Genomics of *Dendroctonus ponderosae* (Coleoptera: Curculionidae) in Alberta

By

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Abstract

Rapid advances in sequencing technologies and analysis methods have greatly increased our understanding of genomic architecture in non-model organisms. The mountain pine beetle (MPB; *Dendroctonus ponderosae*) is a non-model organism that has received intensive genomic study and is of great economic interest in western Canada. I apply next-generation sequencing (NGS) technologies to create a library of single nucleotide polymorphism (SNP) markers, and use the markers to address basic questions concerning population structure in MPB. Then, using the same dataset, I amend standard filtering and analysis techniques for population genomics data to ask questions about genomic architecture and functional genetics. By combined use of linkage network and principal components analysis (PCA), I find new SNP markers for determining sex, and describe a novel method for finding putative islands of genomic divergence that I apply to the major Canadian populations of MPB. Finally, I validate the chromosomal contiguity of these islands of genomic divergence by generating two linkage maps for male- and female-associate sets of MPB SNPs, which I developed using a colony of lab-bred F2 sibling crosses. Both linkage analysis and the viability of experimental crosses suggest the existence of incipient speciation between populations of MPB within their Canadian range. The results described here also contribute to a reassessment of the value of cohorts of loci in tight linkage disequilibrium that have previously been viewed as unusable for population genomics studies.

Preface

The research conducted for this thesis was part of a collaborative effort led by Dr. Felix Sperling at the University of Alberta. The majority of the sampling and laboratory work was performed by me, with some samples in **Chapters 2 and 3** being supplied by Dr. J.K. Janes. **Chapter 2** was co-written by Janes and me, under the supervision of Sperling.

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I was responsible for the laboratory work, data analysis and interpretation, and for co-writing the manuscript. Janes contributed some samples, data interpretation and writing. Sperling was involved in concept formation, data interpretation and manuscript edits.

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I was responsible for concept formation, laboratory work, data analysis, data interpretation, and writing the manuscript. Janes contributed some samples, concept formation, data interpretation and manuscript edits. Data analysis used analytical tools developed by K. Muirhead. Sperling was involved in concept formation, data interpretation and manuscript edits.

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Table of Contents

Abstract ..... **ii**

Preface ..... **iii**

Acknowledgements ..... **iv**

List of Tables ..... **ix**

List of Figures ..... **xi**

List of Abbreviations ..... **xiv**

1. General Introduction **1**

1.1 Overview of population genomics 1

1.1.1 Genomics and genetics 1

1.1.2 Linkage disequilibrium 3

1.1.3 Next generation sequencing techniques 4

1.2 Mountain pine beetle biology 6

1.2.1 Ecology and life history 6

1.2.2 Population genetics 8

1.3 Thesis overview 9

1.4 Literature cited 11

2. Where did mountain pine beetle populations in Jasper Park come from? Tracking beetles with genetics **19**

2.1 Summary 19

2.2 Introduction 19

2.3 Materials and methods 21

2.4 Results and Discussion 23

2.5 Literature cited 28

3. Repurposing population genetics data to discern genomic architecture: A case study of linkage cohort detection in mountain pine beetle (*Dendroctonus ponderosae*) **33**

3.1 Summary 33

3.2 Introduction 34

3.3 Materials and methods 37

3.3.1 Sampling 37

3.3.2 Library preparation 38

3.3.3 Data assembly and alignment 39
3.3.4 Data filtering 39
3.3.5 Multivariate analyses 40
3.3.6 LDna 41
3.3.7 BLAST+ and BLAST2GO 41
3.4 Results 42
3.4.1 Alignment and filtering 42
3.4.2 Principal component analysis 42
3.4.3 LDna results 44
3.4.4 BLAST results 45
3.5 Discussion 46
3.5.1 Overview 46
3.5.2 Population genetic structure 46
3.5.3 Non-geographic clustering - possible sex-linked paralogues in MPB 47
3.5.4 PC 3 – candidate for adaptive selection? 50
3.5.5 Integrating PCA with LD network analysis 51
3.6 Conclusion 53
3.7 Literature Cited 62
4. Preliminary genetic linkage map for the mountain pine beetle (*Dendroctonus ponderosae*) 72
4.1 Summary 72
4.2 Introduction 72
4.3 Materials and methods 74
4.3.1 Sampling 74
4.3.2 Rearing 74
4.3.3 Genotyping 77
4.3.4 Filtering and identity-by-descent 78
4.3.5 Linkage mapping 78
4.3.6 Comparisons among MPB linkage maps and orthology *with Tribolium castaneum* 80
4.4 Results 81
4.4.1 F1 and F2 emergence 81

4.4.2 Genotyping and linkage mapping 81
4.4.3 Linkage map comparisons 82
4.5 Discussion 84
4.5.1 Overview 84
4.5.2 Viability of crosses 84
4.5.3 Linkage map structure 86
4.5.4 Orthology with *Tribolium castaneum* 88
4.6 Conclusion 89
4.7 Literature cited 100
5. General Conclusions 105
5.1 Thesis Overview 105
5.1.1 Introduction 105
5.1.2 Population genomics in mountain pine beetle 105
5.1.3 Genomic architecture and population divergence 106
5.2 Future directions 107
5.2.1 Population genomics 107
5.2.2 Linkage analysis 108
5.3 Conclusion 110
5.4 Literature cited 111
Literature Cited 114
Supplementary Material 133

List of Tables

Table 3.1. Locus counts for the SNP dataset of 175 wild-caught and 13 lab-bred MPB after various filtering treatments. Cutoffs were set to 5% for maximum missing (MM) data, 5% for minor allele frequency (MAF), p=0.000025 for Hardy Weinberg Equilibrium (HWE), and r^2=0.5 for linkage disequilibrium (LD). Final analysis refers to analysis after filtering. 54

Table 3.2. Scaffold distribution of SNPs that contribute significantly to a PC axis (>0.050 PC loading) from a PCA on the 5%-only dataset aligned to the female MPB genome. Numbers indicate how many separate draft genome scaffolds contain SNPs contributing to that PC, with successive rows indicating more SNPs on each scaffold. Only SNPs that are exclusive to PC1 are included in that column; SNPs that are shared with PC3 are included only in the column for PC3. 55

Table 3.3. Gene ontologies for SNPs with significant contributions to PCs 1-4 (PC loading >0.050). PC1 refers only to loci that did not overlap with PC3. Percent given after / for cellular, molecular and biological gene ontology categories include unique ontology results only. Cellular components refer to cellular structures in which a gene product performs a function, molecular functional refers to genes with molecular-level activities performed by gene products, and biological processes refer to larger processes accomplished by multiple molecular activities. 56

Table A.1. Sample information for 175 wild caught mountain pine beetle. 133

Table A.2. Gene Ontologies for 17 loci significant contributions to PC1, but not PC3, of a PCA of 175 wild MPB. 143

Table A.3. Gene Ontologies for 93 loci significant contributions to PC2 of a PCA of 175 wild MPB. 148

Table A.4. Gene Ontologies for 40 loci significant contributions to PC3 of a PCA of 175 wild MPB. 174

Table A.5. Gene Ontologies for 12 loci significant contributions to PC4 of a PCA of 175 wild MPB. 186

Table A.6. Homologous BLAST hits on the genome of *Tribolium castaneum* chromosomes for *D. ponderosae* loci with high-weight contribution to PC axes 1-4 (see **Figure 3.2**). PC1 refers only to loci that did not overlap with PC3. BLAST results for all positive hits on *T. castaneum* are listed, even if mapping and gene annotation for loci was unavailable. Loci that did not have homologous hits on *T. castaneum* are not listed. 191

Table A.7. SNP correspondences among LDna cohorts and PCA cohorts (PC loading >0.050), expanded from those shown in **Figure 3.5**. 192

Table A.8. Pedigree and emergence information for wild P crosses used in the linkage map. Wild BQ bolts were collected from Burnco Quarry, Canmore, AB. SRL bolts were collected from Smokey River Lowlands, Grande Prairie, AB. The number of larval galleries refers only to the main gallery established by researchers, and does not account for beetles colonizing the bolt in a secondary infestation. 193

Table A.9. Pedigrees and emergences for F1 cross used in the linkage map. 195

Table A.10. Parental assignment (CERVUS), and Identity-By-descent (IBD) for 14 *Dendroctonus ponderosae* families used for linkage mapping. 197

Table A.11-24. Identity-by-descent percentages for each of 14 *Dendroctonus ponderosae* F2 families used for linkage mapping. IBD values below the 25% threshold are **bolded**. 198

Table A.25. Linkage group positions for a) 1,729 SNPs and b) 1,638 SNPs from the *Dendroctonus ponderosae* female and male linkage maps, respectively. Overlapping SNPs, found in linkage map construction and population genetics analysis (see **Chapter 3**) are identified in the 'PC' column, which gives the number of the Principal component cohort that SNP belongs to. 212

Table A.26. SNP markers shared between population genetics analysis of *Dendroctonus ponderosae* (**Chapter 3**) and linkage map. LEP-MAP 3 JoinSingles was used to construct the 4,781 SNP linkage map dataset. 250

List of Figures

Figure 2.1. Map of mountain pine beetle collection sites organized by collection year. A total of 175 MPB were collected from 33 sites at 25 localities. Number of specimens sampled is in parentheses. Three U.S. localities are not shown (one specimen from each of Wyoming, Nevada and Washington). 26

Figure 2.2. Principal coordinate analysis of 175 wild-caught mountain pine beetles, plus 13 lab-bred specimens added to simulate intermediates between northern and southern populations. Ellipses give 95% confidence intervals for populations, with the overall northern population sub-divided by colour for areas of particular management interest. 27

Figure 3.1. The mountain pine beetle (*Dendroctonus ponderosae*). Scanning electron micrograph was taken by Jack Scott and is used with permission of the TRIA project. 57

Figure 3.2. Principal component analyses of 175 wild-caught and 13 lab-bred MPB aligned to the female MPB genome. a) FF dataset with 1480 SNPs filtered at 5% MM, 5% MAF, HWE (p=0.000025), LD (r^2=0.5). b-d) 5%-only dataset with 2,077 SNPs filtered at 5% MM and 5% MAF, showing PC1 x PC2, PC1 x PC3, and PC1 x PC4, respectively. 58

Figure 3.3. 2077 SNP loci arranged in descending order of principal component loadings for Axes 1-4 of 175 wild-caught MPB (5% MM, 5% MAF). Locations within PC1 for loci contributing heavily to PCs 2, 3, and 4 are shown in blue, red and green, respectively. 59

Figure 3.4. Linkage disequilibrium network analysis (LDna) for 2,077 SNPs, filtered at 5% MM and 5% MAF. Number of edges (E) is equal to 10. Cluster splitting (φ) is equal to 2. Clustering is depicted as a treespace progressing with increasing support for LD, as indicated by r^2. LDna cohort X at $r^2 = 0.99$, LDna cohort A at $r^2 = 0.54$, and LDna cohort B at $r^2 = 0.24$ are highlighted in blue, red and green, respectively, as they appear along the treespace. 60

Figure 3.5. Correspondence among SNPs with high contributions to PCs 1, 2, 3 and 4 and LDna cohorts X, A and B, based on analysis of 2,077 SNPs in 175 MPB samples from BC and Alberta. SNPs are treated as contributing to an axis if their PC loading weight exceeds 0.050. Combinations with 0 markers are left blank. Two SNPs, which were shared between PC1 and PC3 but not LDna cohort A, are not shown. 61

Figure 4.1. Beetle container used to initiate colonization of bolts, made from 1.5mL microcentrifuge tubes. 90

Figure 4.2. Sampling and family pedigrees used in linkage maps for Dendroctonus ponderosae. a) D. ponderosae in Alberta, showing range and sampling locations, adapted from Bleiker & Hezewjk (2014). b) 14 F2 pedigrees used for linkage mapping, with family sizes and sex ratio (see **Table A.9**). 91

Figure 4.3.a-c. Linkage map of *Dendroctonus ponderosae* using 1729 SNP markers aligned to the female draft genome. Markers are labelled by reference genome scaffold number and position on the reference scaffold (see Keeling *et al*. 2013). Numbers in parentheses, to the right of the marker label, represent additional markers at the same genomic position. SNP markers sharing identity with markers found in Trevoy *et al.* (**Chapter 3**) are highlighted: PC1 - purple, PC2 - blue, PC3 - red, PC4 - green. 92

Figure 4.4.a-c. Linkage map of *Dendroctonus ponderosae* using 1638 SNP markers aligned to the male draft genome. Markers are labelled by reference genome scaffold number and position on the reference scaffold (see Keeling *et al*. 2013). Numbers in parentheses, to the right of the marker label, represent additional markers at the same genomic position. Linkage groups are numbered according to the corresponding female linkage group (see **Figure 4.3**). LG1 & 10 has been split into sections corresponding to LGs 1 and 10 of the female linkage map. SNP markers sharing exact identity with markers found in Trevoy et al. (**Chapter 3**) are highlighted: PC1 - purple, PC2 - blue, PC3 - red, PC4 - green. 95

Figure 4.5. Chord diagram of shared identity between 1408 SNPs in the male (blue) and female (pink) aligned genomes of *D. ponderosae*. Each section represents a separate linkage group (see **Figure 4.3 and 4.4**). (BLASTn analysis, expect value cut-off: 1.0e-10). 98

Figure 4.6. Orthology between *Dendroctonus ponderosae* (red outer arc) and *Tribolium castaneum* (grey outer arc) for 116 orthologues in the female reference genome (a) and 146 in the male reference genome. (BLASTn analysis, expect value cut-off: 1.0e-10). 99

Figure A.1. Principal component analyses of 175 wild-caught MPB aligned to the male MPB genome. a) FF dataset with 1488 SNPs filtered at 5% MM, 5% MAF, HWE (p=0.000025),

LD (r^2=0.5). b-d) 5%-only dataset with 1908 SNPs filtered at 5% MM and 5% MAF, showing PC1 x PC2, PC1 x PC3, and PC1 x PC4, respectively. 250

Figure A.2. Expanded linkage disequilibrium network analysis (LDna) for 2077 SNPs, 5% MM, 5% MAF, aligned to the female draft genome. Number of edges (E) is equal to 10, Cluster splitting (φ) is equal to 2. Clustering is depicted as a treespace progressing with increasing support for LD, as indicated by r2. Cohort X at r^2 = 1.00, Cohort A at r^2 = 0.54, and Cohort B at r^2 = 0.24 are highlighted in blue, red and green, respectively, as in Figure 3. All other highlighted cohorts are comprised of fewer than 20 SNPs and are highlighted in purple. .251

Figure A.3. Distribution of species identified in a BLASTn search of 303 sequences of 200bp from loci with high-weight loadings on the PC2 and PC3 axes of a PCA for *Dendroctonus ponderosae*. 252

Figure A.4. Principal Component Analysis of 5,176 SNPs from 229 *Dendroctonus ponderosae* individuals from 14 families. Preliminary sex assignment of individuals is based on morphology. MM=20%, MAF=5%, ARD=20. 253

List of Abbreviations

ARD: average read depth

bp: base pair

BQ: Burnco Quarry, Canmore Alberta

ddRAD: double-digest restriction-site-associated

cM: centimorgan

GBS: genotyping-by-sequencing

HWE: Hardy-Weinberg equilibrium

IBD: identity-by-descent

LD: linkage disequilibrium

MAF: minor allele frequency

MPB: mountain pine beetle (*Dendroctonus ponderosae*)

MM: maximum missing data

NGS: next-generation sequencing

PCA: principal component analysis

RFB: red four beetle (*Tribolium castaneum*)

SNP: single nucleotide polymorphism

SRL: Smokey River Lowlands, Grande Prairie, AB

Chapter 1

General Introduction

1.1.1 | Overview of population genomics

Population genomics is a sub-discipline of genetics that assesses differences between populations of an organism by comparing many DNA sequences from across their genome. The use of genomic techniques provides an avenue to explore links between genotype, gene function, and evolution at an unprecedented scale. 'Genomics' was first coined by Thomas H. Roderick in 1986 (Kuska 1998); a portmanteau of 'genome' and 'genetic'. Gulcher and Stefansson (1998) are credited with the first use of the term 'population genomics', which they used to describe their work with human genetic diseases. The idea of studying many variable points in an organism's genome was more formally introduced as a new discipline of science three years later by Black *et al*. (2001). Since then, major breakthroughs in genetic sequencing technologies have made it possible to reliably genotype many individuals quickly, accurately, and cheaply. The ability to sequence large, dispersed portions from the genomes of many organisms simultaneously means that thousands of independent markers can be genotyped from hundreds of individuals, allowing genetic analysis on a population-wide scale. This development has allowed study of genome-wide effects, such as migration, genetic drift, and inbreeding within and between populations, furthering our understanding of microevolution (Black *et al.* 2001). These genomic effects differ from localized genetic effects (ie. natural selection, mutation, and recombination) and are a necessary component in understanding phylogenetic history and gene flow (Luikart *et al.* 2003).

Although genomic and genetic techniques differ, the two are not mutually exclusive. Genomic methods have become popular exploratory tools for linking specific variable markers

with a phenotype of research interest. These associative studies, whether quantitative trait loci mapping (QTL; Miles & Wayne 2008) or genome-wide association studies (GWAS; Bush & Moore 2012), scan the genome for markers that covary with a phenotype of interest in order to find candidate genes that influence a phenotypic trait or disease (Haines *et al.* 2005). Markers spanning the genomes of many individuals can similarly be compared to reveal diagnostic markers and areas of genomic differentiation between populations (Turner *et al.* 2005; Nosil *et al.* 2009). This area of study, which seeks to identify genomically localized sites of differentiation between populations, dubbed 'speciation islands', has been an active area of study despite ongoing debates as to its validity (Michel *et al.* 2010; Hahn *et al*. 2012). Still, the speciation islands theory provides an attractive framework to describe and explain sympatric speciation, speciation with introgression, or 'speciation genes' that may be undergoing directional selection (Riesberg *et al*. 2004; Nosil & Feder 2012).

Currently most genomic studies follow three steps: i) sample numerous individuals representing two or more distinct populations of interest; ii) extract DNA and assemble a library of thousands of variable genetic loci across these individuals; and iii) analyse and interpret the resulting data in accordance with the experimental goals. Various filtering and quality assurance methods are employed before analysis to ensure that variant markers are of appropriate quality to lend confidence to results (O'Leary *et al.* 2018). Prevailing wisdom has assumed that neutral, independent markers distributed throughout a genome should be preferred for reliable genomic results (Luikart *et al.* 2003; Baird 2015). However, as population genomics continues to move toward more integrative methods – incorporating knowledge of genomic architecture, evolution, and gene function – these assumptions are being challenged and sometimes overturned. Recent work has demonstrated the validity of adaptive markers for population genomics work (Batista *et*

al. 2016), and the covariance of loci forms the basis for much of the work surrounding islands of genomic divergence (Nosil *et al.* 2009). The use of markers that violate the assumption of independence of loci is of particular interest to this thesis, and builds on prior work using genome scanning methods (**Chapter 3**).

1.1.2 | Linkage Disequilibrium

As sequencing technologies have improved, there has been a marked increase in the number of variable loci that can be reliably genotyped. Genomic datasets can include thousands or tens of thousands of markers and the number of markers per chromosome has increased accordingly (e.g. Lindtke *et al*. 2017; Picq *et al.* 2018). These densely packed marker libraries regularly break the assumption of Mendelian independent assortment (Correns 1900), thereby displaying genetic linkage – the tendency of DNA sequences to be inherited together if they are near each other on a chromosome (Bateson *et al.* 1905; Morgan 1910). Genetic markers are said to be in linkage disequilibrium if two markers are inherited non-randomly.

Markers that are extremely close to each other can be in a state of 'complete linkage', indicating that a recombination event has never been observed between the two markers. However, syntenic markers are not always inherited together if a recombination event redistributes them onto separate chromatids; this is known as 'incomplete linkage'. The further two markers are from each other on a chromosome, the more likely it is that a crossover event will separate the two alleles (Sturtevant 1913). Markers may even display negative linkage disequilibrium, also called 'repulsion', if a crossover event between two loci is abnormally common (Thompson *et al*. 1988). The probability of recombination is expressed in centiMorgans, where 1 cM indicates that two markers are separated onto different chromatids

once per 100 instances of meiosis (Sturtevant 1913). One cM, therefore, is an expression of probability and reflects distance between two markers, but does not correspond directly to a constant physical distance of base pairs. The probability of a crossover event is influenced by distance from the centromere, where recombination is suppressed, or other aspects of genomic architecture specific to the study species (e.g. Turner & Hahn 2010).

Estimation of recombination rates between many markers is used to map where genes are in relation to each other on chromosomes; the resulting diagram is called a linkage map. The first linkage map was developed for a single chromosome of *Drosophila* using only six phenotypic markers (Sturtevant 1913), but modern sequencing and statistical methods allow thousands of markers across an organism's genome to be arranged into detailed linkage maps (e.g. Picq *et al*. 2018). These dense linkage maps are invaluable for exploring genomic architecture. Linkage disequilibrium informs biologists of the potential for genetic hitchhiking of genes near regions that are undergoing directional selection or are in islands of genomic differentiation (Yan *et al*. 1998; Flaxman *et al*. 2013). Construction of linkage maps also allows meaningful comparisons between orthologous genomic regions in distantly related species, providing insights into chromosome evolution (Schubert 2007; Picq *et al.* 2018).

1.1.3 | Next generation sequencing techniques

The ability to reliably determine the order of nucleotides in strands of DNA was first made widely available with the Sanger sequencing method (Sanger *et al.* 1977), but the cost and effort involved was still prohibitive for population genetics work. The first step toward fast and efficient genotyping of many individuals was through PCR (polymerase chain reaction), which allows trace amounts of specific sequences to be multiplied many times over (Mullis *et al*. 1987;

Bartlett & Stirling 2003). This accurate and reliable method of amplifying genetic information was soon followed by a proliferation of methods aimed at evaluating differences between the resulting gene fragments, chief among them SNP arrays (Wang *et al.* 1998), AFLPs (Zabeau & Vos 1993; Vos 1995) and microsatellites (Tautz 1989). Studies of non-model organisms using AFLPs and microsatellites have waned in popularity due to the limited reliability of AFLPs and the time and expense involved in developing microsatellites, but SNP-based genomic approaches continue to enjoy wide acceptance owing to their abundance, ease of automation, and improved accuracy (Luikart *et al*. 2003; Slate *et al*. 2009).

Demand for cheaper, faster methods for sequencing genomes gave rise to next-generation sequencing technologies (NGS), which can leverage massively parallel processes to sequence over a billion base pairs at a time (Grada & Weinbrecht 2013). Several competing NGS methods use different chemistry and detection technologies to sequence DNA, each with distinct advantages over the others (Metzker 2010). For this overview, I focus on Solexa/Illumina dye sequencing, the NGS method used for this thesis.

Dye sequencing takes place in three steps (Bentley *et al.* 2008): (i) DNA is cut into short sequence fragments and tagged with adapter and barcode sequences; (ii) sequences are anchored in an Illumina flow cell and amplified, giving many replicates of each sequence; (iii) nucleotides are added to the flow cells one at a time in order to build complimentary strands to the anchored sequences. Each of the four possible nucleotides is modified with a unique fluorescent tag that is released when the nucleotide binds to the sequence. The resulting fluorescent emission is registered by the machine and interpreted as the corresponding nucleotide. Solexa/Illumina dye sequencing can be performed on as many as 96 individuals at a time, with millions of flow cells simultaneously. This method is highly automated, accurate, and cost-effective in comparison to

other NGS methods. However, the reads used in Illumina dye sequencing are exceedingly short, ranging from 75 bp on the NextSeq500 platform to 100 bp on the Illumina HiSeq2000 platform. These short reads mean that this NGS method cannot accurately genotype repetitive genomic regions such as tandem repeats and chimeric reads (Morozova 2008).

Despite its drawbacks, NGS methods such as Illumina dye sequencing offer a valuable resource for population genomics, especially after the introduction of reduced representation sequencing methods using the same platforms (Elshire *et al.* 2011, Davey *et al.* 2011, Baird *et al.* 2008). Reduced representation sequencing (RRS) is a form of complexity reduction, where DNA is selected for sequencing if it is near a specific short sequence, usually between three and six bps. Restriction enzymes cut the genomes at these specific sequences, and adapters are attached at the restriction site. RRS provides high read depths, lending confidence to results, and many protocols with slight variations have become a popular alternative to more expensive and complex whole genome sequencing approaches (Campbell *et al*. 2018; Andrews *et al*. 2018).

1.2 | Mountain pine beetle biology

1.2.1 | Ecology and life history

The mountain pine beetle (MPB, *Dendroctonus ponderosae* Hopkins: Curculionidae, Scolytinae) is a species of bark beetle that is native to western North America whose range extends from British Colombia and Alberta to northern Mexico (Bentz *et al*., 2010). The beetle feeds on the inner bark of a range of host plants, most notably lodgepole pine (*Pinus contorta* Dougl. ex Loud. var. latifolia) (Safranyik & Carroll, 2006). It is an irruptive species that attacks aging, damaged, or sickly trees when found in low numbers, but periodically enters epidemic

phases where the beetle exhibits pheromone-mediated mass attacks that overwhelm healthy trees (Aukema *et al*. 2008).

MPB is an important forest pest whose latest outbreak has killed millions of hectares of productive forest in British Columbia and Alberta (Safranyik *et al.* 2010). This continuing outbreak is exceptionally large (Taylor & Carroll 2004) and has had a serious, negative effect on biodiversity, forestry, and tourism within western Canada (Ayres & Lombardero 2000). Climate change has enabled colonization of previously marginal landscapes, allowing MPB to expand into higher elevations that were previously too harsh for the beetle (Logan & Bentz 1999; Logan & Powell 2001; Carroll *et al*. 2003; Fauria & Johnson 2009). The MPB has exploited three mountain passes through the Canadian Rockies and, although most populations in British Colombia have receded to endemic numbers, an invasive front has continued to push eastward into Alberta (Janes *et al.* 2014). The beetle has now spread beyond the distribution of its primary host plant, the lodgepole pine, and has entered a landscape where lodgepole pine hybridizes with jack pine (*Pinus banksiana* Lamb) (Cullingham *et al.* 2012). MPB can colonize jack pine within a laboratory environment (Safranyik & Linton 1982), although differences in host plants can have unpredictable effects on the beetle's success (Erbilgin *et al.* 2014). If widespread colonization of jack pine is successful, mountain pine beetle has the potential to spread eastward across Canada to the Atlantic coast (Safranyik *et al.* 2010).

MPB is facultatively univoltine within its Canadian range, overwintering as late instar larvae, pupating in the spring, then emerging in early- or mid-July. The beetles commonly fly a short distance to colonize nearby trees, but have been recorded to fly several kilometers to find suitable hosts (Evenden *et al*. 2014). Female beetles are the pioneering sex, establishing vertical galleries within the inner bark of trees (Safranyik & Carroll 2006). Once underneath the bark,

they infect the tree with blue stain fungus, which the beetles store in mycangia located on their maxillae (Whitney & Farris 1970). The blue stain fungus is one of several species of fungi that form a symbiotic relationship with MPB, assisting in combatting the tree's immune response (Raffa & Berryman 1982). After the tree's defenses have been overcome, a male beetle joins the female inside her gallery and fertilizes her; the male may then either leave the gallery to find another mate or remain and help maintain the gallery. Once fertilized, the female lays eggs singly along the length of the vertical parental gallery (Safranyik & Carroll 2006). Larvae mine along the circumference of the tree, building horizontal galleries to either side of the parental gallery. A single female will lay an average of 60 eggs under normal conditions, but can lay more than 100 eggs under ideal or laboratory conditions (Reid 1962).

1.2.2 | Population genetics

Substantial effort has been made to assess the population structure of MPB (Stock *et al.* 1984; Mock *et al.* 2007; Cullingham *et al.* 2012; Samarasekera *et al.* 2012; Janes *et al.* 2014; Batista et al. 2016). Similarly, the phylogeny of *Dendroctonus* has been well explored (Bentz & Stock 1986; Kelley & Farrell 1998; Cognato 2011; Reeve *et al.* 2012; Victor & Zuniga 2015). Previous work by Samarasekera *et al.* (2012) and Janes *et al.* (2014) identified a north-south split within the beetle's epidemic range, but fine-scale investigations of population structure have shown limited structure (Janes *et al*. 2016). Phylogeographic investigations did not pinpoint a single origin of the recent outbreak, implicating several source populations within the beetle's endemic range (Cullingham *et al.* 2012). Janes *et al.* (2014) noted a lack of bottlenecks or founder effects restricting genetic diversity within Alberta, suggesting the eastward invasion of MPB has not been accompanied by any significant reduction in genetic diversity. In their new

Albertan range, the older northern and southern invasive fronts have been joined by a third invasive front, exploiting the Yellowhead Pass through Jasper National Park in 2015 (Jasper National Park 2016).

