCAGU GGUGGGGGGC
 601 CUUGGCGGCU ACRUGCUGGG AAGUGCCAUG AGCAGGCCCA UCAUACAUUU
 651 CGGCAGUGAC UAUGAGGACY GYUACUAUCG UGAAAACAUG CACCGUUACC
 701 CCAACCAA-- -GUGUACUAC AGGCCCAUGG AUGAGYACAG CAACCAGAAC
 751 AACUUUGUGC ACGACUGCGU CAAUAUCACA AUCAAGCAGC RCACGGUC--
 801 -ACCACAACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACUUCACCGA GACCGACGUU AAGAUGAUGG AGCGCGUGGU UGAGCAGAUG
 901 UGUAUCACCC AGUACGAGAG GGAAUCUCAG GCC---UAUU AC------MA
 951 GAGAGGAUCG AGCAUGGUCC UCUUCUCCUC UCCACCUGUG AUC------C
1001 UUCCUGAUCUC UUUCCUCAUC UUCCUGAUMG UGGGA----- ----------
1051 ---
```

Pan_troglodytes_Common_chimpanzee

```
   1 ------AUGG CAAACCUUGG CUGCUGGAUG CUAGUUCUCU UUGUGGCCAC
  51 AUGGAGUGAC CUGGGCCUCU GCAAGAAG-- -CGCCCGAAG CCU------G
 101 GAGGAUGGAA CACUGGGGGC ---AGCCGA- --------UA CCCGGGGCAG
 151 ---GGCAGCC CUGGAGGCAA CCGCUACCCA CCUCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGUGGUGG CUGGGGG--- CAGCCUCAU- --GGUGGUGG
 351 C------UGG GGGCAG---C CUCAU---GG UGGUGGC--- UGGGGG---C
 401 AGCCCCAU-- -GGUGGUGGC ---UGG---- --------GG A---CAGCCU
 451 CAUGGUGGUG GC-------- -UGGGGUCAA GGA------- --------GG
 501 UGGCACCCAC AGU---CAGU GGAACAAGCC GAGUAAGCCA ---AAAACCA
 551 ACAUGAAGCA CAUGGCUGGU GCUGCAGCAG CUGGGGCAGU GGUGGGGGGC
 601 CUUGGCGGCU ACAUGCUGGG AAGUGCCAUG AGCAGGCCCA UCAUACAUUU
 651 UGGCAGUGAC UAUGAGGACC GUUACUAUCG UGAAAACAUG CACCGUUACC
 701 CCAACCAA-- -GUGUACUAC AGGCCCAUGG AUCAGUACAG CAGCCAGAAC
 751 AACUUUGUGC ACGACUGCGU CAAUAUCACG AUCAAGCAGC ACACGGUC--
 801 -ACCACAACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACUUCACCGA GACCGACGUU AAGAUGAUGG AGCGCGUGGU UGAGCAGAUG
 901 UGUAUCACCC AGUACGAGAG GGAAUCUCAG GCC---UAUU AC------CA
 951 GAGAGGAUCG AGCAUGGUCC UCUUCUCCUC UCCACCUGUG AUC------C
1001 UCCUGAUCUC UUUCCUCAUC UUCCUGAUAG UGGGA----- ----------
1051 ---
```

Gorilla_gorilla_Western_gorilla

```
   1 ------ATGG CGAACCTTGG CTRCTGGATG CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC CTGGGCCTCT GCAAGAAG-- -CGCCCGAAG CCT------G
 101 GAGGATGGAA CACTGGGGGC ---AGCCGA- --------TA CCCGGGGCAG
 151 ---GGCAGCC CTGGAGGCAA CCGCTACCCA CCTCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGTGGTGG CTGGGGG--- CAGCCTCAT- --GGTGGTGG
 351 C------TGG GGGCAG---C CTCAT---GG TGGTGGC--- TGGGGG---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCT
 451 CATGGTGGTG GC-------- -TGGGGTCAA GGA------- --------GG
 501 TGGCACCCAC AGT---CAGT GGAACAAGCC GAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA CATGGCTGGT GCTGCAGCAG CTGGGGCAGT GGTGGGGGGC
 601 CTTGGCGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCCA TCATACATTT
 651 TGGCAGTGAC TATGAGGACC GTTACTATCG TGAAAACATG CACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCCATGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAATATCACA ATCAAGCAGC ACACGGTC--
 801 -ACCACAACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA GACCGACGTT AAGATGATGG AGCGCGTGGT TGAGCAGATG
 901 TGTATCACCC AGTACGAGAG GGAATCTCAG GCC---TATT AC------CA
 951 GAGAGGATCG AGCATGGTCC TCTTCTCCTC TCCACCTGTG ATC------C
1001 TCCTGATCTC TTTCCTCATC TTCCTGATAG TGGGA----- ----------
1051 ---
```

Otolemur_garnettii_Western_greater_galago

```
   1 ------ATGG CGAGACTTGG CTGCTGGATG CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC ATTGGCCTCT GTAAGAAG-- -CGACCGAAG CCT------G
 101 GAGGCTGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGGCAG
 151 ---GGCAGCC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGT------ ---------- --------GG TGGTGGCTGG
 301 GGCCAGCCTC ACGGTGGCAG CTGGGGG--- CAGCCCCAC- --GGTGGCAG
 351 C------TGG GGGCAG---C CCCAT---GG TGGCAGC--- TGGGGA---C
```

```
 401 AGCCCCAC-- -GGTGGTAGC ---TGG---- --------GG ACAGCAGCCT
 451 CATGGTGGTG GT------AG CTGGGGTCAA ---------- --------GG
 501 AGGC------ ------CACT GGAACAAGCC CAGTAAGCCC ---AAGACCA
 551 ACATGAAGCA CGTGGCAGGT GCGGCCGCAG CTGGGGCAGT GGTAGGTGGC
 601 CTTGGTGGCT ACATGCTGGG GAGCGCAATG AGCAGGCCCC TCATCCACTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG AACCGTTACC
 701 CTAGCCAATT GGTGACGTAC AGGCCGGTGG ATCAGTATAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACC ATCAAGCAGC ACACAGTC--
 801 -ACCACCACC ACCAAA---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA GACGGACGTG AAGATAATGG AGCGCATGGT CGAGCAGATG
 901 TGCGTCACCC AGTACCAGAG GGAGTACCAG GCT---GCGT AC------CA
 951 GAGAGGCTCC AGCGTGGTCC TCTTCTCATC ACCACCCGTG ATC------C
1001 TCCTTATCTC CTTCCTCATC TTCCTGATTG TGGGA----- ----------
1051 ---
```

Microcebus_murinus_Gray_mouse-lemur

```
   1 ------AUGG CGAACCUUGG CUGCUGGAUG UUGGUUGUCU UUGUGGCCAC
  51 AUGGAGUGAC GUGGGCCUCU GCAAGAAG-- -CGACCGAAG CCG------G
 101 GAGGCUGGAA CACUGGGGGG ---AGCCGA- --------UA CCCGGGGCAG
 151 ---GGCAGCC CUGGAGGCAA CCGCUACCCA CCGCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGU------ ---------- ---------- ----------
 301 ---------- --GGCGGCGG CUGGGGG--- CAGCCUCAU- --GGCGGUGG
 351 C------UGG GGACAG---C CCCAU---GG GGGUGGC--- UGGGGA---C
 401 AACCCCAC-- -GGGGGCGGC ---UGG---- --------GG A---CAGCCU
 451 CAUGGUGGCG GU------GG UUGGGGUCAA GGA------- --------GG
 501 UGGCUCCCAC GGU---CAGU GGAACAAGCC CAGUAAGCCA ---AAAACCA
 551 ACAUGAAGCA CAUGGCAGGC GCUGCGGCGG CGGGGGCAGU GGUGGGGGGC
```

```
 601 CUUGGCGGCU ACAUGCUGGG GAGCGCCAUG AGCAGGCCCC UCAUGCAUUU
 651 UGGCAAUGAC UAUGAGGACC GUUACUAUCG UGAAAACAUG AACCGUUACC
 701 CCAACCAA-- -GUGUACUAC AAACCGGUGG AUCAGUACAG CAACCAGAAC
 751 AACUUCGUGC ACGACUGCGU CAAUAUCACC AUCAAGCAGC ACACGGUC--
 801 -ACCACCACC ACCAAA---- ---------- ---------- ---GGGGAGA
 851 ACUUCACCGA GACCGACGUC AAGAUGAUGG AGCGCGUGGU GGAGCAGAUG
 901 UGUGUCACCC AGUACCAGAA GGAGUACCAG GCU---GCCU AC------CA
 951 GAGAGGCUCG AGCAUGGUCC UGUUUUCGUC CCCACCCGUG AUC------C
1001 UCCUCAUCUC UUUCCUCAUC UUCCUGAUAG UGGGA----- ----------
1051 ---
```

Ochotona_princeps_American_pika

```
   1 ------AUGG CACACCUCAG CUACUGGCUG CUGGUCCUCU UCGUGGCUGC
  51 AUGGAGUGAC GUGGGCCUUU GCAAGAAG-- -CGGCCAAAG CCC---GGAG
 101 GAGGAUGGAA CACCGGGGGG ---AGCCGA- --------UA CCCGGGUCAG
 151 ---GGCAGCC CAGGAGGCAA CCGUUACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- ---------- ---------- ---------- ----------
 301 ---------- --GGUGGCGG AUGGGGU--- CAGCCCCAU- --GGCGGUGG
 351 C------UGG GGUCAG---C CCCAC---GG UGGUGGC--- UGGGGU---C
 401 AGCCUCAC-- -GGUGGCGGC ---UGG---- --------GG U---CAGCCC
 451 CAUGGUGGCG GC-------- -UGGGGUCAA ---------- --------GG
 501 AGGUACCCAC AAU---CAGU GGGGUAAGCC CAGUAAGCCA ---AAAACCA
 551 ACAUGAAACA UGUGGCAGGU GCCGCCGCGG CGGGGGCAGU GGUUGGGGGU
 601 CUGGGCGGCU ACAUGCUGGG GAGCGCCAUG AGCAGACCCA UCAUACACUU
 651 CGGCAACGAG UACGAGGACC GUUACUAUCG GGAUAACAUG UACCGUUACC
 701 CCAACCAA-- -GUGUAUUAC AAGCCUGUAG ACCAGUACAG CAACCAGAAC
 751 AACUUUGUGC ACGACUGCGU CAACAUCACA AUCAAGCAGC ACACGGUG--
```

```
 801 -ACCACCACC ACCAAA---- ---------- ---------- ---GGAGAGA
 851 ACUUCACCGA GACCGACAUC AAGAUGAUGG AGCGCGUGGU GGAGCAGAUG
 901 UGCGUCACCC AGUACCAGCA GGAGUACCAG GCC---UCCU AC------CA
 951 GAGGGCAGCC AGUGUGGUGG UCUUCUCCUC GCCGCCCGUG AUU------C
1001 UGCUCAUCUC CUUCCUCAUU UUCCUGAUAG UGGGA----- ----------
1051 ---
```

Oryctolagus_cuniculus_European_rabbit

```
   1 ------AUGG CGCACCUCGG CUACUGGAUG CUGCUUCUCU UUGUGGCCAC
  51 GUGGAGUGAC GUGGGCCUCU GCAAGAAG-- -CGGCCGAAG CCU---GGAG
 101 GAGGAUGGAA CACAGGGGGG ---AGCCGG- --------UA CCCGGGUCAG
 151 ---AGCAGCC CUGGAGGCAA CCGCUACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGUGGCGG CUGGGGA--- CAGCCCCAU- --GGCGGCGG
 351 C------UGG GGGCAG---C CUCAC---GG UGGUGGC--- UGGGGA---C
 401 AGCCCCAC-- -GGCGGUGGC ---UGG---- --------GG G---CAGCCC
 451 CACGGUGGUG GC-------- -UGGGGUCAA GGA------- --------GG
 501 UGGUACCCAC AAC---CAGU GGGGCAAGCC CAGUAAGCCG ---AAAACCA
 551 GCAUGAAGCA CGUGGCCGGG GCAGCGGCGG CUGGGGCGGU GGUGGGGGGC
 601 CUCGGCGGCU ACAUGCUGGG GAGCGCCAUG AGCAGGCCCC UCAUCCACUU
 651 CGGCAACGAC UACGAGGACC GCUACUACCG GGAGAACAUG UACCGGUACC
 701 CCAACCAG-- -GUGUACUAC AGGCCCGUGG ACCAGUACAG CAACCAGAAC
 751 AGCUUCGUGC ACGACUGCGU CAACAUCACG GUGAAGCAGC ACACGGUG--
 801 -ACCACCACC ACCAAA---- ---------- ---------- ---GGGGAGA
 851 ACUUCACCGA GACCGACAUC AAGAUCAUGG AGCGCGUGGU GGAGCAGAUG
 901 UGCAUCACGC AGUACCAGCA GGAGUCCCAG GCC---GCCU AC------CA
 951 GAGGGCGGCC GGCGUGCUGC UCUUCUCCUC GCCGCCCGUC AUC------C
```

```
1001 UCCUCAUCUC CUUCCUCAUC UUCCUGAUCG UGGGA----- ----------
1051 ---
```

Mus_musculus_House_mouse

```
   1 ------AUGG CGAACCUUGG CUACUGGCUG CUGGCCCUCU UUGUGACUAU
  51 GUGGACUGAU GUCGGCCUCU GCAAAAAG-- -CGGCCAAAG CCU------G
 101 GAGGGUGGAA CACCGGUGGA ---AGCCGG- --------UA UCCCGGGCAG
 151 ---GGAAGCC CUGGAGGCAA CCGUUACCCA CCUCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- ---------- ---------- ---------- ----------
 301 ---------- --GGUGGCAC CUGGGGG--- CAGCCCCAC- --GGUGGUGG
 351 C------UGG GGACAA---C CCCAU---GG GGGCAGC--- UGGGGA---C
 401 AACCUCAU-- -GGUGGUAGU ---UGG---- --------GG U---CAGCCC
 451 CAUGGCGGUG GA-------- -UGGGGCCAA GGA------- --------GG
 501 GGGUACCCAU AAU---CAGU GGAACAAGCC CAGCAAACCA ---AAAACCA
 551 ACYUCAAGCA UGUGGCAGGG GCUGCGGCAG CUGGGGCAGU AGUGGGGGGC
 601 CUUGGUGGCU ACAUGCUGGG GAGCGCCAUG AGCAGGCCCA UGAUCCAUUU
 651 UGGCAACGAC UGGGAGGACC GCUACUACCG UGAAAACAUG UACCGCUACC
 701 CUAACCAA-- -GUGUACUAC AGGCCAGUGG AUCAGUACAG CAACCAGAAC
 751 AACUUCGUGC ACGACUGCGU CAAUAUCACC AUCAAGCAGC ACACGGUC--
 801 -RYCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACUUCACCGA GACCGAUGUG AAGAUGAUGG AGCGCGUGGU GGAGCAGAUG
 901 UGCGUCACCC AGUACCAGAA GGAGUCCCAG GCC---UAUU ACGACGGGAG
 951 AAGAUCCAGC AGCACCGUGC UUUUCUCCUC CCCUCCUGUC AUC------C
1001 UCCUCAUCUC CUUCCUCAUC UUCCUGAUCG UGGGA----- ----------
1051 ---
```

Rattus_norvegicus_Brown_rat

```
   1 ------AUGG CGAACCUUGG CUACUGGCUG CUGGCCCUCU UUGUGACUAC
  51 AUGUACUGAU GUUGGCCUCU GCAAAAAG-- -CGGCCAAAG CCU------G
 101 GAGGGUGGAA CACUGGUGGA ---AGCCGG- --------UA CCCUGGGCAG
 151 ---GGAAGCC CUGGAGGCAA CCGUUACCCA CCUCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -AGU------ ---------- ---------- ----------
 301 ---------- --GGUGGUAC CUGGGGG--- CAGCCCCAU- --GGUGGUGG
 351 C------UGG GGACAA---C CUCAU---GG UGGUGGC--- UGGGGA---C
 401 AACCUCAU-- -GGUGGUGGC ---UGG---- --------GG U---CAGCCC
 451 CAUGGCGGGG GC-------- -UGGAGUCAA GGA------- --------GG
 501 GGGUACCCAU AAU---CAGU GGAACAAGCC CAGCAAGCCA ---AAAACCA
 551 ACCUCAAGCA UGUGGCAGGG GCUGCCGCAG CUGGGGCAGU AGUGGGGGGC
 601 CUUGGUGGCU ACAUGUUGGG GAGUGCCAUG AGCAGGCCCA UGCUCCAUUU
 651 UGGCAACGAC UGGGAGGACC GCUACUACCG AGAAAACAUG UACCGUUACC
 701 CUAACCAA-- -GUGUACUAC AGGCCGGUGG AUCAGUACAG CAACCAGAAC
 751 AACUUCGUGC ACGACUGUGU CAAUAUCACC AUCAAGCAGC AUACAGUC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACUUCACGGA GACCGACGUG AAGAUGAUGG AGCGUGUGGU GGAGCAGAUG
 901 UGCGUCACCC AGUAUCAGAA GGAGUCCCAG GCC---UAUU ACGAC---GG
 951 GAGAAGAUCU AGCGCCGUGC UUUUCUCCUC CCCUCCUGUG AUC------C
1001 UCCUCAUCUC CUUCCUCAUC UUCCUGAUCG UGGGA----- ----------
1051 ---
```

Cavia_porcellus_Guinea_pig

