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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 (*Ammodramus 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.

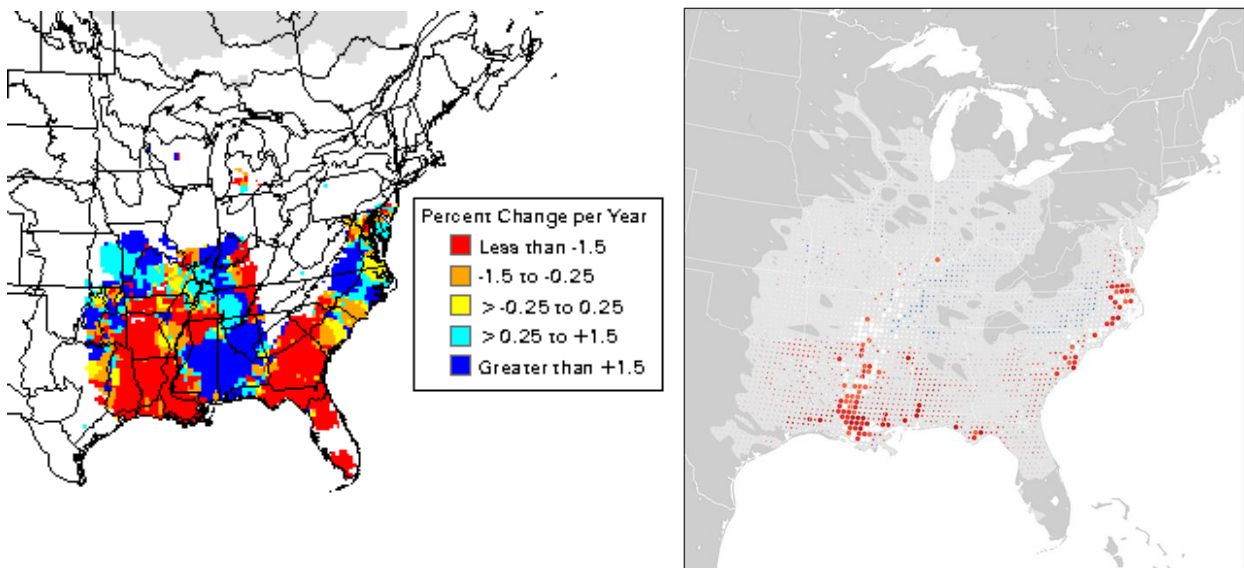


Figure 1: Population trends for breeding Prothonotary Warbler from two different citizen science data sources and time frames. Left: Breeding Bird Survey (BBS) population trends for 1966 - 2019 (Sauer et al., 2020) indicating geographic variation in trends. Right: eBird trends for 2007 – 2021 (Fink et 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.