1.3 | Thesis overview

The goal of this thesis is to apply a genomic approach to finding potential chromosomal regions of adaptation in mountain pine beetle. I explore both conventional and new methods of assessing population structure and genomic architecture, with specific interest in identifying gene linkage and speciation in genome-wide analysis.

This study begins with a basic population genomics approach, characterizing mountain pine beetle in its Canadian range (**Chapter 2:** Trevoy *et al.* 2018). I establish NGS techniques as a viable method for assessing MPB populations, using Illumina dye sequencing to create a library of thousands of variable SNP markers (Elshire *et al.* 2011). These technologies and protocols were chosen due to their low cost, reproducibility, and high degree of genotyping accuracy relative to other methods (Andrews *et al.* 2018). The work presented here is the first genomics study to incorporate the novel invasive population entering Alberta from the Yellowhead Pass. This conventional approach to filtering and analysis is contrasted with later chapters that integrate functional genomic and linkage analysis into the same population genomics dataset.

In **Chapter 3**, I explore the aforementioned SNP library using a combination of principal components analysis (Abdi & Williams 2010) and linkage disequilibrium network analysis (Kemppainen *et al.* 2015) to identify cohorts of sex-linked markers and genes under divergent selection. My work seeks to establish a novel method of assessing groups of covarying SNPs as a

way of identifying islands of genomic differentiation and incipient speciation. Gene ontology is explored for each of the SNP cohorts found in this analysis, offering new insights into traits that may be under directional selection within certain MPB populations.

Finally, I derive linkage maps for the male and female mountain pine beetle, which provide independent evidence of our linkage cohorts (**Chapter 4**). These linkage maps will be a valuable resource for future research into genomic architecture, informing the study of complex traits (Yeaman & Whitlock 2011) and evolution (Feulner *et al.* 2015) in MPB and related species. The linkage maps were constructed using lab-bred pedigrees established using outbred crosses between northern and southern invasive beetles, collected in Alberta, Canada (Samarasekera *et al.* 2012; Janes *et al.* 2014). Recombination rates are more difficult to calculate using an F2 pedigree, relative to a backcross, but due to the difficulty in recovering and retaining specimens over multiple generations, I elected to use an F2 pedigree regime to generate families that could be collected for DNA extraction (Amman 1972; Brunet *et al.* 2014; Picq *et al.* 2018). Techniques and outcomes for colony establishment are discussed in relation to the resulting linkage map and prior population genomics work. Our findings provide evidence of incipient speciation within MPB's invasive Canadian range (**Chapter 3**; Bracewell *et al.* 2011).

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Chapter 2

Where did mountain pine beetle populations in Jasper Park come from? Tracking beetles with genetics

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2.1 | Summary

The invasion of mountain pine beetle (*Dendroctonus ponderosae* Hopk.) into Alberta has been an ongoing concern for forest management. The beetle's recent appearance and spread in Jasper National Park now poses ecological and economic threats to forestry in regions to the east. By applying recent advances in genetic typing and analysis, we show that the beetle population in Jasper is comprised of mixed individuals combining genetic signatures of both northern and southern beetles. Coupled with current monitoring methods, genetic markers can be used to identify the origin of novel populations, facilitate precise monitoring of beetle expansion and potentially inform targeted management strategies.

2. 2 | Introduction

Jasper National Park is a recently affected area in a long series of irruptions by the mountain pine beetle (MPB, *Dendroctonus ponderosae* Hopk.) in western Canada. At least 21,500 ha of forest has been affected (Jasper National Park 2016), creating a corridor for the beetle to potentially spread into highly productive Forest Management Areas (FMAs) to the southeast. Damage to these forests would cause significant social, economic, and ecological

losses, as well as providing more MPB habitat that could exacerbate the current epidemic. Currently, the source of the Jasper infestation has been debated. The infestation may represent a slow spread of beetles from the north, around the Grande Prairie area (Hopkins-Hill 2017), which had extremely high numbers of beetles in 2009 (Pellow *et al.* 2011; Bleiker *et al.* 2011). This northern population is believed to have spread southeast, resulting in an indigenous population near the town of Hinton by 2015 (Jasper National Park 2016). Alternatively, the Jasper infestation could have arrived through affected forests from the west, around Mt. Robson Provincial Park, which have been in active outbreak since at least 2015 (Jasper National Park 2016). Recent research on MPB population genetic structure can contribute to identifying and understanding such movements of MPB on the landscape.

MPB numbers have been rising in Canada since the early 1990's, devastating 16.3 million hectares of forest within British Columbia and western USA by 2011 (Bentz *et al.* 2010; de la Giroday *et al.* 2011). Expansion into northern Alberta in 2006 (Robertson *et al.* 2009; Safranyik *et al*. 2010) has positioned the beetle to colonize a new host species, jack pine (*Pinus banksiana* Lambert) (Cullingham *et al.* 2011), a major component of boreal forest across North America. Expanded research on the MPB system has targeted better prediction, management, and prevention of outbreaks, including studies on their ecological impacts (Carroll *et al.* 2003, Raffa *et al.* 2008), fungal associations (Tsui *et al.* 2010; Roe *et al.* 2010; DiGuistini *et al.* 2011), host suitability and distribution (Cullingham *et al.* 2011; Erbilgin *et al.* 2014; Rosenberger *et al.* 2017a), beetle population dynamics (Hicke *et al.* 2006; Lachowsky & Reid 2014; James *et al.* 2016; Cooke & Carroll 2017; Rosenberger *et al*. 2017b), and population genetic and genomic structure (Samarasekara *et al.* 2012; Keeling *et al.* 2013; Janes *et al.* 2014; Janes *et al.*2016, Batista *et al.* 2016; Janes & Batista 2016).

Here we draw on recent literature and new research to address questions and concerns raised over the 'Jasper beetles'. Using genome-wide sampling of DNA markers, we provide context for the likely source populations of MPB in the Jasper region.

2.3 | Materials and Methods

A total of 175 MPB were collected from 33 sites throughout British Columbia and Alberta between 2007 and 2015 (Figure 2.1; Table A.1). Beetles were either stored in 95% ethanol at -20º C or stored dry at -80º C. In addition, wild-caught MPB from the Smokey River Lowlands (SRL) south of Grande Prairie (54º 21.376'; N 118º 19.112' W) and the Burnco Quarry (BQ) near Canmore (51º 04.026' N; 115º 17.237' W) were used as breeding pairs to produce artificially admixed individuals of northern SRL and southern BQ descent. These sites were chosen to represent the two large-scale beetle populations in Alberta known from prior research (Samarasekara *et al.* 2012; Janes *et al.* 2014). Thirteen offspring from seven of these SRL x BQ crosses (1-3 offspring per pair) were added to the 175 samples, giving a total of 188 samples.

Genomic DNA was extracted using QIAGEN (Toronto, ON, Canada) DNEasy Blood & Tissue kits according to manufacturer's instructions. DNA was quality checked using Qubit flourometric assay (Waltham, MA, USA) and standardized to 20 ng/µl. Samples were genotyped using a double-digest (PstI-MspI), 96-plex genotyping-by-sequencing (GBS) protocol (Elshire *et al.* 2011, Poland *et al*. 2012) at l'Institut de Biologie Intégrative et des Systems (IBIS) of Laval University and the Molecular Biology Services Unit (MBSU) of University of Alberta. A total of 63 samples were sequenced with an Illumina NextSeq 500 for 75 bp single-end reads, and 125 samples were sequenced using an Illumina HiSeq 2000 for 100 bp single-end reads. Campbell *et*

al. (2017) contains further details on library preparation, and supports the consistency and reproducibility of GBS across both preparations and platforms.

Reads (short sequences of DNA) were quality checked using FastQC v0.11.05 (Andrews 2010) and demultiplexed in theSTACKS v1.41 pipeline (Catchen *et al.* 2013). Barcodes and adapters were removed with Cutadapt v1.10 (Martin 2011) to produce a uniform read length of 62 bp for alignment in STACKS (Catchen *et al.* 2013). After removing reads with poor sequence quality and low alignment to the reference genome, 1.1 billion reads remained. GBS data were mapped to the MPB draft reference genome (Keeling *et al.* 2013) using BWA-MEM v0.7.12 (Li & Durbin 2009) with option -c=1 to remove reads that did not uniquely map to the reference. Each sample retained an average of 85.0% of its unique reads. Variants (variable genetic markers in the form of single nucleotide polymorphisms, SNPs) were detected in the STACKS refgen pipeline using default parameters, except for: minor allele frequency ≥ 5%, minimum quality score = 20, and minimum read depth = 7.

VCFtools v0.1.12b (Danecek *et al.* 2011) was used to identify and remove loci containing missing data. A total of 984 variants were identified from these mapped reads, forming the basis for further analysis. An individual-by-individual genetic distance matrix (uncorrected "p") was calculated using PAUP v4.0a152 (Swofford 2002). These genetic distances, which relate to genetic similarity, were visualized using principal coordinates analysis (PCoA) with the ade4 package (Dray *et al.* 2007) in R (R Core Development Team 2009). PCoA is commonly used to explore and visualize the similarity or dissimilarity of among samples, displaying the axes that explain the largest portion of the variation present in the data. For each of the resulting sampling clusters, ellipses based on 95% confidence intervals from the centroid of the cluster were

overlaid using ggplot2 (Wickham 2009). These ellipses provide an additional means of assessing confidence in fit to each cluster.

2.4 | Results and Discussion

Figure 2.2 shows a clear separation of northern (blue and green) and southern (red) populations along axis 1 (45.7% of total variance), in agreement with prior studies using other genetic markers (Samarasekera *et al.* 2012; Janes *et al.* 2014). The northern cluster represents populations from the Peace River region (including Grande Prairie) to north-central Alberta, with samples from the northwest (Terrace, Smithers, and Tumbler Ridge in BC) separated further (Figure 2.2). This suggests a degree of separation by distance over the vast range of the northern MPB population. Beetles from Jasper (purple) and the SRL x BQ (orange) crosses were intermediate to northern and southern populations. Variability among SRL x BQ samples is greater than that of wild-caught Jasper MPB, as shown by its smaller ellipse, nested within SRL x BQ's ellipse (Figure 2.2). Jasper beetles, therefore, fall within the expected variation found within artificially admixed north/south crosses of MPB. The higher degree of variation within SRL x BQ may be explained by pre-emergence mating among siblings within a bolt, a known occurrence in MPB (Bleiker *et al.* 2013; Janes *et al.* 2016).

MPB from Yellowhead County, east of Jasper Park, were most similar to the northern cluster (Figure 2.2), suggesting a northern source for Yellowhead beetles in 2014, a year before MPB numbers were recognized as an outbreak in Jasper. Thus, our data supports the earlier movement of beetles from the Grande Prairie area into Yellowhead County, largely confirming a northern origin for this area. In contrast, the intermediate position of the wild-collected MPB from Jasper suggests either an existing admixed population from BC expanding eastward or

converging invasive fronts meeting secondarily in Jasper. The presence of previously identified intermediate populations around Valemount (Janes *et al.* 2014), in addition to increasing numbers of beetles west of Jasper, appears to support a central BC origin for the Jasper area. While this study has considerably fewer individuals than previous studies of MPB (i.e. Samarasekera *et al.* 2012; Janes *et al.* 2014; Batista *et al.* 2016), we find very similar patterns of genetic diversity and structure suggesting that larger numbers of variants can increase precision and power for low sample numbers. This effect could reduce the need for intensive sampling in future genetic studies. However, to determine the trajectory and genetic composition of the most recent outbreaks additional sampling in leading-edge populations will be necessary.

Regardless of its exact source, the intermediate nature of the MPB population in Jasper provides unique challenges and advantages. For example, admixed populations, even within the same species, are recognized as important evolutionary components in both plants and animals because they can rapidly generate novel genetic material for adaptation (Mallet 2007; Janes & Hamilton 2017). Janes *et al.* (2014) and Batista *et al.* (2016) have consistently identified strong selection differences on known metabolic genes between northern and southern populations. Thus, the intermediate nature of beetles in the Jasper area, if left unmanaged, may contribute to an increased adaptive potential for MPB in Alberta, further facilitating their expansion eastward.

The severity of infestation along the Jasper west park gate suggests the possibility of a new wave of invasion into Alberta (Jasper National Park, 2016) that could, if left unchecked, continue to threaten valuable natural and managed forest resources. In the long term, the signature of admixture may assist future work on management and population genetics in two ways. First, distinct genetic signatures provide a means of tracking beetles as they spread further east and help to identify which areas are contributing to that spread (i.e. south, north, central).

This approach could be used in tandem with traditional assessment methods (i.e. aerial surveys and pheromone traps). Second, the methods we describe could potentially be extended to manage spread risk of MPB long-term. For example, populations of pest species could be managed with the aim of reducing genetic diversity, an inverse of conservation management practices that try to promote genetic diversity in populations to ensure sufficient genetic variation for selection to act on. In conclusion, we describe a means of identifying mixed populations and tracking their spread across the landscape – outcomes that could complement existing management by predicting and reducing spread risk of MPB in the long term.

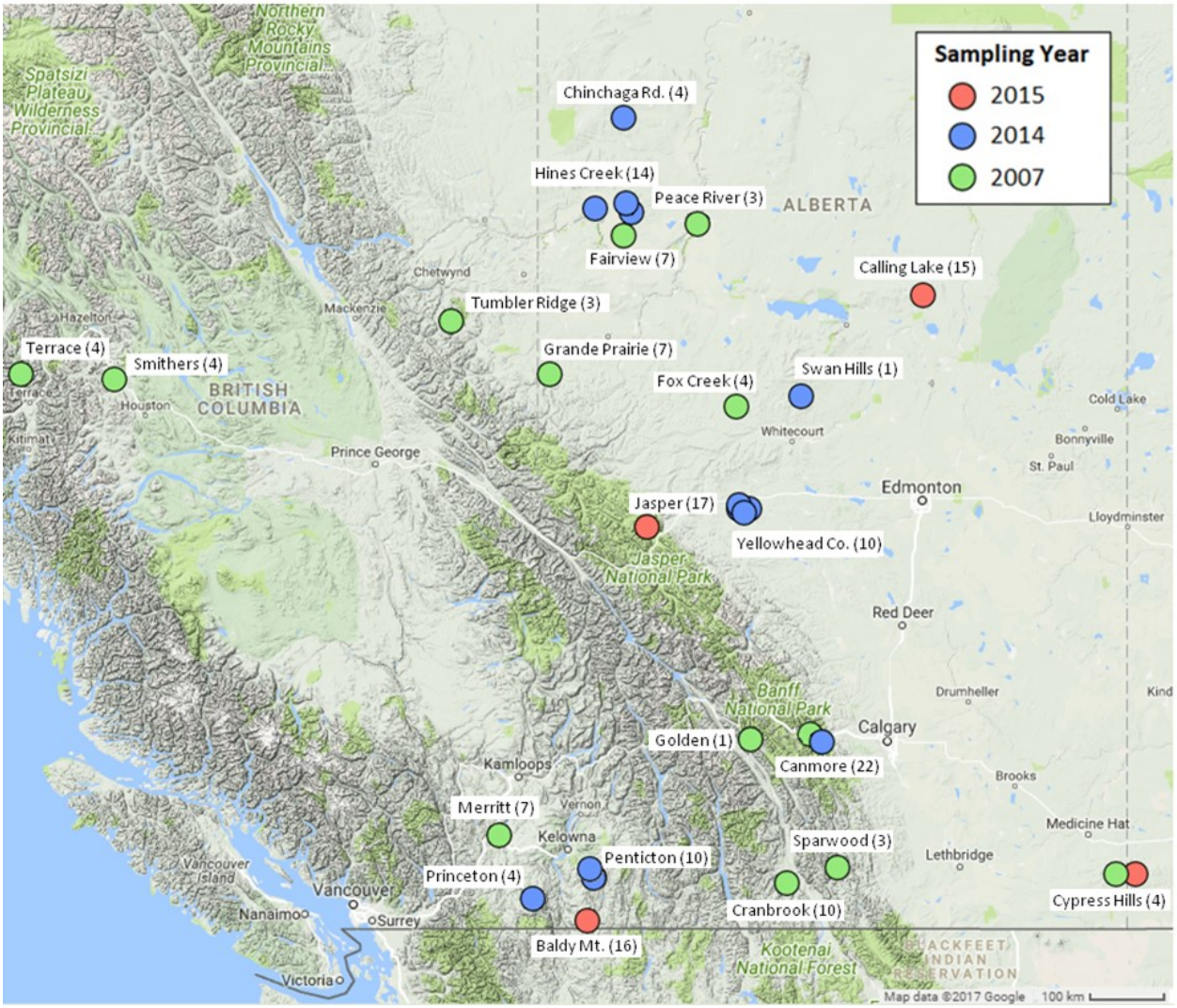

Figure 2.1. Map of mountain pine beetle collection sites organized by collection year. A total of 175 MPB were collected from 33 sites at 25 localities. Number of specimens sampled is in parentheses. Three U.S. localities are not shown (one specimen from each of Wyoming, Nevada and Washington).

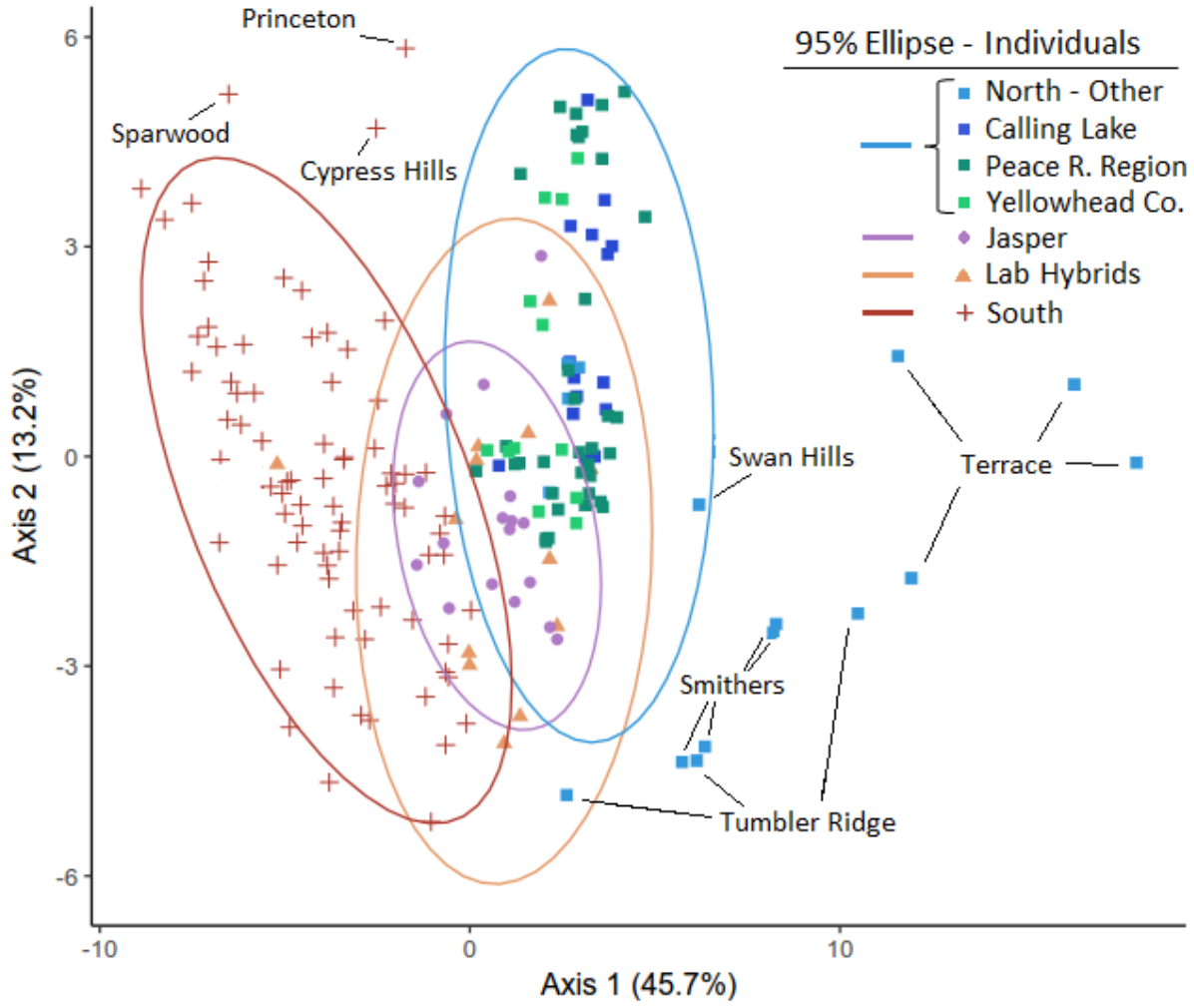

Figure 2.2. Principal coordinate analysis of 175 wild-caught mountain pine beetles, plus 13 lab-bred specimens added to simulate intermediates between northern and southern populations. Ellipses give 95% confidence intervals for populations, with the overall northern population sub-divided by colour for areas of particular management interest.

2.5 | Literature cited

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Chapter 3

Repurposing population genetics data to discern genomic architecture: A case study of linkage cohort detection in mountain pine beetle (*Dendroctonus ponderosae*)

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3.1 | Summary

Genetic surveys of the population structure of species can be used as resources for exploring their genomic architecture. By adjusting filtering assumptions, genome-wide single nucleotide polymorphism (SNP) datasets can be reused to give new insights into the genetic basis of divergence and speciation without targeted resampling of specimens. Filtering only for missing data and minor allele frequency, we used a combination of principal components analysis and linkage disequilibrium network analysis to distinguish three cohorts of variable SNPs in the mountain pine beetle in western Canada, including one that was sex-linked and one that was geographically associated. These marker cohorts indicate genomically localized differentiation, and their detection demonstrates an accessible and intuitive method for discovering potential islands of genomic divergence without *a priori* knowledge of a species' genomic architecture. Thus, this method has utility for directly addressing the genomic architecture of species and generating new hypotheses for functional research.

3.2 | Introduction

Advances in high throughput sequencing have made cost-effective genotyping of thousands of single nucleotide polymorphisms (SNP) possible, allowing a proliferation of population genetics studies (e.g. Baird *et al.* 2008; Davey *et al.* 2011; Elshire *et al.* 2011). Typically, this data is filtered to remove spurious signals, caused by sequence error or repetitive signal, to provide a consistent approach for assessing population genetic structure and a means of comparing data sets (Slate *et al.* 2009; Nielsen *et al.* 2011). However, population genetics studies are concerned primarily with assessing differences between independent markers, often neglecting potential insight into gene function and genomic architecture that can be found in co-related loci (Luikart *et al.* 2003; Stinchcombe & Hoekstra 2008).

A typical study of population structure with SNP data entails the use of three widely applied filtering procedures: 1) minor allele frequency (MAF) cutoffs to reduce the impact of rare alleles or genotyping errors in a population-level analysis (Malenfant *et al.* 2015; Bagley *et al.* 2017); 2) conformance to Hardy-Weinberg equilibrium (HWE) proportions to detect potential genotyping errors and support the assumption of neutrality in most markers (Hosking *et al.* 2004); and 3) linkage disequilibrium (LD) filtering to ensure independence of loci and remove repetitive genetic signal (Barton 2011; Schilling *et al.* 2014; Baird 2015; Lu *et al.* 2016). These methods are not consistently applied, however, and filtering is evaluated on a case-by-case basis depending on research needs and study species (Arnold *et al.* 2013; Narum *et al.* 2013). Although neutral markers are useful for investigations of genetic drift and gene flow, recent work has called into question the value of removing non-neutral markers in SNP assays (Heylar *et al.* 2011; Batista *et al.* 2016). Likewise, filtering out repetitive markers in SNP datasets may

prevent useful genetic signal from being overwhelmed by a few linked markers, but can hinder the reconciliation of genetic differentiation with genomic architecture.

Islands of genomic differentiation, or 'speciation islands', are defined as areas within a genome that have higher allelic variance between populations, most commonly measured by F_{ST} (Turner *et al.* 2005; Wolf & Ellegren 2017). The validity of islands of genomic differentiation is a topic of ongoing debate (Noor & Bennet 2009; Michel *et al.* 2010; Hahn *et al*. 2012). Researchers have observed that markers diverge between populations at different rates in localized genomic regions, but the role that heterogenous genomic regions play in speciation – whether causative, symptomatic, or unrelated – is unclear. Nevertheless, genomic islands of differentiation have become an attractive concept to explain how species boundaries are formed and maintained between sympatric and parapatric populations (Marques *et al.* 2016; Wolf & Ellegren 2017).

The traditional approach for detecting islands of genomic differentiation, known as genome scanning, uses a sliding window of F_{ST} calculations along the length of a genome. However, application of this method is restricted to organisms for which large, contiguous genome sequences have been assembled and is of limited use for the many species with minimal genomic resources (Turner *et al.* 2005; Renaut *et al.* 2011; Feulner *et al.* 2015). Kemppainen *et al.* (2015) recently released a tool for calculating linkage disequilibrium (LDna) that uses network analytical tools to visualize groups of linked loci across a genome. LDna has been used to reduce data dimensionality while searching for QTLs in model organisms (Li *et al*. 2018) and can provide evidence of inversions and islands of genomic differentiation (Benestan *et al.* 2016; Ravinet *et al.* 2017; Lindtke *et al.* 2017). In this paper, we employ a similar approach to reduce dimensionality in our data while looking for cohorts of linked markers undergoing divergence or

directional selection. For the purposes of this thesis, I use the term cohort in its statistical denotation to refer to a group of subjects sharing a defining characteristic.

One species of interest for speciation processes is the mountain pine beetle (MPB, *Dendroctonus ponderosae* Hopkins: Curculionidae, Scolytinae; Figure 1), an irruptive forest pest that has devastated millions of hectares of productive forest within western Canada and the United States (Safranyik & Carroll 2006; Bentz *et al.* 2010, Safranyik *et al.* 2010). Evidence of incipient speciation has been found in US populations surrounding the Great Basin, where three distinct Y-haplotypes result in hybrid male sterility in experimental crosses (Dowle *et al*. 2017; Bracewell *et al.* 2017). These speciation events are driven by rapid degradation of the neo-Y chromosome proceeding independently between populations. In addition to rapid changes in sex chromosomes, changes in climate have expanded MPB's Canadian range northward and eastward into naive landscapes and host plants, providing an opportunity for adaptive radiation (Carroll *et al.* 2003; Fauria & Johnson 2009; Cullingham *et al.* 2011; Janes et al. 2014). Within the beetle's Canadian range, MPB population genetic structure has a well-defined north-south division (Mock *et al*. 2007; Cullingham *et al*. 2011; Samarasekera *et al*. 2012; Janes *et al.* 2014; Batista *et al.* 2016), but lacks fine-scale population structure (Janes *et al.* 2016).

In addition to markers that have allowed extensive population genetics research, modest genomic resources exist for the investigation of MPB genomic architecture. Draft genomes for both a male and female MPB are available, but the sequences are distributed across 8,188 and 6,520 scaffolds, respectively (Keeling *et al.* 2013), and only a few gene families have been annotated (Fraser *et al.* 2017). Research into MPB gene function is aided by comparisons with resources for related species (Richards *et al.* 2008; Vega *et al.* 2015; McKenna *et al.* 2016), and the MPB genome has considerable orthology with that of the red flour beetle (*Tribolium*

castaneum Herbst) (Keeling *et al.* 2013). Synteny has been historically defined as any two genes located on a single chromosome, but has shifted to mean orthologous genes located in the genomes of separate species and sharing common descent (Passarge *et al.* 1999). For the purposes of this paper, we use synteny in its older, more traditional connotation.

The MPB genome is characterized by a karyotype of 11AA + neo-XY (Lanier & Wood 1968). Neo-XY sex-determination arises when an X chromosome fuses with an autosomal chromatid, accompanied by the subsequent loss of the original Y chromosome (Kaiser & Bachtrog 2010; Bracewell *et al.* 2017). The remaining unfused autosomal chromatid then functions as the neo-Y chromosome, becoming a paralogue to part of the neo-X chromosome. Autosomal fusion with sex chromosomes is relatively common in nature (Watson *et al.* 1991; Graves 1998; Henzel *et al.* 2011), and five of the seventeen karyotyped species within *Dendroctonus* possess a neo-XY mechanism (Lanier 1981; Zúñiga *et al.* 2002). However, the 11AA+neo-XY karyotype, in which the neo-XY is derived from fusion with ancestral autosome 1, is unique to *D. ponderosae* and its sister species, *D. jeffreyi* (Jeffrey pine beetle; Hopkins) (Reeve *et al.* 2012; Víctor & Zúñiga 2015).

Our study examines the genomic architecture of MPB using a genome-wide set of SNPs originally developed to survey population structure (**Chapter 2:** Trevoy *et al.* 2018). Previous exploration of sex chromosome evolution in MPB has provided insight into species delimitation, evolutionary biology, and population dynamics (Bracewell *et al.* 2017; Dowle *et al.* 2017). We employ an approach to data filtering that uses multivariate analyses to find additional cohorts of linked SNP markers in the MPB genome, highlighting potential islands of genomic differentiation.