```
   1 ------ATGG CAAATGCCGG CTGCTGGCTG CTGGTTCTTT TTGTGGCCAC
  51 ATGGAGTGAC ACTGGCCTCT GCAAGAAG-- -CGACCAAAA CCA---GGAG
 101 GAGGGTGGAA CACCGGGGGC ---AGCCGT- --------TA CCCATCCCAC
 151 ---------- ---------- ---------- ---------- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -AGC------ ---------- ---------- ----------
 301 ---------- --GGGGGGAC CTGGGGT--- CAGCCCCAT- --GGAGGTAG
 351 C------TGG GGCCAG---C CTCAT---GG TGGTAGC--- TGGGGC---C
 401 AGCCCCAT-- -GGTGGTAGC ---TGG---- --------GG A---CAGCCC
 451 CATGGCGGTG GC-------- -TGGGGCCAT GGA------- --------GG
 501 TGGCTCGTAC AAT---CAGT GGAACAAACC CAGTAAGCCC ---AAAACCA
 551 ACATGAAGCA CATGGCGGGG GCTGCGGCGG CCGGGGCAGT GGTGGGGGGC
 601 CTTGGCGGCT ACATGCTGGG GAGCGCCATG AGCAGGCCCC TCATCCATTT
 651 CGGCAGCGAC TATGAGGACC GTTACTACCG TGAGAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AAGCCCGTGG ATCAGTACAG CAACCAGAAC
 751 AGCTTTGTGC AGGACTGTGT CAACATCACG ATCAAGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAA---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA GACTGACGTG AAGATCATGG AGCGCGTGCT GGAGCAGATG
 901 TGTACCACGC AGTACCAAAA GGAGTCCCAG GCTTACTACT AC------CA
 951 CGGGCGGGCC GGCCTGGTGC TCTTCTCCTC CCCACCCGTG ATC------C
1001 TCCTCATCTC CTTCCTGATC TTCCTGATAG TGGGA----- ----------
1051 ---
```

Sorex_araneus_Common_shrew

```
   1 ATGGTGACGG GCCACCTAGG ATGCTGGCTC CTGGTCCTCT TCATGGCCAC
  51 CTGGAGTGAC GTGGGCCTGT GCAAGAAG-- -AGGCCGAAG CCC---GGCG
 101 GAACCTGGAA CTCTGGGGGG ---AGTCGG- --------TA TCCAGGCCAG
 151 ---GGCGGTT ATGGGGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGCGGAGG CTGGGGT--- CAGCCCCATG GGGGTGGAGG
 351 C------TGG GGTCAG---C CCCATGGCGG CGGAGGC--- TGGGGT---C
```

```
 401 AGCCCCACGG GGGTGGAGGC ---TGG---- --------GG T---CAGCCC
 451 CACGGTGGAG GC-------- -TGGGGCCAA ---------- ----------
 501 -GGCTCCCAC AAC---CAGT GGAATAAGCC CAGCAAGCCC ---AAGACCA
 551 ACATGAAGCA CGTGGCCGGG GCGGCGGCGG CCGGGGCGGT CGTGGGGGGC
 601 CTGGGCGGCT ACATGCTGGG GAGTGCCATG AGCCGGCCCC TCATGCACTT
 651 CGGCAACGAC TACGAGGACC GGTACTACCG TGAGAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AAGCCGGTGG ACCAGTACAG CAACCAGAAC
 751 AACTTCGTGC ACGACTGCGT GAACATGACC GTCAAGCAGC ACACGGTC--
 801 -ACCACCACC AGCAAG---- ---------- ---------- ---GGCGAGA
 851 ACTTCACCGA GACCGACGTC AAGATCATGG AGCGCGTGGT GGAGCAGATG
 901 TGCATCACCC AGTACCGCGA GGCAGCCCAG GCC---TCCT AC------CT
 951 GCAGGGGGAC AGCACAGTCC TCTTCTCCTC CCCGCCCTTC ATC------C
1001 TGCTCATCTC CTTCCTCATC TTCCTGATCG TGGGA----- ----------
1051 ---
```

Erinaceus_europaeus_European_hedgehog

```
   1 ATGGTGAAAA ACCACGTGGG CTGCTGGCTC CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAA GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT------G
 101 GAGGATGGAA CAGTGGGGGA ---AGCCGA- --------TA TCCTGGGCAG
 151 ---GGCAGTT CTGGCAGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGT------ ---------- ---------- ----------
 301 ---------- --GGTGGAGG CTGGGGTCAG CAGCCCCATG CTGGTGGAGG
 351 C------TGG GGTCAGCAGC CCCATGGAGG TGGAGGC--- TGGGGTCAGC
 401 AGCCCCATGG AGGTGGAGGC ---TGG---- --------GG TCAGCAGCCC
 451 CATGGTGGCG GA------GG CTGGGGTCAA ---------- --------GC
 501 TGGCAGCCAC AAC---CAGT GGAACAAGCC CAACAAACCC ---AAAACCA
 551 ACATGAAACA TGTAGCAGGA GCTGCTGCAG CTGGGGCAGT TGTTGGGGGC
```

```
 601 CTTGGTGGCT ACTTAGTGGG GAGTGCCATG AGCAGGCCCC CCATCCACTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAGAACATA AACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AAGCCGGTGG ATCAGTACAG TAACCAGAAC
 751 AACTTCGTGC ATGACTGTGT CAACATCACA GTCAAGCAGC ACACCGTG--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGCGAGA
 851 ACTTCACTGA GACAGACGTC AAGATAATGG AGCGAGTGGT GGAGCAGATG
 901 TGCATCACCC AGTACCAGCA AGCTCGG--- ------GCCT AC------CA
 951 CGACGGGGCC AGCGTGCTCC TCTTCTCCTC CCCCGCTGTG ATT------C
1001 TCCTCATCTC TCTCCTCATC TTCCTGCTAG TGGGA----- ----------
1051 ---
```

Ovis_aries_Domestic_sheep

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGCG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTAGCCAC AGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGACCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
```

```
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATAATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGGGGGGCA AGTGTGATCC TCTTTTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Ovis_canadensis_Bighorn_sheep

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGCG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCYGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CARCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTAGCCAC AGT---CAGY GGAATAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG RGCAGGCCTC TTATACATYT
 651 TGGCAATGAC TATGAGGACC GTTACTATCR TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGACCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CRACATCACA GTCAAKCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATAATGG RGYGAGTGGT GGRGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGGGGGGCA WGTGTGATCC TCTTTTCTTC CCCTCCTGTG ATY------C
```

```
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Capra_hircus_Domestic_goat

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGCG
 101 GAGGATGGAA CACTGKGGGG ---AGCCGA- --------TA CCCRGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTAGCCAC AGT---CRGT GGAACAAGCC CMGTAAGCCA ---AAAMCCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCWGGG AAGTGCCATR AGYAGGCCTC TTAYRCRTTT
 651 TGGCAATGAC TATGAGGACC GTTACTATSV TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGACCAGTGG ATCRGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCMCCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACYGA AACTGACATC AAGATAATGG AGSRAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACMAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AMGGGGGGCA AGTGTGATCC TSTTTTCTYC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Capra_ibex_Alpine_ibex

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGCG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTAGCCAC AGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGTAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGACCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATAATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGGGGGGCA AGTGTGATCC TCTTTTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Rupicapra_rupicapra_Chamois

```
   1 ATGGTGAAAA GCCACATAGG CAGYTGGATC CTRGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTSGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGMG
 101 GAGGATGGAA CACTGGGGGR ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGMAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTASCCAC AGT---CAGT GGAACAAGCC CAGTAARCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCYGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTYGGTGGCT ACATGCTGGG AAGTGCYATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGRCCAGTGG ATCAGTATAR TAACCAGAAC
 751 AMCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACMAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATRATGG AGCGAGTKGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGRGGGGCA AGTGTGATCC TCTTYTCYTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Antilope_cervicapra_Blackbuck

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGA ---AGCCGA- --------TA CCCAGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAACCTCAT- --GGAGGTGG
 351 C------TGG GGTCAG---C CCCAT---GG AGGTGGC--- TGGGGT---C
```

```
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAGTCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Bos_taurus_Domestic_cattle

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCTCAT- --GGAGGTGG
 351 C------TGG GGCCAR---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAAT GGAACAAACC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
```

```
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAGTGAC TATGAGGACC GTTACTATCG TGAAAACATG CACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGGAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATTACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTGATCC TCTTCTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Bison_bison_American_bison

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAY
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCTCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAAT GGAACAAACC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAGTGAC TATGAGGACC GTTACTATCG TGAAAACATG CACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGGAAC ACACAGTC--
```

```
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA

 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG

 901 TGCATTACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA

 951 ACGAGGGGCA AGTGTGATCC TCTTCTCTTC CCCTCCTGTG ATC------C

1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------

1051 ---
```

Syncerus_caffer_caffer_African_cape_buffalo

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGTCAT

  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG

 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGACAG

 151 ---GGCAGTC CTGGAGGCAA CCGTTATCCA TCTCAG---- ----------

 201 ---------- ---------- ---------- ---------- ----------

 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG

 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCTCAT- --GGAGGTGG

 351 C------TGG GGYCAR---C CYCAT---GG AGGTGGC--- TGGGGW---C

 401 AGCCMCAT-- -GGWGGWGGC ---TGG---- --------GG A---CAGCCA

 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG

 501 TGGTACCCAC GGT---CAAT GGAACAAGCC CAGTAAGCCA ---AAAACCA

 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC

 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT

 651 TGGTAATGAC TATGAGGACC GTTACTATCG TGAAAACATG CACCGTTACC

 701 CCAACCAA-- -GTATACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC

 751 ARCTTTGTGC ATGACTGTGT CAACATCACA GTMAAGGAAC ACACAGTC--

 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA

 851 ACTTCACCGA AACTGACGTC AAGATGATGG AGCGAGTGGT GGAGCAAATG

 901 TGCATCACCC AGTACCAGAG RGAATCCSAG GCT---TATT AC------CA

 951 ACGAGGGGCA AGTGTGATCC TCTTCTCTTC CCCTCCTGTG ATC------C
```

```
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Syncerus_caffer_nanus_African_forest_buffalo

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGTCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTATCCA TCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCTCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGAGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAAT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGTAATGAC TATGAGGACC GTTACTATCG TGAAAACATG CACCGTTACC
 701 CCAACCAA-- -GTATACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AGCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGGAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACGTC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCWCCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTGATCC TCTTCTCTTC CCCTCCTRTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Bubalus_bubalis_Water_buffalo

```
   1 AUGGUGAAAA GACACAUAGG CAGUUGGAUC CUGGUUCUCU UUGUGGUCAU
  51 GUGGAGUGAC GUGGGCCUCU GCAAGAAG-- -CGACCAAAA CCU---GGAG
 101 GAGGAUGGAA CACUGGGGGG ---AGCCGA- --------UA CCCRRGACAG
 151 ---GGCAGUC CUGGAGGCAA CCGUUAUCCA UCUCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGAGGGGGU GGCUGGGGUC AGCCCCAUGG AGGUGGCUGG
 301 GGUCAGCCCC AUGGAGGUGG CUGGGGC--- CAGCCUCAU- --GGAGGUGG
 351 C------UGG GGYCAR---C CKCAU---GG WGGUGGC--- UGGGGW---C
 401 AGCCGCAU-- -GGUGGUGGC ---UGG---- --------GG A---CAGCCR
 451 CAUGGUGGUG GA------GG CUGGGGUCAA ---------- --------GG
 501 UGGUACCCAC RGU---CAAU GGAACAAGCC CAGUAAGCCA ---AAAACCA
 551 ACAUGAAGCA UAUGGCAGGA GCUGCUGCAG CUGGAGCAGU GGUAGGGGGC
 601 CUUGGUGGCU ACAUGCUGGG AAGUGCCAUG AGCAGGCCUC UUAUACAUUU
 651 UGGUAAUGAC UAUGAGGACC GUUACUAUCG UGAAAACAUG CACCGUUACC
 701 CCAACCAA-- -GUGUACUAC AGGCCAGUGG AUCAGUAUAG UAACCAGAAC
 751 AACUUUGUGC AUGACUGUGU CAACAUCACA GUCAAGGAAC ACACAGUC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACUUCACYGA AACUGACAUC AAGAUGAUGG AGCGAGUGGU GGAGCAAAUG
 901 UGCAUYACCC AGUACCAGAG AGAAUCCCAG GCU---UAUU AC------CA
 951 ACGAGGGGCA AGUGUGAUCC UCUUCUCUUC CCCUCCUGUG AUC------C
1001 UCCUCAUCUC UUUGCUCAUU UUUCUCAUAG UAGGA----- ----------
1051 ---
```

Bubalus_depressicornis_Anoa

```
   1 ATGGTGAAAA GACACATAGG CAGTTGGATC CTGGTTCYCT TTGTGGTCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTATCCA TCTCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCTCAT- --GGAGGTGG
 351 C------TGG GGCCAG---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCGCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAAT GGAACAAGCC CAGTAAGCCA ---AARACCA
 551 ACATGAAGCA TATGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGTAATGAC TATGAGGACC GTTACTATCG TGAAAACATG CACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCRGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGGAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTGATCC TCTTCTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTGCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Tragelaphus_strepticeros_Greater_kudu

```
   1 ATGGTGAAAA GCCACATAGG CAGWTGGATC CTGGTCCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGSCCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCSA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA YCTCAR---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GRA------ ---------- --------GG GGGTGRCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCCCAT- --GGAGGCGG
 351 C------TGG GGCCAG---C CTCAT---GK AGGTGGC--- TGGGGT---C
```

```
 401 AGCCCCAT-- -GGTGGTGGY ---TGG---- --------GG A---CAGCCR
 451 CATGGTGGTG GA------GG STGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAACA TGTGGCAGGA GCTGCTGCAG CGGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAGTGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAGC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GYT---TATT AC------CA
 951 ACGAGGGGCA AGTGTCATCM TCTTCTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Tragelaphus_oryx_Eland

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTCCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA TCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAG---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGT ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGTG GA------AG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
```

```
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAGTGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAGC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTGATCC TCTTCTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Tragelaphus_angasii_Nyala

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTCCTCT TTGTGGCCAT
  51 GTGGAGTGAT GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA TCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGYCAG---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGT ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAACA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAGTGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAGC ACACAGTC--
```

```
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTCATCC TCTTCTCTTC CCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Tragelaphus_imberbis_Lesser_kudu

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTCCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA TCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCTCAT- --GGAGGTGG
 351 C------TGG GGCCAG---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAGC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTCATCC TCTTCTCTTC CCTCCTGTG ATC------C
```

```
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Boselaphus_tragocamelus_Nilgai

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA TCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTAGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCTCAT- --GGAGGTAG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGC---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CAGGAGCAGT GGTAGGGGGC
 601 CTGGGTGGCT ACATGCTRGG AAGTGCCATG AACAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG CACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC GTGACTGTGT CAACATCACA GTCAAGGAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAC AGAATCCCAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTGGTCC TCTTCTCTTC CCCTCCTGTG GTC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Moschus_chrysogaster_Alpine_musk_deer

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA TCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GCGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCGCAT-- -GGAGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AAT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTCGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ACGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACTGA AACTGACATC AAGATTATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Muntiacus_reevesi_Muntjac

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTAT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCRGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTAGCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTCGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Odocoileus_virginianus_White–tailed_deer

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGRY GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGYTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GRAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
```

```
 401 AGCCCCAT-- -GGWGGTGGC ---TGG---- --------GG G---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAW ---------- --------RG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCR ---AAAACCA
 551 ACATGAAGCA TGTGGSAGGA GCTGCTGCMG CTGGAGCAGT GGTAGGRGGC
 601 CTYGGTGGCT ACATGCTGGG AAGTGCCATG ARCAGRCCTC TTATACATTT
 651 TGGCAAYGAC TATGAGGACY GTTACTATCG TGAAAAYATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATYACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACYGA AACTGACATY AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCMAG GCT---TATT AC------CW
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Odocoileus_hemionus_Mule_deer

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGRC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG G---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCMG CTGGAGCAGT GGTAGGGGGC
```

```
 601 CTYGGTGGCT AYATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAAYGAC TATGAGGACC GTTACTATCG TGAAAAYATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACYGA AACTGACATY AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATYCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATYTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Rangifer_tarandus_Caribou

```
   1 ATGRTGAAAA GCCACATAGG CAGYTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGGGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG G---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------KG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCCG CTGGARCAGT GGTAGGGGGC
 601 CTYRGTGGCT ACATGCTGGG AAGTGCCATG ARCAGGCCTC TTATACATTT
 651 TGGCAAYGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCARTGG ATCAGTATAA TAACCAGRAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
```

```
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATT AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATMCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Alces_alces_European_Elk

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCYCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGG---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG G---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCC ---MAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATT AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
```

```
1001 TCCTMATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Alces_americanus_Moose

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCYCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGG---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG G---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCC ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATT AAGATGATKG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTMATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Hydropotes_inermis_Water_deer

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAA-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGTCAG---C CCCAT---GG AGGTGGC--- TGGGGW---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG T---CAGCCC
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC ART---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT AGTAGGGGGC
 601 CTCGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GCCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Capreolus_capreolus_Roe_deer

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GYAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGAGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAACGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATT AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATATC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Cervus_canadensis_Wapiti

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTYGGCCTCT GCARGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
```

```
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAARCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTCGGTGGCT ACWTGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACRCAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTSATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Cervus_elaphus_Red_deer

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGYGGCCAT
  51 GTGGAGTGAC GTBGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTRG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 ARCCYCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTRCCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
```

```
 601 CTCGGTGGCT ACATGCTGGG AAGTGCYATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGYCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCSAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Cervus_nippon_Sika_deer

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTCGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCYCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC RGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTCGGTGGCT ACATGCTGGG AAGTGCYATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
```

```
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCSAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Dama_dama_Fallow_deer

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGC--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTCGGTGGCT ACATGCTGGG AAGTGCCATG AATAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
```

1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------

1051 ---

Antilocapra_americana_Pronghorn

1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT

51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG

101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGACAG

151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA CCCCAG---- ----------

201 ---------- ---------- ---------- ---------- ----------

251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG

301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCTCAT- --GGAGGTGG

351 C------TGG GGTCAG---C CCCAT---GG TGGTGGC--- TGGGGT---C

401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCC

451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG

501 TGGCACCCAC AGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA

551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC

601 CTCGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT

651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC

701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC

751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACGGTC--

801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA

851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG

901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA

951 AAGAGGAGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C

1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------

1051 ---

Sus_scrofa_Wild_boar

