# Population Structure and Genomic Diversity of the Gila Monster Reflect Ecoregional Patterns



**Final Project Report Prepared for: Clark County, Nevada Department of Environment and Sustainability Desert Conservation Program, Project 2023-USGS-2315H**

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Cover photo of *Heloderma suspectum* from Arizona by Paul A. Maier.

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## Data Availability Statement

Genotype data and sample metadata are available in a U.S. Geological Survey Data Release (Wood and others, 2026; https://doi.org/10.5066/P14XUOJQ) and raw sequences are available in an NCBI Sequence Read Archive (BioProject Accession: PRJNA1529286;https://www.ncbi.nlm.nih.gov/bioproject/1529286).

## Artificial Intelligence Use Disclosure Statement

No artificial intelligence tools were used in the design or implementation of this study, nor in the preparation of this report.

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# Conversion Factors

International System of Units to U.S. customary units

| Multiply | By | To obtain |
|---|---|---|
| | Length | |
| centimeter (cm) | 0.3937 | inch (in.) |
| millimeter (mm) | 0.03937 | inch (in.) |
| meter (m) | 3.281 | foot (ft) |
| kilometer (km) | 0.6214 | mile (mi) |
| kilometer (km) | 0.5400 | mile, nautical (nmi) |
| meter (m) | 1.094 | yard (yd) |
| | Mass | |
| gram (g) | 0.03527 | ounce, avoirdupois (oz) |
| kilogram (kg) | 2.205 | pound avoirdupois (lb) |
| metric ton (t) | 1.102 | ton, short [2,000 lb] |
| metric ton (t) | 0.9842 | ton, long [2,240 lb] |

Temperature in degrees Celsius (°C) may be converted to degrees Fahrenheit (°F) as follows:

°F = (1.8 × °C) + 32.

## Abbreviations

| | |
|---|---|
| DNA | Deoxyribonucleic Acid |
| PCR | Polymerase Chain Reaction |
| RAD | Restriction-Associated DNA |
| SNP | single nucleotide polymorphism |
| US | United States |
| USGS | U.S. Geological Survey |

## Executive Summary

Understanding a species' population structure and contemporary genetic diversity can reveal environmental factors, both natural and anthropogenic, that affect genetic connectivity of populations and can help to inform conservation management. The Gila Monster is a large venomous lizard native to the southwestern United States and northern Mexico. Given its reclusive behavior and patchy distribution throughout its range, the Gila Monster is a notoriously difficult species to study and much remains to be understood regarding genetic population units, diversity, and landscape connectivity. We developed a genomic dataset consisting of 68,154 Single Nucleotide Polymorphic loci (SNPs) and genotyped lizards collected throughout the species range to examine population structure and contemporary patterns of genetic diversity. The regional genetic patterns found in this study emphasize that multiple geographic areas of the Gila Monster's range contain distinct elements of the species' overall genetic diversity. At the broadest level, our findings confirmed the existence of the two traditionally recognized subspecies. In particular, the Banded Gila Monster (*Heloderma suspectum cinctum*) is primarily found in Nevada with a small part of its distribution extending into southwest Utah. Further genetic divisions within each subspecies were supported that divide the range into ecoregionally aligned genetic populations (north and south Mojave, Sonoran, and Chihuahuan clusters), two of which occur in Nevada. Genetic diversity metrics were highest among sites of the Reticulate Gila Monster (*H. s. suspectum*) in the southern portion of the species' range, with a pronounced drop among sites of the Banded Gila Monster (*H. s. cinctum*) in the northern part of the range in Nevada and Utah. Protecting habitats in each region may be crucial to ensure the conservation and representation of genetic diversity across the species.

## Introduction

Habitat loss and fragmentation are among the largest threats to native populations. These impacts can significantly reduce species persistence and population resilience to future environmental change. Habitat fragmentation acts to reduce a species' ability to disperse across the landscape, altering natural movement patterns and landscape use, that can lead to increased risk of population decline, loss of genetic diversity, and extinction for native populations (Frankham, 2005, Fischer and Lindenmayer, 2007). Since genetic diversity and population size are positively linked to population persistence, they represent essential components for species genetic management and recovery programs (Frankham and Ralls, 1998). Therefore, prioritizing populations for conservation requires, in part, an understanding of the current genetic diversity and structure within the species (Petit and others, 1998). Genetic data can help elucidate population connectivity patterns, reveal evolutionary histories, and assist in defining geographic boundaries for the management of unique populations exhibiting high diversity. Nevertheless, investigations of at-risk species frequently concentrate only on regions within the range experiencing population decline or with targeted conservation objectives, which can impede the ability to determine whether focal populations represent distinct genetic lineages or share ancestry with adjacent populations. Furthermore, understanding how environmental factors, both natural and anthropogenic, affect genetic connectivity can assist in identifying important corridors for movement and gene flow and inform habitat restoration efforts (e.g. Epps and others, 2007, Hagerty and others, 2011, Vandergast and others, 2013).

Rapid urban expansion throughout the Mojave Desert has steadily increased over the last century (Hughson, 2009). Within the state of Nevada, rapid growth has resulted in substantial loss of habitat and connectivity in the region (Leu and others, 2008, Webb and others, 2009). The Las

Vegas Valley is the largest metropolitan area in the state and is home to the three largest cities within Clark County: Las Vegas, Henderson and North Las Vegas. Over the span of three decades, population growth in Clark County tripled in size from 700,000 in 1990 to over 3 million in 2024 (US Census Bureau, 2024 Demographic profile data). As human population growth and urbanization are expected to continue to increase in the region, understanding how native species move through this landscape can inform efforts to mitigate impacts to habitat connectivity.

The Gila Monster is a large venomous lizard native to the southwestern United States and northern Mexico (Beck, 2005). Within the U.S., Gila Monsters reach their northern most range limit in Nevada and southwestern Utah. Gila Monsters in Nevada primarily occur in Clark County, with only small portions of their range extending into Nye and Lincoln counties. Despite inhabiting arid environments, these lizards do not tolerate high temperatures and can spend a majority (> 95 percent) of their time seeking refuge in underground shelters (Lowe and others, 1986, Beck, 1990; Beck, 2005), making them among the rarest and most secretive animals in Nevada. Due to this elusiveness, too little is known about population size, structure, and genetic connectivity of populations to evaluate the long-term viability of the Gila Monster throughout Nevada.

### Purpose and Scope

In this study, we developed a larger genomic dataset comprised of Single Nucleotide Polymorphic (SNP) loci and expanded our sampling beyond sites restricted within Nevada (a focus of our previous study; Wood and others, 2023) to include representative sites from throughout the species range. We used this more comprehensive genomic dataset to provide

insight into patterns of regional structure and connectivity, genetic diversity, and genetic population size.

## Methods

### Genomic DNA Collection and NGS Library Preparation

Tissue and blood samples from Gila Monsters were provided to the Western Ecological Research Center (WERC) San Diego Field Station under state permits (Nevada: 497453; Arizona: SP583995 – SP141401; New Mexico: 3914) and under Institutional Animal Care and Use Committee (Protocol numbers 19-012 and 2025068001USGSWERC), and acquired through institutional loans (ASUVTC_2025_01 and MSB Loan 2026.10.Herp). These opportunistic samples were collected between 2002 – 2025 throughout the U.S. portion of the species' range that included Utah, Nevada, Arizona, and New Mexico. Although Gila Monsters have been photographed at several locations in California's eastern Mojave Desert, we are unaware of any tissue samples from these animals being collected for inclusion in this study. These samples were grouped into 64 geographic sites and the number of samples obtained per site ranged from 1 to 36 (Fig. 1, Table S1). We extracted genomic DNA at the WERC San Diego Conservation Genetics Laboratory with Gentra Puregene Kits (Qiagen, Valencia, California) according to manufacturer's protocol with minor modifications that included cell lysis in the presence of Proteinase K and a 20-minute centrifugation step at 21,194g and 4° C.

In total, 287 samples of *Heloderma suspectum* were prepared for sequencing. We followed the 2RAD (restriction-associated DNA) sequencing protocol (Bayona-Vásquez and others, 2019) to generate genome-wide single nucleotide polymorphism (SNP) data. We prepared 2RAD libraries with 100 ng of sample DNA and used the restriction enzymes EcoRI

and MseI. We conducted individual Polymerase Chain Reactions (PCRs), pooled PCR product by volume and size selected fragments between 350 and 450 base pairs (bp) using a Pippin Prep size fractionator (Sage Science). Final libraries were bead-cleaned and quantified using the Qubit fluorometer (Life Technologies) and sequenced (150 bases, paired-end reads) on the Illumina NovaSeq platform at MedGenome, Inc. (Foster City, CA).

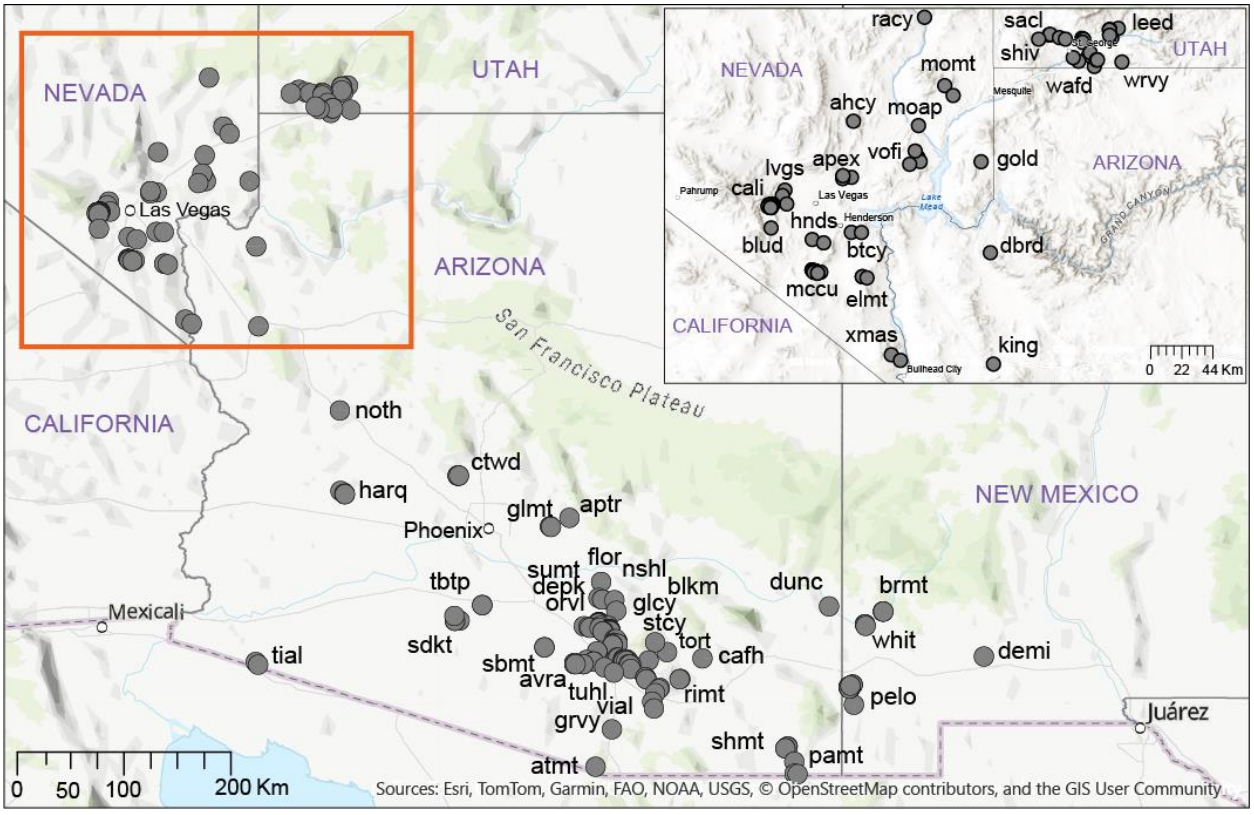



**Figure 1.** Map of sampled occurrences of Gila Monsters throughout Utah, Nevada, Arizona, and New Mexico, USA. Inset map shows a close up of Nevada and Utah occurrences. Site code definitions are listed in the Supplemental Tables.

## Bioinformatics and Data Analysis

Raw sequence demultiplexing, quality filtering, and genotyping were performed on the USGS Hovenweep High Performance Computing platform (Falgout and others, 2023). We used the process_radtag program within Stacks v2.68 (Catchen and others, 2013) to clean and filter raw reads following default settings. We used BWA 0.7.17 to align demultiplexed forward and reverse reads to the *Heloderma suspectum* reference genome (Pinto and others, 2025) using the 'mem' command with default settings. These reads were then exported and sorted as .bam files using SAMtools 1.10 and used as input for the gstacks program within Stacks v2.68 to build a catalog of individual RAD loci. We used the *populations* module within Stacks to generate a Variant Call Format (vcf) file, retaining only loci present in at least 80 percent of individuals, that was used for downstream filtering of datasets. We used the functions within SNPfiltR (DeRaad, 2022) and vcfR (Knaus and Grünwald, 2017) to explore and visualize differing filtering thresholds based on genotype quality, minimum and maximum read depth, allele balance, number of alleles present, missing data per sample and SNP, and genomic distance between SNPs. Final filtering steps removed called genotypes with low confidence by requiring a minimum depth of 5 and a minimum genotype quality of 30, which resulted in the removal of 26.1% and 1.3% of called genotypes, respectively. We then filtered heterozygous genotypes for which an allele balance fell outside the range 0.25-0.75 (Puritz and others, 2014), which removed 9.2% of all heterozygous genotypes (0.5% of all genotypes) from our reference aligned SNP dataset. We set a maximum mean SNP depth cutoff of 70 to remove SNPs with outlier depth values, which removed 0.9% of all SNPs. To identify failed samples, we initially chose to filter out samples with missing SNP calls at more than 80% of their genotypes, and we used vcftools

(Danecek and others, 2011) to compute mean missing data values for the remaining samples, only retaining samples with less than 40 percent missing data. We removed invariant sites generated from removing samples with high missing data. After all filtering steps, we retained genomic data for 266 individuals representing the two subspecies (*H. suspectum suspectum* and *H. s. cinctum*). We also generated a reduced dataset with 104 Gila Monster samples for phylogenetic estimation.

## Population Genetic Structure Analyses

We evaluated population genetic structure with both parametric (model assumptions used) and non-parametric (no model assumptions) approaches. Our parametric approach involved the maximum-likelihood method of ADMIXTURE (Alexander and others, 2009) to estimate the most likely number of genetic clusters (K) given the data assuming Hardy-Weinberg Equilibrium (HWE) within clusters and absence of linkage disequilibrium among markers. We performed 10 replicate analyses to evaluate up to 10 genetic clusters. To assess the best value of K, we performed 10-fold cross-validation and determined the K values with the lowest cross validation error and examined the individual assignment plots. We also used Principal Component Analysis (PCA), a multivariate ordination method that evaluates the optimal number of genetic clusters and because it is a non-parametric approach does not require the assumption of Hardy-Weinberg Equilibrium (HWE) or unlinked markers. We performed PCA in R 4.5.2 (R Core Team, 2025) using adegenet v. 2.1.5 (Jombart and Ahmed 2011).

Population differentiation was estimated using the fixation index ($F_{ST}$) among sites that had at least five sampled individuals and by region. Fixation indices were calculated in R 4.5.2

(R Core Team, 2025) using StAMPP v. 1.6.3 (Pembleton and others, 2013). This package calculates pairwise $F_{ST}$ values along with confidence intervals and P-values (using 10,000 bootstraps) according to the methods described in Weir and Cockerham (1984).

## Genetic Diversity Analyses

Genetic diversity indices including observed heterozygosity (Ho), unbiased expected heterozygosity (uHe) and inbreeding coefficients ($F_{IS}$) were estimated with dartRverse v.1.0.6 (Mijangos and others, 2022) at each sampling location with at least 4 samples and grouped by region. For sites with 8 or more samples, we estimated contemporary effective population size (Ne) using the linkage disequilibrium method (Waples and Do 2008) within the program NeEstimator v. 2.1 (Do and others, 2014). We assumed random mating for each group and limited pairing between markers only on different chromosomes to account for linkage. We calculated 95% confidence intervals for point estimates using the jackknife-across-samples method (Jones and others, 2016), and screened out rare alleles using a critical cut-off value ($P_{crit}$) of 0.01. To diagnose whether Ne estimates of infinity (Inf) were driven by limited sample size or by the chromosome correction formula, we also ran the analysis using the naïve mode, which assumes all markers assort entirely independently.

## Phylogenetic Analyses

We used IQ-TREE 3 (Wong and others, 2026) to estimate the phylogenetic tree based on a concatenated sequence alignment (all nucleotide sites) for 104 samples of *H. suspectum*. We selected one to two samples from each site to maximize the geographic representation of each cluster and representative subspecies. We used the *populations* module and *--phylip-var-all* flag

within Stacks v2.68 (Rochette and Catchen, 2017) to generate a concatenated PHYLIP file. We used ModelFinder (Kalyaanamoorthy and other, 2017) to find the best fit model for the data using Bayesian information criterion. Tree reconstruction was run using the GTR+F+I+G4 model of substitution with 1000 ultrafast bootstrap replicates (Hoang and others, 2018). We used the midpoint root and visualized the output with FigTree v1.4.4 (Rambaut, 2018).

# Results

## Data Quality

A total of 287 samples of *Heloderma suspectum* were sequenced, but 21 samples had greater than 40 percent missing data and were removed prior to any downstream analysis. The final genomic dataset included a total of 266 individuals of *H. suspectum*, with 29 individuals from Utah, 79 individuals from Nevada (76 from Clark County; 3 from Lincoln County), 133 from Arizona, and 25 individuals from New Mexico (Table S1). For all samples, an average of 84% of the total reads were retained, the average coverage per sample was 13.8x (range 3.7 – 84.8x), and missing data across all loci was 8.4%. Stacks processed 186,885 loci (44,116,021 sites) consisting of 321,561 SNPs. After filtering thresholds were implemented with SNPFilter, we obtained 68,154 polymorphic SNPs. For population structure and diversity datasets, we further restricted the data to only a single random SNP per RAD locus, which resulted in 38,008 polymorphic SNPs for the complete dataset and an average of 4% missing data across the 266 samples.

## Genetic Structure

Admixture analyses of the complete dataset identified up to five geographical clusters (Figure 2).

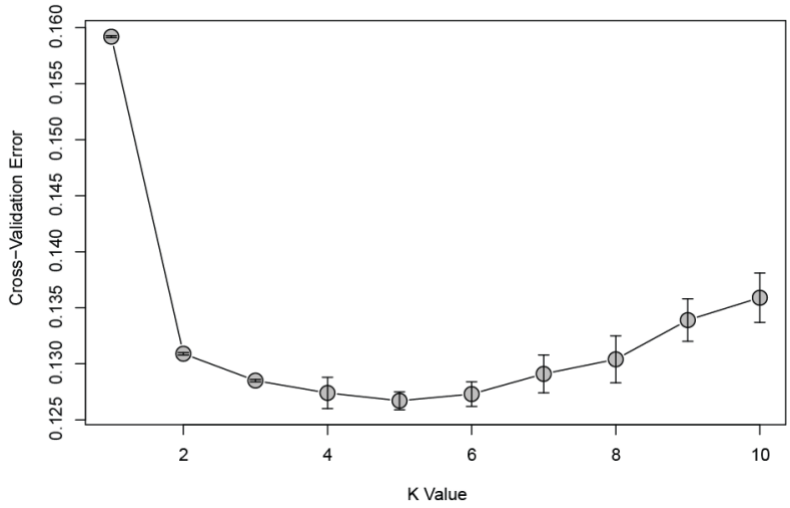



**Figure 2.** Cross validation error (mean and standard error) plotted by assessed K-values (number of clusters) showing lowest error and thus best support for 2-5 genetic clusters of the Gila Monster.

