

Source and spread dynamics of mountain pine beetle in central Alberta,

Canada

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Subject Editor: Barbara Bentz

Abstract

The mountain pine beetle (*Dendroctonus ponderosae* Hopkins) (Coleoptera: Curculionidae) is a significant destructive force in the pine forests of western Canada and has the capacity to spread east into a novel host tree species, jack pine (Pinaceae). New populations have been documented in central Alberta, Canada, but the source populations for these outbreaks have yet to be identified. In this study we use genetic data to identify parent populations for recent outbreak sites near Slave Lake, Lac La Biche, and Hinton, Alberta. We found the northern population cluster that entered Alberta near Grande Prairie was the source of the most eastern established population near Lac La Biche, and the range expansion to this leading-edge population has been too rapid to establish evidence of population structure. However, some dispersal from a population in the Jasper and Hinton area has been detected as far north and east as Slave Lake, Alberta. We also identified two potential source populations for the current outbreak in Hinton: most beetles appear to be from Jasper National Park, Alberta, but some also originated from the northern population cluster. These findings demonstrate the dynamic dispersal capabilities of mountain pine beetle across the Alberta landscape and the potential hazard of increased dispersal to newly established leading-edge populations.

Introduction

The mountain pine beetle, *Dendroctonus ponderosae* Hopkins (Coleoptera: Curculionidae), is a tree-killing bark beetle that has become one of the most significant destructive forest pests in western North America (Natural Resources Canada 2017). Historically, mountain pine beetle populations in Canada have been confined largely to British Columbia and southwestern Alberta within the range of their primary host, lodgepole pine (Pinaceae; Safranyik et al. 2010). However, in the early 2000s, populations expanded and established in northwestern Alberta (Natural Resources Canada 2017), aided by wind updrafts (Jackson et al. 2008; Janes et al. 2014). The species' eastward spread has continued, resulting in more than \$Cdn 500 million being spent on mitigating damage in Alberta alone (Whittaker 2018). Northeastern Alberta is of particular concern because this is where lodgepole pine transitions to jack pine, a naive host species that provides a potential entry point into the boreal pine forests of eastern Canada and the northern United States of America (Cullingham et al. 2011; Bleiker et al. 2014).

Various genetic markers have been used to map mountain pine beetle population structure and range expansions in British Columbia (Mock et al. 2007) and Alberta (Langor and Spence 1991; Cullingham et al. 2012; Samarasekera et al. 2012; Janes et al. 2014; Batista et al. 2016; Janes et al. 2016; Janes et al. 2018). These studies have shown that mountain pine beetle spread into Alberta was composed of

two incursions that are genetically distinct (Samarasekera et al. 2012; Janes et al. 2014; Batista et al. 2016) and of a third incursion that is genetically intermediate (Trevoy et al. 2018). The southern resident population has ranged as far north as Banff and Canmore (Hopping and Mathers 1945), and a more recently established northern population extends eastwards past Grande Prairie (Janes et al. 2014). The intermediate population recently entered Alberta by way of Jasper National Park, and its genetic similarity to lab-produced hybrids between the northern and southern populations suggests that it resulted from admixture between them (Trevoy et al. 2018).

Epidemic populations have been identified in Hinton, west-central Alberta, and Slave Lake, indicating continued northeastwards range expansion in Alberta. Mountain pine beetle has now also been detected at low densities on the eastern edge of Alberta near the border with Saskatchewan, Canada in novel jack pine habitat (MacCormick 2020). It is uncertain if beetles detected near Saskatchewan came from low-density, locally established populations from previous long-range dispersal events or directly from larger outbreak populations to the west. These recently detected populations have not yet been included in demographic studies on mountain pine beetle spread. Determining their sources would allow optimisation of pheromone monitoring (Miller et al. 2005), guide forest management practices to limit localised population increases (Safranyik and Carroll 2006), and better inform assessments of

outbreak risk (Bleiker 2019). In the present study, we use genome-wide single nucleotide polymorphisms (SNPs) to characterise population structure and identify dispersal and spread of mountain pine beetle in northern Alberta, particularly in newly detected northeastern populations.

Methods

Beetle sampling, DNA extraction, and sequencing

A total of 306 specimens were collected at 44 different sites from nine locations during 2014–2018, and specimens were assigned to populations based on proximity to other collection localities (Supplemental materials, Table S1). Beetles were preferentially taken from different trees or egg galleries to reduce the influence of genetic structuring due to the inclusion of siblings from single families. Once collected, beetles were preserved in 90–95% ethanol and placed in a freezer at -20°C until DNA extraction.

DNA extraction used the Qiagen DNEasy Blood & Tissue kit with an optional RNase A treatment. Library preparation of samples collected in 2014–2015 followed the two-enzyme genotyping-by-sequencing protocol of Poland *et al.* (2012), and the library preparation of samples collected in 2016–2018 followed the double digest restriction-site associated DNA sequencing protocol of Peterson *et al.* (2012), according to the general procedure outlined in Campbell *et al.* (2017). Single-end

sequencing of the 2014–2015 samples was performed on an Illumina HiSeq 2000 at the Institut de biologie intégrative et des systèmes (IBIS) at Université Laval, Quebec City, Québec, Canada, whereas single-end sequencing of the 2016–2018 samples was done on an Illumina NextSeq 500 at the University of Alberta Molecular Biology Service Unit, Edmonton, Alberta, Canada.

Data filtering and single nucleotide polymorphism identification

Initial data demultiplexing was conducted in Stacks, version 2.0b (Rochette et al. 2019) on the Graham cluster of Compute Canada (Toronto, Ontario, Canada). The *PstI* restriction sites on the 5' end of each DNA sequence that was read were trimmed using Cutadapt, version 1.9.1 (Martin 2011). Samples sequenced on a NextSeq 500 had a final read length of 67 base pairs after trimming. Following Campbell et al. (2017), longer reads produced on a HiSeq 2000 were additionally truncated on the 3' end to match the length of the NextSeq-generated data. The trimmed sequence reads were then aligned to the female mountain pine beetle draft genome (Keeling et al. 2013) using the alignment algorithm Burrows–Wheeler Aligner Maximal Exact Match (BWA-MEM), version 0.7.17 (Li and Durbin 2009). Alignment quality was checked using SAMtools, version 1.9 (Li et al. 2009).

Single nucleotide polymorphisms were identified using the `ref_map.pl` script in Stacks (Catchen et al. 2011; Rochette et al. 2019). We specified a minimum minor

allele frequency of 0.01 and adhered to the *r80* principle recommended by Paris et al. (2017), which requires a locus to be present in at least 80% of the individuals in a population in order to be retained in the final dataset. At each locus, only a single random SNP was retained. Further filtering of SNP data and samples was conducted in VCFtools, version 0.1.14 (Danecek et al. 2011). Specifically, loci were excluded if they had a genotype-quality score below 30 or if a SNP locus had more than 5% missing data globally. Initial exploratory principal component analysis recovered clustering along PC1 that appeared to be driven by sex (consistent with Trevoy et al. 2019) which largely confounded population-level clustering (Supp. Fig. 2). To remove this signal, we filtered for linkage disequilibrium, following Abdellaoui et al. (2013). Linkage disequilibrium was calculated for all pairwise SNP combinations using the dartR package (Gruber and Georges 2019) in R (R Core Team 2018). For any groups of SNPs that were in linkage disequilibrium ($R^2 > 0.5$), we retained only one random SNP from each to reduce the impact on population-clustering analyses. Finally, we did not distinguish between putatively adaptive and neutral loci for population-clustering analyses because a combination of both has been shown to more accurately reflect population structure in mountain pine beetle (Batista et al. 2016).

Principal component analysis groups specimens based on the extent of covariance in their associated data, and often individuals that are closely related can

confound population structure due to their high rate of covariance (Alhusain and Hafez 2018). Although our sampling procedure was designed to reduce the incidence of multiple specimens from a single family, data visualisation using principal component analysis indicated tight clustering patterns for two groups, consisting of a total of seven individuals, that were consistent with family-level structure (Price et al. 2010; Supplemental materials, Fig. S1). Three clustered individuals came from a single tree (sibling group 1, Supplemental materials, Fig. S1), and four clustered individuals came from two close trees (sibling group 2, Supplemental materials, Fig. S1). No patterns in missing data or poor locus coverage were identified that could explain this structuring. Because female mountain pine beetles are capable of producing multiple egg galleries from a single mating (Reid 1958), these clustered individuals were assumed to be siblings. To reduce the influence of such family structure on population-level analyses, all but one individual in each set of closely related specimens were removed from the dataset.

Population structure analysis

To explore and identify potential signs of population structure across northern Alberta, we used several approaches. A principal component analysis on all samples that passed filtering was performed in the R package Adegenet (Jombart 2008; Jombart and Ahmed 2011) and plotted with ggplot2 (Wickham 2016). This was used

to detect SNP covariance between specimens and to identify population structure among the specimens without *a priori* population assignment. We also used this set of samples to calculate observed heterozygosity, expected heterozygosity, and pairwise population differentiation due to genetic structure (F_{st}) in the R package *dartR*, and the R package *Genepop* (Raymond and Rousset 1995; Rousset 2008) was used to calculate population differentiation based on genetic diversity using an exact G-test of genic differentiation with a Bonferroni correction based on the 36 pairwise tests.

To assess fine-scale population structure across the northernmost locations, we created a northern dataset by removing all southern- and intermediate-cluster population samples, including any putative dispersers. We performed a principal component analysis on this northern dataset, then used discriminant analysis of principal components (Jombart et al. 2010) in *Adegenet* to detect potential weak signals of population structure using *a priori* population assignments based on collection locality and verified by the prior principal component analysis. We then performed isolation-by-distance analysis using the R packages *Geosphere* (Hijmans 2019) and *SNA* (Butts 2016), and calculated a Mantel test in *adegenet*.

The program *Structure*, version 2.3.4 (Pritchard et al. 2000; Falush et al. 2003; Falush et al. 2007; Hubisz et al. 2009) was used to infer genetic population structure among all populations. We subsampled the full dataset to 125 individuals that were arbitrarily selected to represent potential sample-site variation (10 to 16 individuals

from each location) in order to reduce bias due to differences in sampled population sizes (Puechmaille 2016). In this dataset, we attempted to include as many samples as possible for each population while maintaining a roughly equal sample size among the many sampling locations. We used the admixture model without specifying *a priori* population or location information, and we tested values of K from 1 to 10 with 1 million Markov chain Monte Carlo generations and a burn-in period of 250,000. We replicated the analysis for each value of K a total of 10 times and then used CLUMPAK (Kopelman et al. 2015) to average the 10 independent replicates for each value of K . The optimal value of K was assessed using both the difference between the likelihoods of subsequent K values (ΔK) (Evanno et al. 2005), and the mean estimated natural logarithm of the probability of each K value ($\text{Ln}(\text{Pr}K)$) (Pritchard et al. 2000). We then ran a principal component analysis using this subset of data to ensure our Structure results were comparable to the principal component analyses of the full dataset described above.

Results

After filtering, 299 individuals and 2872 genomic SNPs were retained for data analysis (Supplemental materials, Table S1). Average individual read depth was 58.3 (minimum depth = 12.6, maximum depth = 217.3; Supplemental materials, Table S1). Pairwise F_{st} between populations ranged from approximately 0 to 0.13 (Table 1),

with Canmore found to be the most distinct population. Tests for differences in pairwise population genetic differentiation also identified Canmore as having allelic distributions that significantly differed from those of all other tested populations and found some significant differences between intermediate and northern locations (Table 1). Observed heterozygosity was similar among populations, ranging from 0.14 to 0.19, and differences between expected and observed heterozygosity were minimal (Table 1). Some of the most recently detected populations, such as Battle Lake and Lac La Biche, had higher heterozygosity than some older, established populations, such as Grande Prairie and Edson, but no clear trend was evident (Table 1).

In the principal component analysis for the full dataset of 299 individuals (Fig. 1A), beetle sex had strong signal that overwhelmed population structure (Supplemental materials, Fig. S2). All but three specimens could be sexed using methods outlined in Trevoy et al. (2019). For the three ambiguous specimens, we removed all loci containing missing data from sex-related scaffolds, but they remained intermediate between the male and female clusters (Supplemental materials, Fig. S2). Despite this, after filtering for linkage disequilibrium, these specimens clustered as expected, based on sampling location. To focus on geographic population structure, sex-based signal was successfully removed from the dataset by filtering for linkage disequilibrium .