```
   1 ATGGTGAAAA RCCAYATAGG TGGCTGGATC CTCGTTCTCT TTGTGGCCGC
  51 ATGGAGTGAC ATAGGGCTCT GCAAGAAG-- -CGACCAAAG CCT---GGCG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGGCAG
 151 ---GGTAGTC CTGGAGGCAA CCGCTATCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGA--- CAGCCCCAC- --GGAGGTGG
 351 C------TGG GGACAG---C CCCAC---GG AGGCGGC--- TGGGGA---C
 401 AGCCCCAC-- -GGTGGCGGC ---TGG---- --------GG A---CAGCCC
 451 CATGGTGGCG GA------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCTCCCAC GGT---CAGT GGAACAAGCC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGC GCCGCTGCAG CTGGGGCAGT GGTAGGGGGC
 601 CTCGGCGGTT ACATGCTGGG GAGTGCCATG AGCAGACCCC TGATACACTT
 651 TGGCAGTGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AGTTTTGTGC ATGACTGCGT CAACATCACC GTCAAGCAGC ACACAGTG--
 801 -ACCACGACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA GACSGACGTC AAGATGATAG AGCGCGTGGT GGAACAGATG
 901 TGCATCACCC AGTACCAGAA AGAGTACGAG GCR---TACG CC------CA
 951 AAGAGGGGCC AGTGTGATCC TCTTCTCCTC CCCKCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCCTT TTCCTCATAG TGGGC----- ----------
1051 ---
```

Camelus_bactrianus_Bactrian_camel

```
   1 ATGGTGAAAA GCCACATRGG CAGYTGGATC CTGGTTCTCT TTGTGGYCAY
  51 GTGGAGTGAC GTGGGCCTST GCAAGAAG-- -CGMCCAAAR CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCRGGRCAG
 151 ---GGCAGTC CTGGAGGCAA CCGYTATCCA CCYCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGYGGCTGG
 301 GGTCAGCCCC AYGGAGGWGG CTGGGGY--- CAGCCYCAY- --GGAGGYGG
 351 C------TGG GGCCAR---C CYCAY---GG WGGWGGC--- TGGGGY---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGYGGTG GA------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCRCCCAC GGT---CART GGAACAARCC CAGTAAGCCR ---AAAACCA
 551 RCATGAAGCA YGTGGCAGGA GCTGCTGCAG CTGGRGCAGT GGTAGGGGGC
 601 CTYGGYGGCT ACATGCTGGG RAGTGCCATG AGCAGGCCYC TTATACATTT
 651 TGGCARYGAC TATGAGGACC GTTACTATCG WGAAAACATG YACCGTTACC
 701 CCAACCAA-- -GTGTACTAC ARGCCAGTGG ATCAGTAYAG YAACCAGAAC
 751 ARCTTYGTGC ATGACTGYGT CAACATCACA GTCAARSARC ACACRGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACYTCACCGA RACYGACRTC AAGATGATGG AGCGMGTRGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGARTMCCAG GCT---TMKT AC------SR
 951 MMGAGGGGCM AGTGTGATCC TCTTCTCYTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTYCTCATAG TRGGW----- ----------
1051 ---
```

Camelus_dromedarius_Dromedary

```
   1 ATGGTGAAAA GCCACATGGG CAGCTGGATC CTGGTTCTCT TTGTGGTCAC
  51 GTGGAGTGAC GTGGGCCTGT GCAAGAAG-- -CGCCCAAAG CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGCGG CTGGGGT--- CAGCCCCAC- --GGAGGAGG
 351 C------TGG GGTCAG---C CCCAC---GG AGGCGGC--- TGGGGT---C
```

```
 401 AACCCCAC-- -GGAGGCGGC ---TGG---- --------GG C---CAGCCC
 451 CATGGTGGAG GC-------- -TGGGGTCAA GGT------- --------GG
 501 TGGCGCCCAC GGT---CAGT GGAACAAGCC CAGTAAGCCG ---AAAACCA
 551 GCATGAAGCA CGTGGCAGGA GCTGCTGCAG CTGGGGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG GAGTGCCATG AGCAGGCCCC TTATACATTT
 651 TGGCAACGAC TATGAGGACC GTTACTATCG AGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AAGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AGCTTCGTGC ATGACTGCGT CAACATCACA GTCAAACAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA GACCGACGTC AAGATGATGG AGCGCGTAGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAGTACCAG GCT---TCGT AC------GG
 951 CAGAGGGGCC AGTGTGATC- --TTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTCCTCATAG TGGGT----- ----------
1051 ---
```

Equus_asinus_Donkey

```
   1 ATGGTGAAAA GCCACGTAGG CGGCTGGATT CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGGCTCT GCAARAAG-- -CGACCGAAG CCT------G
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCCGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTAYCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGTGGCGG CTGGGGT--- CAACCCCAT- --GGTGGTGG
 351 T------TGG GGTCAG---C CCCAT---GG TGGTGGC--- TGGGGT---C
 401 AGCCGCAY-- -GGTGGTGGT ---TGG---- --------GG A---CAGCCC
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGCTCCCAT GGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCSGCAG CTGGGGCAGT GGTKGGGGGC
```

```
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AGCAGACCCC TCATTCATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCGGTAA ATGAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAAGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 AYTTCACCGA GACCGACGTC AAGATCATGG AGCGCRTGGT GGAGCAGATG
 901 TGCATCACCC AGTACCAGAA AGAGTACGAG GCT---TTTC AA------CA
 951 AAGAGGGGCG AGCGTGGTCC TCTTCTCCTC CCCGCCTGTG RTC------C
1001 TCCTSATCTC TTTCCTCATT TTCCTCATAG TGGGC----- ----------
1051 ---
```

Equus_caballus_Horse

```
   1 ATGGTGAAAA GCCACGTAGG CGGCTGGATT CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGGCTCT GCAAGAAG-- -CGACCGAAG CCT------G
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCCGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGTGGCGG CTGGGGT--- CAACCCCAT- --GGTGGTGG
 351 T------TGG GGTCAG---C CCCAT---GG TGGTGGC--- TGGGGT---C
 401 AGCCGCAT-- -GGTGGTGGT ---TGG---- --------GG A---CAGCCC
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGCTCCCAT GGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCGGCAG CTGGGGCAGT GGTTGGGGGC
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AGCAGACCCC TCATTCATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCGGTAA GTGAGTACAG CAACCAGAAM
 751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAAGCAGC ACACRGTC--
```

```
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA GACCGACGTC AAGATCATGG AGCGCGTGGT GGAGCAGATG
 901 TGCATCACCC AGTACCAGAA AGAGTACGAG GCT---TTTC AA------CA
 951 AAGAGGGGCG AGCGTGGTCC TCTTCTCCTC CCCGCCTGTG GTC------C
1001 TCCTCATCTY TTTCCTCATT TTCCTCATAG TGGGC----- ----------
1051 ---
```

Pteropus_vampyrus_Large_flying_fox

```
   1 ATGGTGAAAA ACTACATAGG CGGTTGGATC CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGCGAC GTGGGTCTCT GCAAGAAA-- -CGACCGAAG CCT---GGAG
 101 GAGGAGGGAG CAGTGGGGGG ---AGCCGA- --------TA CCCGGGGCAG
 151 ---GGGAGTC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGT------ ---------- --------GG TGGTGGCTGG
 301 GGCCAGCCCC ATGGCGGCGG CTGGGGT--- CAGCCCCAC- --GGTGGAGG
 351 C------TGG GGACAG---C CCCAC---GG TGGAGGC--- TGGGGT---C
 401 AGCCCCAC-- -GGTGGAGGC ---TGG---- --------GG A---CAGCCC
 451 CATGGTGGAG GC-------- -TGGGGTCAA GGT------- --------GG
 501 CGGCACCCAC AGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACTTGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGGGCCGT GGTGGGGGGC
 601 CTCGGCGGCT ACATGTTGGG AAGTGCCATG AACAGGCCCC TGTTACATTT
 651 TGGCAATGAC TATGAGGATC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCCGTGG ATCAGTACAA CAACCAGAAC
 751 AGCTTTGTGC ACGACTGCGT CAACATCACG GTCAAGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACTGA GACCGACGTG AAGATGATGG AGCGCGTGGT GGAGCAGATG
 901 TGCATCACCC AGTACCAGCA GGAGTCGCGG GCT---GCGT AC------CA
 951 CAGAGGGGCG AGCGTAGTCG TCTTCTCCTC CCTCCCGTG ATC------C
```

```
1001 TGCTCATTTC TTTCCTCATT TTCCTGATAG TGGGA----- ----------
1051 ---
```

Myotis_lucifugus_Little_brown_bat

```
   1 ATGGTGAAAA GCCTCGTAGG CGGCTGGATA CTGCTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCGAAG CCT---GGAG
 101 GAGGC---AA CACCGGCGGG ---AGCCGA- --------TA CCCGGGGCAG
 151 ---GGTAGTC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- ---------- ---------- ---------- ----------
 301 ---------- --GGCGGCGG CTGGGGT--- CAACCGCAGG GCGGTGGCGG
 351 C------TGG GGTCAG---C CCCATGGTGG TGGAGGC--- TGGGGA---C
 401 AGCCCCATGG TGGTGGAGGC ---TGG---- --------GG A---CAGCCC
 451 CATGGTGGTG GC-------- ---------- ---------- ----------
 501 ----AGCCAC AAT---CAGT GGAACAAGCC AAATAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCCGCGG CCGGGGCAGT GGTGGGGGGC
 601 CTGGGAGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC CCATGCATTT
 651 TGGCAATGAG TATGAGGACC GTTACTACCG TGAAAACATG AACCGTTTCC
 701 CCGACCAA-- -GTGTACTAC AAGCCTGTGG ATCAGTACAA CAACCAGAAC
 751 AACTTCGTGC GCGACTGCGT CAACATCACG GTCAAGCAGC ACACGGTC--
 801 -ACCACCATC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACATCACCGA GACGGACGTC AAGATTATGG AGCGTGTGGT GGAGGAGATG
 901 TGCACCACCC AGTACCAGAA AGAGTACCAG GCT---TCTT AC------CA
 951 AAGAGGGGCG AGCGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTCCTAATAG TGGGG----- ----------
1051 ---
```

Crocuta_crocuta_Spotted_hyena

```
   1 ATGGTGAAAA GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCAAAG CCC---GGCG
 101 GAGGATGGAA CACTGGGGGA ---AGCCGG- --------TA CCCGGGGCAG
 151 ---GGCAGTC CCGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGT------ ---------- ---------- ----------
 301 ---------- --GGGGGCGG CTGGGGT--- CAGCCCCAC- --GGGGGCGG
 351 C------TGG GGACAG---C CCCAC---GG GGGTGGC--- TGGGGT---C
 401 AGCCCCAC-- -GGGGGCGGC ---TGG---- --------GG A---CAGCCC
 451 CATGGTGGAG GT------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCACCCAC AGT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA CATGGCCGGA GCCGCGGCGG CGGGGGCGGT AGTGGGGGGC
 601 CTCGGCGGCT ACATGCTGGG GAGCGCCATG AGCAGGCCCC TCATTCATTT
 651 TGGCAATGAC TACGAGGACC GCTACTACCG CCAAAACATG GACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AAGCCAGTGG ATCAGTACAG CAGCCAGAAC
 751 AACTTCGTGC ACGACTGCGT CAACATCACK GTCAGGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAAA
 851 ACTTCACGGA GACCGACATG AAGATAATGG AACGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAG AGAGTCGGAG GCC---TACT AC------CA
 951 AAGAGGGGCC AGCGTCGTCC TCCTCTCCCC GCCTCCCGTC ATC------C
1001 TCCTCGTCTC GCTCCTCATC CTCCTGATAG TGGGA----- ----------
1051 ---
```

Panthera_leo_Lion

```
   1 ATGGTGAAAG GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGTG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGG- --------TA CCCGGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTACCCA CCCCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- ---------- ---------- ---------- ----------
 301 ---------- ---------- ----GGC--- ---------- --GGCGGCGG
 351 C------TGG GGTCAG---C CCCACGCCGG CGGCGGC--- TGGGGT---C
 401 AGCCCCACGC CGGCGGCGGC ---TGG---- --------GG A---CAGCCC
 451 CACGCCGGCG GC------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCACCCAC AGT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCCGCGGCAG CCGGGGCGGT AGTGGGGGGC
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AACCGGCCCC TCATTCATTT
 651 TGGCAACGAC TACGAGGACC GTTACTACCG TGAAAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAGGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATAATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCC---TACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCTCCCGTG ATT------C
1001 TCCTCCTCTC GCTCCTCATC CTCCTGATCG GGGGT----- ----------
1051 ---
```

Panthera_pardus_saxicolor_Persian_leopard

```
   1 ATGGTGAAAG GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGTG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGG- --------TA CCCGGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGCGGCGG CTGGGGT--- CAGCCCCACG CCGGCGGCGG
 351 C------TGG GGTCAG---C CCCACGCCGG CGGCGGC--- TGGGGA---C
```

```
 401 AGCCCCACGC CGGCGGCGGC ---TGG---- --------GG A---CAGCCC
 451 CACGCCGGCG GC------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCACCCAC AGT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCCGCGGCAG CCGGGGCGGT AGTGGGGGGC
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AACCGGCCCC TCATTCATTT
 651 TGGCAATGAC TACGAGGACC GTTACTACCG TGAAAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAGGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATAATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCC---TACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCTCCCGTG ATT------C
1001 TCCTCCTCTC GCTCCTCATC CTCCTGATAG GGGGT----- ----------
1051 ---
```

Panthera_pardus_orientalis_Amur_leopard

```
   1 ATGGTGAAAG GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGTG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGG- --------TA CCCGGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGCGGCGG CTGGGGT--- CAGCCCCACG CCGGCGGCGG
 351 C------TGG GGTCAG---C CCCACGCCGG CGGCGGC--- TGGGGA---C
 401 AGCCCCACGC CGGCGGTGGC ---TGG---- --------GG A---CAGCCC
 451 CACGCCGGCG GC------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCACCCAC AGT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCCGCGGCAG CCGGGGCGGT AGTGGGGGGC
```

```
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AACCGGCCCC TCATTCATTT
 651 TGGCAACGAC TACGAGGACC GTTACTACCG TGAAAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAGGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATAATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCC---TACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCTCCCGTG ATT------C
1001 TCCTCCTCTC GCTCCTCATC CTCCTGATAG GGGGT----- ----------
1051 ---
```

Panthera_onca_Jaguar

```
   1 ATGGTGAAAG GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGTG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGG- --------TA CCCGGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGCGGCGG CTGGGGT--- CAGCCCCACG CCGGCGGCGG
 351 C------TGG GGTCAG---C CCCACGCCGG CGGCGGC--- TGGGGA---C
 401 AGCCCCACGC CGGCGGCGGC ---TGG---- --------GG A---CAGCCC
 451 CACGCCGGCG GC------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCACCCAC AGT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCCGCAGCAG CCGGGGCGGT AGTGGGGGGC
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AACCGGCCCC TCATTCATTT
 651 TGGCAACGAC TACGAGGACC GTTACTACCG TGAAAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACA GTCAGGCAGC ACACGGTC--
```

```
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATAATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCC---TACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCTCCCGTG ATT------C
1001 TCCTCCTCTC GCTCCTCATC CTCCTGATCG GGGGT----- ----------
1051 ---
```

Panthera_tigris_sumatrae_Sumatran_tiger

```
   1 ATGGTGAAAG GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGTG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGG- --------TA CCCGGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGCGGCGG CTGGGGT--- CAGCCCCACG CCGGCGGCGG
 351 C------TGG GGTCAG---C CCCACGCCGG CGGCGGC--- TGGGGA---C
 401 AGCCCCACGC CGGCGGCGGC ---TGG---- --------GG A---CAGCCC
 451 CACGCCGGCG GC------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCACCCAC AGT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCCGCGGCAG CCGGGGCAGT AGTGGGGGGC
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AACCGGCCCC TCATTCATTT
 651 TGGCAACGAC TACGAGGACC GTTACTACCG TGAAAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAGGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATAATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCC---TACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCTCCCGTG ATT------C
```

1001 TCCTCCTCTC GCTCCTCATC CTCCTGATCG GGGGT----- ----------

1051 ---

Panthera_tigris_altaica_Siberian_tiger

1 ATGGTGAAAG GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC

51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGTG

101 GAGGATGGAA CACTGGGGGG ---AGCCGG- --------TA CCCGGGGCAG

151 ---GGCAGTC CTGGAGGCAA CCGTTACCCA CCCCAG---- ----------

201 ---------- ---------- ---------- ---------- ----------

251 ---------- -GGC------ ---------- ---------- ----------

301 ---------- --GGCGGCGG CTGGGGT--- CAGCCCCACG CCGGCGGCGG

351 C------TGG GGTCAG---C CCCACGCCGG CGGCGGC--- TGGGGA---C

401 AGCCCCACGC CGGCGGCGGC ---TGG---- --------GG A---CAGCCC

451 CACGCCGGCG GC------GG CTGGGGTCAA GGT------- --------GG

501 TGGCACCCAC AGT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA

551 ACATGAAGCA CATGGCAGGA GCCGCGGCAG CCGGGGCAGT AGTGGGGGGC

601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AACCGGCCCC TCATTCATTT

651 TGGCAACGAC TACGAGGACC GTTACTACCG TGAAAACATG TACCGCTACC

701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC

751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAGGCAGC ACACGGTC--

801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA

851 ACTTCACGGA GACCGACATG AAGATAATGG AGCGCGTGGT GGAGCAGATG

901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCC---TACT AC------CA

951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCTCCCGTG ATT------C

1001 TCCTCCTCTC GCTCCTCATC CTCCTGATCG GGGGT----- ----------

1051 ---

Leopardus_wiedii_Margay