3.3 | Methods

3.3.1 | Sampling

A total of 205 wild MPB specimens were selected from 39 sampling events across British Columbia, Alberta, and the northwest USA between 2005 and 2015. Larvae (*N*=139) and adults (*N*=66) were field collected and either placed in 95% ethanol before being stored at -20^{o}C or immediately stored at -80^{o}C. Wild-collected specimens were not sexed prior to DNA extraction. An additional 13 adults from north-south controlled crosses were captive-reared. Further details concerning wild and lab-bred specimens are given in **Chapter 2:** Trevoy *et al.* (2018). To aid in the molecular identification of sex-related markers, the 13 offspring from lab crosses were morphologically sexed by inspection of the sclerotized plectrum found on the beetle's seventh abdominal tergite (Lyon 1958; Safranyik & Carroll 2006; Rosenberger *et al*. 2016).

3.3.2 | Library Preparation

DNA extraction and library preparation methods followed Campbell *et al.* (2017). Extractions from the 2005-2014 samples (Run 1) were sent to l'Institut de Biologie Intégrative et des Systems (IBIS) at Laval University for library preparation and sequencing on an Illumina HiSeq 2000 platform to produce 100 bp single-end sequences. The 2015 and lab-bred samples (Run 2) were extracted and sequenced at the University of Alberta Molecular Biology Services Unit (MBSU) in Edmonton, Alberta, on an Illumina NextSeq500 platform to produce 75 bp single-end sequences. DNA extraction was identical for both runs, but library preparation differed; Run 2 was completed without data normalization or complexity reduction steps.

3.3.3 | Data assembly and alignment

FastQC v0.11.05 (Andrews 2010) was used to view the Illumina sequences and to ensure quality. Reads were demultiplexed using the STACKS v1.41 GBS pipeline (Catchen *et al.* 2013) and custom wrapper scripts written in PERL (see Data Accessibility). We trimmed index-sequence and *PstI* barcode sequence using Cutadapt v1.10 (Martin 2011) to produce reads at a uniform insert size of 62 bp for both GBS runs, as STACKS requires uniform length for variant detection (Catchen *et al.* 2013). Individuals were aligned separately to both the female and male MPB draft genomes (Keeling *et al.* 2013) using BWA-MEM v0.7.12 (Li & Durbin 2009). Reads that did not map uniquely to the draft genome were discarded (BWA-MEM option -c=1), but split hits with fewer than four unique mapping regions were marked as secondary. These secondary hits, along with any chimeric reads, were removed with SAMtools v1.3 (Li *et al.* 2009). Both male- and female-aligned data assemblies were run through the STACKS v1.41 refgen pipeline in order to generate the male and female SNP libraries. Default settings were used, except for a minimum read depth of 7.

3.3.4 | Data filtering

First, to retain a reliable dataset for further analysis, we removed low quality individuals using VCFtools v0.1.12b (Danecek *et al.* 2011). Individuals were deemed unsuitable if they were missing data at >20% of genotyped loci when filtering loci for 20% maximum missing data (MM). Second, we performed additional filtering of the male- and female-aligned datasets to remove loci with >5% MM and <5% MAF using only the female draft genome as a reference. We chose to focus on the female genome because it contains 20% fewer scaffolds but is 3.5% larger than the male draft genome, making it the less fragmented of the two draft genomes

(Keeling *et al.* 2013). Third, LDHeatmap v 0.99-2 (Shin *et al.* 2006) was used to filter the male- and female-aligned datasets for HWE proportions and LD associations. A Bonferroni correction was applied to HWE ($P=2.5x10^{-5}$), while LD filtering used a cutoff of $r^2=0.5$. LDHeatmap was chosen because it can calculate LD without known positions for markers, thus it can detect LD even among high numbers of potentially unlinked scaffolds. The default assumption of 1 kbp separation between markers was used as per the LD Heatmap manual.

In this way, three filtered datasets were obtained for each of the male- and female-aligned datasets: 1) filtered for high quality samples only (referred to as unfiltered); 2) the filtered dataset with 5% MM and 5% MAF filtering applied to loci (referred to as 5%-only); and 3) the 5% filtered dataset with both HWE and LD filtering applied (referred to as FF, fully filtered) (Table 3.1). For subsequent analyses, we use the 5%-only and FF datasets.

3.3.5 | Multivariate Analyses

Principal component analysis (PCA) is a widely used multivariate technique for compressing and distilling complex observations into sets of intercorrelated variables arranged in orthogonal axes, called principal components (PC) (Abdi & Williams 2010). Using ade4 (Dray *et al.* 2007) in R (R Core Development Team 2008), we performed a PCA on both the 5%-only and FF datasets. The thirteen lab-bred individuals were grafted onto the analysis after calculating the PCs, so that lab-bred specimens would not influence overall results. To identify SNP cohorts of potential functional or structural interest within the 5%-only dataset, we plotted SNPs in descending order of PC loading values for the first four axes. Plateaus or steep declines in PC loading were used to delimit groups of SNPs with strong and uniform influence on each PC axis. The scaffold locations and clustering behavior of these cohorts were then assessed.

3.3.6 | LDna

The 5%-only dataset was used in LDna (Kemppainen *et al.* 2015) to explore cohorts of high LD within the dataset, as a means of visualizing results from LD Heatmap and further scrutinizing patterns of LD in our data. LDna presents loci as vertices, and LD as edges between vertices, to graphically represent linkage between genetic markers along increasing levels of LD stringency, calculated using r^2. LD network analyses used default settings (minimum of 10 edges to define cohorts; phi (ϕ) = 2). LDna was not applied to the FF dataset since it had already been filtered for LD using LD Heatmap. The SNP compositions of the cohorts from LDna analyses were then compared to the SNP groups that were identified by high PC loading values.

3.3.7 | BLAST+ and BLAST2GO

In order to identify the SNPs that influence PCs 1-4, scaffold numbers and positions were compiled for all SNPs with a PC loading value that exceeded 0.050. For each SNP of interest, 200 bp of flanking sequence was copied from the draft genome (Keeling *et al.* 2013). Cross-referencing between the draft male and female genome assemblies was performed with BLAST+ (Camacho *et al.* 2008) to determine whether SNPs contributing to substructuring in the data were located on the same scaffolds in the male and female assemblies. SNPs of interest were checked against known protein sequence matches using BLAST2GO v4.0.2 on default settings (Conesa *et al.* 2005); gene ontologies for positive hits were investigated using UniProt.org (The UniProt Consortium 2015; accessed Mar 10, 2018).

3.4 | Results

3.4.1 | Alignment and filtering

A total of 30 low quality samples were removed, leaving 175 wild-collected and 13 lab-bred samples (*N*=188) for further analysis. After trimming barcodes and adapters we obtained 255 million reads of 62 bp in length from 188 samples. On average, 85% of reads were successfully mapped to the reference genome. Quality scores for Run 1 (HiSeq) and Run 2 (NextSeq) were similar, with average phred scores of 36 and 34, respectively. On average, Run 2 had 47% more unique read locations per sample than Run 1, but average read depths in Run 2 were 39% lower. The consistency and reproducibility of GBS across both genotyping platforms is supported by Campbell *et al.* (2017).

Using the draft female reference genome, STACKS yielded 18,503 SNPs for the unfiltered data set (Table 3.1). After removal of loci with 5% MM and MAF (i.e. 5%-only treatment), a total of 2,077 SNPs remained in the 5%-only data set. Further filtering for HWE removed 207 SNPs, and LD filtering removed an additional 388 SNPs from the female-aligned dataset, leaving a total of 1,480 SNPs in the FF data set. Results for the male reference genome were similar (Table 3.1).

3.4.2 | Principal Components Analysis

The FF treatment represents a widely accepted approach to filtering datasets for population genetics questions. The PCA of this set of SNPs showed clustering of individuals by geographic location (mainly latitude) of sampling sites, with a central cluster comprised of samples from Jasper National Park and the majority of lab-bred north-south crosses (Figure 3.2a) (**Chapter 2:** Trevoy *et al*. 2018). All PCA results were replicated using data aligned to the male

MPB reference genome, where similarly partitioned patterns were found (Figure A.1). A single female lab-bred specimen was found in each of the distinct north and south clusters (Figure 3.2a). The PC2 axis did not appear to relate to geography, separating three of 12 samples collected in 2014 near the town of Canmore, Alberta, from the larger southern cluster.

In contrast, the 5%-only dataset aligned to the female MPB genome showed the effect of including SNPs that violated the LD and HWE assumptions. In this PCA plot, the north-south division was reflected in the PC1 axis, but the PC2 axis showed strong nongeographic clustering (Figure 3.2b). PC2 clustered individuals into two groups, with 68 (39%; upper cluster) individuals clearly separated from another group of 107 (61%; lower cluster) (Figure 3.2b). While loadings on the PC1 axis showed a relatively smooth decline (Figure 3.3a), PC2 loadings contained a plateau of 217 loci with values exceeding 0.050 when viewed in descending order of PC loadings (Figure 3.3b). These 217 loci were located on 62 scaffolds on the draft female reference genome, with 56% of the SNPs concentrated on just 10 scaffolds (Table 3.2). This cohort of highly-weighted loci showed a large difference in allele frequency between the two clusters of samples. The individuals in the upper cluster of Figure 3.2b were almost uniformly heterozygous at each of the 217 loci (99.3%), while those in the lower cluster were almost uniformly homozygous (99.9%). Of the thirteen lab-bred individuals, all male beetles were found in the upper cluster while all females were in the lower one (Figure 3.2b). A separate dataset consisting of 157 lab-bred, morphologically sexed MPB specimens contained an axis of similar size that sorted individuals by sex with 98% accuracy (data not shown). The cohort of loci with PC2 loadings of >0.050 accounted for 10.4% of all genotyped loci in the dataset that was filtered only at 5% MAF and 5% MM. These patterns were largely consistent even with varying MAF and MM. For example, 6-12% of loci remained in this cohort when refiltering at various

combinations of MAF (2%-20%) and MM (0%-50%), and when subsampling by subpopulation, genotyping batch, or collection year (data not presented).

The PC3 axis for the 5%-only dataset divided samples into groups that, when viewed in combination with the PC1 axis, gave nine clusters arranged diagonally (Figure 3.2c). Clustering was determined by 88 highly-weighted loci (PC loading >0.050) (Figure 3.3) that were associated partially with north/south sampling location. MAF differed by 80% between the highest (A_2A_2) and lowest (A_1A_1) clusters (Figure 3.2c). Between northern and southern samples, MAF differed by 25%. These 88 loci were on 18 scaffolds in the draft female reference genome, with 64 (73%) of the loci concentrated on three unique scaffolds (Table 3.2). Additionally, 56 of this cohort of 88 SNPs were included within the highly weighted loci from the PC1 axis (Figure 3.3a). Similar to the PC3 axis, the PC4 distribution was influenced by 37 high-weight SNPs, although the clustering of specimens in the PC1 x PC4 plot was less apparent (Figure 3.2d). Most of the loci (78%) comprising the high-weight PC4 cohort were located on two unique scaffolds (Table 3.2). No high-weight loci were shared between the PC2 cohort and those for PCs 1, 3 or 4 (Figure 3.5).

3.4.3 | LDna Results

Linkage disequilibrium network analysis was used to visualize mutually exclusive cohorts of putatively linked loci. Analysis of the 5%-only (2,077 SNPs) data set revealed six SNP cohorts (Figure A.2). We focused on three of the six described cohorts that contained more than 21 loci (1% of the total data) (Figure 3.4). These three LD cohorts, designated LDna X (108 loci), LDna A (71 loci), and LDna B (24 loci), had 100%, 99% and 100% of their SNPs also occurring in the PC2, PC3 and PC4 high-weight SNP cohorts, respectively (Figure 3.5).

3.4.4 | BLAST Results

We identified a total of 390 SNPs with high PC loadings within the 5%-only data set. These SNPs were derived as: 48 SNPs from the PC1 axis only; 217 SNPs from PC2; 88 SNPs from PC 3; and 37 SNPs from PC4 (PC loadings >0.050). However, three SNPs were removed because the variant was too close to the edge of a reference scaffold to extract a flanking sequence of more than 50bps. Thus, a total of 387 SNPs from the 5%-only dataset were used for gene ontology analyses.

Using BLAST2GO, we found matching gene annotations for 140 unique proteins (Table 3.3). The annotations were related to molecular-level activities performed by gene products for 51.4% and 46.3% of SNPs in the PC1 and PC3 cohorts, respectively. The largest portion of genes annotated for the PC2 cohort (44.8%) were components of larger biological processes accomplished by multiple molecular activities, such as oxidation and reduction. Annotations for the PC4 cohort were evenly split between molecular functional genes and biological processes, at 42.9% for each (Table 3.3). At least 12 of the 83 different proteins found for PC2 were related to neurotransmission, either as structural components of neurons or as essential components in the regulation and propagation of signals within the synaptic cleft (Table A.3). The gene annotations for the PC3 cohort included genes for microfilament binding, vesicle formation, and transport of vesicles along microfilaments (Table A.4). No single biological process was noticeably well represented for the PC1 and PC4 cohorts (Table A.2, A.5). The greatest number of annotated hits matched *T. castaneum* and *Anoplophora glabripennis* Motsch (Figure A.3). Of the hits matching the *T. castaneum* genome*,* 79% from the PC2 cohort were located on chromosomes 2 and 4; 69% from PC3 were from chromosome 6; and 70% from PC4 were from chromosome 3 (Table A.6).

3.5 | Discussion

3.5.1 | Overview

In bioinformatics, the choice of filtering methods is informed by the needs of the experimental question (Schilling *et al*. 2014). The SNP dataset shown here was used previously to discern population structure in MPB (**Chapter 2:** Trevoy *et al.* 2018), but continues to provide a basis for further genomics research. Here, we describe a method to uncover genomic regions of interest for future research of gene function and evolution. PCAs of our minimally filtered dataset revealed both nongeographic and geographic clustering of samples (Figure 3.2b, 3.2c) driven by mutually exclusive cohorts of SNP loci in tight LD (Figure 3.4). Comparison between LD network analysis and loadings from PCA showed three major cohorts of SNPs, including one large cohort associated with beetle sex, a second associated loosely with sampling location, and a third with no obvious biological associations (Figure 3.5).

3.5.2 | Population Genetic Structure

When filtered for HWE and LD (i.e. FF dataset), PCA results support a north-south geographic division among the sampling locations (Figure 3.2a), in agreement with prior studies (e.g. Samarasekera *et al.* 2012; Janes *et al.* 2014; Batista *et al.* 2016; **Chapter 2:** Trevoy *et al.* 2018). As demonstrated in **Chapter 2:** Trevoy *et al.* (2018), the Jasper population is intermediate to the north and south populations. This suggests a geographic area of admixture, either from converging invasive fronts meeting in Jasper, or as a result of an existing intermediate population from British Columbia forming a third front of eastward invasion. We find further support for the intermediate nature of Jasper in the placement of lab-bred, north-south crossed specimens, which are intermingled with the Jasper population. The female lab-bred specimens in both the north and

south clusters could be the result of pre-emergence mating among siblings within a bolt, a known occurrence in MPB (Bleiker *et al.* 2013, Janes *et al.* 2016).

3.5.3 | Nongeographic Clustering - Possible Sex-Linked Paralogues in MPB

Datasets that were not filtered based on LD (i.e. the 5%-only) showed additional clustering that did not clearly correspond to sampling locality. The PC2 axis sharply segregated individuals by percent heterozygosity based on 217 SNP loci that had high loadings. The homozygous group contained all the female individuals from the sexed, lab-bred specimens (Figure 3.2b) and included 61% of all samples, while morphologically sexed lab-bred males grouped with the heterozygous PC2 cohort. The division among sexed individuals is consistent with the female-biased sex ratio observed by other researchers in MPB (64%, McGhehey 1969; 62%, Safranyik 1976; 61%, Lachowsky & Reid 2014). We hypothesize that the PC2 axis is driven by recent nucleotide substitutions in sex-linked genes located on the neo-XY chromosomes, with heterozygous loci indicating males, which are the heterogametic sex.

The neo-X chromosome in MPB is thought to be a fusion of the largest ancestral autosome and the ancestral X chromosome, leaving the daughter autosomal chromatid to become the neo-Y after the loss of the ancestral Yp chromosome (Lanier, 1981; Zúñiga *et al.* 2002). This fusion with sex chromatids either inhibits or suspends the autosomal portions from crossing over between sexes, transforming the formerly linked autosomal chromatids into evolutionarily and functionally distinct units (Steinemann & Steinemann 1998; Turner 2005; Kaiser & Bachtrog 2010). Thus, point mutations and fixation of previously variable loci from the ancestrally autosomal fragments would have proceeded independently on each newly fused chromosome

(Kimura 1962; Rice 1996). However, sections of the neo-Y chromosome may still align with homologous regions of the neo-X scaffolds, creating paralogous SNPs.

If the distinct groupings formed by the PC2 cohort are due to SNP paralogues on the historically autosomal portions of the neo-XY complex, this may explain why homologous hits on the genome of *T. castaneum*, another beetle species, are located predominantly on autosomes. Of the 78 BLAST matches between the PC2 cohort and the *T. castaneum* genome, 80% were found on autosomes 2 and 4 (Table A.6). Orthology between MPB and *T. castaneum* has been demonstrated (Keeling *et al*. 2013). However, the two species are widely separated by evolutionary history and karyogamy; evidence for shared autosomal ancestry is only suggestive at this point (Lanier & Wood 1968; Richards *et al.* 2008; McKenna *et al*. 2015).

Despite support for neo-XY paralogues as the source of sex-associated SNPs, there is also evidence to the contrary. For example, scaffolds containing sex-linked SNPs also include some SNPs that were not fully diagnostic for beetle sex. One explanation for this could be that these loci have not yet reached fixation in one or both MPB sexes. It is also possible that incomplete segregation is caused by one or more pseudoautosomal regions of the neo-XY complex that may still undergo recombination (Charlesworth *et al.* 2005). More work is needed to determine if the sex chromosomes of *D. ponderosae* cross over during cell division, as in many other species of plants, animals and fungi (Otto *et al.* 2011; Blavet *et al.* 2012). In any case, our imputed sex-linked scaffolds do not include those predicted by Keeling *et al.* (2013), who suggested six different scaffolds based on their reduced SNP content per kbp. A linkage map or a complete genome sequence assembly for MPB would provide more definitive evaluation of these sex-linked scaffolds (see **Chapter 4**).

The finding that PC2 is associated with sex has various implications and applications. If true, it can be expected that paralogues constitute 6-12% of any given SNP dataset for MPB. Organisms with a neo-XY mechanism like MPB, therefore, pose a unique case for filtering. This paralogous data violates the assumption of locus independence that is commonly applied in population genetics analyses, and these loci may be removed with LD filtering. However, these same evaluations of LD can also provide valuable insight into genomic architecture.

Despite the challenges inherent in filtering paralogous data, these putative neo-XY markers would be useful for determining the sex of samples. Due to the narrow temporal window for collecting postemergence adults, most field samples of MPB are collected in the late larval stage (Carlson & Cole 1965; Safranyik 1968; Safranyik & Carroll 2006), which shows no obvious sexual dimorphism. Within our own analysis, beetles were not sexed prior to genotyping due to the high proportion of larval individuals. Traditional MPB sexing methods (i.e. stridulation and seventh tergite morphology; Lyon 1958) are time-consuming and have some degree of inaccuracy (Rosenberger *et al.* 2016). Both methods call for undamaged adult beetles, but stridulation, a behavioral indicator, further requires specimens to be alive. Meanwhile, genetic methods can be employed on various life-history stages and on physically damaged specimens (Stovall *et al.* 2018). While there is a genetic means of sexing MPB using microsatellites (Davis *et al.* 2009), our results demonstrate a SNP-based sexing method that is easily applied to NGS datasets without the additional cost and labor required to genotype microsatellites. Reliable sexing of MPB is valuable for monitoring and predictive modeling of MPB outbreaks because sex ratio skew is related to outbreak maturity (James *et al.* 2016).

3.5.4 | PC 3 – Candidate for Adaptive Selection?

Unlike the PC2 cohort of SNPs, the SNPs detected by PC3 do not cluster individuals by imputed sex; rather the PC3 axis has substantial geographic signal (Figure 3.2c). The PC3 axis is instead driven by variation in a subset of SNPs already found to contribute significantly to PC1 (Figure 3.3a, 3.3c). LD network analysis shows that LDna SNP cohort A is 96% identical to the portion of the high-weight PC3 cohort that overlaps with high-weight PC1 SNPs (Figure 3/5). This axis is therefore unrelated to sex, but may form an island of genomic differentiation within the geographic signal of the PC1 axis that is concentrated on five autosomal scaffolds of the female MPB genome (Table 3.2). This result complements recent work on divergence in the neo-Y chromosome as a mechanism for speciation (Bracewell *et al.* 2017; Dowle *et al.* 2017). Adding to these studies, our high-weight SNP cohorts from PC axes 1, 3 and 4 provide evidence of autosomal divergence across the Canadian range of MPB.

BLAST2GO analysis suggests that a disproportionate number of the genes associated with the geographically informative PC3 cohort may relate to biological processes of intracellular transport and transcription, but are not linked by ontology or pathway (Table A.4). A possible explanation is that there has been concatenation of adaptive genes into a higher-impact QTL, or supergene – a group of different genes, although often related, that are closely packed on the genome and inherited together. Supergenes were first described for flower morphology in plants (Mather 1950; Yeaman & Whitlock 2011; Hermann *et al.* 2013), but are also key determinants in the coloring of several insect species (Clarke *et al.* 1968; Brown & Benson 1974; Nijhout 2003; Joron *et al.* 2011; Lindtke *et al.* 2017). More conclusive evidence of a multi-gene QTL could make MPB one of the first species described with a metabolic, rather than structural, supergene.

While the differences between northern and southern demes could provide evidence of unique selection pressure, a genomic inversion within one of the populations might also explain why spatially linked loci might appear to be under selection (Giglio *et al*. 2001; McCutchen & von Dohlen 2011). An inversion of genomic sequence does not preclude the existence of selection pressure or a supergene, but does provide an alternative, neutral mechanism. Linkage disequilibrium may also arise through random genetic drift without any functionally active selection (Ohta 1982). Further study of the genes implicated in the detected linkage cohorts could help explain the beetles' expansion into northern Canada through mechanisms like adaptation in metabolic pathways. However, a full linkage map or genome assembly is necessary to determine if the differences between populations are indeed spatially related and whether they are a result of chromosomal inversion (see **Chapter 4**).

3.5.5 | Integrating PCA with LD network analysis

Linkage disequilibrium network analysis detected at least three sizable cohorts of associated markers (Figure 3.4), each of which corresponds with an axis of the PCA on SNPs that were only lightly filtered for missing data and minor allele frequency (5%-only data set) (Figure 3.5). Standard filtering for LD removed these axes. There was substantial concentration of SNPs on a few draft genome scaffolds involved with PC cohorts 2, 3 and 4 and with LDna cohorts X, A, and B, respectively (Table 3.2). Further exploration of genomic differentiation in MPB, using integrated PCA and LD analysis, may discriminate additional SNP cohorts (Figure A.2; Table A.7).

It may be possible to apply this method to other SNP datasets to detect correlated genomic differentiation in subsets of SNPs by 1) partitioning genetic variance among individuals

in a PCA and examining the distribution of PC loadings, and 2) discrimination of SNP cohorts with LD network analysis to verify that correlated SNP cohorts are due to linkage disequilibrium, rather than population structuring. However, studies using more conventional approaches to detect divergence between populations are required to verify the efficacy of this method (Lindtke & Yeaman 2017). Studies using simulated data, with different taxa, traits, sample sizes and loci are also necessary to evaluate the robustness and generality of our method. We note that for MPB the PCA step found more SNPs in each cohort than analysis by LDna alone, while LDna found almost no SNPs that were not in the PC cohorts.

While useful as a means of ensuring independence of loci in classical population genetics surveys, LD analysis can also offer insights into genomic architecture and differentiation, even within nonmodel species (Barton 2011; Kemppainen *et al.* 2015; Baird 2015). Recent work by Li *et al.* (2018) has explored the potential to augment genome-wide association studies (GWAS) in model organisms by imputing loci of interest using PCA to reduce complexity in large datasets, followed by linkage network analysis. Here, we demonstrate an independently developed version of such a method as a tool to detect genomic islands of differentiation in wild populations. The combination of PCA and LDna to detect cohorts of correlated SNP variation has allowed us to circumvent the need for precise knowledge of genomic positions. The use of a draft genome for our research, although useful in supporting our results, was not a requirement for the larger component of our analysis; similar analyses to those shown here are possible with a *de novo* dataset. Although the approach described here is less precise than a genome scan (see Turner *et al.* 2005; Renaut *et al.* 2011; Feulner *et al.* 2015), it offers a means to explore divergence in populations without the need for detailed knowledge of genomic locations, and with the benefit of preexisting or lower-cost genetic marker datasets.

3.6 | Conclusion

Our geographic survey of GBS SNP variation in the mountain pine beetle in western Canada has allowed us to determine both population structure and genomic architecture, as well as to explore functional aspects of population divergence. In addition to replicating previously documented population structure, we uncovered at least three cohorts of genomically linked loci when we dispensed with the traditional approach to filtering for HWE and LD.

The largest cohort of linked SNPs is hypothesized to be composed of paralogous loci from the neo-X and neo-Y regions of the sex chromosomes. This provides a means to determine the sex of individuals. The second SNP cohort is composed of geographically associated loci in tight LD. This SNP cohort yielded several candidate genes for further study of adaptive radiation and selective pressures facing MPB as it expands eastward in Canada. A third cohort of SNPs is independent of the other two, and represents further opportunities for research. Using a procedure related to that of Li *et al*. (2018) to integrate principal components analysis and linkage disequilibrium analyses, we describe a novel approach that can potentially be applied to the burgeoning number of reduced representation SNP datasets to find putative islands of genomic differentiation in nonmodel species.

Table 3.1. Locus counts for the SNP dataset of 175 wild-caught and 13 lab-bred MPB after various filtering treatments were performed (1) or not performed (0). Cutoffs were set to 5% for maximum missing (MM) data, 5% for minor allele frequency (MAF), p=0.000025 for Hardy Weinberg Equilibrium (HWE), and r^2=0.5 for linkage disequilibrium (LD). Final analysis refers to analysis after filtering.

Treatment	MM	MAF	HWE	LD	Female	Male	Final Analysis	Results
unfiltered	0	0	0	0	18 503	18 499	-	-
5%-only	1	1	0	0	2 077	1 908	PCA, LDna	Figure 3.2b, 1c, 1d Figs. 2, 3, 4
FF	1	1	1	1	1 480	1 488	PCA	Figure 3.2a

Table 3.2. Scaffold distribution of SNPs that contribute significantly to a PC axis (>0.050 PC loading) from a PCA on the 5%-only dataset aligned to the female MPB genome. Numbers indicate how many separate draft genome scaffolds contain SNPs contributing to that PC, with successive rows indicating more SNPs on each scaffold. Only SNPs that are exclusive to PC1 are included in that column; SNPs that are shared with PC3 are included only in the column for PC3.

SNPs per Scaffold	PC1 Scaffolds	PC1 SNPs	PC2 Scaffolds	PC2 SNPs	PC3 Scaffolds	PC3 SNPs	PC4 Scaffolds	PC4 SNPs
1-2	33	39	39	48	14	16	5	5
3-5	3	9	13	47	2	8	1	3
6-9	0	0	5	37	1	8	0	0
10-14	0	0	2	24	0	0	1	10
≥15	0	0	3	61	2	56	1	19
Total	36	48	62	217	18	88	8	37

Table 3.3. Gene ontologies for SNPs with significant contributions to PCs 1-4 (PC loading >0.050). PC1 refers only to loci that did not overlap with PC3. Percent given after / for cellular, molecular and biological gene ontology categories include unique ontology results only. Cellular components refer to cellular structures in which a gene product performs a function, molecular functional refers to genes with molecular-level activities performed by gene products, and biological processes refer to larger processes accomplished by multiple molecular activities.

	PC1	PC2	PC3	PC4
Total loci	48	214	88	37
Annotated loci	18	93	40	13
Unique proteins	16	83	29	12
Unique Gene Ontology Terms	37	183	95	42
% cellular components	5 / 13.5%	36 / 19.7%	14 / 14.7%	6 / 14.3%
% molecular functional genes	19 / 51.4%	65 / 35.5%	44 / 46.3%	18 / 42.9%
% biological processes	13 / 35.1%	82 / 44.8%	37 / 38.9%	18 / 42.9%

Figure 3.1. The mountain pine beetle (*Dendroctonus ponderosae*). Scanning electron micrograph was taken by Jack Scott and is used with permission of the TRIA project.