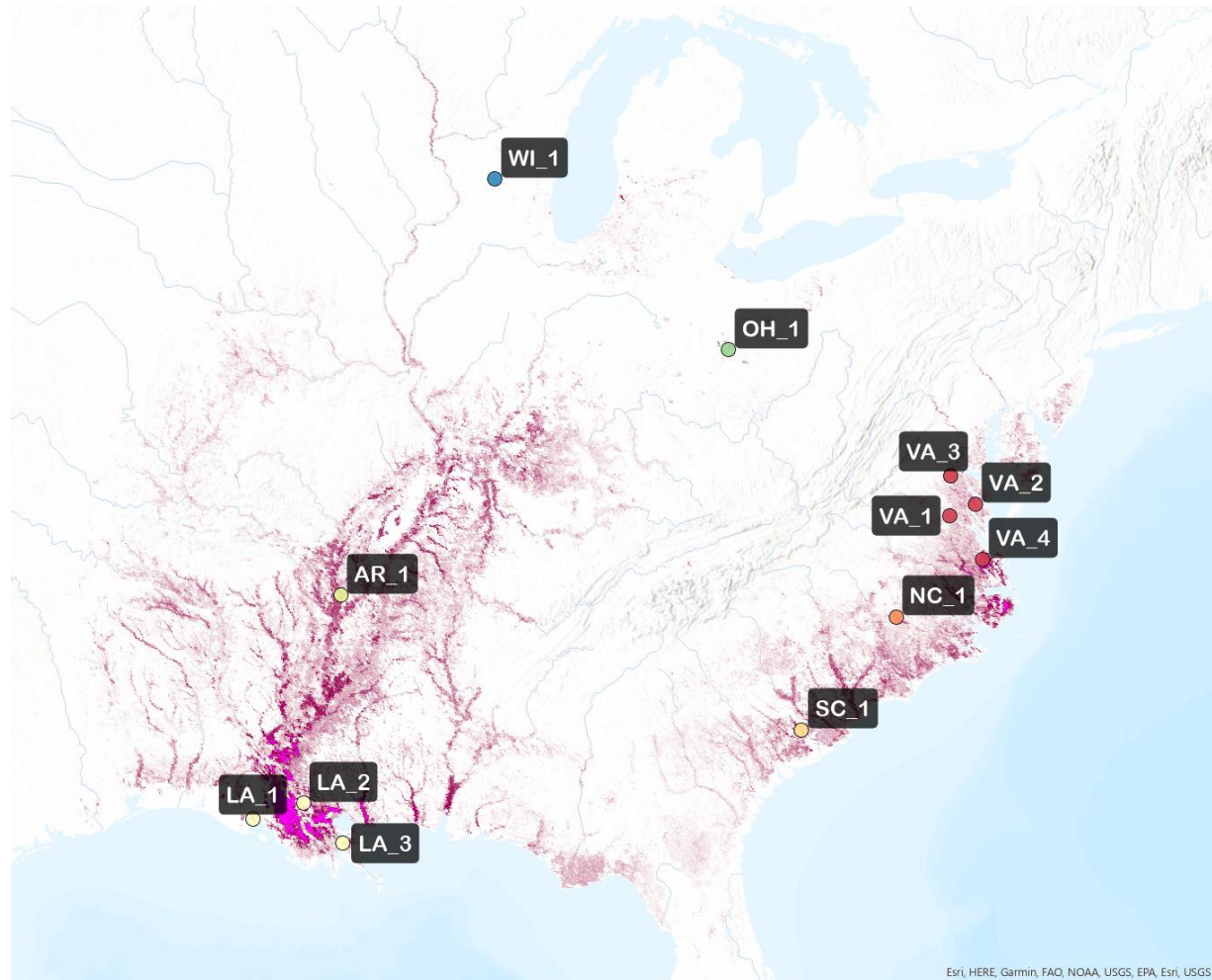


Figure 2: Sampling locations overlaid on map of mean Prothonotary Warbler abundance during the breeding season from eBird (Ebird, 2022). More saturated shades of pink indicate higher mean abundance. Sampling sites are color coded by state; red indicates Virginia, dark orange North Carolina, light orange 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-complements of barcoded reads, and reverse-complement 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 ΔK 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 GEOSPHERE (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 α -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 ($^{\circ}\text{C}$), maximum temperature ($^{\circ}\text{C}$), precipitation (mm), solar radiation ($\text{kJ m}^{-2} \text{ day}^{-1}$), 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 ($\alpha = 0.05$, 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 ($\alpha = 0.05$, 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 ΔK ($L(K=3) = -1,522,670 \pm 10,411$, $\Delta K_{K=3} = 20.777$) (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.