After filtering, the first principal component (PC1), which often relates to geographic location in genetic assessments of population structure (see Abdellaoui et al. 2013), explained 3.6% of the variation in the SNP data and distinguished northern and southern populations as well as a distinct intermediate group between the two; for this study we used $PC1 = -5.5$ and -0.06 to delimit the intermediate cluster. The second principal component explained 1.0% of the remaining variance and related to variation within, rather than between, populations.

No population structure was detected in either principal component analysis or discriminant analysis of principal components when we focussed on a northern dataset that included 206 specimens, after removing individuals from the intermediate and southern clusters (Fig. 1B; Supplemental materials, Fig. S3).

Isolation-by-distance analysis of the northern locations likewise did not indicate any patterns of population differentiation based on geographic distances (Mantel test: $p = 0.75$).

The ΔK values from the Structure analysis indicated an optimal K value of 2, and $\text{Ln}(\text{Pr}K)$ indicated an optimal K of 2 or 3 (Supplemental materials, Fig. S4). A K value of 2 distinguished northern and southern population clusters and identified a genetically and geographically intermediate population of specimens from Jasper, Battle Lake, and Hinton (Fig. 2); K values of three and higher neither further resolved this intermediate population nor indicated any other meaningful geographic

clustering. Thus, $K = 2$ was considered to be optimal (Supplemental materials, Fig. S4). Structure analysis also indicated some individuals that did not cluster according to the locations in which they were collected; one individual that was collected near Edson and one that was collected near Slave Lake grouped with the intermediate population. Principle component analysis using this subset of 125 samples also produced similar divisions to the Structure analysis and closely resembled the patterns shown in Fig. 1A, indicating that the results of the Structure analysis were consistent with the population structure identified through principal component analysis of the full dataset.

Based on the principal component analysis of the full dataset ($n = 299$), we identified several additional individuals that were collected in the northern populations but grouped with the intermediate population cluster, bringing the totals to three beetles from Slave lake, five from Whitecourt, and one from Edson (Supplemental materials, Table S1 and Fig. S5). By chance, none of these Whitecourt individuals were sampled in the subset Structure analysis of 125 individuals; however, a larger Structure analysis of all 299 specimens indicated that these individuals were admixed (Supplemental materials, Fig. S4) and was largely consistent with the results of the principal component analysis presented in Fig. 1A. We also identified 11 specimens collected in Hinton and one collected in Jasper that grouped with the northern cluster. Of these putative dispersers, 81% were female and

19% were male (Supplemental materials, Table S1); the sex ratio of these geographically mismatched individuals is consistent with known sex-biases in mountain pine beetle (Blomquist et al. 2010; James et al. 2016; Fig. 3). No putative dispersers from the intermediate population were found among the newly established Lac La Biche specimens.

Discussion

Our study used population structure to investigate the dispersal dynamics of mountain pine beetle in central Alberta, identifying primary source populations as well as fine-scale dispersal from other regions. We found the same distinct north–south beetle genetic population structure that was previously described for Alberta (Janes et al. 2014; Batista et al. 2016; Trevoy et al. 2018; Figs. 1 and 2). When we focussed on individuals from northern locations, however, we found no evidence of population structure (Fig. 1B). This finding is consistent with a high rate of dispersal and gene flow between these regions. The long-range dispersal capability of mountain pine beetle (Jackson et al. 2008) likely promotes genetic admixture, particularly from west to east, and may have inhibited the further development of genetically distinct populations in this region.

The extensive dispersal of mountain pine beetle also applies to mixing of population clusters. Although we saw no admixture involving the southern cluster, mingling was evident among the north and intermediate populations. We identified

several putative dispersers with affinities to Jasper and Hinton in sites across the northern locations, including as far to the northeast as Slave Lake (Fig. 3; Supplemental materials, Table S1). This illustrates the considerable dispersal capability of these populations and their potential contribution to range expansion in the north. The majority of putative dispersers that we identified were female, which could potentially increase establishment success rate because female beetles can be mated before they disperse (Bleiker et al. 2013) and are the pioneering sex in *D. ponderosae* (Blomquist et al. 2010). Specimens collected in Hinton and one specimen at Jasper showed the reverse pattern, with some beetles having affinities to the northern cluster, indicating that several individuals likely came from a northern source (Fig. 3). These results highlight the importance of considering multiple source populations when determining infestation origins in newly established regions.

Admixture and high dispersal rates from the north and intermediate populations toward the northeast may have important genetic ramifications. In particular, dispersal from the genetically intermediate Jasper and Hinton region is likely to increase genetic diversity in the currently expanding eastern range of mountain pine beetle, which would otherwise be solely composed of the genetically homogenous northern population. Although this introduces the possibility of potential benefits from increased genetic diversity in the leading-edge populations, high rates of dispersal and gene flow may also prevent local adaptation (Lenormand 2002).

Regardless, genetic differences between regions allow us to monitor new populations and to identify the magnitude and composition of the spread of mountain pine beetles toward the northeast from different genetic sources.

Currently, the leading edge of the mountain pine beetle range is found in jack pine forests near Lac La Biche (MacCormick 2020), and this population is genetically indistinguishable from other northern populations as far west as Grande Prairie. This uniformity can be explained by high rates of dispersal and regular waves of reinforcing conspecifics from other populations. In another forest pest, the spruce budworm (*Choristoneura fumiferana* Clemens) (Lepidoptera: Tortricidae), reinforcing waves of dispersers from neighbouring populations may allow endemic populations to become epidemic (Larroque et al. 2020). Although their life histories differ, mountain pine beetle and spruce budworm have similar overall outbreak dynamics, with large increases in population size causing epidemic conditions (Royama 1984; Larroque et al. 2020). In jack pine forests, mountain pine beetle can face intense competition from heterospecifics, such as wood-boring beetles (Klutsch et al. 2016). This may serve to mediate local population growth, but populations near Slave Lake likely make contributions to the Lac La Biche infestation. Continued recruitment in this region risks establishing large, potentially epidemic populations in the eastern jack pine forests.

Mountain pine beetle dispersal has been difficult to predict, but our study has helped to identify large-scale dispersal patterns in central Alberta. We demonstrate that the current Hinton infestation was derived from two sources, these likely being Jasper and, to a lesser degree, Grande Prairie. Although we found no evidence of any dispersal from the southern population cluster, there was a general trend of population expansion from the Jasper region toward the northeast, with occasional dispersal as far northeast as Slave Lake. To date, control efforts in Alberta have been largely successful at slowing the spread of mountain pine beetle, but the beetle nonetheless remains capable of extensive and rapid range expansion. Long-range dispersal may limit population structure within the northernmost regions, but it also may contribute to epidemic population development. Continued focus on reducing current outbreaking populations may be necessary to minimise long-range dispersal and reinforcement of populations at the beetle's leading edge in Alberta.

Acknowledgements. This research was supported by funding awarded to Felix Sperling from the Natural Science and Engineering Research Council of Canada (grant no. NET GP 434810-12) to the TRIA Network, with contributions from Alberta Agriculture and Forestry, fRI Research, Manitoba Conservation and Water Stewardship, Natural Resources Canada – Canadian Forest Service, Northwest Territories Environment and Natural Resources, Ontario Ministry of Natural Resources and Forestry, Saskatchewan Ministry of Environment, West Fraser, and

Weyerhaeuser. An NSERC Discovery Grant to F. Sperling (RGPIN-2018-04920) supported V. Shegelski during preparation of this manuscript.

This research was also funded by the Government of Alberta.

The authors also thank Julian Dupuis, Stephane Bordeleau, Jackson Lai, Dylan Sjolie, Phil Batista, Sebastian Lackey, Devin Letourneau, Melodie Kunegel-Lion, John Haley, Andrew Sperling, William Sperling, Janet Sperling, Stephen Trevoy, Neil Thompson, Jennifer McCormack, and Fraser McKee for their help with sample collection, logistics, and advice on statistical analyses.

This research was enabled in part by support provided by Westgrid (www.westgrid.ca) and Compute Canada (www.computecanada.ca).

Data availability. Raw sequence data in the form of fastq files are available in the National Center for Biotechnology Information Sequence Read Archive (NCBI SRA) under the accession number PRJNA656769 (<https://www.ncbi.nlm.nih.gov/sra/PRJNA656769>).

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Figure & Table Captions

Fig. 1. Principal component analyses results. A, Results for all sampling locations and individuals ($n = 299$), and B, results for northern locations (Edson, Grande Prairie, Lac La Biche, Slave Lake, and Whitecourt), with all intermediate-cluster individuals removed ($n = 201$). In A, ellipses were added to emphasise the south, intermediate and north clusters. These genetic population clusters were divided at $PC1 = -5.5$ and $PC1 = -0.06$ for assignment of individuals in Supplemental materials, Table S1.

Fig. 2. Structure analysis for equivalently sized population subsets, totalling 125 individuals. $K = 2$ was the best supported number of populations. Based on individual assignments, the Edson and Slave Lake populations each include a single admixed individual with a roughly equal assignment to both the northern and southern genetic clusters.

Fig. 3. Population expansion dynamics inferred from genetic evidence based on 299 mountain pine beetle specimens collected from sites across Alberta, Canada.

Pie charts for each sampling location are coloured by proportion of individuals assigned to the north (blue), intermediate (brown), and south (grey) population clusters, as determined using principal component analysis (Fig. 1A).

Table 1. Pairwise population differentiation p -values (above diagonal), F_{st} (below diagonal), and observed (H_o) and expected (H_e) population heterozygosity. Statistics were calculated using n individuals for each population group. Significantly differentiated population pairs (in bold) had genic differentiation values of $p < 0.001$ after Bonferroni correction.

Supplemental materials, Figure S1. Principal component analysis of the full dataset before removal of any individuals displaying potential family structure ($n = 304$). Two clusters (circled in green and orange) of putative siblings are numbered corresponding to sibling groups in Supplemental materials, Table S1.

Supplemental materials, Fig. S2. Principal component analyses results. A, Analysis based on 3372 SNPs using all 299 individuals before filtering for linkage disequilibrium. The first principal component (PC1) separates beetles by sex and shows three individuals with ambiguous sex determination. B, The sex-ambiguous beetles remained intermediate in an analysis based on 3269 SNPs after removing all sites containing missing data on sex-related scaffolds, based on Trevoy et al. (2019). C, Results after filtering for linkage disequilibrium, sex-based signal was removed

and, based on the remaining 2872 SNPs, individuals clustered according to geographic location; males and females were present in each group.