```
   1 ATGGTGAAAG GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGTG
 101 GAGGATGGAA CACTGGGGGA ---AGCCGG- --------TA CCCGGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGTGGCGG CTGGGGT--- CAGCCCCACG CCGGCGGCGG
 351 C------TGG GGTCAG---C CCCACGCCGG CGGAGGC--- TGGGGT---C
 401 AGCCCCACGC CGGCGGTGGC ---TGG---- --------GG T---CAGCCC
 451 CACGCCGGCG GC------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCACCCAC AAT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCTGCGGCAG CCGGGGCGGT AGTGGGGGGC
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AGCCGGCCCC TCATTCATTT
 651 TGGCAACGAC TACGAGGACC GTTACTACCG TGAAAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AGCTTTGTGC ACGACTGCGT CAACATCACG GTCAGGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATAATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCCTACTACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCTCCCGTG ATT------C
1001 TCCTCCTCTC GCTCCTCATC CTCCTGATCG GGGGT----- ----------
1051 ---
```

Puma_concolor_Cougar

```
   1 ATGGTGAAAG GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGTG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGG- --------TA CCCGGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTACCCA CCCCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- ---------- ---------- ---------- ----------
 301 ---------- ---------- ----GGC--- ---------- --GGCGGCGG
 351 C------TGG GGTCAG---C CCCACGCCGG CGGAGGC--- TGGGGT---C
 401 AGCCCCACGC CGGCGGCGGC ---TGG---- --------GG A---CAGCCC
 451 CACGCCGGCG GC------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCACCCAC AGT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCCGCGGCAG CCGGGGCGGT AGTGGGGGGC
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AGCCGGCCCC TCATTCATTT
 651 TGGCAACGAC TACGAGGACC GTTACTACCG TGAAAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAGGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATAATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCC---TACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCTCCCGTG ATT------C
1001 TCCTCCTCTC ACTCCTCATC CTCCTGATCG GGGGT----- ----------
1051 ---
```

Acinonyx_jubatus_Cheetah

```
   1 ATGGTGAAAG GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGTG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGG- --------TA CCCAGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGTGGCGG CTGGGGT--- CAGCCCCACG CCGGCGGCGG
 351 C------TGG GGTCAG---C CCCACGCCGG CGGAGGC--- TGGGGT---C
```

```
 401 AGCCCCACGC CGGCGGTGGC ---TGG---- --------GG A---CAGCCC
 451 CACGCCGGCG GC------GG CTGGGGTCAA GGT------- --------GG
 501 CGGCACCCAC AGT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCCGCGGCAG CCGGGGCGGT AGTGGGGGGC
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AGCCGGCCCC TCATTCATTT
 651 TGGCAACGAC TACGAGGACC GTTACTACCG TGAAAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAGGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATAATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCC---TACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCTCCCGTG ATT------C
1001 TCCTCCTCTC CCTCCTCATC CTCCTGATCG GGGGT----- ----------
1051 ---
```

Neovison_vison_American_mink

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGCTC CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC ATTGGCTTCT GCAAGAAG-- -TGGCCAAAG CCT---GGAG
 101 GAGGCTGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGT------ ---------- ---------- ----------
 301 ---------- --GGTGGCGG CTGGGGC--- CAGCCCCAC- --GGGGGTGG
 351 C------TGG GGACAG---C CCCAC---GG GGGTGGC--- TGGGGT---C
 401 AGCCCCAC-- -GGGGGTGGC ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGCG GT------GG CTGGGGTCAA GGT------- --------GG
 501 TGGGAGCCAC GGT---CAGT GGGGCAAGCC CAGTAAGCCC ---AAAACCA
 551 ACATGAAGCA TGTGGCGGGA GCCGCAGCAG CCGGGGCGGT CGTGGGGGGC
```

```
 601 CTGGGCGGCT ACATGCTGGG GAGCGCCATG AGCAGGCCCC TCATTCATTT
 651 TGGCAACGAC TATGAGGACC GCTACTACCG TGAGAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AAGCCGGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTCGTGC ATGACTGCGT CAACATCACG GTCAAGCAGC ACACGGTG--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGCGAGA
 851 ACTTCACGGA GACCGACATG AAGATCATGG AGCGCGTGGT GGAGCAGATG
 901 TGTGTCACCC AGTACCAGCG AGAGTCCGAG GCT---TACT AC------CA
 951 GAAGGGGGCG AGCGCCATCC TCTTCTCGCC CCCTCCCGTG ATC------C
1001 TCCTCATCTC ACTGCTCATT CTCCTGATAG TGGGA----- ----------
1051 ---
```

Mephitis_mephitis_Striped_skunk

```
   1 ATGGTGGGAA GCCACATAGG CGGCTGGATC CTGATTCTCT TTGTGGCCAC
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCC---GGAG
 101 GAGGCTGGAA CAGYGGTGGA ---AGCCGA- --------TA CCCAGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGTGGCGG CTGGGGT--- CAGCCCCAT- --GGTGGCGG
 351 C------TGG GGACAG---C CCCAC---GG GGGCGGA--- TGGGGT---C
 401 AGCCCCAC-- -GGGGGCGGC ---TGG---- --------GG A---CAGCCT
 451 CACGGTGGCG GT------GG CTGGGGTCAA GGG------- --------GG
 501 TGGCAGCCAT GGT---CAGT GGGGCAAGCC CAGTAAGCCC ---AAAACCA
 551 ACATAAAGCA CATGGCGGGA GCCGCGGCAG CCGGGGCAGT AGTGGGGGGC
 601 CTGGGCGGCT ACATGCTGGG GAGCGCCATG AGCAGGCCCC TCATTCATTT
 651 TGGCAATGAC TATGAGGACC GTTACTACCG TGATAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AAGCCGGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACR GTCCGGCAGC ACACGGTC--
```

```
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATCATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGCG AGAGTCCGAG GCT---TACT AC------CA
 951 GAGGGGGGCG AGCGCCATGC TCTTCTCCCC TCCTCCTGTG ATC------C
1001 TCCTCATCTC ACTGCTCATC CTCCTGATCC TGGGA----- ----------
1051 ---
```

Mustela_putorius_European_polecat

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGCTC CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC ATTGGCTTCT GCAAGAAG-- -CGGCCSAAG CCT---GGAG
 101 GAGGCTGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGT------ ---------- ---------- ----------
 301 ---------- --GGTGGCGG CTGGGGC--- CAGCCCCAC- --GGGGGTGG
 351 C------TGG GGMCAG---C CCCAY---GG GGGTGGC--- TGGGGA---C
 401 AGCCCCAC-- -GGGGGYGGC ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGCG GT------GG CTGGGGTCAA GGT------- --------GG
 501 TGGGAGCCAC GGT---CAGT GGGGCAAGCC CAGTAAGCCT ---AAAACCA
 551 ACATRAAGCA TGTGGCGGGW GCCGCAGCAG CCGGGGCGGT TGTGGGGGGC
 601 CTGGGCGGCT ACATGCTGGG GAGCGCCATG AGCAGGCCCC TCATTCATTT
 651 TGGCAACGAC TATGAGGACC GCTACTACCG TGAGAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AAGCCGGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTKGTGC AYGACTGCGT CAACATCACG GTCAAGCAGC ACACGGTG--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGCGAGA
 851 ACTTCACGGA GACCGACATG AAGATCATGG AGCGCGTGGT GGAGCAGATG
 901 TGTGTCACCC AGTACCAGCR AGAGTCCGAG GCT---TACT AC------CA
 951 GAGGGGGGCG AGCGCCATCC TCTTCTCGCC CCCTCCCGTG ATC------C
```

```
1001 TCCTCATCTC GCTGCTCATT CTCCTGATAG TGGGA----- ----------
1051 ---
```

Mustela_erminea_Stoat

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGCTC CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC ATTGGCTTCT GCAAGAAG-- -CGGCCGAAG CCT---GGAG
 101 GAGGCTGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGT------ ---------- ---------- ----------
 301 ---------- --GGTGGCGG CTGGGGC--- CAGCCCCAC- --GGGGGTGG
 351 C------TGG GGCCAG---C CCCAC---GG GGGTGGC--- TGGGGT---C
 401 AGCCCCAC-- -GGGGGCGGC ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGCG GT------GG CTGGGGTCAA GGT------- --------GG
 501 TGGGAGCCAC GGT---CAGT GGGGCAAGCC CAGTAAGCCC ---AAAACCA
 551 ACATGAAGCA TGTGGCGGGA GCCGCAGCAG CCGGGGCGGT TGTGGGGGGC
 601 CTGGGCGGCT ACATGCTGGG GAGCGCCATG AGCAGGCCCC TCATTCATTT
 651 TGGCAACGAC TATGAGGACC GCTACTACCG TGAGAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AAGCCGGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAAGCAGC ACACGGTG--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGCGAGA
 851 ACTTCACGGA GACCGACATG AAGATCATGG AGCGCGTGGT GGAGCAGATG
 901 TGTGTCACCC AGTACCAGCG AGAGTCCGAG GCT---TACT AC------CA
 951 GAGGGGGGCG AGCGCCATCC TCTTCTCGCC CCCTCCCGTG ATC------C
1001 TCCTCATCTC GCTGCTCATT CTCCTGATAG TGGGA----- ----------
1051 ---
```

Otaria_byronia_South_american_sea_lion

```
   1 ATGGTGAAAA GCCACGTCGG CAGCTGGATC CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGAG
 101 GAGGCTGGAA CACCGGGGGG ---AGCCGA- --------TA CCCAGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGTGGCGG CTGGGGT--- CAGCCCCAT- --GGTGGCGG
 351 C------TGG GGACAG---C CCCACGGTGG TGGCGGC--- TGGGGT---C
 401 AGCCCCACGG TGGTGGCGGC ---TGG---- --------GG A---CAGCCC
 451 CACGGTGGTG GT------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCAGCCAC GGT---CAGT GGGGCAAGCC CAATAAGCCC ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCCGCAGCAG CCGGGGCGGT AGTGGGGGGC
 601 CTGGGTGGCT ACATGCTGGG GAGTGCCATG AGCAGACCCC TCATTCATTT
 651 CGGCAACGAC TATGAGGACC GTTACTATCG TGAGAACATG AACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AAGCCGGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTCGTGC ACGACTGCGT CAACATCACG GTCAAGCAGC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATCATGG AGCGCGTAGT GGAGCAGATG
 901 TGCGTCACCC AATACCAGAG AGAGTCCGAG GCT---TACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCGCC CCCGCCTGTG ATC------C
1001 TCCTCATCTC GCTGCTCATT CTCCTGATAG TGGGA----- ----------
1051 ---
```

Phoca_vitulina_Harbor_seal

```
   1 ATGGTGAAAA GCCACATCGG CGGCTGGATC CTGGTTCTCT TCGTGGCCGC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGAG
 101 GAGGCTGGAA CACCGGGGGA ---AGCCGA- --------TA CCCAGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGAGGCGG CTGGGGT--- CAGCCCCAC- --GGTGGYGG
 351 C------TGG GGACAG---C CCCAY---GG TGGCGGC--- TGGGGT---C
 401 AGCCCCAC-- -GGTGGCGGC ---TGG---- --------GG A---CAGCCG
 451 CACGGTGGTG GT------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCGGCCAC GGT---CAGT GGGGCAAGCC CAATAAGCCC ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCCGCGGCAG CCGGGGCGGT AGTGGGGGGC
 601 CTGGGTGGCT ACATGCTGGG GAGTGCCATG AGCAGGCCCC TCATTCATTT
 651 CGGCAAYGAC TATGAGGACC GTTACTATCG TGAGAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AAGCCGGTGG ATCAGTACAG CAGCCAGAAC
 751 AACTTCGTGC ACGATTGCGT CAACATCACG GTCAAGCAGC ACACAGTG--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATCATGG AGCGCGTAGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCT---TACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCGCCTGTG ATC------C
1001 TCCTCATCTC GCTGCTCATT CTCCTGATAG TGGGA----- ----------
1051 ---
```

Ursus_americanus_American_black_bear

```
   1 ATGGTGAAAA GCCACATAGG CGGCTGGATC CTGGTTCTCT TTGTGGCCAC
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGAG
 101 GCGGCTGGAA CACCGGGGGG ---AGCCGA- --------TA CCCAGGGCAG
 151 ---GGCAGTC CCGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGCGGCGG CTGGGGT--- CAGCCCCAC- --GGGGGCGG
 351 C------TGG GGACAG---C CCCAC---GG GGGTGGC--- TGGGGT---C
```

```
 401 AGCCCCAC-- -GGGGGCGGT ---TGG---- --------GG A---CAGCCG
 451 CACGGGGGCG GT------GG CTGGGGTCAA GGC------- --------GG
 501 GGGCGGCCAC GGT---CAGT GGGGCAAGCC CAGTAAGCCC ---AAAACCA
 551 ACATGAAGCA CGTGGCGGGA GCCGCGGCAG CGGGGGCGGT CGTGGGGGGC
 601 CTTGGCGGCT ACATGCTGGG GAGCGCCATG AGCCGGCCCC TCATTCATTT
 651 TGGCAACGAC TATGAGGACC GTTACTACCG TGAGAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AAGCCGGTGG ATCAGTACAG CAACCAGAAC
 751 AGCTTCGTGC ACGACTGCGT CAACATCACG GTCAAGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATA AAGATCATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAG AGAGGCCGAG GCT---TACT AC------CA
 951 AAGGGGGGCG AGCGCCATCC TCTTCTCCCC GCCCCCGGTG ATC------C
1001 TCCTCATCTC CCTGCTCATT CTCCTGATCG TTGGA----- ----------
1051 ---
```

Ursus_arctos_Brown_bear

```
   1 ATGGTGAAAA GCCACATAGG CGGCTGGATC CTGGTTCTCT TTGTGGCCAC
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGAG
 101 GCGGCTGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGGCAG
 151 ---GGCAGTC CCGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGCGGCGG CTGGGGT--- CAGCCCCAC- --GGGGGCGG
 351 C------TGG GGACAG---C CCCAC---GG GGGTGGC--- TGGGGT---C
 401 AGCCCCAC-- -GGGGGCGGY ---TGG---- --------GG A---CAGCCS
 451 CACGGGGGCG GT------GG CTGGGGTCAA GGC------- --------GG
 501 GGGCGGCCAC GGT---CAGT GGGGCAAGCC CAGTAAGCCC ---AAAACCA
 551 ACATGAAGCA CGTGGCGGGA GCCGCGGCAG CGGGGGCGGT CGTGGGGGGC
```

```
 601 CTCGGCGGCT ACATGCTGGG GAGCGCCATG AGCCGGCCCC TCATTCATTT
 651 TGGCAACGAC TATGAGGACC GTTACTACCG TGAGAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AAGCCGGTGG ATCAGTACAG CAACCAGAAC
 751 AGCTTCGTGC ACGACTGCGT CAACATCACG GTCAAGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATA AAGATCATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAG AGAGGCCGAG GCT---TACT AC------CA
 951 AAGGGGGGCG AGCGCCATCC TCTTCTCCCC GCCSCCGGTG ATC------C
1001 TCCTCATCTC GCTGCTCATT CTCCTGATCG TTGGA----- ----------
1051 ---
```

Canis_lupus_Gray_wolf

```
   1 ATGGTGAAAA GCCACATAGG CGGCTGGATC CTGCTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT------G
 101 GAGGATGGAA CACAGGGGGT GGGAGCCGA- --------TA CCCAGGCCAG
 151 ---GGTAGCC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGTGGTGG CTGGGGT--- CAGCCCCAT- --GGTGGYGG
 351 C------TGG GGTCAG---C CTCAT---GG TGGCGGC--- TGGGGT---C
 401 AGCCCCAC-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GT------GG TTGGGGTCAA GGT------- --------GG
 501 TGGCAGCCAC RGT---CAGT GGGGCAAGCC CAATAAGCCC ---AAAACCA
 551 ACATGAAGCA CGTGGCAGGA GCCGCAGCAG CCGGGGCGGT AGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG GAGTGCCATG AGCAGGCCAC TCATTCATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAGAACATG TACCGCTACC
 701 CCGACCAA-- -GTATACTAC CGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC GTGACTGCGT CAACATCACT GTCAAGCAGC ACACAGTG--
```

```
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACAGA GACCGACATG AAGATCATGG AGCGTGTGGT GGAGCAGATG
 901 TGTGTCACCC AGTACCAGAA GGAGTCCGAG GCT---TACT AC------CA
 951 AAGAGGGGCA AGCGCCATCC TCTTCTCCCC GCCGCCYGTG ATC------C
1001 TCCTCATCTC GCTGCTCATT CTCTTGATAG TGGGA----- ----------
1051 ---
```

Canis_latrans_Coyote

```
   1 ATGGTGAAAA GCCACATAGG CGGCTGGATC CTGCTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT------G
 101 GAGGATGGAA CACAGGGGGT GGGAGCCGA- --------TA CCCAGGCCAG
 151 ---GGTAGCC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGTGGTGG CTGGGGT--- CAGCCCCAT- --GGTGGCGG
 351 C------TGG GGTCAG---C CTCAT---GG TGGCGGC--- TGGGGT---C
 401 AGCCCCAC-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GT------GG TTGGGGTCAA GGT------- --------GG
 501 TGGCAGCCAC RGT---CAGT GGGGCAAGCC CAATAAGCCC ---AAAACCA
 551 ACATGAAGCA CGTGGCAGGA GCCGCAGCAG CCGGGGCGGT AGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG GAGTGCCATG AGCAGGCCAC TCATTCATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAGAACATG TACCGCTACC
 701 CCGACCAA-- -GTATACTAC CGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC GTGACTGCGT CAACATCACT GTCAAGCAGC ACACAGTG--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACAGA GACCGACATG AAGATCATGG AGCGTGTGGT GGAGCAGATG
 901 TGTGTCACCC AGTACCAGAA GGAGTCCGAG GCT---TACT AC------CA
 951 AAGAGGGGCA AGCGCCATCC TCTTCTCCCC GCCGCCCGTG ATC------C
```

```
1001 TCCTCATCTC GCTGCTCATT CTCTTGATAG TGGGA----- ----------
1051 ---
```

