**Final Report for "Development of a CODIS-like Database for the Conservation and Management of Black Bears in Texas"**

## Introduction

Black bears (*Ursus americanus*) were historically distributed throughout most of Texas (Bailey 1905; Schmidly and Bradley 2016). However, due to extensive habitat alteration, human expansion, and unregulated hunting in the 19th and early 20th centuries, black bears were functionally extirpated from the state by the mid-1900s. Their return began in the 1960s when *U. a. luteolus* (Louisiana black bear) emigrated from Louisiana into East Texas. By the 1980s, increasing populations from Arkansas, northern Louisiana, and Oklahoma led to further immigration by *U. a. americanus* into the Pineywoods region of northeast Texas. In the Trans-Pecos region—where bears had been absent for decades—natural recolonization occurred as a result of protection efforts in Mexico (notably in Coahuila and Chihuahua) and Big Bend National Park. This led to the establishment of new populations of *U. a. amblyceps* and *U. a. eremicus* along the southwestern and western edges of Texas.

Despite these population gains, *Ursus americanus* and specifically *U. a. luteolus* remain listed as Threatened by the Texas Parks and Wildlife Department (TPWD). Because TPWD recognizes *U. americanus* as Threatened, all subspecies occurring in Texas are treated with the same status. Although the U.S. Fish and Wildlife Service has removed the species from the federal list of endangered species, bears in Texas still warrant substantial conservation consideration. Increasing reports of human-bear conflicts—particularly in the Trans-Pecos—highlight the need for effective strategies to monitor, manage, and respond to bear populations. Non-lethal identification of individual bears involved in these interactions is crucial for implementing science-based management decisions, including relocation versus removal.

Traditional wildlife monitoring approaches, such as capturing animals for tagging and biopsy, or analyzing scat for diet by morphological methods, are labor-intensive, expensive, and logistically difficult to scale. DNA-based methods offer a powerful and scalable alternative. Advances in genomic and metagenomic sequencing now enable researchers to assess a bear's identity, kinship, population of origin, and diet from non-invasive samples such as hair or scat. Several U.S. states (e.g., California, Washington) have already begun incorporating such technologies into their wildlife management protocols.

## Project Objectives and Relevance to Research Goals

This project directly supported Research Goals outlined by the Texas Comptroller of Public Accounts:

1. **Address knowledge gaps for threatened species** – By developing genetic and ecological profiles of Texas bears, we provide a data-driven foundation for long-term conservation decisions.
2. **Inform ESA (Endangered Species Act) decisions** – Our research supports future species status assessments, listing reviews, and habitat designation by contributing peer-reviewed data.
3. **Provide accessible tools for end-users** – We are delivering a public, extensible online database designed for use by agencies, landowners, and researchers alike.

Our proposal outlined five primary objectives, which remain central to this final report:

**1. Develop a long-term, statewide sampling and archival regime** for bear specimens, with attention to metadata standards and repository archiving at the Natural Science Research Laboratory (NSRL).

**2. Implement genomic methods for individual bear identification**, including whole-genome sequencing of individuals, and kinship inference methods.

**3. Establish a genetic assay for dietary analysis** by applying shotgun metagenomic sequencing of bear scat samples to detect plant and animal taxa consumed.

**4. Development of SNP Chip Technology**, which will have utility for the individual identification of black bears.

**5. Create a CODIS-like Database** that incorporates sample metadata, genetic data, geographic and demographic information that can be used for future management efforts.

**Summary of Research Tasks and Methods**

This work was designed as a pilot project to establish and validate a comprehensive framework for the long-term genetic monitoring and ecological analysis of black bears in Texas. The **five core tasks** of this project were:

- **Task 1:** Coordinate the collection and archival of diverse bear sample types (e.g., tissue, hair, scat) statewide and ensure standardized metadata capture.
- **Task 2:** Generate genomic data and conduct genotyping of individuals across populations.
- **Task 3:** Develop and validate a SNP (single nucleotide polymorphism) assay to allow for high-throughput, cost-effective genotyping and individual identification.

- **Task 4:** Apply metagenomic methods to scat samples to determine dietary composition, including seasonal and geographic variation.
- **Task 5:** Build a publicly accessible, expandable, searchable, and scientifically curated online database of bear sample and genomic data.

Each of these tasks contributes to the overarching goal of building a permanent infrastructure to support wildlife management decisions in Texas. Importantly, our findings are already contributing to the online resource at https://mhenso.shinyapps.io/texas-wildlife, where agencies and researchers can explore bear genomic and ecological data across time and space.

**Methods**

**Objective 1 Develop a long-term, statewide sampling and archival regime**

Between 2022 and 2024, black bear samples were collected across multiple counties in Texas, with a primary focus on the Trans-Pecos region. Sample types included feces, hair, and tissue. Fecal and hair samples were obtained opportunistically and through field surveys, while tissue samples were acquired from organizations such as Texas Parks and Wildlife Department (TPWD) and cooperating landowners. Metadata, including GPS coordinates, sample type, date, elevation, and collection details, were recorded at the time of sampling. All samples were stored in accordance with long-term curation standards set by the Natural Science Research Laboratory (NSRL) at Texas Tech University.

**Objective 2: Implement genomic methods for individual bear identification**

Whole genomic DNA was extracted from bear hair and tissue samples using Qiagen Blood and Tissue Kits following manufacturer protocols. DNA libraries for tissue and hair samples were prepared using SeqWell plexWell96 kits. Due to the substantial presence of exogenous or non-host DNA in fecal samples, shotgun sequencing of fecal DNA typically produces only a small fraction of reads aligning with the host genome. An effort was made to enrich host DNA content using targeted sequence capture techniques for 15 fecal samples. First, total DNA was extracted using the modified protocol from Qiagen QIAamp Fast DNA Stool Minikit (Qiagen, Gaithersburg, MD, USA) and Kingfisher Zymo Kit (Zymo Research, Irvine, CA, USA). Extracted fecal-derived DNA of known quantity was library prepared with the modified protocol from NEBNext Microbiome DNA Enrichment Kit (New England Biolabs Inc, MA, USA). The kit utilizes the methylated CpG-specific binding protein MBD2 which is fused to the Fc fragment of host IgG (MBD2-Fc), to selectively capture CpG-methylated host DNA. The Fc fragment's strong affinity for Protein A facilitates an efficient method for isolating methylated host DNA using A-bound magnetic beads. The host DNA captured in the magnetic beads were eluted and purified via Ampure bead clean-up

process. Following bead cleanup, DNA was quantified with a fluorometer or spectrophotometer. Libraries were pooled and sequenced for paired 150 bp reads in the NovaSeq 6000 (Illumina, Inc. San Diego, CA, USA) at RTL Genomics (Lubbock, TX, USA).

For genomic analysis, raw sequence data were quality filtered using BBDuk (Bushnell 2014) with parameters for adapter removal, quality trimming (Q10), and minimum read length (50 bp). Reads were aligned to the black bear reference genome (GCA_024610735.1) using Bowtie2 (Langmead and Salzberg 2012). Mapping statistics, including total and duplicate reads, were calculated using Picard (https://broadinstitute.github.io/picard/). Genotyping was performed using BCFtools (Danecek et al. 2021). Kinship analysis was performed in R using a custom implementation of the KING-robust kinship estimation (Manichaikul et al. 2010). A reticulated phylogenetic network was inferred using SplitsTree (Huson and Bryant 2006), based on genetic distances calculated in the R package StAMPP (Pembleton et al. 2013). Genetic diversity was estimated as observed heterozygosity from raw genotype data.

**Objective 3: Establish a genetic assay for dietary analysis**

Fecal samples were homogenized by randomly taking material from the interior of the feces while avoiding the outer layer to minimize the risk of contamination. All samples were homogenized in enough pH 8.0 stable saline buffer (TEN solution) containing 10 mM Tris-HCL, 10 mM NaCl, 5 mM CaCl2, 2.5 mM EDTA and 2% SDS. The homogenized samples were subsampled into 300 µl and then DNA was extracted using KingFisher FLEX (Thermo Fisher Scientific, MA, USA) instrument and using a ZymoBIOMICS 96 MagBead DNA kit (Zymo Research, Irvine, CA, USA) according to the manufacturer's guidelines. The extraction protocol was modified to incorporate a mechanical lysis step with a TissueLyser (Qiagen, Gaithersburg, MD, USA). DNA quantity was assessed via Fluorometry (Qubit High Sensitivity Assays) and fragment size were analyzed using TapeStation (Agilent Technologies, Santa Clara, CA, USA). The DNA extracts were further built into libraries using NEBNext® Ultra™ II Library Prep Kit for Illumina® (New England BioLabs, MA, USA) with 20-30ng of material as input, indexed and pooled for Illumina NovaSeq 6000 (Illumina, San Diego, CA, USA) SP Flow Cell generating about 800 million 150 base paired-end reads. Sequencing was carried out at RTL Genomics (Lubbock, TX, USA). For fecal samples intended for bear genome sequencing, bear DNA was enriched using the NEBNext Microbiome DNA Enrichment Kit, following the protocol described by Chiou and Bergey (2018) prior to library preparation.

For metagenomic analysis, quality assessment of the raw shotgun reads was performed using FastQC (Andrews 2010). All samples were of high quality (Q>30), with only a minimal decrease in quality towards the end of the sequences. Host DNA was removed by mapping the reads to a reference black bear genome (Supple et al. 2024) using Bowtie2 (Langmead

and Salzberg 2012) and sequences were analyzed without assembly. Bowtie2 was also used when FASTQ sequences were aligned against a custom reference database containing genomes of plants and animals identified in a previous black bear diet study conducted in the study area based on visual observations of dietary remains from scat samples (McKinney and Villalobos 2014). We removed duplicate reads from the BAM files using Picard's MarkDupliactes to ensure an unbiased estimation of taxa abundance. To account for cases where reads aligned to multiple reference genomes, we evaluated mapping quality (MAPQ) scores in the SAM files. Reads with low-mapping quality (MAPQ < 20) were excluded to ensure reliable taxonomic assignment. The remaining forward and reverse FASTQ sequences were merged and converted into FASTA format.

The FASTA sequences were blasted against the NCBI nucleotide eukaryotic species database using BLASTN (version 2.11.0, Camacho et al. 2009) with the options -outfmt 6, -max_target_seqs 5, and -max hsps 1. We also removed the reads from the FASTA files that had the same start and end positions using seqkit rmdup function. We first filtered the BLAST outputs using stringent criteria, using a similarity threshold of more than 90% and an e-value of less than 0.00001. Under these conditions, over 30% of the reads remained unclassified. To improve classification, we then applied a more relaxed threshold of 70% similarity, which reduced the number of unclassified reads to approximately 16%.

We obtained the complete taxonomy for each GenBank TaxID by querying the NCBI Taxonomy database, retrieving the entire taxonomic lineage for each sample across various taxonomic levels such as kingdom, phylum, class, order, family, genus, and species. Taxonomic classifications were assigned by comparing BLAST hits at each level; if multiple hits disagreed at a given level, the taxonomy was assigned as 'unknown' at that level. This approach assigned over 80% of the reads at the genus level, while the remaining 20% could not be accurately classified (Table S2). The filtered BLAST output was merged with the taxonomy tables to estimate the abundance of taxa. Remaining reads that did not align with the custom or NCBI eukaryote databases were subsequently matched against the PlusPF database, which includes standard reference sequences for archaea, bacteria, viruses, and plasmids. Kraken2 (Wood et al. 2019) was used with default settings to determine the percentage of data aligning to prokaryotic sequences.

The abundance table, taxonomic table and metadata were merged into a relational phyloseq object. We filtered the dataset to remove erroneous reads, including human and other primate sequences. Taxa that could not be identified to at least the family level was excluded, as well as taxa comprising less than 0.01% of the average reads per sample. We also removed any misidentified reads from taxa not present in the study area. Additionally,

potential environmental contaminants, including fungi, algae, and parasitic nematodes were excluded.

**Objective 4: Development of SNP Chip Technology**

To develop SNP genotyping assays, we employed two complementary approaches targeting both kinship inference and population assignment. For kinship, we identified highly informative loci from the variant dataset by filtering for SNPs with high expected heterozygosity (He > 0.4) and low missingness (<20%). To minimize linkage and ensure broad genomic coverage, a 10 kbp thinning threshold was applied, and the top-ranking SNPs were selected to generate panels of various sizes (e.g., 50–500 SNPs). Pairwise kinship coefficients were then estimated using the KING-robust method for each subset, and results were compared to the full dataset to evaluate consistency and performance. For population assignment, we used the variant dataset and generated population-specific allele frequency files using the --keep flag. Within each regional population, we identified SNPs that were fixed or nearly fixed (≥95% allele frequency), selecting approximately 20 ancestry-informative SNPs per region, which were then combined into a final panel of 60 unique markers. These loci were used to assess population structure and genetic lineage assignment.

Primer assays for genotyping were developed using Geneious Prime, guided by standard practices: maintaining GC content between 40–60%, targeting a melting temperature (Tm) of 50–60°C, and ensuring that the difference in Tm between primer pairs did not exceed 5°C. To design primers, we used FASTA files containing 200 bp of flanking sequence upstream and downstream of each SNP, allowing us to target conserved regions and avoid placing primers over variable sites. These optimized primers will be used for downstream genotyping of both kinship and population-informative SNP panels.

**Objective 5: Create a CODIS-like Database**

All curated genotypes, metadata, geographic coordinates, and dietary profiles were integrated into a centralized relational database using R and Shiny. The interface was deployed on shinyapps.io and provides public access to query, visualize, and download sample-level bear data.

**Results and Discussion**

**Objective 1: Develop a long-term, statewide sampling and archival regime**

Over the course of the project, we implemented a comprehensive sampling framework that included fecal, hair, and tissue samples from multiple localities in Texas, with a focus on the Trans-Pecos region. We collaborated with TPWD personnel and private landowners to

gather samples, ensuring adherence to curation and metadata standards set by the Natural Science Research Laboratory (NSRL) at Texas Tech University. As shown in Table 1, 177 samples were collected, and these were archived with associated metadata including geographic location, date, elevation, and sample type.