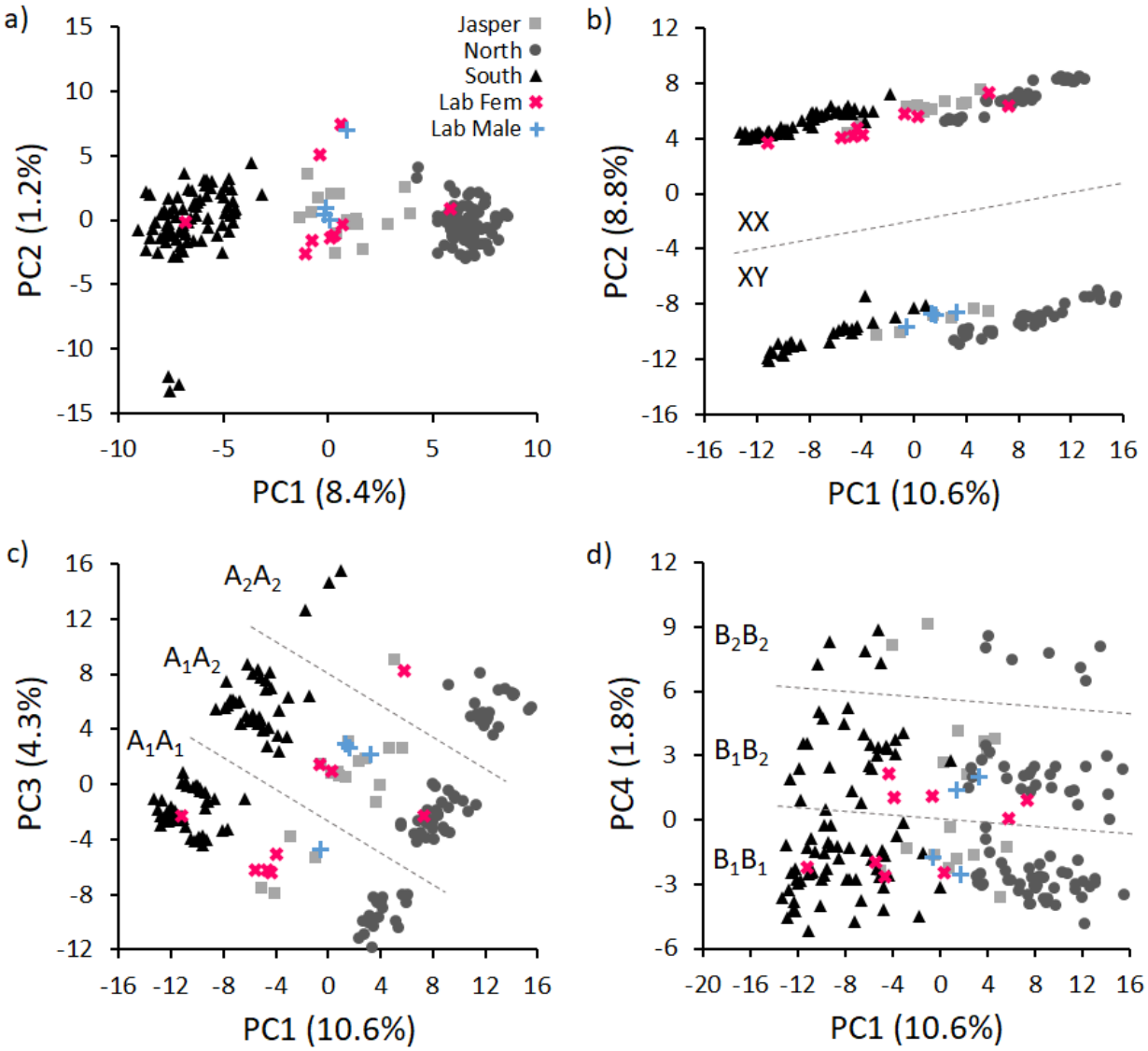

Figure 3.2. Principal component analyses of 175 wild-caught and 13 lab-bred MPB aligned to the female MPB genome. a) FF dataset with 1480 SNPs filtered at 5% MM, 5% MAF, HWE (p=0.000025), LD (r^2=0.5). b-d) 5%-only dataset with 2077 SNPs filtered at 5% MM and 5% MAF, showing PC1 x PC2, PC1 x PC3, and PC1 x PC4, respectively.

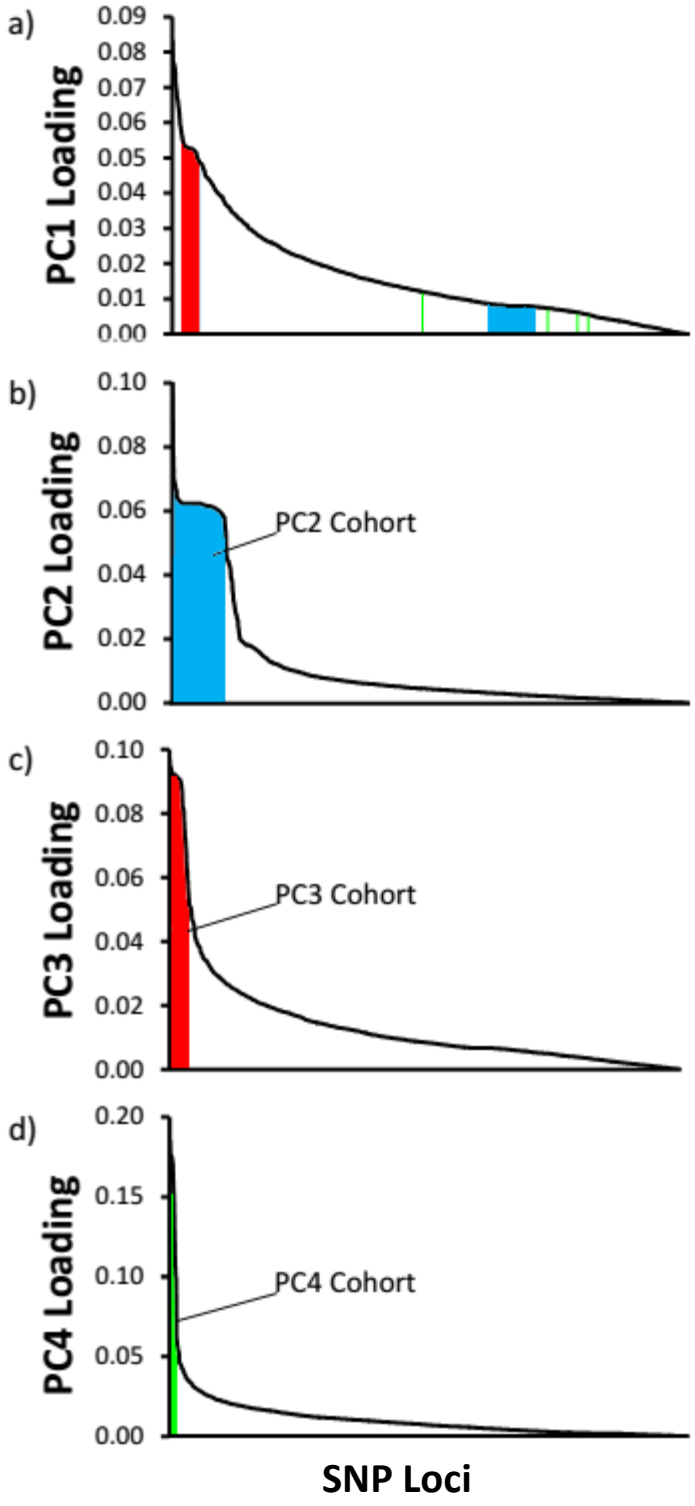

Figure 3.3. 2077 SNP loci arranged in descending order of principal component loadings for Axes 1-4 of 175 wild-caught MPB (5% MM, 5% MAF). Locations within PC1 for loci contributing heavily to PCs 2, 3, and 4 are shown in blue, red and green, respectively.

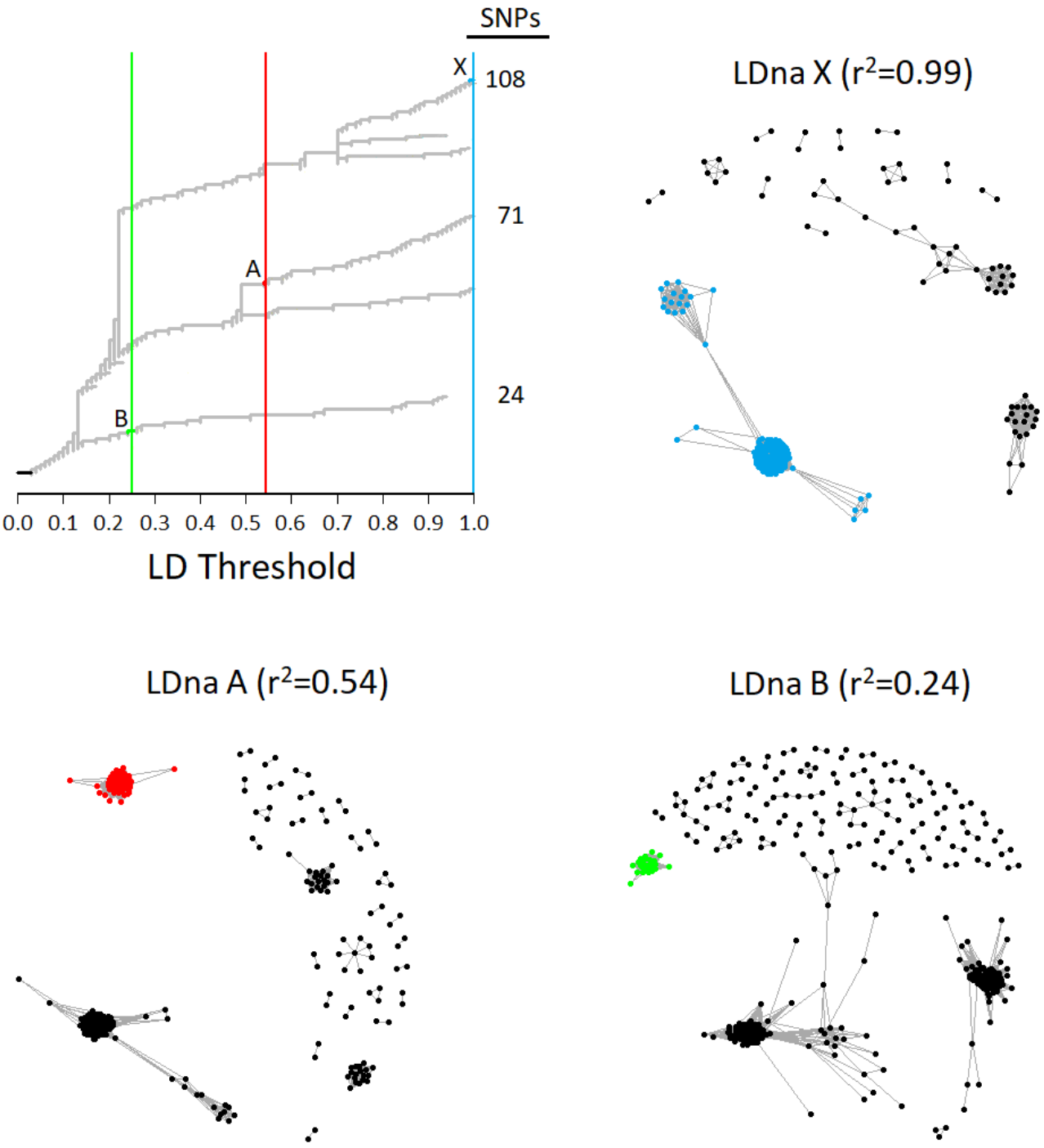

Figure 3.4. Linkage disequilibrium network analysis (LDna) for 2077 SNPs, filtered at 5% MM and 5% MAF. Number of edges (E) is equal to 10, Cluster splitting (φ) is equal to 2. Clustering is depicted as a treespace progressing with increasing support for LD, as indicated by r^2. LDna cohort X at $r^2 = 0.99$, LDna cohort A at $r^2 = 0.54$, and LDna cohort B at $r^2 = 0.24$ are highlighted in blue, red and green, respectively, as they appear along the treespace.

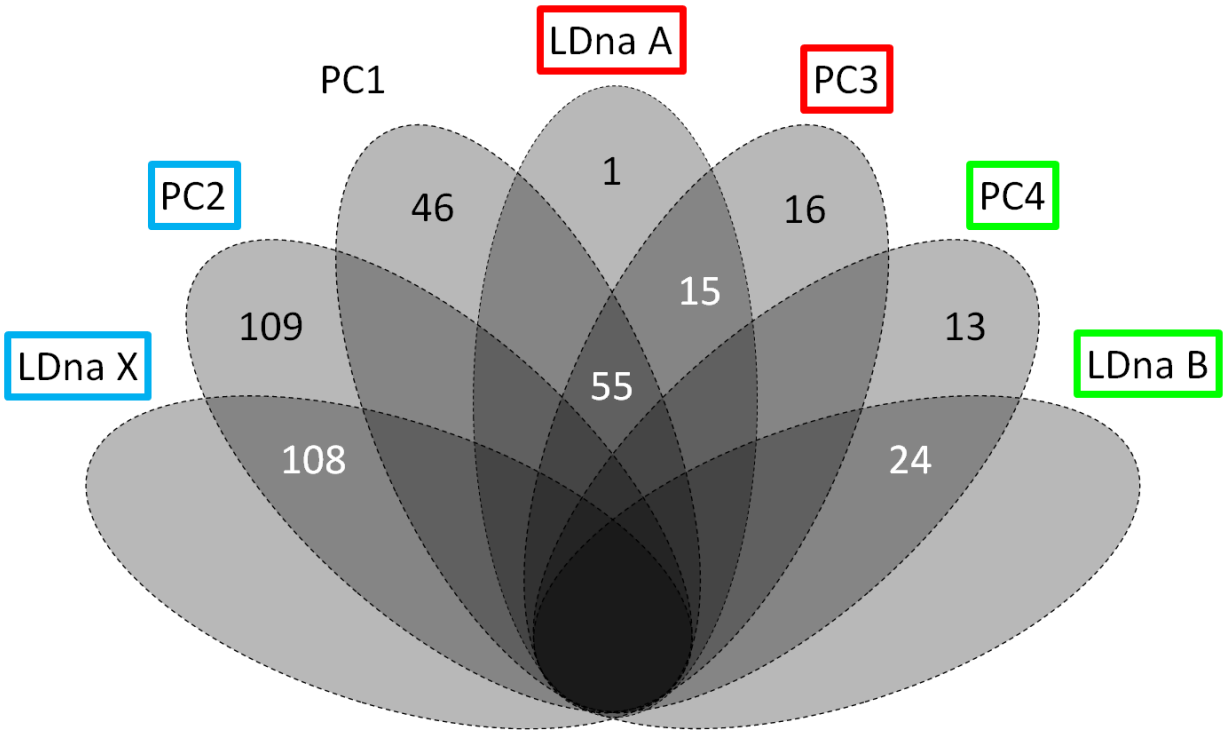

Figure 3.5. Correspondence among SNPs with high contributions to PCs 1, 2, 3 and 4 and LDna cohorts X, A and B, based on analysis of 2077 SNPs in 175 MPB samples from BC and Alberta. SNPs are treated as contributing to an axis if their PC loading weight exceeds 0.050. Combinations with 0 markers are left blank. Two SNPs, which were shared between PC1 and PC3 but not LDna cohort A, are not shown.

3.7 | Literature Cited

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Chapter 4

Preliminary genetic linkage map for the mountain pine beetle (*Dendroctonus ponderosae*)

1.1 | Summary

Linkage maps are a valuable asset for investigations of genomic architecture and evolution. Here, I present a high-density preliminary linkage map for both male and female mountain pine beetle (*Dendroctonus ponderosae*), an irruptive forest pest of particular economic interest. Orthology analysis between the two MPB linkage maps and the linkage map of *Tribolium castaneum*, another beetle species, reveals both highly divergent and conserved genomic regions among the two species. A colony of lab-bred F2 crosses was formed using outbred crosses of wild specimens from two invasive populations. The low success of these lab-bred crosses is compared to previous population genomics work, suggesting incipient speciation within mountain pine beetle's Canadian range.

4.2 | Introduction

By providing the chromosomal locations of genetic markers, linkage maps have been instrumental in answering diverse questions about the role of genomic architecture in evolutionary diversification. For example, genetic linkage maps can inform assessment of genetic hitchhiking (Yan *et al*. 1998; Flaxman *et al*. 2013), the number and distribution of loci that contribute to complex traits (Yeaman & Whitlock 2011; Lindtke *et al*. 2017), and genomic regions with elevated selection and divergence (Turner *et al.* 2005; Fuelner *et al*. 2015). Recent proliferation of high throughput sequencing technologies (Davey *et al.* 2011; Elshire *et al.* 2011) has furthered linkage map construction through cheap and accurate genotyping of thousands of single nucleotide polymorphisms (SNP) (Rastas 2017; Picq *et al*. 2018).

For Coleoptera, investigations of genomic architecture and evolution have been limited by a paucity of genomic resources, despite considerable economic and environmental interest in many beetle species (Richards *et al*. 2008; Keeling *et al*. 2013; McKenna *et al*. 2016). The mountain pine beetle (MPB, *Dendroctonus ponderosae* Hopkins: Curculionidae, Scolytinae), an irruptive forest pest found in western Canada and the United States (Bentz *et al.* 2010; Safranyik *et al.* 2010), illustrates this economic and environmental impact. MPB has recently spread beyond its historical range, expanding north and east into naïve habitats and host species (Cullingham *et al.* 2011; Janes *et al.* 2014; **Chapter 2:** Trevoy *et al*. 2018). Draft genomes for both male and female MPB are available, consisting of 8,188 and 6,520 scaffolds, respectively (Keeling *et al*. 2013). A dense linkage map of MPB would allow these scaffolds to be condensed to a few linkage groups and facilitate exploration of the genomic organization of *Dendroctonus* species. A full linkage map would also allow validation of the potential islands of genomic divergence within MPB that were uncovered in previous population genetics work (**Chapter 3**).

The MPB genome has a karyotype of 11AA + neo-XY, with males as the heterogametic sex (Lanier and Wood 1968). Neo-XY sex-determination results from the fusion of an X chromosome with an autosomal chromatid followed by the loss of the original Y chromosome (Kaiser and Bachtrog 2010; Bracewell *et al.* 2017). The genus *Dendroctonus* is highly variable in karyotype formula, ranging from 14AA + Xyp to 5AA + neoXY (Zúñiga *et al*. 2014). This suggests that novel karyotypes evolve rapidly within *Dendroctonus*. The closest relative of MPB with a well-annotated genetic linkage map is the red flour beetle (RFB, *Tribolium castaneum* Herbst: Tenebrionidae), a stored grains pest that shares partial chromosomal orthology with MPB (Lorenzen *et al*. 2005; Richards *et al*. 2008; Keeling *et al*. 2013).

In this study, several families of MPB were reared in an F2 sibling cross, generating SNP markers for linkage map construction using the draft reference genomes. The two resulting linkage maps, male and female, are then compared to each other and to the existing linkage map for RFB.

4.3 | Materials and methods

4.3.1 | Sampling

A total of eight lodgepole pine trees infested with MPB were selected from the Smokey River Lowlands (SRL), south of Grande Prairie, AB (54º 21.376'; N 118º 19.112' W) and ten lodgepole pine trees from the Burnco Quarry (BQ) near Canmore, AB (51º 04.026' N; 115º 17.237' W). We chose these sites to represent the two genetically divergent populations known from Alberta and maximize the number of genetic markers detected from admixed crosses (Samarasekara *et al.* 2012, Janes *et al.* 2014). Infested trees were felled, cut into 1-meter long bolts, and transported to the University of Alberta (UofA), where the cut ends of the bolts were coated in paraffin wax to reduce desiccation. Bolts were stored at 4º C in a growth chamber at the UofA until the following spring. These wild MPB individuals (F0) served as 'pure' north and south breeding stock for the first crosses.

4.3.2 | Rearing

Larvae of MPB develop beneath the bark of host trees, where they feed on tree phloem, followed by emergence as adults that disperse to find new host plants (Safranyik & Carroll 2006). Females are the pioneers, initiating attacks on a new host tree by constructing the first portion of a larval gallery; males locate females beneath the bark, copulate, and will either leave

to find another female, or remain to help construct the parental gallery. To emulate natural conditions for our crosses, we collected three lodgepole pine trees from Nojack, AB (53º 36.103' N; 115º 35.239' W). These trees, which were free from MPB attacks, were felled and cut into 55cm bolts, and immediately transported to the UofA, where they were coated in paraffin wax to avoid desiccation. These 'clean' bolts served as incubators for the F1 outbred crosses and F2 sibling crosses used in to produce the linkage map.

After the clean bolts were prepared and placed in cold storage, we took the BQ and SRL bolts from cold storage and placed them in opaque plastic emergence boxes (see Mori *et al*. 2011) at room temperature (~22º C) to begin collecting the wild, parental generation (F0). Emerging beetles were collected daily from the emergence boxes and sexed via the auditory sexing technique described by McCambridge (1962). We temporarily stored the beetles at 4º C for up to five days so that sufficient numbers of beetles could be collected to establish crosses. Following the recommendations of C. Whitehouse (pers. comm.), a female beetle from either BQ or SRL was forced onto an uninfested bolt by placing it into a modified 1.5 ml microcentrifuge tube glued directly onto the bolt using hot-melt adhesive (Figure 4.1). If a female failed to burrow into the bolt within 24 hours, we replaced it with a different female. Males from the opposite sampling location were introduced two days after the female successfully bored into the bolt. If the male failed to enter and establish in the gallery it was removed and replaced with a fresh male. In this way, we used a total of 74 female and 69 male MPB to establish 66 BQ x SRL parental crosses (F0), each in their own separate bolt, to create the F1 generation of beetles.

Bolts containing parental crosses were stored upright within a single locked room at room temperature (~22º C) for six weeks, then placed on their sides in emergence boxes. F1 progeny were collected from the emergence boxes over 15 days. Bolts used for F0 crosses were retired

before all beetle emergences could be completed due to storage space limitations; establishing the F1 crosses required that parental bolts be cleared and safely disposed of to make the emergence boxes available for the first F2 emergences. In the six weeks prior to being placed in individual emergence boxes, some F0 beetles abandoned their bolts prematurely and re-established within another bolt. To ensure confidence in our parental pedigrees, we stripped the bark from each bolt and visually inspected the beetle feeding galleries. We counted individual larval feeding tunnels and examined bolts for secondary infestations, evidenced by multiple parental galleries on a single bolt. Parental bolts that contained more than a single adult feeding gallery or had galleries that did not begin at the initial inoculation site were rejected from our F1 crosses.

In the same manner as the F0 crosses, a total of 92 female and 69 male F1 MPB were used to establish 66 F2 full-sibling crosses. After a week inside the bolt, the first 5 cm of the gallery was peeled back to recover the male F1 parent from the packed frass at the bottom of the parental gallery (see Reid, 1958). After extracting the male, the bark was replaced and the cut was sealed with petroleum jelly so the bolt did not dry out. In accordance with Ammon (1972), we expected females to reach the end of their 55 cm bolt in roughly three weeks; at this point they were extracted from the top edge of the bolt in a similar manner to the males. After recovering one or both F1 parents, the bolts were laid on their sides in emergence boxes at room temperature (~22°C) until the F2 progeny were recovered. Specimens were then stored frozen at -20° C. Prior to DNA extraction, all samples were sexed using seventh tergite morphology, as described by Lyon (1958).

4.3.3 | Genotyping

From 66 attempted F1 crosses, 44 crosses produced F2 offspring. From those 44 MPB crosses, 14 were selected for DNA extraction. A family was selected for DNA extraction if it contained more than 10 individuals, and at least one of the F1 parents had been recovered from the bolt. DNA extractions and library preparation methods followed the protocol of Campbell *et al.* (2017), using QIAGEN (Toronto, ON, Canada) DNEasy Blood & Tissue kits according to the manufacturer's instructions. Samples were extracted and sequenced using genotyping-by-sequencing (GBS) as described in Elshire *et al*. (2011). An Illumina NextSeq500 platform was used to produce 75 bp single-end sequences at the University of Alberta Molecular Biology Services Unit (MBSU).

We used FastQC v0.11.05 (Andrews 2010) to view the Illumina sequences and ensure quality. Reads were demultiplexed using the STACKS v2.0 GBS pipeline (Catchen *et al.* 2013), then trimmed using Cutadapt v1.10 (Martin 2011) to remove the index and *PstI* barcode sequences, producing reads at a uniform 62 bp. Individuals were aligned separately to both the female and male MPB draft genomes (Keeling *et al.* 2013) using BWA-MEM v0.7.17 (Li and Durbin 2009). Chimeric reads and reads that did not map uniquely to the draft genome were discarded using the protocol described in **Chapter 2:** Trevoy *et al.* (2018). Assemblies aligned to the male- and female reference genomes, hereafter referred to as the female and male datasets, were run through the STACKS v2.0 refgen pipeline (Catchen *et al.* 2013) to generate SNP libraries. Default settings were used except for a minimum read depth of 5.

4.3.4 | Filtering and identity by descent

To ensure that genotyping errors did not interfere with correct marker ordering and expansion of the linkage map, we removed low-quality reads (Hackett and Broadfoot 2003; Cartwright *et al.* 2007). SNP markers were filtered using VCFtools v0.1.12b (Danecek *et al.* 2011). We employed a cut-off of 20% maximum missing data (MM), 5% minor allele frequency (MAF), and a minimum average read depth (ARD) of 20 per locus. A principal component analysis (PCA) was performed on both male and female datasets, and one principal component was found that sorted the 229 samples by sex with 99.1% accuracy (227/229; Figure A.4). We interpreted the two cases of mismatched sex as an error in our morphological sex determination and amended the sex designation to match our PCA results.

Discrete families are necessary to ensure clear and accurate linkage mapping results (Liu *et al.* 2013). To verify that the individuals used to generate our linkage map were correctly associated with discrete families we used Identity By Descent (IBD) in the Lep-MAP3 IBD and CERVUS programs using default settings (Marshall *et al.* 1998). Individuals were dropped from further analysis if they had less than 25% IBD with at least half of the individuals within their respective families. Parental assignment with CERVUS was useful as confirmation of IBD results, but resulted in fewer rejected samples overall. We relied on the more conservative IBD results going forward.

4.3.5 | Linkage mapping

Linkage maps were generated using Lep-MAP3 (Rastas, 2017). The female linkage map was generated using the SNP dataset obtained using the female reference genome, while the male linkage map used the SNPs from the male reference genome. Prior to creating the linkage

maps, we used the ParentCall2 module of Lep-MAP3 to impute missing or erroneous SNP calls on the F1 parents. After the missing calls were calculated, we used the Filtering2 module to remove markers with high segregation distortion, defined as a data tolerance score of >0.01. Default parameters were used to separate SNP markers into chromosomes, except minimum markers per linkage group (LG) was raised to 10 and LOD scores were adjusted until the number of clusters matched the known number of chromosomes from previous work on MPB karyology (Lanier and Wood 1968). Thus, our linkage maps were generated using a LOD score of 8.5 for the female dataset, and 9.1 for the male dataset. We elected not to use data from the JoinSingles2All program offered by Lep-MAP3 because the program distributed SNP markers from unique reference genome scaffolds onto multiple LGs. The program assigned leftover SNPs onto the existing LG framework, resulting in 22 instances of a single genome scaffold split among 2 or more LGs in the female linkage map, and 28 scaffolds in the male linkage map. Thus, we suspected that this program was overfitting our data. Despite this, the greatly increased number of SNPs from JoinSingles2All was useful when comparing linkage results to earlier population genetics work (Chapter 3).

Once we had our LGs, we used Lep-MAP3's OrderMarkers2 module to determine placement of markers relative to each other along the chromosomes. Marker ordering was done for five replicates of six iterations for each LG separately and the results with the highest likelihood were kept for the final linkage map. We used Haldane's map function, the default for Lep-MAP3, to calculate map distance in cMs. Lone markers on the ends of LGs were trimmed if they contributed >10% of a LG total length. The PCA, previously used to verify the sex of the samples (Figure A.4), was compared with Lep-MAP3's LGs to verify that all SNP markers that were diagnostic for sex in both PCAs were located on a single LG. The implicated LG was then

labeled as the X chromosome; the remaining autosomal LGs in the female linkage map were arranged in descending order of total size in cMs. The male LGs were named and arranged to match the female LG that they corresponded to.