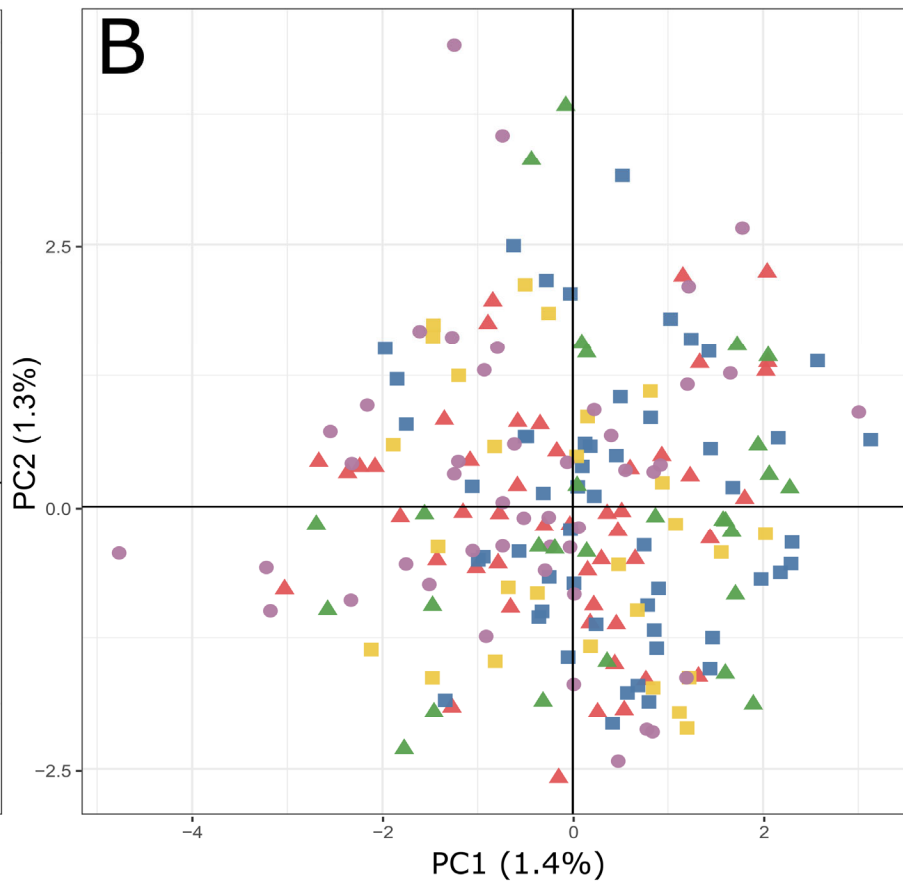
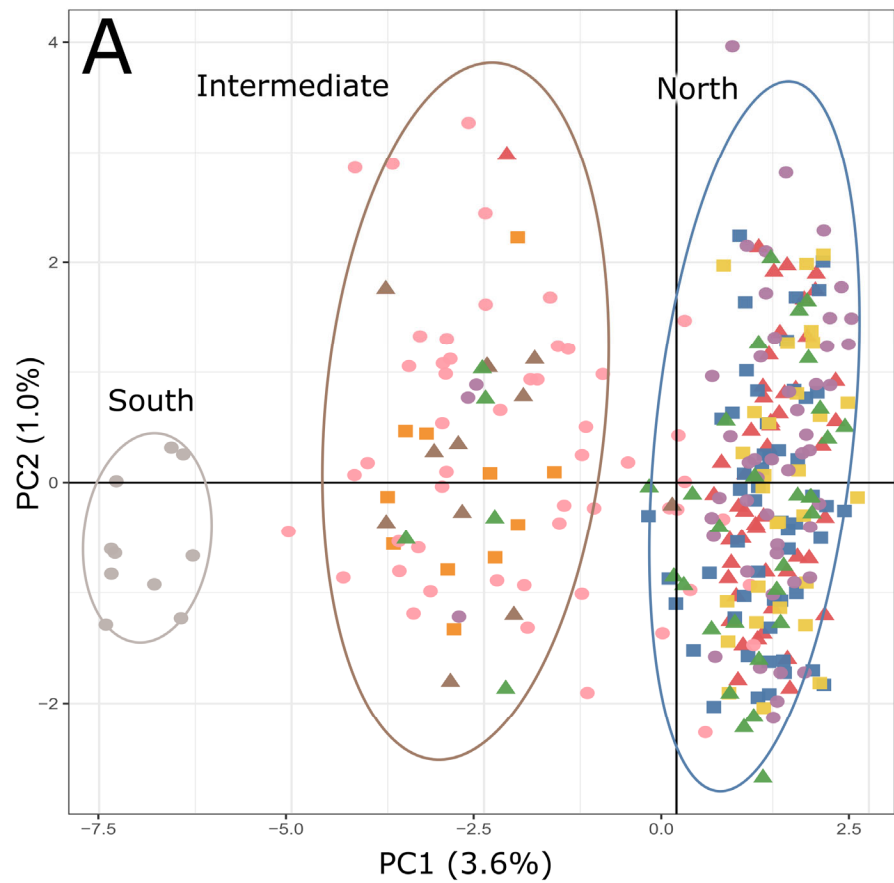
Supplemental materials, Fig. S3. Discriminant analysis of principal components of 206 individuals from five northern populations, excluding intermediate-cluster individuals as in Fig. 1B.

Supplemental materials, Fig. S4. Structure results. A, Results for $K=1$ to $K=10$ using a 125-individual subset from the nine sample locations; B, results for $K=1$ to $K=10$ for a larger analysis containing all 299 specimens.

Supplemental materials, Fig. S5. Principal component analyses of the full dataset of 299 individuals, in which black shading is used to highlight specimens clustered for each individual sampling location.

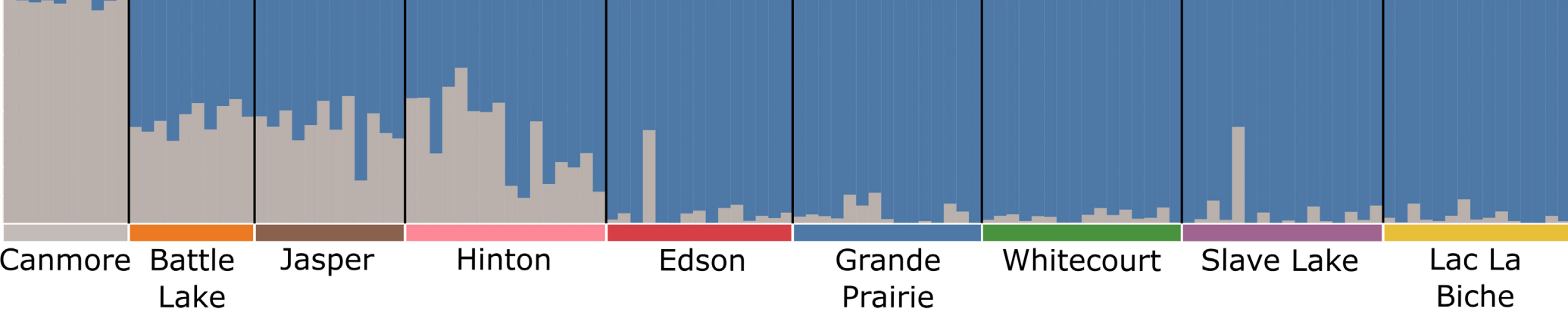
Supplemental materials, Table S1. Specimen collection and analysis summary information.

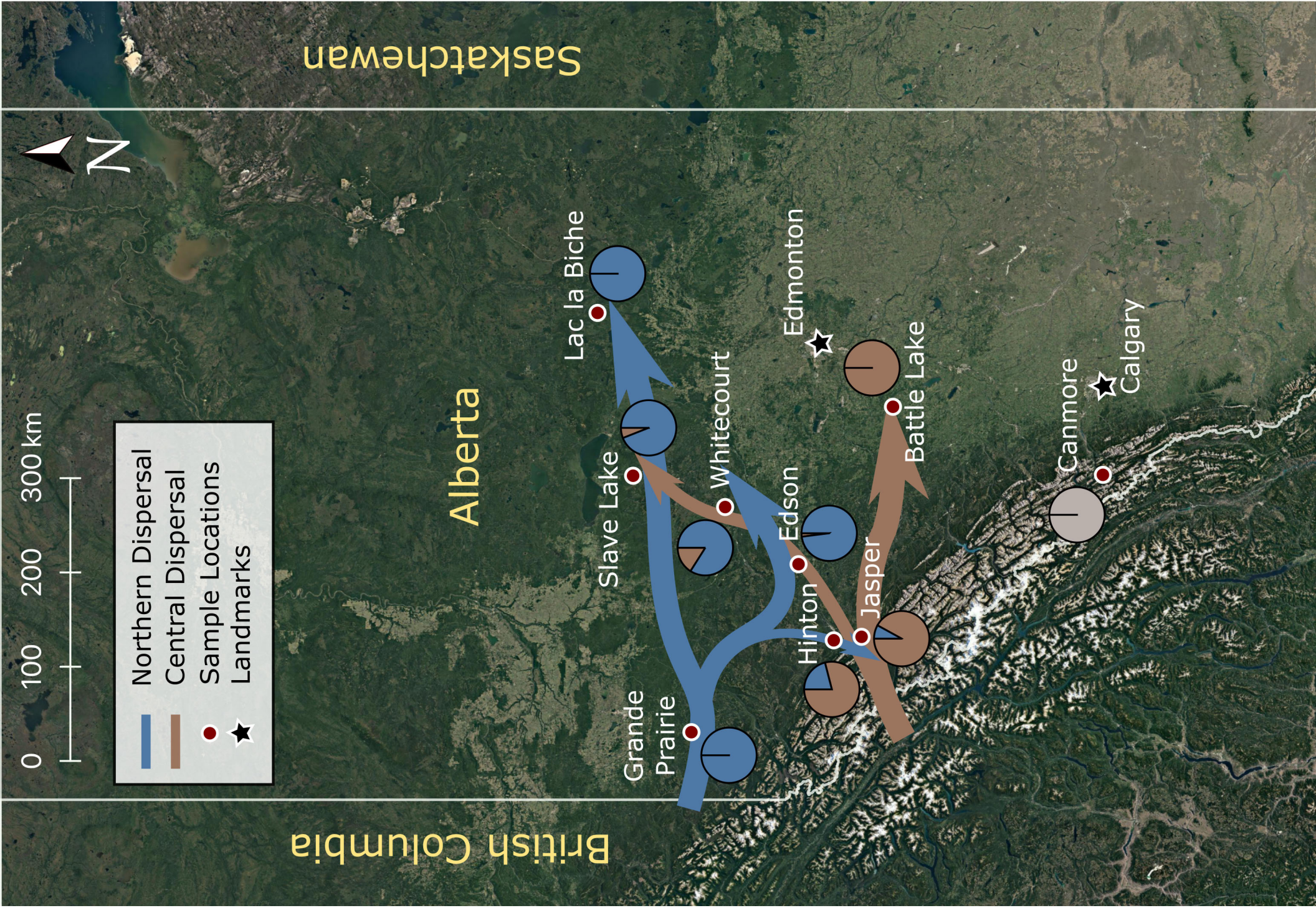
Fst \ Gen D										n	Ho	He
	Battle Lake	Canmore	Edson	Grande Prairie	Hinton	Jasper	Lac La Biche	Slave Lake	Whitecourt			
Battle Lake	--	0.018	0.000	0.000	1.000	1.000	0.000	0.000	0.187	5	0.1	0.1
Canmore	0.053	--	0.000	0.000	0.000	0.000	0.000	0.000	0.000	2	9	9
Edson	0.032	0.128	--	1.000	0.000	0.000	1.000	1.000	1.000	4	0.1	0.1
Grande Prairie	0.032	0.131	0.002	--	0.000	0.000	1.000	1.000	1.000	8	8	8
Hinton	0.002	0.065	0.019	0.018	--	1.000	0.000	0.000	0.000	4	0.1	0.1
Jasper	0.001	0.056	0.028	0.028	0.002	--	0.000	0.000	0.918	9	5	7
Lac La Biche	0.036	0.134	0.003	0.003	0.021	0.031	--	1.000	1.000	5	0.1	0.1
Slave Lake	0.030	0.126	0.001	0.001	0.017	0.024	0.003	--	1.000	3	5	7
Whitecourt	0.021	0.113	0.001	0.001	0.012	0.018	0.003	0.001	--	3	0.1	0.1
										2	4	9
										7	0.1	0.1
										9	8	9
										1	0.1	0.1
										0	7	7
										1	0.1	0.1
										2	4	8
										1	0.1	0.1
										1	6	8



- Battle Lake
- Canmore
- ▲ Edson
- Grande Prairie
- Hinton
- ▲ Jasper
- Lac La Biche
- Slave Lake
- ▲ Whitecourt