The success of this objective was foundational to downstream efforts and demonstrated the feasibility of routine non-invasive and salvage-based sampling for long-term monitoring efforts.

**Objective 2: Implement genomic methods for individual bear identification**

We successfully sequenced tissue, hair, and fecal samples from black bears across multiple regions, including Louisiana, New Mexico, and Texas. A summary of sequencing metrics, including total aligned bases and observed heterozygosity, is presented in Table 2. Sequence data for these samples are available on NCBI SRA at BioprojectPRJNA1276013. A median of about 30 billion base pairs were aligned for each sample, resulting in a median of about 1.6 billion sites genotyped and median heterozygosity of 0.0009.

The enrichment of bear DNA from fecal samples using methylation probes showed modest success. We compared paired samples from bears sequenced from both enriched and total DNA extractions. We found that non-enriched extractions had a median of 3.2% bear DNA (1st quartile: 1.3%, 3rd quartile: 15.8%) while enriched extraction had a median of 23.4% bear DNA (1st quartile: 8.9%, 3rd quartile: 29.3%; Figure 1). We also observed considerable variation among bears in the percentage of bear DNA in fecal samples. Often times enrichment DNA yield was below the detection range of the Qubit High Sensitivity dsDNA fluorometric assay. For such samples, we determined loading concentrations on sequencing runs by first spiking their libraries into pilot runs, and extrapolating their concentration based on the number of reads they generated and by comparison to reads generated by samples for which Qubit readings were possible. Requiring this process for future genetic testing of fecal samples is not ideal, but the SNP genotyping assay we have developed (described below) is expected to be robust to low input concentrations.

DNA obtained from fecal samples tended to have the highest proportion of duplicate reads, indicating a greater effect of PCR artifacts for fecal samples. There was also a significant effect of sample type on the number of sites genotyped ($F = 18.98$, $df = 2,42$, $p < 0.001$), and post-hoc testing confirmed that hair and muscle significantly differed from feces ($p < 0.001$ for both), but hair and muscle did not significantly differ. However, there was no effect of sample type on observed heterozygosity, suggesting that reliable genotypic information can be obtained regardless of sample type.

To visualize genetic relationships among bears, we constructed a reticulated phylogeny based on polymorphic site data (Figure 2). One important result of this effort was that we recovered three main clades of samples representing samples from New Mexico plus Texas Panhandle bears in one clade, Trans-Pecos bears in a second clade, and Louisiana bears in a third clade closely related to the Trans-Pecos clade. These relationships are generally congruent with that reported in the literature (Gould et al. 2022).

Next, we noted in Figure 2 that some samples shared the majority of branch length which is consistent with multiple samples from the same individual or close relatives. In fact, we intentionally included multiple samples from the same bear to test the replicability of our method (TK273908 and TK163843). To further investigate this pattern and help establish our ability to provide individual identification of bears from genetic data, we calculated kinship estimates using R0, R1, and KING-robust statistics. As illustrated in Figure 3, we were able to correctly identify multiple samples from the same bear, as well as delineate close relatives from unrelated bears. Table 2 provides information about relationships among bears.

Because heterozygosity is an important metric for conservation planning, we next calculated observed heterozygosity for each sample. Because we observed distinct phylogenetic separation of groups of bears (Figure 2), we grouped observed heterozygosity measures of bears based on collection origin (New Mexico and Panhandle, Trans-Pecos, and Louisiana). Heterozygosity values ranged from about 0.0005 to 0.0012, with Trans-Pecos bears appearing to have higher heterozygosity than other localities (Figure 4). For reference, 0.001 indicates that 1 out of 1,000 site genotyped were heterozygous. Table 2 provides heterozygosity measures for each sample.

These results confirmed that whole genome sequencing is a viable method for identifying individual bears, assessing relatedness, and evaluating population structure. As expected, tissue samples yielded the highest quality data, followed by hair, with scat samples being the most challenging. Nevertheless, pilot tests confirmed the potential for successful genomic enrichment from scat.

Our findings build upon and expand the genetic insights provided by earlier studies of black bear populations in the southwestern US and northern Mexico. Onorato et al. (2004, 2007) and Van Den Bussche et al. (2009) used mitochondrial DNA and microsatellite markers to examine population structure, genetic diversity, and recolonization patterns in the region. In contrast to these earlier approaches—typically involving few loci and lower-resolution mitochondrial markers—our whole genome sequencing (WGS) approach enabled the genotyping of over 1.6 billion sites per individual. This higher resolution allowed us to detect subtle population structure, identify kin relationships with confidence, and recover

geographically congruent clades with clarity. Furthermore, previous studies relied primarily on tissue from captured bears or recovered carcasses, while our study successfully integrated DNA from fecal, hair and tissue samples using genomic enrichment techniques. This approach not only reduces dependence on invasive sampling but also enables broader monitoring coverage. While our phylogeographic patterns generally align with prior work—recovering clades corresponding to New Mexico, Trans-Pecos, and Louisiana populations—we provide far finer-scale resolution that can better support conservation management decisions. For example, our kinship analysis confirmed repeated sampling of individual bears and delineated first-degree relationships, tools that were not possible using the earlier microsatellite or mtDNA-based approaches. In summary, our WGS-based approach represents a substantial advancement in resolution, individual identification power, and applicability to noninvasively collected samples. These improvements greatly enhance our ability to monitor population structure, track individual bears, and inform regional conservation strategies.

**Objective 3: Establish a genetic assay for dietary analysis**

The raw sequences from 134 fecal samples produced a total of 1,209,561,502 reads, averaging 9,026,910 reads per sample (range: 252,344–52,551,318; SD: 7,553,898). Sequence data for these samples are available on NCBI SRA at BioProject PRJNA1274035. After aligning these reads to the bear genome, 87,091,633 reads were mapped, with a mean of 649,937 ± 121,624 per sample. The remaining non-bear DNA was then aligned to a custom eukaryote genome database, identifying known dietary items, resulting in 55,641,877 mapped sequences (mean = 415,237 ± 96,824). We aligned the remaining reads to the NCBI eukaryotic nucleotide database to identify the unknown dietary items, yielding 370,139,440 reads (mean = 276,223 ±57,824). The rest were classified as either Prokaryotes (499,567,284 reads) or remained unclassified (197,165,780 reads). Across all samples, 841 genera were detected. Rarefaction curves indicated sufficient sampling depth to capture most community diversity, with sequencing depth adequate for taxa detection above 200,000 reads. Good's coverage analysis also showed an average coverage of 92% across samples indicating taxa were well represented across the samples. The distribution of taxa followed a common pattern, with each community dominated by one or a few genera, while the rank abundance curve displayed a long tail of less abundant or rare genera (Figure 5).

In total, 841 unique genera and 465 unique families were identified across all samples. Overall, 71% of the reads matched plants, 12.7% to animal matter, and the remaining 16.3% were unclassified (Figure 6A). In the plant diet, Poaceae accounted for approximately 70% of the identified plant material (Figure 6B). Amaryllidaceae contributed

about 9%, and Anacardiaceae comprised about 8%. While the other plant families collectively represented 15%, indicating a varied but minor contribution from additional taxa. In contrast, the animal diet was primarily composed of Gryllidae, which made up 55% of the total animal-derived dietary components (Figure 6C). Muridae accounted for 15%, followed by Cerviade at 10%, while other animal families collectively contributed 20%. Overall, we found that *Digitaria* and *Sorghum* were the most prevalent genera, appearing in over 25% and 14% of samples, respectively (Figure 7). *Allium* was the next most frequent, occurring in approximately 11% of samples, followed by *Zea* at around 8%. *Gryllus* was also prominent, present in about 7% of samples. All other genera each contributed to less than 5% of the mean relative abundance.

At the genus level for alpha diversity, we observed significant variability in dietary species richness ($Hill_0$), influenced by both season and locality (season: $F = 4.85$, $p = 0.003$; locality: $F = 2.42$, $p = 0.014$), but there was no interaction effect between season and locality ($p > 0.05$). Specifically, dietary richness was higher during the summer and lower during the winter, with notable differences identified between fall and summer, spring and summer, and summer and winter (Figure 8A). At different localities, Terrell exhibited higher richness compared to other locations (Figure 8B), with significant variations between Brewster and Presidio, as well as Brewster and Terrell. Additionally, using Hill1 as a diversity metric, we found significant temporal and spatial effects on dietary diversity (season: $F = 2.49$, $p = 0.02$; locality: $F = 1.67$, $p = 0.05$), however no interaction effect on Hill1. Spring displayed enhanced diversity relative to other seasons, with distinct differences between fall and winter, as well as summer and spring (Figure 8C). In terms of spatial effects on dietary diversity, Brewster showed greater diversity compared to other localities, with significant differences observed between Brewster and Presidio and Brewster and Terrell (Figure 8D).

Diet dissimilarity was assessed using both Jaccard and Bray-Curtis dissimilarity indices to evaluate the effects of temporal and spatial variations on community composition. Permutational analysis of variance (PERMANOVA) based on the Jaccard index revealed that season explained 7.2% of the variation, while locality accounted for 11.7%. Similarly, using the Bray-Curtis index, season was responsible for 9.4% of the variation, and locality for 13.1% (Table 3). No significant interaction effect (season*locality) was observed on diet composition ($p > 0.05$). Post-hoc pairwise tests across seasons and localities identified several significant differences ($p < 0.05$, Table 3).

These findings will inform future work on landscape ecology and trophic interactions of bears in Texas. Manuscript preparation for these results is underway.

Our findings complement and expand upon earlier studies of black bear diet and ecology in Texas and northern Mexico conducted by McKinney and Pittman (1999, 2001), McKinney and Villalobos (2004), and Onorato and Hellgren (2001), which relied primarily on macroscopic and microhistological analyses of scat, along with habitat use and movement data. These earlier efforts documented dominant plant-based food sources—particularly grasses and mast-producing shrubs—as well as seasonal shifts in diet and habitat use. Consistent with these findings, our DNA-based dietary analysis revealed a high prevalence of Poaceae in the plant component of the diet, with *Digitaria* and *Sorghum* appearing frequently across samples. However, our metagenomic approach offers substantially higher taxonomic resolution, capturing both plant and animal dietary components at the genus and family levels, including less detectable taxa such as Gryllidae and Muridae. This approach also allows for quantification of dietary diversity and dissimilarity with greater statistical rigor, enabling robust comparisons across seasons and geographic regions. While our results broadly align with prior observations, the genomic method offers a more detailed and comprehensive view of black bear trophic ecology in the region.

**Objective 4: Development of SNP Chip Technology**

We identified a total of 210 SNPs for targeted genotyping, combining loci selected for kinship inference and population assignment. These SNPs were chosen based on high expected heterozygosity, low missingness, and population-specific allele frequency patterns. For each SNP, we successfully designed primer pairs using flanking regions extracted from the genome. All primers were generated in silico and met standard design criteria, including appropriate GC content, melting temperature range, and primer pair compatibility (Table 4).

**Objective 5: Create a CODIS-like Database**

We developed a public-facing database interface that integrates genetic, geographic, and metadata for all collected samples. The database is hosted online and accessible at:

https://mhenso.shinyapps.io/texas-wildlife

This interactive tool allows researchers and agencies to search, visualize, and download black bear data. The database is designed to be updated as new samples are sequenced and pending ongoing support can be expanded in terms of species represented, data supported, and serve as a long-term resource for conservation genetics and wildlife management in Texas.

Concluding Summary

- Partnership with landowners and Trans-Pecos TPWD biologists established.

- The sampling and archival regime developed.
- Database developed at NSRL for perpetuity analyses.
- Methods for obtaining bear genome from fecal samples were developed and tested.
- Methods for obtaining bear diets from fecal samples were developed and tested.
- A variety of population genetic parameters were obtained.
- A panel of SNPs was developed for future projects.
- This study can serve as a non-invasive blueprint for future studies involving Texas Wildlife where conservation and management are the key outcomes.

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FIGURES

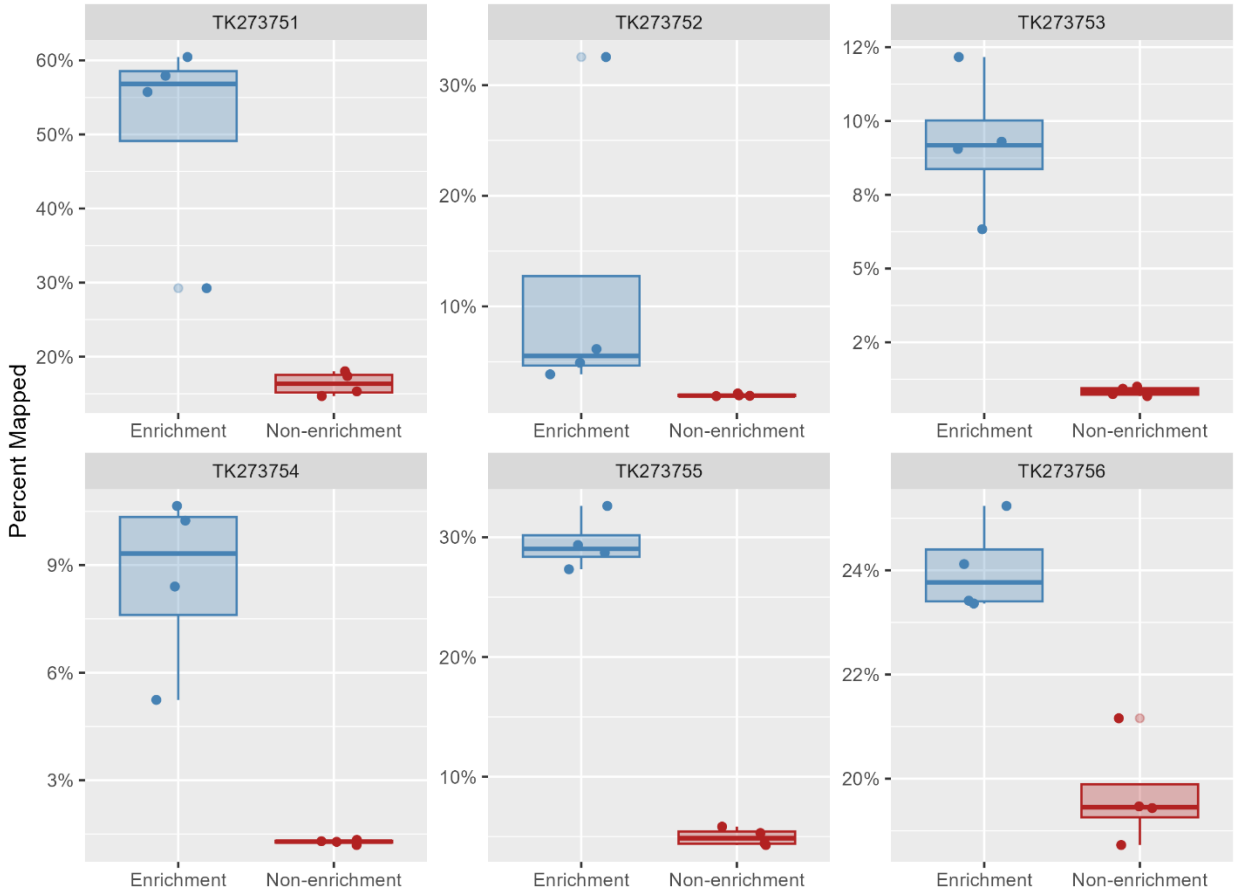



Figure 1. Percent of reads mapped to the black bear reference genome for enriched and non-enriched fecal DNA extractions across six individual samples.