4.3.6 | Comparisons among MPB linkage maps and orthology with Tribolium castaneum

The SNP markers used here to generate the female linkage map were cross-referenced with prior work that found covarying SNP cohorts in a population genomic survey of mountain pine beetle within BC and Alberta (**Chapter 3**). These SNP cohorts were derived using the female reference genome, so we compared them to the linkage map SNPs from the female reference genome. Matches for SNPs were found based on identical alignment positions (reference genome scaffold and base pair number) within both datasets. To compare results between male and female linkage maps, we used BLASTn to search 200 bp of flanking sequence on all SNP markers from the male linkage map against the female linkage map (Altschul *et al.* 1990). Top BLAST hits for each marker were filtered for a minimum of 40 bp of aligned sequence (20% of total sequence length), and a minimum e-value of $1x10^{-10}$. The remaining matches were ordered according to the male linkage map and depicted graphically using a chord diagram generated using Circlize (Gu *et al.* 2014), a package in R (R Core Development Team 2008).

Orthology analysis is valuable for investigating evolutionary history and quantifying genome reshuffling between species (Zdobnov and Bork 2007). In a similar manner to the male-female comparisons, orthology between both MPB linkage maps and RFB was assessed using BLASTn with 200 bp fragments of flanking sequence from the male and female MPB reference genomes. RFB was chosen because RFB remains the most closely-related species to MPB with

both a well-annotated genome and linkage map (Hunt *et al.* 2007; Richards *et al.* 2008). Due to the evolutionary distance between the two species, the minimum alignment length was increased to 60 bp while minimum e-value was kept at $1x10^{-10}$. Chord diagrams for both linkage maps were generated using the same method described for the male-female comparison.

4.4 | Results

4.4.1 | F1 and F2 Emergence

Wild parental families (F0) had an average of 115 larval feeding tunnels per family and produced an average of 27.3 F1 adults during the 15 days of emergence before the bolts were retired (S.D. = 21.7; Table A.8). Numerous teneral F1 adults, pupae, and late-instar larvae were found after the bark was stripped from the bolts. In contrast, the F1 sibling crosses were allowed to proceed to completion and yielded an average of 9.0 F2 beetles per bolt (S.D. = 6.6; Table A.9). Of the 66 attempted F1 crosses, 10 produced three or fewer offspring; another 24 F1 crosses failed to produce any offspring. We recovered at least one F1 parent from 34 of the 66 crosses, but only recovered both F1 parents from three crosses. After rejecting another 20 F1 families, due either to evidence of secondary infestation or insufficient family size (<10 individuals), 14 families containing 229 F1 and F2 individuals were selected for DNA extraction and linkage map construction (Figure 4.2).

4.4.2 | Genotyping and linkage mapping

Genotyping of 229 MPB on the Illumina NextSeq500 produced 414 million reads. Alignment and SNP marker assembly in STACKS yielded 21,521 and 25,563 SNP markers in the male and female datasets, respectively. Filtering for 5% MAF, 20% MM, and 20 ARD left

4,990 and 51,76 SNPs in the male and female datasets, respectively. IBD was used to reject ten individuals, including seven from one family (AK5). All ten samples from AK5 and three singletons from other families were dropped from further analysis, leaving 216 individuals from thirteen families (Table A.10). These filtered datasets were used in all subsequent analysis and linkage map construction.

Lep-MAP3 incorporated 1,645 SNPs from the male reference genome to generate 11 LGs at a LOD score of 9.1 for the male linkage map and 1,740 SNPs to generate 12 LGs at a LOD score of 8.5 in the female map (Figure 4.3; Figure 4.4). Seven and eleven SNPs were trimmed from the ends of the male and female linkage groups, respectively, leaving 1,638 SNPs in the male linkage map, and 1,729 SNPs in the female. The length of LGs in the female linkage map range from 88.8 to 43.1 cM, with an average interlocus length of 0.025 cM; the number of SNP markers per LG ranged from 42 to 365. The male LGs were more variable in size, with LGs ranging from 160.9 to 23.7 cM, and had an average interlocus length of 0.025 cM. The number of SNP markers per LG ranged from 37 to 420 in the male linkage map. Exact SNP positions are in Table A.25. Markers from one LG reliably separated individuals by sex in PCAs of both datasets, providing a means to impute the sex chromosome (Figure A.4).

The expected number of LGs in both linkage maps was informed by prior work on the karyology of MPB (Lanier & Wood 1968). The male linkage map contained one fewer LG than the female linkage map, but comparison between the two indicates that the largest LG in the male linkage map contains LGs 1 and 10 of the female linkage map (Figure 4.5).

4.4.3 | Linkage Map Comparisons

SNPs that overlapped between our linkage map and cohorts found in prior population genomics work with MPB (**Chapter 3**) are highlighted on our linkage maps (Figure 4.3 and 4.4; Table A.26). When comparing 4,781 SNPs assigned to LGs by Lep-MAP3's JoinSingles2All to 445 highly weighted SNPs from the first four PCs of a PCA of wild MPB samples (**Chapter 3**), a total of 402 SNP markers were found that shared exact genomic position on the female reference genome. The highly-weighted population genomics SNPs, defined by their principal component loadings on the first four principal components of a PCA, are referred to as PCs 1-4 (Table A.26). PC2, a suspected sex-linked cohort, was found entirely on LG X of the female linkage map. PC3, a possible genomic region showing geographically divergent frequencies of SNP cohorts, had 94% of its 81 SNP matches located on LG 10. PC4 had 87% of its 30 SNP matches on LG 1. PC1, which carried the strongest north-south signal and had considerable overlap with PC3, had at least one overlapping SNP on each LG, but, like PC3, had the most overlap with LG10.

Of the 1,638 SNPs used to construct the male linkage map, 1,408 (86%) had an equivalent SNP in the female linkage map (Figure 4.5). The longest LG in the male linkage map contained 200 matches with SNPs from the female LG1, 142 from female LG10, and 15 from female LG7. With the exception of male combined LG1&10, LGs from the male linkage map consistently matched with a single LG from the female, with only a few mismatches on the ends of the LGs.

Another beetle species with a well-annotated genome, RFB*,* has an XY sex-determination system and ten autosomal pairs (Lorenzen *et al.* 2005). A BLASTn search of the RFB genome with the 1,638 SNPs from the male MPB linkage map, and 1,729 SNPs from the female linkage map produced 116 and 146 matches, respectively (Figure 4.6). Results from both the male and

female MPB linkage maps were largely consistent with each other, with the reversed order of markers in LGs 9, 7 and 6 reflecting arbitrary computational resolution of the two linkage maps that is not biologically significant. In the female linkage map, all hits on LG 6 and 11 on MPB correspond to LGs 5 and 8 of RFB, respectively. With the exception of three or fewer individual hits, LGs 1, 2, 3, 4, and 8 of MPB correspond to LGs 3, 5, 7, 7, and 3 of RFB, respectively. All matching hits for the X chromosome of RFB came from the X chromosome of MPB, but MPB's X chromosome had additional matches with autosomes 2 and 4 of RFB. There were no matches to LG1 of RFB in either MPB linkage map.

4.5 | Discussion

4.5.1 | Overview

Our study used high throughput sequencing technology to generate SNP markers and build linkage maps for the mountain pine beetle. The resulting linkage maps provide insight into the genomic architecture of MPB, and will be a useful resource for future genetic research on MPB and related beetle species. This linkage map is the third map for a cucujiform beetle species, alongside the red flour beetle (*Tribolium castaneum*; Tenebrionidae; Richards *et al*. 2008) and the potato beetle (*Leptinotarsa decemlineata*; Chrysomelidae; Hawthorne 2001), and the first within Curculionidae.

4.5.2 | Viability of crosses

The F1 sibling crosses used in the construction of the linkage map had unexpectedly low fecundity. The number of larval galleries found in the wild parental crosses was consistent with Reid (1962), who demonstrated that MPB could lay more than 100 eggs under controlled

moisture and temperature conditions. Within two weeks, the parental crosses produced an average of 27.3 offspring, and stripping the bark from the bolts revealed hundreds of larval galleries still developing (Table A.9). The fecundity of the F2 generation, however, was depressed, with an average of nine adult emergences per bolt, excluding crosses that produced no progeny.

The low success of our F1 sibling crosses was dramatic, with 33% of crosses failing to produce more than three F2 offspring, and another 18% of crosses failing to produce any offspring (Table A.9). Several factors may account for the lack fecundity. First, the simplest hypothesis is that the second generation had suboptimal conditions for growth. While the F0 parental crosses were established immediately after collecting the experimental bolts, the F1 sibling crosses were established eight weeks after the bolts were cut. The bolts were sealed with wax and refrigerated, but time spent in cold storage could have negatively impacted the nutrients and suitability of the bolts. Recent studies comparing cut jack pine bolts have shown an increase in monoterpenes and nutrients over time, each of which can negatively impact establishment of adult beetles or development of larvae (Guevara-Rozo *et al*. 2018). Second, recovering the male and female F1 beetles from the bolts could have disrupted the developing F2 larvae; damage to the bolts could have exposed larvae to pathogens or desiccation, drying out the phloem that the beetles fed on despite efforts to re-seal the bolts (Safranyik & Whitney, 1985). A third possibility is inbreeding depression – the increased homozygosity of F2 individuals because their F1 parents were full siblings (Keller and Waller 2002). However, instances of pre-emergence mating occur frequently in wild MPB, which suggests that such inbreeding may not be important to rearing success (Bleiker *et al*. 2013). Finally, the relative inviability of the F2 generation may have been the result of incipient reproductive isolation between the northern and southern Canadian MPB

populations. Recent work by Bracewell *et al.* (2011) has revealed a postzygotic reproductive barrier between some USA populations, with sterile males in crosses between MPB populations in Oregon and Idaho. Thus, partial postzygotic gene flow barriers within the Canadian range of MPB are a possible explanation for their low fecundity.

Controlled crosses of MPB in aged Lodgepole pine bolts would provide an assessment of the likelihood that bolt age negatively impacted the F2 generation. Likewise, crosses without intentional sibling inbreeding of offspring from geographically separate source populations, as well as non-sibling crosses where both parents were taken from the same wild source population, are necessary to assess the effects of inbreeding depression and outbreeding on experimental MPB crosses. If there is reproductive isolation between the two invasive Alberta MPB populations then this could affect ongoing control and modeling efforts. If confirmed using appropriate controlled comparisons, these results would suggest that MPB could be treated as two cryptic subspecies within its Canadian range. Furthermore, concern about northern and southern individuals interbreeding to create a vigorous admixed population in Alberta may be unfounded if this vigor is counteracted by hybrid sterility (see **Chapter 2:** Trevoy *et al.* 2018).

4.5.3 | MPB Linkage map structure

Previous work on sex determination (Lyon 1958) and karyology in MPB (Lanier and Wood 1968) was essential for defining linkage group numbers and sex ratios, respectively. Markers within both male and female datasets were comparable to each other and the linkage groups found were largely consistent, regardless of the reference genome used (Figure 4.5). Despite challenges with establishing adequate pedigrees, the SNP loci used to produce the two linkage maps are high in density and genotyping quality. Although the total number of SNP

markers used in our linkage maps was lower than some contemporary SNP-based linkage maps, the relatively small size of the MPB genome means that the number of SNPs per cM is consistent with these other recent genetic linkage studies (Kumar *et al.* 2017; Picq *et al*. 2018).

The male and female linkage maps were consistent with each other, except that the male linkage map contained one fewer LG, and instead had a single, exceptionally large LG (Figure 4.4). This large chromosome, labeled 'LG1&10', was 160.9 cM long, 2.4 times the size of the next largest chromosome, and was homologous to LGs 1 and 10 of the female linkage map. The karyology of MPB by Lanier & Wood (1968) indicated that there are eleven autosomal chromosomes and that the neo-XY chromosomes should be the largest of the chromosomes. We interpret this chromosome as a combination of LGs 1 and 10, as depicted in the female linkage map (Figure 4.3), which Lep-MAP3 analysis joined erroneously in the male dataset (Figure 4.4).

In the draft genome for MPB, Keeling *et al.* (2013) suggested that six scaffolds within the male genome could be linked to the ancestral autosomal portion of the neo-X chromosome based on their depressed SNP densities. These scaffolds were not recovered in the linkage cohorts of subsequent population genetics work (**Chapter 3**), but all six scaffolds are present within LGX of the male linkage map, thus supporting the methodology of Keeling *et al.* (2013).

The female linkage map provides further insight into SNP cohorts that were described in **Chapter 3**, due to overlap in markers recovered in both SNP libraries. The prior work highlighted several putative SNP cohorts, including a group of possible sex-linked paralogues (PC2; blue on Figure 4.3) and a cohort of markers that were associated with geographic sampling location (PC3; red on Figure 4.3). A third SNP cohort, PC4 (green on Figure 4.3), was not associated with geographic sampling location, but was tightly clustered on few scaffolds and explained 1.8% of variance within the population genomics dataset. These three SNP cohorts had

at least 81% of their SNPs in the female linkage map dataset and provide further evidence that these SNP cohorts are localized on a single chromosome, specifically LGs X, 10, and 1 for PCs 2, 3, and 4, respectively. These results further support the biological nature of the linkage cohorts found in Chapter 3. A confirmed island of genomic divergence would be consistent with early stages of speciation within MPB, as suggested by Bracewell *et al.* (2011).

4.5.4 | *Orthology with* Tribolium castaneum

Diverging an estimated 236 Mya (Hunt *et al.* 2007), RFB is nonetheless the most closely related species to MPB with a well-annotated linkage map (Lorenzen *et al*. 2005). For brevity, our discussion focuses on female MPB linkage map orthology with RFB, because our results differ little among male and female linkage maps.

Analysis of orthology between MPB and RFB provided hits on all LGs in the MPB genome, but not all LGs of RFB were represented (Figure 4.6). Except for one or two hits, MPB LGs 1, 2, 3, 4, 6, 8, and 9 correspond to a single LG of RFB. In contrast, MPB LGs 5, 7, and 10 do not match any single RFB LGs, and are distributed onto two or three LGs within RFB. Hits on these three LGs are interleaved between homologous RFB sequences, suggesting substantial chromosomal rearrangement, inversion or transposition of these chromosomes. LGs within RFB were often split into two separate LGs in MPB, most clearly demonstrated by RFB LGs 5 and 6. The first LG of RFB had no hits on the MPB genome, suggesting either that no identical markers could be found, that RFB LG1 was acquired some time after the RFB's split from MPB, or that the chromosome was lost on the evolutionary branch leading to *D. ponderosae*. Comparisons of

genomic architecture between RFB and representative species from both tenebrionid and scolytid beetles will be necessary to determine which scenario is more likely.

For the sex chromosomes, all hits from the X chromosome of RFB matched the X chromosome of MPB, along with additional hits on autosomal LGs 2 and 4 of RFB (Figure 4.6). Autosomal hits from RFB are expected for the MPB X chromosome because the sex chromosomes in MPB are considered to have undergone a recent fusion with ancestral autosome 1 (Lanier and Wood, 1968; Keeling *et al*. 2013).

4.6 | Conclusion

In this study, SNP markers obtained using NGS methods were employed to generate linkage maps for a destructive forest pest: MPB. Reared MPB lines had declining family sizes in the second generation but further research is needed assign any one of several explanations. Three of the linkage groups found here by classic linkage mapping each contained most of the SNPs in the three linkage cohorts highlighted in Chapter 3, supporting the detection of such cohorts using a combination of PCA and linkage network analysis of data from a basic population genetic survey. Finally, comparisons to the distantly related red flour beetle allow us to infer which chromosomes may be highly conserved, and which have undergone large changes since the two species diverged. The resources generated here provide new insight into the genomic architecture of MPB and related beetle species.

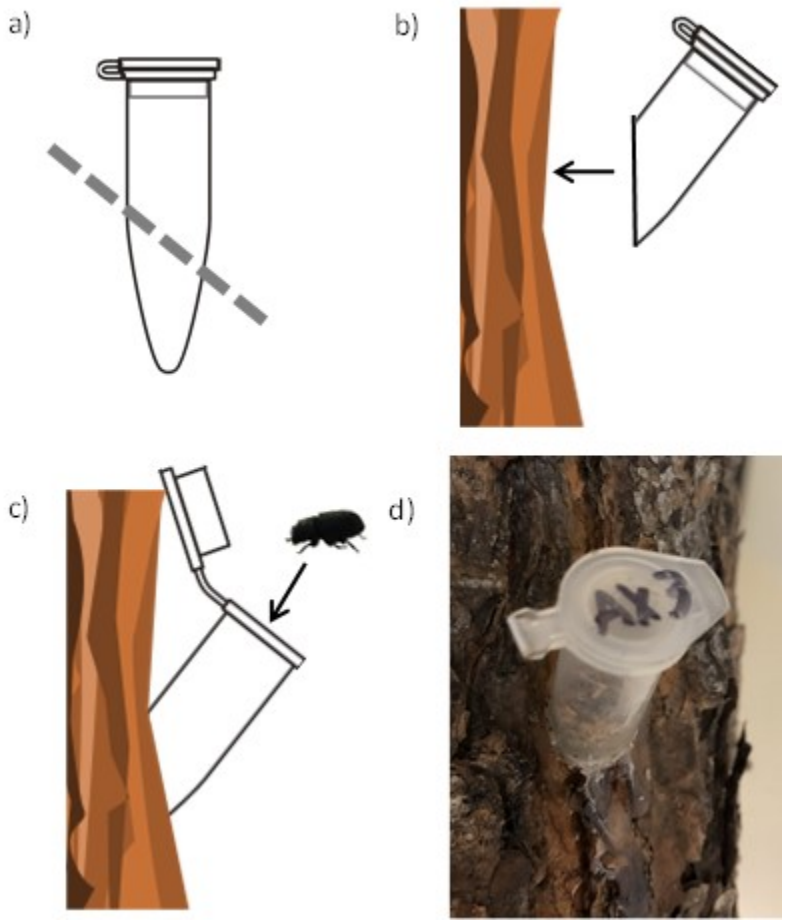


Figure 4.1. Beetle container used to initiate colonization of bolts, made from 1.5mL microcentrifuge tubes.

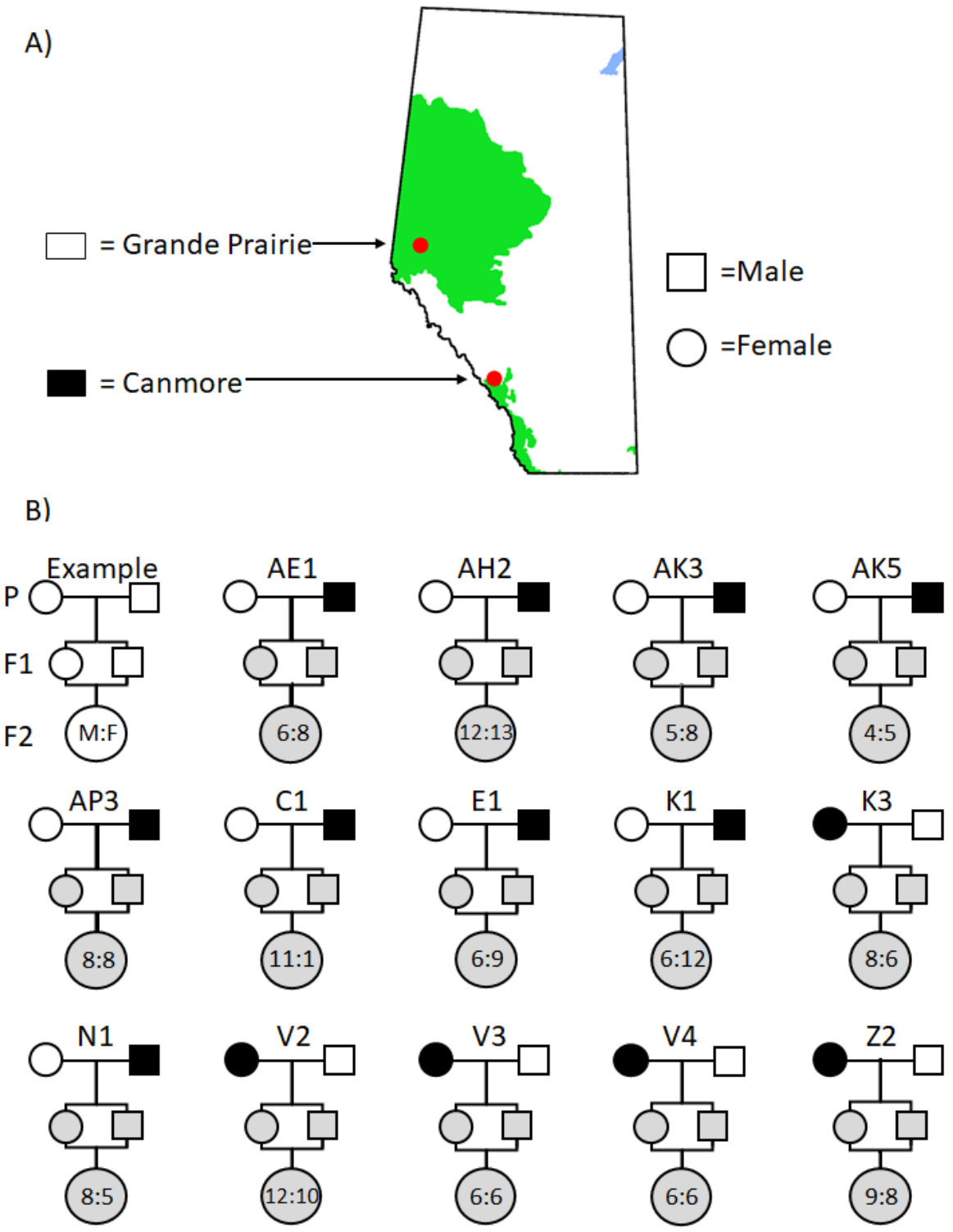


Figure 4.2. Sampling and family pedigrees used in linkage maps for *Dendroctonus ponderosae*. a) *D. ponderosae* in Alberta, showing range and sampling locations, adapted from Bleiker & Hezewjk (2014). b) 14 F2 pedigrees used for linkage mapping, with family sizes and sex ratio (see Table A.9).

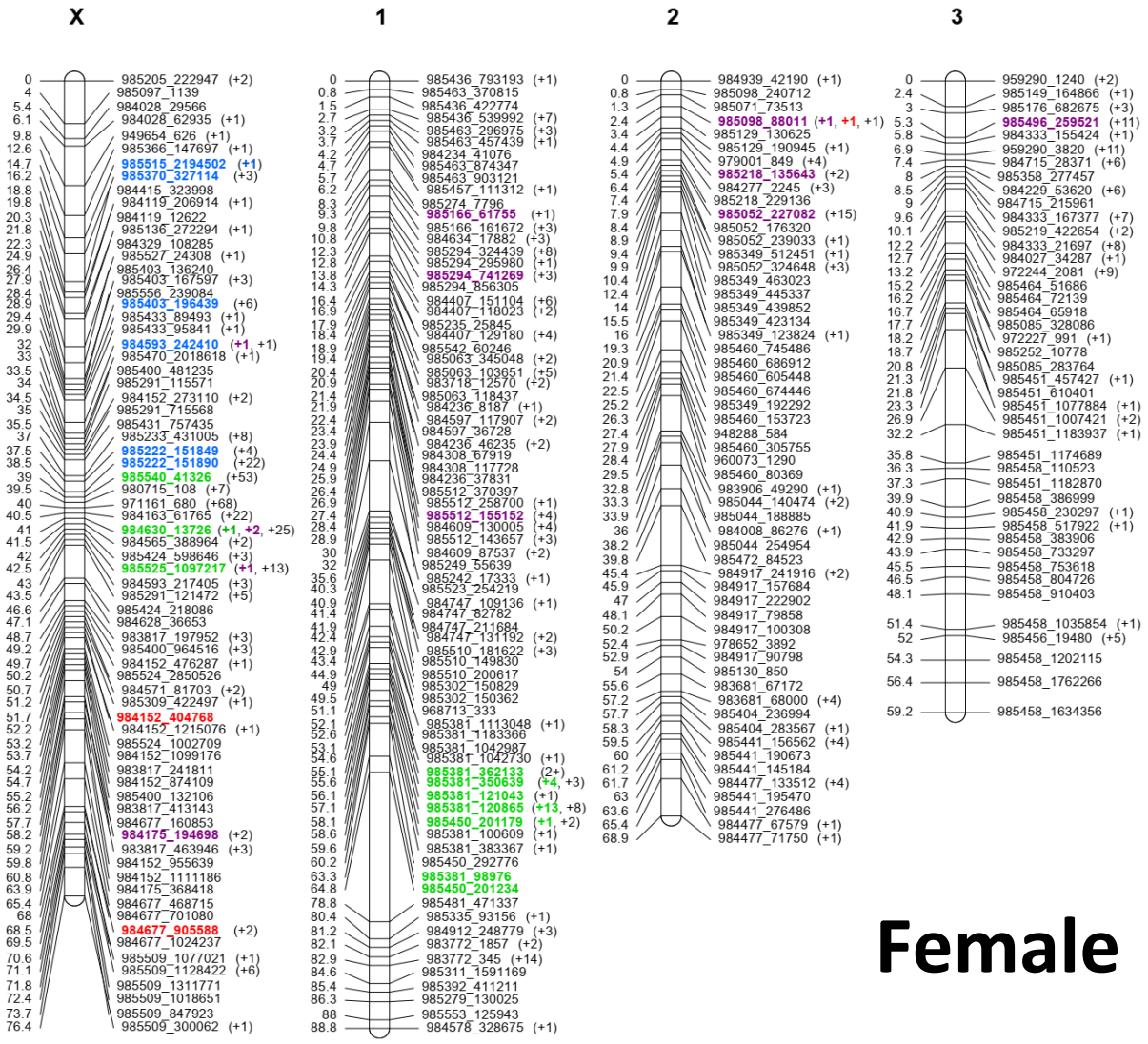


Figure 4.3.a. Linkage map of *Dendroctonus ponderosae* using 1729 SNP markers aligned to the female draft genome. Markers are labelled by reference genome scaffold number and position on the reference scaffold (see Keeling *et al*. 2013). Numbers in parentheses, to the right of the marker label, represent additional markers at the same genomic position. SNP markers sharing identity with markers found in **Chapter 3** are highlighted: PC1 - purple, PC2 - blue, PC3 - red, PC4 - green.