$K = 2$



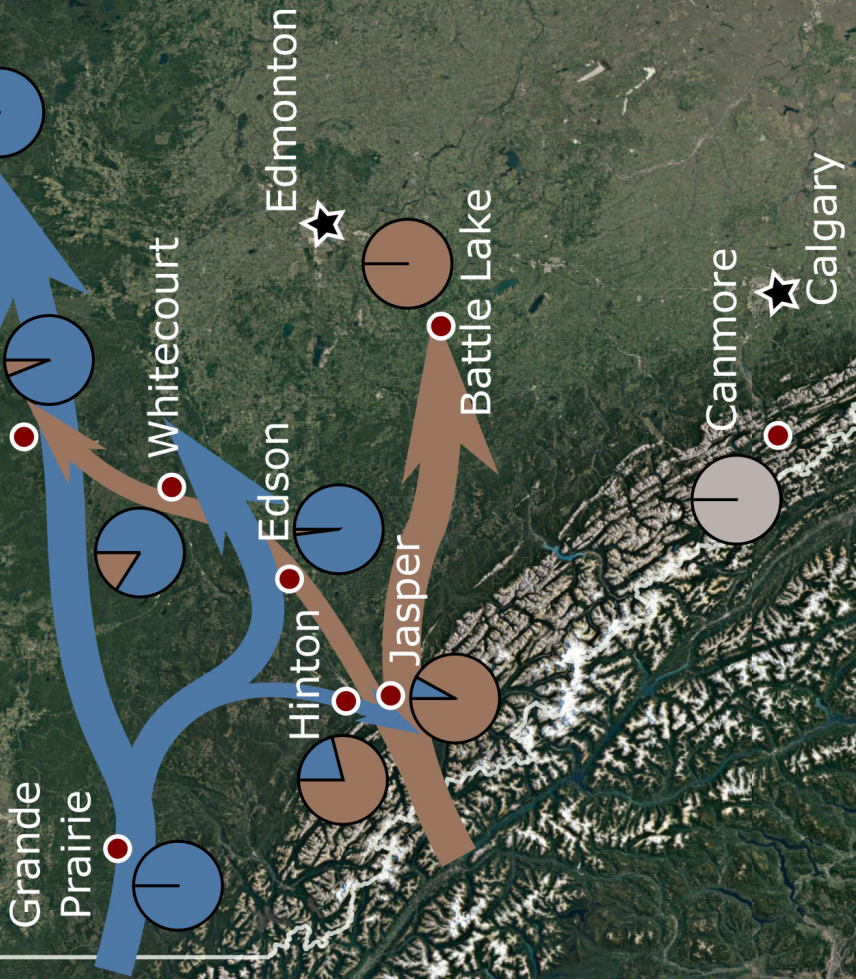


British Columbia

Alberta

Saskatchewan

- Northern Dispersal
- Central Dispersal
- Sample Locations
- Landmarks



Collection Site Data												Read Depth: All Loci before LD filtering	Read Depth: LD Filtered Loci			
Sample ID	Location	Site #	Latitude	Longitude	Collection Year	Cluster Identity (PCA and Structure)	Putative Disperser (Y/-)	PCA Sex	Sexed in Trevoy et al. (2019) (Y/-)	Sibling Group	Structure Sample Subset (Y/-)	# of Loci	Mean Depth	# of Loci	Mean Depth	Removed from final analysis?
12380	Battle Lake	1	52.941	-114.284	2018	Interm.	-	Female	-	-	-	16253	43.4655	2862	82.724	-
12381	Battle Lake	1	52.941	-114.284	2018	Interm.	-	Female	-	-	Y	16012	39.9846	2768	78.9447	-
12382	Battle Lake	1	52.941	-114.284	2018	Interm.	-	Female	-	-	Y	16183	29.1735	2864	55.1994	-
12383	Battle Lake	1	52.941	-114.284	2018	Interm.	-	Male	-	-	Y	16365	37.481	2868	74.8992	-
12384	Battle Lake	1	52.941	-114.284	2018	Interm.	-	Female	-	-	Y	16446	36.82	2869	71.3297	-
12385	Battle Lake	1	52.941	-114.284	2018	Interm.	-	Female	-	-	Y	16463	34.51	2867	65.398	-
12386	Battle Lake	1	52.941	-114.284	2018	Interm.	-	Female	-	-	Y	16431	30.8421	2866	57.8126	-
12387	Battle Lake	1	52.941	-114.284	2018	Interm.	-	Female	-	-	Y	15475	21.2048	2861	44.1615	-
12388	Battle Lake	1	52.941	-114.284	2018	Interm.	-	Female	-	-	Y	16337	27.8837	2869	52.6337	-
12389	Battle Lake	1	52.941	-114.284	2018	Interm.	-	Female	-	-	Y	16292	23.3642	2868	45.0356	-
12390	Battle Lake	1	52.941	-114.284	2018	Interm.	-	Male	-	-	Y	16139	29.3416	2867	54.9111	-
CAN10	Canmore	1	51.067	-115.287	2014	South	-	Female	Y	-	Y	5275	49.8927	2789	60.5034	-
CAN12	Canmore	1	51.067	-115.287	2014	South	-	Female	Y	-	Y	5446	71.3608	2825	88.1763	-
CAN13	Canmore	1	51.067	-115.287	2014	South	-	Male	Y	-	Y	5326	63.4362	2804	76.4326	-
CAN1	Canmore	1	51.067	-115.287	2014	South	-	Female	Y	-	Y	5541	122.351	2838	151.992	-
CAN2	Canmore	1	51.067	-115.287	2014	South	-	Female	Y	-	Y	5446	105.88	2790	132.536	-
CAN4	Canmore	1	51.067	-115.287	2014	South	-	Female	Y	-	Y	5526	107.159	2834	133.19	-
CAN5	Canmore	1	51.067	-115.287	2014	South	-	Female	Y	-	Y	5533	99.7622	2821	124.015	-
CAN6	Canmore	1	51.067	-115.287	2014	South	-	Female	Y	-	Y	5473	96.5167	2826	121.305	-
CAN7	Canmore	1	51.067	-115.287	2014	South	-	Male	Y	-	Y	5309	47.2349	2807	55.7089	-
CAN9	Canmore	1	51.067	-115.287	2014	South	-	Female	Y	-	Y	5540	97.5338	2832	121.204	-
H1_1	Edson	1	53.702	-116.847	2014	North	-	Female	Y	-	Y	6338	115.438	2825	189.487	-
H1_2	Edson	1	53.702	-116.847	2014	North	-	Female	Y	-	-	5884	66.1766	2822	98.3863	-
H1_3	Edson	1	53.702	-116.847	2014	North	-	Female	Y	-	Y	6457	130.719	2836	217.306	-
H2_1	Edson	2	53.770	-116.961	2014	North	-	Female	Y	-	-	5515	44.392	2802	64.6428	-
H2_3	Edson	2	53.770	-116.961	2014	North	-	Male	Y	-	-	5869	57.0421	2815	85.3087	-
H2_4	Edson	2	53.770	-116.961	2014	North	-	Female	Y	-	Y	5693	61.4732	2812	92.4147	-

H3_1	Edson	3	53.777	-116.686	2014	North	-	Male	Y	-	Y	5481	48.3523	2795	68.8279	-
H3_2	Edson	3	53.777	-116.686	2014	North	-	Female	Y	-	-	5624	47.7891	2804	69.8431	-
H3_3	Edson	3	53.777	-116.686	2014	North	-	Female	Y	-	-	5804	54.9254	2816	82.2695	-
H3_4	Edson	3	53.777	-116.686	2014	North	-	Male	Y	-	-	5785	60.7077	2808	89.6368	-
H4_3	Edson	4	53.833	-116.992	2014	North	-	Male	Y	-	Y	5031	30.9646	2754	40.3526	-
H4_4	Edson	4	53.833	-116.992	2014	North	-	Female	Y	-	-	5421	37.9666	2811	53.502	-
xA1A	Edson	5	53.398	-115.850	2016	North	-	Female	-	-	Y	6830	63.081	2871	83.3016	-
xA1B	Edson	5	53.398	-115.850	2016	North	-	Female	-	-	-	6787	37.295	2869	49.4517	-
xA1C	Edson	5	53.398	-115.850	2016	North	-	Male	-	-	-	6780	73.3674	2871	90.6712	-
xA1D	Edson	5	53.398	-115.850	2016	North	-	Male	-	-	-	6815	52.2436	2869	64.5274	-
xA2A	Edson	5	53.398	-115.850	2016	North	-	Male	-	-	Y	6817	73.8147	2869	97.2063	-
xA2B	Edson	5	53.398	-115.850	2016	North	-	Female	-	-	-	6759	28.7661	2865	38.9438	-
xA2C	Edson	5	53.398	-115.850	2016	North	-	Female	-	-	-	6819	55.9207	2869	72.2008	-
xA2D	Edson	5	53.398	-115.850	2016	North	-	Male	-	-	-	6760	30.2969	2863	39.439	-
xA3A	Edson	5	53.398	-115.850	2016	North	-	Female	-	-	Y	6674	27.7881	2868	39.5345	-
xA3B	Edson	5	53.398	-115.850	2016	North	-	Female	-	2	-	6383	16.9452	2862	23.0458	-
xA3C	Edson	5	53.398	-115.850	2016	North	-	Male	-	2	-	6798	30.0484	2868	37.2361	Removed
xA3D	Edson	5	53.398	-115.850	2016	North	-	Female	-	-	-	6795	29.952	2872	38.4143	-
xA4A	Edson	5	53.398	-115.850	2016	Interm.	Y	Female	-	-	Y	6812	41.3062	2869	54.459	-
xA5A	Edson	5	53.398	-115.850	2016	North	-	Female	-	-	Y	6816	37.7707	2869	49.1032	-
xA5B	Edson	5	53.398	-115.850	2016	North	-	Female	-	-	-	6831	46.6061	2868	58.8975	-
xA5C	Edson	5	53.398	-115.850	2016	North	-	Female	-	-	-	6826	46.5381	2869	57.6215	-
xA5D	Edson	5	53.398	-115.850	2016	North	-	Male	-	-	-	6797	42.4673	2868	55.7423	-
xA6A	Edson	5	53.398	-115.850	2016	North	-	Female	-	-	-	6805	40.6642	2865	52.9173	-
xA6B	Edson	5	53.398	-115.850	2016	North	-	Female	-	2	-	6824	49.5299	2870	62.4892	Removed
xA6C	Edson	5	53.398	-115.850	2016	North	-	Male	-	2	-	6810	36.3514	2870	45.6073	Removed
xB1A	Edson	6	53.831	-116.569	2016	North	-	Female	-	-	Y	6701	29.2147	2867	41.2773	-
xB1B	Edson	6	53.831	-116.569	2016	North	-	Female	-	-	-	6709	26.4662	2867	37.0837	-
xB1C	Edson	6	53.831	-116.569	2016	North	-	Male	-	-	-	6782	57.0242	2868	71.4923	-
xB1D	Edson	6	53.831	-116.569	2016	North	-	Male	-	-	-	6785	58.9596	2863	73.8774	-
xB2A	Edson	6	53.831	-116.569	2016	North	-	Female	-	-	Y	6810	45.6078	2871	59.4601	-
xB2B	Edson	6	53.831	-116.569	2016	North	-	Male	-	-	-	6767	34.3501	2871	45.3751	-
xB2C	Edson	6	53.831	-116.569	2016	North	-	Female	-	-	-	6823	51.3948	2868	64.1464	-
xB2D	Edson	6	53.831	-116.569	2016	North	-	Female	-	-	-	6826	46.3541	2868	57.2451	-

xB3A	Edson	6	53.831	-116.569	2016	North	-	Male	-	-	Y	6753	30.2147	2869	40.0136	-
xB3B	Edson	6	53.831	-116.569	2016	North	-	Female	-	-	-	6778	30.0912	2862	40.0402	-
xB3C	Edson	6	53.831	-116.569	2016	North	-	Female	-	-	-	6821	43.5443	2868	56.6492	-
xB3D	Edson	6	53.831	-116.569	2016	North	-	Female	-	-	-	6813	45.2441	2867	58.9522	-
xB4A	Edson	6	53.831	-116.569	2016	North	-	Female	-	-	Y	6683	29.5655	2867	41.76	-
xB4B	Edson	6	53.831	-116.569	2016	North	-	Male	-	-	-	6648	29.0829	2868	40.7737	-
xB4C	Edson	6	53.831	-116.569	2016	North	-	Female	-	-	-	6664	56.2775	2774	73.0397	-
xB4D	Edson	6	53.831	-116.569	2016	North	-	Female	-	-	-	6819	36.6906	2867	46.0105	-
xB5A	Edson	6	53.831	-116.569	2016	North	-	Female	-	-	Y	6745	54.2156	2822	72.3444	-
xB5B	Edson	6	53.831	-116.569	2016	North	-	Female	-	-	-	6829	41.8045	2871	54.4943	-
xB5C	Edson	6	53.831	-116.569	2016	North	-	Female	-	-	-	6616	42.213	2765	53.1374	-
xB5D	Edson	6	53.831	-116.569	2016	North	-	Female	-	-	-	6822	33.9632	2870	42.0753	-
11951	rande Prair	1	54.570	-119.420	2015	North	-	Male	-	-	Y	10989	38.9342	2869	60.6783	-
12101	rande Prair	1	54.570	-119.420	2015	North	-	Female	-	-	Y	11013	34.0285	2871	53.1355	-
12102	rande Prair	1	54.570	-119.420	2015	North	-	Female	-	-	Y	11045	41.9216	2867	65.8148	-
12103	rande Prair	1	54.570	-119.420	2015	North	-	Female	-	-	Y	11026	32.7366	2869	51.0523	-
12104	rande Prair	1	54.570	-119.420	2015	North	-	Female	-	-	Y	11007	37.1044	2867	57.67	-
12105	rande Prair	1	54.570	-119.420	2015	North	-	Female	-	-	-	10789	32.587	2794	51.9384	-
12106	rande Prair	1	54.570	-119.420	2015	North	-	Female	-	-	-	11005	31.9507	2869	49.7292	-
12107	rande Prair	1	54.570	-119.420	2015	North	-	Male	-	-	-	10962	30.1093	2865	46.8876	-
12109	rande Prair	2	54.190	-118.680	2015	North	-	Female	-	-	-	10738	20.0106	2856	31.3403	-
12111	rande Prair	2	54.190	-118.680	2015	North	-	Female	-	-	-	9873	9.51767	2835	13.8621	-
12112	rande Prair	2	54.190	-118.680	2015	North	-	Female	-	-	-	10451	14.2051	2858	21.5794	-
12113	rande Prair	2	54.190	-118.680	2015	North	-	Female	-	-	-	9986	10.3071	2847	15.0948	-
12115	rande Prair	2	54.190	-118.680	2015	North	-	Female	-	-	-	11026	31.6983	2871	50.9478	-
12116	rande Prair	2	54.190	-118.680	2015	North	-	Female	-	-	-	10815	19.5419	2871	30.8157	-
xE1A	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	-	Y	10273	30.2785	2867	47.0527	-
xE1B	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	-	-	10418	30.2878	2866	47.172	-
xE1C	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	-	-	11055	41.7255	2866	60.9714	-
xE1D	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	-	-	11080	35.5255	2870	51.147	-
xE2A	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	-	Y	10283	17.3036	2867	24.5626	-
xE2B	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	-	-	11033	37.3132	2868	54.8368	-
xE2C	rande Prair	3	54.656	-119.007	2016	North	-	Male	-	-	-	10775	36.0033	2867	55.8744	-
xE2D	rande Prair	3	54.656	-119.007	2016	North	-	Male	-	-	-	10819	34.8513	2868	52.2186	-