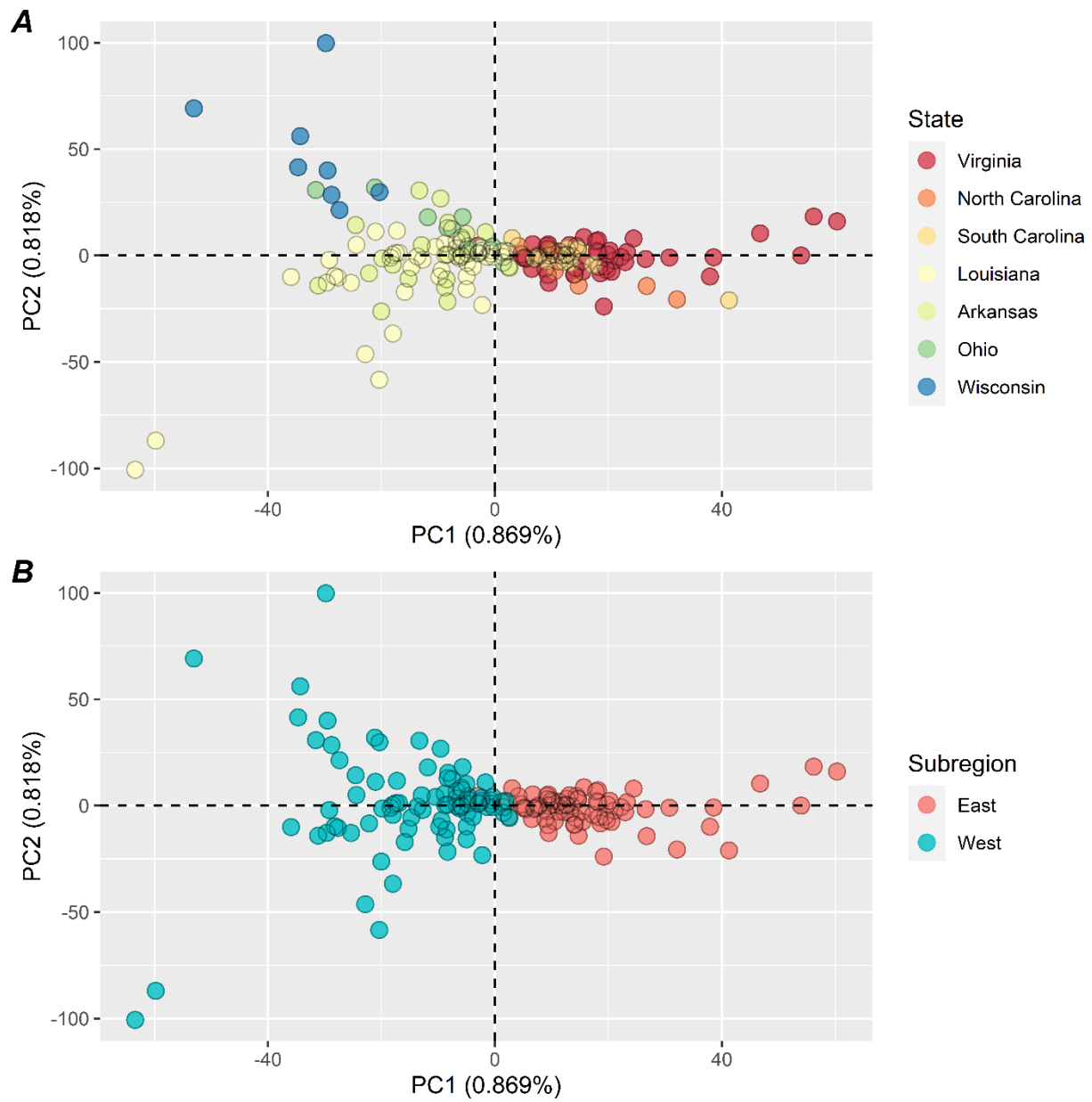


Figure 3: Projection plots of PC1 and PC2 from a multi-locus PCA for the Prothonotary Warbler. Individuals are color-coded by state (A) and by