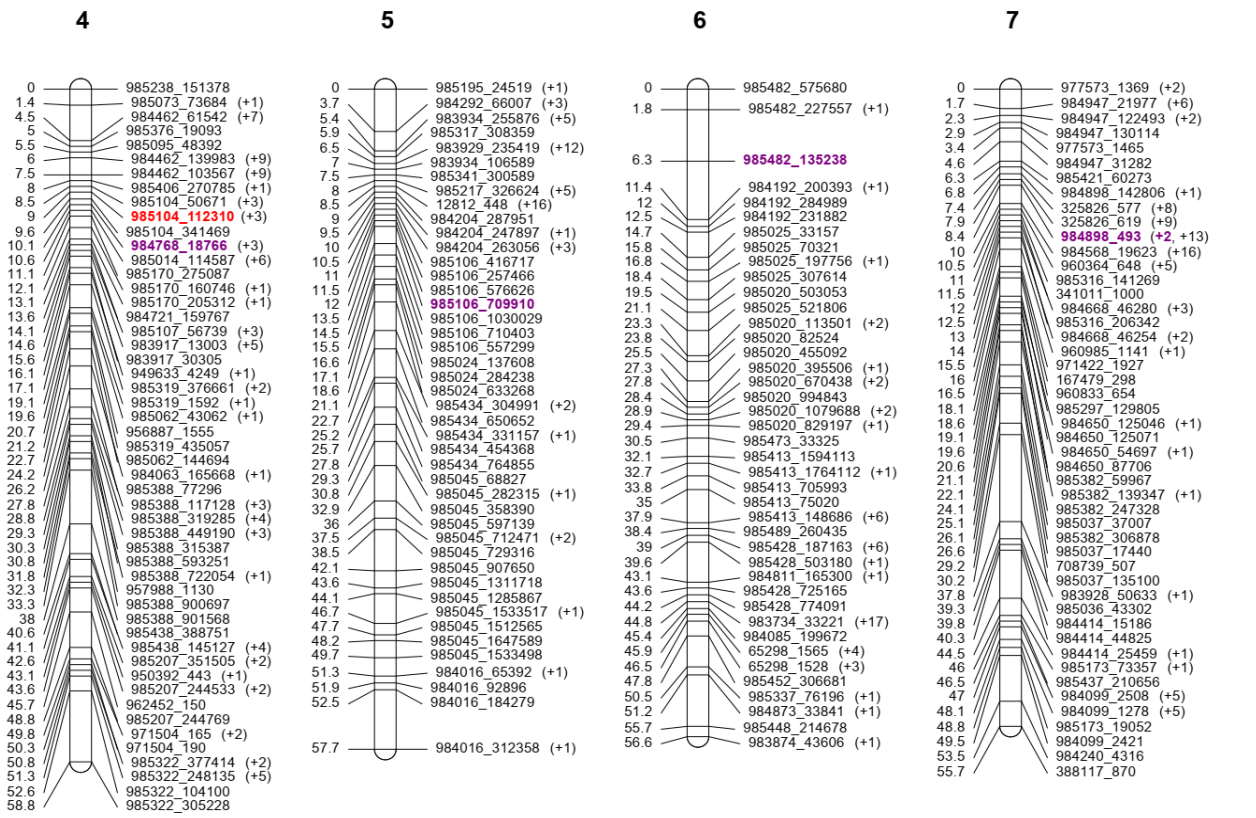
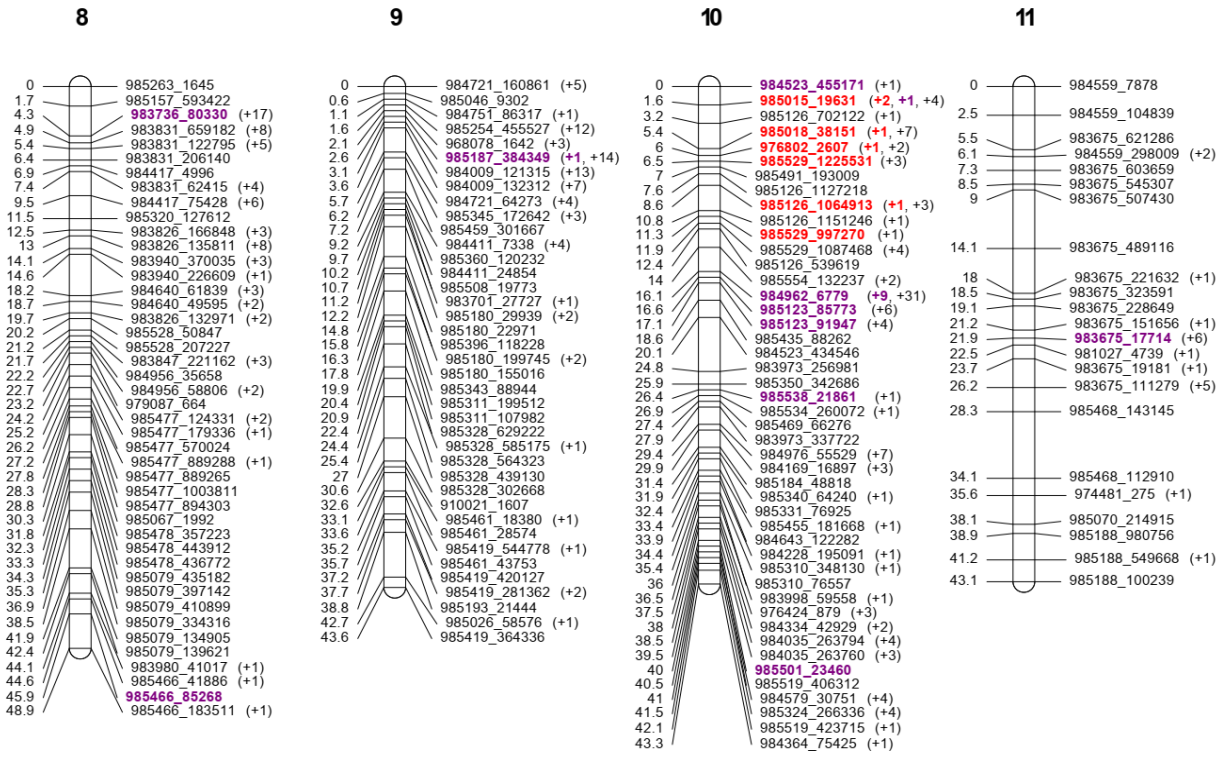


Figure 4.3.b. Linkage map of *Dendroctonus ponderosae* using 1729 SNP markers aligned to the female draft genome. Markers are labelled by reference genome scaffold number and position on the reference scaffold (see Keeling *et al*. 2013). Numbers in parentheses, to the right of the marker label, represent additional markers at the same genomic position. SNP markers sharing identity with markers found in **Chapter 3** are highlighted: PC1 - purple, PC2 - blue, PC3 - red, PC4 - green.



Female

Figure 4.3.c. Linkage map of *Dendroctonus ponderosae* using 1729 SNP markers aligned to the female draft genome. Markers are labelled by reference genome scaffold number and position on the reference scaffold (see Keeling *et al*. 2013). Numbers in parentheses, to the right of the marker label, represent additional markers at the same genomic position. SNP markers sharing identity with markers found in **Chapter 3** are highlighted: PC1 - purple, PC2 - blue, PC3 - red, PC4 - green.

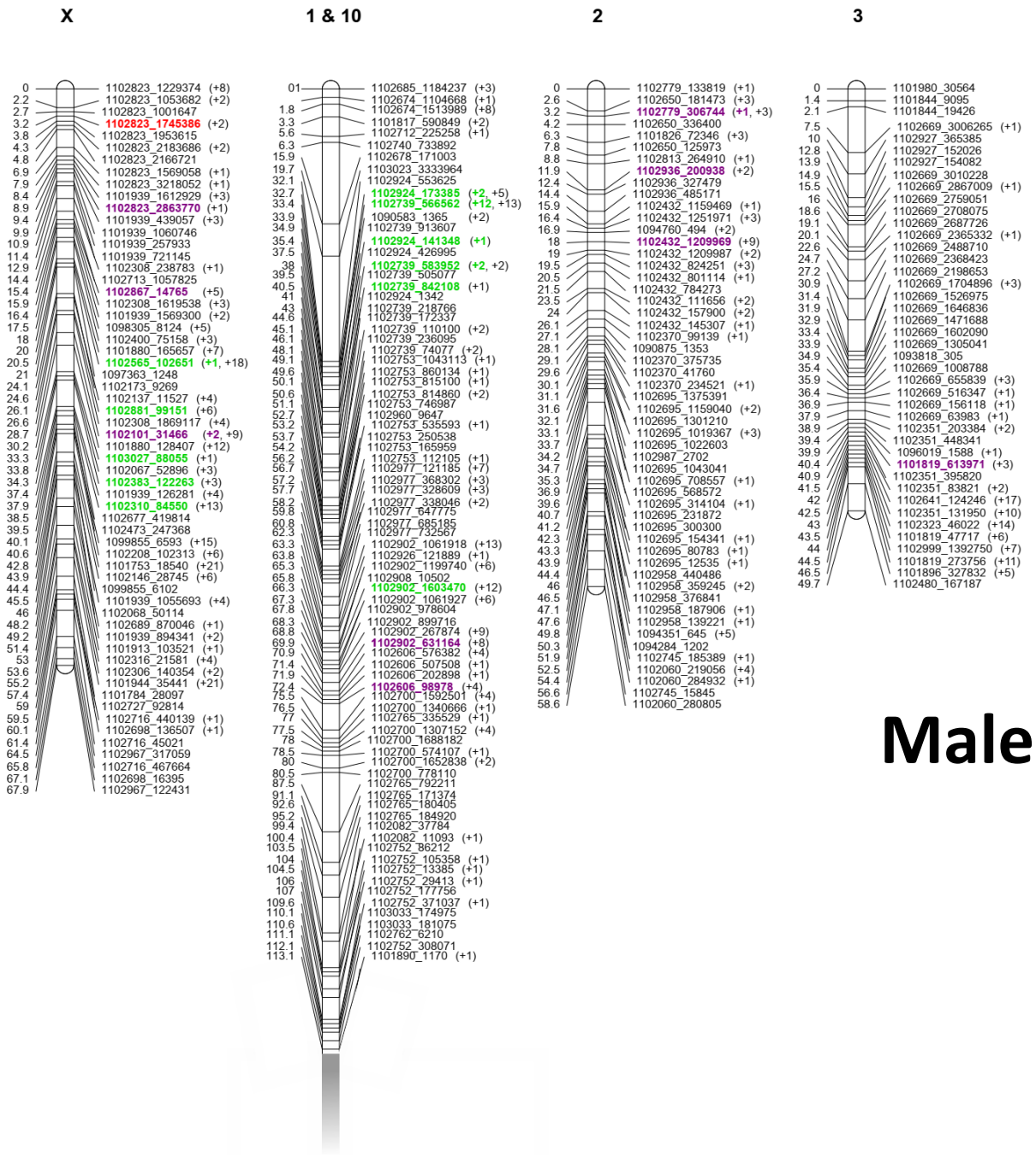


Figure 4.4.a. Linkage map of *Dendroctonus ponderosae* using 1638 SNP markers aligned to the male draft genome. Markers are labelled by reference genome scaffold number and position on the reference scaffold (see Keeling *et al*. 2013). Numbers in parentheses, to the right of the marker label, represent additional markers at the same genomic position. Linkage groups are numbered according to the corresponding female linkage group (see Figure 4.3). LG1 & 10 has been split into sections corresponding to LGs 1 and 10 of the female linkage map. SNP markers sharing exact identity with markers found in **Chapter 3** are highlighted: PC1 - purple, PC2 - blue, PC3 - red, PC4 - green.

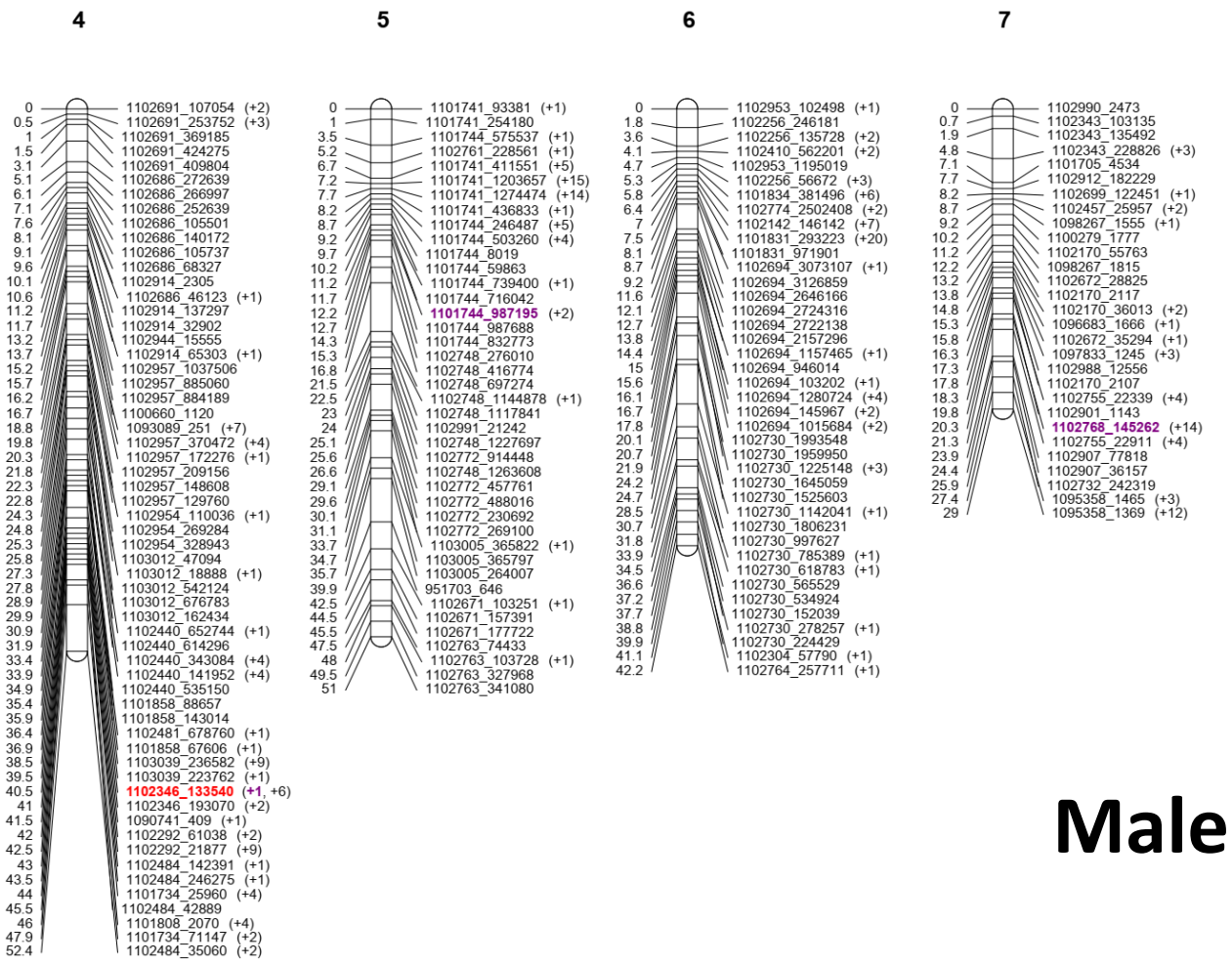


Figure 4.4.b. Linkage map of *Dendroctonus ponderosae* using 1638 SNP markers aligned to the male draft genome. Markers are labelled by reference genome scaffold number and position on the reference scaffold (see Keeling *et al*. 2013). Numbers in parentheses, to the right of the marker label, represent additional markers at the same genomic position. Linkage groups are numbered according to the corresponding female linkage group (see Figure 4.3). LG1 & 10 has been split into sections corresponding to LGs 1 and 10 of the female linkage map. SNP markers sharing exact identity with markers found in **Chapter 3** are highlighted: PC1 - purple, PC2 - blue, PC3 - red, PC4 - green.

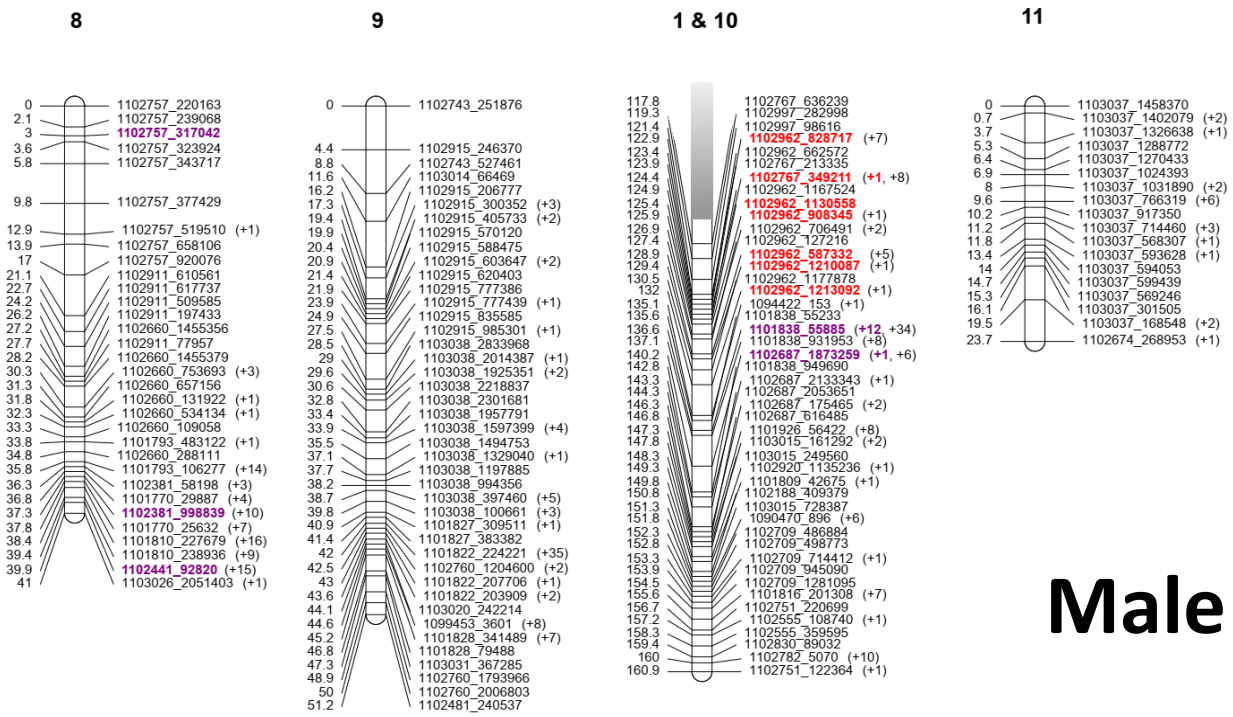


Figure 4.4.c. Linkage map of *Dendroctonus ponderosae* using 1638 SNP markers aligned to the male draft genome. Markers are labelled by reference genome scaffold number and position on the reference scaffold (see Keeling *et al*. 2013). Numbers in parentheses, to the right of the marker label, represent additional markers at the same genomic position. Linkage groups are numbered according to the corresponding female linkage group (see Figure 4.3). LG1 & 10 has been split into sections corresponding to LGs 1 and 10 of the female linkage map. SNP markers sharing exact identity with markers found in **Chapter 3** are highlighted: PC1 - purple, PC2 - blue, PC3 - red, PC4 - green.

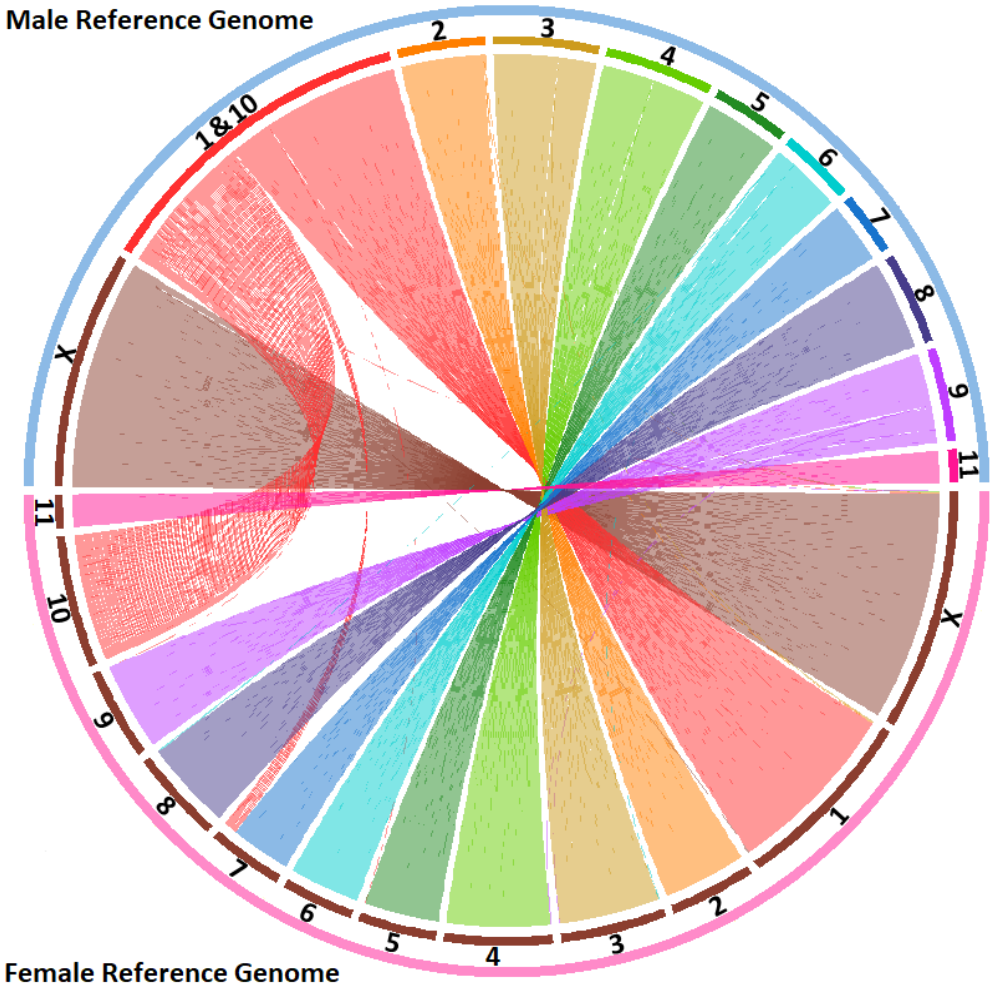


Figure 4.5. Chord diagram of shared identity between 1408 SNPs in the male (blue) and female (pink) aligned genomes of *D. ponderosae*. Each section represents a separate linkage group (see Figure. 4.3 and 4.4). (BLASTn analysis, expect value cut-off: 1.0e-10).

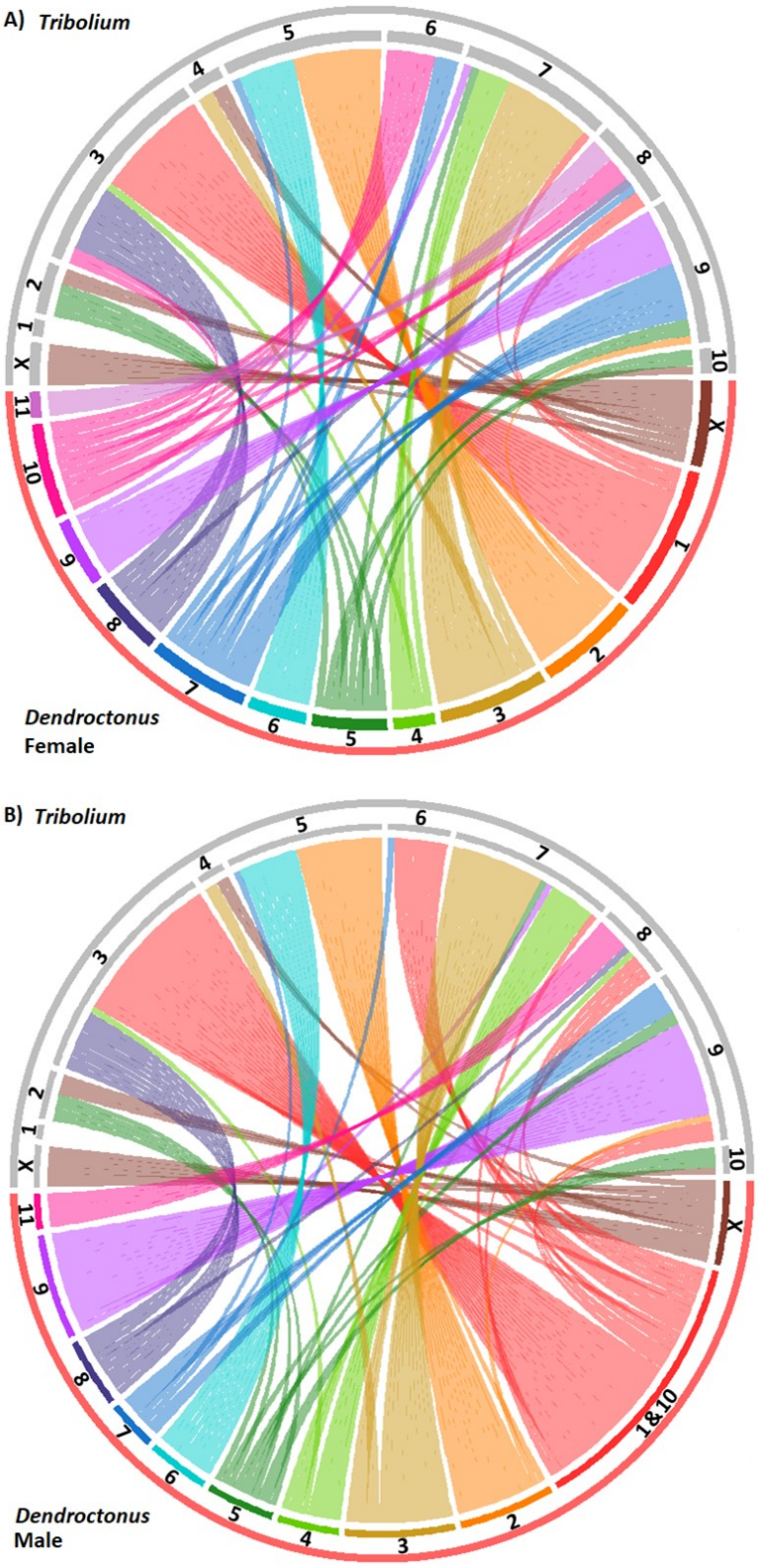


Figure 4.6. Orthology between *Dendroctonus ponderosae* (red outer arc) and *Tribolium castaneum* (grey outer arc) for 116 orthologues in the female reference genome (a) and 146 in the male reference genome. (BLASTn analysis, expect value cut-off: 1.0e-10).

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Chapter 5

General Conclusions

5.1 | Thesis Overview

5.1.1 | Introduction

The mountain pine beetle (MPB, *Dendroctonus ponderosae* Hopkins: Curculionidae, Scolytinae) is a species of particular economic interest to both Canadian and American foresters. The species is spreading east and north to infest novel habitats and has been the subject of intense ecological and genetic inquiry (Fauria & Johnson 2009; Safranyik *et al.* 2010; Janes *et al*. 2016; Cullingham *et al.* 2018). The ongoing expansion of MPB has seen three distinct populations enter the boreal forests of Alberta through separate mountain passes (Janes *et al*. 2014; Trevoy *et al.* 2018). This thesis expands on previous population genomics work on MPB with next-generation sequencing (NGS) techniques, exploring population differences in relation to genomic architecture and genetic linkage.

5.1.2 | Population genomics in mountain pine beetle

Population genomics is valuable for distinguishing the traits and genetic composition of species as they exist on the landscape (Black *et al.* 2001). Biological phenomena such as migration, introgression, inbreeding, and natural selection can be detected using genomic methods, enhancing conservation and monitoring efforts (Luikart *et al.* 2003).

Previous genomic research on MPB has produced many different marker libraries, including 16 microsatellite loci (Davis *et al*. 2009), 1440 unique SNPs from GoldenGate genotyping (Janes *et al*. 2014), and 96 SNPs with Sequenom genotyping (Batista *et al*. 2016). After minimal quality filtering, the NGS method that I employed has yielded 18,503 unique

SNPs for wild MPB. The location of the division between northern and southern populations found within this study is in agreement with prior research (Samarasekera *et al.* 2012; Janes *et al.* 2014), but this newest SNP library also includes the first genetic characterization of a new invasive front entering Alberta from the Yellowhead Pass. Principal coordinate analysis revealed that this population was distinct, but displays signs of north-south admixture, suggesting a central B.C. source population near Valemount, B.C. (see Janes *et al*. 2014). This intermediate population genetic signature could indicate enhanced adaptive potential for these beetles as a result of increased genetic diversity, but also presents a unique admixed signal that could be used to track the population's progress (Mallet 2007; Janes & Hamilton 2017).

5.1.3 | Genomic architecture and population divergence

NGS technologies capture large numbers of both non-neutral and linked markers that allow analysis of genetic linkage, but prior genetics work has stressed the importance of neutrality and independence when selecting markers for genomic research (e.g. Stinchcombe & Hoekstra 2008; Baird 2015). Despite this, both, non-neutral (Batista *et al.* 2016) and genetically linked loci can provide valuable information on the biology of an organism (Barton 2011). Prior research capitalized on the genotyping of covarying SNP markers by using principal component analysis as a complexity reduction step for genome-wide association studies (Li *et al*. 2018). In this thesis, I apply a similar method to identify cohorts of linked markers that vary either by sex or sampling location (**Chapter 3**).

The linkage cohorts detected with this novel approach are supported by a more traditional application of linkage mapping that involves using controlled crosses to arrange variable markers into linkage groups corresponding to chromosomal locations (e.g. Picq *et al.* 2018). MPB

samples were collected from their northern and southern invasive ranges and crossbred in an F2 cross experiment to produce the inbred specimens necessary for linkage map construction (**Chapter 4**). SNP cohorts found in the genomic survey of wild MPB (**Chapter 3**) were recovered within the linkage map dataset aligned to the same reference genome, providing further evidence of the genomic contiguity of these linkage cohorts. MPB linkage maps for both the male and female-derived sets of SNPs were also compared to prior work on *Tribolium castaneum*, a distantly related beetle species with a well-annotated genome (Lorenzen *et al*. 2005; Richards *et al*. 2008). Orthology analysis with *T. castaneum* supported previous work by Keeling *et al.* (2013), showing a high degree of conserved orthology between the two species.

5.2 | Future directions

5.2.1 | Population genomics

The advent of NGS technologies has drastically reduced the cost and effort of genotyping many individuals for population genomics research, including quantification of genome-wide population effects like migration and introgression (Luikart *et al.* 2003). Conservation biology has employed genomics methodology to guide the preservation of diversity in both wild and captive populations (Coates *et al*. 2018), and genomics applications have spread to the study of invasive species as well (Garnas *et al*. 2016; Colautti & Lau 2016). The latest MPB outbreak began at the same time as population genomics methods became tractable for monitoring invasive species (Janes *et a*l. 2014; Batista *et al*. 2016). Consequently, MPB researchers will have a unique opportunity to monitor changes in the biogeography, ecology, and phenotype of MPB as it spreads into novel latitudes and hosts.

The MPB population entering Alberta from the Yellowhead Pass is distinguished from previous invasive populations by its intermediate nature, providing both challenges and opportunities (**Chapter 2:** Trevoy *et al*. 2018). The mixed population displays higher genetic diversity; this poses a risk if the beetles' diversity translates to greater adaptive potential (Mallet 2007; Janes & Hamilton 2017). Although the importance of genetic diversity to the success of a newly invasive species may have been historically overstated (e.g. Rius & Darling 2014; Arca *et al.* 2015), future forest management could target populations with higher genetic diversity in an inverse of established conservation management practices. More concretely, this new population's intermediate nature makes tracking its progress through the landscape practical and could complement existing monitoring and control efforts.