xE3Aa	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	1	-	11073	39.9049	2870	59.5411	-
xE3Ab	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	1	-	10396	33.3814	2870	52.5599	Removed
xE3Ac	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	1	-	10149	24.5168	2870	37.3578	Removed
xE3B	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	-	Y	11070	39.2089	2872	58.1487	-
xE3C	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	-	-	11078	41.0636	2871	59.4037	-
xE3D	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	-	-	11045	33.251	2868	48.6423	-
xE4A	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	-	Y	10404	33.3317	2868	51.4962	-
xE4B	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	-	-	10216	28.7346	2863	45.437	-
xE4C	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	-	-	11068	41.3403	2868	56.5729	-
xE4D	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	-	-	11016	31.3753	2869	44.4102	-
xE5A	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	-	Y	10934	32.9334	2868	49.7169	-
xE5B	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	-	-	10791	25.7331	2865	38.615	-
xE5C	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	-	-	10763	32.1739	2869	49.3991	-
xE5D	rande Prair	3	54.656	-119.007	2016	North	-	Female	-	-	-	10873	39.1902	2868	60.5868	-
xO1A	rande Prair	4	54.606	-118.224	2016	North	-	Female	-	-	Y	11100	43.9413	2869	65.5507	-
xO1B	rande Prair	4	54.606	-118.224	2016	North	-	Male	-	-	-	11005	35.7725	2863	52.6088	-
xO1C	rande Prair	4	54.606	-118.224	2016	North	-	Male	-	-	-	11038	39.8357	2867	58.7949	-
xO1D	rande Prair	4	54.606	-118.224	2016	North	-	Female	-	-	-	11088	40.6703	2870	60.538	-
xO2A	rande Prair	4	54.606	-118.224	2016	North	-	Male	-	-	Y	11064	43.8933	2868	62.5474	-
xO2B	rande Prair	4	54.606	-118.224	2016	North	-	Male	-	-	-	10939	20.9525	2854	30.3805	-
xO2C	rande Prair	4	54.606	-118.224	2016	North	-	Female	-	-	-	11082	33.3657	2867	48.1943	-
xO2D	rande Prair	4	54.606	-118.224	2016	North	-	Female	-	-	-	11070	36.7943	2869	53.9425	-
xO3A	rande Prair	4	54.606	-118.224	2016	North	-	Female	-	-	Y	11073	34.2882	2868	50.4948	-
xO3B	rande Prair	4	54.606	-118.224	2016	North	-	Male	-	-	-	11037	36.6292	2868	53.1363	-
xO3C	rande Prair	4	54.606	-118.224	2016	North	-	Female	-	-	-	11059	34.5043	2869	50.6187	-
xO3D	rande Prair	4	54.606	-118.224	2016	North	-	Female	-	-	-	11056	34.2966	2869	50.5821	-
xO4A	rande Prair	4	54.606	-118.224	2016	North	-	Female	-	-	Y	11040	41.6428	2867	62.0251	-
xO4B	rande Prair	4	54.606	-118.224	2016	North	-	Female	-	-	-	11067	34.0721	2864	50.5422	-
xO4C	rande Prair	4	54.606	-118.224	2016	North	-	Female	-	-	-	11094	39.0969	2870	58.2481	-
xO4D	rande Prair	4	54.606	-118.224	2016	North	-	Female	-	-	-	11081	35.0326	2869	52.19	-
xO5A	rande Prair	4	54.606	-118.224	2016		-	-	-	-	-	437	1.10755	Poorly Sequenced		Removed
xO5B	rande Prair	4	54.606	-118.224	2016	North	-	Female	-	-	Y	11052	21.0258	2869	29.9881	-
xO5C	rande Prair	4	54.606	-118.224	2016	North	-	Male	-	-	-	11007	27.256	2868	39.531	-
xO5D	rande Prair	4	54.606	-118.224	2016	North	-	Female	-	-	-	11108	37.9358	2872	55.6379	-

11904	Hinton	1	53.380	-117.543	2017	Interm.	-	Male	-	-	Y	10120	25.0158	2858	37.1011	-
11906	Hinton	1	53.380	-117.543	2017	Interm.	-	Female	-	-	Y	10244	37.0368	2867	53.9149	-
11909	Hinton	1	53.380	-117.543	2017	Interm.	-	Male	-	-	Y	10206	31.3861	2865	45.0625	-
11910	Hinton	1	53.380	-117.543	2017	Interm.	-	Male	-	-	Y	10176	31.8302	2861	45.8721	-
11911	Hinton	1	53.380	-117.543	2017	Interm.	-	Female	-	-	Y	10269	44.4976	2867	65.7436	-
11912	Hinton	1	53.380	-117.543	2017	Interm.	-	Female	-	-	-	10280	47.6082	2867	69.9229	-
11913	Hinton	1	53.380	-117.543	2017	Interm.	-	Male	-	-	-	10231	39.7592	2864	58.3094	-
11914	Hinton	1	53.380	-117.543	2017	Interm.	-	Female	-	-	-	10246	46.8332	2866	70.141	-
11915	Hinton	1	53.380	-117.543	2017	Interm.	-	Female	-	-	-	10204	31.9509	2866	46.993	-
11916	Hinton	1	53.380	-117.543	2017	Interm.	-	Male	-	-	-	10167	29.8401	2861	43.1797	-
11917	Hinton	1	53.380	-117.543	2017	Interm.	-	Female	-	-	Y	9889	40.9816	2746	62.1533	-
11918	Hinton	1	53.380	-117.543	2017	Interm.	-	Female	-	-	Y	10254	40.6369	2867	59.9121	-
11919	Hinton	1	53.380	-117.543	2017	Interm.	-	Female	-	-	Y	10266	39.5071	2865	58.4129	-
11920	Hinton	1	53.380	-117.543	2017	Interm.	-	Female	-	-	-	10242	32.4982	2866	48.1689	-
11921	Hinton	1	53.380	-117.543	2017	Interm.	-	Male	-	-	-	10241	46.7881	2861	68.7438	-
11922	Hinton	1	53.380	-117.543	2017	Interm.	-	Male	-	-	-	10138	28.9304	2863	42.2263	-
11923	Hinton	1	53.380	-117.543	2017	Interm.	-	Female	-	-	-	10235	29.1069	2868	42.6698	-
11924	Hinton	1	53.380	-117.543	2017	Interm.	-	Female	-	-	-	10264	38.0591	2865	55.7515	-
11925	Hinton	1	53.380	-117.543	2017	Interm.	-	Female	-	-	-	10247	27.8381	2867	40.9299	-
11926	Hinton	1	53.380	-117.543	2017	Interm.	-	Female	-	-	-	10174	24.6102	2865	36.4712	-
11927	Hinton	1	53.380	-117.543	2017	Interm.	-	Female	-	-	-	10224	42.4609	2865	62.6705	-
11928	Hinton	1	53.380	-117.543	2017	Interm.	-	Female	-	-	-	10223	33.6047	2868	50.2371	-
M1A	Hinton	2	53.344	-117.583	2016	North	Y	Male	-	-	Y	6810	13.8671	2814	16.0963	-
M1B	Hinton	2	53.344	-117.583	2016	Interm.	-	Female	-	-	-	7033	15.3036	2825	18.0924	-
M1C	Hinton	2	53.344	-117.583	2016	North	Y	Female	-	-	-	8184	44.6662	2863	61.2546	-
M1D	Hinton	2	53.344	-117.583	2016	Interm.	-	Female	-	-	-	8000	34.944	2855	47.4921	-
M2A	Hinton	2	53.344	-117.583	2016	North	Y	Male	-	-	Y	10188	50.8634	2866	74.7994	-
M2B	Hinton	2	53.344	-117.583	2016	Interm.	-	Female	-	-	-	10277	85.6172	2865	123.458	-
M2C	Hinton	2	53.344	-117.583	2016	Interm.	-	Female	-	-	-	10232	48.0688	2869	69.497	-
M2D	Hinton	2	53.344	-117.583	2016	Interm.	-	Female	-	-	-	10216	43.5035	2864	60.014	-
M3A	Hinton	2	53.344	-117.583	2016	Interm.	-	Female	-	-	Y	10276	89.5317	2865	122.838	-
M3B	Hinton	2	53.344	-117.583	2016	North	Y	Female	-	-	-	10282	70.9663	2860	99.6409	-
M3C	Hinton	2	53.344	-117.583	2016	Interm.	-	Female	-	-	-	10146	37.4568	2866	52.9288	-
M3D	Hinton	2	53.344	-117.583	2016	Interm.	-	Female	-	-	-	10276	53.8124	2869	74.8648	-