putative genetic clusters identified by DeSaix et al. (2019) (B).

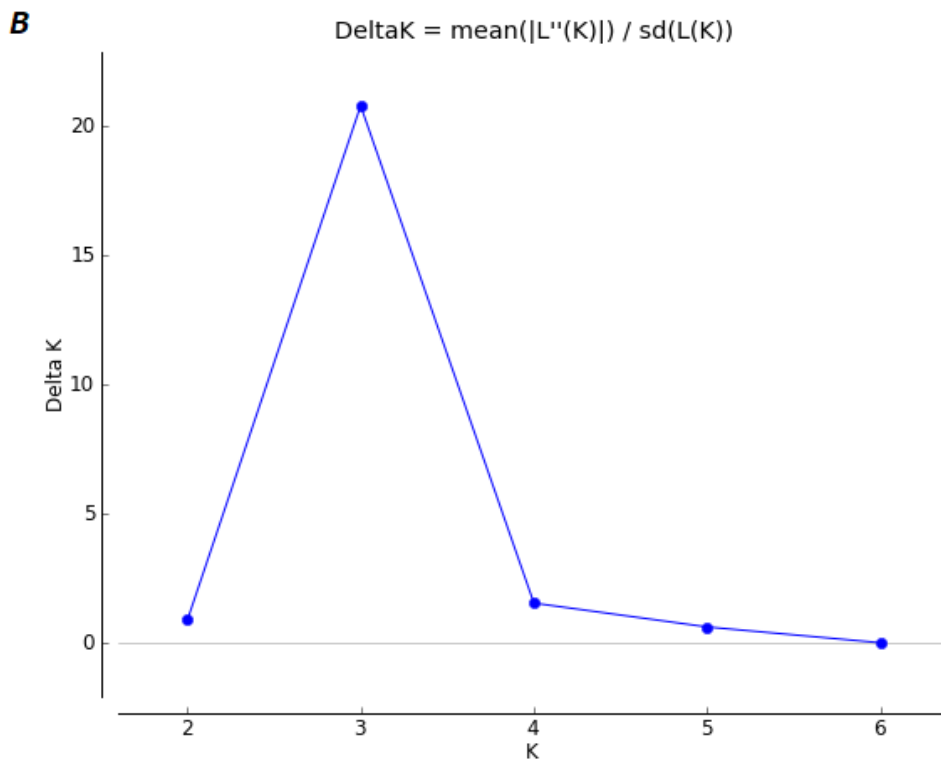
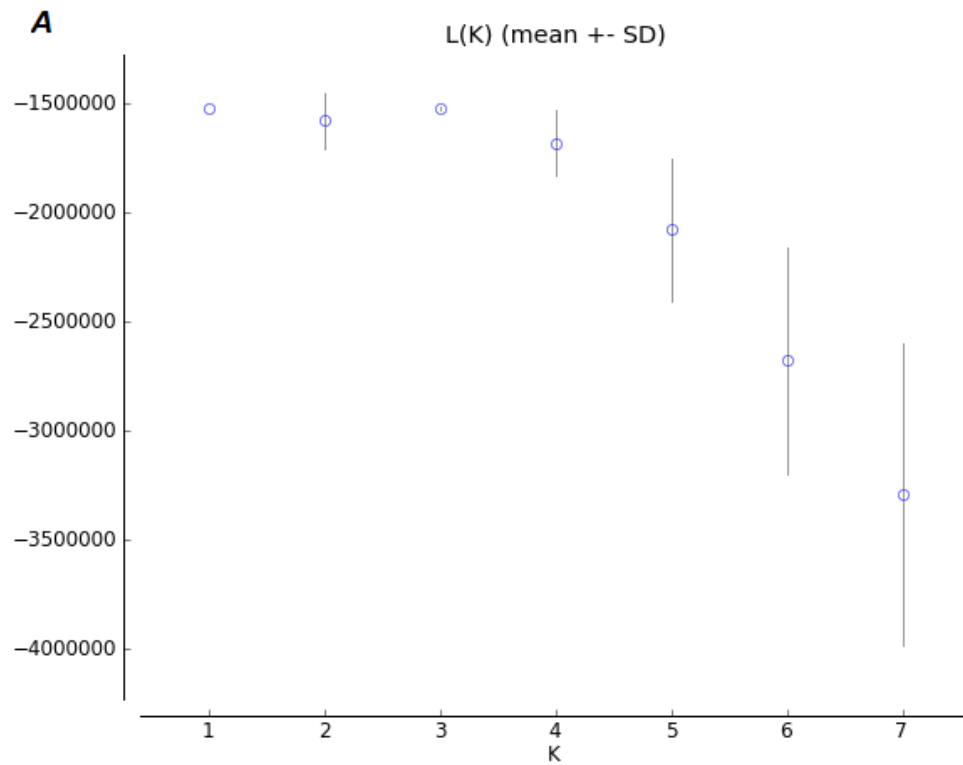
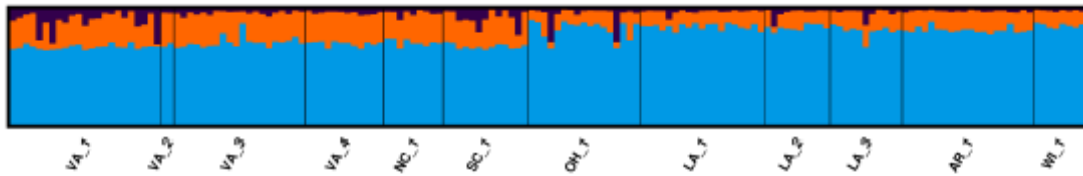