5.2.2 | Linkage analysis

This thesis proposes a new method using the dimensionality reduction of principal component analysis combined with linkage disequilibrium network analysis to confirm genetic linkage in covarying SNP cohorts that clustered individuals by sex and geographic sampling location (**Chapter 3;** Abdi & Williams 2010; Kemppainen *et al.* 2015). The covarying SNP cohorts corresponding to sampling location can be interpreted as possible islands of genomic differentiation between populations (Wolf & Ellegren 2017). This described method can therefore potentially locate genomic regions of interest without prior genomic information and, although a reference genome was used in my study, a de novo assembly would be equally amenable to this approach.

Regions of genomic divergence are of particular interest for evolutionary biology, highlighting genomic points of interest for future research. The number and extent of islands of

genomic differentiation can be indicative of speciation processes and may also be monitored for evidence of adaptive radiation in MPB as its range expands. In addition, the viability of crosses described in **Chapter 4 could** provide further evidence of incipient speciation within the Canadian range of MPB. The low fecundity of the F1 generation of north-south admixed crosses resembles the incipient postzygotic reproductive isolation found between MPB populations in the US (Bracewell *et al.* 2011). However, bolt degradation and the lack of control crosses from the same location preclude any conclusions concerning possible hybrid sterility.

The method demonstrated in **Chapter 3** was partially verified by reproducing the linked SNP cohorts from the population genomic survey by using independent samples from controlled crosses to produce a linkage map (**Chapter 4**). However, more work is needed to show that this method's use is not limited to MPB. Studies that employ the method described in **Chapter 3** will also need to be carried out with simulated data, as well as in studies using more individuals, traits, or taxa, in order to demonstrate wider applicability.

MBP is now the third beetle species with a linkage map, in addition to the red flour beetle (*Tribolium castaneum*; Tenebrionidae; Richards *et al*. 2008) and the potato beetle (*Leptinotarsa decemlineata*; Chrysomelidae; Hawthorne 2001). Linkage maps are useful for studies of genomic architecture and complex traits (Yeaman & Whitlock 2011; Lindtke *et al*. 2017) and are also essential for more stringent analysis of islands of genomic divergence using a genome scan (Turner *et al*. 2005). Genome scans use a sliding window of F_{ST} calculations along the length of a genome to detect localized divergence, and would offer further validation for the islands of genomic differentiation described in **Chapter 3**.

5.3 | Conclusion

In this thesis, I apply NGS methods to study the ongoing outbreak of MPB in western Canada. I used genome-wide SNPs to construct a library of thousands of variable markers and analysed population structure within and between populations of wild MPB. This same dataset was re-used to explore cohorts of linked SNPs using a novel method that combines the dimensionality and complexity-reduction of PCA with linkage disequilibrium network analysis. With this method, three cohorts of SNPs were characterized: a paralogous sex-linked cohort, useful as genetic sexing method, and two possible islands of genomic differentiation between populations of MPB. Finally, I constructed a genetic linkage map for both sexes of MPB using 229 individuals from 14 families generated with an F2 pedigree regime. These linkage maps were compared to prior MPB population and functional genetics work as well as an existing linkage map for *Tribolium castaneum*. The adaptive potential of MPB warrants further research as the pest continues to spread eastward; the methods, markers, and linkage map developed here may provide valuable resources and techniques for further study of a prolific invasive species in the new era of genomics.

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Supplementary Material

Table A.1. Sample information for 175 wild caught mountain pine beetle.

ID	Sex	Province	Location	Date	Collector/facilitator	Data Entry	GPS latitude	GPS longitude
BM1	Female	BC	Baldy Mountain Ski Resort	06/18/15	J. Burke	S. Trevoy	49.10.327	-119.15.119
BM10	Female	BC	Baldy Mountain Ski Resort	06/18/15	J. Burke	S. Trevoy	49.10.327	-119.15.119
BM11	Male	BC	Baldy Mountain Ski Resort	06/18/15	J. Burke	S. Trevoy	49.10.327	-119.15.119
BM12	Female	BC	Baldy Mountain Ski Resort	06/18/15	J. Burke	S. Trevoy	49.10.327	-119.15.119
BM13	Female	BC	Baldy Mountain Ski Resort	06/18/15	J. Burke	S. Trevoy	49.10.327	-119.15.119
BM14	Male	BC	Baldy Mountain Ski Resort	06/18/15	J. Burke	S. Trevoy	49.10.327	-119.15.119
BM15	Male	BC	Baldy Mountain Ski Resort	06/18/15	J. Burke	S. Trevoy	49.10.327	-119.15.119
BM16	Male	BC	Baldy Mountain Ski Resort	06/18/15	J. Burke	S. Trevoy	49.10.327	-119.15.119
BM2	Male	BC	Baldy Mountain Ski Resort	06/18/15	J. Burke	S. Trevoy	49.10.327	-119.15.119
BM3	Female	BC	Baldy Mountain Ski Resort	06/18/15	J. Burke	S. Trevoy	49.10.327	-119.15.119
BM4	Female	BC	Baldy Mountain Ski Resort	06/18/15	J. Burke	S. Trevoy	49.10.327	-119.15.119
BM5	Male	BC	Baldy Mountain Ski Resort	06/18/15	J. Burke	S. Trevoy	49.10.327	-119.15.119
BM6	Female	BC	Baldy Mountain Ski Resort	06/18/15	J. Burke	S. Trevoy	49.10.327	-119.15.119
BM7	Female	BC	Baldy Mountain Ski Resort	06/18/15	J. Burke	S. Trevoy	49.10.327	-119.15.119

BM8	Male	BC	Baldy Mountain Ski Resort	06/18/15	J. Burke	S. Trevoy	49.10.327	-119.15.119
BM9	Male	BC	Baldy Mountain Ski Resort	06/18/15	J. Burke	S. Trevoy	49.10.327	-119.15.119
C1.1	Female	AB	NW of Manning, Chinchaga Forestry Rd.	05/21/14	C. Whitehouse	S. Trevoy	57.23.499	-118.55.345
C1.2	Female	AB	NW of Manning, Chinchaga Forestry Rd.	05/21/14	C. Whitehouse	S. Trevoy	57.23.499	-118.55.345
C1.4	Male	AB	NW of Manning, Chinchaga Forestry Rd.	05/21/14	C. Whitehouse	S. Trevoy	57.23.499	-118.55.345
C1.5	Female	AB	NW of Manning, Chinchaga Forestry Rd.	05/21/14	C. Whitehouse	S. Trevoy	57.23.499	-118.55.345
C2.1	Female	AB	Hines Creek, E of Cleardale	05/23/14	C. Whitehouse	S. Trevoy	56.38.749	-119.02.117
C2.12	Female	AB	Hines Creek, E of Cleardale	05/23/14	C. Whitehouse	S. Trevoy	56.38.749	-119.02.117
C2.13	Male	AB	Hines Creek, E of Cleardale	05/23/14	C. Whitehouse	S. Trevoy	56.38.749	-119.02.117
C2.14	Female	AB	Hines Creek, E of Cleardale	05/23/14	C. Whitehouse	S. Trevoy	56.38.749	-119.02.117
C2.3	Female	AB	Hines Creek, E of Cleardale	05/23/14	C. Whitehouse	S. Trevoy	56.38.749	-119.02.117
C3.1	Female	AB	Hines Creek, Stoney Lake Prov. Park	05/28/14	C. Whitehouse	S. Trevoy	56.44.342	-118.49.903
C3.3	Female	AB	Hines Creek, Stoney Lake Prov. Park	05/28/14	C. Whitehouse	S. Trevoy	56.44.342	-118.49.903
C3.4	Female	AB	Hines Creek, Stoney Lake Prov. Park	05/28/14	C. Whitehouse	S. Trevoy	56.44.342	-118.49.903

C4.1	Female	AB	Hines Creek, NW of Gerry Lake	05/23/14	C. Whitehouse	S. Trevoy	56.35.240	-118.41.156
C4.11	Female	AB	Hines Creek, NW of Gerry Lake	05/23/14	C. Whitehouse	S. Trevoy	56.35.240	-118.41.156
C4.2	Male	AB	Hines Creek, NW of Gerry Lake	05/23/14	C. Whitehouse	S. Trevoy	56.35.240	-118.41.156
C4.3	Male	AB	Hines Creek, NW of Gerry Lake	05/23/14	C. Whitehouse	S. Trevoy	56.35.240	-118.41.156
C4.4	Female	AB	Hines Creek, NW of Gerry Lake	05/23/14	C. Whitehouse	S. Trevoy	56.35.240	-118.41.156
C4.5	Male	AB	Hines Creek, NW of Gerry Lake	05/23/14	C. Whitehouse	S. Trevoy	56.35.240	-118.41.156
CAN1	Female	AB	Canmore, Burnco Quarry	10/06/14	S. Trevoy	S. Trevoy	51.04.026	-115.17.237
CAN10	Female	AB	Canmore, Burnco Quarry	10/06/14	S. Trevoy	S. Trevoy	51.04.026	-115.17.237
CAN12	Female	AB	Canmore, Burnco Quarry	10/06/14	S. Trevoy	S. Trevoy	51.04.026	-115.17.237
CAN13	Male	AB	Canmore, Burnco Quarry	10/06/14	S. Trevoy	S. Trevoy	51.04.026	-115.17.237
CAN2	Female	AB	Canmore, Burnco Quarry	10/06/14	S. Trevoy	S. Trevoy	51.04.026	-115.17.237
CAN3	Female	AB	Canmore, Burnco Quarry	10/06/14	S. Trevoy	S. Trevoy	51.04.026	-115.17.237
CAN4	Female	AB	Canmore, Burnco Quarry	10/06/14	S. Trevoy	S. Trevoy	51.04.026	-115.17.237
CAN5	Female	AB	Canmore, Burnco Quarry	10/06/14	S. Trevoy	S. Trevoy	51.04.026	-115.17.237
CAN6	Female	AB	Canmore, Burnco Quarry	10/06/14	S. Trevoy	S. Trevoy	51.04.026	-115.17.237

CAN7	Male	AB	Canmore, Burnco Quarry	10/06/14	S. Trevoy	S. Trevoy	51.04.026	-115.17.237
CAN8	Female	AB	Canmore, Burnco Quarry	10/06/14	S. Trevoy	S. Trevoy	51.04.026	-115.17.237
CAN9	Female	AB	Canmore, Burnco Quarry	10/06/14	S. Trevoy	S. Trevoy	51.04.026	-115.17.237
CanH.11	Male	AB	Canmore, Harvey Heights	06/29/05	-	A. Roe	51.12.990	-115.37.950
CanH.12	Female	AB	Canmore, Harvey Heights	06/29/05	-	A. Roe	51.12.990	-115.37.950
CanH.13	Male	AB	Canmore, Harvey Heights	06/29/05	-	A. Roe	51.12.990	-115.37.950
CanH.14	Female	AB	Canmore, Harvey Heights	06/29/05	-	A. Roe	51.12.990	-115.37.950
CanH.15	Female	AB	Canmore, Harvey Heights	06/29/05	-	A. Roe	51.12.990	-115.37.950
CanH.16	Male	AB	Canmore, Harvey Heights	06/29/05	-	A. Roe	51.12.990	-115.37.950
CanH.17	Male	AB	Canmore, Harvey Heights	06/29/05	-	A. Roe	51.12.990	-115.37.950
CanH.18	Male	AB	Canmore, Harvey Heights	06/29/05	-	A. Roe	51.12.990	-115.37.950
CanH.19	Female	AB	Canmore, Harvey Heights	06/29/05	-	A. Roe	51.12.990	-115.37.950
CanH.20	Male	AB	Canmore, Harvey Heights	06/29/05	-	A. Roe	51.12.990	-115.37.950
CB1	Female	BC	Cranbrook, Gold Creek Rd.	06/27/05	-	A. Roe	49.40.860	-115.64.620
CB10	Male	BC	Cranbrook, Gold Creek Rd.	06/27/05	-	A. Roe	49.40.860	-115.64.620
CB11	Male	BC	Cranbrook, Gold Creek Rd.	06/27/05	-	A. Roe	49.40.860	-115.64.620
CB2	Male	BC	Cranbrook, Gold Creek Rd.	06/27/05	-	A. Roe	49.40.860	-115.64.620

CB4	Male	BC	Cranbrook, Gold Creek Rd.	06/27/05	-	A. Roe	49.40.860	-115.64.620
CB5	Female	BC	Cranbrook, Gold Creek Rd.	06/27/05	-	A. Roe	49.40.860	-115.64.620
CB6	Female	BC	Cranbrook, Gold Creek Rd.	06/27/05	-	A. Roe	49.40.860	-115.64.620
CB7	Male	BC	Cranbrook, Gold Creek Rd.	06/27/05	-	A. Roe	49.40.860	-115.64.620
CB8	Male	BC	Cranbrook, Gold Creek Rd.	06/27/05	-	A. Roe	49.40.860	-115.64.620
CB9	Female	BC	Cranbrook, Gold Creek Rd.	06/27/05	-	A. Roe	49.40.860	-115.64.620
CH17	Male	AB	Cypress Hills Prov. Park	06/29/05	-	A. Roe	49.61.000	-110.19.000
CH9	Female	AB	Cypress Hills Prov. Park	06/29/05	-	A. Roe	49.60.480	-110.29.980
CL1	Female	BC	Calling Lake, 40km N of town	10/21/15	T. Hutchison, B. Cooke, R. McIntosh, F. McKee	S. Trevoy	55.56.890	-113.45.910
CL10	Female	BC	Calling Lake, 40km N of town	10/21/15	T. Hutchison, B. Cooke, R. McIntosh, F. McKee	S. Trevoy	55.56.930	-113.45.880
CL11	Male	BC	Calling Lake, 40km N of town	10/21/15	T. Hutchison, B. Cooke, R. McIntosh, F. McKee	S. Trevoy	55.56.930	-113.45.880
CL12	Male	BC	Calling Lake, 40km N of town	10/21/15	T. Hutchison, B. Cooke, R. McIntosh, F. McKee	S. Trevoy	55.56.930	-113.45.880
CL13	Male	BC	Calling Lake, 40km N of town	10/21/15	T. Hutchison, B. Cooke, R. McIntosh, F. McKee	S. Trevoy	55.56.930	-113.45.880
CL15	Female	BC	Calling Lake, 40km N of town	10/21/15	T. Hutchison, B. Cooke, R. McIntosh, F. McKee	S. Trevoy	55.56.930	-113.45.880
CL16	Male	BC	Calling Lake, 40km N of town	10/21/15	T. Hutchison, B. Cooke, R. McIntosh, F. McKee	S. Trevoy	55.56.930	-113.45.880

CL2	Female	BC	Calling Lake, 40km N of town	10/21/15	T. Hutchison, B. Cooke, R. McIntosh, F. McKee	S. Trevoy	55.56.890	-113.45.910
CL3	Female	BC	Calling Lake, 40km N of town	10/21/15	T. Hutchison, B. Cooke, R. McIntosh, F. McKee	S. Trevoy	55.56.890	-113.45.910
CL4	Female	BC	Calling Lake, 40km N of town	10/21/15	T. Hutchison, B. Cooke, R. McIntosh, F. McKee	S. Trevoy	55.56.890	-113.45.910
CL5	Male	BC	Calling Lake, 40km N of town	10/21/15	T. Hutchison, B. Cooke, R. McIntosh, F. McKee	S. Trevoy	55.56.890	-113.45.910
CL6	Male	BC	Calling Lake, 40km N of town	10/21/15	T. Hutchison, B. Cooke, R. McIntosh, F. McKee	S. Trevoy	55.56.890	-113.45.910
CL7	Female	BC	Calling Lake, 40km N of town	10/21/15	T. Hutchison, B. Cooke, R. McIntosh, F. McKee	S. Trevoy	55.56.930	-113.45.880
CL8	Female	BC	Calling Lake, 40km N of town	10/21/15	T. Hutchison, B. Cooke, R. McIntosh, F. McKee	S. Trevoy	55.56.930	-113.45.880
CL9	Female	BC	Calling Lake, 40km N of town	10/21/15	T. Hutchison, B. Cooke, R. McIntosh, F. McKee	S. Trevoy	55.56.930	-113.45.880
CyHi1	Female	SK	Cypress Hills Prov. Park	05/20/15	Brogan Waldner /R. McIntosh	S. Trevoy	49.61.116	-109.86.372
CyHi6	Female	SK	Cypress Hills Prov. Park	05/20/15	Brogan Waldner /R. McIntosh	S. Trevoy	49.61.116	-109.86.372
F11	Female	AB	Fairview, SE of Sand Lake Nat. Area	06/29/05	-	A. Roe	56.12.840	-118.54.750
F12	Male	AB	Fairview, SE of Sand Lake Nat. Area	06/29/05	-	A. Roe	56.12.840	-118.54.750
F14	Male	AB	Fairview, SE of Sand Lake Nat. Area	06/29/05	-	A. Roe	56.12.840	-118.54.750
F15	Female	AB	Fairview, SE of Sand Lake Nat. Area	06/29/05	-	A. Roe	56.12.840	-118.54.750
F16	Female	AB	Fairview, SE of Sand Lake Nat. Area	06/29/05	-	A. Roe	56.12.840	-118.54.750

F17	Male	AB	Fairview, SE of Sand Lake Nat. Area	06/29/05	-	A. Roe	56.12.840	-118.54.750
F19	Male	AB	Fairview, SE of Sand Lake Nat. Area	06/29/05	-	A. Roe	56.12.840	-118.54.750
FC1	Female	AB	Fox Creek, Raspberry Lake	06/29/05	-	A. Roe	54.48.060	-116.63.480
FC3	Male	AB	Fox Creek, Raspberry Lake	06/29/05	-	A. Roe	54.48.060	-116.63.480
FC4	Female	AB	Fox Creek, Raspberry Lake	06/29/05	-	A. Roe	54.48.060	-116.63.480
FC6	Male	AB	Fox Creek, Raspberry Lake	06/29/05	-	A. Roe	54.48.060	-116.63.480
G2	Male	BC	Golden, Mkeeman Peak	06/29/05	-	A. Roe	51.07.000	-116.38.000
GP13	Male	AB	Grande Prairie, Lingrell Lake	06/29/05	-	A. Roe	54.80.000	-119.79.000
GP14	Female	AB	Grande Prairie, Lingrell Lake	06/29/05	-	A. Roe	54.80.000	-119.79.000
GP15	Male	AB	Grande Prairie, Lingrell Lake	06/29/05	-	A. Roe	54.80.000	-119.79.000
GP16	Male	AB	Grande Prairie, Lingrell Lake	06/29/05	-	A. Roe	54.80.000	-119.79.000
GP18	Female	AB	Grande Prairie, Lingrell Lake	06/29/05	-	A. Roe	54.80.000	-119.79.000
GP19	Female	AB	Grande Prairie, Lingrell Lake	06/29/05	-	A. Roe	54.80.000	-119.79.000
GP20	Female	AB	Grande Prairie, Lingrell Lake	06/29/05	-	A. Roe	54.80.000	-119.79.000
H1.1	Female	AB	Edson, 15km SW	07/17/14	/E. Samis	S. Trevoy	53.42.131	-116.50.803
H1.2	Female	AB	Edson, 15km SW	07/17/14	/E. Samis	S. Trevoy	53.42.131	-116.50.803
H1.3	Female	AB	Edson, 15km SW	07/17/14	/E. Samis	S. Trevoy	53.42.131	-116.50.803
H2.1	Female	AB	Edson, 10km SW	07/17/14	/E. Samis	S. Trevoy	53.49.970	-116.59.544
H2.3	Male	AB	Edson, 10km SW	07/17/14	/E. Samis	S. Trevoy	53.49.970	-116.59.544
H2.4	Female	AB	Edson, 10km SW	07/17/14	/E. Samis	S. Trevoy	53.49.970	-116.59.544

H3.1	Male	AB	Edson, 15km S	07/17/14	/E. Samis	S. Trevoy	53.46.608	-116.41.185
H3.2	Female	AB	Edson, 15km S	07/17/14	/E. Samis	S. Trevoy	53.46.608	-116.41.185
H3.3	Female	AB	Edson, 15km S	07/17/14	/E. Samis	S. Trevoy	53.46.608	-116.41.185
H3.4	Male	AB	Edson, 15km S	07/17/14	/E. Samis	S. Trevoy	53.46.608	-116.41.185
H4.3	Male	AB	Edson, 15km S	07/17/14	/E. Samis	S. Trevoy	53.46.188	-116.57.686
H4.4	Female	AB	Edson, 15km S	07/17/14	/E. Samis	S. Trevoy	53.46.188	-116.57.686
J.BrNF1	Female	WY (USA)	Bridger National Forest	07/03/05	-	C. Boone	43.92.399	-110.28.763
J.CMt1	Male	WA (USA)	Okanagan-Wenatchee NF, Cooper Mountain	07/03/05	-	C. Boone	48.01.125	-120.19.130
J.HC1	Male	AB	Hines Creek, 25km NW	09/03/08	C. MacQuarrie, C. Myrholm, A. Rice, A. Roe/	A. Roe	56.47.997	-118.51.837
J.HC2	Female	AB	Hines Creek, 25km NW	09/03/08	C. MacQuarrie, C. Myrholm, A. Rice, A. Roe/	A. Roe	56.47.997	-118.51.837
J.HC3	Female	AB	Hines Creek, 25km NW	09/03/08	C. MacQuarrie, C. Myrholm, A. Rice, A. Roe/	A. Roe	56.47.997	-118.51.837
J.MtR1	Female	NV (USA)	Mount Rose Ski Resort	07/03/05	-	C. Boone	39.34.372	-119.91.715
J1	Female	AB	Jasper, Mt. Aeolus	09/21/15	C. Whitehouse	S. Trevoy	53.27.806	-118.14.242
J10	Male	AB	Jasper, Mt. Aeolus	09/21/15	C. Whitehouse	S. Trevoy	53.30.171	-117.44.036
J11	Female	AB	Jasper, Mt. Aeolus	09/21/15	C. Whitehouse	S. Trevoy	53.23.997	-117.47.824
J12	Female	AB	Jasper, Mt. Aeolus	09/21/15	C. Whitehouse	S. Trevoy	53.23.997	-117.47.824
J16	Female	AB	Jasper, Mt. Aeolus	09/21/15	C. Whitehouse	S. Trevoy	53.23.997	-117.47.824
J17	Female	AB	Jasper, Mt. Aeolus	09/21/15	C. Whitehouse	S. Trevoy	53.09.573	-117.31.828
J18	Male	AB	Jasper, Mt. Aeolus	09/21/15	C. Whitehouse	S. Trevoy	53.09.573	-117.31.828
J2	Female	AB	Jasper, Mt. Aeolus	09/21/15	C. Whitehouse	S. Trevoy	53.27.806	-118.14.242
J20	Female	AB	Jasper, Mt. Aeolus	09/21/15	C. Whitehouse	S. Trevoy	53.09.573	-117.31.828
J22	Male	AB	Jasper, Mt. Aeolus	09/21/15	C. Whitehouse	S. Trevoy	53.20.801	-117.34.787

J23	Male	AB	Jasper, Mt. Aeolus	09/21/15	C. Whitehouse	S. Trevoy	53.20.801	-117.34.787
J24	Female	AB	Jasper, Mt. Aeolus	09/21/15	C. Whitehouse	S. Trevoy	53.20.801	-117.34.787
J3	Female	AB	Jasper, Mt. Aeolus	09/21/15	C. Whitehouse	S. Trevoy	53.27.806	-118.14.242
J4	Male	AB	Jasper, Mt. Aeolus	09/21/15	C. Whitehouse	S. Trevoy	53.27.806	-118.14.242
J5	Male	AB	Jasper, Mt. Aeolus	09/21/15	C. Whitehouse	S. Trevoy	53.27.806	-118.14.242
J8	Female	AB	Jasper, Mt. Aeolus	09/21/15	C. Whitehouse	S. Trevoy	53.30.171	-117.44.036
J9	Female	AB	Jasper, Mt. Aeolus	09/21/15	C. Whitehouse	S. Trevoy	53.30.171	-117.44.036
K.S1T1	Male	BC	Penticton, Nipple Mt.	06/24/14	G. Smith /K. Bleiker	S. Trevoy	49.56.126	-119.05.319
K.S1T2	Female	BC	Penticton, Nipple Mt.	06/24/14	G. Smith /K. Bleiker	S. Trevoy	49.56.126	-119.05.319
K.S1T3	Female	BC	Penticton, Nipple Mt.	06/24/14	G. Smith /K. Bleiker	S. Trevoy	49.56.126	-119.05.319
K.S1T3.2	Female	BC	Penticton, Nipple Mt.	06/24/14	G. Smith /K. Bleiker	S. Trevoy	49.56.126	-119.05.319
K.S1T4	Female	BC	Penticton, Nipple Mt.	06/24/14	G. Smith /K. Bleiker	S. Trevoy	49.56.126	-119.05.319
K.S1T5	Male	BC	Penticton, Nipple Mt.	06/24/14	G. Smith /K. Bleiker	S. Trevoy	49.56.126	-119.05.319
K.S1T6	Female	BC	Penticton, Nipple Mt.	06/24/14	G. Smith /K. Bleiker	S. Trevoy	49.56.126	-119.05.319
K.S1T6.2	Female	BC	Penticton, Nipple Mt.	06/24/14	G. Smith /K. Bleiker	S. Trevoy	49.56.126	-119.05.319
K.S2T1A	Female	BC	Penticton, Nipple Mt.	06/24/14	G. Smith /K. Bleiker	S. Trevoy	49.58.299	-119.04.395
K.S2T1B	Female	BC	Penticton, Nipple Mt.	06/24/14	G. Smith /K. Bleiker	S. Trevoy	49.58.299	-119.04.395
M1	Female	BC	Merritt, Selish Mt.	06/29/05	-	C. Boone	50.03.524	-120.65.615
M2	Female	BC	Merritt, Selish Mt.	06/29/05	-	C. Boone	50.03.524	-120.65.615
M4	Female	BC	Merritt, Selish Mt.	06/29/05	-	C. Boone	50.03.524	-120.65.615
M6	Female	BC	Merritt, Selish Mt.	06/29/05	-	C. Boone	50.03.524	-120.65.615
M7	Female	BC	Merritt, Selish Mt.	06/29/05	-	C. Boone	50.03.524	-120.65.615
M8	Female	BC	Merritt, Selish Mt.	06/29/05	-	C. Boone	50.03.524	-120.65.615

M9	Female	BC	Merritt, Selish Mt.	06/29/05	-	C. Boone	50.03.524	-120.65.615
PR10	Female	BC	Princeton, Hedley	06/24/14	G. Smith /K. Bleiker	S. Trevoy	49.33.884	-120.08.923
PR2	Female	BC	Princeton, Hedley	06/24/14	G. Smith /K. Bleiker	S. Trevoy	49.33.884	-120.08.923
PR3	Female	BC	Princeton, Hedley	06/24/14	G. Smith /K. Bleiker	S. Trevoy	49.33.884	-120.08.923
PR7	Female	BC	Princeton, Hedley	06/24/14	G. Smith /K. Bleiker	S. Trevoy	49.33.884	-120.08.923
SL1	Female	AB	Slave Lake, Swan Hills	07/17/14	/E. Samis	S. Trevoy	54.58.302	-115.53.486
Sm1	Male	BC	Smithers, Hudson Bay Mt Resort Access	06/27/05	-	C. Boone	54.78.236	-127.16.855
Sm11	Male	BC	Smithers, Hudson Bay Mt Resort Access	06/27/05	-	C. Boone	54.78.236	-127.16.855
Sm2	Male	BC	Smithers, Hudson Bay Mt Resort Access	06/27/05	-	C. Boone	54.78.236	-127.16.855
Sm3	Male	BC	Smithers, Hudson Bay Mt Resort Access	06/27/05	-	C. Boone	54.78.236	-127.16.855
SW3	Male	BC	Sparwood	06/29/05	-	A. Roe	49.68.000	-114.91.000
SW4	Female	BC	Sparwood	06/29/05	-	A. Roe	49.68.000	-114.91.000
SW5	Female	BC	Sparwood	06/29/05	-	A. Roe	49.68.000	-114.91.000
TeRo2	Male	BC	Terrace, Rosswood	06/29/05	-	A. Roe	54.80.427	-128.76.349
TeRo3	Male	BC	Terrace, Rosswood	06/29/05	-	A. Roe	54.80.427	-128.76.349
TeRo4	Female	BC	Terrace, Rosswood	06/29/05	-	A. Roe	54.80.427	-128.76.349
TeRo5	Male	BC	Terrace, Rosswood	06/29/05	-	A. Roe	54.80.427	-128.76.349
TR1	Female	BC	Tumbler Ridge 1, Gwyllim Lake	06/29/05	-	A. Roe	55.31.780	-121.45.530
TR2	Male	BC	Tumbler Ridge 1, Gwyllim Lake	06/29/05	-	A. Roe	55.31.780	-121.45.530
TR5	Male	BC	Tumbler Ridge 2, Gwyllim Lake	06/29/05	-	A. Roe	54.91.000	-121.23.000

Table A.2. Gene Ontologies for 17 loci significant contributions to PC1, but not PC3, of a PCA of 175 wild MPB.