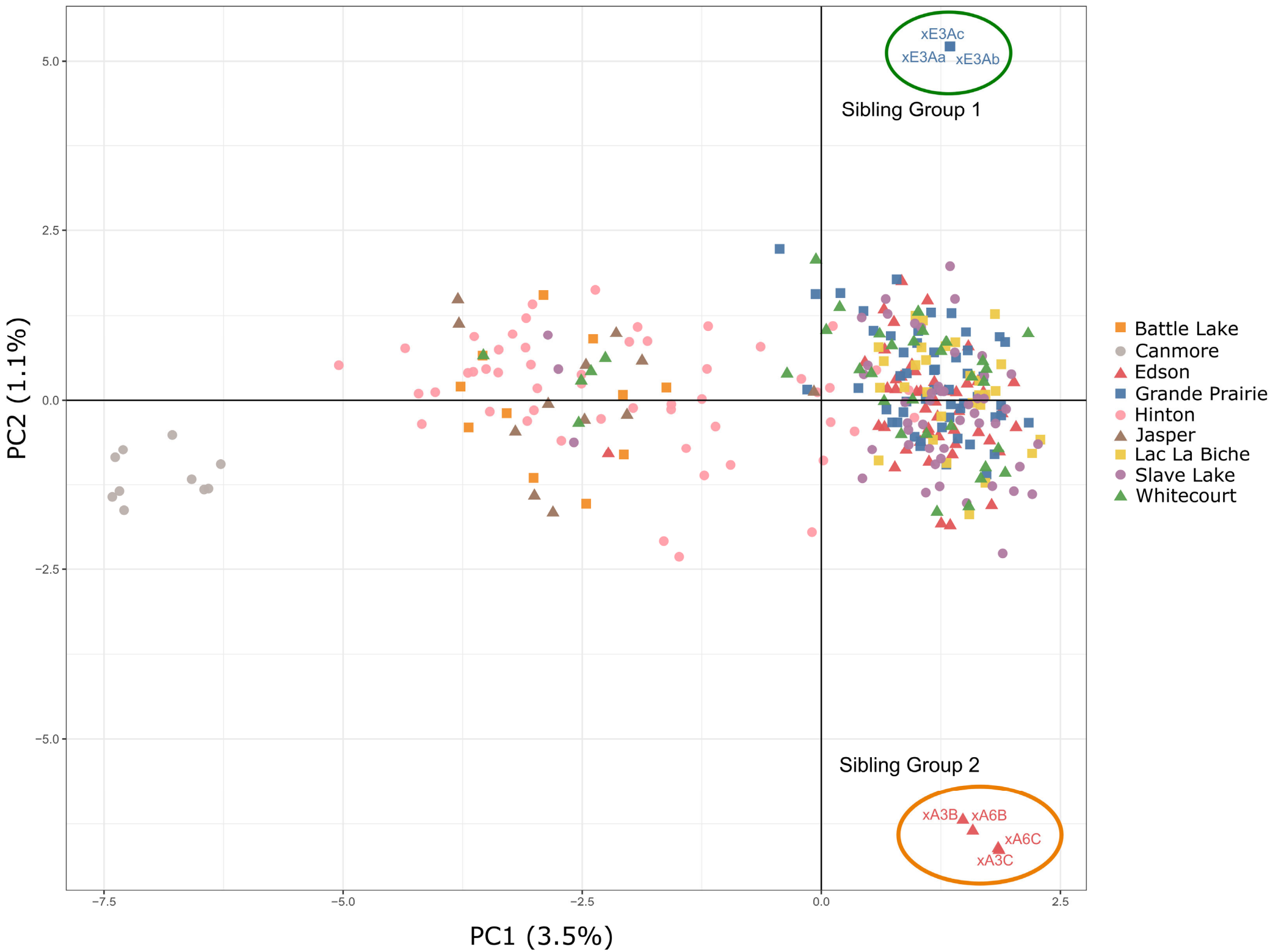
M4A	Hinton	2	53.344	-117.583	2016	North	Y	Female	-	-	Y	7315	17.6167	2838	21.655	-
M4B	Hinton	2	53.344	-117.583	2016	Interm.	-	Female	-	-	-	6444	11.5178	2742	12.7991	-
M4C	Hinton	2	53.344	-117.583	2016	North	Y	Female	-	-	-	7971	34.834	2863	46.9521	-
M4D	Hinton	2	53.344	-117.583	2016	North	Y	Male	-	-	-	7569	31.7067	2850	40.4196	-
M5A	Hinton	2	53.344	-117.583	2016	Interm.	-	Female	-	-	Y	10281	79.9264	2865	115.405	-
M5B	Hinton	2	53.344	-117.583	2016	Interm.	-	Female	-	-	-	9969	31.3367	2860	46.3913	-
M5C	Hinton	2	53.344	-117.583	2016	Interm.	-	Female	-	-	-	10250	65.2704	2869	93.0359	-
M5D	Hinton	2	53.344	-117.583	2016	North	Y	Female	-	-	-	10053	19.2981	2863	27.6678	-
M6B	Hinton	2	53.344	-117.583	2016	Interm.	-	Female	-	-	Y	10007	11.9142	2827	13.5607	-
M6C	Hinton	2	53.344	-117.583	2016	Interm.	-	Male	-	-	-	10248	23.8892	2861	27.8291	-
M6D	Hinton	2	53.344	-117.583	2016	North	Y	Female	-	-	-	10226	17.101	2858	19.8628	-
M7A	Hinton	2	53.344	-117.583	2016	Interm.	-	Male	-	-	Y	10148	16.1649	2857	18.8474	-
M7B	Hinton	2	53.344	-117.583	2016	Interm.	-	Female	-	-	-	10183	16.1745	2849	19.0534	-
M7C	Hinton	2	53.344	-117.583	2016	Interm.	-	Female	-	-	-	9957	10.9226	2836	12.7031	-
M7D	Hinton	2	53.344	-117.583	2016	Interm.	-	Female	-	-	-	9825	22.5322	2711	26.7348	-
M8A	Hinton	2	53.344	-117.583	2016	North	Y	Female	-	-	Y	9911	10.6579	2814	12.1848	-
M8B	Hinton	2	53.344	-117.583	2016	North	Y	Male	-	-	-	10135	15.4883	2846	17.6311	-
M8C	Hinton	2	53.344	-117.583	2016	Interm.	-	Female	-	-	-	10080	14.7842	2841	17.3365	-
J1	Jasper	1	53.463	-118.237	2015	Interm.	-	Female	Y	-	Y	10173	32.0467	2868	51.2402	-
J2	Jasper	1	53.463	-118.237	2015	Interm.	-	Female	Y	-	Y	10183	36.1	2865	58.1937	-
J10	Jasper	2	53.160	-117.530	2015	Interm.	-	Male	Y	-	Y	10136	36.3676	2868	58.0927	-
J8	Jasper	2	53.160	-117.530	2015	Interm.	-	Female	Y	-	Y	9962	27.7519	2866	43.8465	-
J9	Jasper	2	53.160	-117.530	2015	Interm.	-	Female	Y	-	Y	10115	32.9129	2864	53.8076	-
J17	Jasper	3	53.208	-117.348	2015	Interm.	-	Female	Y	-	Y	10071	33.9267	2866	55.7216	-
J18	Jasper	3	53.208	-117.348	2015	Interm.	-	Male	Y	-	Y	10144	38.425	2864	61.3795	-
J20	Jasper	3	53.208	-117.348	2015	Interm.	-	Female	Y	-	Y	10085	26.3551	2867	42.76	-
J12	Jasper	4	53.400	-117.247	2015	Interm.	-	Female	Y	-	Y	10066	28.4356	2867	45.0938	-
J22	Jasper	5	53.503	-117.734	2015	Interm.	-	Male	Y	-	Y	10212	39.1384	2866	62.4637	-
J23	Jasper	5	53.503	-117.734	2015	Interm.	-	Male	Y	-	Y	10101	33.6657	2859	54.5075	-
J24	Jasper	5	53.503	-117.734	2015	North	Y	Female	Y	-	Y	10243	35.6414	2868	57.2197	-
12351	Lac La Biche	1	55.622	-112.881	2018	North	-	Male	-	-	Y	14460	26.8271	2864	56.8115	-
12352	Lac La Biche	1	55.622	-112.881	2018	North	-	Female	-	-	Y	16385	40.1901	2867	70.4332	-
12371	Lac La Biche	1	55.622	-112.881	2018	North	-	Female	-	-	-	16074	21.9841	2868	39.3755	-
12374	Lac La Biche	1	55.622	-112.881	2018	North	-	Female	-	-	-	16139	30.1936	2869	57.2496	-

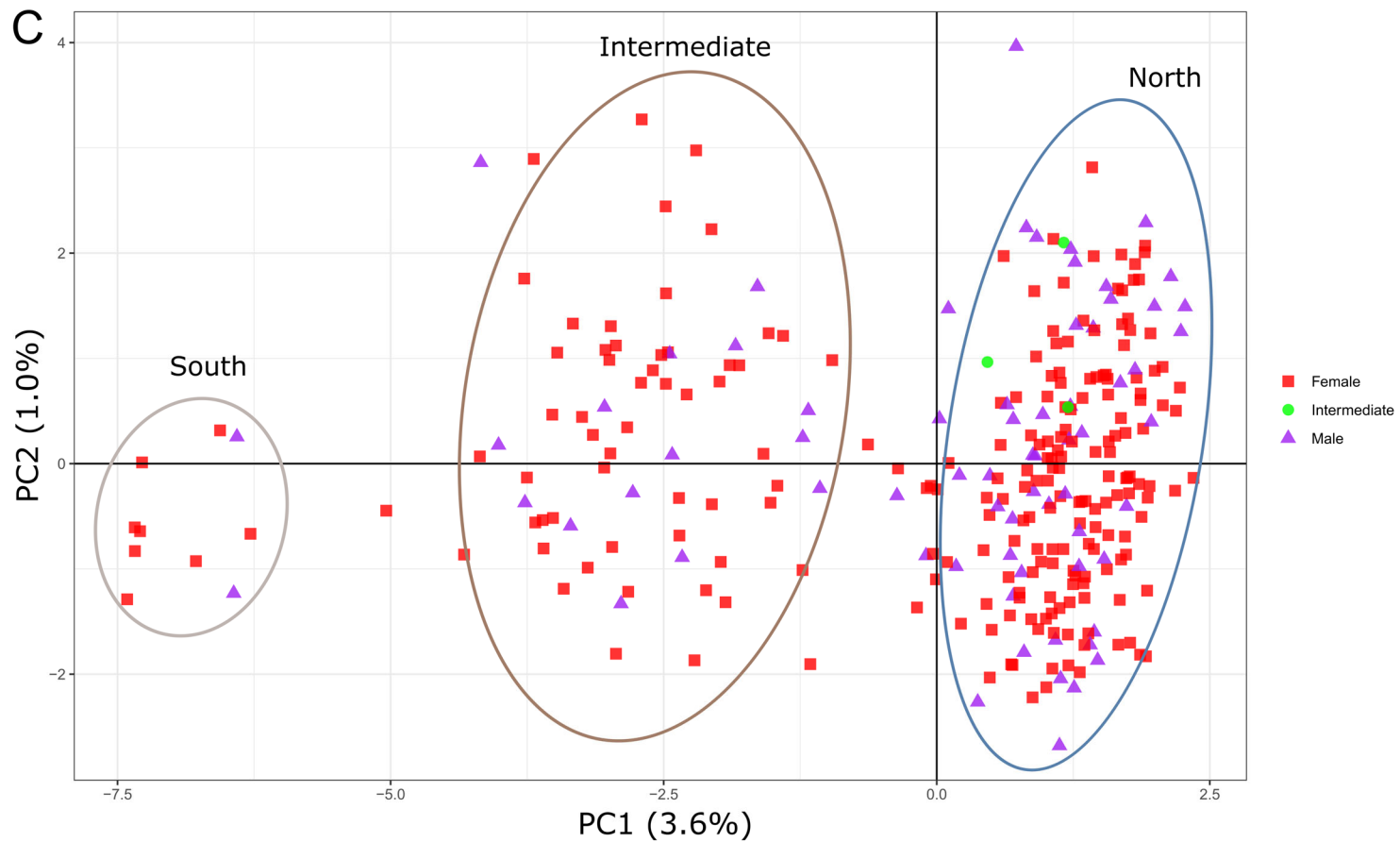
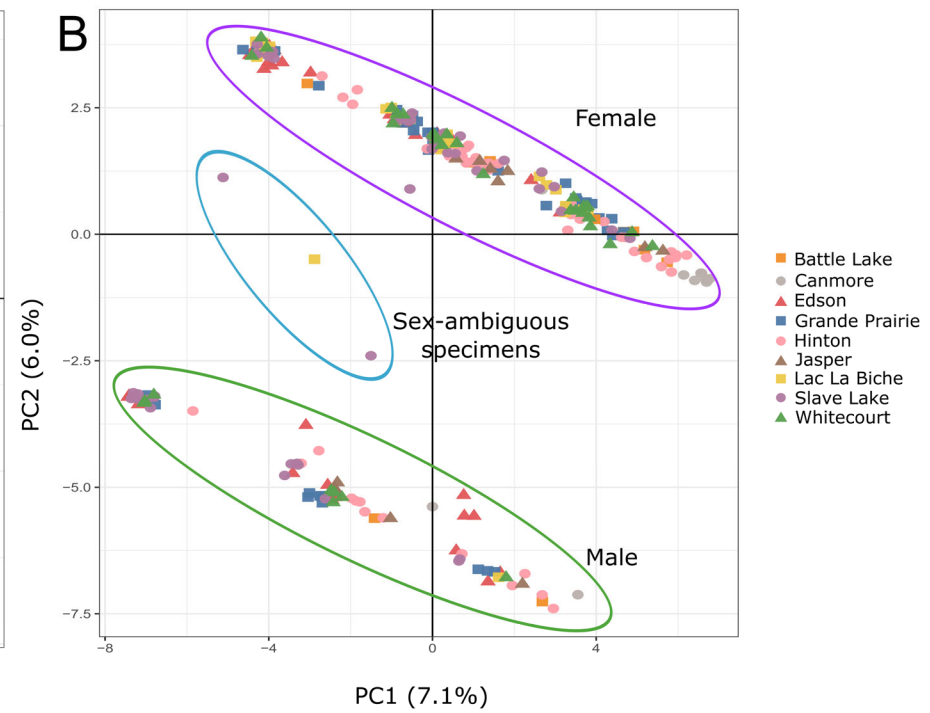
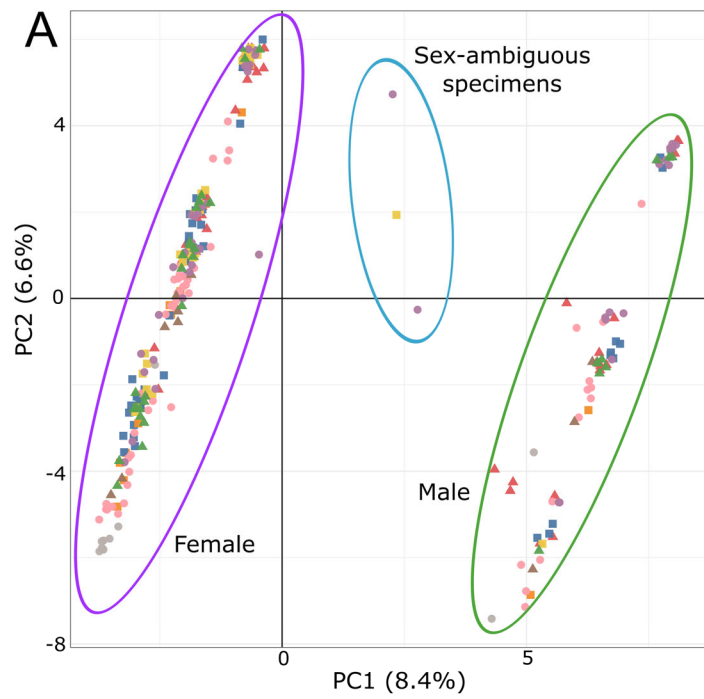
12377	Lac La Biche	1	55.622	-112.881	2018	North	-	Female	-	-	-	16291	34.5529	2870	64.5031	-
12379	Lac La Biche	1	55.622	-112.881	2018	North	-	Female	-	-	-	16228	30.8786	2871	57.2198	-
12353	Lac La Biche	2	55.389	-112.976	2018	North	-	Female	-	-	Y	16259	34.1916	2869	65.2489	-
12360	Lac La Biche	2	55.389	-112.976	2018	North	-	Female	-	-	Y	16275	29.9264	2871	55.0146	-
12367	Lac La Biche	2	55.389	-112.976	2018	North	-	Female	-	-	Y	16402	41.1872	2870	75.9599	-
12356	Lac La Biche	3	55.382	-112.990	2018	North	-	Female	-	-	Y	16262	30.4428	2870	54.0829	-
12363	Lac La Biche	3	55.382	-112.990	2018	North	-	Female	-	-	Y	16247	31.7365	2868	58.696	-
12370	Lac La Biche	3	55.382	-112.990	2018	North	-	Female	-	-	-	16172	27.0252	2871	49.4396	-
12372	Lac La Biche	3	55.382	-112.990	2018	North	-	Female	-	-	-	16252	30.8622	2867	57.79	-
12378	Lac La Biche	3	55.382	-112.990	2018	North	-	Female	-	-	-	16330	37.1962	2866	68.6923	-
12362	Lac La Biche	4	55.397	-112.972	2018	North	-	Female	-	-	-	16205	37.2382	2866	77.2327	-
12365	Lac La Biche	4	55.397	-112.972	2018	North	-	ntermediat	-	-	-	13945	9.46447	2748	16.1223	-
12369	Lac La Biche	4	55.397	-112.972	2018	North	-	Female	-	-	-	16019	40.1006	2872	83.891	-
12373	Lac La Biche	4	55.397	-112.972	2018	North	-	Female	-	-	-	16238	24.3048	2867	43.5033	-
12375	Lac La Biche	4	55.397	-112.972	2018	North	-	Female	-	-	-	16204	28.924	2866	54.053	-
12366	Lac La Biche	5	55.395	-112.972	2018	North	-	Female	-	-	Y	16245	32.3689	2870	60.0561	-
12368	Lac La Biche	5	55.395	-112.972	2018	North	-	Female	-	-	-	16373	38.4566	2870	71.0645	-
12376	Lac La Biche	5	55.395	-112.972	2018	North	-	Female	-	-	-	16129	26.1264	2863	48.2801	-
12364	Lac La Biche	6	55.390	-112.989	2018	North	-	Female	-	-	Y	16346	41.5267	2868	78.3368	-
12359	Lac La Biche	7	55.431	-112.072	2018	North	-	Female	-	-	Y	15025	27.8087	2859	64.929	-
12354	Lac La Biche	8	55.413	-112.005	2018	North	-	Female	-	-	Y	16322	32.7734	2868	57.1457	-
12355	Lac La Biche	8	55.413	-112.005	2018	North	-	Female	-	-	Y	16185	24.3249	2869	42.2788	-
12357	Lac La Biche	8	55.413	-112.005	2018	North	-	Female	-	-	Y	16278	29.3537	2870	50.3439	-
12358	Lac La Biche	8	55.413	-112.005	2018	North	-	Female	-	-	Y	16173	29.2092	2871	54.4619	-
12361	Lac La Biche	8	55.413	-112.005	2018	North	-	Female	-	-	Y	16354	37.7823	2866	69.8583	-
11929	Slave Lake	1	54.863	-115.163	2017	North	-	Male	-	-	-	9808	28.5945	2865	40.5462	-
11930	Slave Lake	1	54.863	-115.163	2017	North	-	Female	-	-	-	9884	53.065	2867	76.1768	-
11931	Slave Lake	1	54.863	-115.163	2017	North	-	Male	-	-	-	9794	36.9059	2866	52.6424	-
11932	Slave Lake	1	54.863	-115.163	2017	North	-	Female	-	-	-	9829	36.06	2867	50.8985	-
11933	Slave Lake	1	54.863	-115.163	2017	North	-	ntermediat	-	-	-	9551	46.1553	2783	67.0762	-
11935	Slave Lake	1	54.863	-115.163	2017	North	-	Female	-	-	-	9858	40.5492	2869	59.793	-
11937	Slave Lake	1	54.863	-115.163	2017	North	-	Female	-	-	-	9824	41.9161	2865	60.934	-
11938	Slave Lake	1	54.863	-115.163	2017	North	-	Female	-	-	-	9871	37.4348	2866	53.7153	-
11940	Slave Lake	1	54.863	-115.163	2017	North	-	Male	-	-	-	9839	40.8678	2869	58.7334	-