Chrysocyon_brachyurus_Maned_wolf

```
   1 ATGGTGAAAA GCCACATAGG CGGCTGGATC CTGCTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT------G
 101 GAGGATGGAA TACAGGGGGT GGGAGCCGA- --------TA CCCAGGCCAG
 151 ---GGTAGCC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGTGGTGG CTGGGGT--- CAGCCTCAC- --GGTGGCGG
 351 C------TGG GGTCAG---C CTCAC---GG TGGCGGC--- TGGGGT---C
 401 AGCCCCAC-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CACGGTGGTG GT------GG TTGGGGTCAA GGT------- --------GG
 501 TGGCAGCCAC AGT---CAGT GGGGCAAGCC CAATAAGCCC ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCCGCAGCAG CCGGGGCGGT AGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG GAGTGCCATG AGCAGGCCAC TCATTCATTT
 651 TGGCAATGAT TATGAGGACC GTTACTATCG TGAGAACATG TACCGCTACC
 701 CCGACCAA-- -GTATACTAC CGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTAC GTGACTGCGT CAACATCACT GTCAAGCAGC ACACAGTG--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACAGA GACCGACATG AAGATCATGG AGCGTGTGGT GGAGCAGATG
 901 TGTGTCACCC AGTACCAGAA GGAGTCCGAG GCT---TACT AC------CA
 951 AAGAGGGGCA AGCGCCATCC TCTTCTCTCC GCCGCCCGTG ATC------C
1001 TCCTCATCTC GCTGCTCATT CTCCTGATAG TGGGA----- ----------
1051 ---
```

Speothos_venaticus_Bush_dog

```
   1 ATGGTGAAAA GCCACATAGG CGGCTGGATC CTGCTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT------G
 101 GAGGATGGAA TACAGGGGGT GGGAGCCGA- --------TA CCCAGGCCAG
 151 ---GGTAGCC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGTGGTGG CTGGGGT--- CAGCCCCAT- --GGTGGCGG
 351 C------TGG GGTCAG---C CTCAC---GG TGGCGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CACGGTGGTG GT------GG TTGGGGTCAA GGT------- --------GG
 501 TGGCAGCCAC AGT---CAGT GGGGCAAGCC CAATAAGCCC ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCCGCAGCAG CCGGGGCGGT AGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG GAGTGCCATG AGCAGGCCAC TCATTCATTT
 651 TGGCAATGAT TATGAGGACC GTTACTATCG TGAGAACATG TACCGCTACC
 701 CCGACCAA-- -GTATACTAC CGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC GTGACTGCGT CAACATCACT GTCAAGCAGC ACACAGTG--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACAGA GACCGACATG AAGATCATGG AGCGTGTGGT GGAGCAGATG
 901 TGTGTCACCC AGTACCAGAA GGAGTCCGAG GCT---TACT AC------CA
 951 AAGAGGGGCA AGCGCCATCC TCTTCTCTCC GCCGCCCATG ATC------C
1001 TCCTCATCTC GCTGCTCATT CTCTTGATAG TGGGA----- ----------
1051 ---
```

Vulpes_lagopus_Arctic_fox

```
   1 ATGGTGAAAA GCCACATAGG CGGCTGGATC CTGCTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT------G
 101 GAGGATGGAA CACAGGGGGT GGGAGCCGA- --------TA CCCAGGCCAG
 151 ---GGTAGCC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGTGGTGG GTGGGGT--- CAGCCCCAT- --GGTGGCGG
 351 C------TGG GGTCAG---C CTCAC---GG TGGCGGC--- TGGGGA---C
 401 AGCCCCAC-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CACGGTGGTG GT------GG TTGGGGTCAA GGT------- --------GG
 501 TGGCAGCCAC GGT---CAGT GGGGGAAGCC CAATAAGCCC ---AAAACCA
 551 ACATGAAGCA CGTGGCAGGA GCCGCAGCAG CCGGGGCGGT AGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG GAGTGCCATG AGCAGGCCAC TCATTCATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAGAACATG TACCGCTACC
 701 CCGACCAA-- -GTATACTAC CGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC GTGACTGCGT CAACATCACT GTCAAGCAGC ACACAGTG--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACAGA GACCGACATG AAGATCATGG AGCGTGTGGT GGAGCAGATG
 901 TGTGTCACCC AGTACCAGAA GGAGTCCGAG GCT---TACT AC------CA
 951 AAGAGGGGCA AGCGCCATCC TCTTCTCCCC ACCGCCCGTG ATC------C
1001 TCCTCATCTC GCTGCTCATT CTCTTGATAG TGGGA----- ----------
1051 ---
```

Vulpes_vulpes_Red_Fox

```
   1 ATGGTGAAAA GCCACATAGG CGGCTGGATC CTGCTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT------G
 101 GAGGATGGAA CACAGGGGGT GGGAGCCGA- --------TA CCCAGGCCAG
 151 ---GGTAGCC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGTGGTGG GTGGGGT--- CAGCCCCAT- --GGTGGCGG
 351 C------TGG GGTCAG---C CTCAC---GG TGGCGGC--- TGGGGA---C
```

```
 401 AGCCCCAC-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CACGGTGGTG GT------GG TTGGGGTCAA GGT------- --------GG
 501 TGGCAGCCAC GGT---CAGT GGGGSAAGCC CAATAAGCCC ---AAAACCA
 551 ACATGAAGCA CGTGGCAGGA GCCGCAGCAG CCGGGGCGGT AGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG GAGTGCCATG AGCAGGCCAC TCATTCATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAGAACATG TACCGCTACC
 701 CCGACCAA-- -GTATACTAC CGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC GTGACTGCGT CAACATCACT GTCAAGCAGC ACACAGTG--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACAGA GACCGACATG AAGATCATGG AGCGTGTGGT GGAGCAGATG
 901 TGTGTCACCC AGTACCAGAA GGAGTCCGAG GCT---TACT AC------CA
 951 AAGAGGGGCA AGCGCCATCC TCTTCTCCCC RCCGCCCGTG ATC------C
1001 TCCTCATCTC GCTGCTCATT CTCYTGATAG TGGGA----- ----------
1051 ---;
```

Appendix B

Small *Prnp* Alignment

Complete Sequences Used for PAML Analysis

Macaca_assamensis_Assam_macaque1

```
   1 ------ATGG CGAACCTTGG CTGCTGGATG CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC CTGGGCCTCT GCAAGAAG-- -CGCCCAAAG CCT------G
 101 GAGGATGGAA CACTGGAGGC ---AGCCGA- --------TA CCCGGGGCAG
 151 ---GGCAGCC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGT------ ---------- ---------- ----------
 301 ---------- --GGTGGTGG CTGGGGG--- CAGCCTCAT- --GGTGGTGG
 351 C------TGG GGGCAA---C CCCAT---GG TGGCGGC--- TGGGGA---C
 401 AGCCTCAT-- -GGTGGCGGC ---TGG---- --------GG A---CAGCCT
 451 CATGGTGGTG GC-------- -TGGGGTCAA GGA------- --------GG
 501 TGGCACCCAC AAT---CAGT GGCACAAGCC CAGTAAGCCA ---AAAACCA
 551 GCATGAAGCA CATGGCTGGT GCTGCAGCAG CTGGGGCAGT GGTGGGGGGC
 601 CTTGGCGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCCC TCATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCTGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAATATCACA ATTAAGCAGC ACACAGTC--
 801 -ACCACCACC ACCAAA---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA GACCGACGTT AAGATGATGG AGCGCGTGGT TGAGCAGATG
 901 TGTATCACCC AGTACGAGAA GGAATCACAG GCC---TATT AT------CA
 951 GAGAGGATCG AGCATGGTCC TGTTCTCCTC CCCGCCTGTG ATC------C
1001 TCCTGATTTC TTTCCTCATC TTCCTGATAG TGGGA----- ----------
1051 ---
```

Macaca_assamensis_Assam_macaque2

```
   1 ------ATGG CGAACCTTGG CTGCTGGATG CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC CTGGGCCTCT GCAAGAAG-- -CGCCCAAAG CCT------G
 101 GAGGATGGAA CACTGGAGGC ---AGCCGA- --------TA CCCGGGGCAG
 151 ---GGCAGCC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGT------ ---------- ---------- ----------
 301 ---------- --GGTGGTGG CTGGGG---- CAGCCTCAT- --GGTGGTGG
 351 C------TGG GGGCAA---C CCCAT---GG TGGCGGC--- TGGGGA---C
 401 AGCCTCAT-- -GGTGGCGGC ---TGG---- --------GG A---CAGCCT
 451 CATGGTGGTG GC-------- -TGGGGTCAA GGA------- --------GG
 501 TGGCACCCAC AAT---CAGT GGCACAAGCC CAGTAAGCCA ---AAAACCA
 551 GCATGAAGCA CATGGCTGGT GCTGCAGCAG CTGGGGCAGT GGTGGGGGGC
 601 CTTGGCGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCCC TCATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCTGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAATATCACA ATTAAGCAGC ACACAGTC--
 801 -ACCACCACC ACCAAA---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA GACCGACGTT AAGATGATGG AGCGCGTGGT TGAGCAGATG
 901 TGTATCACCC AGTACGAGAA GGAATCACAG GCC---TATT AT------CA
 951 GAGAGGATCG AGCATGGTCC TGTTCTCCTC CCCGCCTGTG ATC------C
1001 TCCTGATTTC TTTCCTCATC TTCCTGATAG TGGGA----- ----------
1051 ---
```

Macaca_mulatta_Rhesus_macaque1

```
   1 ------AUGG CGAACCUUGG CUGCUGGAUG CUGGUUCUCU UUGUGGCCAC
  51 AUGGAGUGAC CUGGGCCUCU GCAAGAAG-- -CGCCCAAAG CCU------G
 101 GAGGAUGGAA CACUGGAGGC ---AGCCGA- --------UA CCCGGGGCAG
```

```
 151 ---GGCAGCC CUGGAGGCAA CCGCUACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGU------ ---------- ---------- ----------
 301 ---------- --GGUGGUGG CUGGGGG--- CAGCCUCAU- --GGUGGUGG
 351 C------UGG GGGCAA---C CCCAU---GG UGGCGGC--- UGGGGA---C
 401 AGCCUCAU-- -GGUGGCGGC ---UGG---- --------GG A---CAGCCU
 451 CAUGGUGGUG GC-------- -UGGGGUCAA GGA------- --------GG
 501 UGGCACCCAC AAU---CAGU GGCACAAGCC CAGUAAGCCA ---AAAACCA
 551 GCAUGAAGCA CAUGGCUGGU GCUGCAGCAG CUGGGGCAGU GGUGGGGGGC
 601 CUUGGCGGCU ACAUGCUGGG AAGUGCCAUG AGCAGGCCCC UCAUACAUUU
 651 UGGCAAUGAC UAUGAGGACC GUUACUAUCG UGAAAACAUG UACCGUUACC
 701 CCAACCAA-- -GUGUACUAC AGGCCUGUGG AUCAGUACAG CAACCAGAAC
 751 AACUUUGUGC ACGACUGCGU CAAUAUCACG AUUAAGCAGC ACACAGUC--
 801 -ACCACCACC ACCAAA---- ---------- ---------- ---GGGGAGA
 851 ACUUCACCGA GACCGACGUU AAGAUGAUGG AGCGCGUGGU UGAGCAGAUG
 901 UGUAUCACCC AGUACGAGAA GGAAUCACAG GCC---UAUU AU------CA
 951 GAGAGGAUCG AGCAUGGUCC UCUUCUCCUC CCCGCCUGUG AUC------C
1001 UCCUGAUUUC UUUCCUCAUC UUCCUGAUAG UGGGA----- ----------
1051 ---
```

Macaca_mulatta_Rhesus_macaque2

```
   1 ------AUGG CGAACCUUGG CUGCUGGAUG CUGGUUCUCU UUGUGGCCAC
  51 AUGGAGUGAC CUGGGCCUCU GCAAGAAG-- -CGCCCAAAG CCU------G
 101 GAGGAUGGAA CACUGGAGGC ---AGCCGA- --------UA CCCGGGGCAG
 151 ---GGCAGCC CUGGAGGCAA CCGCUACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGU------ ---------- ---------- ----------
 301 ---------- --GGUGGUGG CUGGGGG--- CAGCCUCAU- --GGUGGUGG
```

```
 351 C------UGG GGGCAA---C CCCAU---GG UGGCGGC--- UGGGGA---C
 401 AGCCUCAU-- -GGUGGCGGC ---UGG---- --------GG A---CAGCCU
 451 CAUGGUGGUG GC-------- -UGGGGUCAA GGA------- --------GG
 501 UGGCACCCAC AAU---CAGU GGCACAAGCC CAGUAAGCCA ---AAAACCA
 551 GCAUGAAGCA CAUGGCUGGU GCUGCAGCAG CUGGGGCAGU GGUGGGGGGC
 601 CUUGGCGGCU ACAUGCUGGG AAGUGCCAUG AGCAGGCCCC UCAUACAUUU
 651 UGGCAAUGAC UAUGAGGACC GUUACUAUCG UGAAAACAUG UACCGUUACC
 701 CCAACCAA-- -GUGUACUAC AGGCCUGUGG AUCAGUACAG CAACCAGAAC
 751 AACUUUGUGC ACGACUGCGU CAAUAUCACG AUUAAGCAGC ACACAGUC--
 801 -ACCACCACC ACCAAA---- ---------- ---------- ---GGGGAGA
 851 ACUUCACCGA GACCGACGUU AAGAUGAUGG AGCGCGUGGU UGAGCAGAUG
 901 UGUAUCACCC AGUACGAGAA GGAAUCACAG GCC---UAUU AU------CA
 951 GAGAGGAUCG AGCAUGGUCC UCUUCUCCUC CCCGCCUGUG AUC------C
1001 UCCUGAUUUC UUUCCUCAUC UUCCUGAUAG UGGGA----- ----------
1051 ---
```

Pongo_pygmaeus_Bornean_orangutan1

```
   1 ------AUGG CGAACCUUGG CUGCUGGAUG CUGGUUCUCU UUGUGGCCAC
  51 AUGGAGUAAC CUGGGCCUCU GCAAGAAG-- -CGCCCAAAG CCU------G
 101 GAGGAUGGAA CACUGGGGGC ---AGCCGA- --------UA CCCGGGGCAG
 151 ---GGCAGCC CUGGAGGCAA CCGCUACCCA CCUCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGUGGUGG CUGGGGG--- CAGCCUCAU- --GGUGGUGG
 351 C------UGG GGGCAG---C CUCAU---GG UGGUGGC--- UGGGGG---C
 401 AGCCCCAU-- -GGUGGUGGC ---UGG---- --------GG G---CAGCCU
 451 CAUGGUGGUG GC-------- -UGGGGUCAA GGA------- --------GG
 501 UGGUACCCAC AGU---CAGU GGAACAAGCC CAGUAAGCCA ---AAAACCA
```

```
 551 ACAUGAAGCA CAUGGCUGGU GCUGCAGCAG CUGGGGCAGU GGUGGGGGGC
 601 CUUGGUGGCU ACAUGCUGGG AAGUGCCAUG AGCAGGCCCA UCAUACAUUU
 651 UGGCAAUGAC UAUGAGGACC GUUACUAUCG UGAAAACAUG UACCGUUACC
 701 CCAACCAA-- -GUGUACUAC AGGCCCGUGG AUCAGUACAG CAACCAGAAC
 751 AACUUUGUGC ACGACUGCGU CAAUAUCACA AUCAAGCAGC ACACAGUC--
 801 -ACCACAACC ACCAAA---- ---------- ---------- ---GGGGAGA
 851 ACUUCACCGA GACCGACGUU AAGAUGAUGG AGCGUGUGGU UGAGCAGAUG
 901 UGUAUCACGC AGUACGAGAG GGAAUCUCAG GCC---UAUU AC------CA
 951 GAGAGGAUCG AGCAUGGUCC UCUUCUCCUC CCCACCUGUG AUC------C
1001 UCCUGAUCUC UUUCCUCAUC UUCCUAAUAG UGGGA----- ----------
1051 ---
```

Pongo_pygmaeus_Bornean_orangutan2

```
   1 ------AUGG CGAACCUUGG CUGCUGGAUG CUGGUUCUCU UUGUGGCCAC
  51 AUGGAGUAAC CUGGGCCUCU GCAAGAAG-- -CGCCCAAAG CCU------G
 101 GAGGAUGGAA CACUGGGGGC ---AGCCGA- --------UA CCCGGGGCAG
 151 ---GGCAGCC CUGGAGGCAA CCGCUACCCA CCUCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGUGGUGG CUGGGGG--- CAGCCUCAU- --GGUGGUGG
 351 C------UGG GGGCAG---C CUCAU---GG UGGUGGC--- UGGGGG---C
 401 AGCCCCAU-- -GGUGGUGGC ---UGG---- --------GG G---CAGCCU
 451 CAUGGUGGUG GC-------- -UGGGGUCAA GGA------- --------GG
 501 UGGUACCCAC AGU---CAGU GGAACAAGCC CAGUAAGCCA ---AAAACCA
 551 ACAUGAAGCA CAUGGCUGGU GCUGCAGCAG CUGGGGCAGU GGUGGGGGGC
 601 CUUGGUGGCU ACAUGCUGGG AAGUGCCAUG AGCAGGCCCA UCAUACAUUU
 651 UGGCAAUGAC UAUGAGGACC GUUACUAUCG UGAAAACAUG UACCGUUACC
 701 CCAACCAA-- -GUGUACUAC AGGCCCGUGG AUCAGUACAG CAACCAGAAC
```

```
 751 AACUUUGUGC ACGACUGCGU CAAUAUCACA AUCAAGCAGC ACACAGUC--
 801 -ACCACAACC ACCAAA---- ---------- ---------- ---GGGGAGA
 851 ACUUCACCGA GACCGACGUU AAGAUGAUGG AGCGUGUGGU UGAGCAGAUG
 901 UGUAUCACGC AGUACGAGAG GGAAUCUCAG GCC---UAUU AC------CA
 951 GAGAGGAUCG AGCAUGGUCC UCUUCUCCUC CCCACCUGUG AUC------C
1001 UCCUGAUCUC UUUCCUCAUC UUCCUAAUAG UGGGA----- ----------
1051 ---
```