Figure 4: Plots of mean $L(K)$ (A), and ΔK (B) given K genetic clusters after conducting subsequent MCMC simulations for values of K 2 through 6 and discarding low $L(K)$ runs for values of K 2 through 4.

K=2



K=3



K=4

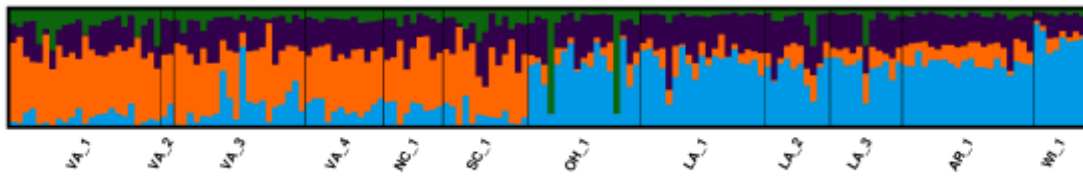


Figure 5: STRUCTURE cluster assignment plots showing individual population assignment probabilities for values of K ranging 2 through 4.

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.

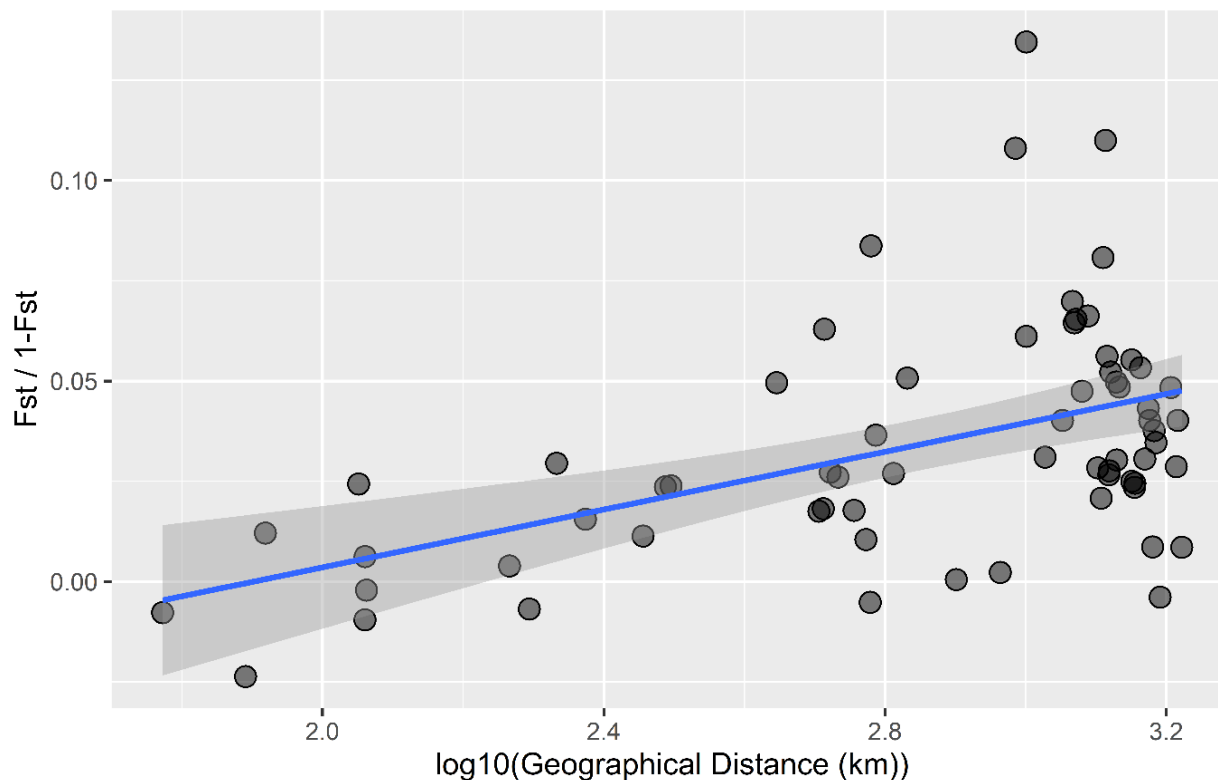


Figure 6: Linear regression of pairwise $\log_{10}(\text{Geographical Distance})$ against pairwise genetic distance ($F_{ST} / 1 - F_{ST}$) for all sampling sites, standard error bands shown in dark gray.

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

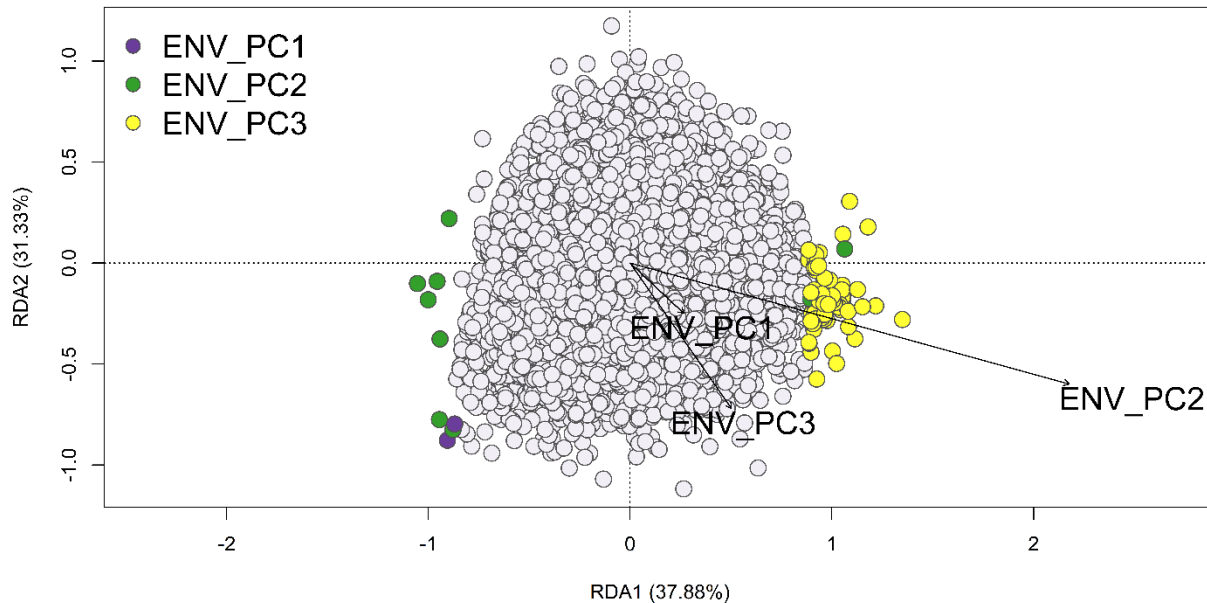


Figure 7: pRDA projection for axes 1 and 2. Gray circles depict SNPs, with colored circles overlaid for outlier SNPs on the first RDA axis; outliers are color-coded by the environmental predictor they show the strongest correlation with. Arrows depict environmental predictors. The arrangement of these 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 ($F_{RDA3} = 0.986$, $df = 1$, $P_{RDA3} = 0.665$) 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 & Reaser, 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 ΔK . The standard deviations of both $L(K)$ estimates overlap, and ΔK 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.

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Appendix - Supplementary Tables and Figures:

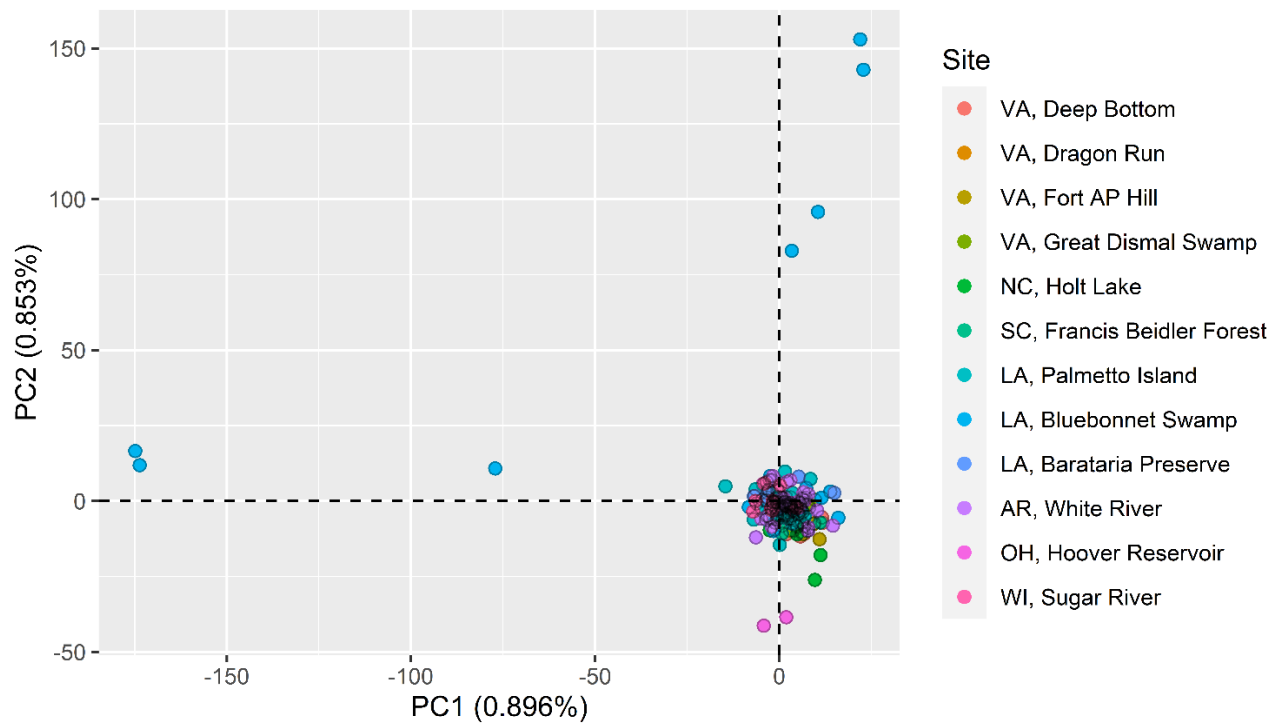


Figure S.1: Projection plot of PC1 and PC2 from initial multi-locus PCA before filtering out birds whose PCA coordinates exceeded six standard deviations from the mean of the first ten principal components over four iterations.

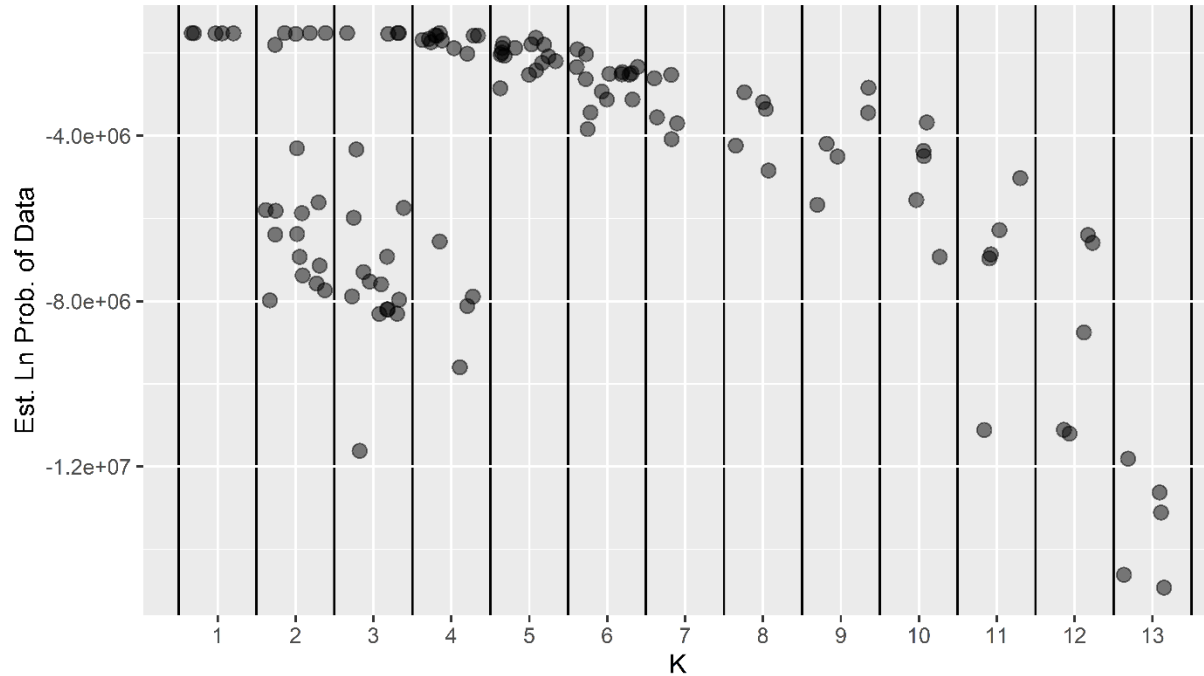


Figure S.2: Scatterplot of $L(K)$ for all STRUCTURE MCMC runs.