11942	Slave Lake	1	54.863	-115.163	2017	North	-	Male	-	-	-	9788	26.688	2869	37.5037	-
11943	Slave Lake	1	54.863	-115.163	2017	North	-	Female	-	-	-	9810	28.9635	2867	41.2469	-
11947	Slave Lake	1	54.863	-115.163	2017	North	-	Male	-	-	-	9806	37.1354	2867	53.971	-
11948	Slave Lake	1	54.863	-115.163	2017	North	-	Male	-	-	-	9786	27.7559	2867	39.5148	-
12395	Slave Lake	2	55.139	-115.343	2018	Interm.	Y	Female	-	-	Y	9859	53.8491	2867	70.4179	-
12396	Slave Lake	2	55.139	-115.343	2018	North	-	Female	-	-	Y	9867	48.442	2868	63.3884	-
12397	Slave Lake	2	55.139	-115.343	2018	North	-	Female	-	-	Y	9703	57.2403	2794	77.0787	-
12398	Slave Lake	2	55.139	-115.343	2018	North	-	Male	-	-	Y	9867	49.51	2866	64.0837	-
12399	Slave Lake	2	55.139	-115.343	2018	North	-	Female	-	-	-	9885	56.2642	2864	76.0548	-
12391	Slave Lake	3	54.933	-115.452	2018	North	-	Female	-	-	Y	9883	42.7261	2866	55.9986	-
12392	Slave Lake	3	54.933	-115.452	2018	North	-	Female	-	-	Y	9892	42.6326	2869	55.2579	-
12393	Slave Lake	3	54.933	-115.452	2018	North	-	Female	-	-	Y	9883	41.3565	2870	54.3829	-
12394	Slave Lake	3	54.933	-115.452	2018	North	-	Female	-	-	Y	9851	54.0568	2869	69.9184	-
12400	Slave Lake	4	54.744	-115.798	2018	Interm.	Y	Female	-	-	-	9857	51.4387	2865	67.178	-
12401	Slave Lake	4	54.744	-115.798	2018	Interm.	Y	Female	-	-	-	9860	56.5253	2862	73.884	-
12402	Slave Lake	4	54.744	-115.798	2018	North	-	Female	-	-	-	9897	41.2591	2867	53.9316	-
12403	Slave Lake	4	54.744	-115.798	2018	North	-	Female	-	-	-	9810	28.87	2869	37.694	-
12404	Slave Lake	4	54.744	-115.798	2018	North	-	Female	-	-	-	9888	44.4801	2864	57.6459	-
12411	Slave Lake	4	54.744	-115.798	2018	North	-	Female	-	-	-	9299	13.2281	2834	20.0025	-
12412	Slave Lake	4	54.744	-115.798	2018	North	-	Female	-	-	-	9896	55.7983	2867	71.9658	-
S1A	Slave Lake	5	55.613	-114.326	2016	North	-	Female	-	-	Y	8962	32.4686	2869	45.5406	-
S1B	Slave Lake	5	55.613	-114.326	2016	North	-	Female	-	-	Y	8779	26.4868	2864	35.4797	-
S1C	Slave Lake	5	55.613	-114.326	2016	North	-	Female	-	-	Y	9834	46.9879	2867	63.9466	-
S1D	Slave Lake	5	55.613	-114.326	2016	North	-	Male	-	-	Y	9814	36.3225	2868	49.1468	-
S2A	Slave Lake	5	55.613	-114.326	2016	North	-	Male	-	-	Y	8687	28.0807	2859	38.6198	-
S2B	Slave Lake	5	55.613	-114.326	2016	North	-	Female	-	-	Y	9241	36.6773	2868	52.8145	-
S2C	Slave Lake	5	55.613	-114.326	2016	North	-	Female	-	-	Y	9760	53.119	2871	74.4326	-
S2D	Slave Lake	5	55.613	-114.326	2016	North	-	Male	-	-	Y	9789	42.69	2868	59.6029	-
S3A	Slave Lake	5	55.613	-114.326	2016	North	-	Female	-	-	-	8302	26.7903	2857	35.9797	-
S3B	Slave Lake	5	55.613	-114.326	2016	North	-	Female	-	-	-	8705	30.0449	2867	42.2225	-
S3C	Slave Lake	5	55.613	-114.326	2016	North	-	Male	-	-	-	9738	45.4056	2864	64.279	-
S3D	Slave Lake	5	55.613	-114.326	2016	North	-	Male	-	-	-	9803	42.962	2862	60.5479	-
S4A	Slave Lake	5	55.613	-114.326	2016	North	-	Female	-	-	-	9146	41.6804	2870	59.599	-
S4B	Slave Lake	5	55.613	-114.326	2016	North	-	Female	-	-	-	9169	39.6859	2867	56.8859	-