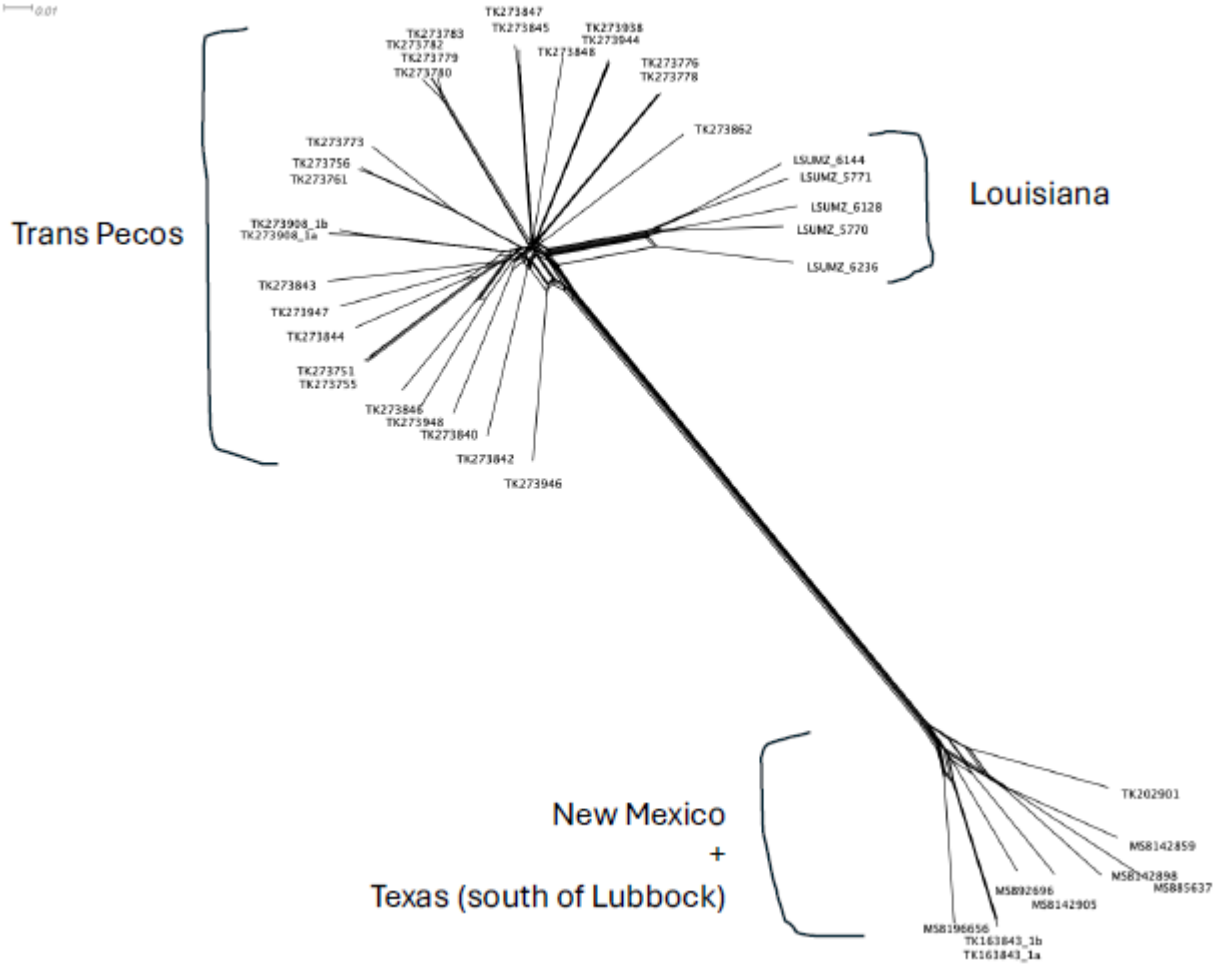



Figure 2. Reticulated phylogeny illustrating evolutionary relationships among bear samples based on whole genome sequencing. Labels are museum accession numbers, branch length is proportional to genetic distance, and reticulations (i.e., closed polygons connecting edges) represent uncertainty in relationships.

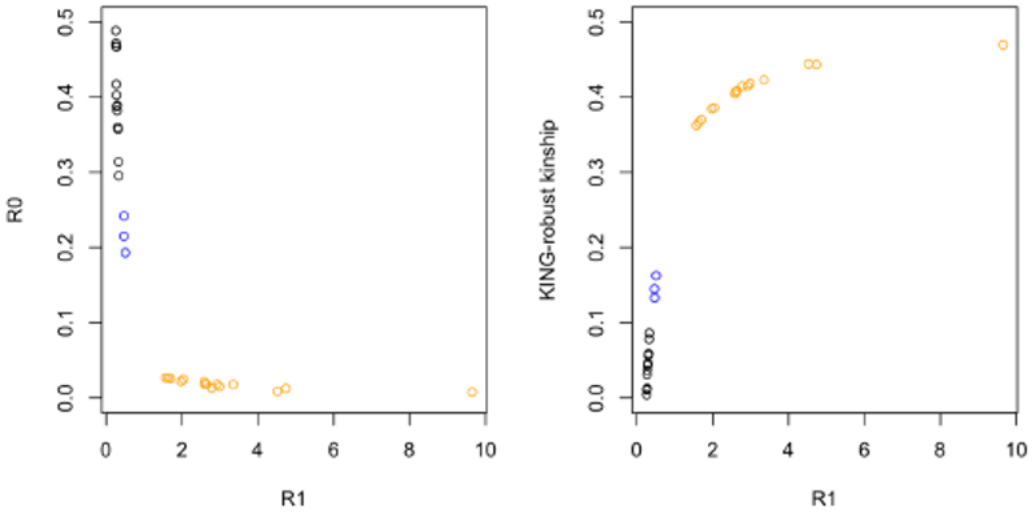



Figure 3. Kinship inference based on pairwise genotype comparisons.
Left panel shows the relationship between R0 (proportion of loci with zero shared alleles) and R1 (proportion with one shared allele). Right panel shows KING-robust kinship coefficient versus R1. Orange points represent comparisons between the same individual (identical genotypes), while blue points indicate close kin relationships such as half-siblings, avuncular pairs, or grandparent–grandchild. Black points represent unrelated individuals.

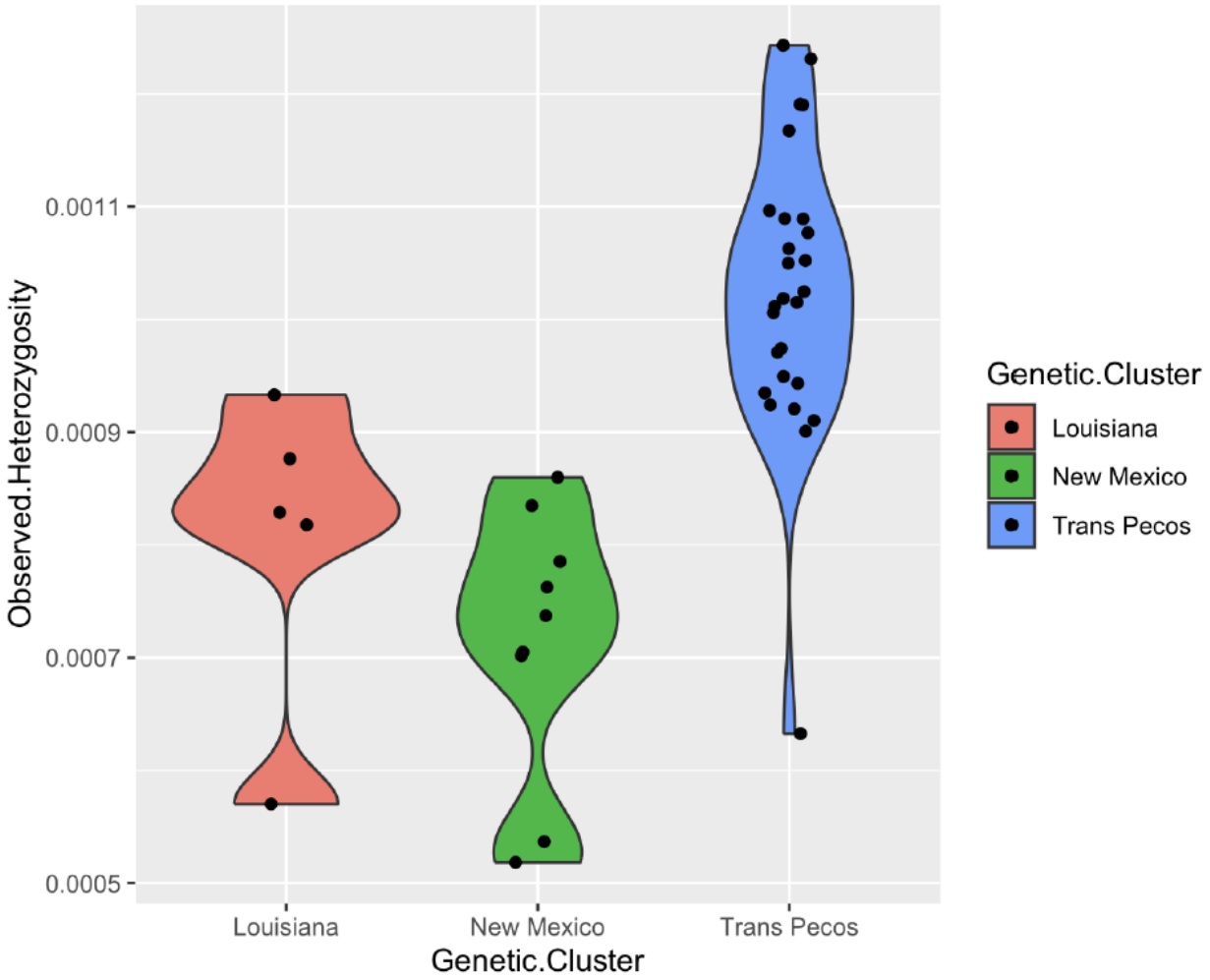



Figure 4. Violin plot of observed heterozygosity for each bear sample grouped by broad-scale geographic origin. The thickness of the colored plots illustrates the proportion of samples occurring at that location on the y-axis. Observed heterozygosity is on the scale of observed heterozygous sites per one thousand sites observed.

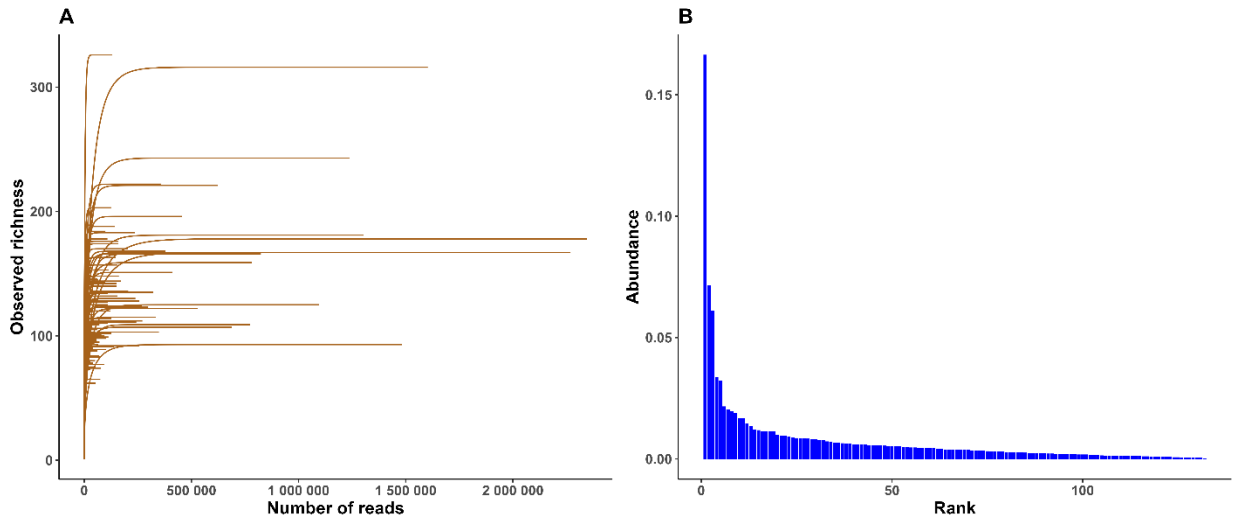



Figure 5. Diversity estimates through rarefaction curve and rank abundance plot. (A) Rarefaction curves depicting the number of genera as a function of sequence depth for each sample, subsampled between 500 and 2,000,000 reads with a step size of 250. (B) Distribution pattern of genera illustrated by a rank abundance plot, showing ranked genera from highest to lowest based on mean relative abundance across samples.