At the lowest clustering level (K=2), Admixture analyses separate the Banded Gila Monster (*Heloderma suspectum cinctum*) from the Reticulate Gila Monster (*H. s. suspectum*), with sites along the boundary of contact (vicinity of the Mojave and Sonoran desert ecotone) showing mixed ancestry coefficients between the two subspecies (Figure 3 and Figure 4). At the highest clustering level (K= 5), the inferred clusters partition populations within different desert boundaries that included a 'north Mojave' cluster containing sites within Utah and southeastern Nevada, a 'south Mojave' cluster consisting of the remaining Mojave Desert sites within southern Nevada, an 'ecotone' cluster comprising sites along the Mojave and Sonoran desert ecotone along the western and northwestern portion of Arizona, a "Sonoran" cluster encompassing sites within the Sonoran Desert in Arizona, and a "Chihuahuan" cluster containing

sites within southeastern Arizona and New Mexico. The average majority ancestry coefficient values for each cluster (K=5) ranged from 0.85 – 0.99, with the ecotone cluster being the most admixed (average ancestry coefficient = 0.85, SD = 0.18, n = 19), and the Chihuahuan cluster the least admixed (ancestry coefficient = 0.99, SD = 0.03, n = 26). At K=4, the inferred geographic clusters were largely the same as in K=5 except sites (dbrd, king, noth, harq, ctwd, tial, glmt, and aptr) that were assigned to the ecotone cluster at K=5 were admixed across the four identified clusters (average ancestry coefficient = 0.63, SD = 0.11, n = 18).

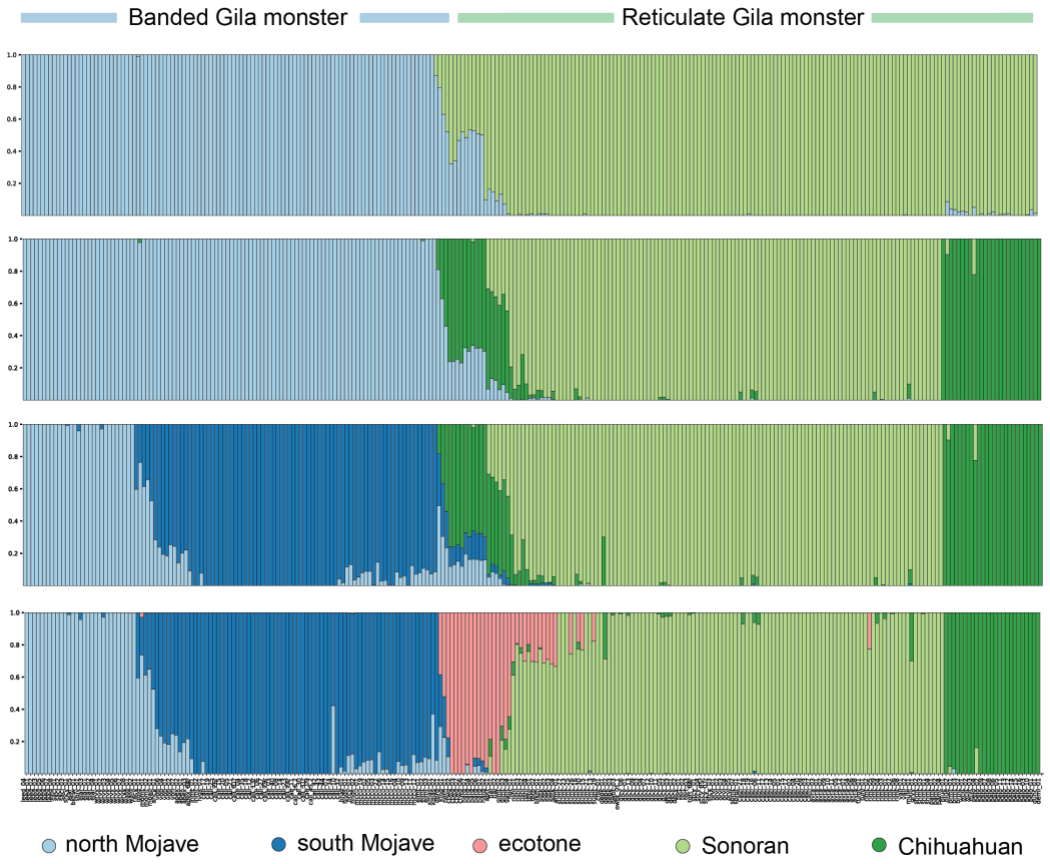



**Figure 3.** Ancestry assignment plots of the Gila Monster from admixture analysis from K = 2 to K=5. Individuals are arranged by occurrence from north to south. At K=5 the inferred clusters partition populations within different desert boundaries noted by the different colors: north Mojave (light blue), south Mojave (dark blue), ecotone (pink), Sonoran (light green), and Chihuahuan (dark green).

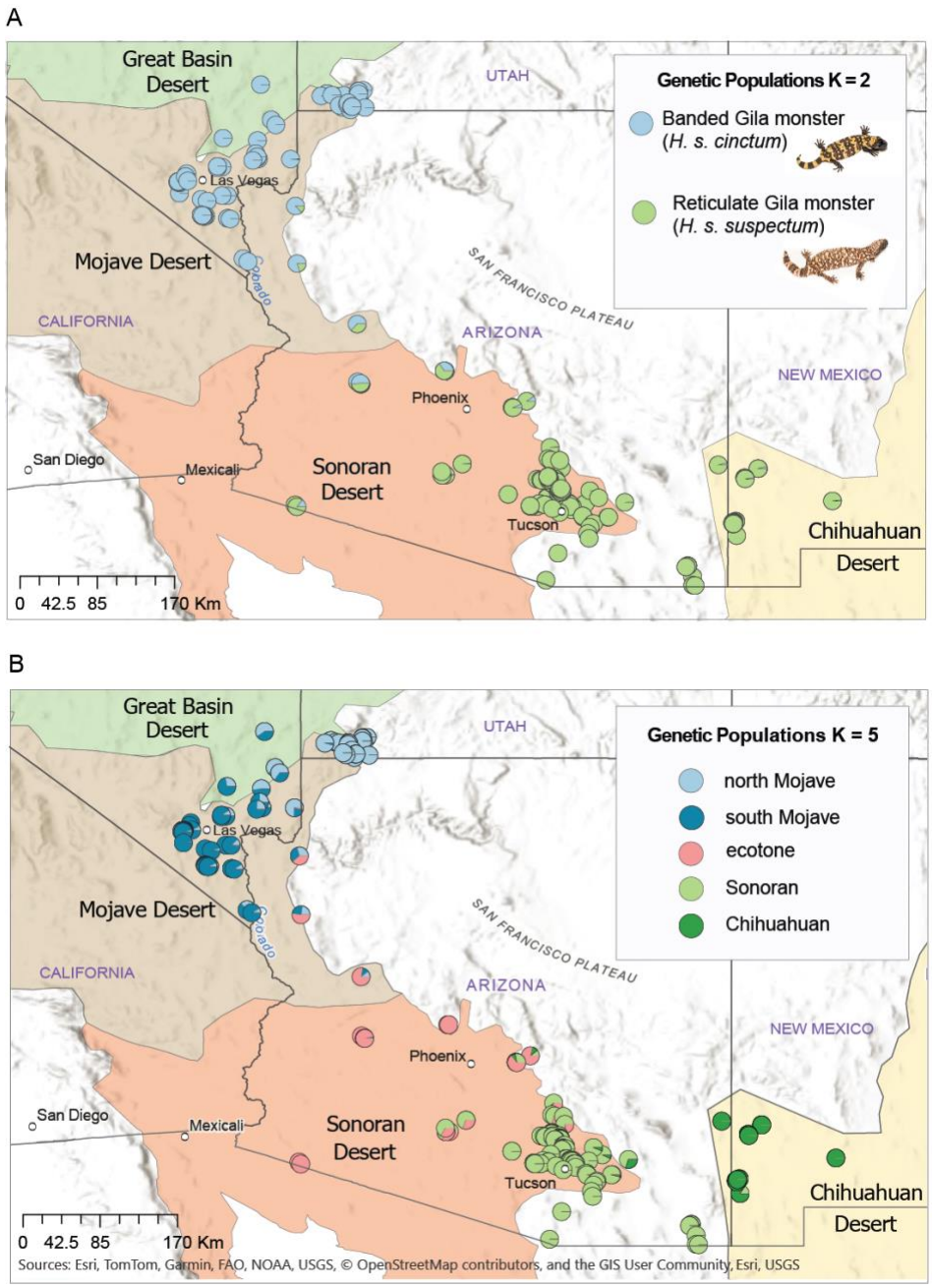



**Figure 4.** Maps of the genetic structure of the Gila Monster from Admixture analysis. Pie charts represent individual ancestry assignment proportions at (A.) K=2 that depicts the genetic support for the Banded and Reticulate Gila Monster subspecies, and at (B.) K=5 that depicts the genetic support for the ecoregionally aligned desert groups. Colored polygons delineate the boundaries of the four desert biomes in southwestern USA. Photographs of Gila Monsters by Paul A. Maier

In the PCAs, structuring among five main desert groups were similar to the Admixture results (Figure 5). The first principal component (PC) axis (18.5%) separated the Sonoran and Chihuahuan clusters from the north and south Mojave clusters, with sites aligned to the ecotone cluster structured intermediate between these four groups. The second PC axis (3.04%) separated samples between the Sonoran and Chihuahuan clusters. The third PC axis (2.43%) differentiated between samples belonging to the north and south Mojave cluster, with samples of the south Mojave group tending toward positive loadings and samples of the north Mojave group tending toward negative loadings.

Population differentiation from pairwise $F_{ST}$ estimates (Table 1) increased with geographic distance, with Mojave (north & south) and Chihuahuan clusters being the most differentiated ($F_{ST}$ = 0.301 - 0.315) and adjacent ecotone and Sonoran clusters being the least ($F_{ST}$ = 0.062). The Reticulate Gila Monster exhibited lower differentiation among sites throughout its range ($F_{ST}$ = 0.006 – 0.138) compared to differentiation among sites within the Banded Gila Monster ($F_{ST}$ = 0.075 – 0.227). Pairwise $F_{ST}$ estimates between all sites with at least 5 samples were mostly significant and ranged from 0.006 to 0.370 (Table S2). Population differentiation between the two Nevada focal sites was low (cali and mccu, $F_{ST}$ = 0.095), although pairwise estimates among cali and all the other sites resulted in the highest differentiation values suggesting this site may be more isolated than mccu.

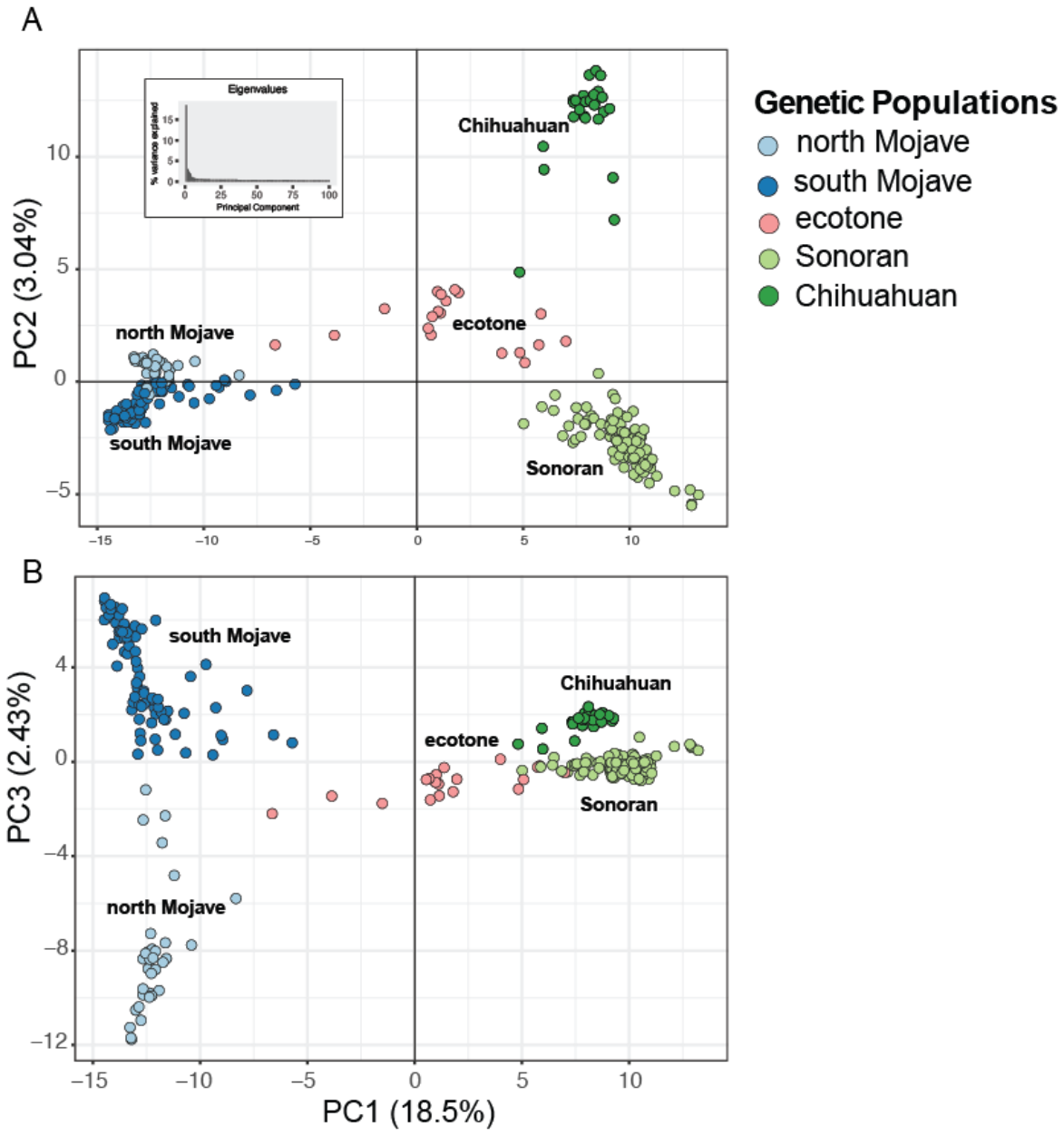



**Figure 5.** Principal Components Analysis (PCA) results showing the separation of the four biome-align genetic populations within the Gila Monster. (A.) Principal Component (PC) 1 and 2 separated four genetic groups (north + south Mojave; ecotone; Sonoran; Chihuahuan). (B) PC 3 further distinguishes north and south Mojave. Inset graph shows the percentage of variation explained by each principal component.

**Table 1.** Mean pairwise differentiation ($F_{ST}$) values for genetic population pairs and subspecies of the Gila Monster calculated in StAMPP.

| Population pairs | $F_{ST}$ value |
|---|---|
| north Mojave - south Mojave | 0.115 |
| north Mojave - ecotone | 0.189 |
| north Mojave - Sonoran | 0.215 |
| north Mojave - Chihuahuan | 0.301 |
| south Mojave - ecotone | 0.200 |
| south Mojave - Sonoran | 0.226 |
| south Mojave - Chihuahuan | 0.315 |
| ecotone - Sonoran | 0.062 |
| ecotone - Chihuahuan | 0.096 |
| Sonoran - Chihuahuan | 0.083 |
| Banded Gila Monster – Reticulate Gila Monster | 0.209 |
| Banded Gila Monster - ecotone | 0.203 |
| Reticulate Gila Monster - ecotone | 0.071 |

## Genetic Diversity

Diversity statistics, including percent polymorphic loci and observed and expected heterozygosity were highest in the southern portion of the range and lower in the north (Table 2, Figure 6). A sharp decline in diversity occurred within the ecotone region (ctwd and harq) where diversity was lower than sites to the south, and another sharp drop in diversity occurred among sites to the north in the Mojave Desert region. This shift in diversity also coincides with the change in subspecies range from the Reticulate Gila Monster (high diversity) to the Banded Gila Monster (low diversity).

**Table 2.** Genetic diversity statistics for sampled sites and populations with ≥ four individuals of the Gila Monster arranged from north to south. We report the number of individuals analyzed (N), number of loci (N Loci), percentage of polymorphic loci (% Poly), observed heterozygosity (Ho), unbiased expected heterozygosity (uHe), inbreeding coefficient ($F_{IS}$), and the effective population size (Ne) and 95% Confidence Intervals (95%CI), no estimate was attempted (—). Site code names are defined in Table S1.

| Sites (n > 4 samples) | N | N Loci | % Poly | Ho | uHe | $F_{IS}$ | Ne | Ne 95%CI |
|---|---|---|---|---|---|---|---|---|
| leed | 8 | 32861 | 8.85 | 0.030 | 0.029 | -0.010 | 3 | 3.3 - Inf |
| elar | 4 | 32857 | 10.50 | 0.036 | 0.036 | -0.015 | — | — |
| wrvy | 8 | 32861 | 10.38 | 0.034 | 0.034 | 0.000 | 28 | 10.2 - Inf |
| vofi | 5 | 32861 | 9.63 | 0.033 | 0.035 | 0.030 | — | — |
| apex | 4 | 32860 | 8.62 | 0.035 | 0.034 | -0.014 | — | — |
| cali | 36 | 32861 | 15.15 | 0.032 | 0.031 | -0.014 | 16 | 10 - 26 |
| mccu | 16 | 32861 | 13.46 | 0.036 | 0.035 | -0.002 | 22 | 9 - 245 |
| ctwd | 4 | 32858 | 15.58 | 0.066 | 0.061 | -0.059 | — | — |
| harq | 6 | 32861 | 19.14 | 0.061 | 0.060 | -0.011 | — | — |
| nshl | 4 | 32860 | 20.61 | 0.072 | 0.072 | -0.001 | — | — |
| sdtk | 4 | 32861 | 21.32 | 0.074 | 0.074 | 0.005 | — | — |
| sumt | 10 | 32861 | 30.91 | 0.071 | 0.070 | -0.007 | Inf | Inf |
| glcy | 12 | 32861 | 32.44 | 0.070 | 0.072 | 0.013 | 55 | 16.4 - Inf |
| tort | 4 | 32861 | 20.04 | 0.071 | 0.072 | 0.004 | — | — |
| stcy | 5 | 32861 | 22.75 | 0.072 | 0.072 | -0.002 | — | — |
| orvl | 5 | 32861 | 22.43 | 0.070 | 0.070 | 0.008 | — | — |
| cafh | 19 | 32861 | 39.23 | 0.070 | 0.071 | 0.009 | 33 | 10.5 - Inf |
| avra | 12 | 32861 | 33.35 | 0.070 | 0.073 | 0.035 | 10 | 1.7 - Inf |
| rimt | 9 | 32861 | 29.62 | 0.071 | 0.072 | 0.013 | 43 | 3 - Inf |
| shmt | 4 | 32859 | 16.65 | 0.063 | 0.064 | 0.011 | — | — |
| pelo | 16 | 32861 | 24.69 | 0.059 | 0.059 | 0.001 | 26 | 8 - Inf |
| **Genetic populations** | | | | | | | | |
| North Mojave | 34 | 6233 | 16.40 | 0.028 | 0.030 | 0.042 | 25 | 13.1 - 61.2 |
| South Mojave | 74 | 8071 | 21.24 | 0.029 | 0.030 | 0.032 | 37 | 27.2 - 52.2 |
| ecotone | 19 | 12805 | 33.69 | 0.053 | 0.056 | 0.034 | 71 | 20.4 - Inf |
| Sonoran | 113 | 26159 | 68.82 | 0.061 | 0.064 | 0.033 | 190 | 116.8 - 419 |
| Chihuahuan | 26 | 9796 | 25.77 | 0.050 | 0.052 | 0.030 | 50 | 26.1 - 191.6 |
| Banded Gila Monster | 110 | 11195 | 29.45 | 0.029 | 0.032 | 0.054 | 32 | 26 - 38.6 |
| "admixed" | 11 | 8909 | 23.44 | 0.054 | 0.054 | 0.001 | 38 | 3.4 - Inf |
| Reticulate Gila Monster | 145 | 28909 | 76.06 | 0.058 | 0.063 | 0.044 | 138 | 102.3 - 197.3 |