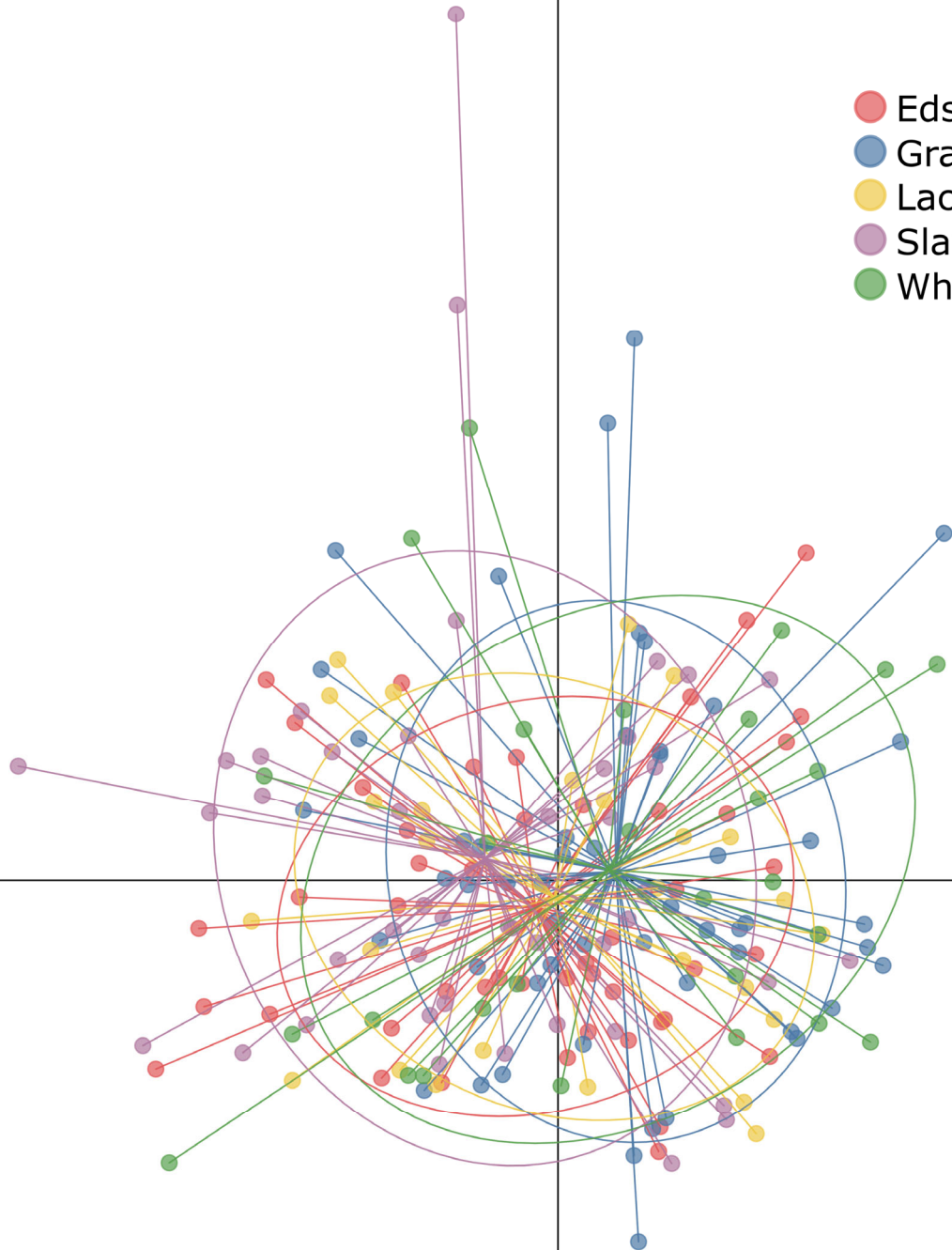
S4C	Slave Lake	5	55.613	-114.326	2016	North	-	Female	-	-	-	9610	46.1901	2798	63.2598	-
S4D	Slave Lake	5	55.613	-114.326	2016	North	-	Male	-	-	-	9543	22.1935	2869	28.7598	-
S5A	Slave Lake	5	55.613	-114.326	2016	North	-	Male	-	-	-	9151	42.7492	2792	63.1848	-
S5B	Slave Lake	5	55.613	-114.326	2016	North	-	Male	-	-	-	8597	22.1805	2863	29.971	-
S5C	Slave Lake	5	55.613	-114.326	2016	North	-	Intermediate	-	-	-	9458	47.5605	2766	68.4631	-
S5D	Slave Lake	5	55.613	-114.326	2016	North	-	Male	-	-	-	9788	36.7975	2869	50.4977	-
12406	Whitecourt	1	54.393	-116.286	2018	North	-	Female	-	-	Y	11194	39.7926	2871	58.7736	-
12413	Whitecourt	1	54.393	-116.286	2018	North	-	Female	-	-	Y	10825	29.6991	2760	42.2725	-
12415	Whitecourt	1	54.393	-116.286	2018	Interm.	Y	Female	-	-	-	11185	57.7738	2872	79.3357	-
12420	Whitecourt	1	54.393	-116.286	2018	Interm.	Y	Female	-	-	-	11185	35.5714	2865	48.3571	-
12422	Whitecourt	1	54.393	-116.286	2018	North	-	Female	-	-	-	11047	22.3404	2868	30.9808	-
12405	Whitecourt	2	54.354	-115.782	2018	North	-	Female	-	-	Y	11094	25.8734	2868	40.9962	-
12408	Whitecourt	2	54.354	-115.782	2018	North	-	Female	-	-	Y	11180	41.0472	2870	56.9331	-
12409	Whitecourt	2	54.354	-115.782	2018	North	-	Female	-	-	Y	11185	44.8059	2867	61.6243	-
12414	Whitecourt	2	54.354	-115.782	2018	North	-	Female	-	-	Y	11211	46.4125	2868	64.8494	-
12421	Whitecourt	2	54.354	-115.782	2018	North	-	Female	-	-	-	11219	42.6333	2868	58.6625	-
12407	Whitecourt	3	54.493	-115.538	2018	North	-	Female	-	-	Y	11230	42.6378	2868	58.9962	-
12410	Whitecourt	3	54.493	-115.538	2018	North	-	Female	-	-	Y	11242	50.8857	2868	69.355	-
12416	Whitecourt	3	54.493	-115.538	2018	Interm.	Y	Female	-	-	-	11189	48.6918	2864	67.7853	-
12417	Whitecourt	3	54.493	-115.538	2018	Interm.	Y	Female	-	-	-	11004	32.4069	2839	45.3797	-
12418	Whitecourt	3	54.493	-115.538	2018	Interm.	Y	Female	-	-	-	11171	36.0057	2867	49.7537	-
Y1A	Whitecourt	4	54.376	-115.691	2016	North	-	Male	-	-	-	9954	33.2206	2868	51.3546	-
Y1B	Whitecourt	4	54.376	-115.691	2016	North	-	Male	-	-	Y	9929	32.9941	2871	50.7318	-
Y1C	Whitecourt	4	54.376	-115.691	2016		-	-	-	-	-	1966	1.45371	Poorly Sequenced	Removed	
Y1D	Whitecourt	4	54.376	-115.691	2016	North	-	Male	-	-	-	11155	61.9705	2870	93.9592	-
Y2A	Whitecourt	4	54.376	-115.691	2016	North	-	Female	-	-	Y	11078	69.0167	2867	108.653	-
Y2B	Whitecourt	4	54.376	-115.691	2016	North	-	Female	-	-	-	11001	49.744	2869	77.8233	-
Y2C	Whitecourt	4	54.376	-115.691	2016	North	-	Female	-	-	-	11224	67.5699	2870	100.644	-
Y2D	Whitecourt	4	54.376	-115.691	2016	North	-	Male	-	-	-	11156	59.4958	2869	87.6511	-
Y3A	Whitecourt	4	54.376	-115.691	2016	North	-	Female	-	-	Y	11084	65.8665	2867	105.755	-
Y3B	Whitecourt	4	54.376	-115.691	2016	North	-	Female	-	-	-	11083	61.1661	2868	97.1437	-
Y3C	Whitecourt	4	54.376	-115.691	2016	North	-	Female	-	-	-	11182	72.3391	2864	111.834	-
Y3D	Whitecourt	4	54.376	-115.691	2016	North	-	Female	-	-	-	11175	70.5556	2864	108.883	-
Y4A	Whitecourt	4	54.376	-115.691	2016	North	-	Male	-	-	Y	10498	51.2177	2868	83.8093	-

Y4B	Whitecourt	4	54.376	-115.691	2016	North	-	Female	-	-	Y	10065	35.7254	2866	56.4382	-
Y4C	Whitecourt	4	54.376	-115.691	2016	North	-	Male	-	-	Y	11073	49.7395	2866	73.9522	-
Y4D	Whitecourt	4	54.376	-115.691	2016	North	-	Male	-	-	-	11122	50.4838	2859	75.8328	-
Y5A	Whitecourt	4	54.376	-115.691	2016	North	-	Female	-	-	-	11099	59.6583	2870	93.0091	-
Y5B	Whitecourt	4	54.376	-115.691	2016	North	-	Male	-	-	-	10834	41.8858	2863	63.2403	-
Y5C	Whitecourt	4	54.376	-115.691	2016	North	-	Female	-	-	Y	10113	10.5088	2849	12.5795	-
Y5D	Whitecourt	4	54.376	-115.691	2016	North	-	Female	-	-	Y	10905	30.5934	2864	38.6666	-

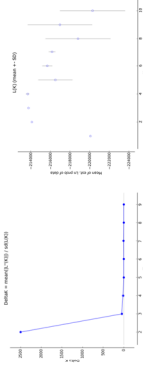




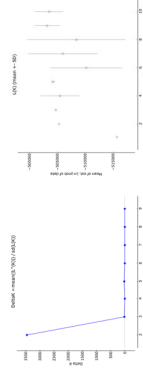
- Edson
- Grande Prairie
- Lac La Biche
- Slave Lake
- Whitecourt



A Data set with roughly equal sample sizes (n=125)

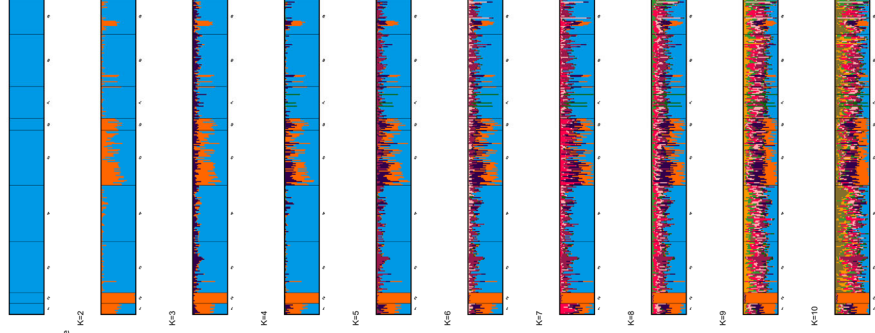
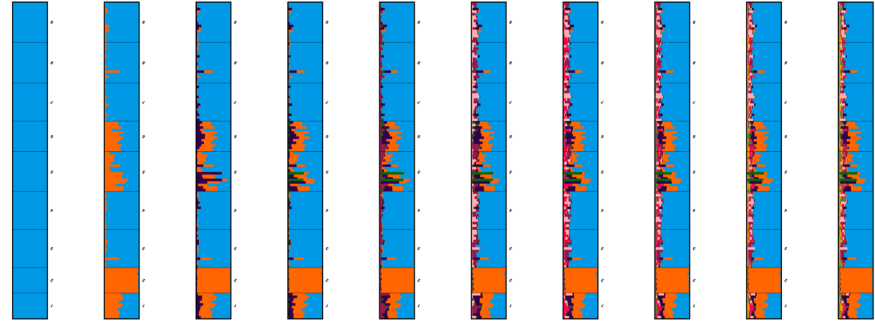


B Complete data set with unequal sample sizes (n=306)



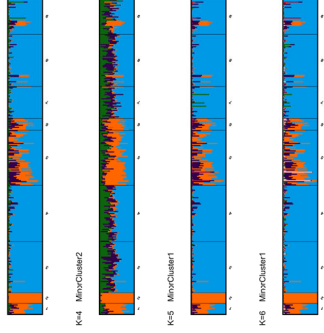
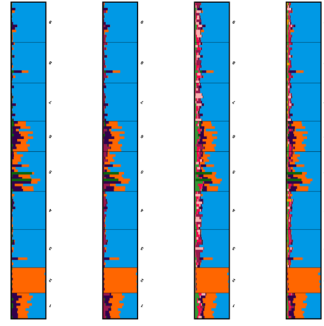
Major modes for the uploaded data:

- 1 - Battle Lake
- 2 - Canmore
- 3 - Grande Prairie
- 4 - Grande Prairie
- 5 - Hinton
- 6 - Jasper
- 7 - Jasper
- 8 - Slave Lake
- 9 - Whitecourt

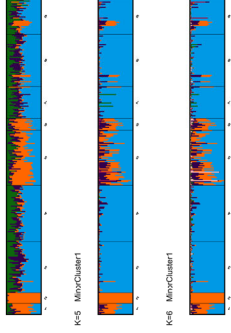
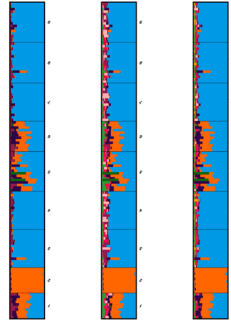


Minor modes for the uploaded data:

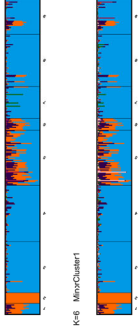
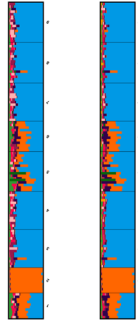
- Kc4_MicroCluster1



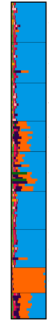
- Kc4_MicroCluster2



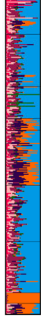
- Kc6_MicroCluster1



- Kc6_MicroCluster1



- Kc7_MicroCluster1



- Kc7_MicroCluster2



- Kc8_MicroCluster1



- Kc8_MicroCluster1



- Kc10_MicroCluster1



Division of runs by mode:

Kc1	1000
Kc2	1000
Kc3	1500, 165, 110
Kc4	700, 210
Kc5	800, 210, 210
Kc6	700, 210
Kc7	700, 210
Kc8	700, 210
Kc9	500, 210
Kc10	500, 210