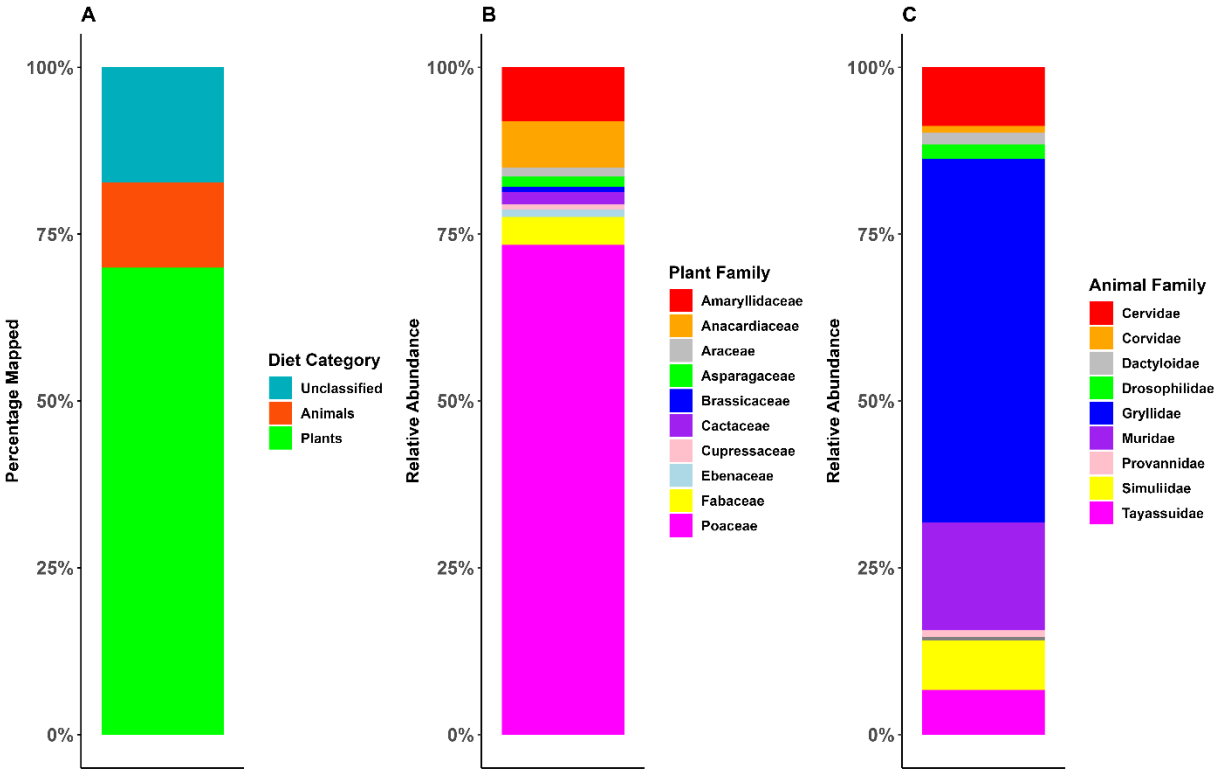



Figure 6. Bar plots showing the dietary items of black bears. (A) Percentage of reads aligned to different diet categories. (B) Proportion of top ten plant families consumed by black bears. (C) Proportion of top ten animal families consumed by black bears.

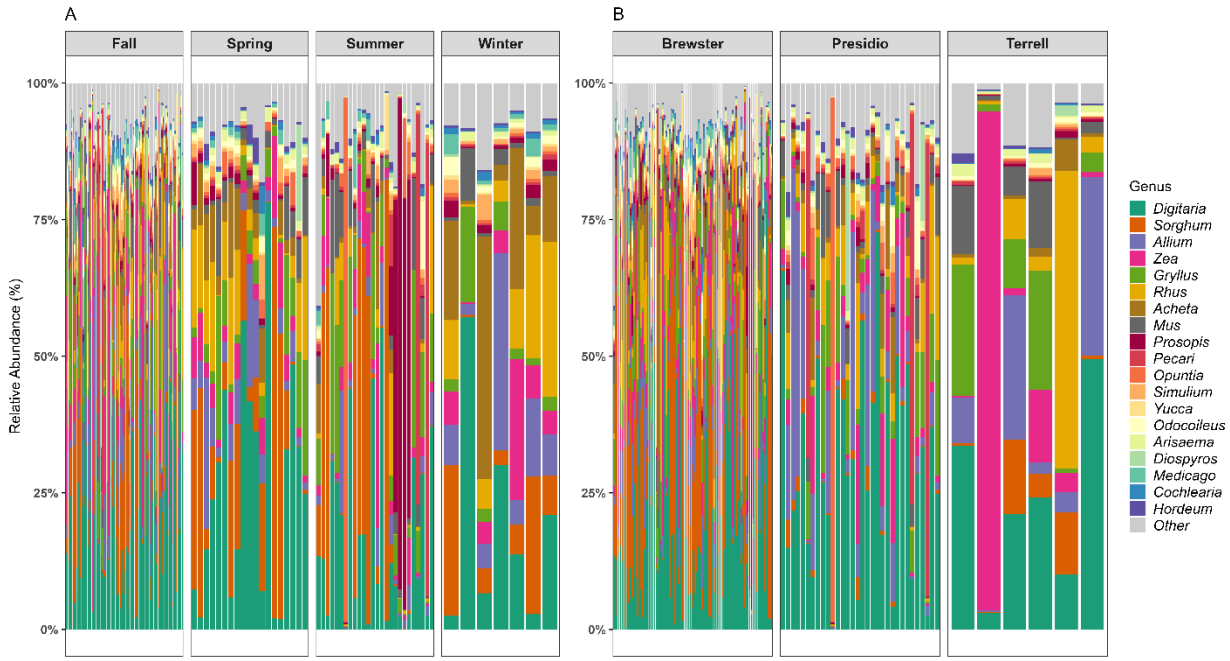



Figure 7. Relative abundance of dietary items across different (A) seasons and (B) localities, highlighting the most abundant genera identified from the custom eukaryote reference genomes and the NCBI nucleotide eukaryotes database.

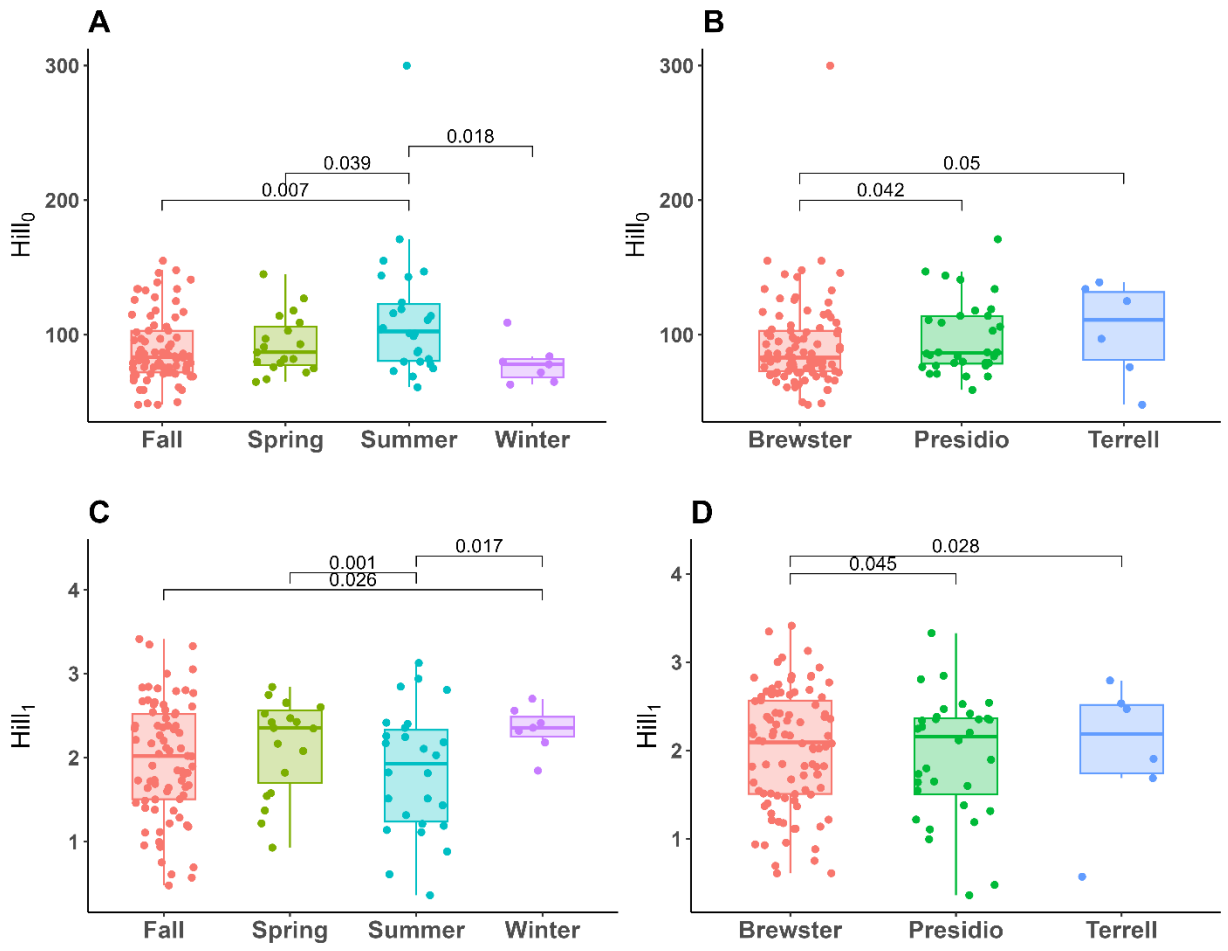



Figure 8. Dietary diversity, as measured by $Hill_0$ and $Hill_1$, is grouped by season (A and C) and locality (B and D). Boxplots are outlined by the interquartile range (IQR), with medians indicated by horizontal lines within the boxes and whiskers extend to 1.5 times the IQR. Pairwise comparisons are adjusted for multiple testing using Benjamini-Hochberg adjusted p-values derived from Tukey's HSD tests.

Table 1. Summary of samples collected during this project.

| TK | Sample | Date | Lat | Long | Elevation | County |
|---|---|---|---|---|---|---|
| TK273751 | Feces | 5-Aug-22 | 29.46725 | -102.8816694 | 2042 | Brewster |
| TK273752 | Feces | 31-Jul-22 | 29.4278556 | -102.8700972 | 1837 | Brewster |
| TK273753 | Feces | 1-Aug-22 | 29.4830306 | -102.8880556 | 2139 | Brewster |
| TK273754 | Feces | 31-Jul-22 | 29.4626472 | -102.8788167 | 2022 | Brewster |
| TK273755 | Feces | 31-Jul-22 | 29.4260861 | -102.87035 | 1856 | Brewster |
| TK273756 | Feces | 3-Aug-22 | 29.426525 | -102.8685778 | 1837 | Brewster |
| TK273757 | Feces | 3-Aug-22 | 29.426525 | -102.8685778 | 1837 | Brewster |
| TK273758 | Feces | 5-Aug-22 | 29.426525 | -102.8685778 | 1837 | Brewster |
| TK273759 | Feces | 2-Aug-22 | 29.4830306 | -102.8880556 | 2139 | Brewster |

| | | | | | | |
|---|---|---|---|---|---|---|
| TK273761 | Feces | 2-Aug-22 | 29.4830306 | -102.8880556 | 2139 | Brewster |
| TK273762 | Feces | 2-Aug-22 | 29.4830306 | -102.8880556 | 2139 | Brewster |
| TK273763 | Feces | 6-Aug-22 | 29.4830306 | -102.8880556 | 2139 | Brewster |
| TK273764 | Feces | 8-Aug-22 | 29.409475 | -102.8366722 | 1728 | Brewster |
| TK273765 | Feces | 9-Aug-22 | 29.4768667 | -102.8856722 | 2126 | Brewster |
| TK273766 | Feces | 16-Aug | 29.4076583 | -102.8392611 | 1772 | Brewster |
| TK273767 | Feces | 20-Aug-22 | 29.409475 | -102.8366722 | 1728 | Brewster |
| TK273768 | Feces | 20-Aug-22 | 29.4209028 | -102.8624639 | 1803 | Brewster |
| TK273769 | Feces | 25-Aug-22 | 29.4116972 | -102.8498444 | 1781 | Brewster |
| TK273770 | Feces | 25-Aug-22 | 29.4116972 | -102.8498444 | 1781 | Brewster |

| | | | | | | |
|---|---|---|---|---|---|---|
| TK273771 | Feces | 27-Aug-22 | 29.4785611 | -102.8876472 | 2149 | Brewster |
| TK273772 | Feces | 28-Aug-22 | 29.4070889 | -102.8368194 | 1769 | Brewster |
| TK273773 | Feces | 30-Aug-22 | 29.4077333 | -102.8387556 | 1772 | Brewster |
| TK273774 | Feces | 30-Aug-22 | 29.4089389 | -102.8376028 | 1736 | Brewster |
| TK273775 | Feces | 9-Sep-22 | 29.426525 | -102.8685778 | 1837 | Brewster |
| TK273776 | Feces | 11-Sep-22 | 29.4101306 | -102.8390333 | 1725 | Brewster |
| TK273777 | Feces | 11-Sep-22 | 29.4276361 | -102.8685778 | 1837 | Brewster |
| TK273778 | Feces | 11-Sep-22 | 29.4101028 | -102.8397167 | 1743 | Brewster |
| TK273779 | Feces | 12-Sep-22 | 29.4079167 | -102.8387861 | 1772 | Brewster |
| TK273780 | Feces | 12-Sep-22 | 29.4132778 | -102.8469583 | 1746 | Brewster |

| | | | | | | |
|---|---|---|---|---|---|---|
| TK273781 | Feces | 13-Sep-22 | 29.4079167 | -102.8387861 | 1772 | Brewster |
| TK273782 | Feces | 23-Sep-22 | 29.4653194 | -102.879725 | 2029 | Brewster |
| TK273783 | Feces | 25-Sep-22 | 29.4711778 | -102.9137833 | 2922 | Brewster |
| TK273784 | Feces | 25-Sep-22 | 29.4079167 | -102.8387861 | 1772 | Brewster |
| TK273785 | Feces | 1-Oct-22 | 29.4079472 | -102.8393972 | 1770 | Brewster |
| TK273786 | Feces | 1-Oct-22 | 29.426525 | -102.8685778 | 1837 | Brewster |
| TK273787 | Feces | 2-Oct-22 | 29.4077333 | -102.8387556 | 1772 | Brewster |
| TK273788 | Feces | 4-Oct-22 | 29.4297389 | -102.8560083 | 1828 | Brewster |
| TK273789 | Feces | 4-Oct-22 | 29.4284889 | -102.8562278 | 1819 | Brewster |
| TK273790 | Feces | 4-Oct-22 | 29.4278778 | -102.8555333 | 1819 | Brewster |