Homo_sapiens_Human1

```
   1 ------AUGG CGAACCUUGG CUACUGGAUG CUGGUUCUCU UUGUGGCCAC
  51 AUGGAGUGAC CUGGGCCUCU GCAAGAAG-- -CGCCCGAAG CCU------G
 101 GAGGAUGGAA CACUGGGGGC ---AGCCGA- --------UA CCCGGGGCAG
 151 ---GGCAGCC CUGGAGGCAA CCGCUACCCA CCUCAGGGCG GUGGUGGCUG
 201 GGGGCAGCCU CAUGGUGGUG GCUGGGGGCA GCCUCAUGGU GGUGGCUGGG
 251 GGCAGCCCCA UGGU------ ---------- ---------- -GGUGGCUGG
 301 GGGCAGCCUC AUGGUGGUGG CUGGGGA--- CAGCCUCAU- --GGUGGUGG
 351 C------UGG GGGCAG---C CUCAU---GG UGGUGGC--- UGGGGG---C
 401 AGCCCCAU-- -GGUGGUGGC ---UGG---- --------GG A---CAGCCU
 451 CAUGGUGGUG GC-------- -UGGGGUCAA GGA------- --------GG
 501 UGGCACCCAC AGU---CAGC GGAACAAGCC GAGUAAGCCA ---AAAACCA
 551 ACAUGAAGCA CAUGGCUGGU GCAGCAGCAG CUGGGGCAGU GGUGGGGGGC
 601 CUUGGCGGCU ACAUGCUGGG AAGUGCCAUG AGCAGGCCCA UCAUACAUUU
 651 CGGCAGUGAC UAUGAGGACC GCUACUAUCG UGAAAACAUG CACCGUUACC
 701 CCAACCAA-- -GUGUACUAC AGGCCCAUGG AUGAGCACAG CAACCAGAAC
 751 AACUUUGUGC ACGACUGCGU CAAUAUCACA AUCAAGCAGC ACACGGUC--
 801 -ACCACAACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACUUCACCGA GACCGACGUU AAGAUGAUGG AGCGCGUGGU UGAGCAGAUG
 901 UGUAUCACCC AGUACGAGAG GGAAUCUCAG GCC---UAUU AC------AA
```

```
 951 GAGAGGAUCG AGCAUGGUCC UCUUCUCCUC UCCACCUGUG AUC------C
1001 UCCUGAUCUC UUUCCUCAUC UUCCUGAUAG UGGGA----- ----------
1051 ---
```

Homo_sapiens_Human2

```
   1 ------AUGG CGAACCUUGG CUGCUGGAUG CUGGUUCUCU UUGUGGCCAC
  51 AUGGAGUGAC CUGGGCCUCU GCAAGAAG-- -CGCCCGAAG CCU------G
 101 GAGGAUGGAA CACUGGGGGC ---AGCCGA- --------UA CCCGGGGCAG
 151 ---GGCAGCC CUGGAGGCAA CCGCUACCCA CCUCAGGGCG GUGGUGGCUG
 201 GGGGCAGCCU CAUGGUGGUG GCUGGGGGCA GCCUCAUGGU GGUGGCUGGG
 251 GGCAGCCCCA UGGU------ ---------- ---------- -GGUGGCUGG
 301 GGGCAGCCUC AUGGUGGUGG CUGGGGG--- CAGCCUCAU- --GGUGGUGG
 351 C------UGG GGGCAG---C CUCAU---GG UGGUGGC--- UGGGGG---C
 401 AGCCCCAU-- -GGUGGUGGC ---UGG---- --------GG A---CAGCCU
 451 CAUGGUGGUG GC-------- -UGGGGUCAA GGA------- --------GG
 501 UGGCACCCAC AGU---CAGT GGAACAAGCC GAGUAAGCCA ---AAAACCA
 551 ACAUGAAGCA CAUGGCUGGU GCTGCAGCGG CUGGGGCAGU GGUGGGGGGC
 601 CUUGGCGGCU ACGUGCUGGG AAGUGCCAUG AGCAGGCCCA UCAUACAUUU
 651 CGGCAGUGAC UAUGAGGACT GTUACUAUCG UGAAAACAUG CACCGUUACC
 701 CCAACCAA-- -GUGUACUAC AGGCCCAUGG AUGAGTACAG CAACCAGAAC
 751 AACUUUGUGC ACGACUGCGU CAAUAUCACA AUCAAGCAGC GCACGGUC--
 801 -ACCACAACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACUUCACCGA GACCGACGUU AAGAUGAUGG AGCGCGUGGU UGAGCAGAUG
 901 UGUAUCACCC AGUACGAGAG GGAAUCUCAG GCC---UAUU AC------CA
 951 GAGAGGAUCG AGCAUGGUCC UCUUCUCCUC UCCACCUGUG AUC------C
1001 UCCUGAUCUC UUUCCUCAUC UUCCUGAUCG UGGGA----- ----------
1051 ---
```

Pan_troglodytes_Common_chimpanzee1

```
   1 ------AUGG CAAACCUUGG CUGCUGGAUG CUAGUUCUCU UUGUGGCCAC
  51 AUGGAGUGAC CUGGGCCUCU GCAAGAAG-- -CGCCCGAAG CCU------G
 101 GAGGAUGGAA CACUGGGGGC ---AGCCGA- --------UA CCCGGGGCAG
 151 ---GGCAGCC CUGGAGGCAA CCGCUACCCA CCUCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGUGGUGG CUGGGGG--- CAGCCUCAU- --GGUGGUGG
 351 C------UGG GGGCAG---C CUCAU---GG UGGUGGC--- UGGGGG---C
 401 AGCCCCAU-- -GGUGGUGGC ---UGG---- --------GG A---CAGCCU
 451 CAUGGUGGUG GC-------- -UGGGGUCAA GGA------- --------GG
 501 UGGCACCCAC AGU---CAGU GGAACAAGCC GAGUAAGCCA ---AAAACCA
 551 ACAUGAAGCA CAUGGCUGGU GCUGCAGCAG CUGGGGCAGU GGUGGGGGGC
 601 CUUGGCGGCU ACAUGCUGGG AAGUGCCAUG AGCAGGCCCA UCAUACAUUU
 651 UGGCAGUGAC UAUGAGGACC GUUACUAUCG UGAAAACAUG CACCGUUACC
 701 CCAACCAA-- -GUGUACUAC AGGCCCAUGG AUCAGUACAG CAGCCAGAAC
 751 AACUUUGUGC ACGACUGCGU CAAUAUCACG AUCAAGCAGC ACACGGUC--
 801 -ACCACAACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACUUCACCGA GACCGACGUU AAGAUGAUGG AGCGCGUGGU UGAGCAGAUG
 901 UGUAUCACCC AGUACGAGAG GGAAUCUCAG GCC---UAUU AC------CA
 951 GAGAGGAUCG AGCAUGGUCC UCUUCUCCUC UCCACCUGUG AUC------C
1001 UCCUGAUCUC UUUCCUCAUC UUCCUGAUAG UGGGA----- ----------
1051 ---
```

Pan_troglodytes_Common_chimpanzee2

```
   1 ------AUGG CAAACCUUGG CUGCUGGAUG CUAGUUCUCU UUGUGGCCAC
  51 AUGGAGUGAC CUGGGCCUCU GCAAGAAG-- -CGCCCGAAG CCU------G
 101 GAGGAUGGAA CACUGGGGGC ---AGCCGA- --------UA CCCGGGGCAG
 151 ---GGCAGCC CUGGAGGCAA CCGCUACCCA CCUCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGUGGUGG CUGGGGG--- CAGCCUCAU- --GGUGGUGG
 351 C------UGG GGGCAG---C CUCAU---GG UGGUGGC--- UGGGGG---C
 401 AGCCCCAU-- -GGUGGUGGC ---UGG---- --------GG A---CAGCCU
 451 CAUGGUGGUG GC-------- -UGGGGUCAA GGA------- --------GG
 501 UGGCACCCAC AGU---CAGU GGAACAAGCC GAGUAAGCCA ---AAAACCA
 551 ACAUGAAGCA CAUGGCUGGU GCUGCAGCAG CUGGGGCAGU GGUGGGGGGC
 601 CUUGGCGGCU ACAUGCUGGG AAGUGCCAUG AGCAGGCCCA UCAUACAUUU
 651 UGGCAGUGAC UAUGAGGACC GUUACUAUCG UGAAAACAUG CACCGUUACC
 701 CCAACCAA-- -GUGUACUAC AGGCCCAUGG AUCAGUACAG CAGCCAGAAC
 751 AACUUUGUGC ACGACUGCGU CAAUAUCACG AUCAAGCAGC ACACGGUC--
 801 -ACCACAACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACUUCACCGA GACCGACGUU AAGAUGAUGG AGCGCGUGGU UGAGCAGAUG
 901 UGUAUCACCC AGUACGAGAG GGAAUCUCAG GCC---UAUU AC------CA
 951 GAGAGGAUCG AGCAUGGUCC UCUUCUCCUC UCCACCUGUG AUC------C
1001 UCCUGAUCUC UUUCCUCAUC UUCCUGAUAG UGGGA----- ----------
1051 ---
```

Gorilla_gorilla_Western_gorilla1

```
   1 ------ATGG CGAACCTTGG CTACTGGATG CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC CTGGGCCTCT GCAAGAAG-- -CGCCCGAAG CCT------G
 101 GAGGATGGAA CACTGGGGGC ---AGCCGA- --------TA CCCGGGGCAG
 151 ---GGCAGCC CTGGAGGCAA CCGCTACCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGTGGTGG CTGGGGG--- CAGCCTCAT- --GGTGGTGG
 351 C------TGG GGGCAG---C CTCAT---GG TGGTGGC--- TGGGGG---C
```

```
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCT
 451 CATGGTGGTG GC-------- -TGGGGTCAA GGA------- --------GG
 501 TGGCACCCAC AGT---CAGT GGAACAAGCC GAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA CATGGCTGGT GCTGCAGCAG CTGGGGCAGT GGTGGGGGGC
 601 CTTGGCGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCCA TCATACATTT
 651 TGGCAGTGAC TATGAGGACC GTTACTATCG TGAAAACATG CACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCCATGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAATATCACA ATCAAGCAGC ACACGGTC--
 801 -ACCACAACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA GACCGACGTT AAGATGATGG AGCGCGTGGT TGAGCAGATG
 901 TGTATCACCC AGTACGAGAG GGAATCTCAG GCC---TATT AC------CA
 951 GAGAGGATCG AGCATGGTCC TCTTCTCCTC TCCACCTGTG ATC------C
1001 TCCTGATCTC TTTCCTCATC TTCCTGATAG TGGGA----- ----------
1051 ---
```

Gorilla_gorilla_Western_gorilla2

```
   1 ------ATGG CGAACCTTGG CTGCTGGATG CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC CTGGGCCTCT GCAAGAAG-- -CGCCCGAAG CCT------G
 101 GAGGATGGAA CACTGGGGGC ---AGCCGA- --------TA CCCGGGGCAG
 151 ---GGCAGCC CTGGAGGCAA CCGCTACCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGTGGTGG CTGGGGG--- CAGCCTCAT- --GGTGGTGG
 351 C------TGG GGGCAG---C CTCAT---GG TGGTGGC--- TGGGGG---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCT
 451 CATGGTGGTG GC-------- -TGGGGTCAA GGA------- --------GG
 501 TGGCACCCAC AGT---CAGT GGAACAAGCC GAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA CATGGCTGGT GCTGCAGCAG CTGGGGCAGT GGTGGGGGGC
```

```
 601 CTTGGCGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCCA TCATACATTT
 651 TGGCAGTGAC TATGAGGACC GTTACTATCG TGAAAACATG CACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCCATGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAATATCACA ATCAAGCAGC ACACGGTC--
 801 -ACCACAACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA GACCGACGTT AAGATGATGG AGCGCGTGGT TGAGCAGATG
 901 TGTATCACCC AGTACGAGAG GGAATCTCAG GCC---TATT AC------CA
 951 GAGAGGATCG AGCATGGTCC TCTTCTCCTC TCCACCTGTG ATC------C
1001 TCCTGATCTC TTTCCTCATC TTCCTGATAG TGGGA----- ----------
1051 ---
```

Ovis_aries_Domestic_sheep1

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGCG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTAGCCAC AGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGACCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
```

```
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATAATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGGGGGGCA AGTGTGATCC TCTTTTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Ovis_aries_Domestic_sheep2

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGCG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTAGCCAC AGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGACCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATAATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGGGGGGCA AGTGTGATCC TCTTTTCTTC CCCTCCTGTG ATC------C
```

```
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Ovis_canadensis_Bighorn_sheep1

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGCG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAACCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTAGCCAC AGT---CAGC GGAATAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATCT
 651 TGGCAATGAC TATGAGGACC GTTACTATCA TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGACCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATAATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGGGGGGCA AGTGTGATCC TCTTTTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Ovis_canadensis_Bighorn_sheep2

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGCG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCTGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTAGCCAC AGT---CAGT GGAATAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG GGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGACCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CGACATCACA GTCAATCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATAATGG GGCGAGTGGT GGGGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGGGGGGCA TGTGTGATCC TCTTTTCTTC CCCTCCTGTG ATT------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Capra_hircus_Domestic_goat1

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGCG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTAGCCAC AGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCAGGG AAGTGCCATA AGCAGGCCTC TTACACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCV TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGACCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATAATGG AGCAAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACAAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGGGGGGCA AGTGTGATCC TCTTTTCTCC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Capra_hircus_Domestic_goat2

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGCG
 101 GAGGATGGAA CACTGTGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
```

```
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTAGCCAC AGT---CGGT GGAACAAGCC CCGTAAGCCA ---AAACCCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGTAGGCCTC TTATGCGTTT
 651 TGGCAATGAC TATGAGGACC GTTACTATGV TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGACCAGTGG ATCGGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCCCCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACTGA AACTGACATC AAGATAATGG AGGGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 ACGGGGGGCA AGTGTGATCC TGTTTTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Capra_ibex_Alpine_ibex1

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGCG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTAGCCAC AGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
```

```
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGTAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGACCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATAATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGGGGGGCA AGTGTGATCC TCTTTTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Capra_ibex_Alpine_ibex2

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGCG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTAGCCAC AGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGTAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGACCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
```

```
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATAATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGGGGGGCA AGTGTGATCC TCTTTTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Bos_taurus_Domestic_cattle1

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCTCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAAT GGAACAAACC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAGTGAC TATGAGGACC GTTACTATCG TGAAAACATG CACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGGAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATTACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTGATCC TCTTCTCTTC CCCTCCTGTG ATC------C
```

```
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Bos_taurus_Domestic_cattle2

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCTCAT- --GGAGGTGG
 351 C------TGG GGCCAG---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAAT GGAACAAACC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAGTGAC TATGAGGACC GTTACTATCG TGAAAACATG CACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGGAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATTACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTGATCC TCTTCTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Bison_bison_American_bison1

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAC
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCTCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAAT GGAACAAACC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAGTGAC TATGAGGACC GTTACTATCG TGAAAACATG CACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGGAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATTACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTGATCC TCTTCTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Bison_bison_American_bison2

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTATCCA CCTCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCTCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAAT GGAACAAACC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAGTGAC TATGAGGACC GTTACTATCG TGAAAACATG CACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGGAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATTACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTGATCC TCTTCTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Syncerus_caffer_caffer_African_cape_buffalo1

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGTCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTATCCA TCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCTCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CCCAT---GG AGGTGGC--- TGGGGA---C
```

```
 401 AGCCACAT-- -GGAGGAGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAAT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGTAATGAC TATGAGGACC GTTACTATCG TGAAAACATG CACCGTTACC
 701 CCAACCAA-- -GTATACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTAAAGGAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACGTC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTGATCC TCTTCTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Syncerus_caffer_caffer_African_cape_buffalo2

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGTCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTATCCA TCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCTCAT- --GGAGGTGG
 351 C------TGG GGTCAG---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAAT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
```

```
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGTAATGAC TATGAGGACC GTTACTATCG TGAAAACATG CACCGTTACC
 701 CCAACCAA-- -GTATACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AGCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGGAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACGTC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG GGAATCCGAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTGATCC TCTTCTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Syncerus_caffer_nanus_African_forest_buffalo1

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGTCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTATCCA TCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCTCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGAGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAAT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGTAATGAC TATGAGGACC GTTACTATCG TGAAAACATG CACCGTTACC
 701 CCAACCAA-- -GTATACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AGCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGGAAC ACACAGTC--
```

```
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACGTC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTGATCC TCTTCTCTTC CCCTCCTATG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Syncerus_caffer_nanus_African_forest_buffalo2

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTTCTCT TTGTGGTCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTATCCA TCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCTCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGAGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAAT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGTAATGAC TATGAGGACC GTTACTATCG TGAAAACATG CACCGTTACC
 701 CCAACCAA-- -GTATACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AGCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGGAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACGTC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCTCCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTGATCC TCTTCTCTTC CCCTCCTGTG ATC------C
```