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	-	-	-	-	-	-	-	-	-	-	-	-

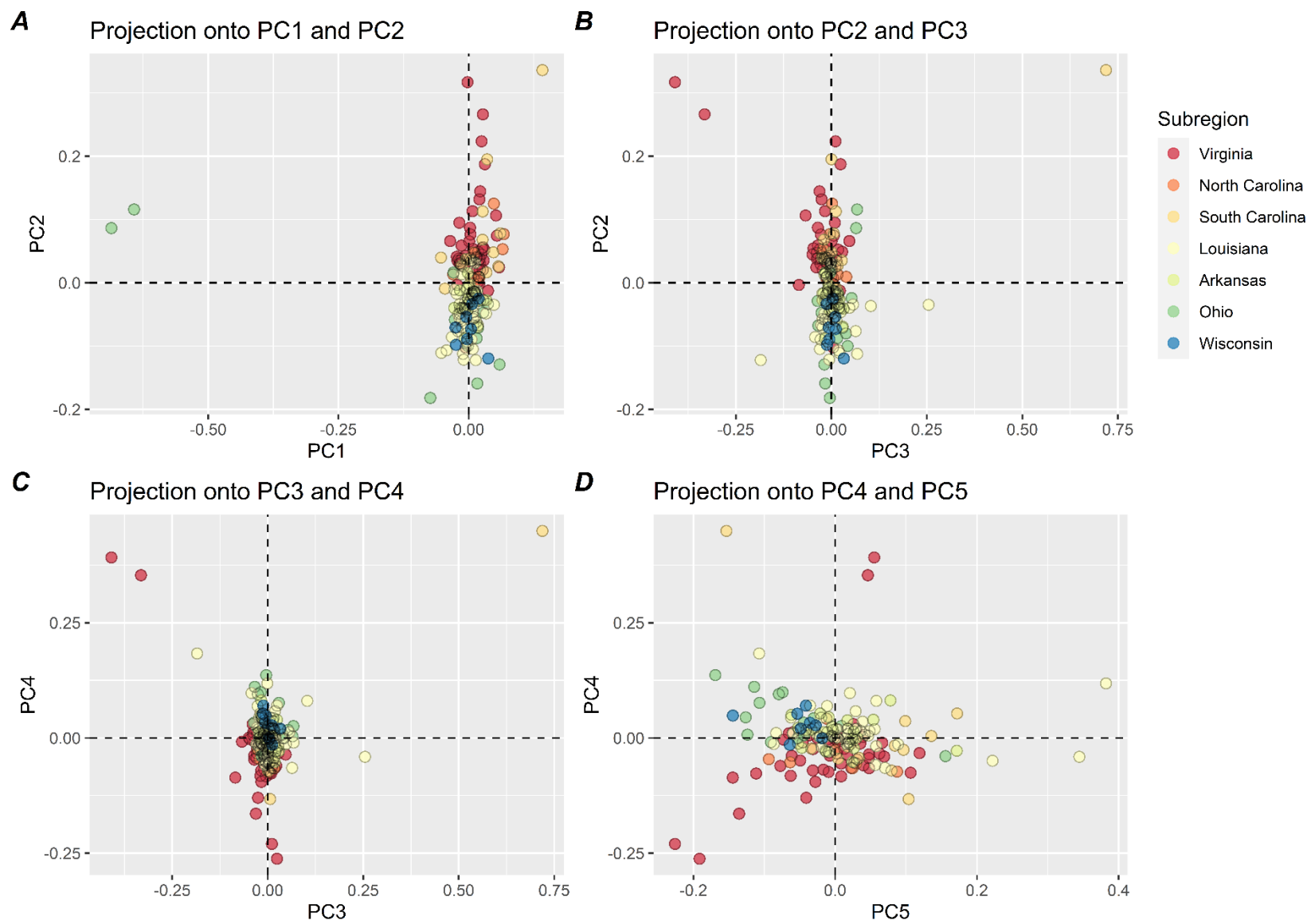


Figure S.3: PCADAPT projection plots for PCs 1 through 5.