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|---|---|---|---|---|---|---|
| TK273791 | Feces | 4-Oct-22 | 29.4258111 | -102.8555333 | 1806 | Brewster |
| TK273792 | Feces | 4-Oct-22 | 29.4246222 | -102.8558417 | 1799 | Brewster |
| TK273793 | Feces | 4-Oct-22 | 29.4227889 | -102.8548333 | 1789 | Brewster |
| TK273794 | Feces | 6-Oct-22 | 29.4191361 | -102.8629861 | 1808 | Brewster |
| TK273795 | Feces | 6-Oct-22 | 29.4078333 | -102.83885 | 1772 | Brewster |
| TK273796 | Feces | 6-Oct-22 | 29.4077639 | -102.8387056 | 1773 | Brewster |
| TK273797 | Feces | 6-Oct-22 | 29.40775 | -102.8386667 | 1773 | Brewster |
| TK273798 | Feces | 6-Oct-22 | 29.4762833 | -102.8848639 | 2113 | Brewster |
| TK273799 | Feces | 6-Oct-22 | 29.4263194 | -102.8687639 | 1840 | Brewster |
| TK273800 | Feces | 6-Oct-22 | 29.4264861 | -102.8688472 | 1835 | Brewster |

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|---|---|---|---|---|---|---|
| TK273801 | Feces | 10-Oct-22 | 29.4077639 | -102.8387056 | 1773 | Brewster |
| TK273802 | Feces | 14-Oct-22 | 29.4394139 | -102.8661778 | 1887 | Brewster |
| TK273803 | Feces | 14-Oct-22 | 29.4340778 | -102.8659417 | 1860 | Brewster |
| TK273804 | Feces | 20-Oct-22 | 29.40755 | -102.8401083 | 1769 | Brewster |
| TK273805 | Feces | 24-Oct-22 | 29.4713639 | -102.8835694 | 2076 | Brewster |
| TK273806 | Feces | 29-Oct-22 | 29.4294861 | -102.8559528 | 1827 | Brewster |
| TK273807 | Feces | 30-Oct-22 | 29.4070111 | -102.8364028 | 1768 | Brewster |
| TK273808 | Feces | 31-Oct-22 | 29.4114278 | -102.8389222 | 1724 | Brewster |
| TK273809 | Feces | 9-Nov-22 | 29.4092806 | -102.8363472 | 1729 | Brewster |
| TK273810 | Feces | 9-Nov-22 | 29.4096028 | -102.8370111 | 1728 | Brewster |

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|---|---|---|---|---|---|---|
| TK273811 | Feces | 10-Nov-22 | 29.4174333 | -102.8564972 | 1784 | Brewster |
| TK273812 | Feces | 1-Dec-22 | 29.4101917 | -102.8394361 | 1726 | Brewster |
| TK273813 | Feces | 13-Dec-22 | 29.4109806 | -102.8476389 | 1765 | Brewster |
| TK273814 | Feces | 28-Dec-22 | 29.4080361 | -102.8387056 | 1772 | Brewster |
| TK273815 | Feces | 3-Jan-23 | 29.4080111 | -102.8365806 | 1773 | Brewster |
| TK273816 | Feces | 8-Jan-23 | 29.4096028 | -102.8368083 | 1727 | Brewster |
| TK273817 | Feces | 8-Jan-23 | 29.4096861 | -102.8368083 | 1729 | Brewster |
| TK273818 | Feces | 13-Jan-23 | 29.426525 | -102.8685778 | 1838 | Brewster |
| TK273819 | Feces | 14-Mar-23 | 29.4297389 | -102.8560139 | 1829 | Brewster |
| TK273820 | Feces | 14-Mar-23 | 29.4297389 | -102.8560139 | 1829 | Brewster |

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|---|---|---|---|---|---|---|
| TK273821 | Feces | 14-Mar-23 | 29.4297389 | -102.8560139 | 1829 | Brewster |
| TK273822 | Feces | 14-Mar-23 | 29.4297389 | -102.8560139 | 1829 | Brewster |
| TK273823 | Feces | 14-Mar-23 | 29.4297389 | -102.8560139 | 1829 | Brewster |
| TK273824 | Feces | 14-Mar-23 | 29.4297389 | -102.8560139 | 1829 | Brewster |
| TK273825 | Feces | 14-Mar-23 | 29.4297389 | -102.8560139 | 1829 | Brewster |
| TK273826 | Feces | 14-Mar-23 | 29.4297389 | -102.8560139 | 1829 | Brewster |
| TK273827 | Feces | 14-Mar-23 | 29.4297389 | -102.8560139 | 1829 | Brewster |
| TK273828 | Feces | 14-Mar-23 | 29.4297389 | -102.8560139 | 1829 | Brewster |
| TK273829 | Feces | | 29.573743 | -103.812902 | | Presidio |
| TK273830 | Feces | 14-Nov-22 | | | | Brewster |

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|---|---|---|---|---|---|
| TK273831 | Feces | 1-Nov-22 | 29.576265 | -103.80963 | Presidio |
| TK273832 | Feces | 13-Oct-22 | | | Brewster |
| TK273833 | Feces | 1-Nov-22 | 29.562627 | -103.817733 | Presidio |
| TK273834 | Feces | 13-Oct-22 | | | Brewster |
| TK273835 | Feces | 13-Oct-22 | | | Brewster |
| TK273836 | Feces | 13-Oct-22 | | | Brewster |
| TK273837 | Feces | 1-Nov-22 | | | Presidio |
| TK273838 | Feces | 25-Oct-22 | | | Terrell |
| TK273839 | Feces | | | | Jeff Davis |
| TK273840 | Tissue | 1-Dec-22 | | | Brewster |

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|---|---|---|---|---|---|
| TK273841 | Skull | 28-Nov-22 | 29.93018 | -102.44162 | Brewster |
| TK273842 | Tissue | 17-Jun-19 | | | Jeff Davis |
| TK273843 | Hair | 18-Sep-20 | 30.0783333 | -102.3969444 | Terrell |
| TK273844 | Hair | 15-Jun-18 | | | Brewster |
| TK273845 | Tissue | 6-Sep-19 | | | Brewster |
| TK273846 | Hair | 8-Nov-19 | | | Brewster |
| TK273847 | Hair | 6-Sep-19 | | | Brewster |
| TK273848 | Hair | 9-Nov-17 | | | Brewster |
| TK273849 | Hair | | | | Brewster |
| TK273850 | Feces | 1-Nov-22 | | | Presidio |

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|---|---|---|---|
| TK273851 | Feces | 1-Nov-22 | Presidio |
| TK273852 | Feces | 1-Nov-22 | Presidio |
| TK273853 | Feces | 1-Nov-22 | Presidio |
| TK273854 | Feces | 1-Nov-22 | Presidio |
| TK273855 | Feces | 13-Oct-22 | Brewster |
| TK273856 | Feces | 13-Oct-22 | Brewster |
| TK273857 | Feces | 13-Oct-22 | Brewster |
| TK273858 | Feces | 13-Oct-22 | Brewster |
| TK273859 | Feces | 13-Oct-22 | Brewster |
| TK273860 | Feces | 13-Oct-22 | Brewster |

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|---|---|---|---|---|---|
| TK273861 | Tissue | 28-Jun-23 | | | Presidio |
| TK273862 | Hair | 29-Apr-23 | | | Brewster |
| TK273863 | Feces | 25-Oct-22 | | | Terrell |
| TK273864 | Feces | 25-Oct-22 | | | Terrell |
| TK273865 | Feces | 25-Oct-22 | | | Terrell |
| TK273866 | Feces | 25-Oct-22 | | | Terrell |
| TK273867 | Feces | 25-Oct-22 | | | Terrell |
| TK273868 | Feces | 1-Nov-22 | 29.562627 | -103.817733 | Presidio |
| TK273869 | Feces | 1-Nov-22 | 29.562627 | -103.817733 | Presidio |
| TK273870 | Feces | 1-Nov-22 | 29.562627 | -103.817733 | Presidio |

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|---|---|---|---|---|---|
| TK273871 | Feces | 1-Nov-22 | 29.562627 | -103.817733 | Presidio |
| TK273872 | Feces | 1-Nov-22 | 29.562627 | -103.817733 | Presidio |
| TK273873 | Feces | 13-Oct-22 | | | Brewster |
| TK273874 | Feces | 13-Oct-22 | | | Brewster |
| TK273875 | Feces | 13-Oct-22 | | | Brewster |
| TK273876 | Feces | 19-Jul-21 | | | Brewster |
| TK273877 | Feces | 19-Jul-23 | | | Brewster |
| TK273878 | Feces | 19-Jul-23 | | | Brewster |
| TK273879 | Feces | 19-Jul-23 | | | Brewster |
| TK273880 | Feces | 19-Jul-23 | | | Brewster |

| | | | | | |
|---|---|---|---|---|---|
| TK273881 | Feces | 19-Jul-23 | | | Brewster |
| TK273882 | Feces | 20-Jul-23 | | | Brewster |
| TK273883 | Feces | 21-Jul-23 | | | Brewster |
| TK273884 | Feces | 1-Nov-22 | 29.576265 | -103.80963 | Presidio |
| TK273885 | Feces | 1-Nov-22 | 29.576265 | -103.80963 | Presidio |
| TK273886 | Feces | 1-Nov-22 | 29.576265 | -103.80963 | Presidio |
| TK273887 | Feces | 1-Nov-22 | 29.576265 | -103.80963 | Presidio |
| TK273888 | Feces | 1-Nov-22 | 29.576265 | -103.80963 | Presidio |
| TK273889 | Feces | 1-Nov-22 | 29.576265 | -103.80963 | Presidio |
| TK273890 | Feces | 1-Nov-22 | 29.576265 | -103.80963 | Presidio |

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|---|---|---|---|---|---|
| TK273891 | Feces | 1-Nov-22 | 29.576265 | -103.80963 | Presidio |
| TK273892 | Feces | 1-Nov-22 | 29.576265 | -103.80963 | Presidio |
| TK273893 | Feces | 13-Oct-22 | | | Brewster |
| TK273894 | Feces | 13-Oct-22 | | | Brewster |
| TK273895 | Feces | 13-Oct-22 | | | Brewster |
| TK273896 | Feces | 13-Oct-22 | | | Brewster |
| TK273897 | Feces | 13-Oct-22 | | | Brewster |
| TK273898 | Feces | 13-Oct-22 | | | Brewster |
| TK273899 | Feces | 13-Oct-22 | | | Brewster |
| TK273900 | Feces | 13-Oct-22 | | | Brewster |

| | | | | | | |
|---|---|---|---|---|---|---|
| TK273901 | Feces | 13-Oct-22 | | | | Brewster |
| TK273902 | Feces | 10-May-22 | 29.409108 | -102.883266 | 2158 | Brewster |
| TK273903 | Feces | 14-May-22 | 29.460241 | -102.884438 | 2191 | Brewster |
| TK273904 | Feces | 10-May-22 | 29.409108 | -102.883266 | 2158 | Brewster |
| TK273905 | Feces | 10-May-22 | 29.4121583 | -102.8746388 | 2124 | Brewster |
| TK273906 | Feces | 10-May-22 | 29.409108 | -102.883266 | 2158 | Brewster |
| TK273907 | Feces | 10-May-22 | 29.409108 | -102.883266 | 2158 | Brewster |
| TK273908 | Tissue, hair | 12-Jul-23 | | | | Pecos |
| TK202901 | Tissue | 7-Aug-20 | 32.859583 | -101.023722 | | Scurry |
| TK163843 | Tissue, colon, hair | 21-May-22 | 36.938863 | -105.198777 | | Hudspeth |

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|---|---|---|---|
| TK273926 | Feces | 31-May-22 | Presidio |
| TK273927 | Feces | 3-Jun-20 | Presidio |
| TK273928 | Feces | 3-Jun-20 | Presidio |
| TK273929 | Feces | 3-Jun-21 | Presidio |
| TK273930 | Feces | 31-May-22 | Presidio |
| TK273931 | Feces | 3-Jun-21 | Presidio |
| TK273932 | Feces | 5-Jun-23 | Presidio |
| TK273933 | Feces | 7-Jun-23 | Presidio |
| TK273934 | Feces | 3-Jun-20 | Presidio |
| TK273935 | Feces | 16-May-17 | Presidio |

| | | | | | |
|---|---|---|---|---|---|
| TK273936 | Feces | 3-Jun-21 | | | Presidio |
| TK273937 | Feces | 28-Oct-23 | | | Val Verde |
| TK273938 | Hair | 30-Sep-23 | | | Uvalde |
| TK273944 | Liver | 19-Dec-23 | | | Brewster |
| TK273945 | Muscle | 3-Jun-24 | 30.05104 | -103.28088 | Brewster |
| TK273946 | Hair | 16-Jul-24 | 30.0725 | -102.85681 | Brewster |
| TK273947 | Hair | 9-May-24 | 29.74835 | -102.7438 | Brewster |
| TK273948 | Hair | 22-Jul-24 | | | Brewster |