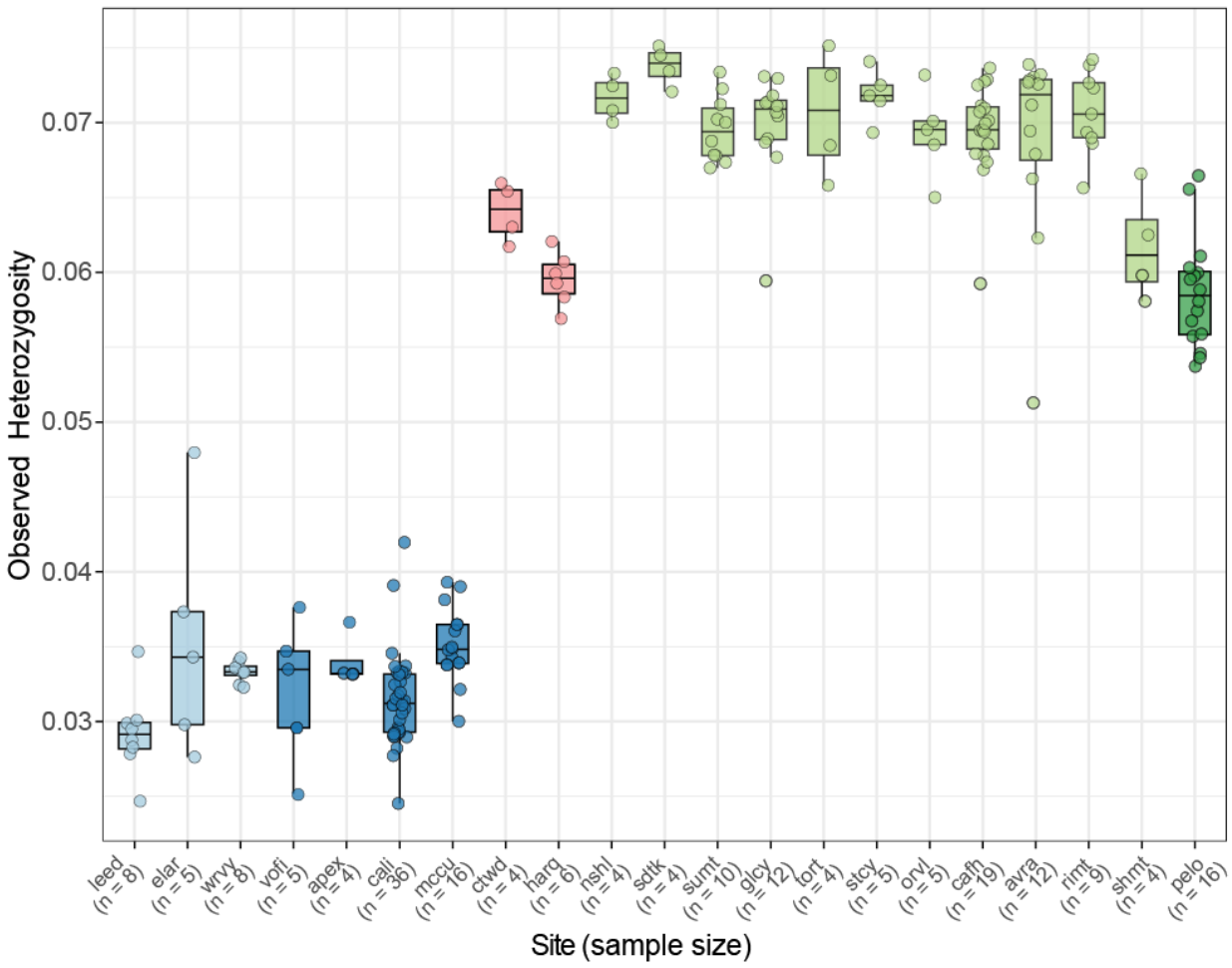



**Figure 6.** Observed heterozygosity across 21 sites and their sample sizes arranged from north to south. Site codes follow Figure 1 and colors follow the 5 ecoregionally aligned genetic populations identified in the population structure analyses (light blue = north Mojave; dark blue = south Mojave; pink = ecotone; light green = Sonoran; dark green = Chihuahuan). Box plots represent the interquartile range with a horizontal line indicating the median, and the whiskers extend to the 90$^{th}$ and 10$^{th}$ percentiles, respectively. The colored circles indicate all samples used for each box plot.

Effective population size (Ne) estimates followed a similar pattern to other diversity statistics (Table 2), where the lowest estimate was recovered in the north (Ne = 25, north Mojave) and increased in the south (Ne = 190, Sonoran), and higher overall estimates were recovered within the range of the Reticulate Gila Monster. Effective population size (Ne) estimates at the two focal sites in Nevada were low (Ne =16-22), but the upper confidence interval was much larger for mccu (upper 95% CI = 245) than cali (upper 95% CI = 26). We could not obtain reliable upper confidence estimates (Inf) at any other sites. Based on our analyses using the naïve mode within NeEstimator, our Ne upper confidence estimates of infinity (Inf) were driven by limited sample size, suggesting that not enough information was available in the sample.

## Phylogenetic Analyses

The concatenated tree estimated in IQ-TREE3 showed good correspondence with the population structure results in supporting clades by desert region (Figure 7). When applying the midpoint rooting, the two traditionally recognized Reticulate and Banded Gila Monster subspecies are supported as well. However, sites along the contact zone of these two subspecies are placed on intermediate branches (labeled 'ecotone' in Figure 7) between the two major clades in a manner consistent with the sampling geography—sites furthest south in the contact zone associate more closely with the Reticulate Gila Monster, and those to the north associate with the Banded Gila Monster.

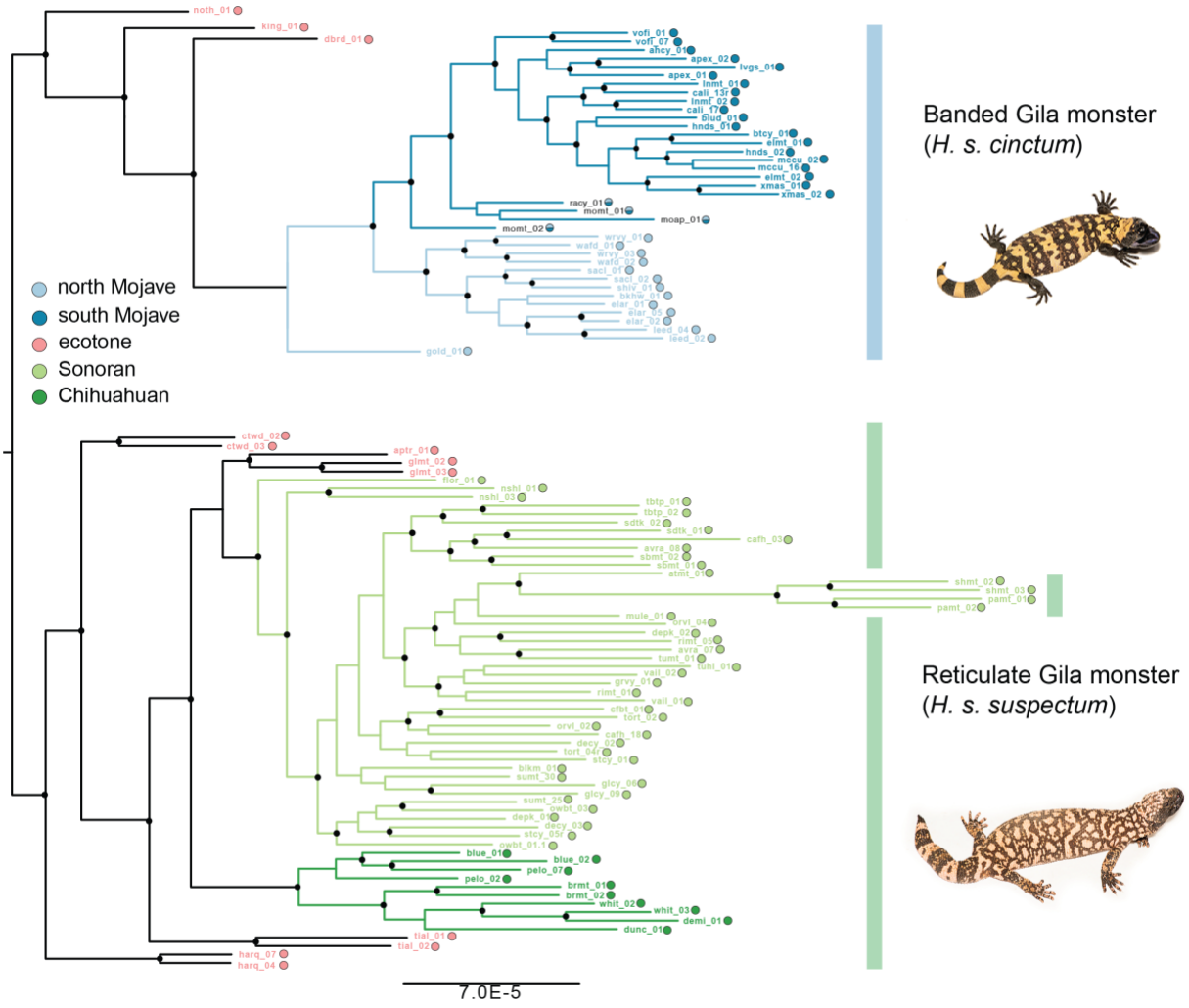



**Figure 7.** Phylogenetic relationships of concatenated SNP loci within the Gila Monster estimated in IQ-TREE3 and rooted at the midpoint. Nodes with black dots indicate bootstrap support ≥ 0.90. Photographs of Gila Monsters by Paul A. Maier.

# Discussion

Knowledge of evolutionary history and the distribution of genetic variation across a species' range can inform conservation and management. Genetic data can reveal patterns of population connectivity, unravel evolutionary histories, and help to determine appropriate geographic boundaries for management of unique genetic lineages and populations of high diversity (Waples and Gaggiotti 2006; Doak and others, 2015). However, genetic studies on at-risk species often focus only on parts of the range where populations are declining or where specific conservation objectives are located (Wood and others, 2025). Without sampling across the entire range, including regions with stable populations or admixture between neighboring populations, it becomes challenging to determine whether the populations of interest represent demographically independent lineages. This can limit the effectiveness of conservation strategies, as broader patterns of connectivity may be critical for understanding how populations have historically interacted and evolved. To address this issue in the Gila Monster, we expanded on our previous study (Wood and others, 2023) that focused primarily on conservation genetics of Nevada populations to include occupied sites from throughout the range of the species in the U.S. This expanded dataset provides new insights into the population structure and diversity of Gila Monster populations along the northern periphery of the range. Below we detail these findings and discuss their implications for management.

## Regional Population Structure

While Gila Monsters are a conspicuous component of the desert southwest, their secretive nature make them difficult to study (Beck 2005). As a result, genetic investigations involving this species have been limited. Douglas and others (2010) used nuclear and

mitochondrial genes to study the evolutionary history and diversification of the Gila Monster (*Heloderma suspectum*) and their allies. Their results had insufficient phylogenetic signal to support the traditional subspecific taxonomy, and they reported low levels of genetic diversity across the species' range. Based on these findings, Douglas and others (2010) presumed regional population structure across the range of the Gila Monster was unlikely.

Our results support that Gila monsters are comprised of two major lineages that align with the ranges of the formerly recognized subspecies, with the Banded Gila Monster (*H. s. cinctum*) occupying areas across southern Nevada and southwestern Utah in the Mojave Desert and the Reticulate Gila Monster (*H. s. suspectum*) occupying sites across Arizona and New Mexico in the Sonoran and Chihuahuan Deserts. Admixed individuals sampled along the contact zone of the two subspecies, a region that coincides with the shift from the Sonoran to the Mojave Desert, provide evidence of past or ongoing gene flow between the two lineages. This pattern was also reflected in our tree-based analysis, where individuals within the contact zone were more closely related to members of one lineage or the other depending on the sampling location. Phylogenetic methods and genetic data are often used to evaluate subspecies limits, and numerous studies have demonstrated that phenotypic subspecies (described on the basis of color pattern and other morphological characters) often fail to correspond to monophyletic genetic lineages (Burbrink and others, 2000; Janzen and others, 2002; Kodandaramaiah and others, 2012). However, others have criticized the use of monophyletic lineages as too stringent of a criterion for subspecies, because introgression and incomplete lineage sorting between diverging populations can lead to incongruent gene trees at the species-subspecies boundary (Haig and others, 2006; Patten, 2010). Relying solely on historical isolation also tends to ignore other factors contributing to phenotypic and genetic differences that may be important for

conservation. For example, local adaptation may contribute to genetic divergence but may be so recent that insufficient time has passed to achieve monophyletic gene trees. Similarly, even though lineages may have diverged to the point of having some diagnosable differences (i.e., phenotypic and/or genetic), these lineages may not be sufficiently reproductively isolated to prevent gene flow in areas of secondary contact. Such admixture can create fuzzy boundaries along these zones of contact. This is likely the case for this species, as diversification within the Gila Monster is thought to be relatively recent, during late Pleistocene at the earliest (Douglas and others, 2010; Reiserer and others, 2013). Despite this recent diversification, we found compelling evidence for two divergent groups that have broadly concordant boundaries with the two morphologically defined subspecies unlike in previous genetic studies (Douglas and others, 2010).

We found further divisions within each of these subspecies that partitioned populations into multiple genetic clusters and well-supported clades that are concordant with the Mojave, Sonoran, and Chihuahuan Desert ecoregions. These results highlight that each geographic region contains unique components of genetic diversity within this species. Protection within each of these areas could maximize the conservation of geographic and genetic representation within the species. Metrics of individual genetic diversity, such as heterozygosity and proportion of variable SNPs, were ~2X higher in the Sonoran and Chihuahuan populations compared to populations at the northern periphery of the species' range in the Mojave Desert. Similarly, estimates of effective population size across genetic clusters and subspecies all reflect a similar pattern, where larger estimates occur in the southern portion of the species range and lower estimates in the northern portion. This pattern of diversity is consistent with a latitudinal shift model (Hewitt 2004; DeChaine and other, 2006) where genetic diversity decreases with increasing latitude

because of northward range expansions and genetic drift. Under this scenario, southern populations may have expanded northward in conjunction with recent aridification and northward expansion of desert scrub habitats throughout the southwestern deserts (Douglas and others, 2010; Reiserer and others, 2013). Given this biogeographic history, it is likely that low levels of genetic diversity in much of Nevada and Utah reflect this process of historical range expansion, although this could also be influenced by more recent fragmentation and population reductions.

Within the Mojave Desert biome, our results supported two regional subgroups that partitioned sampled sites into separate clusters. The northernmost cluster was composed of lizards that inhabit the extreme southwestern region of Utah, while lizards across Clark County in southern Nevada were grouped into the south cluster. Occupied sites between these clusters exhibited mixed ancestry indicative of widespread historical connectivity across this region. Our previous study (Wood and others, 2023) found strong isolation by distance among sites throughout this region consistent with a stepping-stone pattern of movement and gene flow. Combined with the current understanding of limited above ground activity, small home range size and short movement distances (Stalker and other, 2023; Hromada and others, 2025), low genetic connectivity is likely a result of continued occupancy and limited individual movements over generations in areas of suitable habitat, similar to that described in Mojave desert tortoises (Dutcher and others, 2020; Hagerty and others, 2011). In addition, habitat loss and fragmentation due to recent urbanization, and other development may be further restricting gene flow. Highways, for example, were significantly associated with greater genetic differentiation among individuals across Clark County (Wood and others, 2023), even after accounting for geographic distance and climatic differences across the species' range.

This is particularly the case within the south Mojave cluster, where the majority of previously available habitat in the area is now developed. Remaining open space with suitable habitat between sites is constrained to narrow corridors south of Las Vegas and Henderson, that extend along the Calico and Blue Diamond hills southeast to North McCullough and Sloan Canyon Wilderness Areas. This region could be of importance for maintaining or enhancing gene exchange among occupied sites. This corridor is bisected by Highway 160 and Interstate Highway 15, both of which likely present barriers to connectivity along the Vegas Valley corridor. There is limited published information on the effects of urbanization on Gila Monsters, but one study in the Phoenix area found that Gila Monsters readily crossed narrow roads, and that movement rates and home range sizes were unaffected at more highly urbanized study sites (Kwiatkowski and others, 2008). However, this same study reported female-skewed sex ratios in urbanized areas and suggested that higher mortality rates associated with higher movement rates in males could contribute to this pattern. Another study of road kill near Saguaro National park found that Gila Monster road mortalities were correlated with traffic density (Paredes 2017). Existing culverts or other undercrossing structures and fencing along major roads and highways could be assessed to better understand if existing structures are useful or could be enhanced to support regional connectivity. Our previous analysis also associated genetic distance with climate differences, notably temperature (Wood and others, 2023).

## Effective Population Sizes

Effective population size (Ne) is an important parameter for conservation management because it provides a way to measure the influence of genetic drift (chance loss of alleles through time) and inbreeding in a population (Frankham and others, 2017). Thus, effective population size provides a measure of the ability of populations to maintain genetic diversity over future

generations. We focused our efforts across two focal sites in Nevada (cali and mccu) but also attempted to estimate Ne from across the species' range at sites with greater than 10 individuals for comparative purposes. The contemporary effective population size estimate at cali and mccu were both small (16 and 22 respectively) but upper 95% confidence intervals between the two sites differed considerably, ranging from 26 at cali to 245 at mccu. The higher Ne upper confidence limit at mccu is consistent with that of effective size (95% CI ranged from 78-137) from a protected population located in the core of the species range at Saguaro National Park, Arizona (Farrar and others, 2017), which makes the smaller upper Ne estimate at cali more striking. Differences in habitat, resource availability, and genetic connectivity to neighboring sites may drive the disparity between these two Nevada sites. Mccu is a lower elevation site, between 400-900 m, and is sparsely vegetated, while cali lies between 1,000-1,500 m, is bordered by a residential area, and has a spring which supplies water most of the year, encouraging continual and diverse vegetation growth. Stalker and others (2023) found that lizards at cali had smaller home ranges compared to mccu and that the habitat heterogeneity and resource differences across these sites likely drive these space use differences. These factors suggest that lizards at cali may be more isolated from neighboring populations than lizards at mccu, which may contribute to lower immigration and higher rates of inbreeding at cali. The cali Ne estimates fall outside the recommended range (Ne = 50 – 100) to avoid short-term inbreeding effects (Franklin 1980, Frankham and others, 2014) which may be accelerating genetic drift at this site (Allendorf, 1986; Slatkin, 1987) and that more effective management of this site might be achieved by taking this into account. Studies have shown that an ideal, genetically healthy population is one that has a sufficiently large Ne coupled with moderate connectivity to other

populations to maintain gene exchange and counter the effects of genetic drift (Wright, 1931; Lowe and others, 2010).

All other site estimates of effective size estimates across the range resulted in unbounded upper confidence intervals. The lack of an upper bound in the confidence interval suggests that the sample sizes were too small (see Waples and Do, 2010), a deficit that could be improved with additional sampling at sites of interest. Nonetheless, when sites were grouped by genetic populations, we recovered much lower Ne estimates in the northern periphery of the species range. This pattern could be influenced by demographic instability, small population sizes, nonrandom reproductive success, inbreeding, and loss of connectivity from habitat disturbances across the region. Alternatively, lower diversity and small Ne in the northern periphery may also be influenced by historical demography. Historical range expansions can reduce genetic diversity and effective population size through founder effects, where only a small fraction of the species' genetic diversity is passed into these range edge populations. Overall, our results highlight the value of continued population monitoring across the range to better understand population sizes and densities and how they are affected by landscape connectivity and historical demographic processes.

## Management Implications

This study provides baseline genomic metrics for future monitoring of population status and to help inform effective mitigation measures to maintain species viability. This study focused on the genetic diversity of the species across its entire range, investigating whether it is divided into distinct genetic regions and examining how these regions are evolutionarily connected to each other. The regional genetic structure detected here highlights that each geographic region contains unique components of the overall genetic diversity within Gila

Monsters. On the largest scale, our results supported the traditionally described subspecies, including the Banded Gila Monster (*Heloderma suspectum cinctum*), which is mostly found in Nevada, with a small part of its range extending into southwest Utah. We also identified two separate genetic groups within Nevada. Protecting habitats in each region could help ensure the conservation and representation of genetic diversity across the species. Comparing the two best-sampled focal locations (mccu and cali), effective population size estimates were lower at cali, suggesting that genetic drift may be occurring more rapidly at this site and indicating that population augmentation could be necessary. It remains unclear whether this finding is unique to cali or representative of other occupied sites throughout Nevada and Utah, as sample sizes are still insufficient to reliably estimate local effective population sizes at most locations. The lower genetic diversity and smaller effective population sizes observed at the species' northern range boundary are notable. Further research is needed to determine the relative contributions of contemporary and historical processes to the patterns of diversity in this region.

Gaining more insight into how common and widespread Gila Monsters are in Clark County may reveal areas with more robust populations. Surveys could be directed toward regions with suitable habitats and signs of historical genetic connections or mixing. This could be particularly relevant in northeastern Clark County, through the region encompassing the Moapa Valley, Valley of Fire, Muddy Mountains and Gale Hills, and west of Interstate Highway 15 through the Dry Lake Range. This region is still relatively free from urban development and appears to be a region of high historical admixture between the north and south Mojave clusters. Additional blood collection and genetic sampling efforts (approx. 20+ individuals per population center) could provide more robust estimates of Ne in these locations, as we estimated for mccu and cali. Previous study results, that roads are associated with greater genetic divergence (Wood

and others, 2023), together with other studies of road mortalities and links between sex ratio and urban development in Gila Monsters, support efforts to identify corridors and structures for highway avoidance and crossings. Should managers determine that future translocation and augmentation initiatives are necessary in Nevada, the data presented regarding the north and south Mojave clusters may serve to identify suitable source sites within the corresponding regional genetic cluster.

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## Supplementary Tables

**Table S1.** Individual per sample sequencing statistics after alignment to a reference genome (Heloderma suspectum; GCA_022577455.1) using the Stacks bioinformatics pipeline for restriction-enzyme based data. See Table S3 for site information. (Continued on multiple pages)

| Sample | Alignments obtained | Alignments kept | Fraction kept | Unmapped alignments | Number of loci | Mean coverage | Percent Missing | Passed Filtering |
|---|---|---|---|---|---|---|---|---|
| ahcy_01 | 7,526,006 | 6,320,392 | 0.84 | 23,602 | 390,053 | 10.6 | 0.3% | Pass |
| apex_01 | 26,550,608 | 22,721,416 | 0.856 | 23,252 | 523,541 | 32.9 | 0.0% | Pass |
| apex_02 | 8,001,569 | 6,644,510 | 0.83 | 98,518 | 392,306 | 11.1 | 0.2% | Pass |
| apex_03 | 9,060,643 | 7,598,413 | 0.839 | 33,139 | 410,322 | 12.4 | 0.1% | Pass |
| apex_04r | 1,537,456 | 1,278,265 | 0.831 | 12,240 | 184,415 | 3.8 | 36.5% | Pass |
| aptr_01 | 3,170,613 | 2,630,815 | 0.83 | 21,495 | 272,380 | 5.8 | 4.6% | Pass |
| atmt_01 | 7,595,553 | 5,935,430 | 0.781 | 4,672 | 401,209 | 10.2 | 0.5% | Pass |
| avra_01 | 8,578,300 | 7,358,010 | 0.858 | 14,746 | 399,706 | 12.5 | 0.2% | Pass |
| avra_02 | 1,579,074 | 1,359,649 | 0.861 | 3,247 | 195,837 | 3.9 | 33.5% | Pass |
| avra_03 | 3,594,211 | 3,056,826 | 0.85 | 8,485 | 287,162 | 6.6 | 4.4% | Pass |
| avra_04 | 4,109,260 | 3,536,349 | 0.861 | 3,408 | 304,450 | 7.1 | 1.8% | Pass |
| avra_05 | 4,466,009 | 3,798,262 | 0.85 | 7,718 | 305,755 | 7.7 | 1.3% | Pass |
| avra_06 | 8,767,519 | 7,395,646 | 0.844 | 9,133 | 402,410 | 12.3 | 0.2% | Pass |
| avra_07 | 11,563,949 | 9,700,827 | 0.839 | 35,122 | 441,042 | 15.1 | 0.2% | Pass |
| avra_08 | 5,226,422 | 4,465,188 | 0.854 | 4,214 | 327,011 | 8.5 | 1.0% | Pass |
| avra_09 | 11,316,562 | 9,575,611 | 0.846 | 28,934 | 428,655 | 15.5 | 0.2% | Pass |
| avra_10 | 4,245,649 | 3,602,438 | 0.849 | 6,909 | 295,644 | 7.6 | 1.9% | Pass |
| avra_11 | 11,098,302 | 8,957,181 | 0.807 | 67,004 | 459,097 | 14.2 | 0.2% | Pass |
| avra_12 | 8,401,627 | 7,116,602 | 0.847 | 15,079 | 392,336 | 12.5 | 0.3% | Pass |
| bkhw_01 | 10,729,615 | 8,949,558 | 0.834 | 17,867 | 436,843 | 14.0 | 0.1% | Pass |
| blkm_01 | 3,064,476 | 2,669,847 | 0.871 | 4,119 | 261,764 | 6.0 | 5.1% | Pass |
| blud_01 | 24,225,112 | 20,646,418 | 0.852 | 63,237 | 514,443 | 30.5 | 0.1% | Pass |
| blue_01 | 1,528,434 | 1,311,285 | 0.858 | 3,869 | 188,321 | 3.9 | 34.6% | Pass |
| blue_02 | 9,552,711 | 8,147,191 | 0.853 | 21,916 | 406,832 | 13.5 | 0.2% | Pass |
| brmt_01 | 2,931,846 | 2,487,688 | 0.849 | 8,628 | 254,660 | 5.7 | 6.4% | Pass |
| brmt_02 | 5,474,389 | 4,589,749 | 0.838 | 11,454 | 344,856 | 8.7 | 0.7% | Pass |
| brmt_03 | 7,302,528 | 6,240,364 | 0.855 | 16,632 | 369,616 | 11.1 | 0.4% | Pass |
| btcy_01 | 16,014,969 | 13,508,808 | 0.844 | 34,990 | 471,444 | 20.8 | 0.1% | Pass |
| cafh_01 | 5,512,616 | 4,777,085 | 0.867 | 94,287 | 322,765 | 9.2 | 0.6% | Pass |

| Sample | Alignments obtained | Alignments kept | Fraction kept | Unmapped alignments | Number of loci | Mean coverage | Percent Missing | Passed Filtering |
|---|---|---|---|---|---|---|---|---|
| cafh_02 | 4,801,417 | 4,164,285 | 0.867 | 4,982 | 316,733 | 8.1 | 1.4% | Pass |
| cafh_03 | 5,520,221 | 4,806,949 | 0.871 | 18,956 | 327,930 | 9.2 | 0.7% | Pass |
| cafh_04 | 20,716,813 | 17,906,826 | 0.864 | 29,953 | 504,282 | 26.3 | 0.1% | Pass |
| cafh_05 | 9,683,474 | 8,258,210 | 0.853 | 12,603 | 431,426 | 13.2 | 0.2% | Pass |
| cafh_06 | 4,691,757 | 4,071,935 | 0.868 | 11,591 | 310,398 | 8.1 | 1.1% | Pass |
| cafh_07 | 5,074,058 | 4,355,551 | 0.858 | 39,524 | 329,744 | 8.3 | 1.0% | Pass |
| cafh_09 | 2,226,352 | 1,857,938 | 0.835 | 19,408 | 236,329 | 4.5 | 16.3% | Pass |
| cafh_11 | 2,179,395 | 1,838,257 | 0.843 | 4,755 | 229,465 | 4.6 | 18.6% | Pass |
| cafh_12 | 5,855,332 | 5,004,987 | 0.855 | 8,627 | 342,186 | 9.4 | 0.5% | Pass |
| cafh_13 | 2,335,330 | 2,009,582 | 0.861 | 2,901 | 244,053 | 4.8 | 13.4% | Pass |
| cafh_14 | 5,267,513 | 4,550,196 | 0.864 | 3,419 | 321,316 | 8.8 | 1.1% | Pass |
| cafh_15 | 9,044,903 | 7,887,841 | 0.872 | 12,003 | 400,229 | 13.2 | 0.2% | Pass |
| cafh_16 | 5,374,255 | 4,722,898 | 0.879 | 7,293 | 328,182 | 9.0 | 0.6% | Pass |
| cafh_17 | 3,842,728 | 3,345,090 | 0.87 | 7,055 | 285,220 | 7.1 | 2.3% | Pass |
| cafh_18 | 16,758,144 | 14,343,062 | 0.856 | 40,407 | 497,506 | 21.4 | 0.1% | Pass |
| cafh_19 | 2,996,539 | 2,423,754 | 0.809 | 2,142 | 274,820 | 5.4 | 10.0% | Pass |
| cafh_20 | 11,052,760 | 9,578,229 | 0.867 | 9,404 | 414,175 | 15.7 | 0.2% | Pass |
| cafh_21 | 6,741,893 | 5,851,185 | 0.868 | 18,781 | 365,698 | 10.3 | 0.4% | Pass |
| cali_01r | 3,092,181 | 2,640,030 | 0.854 | 16,723 | 227,542 | 6.6 | 11.7% | Pass |
| cali_03 | 11,647,894 | 9,947,347 | 0.854 | 28,751 | 433,750 | 15.8 | 0.1% | Pass |
| cali_04 | 11,595,058 | 9,892,514 | 0.853 | 14,339 | 430,402 | 15.7 | 0.1% | Pass |
| cali_05 | 6,375,799 | 5,374,638 | 0.843 | 10,493 | 359,333 | 9.8 | 0.7% | Pass |
| cali_06 | 5,197,603 | 4,390,865 | 0.845 | 11,448 | 328,200 | 8.4 | 0.7% | Pass |
| cali_07 | 4,697,036 | 3,965,105 | 0.844 | 4,255 | 321,574 | 7.6 | 1.1% | Pass |
| cali_08 | 14,922,086 | 12,717,503 | 0.852 | 18,093 | 480,030 | 19.4 | 0.1% | Pass |
| cali_09 | 30,725,582 | 25,763,627 | 0.839 | 46,664 | 562,185 | 36.2 | 0.0% | Pass |
| cali_10 | 13,642,124 | 11,758,116 | 0.862 | 20,037 | 450,975 | 18.6 | 0.0% | Pass |
| cali_11 | 12,452,879 | 10,466,670 | 0.841 | 19,110 | 448,834 | 16.2 | 0.1% | Pass |
| cali_12 | 8,402,398 | 7,103,247 | 0.845 | 8,008 | 383,445 | 12.2 | 0.1% | Pass |
| cali_13r | 2,310,625 | 1,909,118 | 0.826 | 34,092 | 223,642 | 4.8 | 17.3% | Pass |
| cali_14 | 4,035,653 | 3,436,360 | 0.852 | 8,499 | 296,193 | 7.1 | 1.2% | Pass |
| cali_15 | 6,218,908 | 5,243,031 | 0.843 | 18,914 | 358,750 | 9.4 | 0.4% | Pass |
| cali_16.2 | 5,809,724 | 4,948,909 | 0.852 | 7,764 | 349,684 | 9.1 | 0.7% | Pass |

| Sample | Alignments obtained | Alignments kept | Fraction kept | Unmapped alignments | Number of loci | Mean coverage | Percent Missing | Passed Filtering |
|---|---|---|---|---|---|---|---|---|
| cali_17 | 4,350,216 | 3,711,072 | 0.853 | 3,805 | 305,599 | 7.5 | 1.9% | Pass |
| cali_18 | 21,664,604 | 18,973,476 | 0.876 | 17,043 | 488,306 | 28.6 | 0.0% | Pass |
| cali_19 | 12,358,880 | 10,371,070 | 0.839 | 20,544 | 447,670 | 16.0 | 0.1% | Pass |
| cali_20 | 8,105,629 | 6,854,256 | 0.846 | 7,847 | 384,167 | 11.7 | 0.1% | Pass |
| cali_21 | 10,847,645 | 9,027,890 | 0.832 | 17,718 | 433,637 | 14.2 | 0.1% | Pass |
| cali_23 | 5,544,523 | 4,576,282 | 0.825 | 31,695 | 346,276 | 8.4 | 0.3% | Pass |
| cali_24r | 4,924,151 | 4,133,159 | 0.839 | 28,677 | 293,404 | 8.4 | 3.6% | Pass |
| cali_25 | 3,276,342 | 2,561,490 | 0.782 | 1,856 | 285,448 | 5.4 | 6.7% | Pass |
| cali_26r | 5,594,161 | 4,615,859 | 0.825 | 53,165 | 313,782 | 8.9 | 1.1% | Pass |
| cali_27 | 3,023,117 | 2,480,637 | 0.821 | 2,265 | 271,060 | 5.5 | 5.7% | Pass |
| cali_29r | 12,606,628 | 10,415,605 | 0.826 | 29,571 | 391,925 | 17.3 | 0.1% | Pass |
| cali_30 | 3,597,086 | 3,010,244 | 0.837 | 2,421 | 291,398 | 6.4 | 3.5% | Pass |
| cali_31r | 32,833,969 | 27,077,931 | 0.825 | 68,328 | 487,724 | 40.7 | 0.1% | Pass |
| cali_32 | 6,217,623 | 4,913,008 | 0.79 | 3,477 | 393,486 | 8.3 | 0.9% | Pass |
| cali_34 | 2,454,050 | 1,890,145 | 0.77 | 1,211 | 257,280 | 4.3 | 16.0% | Pass |
| cali_35 | 6,587,097 | 5,685,077 | 0.863 | 10,442 | 345,583 | 10.5 | 0.3% | Pass |
| cali_40 | 5,856,782 | 5,035,111 | 0.86 | 5,636 | 327,189 | 9.7 | 0.5% | Pass |
| cali_42 | 4,219,372 | 3,530,452 | 0.837 | 7,891 | 316,657 | 6.9 | 1.9% | Pass |
| cali_43 | 1,782,103 | 1,486,338 | 0.834 | 5,773 | 216,233 | 3.9 | 27.5% | Pass |
| cali_44 | 2,206,375 | 1,860,598 | 0.843 | 2,559 | 230,417 | 4.7 | 19.7% | Pass |
| cali_45.2 | 14,603,881 | 12,494,013 | 0.856 | 33,217 | 434,742 | 20.2 | 0.0% | Pass |
| cfbt_01 | 5,069,817 | 4,398,833 | 0.868 | 8,155 | 319,510 | 8.5 | 0.9% | Pass |
| ctwd_02 | 3,467,165 | 2,562,065 | 0.739 | 4,085 | 298,703 | 5.3 | 6.8% | Pass |
| ctwd_03 | 2,476,927 | 1,929,239 | 0.779 | 2,093 | 251,870 | 4.5 | 16.5% | Pass |
| ctwd_06 | 4,648,861 | 3,429,828 | 0.738 | 3,652 | 358,629 | 6.2 | 3.2% | Pass |
| ctwd_07 | 38,177,598 | 31,069,031 | 0.814 | 35,323 | 647,529 | 43.0 | 0.1% | Pass |
| dbrd_01 | 7,927,085 | 6,622,887 | 0.835 | 6,912 | 382,694 | 11.5 | 0.2% | Pass |
| decy_01 | 4,921,317 | 4,270,634 | 0.868 | 25,228 | 308,032 | 8.5 | 1.1% | Pass |
| decy_02 | 17,539,926 | 15,196,733 | 0.866 | 64,502 | 485,832 | 22.7 | 0.1% | Pass |
| decy_03 | 6,255,257 | 5,468,848 | 0.874 | 8,087 | 341,414 | 10.1 | 0.4% | Pass |
| demi_01 | 15,707,937 | 12,902,618 | 0.821 | 61,383 | 423,894 | 20.6 | 0.2% | Pass |
| depk_01 | 2,127,190 | 1,805,226 | 0.849 | 1,858 | 229,910 | 4.5 | 17.3% | Pass |
| depk_02 | 5,491,812 | 4,761,470 | 0.867 | 8,159 | 344,929 | 8.7 | 0.7% | Pass |

| Sample | Alignments obtained | Alignments kept | Fraction kept | Unmapped alignments | Number of loci | Mean coverage | Percent Missing | Passed Filtering |
|---|---|---|---|---|---|---|---|---|
| depk_03 | 2,195,716 | 1,917,267 | 0.873 | 3,339 | 225,192 | 4.9 | 15.6% | Pass |
| dunc_01 | 12,967,323 | 10,835,629 | 0.836 | 54,977 | 379,036 | 18.5 | 0.2% | Pass |
| elar_01 | 2,734,972 | 2,170,528 | 0.794 | 1,356 | 261,733 | 4.9 | 11.9% | Pass |
| elar_02 | 2,243,162 | 1,762,073 | 0.786 | 1,347 | 243,526 | 4.2 | 21.6% | Pass |
| elar_03 | 3,650,827 | 2,877,228 | 0.788 | 1,930 | 300,652 | 5.9 | 3.7% | Pass |
| elar_04 | 6,069,207 | 4,900,225 | 0.807 | 2,814 | 363,470 | 8.8 | 0.4% | Pass |
| elar_05 | 3,812,057 | 3,129,675 | 0.821 | 3,874 | 299,594 | 6.4 | 3.1% | Pass |
| elmt_01 | 38,628,743 | 32,504,434 | 0.841 | 118,811 | 573,740 | 45.6 | 0.1% | Pass |
| elmt_02 | 13,474,838 | 11,139,407 | 0.827 | 40,737 | 467,916 | 17.0 | 0.1% | Pass |
| elmt_03 | 4,342,064 | 3,597,382 | 0.828 | 4,759 | 310,423 | 7.3 | 1.7% | Pass |
| flor_01 | 12,705,014 | 10,896,363 | 0.858 | 27,447 | 446,591 | 16.9 | 0.1% | Pass |
| glcy_01 | 5,686,372 | 4,889,459 | 0.86 | 9,850 | 351,196 | 8.8 | 0.6% | Pass |
| glcy_02 | 14,230,716 | 12,179,813 | 0.856 | 97,277 | 460,657 | 18.6 | 0.1% | Pass |
| glcy_03 | 10,329,687 | 8,902,324 | 0.862 | 20,069 | 420,323 | 14.3 | 0.2% | Pass |
| glcy_04 | 7,150,160 | 6,045,564 | 0.846 | 51,682 | 380,601 | 10.4 | 0.5% | Pass |
| glcy_05 | 3,897,710 | 3,247,576 | 0.833 | 23,857 | 299,818 | 6.6 | 2.8% | Pass |
| glcy_06 | 6,508,552 | 5,613,296 | 0.862 | 10,293 | 349,882 | 10.2 | 0.4% | Pass |
| glcy_07 | 6,090,674 | 5,291,640 | 0.869 | 14,524 | 339,020 | 9.9 | 0.4% | Pass |
| glcy_09 | 6,695,388 | 5,794,457 | 0.865 | 47,228 | 352,204 | 10.5 | 0.4% | Pass |
| glcy_10 | 16,675,733 | 14,340,437 | 0.86 | 29,211 | 476,838 | 21.6 | 0.1% | Pass |
| glcy_11 | 4,821,557 | 4,164,323 | 0.864 | 30,934 | 320,265 | 8.0 | 0.9% | Pass |
| glcy_12 | 5,275,158 | 4,551,873 | 0.863 | 69,079 | 325,042 | 8.7 | 0.6% | Pass |
| glcy_13 | 7,084,096 | 6,030,433 | 0.851 | 60,843 | 371,335 | 10.5 | 0.3% | Pass |
| glmt_02 | 2,934,715 | 2,524,300 | 0.86 | 12,190 | 262,137 | 5.7 | 7.0% | Pass |
| glmt_03 | 1,752,937 | 1,527,502 | 0.871 | 3,445 | 205,861 | 4.2 | 26.7% | Pass |
| glmt_04 | 4,538,690 | 3,930,107 | 0.866 | 8,950 | 307,248 | 7.9 | 1.2% | Pass |
| gold_01 | 24,138,170 | 20,941,712 | 0.868 | 21,290 | 527,612 | 30.8 | 0.1% | Pass |
| grvy_01 | 3,124,895 | 2,628,635 | 0.841 | 6,875 | 271,586 | 5.8 | 4.9% | Pass |
| harq_01 | 3,160,124 | 2,746,010 | 0.869 | 13,104 | 260,461 | 6.2 | 4.9% | Pass |
| harq_02 | 7,733,621 | 6,739,360 | 0.871 | 14,749 | 375,789 | 11.7 | 0.3% | Pass |
| harq_04 | 6,319,133 | 5,447,960 | 0.862 | 26,392 | 354,758 | 9.8 | 0.4% | Pass |
| harq_05 | 1,897,118 | 1,647,860 | 0.869 | 7,246 | 208,872 | 4.5 | 22.4% | Pass |
| harq_06 | 1,860,618 | 1,619,051 | 0.87 | 4,883 | 207,209 | 4.4 | 23.9% | Pass |

| Sample | Alignments obtained | Alignments kept | Fraction kept | Unmapped alignments | Number of loci | Mean coverage | Percent Missing | Passed Filtering |
|---|---|---|---|---|---|---|---|---|
| harq_07 | 3,103,019 | 2,719,040 | 0.876 | 6,677 | 258,386 | 6.2 | 5.2% | Pass |
| hnds_01 | 2,012,911 | 1,712,991 | 0.851 | 4,730 | 212,998 | 4.6 | 18.6% | Pass |
| hnds_02 | 2,905,820 | 2,330,882 | 0.802 | 3,570 | 265,380 | 5.3 | 10.0% | Pass |
| king_01 | 2,533,937 | 2,191,909 | 0.865 | 2,619 | 242,882 | 5.2 | 8.5% | Pass |
| leed_01 | 5,863,742 | 4,833,299 | 0.824 | 3,398 | 364,072 | 8.7 | 0.5% | Pass |
| leed_02 | 14,157,106 | 11,886,315 | 0.84 | 18,634 | 490,082 | 18.3 | 0.1% | Pass |
| leed_03 | 21,091,054 | 17,678,024 | 0.838 | 27,408 | 551,841 | 25.8 | 0.1% | Pass |
| leed_04 | 23,171,799 | 19,859,104 | 0.857 | 21,819 | 502,998 | 29.7 | 0.1% | Pass |
| leed_05 | 4,168,066 | 3,528,427 | 0.847 | 12,180 | 297,742 | 7.2 | 1.5% | Pass |
| leed_06 | 5,207,086 | 4,480,075 | 0.86 | 8,724 | 313,953 | 8.8 | 0.4% | Pass |
| leed_07 | 6,295,797 | 5,412,936 | 0.86 | 13,933 | 333,416 | 10.3 | 0.3% | Pass |
| leed_08 | 5,537,775 | 4,748,351 | 0.857 | 4,794 | 328,884 | 9.0 | 0.5% | Pass |
| lnmt_01 | 4,198,347 | 3,347,276 | 0.797 | 2,223 | 343,917 | 6.6 | 2.4% | Pass |
| lnmt_02 | 7,842,533 | 6,865,175 | 0.875 | 14,079 | 366,020 | 12.2 | 0.1% | Pass |
| lvgs_01 | 7,611,272 | 6,454,082 | 0.848 | 7,435 | 380,186 | 11.2 | 0.2% | Pass |
| mccu_01 | 6,361,420 | 5,470,237 | 0.86 | 4,897 | 347,904 | 10.0 | 0.3% | Pass |
| mccu_02 | 7,650,095 | 6,486,133 | 0.848 | 12,452 | 381,004 | 11.5 | 0.2% | Pass |
| mccu_03 | 21,534,361 | 18,023,444 | 0.837 | 75,770 | 515,112 | 26.1 | 0.1% | Pass |
| mccu_04 | 7,822,279 | 6,616,264 | 0.846 | 20,352 | 374,623 | 11.6 | 0.2% | Pass |
| mccu_05 | 2,491,445 | 1,944,227 | 0.78 | 1,669 | 265,368 | 4.4 | 16.5% | Pass |
| mccu_06 | 4,286,742 | 3,607,004 | 0.841 | 10,959 | 305,271 | 7.3 | 1.0% | Pass |
| mccu_09 | 12,354,610 | 10,744,195 | 0.87 | 45,229 | 421,845 | 17.6 | 0.1% | Pass |
| mccu_10 | 7,500,672 | 6,454,252 | 0.86 | 6,296 | 375,225 | 11.3 | 0.2% | Pass |
| mccu_11 | 56,238,302 | 48,429,474 | 0.861 | 529,481 | 615,223 | 67.5 | 0.1% | Pass |
| mccu_12 | 3,535,783 | 3,019,710 | 0.854 | 29,025 | 272,268 | 6.6 | 3.2% | Pass |
| mccu_13 | 29,984,729 | 26,138,314 | 0.872 | 40,283 | 533,716 | 38.5 | 0.1% | Pass |
| mccu_14 | 71,149,405 | 61,605,804 | 0.866 | 288,152 | 647,132 | 84.8 | 0.0% | Pass |
| mccu_15 | 6,786,928 | 5,916,117 | 0.872 | 30,822 | 346,620 | 10.9 | 0.2% | Pass |
| mccu_16 | 3,289,768 | 2,844,675 | 0.865 | 12,693 | 272,196 | 6.2 | 5.2% | Pass |
| mccu_19 | 6,560,822 | 5,551,084 | 0.846 | 14,261 | 355,628 | 10.0 | 0.2% | Pass |
| mccu_22 | 26,050,055 | 21,914,087 | 0.841 | 40,525 | 532,915 | 31.2 | 0.0% | Pass |
| moap_01 | 20,167,372 | 16,892,149 | 0.838 | 35,349 | 508,807 | 24.7 | 0.1% | Pass |
| momt_01 | 3,447,731 | 2,967,687 | 0.861 | 5,855 | 269,676 | 6.6 | 3.2% | Pass |

| Sample | Alignments obtained | Alignments kept | Fraction kept | Unmapped alignments | Number of loci | Mean coverage | Percent Missing | Passed Filtering |
|---|---|---|---|---|---|---|---|---|
| momt_02 | 4,620,001 | 3,981,718 | 0.862 | 19,026 | 310,691 | 7.9 | 1.5% | Pass |
| mule_01 | 2,004,462 | 1,678,059 | 0.837 | 4,600 | 221,793 | 4.4 | 22.4% | Pass |
| noth_01 | 10,784,417 | 9,434,355 | 0.875 | 14,145 | 424,001 | 15.2 | 0.1% | Pass |
| nshl_01 | 12,969,777 | 10,849,078 | 0.836 | 23,827 | 460,790 | 16.7 | 0.2% | Pass |
| nshl_02 | 3,296,506 | 2,667,952 | 0.809 | 5,393 | 293,073 | 5.5 | 6.2% | Pass |
| nshl_03 | 5,961,851 | 5,109,331 | 0.857 | 13,227 | 337,550 | 9.6 | 0.6% | Pass |
| nshl_04 | 33,702,069 | 28,294,018 | 0.84 | 50,425 | 570,210 | 39.6 | 0.1% | Pass |
| orvl_01 | 4,295,561 | 3,722,114 | 0.867 | 7,020 | 298,233 | 7.6 | 1.7% | Pass |
| orvl_02 | 2,551,090 | 2,142,247 | 0.84 | 8,585 | 244,668 | 5.1 | 11.6% | Pass |
| orvl_03 | 7,280,746 | 6,199,820 | 0.852 | 17,617 | 383,910 | 11.0 | 0.4% | Pass |
| orvl_04 | 5,182,933 | 4,523,609 | 0.873 | 6,391 | 325,040 | 8.7 | 0.8% | Pass |
| orvl_05 | 13,946,970 | 12,076,331 | 0.866 | 15,162 | 463,409 | 18.5 | 0.1% | Pass |
| owbt_01.1 | 3,244,137 | 2,804,545 | 0.864 | 14,704 | 272,655 | 6.1 | 5.3% | Pass |
| owbt_03 | 12,896,265 | 11,141,806 | 0.864 | 16,073 | 453,153 | 17.5 | 0.1% | Pass |
| pamt_01 | 14,415,242 | 11,888,705 | 0.825 | 21,971 | 477,456 | 18.2 | 0.3% | Pass |
| pamt_02 | 5,794,243 | 4,830,614 | 0.834 | 17,944 | 355,600 | 8.7 | 1.8% | Pass |
| pamt_04 | 4,616,921 | 4,012,108 | 0.869 | 9,771 | 309,573 | 7.9 | 1.1% | Pass |
| pelo_01 | 3,211,234 | 2,651,956 | 0.826 | 2,563 | 278,033 | 5.8 | 7.6% | Pass |
| pelo_02 | 2,990,603 | 2,556,201 | 0.855 | 2,609 | 349,713 | 5.3 | 11.4% | Pass |
| pelo_03 | 10,558,600 | 9,047,850 | 0.857 | 11,860 | 428,252 | 14.6 | 0.2% | Pass |
| pelo_04 | 5,614,146 | 4,731,566 | 0.843 | 16,806 | 346,353 | 8.7 | 0.8% | Pass |
| pelo_05 | 9,183,502 | 7,826,681 | 0.852 | 11,510 | 398,783 | 13.1 | 0.3% | Pass |
| pelo_06 | 6,049,749 | 5,139,115 | 0.849 | 14,858 | 351,682 | 9.3 | 0.6% | Pass |
| pelo_07 | 5,605,485 | 4,807,807 | 0.858 | 9,153 | 329,355 | 9.3 | 0.6% | Pass |
| pelo_08 | 4,111,058 | 3,552,005 | 0.864 | 3,800 | 293,906 | 7.4 | 2.8% | Pass |
| pelo_09 | 13,407,253 | 11,432,584 | 0.853 | 31,679 | 443,560 | 18.0 | 0.1% | Pass |
| pelo_10 | 10,752,957 | 9,260,195 | 0.861 | 15,951 | 415,145 | 15.3 | 0.1% | Pass |
| pelo_11 | 11,396,756 | 9,607,244 | 0.843 | 17,271 | 440,622 | 15.0 | 0.2% | Pass |
| pelo_12 | 9,582,151 | 8,274,683 | 0.864 | 16,043 | 387,448 | 14.2 | 0.2% | Pass |
| pelo_13 | 5,348,894 | 4,599,037 | 0.86 | 8,997 | 325,807 | 8.9 | 0.8% | Pass |
| pelo_14 | 9,371,263 | 7,999,121 | 0.854 | 17,221 | 399,154 | 13.3 | 0.2% | Pass |
| pelo_15 | 22,025,800 | 18,409,025 | 0.836 | 92,634 | 440,019 | 28.8 | 0.1% | Pass |
| pelo_16 | 16,653,844 | 14,055,438 | 0.844 | 24,105 | 394,900 | 23.4 | 0.1% | Pass |

| Sample | Alignments obtained | Alignments kept | Fraction kept | Unmapped alignments | Number of loci | Mean coverage | Percent Missing | Passed Filtering |
|---|---|---|---|---|---|---|---|---|
| racy_01 | 9,591,920 | 8,049,824 | 0.839 | 28,655 | 413,489 | 13.1 | 0.1% | Pass |
| rimt_01 | 2,094,891 | 1,798,875 | 0.859 | 14,441 | 225,346 | 4.6 | 16.4% | Pass |
| rimt_02 | 2,400,886 | 2,068,792 | 0.862 | 3,338 | 235,279 | 5.1 | 12.4% | Pass |
| rimt_03 | 12,238,030 | 10,245,694 | 0.837 | 25,818 | 441,451 | 16.1 | 0.2% | Pass |
| rimt_04 | 16,105,030 | 13,528,912 | 0.84 | 155,194 | 460,144 | 21.0 | 0.1% | Pass |
| rimt_05 | 39,677,928 | 33,034,252 | 0.833 | 361,544 | 583,557 | 46.0 | 0.1% | Pass |
| rimt_06 | 9,951,988 | 7,787,860 | 0.783 | 12,753 | 439,286 | 12.3 | 0.3% | Pass |
| rimt_07 | 15,757,449 | 13,061,555 | 0.829 | 472,990 | 471,145 | 19.7 | 0.2% | Pass |
| rimt_08 | 14,733,287 | 12,414,542 | 0.843 | 89,824 | 487,941 | 18.9 | 0.1% | Pass |
| rimt_09 | 14,694,893 | 12,400,066 | 0.844 | 31,231 | 459,813 | 19.1 | 0.1% | Pass |
| sacl_01 | 4,287,117 | 3,493,693 | 0.815 | 1,982 | 311,260 | 7.0 | 1.6% | Pass |
| sacl_02 | 11,318,410 | 9,388,486 | 0.829 | 31,009 | 423,798 | 15.4 | 0.1% | Pass |
| sacl_03 | 5,389,957 | 4,611,830 | 0.856 | 11,257 | 324,773 | 9.0 | 0.4% | Pass |
| sbmt_01 | 13,307,779 | 11,190,243 | 0.841 | 11,863 | 447,055 | 17.6 | 0.1% | Pass |
| sbmt_02 | 7,305,923 | 6,142,252 | 0.841 | 45,129 | 365,258 | 10.9 | 0.4% | Pass |
| sdtk_01 | 22,549,344 | 19,011,429 | 0.843 | 33,786 | 522,388 | 27.5 | 0.1% | Pass |
| sdtk_02 | 29,068,851 | 24,484,929 | 0.842 | 73,594 | 625,211 | 35.0 | 0.1% | Pass |
| sdtk_03 | 10,505,877 | 8,907,387 | 0.848 | 30,662 | 407,719 | 14.8 | 0.2% | Pass |
| sdtk_04 | 37,749,491 | 32,205,338 | 0.853 | 158,688 | 570,298 | 45.4 | 0.2% | Pass |
| shiv_01 | 16,590,157 | 13,846,381 | 0.835 | 26,333 | 489,923 | 20.6 | 0.1% | Pass |
| shmt_01 | 5,383,250 | 4,620,086 | 0.858 | 10,919 | 339,093 | 8.5 | 0.9% | Pass |
| shmt_02 | 7,219,464 | 6,135,054 | 0.85 | 9,031 | 377,176 | 10.6 | 0.5% | Pass |
| shmt_03 | 66,943,052 | 57,769,524 | 0.863 | 86,015 | 635,839 | 79.8 | 0.2% | Pass |
| shmt_04 | 3,321,626 | 2,798,062 | 0.842 | 10,070 | 273,046 | 6.1 | 4.8% | Pass |
| sncy_01 | 20,779,812 | 17,359,042 | 0.835 | 30,716 | 532,523 | 25.1 | 0.1% | Pass |
| stcy_01 | 7,329,466 | 5,914,539 | 0.807 | 10,281 | 373,007 | 10.3 | 0.4% | Pass |
| stcy_03 | 34,442,672 | 28,608,973 | 0.831 | 235,099 | 568,900 | 40.4 | 0.1% | Pass |
| stcy_04 | 38,215,655 | 32,127,433 | 0.841 | 125,913 | 686,490 | 45.3 | 0.1% | Pass |
| stcy_05r | 4,673,832 | 3,058,092 | 0.654 | 68,201 | 305,921 | 6.2 | 16.9% | Pass |
| stcy_07r | 18,842,354 | 15,920,703 | 0.845 | 59,142 | 400,642 | 26.2 | 0.1% | Pass |
| sumt_13 | 3,353,082 | 2,894,979 | 0.863 | 12,782 | 271,011 | 6.4 | 4.3% | Pass |
| sumt_15 | 3,728,610 | 3,126,303 | 0.838 | 27,638 | 293,895 | 6.5 | 3.4% | Pass |
| sumt_16 | 2,961,473 | 2,562,594 | 0.865 | 6,202 | 267,060 | 5.7 | 6.4% | Pass |

| Sample | Alignments obtained | Alignments kept | Fraction kept | Unmapped alignments | Number of loci | Mean coverage | Percent Missing | Passed Filtering |
|---|---|---|---|---|---|---|---|---|
| sumt_21 | 3,561,659 | 3,008,709 | 0.845 | 8,934 | 294,010 | 6.2 | 4.1% | Pass |
| sumt_23r | 12,259,459 | 10,268,218 | 0.838 | 86,436 | 366,389 | 17.8 | 0.2% | Pass |
| sumt_25 | 1,658,586 | 1,415,027 | 0.853 | 1,673 | 195,798 | 4.1 | 29.5% | Pass |
| sumt_26 | 6,845,027 | 5,888,415 | 0.86 | 7,513 | 372,367 | 10.3 | 0.5% | Pass |
| sumt_27 | 15,474,835 | 13,050,500 | 0.843 | 22,650 | 493,639 | 19.4 | 0.1% | Pass |
| sumt_29 | 3,953,841 | 3,346,172 | 0.846 | 33,864 | 294,852 | 6.9 | 2.2% | Pass |
| sumt_30 | 2,391,513 | 1,971,119 | 0.824 | 22,609 | 252,849 | 4.6 | 17.7% | Pass |
| tbtp_01 | 12,309,553 | 9,728,723 | 0.79 | 7,249 | 446,915 | 15.4 | 0.2% | Pass |
| tbtp_02 | 12,483,283 | 10,157,486 | 0.814 | 29,892 | 481,029 | 16.4 | 0.2% | Pass |
| tial_01 | 8,973,753 | 7,689,641 | 0.857 | 15,730 | 384,554 | 13.4 | 0.2% | Pass |
| tial_02 | 19,557,747 | 16,800,791 | 0.859 | 16,297 | 482,314 | 25.6 | 0.1% | Pass |
| tort_01 | 17,046,747 | 14,640,946 | 0.859 | 44,241 | 465,236 | 22.6 | 0.1% | Pass |
| tort_02 | 11,723,496 | 9,844,361 | 0.84 | 19,632 | 457,822 | 16.1 | 0.1% | Pass |
| tort_03 | 10,425,158 | 8,954,445 | 0.859 | 53,255 | 397,928 | 15.0 | 0.2% | Pass |
| tort_04r | 2,687,174 | 2,235,900 | 0.832 | 8,882 | 229,974 | 5.5 | 12.3% | Pass |
| tuhl_01 | 15,631,674 | 13,254,524 | 0.848 | 135,409 | 457,415 | 20.8 | 0.1% | Pass |
| tumt_01 | 11,870,676 | 10,014,894 | 0.844 | 25,679 | 439,150 | 16.4 | 0.2% | Pass |
| vail_01 | 10,115,982 | 8,654,321 | 0.856 | 10,085 | 412,951 | 14.5 | 0.2% | Pass |
| vail_02 | 5,029,144 | 4,244,607 | 0.844 | 6,466 | 321,572 | 8.3 | 2.4% | Pass |
| vofi_01 | 6,074,659 | 4,323,461 | 0.712 | 3,628 | 438,332 | 7.4 | 1.8% | Pass |
| vofi_02 | 4,733,004 | 3,915,066 | 0.827 | 6,819 | 314,499 | 7.8 | 1.1% | Pass |
| vofi_04 | 2,110,338 | 1,784,906 | 0.846 | 5,002 | 221,200 | 4.7 | 17.4% | Pass |
| vofi_06 | 2,856,462 | 2,449,995 | 0.858 | 6,505 | 258,397 | 5.6 | 6.9% | Pass |
| vofi_07 | 8,844,159 | 7,360,451 | 0.832 | 29,302 | 407,560 | 12.0 | 0.1% | Pass |
| wafd_01 | 31,934,342 | 27,382,196 | 0.857 | 37,241 | 581,349 | 39.0 | 0.0% | Pass |
| wafd_02 | 13,135,768 | 11,211,389 | 0.854 | 36,309 | 459,120 | 17.6 | 0.1% | Pass |
| whit_01 | 9,051,429 | 7,680,329 | 0.849 | 25,618 | 328,178 | 14.3 | 0.5% | Pass |
| whit_02 | 4,919,371 | 4,117,467 | 0.837 | 43,411 | 285,827 | 8.5 | 1.3% | Pass |
| whit_03 | 8,662,630 | 7,235,680 | 0.835 | 35,151 | 348,843 | 12.8 | 0.3% | Pass |
| wrvy_01 | 7,950,548 | 6,362,422 | 0.8 | 4,794 | 428,449 | 10.3 | 0.4% | Pass |
| wrvy_02 | 4,260,033 | 3,694,909 | 0.867 | 6,908 | 294,998 | 7.6 | 1.1% | Pass |
| wrvy_03 | 11,214,600 | 9,418,681 | 0.84 | 36,110 | 427,248 | 15.0 | 0.1% | Pass |
| wrvy_04 | 4,246,438 | 3,590,134 | 0.845 | 3,817 | 308,463 | 7.2 | 1.7% | Pass |

| Sample | Alignments obtained | Alignments kept | Fraction kept | Unmapped alignments | Number of loci | Mean coverage | Percent Missing | Passed Filtering |
|---|---|---|---|---|---|---|---|---|
| wrvy_05 | 12,634,737 | 10,251,802 | 0.811 | 18,234 | 534,910 | 15.7 | 0.1% | Pass |
| wrvy_06 | 8,308,143 | 7,196,258 | 0.866 | 7,585 | 386,156 | 12.3 | 0.1% | Pass |
| wrvy_07 | 6,296,635 | 5,288,628 | 0.84 | 19,031 | 348,991 | 9.7 | 0.2% | Pass |
| wrvy_08 | 7,726,904 | 6,688,452 | 0.866 | 11,936 | 371,646 | 11.8 | 0.1% | Pass |
| xmas_01 | 1,511,747 | 1,255,111 | 0.83 | 18,755 | 190,435 | 3.7 | 38.5% | Pass |
| xmas_02 | 15,515,806 | 13,216,202 | 0.852 | 35,831 | 444,800 | 21.2 | 0.0% | Pass |
| avra_13r | 28,932 | 189 | 0.007 | 2,592 | 92 | 1.0 | NA | Fail |
| cafh_10 | 1,470,372 | 1,265,412 | 0.861 | 1,983 | 198,370 | 3.6 | 40.3% | Fail |
| cali_33r | 310,820 | 257,010 | 0.827 | 4,961 | 71,658 | 1.8 | NA | Fail |
| ctwd_01 | 1,620,442 | 1,147,221 | 0.708 | 3,155 | 209,913 | 3.1 | NA | Fail |
| ctwd_05 | 1,539,528 | 1,120,048 | 0.728 | 1,326 | 203,250 | 3.1 | NA | Fail |
| glcy_14 | 1,260,941 | 1,085,912 | 0.861 | 7,496 | 173,726 | 3.4 | 47.2% | Fail |
| glmt_01 | 1,384,029 | 1,171,365 | 0.846 | 35,313 | 178,940 | 3.6 | 41.0% | Fail |
| glob_01r | 1,274,909 | 588,403 | 0.462 | 13,958 | 155,502 | 2.1 | NA | Fail |
| harq_03 | 1,174,283 | 1,016,516 | 0.866 | 1,970 | 171,058 | 3.3 | 49.7% | Fail |
| mccu_08r | 11,358 | 5,062 | 0.446 | 2,283 | 2,070 | 1.2 | NA | Fail |
| mccu_18 | 160,884 | 104,438 | 0.649 | 459 | 33,915 | 1.7 | NA | Fail |
| nsrd_01r | 1,082,066 | 894,089 | 0.826 | 13,711 | 158,150 | 3.0 | NA | Fail |
| pamt_03 | 1,505,891 | 1,248,658 | 0.829 | 5,664 | 197,786 | 3.5 | 39.8% | Fail |
| stcy_02r | 533,848 | 283,806 | 0.532 | 2,735 | 87,987 | 1.7 | NA | Fail |
| stcy_06 | 1,906,207 | 1,211,794 | 0.636 | 62,796 | 225,763 | 3.1 | 51.2% | Fail |
| sumt_14r | 24,516,435 | 173,580 | 0.007 | 10,210,396 | 2,512 | 18.8 | NA | Fail |
| sumt_24 | 577,307 | 311,168 | 0.539 | 448 | 103,156 | 1.6 | NA | Fail |
| sumt_28 | 1,411,644 | 1,169,971 | 0.829 | 8,822 | 189,516 | 3.4 | 44.6% | Fail |
| vofi_03r | 309,565 | 231,227 | 0.747 | 1,427 | 68,605 | 1.7 | NA | Fail |
| xmas_03r | 42,584 | 11,229 | 0.264 | 24,930 | 4,400 | 1.3 | NA | Fail |
| xmas_04r | 24,969 | 8,897 | 0.356 | 5,475 | 3,570 | 1.2 | NA | Fail |

**Table S2**. Mean pairwise differentiation ($F_{ST}$) values for genetic population pairs for sites with at least 5 individuals calculated in StAMPP. See Table S3 for site information.

| | leed | wrvy | vofi | cali | mccu | harq | sumt | glcy | stcy | orvl | cafh | avra | rimt | pelo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **leed** | — | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.000 | < 0.000 | < 0.000 | < 0.000 | < 0.000 | < 0.000 | < 0.000 | < 0.000 |
| **wrvy** | 0.075 | — | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 |
| **vofi** | 0.185 | 0.126 | — | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 |
| **cali** | 0.227 | 0.184 | 0.091 | — | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 |
| **mccu** | 0.191 | 0.147 | 0.075 | 0.095 | — | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 |
| **harq** | 0.242 | 0.191 | 0.151 | 0.253 | 0.190 | — | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 |
| **sumt** | 0.276 | 0.241 | 0.204 | 0.322 | 0.257 | 0.090 | — | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 |
| **glcy** | 0.275 | 0.244 | 0.206 | 0.326 | 0.260 | 0.097 | 0.012 | — | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 |
| **stcy** | 0.331 | 0.288 | 0.241 | 0.370 | 0.302 | 0.107 | 0.011 | 0.012 | — | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 |
| **orvl** | 0.328 | 0.285 | 0.239 | 0.367 | 0.299 | 0.102 | 0.008 | 0.011 | 0.006 | — | < 0.0001 | < 0.0001 | < 0.0001 | < 0.0001 |
| **cafh** | 0.257 | 0.230 | 0.198 | 0.304 | 0.243 | 0.096 | 0.015 | 0.019 | 0.012 | 0.006 | — | < 0.0001 | < 0.0001 | < 0.0001 |
| **avra** | 0.276 | 0.244 | 0.206 | 0.329 | 0.262 | 0.100 | 0.015 | 0.021 | 0.011 | 0.007 | 0.015 | — | < 0.0001 | < 0.0001 |
| **rimt** | 0.291 | 0.258 | 0.218 | 0.346 | 0.278 | 0.105 | 0.024 | 0.026 | 0.021 | 0.017 | 0.018 | 0.022 | — | < 0.0001 |
| **pelo** | 0.317 | 0.286 | 0.257 | 0.356 | 0.296 | 0.138 | 0.107 | 0.109 | 0.118 | 0.113 | 0.108 | 0.116 | 0.114 | — |

**Table S3**: List of the 266 samples which passed quality filtering and were included in genomic analyses: Sample and Site Name, sample and site names used to refers to the localities on the sampling map (Figure 1; Table S1); VCF POS, the position of the sample in the vcf file; Museum Number, voucher numbers for museum samples (na = not applicable); Location, detailed location information for the sample; Cluster (K2 and K5), the cluster assignment of the sample.

| Sample | VCF POS | Museum Number | Site Name | Location | Cluster Assignment (K2) | Cluster Assignment (K5) | Collection Date | Sex | Collector | DNA source |
|---|---|---|---|---|---|---|---|---|---|---|
| leed_04 | 1 | na | leed | USA: Utah, Washington Co, Toquerville | cinc | north Mojave | 29-Jun-2010 | Unknown | Ben Ewell | muscle |
| leed_01 | 2 | na | leed | USA: Utah, Washington Co, Leeds | cinc | north Mojave | 18-May-2024 | Male | C. Rognan | blood |
| leed_02 | 3 | na | leed | USA: Utah, Washington Co, Leeds | cinc | north Mojave | 4-May-2024 | Unknown | C. Rognan | blood |
| leed_03 | 4 | na | leed | USA: Utah, Washington Co, Gould Wash | cinc | north Mojave | 11-Jun-2019 | Unknown | M. Weston, M. Kelso | muscle |
| leed_05 | 5 | na | leed | USA: Utah, Washington Co, Leeds | cinc | north Mojave | 15-Apr-2025 | Unknown | C. Rognan | blood |
| leed_06 | 6 | na | leed | USA: Utah, Washington Co, Leeds | cinc | north Mojave | 25-Apr-2025 | Unknown | C. Rognan | blood |
| leed_07 | 7 | na | leed | USA: Utah, Washington Co, Leeds | cinc | north Mojave | 8-May-2025 | Unknown | C. Rognan | blood |
| leed_08 | 8 | na | leed | USA: Utah, Washington Co, Babylon- Sand Cove | cinc | north Mojave | 2-Jun-2025 | Female | C. Rognan | blood |
| sacl_01 | 9 | na | sacl | USA: Utah, Washington Co, St. George | cinc | north Mojave | 1-May-2020 | Male | not collected | blood |
| sacl_02 | 10 | na | sacl | USA: Utah, Washington Co, St. George | cinc | north Mojave | 10-Jun-2021 | Male | C. Rognan | blood |
| sacl_03 | 11 | na | sacl | USA: Utah, Washington Co, St. George | cinc | north Mojave | 23-May-2024 | Female | C. Rognan | blood |
| sncy_01 | 12 | na | sncy | USA: Utah, Washington Co, Snow Canyon SP | cinc | north Mojave | 23-Jun-2017 | Unknown | R. Olroyd, J. Stuck | muscle |
| elar_05 | 13 | na | elar | USA: Utah, Washington Co, East Mill Creek | cinc | north Mojave | 8-May-2019 | Unknown | not collected | blood |
| bkhw_01 | 14 | na | bkhw | USA: Utah, Washington Co, Buckskin Hollow | cinc | north Mojave | 14-May-2024 | Female | C. Rognan | blood |
| shiv_01 | 15 | na | shiv | USA: Utah, Washington Co, Shivwits/Highway 91 | cinc | north Mojave | 5-Jun-2024 | Unknown | Seth Topham | muscle |
| elar_03 | 16 | na | elar | USA: Utah, Washington Co, Elephant Arch, RCDR | cinc | north Mojave | 10-May-2020 | Male | B. Heyborne, C. Rognan, C. Gardner | blood |

| Sample | VCF POS | Museum Number | Site Name | Location | Cluster Assignment (K2) | Cluster Assignment (K5) | Collection Date | Sex | Collector | DNA source |
|---|---|---|---|---|---|---|---|---|---|---|
| elar_01 | 17 | na | elar | USA: Utah, Washington Co, Elephant Arch, RCDR | cinc | north Mojave | 1-May-2020 | Female | Bill H. | blood |
| elar_02 | 18 | na | elar | USA: Utah, Washington Co, Elephant Arch, RCDR | cinc | north Mojave | 17-May-2020 | Male | B. Heyborne | blood |
| elar_04 | 19 | na | elar | USA: Utah, Washington Co, Dino Cliffs | cinc | north Mojave | 10-May-2020 | Female | B. Heyborne, C. Rognan, C. Gardner | blood |
| wrvy_01 | 20 | na | wrvy | USA: Utah, Washington Co, Warner Valley | cinc | north Mojave | 22-May-2020 | Female | C. Rognan, C. Gardner, L.H., W.H. | blood |
| wrvy_02 | 21 | na | wrvy | USA: Utah, Washington Co, Warner Valley | cinc | north Mojave | 24-Apr-2021 | Male | C. Rognan, S. M. Mangum | blood |
| wrvy_03 | 22 | na | wrvy | USA: Utah, Washington Co, Warner Valley | cinc | north Mojave | 24-Apr-2021 | Female | J. L. Jones, C. Rognan | blood |
| wrvy_04 | 23 | na | wrvy | USA: Utah, Washington Co, Warner Valley | cinc | north Mojave | 4-May-2024 | Female | C. Rognan | blood |
| wrvy_05 | 24 | na | wrvy | USA: Utah, Washington Co, Warner Valley | cinc | north Mojave | 8-Jun-2016 | Unknown | D. Smith | muscle |
| wrvy_06 | 25 | na | wrvy | USA: Utah, Washington Co, Warner Valley | cinc | north Mojave | 18-May-2024 | Female | C. Rognan | blood |
| wrvy_07 | 26 | na | wrvy | USA: Utah, Washington Co, Warner Valley | cinc | north Mojave | 25-May-2024 | Male | C. Rognan | blood |
| wrvy_08 | 27 | na | wrvy | USA: Utah, Washington Co, Warner Valley | cinc | north Mojave | 25-May-2024 | Female | C. Rognan | blood |
| wafd_01 | 28 | na | wafd | USA: Utah, Washington Co, Washington Fields | cinc | north Mojave | 22-Apr-2023 | Unknown | L. Matschek | muscle |
| wafd_02 | 29 | na | wafd | USA: Utah, Washington Co, Washington Fields | cinc | north Mojave | 9-May-2002 | Unknown | J. Schiff | muscle |
| racy_01 | 30 | na | racy | USA: Nevada, Lincoln Co, Rainbow Canyon | cinc | north Mojave | 13-May-2017 | Unknown | not collected | blood |
| gold_01 | 31 | na | gold | USA: Nevada, Clark Co, Thomas Gap, Gold Butte | cinc | north Mojave | 22-May-1994 | Unknown | not collected | blood |
| momt_01 | 32 | na | momt | USA: Nevada, Lincoln Co, Mormon Mountains | cinc | north Mojave | 23-Apr-2019 | Unknown | not collected | blood |
| momt_02 | 33 | na | momt | USA: Nevada, Lincoln Co, Mormon Mountains | cinc | north Mojave | 20-Jul-2020 | Female | Jason L. Jones | blood |
| moap_01 | 34 | na | moap | USA: Nevada, Clark Co, Moapa | cinc | north Mojave | 11-Apr-2018 | Unknown | not collected | blood |
| ahcy_01 | 35 | na | ahcy | USA: Nevada, Clark Co, Arrowhead Canyon | cinc | south Mojave | 12-May-2013 | Unknown | not collected | blood |
| vofi_06 | 36 | na | vofi | USA: Nevada, Clark Co, Valley of Fire | cinc | south Mojave | 28-May-2025 | Unknown | C.M. Geinger | blood |
| vofi_04 | 37 | na | vofi | USA: Nevada, Clark Co, Valley of Fire | cinc | south Mojave | 12-Oct-2020 | Female | Jason L. Jones | blood |

| Sample | VCF POS | Museum Number | Site Name | Location | Cluster Assignment (K2) | Cluster Assignment (K5) | Collection Date | Sex | Collector | DNA source |
|---|---|---|---|---|---|---|---|---|---|---|
| vofi_01 | 38 | na | vofi | USA: Nevada, Clark Co, Valley of Fire | cinc | south Mojave | 5-Jun-2016 | Unknown | not collected | blood |
| vofi_02 | 39 | na | vofi | USA: Nevada, Clark Co, Valley of Fire | cinc | south Mojave | 25-May-2020 | Male | S. Cohen | blood |
| vofi_07 | 40 | na | vofi | USA: Nevada, Clark Co, Valley of Fire | cinc | south Mojave | 9-Jun-2022 | Unknown | K. Wolff | blood |
| apex_02 | 41 | na | apex | USA: Nevada, Clark Co, Apex | cinc | south Mojave | 30-Apr-2014 | Unknown | not collected | blood |
| apex_01 | 42 | na | apex | USA: Nevada, Clark Co, Apex | cinc | south Mojave | 9-Jul-2018 | Unknown | not collected | blood |
| apex_03 | 43 | na | apex | USA: Nevada, Clark Co, Apex | cinc | south Mojave | 17-Apr-2017 | Unknown | not collected | blood |
| apex_04r | 44 | na | apex | USA: Nevada, Clark Co, Apex | cinc | south Mojave | 28-Apr-2014 | Unknown | not collected | blood |
| lnmt_01 | 45 | na | lnmt | USA: Nevada, Clark Co, Lone Mountain | cinc | south Mojave | 9-Jun-2020 | Unknown | J. Stalker | blood |
| lnmt_02 | 46 | na | lnmt | USA: Nevada, Clark Co, Lone Mountain | cinc | south Mojave | 24-May-2023 | Unknown | Jason L. Jones | blood |
| lvgs_01 | 47 | BYU:Herp:70808 | lvgs | USA: Nevada, Clark Co, Las Vegas | cinc | south Mojave | 24-Jul-2009 | Unknown | not collected | blood |
| cali_17 | 48 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 22-May-2018 | Unknown | not collected | blood |
| cali_19 | 49 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 29-Sep-2019 | Unknown | not collected | blood |
| cali_25 | 50 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 6-Apr-2020 | Female | C.M. Geinger | blood |
| cali_26r | 51 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 9-Apr-20 | Female | Jason L. Jones | blood |
| cali_15 | 52 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 21-May-2018 | Unknown | not collected | blood |
| cali_20 | 53 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 21-May-2019 | Female | not collected | blood |
| cali_05 | 54 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 18-May-2019 | Female | not collected | blood |
| cali_21 | 55 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 1-Jun-2019 | Unknown | not collected | blood |
| cali_01r | 56 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 21-Jun-2019 | Unknown | not collected | blood |
| cali_04 | 57 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 1-Jul-2019 | Unknown | not collected | blood |
| cali_35 | 58 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 1-Sep-2017 | Unknown | not collected | blood |
| cali_18 | 59 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 26-Mar-2019 | Female | not collected | blood |
| cali_12 | 60 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 1-Jun-2017 | Unknown | not collected | blood |
| cali_13r | 61 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 16-May-18 | Unknown | not collected | blood |
| cali_06 | 62 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 13-May-2016 | Unknown | not collected | blood |

| Sample | VCF POS | Museum Number | Site Name | Location | Cluster Assignment (K2) | Cluster Assignment (K5) | Collection Date | Sex | Collector | DNA source |
|---|---|---|---|---|---|---|---|---|---|---|
| cali_27 | 63 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 20-Apr-2020 | Female | Jason L. Jones | blood |
| cali_29r | 64 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 10-May-20 | Unknown | Jason L. Jones | blood |
| cali_03 | 65 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 21-May-2015 | Unknown | not collected | blood |
| cali_40 | 66 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 10-Apr-2025 | Unknown | C.S. Stratton | blood |
| cali_08 | 67 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 2-Aug-2016 | Unknown | not collected | blood |
| cali_14 | 68 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 23-May-2016 | Unknown | not collected | blood |
| cali_23 | 69 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 4-May-2018 | Male | not collected | blood |
| cali_24r | 70 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 19-Jun-19 | Female | not collected | blood |
| cali_11 | 71 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 8-May-2019 | Unknown | not collected | blood |
| cali_16.2 | 72 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 26-May-2025 | Unknown | C.S. Stratton | blood |
| cali_30 | 73 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 14-May-2020 | Unknown | Jason L. Jones | blood |
| cali_31r | 74 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 2-Jun-2020 | Female | Jason L. Jones, J. Stalker | blood |
| cali_09 | 75 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 5-Apr-2017 | Female | not collected | blood |
| cali_45.2 | 76 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 11-May-2025 | Unknown | J. Jones, S. Jones | blood |
| cali_42 | 77 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 12-May-2025 | Unknown | C.S. Stratton | blood |
| cali_43 | 78 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 13-May-2025 | Unknown | C.S. Stratton | blood |
| cali_44 | 79 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 14-May-2025 | Unknown | C.S. Stratton | blood |
| cali_07 | 80 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 22-May-2016 | Unknown | not collected | blood |
| cali_34 | 81 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 19-May-2020 | Unknown | Jason L. Jones | blood |
| cali_10 | 82 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 10-May-2017 | Male | not collected | blood |
| cali_32 | 83 | na | cali | USA: Nevada, Clark Co, Red Rocks | cinc | south Mojave | 17-May-2020 | Unknown | B. Brown | blood |
| blud_01 | 84 | na | blud | USA: Nevada, Clark Co, south Red Rocks | cinc | south Mojave | 24-May-2018 | Male | not collected | blood |
| hnds_01 | 85 | na | hnds | USA: Nevada, Clark Co, Henderson | cinc | south Mojave | 1-Jun-2009 | Male | not collected | blood |
| btcy_01 | 86 | na | btcy | USA: Nevada, Clark Co, Bootleg Canyon | cinc | south Mojave | 20-Apr-2016 | Unknown | not collected | blood |
| hnds_02 | 87 | na | hnds | USA: Nevada, Clark Co, Henderson | cinc | south Mojave | 13-Jun-2016 | Unknown | not collected | blood |

| Sample | VCF POS | Museum Number | Site Name | Location | Cluster Assignment (K2) | Cluster Assignment (K5) | Collection Date | Sex | Collector | DNA source |
|---|---|---|---|---|---|---|---|---|---|---|
| mccu_01 | 88 | na | mccu | USA: Nevada, Clark Co, McCullough Mountains | cinc | south Mojave | 3-Jun-2019 | Unknown | not collected | blood |
| mccu_19 | 89 | na | mccu | USA: Nevada, Clark Co, McCullough Mountains | cinc | south Mojave | 2-Jul-2019 | Unknown | not collected | blood |
| mccu_02 | 90 | na | mccu | USA: Nevada, Clark Co, McCullough Mountains | cinc | south Mojave | 22-Apr-2013 | Unknown | not collected | blood |
| mccu_05 | 91 | na | mccu | USA: Nevada, Clark Co, McCullough Mountains | cinc | south Mojave | 29-Apr-2013 | Female | not collected | blood |
| mccu_03 | 92 | na | mccu | USA: Nevada, Clark Co, McCullough Mountains | cinc | south Mojave | 30-Apr-2013 | Male | not collected | blood |
| mccu_22 | 93 | na | mccu | USA: Nevada, Clark Co, McCullough Mountains | cinc | south Mojave | 12-May-2018 | Female | not collected | blood |
| mccu_06 | 94 | na | mccu | USA: Nevada, Clark Co, McCullough Mountains | cinc | south Mojave | 11-Jun-2013 | Unknown | not collected | blood |
| mccu_14 | 95 | na | mccu | USA: Nevada, Clark Co, McCullough Mountains | cinc | south Mojave | 31-May-2015 | Unknown | not collected | blood |
| mccu_15 | 96 | na | mccu | USA: Nevada, Clark Co, McCullough Mountains | cinc | south Mojave | 31-May-2015 | Unknown | not collected | blood |
| mccu_16 | 97 | na | mccu | USA: Nevada, Clark Co, McCullough Mountains | cinc | south Mojave | 31-May-2015 | Unknown | not collected | blood |
| mccu_04 | 98 | na | mccu | USA: Nevada, Clark Co, McCullough Mountains | cinc | south Mojave | 1-May-2013 | Male | not collected | blood |
| mccu_10 | 99 | na | mccu | USA: Nevada, Clark Co, McCullough Mountains | cinc | south Mojave | 5-May-2017 | Unknown | not collected | blood |
| mccu_09 | 100 | na | mccu | USA: Nevada, Clark Co, McCullough Mountains | cinc | south Mojave | 6-Oct-2014 | Unknown | not collected | blood |
| mccu_13 | 101 | na | mccu | USA: Nevada, Clark Co, McCullough Mountains | cinc | south Mojave | 20-May-2015 | Unknown | not collected | blood |
| mccu_11 | 102 | na | mccu | USA: Nevada, Clark Co, McCullough Mountains | cinc | south Mojave | 20-May-2018 | Male | not collected | blood |
| mccu_12 | 103 | na | mccu | USA: Nevada, Clark Co, McCullough Mountains | cinc | south Mojave | 20-May-2015 | Unknown | not collected | blood |
| elmt_01 | 104 | na | elmt | USA: Nevada, Clark Co, Eldorado | cinc | south Mojave | 9-May-2019 | Unknown | not collected | blood |
| elmt_02 | 105 | na | elmt | USA: Nevada, Clark Co, Nelson | cinc | south Mojave | 3-Apr-2016 | Unknown | not collected | blood |
| elmt_03 | 106 | na | elmt | USA: Nevada, Clark Co, Nelson | cinc | south Mojave | 3-Apr-2016 | Unknown | not collected | blood |
| xmas_01 | 107 | na | xmas | USA: Nevada, Clark Co, Christmas Tree Pass | cinc | south Mojave | 22-May-2008 | Unknown | not collected | blood |
| xmas_02 | 108 | na | xmas | USA: Nevada, Clark Co, Christmas Tree Pass | cinc | south Mojave | 30-May-2009 | Unknown | not collected | blood |
| dbrd_01 | 109 | na | dbrd | USA: Arizona, Mohave Co, Diamond bar road | cinc | ecotone | 26-Jun-2025 | Unknown | J. Kurilara | muscle |

| Sample | VCF POS | Museum Number | Site Name | Location | Cluster Assignment (K2) | Cluster Assignment (K5) | Collection Date | Sex | Collector | DNA source |
|---|---|---|---|---|---|---|---|---|---|---|
| king_01 | 110 | ASUVTC002931 | king | USA: Arizona, Mohave Co, Kingman | cinc | ecotone | 9-Jul-2014 | Male | not collected | blood |
| noth_01 | 111 | ASUVTC002924 | noth | USA: Arizona, Mohave Co, Nothing | cinc | ecotone | 1-Jul-2013 | Female | M. Ardlich | blood |
| ctwd_02 | 112 | na | ctwd | USA: Arizona, Yavapai Co, Cottonwood Creek | admx | ecotone | 24-Mar-2004 | Male | F.R. Hensley, T.R. Jones | blood |
| ctwd_03 | 113 | na | ctwd | USA: Arizona, Yavapai Co, Cottonwood Creek | admx | ecotone | 2-May-2003 | Unknown | C. LiWanPo | blood |
| ctwd_07 | 114 | na | ctwd | USA: Arizona, Yavapai Co, Cottonwood Creek | admx | ecotone | 2-May-2003 | Unknown | C. LiWanPo | blood |
| ctwd_06 | 115 | na | ctwd | USA: Arizona, Yavapai Co, Cottonwood Creek | admx | ecotone | 3-May-2003 | Male | C. LiWanPo, L.V. Giessen | blood |
| harq_07 | 116 | ASUVTC002945 | harq | USA: Arizona, Maricopa Co, Harquahala Mtns | admx | ecotone | 25-Apr-2015 | Male | D. DeNardo | blood |
| harq_04 | 117 | ASUVTC002942 | harq | USA: Arizona, Maricopa Co, Harquahala Mtns | admx | ecotone | 25-Apr-2015 | Male | D. DeNardo | blood |
| harq_05 | 118 | ASUVTC002943 | harq | USA: Arizona, Maricopa Co, Harquahala Mtns | admx | ecotone | 25-Apr-2015 | Male | D. DeNardo | blood |
| harq_06 | 119 | ASUVTC002944 | harq | USA: Arizona, Maricopa Co, Harquahala Mtns | admx | ecotone | 25-Apr-2015 | Male | M. Feldner | blood |
| harq_01 | 120 | ASUVTC002939 | harq | USA: Arizona, Maricopa Co, Harquahala Mtns | admx | ecotone | 24-Apr-2015 | Male | D. DeNardo | blood |
| harq_02 | 121 | ASUVTC002940 | harq | USA: Arizona, Maricopa Co, Harquahala Mtns | admx | ecotone | 24-Apr-2015 | Male | D. DeNardo | blood |
| aptr_01 | 122 | ASUVTC002965 | aptr | USA: Arizona, Maricopa Co, Tortilla Flats, Apache Trail | susp | ecotone | 17-Aug-2018 | Male | S. Hurd, D. DeNardo | blood |
| tial_01 | 123 | ASUVTC002891 | tial | USA: Arizona, Yuma Co, Tinajas Altas | susp | ecotone | 22-Mar-2013 | Unknown | M. Green | blood |
| tial_02 | 124 | ASUVTC002968 | tial | USA: Arizona, Yuma Co, Tinajas Altas | susp | ecotone | 6-Apr-2019 | Unknown | M. Feldner, J. Slone | blood |
| glmt_02 | 125 | ASUVTC002998 | glmt | USA: Arizona, Maricopa Co, Goldfield Mtns | susp | ecotone | 10-Sep-2022 | Unknown | S. Hurd | blood |
| glmt_03 | 126 | ASUVTC002999 | glmt | USA: Arizona, Maricopa Co, Goldfield Mtns | susp | ecotone | 10-Sep-2022 | Unknown | S. Hurd | blood |
| glmt_04 | 127 | ASUVTC003011 | glmt | USA: Arizona, Maricopa Co, Goldfield Mtns | susp | ecotone | 28-Apr-2024 | Unknown | S. Hurd | blood |
| flor_01 | 128 | ASUVTC002958 | flor | USA: Arizona, Pinal Co, Florence | susp | Sonoran | 31-Mar-2018 | Unknown | M. Feldner | blood |
| nshl_01 | 129 | ASUVTC002936 | nshl | USA: Arizona, Pinal Co, Ninetysix Hills | susp | Sonoran | 22-Mar-2015 | Unknown | R. Repp, M. Feldner | toes |
| nshl_03 | 130 | ASUVTC002962 | nshl | USA: Arizona, Pinal Co, Ninetysix Hills | susp | Sonoran | 20-Jul-2018 | Female | R. Repp | blood |

| Sample | VCF POS | Museum Number | Site Name | Location | Cluster Assignment (K2) | Cluster Assignment (K5) | Collection Date | Sex | Collector | DNA source |
|---|---|---|---|---|---|---|---|---|---|---|
| nshl_02 | 131 | ASUVTC002959 | nshl | USA: Arizona, Pinal Co, Ninetysix Hills | susp | Sonoran | 4-Apr-2018 | Unknown | R. Repp | blood |
| nshl_04 | 132 | ASUVTC002977 | nshl | USA: Arizona, Pinal Co, Ninetysix Hills | susp | Sonoran | 23-Mar-2020 | Unknown | R. Repp | blood |
| tbtp_01 | 133 | ASUVTC002970 | tbtp | USA: Arizona, Pinal Co, Table Top Mtn | susp | Sonoran | 1-Jun-2019 | Unknown | M. Feldner | blood |
| tbtp_02 | 134 | ASUVTC002971 | tbtp | USA: Arizona, Pinal Co, Table Top Mtn | susp | Sonoran | 1-Jun-2019 | Unknown | M. Feldner | blood |
| blkm_01 | 135 | na | blkm | USA: Arizona, Pinal Co, Black Mtn | susp | Sonoran | 4-Apr-2020 | Unknown | M. Feldner | blood |
| sdtk_01 | 136 | ASUVTC002981 | sdtk | USA: Arizona, Maricopa Co, Sand Tank Mtns | susp | Sonoran | 9-May-2020 | Unknown | M. Feldner | blood |
| sdtk_02 | 137 | ASUVTC002982 | sdtk | USA: Arizona, Maricopa Co, Sand Tank Mtns | susp | Sonoran | 9-May-2020 | Unknown | M. Feldner | blood |
| sdtk_03 | 138 | ASUVTC002983 | sdtk | USA: Arizona, Maricopa Co, Sand Tank Mtns | susp | Sonoran | 9-May-2020 | Unknown | M. Feldner | blood |
| sdtk_04 | 139 | ASUVTC002989 | sdtk | USA: Arizona, Maricopa Co, Sand Tank Mtns | susp | Sonoran | 9-Apr-2021 | Female | I. Latella | blood |
| atmt_01 | 140 | na | atmt | USA: Arizona, Santa Cruz Co, Atascosa Mtns | susp | Sonoran | 18-Aug-2007 | Female | T.R. Jones, R.J. Timmons | blood |
| sumt_27 | 141 | ASUVTC002925 | sumt | USA: Arizona, Pinal Co, Iron Mine Hill / Suizo Mtns | susp | Sonoran | 16-Aug-2013 | Female | D. DeNardo | blood |
| sumt_23 | 142 | ASUVTC002901 | sumt | USA: Arizona, Pinal Co, Iron Mine Hill / Suizo Mtns | susp | Sonoran | 30-Mar-2013 | Female | G. Schuett | blood |
| sumt_25 | 143 | ASUVTC002919 | sumt | USA: Arizona, Pinal Co, Iron Mine Hill / Suizo Mtns | susp | Sonoran | 7-Jun-2013 | Female | R. Repp, G. Schuett | blood |
| sumt_26 | 144 | ASUVTC002923 | sumt | USA: Arizona, Pinal Co, Iron Mine Hill / Suizo Mtns | susp | Sonoran | 29-Jun-2013 | Unknown | M. Feldner | blood |
| sumt_16 | 145 | ASUVTC002887 | sumt | USA: Arizona, Pinal Co, Iron Mine Hill / Suizo Mtns | susp | Sonoran | 4-Jun-2010 | Female | R. Repp, G. Schuett | blood |
| sumt_30 | 146 | ASUVTC002976 | sumt | USA: Arizona, Pinal Co, Iron Mine Hill / Suizo Mtns | susp | Sonoran | 4-Mar-2020 | Female | R. Repp | blood |
| sumt_15 | 147 | ASUVTC002886 | sumt | USA: Arizona, Pinal Co, Iron Mine Hill / Suizo Mtns | susp | Sonoran | 12-Mar-2010 | Male | R. Repp, G. Schuett | blood |
| sumt_21 | 148 | ASUVTC002896 | sumt | USA: Arizona, Pinal Co, Iron Mine Hill / Suizo Mtns | susp | Sonoran | 30-Mar-2013 | Female | H.W. Herrmann | blood |
| sumt_13 | 149 | ASUVTC002889 | sumt | USA: Arizona, Pinal Co, Iron Mine Hill / Suizo Mtns | susp | Sonoran | 2-Aug-2012 | Female | R. Repp, G. Schuett | blood |
| sumt_29 | 150 | ASUVTC002927 | sumt | USA: Arizona, Pinal Co, Iron Mine Hill / Suizo Mtns | susp | Sonoran | 31-Aug-2013 | Male | R. Repp | blood |
| cfbt_01 | 151 | ASUVTC002910 | cfbt | USA: Arizona, Pinal Co, E of Chief Buttes | susp | Sonoran | 4-May-2013 | Male | K. Moeller | blood |

| Sample | VCF POS | Museum Number | Site Name | Location | Cluster Assignment (K2) | Cluster Assignment (K5) | Collection Date | Sex | Collector | DNA source |
|---|---|---|---|---|---|---|---|---|---|---|
| depk_01 | 152 | ASUVTC002917 | depk | USA: Arizona, Pinal Co, Desert Peak area | susp | Sonoran | 16-May-2013 | Male | M. Feldner | blood |
| depk_02 | 153 | ASUVTC002996 | depk | USA: Arizona, Pinal Co, Cattle Tank Rd | susp | Sonoran | 18-May-2022 | Male | D. DeNardo | blood |
| depk_03 | 154 | ASUVTC003010 | depk | USA: Arizona, Pinal Co, Cattle Tank Rd | susp | Sonoran | 5-Aug-2023 | Female | D. DeNardo | blood |
| owbt_03 | 155 | ASUVTC002888 | owbt | USA: Arizona, Pinal Co, Owl Head Buttes | susp | Sonoran | 23-May-2012 | Unknown | D. DeNardo | toes |
| owbt_01.1 | 156 | ASUVTC002994 | owbt | USA: Arizona, Pinal Co, Owl Head Buttes | susp | Sonoran | 31-Mar-2022 | Female | D. DeNardo | blood |
| glcy_06 | 157 | ASUVTC002906 | glcy | USA: Arizona, Pinal Co, Guild Canyon, Tortolita Mtns | susp | Sonoran | 25-Apr-2013 | Female | G. Demare | blood |
| glcy_01 | 158 | ASUVTC002898 | glcy | USA: Arizona, Pinal Co, Guild Canyon, Tortolita Mtns | susp | Sonoran | 6-Apr-2013 | Female | M. Feldner | blood |
| glcy_13 | 159 | ASUVTC002922 | glcy | USA: Arizona, Pinal Co, Guild Canyon, Tortolita Mtns | susp | Sonoran | 27-Jun-2013 | Male | M. Feldner | blood |
| glcy_09 | 160 | ASUVTC002911 | glcy | USA: Arizona, Pinal Co, Guild Canyon, Tortolita Mtns | susp | Sonoran | 5-May-2013 | Female | K. Moeller | blood |
| glcy_03 | 161 | ASUVTC002900 | glcy | USA: Arizona, Pinal Co, Guild Canyon, Tortolita Mtns | susp | Sonoran | 6-Apr-2013 | Unknown | M. Feldner | blood |
| glcy_04 | 162 | ASUVTC002904 | glcy | USA: Arizona, Pinal Co, Guild Canyon, Tortolita Mtns | susp | Sonoran | 23-Apr-2013 | Male | K. Moeller | blood |
| glcy_07 | 163 | ASUVTC002908 | glcy | USA: Arizona, Pinal Co, Guild Canyon, Tortolita Mtns | susp | Sonoran | 28-Apr-2013 | Male | G. Demare | blood |
| glcy_12 | 164 | ASUVTC002920 | glcy | USA: Arizona, Pinal Co, Guild Canyon, Tortolita Mtns | susp | Sonoran | 21-Jun-2013 | Male | M. Feldner | blood |
| glcy_10 | 165 | ASUVTC002912 | glcy | USA: Arizona, Pinal Co, Guild Canyon, Tortolita Mtns | susp | Sonoran | 11-May-2013 | Female | K. Moeller | blood |
| glcy_11 | 166 | ASUVTC002913 | glcy | USA: Arizona, Pinal Co, Guild Canyon, Tortolita Mtns | susp | Sonoran | 11-May-2013 | Female | K. Moeller | blood |
| glcy_05 | 167 | ASUVTC002905 | glcy | USA: Arizona, Pinal Co, Guild Canyon, Tortolita Mtns | susp | Sonoran | 25-Apr-2013 | Male | G. Demare | blood |
| glcy_02 | 168 | ASUVTC002899 | glcy | USA: Arizona, Pinal Co, Guild Canyon, Tortolita Mtns | susp | Sonoran | 6-Apr-2013 | Male | M. Feldner | blood |
| decy_03 | 169 | ASUVTC002985 | decy | USA: Arizona, Pinal Co, Derrio Canyon, Tortolita Mtns | susp | Sonoran | 22-May-2020 | Unknown | D. DeNardo | blood |
| decy_01 | 170 | ASUVTC002979 | decy | USA: Arizona, Pinal Co, Derrio Canyon, Tortolita Mtns | susp | Sonoran | 2-May-2020 | Male | J. Servoss | blood |
| decy_02 | 171 | ASUVTC002980 | decy | USA: Arizona, Pinal Co, Derrio Canyon, Tortolita Mtns | susp | Sonoran | 2-May-2020 | Male | D. DeNardo | blood |
| tort_01 | 172 | ASUVTC002997 | tort | USA: Arizona, Pima Co, Tortolita Mtns east side | susp | Sonoran | 31-Aug-2022 | Unknown | M. Feldner | blood |

| Sample | VCF POS | Museum Number | Site Name | Location | Cluster Assignment (K2) | Cluster Assignment (K5) | Collection Date | Sex | Collector | DNA source |
|---|---|---|---|---|---|---|---|---|---|---|
| tort_02 | 173 | ASUVTC003001 | tort | USA: Arizona, Pima Co, Tortolita Mtns east side | susp | Sonoran | 23-Apr-2023 | Unknown | M. Feldner | blood |
| tort_03 | 174 | ASUVTC003002 | tort | USA: Arizona, Pima Co, Tortolita Mtns east side | susp | Sonoran | 23-Apr-2023 | Unknown | M. Feldner | blood |
| tort_04r | 175 | ASUVTC003012 | tort | USA: Arizona, Pima Co, Tortolita Mtns east side | susp | Sonoran | 30-Aug-2024 | Unknown | D. Benson, D. DeNardo | blood |
| stcy_01 | 176 | ASUVTC002892 | stcy | USA: Arizona, Pima Co, Stone Canyon Club | susp | Sonoran | 28-Mar-2013 | Female | M. Goode | blood |
| stcy_04 | 177 | ASUVTC002902 | stcy | USA: Arizona, Pima Co, Stone Canyon Club | susp | Sonoran | 17-Apr-2013 | Male | M. Goode | blood |
| stcy_05r | 178 | ASUVTC002894 | stcy | USA: Arizona, Pima Co, Stone Canyon Club | susp | Sonoran | 28-Mar-2013 | Female | M. Goode | blood |
| stcy_07r | 179 | ASUVTC002921 | stcy | USA: Arizona, Pima Co, Stone Canyon Club | susp | Sonoran | 25-Jun-2013 | Unknown | M. Goode | blood |
| stcy_03 | 180 | ASUVTC002907 | stcy | USA: Arizona, Pima Co, Stone Canyon Club | susp | Sonoran | 26-Apr-2013 | Female | M. Goode | blood |
| orvl_01 | 181 | ASUVTC002881 | orvl | USA: Arizona, Pima Co, Oro Valley | susp | Sonoran | 7-Jul-2005 | Unknown | M. Feldner | toes |
| orvl_02 | 182 | ASUVTC002882 | orvl | USA: Arizona, Pima Co, Oro Valley | susp | Sonoran | 7-Jul-2005 | Unknown | M. Feldner | toes |
| orvl_03 | 183 | ASUVTC002883 | orvl | USA: Arizona, Pima Co, Oro Valley | susp | Sonoran | 7-Jul-2005 | Unknown | M. Feldner | toes |
| orvl_04 | 184 | ASUVTC002884 | orvl | USA: Arizona, Pima Co, Oro Valley | susp | Sonoran | 7-Jul-2005 | Unknown | M. Feldner | toes |
| orvl_05 | 185 | ASUVTC002885 | orvl | USA: Arizona, Pima Co, Oro Valley | susp | Sonoran | 7-Jul-2005 | Unknown | M. Feldner | toes |
| sbmt_02 | 186 | ASUVTC003004 | sbmt | USA: Arizona, Pima Co, Silver Bell Mountains | susp | Sonoran | 14-May-2023 | Unknown | M. Feldner | blood |
| sbmt_01 | 187 | ASUVTC003003 | sbmt | USA: Arizona, Pima Co, Silver Bell Mountains | susp | Sonoran | 14-May-2023 | Unknown | M. Feldner | blood |
| cafh_21 | 188 | ASUVTC003007 | cafh | USA: Arizona, Pima Co, Catalina Foothills | susp | Sonoran | 11-Jun-2023 | Unknown | M. Feldner | blood |
| cafh_18 | 189 | ASUVTC002993 | cafh | USA: Arizona, Pima Co, Catalina Foothills | susp | Sonoran | 18-Jul-2021 | Unknown | not collected | toes |
| cafh_19 | 190 | ASUVTC003008 | cafh | USA: Arizona, Pima Co, Catalina Foothills | susp | Sonoran | not collected | Unknown | not collected | toes |
| cafh_16 | 191 | ASUVTC002986 | cafh | USA: Arizona, Pima Co, Catalina Foothills | susp | Sonoran | 30-May-2020 | Unknown | M. Feldner | blood |
| cafh_06 | 192 | ASUVTC002948 | cafh | USA: Arizona, Pima Co, Catalina Foothills | susp | Sonoran | 17-May-2016 | Unknown | M. Feldner | toes |
| cafh_11 | 193 | ASUVTC002953 | cafh | USA: Arizona, Pima Co, Catalina Foothills | susp | Sonoran | 28-Oct-2016 | Unknown | R. Repp | blood |

| Sample | VCF POS | Museum Number | Site Name | Location | Cluster Assignment (K2) | Cluster Assignment (K5) | Collection Date | Sex | Collector | DNA source |
|---|---|---|---|---|---|---|---|---|---|---|
| cafh_12 | 194 | ASUVTC002954 | cafh | USA: Arizona, Pima Co, Catalina Foothills | susp | Sonoran | 28-Oct-2016 | Unknown | R. Repp | blood |
| cafh_13 | 195 | ASUVTC002955 | cafh | USA: Arizona, Pima Co, Catalina Foothills | susp | Sonoran | 28-Oct-2016 | Unknown | R. Repp | blood |
| cafh_14 | 196 | ASUVTC002956 | cafh | USA: Arizona, Pima Co, Catalina Foothills | susp | Sonoran | 28-Oct-2016 | Unknown | R. Repp | blood |
| cafh_05 | 197 | ASUVTC002946 | cafh | USA: Arizona, Pima Co, Catalina Foothills | susp | Sonoran | 30-May-2015 | Unknown | not collected | toes |
| cafh_01 | 198 | ASUVTC002909 | cafh | USA: Arizona, Pima Co, Catalina Foothills | susp | Sonoran | 2-May-2013 | Male | not collected | blood |
| cafh_15 | 199 | ASUVTC002957 | cafh | USA: Arizona, Pima Co, Catalina Foothills | susp | Sonoran | 1-May-2017 | Unknown | not collected | toes |
| cafh_17 | 200 | ASUVTC002991 | cafh | USA: Arizona, Pima Co, Catalina Foothills | susp | Sonoran | 22-May-2021 | Unknown | not collected | toes |
| cafh_02 | 201 | ASUVTC002932 | cafh | USA: Arizona, Pima Co, Catalina Foothills | susp | Sonoran | 10-Jul-2014 | Unknown | M. Feldner | toes |
| cafh_04 | 202 | ASUVTC002938 | cafh | USA: Arizona, Pima Co, Catalina Foothills | susp | Sonoran | 24-Apr-2015 | Unknown | J. Servoss | toes |
| cafh_20 | 203 | ASUVTC003005 | cafh | USA: Arizona, Pima Co, Catalina Foothills | susp | Sonoran | 17-May-2023 | Unknown | M. Feldner | toes |
| cafh_09 | 204 | ASUVTC002960 | cafh | USA: Arizona, Pima Co, Catalina Foothills | susp | Sonoran | 26-Apr-2018 | Unknown | M. Feldner | blood |
| cafh_03 | 205 | ASUVTC002937 | cafh | USA: Arizona, Pima Co, Catalina Foothills | susp | Sonoran | 1-Apr-2015 | Unknown | M. Feldner | toes |
| cafh_07 | 206 | ASUVTC002950 | cafh | USA: Arizona, Pima Co, Catalina Foothills | susp | Sonoran | 22-Jul-2016 | Unknown | M. Feldner | toes |
| avra_03 | 207 | ASUVTC002984 | avra | USA: Arizona, Pima Co, Silverbell Rd, SE of Marana | susp | Sonoran | 21-May-2020 | Unknown | R. Repp | toes |
| avra_01 | 208 | ASUVTC002933 | avra | USA: Arizona, Pima Co, Silverbell Rd, SE of Marana | susp | Sonoran | 14-Jul-2014 | Unknown | M. Feldner | toes |
| avra_02 | 209 | ASUVTC002961 | avra | USA: Arizona, Pima Co, Silverbell Rd, SE of Marana | susp | Sonoran | 28-May-2018 | Unknown | J. Slone | blood |
| avra_09 | 210 | na | avra | USA: Arizona, Pima Co, Tuscon | susp | Sonoran | 5-Aug-2022 | Unknown | P. A. Maier | blood |
| avra_10 | 211 | na | avra | USA: Arizona, Pima Co, Tuscon | susp | Sonoran | 16-Aug-2022 | Unknown | P. A. Maier | blood |
| avra_11 | 212 | na | avra | USA: Arizona, Pima Co, Tuscon | susp | Sonoran | 21-Jul-2024 | Unknown | P. A. Maier | blood |
| avra_05 | 213 | na | avra | USA: Arizona, Pima Co, Tuscon | susp | Sonoran | 29-May-2023 | Unknown | P. A. Maier | blood |
| avra_12 | 214 | na | avra | USA: Arizona, Pima Co, Tuscon | susp | Sonoran | 12-Aug-2024 | Unknown | P. A. Maier | blood |
| avra_07 | 215 | na | avra | USA: Arizona, Pima Co, Tuscon | susp | Sonoran | 18-Jun-2023 | Unknown | P. A. Maier | blood |

| Sample | VCF POS | Museum Number | Site Name | Location | Cluster Assignment (K2) | Cluster Assignment (K5) | Collection Date | Sex | Collector | DNA source |
|---|---|---|---|---|---|---|---|---|---|---|
| avra_04 | 216 | ASUVTC003009 | avra | USA: Arizona, Pima Co, Manville Rd, S of Marana | susp | Sonoran | 29-May-2023 | Male | P. A. Maier | toes |
| avra_06 | 217 | na | avra | USA: Arizona, Pima Co, Tuscon | susp | Sonoran | 29-May-2023 | Unknown | P. A. Maier | blood |
| avra_08 | 218 | na | avra | USA: Arizona, Pima Co, Tuscon | susp | Sonoran | 21-Jun-2023 | Unknown | P. A. Maier | blood |
| tumt_01 | 219 | ASUVTC002935 | tumt | USA: Arizona, Pima Co, Tucson Mtns, Tucson | susp | Sonoran | 14-Aug-2014 | Male | J. Schmidt (via R. Repp) | toes |
| tuhl_01 | 220 | ASUVTC002903 | tuhl | USA: Arizona, Pima Co, Tumamoc Hill, Tucson | susp | Sonoran | 17-Apr-2013 | Female | M. Goode | blood |
| rimt_02 | 221 | ASUVTC002916 | rimt | USA: Arizona, Pima Co, Rincon Mtns | susp | Sonoran | 13-May-2013 | Female | K. Bonine | blood |
| rimt_05 | 222 | ASUVTC002951 | rimt | USA: Arizona, Pima Co, Rincon Mtns | susp | Sonoran | 23-Aug-2016 | Unknown | K. Bonine | blood |
| rimt_09 | 223 | ASUVTC003006 | rimt | USA: Arizona, Cochise Co, Rincon Mtns - Paige Creek | susp | Sonoran | 4-Jun-2023 | Unknown | M. Feldner | blood |
| rimt_04 | 224 | ASUVTC002934 | rimt | USA: Arizona, Pima Co, Rincon Mtns | susp | Sonoran | 1-Aug-2014 | Female | K. Bonine | blood |
| rimt_03 | 225 | ASUVTC002928 | rimt | USA: Arizona, Cochise Co, Rincon Mtns - Paige Creek | susp | Sonoran | 28-Sep-2013 | Unknown | R. Repp, M. Feldner | blood |
| rimt_01 | 226 | ASUVTC002915 | rimt | USA: Arizona, Pima Co, Rincon Mtns | susp | Sonoran | 13-May-2013 | Male | K. Bonine | blood |
| rimt_07 | 227 | ASUVTC002987 | rimt | USA: Arizona, Pima Co, Rincon Mtns | susp | Sonoran | 16-Aug-2020 | Unknown | M. Feldner | blood |
| rimt_06 | 228 | ASUVTC002974 | rimt | USA: Arizona, Pima Co, Rincon Mtns | susp | Sonoran | 20-Aug-2019 | Unknown | M. Feldner | blood |
| rimt_08 | 229 | ASUVTC002988 | rimt | USA: Arizona, Pima Co, Rincon Mtns | susp | Sonoran | 3-Sep-2020 | Unknown | M. Feldner, J. Servoss | blood |
| vail_01 | 230 | ASUVTC003000 | vail | USA: Arizona, Pima Co, Vail | susp | Sonoran | 18-Sep-2022 | Unknown | M. Feldner | toes |
| vail_02 | 231 | ASUVTC002992 | vail | USA: Arizona, Pima Co, Vail | susp | Sonoran | 5-Jul-2021 | Unknown | M. Feldner | toes |
| mule_01 | 232 | ASUVTC002918 | mule | USA: Arizona, Cochise Co, Muleshoe | susp | Sonoran | 17-May-2013 | Female | M. Feldner, R. Repp | blood |
| grvy_01 | 233 | ASUVTC002949 | grvy | USA: Arizona, Pima Co, south of Green Valley | susp | Sonoran | 30-Jun-2016 | Unknown | M. Feldner | toes |
| shmt_02 | 234 | ASUVTC002969 | shmt | USA: Arizona, Cochise Co, N of Douglas | susp | Sonoran | 26-Apr-2019 | Female | B. Radke | blood |
| shmt_03 | 235 | ASUVTC002972 | shmt | USA: Arizona, Cochise Co, N of Douglas | susp | Sonoran | 17-Jul-2019 | Male | B. Radke | blood |
| shmt_01 | 236 | ASUVTC002964 | shmt | USA: Arizona, Cochise Co, N of Douglas | susp | Sonoran | 31-Jul-2018 | Female | B. Radke | blood |
| shmt_04 | 237 | ASUVTC002973 | shmt | USA: Arizona, Cochise Co, N of Douglas | susp | Sonoran | 12-Aug-2019 | Female | B. Radke | blood |

| Sample | VCF POS | Museum Number | Site Name | Location | Cluster Assignment (K2) | Cluster Assignment (K5) | Collection Date | Sex | Collector | DNA source |
|---|---|---|---|---|---|---|---|---|---|---|
| pamt_01 | 238 | ASUVTC002963 | pamt | USA: Arizona, Cochise Co, Parilla Mountains | susp | Sonoran | 23-Jul-2018 | Unknown | B. Radke | toes |
| pamt_02 | 239 | ASUVTC002966 | pamt | USA: Arizona, Cochise Co, Parilla Mountains | susp | Sonoran | 7-Sep-2018 | Female | B. Radke | blood |
| pamt_04 | 240 | ASUVTC002975 | pamt | USA: Arizona, Cochise Co, Parilla Mountains | susp | Sonoran | 3-Oct-2019 | Male | B. Radke | blood |
| blue_01 | 241 | na | blue | USA: New Mexico, Hidalgo Co, Blue Mountain | susp | Chihuahuan | 17-Jul-2025 | Unknown | not collected | blood |
| blue_02 | 242 | na | blue | USA: New Mexico, Hidalgo Co, Blue Mountain | susp | Chihuahuan | 17-Jul-2025 | Unknown | not collected | blood |
| brmt_01 | 243 | na | brmt | USA: New Mexico, Hidalgo Co, Brushy Mountain | susp | Chihuahuan | 26-Apr-2025 | Unknown | not collected | blood |
| brmt_03 | 244 | na | brmt | USA: New Mexico, Hidalgo Co, Brushy Mountain | susp | Chihuahuan | 27-Apr-2025 | Unknown | not collected | blood |
| brmt_02 | 245 | na | brmt | USA: New Mexico, Hidalgo Co, Brushy Mountain | susp | Chihuahuan | 27-Apr-2025 | Unknown | not collected | blood |
| whit_01 | 246 | MSB:Herp:98819 | whit | USA: New Mexico, Grant Co, White Rock Canyon | susp | Chihuahuan | 17-May-2017 | Unknown | JTG | blood |
| whit_02 | 247 | MSB:Herp:98824 | whit | USA: New Mexico, Grant Co, White Rock Canyon | susp | Chihuahuan | 1-Jun-2017 | Unknown | JTG | blood |
| whit_03 | 248 | MSB:Herp:98831 | whit | USA: New Mexico, Grant Co, White Rock Canyon | susp | Chihuahuan | 31-May-2017 | Unknown | JTG | blood |
| pelo_04 | 249 | na | pelo | USA: New Mexico, Hidalgo Co, Peloncillo Mtns | susp | Chihuahuan | 8-Aug-2024 | Unknown | A. Pawlicki | blood |
| pelo_02 | 250 | na | pelo | USA: New Mexico, Hidalgo Co, Peloncillo Mtns | susp | Chihuahuan | 5-Jul-2024 | Unknown | A. Pawlicki | blood |
| pelo_09 | 251 | na | pelo | USA: New Mexico, Hidalgo Co, Peloncillo Mtns | susp | Chihuahuan | 13-May-2025 | Unknown | A. Pawlicki | blood |
| pelo_07 | 252 | na | pelo | USA: New Mexico, Hidalgo Co, Peloncillo Mtns | susp | Chihuahuan | 4-May-2025 | Unknown | A. Pawlicki | blood |
| pelo_08 | 253 | na | pelo | USA: New Mexico, Hidalgo Co, Peloncillo Mtns | susp | Chihuahuan | 7-May-2025 | Unknown | A. Pawlicki | blood |
| pelo_06 | 254 | na | pelo | USA: New Mexico, Hidalgo Co, Peloncillo Mtns | susp | Chihuahuan | 12-Apr-2025 | Unknown | A. Pawlicki | blood |
| pelo_05 | 255 | na | pelo | USA: New Mexico, Hidalgo Co, Peloncillo Mtns | susp | Chihuahuan | 11-Apr-2025 | Unknown | A. Pawlicki | blood |
| pelo_11 | 256 | na | pelo | USA: New Mexico, Hidalgo Co, Peloncillo Mtns | susp | Chihuahuan | 17-May-2025 | Unknown | A. Pawlicki | blood |
| pelo_13 | 257 | na | pelo | USA: New Mexico, Hidalgo Co, Peloncillo Mtns | susp | Chihuahuan | 16-Jul-2025 | Unknown | A. Pawlicki | blood |
| pelo_12 | 258 | na | pelo | USA: New Mexico, Hidalgo Co, Peloncillo Mtns | susp | Chihuahuan | 16-Jul-2025 | Unknown | A. Pawlicki | blood |

| Sample | VCF POS | Museum Number | Site Name | Location | Cluster Assignment (K2) | Cluster Assignment (K5) | Collection Date | Sex | Collector | DNA source |
|---|---|---|---|---|---|---|---|---|---|---|
| pelo_14 | 259 | na | pelo | USA: New Mexico, Hidalgo Co, Peloncillo Mtns | susp | Chihuahuan | 17-Jul-2025 | Unknown | A. Pawlicki | blood |
| pelo_15 | 260 | MSB:Herp: 97864 | pelo | USA: New Mexico, Hidalgo Co, Peloncillo Mtns | susp | Chihuahuan | 30-Jul-2016 | Unknown | B. Christman | muscle |
| pelo_16 | 261 | MSB:Herp: 100282 | pelo | USA: New Mexico, Hidalgo Co, Peloncillo Mtns | susp | Chihuahuan | 27-Jul-2019 | Unknown | B. Christman | muscle |
| pelo_03 | 262 | na | pelo | USA: New Mexico, Hidalgo Co, Peloncillo Mtns | susp | Chihuahuan | 27-Jul-2024 | Unknown | A. Pawlicki | blood |
| pelo_10 | 263 | na | pelo | USA: New Mexico, Hidalgo Co, Peloncillo Mtns | susp | Chihuahuan | 17-May-2025 | Unknown | A. Pawlicki | blood |
| pelo_01 | 264 | na | pelo | USA: New Mexico, Hidalgo Co, Peloncillo Mtns | susp | Chihuahuan | 27-Jul-2019 | Unknown | J.L. Jones, B. Christman, M. Christman, L. Patterson | blood |
| dunc_01 | 265 | MSB:Herp: 97865 | dunc | USA: Arizona, Greenlee Co, 3.1 miles W of Duncan | susp | Chihuahuan | 31-Jul-2016 | Unknown | B. Christman | muscle |
| demi_01 | 266 | MSB:Herp: 108522 | demi | USA: New Mexico, Luna Co, Deming | susp | Chihuahuan | 17-May-2023 | Unknown | B. Christman | muscle |