```
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Tragelaphus_strepticeros_Greater_kudu1

```
   1 ATGGTGAAAA GCCACATAGG CAGATGGATC CTGGTCCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGCCCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCCA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA CCTCAA---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GAA------ ---------- --------GG GGGTGACTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCCCAT- --GGAGGCGG
 351 C------TGG GGCCAG---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAACA TGTGGCAGGA GCTGCTGCAG CGGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAGTGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAGC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTCATCA TCTTCTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Tragelaphus_strepticeros_Greater_kudu2

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTCCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGCCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA TCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCCCAT- --GGAGGCGG
 351 C------TGG GGCCAG---C CTCAT---GT AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGT ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGTG GA------GG GTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAACA TGTGGCAGGA GCTGCTGCAG CGGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAGTGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAGC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GTT---TATT AC------CA
 951 ACGAGGGGCA AGTGTCATCC TCTTCTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Tragelaphus_oryx_Eland1

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTCCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA TCTCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAG---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGT ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGTG GA------AG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAGTGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAGC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTGATCC TCTTCTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Tragelaphus_oryx_Eland2

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTCCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA TCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAG---C CTCAT---GG AGGTGGC--- TGGGGT---C
```

```
 401 AGCCCCAT-- -GGTGGTGGT ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGTG GA------AG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAGTGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAGC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTGATCC TCTTCTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Tragelaphus_angasii_Nyala1

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTCCTCT TTGTGGCCAT
  51 GTGGAGTGAT GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA TCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAG---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGT ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAACA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
```

```
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAGTGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAGC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTCATCC TCTTCTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Tragelaphus_angasii_Nyala2

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTCCTCT TTGTGGCCAT
  51 GTGGAGTGAT GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA TCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGTCAG---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGT ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAACA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAGTGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAGC ACACAGTC--
```

```
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTCATCC TCTTCTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Tragelaphus_imberbis_Lesser_kudu1

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTCCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA TCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCTCAT- --GGAGGTGG
 351 C------TGG GGCCAG---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAGC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTCATCC TCTTCTCTTC CCCTCCTGTG ATC------C
```

```
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Tragelaphus_imberbis_Lesser_kudu2

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTGGTCCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTATCCA TCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- --------GG GGGTGGCTGG
 301 GGTCAGCCCC ATGGAGGTGG CTGGGGC--- CAGCCTCAT- --GGAGGTGG
 351 C------TGG GGCCAG---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAGT GGAACAAGCC CAGTAAGCCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAG TAACCAGAAC
 751 AACTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAGC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTGGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GCT---TATT AC------CA
 951 ACGAGGGGCA AGTGTCATCC TCTTCTCTTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Muntiacus_reevesi_Muntjac1

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTAT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTAGCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTCGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Muntiacus_reevesi_Muntjac2

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTAT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTAGCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTCGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Odocoileus_virginianus_White–tailed_deer1

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GAAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
```

```
 401 AGCCCCAT-- -GGAGGTGGC ---TGG---- --------GG G---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------AG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGAGGC
 601 CTCGGTGGCT ACATGCTGGG AAGTGCCATG AACAGACCTC TTATACATTT
 651 TGGCAACGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCAAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Odocoileus_virginianus_White–tailed_deer2

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGGT GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGTTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG G---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAT ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCG ---AAAACCA
 551 ACATGAAGCA TGTGGGAGGA GCTGCTGCCG CTGGAGCAGT GGTAGGGGGC
```

```
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACT GTTACTATCG TGAAAATATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATTACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACTGA AACTGACATT AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CT
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Odocoileus_hemionus_Mule_deer1

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG G---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTCGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAACGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
```

```
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Odocoileus_hemionus_Mule_deer2

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGGC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG G---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCCG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ATATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAATATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACTGA AACTGACATT AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATTCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
```

```
1001 TCCTCATTTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Rangifer_tarandus_Caribou1

```
   1 ATGATGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGGGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG G---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCCG CTGGAACAGT GGTAGGGGGC
 601 CTCAGTGGCT ACATGCTGGG AAGTGCCATG AACAGGCCTC TTATACATTT
 651 TGGCAACGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAATGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATT AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATACCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Rangifer_tarandus_Caribou2

```
   1 ATGGTGAAAA GCCACATAGG CAGTTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGGGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG G---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------TG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCCG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGGAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATT AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Alces_alces_European_elk1

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGG---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG G---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCC ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATT AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTAATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Alces_alces_European_elk2

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCTCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGG---C
```

```
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG G---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCC ---CAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATT AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Alces_americanus_Moose1

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGG---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG G---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCC ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
```

```
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATT AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTAATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Alces_americanus_Moose2

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCTCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGG---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG G---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCC ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
```

```
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATT AAGATGATTG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Hydropotes_inermis_Water_deer1

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAA-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGTCAG---C CCCAT---GG AGGTGGC--- TGGGGA---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG T---CAGCCC
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AAT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT AGTAGGGGGC
 601 CTCGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GCCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
```

```
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Hydropotes_inermis_Water_deer2

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAA-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGTCAG---C CCCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG T---CAGCCC
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT AGTAGGGGGC
 601 CTCGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GCCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Capreolus_capreolus_Roe_deer1

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGAGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAACGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATT AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATATC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Capreolus_capreolus_Roe_deer2

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GTAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGAGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTTGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAACGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATT AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATATC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Cervus_canadensis_Wapiti1

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTCGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
```

```
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAACC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTCGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Cervus_canadensis_Wapiti2

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTTGGCCTCT GCAGGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
```

```
 601 CTCGGTGGCT ACTTGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACGCAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTGATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Cervus_elaphus_Red_deer1

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGCGGCCAT
  51 GTGGAGTGAC GTBGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTAG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AACCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTCGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
```

```
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Cervus_elaphus_Red_deer2

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTBGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCTCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTGCCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTCGGTGGCT ACATGCTGGG AAGTGCTATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGTCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
```

```
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Cervus_nippon_Sika_deer1

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTCGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTCGGTGGCT ACATGCTGGG AAGTGCCATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCCAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Cervus_nippon_Sika_deer2

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTCGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGT--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCTCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC GGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTCGGTGGCT ACATGCTGGG AAGTGCTATG AGCAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Dama_dama_Fallow_deer1

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGC--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTCGGTGGCT ACATGCTGGG AAGTGCCATG AATAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Dama_dama_Fallow_deer2

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
  51 GTGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGACCAAAA CCT---GGAG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGA- --------TA CCCGGGACAG
 151 ---GGAAGTC CTGGAGGCAA CCGCTATCCA CCTCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGA------ ---------- ---------- ----------
 301 ---------- --GGGGGTGG CTGGGGC--- CAGCCCCAT- --GGAGGTGG
 351 C------TGG GGCCAA---C CTCAT---GG AGGTGGC--- TGGGGT---C
```

```
 401 AGCCCCAT-- -GGTGGTGGC ---TGG---- --------GG A---CAGCCA
 451 CATGGTGGTG GA------GG CTGGGGTCAA ---------- --------GG
 501 TGGTACCCAC AGT---CAGT GGAACAAGCC CAGTAAACCA ---AAAACCA
 551 ACATGAAGCA TGTGGCAGGA GCTGCTGCAG CTGGAGCAGT GGTAGGGGGC
 601 CTCGGTGGCT ACATGCTGGG AAGTGCCATG AATAGGCCTC TTATACATTT
 651 TGGCAATGAC TATGAGGACC GTTACTATCG TGAAAACATG TACCGTTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTATAA TAACCAGAAC
 751 ACCTTTGTGC ATGACTGTGT CAACATCACA GTCAAGCAAC ACACAGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACCGA AACTGACATC AAGATGATGG AGCGAGTTGT GGAGCAAATG
 901 TGCATCACCC AGTACCAGAG AGAATCCGAG GCT---TATT AC------CA
 951 AAGAGGGGCA AGTGTGATCC TCTTCTCCTC CCCTCCTGTG ATC------C
1001 TCCTCATCTC TTTCCTCATT TTTCTCATAG TAGGA----- ----------
1051 ---
```

Panthera_tigris_sumatrae_Sumatran_tiger1

```
   1 ATGGTGAAAG GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGTG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGG- --------TA CCCGGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGCGGCGG CTGGGGT--- CAGCCCCACG CCGGCGGCGG
 351 C------TGG GGTCAG---C CCCACGCCGG CGGCGGC--- TGGGGA---C
 401 AGCCCCACGC CGGCGGCGGC ---TGG---- --------GG A---CAGCCC
 451 CACGCCGGCG GC------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCACCCAC AGT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCCGCGGCAG CCGGGGCAGT AGTGGGGGGC
```

```
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AACCGGCCCC TCATTCATTT
 651 TGGCAACGAC TACGAGGACC GTTACTACCG TGAAAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAGGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATAATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCC---TACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCTCCCGTG ATT------C
1001 TCCTCCTCTC GCTCCTCATC CTCCTGATCG GGGGT----- ----------
1051 ---
```

Panthera_tigris_sumatrae_Sumatran_tiger2

```
   1 ATGGTGAAAG GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGTG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGG- --------TA CCCGGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGCGGCGG CTGGGGT--- CAGCCCCACG CCGGCGGCGG
 351 C------TGG GGTCAG---C CCCACGCCGG CGGCGGC--- TGGGGA---C
 401 AGCCCCACGC CGGCGGCGGC ---TGG---- --------GG A---CAGCCC
 451 CACGCCGGCG GC------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCACCCAC AGT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCCGCGGCAG CCGGGGCAGT AGTGGGGGGC
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AACCGGCCCC TCATTCATTT
 651 TGGCAACGAC TACGAGGACC GTTACTACCG TGAAAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAGGCAGC ACACGGTC--
```

```
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATAATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCC---TACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCTCCCGTG ATT------C
1001 TCCTCCTCTC GCTCCTCATC CTCCTGATCG GGGGT----- ----------
1051 ---
```

Panthera_tigris_altaica_Siberian_tiger1

```
   1 ATGGTGAAAG GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGTG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGG- --------TA CCCGGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGCGGCGG CTGGGGT--- CAGCCCCACG CCGGCGGCGG
 351 C------TGG GGTCAG---C CCCACGCCGG CGGCGGC--- TGGGGA---C
 401 AGCCCCACGC CGGCGGCGGC ---TGG---- --------GG A---CAGCCC
 451 CACGCCGGCG GC------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCACCCAC AGT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCCGCGGCAG CCGGGGCAGT AGTGGGGGGC
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AACCGGCCCC TCATTCATTT
 651 TGGCAACGAC TACGAGGACC GTTACTACCG TGAAAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAGGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATAATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCC---TACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCTCCCGTG ATT------C
```

```
1001 TCCTCCTCTC GCTCCTCATC CTCCTGATCG GGGGT----- ----------
1051 ---
```

Panthera_tigris_altaica_Siberian_tiger2

```
   1 ATGGTGAAAG GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGTG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGG- --------TA CCCGGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGCGGCGG CTGGGGT--- CAGCCCCACG CCGGCGGCGG
 351 C------TGG GGTCAG---C CCCACGCCGG CGGCGGC--- TGGGGA---C
 401 AGCCCCACGC CGGCGGCGGC ---TGG---- --------GG A---CAGCCC
 451 CACGCCGGCG GC------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCACCCAC AGT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCCGCGGCAG CCGGGGCAGT AGTGGGGGGC
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AACCGGCCCC TCATTCATTT
 651 TGGCAACGAC TACGAGGACC GTTACTACCG TGAAAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAGGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATAATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCC---TACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCTCCCGTG ATT------C
1001 TCCTCCTCTC GCTCCTCATC CTCCTGATCG GGGGT----- ----------
1051 ---
```

Leopardus_wiedii_Margay1

```
   1 ATGGTGAAAG GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGTG
 101 GAGGATGGAA CACTGGGGGA ---AGCCGG- --------TA CCCGGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGTGGCGG CTGGGGT--- CAGCCCCACG CCGGCGGCGG
 351 C------TGG GGTCAG---C CCCACGCCGG CGGAGGC--- TGGGGT---C
 401 AGCCCCACGC CGGCGGTGGC ---TGG---- --------GG T---CAGCCC
 451 CACGCCGGCG GC------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCACCCAC AAT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCTGCGGCAG CCGGGGCGGT AGTGGGGGGC
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AGCCGGCCCC TCATTCATTT
 651 TGGCAACGAC TACGAGGACC GTTACTACCG TGAAAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AGCTTTGTGC ACGACTGCGT CAACATCACG GTCAGGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATAATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCCTACTACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCTCCCGTG ATT------C
1001 TCCTCCTCTC GCTCCTCATC CTCCTGATCG GGGGT----- ----------
1051 ---
```

Leopardus_wiedii_Margay2

```
   1 ATGGTGAAAG GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGTG
 101 GAGGATGGAA CACTGGGGGA ---AGCCGG- --------TA CCCGGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTACCCA CCCCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGTGGCGG CTGGGGT--- CAGCCCCACG CCGGCGGCGG
 351 C------TGG GGTCAG---C CCCACGCCGG CGGAGGC--- TGGGGT---C
 401 AGCCCCACGC CGGCGGTGGC ---TGG---- --------GG T---CAGCCC
 451 CACGCCGGCG GC------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCACCCAC AAT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCTGCGGCAG CCGGGGCGGT AGTGGGGGGC
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AGCCGGCCCC TCATTCATTT
 651 TGGCAACGAC TACGAGGACC GTTACTACCG TGAAAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AGCTTTGTGC ACGACTGCGT CAACATCACG GTCAGGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATAATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCCTACTACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCTCCCGTG ATT------C
1001 TCCTCCTCTC GCTCCTCATC CTCCTGATCG GGGGT----- ----------
1051 ---
```

Puma_concolor_Cougar1

```
   1 ATGGTGAAAG GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGTG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGG- --------TA CCCGGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- ---------- ---------- ---------- ----------
 301 ---------- ---------- ----GGC--- ---------- --GGCGGCGG
 351 C------TGG GGTCAG---C CCCACGCCGG CGGAGGC--- TGGGGT---C
```

```
 401 AGCCCCACGC CGGCGGCGGC ---TGG---- --------GG A---CAGCCC
 451 CACGCCGGCG GC------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCACCCAC AGT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCCGCGGCAG CCGGGGCGGT AGTGGGGGGC
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AGCCGGCCCC TCATTCATTT
 651 TGGCAACGAC TACGAGGACC GTTACTACCG TGAAAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAGGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATAATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCC---TACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCTCCCGTG ATT------C
1001 TCCTCCTCTC ACTCCTCATC CTCCTGATCG GGGGT----- ----------
1051 ---
```

Puma_concolor_Cougar2

```
   1 ATGGTGAAAG GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGTG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGG- --------TA CCCGGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- ---------- ---------- ---------- ----------
 301 ---------- ---------- ----GGC--- ---------- --GGCGGCGG
 351 C------TGG GGTCAG---C CCCACGCCGG CGGAGGC--- TGGGGT---C
 401 AGCCCCACGC CGGCGGCGGC ---TGG---- --------GG A---CAGCCC
 451 CACGCCGGCG GC------GG CTGGGGTCAA GGT------- --------GG
 501 TGGCACCCAC AGT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCCGCGGCAG CCGGGGCGGT AGTGGGGGGC
```

```
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AGCCGGCCCC TCATTCATTT
 651 TGGCAACGAC TACGAGGACC GTTACTACCG TGAAAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAGGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATAATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCC---TACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCTCCCGTG ATT------C
1001 TCCTCCTCTC ACTCCTCATC CTCCTGATCG GGGGT----- ----------
1051 ---
```

Acinonyx_jubatus_Cheetah1

```
   1 ATGGTGAAAG GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGTG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGG- --------TA CCCAGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGTGGCGG CTGGGGT--- CAGCCCCACG CCGGCGGCGG
 351 C------TGG GGTCAG---C CCCACGCCGG CGGAGGC--- TGGGGT---C
 401 AGCCCCACGC CGGCGGTGGC ---TGG---- --------GG A---CAGCCC
 451 CACGCCGGCG GC------GG CTGGGGTCAA GGT------- --------GG
 501 CGGCACCCAC AGT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCCGCGGCAG CCGGGGCGGT AGTGGGGGGC
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AGCCGGCCCC TCATTCATTT
 651 TGGCAACGAC TACGAGGACC GTTACTACCG TGAAAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAGGCAGC ACACGGTC--
```

```
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATAATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCC---TACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCTCCCGTG ATT------C
1001 TCCTCCTCTC CCTCCTCATC CTCCTGATCG GGGGT----- ----------
1051 ---
```

Acinonyx_jubatus_Cheetah2

```
   1 ATGGTGAAAG GCCACATAGG CGGCTGGATC CTGGTTCTGT TTGTGGCCAC
  51 ATGGAGTGAC GTGGGCCTCT GCAAGAAG-- -CGGCCGAAG CCT---GGTG
 101 GAGGATGGAA CACTGGGGGG ---AGCCGG- --------TA CCCAGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGTTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGC------ ---------- ---------- ----------
 301 ---------- --GGTGGCGG CTGGGGT--- CAGCCCCACG CCGGCGGCGG
 351 C------TGG GGTCAG---C CCCACGCCGG CGGAGGC--- TGGGGT---C
 401 AGCCCCACGC CGGCGGTGGC ---TGG---- --------GG A---CAGCCC
 451 CACGCCGGCG GC------GG CTGGGGTCAA GGT------- --------GG
 501 CGGCACCCAC AGT---CAGT GGGGCAAACC CAGTAAGCCG ---AAAACCA
 551 ACATGAAGCA CATGGCAGGA GCCGCGGCAG CCGGGGCGGT AGTGGGGGGC
 601 CTCGGCGGCT ACATGCTGGG GAGTGCCATG AGCCGGCCCC TCATTCATTT
 651 TGGCAACGAC TACGAGGACC GTTACTACCG TGAAAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AGGCCAGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAGGCAGC ACACGGTC--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGGGAGA
 851 ACTTCACGGA GACCGACATG AAGATAATGG AGCGCGTGGT GGAGCAGATG
 901 TGCGTCACCC AGTACCAGAA AGAGTCCGAG GCC---TACT AC------CA
 951 AAGAGGGGCG AGCGCCATCC TCTTCTCCCC GCCTCCCGTG ATT------C
```

```
1001 TCCTCCTCTC CCTCCTCATC CTCCTGATCG GGGGT----- ----------
1051 ---
```