Table 2. Summary of bear genome sequencing effort.

| ID | Tissue Type | Sum Aligned bp | Duplicate Proportion | Sites Genotyped | Observed Heterozygosity | Genetic Cluster |
|---|---|---|---|---|---|---|
| LSUMZ_5770 | Muscle | 63782325665 | 0.143853 | 2263433566 | 0.000933062 | Louisiana |
| LSUMZ_5771 | Muscle | 45747592701 | 0.15137 | 2241096634 | 0.000828656 | Louisiana |
| LSUMZ_6128 | Muscle | 43863916015 | 0.171493 | 2218586943 | 0.00087634 | Louisiana |
| LSUMZ_6144 | Muscle | 36186528959 | 0.169208 | 2185323129 | 0.000817717 | Louisiana |
| LSUMZ_6235 | Muscle | 3434524948 | 0.573077 | 45166275 | 0.000657544 | |
| LSUMZ_6236 | Muscle | 15453323282 | 0.132962 | 1054830909 | 0.000570011 | Louisiana |
| MSB142859 | Muscle | 55579859321 | 0.15157 | 2269366281 | 0.000860047 | New Mexico |
| MSB142898 | Muscle | 32428247605 | 0.144349 | 2162731671 | 0.000785306 | New Mexico |
| MSB142905 | Muscle | 38313365649 | 0.121055 | 2136098118 | 0.000737145 | New Mexico |
| MSB196656 | Muscle | 14196856974 | 0.432272 | 429116822 | 0.000536662 | New Mexico |
| MSB85637 | Muscle | 19751311061 | 0.150778 | 944196014 | 0.000518251 | New Mexico |
| MSB92696 | Muscle | 25489660892 | 0.151326 | 1736253851 | 0.000704724 | New Mexico |
| TK163843_1a | Muscle | 21024094708 | 0.099054 | 1598930424 | 0.000701731 | New Mexico |
| TK163843_1b | Hair | 48645412159 | 0.169947 | 2225060508 | 0.000762581 | New Mexico |
| TK202901 | Muscle | 20757540199 | 0.111471 | 1622151001 | 0.000834946 | New Mexico |
| TK273751 | Feces | 21157072039 | 0.611516 | 437296541 | 0.001190466 | Trans Pecos |
| TK273755 | Feces | 15024584016 | 0.300705 | 192992586 | 0.001167482 | Trans Pecos |
| TK273756 | Feces | 13247859430 | 0.325736 | 135542836 | 0.001190852 | Trans Pecos |
| TK273758 | Feces | 10759036268 | 0.540833 | 81432894 | 0.001256919 | |
| TK273761 | Feces | 10521974173 | 0.368729 | 271971141 | 0.00091028 | Trans Pecos |
| TK273773 | Feces | 10665133103 | 0.562533 | 212140602 | 0.001243209 | Trans Pecos |
| TK273776 | Feces | 36953445486 | 0.412841 | 466037084 | 0.001089122 | Trans Pecos |
| TK273777 | Feces | 4784299117 | 0.697924 | 55060813 | 0.00116226 | |
| TK273778 | Feces | 29949078757 | 0.416439 | 499186013 | 0.001231184 | Trans Pecos |
| TK273779 | Feces | 48625959755 | 0.407197 | 1437716274 | 0.001011757 | Trans Pecos |
| TK273780 | Feces | 30031525967 | 0.607023 | 1183272276 | 0.001015276 | Trans Pecos |
| TK273782 | Feces | 8803599393 | 0.378632 | 341411843 | 0.000924117 | Trans Pecos |

| | | | | | | |
|---|---|---|---|---|---|---|
| TK273783 | Feces | 19434889386 | 0.424289 | 1327750910 | 0.00097088 | Trans Pecos |
| TK273840 | Muscle | 29389087228 | 0.090172 | 1903105921 | 0.000949461 | Trans Pecos |
| TK273842 | Muscle | 14380545670 | 0.087918 | 944426221 | 0.00093471 | Trans Pecos |
| TK273843 | Hair | 44376328168 | 0.181458 | 2247786707 | 0.001018738 | Trans Pecos |
| TK273844 | Hair | 50490185037 | 0.266282 | 2250526944 | 0.001076706 | Trans Pecos |
| TK273845 | Muscle | 34919763180 | 0.112415 | 2054555474 | 0.000974265 | Trans Pecos |
| TK273846 | Hair | 48401665957 | 0.19797 | 2238240084 | 0.001049805 | Trans Pecos |
| TK273847 | Hair | 28546368734 | 0.354627 | 1914224807 | 0.000920728 | Trans Pecos |
| TK273848 | Hair | 40903202326 | 0.477104 | 2196697445 | 0.001062787 | Trans Pecos |
| TK273862 | Hair | 30461540684 | 0.221178 | 2053757803 | 0.00100591 | Trans Pecos |
| TK273908_1a | Muscle | 16492882337 | 0.089175 | 1332227925 | 0.000900746 | Trans Pecos |
| TK273908_1b | Hair | 20364065165 | 0.169691 | 1574710251 | 0.000943176 | Trans Pecos |
| TK273938 | Hair | 34358518015 | 0.286353 | 2153772561 | 0.001024639 | Trans Pecos |
| TK273944 | Muscle | 59335314746 | 0.248836 | 2268456987 | 0.001096491 | Trans Pecos |
| TK273945 | Muscle | 981400369 | 0.826865 | 1323502 | 0.000544915 | |
| TK273946 | Hair | 9304178892 | 0.229667 | 503154507 | 0.000632414 | Trans Pecos |
| TK273947 | Hair | 71132612402 | 0.345016 | 2272604152 | 0.001089501 | Trans Pecos |
| TK273948 | Hair | 60032236141 | 0.208819 | 2250000996 | 0.001052185 | Trans Pecos |

Table 3: Pairwise Test results examining the impact of temporal and spatial factors on diet composition, using Jaccard and Bray-Curtis dissimilarity indices.

| **Dissimilarity index** | **Season** | **F** | **$R^2$** | **P-value** |
|---|---|---|---|---|
| Jaccard | Summer vs Fall | 2.55 | 0.043 | 0.015* |
| | Summer vs Winter | 1.77 | 0.037 | 0.007* |
| | Summer vs Spring | 2.09 | 0.049 | 0.046* |
| | Fall vs Winter | 1.21 | 0.014 | 0.283 |
| | Fall vs Spring | 0.78 | 0.008 | 0.567 |
| | Winter vs Spring | 0.95 | 0.038 | 0.393 |
| | **Locality** | | | |
| | Brewster vs Presidio | 3.41 | 0.062 | 0.006* |
| | Brewster vs Terrell | 2.07 | 0.057 | 0.04* |
| | Presidio vs Terrell | 1.45 | 0.038 | 0.16 |
| Bray-Curtis | **Season** | **F** | **$R^2$** | **P-value** |
| | Summer vs Fall | 2.92 | 0.067 | 0.017* |
| | Summer vs Winter | 1.81 | 0.045 | 0.012* |
| | Summer vs Spring | 2.23 | 0.059 | 0.009* |
| | Fall vs Winter | 1.00 | 0.012 | 0.35 |
| | Fall vs Spring | 0.64 | 0.006 | 0.654 |
| | Winter vs Spring | 0.88 | 0.035 | 0.435 |
| | **Locality** | | | |
| | Brewster vs Presidio | 3.98 | 0.081 | 0.005* |
| | Brewster vs Terrell | 2.38 | 0.073 | 0.042* |
| | Presidio vs Terrell | 1.63 | 0.043 | 0.127 |

Table 4. Primer sequences with Illumina overhang adapters used for SNP genotyping of black bear samples.

| Sequence Name | Direction | Primer with Overhang |
|---|---|---|
| kinship_snp1 - 100 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGAGCTCAGCAGGGACAGT |
| kinship_snp1 - 309 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCTCAAGCGGTGGAAGCA |
| kinship_snp2 - 99 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGTAGGCCATCTCACCACG |
| kinship_snp2 - 293 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTAGTGCTCTGTGTTTTCGC |
| kinship_snp3 - 126 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGAAGATGACAGTGTAGCCT |
| kinship_snp3 - 325 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGAGGGAGGGAGAACATG |
| kinship_snp4 - 96 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGTACAGGGCTCTGGCATTG |
| kinship_snp4 - 295 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCCCTTGTTTCTCAGCCTTG |
| kinship_snp5 - 93 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCATCACAGCGGCGGTTTTC |
| kinship_snp5 - 284 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGACCCCAGGTTGATGAAACACA |
| kinship_snp6 - 101 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGAGCAGCCACGATATTTCAAC |
| kinship_snp6 - 300 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGCAGGGGTGGGACTTAAG |
| kinship_snp7 - 106 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCACAGCTCCTAAGGTCGTGAG |
| kinship_snp7 - 262 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGACAGCTCTGGGGGAACAAGG |
| kinship_snp8 - 104 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGAAGCTTTCACTGGCCTTTTAC |
| kinship_snp8 - 303 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGCTCCTGTCCCTGACTTG |
| kinship_snp9 - 103 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACTGAATAAAAAGTCCCCTTCTGG |
| kinship_snp9 - 301 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAAGCTGGGGTCCCTGTGTA |

| | | |
|---|---|---|
| kinship_snp10 - 157 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACAAAAAGCAGACGACATGAAG |
| kinship_snp10 - 325 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCACTGGCTCCCATTTTCTC |
| kinship_snp11 - 110 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCTGCACGGACATCCTCTC |
| kinship_snp11 - 307 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTCAGAGGAGCATGGGGAC |
| kinship_snp12 - 95 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGCTTTTTAAAAGGGTCACGC |
| kinship_snp12 - 294 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCGACCTACGCTTCAAGAAAAG |
| kinship_snp13 - 125 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGCTCACCCCACAGGATTG |
| kinship_snp13 - 324 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCACACACACATTGCGGCAC |
| kinship_snp14 - 90 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATAGTTGGGAGGTGGGGTG |
| kinship_snp14 - 292 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCAAGCTGGTGGCCTTTG |
| kinship_snp15 - 82 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGTCCCATAGCGCATGTC |
| kinship_snp15 - 281 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTCTTTTGAGGTCTGCTTGG |
| kinship_snp16 - 111 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGATTCAGGCTTAGGAGGTC |
| kinship_snp16 - 310 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCACTTAGAGTCAGGTGGC |
| kinship_snp17 - 118 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCACTTCTTGGTACATCCTGTTTG |
| kinship_snp17 - 317 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAAAATCCCCGCACCTACCA |
| kinship_snp18 - 122 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGTCTCAGGAGTGCGTGGAC |
| kinship_snp18 - 312 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTCTCGTCAGACACACGCTC |
| kinship_snp19 - 126 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGTTTGCTGGAGGCTGAGTC |
| kinship_snp19 - 325 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCCTCCACCTTAATGAAGAGC |
| kinship_snp20 - 108 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGACACCTTCCTTCACGTCC |
| kinship_snp20 - 307 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCTTCCCCGACTCAGTCTTC |
| kinship_snp21 - 108 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCTGAGTCTCCTGGGAAGG |
| kinship_snp21 - 307 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGGAAATGAGAAGCGAGCCTC |
| kinship_snp22 - 57 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGTATATCTCCCTGCGGCTGTC |
| kinship_snp22 - 272 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCCAAGTCCTTCTCGGCCAG |
| kinship_snp23 - 112 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGAAACAGGGTAGGGTGAAGC |
| kinship_snp23 - 311 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGGTGGGAGAAGGATGCAG |
| kinship_snp24 - 117 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCCTCTAGGAAGGGTCATGA |
| kinship_snp24 - 316 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTCCACTGTGATTTCCCCAC |
| kinship_snp25 - 108 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTTTTCTAGTTGTACACAGGCC |
| kinship_snp25 - 307 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTGTCCCAGCATCAATGTGA |
| kinship_snp26 - 77 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCATTAACCCTTGGTGCAGC |
| kinship_snp26 - 239 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCGCTGCAGAAACACATGAC |
| kinship_snp27 - 116 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACATGAGAATCTCCCACTCTG |
| kinship_snp27 - 315 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAAGTCCCTCTCCAGTGTCG |
| kinship_snp28 - 116 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGGCACGCTGAATCCTCCT |
| kinship_snp28 - 308 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCAGCAAGGACGTGAAGGCA |
| kinship_snp29 - 121 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAAGGTGACGGGTGCATAC |
| kinship_snp29 - 320 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCGCTTAACCAACTGAGCCC |
| kinship_snp30 - 86 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCAGCTGGCACTTTCATGG |
| kinship_snp30 - 262 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCATGCCAGCAAAGCCACA |
| kinship_snp31 - 131 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACCACCAGCCAGTTCGCTA |
| kinship_snp31 - 311 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTGATCTGCCAGCTGTGCA |
| kinship_snp32 - 119 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACAATAGTCCTGGGGTCCA |
| kinship_snp32 - 319 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAACACTACGGCAGACATGG |

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|---|---|---|
| kinship_snp33 - 97 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCACACACTCGGCTTCTAACC |
| kinship_snp33 - 296 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCGACGCCCACCTAGGATTC |
| kinship_snp34 - 103 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGCTTGGGATCTTGTGGAT |
| kinship_snp34 - 303 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTGGGAGAGGAAGAAGCAG |
| kinship_snp35 - 60 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCAACTGGAGCAGAGCCGAGA |
| kinship_snp35 - 254 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGCTCCCCATTCTATAGCTAAGGC |
| kinship_snp36 - 95 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCAAAAAGATGCGGGAAGAGC |
| kinship_snp36 - 294 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAAGAAGGCTGTGCGGTTG |
| kinship_snp37 - 110 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCATTTGAGGGAGAGAGCG |
| kinship_snp37 - 309 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGCCTTGGGTGCTTCTAAATC |
| kinship_snp38 - 61 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAAGGACAGAGGGAGAGAGG |
| kinship_snp38 - 260 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTGTGTCCTGTGATGATTCTCA |
| kinship_snp39 - 77 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGACAAGGTTCTCAGGCAGTC |
| kinship_snp39 - 268 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGTCCAAAAGGCCACCAAAG |
| kinship_snp40 - 67 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACAGACGCCAAGGCACAGA |
| kinship_snp40 - 271 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGCCCTCGGAAGGTGTTTAC |
| kinship_snp41 - 83 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTGCGTGCATTTCTTTTAGA |
| kinship_snp41 - 282 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGAGACACAACAGCCGAAG |
| kinship_snp42 - 120 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGCAGGCATCAGCAGAGTG |
| kinship_snp42 - 321 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTTTCCTCAGCTGTAAAATGGAAC |
| kinship_snp43 - 86 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTTTTCCCTAGGTGGCAGGC |
| kinship_snp43 - 266 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGAGCGTCACACCGAACCTTC |
| kinship_snp44 - 82 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGATGATGGGCAGGGAAAG |
| kinship_snp44 - 281 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCGCAGAAGAGAGAAGGCTTG |
| kinship_snp45 - 113 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCAGGGAAATCAATGTCCTGC |
| kinship_snp45 - 312 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCAGCTAGAACCATTTTCGGT |
| kinship_snp46 - 117 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAAGAGACAAAAGGAGCCCAG |
| kinship_snp46 - 316 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCCATCCGGACTGAAAGATG |
| kinship_snp47 - 113 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTGCTCGAGAAATGGCCCTG |
| kinship_snp47 - 312 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTGCAGGCTATTTCCCGCA |
| kinship_snp48 - 79 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACATAGACAGAGACAGCCAG |
| kinship_snp48 - 278 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTCGATCCTGCCATACACTG |
| kinship_snp49 - 75 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCATCTGGGCCACTACTCTG |
| kinship_snp49 - 274 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGAGTAATGAAGGTCATGTGCAG |
| kinship_snp50 - 93 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGGCTCCACTTAGGACCAAG |
| kinship_snp50 - 292 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCAGGCCACAAATCATTCATTAGC |
| kinship_snp51 - 77 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGGGACAAGAGTGAGTATAAGTG |
| kinship_snp51 - 227 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGGACGGGCAAAGAGAAGAGA |
| kinship_snp52 - 84 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGAAAGAACTTGTAAGGCTGC |
| kinship_snp52 - 281 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTTTGCCCCCAAACTCCAG |
| kinship_snp53 - 85 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGAAGGTCCTAGAATCAGTGCG |
| kinship_snp53 - 284 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGATTGGAAACCCTGTTGCAAC |
| kinship_snp54 - 103 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGAACCGTTGAAACACGAAGG |
| kinship_snp54 - 302 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGGGACAGATTAGAGCCACG |
| kinship_snp55 - 151 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCGAACACGAGGGTTAGG |
| kinship_snp55 - 324 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCGCTGAGATCTTCCTCCTG |

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|---|---|---|
| kinship_snp56 - 85 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGTCCTATACCCGCAGAAGG |
| kinship_snp56 - 285 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGCGTAAAGAGTCTTGGCTTA |
| kinship_snp57 - 114 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGCTCGTGGAGACTCCTAAT |
| kinship_snp57 - 313 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTTTGCCCGTCTTCCAGGT |
| kinship_snp58 - 77 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCGGACTCGTAGACAGTCAC |
| kinship_snp58 - 272 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCAGCACATCTCTGTCCTTTGT |
| kinship_snp59 - 96 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGCAGCTTTCACGCTACG |
| kinship_snp59 - 295 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGGATCTCGGCACAACGA |
| kinship_snp60 - 120 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCTGGGAAGACGGAGAGCTG |
| kinship_snp60 - 319 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTGGGAGGTTCTTGCAAAAGT |
| kinship_snp61 - 105 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACGGAGAGTCTCACGTACG |
| kinship_snp61 - 304 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTCCTTGAGCCCTGTGTTC |
| kinship_snp62 - 132 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGGAAGAGGGAGAGGTGTGC |
| kinship_snp62 - 325 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTGTTCTCTAGGTCTTCAGCTACC |
| kinship_snp63 - 70 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCTTGCGGATTCTTTTCCATC |
| kinship_snp63 - 269 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTTCTTGGCGTCCATGGAG |
| kinship_snp64 - 82 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGAATGACCCTTCCTCACGC |
| kinship_snp64 - 281 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGACTTAGCAGAGCAGGAACC |
| kinship_snp65 - 104 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGAGTAGGCAAGTGGACAGTG |
| kinship_snp65 - 303 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGACTAAGGGTTCACGGAGAC |
| kinship_snp66 - 141 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCGAGTCCGGAAGCAACAAGTG |
| kinship_snp66 - 342 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGGGGACGAGAGGCAAGCT |
| kinship_snp67 - 78 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTCGAGGGAAGAGATCTGC |
| kinship_snp67 - 277 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGATTGTTACACACTTCCTGC |
| kinship_snp68 - 110 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAAACAAAAGGGGGAGGCC |
| kinship_snp68 - 316 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCACTATACCTCAGCCCTG |
| kinship_snp69 - 87 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTGACATACAGGGAGACAC |
| kinship_snp69 - 286 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTCCTCTAGACTGCTGGAA |
| kinship_snp70 - 78 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCGCGTCACATACTAAGTGTTC |
| kinship_snp70 - 277 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGTGGTTCATTCATACCCCG |
| kinship_snp71 - 124 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCAAAGAGCAACGGTTCAGATC |
| kinship_snp71 - 323 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGCTGTCACGGGCTTATAGGA |
| kinship_snp72 - 105 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCGGAGATGTTCTGTCCCCA |
| kinship_snp72 - 304 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTGGGAAAGGTCCTTGAGAC |
| kinship_snp73 - 87 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCCTCTTTGTCTGACTGCAC |
| kinship_snp73 - 286 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGACCCTGCCCTATCGAGTTC |
| kinship_snp74 - 125 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTGGGTCAGCTGTGAGTCAC |
| kinship_snp74 - 323 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCAGTGGAAATGATACTGGGCC |
| kinship_snp75 - 83 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGAAACATTCGCTCCACCG |
| kinship_snp75 - 282 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTACTGGTCTCTGTCCCGAT |
| kinship_snp76 - 126 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGTGACAGGAAGTGATCAGGC |
| kinship_snp76 - 325 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCAACAGCACCTCAGAGGCT |
| kinship_snp77 - 75 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCCTCTGGTGTTTCCTGTG |
| kinship_snp77 - 265 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGCGAGCAGATTCCACCT |
| kinship_snp78 - 102 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATCTACGCCTCAGGGAAGTG |
| kinship_snp78 - 301 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGTCCCCACCTCTGAAGAC |

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|---|---|---|
| kinship_snp79 - 109 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTCCTCTGTGCTCCTGTGC |
| kinship_snp79 - 308 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCTGGTCAATTTTCAAGTCGC |
| kinship_snp80 - 92 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATCCTCCAAGATGCTCTTTGG |
| kinship_snp80 - 291 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGCTCCATCTGAGTTGAATCC |
| kinship_snp81 - 121 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGGAAGAGGCATGTAAGATGAAG |
| kinship_snp81 - 317 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCAGGCGAGTGAGAGAGGAAG |
| kinship_snp82 - 122 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTAGCCCCATGTTCTAACCAG |
| kinship_snp82 - 321 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGGAAGCCTCAGAAATGACC |
| kinship_snp83 - 75 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGCTCAACGTGTCCAGAAC |
| kinship_snp83 - 274 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGCACTAAGGATGAGCGTGAG |
| kinship_snp84 - 109 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCGACATGGACCCACAATATG |
| kinship_snp84 - 309 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAACACGAGAAGCTGGGAAAG |
| kinship_snp85 - 76 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACGTTGGAACCCCTGAGATC |
| kinship_snp85 - 272 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGGGGCTAAATACACACCCG |
| kinship_snp86 - 107 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTCTCGGTGTAAAGGAGGAC |
| kinship_snp86 - 306 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCCCCTATTCTGTAGGCATC |
| kinship_snp87 - 123 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCACCTGTCAAGTCTGAAGC |
| kinship_snp87 - 322 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAAAGAAGCAGAGACGGCAG |
| kinship_snp88 - 80 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCCAGTCTGCTCTTTGTTGG |
| kinship_snp88 - 279 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGCCTCCATGTTGCTTATGAG |
| kinship_snp89 - 88 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATCTCCAATAAAGTCACGGTCC |
| kinship_snp89 - 287 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAAACGCTGGGCAACATCC |
| kinship_snp90 - 61 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGCATGAAGCCTGCAGGAC |
| kinship_snp90 - 240 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGGGACACCGTGACCTTAGAG |
| kinship_snp91 - 108 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGTTCTGGCACTGGAGACTG |
| kinship_snp91 - 304 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGGAGATCCTTTCCAGAACC |
| kinship_snp92 - 93 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGCAGCAATGCTCGGGAAG |
| kinship_snp92 - 292 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCTGTAGCCTGTTCGTAGCC |
| kinship_snp93 - 85 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCATCTGCCACATACGGGGAC |
| kinship_snp93 - 286 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCAAGTCCAAGGCCTCCCAG |
| kinship_snp94 - 106 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCGTTACTGAATCTCCCTTCTG |
| kinship_snp94 - 306 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTAAATGAACTCGCTGGGTG |
| kinship_snp95 - 83 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGGGCGTAAATAAGTCAGAG |
| kinship_snp95 - 282 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGCCTTGGTCACGTTATCC |
| kinship_snp96 - 116 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCGACATTGCCTCCCTTTCG |
| kinship_snp96 - 315 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGAGATCAGAGAGGTTAAGCCAC |
| kinship_snp97 - 75 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCGGAAATGCCTCCCTTC |
| kinship_snp97 - 274 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTCCCCATTCCTCATCTGC |
| kinship_snp98 - 76 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATGGGAGACAGAGGCAGTG |
| kinship_snp98 - 283 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCCGTAAGCTAAGGGACGC |
| kinship_snp99 - 128 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGTGGGCGACATCATGGCT |
| kinship_snp99 - 325 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCTGGCACCGAAGAAGGAAAG |
| kinship_snp100 - 77 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCAGAACGAGCCACTCACACC |
| kinship_snp100 - 280 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCACAGCAAACCCTCGGGATC |
| kinship_snp101 - 82 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTCTCCCTTCAATGAGTTTACCTG |
| kinship_snp101 - 279 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCTAGCACCGGCACTCTGA |

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|---|---|---|
| kinship_snp102 - 118 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCCTCTTAATAATGCTCTCTCTG |
| kinship_snp102 - 317 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTCTTTCACACTCAGTCCTTG |
| kinship_snp103 - 131 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACAGCAGGCATTTCCCAC |
| kinship_snp103 - 330 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCGTTGGTTCAGCAGCTGATA |
| kinship_snp104 - 130 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTAAAGTCTGCTGTTACAGGCC |
| kinship_snp104 - 329 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGCAGCAGTGTCGAGTTTC |
| kinship_snp105 - 39 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTAAGGCTAGGGATGGGGCT |
| kinship_snp105 - 238 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCTGCCACTTAGAAACCTGC |
| kinship_snp106 - 99 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCTATTAGGAAAGCTTGGGGAAG |
| kinship_snp106 - 297 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGGGACAAGTGACCACCAAAC |
| kinship_snp107 - 126 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCAGATCTCATGCAGACATC |
| kinship_snp107 - 328 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCTGACTTTGTTGTTGTCTTTG |
| kinship_snp108 - 80 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGAAGAAGACCAGTACCCCCA |
| kinship_snp108 - 279 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTTGATCGATGGCCCCTAAC |
| kinship_snp109 - 129 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCTCTCGTCTCTGCCTTTAC |
| kinship_snp109 - 329 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTGAGTGTGACCTTATTTCCA |
| kinship_snp110 - 81 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGACGTCACAGCCACCAATG |
| kinship_snp110 - 257 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGCTTGGTAGGATGTGGGACG |
| kinship_snp111 - 108 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATGTGCCAAAACTTCCCTGC |
| kinship_snp111 - 307 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTCTGACGCTGCAAACTAGG |
| kinship_snp112 - 75 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGGACTCAGACGATGCAGC |
| kinship_snp112 - 279 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAAAGTGCGTCCACCAAGC |
| kinship_snp113 - 52 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGAGTGCAGATAGACAGGCG |
| kinship_snp113 - 208 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGTGACCTGGCGTGTCTCTC |
| kinship_snp114 - 112 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGCCTCTGTGATGAAAGCTC |
| kinship_snp114 - 311 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCGCAGTTCAAAGGTCTCCTC |
| kinship_snp115 - 131 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAATGAGGGGAGCAGTGTGAC |
| kinship_snp115 - 330 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGATCGTGGGCTTACAAATCTTTAG |
| kinship_snp116 - 103 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGGAAGAAGAGCTTGGAGC |
| kinship_snp116 - 306 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGATAGGACACCACGACTGAC |
| kinship_snp117 - 122 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGCAGATGAAGCAGTGGAAG |
| kinship_snp117 - 323 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTATCCGGCGGTTACTGTGTG |
| kinship_snp118 - 116 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATGTGAACGGTGTGTGATGG |
| kinship_snp118 - 315 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCTGCAGAGATGGGGAAGAG |
| kinship_snp119 - 135 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCCGTACCCCGTGATTCAT |
| kinship_snp119 - 328 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGGGTCCACTGATACAGCTC |
| kinship_snp120 - 136 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCCGTTAGCTCACTCTGTC |
| kinship_snp120 - 329 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCGTAGTTGAGCATGGCAG |
| kinship_snp121 - 96 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGTCTGCGAGGCTTTCTAGG |
| kinship_snp121 - 298 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCCGCGCACATAAACAAAAC |
| kinship_snp122 - 99 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGCAAGAAATGTCACAAACTCC |
| kinship_snp122 - 298 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGGGCCTTACGTTGGAAAAG |
| kinship_snp123 - 117 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACTCACCGGTCACATCAGA |
| kinship_snp123 - 315 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAAAGAAATAGACCACATCCCAC |
| kinship_snp124 - 102 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTGTGCTGAGTGTCGCCTG |
| kinship_snp124 - 303 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTGTTGGTCTCGGTCCTCA |

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|---|---|---|
| kinship_snp125 - 91 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGCTCCATCCGTCAGAAG |
| kinship_snp125 - 290 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAACTGAACCTATTTCCATGCG |
| kinship_snp126 - 119 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCTTTTGCCCTGTTTGGTCT |
| kinship_snp126 - 318 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGTGAAGCCAGCCCAAAAG |
| kinship_snp127 - 120 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCATCCTGCCAAGACCAGAC |
| kinship_snp127 - 317 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGGATGCCCTGACTGTTTGC |
| kinship_snp128 - 92 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGAGGACCACACCTTCGAGAG |
| kinship_snp128 - 291 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTGGACATCGGTTACCTTTGC |
| kinship_snp129 - 111 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCTTTGTCGCTTCCCAGC |
| kinship_snp129 - 315 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCAGAGCGTGTTGTCGTGT |
| kinship_snp130 - 104 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCATACTTGGAGCCCTCTCG |
| kinship_snp130 - 302 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCGACTGTCCTACATGCCAC |
| kinship_snp131 - 126 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACCCATGTCAGTCCTTCAGG |
| kinship_snp131 - 325 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTATCCTTCCTCACGTCCTGC |
| kinship_snp132 - 104 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGAACACGGCGATACTGTAAC |
| kinship_snp132 - 303 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTTCTTTTTCGTGGGTGTGG |
| kinship_snp133 - 117 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGTGACACGACTTCGAGCATC |
| kinship_snp133 - 302 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAAACTGAGGCCTCCACCGA |
| kinship_snp134 - 125 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACTCTGCCAGGATCGTGTTC |
| kinship_snp134 - 321 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTGACAGCGGGGTATTAGC |
| kinship_snp135 - 123 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCAGGCATCACACCGAGGAG |
| kinship_snp135 - 322 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGACGATCTGGAAGCCACTTCTC |
| kinship_snp136 - 70 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGGAATACTGCTGAGGTAG |
| kinship_snp136 - 273 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGAAAGGGGTGTGCTTTAGG |
| kinship_snp137 - 75 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTCATGGATCCCAAACAGG |
| kinship_snp137 - 268 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTTGTGGTGGCTCTGCTA |
| kinship_snp138 - 108 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTTAGGAAGGGACCCTCAG |
| kinship_snp138 - 316 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTATTCAGGGCAGGAGAATGG |
| kinship_snp139 - 93 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCCGCTCTTCCTCTCCGAAG |
| kinship_snp139 - 298 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCGAGAGTCCATGGTCACCG |
| kinship_snp140 - 101 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCGTTCTTAGCGGGGAAATGG |
| kinship_snp140 - 300 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGAGAGAGGAAGAAGCAGGC |
| kinship_snp141 - 99 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAACCATAAGACTGGAAGAAACCG |
| kinship_snp141 - 298 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGATCTTTTTGGCGCGTTG |
| kinship_snp142 - 125 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTAAGAATAAGGGTCCACTGCGG |
| kinship_snp142 - 324 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGGTGCTGCGTCTTCCATC |
| kinship_snp143 - 93 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCAAGTGGGTCTTCGATCAAC |
| kinship_snp143 - 292 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGTTTTCTAAGCGGGCCTG |
| kinship_snp144 - 103 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCATCTGATCTGTGAACATCCTG |
| kinship_snp144 - 302 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCTCCTCTTCTGGTTGCTTC |
| kinship_snp145 - 137 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGTAAGAGGCCAGGGTCTG |
| kinship_snp145 - 347 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGCATCTCACAACCCAGTAGG |
| kinship_snp146 - 124 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATCTTGACCGAGTGCGTC |
| kinship_snp146 - 324 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGACAGTCCTGGTATGGGTCTG |
| kinship_snp147 - 80 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTCGTGTGAATCCCATGAAAAG |
| kinship_snp147 - 279 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTATCTCCTTCCCTGGCCAC |

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| kinship_snp148 - 87 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGATTCACAGCCCCTCACAG |
| kinship_snp148 - 286 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGGCTCCTCCTTTTGCACAG |
| kinship_snp149 - 89 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTTCGAAGGAGACCATCGCC |
| kinship_snp149 - 284 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAAGGGTGAGTCCAGCGTTG |
| kinship_snp150 - 129 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCCCGGGGGCTAACACTAAC |
| kinship_snp150 - 291 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCCTGAATGACCAGCGACG |
| structure_snp1 - 79 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCGTGTTGTTTAAGGGTCAACTC |
| structure_snp1 - 278 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTCAACTGCACCTTCCACG |
| structure_snp3 - 102 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGACACTGACACCCAAGCT |
| structure_snp3 - 306 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTGTGAGAGAGTTTTCGAGAG |
| structure_snp4 - 138 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCTGGGTGTTCTTGCTGATC |
| structure_snp4 - 337 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGATTGGGAGGCCATCATCTTTG |
| structure_snp5 - 95 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTGAGCCAGGTATTTTCCTTTC |
| structure_snp5 - 294 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCACCTTCATCCCATTCTCC |
| structure_snp6 - 75 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGAGTGTGGAGCAGTTGTG |
| structure_snp6 - 274 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGGGCTGGTTAGGGAACTTG |
| structure_snp7 - 102 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCAGCAGTGAATCATGGATGC |
| structure_snp7 - 301 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCAATGCTGTGGATTATGAAGGC |
| structure_snp8 - 96 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGAGGAAACTGACGGAGAGG |
| structure_snp8 - 295 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAACATCTAGTGCAGTGCCTG |
| structure_snp9 - 89 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTTGGAGAGAAGAACTATTTGG |
| structure_snp9 - 304 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGACACTGAATAAAGGCGCAG |
| structure_snp10 - 77 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTCTCTGTACCTTTGTCGTACTC |
| structure_snp10 - 276 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGGAAGACACGTGCTTTCCG |
| structure_snp11 - 106 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGTAAAGATAGTCCCAGGCTG |
| structure_snp11 - 305 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTTTTCATCGAAACCTCCCTTG |
| structure_snp12 - 93 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCAGACAACTCCCCAGTTAC |
| structure_snp12 - 292 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCATGACACTTCCCTCCTGG |
| structure_snp13 - 75 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACCCTTCAATCAAATGCACAAC |
| structure_snp13 - 274 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTCCCAAAGCAACTGGTGAT |
| structure_snp14 - 118 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGTGCCTGGCTCATTAAACG |
| structure_snp14 - 317 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTGGCTAGAGATCCTTGGAC |
| structure_snp15 - 104 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACTGAAGGCAATAGCTTCACT |
| structure_snp15 - 303 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTTTAAGTGGACGACCCCTC |
| structure_snp16 - 62 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCCCGATGGTGAACTGTCA |
| structure_snp16 - 227 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGCCAAGCCCAGCTGAAGT |
| structure_snp17 - 112 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTCAGCAGATGACCTCCAAG |
| structure_snp17 - 311 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGAACTCAAAATGCCCAACAC |
| structure_snp18 - 83 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCCCAGAGAGGAGAGAGAAG |
| structure_snp18 - 282 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGGGGTTCTGTAAAGTCGGA |
| structure_snp19 - 100 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCCCTCAGCCTTTCTTACCTG |
| structure_snp19 - 299 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCAAGGAGAGGTGGTGTGTG |
| structure_snp20 - 95 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCAAACCCACTGCCAAGGAG |
| structure_snp20 - 294 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTCCTTCTTTGCGTGCCAAG |
| structure_snp21 - 106 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCGGCTTGATATTCCTGAAC |
| structure_snp21 - 307 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAAAATGCCTTCCTCTCTGCA |

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|---|---|---|
| structure_snp22 - 110 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGGAGTGGCTGCATTGTAC |
| structure_snp22 - 309 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTGATGCCCTGAGGAGAATG |
| structure_snp23 - 118 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGAGCAGAGCTACCAGGAG |
| structure_snp23 - 317 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGACCAGGGCGTTACATAGTAAAG |
| structure_snp24 - 84 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGTCTGGGTTCACTTTTGGATC |
| structure_snp24 - 283 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGATTATTGCTGGCTGCTGTGT |
| structure_snp25 - 84 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTACTTCCTCGAGATCTGCC |
| structure_snp25 - 283 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTATTTTAACCCGGTTCGTAGC |
| structure_snp26 - 105 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGATTTTGAGCAATCCCCAC |
| structure_snp26 - 304 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCATATCAGAAAGAGACGCGA |
| structure_snp27 - 77 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGGATCCAACCCCTCTTACTC |
| structure_snp27 - 244 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGACAACCGTTCAAAACCCTGT |
| structure_snp28 - 116 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCAGCCAATGGAGGTCAGCA |
| structure_snp28 - 317 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGTGGCATGTTCTAGCAAGAG |
| structure_snp29 - 77 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGCTTTAGGGAGACACACC |
| structure_snp29 - 280 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCGGGTCGATTCCTACCTACT |
| structure_snp30 - 95 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCTGTTGAGGACTCCCAAAGA |
| structure_snp30 - 297 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTCTCAGACGGAATGCCCTG |
| structure_snp31 - 115 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTTCCTGTAGCCTCATCTGAG |
| structure_snp31 - 314 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCTTTAGCCTCAGGAGCAGG |
| structure_snp32 - 96 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATCCTTGGCAAAGCAGCAC |
| structure_snp32 - 295 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCCCTGCTGTTTAAAACCCA |
| structure_snp33 - 125 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTCAGAGATCTCTCCTGTGTG |
| structure_snp33 - 324 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGAAGGAGAGAGGAAGGGGA |
| structure_snp34 - 117 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTTCCCCCAAAGCGTTCG |
| structure_snp34 - 316 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAAGAAAGTCTGGGGATGTGG |
| structure_snp35 - 151 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTGGCTAGCTCCAGGACCA |
| structure_snp35 - 350 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGAAGGAGCAACTGCCATCC |
| structure_snp36 - 103 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCTACGGAAGCTATGAATAATCCT |
| structure_snp36 - 302 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGATGCCCCCAACAAGCAGA |
| structure_snp37 - 113 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAAACTCTGTCATGGGTCAGAC |
| structure_snp37 - 312 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGTCAGCTGAAAGGATGTAGC |
| structure_snp38 - 106 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGATATTTTAAGGGGCGCCTG |
| structure_snp38 - 285 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGATTTATGTGACAGAGAGACAGC |
| structure_snp39 - 88 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGACCAGTTAATGAGTGTTTGAG |
| structure_snp39 - 289 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTTTTGAGCCTCCTAAAAACTG |
| structure_snp40 - 104 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCATGACCACTGGCTTATGTG |
| structure_snp40 - 303 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCCTTCTGAACTGCTTCAAC |
| structure_snp41 - 129 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGGCGGTTTCATGGGGTAT |
| structure_snp41 - 325 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAAAAGTGTCCTGCTCCCCTC |
| structure_snp42 - 107 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGGGTATCTTCTGGAGCCTC |
| structure_snp42 - 306 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCAAGGGCTCCTAAATGCTG |
| structure_snp43 - 121 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATGTGGGGCTCGATCCAAG |
| structure_snp43 - 320 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCTGCATGAGATTCTCTCCCTC |
| structure_snp44 - 111 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACCTGAGTTCTTGCCCTGG |
| structure_snp44 - 310 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCAGTTCCACACATGCAGC |

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| structure_snp45 - 102 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCTGAGACTTGGAGCCAGC |
| structure_snp45 - 302 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGGCGTGACAATAAAACGACA |
| structure_snp46 - 140 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCGCTTGTTGGGTTTGGTC |
| structure_snp46 - 324 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAACCCTCAAGTCTACTCCG |
| structure_snp47 - 115 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCATAAAACAATAGCTCCCCAAC |
| structure_snp47 - 314 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGACATTCTGACATATGCTACGG |
| structure_snp48 - 83 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGACAGACAGAGGTTGAGC |
| structure_snp48 - 282 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCTCTGACATGGGACTCCTC |
| structure_snp49 - 72 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGTTTTGCCTTGCTGAATGG |
| structure_snp49 - 250 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTTTACAATTTGCTCTCCTGAG |
| structure_snp50 - 80 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCTTTAGCTAAACAGCCCAAAGA |
| structure_snp50 - 264 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGATGTGCAGTCCCACCCCTA |
| structure_snp51 - 112 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGAAGTTGCCCTGGGTGAAG |
| structure_snp51 - 311 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAATGGAGGCCTGGAAAATGG |
| structure_snp52 - 119 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGCTCTCAGGAATCCCTCTC |
| structure_snp52 - 318 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGAATGAATGAGGGCAACACTG |
| structure_snp53 - 130 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCTTGATCCCAGAACGCTG |
| structure_snp53 - 311 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAAGGGTATATCCAACAATCCATCC |
| structure_snp54 - 119 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGATGCAGGGGAGACATGGA |
| structure_snp54 - 317 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGATGCTTCCTAAAATGGGCC |
| structure_snp55 - 122 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGTCTCTCCCACTCTAACAAAG |
| structure_snp55 - 321 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGAGGAGGCTTCACTGATGAC |
| structure_snp56 - 76 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCGGGTGATAGTTGGAGCTG |
| structure_snp56 - 275 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCTCCTTCAAGGGCAGGAATG |
| structure_snp57 - 113 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGCCCCAACAATCAGAATCA |
| structure_snp57 - 312 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCGGTAGGATTTGTTGCTAACAG |
| structure_snp58 - 122 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCACTACGCTGTCACTTGAGC |
| structure_snp58 - 321 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTGCTCCCTCCCCAAATATTC |
| structure_snp59 - 79 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTGGTAGGCGGCATGTAAG |
| structure_snp59 - 278 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTTATTTGAGAGAGGAGGAGAGC |
| structure_snp60 - 92 F | F | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCAGCCTCCTGTGCGATAAC |
| structure_snp60 - 291 R | R | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGCTTCAAAGGTGGCAGAAGG |