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# Evaluating Population Genetic Structure and Potential Genomic Signals of Natural Selection in a Migratory Songbird (Protonotaria citrea)

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# **Evaluating Population Genetic Structure and Potential Genomic Signals of Natural Selection in a Migratory Songbird (*Protonotaria citrea*)**

A thesis submitted in partial fulfillment of the requirements for the degree of Master of Science at Virginia Commonwealth University.

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## Abstract:

In this study I attempted to further resolve the population genetic structure in the Prothonotary Warbler (*Protonotaria citrea*), and conducted an outlier SNP analysis and exploratory gene ontology analysis to investigate potential ongoing natural selection in the species. This analysis of population structure confirms previous work by DeSaix et al. (2019), where weak population structure was observed between eastern sites along the Atlantic Coastal Plain, and western sites in the Mississippi Alluvial Valley, possibly due to a genetic discontinuity across the Appalachian Mountains. I conducted two forms of outlier SNP analyses, a principal component analysis (PCA)-based approach to identify SNPs associated with local adaptation, and a partial redundancy analysis (pRDA) to identify SNPs associated with site-specific environmental factors. I then performed an exploratory gene ontology analysis of the top ten outliers identified from both methods. I found two of the top outliers both fell within gene structures that aligned to proteins localized to the eye, which I suggest may be due to selective pressure on the visual system of the Prothonotary Warbler, perhaps due to sexual selection or adaptation to light pollution. Further investigation is needed to determine whether this signal is not a false positive, and if so, determine what selective pressures are acting on the Prothonotary Warbler visual system. There did not appear to any other discernible patterns in the gene ontologies of the top outlier SNPs, but a full gene ontology analysis may be able to reveal additional selective pressures for further investigation.

## Introduction:

Studies on geographic variation at the genomic level can allow us insight into the potential mechanisms by which populations may adapt to environmental change at a level of detail that is not obtainable through more traditional studies of morphological or behavioral variation. Population genetic and genotype-association studies allow us to observe evolutionary and ecological processes at the molecular level. Through such studies we can identify regions of the genome potentially under selective pressure, identify patterns of gene flow between sub-populations (Reid et al., 2016; Walsh et al., 2018; Wagner et al., 2020), and predict a given population's vulnerability to environmental change and habitat fragmentation (Chen et al., 2016; Bay et al., 2018).

One study that conducted an ontology analysis of alleles introgressing between two closely related tidal marsh sparrow species, Saltmarsh Sparrows (*Ammospiza caudacuta*) and Nelson's Sparrows (*A. nelsoni*), found that alleles displaying the highest rates of introgression were associated with ontologies conferring adaptation to high salinity environments (Walsh et al., 2018). Both species breed in tidal wetlands and are particularly vulnerable to habitat loss and sea level rise, and the authors of this study concluded that conservation of suitable habitat for both species is likely necessary for either's long term survival (Walsh et al., 2018). Another study in a pedigreed population of the endangered Florida Scrub-jay (*Aphelocoma coerulescens*) found a negative relationship between metrics of inbreeding such as parental identity by descent (IBD) and various metrics of offspring fitness (Chen et al., 2016). While their study population has remained stable over time, human-mediated habitat destruction and fragmentation has caused steep population declines in the surrounding area (Chen et al., 2016). Florida Scrub-jays have low offspring dispersal, and as these satellite populations have declined, new immigrants to the study population have decreased and metrics of inbreeding have increased (Chen et al., 2016). This coupled with the observed patterns of inbreeding depression led Chen et al. (2016) to recommend preservation of small and even inbred satellite populations should be prioritized, as they can play a vital role in preserving genetic variation in larger seemingly stable populations.

The Prothonotary Warbler is a vibrant yellow, insectivorous, cavity-nesting migratory songbird of the *Parulidae* family (Petit, 2020). Prothonotary Warblers breed in bottomland hardwood forests in Eastern North America and overwinter in mangroves and flooded forests throughout Central America, Northern South America, and the Caribbean. Prothonotary Warblers are estimated to number ~2,100,000 globally (Partners in Flight, 2020), and like many other neotropical migrant passerines, Prothonotary Warblers are vulnerable to habitat loss and fragmentation in their breeding range and throughout their migration path and wintering grounds (Petit, 2020). Only 10% of the original bottomland hardwood forest in the continental U.S. remain (Petit, 2020), and Prothonotary Warblers exhibit moderate forest area sensitivity, avoiding forest tracts less than 100ha and riparian woodlands less than 30m wide (Petit, 2020). Breeding Bird Survey (BBS) data between 1966 and 2019 indicate a range-wide decline in Prothonotary Warblers by -0.7% (-1.2 - -0.26) annually (Sauer et al., 2020), and population trends based on eBird data also show range-wide declines between 2007 and 2021 (Figure 1). However, the longer-term population trends (BBS) vary significantly across the breeding range. Such geographic variation in population trends may indicate concomitant variation in limiting factors and/or selective pressures.

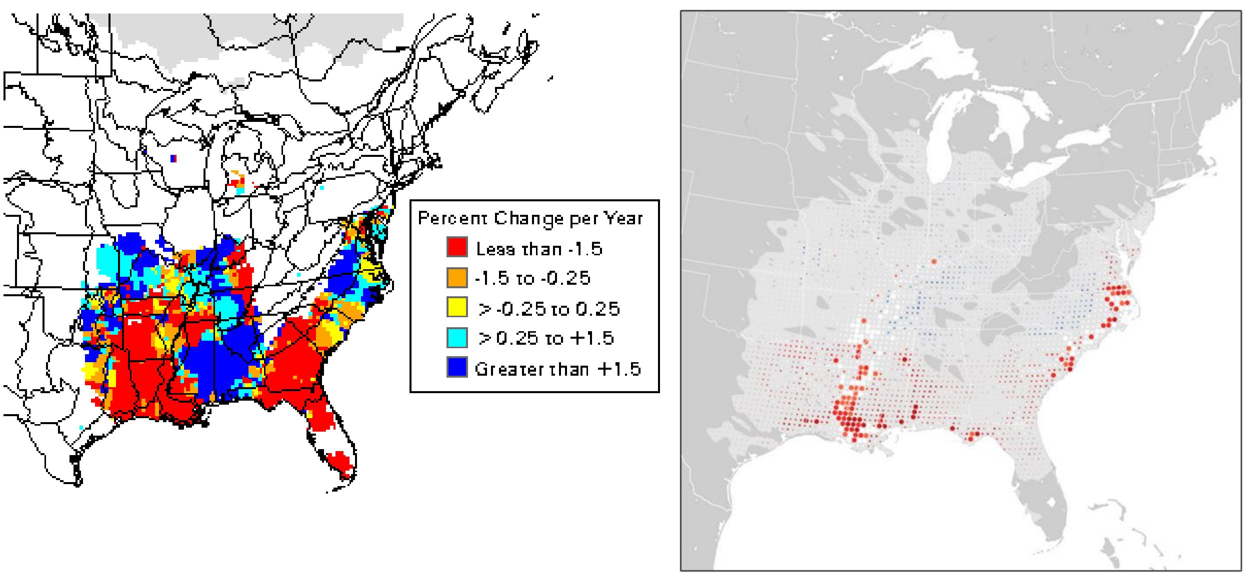


**Figure 1:** Population trends for breeding Prothonotary Warbler from two different citizen science data sources and time frames. Left: Breeding Bird Survey (BBS) population trends for 1966 - 2019 (Sauer et al., 2020) indicating geographic variation in trends. Right: eBird trends for 2007 – 2021 (Fink et al., 2022) with circles representing 27km x 27km regions. Red indicates decline and blue indicates increase. The darker the color, the stronger the trend. White circles represent locations where the trend estimate is not significantly different from zero (i.e., the 80% confidence interval contains zero). Circle sizes are scaled by the estimated relative abundance at the middle of the time period.

To assess whether geographic variation in population trends may be related to differences in overwintering locations, DeSaix et al. (2019) used population assignment by genotype to investigate migratory connectivity in Prothonotary Warblers. Migratory connectivity is the degree to which breeding populations are distinct or intermix with other breeding populations during the non-breeding season. They found regional genetic structure between the eastern/Atlantic and the Mississippi River Alluvial Valley breeding populations, and that warblers throughout the breeding grounds intermix in a relatively small geographic area on the nonbreeding grounds.

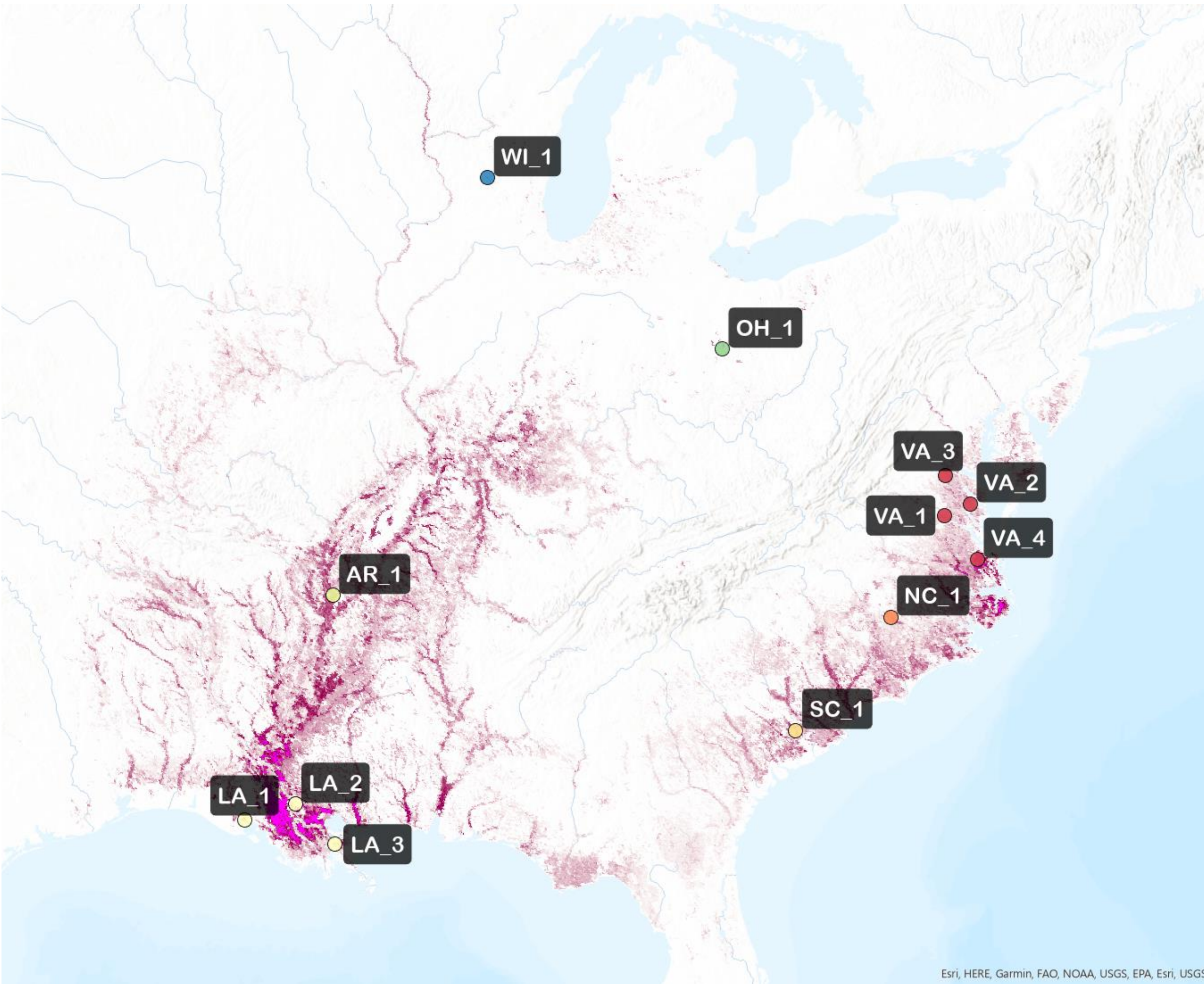


**Figure 2:** Sampling locations overlaid on map of mean Prothonotary Warbler abundance during the breeding season from eBird (Ebird, 2022). More saturated shades of pink indicate higher mean abundance. Sampling sites are color coded by state; red indicates Virginia, dark orange North Carolina, light orange South Carolina, yellow Louisiana, lime green Arkansas, green Ohio, and blue Wisconsin. It is important to note that in addition to covering a geographically diverse selection of the Prothonotary Warbler's breeding distribution, the species' mean local abundance also varies greatly between sampling sites. Map rendered using ArcGIS PRO (Esri Inc., 2022).

In this study, I used the sequence libraries provided by DeSaix et al. (2019) to (1) attempt to further resolve population genetic structure of the Prothonotary Warbler by aligning reads to a reference genome during SNP catalog assembly, and (2) identify gene ontologies under selective pressure in the Prothonotary Warbler. Ideally, these gene ontology associations may be used to assess potential mechanisms for adaptation to a changing environment, which could help inform wildlife management decisions for this species and possibly other related migratory bird species.

## **Methods:**

### *SNP Catalog Assembly and Filtering:*

Blood samples were obtained by DeSaix et al. (2019) from 288 *P. citrea* individuals across 12 breeding sites split between the Atlantic Seaboard and Mississippi River Valley, and 6 wintering sites in Panama and Colombia. The raw sequence libraries were received directly from Matthew DeSaix. Two individuals sampled from Bluebonnet Swamp in Louisiana were labelled with the same individual I.D. in the barcode file, and therefore their sampling location could not be known with certainty as either or both samples had been mislabeled. These two birds were removed from the data set. I also subset the data set to include only birds sampled on the breeding grounds as it cannot be known for certain to which breeding or wintering population migratory individuals belong. This resulted in 182 birds sampled from 12 sites throughout the eastern United States (Figure 2, Table 2).

I used a custom Python script (Hohenstein, 2022; code provided by Lindsey Miles, pers. communication, 2020) to parse the raw sequence libraries for reverse-compliments of barcoded reads, and reverse-compliment those sequences so that they would be recognizable as barcoded reads by STACKS ver. 2.60 (Catchen et al., 2013). I then used fastQC ver. 0.11.9 (Andrews, 2010) to assess the read quality of the sequence libraries and to help determine trim length. The sequence libraries were then demultiplexed using STACKS, trimming reads to 60 bases in length.

To assemble the SNP catalog, I used dDocent ver. 2.8.13 (Puritz et al., 2013) with minimal filtering thresholds of 3x coverage per locus and presence of loci in at least 10 individuals, yielding 163,418 putative SNPs. I removed indels from the SNP catalog and filtered for a minimum Phred quality score of 20 and biallelic variants only using VCFtools ver. 0.1.16 (Danecek et al., 2011), retaining 122,173 SNPs.

The closest related genome to the Prothonotary Warbler assembled at the chromosome level is the Yellow-rumped Warbler (*Setophaga coronata)* (Baiz et al., 2021). I chose this as the reference genome to align consensus sequences to obtain positional information for the SNP catalog. This alignment was done in Bowtie2 ver. 2.1.0 (Langmead & Salzberg, 2012) on very-sensitive local alignment presets. The consensus sequences aligned to the Yellow-rumped Warbler genome at an overall rate of 82.69%.

I then used a custom R script (Hohenstein, 2022) to filter the SNP catalog. I first removed SNP loci from contigs that did not align to Yellow-rumped warbler reference genome. I then removed individuals with > 90% missing data, and removed SNP loci if they had minor allele frequencies less than 0.01, greater than 50% missing data, or Wright's *F* values greater than |0.5|. I further filtered the SNP catalog to retain only one SNP per RAD tag to avoid issues with linkage disequilibrium. The resulting SNP catalog retained 22,788 SNPs across 175 birds (Table 1).

**Table 1:** Comparisons between SNP filtering choices and results between this study and those of DeSaix et al. (2019). "Raw SNPs" denote the initial number of putative SNPs in each catalog after assembly. Other than discarding SNPs from contigs that did not align to the Yellow-rumped Warbler genome in this study, all other filtering parameters remained the same between both studies; the numbers of SNPs in each catalog if all filtering parameters remained the same in both analyses are denoted by "same filtering parameters." The number of SNPs retained in this study after discarding SNPs from unplaced contigs are denoted by "after discarding unplaced contigs". Later in their analysis, DeSaix et al. (2019) opted to use a reduced SNP set, denoted here as "high $F_{ST}$ SNP set," selected by $F_{ST}$ for use in population assignment for the purposes of assessing migratory connectivity.

| | this study | DeSaix et al. (2019) |
|---|---|---|
| **raw SNPs** | 163,418 | 145,260 |
| **same filtering parameters** | 27,781 | 26,189 |
| **after discarding unplaced contigs** | 22,788 | - |
| **high $F_{ST}$ SNP set** | - | 600 |

*Population Structure:*

To assess population structure, I first conducted a principal component analysis (PCA) of multi-locus genotypes following the methods described by Patterson et al. (2006). Missing data were imputed as the centered and standardized mean. In the initial PCA, most individuals were tightly clustered around the centroid except for seven outliers, all from Bluebonnet Swamp in Louisiana (Figure S.1). I removed these birds as well as those whose PCA coordinates exceeded six standard deviations from the mean of the first ten principal components over four iterations, three from Hoover Reservoir, Ohio, and one from Sugar River, Wisconsin. This resulted in a final sample size of 164 individuals across 12 sampling sites (Table 2). I then generated projection plots for the first two principal components (PCs) to visualize population structure.

I further evaluated genetic structure using the program STRUCTURE (Pritchard et al., 2000). I initially ran STRUCTURE with 10,000 burn-in iterations and 20,000 Markov chain Monte Carlo (MCMC) steps for the number of clusters (*K*) ranging from 1 through 13, with five MCMC simulations for each value of *K*. After visual assessment of the mean estimated log probabilities of the data for each value of *K* (L(*K*)) using STRUCTURE Harvester (Earl & VonHoldt, 2012), I then conducted an additional ten runs for values of *K* ranging from 2 through 6 with 10,000 burn-in iterations and 20,000 MCMC steps to account for the high standard deviations of mean L(*K*) observed across those values of *K*. Visual inspection of the L(*K*) for all simulations (Figure S.2) revealed a bimodal distribution of L(*K*) for values of *K* ranging from 2 through 4. To account for this, I discarded runs with estimated log probabilities below -4e6 for values of *K* ranging 2 through 4. To account for the low number of simulations remaining for values of *K* 2 and 3, I conducted additional MCMC simulations for values of *K* 2 and 3 with 50,000 burn-in iterations and 100,000 MCMC steps. I then produced cluster assignment bar plots to visualize individual cluster assignment probabilities from the retained simulations using the web-tool CLUMPAK

(Kopelman et al., 2015), and determined the most likely value of $K$ with the $\Delta K$ method described by Evanno et al. (2005), and by inspection of the relationship of the log probability of the data given $K$ (Figure 5).

**Table 2:** Sampling site information. "Subregion" denotes which regional genotype cluster identified by DeSaix et al. (2019) each site belongs to, East being the Atlantic Seaboard and West being the Mississippi Alluvial Valley. Latitude and longitude for sampling sites are specified in decimal degrees. The last column, "*n*," denotes the number of birds from each site retained in the final data set.

| Site Name | Site ID | State | Subregion | Latitude | Longitude | *n* |
|---|---|---|---|---|---|---|
| VA, Deep Bottom | VA_1 | Virginia | East | 37.407 | -77.305 | 23 |
| VA, Dragon Run | VA_2 | Virginia | East | 37.652 | -76.710 | 2 |
| VA, Fort AP Hill | VA_3 | Virginia | East | 38.155 | -77.324 | 20 |
| VA, Great Dismal Swamp | VA_4 | Virginia | East | 36.631 | -76.491 | 12 |
| NC, Holt Lake | NC_1 | North Carolina | East | 35.469 | -78.403 | 9 |
| SC, Francis Beidler Forest | SC_1 | South Carolina | East | 33.221 | -80.354 | 13 |
| LA, Palmetto Island | LA_1 | Louisiana | West | 29.864 | -92.150 | 19 |
| LA, Bluebonnet Swamp | LA_2 | Louisiana | West | 30.368 | -91.107 | 10 |
| LA, Barataria Preserve | LA_3 | Louisiana | West | 29.784 | -90.115 | 11 |
| AR, White River | AR_1 | Arkansas | West | 34.358 | -91.091 | 20 |
| OH, Hoover Reservoir | OH_1 | Ohio | West | 40.107 | -82.886 | 17 |
| WI, Sugar River | WI_1 | Wisconsin | West | 42.530 | -89.329 | 8 |

I also described population structure by estimating hierarchical $F$-statistics (Weir and Cockerham, 1984). I estimated pairwise multi-locus $F_{ST}$ between sampling sites and global hierarchical $F$-statistics subset by sampling sites and nested within the eastern and western subregions identified as genetic clusters by DeSaix et al. (2019), using the R package HIERFSTAT (Goudet, 2005). I calculated the Vincenty ellipsoid geographical distance between sites using the R package GEOSPERE (Hijmans et al., 2017), and plotted pairwise genetic distance ($F_{ST}$ / 1- $F_{ST}$) against $\log_{10}$(geographical distance) to visualize the relationship between genetic and geographical distance. I performed a Mantel test with 1,000 permutations to test the statistical significance of this relationship using the R package VEGAN (Dixon, 2003), using a nominal $\alpha$-threshold of 0.05.

*Outlier SNP Analysis:*

Following the methods specified by Privé et al. (2020), I used PCADAPT (Luu et al., 2017) to detect outlier SNPs. PCADAPT is an R package that provides PCA-based statistical tools for outlier SNP detection on the basis of local adaptation. In this outlier SNP analysis, after visual assessment of a scree plot of the percent variance explained, quantile plots, and PCA projection plots generated through PCADAPT (Figure S.3), I searched for outliers across the first five PCs.

The test statistic used by PCADAPT in detecting outlier SNPs is the Mahalanobis distance, which is a multi-dimensional approach that measures the distance between a point and the mean. After calculating the Mahalanobis distance and corresponding p-values for all SNPs I assessed diagnostic plots to examine the distribution of p-values for the test statistic and determine the presence of outlier SNPs. I then reported two lists of candidate outlier SNPs, one utilizing Benjamini-Hochberg corrected p-values, and the other utilizing Bonferroni corrected p-values, both based on a nominal α-threshold of 0.05 (Table S.6) following the methods specified by Privé et al. (2020).

To complement this PCA-based outlier SNP analysis, I conducted a partial redundancy analysis using the R package VEGAN (Dixon, 2003), to examine associations between site-specific bioclimatic factors and genetic variation. This framework was also used to identify outlier SNPs specifically associated with site-specific bioclimatic factors. Redundancy analysis (RDA) is an extension of multiple regression to model multivariate response data (Legendre & Legendre, 2012). Partial RDA (pRDA) is the analysis of a set of response variables by a set of explanatory variables, conditioned on an additional set of explanatory covariables (Legendre & Legendre, 2012). Following the methods suggested by Forester et al. (2018), I conducted a pRDA with site-specific environmental variables as explanatory variables, with site latitude and longitude as covariables and the centered and standardized SNP catalog matrix used in the multi-locus PCA as response variables. For environmental variables, I obtained historical climate data for 1970-2000 for the sampling sites from WorldClim 2.1 (Fick et al., 2017) at a resolution of 30 seconds. I selected five historical climate indices describing monthly temperature (°C), maximum temperature (°C), precipitation (mm), solar radiation (kJ m-2 day-1), and water vapor pressure (kPa) for April through July for use as environmental predictors. I chose these specific predictors in order to cover a broad range of site-specific environmental variation for the months that Prothonotary Warblers are on breeding grounds. To reduce the dimensionality of these predictors for use in the pRDA, I conducted a PCA of these historical climate indices and elected to use the first three environmental PCs as predictor variables for the pRDA, as these three PCs explained >90% of the environmental variation of the sampling sites; the first environmental PC accounting for 78.30% of the variation, the second for 9.55%, and the third for 5.87%.

I assessed the global significance of the pRDA model using an ANOVA-like permutation test (α = 0.05, 1,000 permutations) in the R package VEGAN (Dixon, 2003), with the null hypothesis being that there is no linear relationship between the SNP data and the environmental predictors. The significance of each of the constrained pRDA axes, and of each of the predictors was also independently assessed using the same ANOVA-like permutation test (α = 0.05, 1,000 permutations), where each constrained axis was tested using all previous constrained axes as conditions, and each predictor was tested in sequential order. It is important to note that in this permutation test, the order in which the predictor variables are tested can affect their significance (Dixon, 2003).

I then reported all SNPs that fell more than three standard deviations outside the mean for all significant pRDA axes as candidate outliers, as suggested by Forester et al. (2018).

*Gene Ontology Analysis:*

To perform an exploratory analysis of biological processes represented by the identified outlier SNPs, I first searched for gene structures within 30,000 bases of the top ten highest loaded outlier SNPs in the Yellow-rumped Warbler genome assembly for both the PCADAPT and pRDA outlier SNP detection methods. I then compiled the DNA sequences of these gene structures using a custom Python script (Hohenstein, 2022). These sequences were then queried against the Zebra Finch (*Taeniopygia guttata*) reference proteome (Warren et al., 2010) using BlastX (Camacho et al., 2009) to identify known proteins encoded by these gene structures. I then compiled descriptions of these genes' functions from GeneCards (Safran et al., 2021), as well as gene ontologies of orthologs in the Red Junglefowl (*Gallus gallus*) using EggNOG (Huerta-Cepas et al., 2019) and OrthoDB (Kriventseva et al., 2019).

## Results:

*Population Structure:*

In the multi-locus PCA, after removing outlier individuals, the first two PCs explained 0.87% and 0.82% of the genetic variation of the sample population, respectively. Projection plots of the first two PCs show weak structure between individuals sampled from the Atlantic Seaboard in the east and the Mississippi Alluvial Valley in the west on PC1 (Figure 3B). Among western individuals there appears to be some weak latitudinal structure on PC2, with northern individuals being more positively loaded and southern individuals being more negatively loaded (Figure 3A). This latitudinal structure along PC2 is not apparent in eastern individuals.

In the STRUCTURE analysis I found conflicting results in determining the best value of $K$ genetic clusters. $K = 3$ is the most likely based on $\Delta K$ ($L(K{=}3) = -1{,}522{,}670 \pm 10{,}411$, $\Delta K_{K=3} = 20.777$) (Figure 4), but the highest $L(K)$ value observed was $K = 1$ ($L(K{=}1) = -1{,}522{,}332 \pm 2{,}794$). The $L(K)$ estimates for both values of $K$ overlap when accounting for standard deviation, and ΔK cannot be calculated for $K = 1$ as it is a quantity based on the second order rate of change with respect to K of the likelihood function (Evanno et al., 2005). Inspection of assignment plots showing individual cluster assignment probabilities (Figure 5) averaged across MCMC runs for $K = 3$ reveals weak longitudinal structure between eastern and western sites; however, all birds in the cluster assignment barplot for $K = 3$ were still most likely to be assigned to the first of three genetic clusters. This weak longitudinal structure is also apparent in assignment plots for higher values of $K$. Two Ohio birds are distinguished by their cluster assignment probabilities from other Ohio individuals and the rest of the population for values of $K = 3$ and above (Figure 5). These same two Ohio birds also cluster on the first PC axis in the PCADAPT PCA projection plots (Figure S.3). These two birds were not found to differentiate from the rest of the population on any of the first 10 PCs in the multi-locus PCA, and inspection of missing SNP loci in these two individuals did not reveal any patterns of missing data not found in the rest of the population.

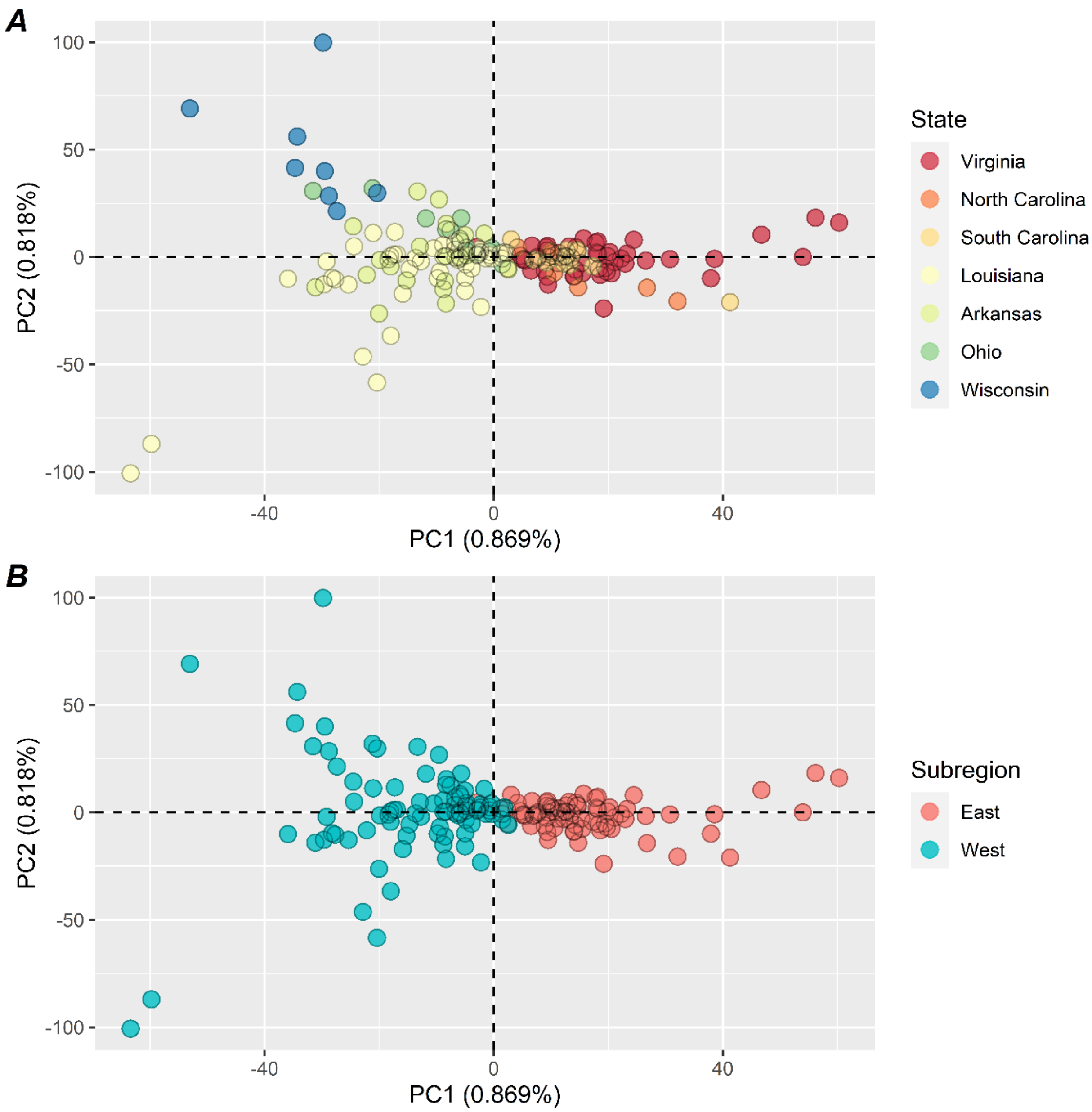


**Figure 3:** Projection plots of PC1 and PC2 from a multi-locus PCA for the Prothonotary Warbler. Individuals are color-coded by state (A) and by putative genetic clusters identified by DeSaix et al. (2019) (B).

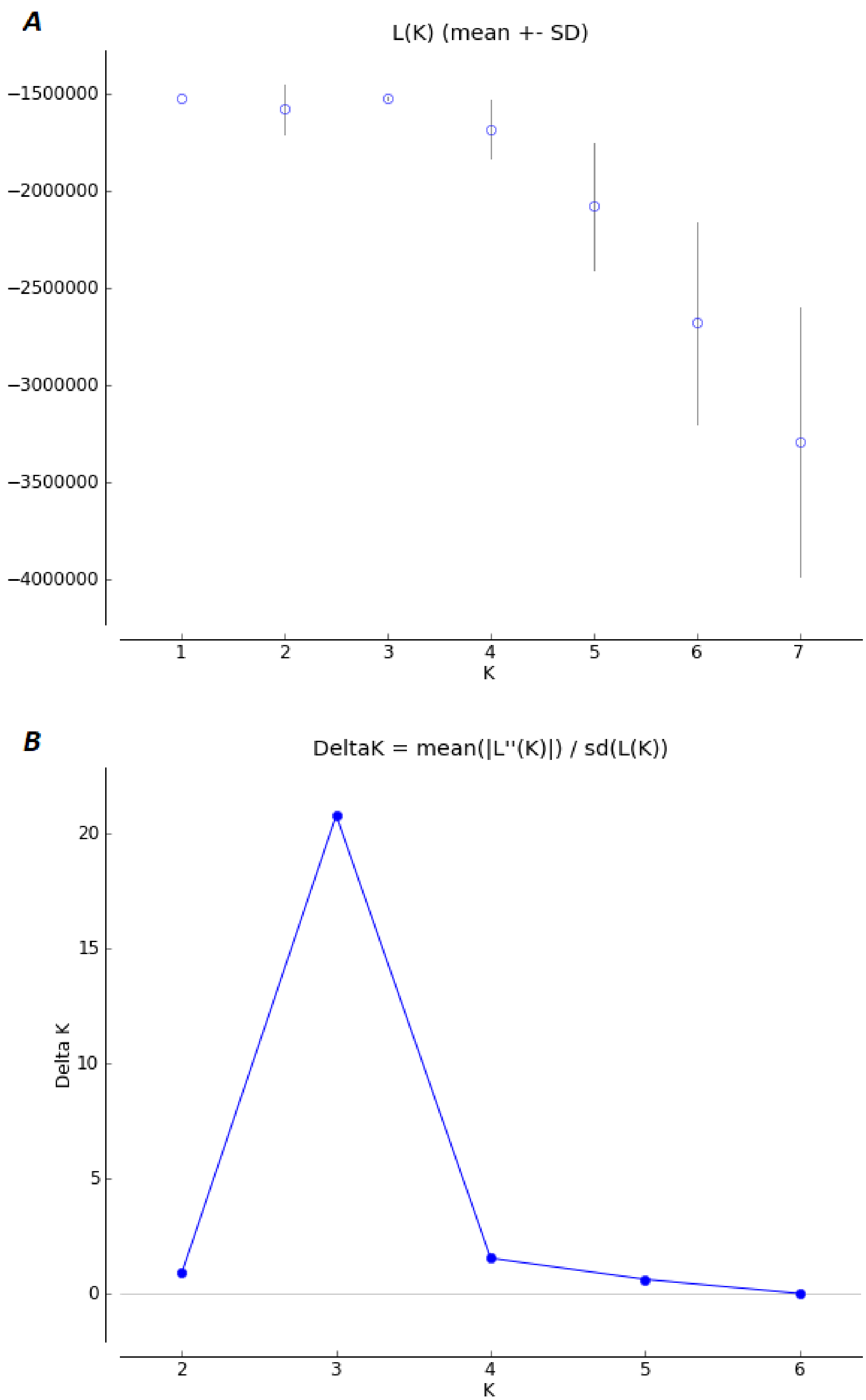


**Figure 4:** Plots of mean L(*K*) (A), and Δ*K* (B) given *K* genetic clusters after conducting subsequent MCMC simulations for values of *K* 2 through 6 and discarding low L(*K*) runs for values of *K* 2 through 4.

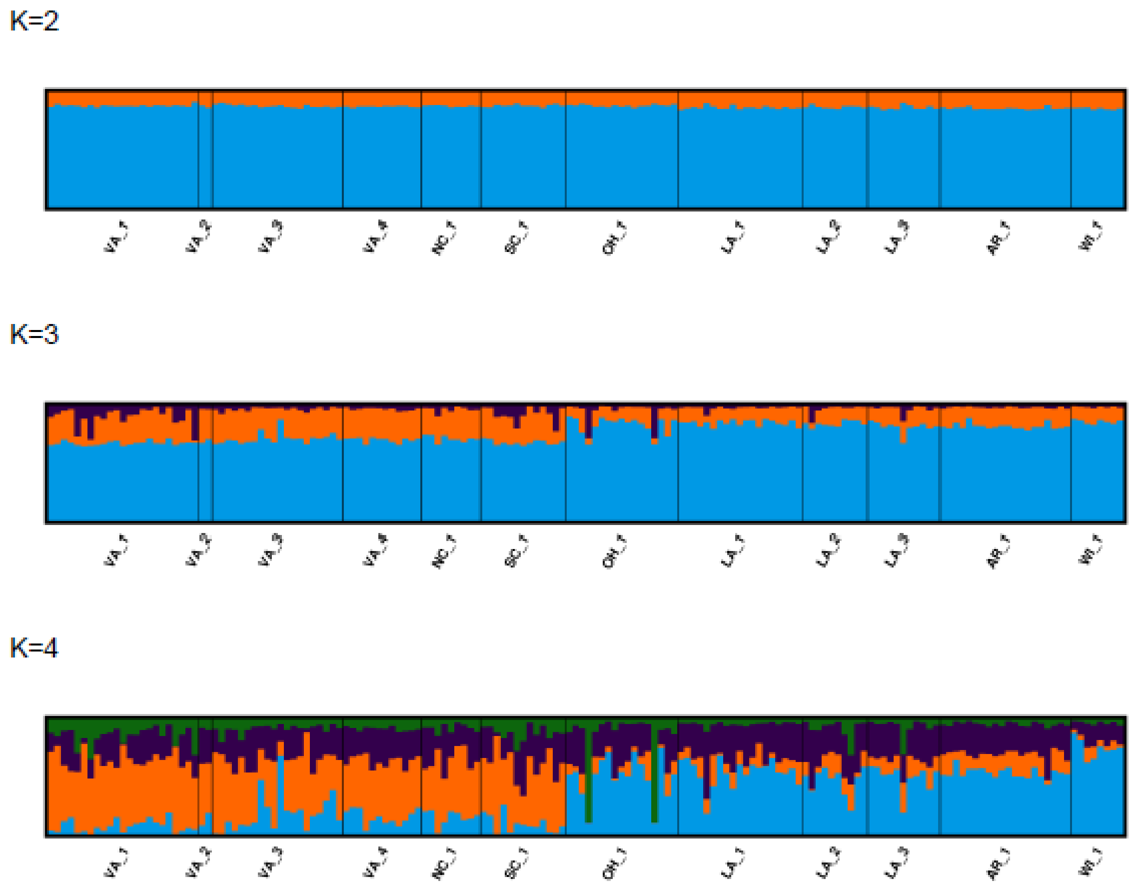


**Figure 5:** STRUCTURE cluster assignment plots showing individual population assignment probabilities for values of *K* ranging 2 through 4.

In PCA projection plots generated through PCADAPT (Figure S.3), I found the first PC to mainly differentiate between two Ohio individuals and the rest of the population. The second and fourth PCs show weak longitudinal structure, and the fifth PC shows weak latitudinal structure, similar to what was observed in the first two PCs of the multi-locus PCA. The third PCADAPT PC however, did not show any recognizable spatial population structure.

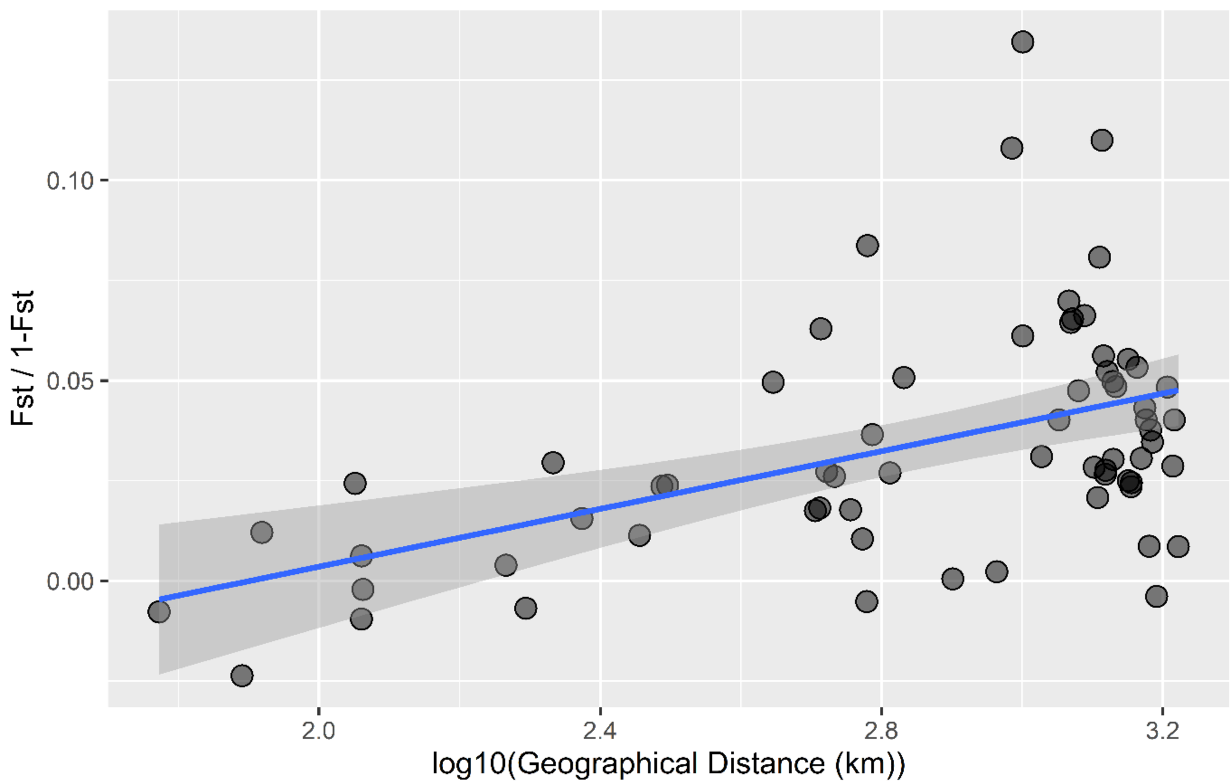


**Figure 6:** Linear regression of pairwise log10(Geographical Distance) against pairwise genetic distance ($F_{ST}$ / 1 – $F_{ST}$) for all sampling sites, standard error bands shown in dark gray.

I found pairwise genetic distance (Table S.1) is positively correlated with geographical distance between sites (Figure 6: Mantel's $r$ = 0.481, P = 0.002). Global hierarchical $F$-statistics subset by sampling site and eastern and western subregions (Table 3) show the sampling site to account for the same amount of deviation from Hardy-Weinberg equilibrium ($F_{SC}$ = 0.0028) than that of subregion ($F_{CT}$ = 0.0028), with both showing weak deviation overall ($F_{ST}$ = 0.0055).

**Table 3:** Hierarchical $F$-statistics

| | Subregion | Site | Individual |
|---|---|---|---|
| **Total** | 0.0028 | 0.0055 | -0.1391 |
| **Subregion** | - | 0.0028 | -0.1423 |
| **Site** | - | - | -0.1454 |

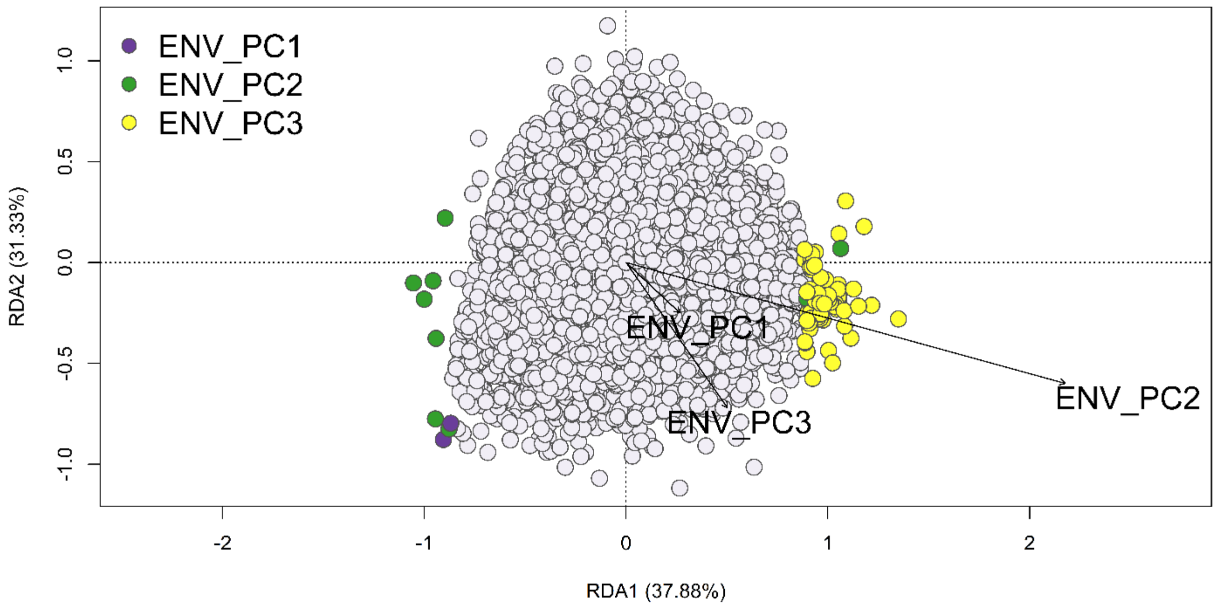


**Figure 7:** pRDA projection for axes 1 and 2. Gray circles depict SNPs, with colored circles overlayed for outlier SNPs on the first RDA axis; outliers are color-coded by the environmental predictor they show the strongest correlation with. Arrows depict environmental predictors. The arrangement of these items in the ordination space depicts their relationship with the ordination axes, which are linear combinations of the predictor variables.

*Outlier SNP Analysis:*

In the PCADAPT outlier SNP analysis I initially found 827 outlier SNPs with $P < 0.05$ using the Benjamini-Hochberg procedure; of those, 286 were retained after Bonferroni correction (Table S.6). In the Benjamini-Hochberg corrected list of outlier SNPs I found 281 SNPs associated with the first PCADAPT PC, 89 with the second PC, 293 with the third PC, 111 with the fourth PC, and 53 with the fifth PC. In the Bonferroni corrected list of outlier SNPs I found 83 SNPs associated with the first PC, 26 with the second PC, 144 with the third PC, 27 with the fourth PC, and 6 with the fifth PC. Out of the top ten PCADAPT outliers by Bonferroni corrected P-value, 6 were associated the third PC, 2 with the fourth PC, and 1 each with the first and second PCs (Table S.2).

In the environmental PCA that was used to generate the predictors for the pRDA outlier SNP analysis, ENV_PC1 was positively loaded for all of its component site-specific environmental variables (Figure S.4). ENV_PC2 was primarily positively loaded for precipitation in spring (April/May) and negatively loaded precipitation in summer (June/July) as well as positively loaded for solar radiation in summer. ENV_PC3 was primarily negatively loaded for precipitation in April through July and positively loaded for solar radiation in April through June; and positively loaded for maximum temperature in April through July.

The pRDA model (Figure 7) had an $R^2$ of 0.0196 and an adjusted $R^2$ of 0.0013. I found the full pRDA model to be significant ($F = 1.068$, df = 3, P < 0.001), and I found the first constrained RDA axis to be significant ($F_{RDA1} = 1.214$, df = 1, $P_{RDA1} < 0.001$), while RDA2 ($F_{RDA2} = 1.004$, df = 1, $P_{RDA2} = 0.842$) and RDA3 ($F_{RDA2} = 0.986$, df = 1, $P_{RDA2} = 0.665$) were not found to be significant. Significance in this case is defined as how well the full model, a given constrained axis, or a given predictor explains genetic variance that is not explained by latitude or longitude. The first two predictors, ENV_PC1 ($F_{ENV\_PC1} = 1.088$, df = 1, $P_{ENV\_PC1} < 0.001$) and ENV_PC2 ($F_{ENV\_PC2} = 1.124$, df = 1, $P_{ENV\_PC2} < 0.001$) were found to be significant, while I did not find ENV_PC3 ($F_{ENV\_PC3} = 0.992$, df = 1, $P_{ENV\_PC3} = 0.603$) to be significant.

In the pRDA, I found 87 unique SNPs to fall more than three standard deviations outside the mean loading on the first RDA axis. Of these, 2 SNPs were most correlated with ENV_PC1, 9 with ENV_PC2, and 76 with ENV_PC3 (Figure 7, Table S.7). Out of the top ten highest loaded pRDA outliers, 9 were most correlated with ENV_PC3, and 1 was most correlated with ENV_PC2, all were more correlated with both ENV_PC2 and ENV_PC3 than ENV_PC1 (Table S.3). There was one common outlier SNP between the Benjamini-Hochberg corrected PCADAPT outlier SNP set and the pRDA outliers, and there were no common outliers between the Bonferroni corrected PCADAPT outliers and the pRDA outliers.

*Gene Ontology Analysis:*

Out of the top ten outlier SNPs identified through the PCADAPT analysis, two fell within gene structures in the Yellow-rumped Warbler genome assembly and aligned to proteins in the eye when queried against the Zebra Finch proteome. LGSN is localized to the lens of the eye and PDE6C is localized to cone cells in the retina (O'Leary et al., 2016) (Table S.4). Both of these outlier SNPs were associated with the fourth PCADAPT PC (Table S.2).

Additionally, while they didn't fall directly within gene structures, two more of the top ten outlier SNPs identified with PCADAPT fell within 30,000 bases of gene structures in the Yellow-rumped Warbler genome assembly. The two nearest gene structures were 6,178 and 10,020 bases away and aligned to the proteins CABLES2 and MTF1, respectively, in the Zebra Finch proteome (Table S.4). CABLES2 is thought to be involved in regulation of the cell cycle and MTF1 is involved in the homeostatic regulation of heavy metals (O'Leary et al., 2016)

Of the top ten highest loaded pRDA outlier SNPs (Table S.3), three fell within gene structures in the Yellow-rumped Warbler genome assembly. These three gene structures aligned to the proteins OSBPL3, PALMD, and CDH22 (Table S.5). OSBPL3 is involved in cell adhesion and organization of the actin cytoskeleton, PALMD is predicted to be involved in regulation of cell shape, and CDH22 is involved in cell adhesion, primarily in neural and non-neural cells in the brain and neuroendocrine organs (O'Leary et al., 2016). SNP_94159 which fell within a gene structure aligning to CDH22, also fell within 30,000 bases of another gene structure that also aligned to CDH22 at a distance 21,968 bases (Table S.5).

An additional three out of the top ten outlier SNPs identified through pRDA fell within 30,000 bases of gene structures in the Yellow-rumped Warbler genome. The nearest gene structures to these three SNPs aligned to the proteins COPS4, FGGY, and INPP5K in the Zebra Finch proteome at distances of 28,356, 6,867, and 2,082 bases respectively (Table S.5). COPS4 encodes for a subunit of the COP9 signalosome which is an important regulator in multiple signaling pathways, FGGY is involved in carbohydrate phosphorylation, and INPP5K is predicted to be involved in regulation of the actin-cytoskeleton (O'Leary et al., 2016).

## Discussion:

### *Population Structure:*

My multi-locus PCA results support DeSaix et al (2019) in that I found weak population structure across the Prothonotary Warbler breeding range, primarily showing differentiation between eastern and western sites. This analysis also suggests there may be weak latitudinal structure among the western sites. I also found a positive correlation between genetic variation and geographic variation, demonstrating genetic variation in the species is in part explained by isolation by distance. This is consistent with Prothonotary Warblers showing high site fidelity and short natal dispersal distances (Hoover, 2003; McKim-Louder et al., 2013; Petit, 2020; Wood & Reasor, 2006).

I found conflicting results in determining the most likely number of genetic clusters in the STRUCTURE analysis, with $K = 1$ being the most likely based on L($K$), and $K = 3$ based on $\Delta K$. The standard deviations of both L($K$) estimates overlap, and $\Delta K$ cannot be calculated for $K = 1$. Performing more STRUCTURE runs with a higher number of MCMC steps could provide more accurate L($K$) estimates and might help resolve this discrepancy. Three clusters would match the PCA results showing weak structure longitudinally and latitudinal structure in the west, however that was not the case. Cluster assignment for $K = 3$ showed weak structure between eastern and western sites, and all birds had the highest assignment probability for the first of the three clusters. Two Ohio individuals were differentiated from the rest of the population in both the STRUCTURE analysis and the PCADAPT PCA projection plots, but were not observed to differentiate from the rest of the population in the multi-locus PCA. In cluster assignment barplots for $K = 3$, these two Ohio individuals along with three Virginia individuals had the highest assignment probabilities out of the entire population for the third of the three clusters.

These results differ from that of DeSaix et al. (2019), who found two to be the most likely number of genetic clusters with weak support for $K = 4$. I found cluster assignment plots in this study provide some support for the presence of two genetic clusters in the species in the Atlantic Seaboard and Mississippi alluvial valley. For $K = 4$, DeSaix et al. (2019) found additional clusters in Ohio and Virginia, similar to the Virginia and Ohio birds I found to differentiate for $K = 3$. The differences in results between this STRUCTURE analysis and those of DeSaix et al (2019) are most likely because I used my full SNP catalog in this STRUCTURE analysis while DeSaix et al. (2019) used a reduced set of 600 SNPs selected by $F_{ST}$.

Generally, most SNP loci in a catalog are neutral with regard to population structure; using a reduced SNP set selected by high $F_{ST}$ values introduces bias towards observing results displaying stronger population structure in a STRUCTURE analysis. Indeed, DeSaix et al. (2019) specifically elected to perform their STRUCTURE analysis with their reduced high $F_{ST}$ catalog for this reason, as the purpose of their study was to assess migratory connectivity in the Prothonotary Warbler. Given the weak population structure of the species as observed in all other assessments of population structure, the decision to use such a reduced SNP catalog by

DeSaix et al. (2019) for their STRUCTURE analysis facilitated the accuracy of their cluster assignments later in their analysis. However, the goal of this study was to assess population structure and identify potential genes under selection; therefore, I used the full SNP catalog in this STRUCTURE analysis. The differences between the two analyses might also be because I aligned reads to a reference genome during SNP catalog assembly, or because I used fewer MCMC steps. DeSaix et al. (2019) used 50,000 burn-in iterations and 100,000 MCMC steps, in comparison to 10,000 burn-ins and 20,000 MCMC steps in my initial runs. Again, conducting more STRUCTURE runs with a higher number of MCMC steps might improve the accuracy of my STRUCTURE analysis and help resolve the discrepancies between the two analyses.

Hierarchical estimations of genetic variation due to site ($F_{SC}$) and subregion ($F_{CT}$) indicated that sampling site and subregion account for equal amounts of deviation from Hardy-Weinberg equilibrium, with both showing weak genetic differentiation overall. If there were distinct subpopulations among Prothonotary Warblers, one would expect these hierarchical levels to account for a greater amount of genetic differentiation. This coupled with the lack of strong differentiation between eastern and western genetic clusters in my multi-locus PCA and STRUCTURE analysis suggests that there is substantial ongoing gene flow across the Prothonotary warbler breeding range and/or a recent divergence of large ancestral populations (Marko & Hart, 2011). These patterns of weak population structure are consistent with those observed in other Parulid species in the southeastern U.S. which show weak or no population structure across their ranges (Ball & Avise, 1992; Deane et al., 2013; Klein & Brown, 1994; Winker et al., 2000).

Although a previous study of southeastern North America seeking to identify phylogeographic barriers during the last glacial maximum did not identify any genetic discontinuities across the Appalachian Mountains in any of the avian species evaluated (Soltis et al., 2006), it would make sense to observe such a discontinuity in a bottomland forest specialist like the Prothonotary Warbler, as highlands such as the Appalachian Mountains present little suitable breeding habitat. This, paired with the high breeding site fidelity and short dispersal distances for offspring recruited as breeding adults observed in the species, could explain the longitudinal differentiation in population structure I observed.

*Outlier SNP Analysis:*

I found the PCs in the PCADAPT analysis to explain weak spatial population structure similar to that observed in the multi-locus PCA and STRUCTURE analysis, with the first PC highlighting the two Ohio birds noted above as being distinct from the rest of the population. As such, outlier SNPs found on these PC axes can likely be attributed to spatial adaptation, assuming they are not false positives. However, the majority of the top ten PCADAPT outliers were outliers on the third PC, which did not display any apparent spatial population structure. Further evaluation of this third PC is necessary to determine whether and what kind of population structure it describes.

The low $R^2$ values observed for the full model in the pRDA was not unexpected, considering it would be expected that most SNPs in the catalog would not show a relationship with the environmental predictors, (e.g., most SNPs will be neutrally loaded in the pRDA ordination space) (Forester et al., 2018). ANOVA-like permutation tests showed the full model, first constrained RDA axis, and first two environmental PCs to be significant in explaining genetic variance that was not explained by latitude and longitude. All of the pRDA outliers were found on RDA1, as this was the only constrained axis found to be significant.

As noted in my methods, in the variety of permutation test used here to evaluate predictor significance, the order in which the predictors are tested can affect their estimated significance. It may be that the third environmental PC was also significant in explaining genetic variance; further evaluation will be needed to determine if this is the case.

Despite finding ENV_PC3 to not be significant, the vast majority of the pRDA outliers were most correlated with ENV_PC3. Additionally, most pRDA outliers were more strongly correlated with ENV_PC2 and ENV_PC3 than ENV_PC1, despite ENV_PC1 accounting for the vast majority of variation explained in the environmental PCA. Given this pRDA was conditioned on latitude and longitude as covariates, the mismatch between the high proportion of environmental variation explained by ENV_PC1 in the environmental PCA with the low number of outliers found to be associated with ENV_PC1 could be explained by ENV_PC1 accounting for environmental variation due to latitude and longitude. Inspection of variable loadings for ENV_PC1 showed positive loadings for all environmental variables, which is what might be expected if ENV_PC1 primarily explained environmental variation between sites due to latitude and longitude. Inspection of variable loadings also show ENV_PC2 and ENV_PC3 appear to account for variation in precipitation and solar radiation in different periods of the breeding season, suggesting they may explain environmental variation that does not covary with latitude and longitude, which would explain why most of the pRDA outliers are more strongly correlated with them than ENV_PC1. Given the variable loadings of ENV_PC2 and ENV_PC3, it is possible that outlier SNPs correlated with either predictor are associated with variation in the seasonality of precipitation and solar radiation throughout the Prothonotary Warbler breeding range.

That there were almost no outlier SNPs shared in common between the two outlier SNP discovery methods is not unexpected. PCADAPT is intended for use in identifying outliers as a result of local adaptation (Luu et al., 2017), and the pRDA was conditioned on latitude and longitude in order to identify outlier SNPs solely associated with environment and not explained by geography. It should also be noted that the PCADAPT outliers are more likely to be false positive signals of selection, with an estimated false discovery rate of ~10% using these methods (Luu et al., 2020), than the pRDA outliers which have been shown to be very robust to false outlier discovery (Forester et al., 2018).

*Gene Ontology Analysis:*

Assuming outlier SNPs are true signals of selection, ontology analyses can still be unreliable at revealing biological processes under selection (Pavlidis et al., 2012). Although biological processes under selection could be revealed by the functions of genes near outlier loci due to linkage equilibrium or upstream regulatory sites, nuclear DNA is a complex molecular machine and it is possible for outlier loci to be true signals of selection while not being directly associated with the biological processes mediated by nearby genes. A 2012 simulation study found that there are practically unlimited interpretations of ontology results, and that it is easy to spin logical narratives of biological processes under selective pressure from false positive data (Pavlidis et al., 2012).

Acknowledging the possibility that the ontological signals identified in this study may not be indicators of biological processes under selection, it is interesting that out of the top ten lowest P-value SNPs from the PCADAPT analysis, the two SNPs that did fall within gene structures both aligned to proteins localized to the eye. Additionally, both of these outlier SNPs were the only two out of the top ten that were identified as outliers on the fourth PCADAPT PC, which showed weak longitudinal structure in projection plots. Beyond this being a false positive signal, possible explanations for why genes encoding proteins localized to the eye are hard to pin down without further investigation; however, I postulate some potential selective pressures relating to avian vision. Sexual selection is an important driver of evolution in birds, and among passerine birds, sensory system changes in females have been found to co-evolve with male plumage and display, presumably impacting female choice (Bloch, 2015; Fusani et al., 2014). One study investigating the expression of cone opsin proteins, which mediate color vision, in the retinas of sixteen species in *Parulidae* found the level of opsin expression in females across species to be associated with the degree of plumage dichromatism between males and females (Bloch, 2015). Given that selection on the sensory system due to female choice is already documented in other Parulid species, it may be that this is the mechanism that is applying selective pressure on these proteins localized to the eye in Prothonotary Warblers. A previous study found differences in carotenoid-based plumage coloration of both male and female Prothonotary Warblers, and different relationships between female coloration and metrics of individual quality such as reproductive success and apparent annual survival between populations in Arkansas and Virginia (Slevin et al., 2019). Given this evidence for longitudinal variation in sexual selection in Prothonotary Warblers, and that the fourth PC in the PCADAPT analysis showed weak longitudinal structure, this may indicate that the two outlier SNPs are a genomic signal of differences in sexual selection across the Prothonotary Warbler breeding range.

Light pollution poses challenges for several aspects of the biology and ecology of migratory songbirds. For nocturnally migrating songbirds like Prothonotary Warblers, light pollution can disrupt circadian rhythms, and cause disorientation during flight to the point where birds can be trapped by bright artificial sources of light when migrating over urban areas (Cabrera-Cruz et al., 2018). Prothonotary Warblers breeding in Atlantic and Mississippi Alluvial Valley regions could be experiencing differing levels of light pollution during annual migrations between their breeding and non-breeding sites. Light pollution is most apparent in the Atlantic Seaboard; light pollution appears to be less apparent in the Mississippi alluvial valley, albeit still pronounced (Horton et al., 2019; La Sorte et al., 2022). It may be that differing levels in light pollution experienced by eastern and western-breeding Prothonotary Warblers during migration are applying selective pressure to the sensory system as they are forced to navigate these hazards.

*Future Steps:*

For future population structure analyses in the Prothonotary Warbler, I recommend sampling birds from more sites across the breeding range, including locations at the farthest extents of the breeding range and from more inland sites away from the Atlantic Coastal Plain and Mississippi Alluvial Valley. These additional samples may determine if the longitudinal population structure observed in this study and by DeSaix et al. (2019) is also present in the east and may also highlight additional selective pressures away from the core of the breeding range. Additionally, as it appears that the Appalachian Mountains are a barrier to gene flow in the species, it would be interesting to sample birds across the Ouchitas and the Ozarks, to see if these mountains may have served as a barrier to dispersal.

In this study I aligned the reads to the Yellow-rumped Warbler genome assembly, which has been assembled to the chromosome level. Assuming synteny between the Yellow-rumped and Prothonotary Warbler genomes, this can be used to estimate the relative position of SNPs within the Prothonotary Warbler genome. In the future, SNPs should be filtered by linkage disequilibrium coefficient instead of only retaining one SNP per RAD tag. This method might allow retention of more SNPs in the final SNP catalog, which could further resolve the population structure of the species. Additionally, an assembly of the Prothonotary Warbler genome was recently published (Antonson et al., 2022). Although this genome has not yet been assembled to the chromosome level nor annotated, once this has occurred, aligning reads to the Prothonotary Warbler genome instead of the Yellow-rumped Warbler could provide a higher quality SNP catalog, allowing for better resolution of population genetic structure.

My outlier SNP gene ontology analysis was largely exploratory in nature. Further work is necessary to verify that the outlier genes identified are not false positives, and if so, determine what selective pressures are responsible. Complementing this PCADAPT analysis with an $F_{ST}$-based outlier SNP detection method, such as OUTFLANK (Whitlock & Lotterhos, 2015), may allow better identification of false positive outliers among the outlier SNP set. Conducting a full gene ontology analysis for all outlier SNPs may reveal patterns in ontologies under selective pressure that may not have been apparent from viewing only the top ten outliers from each detection method. These gene ontologies could be compared to a complementary gene ontology analysis of the entire SNP catalog to determine whether any ontologies are represented more than would be expected if the outliers were false positives. These steps would allow us to more firmly identify ontologies that are likely undergoing selective pressure.

Future Prothonotary Warbler gene expression and genotype-phenotype association studies could help resolve whether gene ontologies identified as being under selective pressure are not false positives. For example, while retinal gene expression studies have been conducted in other *Parulidae* species to investigate the relationship between female mate choice on sensory system evolution (Bloch, 2015), none have been done in Prothonotary Warblers. Previous morphological studies have demonstrated variation in plumage (Slevin et al., 2019) and body/egg size (Youtz et al., 2020) throughout the Prothonotary Warbler breeding range; future genome-wide association studies could help reveal a genomic mechanism for this variation.

*Conclusion:*

In this study, I observed similar patterns of weak longitudinal population structure as DeSaix et al. (2019) across various assessments of population structure in the Prothonotary Warbler. Only my STRUCTURE results differed significantly from the findings of DeSaix et al. (2019). The differences between these results were likely due to DeSaix et al. (2019) electing to use a reduced set of SNPs selected by high $F_{ST}$ values for their STRUCTURE analysis, in order to facilitate the accuracy of their cluster assignments for the purposes of assessing migratory connectivity.

I also conducted an exploratory analysis of gene ontologies potentially under selective pressure in the species, highlighting traits involving vision; however, further analysis is necessary to determine whether or not this signal is a false positive. Future gene expression and genome-wide association studies could be used to discern genomic mechanisms underpinning natural selection in the species, and confirm whether the ontologies identified in this exploratory analysis are false positives or not. A wider gene ontology analysis might also be able to reveal additional selective pressures for further investigation.

## Literature Cited:


"Alliance of Genome Resources Portal: unified model organism research platform." Nucleic acids research 48, no. D1 (2020): D650-D658.

Andrews, S. (2010). FastQC: a quality control tool for high throughput sequence data.

Antonson, N. D., Hauber, M. E., Schelsky, W. M., Scharf, H. M., Bulluck, L., Viverette, C., ... & Boves, T. J. (2022). The Complete Genome Sequence of Protonotaria citrea, the Prothonotary Warbler. Biodiversity Genomes.

Ball Jr, R. M., & Avise, J. C. (1992). Mitochondrial DNA phylogeographic differentiation among avian populations and the evolutionary significance of subspecies. The Auk, 109(3), 626-636.

Baiz, M. D., Wood, A. W., Brelsford, A., Lovette, I. J., & Toews, D. P. (2021). Pigmentation genes show evidence of repeated divergence and multiple bouts of introgression in Setophaga warblers. Current Biology, 31(3), 643-649.

Bay, R. A., Harrigan, R. J., Le Underwood, V., Gibbs, H. L., Smith, T. B., & Ruegg, K. (2018). Genomic signals of selection predict climate-driven population declines in a migratory bird. *Science*, *359*(6371), 83-86.

Bloch, N. I. (2015). Evolution of opsin expression in birds driven by sexual selection and habitat. Proceedings of the Royal Society B: Biological Sciences, 282(1798), 20142321.

Cabrera-Cruz, S. A., Smolinsky, J. A., & Buler, J. J. (2018). Light pollution is greatest within migration passage areas for nocturnally-migrating birds around the world. Scientific reports, 8(1), 1-8.

Catchen, J., Hohenlohe, P. A., Bassham, S., Amores, A., & Cresko, W. A. (2013). Stacks: an analysis tool set for population genomics. Molecular ecology, 22(11), 3124-3140.

Camacho, C., Coulouris, G., Avagyan, V., Ma, N., Papadopoulos, J., Bealer, K., & Madden, T. L. (2009). BLAST+: architecture and applications. BMC bioinformatics, 10(1), 1-9.

Danecek, P., Auton, A., Abecasis, G., Albers, C. A., Banks, E., DePristo, M. A., ... & McVean, G. (2011). The variant call format and VCFtools. Bioinformatics, 27(15), 2156-2158.

Deane, P. E., Mccoy, K. D., Robertson, R. J., Birt, T. P., & Friesen, V. L. (2013). Minimal Genetic Structure in the Cerulean Warbler Despite Evidence for Ecological Differentiation Among Populations: Estructura Genética Minima en Setophaga cerulea a Pesar de Evidencia de Diferenciación Ecológica entre Poblaciones. The Condor, 115(1), 178-185.

DeSaix, M. G., Bulluck, L. P., Eckert, A. J., Viverette, C. B., Boves, T. J., Reese, J. A., ... & Dyer, R. J. (2019). Population assignment reveals low migratory connectivity in a weakly structured songbird. Molecular ecology, 28(9), 2122-2135.

Dixon, P. (2003). VEGAN, a package of R functions for community ecology. *Journal of Vegetation Science*, *14*(6), 927-930.

Earl, D. A., & VonHoldt, B. M. (2012). STRUCTURE HARVESTER: a website and program for visualizing STRUCTURE output and implementing the Evanno method. Conservation genetics resources, 4(2), 359-361.

Ebird. (2017). eBird: An online database of bird distribution and abundance. eBird, Cornell Lab of Ornithology. (Accessed: July 22, 2022).

Esri Inc. (2022). ArcGIS Pro (Version 3.0). Esri Inc. https://www.esri.com/en-us/arcgis/products/arcgis-pro/overview.

Evanno, G., Regnaut, S., & Goudet, J. (2005). Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. Molecular ecology, 14(8), 2611-2620.

Fick, S.E. and R.J. Hijmans, 2017. WorldClim 2: new 1km spatial resolution climate surfaces for global land areas

Fink, D., T. Auer, A. Johnston, M. Strimas-Mackey, S. Ligocki, O. Robinson, W. Hochachka, L. Jaromczyk, A. Rodewald, C. Wood, I. Davies, A. Spencer. (2022). eBird Status and Trends, Data Version: 2021; Released: 2022. Cornell Lab of Ornithology, Ithaca, New York. https://doi.org/10.2173/ebirdst.2021

Forester, B. R., Lasky, J. R., Wagner, H. H., & Urban, D. L. (2018). Comparing methods for detecting multi-locus adaptation with multivariate genotype–environment associations. Molecular Ecology, 27(9), 2215-2233.

Fusani, L., Barske, J., Day, L. D., Fuxjager, M. J., & Schlinger, B. A. (2014). Physiological control of elaborate male courtship: female choice for neuromuscular systems. Neuroscience & Biobehavioral Reviews, 46, 534-546.

Goudet, J. (2005). Hierfstat, a package for R to compute and test hierarchical F statistics. *Molecular ecology notes*, *5*(1), 184-186.

Hijmans, R. J., Williams, E., Vennes, C., & Hijmans, M. R. J. (2017). Package ‘geosphere’. Spherical trigonometry, 1(7).

Huerta-Cepas, J., Szklarczyk, D., Heller, D., Hernández-Plaza, A., Forslund, S. K., Cook, H., ... & Bork, P. (2019). eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. Nucleic acids research, 47(D1), D309-D314.

Hohenstein, T.A. (2022). PROW_thesis_materials.

https://github.com/Tyler-Hohenstein/PROW_thesis_materials
Hoover, J. P. (2003). Decision rules for site fidelity in a migratory bird, the prothonotary warbler. Ecology, 84(2), 416-430.
Horton, K. G., Nilsson, C., Van Doren, B. M., La Sorte, F. A., Dokter, A. M., & Farnsworth, A. (2019). Bright lights in the big cities: migratory birds' exposure to artificial light. Frontiers in Ecology and the Environment, 17(4), 209-214.
Klein, N. K., & Brown, W. M. (1994). Intraspecific molecular phylogeny in the yellow warbler (Dendroica petechia), and implications for avian biogeography in the West Indies. Evolution, 48(6), 1914-1932.
Kopelman, N. M., Mayzel, J., Jakobsson, M., Rosenberg, N. A., & Mayrose, I. (2015). Clumpak: a program for identifying clustering modes and packaging population structure inferences across K. Molecular ecology resources, 15(5), 1179-1191.
Kriventseva, E. V., Kuznetsov, D., Tegenfeldt, F., Manni, M., Dias, R., Simão, F. A., & Zdobnov, E. M. (2019). OrthoDB v10: sampling the diversity of animal, plant, fungal, protist, bacterial and viral genomes for evolutionary and functional annotations of orthologs. Nucleic acids research, 47(D1), D807-D811.
de Lacerda, L. D., Borges, R., & Ferreira, A. C. (2019). Neotropical mangroves: Conservation and sustainable use in a scenario of global climate change. Aquatic Conservation: Marine and Freshwater Ecosystems, 29(8), 1347-1364.
Langmead, B., & Salzberg, S. L. (2012). Fast gapped-read alignment with Bowtie 2. *Nature methods*, *9*(4), 357-359.
La Sorte, F. A., Horton, K. G., Johnston, A., Fink, D., & Auer, T. (2022). Seasonal associations with light pollution trends for nocturnally migrating bird populations. Ecosphere, 13(3), e3994.
Legendre, P., & Legendre, L. (2012). Numerical ecology. Elsevier.
Luu, K., Bazin, E., & Blum, M. G. (2017). pcadapt: an R package to perform genome scans for selection based on principal component analysis. Molecular ecology resources, 17(1), 67-
Marko, P. B., & Hart, M. W. (2011). The complex analytical landscape of gene flow inference. Trends in ecology & evolution, 26(9), 448-456.
McKim-Louder, M. I., Hoover, J. P., Benson, T. J., & Schelsky, W. M. (2013). Juvenile survival in a Neotropical migratory songbird is lower than expected. PLoS One, 8(2), e56059.
O'Leary, N. A., Wright, M. W., Brister, J. R., Ciufo, S., Haddad, D., McVeigh, R., ... & Pruitt, K. D. (2016). Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic acids research, 44(D1), D733-D745.
Pardieck, K. L., D. J. Ziolkowski Jr., M. Lutmerding, V. I. Aponte, and M-A. R. Hudson (2020). North American Breeding Bird Survey Dataset 1966–2019: U.S. Geological Survey data release.
Partners in Flight. (2020). Population Estimates Database, version 3.1. Available at http://pif.birdconservancy.org/PopEstimates. (Accessed: December 10, 2022) .
Pavlidis, P., Jensen, J. D., Stephan, W., & Stamatakis, A. (2012). A critical assessment of storytelling: gene ontology categories and the importance of validating genomic scans. Molecular biology and evolution, 29(10), 3237-3248.

Petit, L. J. (2020). Prothonotary Warbler (Protonotaria citrea), version 1.0. In Birds of the World (A. F. Poole and F. B. Gill, Editors). Cornell Lab of Ornithology, Ithaca, NY, USA.
Puritz, J. B., Hollenbeck, C. M., & Gold, J. R. (2014). dDocent: a RADseq, variant-calling pipeline designed for population genomics of non-model organisms. PeerJ, 2, e431.
Pritchard, J. K., Stephens, M., & Donnelly, P. (2000). Inference of population structure using multi-locus genotype data. Genetics, 155(2), 945-959.
Privé, F., Luu, K., Vilhjálmsson, B. J., & Blum, M. G. (2020). Performing highly efficient genome scans for local adaptation with R package pcadapt version 4. Molecular Biology and Evolution, 37(7), 2153-2154.
Reid, N. M., Proestou, D. A., Clark, B. W., Warren, W. C., Colbourne, J. K., Shaw, J. R., ... & Whitehead, A. (2016). The genomic landscape of rapid repeated evolutionary adaptation to toxic pollution in wild fish. Science, 354(6317), 1305-1308.
Safran, M., Rosen, N., Twik, M., BarShir, R., Stein, T. I., Dahary, D., ... & Lancet, D. (2021). The genecards suite. In Practical guide to life science databases (pp. 27-56). Springer, Singapore.
Sauer, J.R., Link, W.A., and Hines, J.E. (2020). The North American Breeding Bird Survey, Analysis Results 1966 - 2019: U.S. Geological Survey data release, https://doi.org/10.5066/P96A7675.
Slevin, M. C., Bulluck, L. P., Matthews, A. E., & Boves, T. J. (2019). Spatial variation in carotenoid plumage coloration and relationships between female coloration and quality in Prothonotary Warblers (Protonotaria citrea). The Auk: Ornithological Advances, 136(2), ukz011.
Soltis, D. E., Morris, A. B., McLachlan, J. S., Manos, P. S., & Soltis, P. S. (2006). Comparative phylogeography of unglaciated eastern North America. Molecular ecology, 15(14), 4261-4293.
Toews, D. P., Taylor, S. A., Vallender, R., Brelsford, A., Butcher, B. G., Messer, P. W., & Lovette, I. J. (2016). Plumage genes and little else distinguish the genomes of hybridizing warblers. *Current Biology*, *26*(17), 2313-2318.
Wagner, D. N., Curry, R. L., Chen, N., Lovette, I. J., & Taylor, S. A. (2020). Genomic regions underlying metabolic and neuronal signaling pathways are temporally consistent in a moving avian hybrid zone. Evolution, 74(7), 1498-1513.
Walsh, J., Kovach, A. I., Olsen, B. J., Shriver, W. G., & Lovette, I. J. (2018). Bidirectional adaptive introgression between two ecologically divergent sparrow species. Evolution, 72(10), 2076-2089.
Warren, W. C., Clayton, D. F., Ellegren, H., Arnold, A. P., Hillier, L. W., Künstner, A., ... & Wilson, R. K. (2010). The genome of a songbird. Nature, 464(7289), 757-762.
Whitlock, M. C., & Lotterhos, K. E. (2015). Reliable detection of loci responsible for local adaptation: Inference of a null model through trimming the distribution of F ST. The American Naturalist, 186(S1), S24-S36.
Winker, K., Graves, G. R., & Braun, M. J. (2000). Genetic differentiation among populations of a migratory songbird: Limnothlypis swainsonii. Journal of Avian Biology, 31(3), 319-328.
Wood, D. R., & Reasor, J. (2006). Prothonotary Warbler reproductive success and site fidelity in

a fragmented Oklahoma landscape. North American Bird Bander, 31(1).
Youtz, J., Miller, K. D., Bowers, E. K., Rogers, S. L., Bulluck, L. P., Johnson, M., ... & Boves, T. J. (2020). Bergmann's rule is followed at multiple stages of postembryonic development in a long-distance migratory songbird. Ecology and Evolution, 10(19), 10672-10686.

**Appendix - Supplementary Tables and Figures:**

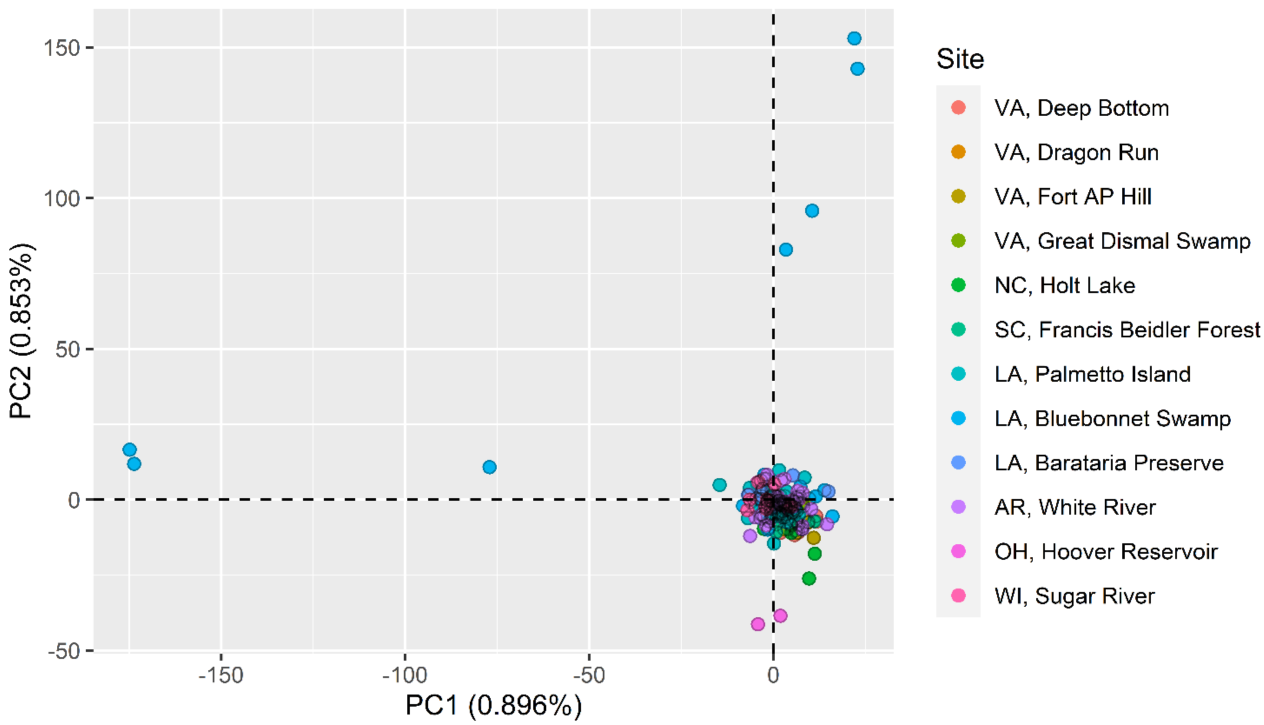


**Figure S.1:** Projection plot of PC1 and PC2 from initial multi-locus PCA before filtering out birds whose PCA coordinates exceeded six standard deviations from the mean of the first ten principal components over four iterations.

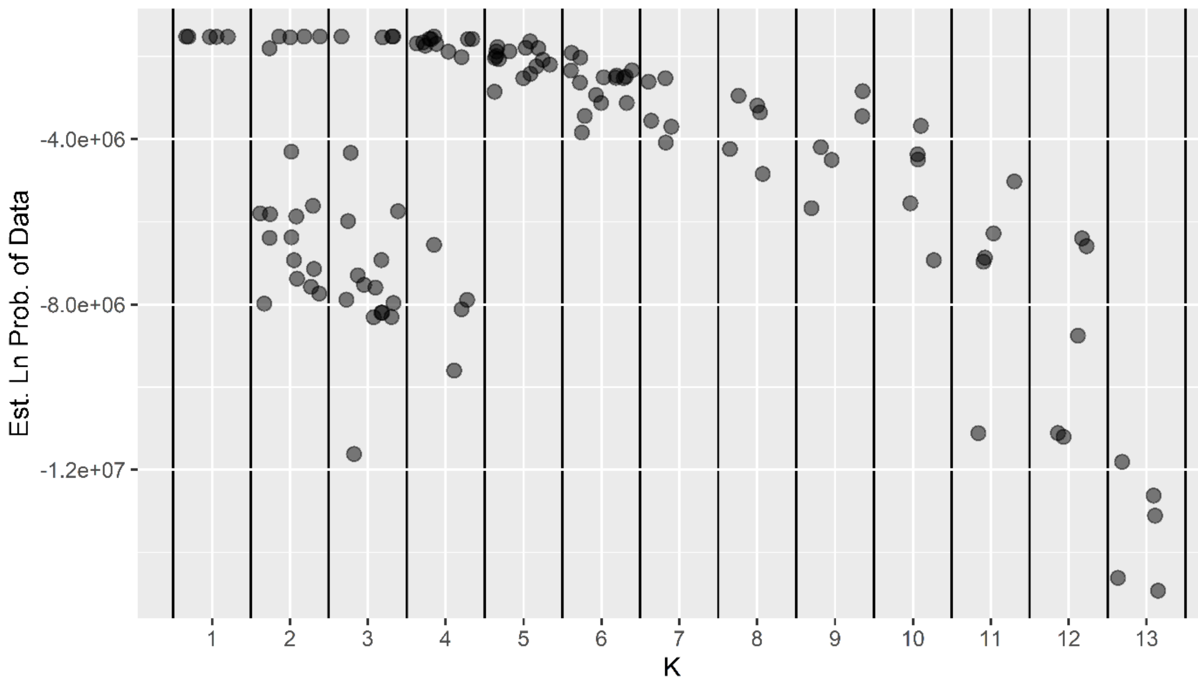


**Figure S.2:** Scatterplot of L(*K*) for all STRUCTURE MCMC runs.

**Table S.1:** Pairwise $F_{ST}$ by site.

| | VA_1 | VA_2 | VA_3 | VA_4 | NC_1 | SC_1 | LA_1 | LA_2 | LA_3 | AR_1 | OH_1 | WI_1 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **VA_1** | - | -0.0078 | 0.0120 | 0.0238 | 0.0153 | 0.0254 | 0.0462 | 0.0414 | 0.0506 | 0.0747 | 0.0174 | 0.0606 |
| **VA_2** | - | - | -0.0242 | -0.0096 | 0.0112 | 0.0104 | 0.0085 | -0.0039 | 0.0086 | 0.0474 | -0.0052 | 0.0453 |
| **VA_3** | - | - | - | 0.0039 | 0.0233 | 0.0352 | 0.0386 | 0.0335 | 0.0386 | 0.0532 | 0.0266 | 0.0386 |
| **VA_4** | - | - | - | - | 0.0287 | 0.0592 | 0.0279 | 0.0363 | 0.0297 | 0.0294 | 0.0483 | 0.0204 |
| **NC_1** | - | - | - | - | - | 0.0231 | 0.0240 | 0.0269 | 0.0276 | 0.0653 | 0.0262 | 0.0621 |
| **SC_1** | - | - | - | - | - | - | 0.0614 | 0.0301 | 0.0576 | 0.1186 | 0.0005 | 0.0991 |
| **LA_1** | - | - | - | - | - | - | - | 0.0062 | -0.0069 | 0.0172 | 0.0524 | 0.0230 |
| **LA_2** | - | - | - | - | - | - | - | - | -0.002 | 0.0473 | 0.0259 | 0.0462 |
| **LA_3** | - | - | - | - | - | - | - | - | - | 0.0179 | 0.0497 | 0.0244 |
| **AR_1** | - | - | - | - | - | - | - | - | - | - | 0.0975 | 0.0023 |
| **OH_1** | - | - | - | - | - | - | - | - | - | - | - | 0.0772 |
| **WI_1** | - | - | - | - | - | - | - | - | - | - | - | - |

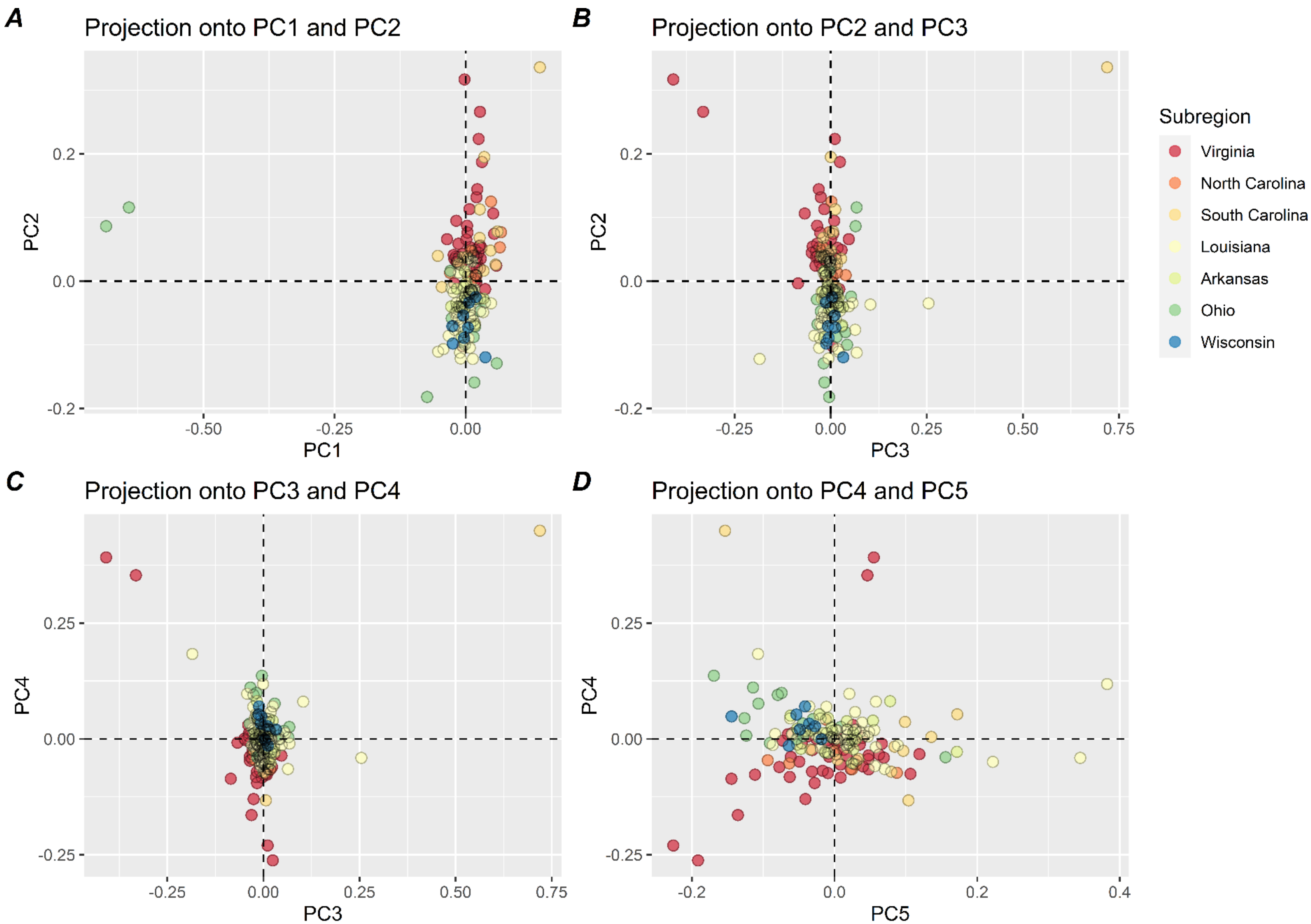


**Figure S.3:** PCADAPT projection plots for PCs 1 through 5.

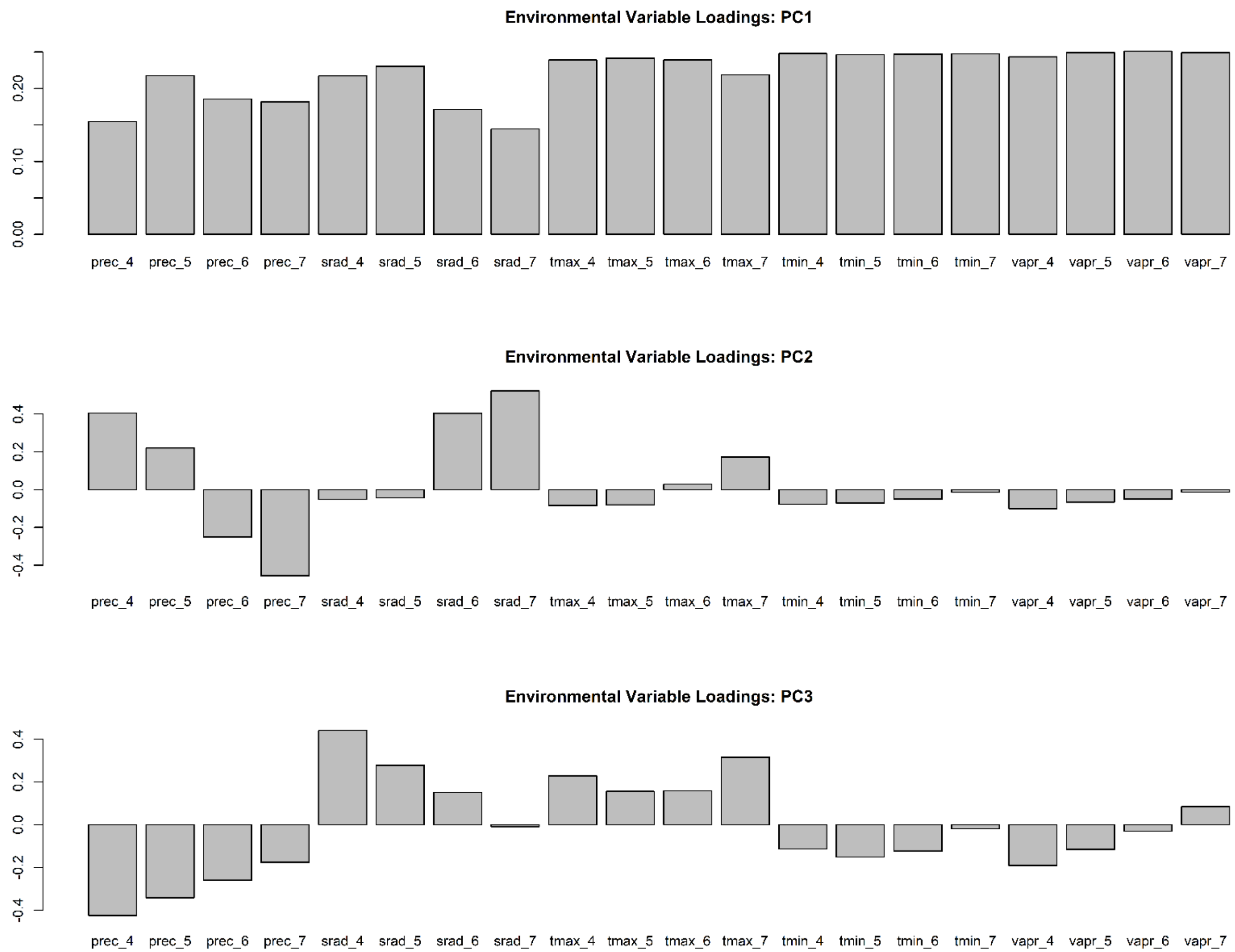


**Figure S.4:** Barplots of variable loadings from PCA of historical climate variables for the months of April through July (4 through 7, respectively); "prec" signifies monthly precipitation (mm), "srad" signifies monthly solar radiation (kJ $m^{-2}$ $day^{-1}$), "tmax" signifies maximum monthly temperature (°C), "tmin" signifies minimum monthly temperature (°C), and "vapr" signifies average monthly water vapor pressure (kPa).

**Table S.2:** PCADAPT candidate outlier SNPs with the top ten lowest Bonferroni-corrected P-values; "PC" denotes which PC axis on which the SNP was identified as an outlier in the PCADAPT analysis.

| SNP | contig | chromosome | position | PC | P |
|---|---|---|---|---|---|
| SNP_9302 | dDocent_Contig_6456 | CM027508.1 | 147575996 | 3 | 1.7634E-27 |
| SNP_5476 | dDocent_Contig_3929 | CM027509.1 | 3635042 | 3 | 5.1013E-27 |
| SNP_21015 | dDocent_Contig_14503 | CM027509.1 | 97802727 | 4 | 1.0398E-26 |
| SNP_40840 | dDocent_Contig_32337 | CM027512.1 | 19594425 | 4 | 9.5670E-26 |
| SNP_90741 | dDocent_Contig_86764 | CM027514.1 | 701148 | 3 | 2.1741E-24 |
| SNP_49978 | dDocent_Contig_41454 | CM027515.1 | 18211031 | 3 | 2.3744E-24 |
| SNP_5436 | dDocent_Contig_3906 | CM027516.1 | 17602659 | 2 | 6.0607E-23 |
| SNP_7077 | dDocent_Contig_5019 | CM027524.1 | 8372929 | 3 | 1.5116E-22 |
| SNP_32256 | dDocent_Contig_24103 | CM027525.1 | 10144679 | 1 | 5.6436E-22 |
| SNP_55945 | dDocent_Contig_47226 | CM027528.1 | 3229105 | 3 | 4.4306E-19 |

**Table S.3:** pRDA candidate outlier SNPs with the top ten highest loadings; "ENV_PC1," "ENV_PC2," and "ENV_PC3" show a given SNP's correlation coefficient with each of the three environmental PC predictor variables.

| SNP | contig | chromosome | Position | loading | ENV_PC1 | ENV_PC2 | ENV_PC3 |
|---|---|---|---|---|---|---|---|
| SNP_11960 | dDocent_Contig_69825 | CM027508.1 | 33004947 | 0.1162 | 0.0115 | 0.2108 | -0.3966 |
| SNP_79484 | dDocent_Contig_61975 | CM027510.1 | 55663997 | 0.1048 | -0.0422 | 0.2594 | -0.2790 |
| SNP_105087 | dDocent_Contig_125352 | CM027510.1 | 70915197 | 0.1015 | -0.0263 | 0.2315 | -0.2414 |
| SNP_96236 | dDocent_Contig_94189 | CM027537.1 | 17954856 | 0.0992 | -0.0116 | 0.1844 | -0.3183 |
| SNP_116288 | dDocent_Contig_72719 | CM027514.1 | 12384366 | 0.0971 | 0.0131 | 0.1932 | -0.3061 |
| SNP_69842 | dDocent_Contig_107075 | CM027514.1 | 27602081 | 0.0960 | 0.0108 | 0.1844 | -0.3030 |
| SNP_77047 | dDocent_Contig_8151 | CM027515.1 | 21092067 | 0.0937 | 0.0694 | 0.2213 | -0.2369 |
| SNP_94159 | dDocent_Contig_73524 | CM027517.1 | 16760017 | 0.0932 | -0.0108 | 0.1711 | -0.3704 |
| SNP_94924 | dDocent_Contig_91220 | CM027524.1 | 5020330 | 0.0930 | 0.0219 | 0.1759 | -0.3287 |
| SNP_80255 | dDocent_Contig_92198 | MDLI02000885.1 | 276 | 0.0916 | -0.0451 | 0.2428 | -0.1620 |

**Table S.4:** Annotation table for PCADAPT candidate outlier SNPs with lowest P-values. This table shows functional annotations for the SNPs listed in Table S.2 that fell within gene structures when aligned to the Yellow-rumped Warbler genome assembly. Rows in green indicate gene structures that overlapped with outlier SNP positions, while rows in blue indicate the closest gene structures to a given SNP in the absence of a gene structure overlapping with that SNP position. "Top BlastX result" lists the best protein alignment for a given gene structure when queried against the Zebra Finch proteome, with the e-value for that alignment given under "e-value." "Protein function" lists the functional annotation for the top BlastX result as given by GeneCards. "Ontology" lists functional ontology categories for the top BlastX result obtained from EggNOG (Huerta-Cepas et al., 2019) or OrthoDB (Kriventseva et al., 2019).

| SNP | gene distance | top BlastX result (gene) | e-value | protein function | ontology |
|---|---|---|---|---|---|
| SNP_21015 | 0 | LGSN | 0 | This gene encodes a protein with similarity to the GS I members of the glutamine synthetase superfamily. The encoded protein is referred to as a pseudo-glutamine synthetase because it has no glutamine synthesis activity and may function as a chaperone protein. This protein is localized to the lens and may be associated with cataract disease. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Jan 2009] | Amino acid transport and metabolism; glutamine synthetase [EggNOG]; localized to lens of eye |
| SNP_40840 | 0 | PDE6C | 3E-84 | This gene encodes the alpha-prime subunit of cone phosphodiesterase, which is composed of a homodimer of two alpha-prime subunits and 3 smaller proteins of 11, 13, and 15 kDa. Mutations in this gene are associated with cone dystrophy type 4 (COD4). [provided by RefSeq, Mar 2010] | Signal transduction mechanisms; 3',5'-cyclic-nucleotide phosphodiesterase activity [EggNOG]; localized to cone cells in the retina |

| | | | | | |
|---|---|---|---|---|---|
| SNP_40840 | 11415 | FRA10AC1 | 3E-16 | The protein encoded by this gene is a nuclear phosphoprotein of unknown function. This gene contains a tandem CGG repeat region within a CpG island that normally consists of 8-14 repeats but can expand to over 200 repeats. The repeat region is within the 5' UTR of some transcript variants, but is intronic to another variant. The expanded repeat allele is a fragile site and becomes hypermethylated, causing a reduction in gene expression. A disease phenotype has not been associated with expanded alleles. This gene is found within the rare FRA10A folate-sensitive fragile site. [provided by RefSeq, Dec 2016] | Posttranslational modification, protein turnover, chaperones; Transcription [OrthoDB] |
| SNP_40840 | 26115 | FFAR4 | 4E-69 | This gene encodes a G protein-coupled receptor (GPR) which belongs to the rhodopsin family of GPRs. The encoded protein functions as a receptor for free fatty acids, including omega-3, and participates in suppressing anti-inflammatory responses and insulin sensitizing. Multiple transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Feb 2012] | Post-translational modification, protein turnover, and chaperones; G-protein coupled receptor activity [EggNOG] |

| | | | | | |
|---|---|---|---|---|---|
| SNP_32256 | 6178 | CABLES2 | 1E-35 | Predicted to be involved in cell division and regulation of cell cycle. [provided by Alliance of Genome Resources, Apr 2022] | Post-translational modification, protein turnover, and chaperones; regulation of cell cycle [EggNOG] |
| SNP_55945 | 10020 | MTF1 | 3E-79 | This gene encodes a transcription factor that induces expression of metallothioneins and other genes involved in metal homeostasis in response to heavy metals such as cadmium, zinc, copper, and silver. The protein is a nucleocytoplasmic shuttling protein that accumulates in the nucleus upon heavy metal exposure and binds to promoters containing a metal-responsive element (MRE). [provided by RefSeq, Jul 2008] | Chromatin structure and dynamics; DNA binding [EggNOG] |
| SNP_55945 | 23585 | INPP5B | 8E-67 | This gene encodes a member of a family of inositol polyphosphate-5-phosphatases. These enzymes function in the regulation of calcium signaling by inactivating inositol phosphates. The encoded protein is localized to the cytosol and mitochondria, and associates with membranes through an isoprenyl modification near the C-terminus. Alternatively spliced transcript variants of this gene have been described. [provided by RefSeq, Jul 2014] | Function unknown; GTPase activator activity [EggNOG] |

| | | | | | |
|---|---|---|---|---|---|
| SNP_55945 | 26444 | YRDC | 3E-135 | Predicted to enable nucleotidyltransferase activity and tRNA binding activity. Acts upstream of or within negative regulation of transport. Predicted to be located in membrane and mitochondrion. Predicted to be active in cytoplasm. [provided by Alliance of Genome Resources, Apr 2022] | Translation, ribosomal structure and biogenesis; L-threonylcarbamoyladenylate synthase [EggNOG] |

**Table S.5:** Annotation table for pRDA candidate outlier SNPs with highest loadings. This table shows functional annotations for the SNPs listed in Table S.3 that fell within gene structures when aligned to the Yellow-rumped Warbler genome assembly. Rows in green indicate gene structures that overlapped with outlier SNP positions, while rows in blue indicate the closest gene structures to a given SNP in the absence of a gene structure overlapping with that SNP position. "Top BlastX result" lists the best protein alignment for a given gene structure when queried against the Zebra Finch proteome, with the e-value for that alignment given under "e-value." "Protein function" lists the functional annotation for the top BlastX result as given by GeneCards. "Ontology" lists functional ontology categories for the top BlastX result obtained from EggNOG (Huerta-Cepas et al., 2019) or OrthoDB (Kriventseva et al., 2019).

| SNP | gene distance | top blastx result (gene) | e-value | protein function | ontology |
|---|---|---|---|---|---|
| SNP_11960 | 0 | OSBPL3 | 2E-44 | This gene encodes a member of the oxysterol-binding protein (OSBP) family, a group of intracellular lipid receptors. Most members contain an N-terminal pleckstrin homology domain and a highly conserved C-terminal OSBP-like sterol-binding domain. The encoded protein is involved in the regulation of cell adhesion and organization of the actin cytoskeleton. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Aug 2013] | lipid transport [EggNOG] |
| SNP_11960 | 26382 | GSDME | 1E-37 | Hearing impairment is a heterogeneous condition with over 40 loci described. The protein encoded by this gene is expressed in fetal cochlea, however, its function is not known. Nonsyndromic hearing impairment is associated with a mutation in this gene. Three transcript variants encoding two different isoforms | transcription; sensory perception of sound [OrthoDB] |

| | | | | | |
|---|---|---|---|---|---|
| | | | | have been found for this gene. [provided by RefSeq, Jul 2008] | |
| SNP_79484 | 28356 | COPS4 | 5E-30 | This gene encodes one of eight subunits composing COP9 signalosome, a highly conserved protein complex that functions as an important regulator in multiple signaling pathways. The structure and function of COP9 signalosome is similar to that of the 19S regulatory particle of 26S proteasome. COP9 signalosome has been shown to interact with SCF-type E3 ubiquitin ligases and act as a positive regulator of E3 ubiquitin ligases. Two transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Apr 2012] | protein deneddylation [EggNOG] |
| SNP_116288 | 0 | PALMD | 0 | Predicted to be involved in regulation of cell shape. Predicted to be located in dendrite. Predicted to be active in cytoplasm. [provided by Alliance of Genome Resources, Apr 2022] | regulation of cell shape [EggNOG] |

| | | | | | |
|---|---|---|---|---|---|
| SNP_69842 | 6867 | FGGY | 1E-25 | This gene encodes a protein that phosphorylates carbohydrates such as ribulose, ribitol, and L-arabinitol. Genome-wide association studies in some populations have found an association between polymorphisms in this gene and sporadic amyotrophic lateral sclerosis, but studies of other populations have not been able to replicate this association. Alternative splicing results in multiple transcript variants. [provided by RefSeq, May 2013] | energy production and conversion; glycerol kinase activity [EggNOG] |
| SNP_77047 | 2082 | INPP5K | 2E-29 | This gene encodes a protein with 5-phosphatase activity toward polyphosphate inositol. The protein localizes to the cytosol in regions lacking actin stress fibers. It is thought that this protein may negatively regulate the actin cytoskeleton. Alternatively spliced transcript variants encoding different isoforms have been identified. [provided by RefSeq, Oct 2008] | signal transduction mechanisms; phosphatidylinositol dephosphorylation [EggNOG] |

| | | | | | |
|---|---|---|---|---|---|
| SNP_77047 | 22512 | MYO1C | 8E-33 | This gene encodes a member of the unconventional myosin protein family, which are actin-based molecular motors. The protein is found in the cytoplasm, and one isoform with a unique N-terminus is also found in the nucleus. The nuclear isoform associates with RNA polymerase I and II and functions in transcription initiation. The mouse ortholog of this protein also functions in intracellular vesicle transport to the plasma membrane. Multiple transcript variants encoding different isoforms have been found for this gene. The related gene myosin IE has been referred to as myosin IC in the literature, but it is a distinct locus on chromosome 19. [provided by RefSeq, Jul 2008] | microtubule-based movement [OrthoDB] |
| SNP_77047 | 24081 | PITPNA | 8E-29 | This gene encodes a member of a family of lipid-binding proteins that transfer molecules of phosphatidylinositol or phosphatidylcholine between membrane surfaces. The protein is implicated in phospholipase C signaling and in the production of phosphatidylinositol 3,4,5-trisphosphate (PIP3) by phosphoinositide-3-kinase.[provided by RefSeq, Sep 2009] | phospholipid transport [OrthoDB] |

| | | | | | |
|---|---|---|---|---|---|
| SNP_94159 | 0 | CDH22 | 3E-43 | This gene is a member of the cadherin superfamily. The gene product is composed of five cadherin repeat domains and a cytoplasmic tail similar to the highly conserved cytoplasmic region of classical cadherins. Expressed predominantly in the brain, this putative calcium-dependent cell adhesion protein may play an important role in morphogenesis and tissue formation in neural and non-neural cells during development and maintenance of the brain and neuroendocrine organs. [provided by RefSeq, Jul 2008] | homophilic cell adhesion via plasma membrane adhesion molecules [OrthoDB] |
| SNP_94159 | 21968 | CDH22 | 5E-92 | see above | see above |

**Table S.6:** PCADAPT candidate outlier SNPs; “PC” signifies which PC axis the SNP was identified as an outlier on; “P” denotes a SNP’s Bonferroni corrected P-value; a 1 under “Bonferroni correction” indicates that the SNP’s Bonferroni corrected P-value still fell below a nominal α-value of 0.05, a 0 indicates that the SNP was only included in the wider Benjamini-Hochberg corrected outlier SNP set.

| SNP | contig | chromosome | chromosome position | PC | P | Bonferroni correction |
|---|---|---|---|---|---|---|
| SNP_56 | dDocent_Contig_97 | CM027535.1 | 22805723 | 3 | 1.5380E-01 | 0 |
| SNP_828 | dDocent_Contig_593 | CM027510.1 | 41120210 | 2 | 9.0339E-03 | 1 |
| SNP_1197 | dDocent_Contig_914 | CM027507.1 | 83374609 | 3 | 2.0129E-01 | 0 |
| SNP_1295 | dDocent_Contig_974 | CM027514.1 | 412048 | 1 | 1.0008E-05 | 1 |
| SNP_1481 | dDocent_Contig_1137 | CM027508.1 | 6547169 | 3 | 2.2495E-10 | 1 |
| SNP_1613 | dDocent_Contig_1239 | CM027518.1 | 19681928 | 3 | 1.0000E+00 | 0 |
| SNP_1619 | dDocent_Contig_1244 | CM027509.1 | 11964998 | 1 | 1.3615E-05 | 1 |
| SNP_1856 | dDocent_Contig_1433 | CM027515.1 | 4684365 | 5 | 1.0000E+00 | 0 |
| SNP_1861 | dDocent_Contig_1435 | CM027510.1 | 56953055 | 3 | 2.0605E-09 | 1 |
| SNP_2120 | dDocent_Contig_1616 | CM027522.1 | 6403537 | 1 | 4.0459E-02 | 1 |
| SNP_2163 | dDocent_Contig_1640 | CM027508.1 | 10926149 | 2 | 2.1658E-10 | 1 |
| SNP_2353 | dDocent_Contig_1770 | CM027524.1 | 5154294 | 1 | 1.8509E-01 | 0 |
| SNP_2377 | dDocent_Contig_1790 | CM027528.1 | 6305063 | 1 | 1.9869E-07 | 1 |
| SNP_2493 | dDocent_Contig_1888 | CM027535.1 | 72316462 | 3 | 1.0000E+00 | 0 |
| SNP_2609 | dDocent_Contig_1973 | CM027536.1 | 19820062 | 2 | 1.0000E+00 | 0 |
| SNP_2643 | dDocent_Contig_1997 | CM027518.1 | 683762 | 1 | 1.8548E-16 | 1 |
| SNP_2655 | dDocent_Contig_2009 | CM027518.1 | 10092643 | 2 | 2.9248E-06 | 1 |
| SNP_2899 | dDocent_Contig_2203 | CM027511.1 | 60039528 | 1 | 1.0000E+00 | 0 |
| SNP_2921 | dDocent_Contig_2217 | CM027511.1 | 58550262 | 3 | 1.5243E-05 | 1 |
| SNP_3050 | dDocent_Contig_2326 | CM027532.1 | 3613275 | 3 | 3.2378E-01 | 0 |
| SNP_3060 | dDocent_Contig_2333 | CM027517.1 | 14087844 | 2 | 1.8046E-14 | 1 |
| SNP_3092 | dDocent_Contig_2355 | CM027531.1 | 3610395 | 1 | 3.5590E-01 | 0 |
| SNP_3238 | dDocent_Contig_2451 | CM027508.1 | 8207604 | 1 | 9.8747E-03 | 1 |
| SNP_3267 | dDocent_Contig_2483 | CM027508.1 | 53037454 | 1 | 4.7352E-05 | 1 |
| SNP_3285 | dDocent_Contig_2490 | CM027523.1 | 1725848 | 3 | 4.2269E-03 | 1 |
| SNP_3357 | dDocent_Contig_2537 | CM027513.1 | 1153248 | 3 | 1.0000E+00 | 0 |

| | | | | | | |
|---|---|---|---|---|---|---|
| SNP_3427 | dDocent_Contig_2594 | CM027512.1 | 718725 | 3 | 1.0000E+00 | 0 |
| SNP_3642 | dDocent_Contig_2758 | CM027529.1 | 2164220 | 1 | 7.4298E-10 | 1 |
| SNP_3677 | dDocent_Contig_2776 | CM027516.1 | 1519311 | 1 | 2.2830E-01 | 0 |
| SNP_3918 | dDocent_Contig_2936 | CM027518.1 | 1779461 | 1 | 3.8923E-02 | 1 |
| SNP_3938 | dDocent_Contig_2944 | CM027508.1 | 2479233 | 3 | 1.0000E+00 | 0 |
| SNP_3983 | dDocent_Contig_2971 | CM027522.1 | 11057494 | 2 | 5.7310E-03 | 1 |
| SNP_4003 | dDocent_Contig_2989 | CM027525.1 | 10828110 | 3 | 1.0000E+00 | 0 |
| SNP_4052 | dDocent_Contig_3025 | CM027517.1 | 15618714 | 1 | 9.3928E-03 | 1 |
| SNP_4231 | dDocent_Contig_3147 | CM027511.1 | 8377310 | 3 | 7.9299E-02 | 0 |
| SNP_4431 | dDocent_Contig_3278 | CM027512.1 | 6811836 | 3 | 1.0000E+00 | 0 |
| SNP_4485 | dDocent_Contig_3305 | CM027525.1 | 6107052 | 3 | 1.0013E-02 | 1 |
| SNP_4575 | dDocent_Contig_3352 | CM027535.1 | 64068649 | 5 | 1.1526E-01 | 0 |
| SNP_4816 | dDocent_Contig_3493 | CM027508.1 | 1.49E+08 | 4 | 2.5172E-06 | 1 |
| SNP_4992 | dDocent_Contig_3606 | CM027530.1 | 1631335 | 3 | 8.3050E-05 | 1 |
| SNP_5044 | dDocent_Contig_3642 | CM027536.1 | 64334702 | 1 | 2.2079E-01 | 0 |
| SNP_5101 | dDocent_Contig_3683 | CM027514.1 | 20048043 | 3 | 9.2254E-04 | 1 |
| SNP_5103 | dDocent_Contig_3685 | CM027536.1 | 4206382 | 1 | 3.7935E-01 | 0 |
| SNP_5179 | dDocent_Contig_3732 | CM027507.1 | 6606986 | 3 | 6.4070E-16 | 1 |
| SNP_5302 | dDocent_Contig_3827 | CM027529.1 | 846438 | 1 | 7.8072E-01 | 0 |
| SNP_5407 | dDocent_Contig_3891 | CM027517.1 | 11341196 | 1 | 3.3073E-06 | 1 |
| SNP_5436 | dDocent_Contig_3906 | CM027512.1 | 19594425 | 2 | 6.0607E-23 | 1 |
| SNP_5473 | dDocent_Contig_3926 | CM027520.1 | 8622956 | 1 | 1.0000E+00 | 0 |
| SNP_5476 | dDocent_Contig_3929 | CM027515.1 | 18211031 | 3 | 5.1013E-27 | 1 |
| SNP_5517 | dDocent_Contig_3957 | CM027520.1 | 5587659 | 1 | 1.0000E+00 | 0 |
| SNP_5536 | dDocent_Contig_3969 | CM027509.1 | 85467336 | 1 | 2.0052E-03 | 1 |
| SNP_5629 | dDocent_Contig_4024 | CM027518.1 | 778791 | 3 | 1.0000E+00 | 0 |
| SNP_5696 | dDocent_Contig_4058 | CM027511.1 | 10338547 | 4 | 1.0000E+00 | 0 |
| SNP_6254 | dDocent_Contig_4441 | CM027516.1 | 11964968 | 3 | 1.0000E+00 | 0 |
| SNP_6297 | dDocent_Contig_4468 | CM027537.1 | 55452 | 1 | 1.0000E+00 | 0 |
| SNP_6434 | dDocent_Contig_4560 | CM027525.1 | 10505041 | 3 | 1.0388E-05 | 1 |
| SNP_6570 | dDocent_Contig_4654 | CM027523.1 | 5174459 | 3 | 2.9006E-03 | 1 |

| | | | | | | |
|---|---|---|---|---|---|---|
| SNP_6575 | dDocent_Contig_4656 | CM027511.1 | 15641457 | 3 | 1.0000E+00 | 0 |
| SNP_6578 | dDocent_Contig_4659 | CM027510.1 | 61753849 | 3 | 1.5005E-07 | 1 |
| SNP_6756 | dDocent_Contig_4788 | CM027518.1 | 3177524 | 2 | 1.0000E+00 | 0 |
| SNP_6975 | dDocent_Contig_4930 | CM027510.1 | 64797379 | 1 | 2.7333E-07 | 1 |
| SNP_7064 | dDocent_Contig_5013 | CM027518.1 | 19219346 | 5 | 1.0000E+00 | 0 |
| SNP_7077 | dDocent_Contig_5019 | CM027528.1 | 3229105 | 3 | 1.5116E-22 | 1 |
| SNP_7147 | dDocent_Contig_5063 | CM027518.1 | 16102044 | 2 | 1.0000E+00 | 0 |
| SNP_7290 | dDocent_Contig_5152 | CM027529.1 | 734154 | 1 | 1.4830E-02 | 1 |
| SNP_7296 | dDocent_Contig_5155 | CM027515.1 | 23410678 | 4 | 3.5491E-09 | 1 |
| SNP_7553 | dDocent_Contig_5327 | CM027507.1 | 99543943 | 3 | 5.0282E-05 | 1 |
| SNP_7596 | dDocent_Contig_5351 | CM027515.1 | 24235541 | 3 | 8.2714E-05 | 1 |
| SNP_7608 | dDocent_Contig_5361 | CM027522.1 | 1697085 | 4 | 4.0954E-04 | 1 |
| SNP_7676 | dDocent_Contig_5394 | CM027519.1 | 3720021 | 1 | 1.4891E-03 | 1 |
| SNP_7743 | dDocent_Contig_5439 | CM027518.1 | 4821602 | 3 | 2.7369E-06 | 1 |
| SNP_7753 | dDocent_Contig_5446 | CM027515.1 | 21696524 | 1 | 1.0000E+00 | 0 |
| SNP_7865 | dDocent_Contig_5530 | CM027516.1 | 9205418 | 3 | 2.7098E-03 | 1 |
| SNP_7867 | dDocent_Contig_5533 | CM027507.1 | 73661275 | 1 | 9.1578E-05 | 1 |
| SNP_7915 | dDocent_Contig_5560 | CM027517.1 | 1861100 | 3 | 1.0000E+00 | 0 |
| SNP_7934 | dDocent_Contig_5568 | CM027507.1 | 35084218 | 4 | 1.0000E+00 | 0 |
| SNP_7958 | dDocent_Contig_5599 | CM027516.1 | 11025395 | 3 | 1.2859E-03 | 1 |
| SNP_7970 | dDocent_Contig_5610 | CM027510.1 | 61123902 | 1 | 6.9180E-07 | 1 |
| SNP_8081 | dDocent_Contig_5701 | CM027509.1 | 30539779 | 3 | 1.0000E+00 | 0 |
| SNP_8144 | dDocent_Contig_5744 | CM027509.1 | 40529034 | 1 | 1.0000E+00 | 0 |
| SNP_8212 | dDocent_Contig_5788 | CM027520.1 | 1157051 | 1 | 1.0000E+00 | 0 |
| SNP_8219 | dDocent_Contig_5791 | CM027524.1 | 2455427 | 3 | 9.1500E-16 | 1 |
| SNP_8226 | dDocent_Contig_5795 | CM027529.1 | 836274 | 3 | 2.5084E-08 | 1 |
| SNP_8319 | dDocent_Contig_5848 | CM027519.1 | 1150984 | 2 | 1.2794E-05 | 1 |
| SNP_8367 | dDocent_Contig_5885 | CM027507.1 | 1.08E+08 | 3 | 4.4862E-03 | 1 |
| SNP_8424 | dDocent_Contig_5927 | CM027514.1 | 25486126 | 3 | 6.9477E-09 | 1 |
| SNP_8440 | dDocent_Contig_5940 | CM027507.1 | 97207313 | 4 | 6.1338E-04 | 1 |
| SNP_8505 | dDocent_Contig_5977 | CM027518.1 | 17176531 | 3 | 1.0000E+00 | 0 |

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| SNP_8528 | dDocent_Contig_5988 | CM027537.1 | 8745674 | 3 | 1.0000E+00 | 0 |
| SNP_8708 | dDocent_Contig_6096 | CM027521.1 | 6105638 | 3 | 3.1820E-02 | 1 |
| SNP_8725 | dDocent_Contig_6105 | MDLI02001798.1 | 735 | 1 | 9.9832E-01 | 0 |
| SNP_8735 | dDocent_Contig_6109 | CM027509.1 | 18923206 | 1 | 1.0000E+00 | 0 |
| SNP_8809 | dDocent_Contig_6153 | CM027508.1 | 1.13E+08 | 1 | 1.0000E+00 | 0 |
| SNP_8826 | dDocent_Contig_6160 | CM027507.1 | 1.09E+08 | 3 | 6.5715E-04 | 1 |
| SNP_8842 | dDocent_Contig_6171 | CM027512.1 | 28478792 | 3 | 3.1166E-04 | 1 |
| SNP_8976 | dDocent_Contig_6249 | CM027537.1 | 19312253 | 1 | 1.0000E+00 | 0 |
| SNP_9086 | dDocent_Contig_6325 | CM027508.1 | 1.34E+08 | 1 | 1.0000E+00 | 0 |
| SNP_9128 | dDocent_Contig_6349 | CM027536.1 | 2179365 | 1 | 1.0000E+00 | 0 |
| SNP_9184 | dDocent_Contig_6389 | MDLI02000061.1 | 18982 | 4 | 1.0000E+00 | 0 |
| SNP_9302 | dDocent_Contig_6456 | CM027514.1 | 701148 | 3 | 1.7634E-27 | 1 |
| SNP_9308 | dDocent_Contig_6458 | CM027529.1 | 3650690 | 3 | 1.0000E+00 | 0 |
| SNP_9538 | dDocent_Contig_6599 | CM027531.1 | 5929584 | 5 | 1.0000E+00 | 0 |
| SNP_9559 | dDocent_Contig_6611 | CM027511.1 | 25967719 | 4 | 3.0787E-01 | 0 |
| SNP_9596 | dDocent_Contig_6638 | CM027515.1 | 4785564 | 2 | 6.7268E-02 | 0 |
| SNP_9742 | dDocent_Contig_6739 | CM027508.1 | 1.16E+08 | 3 | 1.0000E+00 | 0 |
| SNP_9806 | dDocent_Contig_6772 | CM027512.1 | 9792139 | 1 | 1.0000E+00 | 0 |
| SNP_9832 | dDocent_Contig_6788 | CM027533.1 | 3690683 | 2 | 1.0000E+00 | 0 |
| SNP_9965 | dDocent_Contig_6867 | CM027533.1 | 4190528 | 1 | 7.5388E-01 | 0 |
| SNP_10165 | dDocent_Contig_6985 | CM027527.1 | 2402085 | 3 | 1.0000E+00 | 0 |
| SNP_10218 | dDocent_Contig_7023 | CM027521.1 | 6899031 | 1 | 1.0000E+00 | 0 |
| SNP_10310 | dDocent_Contig_7103 | CM027512.1 | 29385488 | 3 | 5.3444E-01 | 0 |
| SNP_10370 | dDocent_Contig_7134 | CM027508.1 | 1.16E+08 | 3 | 8.5158E-04 | 1 |
| SNP_10382 | dDocent_Contig_7143 | CM027537.1 | 18579310 | 3 | 1.2478E-03 | 1 |
| SNP_10446 | dDocent_Contig_7179 | CM027507.1 | 98689017 | 1 | 1.0000E+00 | 0 |
| SNP_10561 | dDocent_Contig_7264 | CM027525.1 | 14792722 | 1 | 1.0000E+00 | 0 |
| SNP_10658 | dDocent_Contig_7330 | CM027507.1 | 1.01E+08 | 4 | 4.4651E-01 | 0 |
| SNP_10737 | dDocent_Contig_7380 | CM027531.1 | 2023566 | 5 | 1.0000E+00 | 0 |
| SNP_10768 | dDocent_Contig_7398 | CM027509.1 | 94542963 | 3 | 1.0000E+00 | 0 |
| SNP_10775 | dDocent_Contig_7405 | CM027510.1 | 2196662 | 1 | 2.6894E-06 | 1 |

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|---|---|---|---|---|---|---|
| SNP_10805 | dDocent_Contig_7418 | CM027527.1 | 741430 | 3 | 1.0000E+00 | 0 |
| SNP_10839 | dDocent_Contig_7434 | CM027507.1 | 20390091 | 1 | 1.0000E+00 | 0 |
| SNP_10955 | dDocent_Contig_7503 | CM027515.1 | 134176 | 1 | 1.1643E-05 | 1 |
| SNP_10987 | dDocent_Contig_7547 | CM027512.1 | 6456483 | 3 | 8.8442E-11 | 1 |
| SNP_11003 | dDocent_Contig_7555 | CM027511.1 | 3598760 | 4 | 1.9760E-01 | 0 |
| SNP_11024 | dDocent_Contig_7570 | CM027522.1 | 5316663 | 3 | 6.0618E-03 | 1 |
| SNP_11120 | dDocent_Contig_7629 | CM027512.1 | 28987921 | 3 | 3.4300E-07 | 1 |
| SNP_11151 | dDocent_Contig_7641 | CM027513.1 | 27224225 | 3 | 1.1531E-04 | 1 |
| SNP_11244 | dDocent_Contig_7682 | CM027509.1 | 645674 | 3 | 1.0000E+00 | 0 |
| SNP_11248 | dDocent_Contig_7687 | CM027510.1 | 61202394 | 1 | 1.7062E-02 | 1 |
| SNP_11263 | dDocent_Contig_7696 | CM027513.1 | 23389789 | 3 | 5.9278E-04 | 1 |
| SNP_11588 | dDocent_Contig_7912 | CM027510.1 | 4181058 | 4 | 1.0000E+00 | 0 |
| SNP_11608 | dDocent_Contig_7922 | CM027524.1 | 9941138 | 3 | 2.9197E-03 | 1 |
| SNP_11657 | dDocent_Contig_7961 | CM027537.1 | 4559369 | 3 | 1.0299E-04 | 1 |
| SNP_11721 | dDocent_Contig_7994 | CM027510.1 | 55294989 | 3 | 1.0000E+00 | 0 |
| SNP_11739 | dDocent_Contig_8005 | CM027536.1 | 54749060 | 3 | 1.0523E-03 | 1 |
| SNP_11752 | dDocent_Contig_8030 | CM027524.1 | 11260812 | 1 | 1.0000E+00 | 0 |
| SNP_11786 | dDocent_Contig_8050 | CM027508.1 | 1.24E+08 | 1 | 1.0000E+00 | 0 |
| SNP_11843 | dDocent_Contig_8088 | CM027515.1 | 4825701 | 2 | 1.0000E+00 | 0 |
| SNP_12106 | dDocent_Contig_8243 | CM027536.1 | 37870863 | 1 | 1.1314E-09 | 1 |
| SNP_12119 | dDocent_Contig_8269 | CM027507.1 | 25081838 | 4 | 4.4107E-05 | 1 |
| SNP_12178 | dDocent_Contig_8305 | CM027518.1 | 3094459 | 1 | 3.3849E-06 | 1 |
| SNP_12201 | dDocent_Contig_8320 | CM027513.1 | 29770011 | 2 | 1.3269E-12 | 1 |
| SNP_12335 | dDocent_Contig_8399 | CM027532.1 | 2335785 | 1 | 2.1067E-03 | 1 |
| SNP_12393 | dDocent_Contig_8439 | CM027537.1 | 9665534 | 3 | 2.8233E-04 | 1 |
| SNP_12443 | dDocent_Contig_8473 | CM027507.1 | 1.11E+08 | 3 | 1.0346E-02 | 1 |
| SNP_12483 | dDocent_Contig_8519 | CM027537.1 | 8338695 | 5 | 1.0000E+00 | 0 |
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| SNP_12640 | dDocent_Contig_8630 | CM027533.1 | 1101986 | 1 | 1.0000E+00 | 0 |
| SNP_12836 | dDocent_Contig_8743 | CM027508.1 | 4398557 | 3 | 1.3848E-02 | 1 |
| SNP_12993 | dDocent_Contig_8850 | CM027513.1 | 9968550 | 3 | 1.0114E-06 | 1 |

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|---|---|---|---|---|---|---|
| SNP_13009 | dDocent_Contig_8861 | CM027534.1 | 204460 | 1 | 1.0000E+00 | 0 |
| SNP_13076 | dDocent_Contig_8902 | CM027510.1 | 61921735 | 2 | 2.4833E-14 | 1 |
| SNP_13142 | dDocent_Contig_8950 | CM027507.1 | 567534 | 3 | 1.0000E+00 | 0 |
| SNP_13151 | dDocent_Contig_8955 | CM027507.1 | 40574819 | 1 | 1.2448E-03 | 1 |
| SNP_13209 | dDocent_Contig_8997 | CM027532.1 | 843560 | 4 | 7.5617E-01 | 0 |
| SNP_13213 | dDocent_Contig_8999 | CM027515.1 | 3105088 | 4 | 6.1452E-06 | 1 |
| SNP_13250 | dDocent_Contig_9019 | CM027517.1 | 16629963 | 1 | 1.0000E+00 | 0 |
| SNP_13537 | dDocent_Contig_9230 | CM027521.1 | 1511552 | 3 | 1.0000E+00 | 0 |
| SNP_13550 | dDocent_Contig_9243 | CM027512.1 | 9441044 | 1 | 1.0000E+00 | 0 |
| SNP_13564 | dDocent_Contig_9252 | CM027507.1 | 1.06E+08 | 3 | 1.4417E-11 | 1 |
| SNP_13732 | dDocent_Contig_9375 | CM027512.1 | 10180537 | 1 | 1.0000E+00 | 0 |
| SNP_13867 | dDocent_Contig_9475 | CM027533.1 | 2392602 | 1 | 5.7574E-06 | 1 |
| SNP_13969 | dDocent_Contig_9540 | CM027518.1 | 7114452 | 3 | 1.0000E+00 | 0 |
| SNP_14201 | dDocent_Contig_9683 | CM027528.1 | 227333 | 5 | 1.0000E+00 | 0 |
| SNP_14293 | dDocent_Contig_9733 | CM027509.1 | 71320427 | 1 | 1.4005E-02 | 1 |
| SNP_14303 | dDocent_Contig_9739 | CM027510.1 | 7573692 | 3 | 3.2090E-06 | 1 |
| SNP_14390 | dDocent_Contig_9792 | CM027512.1 | 2855064 | 3 | 1.1879E-06 | 1 |
| SNP_14493 | dDocent_Contig_9877 | CM027511.1 | 45494116 | 3 | 3.1490E-01 | 0 |
| SNP_14541 | dDocent_Contig_9908 | CM027536.1 | 20773411 | 3 | 2.2278E-07 | 1 |
| SNP_14617 | dDocent_Contig_9957 | CM027507.1 | 58901627 | 1 | 1.2051E-02 | 1 |
| SNP_14634 | dDocent_Contig_9971 | CM027509.1 | 4855155 | 3 | 1.0000E+00 | 0 |
| SNP_14674 | dDocent_Contig_9997 | CM027520.1 | 16249330 | 3 | 4.2433E-13 | 1 |
| SNP_14830 | dDocent_Contig_10087 | CM027522.1 | 11107443 | 4 | 1.0000E+00 | 0 |
| SNP_14838 | dDocent_Contig_10092 | CM027533.1 | 4649697 | 3 | 9.8575E-04 | 1 |
| SNP_14862 | dDocent_Contig_10103 | CM027536.1 | 56435804 | 1 | 1.0000E+00 | 0 |
| SNP_14884 | dDocent_Contig_10143 | CM027514.1 | 24765260 | 3 | 7.8863E-06 | 1 |
| SNP_14948 | dDocent_Contig_10190 | CM027514.1 | 25567119 | 4 | 3.6407E-01 | 0 |
| SNP_15007 | dDocent_Contig_10234 | CM027537.1 | 5527273 | 3 | 1.0000E+00 | 0 |
| SNP_15039 | dDocent_Contig_10254 | CM027507.1 | 6254728 | 3 | 7.2486E-12 | 1 |
| SNP_15045 | dDocent_Contig_10259 | CM027508.1 | 6729219 | 3 | 1.0000E+00 | 0 |
| SNP_15111 | dDocent_Contig_10304 | CM027529.1 | 1637812 | 5 | 1.0000E+00 | 0 |

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|---|---|---|---|---|---|---|
| SNP_15138 | dDocent_Contig_10324 | CM027510.1 | 10689696 | 3 | 3.8671E-06 | 1 |
| SNP_15183 | dDocent_Contig_10354 | CM027512.1 | 27111819 | 5 | 1.0000E+00 | 0 |
| SNP_15216 | dDocent_Contig_10367 | CM027521.1 | 4028145 | 1 | 1.0000E+00 | 0 |
| SNP_15262 | dDocent_Contig_10424 | CM027510.1 | 3822185 | 4 | 4.6683E-01 | 0 |
| SNP_15494 | dDocent_Contig_10591 | CM027512.1 | 28039564 | 1 | 1.0000E+00 | 0 |
| SNP_15650 | dDocent_Contig_10702 | CM027507.1 | 52091346 | 2 | 3.0022E-02 | 1 |
| SNP_15678 | dDocent_Contig_10716 | CM027536.1 | 68531401 | 1 | 1.0000E+00 | 0 |
| SNP_15691 | dDocent_Contig_10722 | CM027526.1 | 194385 | 1 | 3.0102E-04 | 1 |
| SNP_15764 | dDocent_Contig_10775 | CM027536.1 | 5744475 | 1 | 1.0000E+00 | 0 |
| SNP_15804 | dDocent_Contig_10798 | CM027514.1 | 3724905 | 1 | 3.8340E-01 | 0 |
| SNP_15823 | dDocent_Contig_10810 | CM027525.1 | 1646131 | 1 | 1.0000E+00 | 0 |
| SNP_15855 | dDocent_Contig_10833 | CM027529.1 | 4068073 | 4 | 8.0236E-01 | 0 |
| SNP_15898 | dDocent_Contig_10857 | CM027508.1 | 1.09E+08 | 1 | 2.2807E-05 | 1 |
| SNP_15933 | dDocent_Contig_10889 | CM027519.1 | 12403667 | 2 | 1.0000E+00 | 0 |
| SNP_15939 | dDocent_Contig_10894 | CM027535.1 | 43093065 | 1 | 1.0000E+00 | 0 |
| SNP_16046 | dDocent_Contig_11002 | CM027531.1 | 5535552 | 3 | 3.9537E-01 | 0 |
| SNP_16063 | dDocent_Contig_11016 | CM027507.1 | 86063389 | 4 | 5.8208E-03 | 1 |
| SNP_16074 | dDocent_Contig_11024 | CM027512.1 | 30044817 | 3 | 1.0000E+00 | 0 |
| SNP_16088 | dDocent_Contig_11034 | CM027509.1 | 24661948 | 1 | 3.9100E-02 | 1 |
| SNP_16110 | dDocent_Contig_11049 | CM027536.1 | 60152528 | 4 | 9.8834E-02 | 0 |
| SNP_16127 | dDocent_Contig_11064 | CM027512.1 | 816273 | 1 | 3.5130E-02 | 1 |
| SNP_16175 | dDocent_Contig_11089 | CM027508.1 | 1.33E+08 | 1 | 1.6858E-06 | 1 |
| SNP_16212 | dDocent_Contig_11115 | CM027511.1 | 38532232 | 3 | 4.2714E-02 | 1 |
| SNP_16227 | dDocent_Contig_11133 | CM027509.1 | 22018202 | 4 | 1.0000E+00 | 0 |
| SNP_16284 | dDocent_Contig_11167 | CM027518.1 | 3309780 | 3 | 4.1941E-05 | 1 |
| SNP_16548 | dDocent_Contig_11365 | CM027516.1 | 1090001 | 4 | 6.5571E-01 | 0 |
| SNP_16606 | dDocent_Contig_11402 | MDLI02000991.1 | 1680 | 1 | 1.0000E+00 | 0 |
| SNP_16703 | dDocent_Contig_11446 | CM027509.1 | 1.1E+08 | 3 | 1.0000E+00 | 0 |
| SNP_17120 | dDocent_Contig_11724 | CM027523.1 | 11445567 | 3 | 4.6604E-04 | 1 |
| SNP_17149 | dDocent_Contig_11743 | CM027520.1 | 6939757 | 1 | 1.0000E+00 | 0 |
| SNP_17171 | dDocent_Contig_11759 | CM027515.1 | 2844252 | 3 | 9.1838E-07 | 1 |

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|---|---|---|---|---|---|---|
| SNP_17282 | dDocent_Contig_11838 | MDLI02000034.1 | 59669 | 3 | 1.0369E-09 | 1 |
| SNP_17473 | dDocent_Contig_11994 | CM027511.1 | 54355487 | 2 | 1.0000E+00 | 0 |
| SNP_17587 | dDocent_Contig_12063 | CM027531.1 | 4133907 | 5 | 1.0000E+00 | 0 |
| SNP_17612 | dDocent_Contig_12073 | CM027536.1 | 885644 | 3 | 7.9314E-01 | 0 |
| SNP_17615 | dDocent_Contig_12075 | CM027533.1 | 1248792 | 5 | 1.0000E+00 | 0 |
| SNP_17670 | dDocent_Contig_12118 | CM027509.1 | 1.1E+08 | 1 | 5.9952E-14 | 1 |
| SNP_17777 | dDocent_Contig_12209 | CM027512.1 | 4407415 | 3 | 1.0000E+00 | 0 |
| SNP_17867 | dDocent_Contig_12268 | CM027525.1 | 9047058 | 1 | 5.0806E-17 | 1 |
| SNP_17886 | dDocent_Contig_12285 | CM027511.1 | 15348493 | 3 | 1.2859E-03 | 1 |
| SNP_18015 | dDocent_Contig_12357 | CM027509.1 | 93526151 | 3 | 1.0000E+00 | 0 |
| SNP_18067 | dDocent_Contig_12388 | CM027517.1 | 8272527 | 4 | 1.0938E-01 | 0 |
| SNP_18206 | dDocent_Contig_12505 | CM027524.1 | 10007810 | 1 | 1.0000E+00 | 0 |
| SNP_18327 | dDocent_Contig_12581 | CM027526.1 | 3323233 | 3 | 1.0000E+00 | 0 |
| SNP_18338 | dDocent_Contig_12589 | CM027516.1 | 2117078 | 1 | 4.0664E-02 | 1 |
| SNP_18499 | dDocent_Contig_12688 | CM027532.1 | 2887255 | 4 | 1.0000E+00 | 0 |
| SNP_18525 | dDocent_Contig_12704 | CM027510.1 | 6581237 | 3 | 1.2734E-04 | 1 |
| SNP_18547 | dDocent_Contig_12711 | CM027510.1 | 11044025 | 1 | 1.0000E+00 | 0 |
| SNP_18601 | dDocent_Contig_12745 | CM027521.1 | 13213412 | 1 | 5.1337E-05 | 1 |
| SNP_18602 | dDocent_Contig_12746 | CM027525.1 | 12246827 | 2 | 5.8872E-05 | 1 |
| SNP_18763 | dDocent_Contig_12882 | CM027511.1 | 46854039 | 3 | 6.3427E-04 | 1 |
| SNP_19008 | dDocent_Contig_13036 | CM027522.1 | 10823585 | 3 | 9.4563E-01 | 0 |
| SNP_19083 | dDocent_Contig_13090 | CM027508.1 | 1.09E+08 | 4 | 3.1117E-07 | 1 |
| SNP_19111 | dDocent_Contig_13108 | CM027509.1 | 1867691 | 4 | 2.6367E-02 | 1 |
| SNP_19188 | dDocent_Contig_13154 | CM027526.1 | 2395683 | 1 | 1.0000E+00 | 0 |
| SNP_19224 | dDocent_Contig_13220 | CM027508.1 | 1.49E+08 | 4 | 1.0000E+00 | 0 |
| SNP_19258 | dDocent_Contig_13239 | CM027509.1 | 899293 | 5 | 8.2291E-02 | 0 |
| SNP_19407 | dDocent_Contig_13332 | CM027517.1 | 1369709 | 1 | 9.6471E-01 | 0 |
| SNP_19427 | dDocent_Contig_13341 | CM027509.1 | 17098624 | 5 | 1.0000E+00 | 0 |
| SNP_19538 | dDocent_Contig_13404 | CM027512.1 | 34134748 | 5 | 9.1311E-01 | 0 |
| SNP_19623 | dDocent_Contig_13467 | CM027510.1 | 12015258 | 3 | 1.5326E-12 | 1 |
| SNP_19649 | dDocent_Contig_13486 | CM027520.1 | 10803330 | 3 | 2.4539E-01 | 0 |

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| SNP_19807 | dDocent_Contig_13627 | CM027536.1 | 568487 | 3 | 1.0000E+00 | 0 |
| SNP_19909 | dDocent_Contig_13686 | CM027521.1 | 3379410 | 3 | 6.4125E-04 | 1 |
| SNP_20025 | dDocent_Contig_13754 | CM027510.1 | 55898851 | 3 | 1.1378E-06 | 1 |
| SNP_20032 | dDocent_Contig_13758 | CM027536.1 | 10564169 | 1 | 1.0000E+00 | 0 |
| SNP_20066 | dDocent_Contig_13780 | CM027511.1 | 14077592 | 1 | 1.0000E+00 | 0 |
| SNP_20275 | dDocent_Contig_13964 | CM027531.1 | 4984447 | 1 | 1.0000E+00 | 0 |
| SNP_20306 | dDocent_Contig_13990 | CM027507.1 | 1.13E+08 | 3 | 6.7031E-01 | 0 |
| SNP_20374 | dDocent_Contig_14036 | CM027527.1 | 3346318 | 3 | 1.2555E-01 | 0 |
| SNP_20507 | dDocent_Contig_14113 | CM027513.1 | 36233266 | 1 | 1.0000E+00 | 0 |
| SNP_20519 | dDocent_Contig_14128 | CM027509.1 | 1005704 | 3 | 1.0000E+00 | 0 |
| SNP_20529 | dDocent_Contig_14132 | CM027520.1 | 7816210 | 3 | 1.0000E+00 | 0 |
| SNP_20558 | dDocent_Contig_14154 | CM027514.1 | 30280042 | 2 | 1.0000E+00 | 0 |
| SNP_20589 | dDocent_Contig_14171 | CM027508.1 | 1.22E+08 | 1 | 9.8416E-05 | 1 |
| SNP_20644 | dDocent_Contig_14203 | CM027509.1 | 1.07E+08 | 3 | 1.0000E+00 | 0 |
| SNP_20723 | dDocent_Contig_14255 | CM027508.1 | 7610698 | 1 | 1.0000E+00 | 0 |
| SNP_20909 | dDocent_Contig_14429 | CM027535.1 | 68177589 | 2 | 1.0563E-02 | 1 |
| SNP_21000 | dDocent_Contig_14493 | CM027522.1 | 6556008 | 1 | 4.0300E-04 | 1 |
| SNP_21015 | dDocent_Contig_14503 | CM027508.1 | 1.48E+08 | 4 | 1.0398E-26 | 1 |
| SNP_21393 | dDocent_Contig_14790 | CM027508.1 | 1.38E+08 | 3 | 2.0777E-15 | 1 |
| SNP_21401 | dDocent_Contig_14800 | CM027536.1 | 64070660 | 1 | 1.0000E+00 | 0 |
| SNP_21424 | dDocent_Contig_14818 | CM027526.1 | 3872710 | 3 | 5.8645E-08 | 1 |
| SNP_21440 | dDocent_Contig_14833 | CM027515.1 | 18512703 | 1 | 1.0000E+00 | 0 |
| SNP_21509 | dDocent_Contig_14877 | CM027513.1 | 9835555 | 3 | 1.0000E+00 | 0 |
| SNP_21511 | dDocent_Contig_14879 | CM027521.1 | 7616577 | 1 | 6.8496E-02 | 0 |
| SNP_21517 | dDocent_Contig_14883 | CM027512.1 | 32335828 | 2 | 1.0000E+00 | 0 |
| SNP_21523 | dDocent_Contig_14887 | CM027520.1 | 9534285 | 2 | 1.0000E+00 | 0 |
| SNP_21609 | dDocent_Contig_14944 | CM027507.1 | 24599663 | 3 | 9.6879E-02 | 0 |
| SNP_21633 | dDocent_Contig_14960 | CM027536.1 | 38466628 | 1 | 1.0000E+00 | 0 |
| SNP_21663 | dDocent_Contig_14979 | CM027507.1 | 868127 | 1 | 1.1520E-02 | 1 |
| SNP_21690 | dDocent_Contig_14999 | CM027513.1 | 6634450 | 3 | 1.9123E-09 | 1 |
| SNP_21731 | dDocent_Contig_15086 | CM027507.1 | 1.11E+08 | 3 | 1.7824E-05 | 1 |

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| SNP_21758 | dDocent_Contig_15105 | CM027535.1 | 8182128 | 4 | 9.3645E-03 | 1 |
| SNP_21839 | dDocent_Contig_15160 | CM027513.1 | 2587083 | 4 | 1.3626E-01 | 0 |
| SNP_21874 | dDocent_Contig_15184 | CM027511.1 | 56730221 | 3 | 3.4372E-16 | 1 |
| SNP_21886 | dDocent_Contig_15190 | CM027508.1 | 1.42E+08 | 4 | 1.0000E+00 | 0 |
| SNP_21956 | dDocent_Contig_15233 | CM027507.1 | 22814669 | 3 | 6.8481E-13 | 1 |
| SNP_22048 | dDocent_Contig_15294 | CM027523.1 | 11231200 | 5 | 1.0000E+00 | 0 |
| SNP_22155 | dDocent_Contig_15361 | CM027520.1 | 2462994 | 3 | 2.4441E-04 | 1 |
| SNP_22356 | dDocent_Contig_15545 | CM027536.1 | 63713240 | 1 | 4.9163E-03 | 1 |
| SNP_22393 | dDocent_Contig_15570 | CM027515.1 | 24287309 | 2 | 1.5287E-01 | 0 |
| SNP_22436 | dDocent_Contig_15600 | CM027518.1 | 12486363 | 1 | 1.0000E+00 | 0 |
| SNP_22441 | dDocent_Contig_15603 | CM027509.1 | 94505130 | 1 | 3.5612E-13 | 1 |
| SNP_22534 | dDocent_Contig_15648 | CM027520.1 | 14941261 | 1 | 1.0000E+00 | 0 |
| SNP_22747 | dDocent_Contig_15790 | CM027518.1 | 20136657 | 3 | 2.3099E-03 | 1 |
| SNP_22786 | dDocent_Contig_15824 | CM027536.1 | 241199 | 3 | 4.5208E-07 | 1 |
| SNP_22830 | dDocent_Contig_15925 | CM027512.1 | 16388378 | 2 | 1.4778E-02 | 1 |
| SNP_23030 | dDocent_Contig_16035 | CM027513.1 | 11382563 | 1 | 1.0000E+00 | 0 |
| SNP_23109 | dDocent_Contig_16076 | CM027508.1 | 98516756 | 1 | 1.0000E+00 | 0 |
| SNP_23132 | dDocent_Contig_16093 | CM027512.1 | 32029421 | 5 | 1.0000E+00 | 0 |
| SNP_23172 | dDocent_Contig_16121 | CM027518.1 | 15431571 | 1 | 1.0000E+00 | 0 |
| SNP_23177 | dDocent_Contig_16124 | CM027524.1 | 834860 | 5 | 1.0000E+00 | 0 |
| SNP_23216 | dDocent_Contig_16152 | CM027507.1 | 1.12E+08 | 4 | 1.0000E+00 | 0 |
| SNP_23241 | dDocent_Contig_16164 | CM027508.1 | 81058339 | 2 | 1.0000E+00 | 0 |
| SNP_23299 | dDocent_Contig_16202 | CM027536.1 | 3645229 | 3 | 1.5367E-05 | 1 |
| SNP_23311 | dDocent_Contig_16211 | CM027513.1 | 26740168 | 3 | 1.0000E+00 | 0 |
| SNP_23383 | dDocent_Contig_16251 | CM027511.1 | 59692648 | 1 | 6.0171E-05 | 1 |
| SNP_23401 | dDocent_Contig_16264 | CM027512.1 | 17702504 | 1 | 1.0000E+00 | 0 |
| SNP_23509 | dDocent_Contig_16411 | CM027523.1 | 7980344 | 1 | 3.8109E-01 | 0 |
| SNP_23514 | dDocent_Contig_16413 | CM027512.1 | 33089001 | 5 | 4.2056E-01 | 0 |
| SNP_23539 | dDocent_Contig_16429 | CM027513.1 | 32338509 | 2 | 1.0000E+00 | 0 |
| SNP_23558 | dDocent_Contig_16441 | CM027509.1 | 42164935 | 1 | 2.7081E-08 | 1 |
| SNP_23689 | dDocent_Contig_16520 | CM027518.1 | 17305395 | 2 | 1.0000E+00 | 0 |

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| SNP_23702 | dDocent_Contig_16526 | MDLI02000105.1 | 8668 | 1 | 1.0000E+00 | 0 |
| SNP_23740 | dDocent_Contig_16545 | CM027507.1 | 11210391 | 1 | 9.9109E-01 | 0 |
| SNP_23776 | dDocent_Contig_16571 | CM027513.1 | 22456108 | 5 | 2.8664E-02 | 1 |
| SNP_24052 | dDocent_Contig_16842 | CM027514.1 | 980865 | 5 | 3.8365E-01 | 0 |
| SNP_24139 | dDocent_Contig_16895 | CM027523.1 | 7991711 | 1 | 1.1324E-01 | 0 |
| SNP_24143 | dDocent_Contig_16899 | CM027509.1 | 41105636 | 3 | 8.5950E-09 | 1 |
| SNP_24257 | dDocent_Contig_16971 | CM027520.1 | 13359476 | 1 | 1.0000E+00 | 0 |
| SNP_24314 | dDocent_Contig_17008 | CM027526.1 | 7241956 | 3 | 3.6113E-03 | 1 |
| SNP_24321 | dDocent_Contig_17012 | CM027523.1 | 8129121 | 2 | 4.0463E-01 | 0 |
| SNP_24696 | dDocent_Contig_17320 | CM027523.1 | 3751573 | 1 | 1.0000E+00 | 0 |
| SNP_24730 | dDocent_Contig_17344 | CM027513.1 | 16230870 | 5 | 7.5153E-03 | 1 |
| SNP_24991 | dDocent_Contig_17517 | CM027514.1 | 30347022 | 1 | 1.0000E+00 | 0 |
| SNP_25026 | dDocent_Contig_17534 | CM027513.1 | 1561945 | 1 | 1.0000E+00 | 0 |
| SNP_25037 | dDocent_Contig_17544 | CM027508.1 | 1.38E+08 | 4 | 9.2909E-05 | 1 |
| SNP_25068 | dDocent_Contig_17569 | CM027518.1 | 14894651 | 2 | 1.0000E+00 | 0 |
| SNP_25245 | dDocent_Contig_17753 | CM027516.1 | 13283275 | 5 | 1.0000E+00 | 0 |
| SNP_25270 | dDocent_Contig_17765 | CM027524.1 | 520992 | 1 | 1.0000E+00 | 0 |
| SNP_25308 | dDocent_Contig_17786 | CM027508.1 | 85373513 | 1 | 1.0000E+00 | 0 |
| SNP_25641 | dDocent_Contig_18025 | CM027508.1 | 89275308 | 1 | 1.0000E+00 | 0 |
| SNP_25706 | dDocent_Contig_18069 | CM027518.1 | 14477943 | 1 | 1.0000E+00 | 0 |
| SNP_25818 | dDocent_Contig_18229 | CM027517.1 | 8623907 | 1 | 1.3257E-07 | 1 |
| SNP_25819 | dDocent_Contig_18231 | CM027524.1 | 5211762 | 5 | 1.0000E+00 | 0 |
| SNP_25877 | dDocent_Contig_18271 | CM027530.1 | 1072954 | 2 | 1.0000E+00 | 0 |
| SNP_26000 | dDocent_Contig_18349 | CM027507.1 | 58248653 | 3 | 8.4568E-01 | 0 |
| SNP_26038 | dDocent_Contig_18366 | CM027511.1 | 18724963 | 3 | 6.0099E-09 | 1 |
| SNP_26153 | dDocent_Contig_18431 | CM027523.1 | 1835125 | 1 | 1.0000E+00 | 0 |
| SNP_26200 | dDocent_Contig_18476 | CM027536.1 | 68745796 | 3 | 1.0000E+00 | 0 |
| SNP_26340 | dDocent_Contig_18564 | CM027508.1 | 13849314 | 4 | 1.0000E+00 | 0 |
| SNP_26352 | dDocent_Contig_18571 | CM027518.1 | 15659077 | 5 | 4.9643E-01 | 0 |
| SNP_26460 | dDocent_Contig_18766 | CM027507.1 | 40800887 | 1 | 1.0000E+00 | 0 |
| SNP_26588 | dDocent_Contig_18855 | CM027517.1 | 4518373 | 3 | 1.1129E-02 | 1 |

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|---|---|---|---|---|---|---|
| SNP_26680 | dDocent_Contig_18910 | CM027511.1 | 49094477 | 1 | 1.0000E+00 | 0 |
| SNP_26816 | dDocent_Contig_19005 | CM027508.1 | 48710820 | 3 | 2.8681E-01 | 0 |
| SNP_26840 | dDocent_Contig_19030 | CM027519.1 | 4506097 | 1 | 1.0000E+00 | 0 |
| SNP_26864 | dDocent_Contig_19041 | CM027521.1 | 9144923 | 3 | 1.0000E+00 | 0 |
| SNP_26919 | dDocent_Contig_19073 | CM027537.1 | 14518129 | 2 | 1.0000E+00 | 0 |
| SNP_26947 | dDocent_Contig_19090 | CM027536.1 | 21285456 | 3 | 1.0000E+00 | 0 |
| SNP_27065 | dDocent_Contig_19293 | CM027531.1 | 58779 | 1 | 1.5806E-01 | 0 |
| SNP_27367 | dDocent_Contig_19486 | CM027510.1 | 46520781 | 2 | 2.9292E-01 | 0 |
| SNP_27541 | dDocent_Contig_19598 | CM027522.1 | 5912324 | 3 | 5.0853E-02 | 0 |
| SNP_27544 | dDocent_Contig_19600 | CM027507.1 | 2081873 | 1 | 1.0000E+00 | 0 |
| SNP_27577 | dDocent_Contig_19630 | CM027525.1 | 7342028 | 4 | 2.4973E-07 | 1 |
| SNP_27661 | dDocent_Contig_19810 | CM027515.1 | 22365863 | 2 | 1.0000E+00 | 0 |
| SNP_27667 | dDocent_Contig_19814 | MDLI02000204.1 | 331 | 1 | 1.0000E+00 | 0 |
| SNP_27713 | dDocent_Contig_19848 | CM027518.1 | 2570729 | 3 | 1.0000E+00 | 0 |
| SNP_27790 | dDocent_Contig_19894 | CM027512.1 | 1588093 | 3 | 2.4383E-05 | 1 |
| SNP_27858 | dDocent_Contig_19943 | CM027536.1 | 69129577 | 4 | 3.9580E-01 | 0 |
| SNP_28130 | dDocent_Contig_20127 | CM027536.1 | 28055442 | 2 | 1.0000E+00 | 0 |
| SNP_28143 | dDocent_Contig_20137 | CM027525.1 | 13184950 | 3 | 7.5309E-01 | 0 |
| SNP_28198 | dDocent_Contig_20194 | CM027510.1 | 16234944 | 2 | 2.8630E-01 | 0 |
| SNP_28264 | dDocent_Contig_20344 | CM027536.1 | 53298787 | 1 | 7.1002E-01 | 0 |
| SNP_28322 | dDocent_Contig_20378 | CM027508.1 | 52066019 | 1 | 1.0000E+00 | 0 |
| SNP_28491 | dDocent_Contig_20493 | CM027508.1 | 1.24E+08 | 3 | 9.4654E-01 | 0 |
| SNP_28538 | dDocent_Contig_20521 | CM027515.1 | 25282599 | 4 | 1.0000E+00 | 0 |
| SNP_28779 | dDocent_Contig_20695 | CM027508.1 | 1823094 | 4 | 1.0000E+00 | 0 |
| SNP_29082 | dDocent_Contig_21015 | CM027537.1 | 12860235 | 1 | 6.1597E-02 | 0 |
| SNP_29135 | dDocent_Contig_21050 | CM027509.1 | 47639130 | 1 | 1.0000E+00 | 0 |
| SNP_29165 | dDocent_Contig_21071 | CM027519.1 | 17084354 | 3 | 1.0000E+00 | 0 |
| SNP_29203 | dDocent_Contig_21093 | CM027528.1 | 2811409 | 3 | 1.0000E+00 | 0 |
| SNP_29318 | dDocent_Contig_21172 | CM027507.1 | 66756918 | 2 | 1.0000E+00 | 0 |
| SNP_29346 | dDocent_Contig_21196 | CM027507.1 | 1.04E+08 | 1 | 8.7817E-02 | 0 |
| SNP_29370 | dDocent_Contig_21212 | CM027510.1 | 65912923 | 1 | 3.9449E-01 | 0 |

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|---|---|---|---|---|---|---|
| SNP_29548 | dDocent_Contig_21485 | CM027522.1 | 633473 | 3 | 5.3685E-01 | 0 |
| SNP_29661 | dDocent_Contig_21567 | CM027525.1 | 4742934 | 4 | 1.0000E+00 | 0 |
| SNP_29766 | dDocent_Contig_21623 | CM027513.1 | 1830996 | 1 | 1.0000E+00 | 0 |
| SNP_29775 | dDocent_Contig_21626 | CM027508.1 | 38358647 | 3 | 9.4787E-09 | 1 |
| SNP_29854 | dDocent_Contig_21680 | CM027512.1 | 32558822 | 3 | 8.9025E-01 | 0 |
| SNP_29930 | dDocent_Contig_21725 | CM027511.1 | 6173203 | 4 | 5.7922E-05 | 1 |
| SNP_29937 | dDocent_Contig_21728 | CM027509.1 | 10613660 | 5 | 1.0000E+00 | 0 |
| SNP_29943 | dDocent_Contig_21740 | CM027535.1 | 25340680 | 3 | 1.1144E-08 | 1 |
| SNP_30092 | dDocent_Contig_21857 | CM027524.1 | 6566472 | 3 | 7.2739E-13 | 1 |
| SNP_30145 | dDocent_Contig_22051 | CM027508.1 | 1.04E+08 | 2 | 2.3847E-06 | 1 |
| SNP_30307 | dDocent_Contig_22162 | CM027510.1 | 43814745 | 1 | 1.0000E+00 | 0 |
| SNP_30345 | dDocent_Contig_22189 | CM027524.1 | 8425755 | 1 | 6.5130E-02 | 0 |
| SNP_30503 | dDocent_Contig_22334 | CM027523.1 | 9571515 | 3 | 1.0000E+00 | 0 |
| SNP_30509 | dDocent_Contig_22343 | CM027526.1 | 5674073 | 1 | 1.0000E+00 | 0 |
| SNP_30557 | dDocent_Contig_22374 | CM027511.1 | 53395597 | 1 | 8.1251E-04 | 1 |
| SNP_30597 | dDocent_Contig_22399 | CM027508.1 | 8035491 | 1 | 1.3896E-03 | 1 |
| SNP_30618 | dDocent_Contig_22418 | CM027536.1 | 47939008 | 1 | 1.0751E-02 | 1 |
| SNP_30641 | dDocent_Contig_22433 | CM027509.1 | 12265345 | 3 | 2.4956E-02 | 1 |
| SNP_30832 | dDocent_Contig_22721 | CM027516.1 | 3677675 | 3 | 2.7536E-03 | 1 |
| SNP_30933 | dDocent_Contig_22784 | CM027519.1 | 584503 | 3 | 1.0000E+00 | 0 |
| SNP_31015 | dDocent_Contig_22857 | CM027510.1 | 16229542 | 3 | 5.4334E-01 | 0 |
| SNP_31085 | dDocent_Contig_22905 | CM027512.1 | 25454444 | 2 | 6.4413E-02 | 0 |
| SNP_31089 | dDocent_Contig_22908 | CM027537.1 | 14420042 | 1 | 1.0000E+00 | 0 |
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| SNP_31344 | dDocent_Contig_23188 | CM027508.1 | 34690195 | 5 | 1.0000E+00 | 0 |
| SNP_31405 | dDocent_Contig_23306 | CM027511.1 | 27273243 | 4 | 1.0000E+00 | 0 |
| SNP_31417 | dDocent_Contig_23325 | CM027510.1 | 1446446 | 2 | 1.0000E+00 | 0 |
| SNP_31430 | dDocent_Contig_23333 | CM027507.1 | 3377611 | 3 | 1.0000E+00 | 0 |
| SNP_31445 | dDocent_Contig_23345 | CM027511.1 | 60846703 | 4 | 8.2018E-01 | 0 |
| SNP_31561 | dDocent_Contig_23428 | CM027507.1 | 26388270 | 2 | 1.0000E+00 | 0 |
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| SNP_32204 | dDocent_Contig_24065 | CM027508.1 | 1.48E+08 | 3 | 1.0000E+00 | 0 |
| SNP_32209 | dDocent_Contig_24068 | CM027513.1 | 36832138 | 1 | 1.0000E+00 | 0 |
| SNP_32256 | dDocent_Contig_24103 | CM027516.1 | 17602659 | 1 | 5.6436E-22 | 1 |
| SNP_32299 | dDocent_Contig_24131 | CM027514.1 | 30326496 | 1 | 1.0000E+00 | 0 |
| SNP_32309 | dDocent_Contig_24137 | CM027512.1 | 4610485 | 1 | 1.0000E+00 | 0 |
| SNP_32400 | dDocent_Contig_24191 | CM027515.1 | 8729641 | 4 | 1.0000E+00 | 0 |
| SNP_32573 | dDocent_Contig_24302 | CM027508.1 | 1.41E+08 | 4 | 1.0000E+00 | 0 |
| SNP_32866 | dDocent_Contig_24716 | CM027509.1 | 28542550 | 3 | 4.1303E-01 | 0 |
| SNP_32944 | dDocent_Contig_24768 | CM027524.1 | 2070933 | 2 | 3.1164E-01 | 0 |
| SNP_33014 | dDocent_Contig_24824 | CM027524.1 | 1118282 | 2 | 4.7775E-07 | 1 |
| SNP_33265 | dDocent_Contig_25028 | CM027515.1 | 15123370 | 1 | 8.2658E-03 | 1 |
| SNP_33326 | dDocent_Contig_25227 | CM027535.1 | 24480254 | 3 | 3.6584E-02 | 1 |
| SNP_33523 | dDocent_Contig_25382 | CM027521.1 | 8275186 | 3 | 1.6699E-12 | 1 |
| SNP_33621 | dDocent_Contig_25458 | CM027507.1 | 42221715 | 3 | 1.0000E+00 | 0 |
| SNP_33655 | dDocent_Contig_25489 | CM027516.1 | 968486 | 1 | 1.0000E+00 | 0 |
| SNP_33699 | dDocent_Contig_25518 | CM027508.1 | 59040865 | 1 | 1.0000E+00 | 0 |
| SNP_33726 | dDocent_Contig_25536 | CM027515.1 | 23365669 | 1 | 4.3507E-02 | 1 |
| SNP_33819 | dDocent_Contig_25602 | CM027511.1 | 11155025 | 1 | 1.0000E+00 | 0 |
| SNP_33823 | dDocent_Contig_25609 | CM027508.1 | 46076971 | 3 | 3.2060E-05 | 1 |
| SNP_33848 | dDocent_Contig_25620 | CM027536.1 | 64585189 | 4 | 1.0000E+00 | 0 |
| SNP_33908 | dDocent_Contig_25663 | CM027514.1 | 25684347 | 1 | 1.0000E+00 | 0 |
| SNP_34092 | dDocent_Contig_25957 | CM027519.1 | 4448106 | 1 | 2.3693E-01 | 0 |
| SNP_34204 | dDocent_Contig_26040 | CM027536.1 | 30547629 | 1 | 1.0000E+00 | 0 |
| SNP_34269 | dDocent_Contig_26093 | CM027524.1 | 2168924 | 4 | 9.0923E-01 | 0 |
| SNP_34493 | dDocent_Contig_26239 | CM027532.1 | 1192518 | 4 | 1.0000E+00 | 0 |
| SNP_34523 | dDocent_Contig_26258 | CM027510.1 | 14858361 | 3 | 6.6521E-07 | 1 |
| SNP_34804 | dDocent_Contig_26642 | CM027507.1 | 10662560 | 1 | 1.0000E+00 | 0 |
| SNP_35073 | dDocent_Contig_26839 | CM027536.1 | 65512443 | 3 | 4.6563E-05 | 1 |
| SNP_35284 | dDocent_Contig_26984 | CM027510.1 | 2057024 | 4 | 1.0000E+00 | 0 |
| SNP_35337 | dDocent_Contig_27026 | CM027509.1 | 66369722 | 3 | 7.1406E-03 | 1 |
| SNP_35347 | dDocent_Contig_27034 | CM027509.1 | 16730136 | 3 | 1.0000E+00 | 0 |

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| SNP_35382 | dDocent_Contig_27053 | CM027508.1 | 10346741 | 1 | 1.0000E+00 | 0 |
| SNP_35519 | dDocent_Contig_27298 | CM027525.1 | 10299483 | 3 | 1.3823E-10 | 1 |
| SNP_35827 | dDocent_Contig_27514 | CM027532.1 | 2050244 | 1 | 1.0000E+00 | 0 |
| SNP_35904 | dDocent_Contig_27565 | CM027517.1 | 18033073 | 2 | 1.0000E+00 | 0 |
| SNP_36137 | dDocent_Contig_27718 | CM027536.1 | 11874648 | 3 | 1.0000E+00 | 0 |
| SNP_36178 | dDocent_Contig_27746 | MDLI02000076.1 | 23762 | 3 | 7.9035E-12 | 1 |
| SNP_36201 | dDocent_Contig_27758 | CM027524.1 | 11261398 | 3 | 5.0408E-03 | 1 |
| SNP_36403 | dDocent_Contig_28088 | CM027518.1 | 2977833 | 1 | 3.7783E-05 | 1 |
| SNP_36464 | dDocent_Contig_28125 | CM027507.1 | 54733248 | 3 | 1.0478E-04 | 1 |
| SNP_36610 | dDocent_Contig_28231 | MDLI02000525.1 | 604 | 1 | 4.8278E-02 | 1 |
| SNP_36655 | dDocent_Contig_28255 | CM027511.1 | 17441466 | 1 | 1.0000E+00 | 0 |
| SNP_36813 | dDocent_Contig_28353 | CM027516.1 | 3542676 | 4 | 8.6313E-05 | 1 |
| SNP_37143 | dDocent_Contig_28752 | CM027516.1 | 18023024 | 3 | 1.9174E-01 | 0 |
| SNP_37147 | dDocent_Contig_28753 | CM027524.1 | 5165925 | 1 | 1.0000E+00 | 0 |
| SNP_37165 | dDocent_Contig_28768 | CM027510.1 | 46046852 | 2 | 1.0000E+00 | 0 |
| SNP_37175 | dDocent_Contig_28773 | CM027507.1 | 92974096 | 3 | 1.2270E-02 | 1 |
| SNP_37246 | dDocent_Contig_28833 | CM027536.1 | 7758090 | 1 | 1.0000E+00 | 0 |
| SNP_37305 | dDocent_Contig_28875 | CM027518.1 | 1095295 | 1 | 1.0000E+00 | 0 |
| SNP_37351 | dDocent_Contig_28901 | CM027509.1 | 33986075 | 3 | 1.4765E-08 | 1 |
| SNP_37509 | dDocent_Contig_29015 | CM027534.1 | 579073 | 1 | 2.2354E-03 | 1 |
| SNP_37579 | dDocent_Contig_29062 | CM027522.1 | 8698030 | 2 | 1.0000E+00 | 0 |
| SNP_37625 | dDocent_Contig_29091 | CM027513.1 | 10997999 | 3 | 1.0000E+00 | 0 |
| SNP_37649 | dDocent_Contig_29118 | CM027508.1 | 94865841 | 3 | 1.0000E+00 | 0 |
| SNP_37654 | dDocent_Contig_29124 | CM027537.1 | 18116124 | 1 | 5.2087E-06 | 1 |
| SNP_37871 | dDocent_Contig_29481 | CM027517.1 | 19326915 | 3 | 4.5267E-01 | 0 |
| SNP_37875 | dDocent_Contig_29483 | CM027507.1 | 97827375 | 4 | 1.0000E+00 | 0 |
| SNP_37953 | dDocent_Contig_29546 | CM027523.1 | 4109214 | 1 | 2.1189E-06 | 1 |
| SNP_38050 | dDocent_Contig_29613 | CM027511.1 | 54633046 | 1 | 1.0000E+00 | 0 |
| SNP_38093 | dDocent_Contig_29637 | CM027513.1 | 37282336 | 2 | 5.2822E-01 | 0 |
| SNP_38377 | dDocent_Contig_29848 | CM027508.1 | 1.41E+08 | 3 | 4.4901E-04 | 1 |
| SNP_38412 | dDocent_Contig_29873 | CM027508.1 | 1.19E+08 | 1 | 1.0000E+00 | 0 |

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| SNP_38417 | dDocent_Contig_29875 | CM027515.1 | 14021463 | 4 | 7.9634E-08 | 1 |
| SNP_38614 | dDocent_Contig_30221 | CM027531.1 | 614488 | 2 | 6.2055E-01 | 0 |
| SNP_38673 | dDocent_Contig_30266 | CM027517.1 | 14216651 | 2 | 1.0000E+00 | 0 |
| SNP_38686 | dDocent_Contig_30273 | CM027510.1 | 42515018 | 5 | 1.0000E+00 | 0 |
| SNP_39424 | dDocent_Contig_31057 | CM027528.1 | 1332493 | 2 | 1.0000E+00 | 0 |
| SNP_39436 | dDocent_Contig_31065 | CM027508.1 | 7661031 | 3 | 2.0170E-04 | 1 |
| SNP_39650 | dDocent_Contig_31211 | CM027517.1 | 1737909 | 5 | 2.9081E-03 | 1 |
| SNP_39680 | dDocent_Contig_31229 | CM027508.1 | 1.32E+08 | 3 | 1.0000E+00 | 0 |
| SNP_39994 | dDocent_Contig_31481 | CM027509.1 | 28732974 | 3 | 2.0069E-01 | 0 |
| SNP_40187 | dDocent_Contig_31820 | CM027510.1 | 21421609 | 4 | 1.0000E+00 | 0 |
| SNP_40213 | dDocent_Contig_31841 | CM027529.1 | 1613579 | 3 | 1.2999E-04 | 1 |
| SNP_40722 | dDocent_Contig_32232 | CM027511.1 | 14972219 | 3 | 3.6900E-02 | 1 |
| SNP_40820 | dDocent_Contig_32323 | CM027517.1 | 20030759 | 1 | 1.0000E+00 | 0 |
| SNP_40840 | dDocent_Contig_32337 | CM027525.1 | 10144679 | 4 | 9.5670E-26 | 1 |
| SNP_40919 | dDocent_Contig_32597 | CM027511.1 | 26990879 | 4 | 1.2232E-04 | 1 |
| SNP_41076 | dDocent_Contig_32716 | CM027508.1 | 98794215 | 3 | 2.2546E-01 | 0 |
| SNP_41123 | dDocent_Contig_32738 | CM027508.1 | 14032671 | 3 | 1.0000E+00 | 0 |
| SNP_41171 | dDocent_Contig_32785 | CM027524.1 | 7826608 | 3 | 3.8835E-13 | 1 |
| SNP_41253 | dDocent_Contig_32858 | CM027526.1 | 5032571 | 1 | 1.0000E+00 | 0 |
| SNP_41358 | dDocent_Contig_32944 | CM027516.1 | 14894948 | 4 | 7.6326E-01 | 0 |
| SNP_41576 | dDocent_Contig_33112 | CM027523.1 | 12133765 | 3 | 1.0000E+00 | 0 |
| SNP_41610 | dDocent_Contig_33140 | CM027516.1 | 9465400 | 3 | 3.5401E-16 | 1 |
| SNP_41671 | dDocent_Contig_33394 | CM027515.1 | 13740836 | 1 | 1.0000E+00 | 0 |
| SNP_41761 | dDocent_Contig_33452 | CM027507.1 | 96036615 | 2 | 1.0000E+00 | 0 |
| SNP_41789 | dDocent_Contig_33477 | CM027523.1 | 2463603 | 1 | 1.4112E-01 | 0 |
| SNP_41841 | dDocent_Contig_33522 | MDLI02000316.1 | 308 | 2 | 1.0000E+00 | 0 |
| SNP_41844 | dDocent_Contig_33523 | CM027537.1 | 5464259 | 1 | 1.2909E-05 | 1 |
| SNP_41880 | dDocent_Contig_33553 | CM027522.1 | 328411 | 1 | 1.0000E+00 | 0 |
| SNP_41944 | dDocent_Contig_33605 | CM027511.1 | 10855737 | 3 | 1.2095E-05 | 1 |
| SNP_42051 | dDocent_Contig_33676 | CM027522.1 | 7356383 | 4 | 1.0000E+00 | 0 |
| SNP_42193 | dDocent_Contig_33803 | CM027507.1 | 67597754 | 1 | 1.0000E+00 | 0 |

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| SNP_42221 | dDocent_Contig_33824 | CM027508.1 | 92494906 | 1 | 3.0033E-02 | 1 |
| SNP_42389 | dDocent_Contig_33940 | CM027510.1 | 46293100 | 5 | 8.2150E-06 | 1 |
| SNP_42425 | dDocent_Contig_33972 | CM027517.1 | 19897717 | 1 | 3.9738E-01 | 0 |
| SNP_42458 | dDocent_Contig_34181 | CM027526.1 | 4629902 | 4 | 1.0000E+00 | 0 |
| SNP_42459 | dDocent_Contig_34182 | CM027512.1 | 31619809 | 4 | 1.0000E+00 | 0 |
| SNP_42476 | dDocent_Contig_34196 | CM027508.1 | 49083329 | 3 | 1.0000E+00 | 0 |
| SNP_42550 | dDocent_Contig_34237 | CM027508.1 | 51595709 | 4 | 1.0000E+00 | 0 |
| SNP_42628 | dDocent_Contig_34295 | CM027508.1 | 1.44E+08 | 1 | 7.0115E-01 | 0 |
| SNP_42664 | dDocent_Contig_34322 | CM027536.1 | 46543511 | 2 | 1.0000E+00 | 0 |
| SNP_42774 | dDocent_Contig_34410 | CM027515.1 | 24874428 | 1 | 7.8460E-02 | 0 |
| SNP_42788 | dDocent_Contig_34424 | CM027519.1 | 12053545 | 3 | 1.5619E-06 | 1 |
| SNP_42798 | dDocent_Contig_34428 | CM027525.1 | 14199227 | 1 | 1.0000E+00 | 0 |
| SNP_42814 | dDocent_Contig_34436 | CM027509.1 | 39353026 | 4 | 3.4464E-02 | 1 |
| SNP_42890 | dDocent_Contig_34483 | CM027515.1 | 10015123 | 4 | 1.0000E+00 | 0 |
| SNP_42953 | dDocent_Contig_34523 | CM027507.1 | 10638830 | 3 | 1.0000E+00 | 0 |
| SNP_43194 | dDocent_Contig_34682 | CM027518.1 | 7933816 | 2 | 2.1771E-08 | 1 |
| SNP_43217 | dDocent_Contig_34702 | CM027509.1 | 78402711 | 3 | 1.0000E+00 | 0 |
| SNP_43324 | dDocent_Contig_34799 | CM027512.1 | 15955877 | 5 | 6.5027E-02 | 0 |
| SNP_43326 | dDocent_Contig_34800 | CM027509.1 | 16184464 | 5 | 1.0000E+00 | 0 |
| SNP_43467 | dDocent_Contig_35088 | CM027518.1 | 19018857 | 1 | 1.8444E-03 | 1 |
| SNP_43538 | dDocent_Contig_35136 | CM027508.1 | 36979122 | 3 | 3.8823E-01 | 0 |
| SNP_43768 | dDocent_Contig_35321 | CM027517.1 | 19008674 | 2 | 6.1616E-02 | 0 |
| SNP_43798 | dDocent_Contig_35345 | CM027514.1 | 6369061 | 1 | 1.0000E+00 | 0 |
| SNP_43818 | dDocent_Contig_35366 | CM027513.1 | 33452387 | 1 | 1.0000E+00 | 0 |
| SNP_43901 | dDocent_Contig_35427 | CM027507.1 | 2699944 | 3 | 1.0000E+00 | 0 |
| SNP_44093 | dDocent_Contig_35571 | CM027508.1 | 42216914 | 5 | 1.0000E+00 | 0 |
| SNP_44117 | dDocent_Contig_35586 | CM027513.1 | 29118546 | 3 | 1.0000E+00 | 0 |
| SNP_44234 | dDocent_Contig_35880 | CM027514.1 | 18913538 | 3 | 5.0868E-01 | 0 |
| SNP_44483 | dDocent_Contig_36066 | CM027507.1 | 97550322 | 1 | 3.9681E-02 | 1 |
| SNP_44661 | dDocent_Contig_36202 | CM027531.1 | 4612040 | 1 | 1.0000E+00 | 0 |
| SNP_44744 | dDocent_Contig_36258 | CM027509.1 | 43020121 | 5 | 1.0000E+00 | 0 |

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| SNP_45162 | dDocent_Contig_36774 | CM027512.1 | 20090170 | 1 | 1.0000E+00 | 0 |
| SNP_45173 | dDocent_Contig_36782 | CM027507.1 | 1.05E+08 | 1 | 1.0000E+00 | 0 |
| SNP_45231 | dDocent_Contig_36827 | CM027531.1 | 5731621 | 1 | 1.0000E+00 | 0 |
| SNP_45523 | dDocent_Contig_37082 | CM027521.1 | 4202711 | 3 | 8.7899E-02 | 0 |
| SNP_45545 | dDocent_Contig_37094 | CM027536.1 | 62388058 | 4 | 1.0000E+00 | 0 |
| SNP_45609 | dDocent_Contig_37146 | CM027524.1 | 6825282 | 2 | 2.0811E-02 | 1 |
| SNP_45748 | dDocent_Contig_37260 | CM027536.1 | 38996481 | 4 | 1.0000E+00 | 0 |
| SNP_45847 | dDocent_Contig_37332 | CM027513.1 | 25618317 | 3 | 1.0000E+00 | 0 |
| SNP_45849 | dDocent_Contig_37333 | CM027515.1 | 21820437 | 5 | 1.0000E+00 | 0 |
| SNP_46536 | dDocent_Contig_38066 | CM027511.1 | 10265415 | 3 | 1.3773E-06 | 1 |
| SNP_46598 | dDocent_Contig_38097 | CM027510.1 | 45397797 | 5 | 1.0000E+00 | 0 |
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| SNP_46878 | dDocent_Contig_38314 | CM027507.1 | 28673538 | 2 | 1.0000E+00 | 0 |
| SNP_47141 | dDocent_Contig_38719 | CM027512.1 | 9674509 | 3 | 1.0000E+00 | 0 |
| SNP_47244 | dDocent_Contig_38808 | CM027519.1 | 2932381 | 1 | 1.0000E+00 | 0 |
| SNP_47440 | dDocent_Contig_38956 | CM027507.1 | 43114258 | 3 | 1.0000E+00 | 0 |
| SNP_47767 | dDocent_Contig_39225 | CM027515.1 | 25584195 | 1 | 4.3961E-02 | 1 |
| SNP_47845 | dDocent_Contig_39297 | CM027517.1 | 4225999 | 2 | 1.0000E+00 | 0 |
| SNP_47888 | dDocent_Contig_39527 | CM027523.1 | 1023936 | 1 | 1.0000E+00 | 0 |
| SNP_47909 | dDocent_Contig_39540 | CM027514.1 | 26332883 | 1 | 1.0000E+00 | 0 |
| SNP_47911 | dDocent_Contig_39542 | CM027510.1 | 3123556 | 3 | 1.5810E-03 | 1 |
| SNP_48687 | dDocent_Contig_40166 | CM027517.1 | 8816989 | 1 | 1.0000E+00 | 0 |
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| SNP_48869 | dDocent_Contig_40457 | CM027510.1 | 67370171 | 3 | 1.0000E+00 | 0 |
| SNP_48959 | dDocent_Contig_40529 | CM027507.1 | 1.09E+08 | 4 | 8.0684E-05 | 1 |
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| SNP_49001 | dDocent_Contig_40557 | CM027508.1 | 59737445 | 1 | 1.0000E+00 | 0 |
| SNP_49027 | dDocent_Contig_40572 | CM027509.1 | 1.02E+08 | 4 | 1.0000E+00 | 0 |
| SNP_49124 | dDocent_Contig_40643 | CM027512.1 | 26276029 | 4 | 1.0000E+00 | 0 |

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| SNP_49203 | dDocent_Contig_40698 | CM027508.1 | 18686784 | 3 | 8.9833E-15 | 1 |
| SNP_49364 | dDocent_Contig_40811 | CM027523.1 | 4833908 | 1 | 7.4502E-02 | 0 |
| SNP_49417 | dDocent_Contig_40849 | CM027514.1 | 16000270 | 3 | 1.0000E+00 | 0 |
| SNP_49539 | dDocent_Contig_40959 | CM027525.1 | 12368813 | 4 | 1.0000E+00 | 0 |
| SNP_49656 | dDocent_Contig_41057 | CM027511.1 | 7690812 | 3 | 1.0000E+00 | 0 |
| SNP_49679 | dDocent_Contig_41068 | CM027536.1 | 59692986 | 1 | 1.0000E+00 | 0 |
| SNP_49844 | dDocent_Contig_41177 | CM027511.1 | 46822876 | 3 | 2.5623E-10 | 1 |
| SNP_49920 | dDocent_Contig_41406 | CM027509.1 | 78219677 | 3 | 9.3200E-02 | 0 |
| SNP_49978 | dDocent_Contig_41454 | CM027509.1 | 97802727 | 3 | 2.3744E-24 | 1 |
| SNP_50036 | dDocent_Contig_41496 | CM027537.1 | 14765393 | 3 | 3.2007E-11 | 1 |
| SNP_50176 | dDocent_Contig_41618 | CM027520.1 | 10108537 | 4 | 6.0001E-01 | 0 |
| SNP_50177 | dDocent_Contig_41619 | CM027511.1 | 3310135 | 1 | 1.1804E-02 | 1 |
| SNP_50457 | dDocent_Contig_41817 | CM027514.1 | 28448078 | 1 | 1.0000E+00 | 0 |
| SNP_50463 | dDocent_Contig_41821 | CM027514.1 | 19811094 | 4 | 6.3704E-02 | 0 |
| SNP_50714 | dDocent_Contig_42006 | CM027508.1 | 1.47E+08 | 5 | 6.1543E-03 | 1 |
| SNP_50946 | dDocent_Contig_42371 | CM027507.1 | 4537188 | 3 | 9.1495E-16 | 1 |
| SNP_51158 | dDocent_Contig_42540 | CM027517.1 | 7335952 | 1 | 4.3099E-01 | 0 |
| SNP_51267 | dDocent_Contig_42657 | CM027515.1 | 8260396 | 4 | 1.0000E+00 | 0 |
| SNP_51531 | dDocent_Contig_42844 | CM027512.1 | 5944856 | 3 | 1.0000E+00 | 0 |
| SNP_51587 | dDocent_Contig_42890 | CM027509.1 | 71818722 | 3 | 1.0000E+00 | 0 |
| SNP_51722 | dDocent_Contig_43007 | CM027537.1 | 2626951 | 3 | 1.0000E+00 | 0 |
| SNP_51967 | dDocent_Contig_43378 | CM027519.1 | 5669637 | 4 | 7.6345E-04 | 1 |
| SNP_51990 | dDocent_Contig_43400 | CM027507.1 | 14676287 | 1 | 1.0000E+00 | 0 |
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| SNP_52084 | dDocent_Contig_43489 | CM027511.1 | 44428156 | 4 | 1.0000E+00 | 0 |
| SNP_52451 | dDocent_Contig_43735 | CM027507.1 | 36301663 | 1 | 1.0000E+00 | 0 |
| SNP_52498 | dDocent_Contig_43774 | CM027526.1 | 694918 | 5 | 1.0000E+00 | 0 |
| SNP_52666 | dDocent_Contig_43918 | CM027507.1 | 35683921 | 1 | 3.0220E-01 | 0 |
| SNP_52852 | dDocent_Contig_44071 | CM027508.1 | 33231383 | 5 | 9.4347E-01 | 0 |
| SNP_53097 | dDocent_Contig_44468 | CM027512.1 | 17436089 | 3 | 1.0000E+00 | 0 |

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| SNP_53287 | dDocent_Contig_44639 | CM027520.1 | 3392452 | 1 | 4.2062E-02 | 1 |
| SNP_53381 | dDocent_Contig_44732 | CM027514.1 | 23048656 | 1 | 2.0013E-03 | 1 |
| SNP_53962 | dDocent_Contig_45414 | CM027507.1 | 35646796 | 3 | 1.6691E-04 | 1 |
| SNP_54164 | dDocent_Contig_45567 | CM027537.1 | 3819044 | 3 | 4.6962E-01 | 0 |
| SNP_54239 | dDocent_Contig_45637 | CM027513.1 | 14433504 | 5 | 1.0000E+00 | 0 |
| SNP_54388 | dDocent_Contig_45782 | CM027512.1 | 6909998 | 1 | 1.0000E+00 | 0 |
| SNP_54453 | dDocent_Contig_45831 | CM027536.1 | 61414164 | 3 | 1.0149E-06 | 1 |
| SNP_54458 | dDocent_Contig_45834 | CM027536.1 | 54209764 | 3 | 1.0000E+00 | 0 |
| SNP_54525 | dDocent_Contig_45894 | CM027510.1 | 18259383 | 3 | 1.0000E+00 | 0 |
| SNP_54540 | dDocent_Contig_45904 | CM027511.1 | 10407721 | 1 | 1.0000E+00 | 0 |
| SNP_54725 | dDocent_Contig_46051 | CM027508.1 | 4256023 | 1 | 1.0000E+00 | 0 |
| SNP_54838 | dDocent_Contig_46134 | CM027526.1 | 3358293 | 3 | 7.2934E-12 | 1 |
| SNP_54868 | dDocent_Contig_46153 | CM027509.1 | 36477219 | 3 | 1.5629E-05 | 1 |
| SNP_55088 | dDocent_Contig_46527 | CM027514.1 | 10258368 | 4 | 1.0000E+00 | 0 |
| SNP_55143 | dDocent_Contig_46575 | CM027525.1 | 3010175 | 3 | 3.4396E-04 | 1 |
| SNP_55320 | dDocent_Contig_46740 | CM027516.1 | 13093140 | 3 | 1.0000E+00 | 0 |
| SNP_55462 | dDocent_Contig_46850 | CM027510.1 | 50384739 | 1 | 7.3406E-04 | 1 |
| SNP_55502 | dDocent_Contig_46890 | CM027517.1 | 7953913 | 3 | 1.8524E-15 | 1 |
| SNP_55792 | dDocent_Contig_47088 | CM027536.1 | 25738722 | 2 | 1.0000E+00 | 0 |
| SNP_55859 | dDocent_Contig_47149 | CM027513.1 | 24024988 | 1 | 1.0000E+00 | 0 |
| SNP_55889 | dDocent_Contig_47170 | CM027508.1 | 18034819 | 2 | 9.7880E-01 | 0 |
| SNP_55945 | dDocent_Contig_47226 | CM027509.1 | 3635042 | 3 | 4.4306E-19 | 1 |
| SNP_56040 | dDocent_Contig_47304 | CM027511.1 | 13584400 | 4 | 3.2091E-06 | 1 |
| SNP_56324 | dDocent_Contig_47757 | CM027514.1 | 6402659 | 1 | 1.0000E+00 | 0 |
| SNP_56404 | dDocent_Contig_47824 | CM027515.1 | 20034643 | 3 | 5.0863E-03 | 1 |
| SNP_56488 | dDocent_Contig_47899 | CM027519.1 | 8294168 | 4 | 1.0000E+00 | 0 |
| SNP_56544 | dDocent_Contig_47944 | CM027508.1 | 60651048 | 2 | 1.0000E+00 | 0 |
| SNP_56669 | dDocent_Contig_48053 | CM027533.1 | 4637106 | 5 | 1.0000E+00 | 0 |
| SNP_56757 | dDocent_Contig_48126 | CM027508.1 | 66099921 | 3 | 2.5077E-06 | 1 |
| SNP_56939 | dDocent_Contig_48277 | CM027522.1 | 609458 | 3 | 8.8796E-01 | 0 |
| SNP_57240 | dDocent_Contig_48727 | CM027512.1 | 33672891 | 2 | 8.0848E-04 | 1 |

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| SNP_57273 | dDocent_Contig_48752 | CM027513.1 | 27914042 | 3 | 1.0000E+00 | 0 |
| SNP_57297 | dDocent_Contig_48786 | CM027507.1 | 220043 | 2 | 1.4823E-14 | 1 |
| SNP_57376 | dDocent_Contig_48858 | CM027509.1 | 1.09E+08 | 1 | 1.0000E+00 | 0 |
| SNP_57511 | dDocent_Contig_48984 | CM027508.1 | 55165470 | 5 | 6.2147E-01 | 0 |
| SNP_57641 | dDocent_Contig_49086 | CM027507.1 | 77524 | 1 | 1.9315E-01 | 0 |
| SNP_57819 | dDocent_Contig_49240 | CM027508.1 | 1.38E+08 | 3 | 4.4072E-04 | 1 |
| SNP_58012 | dDocent_Contig_49400 | CM027536.1 | 40068231 | 2 | 1.0000E+00 | 0 |
| SNP_58019 | dDocent_Contig_49408 | CM027507.1 | 34552226 | 3 | 9.4772E-18 | 1 |
| SNP_58320 | dDocent_Contig_49854 | CM027517.1 | 2713662 | 2 | 8.5760E-01 | 0 |
| SNP_58353 | dDocent_Contig_49879 | CM027515.1 | 25697068 | 1 | 9.4170E-04 | 1 |
| SNP_58449 | dDocent_Contig_49947 | CM027508.1 | 1.03E+08 | 1 | 2.9750E-06 | 1 |
| SNP_58465 | dDocent_Contig_49961 | CM027516.1 | 974168 | 1 | 1.0000E+00 | 0 |
| SNP_58627 | dDocent_Contig_50106 | CM027508.1 | 62965839 | 3 | 1.0000E+00 | 0 |
| SNP_58631 | dDocent_Contig_50110 | CM027515.1 | 8853476 | 1 | 1.0000E+00 | 0 |
| SNP_58888 | dDocent_Contig_50359 | CM027513.1 | 23881462 | 1 | 5.0144E-01 | 0 |
| SNP_59055 | dDocent_Contig_50507 | CM027516.1 | 4443657 | 3 | 1.0000E+00 | 0 |
| SNP_59218 | dDocent_Contig_50661 | CM027511.1 | 51476826 | 1 | 1.0000E+00 | 0 |
| SNP_59271 | dDocent_Contig_50707 | CM027522.1 | 1834850 | 1 | 1.9810E-04 | 1 |
| SNP_59378 | dDocent_Contig_50800 | CM027512.1 | 18997279 | 3 | 1.0000E+00 | 0 |
| SNP_59604 | dDocent_Contig_51194 | CM027509.1 | 48262080 | 1 | 7.8862E-01 | 0 |
| SNP_59654 | dDocent_Contig_51225 | CM027532.1 | 1452453 | 1 | 1.0000E+00 | 0 |
| SNP_59834 | dDocent_Contig_51387 | CM027525.1 | 4677635 | 1 | 1.3868E-01 | 0 |
| SNP_59846 | dDocent_Contig_51397 | CM027507.1 | 58855044 | 5 | 6.5473E-01 | 0 |
| SNP_60347 | dDocent_Contig_51815 | CM027516.1 | 10103149 | 4 | 1.0000E+00 | 0 |
| SNP_60840 | dDocent_Contig_52427 | CM027512.1 | 20521240 | 4 | 1.0000E+00 | 0 |
| SNP_60864 | dDocent_Contig_52446 | CM027512.1 | 17228989 | 3 | 1.0000E+00 | 0 |
| SNP_60958 | dDocent_Contig_52536 | CM027511.1 | 60666083 | 3 | 1.0000E+00 | 0 |
| SNP_61111 | dDocent_Contig_52659 | CM027507.1 | 596737 | 5 | 1.0000E+00 | 0 |
| SNP_61374 | dDocent_Contig_52882 | CM027515.1 | 8883073 | 1 | 1.2339E-01 | 0 |
| SNP_61813 | dDocent_Contig_53273 | CM027527.1 | 2116354 | 3 | 5.2017E-01 | 0 |
| SNP_61860 | dDocent_Contig_53326 | CM027524.1 | 531944 | 1 | 1.0000E+00 | 0 |

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| SNP_61919 | dDocent_Contig_53386 | CM027531.1 | 4069415 | 4 | 1.0000E+00 | 0 |
| SNP_61978 | dDocent_Contig_53624 | CM027521.1 | 4675061 | 4 | 5.5750E-02 | 0 |
| SNP_62027 | dDocent_Contig_53661 | CM027520.1 | 11936214 | 3 | 5.0847E-19 | 1 |
| SNP_62114 | dDocent_Contig_53740 | CM027536.1 | 45869633 | 1 | 4.6321E-05 | 1 |
| SNP_62285 | dDocent_Contig_53891 | CM027537.1 | 1790456 | 1 | 4.5084E-02 | 1 |
| SNP_62308 | dDocent_Contig_53913 | CM027507.1 | 62053287 | 4 | 1.0000E+00 | 0 |
| SNP_62534 | dDocent_Contig_54116 | CM027508.1 | 1.38E+08 | 1 | 1.0000E+00 | 0 |
| SNP_62735 | dDocent_Contig_54275 | CM027513.1 | 1386041 | 3 | 9.7738E-02 | 0 |
| SNP_62990 | dDocent_Contig_54505 | CM027509.1 | 9950438 | 5 | 1.0780E-01 | 0 |
| SNP_63012 | dDocent_Contig_54515 | CM027508.1 | 38356662 | 4 | 5.4431E-02 | 0 |
| SNP_63090 | dDocent_Contig_54592 | CM027517.1 | 4433534 | 1 | 1.0000E+00 | 0 |
| SNP_63103 | dDocent_Contig_54597 | CM027511.1 | 13221322 | 3 | 1.0000E+00 | 0 |
| SNP_63166 | dDocent_Contig_54672 | CM027510.1 | 46812152 | 1 | 1.0000E+00 | 0 |
| SNP_63240 | dDocent_Contig_54934 | CM027509.1 | 53545111 | 1 | 1.9790E-01 | 0 |
| SNP_63377 | dDocent_Contig_55054 | CM027507.1 | 92405830 | 1 | 1.0000E+00 | 0 |
| SNP_63398 | dDocent_Contig_55072 | CM027519.1 | 1067088 | 3 | 2.0364E-01 | 0 |
| SNP_63419 | dDocent_Contig_55100 | CM027512.1 | 27627138 | 1 | 1.0000E+00 | 0 |
| SNP_63529 | dDocent_Contig_55217 | CM027510.1 | 60083546 | 3 | 6.0088E-07 | 1 |
| SNP_64129 | dDocent_Contig_55780 | CM027520.1 | 3321011 | 1 | 1.0000E+00 | 0 |
| SNP_64440 | dDocent_Contig_56071 | CM027536.1 | 59771429 | 1 | 1.0000E+00 | 0 |
| SNP_64782 | dDocent_Contig_56532 | CM027523.1 | 2463609 | 4 | 9.0964E-01 | 0 |
| SNP_64803 | dDocent_Contig_56552 | CM027536.1 | 1782551 | 4 | 2.8062E-01 | 0 |
| SNP_65178 | dDocent_Contig_56895 | CM027509.1 | 70157491 | 5 | 1.0000E+00 | 0 |
| SNP_65216 | dDocent_Contig_56929 | CM027508.1 | 8028508 | 3 | 4.6392E-12 | 1 |
| SNP_65280 | dDocent_Contig_56976 | CM027526.1 | 7459979 | 3 | 3.0695E-01 | 0 |
| SNP_65412 | dDocent_Contig_57112 | CM027511.1 | 61066012 | 1 | 1.0000E+00 | 0 |
| SNP_65437 | dDocent_Contig_57130 | CM027536.1 | 26161044 | 3 | 1.0000E+00 | 0 |
| SNP_65471 | dDocent_Contig_57164 | CM027509.1 | 1.08E+08 | 1 | 1.0000E+00 | 0 |
| SNP_65617 | dDocent_Contig_57324 | CM027514.1 | 16984389 | 4 | 1.0000E+00 | 0 |
| SNP_65643 | dDocent_Contig_57354 | CM027508.1 | 52789624 | 4 | 3.2387E-03 | 1 |
| SNP_65850 | dDocent_Contig_57678 | CM027536.1 | 32118667 | 3 | 7.0501E-18 | 1 |

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|---|---|---|---|---|---|---|
| SNP_66059 | dDocent_Contig_57871 | CM027509.1 | 38244150 | 3 | 1.0000E+00 | 0 |
| SNP_66253 | dDocent_Contig_58054 | CM027513.1 | 30206166 | 2 | 1.0000E+00 | 0 |
| SNP_66676 | dDocent_Contig_58446 | CM027508.1 | 48606964 | 4 | 1.0000E+00 | 0 |
| SNP_66701 | dDocent_Contig_58470 | CM027508.1 | 62354747 | 3 | 1.0000E+00 | 0 |
| SNP_67314 | dDocent_Contig_59210 | CM027521.1 | 7373275 | 3 | 1.0000E+00 | 0 |
| SNP_67505 | dDocent_Contig_59415 | CM027535.1 | 22058553 | 3 | 1.0000E+00 | 0 |
| SNP_67572 | dDocent_Contig_59468 | CM027510.1 | 33748506 | 2 | 1.0000E+00 | 0 |
| SNP_67601 | dDocent_Contig_59493 | CM027515.1 | 23371931 | 1 | 1.0000E+00 | 0 |
| SNP_67876 | dDocent_Contig_59725 | CM027520.1 | 2457430 | 1 | 1.0000E+00 | 0 |
| SNP_67931 | dDocent_Contig_59769 | CM027507.1 | 49102109 | 2 | 3.7179E-01 | 0 |
| SNP_68137 | dDocent_Contig_59957 | CM027529.1 | 2589637 | 4 | 6.4832E-01 | 0 |
| SNP_68377 | dDocent_Contig_60198 | CM027515.1 | 11802655 | 4 | 1.3638E-01 | 0 |
| SNP_68454 | dDocent_Contig_60262 | CM027507.1 | 86232814 | 1 | 9.4220E-01 | 0 |
| SNP_68611 | dDocent_Contig_60587 | CM027508.1 | 90253882 | 4 | 1.0000E+00 | 0 |
| SNP_68633 | dDocent_Contig_60609 | CM027507.1 | 34527930 | 1 | 1.0000E+00 | 0 |
| SNP_68807 | dDocent_Contig_60815 | CM027510.1 | 2773836 | 3 | 1.0000E+00 | 0 |
| SNP_69274 | dDocent_Contig_61268 | CM027507.1 | 94233473 | 3 | 1.0000E+00 | 0 |
| SNP_69305 | dDocent_Contig_61301 | CM027514.1 | 13902793 | 4 | 1.0000E+00 | 0 |
| SNP_69456 | dDocent_Contig_61440 | CM027536.1 | 44626708 | 2 | 1.0000E+00 | 0 |
| SNP_69511 | dDocent_Contig_61481 | CM027507.1 | 45663788 | 3 | 1.0000E+00 | 0 |
| SNP_69942 | dDocent_Contig_62056 | CM027511.1 | 8533653 | 3 | 2.2048E-01 | 0 |
| SNP_70685 | dDocent_Contig_62839 | CM027509.1 | 93815159 | 2 | 4.9484E-01 | 0 |
| SNP_70694 | dDocent_Contig_62851 | CM027523.1 | 2720338 | 1 | 1.0000E+00 | 0 |
| SNP_70750 | dDocent_Contig_62913 | CM027507.1 | 1468429 | 3 | 5.0153E-01 | 0 |
| SNP_70845 | dDocent_Contig_62988 | CM027510.1 | 51159161 | 1 | 1.0000E+00 | 0 |
| SNP_70997 | dDocent_Contig_63135 | CM027511.1 | 12161066 | 2 | 9.2982E-04 | 1 |
| SNP_71417 | dDocent_Contig_63684 | CM027509.1 | 43559120 | 5 | 1.0000E+00 | 0 |
| SNP_71612 | dDocent_Contig_63887 | CM027527.1 | 700673 | 1 | 4.8571E-03 | 1 |
| SNP_72060 | dDocent_Contig_64317 | CM027510.1 | 1177665 | 3 | 1.8418E-02 | 1 |
| SNP_72134 | dDocent_Contig_64394 | CM027527.1 | 952746 | 2 | 1.0000E+00 | 0 |
| SNP_72161 | dDocent_Contig_64411 | CM027508.1 | 1.21E+08 | 3 | 1.1691E-01 | 0 |

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|---|---|---|---|---|---|---|
| SNP_72321 | dDocent_Contig_64581 | CM027537.1 | 14327864 | 1 | 1.8606E-01 | 0 |
| SNP_72474 | dDocent_Contig_64745 | CM027526.1 | 4053055 | 4 | 1.0000E+00 | 0 |
| SNP_72478 | dDocent_Contig_64747 | CM027510.1 | 17814924 | 4 | 1.0000E+00 | 0 |
| SNP_72617 | dDocent_Contig_64868 | CM027537.1 | 3521235 | 3 | 1.0000E+00 | 0 |
| SNP_73093 | dDocent_Contig_65515 | CM027515.1 | 11281295 | 1 | 3.1212E-04 | 1 |
| SNP_73175 | dDocent_Contig_65582 | CM027525.1 | 3672919 | 1 | 9.9599E-06 | 1 |
| SNP_73215 | dDocent_Contig_65645 | CM027520.1 | 1867148 | 3 | 1.0000E+00 | 0 |
| SNP_73491 | dDocent_Contig_65910 | CM027509.1 | 57019131 | 2 | 3.0703E-10 | 1 |
| SNP_73501 | dDocent_Contig_65923 | CM027508.1 | 1.12E+08 | 5 | 1.0000E+00 | 0 |
| SNP_74381 | dDocent_Contig_66957 | CM027537.1 | 14114178 | 5 | 1.0000E+00 | 0 |
| SNP_74447 | dDocent_Contig_67025 | CM027509.1 | 84629047 | 2 | 1.0000E+00 | 0 |
| SNP_74483 | dDocent_Contig_67069 | CM027510.1 | 41098585 | 1 | 9.8343E-01 | 0 |
| SNP_74509 | dDocent_Contig_67092 | CM027511.1 | 27220889 | 1 | 1.0000E+00 | 0 |
| SNP_75019 | dDocent_Contig_67555 | CM027508.1 | 42161372 | 3 | 2.6080E-04 | 1 |
| SNP_75136 | dDocent_Contig_67684 | CM027512.1 | 31041223 | 3 | 1.0314E-11 | 1 |
| SNP_75468 | dDocent_Contig_68014 | CM027509.1 | 32678197 | 1 | 1.0000E+00 | 0 |
| SNP_75484 | dDocent_Contig_68036 | CM027536.1 | 39520480 | 4 | 1.0000E+00 | 0 |
| SNP_75514 | dDocent_Contig_68076 | CM027508.1 | 17869644 | 1 | 1.0000E+00 | 0 |
| SNP_75777 | dDocent_Contig_68481 | CM027519.1 | 14873748 | 3 | 2.4905E-01 | 0 |
| SNP_75920 | dDocent_Contig_68682 | CM027507.1 | 1.08E+08 | 1 | 2.4091E-02 | 1 |
| SNP_76145 | dDocent_Contig_68926 | MDLI02000246.1 | 9760 | 3 | 1.0000E+00 | 0 |
| SNP_76403 | dDocent_Contig_69161 | CM027519.1 | 3916238 | 1 | 9.6008E-03 | 1 |
| SNP_76480 | dDocent_Contig_69224 | CM027512.1 | 2436272 | 3 | 6.6694E-04 | 1 |
| SNP_77035 | dDocent_Contig_69812 | CM027507.1 | 66397735 | 2 | 1.7354E-07 | 1 |
| SNP_77846 | dDocent_Contig_70856 | CM027507.1 | 1.02E+08 | 3 | 1.0000E+00 | 0 |
| SNP_77859 | dDocent_Contig_70867 | CM027509.1 | 15197356 | 2 | 3.7477E-01 | 0 |
| SNP_78689 | dDocent_Contig_71749 | CM027523.1 | 1661171 | 4 | 1.0000E+00 | 0 |
| SNP_79469 | dDocent_Contig_72698 | CM027513.1 | 12769812 | 1 | 1.0000E+00 | 0 |
| SNP_79521 | dDocent_Contig_72753 | CM027536.1 | 12213640 | 3 | 1.0000E+00 | 0 |
| SNP_79548 | dDocent_Contig_72787 | CM027508.1 | 56515200 | 3 | 1.0000E+00 | 0 |
| SNP_79565 | dDocent_Contig_72818 | CM027524.1 | 2048994 | 3 | 3.1341E-02 | 1 |

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|---|---|---|---|---|---|---|
| SNP_79719 | dDocent_Contig_72995 | CM027507.1 | 15564103 | 1 | 1.9521E-03 | 1 |
| SNP_79789 | dDocent_Contig_73062 | CM027509.1 | 83677318 | 3 | 4.5793E-02 | 1 |
| SNP_79795 | dDocent_Contig_73066 | CM027519.1 | 13476315 | 3 | 1.0000E+00 | 0 |
| SNP_79826 | dDocent_Contig_73102 | CM027520.1 | 14560099 | 2 | 2.6090E-04 | 1 |
| SNP_80064 | dDocent_Contig_73350 | CM027510.1 | 3849779 | 2 | 1.0000E+00 | 0 |
| SNP_80502 | dDocent_Contig_73831 | CM027523.1 | 4285006 | 4 | 1.0000E+00 | 0 |
| SNP_80541 | dDocent_Contig_73868 | CM027524.1 | 10576727 | 3 | 1.3326E-10 | 1 |
| SNP_80556 | dDocent_Contig_73890 | CM027511.1 | 1705010 | 3 | 1.0000E+00 | 0 |
| SNP_81309 | dDocent_Contig_74909 | CM027510.1 | 21964191 | 1 | 9.2951E-02 | 0 |
| SNP_81611 | dDocent_Contig_75241 | CM027524.1 | 9830295 | 3 | 3.0258E-02 | 1 |
| SNP_81628 | dDocent_Contig_75251 | CM027524.1 | 2176887 | 1 | 1.0000E+00 | 0 |
| SNP_82431 | dDocent_Contig_76135 | CM027511.1 | 12842357 | 1 | 1.0000E+00 | 0 |
| SNP_82621 | dDocent_Contig_76574 | CM027527.1 | 3123059 | 4 | 1.0000E+00 | 0 |
| SNP_82814 | dDocent_Contig_76785 | CM027515.1 | 22027604 | 4 | 1.0000E+00 | 0 |
| SNP_82821 | dDocent_Contig_76791 | CM027508.1 | 1.06E+08 | 4 | 1.0000E+00 | 0 |
| SNP_83103 | dDocent_Contig_77136 | CM027510.1 | 36551712 | 1 | 1.0000E+00 | 0 |
| SNP_83748 | dDocent_Contig_77829 | CM027512.1 | 24443952 | 3 | 1.0000E+00 | 0 |
| SNP_84076 | dDocent_Contig_78216 | CM027536.1 | 67732963 | 1 | 1.0000E+00 | 0 |
| SNP_84357 | dDocent_Contig_78747 | CM027511.1 | 2856194 | 1 | 9.7425E-01 | 0 |
| SNP_84421 | dDocent_Contig_78803 | CM027508.1 | 10725916 | 4 | 5.4312E-09 | 1 |
| SNP_85048 | dDocent_Contig_79494 | CM027536.1 | 63594487 | 4 | 1.0000E+00 | 0 |
| SNP_86793 | dDocent_Contig_81735 | CM027528.1 | 5233009 | 4 | 1.0000E+00 | 0 |
| SNP_87312 | dDocent_Contig_82267 | CM027517.1 | 5047663 | 3 | 1.0000E+00 | 0 |
| SNP_87413 | dDocent_Contig_82429 | CM027520.1 | 5785811 | 5 | 1.0000E+00 | 0 |
| SNP_88017 | dDocent_Contig_83300 | CM027518.1 | 15628146 | 2 | 1.0000E+00 | 0 |
| SNP_88203 | dDocent_Contig_83551 | CM027537.1 | 3307285 | 1 | 1.0633E-11 | 1 |
| SNP_89032 | dDocent_Contig_84578 | CM027537.1 | 16677460 | 5 | 6.5106E-03 | 1 |
| SNP_89503 | dDocent_Contig_85129 | CM027513.1 | 36131825 | 1 | 5.0905E-02 | 0 |
| SNP_89634 | dDocent_Contig_85263 | CM027525.1 | 14519095 | 1 | 1.0000E+00 | 0 |
| SNP_89657 | dDocent_Contig_85281 | CM027536.1 | 19590822 | 1 | 1.1053E-06 | 1 |
| SNP_89681 | dDocent_Contig_85312 | CM027510.1 | 12529772 | 4 | 1.8223E-01 | 0 |

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|---|---|---|---|---|---|---|
| SNP_89706 | dDocent_Contig_85334 | CM027535.1 | 8872364 | 1 | 1.0000E+00 | 0 |
| SNP_90375 | dDocent_Contig_86312 | CM027507.1 | 27686518 | 2 | 1.0000E+00 | 0 |
| SNP_90741 | dDocent_Contig_86764 | CM027524.1 | 8372929 | 3 | 2.1741E-24 | 1 |
| SNP_90749 | dDocent_Contig_86768 | CM027517.1 | 18047746 | 4 | 3.9686E-01 | 0 |
| SNP_91400 | dDocent_Contig_87475 | CM027523.1 | 7738978 | 1 | 3.3355E-01 | 0 |
| SNP_92060 | dDocent_Contig_88425 | CM027518.1 | 13348835 | 2 | 1.0000E+00 | 0 |
| SNP_92111 | dDocent_Contig_88474 | CM027532.1 | 4701886 | 3 | 5.4252E-03 | 1 |
| SNP_93247 | dDocent_Contig_89873 | CM027537.1 | 15143890 | 2 | 1.0000E+00 | 0 |
| SNP_93370 | dDocent_Contig_90012 | CM027508.1 | 1.33E+08 | 1 | 1.0000E+00 | 0 |
| SNP_93844 | dDocent_Contig_90582 | CM027507.1 | 25037106 | 4 | 1.0000E+00 | 0 |
| SNP_94043 | dDocent_Contig_91010 | CM027535.1 | 58489079 | 4 | 7.1977E-03 | 1 |
| SNP_94181 | dDocent_Contig_91254 | CM027516.1 | 19323224 | 1 | 4.2483E-05 | 1 |
| SNP_94719 | dDocent_Contig_91893 | CM027509.1 | 24526118 | 3 | 2.5836E-18 | 1 |
| SNP_94743 | dDocent_Contig_91923 | CM027508.1 | 55124969 | 5 | 1.0000E+00 | 0 |
| SNP_95382 | dDocent_Contig_92806 | CM027517.1 | 3899943 | 3 | 9.4615E-01 | 0 |
| SNP_95479 | dDocent_Contig_92940 | CM027515.1 | 12270647 | 3 | 3.0419E-02 | 1 |
| SNP_95529 | dDocent_Contig_93018 | CM027512.1 | 6444038 | 1 | 1.0000E+00 | 0 |
| SNP_95621 | dDocent_Contig_93137 | CM027521.1 | 2344054 | 3 | 6.8962E-03 | 1 |
| SNP_96944 | dDocent_Contig_95134 | CM027508.1 | 1.36E+08 | 2 | 1.0000E+00 | 0 |
| SNP_96992 | dDocent_Contig_95197 | CM027508.1 | 3516158 | 3 | 1.0000E+00 | 0 |
| SNP_97269 | dDocent_Contig_95594 | CM027508.1 | 1.25E+08 | 3 | 1.6044E-10 | 1 |
| SNP_97503 | dDocent_Contig_95898 | CM027516.1 | 18151961 | 1 | 1.0000E+00 | 0 |
| SNP_97532 | dDocent_Contig_95955 | CM027537.1 | 10447404 | 4 | 3.4073E-01 | 0 |
| SNP_97881 | dDocent_Contig_96452 | CM027509.1 | 37522848 | 3 | 6.1049E-02 | 0 |
| SNP_98673 | dDocent_Contig_97720 | CM027511.1 | 41699953 | 2 | 1.5518E-02 | 1 |
| SNP_99881 | dDocent_Contig_99411 | CM027516.1 | 18974873 | 1 | 1.4172E-01 | 0 |
| SNP_99945 | dDocent_Contig_99481 | CM027536.1 | 25124597 | 3 | 3.2295E-04 | 1 |
| SNP_100779 | dDocent_Contig_100819 | CM027509.1 | 90493768 | 1 | 2.9732E-01 | 0 |
| SNP_100858 | dDocent_Contig_100937 | CM027507.1 | 82225975 | 4 | 4.1023E-02 | 1 |
| SNP_102065 | dDocent_Contig_102621 | CM027528.1 | 6114760 | 1 | 1.0000E+00 | 0 |
| SNP_102220 | dDocent_Contig_102837 | CM027507.1 | 97175594 | 1 | 1.0000E+00 | 0 |

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|---|---|---|---|---|---|---|
| SNP_103057 | dDocent_Contig_104029 | CM027536.1 | 64735264 | 2 | 1.0000E+00 | 0 |
| SNP_105068 | dDocent_Contig_107053 | CM027536.1 | 68746801 | 5 | 1.0000E+00 | 0 |
| SNP_105183 | dDocent_Contig_107210 | CM027511.1 | 20539576 | 4 | 1.0000E+00 | 0 |
| SNP_105740 | dDocent_Contig_108010 | CM027508.1 | 95422921 | 3 | 7.7483E-06 | 1 |
| SNP_105892 | dDocent_Contig_108177 | CM027511.1 | 40202177 | 4 | 1.0000E+00 | 0 |
| SNP_107063 | dDocent_Contig_110074 | CM027507.1 | 52935345 | 1 | 6.6308E-01 | 0 |
| SNP_107954 | dDocent_Contig_111304 | CM027525.1 | 14303421 | 2 | 4.6466E-03 | 1 |
| SNP_108499 | dDocent_Contig_112033 | CM027537.1 | 7057595 | 1 | 1.0000E+00 | 0 |
| SNP_108570 | dDocent_Contig_112141 | CM027537.1 | 14119500 | 4 | 1.0000E+00 | 0 |
| SNP_108591 | dDocent_Contig_112175 | CM027508.1 | 1.28E+08 | 1 | 1.2628E-05 | 1 |
| SNP_110242 | dDocent_Contig_114934 | CM027508.1 | 75967799 | 3 | 4.4535E-01 | 0 |
| SNP_111032 | dDocent_Contig_116245 | CM027522.1 | 5611545 | 3 | 8.8286E-04 | 1 |
| SNP_111324 | dDocent_Contig_116653 | CM027518.1 | 13179119 | 3 | 1.0000E+00 | 0 |
| SNP_112196 | dDocent_Contig_118440 | CM027519.1 | 14975052 | 1 | 1.0000E+00 | 0 |
| SNP_113356 | dDocent_Contig_120347 | CM027507.1 | 1.14E+08 | 1 | 1.0000E+00 | 0 |
| SNP_113648 | dDocent_Contig_120812 | CM027507.1 | 34887473 | 3 | 1.0000E+00 | 0 |
| SNP_114546 | dDocent_Contig_122198 | CM027509.1 | 95449589 | 3 | 1.0000E+00 | 0 |
| SNP_114755 | dDocent_Contig_122531 | CM027508.1 | 38536557 | 3 | 1.0000E+00 | 0 |
| SNP_115083 | dDocent_Contig_122962 | CM027510.1 | 9370098 | 3 | 5.2087E-04 | 1 |
| SNP_115115 | dDocent_Contig_123413 | CM027509.1 | 97665553 | 3 | 4.0249E-01 | 0 |
| SNP_116225 | dDocent_Contig_125245 | CM027508.1 | 53821303 | 3 | 3.0408E-02 | 1 |
| SNP_116609 | dDocent_Contig_125944 | CM027514.1 | 19719379 | 1 | 1.0000E+00 | 0 |
| SNP_118274 | dDocent_Contig_128826 | CM027514.1 | 9987914 | 5 | 1.0000E+00 | 0 |
| SNP_118397 | dDocent_Contig_129030 | CM027537.1 | 16094845 | 3 | 1.0000E+00 | 0 |
| SNP_121829 | dDocent_Contig_135366 | CM027510.1 | 69434120 | 1 | 7.0342E-03 | 1 |
| SNP_121986 | dDocent_Contig_135623 | CM027509.1 | 83600666 | 1 | 2.5505E-06 | 1 |

**Table S.7:** pRDA candidate outlier SNPs; "loading" denotes a given SNP's overall loading on the first RDA axis; "ENV_PC1," "ENV_PC2," and "ENV_PC3" each denote a SNP's correlation coefficients for each environmental predictor; "predictor" lists which environmental predictor had the strongest correlation coefficient for each SNP.

| SNP | contig | chromosome | chromosome position | loading | ENV_PC1 | ENV_PC2 | ENV_PC3 | predictor |
|---|---|---|---|---|---|---|---|---|
| SNP_11960 | dDocent_Contig_8151 | CM027515.1 | 21092067 | 0.1162 | 0.0115 | 0.2108 | -0.3966 | ENV_PC3 |
| SNP_79484 | dDocent_Contig_72719 | CM027514.1 | 12384366 | 0.1048 | -0.0422 | 0.2594 | -0.2790 | ENV_PC3 |
| SNP_105087 | dDocent_Contig_107075 | CM027514.1 | 27602081 | 0.1015 | -0.0263 | 0.2315 | -0.2414 | ENV_PC3 |
| SNP_96236 | dDocent_Contig_94189 | CM027537.1 | 17954856 | 0.0992 | -0.0116 | 0.1844 | -0.3183 | ENV_PC3 |
| SNP_116288 | dDocent_Contig_125352 | CM027510.1 | 70915197 | 0.0971 | 0.0131 | 0.1932 | -0.3061 | ENV_PC3 |
| SNP_69842 | dDocent_Contig_61975 | CM027510.1 | 55663997 | 0.0960 | 0.0108 | 0.1844 | -0.3030 | ENV_PC3 |
| SNP_77047 | dDocent_Contig_69825 | CM027508.1 | 33004947 | 0.0937 | 0.0694 | 0.2213 | -0.2369 | ENV_PC3 |
| SNP_94159 | dDocent_Contig_91220 | CM027524.1 | 5020330 | 0.0932 | -0.0108 | 0.1711 | -0.3704 | ENV_PC3 |
| SNP_94924 | dDocent_Contig_92198 | MDLI02000885.1 | 276 | 0.0930 | 0.0219 | 0.1759 | -0.3287 | ENV_PC3 |
| SNP_80255 | dDocent_Contig_73524 | CM027517.1 | 16760017 | 0.0916 | -0.0451 | 0.2428 | -0.1620 | ENV_PC2 |
| SNP_28524 | dDocent_Contig_20511 | CM027526.1 | 6777904 | 0.0908 | 0.0499 | 0.1991 | -0.2578 | ENV_PC3 |
| SNP_71464 | dDocent_Contig_63736 | CM027522.1 | 7949396 | -0.0908 | 0.0991 | -0.3463 | 0.0588 | ENV_PC2 |
| SNP_57842 | dDocent_Contig_49272 | CM027509.1 | 61285754 | 0.0907 | -0.0160 | 0.1752 | -0.2885 | ENV_PC3 |
| SNP_43688 | dDocent_Contig_35264 | CM027508.1 | 67188270 | 0.0906 | 0.0401 | 0.1412 | -0.3033 | ENV_PC3 |
| SNP_40629 | dDocent_Contig_32166 | CM027511.1 | 56393163 | 0.0906 | 0.0541 | 0.1456 | -0.2778 | ENV_PC3 |
| SNP_60429 | dDocent_Contig_51875 | CM027509.1 | 57817059 | 0.0904 | 0.0233 | 0.1676 | -0.2557 | ENV_PC3 |
| SNP_27336 | dDocent_Contig_19464 | CM027524.1 | 8276975 | 0.0901 | 0.0053 | 0.1680 | -0.2946 | ENV_PC3 |
| SNP_54163 | dDocent_Contig_45565 | CM027508.1 | 38162244 | 0.0901 | 0.0407 | 0.1956 | -0.2976 | ENV_PC3 |
| SNP_21602 | dDocent_Contig_14938 | CM027510.1 | 62333482 | 0.0899 | 0.0125 | 0.1664 | -0.3059 | ENV_PC3 |
| SNP_61567 | dDocent_Contig_53063 | CM027524.1 | 4574179 | 0.0894 | 0.0058 | 0.1712 | -0.2895 | ENV_PC3 |
| SNP_77247 | dDocent_Contig_70030 | CM027537.1 | 6822641 | 0.0892 | -0.0076 | 0.1741 | -0.2869 | ENV_PC3 |
| SNP_29072 | dDocent_Contig_21011 | CM027522.1 | 6911498 | 0.0891 | -0.0043 | 0.1367 | -0.2895 | ENV_PC3 |
| SNP_47244 | dDocent_Contig_38808 | CM027519.1 | 2932381 | 0.0881 | 0.0194 | 0.1007 | -0.2636 | ENV_PC3 |
| SNP_54617 | dDocent_Contig_45955 | CM027511.1 | 23151602 | 0.0881 | -0.0102 | 0.1676 | -0.2831 | ENV_PC3 |
| SNP_52902 | dDocent_Contig_44120 | CM027537.1 | 11007865 | 0.0874 | -0.0015 | 0.1728 | -0.2812 | ENV_PC3 |
| SNP_82076 | dDocent_Contig_75740 | CM027507.1 | 73511283 | 0.0873 | -0.0105 | 0.1736 | -0.2771 | ENV_PC3 |
| SNP_50050 | dDocent_Contig_41504 | CM027521.1 | 1276357 | 0.0872 | 0.0117 | 0.1551 | -0.3009 | ENV_PC3 |

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|---|---|---|---|---|---|---|---|---|
| SNP_34926 | dDocent_Contig_26724 | CM027536.1 | 5924411 | 0.0866 | 0.0036 | 0.1608 | -0.2829 | ENV_PC3 |
| SNP_85169 | dDocent_Contig_79656 | CM027535.1 | 5491350 | 0.0865 | 0.0027 | 0.1873 | -0.2543 | ENV_PC3 |
| SNP_21232 | dDocent_Contig_14686 | CM027515.1 | 1992099 | 0.0864 | 0.0000 | 0.1670 | -0.2566 | ENV_PC3 |
| SNP_91891 | dDocent_Contig_88245 | CM027507.1 | 62509756 | 0.0863 | -0.0188 | 0.1708 | -0.2791 | ENV_PC3 |
| SNP_42654 | dDocent_Contig_34314 | CM027508.1 | 44646223 | -0.0862 | 0.0277 | -0.2725 | 0.0554 | ENV_PC2 |
| SNP_34080 | dDocent_Contig_25948 | CM027515.1 | 15572393 | 0.0861 | -0.0177 | 0.2135 | -0.2214 | ENV_PC3 |
| SNP_70707 | dDocent_Contig_62861 | CM027507.1 | 45900850 | 0.0857 | 0.0060 | 0.1607 | -0.2686 | ENV_PC3 |
| SNP_69802 | dDocent_Contig_61745 | CM027518.1 | 19609566 | 0.0852 | 0.1049 | 0.1690 | -0.2869 | ENV_PC3 |
| SNP_43434 | dDocent_Contig_35053 | CM027509.1 | 94552559 | 0.0848 | 0.0022 | 0.1532 | -0.2834 | ENV_PC3 |
| SNP_116598 | dDocent_Contig_125931 | CM027520.1 | 2105262 | 0.0846 | 0.0156 | 0.1759 | -0.2655 | ENV_PC3 |
| SNP_34509 | dDocent_Contig_26248 | CM027511.1 | 57553235 | 0.0845 | 0.0008 | 0.1555 | -0.2813 | ENV_PC3 |
| SNP_5191 | dDocent_Contig_3742 | CM027516.1 | 18343540 | 0.0840 | -0.0033 | 0.2011 | -0.2596 | ENV_PC3 |
| SNP_17554 | dDocent_Contig_12048 | CM027517.1 | 19214857 | 0.0839 | 0.0073 | 0.1552 | -0.2844 | ENV_PC3 |
| SNP_62957 | dDocent_Contig_54478 | CM027507.1 | 44465716 | 0.0838 | 0.0045 | 0.1543 | -0.2795 | ENV_PC3 |
| SNP_108087 | dDocent_Contig_111459 | CM027512.1 | 26366551 | 0.0831 | 0.0213 | 0.1561 | -0.2599 | ENV_PC3 |
| SNP_96753 | dDocent_Contig_94904 | CM027523.1 | 10420758 | 0.0831 | -0.0058 | 0.1566 | -0.2734 | ENV_PC3 |
| SNP_70319 | dDocent_Contig_62471 | CM027508.1 | 73474547 | 0.0829 | 0.0047 | 0.2030 | -0.2546 | ENV_PC3 |
| SNP_102349 | dDocent_Contig_103031 | CM027518.1 | 5876432 | 0.0828 | -0.0297 | 0.1578 | -0.2181 | ENV_PC3 |
| SNP_82583 | dDocent_Contig_76513 | CM027537.1 | 4750876 | -0.0824 | 0.0154 | -0.3580 | 0.0249 | ENV_PC2 |
| SNP_72350 | dDocent_Contig_64607 | CM027511.1 | 17792913 | 0.0820 | -0.0115 | 0.1558 | -0.2745 | ENV_PC3 |
| SNP_91892 | dDocent_Contig_88246 | CM027509.1 | 25915821 | 0.0819 | -0.0012 | 0.1591 | -0.2589 | ENV_PC3 |
| SNP_48935 | dDocent_Contig_40510 | CM027536.1 | 1260125 | -0.0814 | -0.2103 | -0.3159 | -0.1066 | ENV_PC2 |
| SNP_111724 | dDocent_Contig_117340 | CM027529.1 | 7171298 | -0.0812 | -0.2276 | -0.3101 | -0.0621 | ENV_PC2 |
| SNP_31044 | dDocent_Contig_22877 | CM027514.1 | 28556463 | 0.0808 | -0.0172 | 0.1724 | -0.2082 | ENV_PC3 |
| SNP_78653 | dDocent_Contig_71710 | CM027514.1 | 13010474 | 0.0807 | 0.0008 | 0.1637 | -0.2513 | ENV_PC3 |
| SNP_24147 | dDocent_Contig_16901 | CM027507.1 | 23173284 | 0.0805 | -0.0253 | 0.1749 | -0.2236 | ENV_PC3 |
| SNP_119771 | dDocent_Contig_131726 | CM027525.1 | 9800134 | 0.0804 | -0.0118 | 0.1690 | -0.2194 | ENV_PC3 |
| SNP_35088 | dDocent_Contig_26846 | CM027512.1 | 2922947 | 0.0803 | 0.0488 | 0.1208 | -0.3102 | ENV_PC3 |
| SNP_25338 | dDocent_Contig_17804 | CM027518.1 | 8880683 | 0.0800 | -0.0190 | 0.1765 | -0.2150 | ENV_PC3 |
| SNP_35858 | dDocent_Contig_27529 | CM027511.1 | 45163416 | 0.0797 | 0.0095 | 0.1990 | -0.1995 | ENV_PC3 |
| SNP_82623 | dDocent_Contig_76575 | CM027507.1 | 38238887 | 0.0793 | 0.0060 | 0.1659 | -0.2419 | ENV_PC3 |

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|---|---|---|---|---|---|---|---|---|
| SNP_110559 | dDocent_Contig_115491 | CM027519.1 | 5826585 | 0.0793 | -0.0106 | 0.1839 | -0.2100 | ENV_PC3 |
| SNP_90353 | dDocent_Contig_86291 | CM027536.1 | 68713771 | 0.0791 | 0.0419 | 0.1939 | -0.2187 | ENV_PC3 |
| SNP_41696 | dDocent_Contig_33409 | CM027511.1 | 57955833 | 0.0789 | -0.0020 | 0.1707 | -0.2220 | ENV_PC3 |
| SNP_33750 | dDocent_Contig_25562 | CM027512.1 | 8285916 | 0.0789 | -0.0059 | 0.1613 | -0.2479 | ENV_PC3 |
| SNP_41356 | dDocent_Contig_32938 | CM027514.1 | 5319329 | 0.0789 | -0.0212 | 0.1773 | -0.2058 | ENV_PC3 |
| SNP_72487 | dDocent_Contig_64755 | CM027507.1 | 7428780 | 0.0787 | 0.0658 | 0.1496 | -0.2656 | ENV_PC3 |
| SNP_31446 | dDocent_Contig_23346 | CM027525.1 | 5199234 | 0.0787 | -0.0119 | 0.1655 | -0.2178 | ENV_PC3 |
| SNP_28649 | dDocent_Contig_20602 | CM027520.1 | 4135893 | 0.0787 | -0.0227 | 0.0813 | -0.2425 | ENV_PC3 |
| SNP_74672 | dDocent_Contig_67230 | CM027512.1 | 25447573 | 0.0786 | 0.0350 | 0.1831 | -0.2468 | ENV_PC3 |
| SNP_87929 | dDocent_Contig_83185 | CM027519.1 | 6404692 | 0.0785 | -0.0256 | 0.1792 | -0.2051 | ENV_PC3 |
| SNP_75368 | dDocent_Contig_67914 | CM027520.1 | 4432077 | 0.0784 | -0.0278 | 0.1855 | -0.2348 | ENV_PC3 |
| SNP_19563 | dDocent_Contig_13423 | CM027509.1 | 1.1E+08 | 0.0783 | -0.0044 | 0.0946 | -0.2485 | ENV_PC3 |
| SNP_104649 | dDocent_Contig_106538 | CM027536.1 | 57288515 | 0.0780 | 0.0168 | 0.1468 | -0.2172 | ENV_PC3 |
| SNP_56583 | dDocent_Contig_47983 | MDLI02000298.1 | 4254 | -0.0780 | -0.3222 | -0.3078 | -0.1161 | ENV_PC1 |
| SNP_71774 | dDocent_Contig_64043 | CM027507.1 | 53933730 | 0.0780 | 0.0327 | 0.1753 | -0.2468 | ENV_PC3 |
| SNP_54459 | dDocent_Contig_45835 | CM027509.1 | 89185302 | 0.0774 | 0.0052 | 0.1559 | -0.2604 | ENV_PC3 |
| SNP_56511 | dDocent_Contig_47924 | CM027513.1 | 11624576 | -0.0773 | -0.1417 | -0.3010 | -0.0389 | ENV_PC2 |
| SNP_118990 | dDocent_Contig_130440 | CM027520.1 | 15470227 | 0.0772 | 0.0387 | 0.1272 | -0.2398 | ENV_PC3 |
| SNP_15473 | dDocent_Contig_10579 | CM027509.1 | 2009845 | 0.0772 | -0.0348 | 0.1509 | -0.2064 | ENV_PC3 |
| SNP_29812 | dDocent_Contig_21654 | CM027518.1 | 2188806 | 0.0772 | 0.0002 | 0.1730 | -0.2443 | ENV_PC3 |
| SNP_117543 | dDocent_Contig_127591 | CM027511.1 | 13427124 | 0.0772 | 0.0408 | 0.1320 | -0.2474 | ENV_PC3 |
| SNP_49976 | dDocent_Contig_41451 | CM027507.1 | 1.07E+08 | 0.0771 | 0.0810 | 0.2354 | -0.0097 | ENV_PC2 |
| SNP_3749 | dDocent_Contig_2827 | CM027519.1 | 87957 | 0.0767 | -0.0816 | 0.1798 | -0.2062 | ENV_PC3 |
| SNP_102660 | dDocent_Contig_103454 | CM027537.1 | 12718720 | 0.0764 | -0.0160 | 0.1895 | -0.2244 | ENV_PC3 |
| SNP_105781 | dDocent_Contig_108060 | CM027513.1 | 5094538 | 0.0763 | 0.0511 | 0.1312 | -0.2133 | ENV_PC3 |
| SNP_113472 | dDocent_Contig_120533 | CM027513.1 | 1937036 | 0.0762 | 0.0066 | 0.1658 | -0.1978 | ENV_PC3 |
| SNP_14484 | dDocent_Contig_9873 | CM027521.1 | 2112556 | 0.0761 | 0.0415 | 0.1328 | -0.2627 | ENV_PC3 |
| SNP_91120 | dDocent_Contig_87131 | CM027533.1 | 2964288 | -0.0756 | -0.2941 | -0.2953 | -0.1035 | ENV_PC2 |
| SNP_102637 | dDocent_Contig_103412 | CM027511.1 | 19632308 | -0.0749 | -0.3014 | -0.2966 | -0.1240 | ENV_PC1 |

Hi, thanks for taking the time to read my thesis. It'd be cool to have a chat and hear your thoughts on it. If you want, shoot me an email or text, or maybe mail me a letter if you want to contact me in the distant future.

Cheers,
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