Mustela_putorius_European_polecat1

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGCTC CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC ATTGGCTTCT GCAAGAAG-- -CGGCCCAAG CCT---GGAG
 101 GAGGCTGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGT------ ---------- ---------- ----------
 301 ---------- --GGTGGCGG CTGGGGC--- CAGCCCCAC- --GGGGGTGG
 351 C------TGG GGACAG---C CCCAC---GG GGGTGGC--- TGGGGA---C
 401 AGCCCCAC-- -GGGGGCGGC ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGCG GT------GG CTGGGGTCAA GGT------- --------GG
 501 TGGGAGCCAC GGT---CAGT GGGGCAAGCC CAGTAAGCCT ---AAAACCA
 551 ACATAAAGCA TGTGGCGGGA GCCGCAGCAG CCGGGGCGGT TGTGGGGGGC
 601 CTGGGCGGCT ACATGCTGGG GAGCGCCATG AGCAGGCCCC TCATTCATTT
 651 TGGCAACGAC TATGAGGACC GCTACTACCG TGAGAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AAGCCGGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTGGTGC ACGACTGCGT CAACATCACG GTCAAGCAGC ACACGGTG--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGCGAGA
 851 ACTTCACGGA GACCGACATG AAGATCATGG AGCGCGTGGT GGAGCAGATG
 901 TGTGTCACCC AGTACCAGCA AGAGTCCGAG GCT---TACT AC------CA
 951 GAGGGGGGCG AGCGCCATCC TCTTCTCGCC CCCTCCCGTG ATC------C
1001 TCCTCATCTC GCTGCTCATT CTCCTGATAG TGGGA----- ----------
1051 ---
```

Mustela_putorius_European_polecat2

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGCTC CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC ATTGGCTTCT GCAAGAAG-- -CGGCCGAAG CCT---GGAG
 101 GAGGCTGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGT------ ---------- ---------- ----------
 301 ---------- --GGTGGCGG CTGGGC---- CAGCCCCAC- --GGGGGTGG
 351 C------TGG GGCCAG---C CCCAT---GG GGGTGGC--- TGGGGA---C
 401 AGCCCCAC-- -GGGGGTGGC ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGCG GT------GG CTGGGGTCAA GGT------- --------GG
 501 TGGGAGCCAC GGT---CAGT GGGGCAAGCC CAGTAAGCCT ---AAAACCA
 551 ACATGAAGCA TGTGGCGGGT GCCGCAGCAG CCGGGGCGGT TGTGGGGGGC
 601 CTGGGCGGCT ACATGCTGGG GAGCGCCATG AGCAGGCCCC TCATTCATTT
 651 TGGCAACGAC TATGAGGACC GCTACTACCG TGAGAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AAGCCGGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ATGACTGCGT CAACATCACG GTCAAGCAGC ACACGGTG--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGCGAGA
 851 ACTTCACGGA GACCGACATG AAGATCATGG AGCGCGTGGT GGAGCAGATG
 901 TGTGTCACCC AGTACCAGCG AGAGTCCGAG GCT---TACT AC------CA
 951 GAGGGGGGCG AGCGCCATCC TCTTCTCGCC CCCTCCCGTG ATC------C
1001 TCCTCATCTC GCTGCTCATT CTCCTGATAG TGGGA----- ----------
1051 ---
```

Mustela_erminea_Stoat1

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGCTC CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC ATTGGCTTCT GCAAGAAG-- -CGGCCGAAG CCT---GGAG
 101 GAGGCTGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
```

```
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGT------ ---------- ---------- ----------
 301 ---------- --GGTGGCGG CTGGGGC--- CAGCCCCAC- --GGGGGTGG
 351 C------TGG GGCCAG---C CCCAC---GG GGGTGGC--- TGGGGT---C
 401 AGCCCCAC-- -GGGGGCGGC ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGCG GT------GG CTGGGGTCAA GGT------- --------GG
 501 TGGGAGCCAC GGT---CAGT GGGGCAAGCC CAGTAAGCCC ---AAAACCA
 551 ACATGAAGCA TGTGGCGGGA GCCGCAGCAG CCGGGGCGGT TGTGGGGGGC
 601 CTGGGCGGCT ACATGCTGGG GAGCGCCATG AGCAGGCCCC TCATTCATTT
 651 TGGCAACGAC TATGAGGACC GCTACTACCG TGAGAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AAGCCGGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAAGCAGC ACACGGTG--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGCGAGA
 851 ACTTCACGGA GACCGACATG AAGATCATGG AGCGCGTGGT GGAGCAGATG
 901 TGTGTCACCC AGTACCAGCG AGAGTCCGAG GCT---TACT AC------CA
 951 GAGGGGGGCG AGCGCCATCC TCTTCTCGCC CCCTCCCGTG ATC------C
1001 TCCTCATCTC GCTGCTCATT CTCCTGATAG TGGGA----- ----------
1051 ---
```

Mustela_erminea_Stoat2

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGCTC CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC ATTGGCTTCT GCAAGAAG-- -CGGCCGAAG CCT---GGAG
 101 GAGGCTGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGT------ ---------- ---------- ----------
 301 ---------- --GGTGGCGG CTGGGGC--- CAGCCCCAC- --GGGGGTGG
 351 C------TGG GGCCAG---C CCCAC---GG GGGTGGC--- TGGGGT---C
```

```
 401 AGCCCCAC-- -GGGGGCGGC ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGCG GT------GG CTGGGGTCAA GGT------- --------GG
 501 TGGGAGCCAC GGT---CAGT GGGGCAAGCC CAGTAAGCCC ---AAAACCA
 551 ACATGAAGCA TGTGGCGGGA GCCGCAGCAG CCGGGGCGGT TGTGGGGGGC
 601 CTGGGCGGCT ACATGCTGGG GAGCGCCATG AGCAGGCCCC TCATTCATTT
 651 TGGCAACGAC TATGAGGACC GCTACTACCG TGAGAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AAGCCGGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTTGTGC ACGACTGCGT CAACATCACG GTCAAGCAGC ACACGGTG--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGCGAGA
 851 ACTTCACGGA GACCGACATG AAGATCATGG AGCGCGTGGT GGAGCAGATG
 901 TGTGTCACCC AGTACCAGCG AGAGTCCGAG GCT---TACT AC------CA
 951 GAGGGGGGCG AGCGCCATCC TCTTCTCGCC CCCTCCCGTG ATC------C
1001 TCCTCATCTC GCTGCTCATT CTCCTGATAG TGGGA----- ----------
1051 ---
```

Neovison_vison_American_mink1

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGCTC CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC ATTGGCTTCT GCAAGAAG-- -TGGCCAAAG CCT---GGAG
 101 GAGGCTGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGT------ ---------- ---------- ----------
 301 ---------- --GGTGGCGG CTGGGGC--- CAGCCCCAC- --GGGGGTGG
 351 C------TGG GGACAG---C CCCAC---GG GGGTGGC--- TGGGGT---C
 401 AGCCCCAC-- -GGGGGTGGC ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGCG GT------GG CTGGGGTCAA GGT------- --------GG
 501 TGGGAGCCAC GGT---CAGT GGGGCAAGCC CAGTAAGCCC ---AAAACCA
 551 ACATGAAGCA TGTGGCGGGA GCCGCAGCAG CCGGGGCGGT CGTGGGGGGC
```

```
 601 CTGGGCGGCT ACATGCTGGG GAGCGCCATG AGCAGGCCCC TCATTCATTT
 651 TGGCAACGAC TATGAGGACC GCTACTACCG TGAGAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AAGCCGGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTCGTGC ATGACTGCGT CAACATCACG GTCAAGCAGC ACACGGTG--
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGCGAGA
 851 ACTTCACGGA GACCGACATG AAGATCATGG AGCGCGTGGT GGAGCAGATG
 901 TGTGTCACCC AGTACCAGCG AGAGTCCGAG GCT---TACT AC------CA
 951 GAAGGGGGCG AGCGCCATCC TCTTCTCGCC CCCTCCCGTG ATC------C
1001 TCCTCATCTC ACTGCTCATT CTCCTGATAG TGGGA----- ----------
1051 ---
```

Neovison_vison_American_mink2

```
   1 ATGGTGAAAA GCCACATAGG CAGCTGGCTC CTGGTTCTCT TTGTGGCCAC
  51 ATGGAGTGAC ATTGGCTTCT GCAAGAAG-- -TGGCCAAAG CCT---GGAG
 101 GAGGCTGGAA CACTGGGGGG ---AGCCGA- --------TA CCCAGGGCAG
 151 ---GGCAGTC CTGGAGGCAA CCGCTACCCA CCCCAG---- ----------
 201 ---------- ---------- ---------- ---------- ----------
 251 ---------- -GGT------ ---------- ---------- ----------
 301 ---------- --GGTGGCGG CTGGGGC--- CAGCCCCAC- --GGGGGTGG
 351 C------TGG GGACAG---C CCCAC---GG GGGTGGC--- TGGGGT---C
 401 AGCCCCAC-- -GGGGGTGGC ---TGG---- --------GG A---CAGCCG
 451 CATGGTGGCG GT------GG CTGGGGTCAA GGT------- --------GG
 501 TGGGAGCCAC GGT---CAGT GGGGCAAGCC CAGTAAGCCC ---AAAACCA
 551 ACATGAAGCA TGTGGCGGGA GCCGCAGCAG CCGGGGCGGT CGTGGGGGGC
 601 CTGGGCGGCT ACATGCTGGG GAGCGCCATG AGCAGGCCCC TCATTCATTT
 651 TGGCAACGAC TATGAGGACC GCTACTACCG TGAGAACATG TACCGCTACC
 701 CCAACCAA-- -GTGTACTAC AAGCCGGTGG ATCAGTACAG CAACCAGAAC
 751 AACTTCGTGC ATGACTGCGT CAACATCACG GTCAAGCAGC ACACGGTG--
```

```
 801 -ACCACCACC ACCAAG---- ---------- ---------- ---GGCGAGA
 851 ACTTCACGGA GACCGACATG AAGATCATGG AGCGCGTGGT GGAGCAGATG
 901 TGTGTCACCC AGTACCAGCG AGAGTCCGAG GCT---TACT AC------CA
 951 GAAGGGGGCG AGCGCCATCC TCTTCTCGCC CCCTCCCGTG ATC------C
1001 TCCTCATCTC ACTGCTCATT CTCCTGATAG TGGGA----- ----------
1051 ---
```

Appendix C

Observed *Prnp* Haplotypes

Complete Sequences of *Prnp* Haplotypes (Alleles) Inferred from Field Observations of Free-Ranging Colorado Mule Deer (*Odocoileus hemionus*)

Prnp_DF

1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT

51 GTGGAGTGAC GTGGGCCTCT GCAAGAAGCG ACCAAAACCT GGAGGAGGAT

101 GGAACACTGG GGGGAGCCGA TACCCGGGAC AGGGAAGTCC TGGAGGCAAC

151 CGCTATCCAC CTCAGGGAGG GGGTGGCTGG GGTCAGCCCC ATGGAGGTGG

201 CTGGGGCCAA CCTCATGGAG GTGGCTGGGG TCAGCCCCAT GGTGGTGGCT

251 GGGGGCAGCC ACATGGTGGT GGAGGCTGGG GTCAAGGTGG TACCCACAGT

301 CAGTGGAACA AGCCCAGTAA ACCAAAAACC AACATGAAGC ATGTGGCAGG

351 AGCTGCTGCC GCTGGAGCAG TGGTAGGGGG CCTTGGTGGC TAYATGCTGG

401 GAAGTGCCAT GAGCAGGCCT CTTATACATT TTGGCAACGA CTATGAGGAC

451 CGTTACTATC GTGAAAATAT GTACCGTTAC CCCAACCAAG TGTACTACAG

501 GCCAGTGGAT CAGTATAATA ACCAGAACAC CTTTGTGCAT GACTGTGTCA

551 ACATCACAGT CAAGCAACAC ACAGTCACCA CCACCACCAA GGGGGAGAAC

601 TTCACTGAAA CTGACATTAA GATGATGGAG CGAGTTGTGG AGCAAATGTG

651 CATCACCCAG TACCAGAGAG AATTCCAGGC TTATTACCAA AGAGGGGCAA

701 GTGTGATCCT CTTCTCCTCC CCTCCTGTGA TCCTCCTCAT YTCTTTCCTC

751 ATTTTTCTCA TAGTAGGATA G

Prnp_GS

1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT

51 GTGGAGTGGC GTGGGCCTCT GCAAGAAGCG ACCAAAACCT GGAGGAGGAT

101 GGAACACTGG GGGGAGCCGA TACCCGGGAC AGGGAAGTCC TGGAGGCAAC

151 CGCTATCCAC CTCAGGGAGG GGGTGGCTGG GGTCAGCCCC ATGGAGGTGG

```
201 CTGGGGCCAA CCTCATGGAG GTGGCTGGGG TCAGCCCCAT GGTGGTGGCT
251 GGGGGCAGCC ACATGGTGGT GGAGGCTGGG GTCAAGGTGG TACCCACAGT
301 CAGTGGAACA AGCCCAGTAA ACCAAAAACC AACATGAAGC ATGTGGCAGG
351 AGCTGCTGCC GCTGGAGCAG TGGTAGGGGG CCTTGGTGGC TAYATGCTGG
401 GAAGTGCCAT GAGCAGGCCT CTTATACATT TTGGCAACGA CTATGAGGAC
451 CGTTACTATC GTGAAAATAT GTACCGTTAC CCCAACCAAG TGTACTACAG
501 GCCAGTGGAT CAGTATAATA ACCAGAACAC CTTTGTGCAT GACTGTGTCA
551 ACATCACAGT CAAGCAACAC ACAGTCACCA CCACCACCAA GGGGGAGAAC
601 TTCACTGAAA CTGACATTAA GATGATGGAG CGAGTTGTGG AGCAAATGTG
651 CATCACCCAG TACCAGAGAG AATCCCAGGC TTATTACCAA AGAGGGGCAA
701 GTGTGATCCT CTTCTCCTCC CCTCCTGTGA TCCTCCTCAT YTCTTTCCTC
751 ATTTTTCTCA TAGTAGGATA G
```

Prnp_DS

```
  1 ATGGTGAAAA GCCACATAGG CAGCTGGATC CTAGTTCTCT TTGTGGCCAT
 51 GTGGAGTGAC GTGGGCCTCT GCAAGAAGCG ACCAAAACCT GGAGGAGGAT
101 GGAACACTGG GGGGAGCCGA TACCCGGGAC AGGGAAGTCC TGGAGGCAAC
151 CGCTATCCAC CTCAGGGAGG GGGTGGCTGG GGTCAGCCCC ATGGAGGTGG
201 CTGGGGCCAA CCTCATGGAG GTGGCTGGGG TCAGCCCCAT GGTGGTGGCT
251 GGGGGCAGCC ACATGGTGGT GGAGGCTGGG GTCAAGGTGG TACCCACAGT
301 CAGTGGAACA AGCCCAGTAA ACCAAAAACC AACATGAAGC ATGTGGCAGG
351 AGCTGCTGCC GCTGGAGCAG TGGTAGGGGG CCTTGGTGGC TAYATGCTGG
401 GAAGTGCCAT GAGCAGGCCT CTTATACATT TTGGCAACGA CTATGAGGAC
451 CGTTACTATC GTGAAAATAT GTACCGTTAC CCCAACCAAG TGTACTACAG
501 GCCAGTGGAT CAGTATAATA ACCAGAACAC CTTTGTGCAT GACTGTGTCA
551 ACATCACAGT CAAGCAACAC ACAGTCACCA CCACCACCAA GGGGGAGAAC
601 TTCACTGAAA CTGACATTAA GATGATGGAG CGAGTTGTGG AGCAAATGTG
651 CATCACCCAG TACCAGAGAG AATCCCAGGC TTATTACCAA AGAGGGGCAA
```

701 GTGTGATCCT CTTCTCCTCC CCTCCTGTGA TCCTCCTCAT YTCTTTCCTC

751 ATTTTTCTCA TAGTAGGATA G

Appendix D

Supplemental Model Details

Full transition matrix, $\boldsymbol{M} =$

$$\begin{bmatrix}
0 & 0 & 0 & r\left(SS{+}SF\right) & r\frac{1}{4}SF & 0 & r\left(SS{+}SF\right) & r\frac{1}{4}SF & 0 \\
0 & 0 & 0 & r\left(SF{+}2FF\right) & r\left(\frac{1}{2}SF{+}FF\right) & 0 & r\left(SF{+}2FF\right) & r\left(\frac{1}{2}SF{+}FF\right) & 0 \\
0 & 0 & 0 & 0 & r\frac{1}{4}SF & r\left(FF{+}SF\right) & 0 & r\frac{1}{4}SF & r\left(FF{+}SF\right) \\
\phi_J\left(1{-}\psi_{SS}\right) & 0 & 0 & \phi_S\left(1{-}\psi_{SS}\right) & 0 & 0 & 0 & 0 & 0 \\
0 & \phi_J\left(1{-}\psi_{F*}\right) & 0 & 0 & \phi_S\left(1{-}\psi_{F*}\right) & 0 & 0 & 0 & 0 \\
0 & 0 & \phi_S\left(1{-}\psi_{F*}\right) & 0 & 0 & \phi_S\left(1{-}\psi_{F*}\right) & 0 & 0 & 0 \\
\phi_S^{\left(\frac{1}{2}\right)}\phi_I^{\left(\frac{1}{2}\right)}\left(\psi_{SS}\right) & 0 & 0 & \phi_S^{\left(\frac{1}{2}\right)}\phi_I^{\left(\frac{1}{2}\right)}\left(\psi_{SS}\right) & 0 & 0 & \phi_I & 0 & 0 \\
0 & \phi_S^{\left(\frac{1}{2}\right)}\phi_I^{\left(\frac{1}{2}\right)}\left(\psi_{F*}\right) & 0 & 0 & \phi_S^{\left(\frac{1}{2}\right)}\phi_I^{\left(\frac{1}{2}\right)}\left(\psi_{F*}\right) & 0 & 0 & \phi_I & 0 \\
0 & 0 & \phi_S^{\left(\frac{1}{2}\right)}\phi_I^{\left(\frac{1}{2}\right)}\left(\psi_{F*}\right) & 0 & 0 & \phi_S^{\left(\frac{1}{2}\right)}\phi_I^{\left(\frac{1}{2}\right)}\left(\psi_{F*}\right) & 0 & 0 & \phi_I
\end{bmatrix}$$

Where r is recruitment to census, ϕ_S is uninfected survival, ϕ_I CWD-infected survival, ψ annual disease risk across genotypic categories, and SS, SF, and FF, refer to genotype frequencies. For our forecasts, heterozygotes, 225SF, and rare homozygotes, 225FF, experience the same annual disease risk, notated ψ_{F*}.