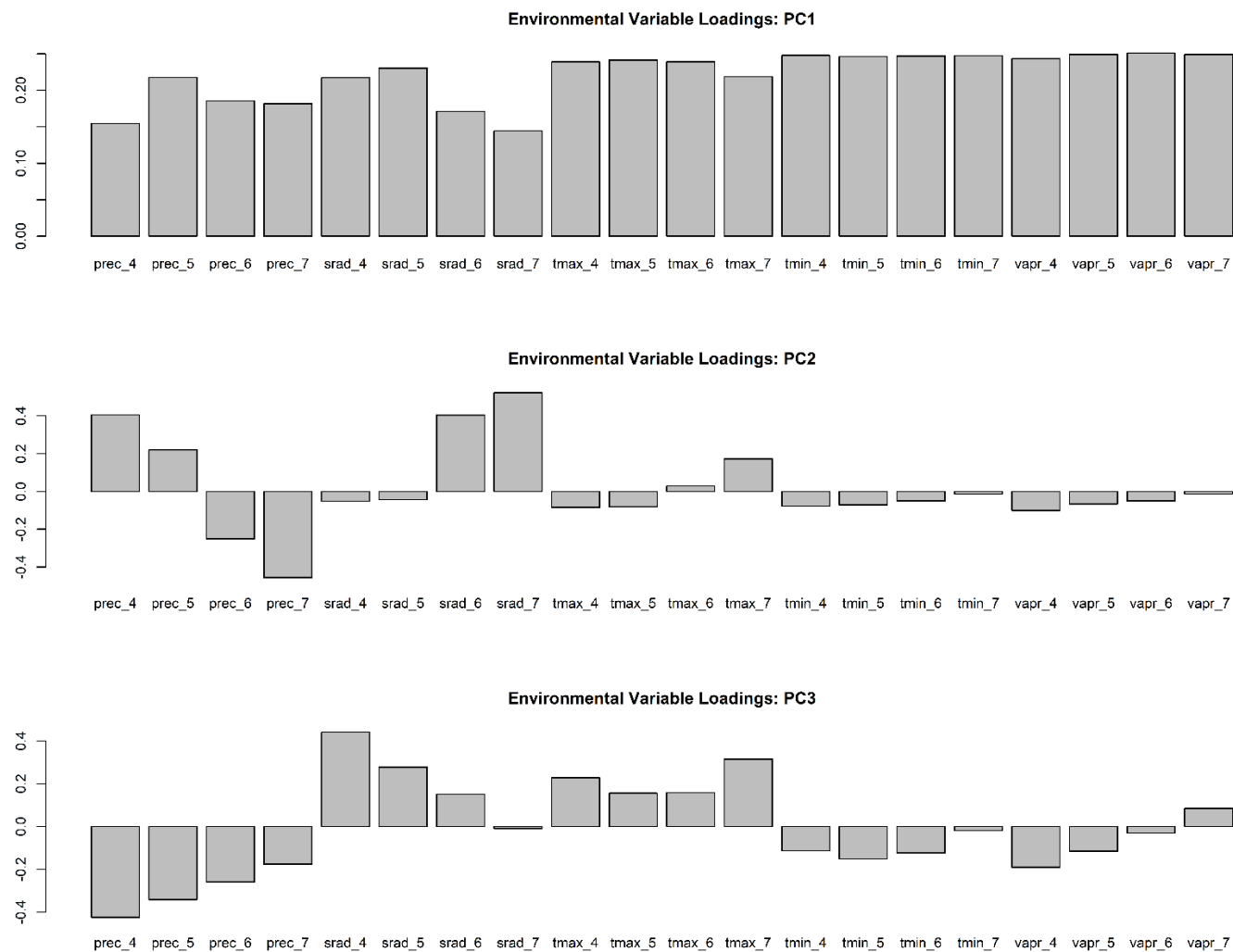


Figure S.4: Barplots of variable loadings from PCA of historical climate variables for the months of April through July (4 through 7, respectively); “prec” signifies monthly precipitation (mm), “srad” signifies monthly solar radiation ($\text{kJ m}^{-2} \text{day}^{-1}$), “tmax” signifies maximum monthly temperature ($^{\circ}\text{C}$), “tmin” signifies minimum monthly temperature ($^{\circ}\text{C}$), 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]
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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	<p>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]</p>	<p>energy production and conversion; glycerol kinase activity [EggNOG]</p>
SNP_77047	2082	INPP5K	2E-29	<p>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]</p>	<p>signal transduction mechanisms; phosphatidylinositol dephosphorylation [EggNOG]</p>

SNP_77047	22512	MYO1C	8E-33	<p>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]</p>	microtubule-based movement [OrthoDB]
SNP_77047	24081	PITPNA	8E-29	<p>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]</p>	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

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

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
SNP_12549	dDocent_Contig_8568	CM027515.1	801477	2	1.3074E-06	1
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

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

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

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

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

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

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

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

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
SNP_31315	dDocent_Contig_23064	CM027513.1	17200542	1	7.4688E-04	1
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
SNP_32192	dDocent_Contig_24053	CM027509.1	1.06E+08	2	2.9659E-01	0

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

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

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

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

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
SNP_46729	dDocent_Contig_38208	CM027509.1	34672947	3	3.4046E-11	1
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
SNP_48790	dDocent_Contig_40232	CM027509.1	42164989	3	4.7971E-08	1
SNP_48821	dDocent_Contig_40259	CM027536.1	34452550	1	1.5886E-07	1
SNP_48838	dDocent_Contig_40266	CM027509.1	1659790	4	1.6006E-12	1
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
SNP_48971	dDocent_Contig_40533	CM027515.1	3726388	2	5.8725E-01	0
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

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
SNP_51999	dDocent_Contig_43404	CM027520.1	1675102	1	2.2446E-01	0
SNP_52034	dDocent_Contig_43426	CM027508.1	64232108	3	1.3034E-16	1
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

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

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

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

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

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

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

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

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

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

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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