Genome Scaffold	Scaffold Position	Description	#Hits
983032	57335	endothelin-converting enzyme 1 isoform X2	20
983675	17713	PREDICTED: uncharacterized protein LOC109545326	3
984898	492	peroxisomal acyl-coenzyme A oxidase 3	20
984898	6778	carboxypeptidase B-like	20
985123	79611	serine/threonine-protein kinase WNK1-like	20
985123	91946	hypothetical protein D910_05189, partial	3
985322	393287	glucose dehydrogenase [FAD, quinone]-like	20
985350	265965	tyrosine-protein phosphatase non-receptor type 5-like	20
985375	15824	huntingtin-interacting protein 1 isoform X1	20
985379	8007	ubiquitin carboxyl-terminal hydrolase 32 isoform X2	20
985379	357530	lisH domain and HEAT repeat-containing protein KIAA1468 homolog	18
985379	153935	zinc finger protein castor homolog 1-like isoform X1	20
985400	481002	tyrosine-protein kinase receptor torso	20
985400	481268	vascular endothelial growth factor receptor 2-like isoform X1	20
985435	400431	brachyurin-like	20
985466	85267	MOG interacting and ectopic P-granules protein 1 isoform X1	20
985556	93079	amphoterin-induced protein 1-like	5

Genome Scaffold	e-Value	sim mean	#GO	GO IDs
983032	9.57E-17	93.2	3	C:GO:0016021; P:GO:0016486; F:GO:0004222
983675	1.82E-18	100	3	F:GO:0008061; P:GO:0006030; C:GO:0005576
984898	1.01E-23	73.55	4	F:GO:0071949; C:GO:0005777; F:GO:0003997; P:GO:0006635
984898	5.70E-28	79.25	3	F:GO:0008270; F:GO:0004181; P:GO:0006508
985123	1.11E-09	89	3	F:GO:0005524; F:GO:0004674; P:GO:0006468
985123	5.05E-21	97.33	3	F:GO:0005524; F:GO:0004674; P:GO:0006468
985322	5.74E-20	80.3	3	F:GO:0050660; P:GO:0055114; F:GO:0008812
985350	1.01E-25	85.2	3	F:GO:0004725; C:GO:0016021; P:GO:0035335
985375	1.60E-19	66.45	1	F:GO:0005488
985379	5.82E-43	89.1	4	F:GO:0004843; P:GO:0016579; F:GO:0005509; P:GO:0006511
985379	1.28E-22	75.56	4	P:GO:0006627; C:GO:0005759; F:GO:0046872; F:GO:0004222
985379	2.29E-36	82.2	1	F:GO:0003676
985400	2.76E-24	92	3	F:GO:0005524; P:GO:0018108; F:GO:0004713
985400	1.69E-37	64.75	4	F:GO:0005524; P:GO:0018108; F:GO:0004713; C:GO:0016021
985435	1.09E-36	77.65	2	P:GO:0006508; F:GO:0004252
985466	8.12E-16	95.55	1	F:GO:0003676
985556	4.07E-35	86.8	3	F:GO:0003824; P:GO:0008152; C:GO:0016021

Genome Scaffold	GO Names
983032	C:integral component of membrane; P:peptide hormone processing; F:metalloendopeptidase activity
983675	F:chitin binding; P:chitin metabolic process; C:extracellular region
984898	F:FAD binding; C:peroxisome; F:acyl-CoA oxidase activity; P:fatty acid beta-oxidation
984898	F:zinc ion binding; F:metallocarboxypeptidase activity; P:proteolysis
985123	F:ATP binding; F:protein serine/threonine kinase activity; P:protein phosphorylation
985123	F:ATP binding; F:protein serine/threonine kinase activity; P:protein phosphorylation
985322	F:flavin adenine dinucleotide binding; P:oxidation-reduction process; F:choline dehydrogenase activity
985350	F:protein tyrosine phosphatase activity; C:integral component of membrane; P:peptidyl-tyrosine dephosphorylation
985375	F:binding
985379	F:thiol-dependent ubiquitin-specific protease activity; P:protein deubiquitination; F:calcium ion binding; P:ubiquitin-dependent protein catabolic process
985379	P:protein processing involved in protein targeting to mitochondrion; C:mitochondrial matrix; F:metal ion binding; F:metalloendopeptidase activity
985379	F:nucleic acid binding
985400	F:ATP binding; P:peptidyl-tyrosine phosphorylation; F:protein tyrosine kinase activity
985400	F:ATP binding; P:peptidyl-tyrosine phosphorylation; F:protein tyrosine kinase activity; C:integral component of membrane
985435	P:proteolysis; F:serine-type endopeptidase activity
985466	F:nucleic acid binding
985556	F:catalytic activity; P:metabolic process; C:integral component of membrane

Genome Scaffold	Enzyme Codes	Enzyme Names	InterPro IDs
983032	EC:3.4.24	Acting on peptide bonds (peptidases)	IPR024079 (G3DSA:3.40.390.GENE3D)
983675			no IPS match
984898	EC:1.3.3.6	Acyl-CoA oxidase	IPR002655 (PFAM); G3DSA:1.20.140.10 (GENE3D); PTHR10909:SF315 (PANTHER); PTHR10909 (PANTHER); IPR036250 (SUPERFAMILY)
984898	EC:3.4.17	Acting on peptide bonds (peptidases)	G3DSA:3.40.630.10 (GENE3D); IPR000834 (PFAM); PTHR11705:SF86 (PANTHER); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
985123	EC:2.7.11	Transferring phosphorus-containing groups	no IPS match
985123	EC:2.7.11	Transferring phosphorus-containing groups	mobidb-lite (MOBIDB_LITE)
985322	EC:1.1.99.1	Choline dehydrogenase	IPR000172 (PFAM); IPR036188 (G3DSA:3.50.50.GENE3D); PTHR11552:SF198 (PANTHER); PTHR11552 (PANTHER); IPR036188 (SUPERFAMILY)
985350	EC:3.1.3.16; EC:3.1.3.48; EC:3.1.3.41	Protein-serine/threonine phosphatase; Protein-tyrosine-phosphatase; 4-nitrophenylphosphatase	IPR029021 (G3DSA:3.90.190.GENE3D); IPR029021 (SUPERFAMILY)
985375			mobidb-lite (MOBIDB_LITE)
985379	EC:3.4.19.12	Ubiquitinyl hydrolase 1	PTHR44893 (PANTHER)
985379	EC:3.4.24	Acting on peptide bonds (peptidases)	no IPS match
985379	---	---	IPR013087 (PROSITE_PROFILES); IPR036236 (SUPERFAMILY)
985400	EC:2.7.10	Transferring phosphorus-containing groups	IPR001245 (PRINTS); IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24416:SF400 (PANTHER); PTHR24416 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
985400	EC:2.7.10	Transferring phosphorus-containing groups	G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
985435	EC:3.4.21	Acting on peptide bonds (peptidases)	no IPS match
985466	---	---	mobidb-lite (MOBIDB_LITE)
985556	---	---	no IPS match

Genome Scaffold	InterPro GO IDs	InterPro GO Names
983032	F:GO:0008237	F:metallopeptidase activity
983675	no IPS match	no IPS match
984898	C:GO:0005777; P:GO:0006635; F:GO:0003997; F:GO:0016627; P:GO:0055114	C:peroxisome; P:fatty acid beta-oxidation; F:acyl-CoA oxidase activity; F:oxidoreductase activity, acting on the CH-CH group of donors; P:oxidation-reduction process
984898	F:GO:0008270; F:GO:0004181; P:GO:0006508	F:zinc ion binding; F:metallocarboxypeptidase activity; P:proteolysis
985123	no IPS match	no IPS match
985123	no GO terms	no GO terms
985322	F:GO:0016614; F:GO:0050660; P:GO:0055114	F:oxidoreductase activity, acting on CH-OH group of donors; F:flavin adenine dinucleotide binding; P:oxidation-reduction process
985350	no GO terms	no GO terms
985375	no GO terms	no GO terms
985379	no GO terms	no GO terms
985379	no IPS match	no IPS match
985379	F:GO:0003676	F:nucleic acid binding
985400	F:GO:0005524; F:GO:0004672; P:GO:0006468	F:ATP binding; F:protein kinase activity; P:protein phosphorylation
985400	F:GO:0005524; F:GO:0004672; P:GO:0006468	F:ATP binding; F:protein kinase activity; P:protein phosphorylation
985435	no IPS match	no IPS match
985466	no GO terms	no GO terms
985556	no IPS match	no IPS match

Table A.3. Gene Ontologies for 93 loci significant contributions to PC2 of a PCA of 175 wild MPB.

Genome Scaffold	Scaffold Position	Description	#Hits
962832	1722	spondin-1	20
974948	2303	cyclin-K	20
983688	188545	cytoplasmic dynein 2 heavy chain 1	20
983860	92671	homeodomain-interacting kinase 2-	13
984571	112321	cadherin-23	20
984762	948054	mago nashi homolog	20
984762	1137923	diacylglycerol kinase theta isoform X7	20
984762	1140752	diacylglycerol kinase theta isoform X2	20
984762	1310481	myosin-I heavy chain	3
984762	1316648	unconventional myosin-IXb isoform X1	20
984762	412689	Scy1	20
984762	1137743	diacylglycerol kinase theta isoform X1	20
984762	1287565	soluble guanylate cyclase 89Db-like isoform X1	20
984762	1317194	unconventional myosin-IXa isoform X2	15
984762	96633	ATP-dependent RNA helicase DDX54	20
985141	163415	hypothetical protein YQE_09634, partial	3
985155	328412	proton-coupled amino acid transporter pathetic isoform X2	18
985222	151848	neurogenic mastermind-like	4
985222	151889	neurogenic mastermind-like	4
985222	151591	neurogenic mastermind-like	4
985250	85683	endonuclease-reverse transcriptase	11
985266	212238	transmembrane and TPR repeat-containing CG4341-	5
985291	436191	B-cell lymphoma leukemia 11A-like	20
985291	121293	trans-1,2-dihydrobenzene-1,2-diol dehydrogenase-like	20
985291	60146	mitogen-activated kinase kinase kinase 11-like isoform X1	20
985291	192351	stoned-B isoform X2	20

Genome Scaffold	Scaffold Position	Description	#Hits
985291	139998	otopetrin-2-like isoform X3	20
985293	912982	dachsous	20
985293	913707	Dachsous	20
985293	58266	cytochrome P450 4g15-like	20
985293	672230	hypothetical protein YQE_03943, partial	4
985293	913039	dachsous	20
985304	39996	peroxiredoxin- mitochondrial	20
985309	358525	myc box-dependent-interacting 1 isoform X2	20
985370	327113	PO11_POPJA ame: Full=Retrovirus-related Pol poly from type-1 retrotransposable element R1 ame: Full=Retrovirus-related Pol poly from type I retrotransposable element R1 Includes: ame: Full=Reverse transcriptase Includes: ame: Full=Endonuclease	8
985370	447622	E3 ubiquitin- ligase RNF19A-like isoform X1	13
985400	769115	zinc finger RNA-binding isoform X3	20
985400	480826	proto-oncogene tyrosine- kinase receptor Ret	20
985400	620247	gastrula zinc finger -like	20
985402	428981	synaptic vesicle glyco 2B-like	20
985402	190923	ribosomal S6 kinase alpha-2 isoform X1	20
985402	282189	60S ribosomal L18a	20
985402	279224	major facilitator superfamily domain-containing 8	20
985403	401559	hypothetical protein D910_08565	13
985403	568459	YIPF6	20
985403	621029	activating transcription factor 3	20
985403	775083	peptidyl-prolyl cis-trans isomerase D	20
985403	829248	multiple epidermal growth factor-like domains 10 isoform X1	20
985403	829167	draper isoform X1	20
985403	196438	venom acid phosphatase Acph-1-like	20
985424	334459	cytochrome P450 4g15	20

Genome Scaffold	Scaffold Position	Description	#Hits
985424	533292	inorganic phosphate cotransporter	20
985433	814518	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase classes I and II-	8
985433	1379829	pericentriolar material 1 isoform X4	20
985433	81342	zinc transporter 1 isoform X1	16
985433	193585	leucine-rich repeat-containing 24-like	20
985433	1401217	dynein heavy chain axonemal-	20
985433	1440113	syntaxin-5	20
985433	1483607	spermine oxidase	5
985433	174402	tumor suppressor candidate 3	20
985433	813771	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase classes I and II-	20
985433	637112	DNA-binding D-ETS-4 isoform X1	11
985433	57863	inhibitor of growth 1-like	4
985433	120139	hypothetical protein YQE_00438, partial	20
985462	373281	RING finger 141-like	20
985462	294774	hypothetical protein D910_10178	1
985479	283639	glycogen phosphorylase	20
985498	1193249	leucine--tRNA cytoplasmic	20
985499	705080	sorting nexin-25	20
985499	776289	isoform A	18
985500	440850	hypothetical protein D910_11139	20
985500	888471	T-complex 1 subunit eta-like	20
985500	3296395	endopolygalacturonase A-like	7
985500	1130812	U4 U6 small nuclear ribonucleo Prp4	20
985500	2741139	Histone-lysine N-methyltransferase	20
985515	817043	esterase FE4-like	20
985515	2223086	myb P	20
985515	383371	beta-glucuronidase-like isoform X2	20

Genome Scaffold	Scaffold Position	Description	#Hits
985515	2300659	fork head domain transcription factor slp2-like	6
985516	545872	larval cuticle A2B-like	20
985522	272799	methyl- -binding domain 5 isoform X1	20
985525	965720	15-hydroxyprostaglandin dehydrogenase [NAD(+)]-like	18
985526	95381	BTB POZ domain-containing KCTD12	20
985527	242956	kinesin CG14535	20
985535	76477	S-methyl-5 -thioadenosine phosphorylase-like	20
985535	126206	catalase-like	20
985535	515098	gamma-aminobutyric acid type B receptor subunit 1 isoform X1	20
985535	76287	S-methyl-5 -thioadenosine phosphorylase-like	20
985545	383125	signal recognition particle receptor subunit alpha homolog	20
985556	223742	phosphatidylinositol-binding clathrin assembly LAP-like	20
985556	89493	organic solute transporter alpha	5
985558	19191	hypothetical protein D910_12819	5
985558	21181	tetraspanin-9	20

Genome Scaffold	e-Value	sim mean	#GO	GO IDs
962832	2.87E-30	85.6	2	F:GO:0004867; P:GO:0010951
974948	4.57E-41	96.7	1	C:GO:0005634
983688	1.12E-23	79.7	5	F:GO:0016887; F:GO:0005524; F:GO:0003777; C:GO:0030286; P:GO:0007018
983860	5.04E-39	68.92	3	F:GO:0005524; F:GO:0004672; P:GO:0006468
984571	2.53E-22	78.4	4	F:GO:0005509; C:GO:0016021; P:GO:0007156; C:GO:0005886
984762	3.04E-22	98	6	C:GO:0035145; P:GO:0008380; F:GO:0003723; C:GO:0071013; P:GO:0006397; P:GO:0051028
984762	5.83E-41	98.2	7	F:GO:0000166; F:GO:0003676; F:GO:0004143; P:GO:0016310; P:GO:0007205; C:GO:0005622; P:GO:0035556
984762	2.19E-30	91.05	4	F:GO:0005524; F:GO:0004143; P:GO:0016310; P:GO:0007205
984762	2.02E-19	100	4	C:GO:0016459; F:GO:0005524; F:GO:0003779; F:GO:0003774
984762	4.59E-40	94.15	4	C:GO:0016459; F:GO:0005524; F:GO:0003779; F:GO:0003774
984762	1.49E-37	90.6	4	F:GO:0005524; C:GO:0016021; F:GO:0004672; P:GO:0006468
984762	2.65E-14	89.35	4	F:GO:0005524; F:GO:0004143; P:GO:0016310; P:GO:0007205
984762	2.45E-11	92.65	2	P:GO:0006508; F:GO:0004252
984762	5.06E-20	67.33	3	C:GO:0016459; F:GO:0005524; F:GO:0003774
984762	3.09E-18	91.4	14	F:GO:0005272; F:GO:0004672; C:GO:0005730; P:GO:0000027; P:GO:0006468; P:GO:1902626; P:GO:0000466; F:GO:0004004; P:GO:0000463; F:GO:0005524; F:GO:0003723; C:GO:0016020; P:GO:0035725; C:GO:0030687
985141	4.72E-26	85	4	F:GO:0005524; F:GO:0003777; C:GO:0030286; P:GO:0007018
985155	3.93E-16	82.5	1	C:GO:0016021
985222	9.61E-13	97	4	P:GO:0007219; F:GO:0003713; C:GO:0016607; P:GO:0045944
985222	1.24E-17	97.5	4	P:GO:0007219; F:GO:0003713; C:GO:0016607; P:GO:0045944
985222	3.61E-09	97	4	P:GO:0007219; F:GO:0003713; C:GO:0016607; P:GO:0045944
985250	4.47E-09	77.91	2	P:GO:0090304; F:GO:0003824

Genome Scaffold	e-Value	sim mean	#GO	GO IDs
985266	4.35E-26	98.6	1	C:GO:0016021
985291	7.20E-30	87.8	2	F:GO:0003676; F:GO:0046872
985291	7.76E-39	85.25	2	F:GO:0016491; P:GO:0055114
985291	2.77E-15	95.2	3	F:GO:0005524; F:GO:0004674; P:GO:0006468
985291	4.08E-29	97	12	C:GO:0030139; F:GO:0097110; P:GO:0016183; C:GO:0008021; P:GO:1900242; C:GO:0016021; C:GO:0030131; C:GO:0048788; P:GO:0006886; C:GO:0030135; C:GO:0005886; P:GO:0007269
985291	3.16E-25	98.3	1	C:GO:0016021
985293	3.21E-35	94.05	4	F:GO:0005509; C:GO:0016021; P:GO:0007156; C:GO:0005886
985293	4.78E-37	91.2	4	F:GO:0005509; C:GO:0016021; P:GO:0007156; C:GO:0005886
985293	2.96E-18	63.35	2	F:GO:0016491; F:GO:0005488
985293	5.20E-08	100	4	F:GO:0005509; C:GO:0016021; P:GO:0007156; C:GO:0005886
985293	5.72E-36	96.5	4	F:GO:0005509; C:GO:0016021; P:GO:0007156; C:GO:0005886
985304	2.32E-13	92.45	2	F:GO:0016491; P:GO:0055114
985309	2.62E-32	93.9	4	F:GO:0005525; P:GO:0072583; C:GO:0005737; F:GO:0003924
985370	1.78E-10	59.25	4	P:GO:0048015; P:GO:0046854; F:GO:0016301; C:GO:0005622
985370	2.70E-38	83.23	3	F:GO:0004842; F:GO:0016874; P:GO:0016567
985400	7.09E-08	97.7	2	F:GO:0003676; F:GO:0008270
985400	3.76E-38	56.8	1	F:GO:0016301
985400	7.91E-25	77	5	F:GO:0003676; C:GO:0005634; F:GO:0003700; F:GO:0008270; P:GO:0006355
985402	2.62E-27	75.75	3	P:GO:0055085; F:GO:0022857; C:GO:0016021
985402	5.27E-16	96.25	23	P:GO:0060047; C:GO:0008540; P:GO:0008285; P:GO:0045835; P:GO:0002035; C:GO:0005654; P:GO:0006511; F:GO:0000287; F:GO:0004711; F:GO:0005524; P:GO:0007507; C:GO:0031965; F:GO:0004712; P:GO:0001556; P:GO:0010659; C:GO:0005737; P:GO:0071322; P:GO:0010628; P:GO:0043065; C:GO:0005819; P:GO:0018105;

Genome Scaffold	e-Value	sim mean	#GO	GO IDs
				P:GO:0035556; P:GO:0070613
985402	3.49E-22	95.95	3	F:GO:0003735; C:GO:0005840; P:GO:0006412
985402	8.74E-38	85.35	2	P:GO:0055085; C:GO:0016021
985403	1.79E-18	85.46	1	C:GO:0016021
985403	4.93E-21	70.9	1	C:GO:0016020
985403	1.62E-15	89.75	3	F:GO:0003700; F:GO:0043565; P:GO:0006357
985403	1.05E-29	69.25	3	F:GO:0003755; P:GO:0000413; P:GO:0006457
985403	9.57E-40	86.85	1	C:GO:0016021
985403	4.74E-26	86.95	1	C:GO:0016021
985403	8.99E-40	81	2	P:GO:0016311; F:GO:0003993
985424	1.04E-27	88.1	6	F:GO:0005506; F:GO:0016705; C:GO:0016021; P:GO:0055114; F:GO:0004497; F:GO:0020037
985424	3.17E-23	73.5	2	P:GO:0055085; C:GO:0016021
985433	2.16E-24	99.63	6	F:GO:0004435; F:GO:0005509; P:GO:0016042; F:GO:0004871; C:GO:0005622; P:GO:0035556
985433	1.13E-30	89.6	3	C:GO:0005813; P:GO:0034454; P:GO:0071539
985433	1.10E-15	78.94	3	P:GO:0098655; C:GO:0016021; F:GO:0008324
985433	5.87E-31	79.25	1	C:GO:0016021
985433	3.00E-37	88.6	5	F:GO:0016887; F:GO:0005524; F:GO:0003777; C:GO:0005858; P:GO:0003341
985433	2.59E-21	65.7	2	C:GO:0016020; P:GO:0006810
985433	1.46E-24	84.6	2	F:GO:0016491; P:GO:0055114
985433	2.60E-26	85.65	2	C:GO:0016021; F:GO:0016740
985433	1.72E-14	96.2	6	F:GO:0004435; F:GO:0005509; P:GO:0016042; F:GO:0004871; C:GO:0005622; P:GO:0035556
985433	6.71E-36	73.64	4	C:GO:0005634; F:GO:0003700; P:GO:0006355; F:GO:0043565
985433	5.78E-21	97.5	2	C:GO:0005634; F:GO:0008270
985433	3.35E-29	93.75	2	P:GO:0007165; C:GO:0016021
985462	3.01E-28	84.05	1	F:GO:0008270

Genome Scaffold	e-Value	sim mean	#GO	GO IDs
985462	2.90E-11	100	2	F:GO:0008270; C:GO:0005622
985479	6.15E-38	92.55	4	F:GO:0008184; F:GO:0030170; C:GO:0005737; P:GO:0005980
985498	1.82E-17	94.6	10	F:GO:0005524; P:GO:0006429; F:GO:0004823; P:GO:0042060; C:GO:0005759; P:GO:0006450; F:GO:0002161; C:GO:0017101; P:GO:0022008; C:GO:0005875
985499	8.36E-37	85.35	3	P:GO:0090101; C:GO:0016021; F:GO:0035091
985499	3.11E-20	88.61	1	C:GO:0016021
985500	2.84E-37	82.95	1	C:GO:0016021
985500	4.37E-25	96.15	8	F:GO:0005524; P:GO:0007052; C:GO:0005829; F:GO:0051082; P:GO:0022008; P:GO:0031122; P:GO:0006457; C:GO:0005875
985500	1.31E-11	95.86	4	P:GO:0005975; F:GO:0004650; P:GO:0071555; C:GO:0005576
985500	4.22E-40	91.3	2	C:GO:0030529; C:GO:0019013
985500	1.44E-16	83.4	2	F:GO:0008168; P:GO:0032259
985515	7.00E-19	55.9	2	F:GO:0003824; P:GO:0009987
985515	2.38E-25	77.85	3	P:GO:0002098; F:GO:0016300; P:GO:0030488
985515	1.16E-14	76.3	3	P:GO:0005975; F:GO:0004566; C:GO:0005764
985515	3.51E-21	82	3	F:GO:0003700; P:GO:0006355; F:GO:0043565
985516	6.43E-09	93.9	1	F:GO:0042302
985522	1.92E-22	92.1	2	C:GO:0005634; F:GO:0003677
985525	5.53E-12	84.72	2	P:GO:0055114; F:GO:0004022
985526	3.54E-26	78.95	6	P:GO:0090327; P:GO:0008049; P:GO:0051260; P:GO:0030431; P:GO:0002121; C:GO:0005886
985527	1.17E-20	93.9	5	F:GO:0005524; F:GO:0003777; P:GO:0007018; C:GO:0005874; F:GO:0008017
985535	3.70E-18	73.1	4	C:GO:0005634; F:GO:0017061; C:GO:0005737; P:GO:0006166
985535	4.55E-27	80.4	8	P:GO:0006979; F:GO:0046872; F:GO:0004096; P:GO:0098869; P:GO:0055114; P:GO:0006952; F:GO:0020037; P:GO:0042744
985535	4.53E-20	87	3	F:GO:0004965; P:GO:0007186; C:GO:0016021

Genome Scaffold	e-Value	sim mean	#GO	GO IDs
985535	2.51E-24	82.4	4	C:GO:0005634; F:GO:0017061; C:GO:0005737; P:GO:0006166
985545	9.73E-14	89.15	5	F:GO:0005525; P:GO:0006614; F:GO:0003924; C:GO:0005785; F:GO:0005047
985556	4.94E-38	92.2	5	P:GO:0048268; C:GO:0016021; F:GO:0030276; C:GO:0030136; F:GO:0005545
985556	5.38E-25	100	1	C:GO:0016021
985558	4.38E-26	76.8	2	C:GO:0005634; P:GO:0051028
985558	1.63E-27	79.55	1	C:GO:0016021

Genome Scaffold	GO Names
962832	F:serine-type endopeptidase inhibitor activity; P:negative regulation of endopeptidase activity
974948	C:nucleus
983688	F:ATPase activity; F:ATP binding; F:microtubule motor activity; C:dynein complex; P:microtubule-based movement
983860	F:ATP binding; F:protein kinase activity; P:protein phosphorylation
984571	F:calcium ion binding; C:integral component of membrane; P:homophilic cell adhesion via plasma membrane adhesion molecules; C:plasma membrane
984762	C:exon-exon junction complex; P:RNA splicing; F:RNA binding; C:catalytic step 2 spliceosome; P:mRNA processing; P:mRNA transport
984762	F:nucleotide binding; F:nucleic acid binding; F:diacylglycerol kinase activity; P:phosphorylation; P:protein kinase C-activating G-protein coupled receptor signaling pathway; C:intracellular; P:intracellular signal transduction
984762	F:ATP binding; F:diacylglycerol kinase activity; P:phosphorylation; P:protein kinase C-activating G-protein coupled receptor signaling pathway
984762	C:myosin complex; F:ATP binding; F:actin binding; F:motor activity
984762	C:myosin complex; F:ATP binding; F:actin binding; F:motor activity
984762	F:ATP binding; C:integral component of membrane; F:protein kinase activity; P:protein phosphorylation
984762	F:ATP binding; F:diacylglycerol kinase activity; P:phosphorylation; P:protein kinase C-activating G-protein coupled receptor signaling pathway
984762	P:proteolysis; F:serine-type endopeptidase activity
984762	C:myosin complex; F:ATP binding; F:motor activity
984762	F:sodium channel activity; F:protein kinase activity; C:nucleolus; P:ribosomal large subunit assembly; P:protein phosphorylation; P:assembly of large subunit precursor of preribosome; P:maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA); F:ATP-dependent RNA helicase activity; P:maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA); F:ATP binding; F:RNA binding; C:membrane; P:sodium ion transmembrane transport; C:preribosome, large subunit precursor

Genome Scaffold	GO Names
985141	F:ATP binding; F:microtubule motor activity; C:dynein complex; P:microtubule-based movement
985155	C:integral component of membrane
985222	P:Notch signaling pathway; F:transcription coactivator activity; C:nuclear speck; P:positive regulation of transcription from RNA polymerase II promoter
985222	P:Notch signaling pathway; F:transcription coactivator activity; C:nuclear speck; P:positive regulation of transcription from RNA polymerase II promoter
985222	P:Notch signaling pathway; F:transcription coactivator activity; C:nuclear speck; P:positive regulation of transcription from RNA polymerase II promoter
985250	P:nucleic acid metabolic process; F:catalytic activity
985266	C:integral component of membrane
985291	F:nucleic acid binding; F:metal ion binding
985291	F:oxidoreductase activity; P:oxidation-reduction process
985291	F:ATP binding; F:protein serine/threonine kinase activity; P:protein phosphorylation
985291	C:endocytic vesicle; F:scaffold protein binding; P:synaptic vesicle coating; C:synaptic vesicle; P:regulation of synaptic vesicle endocytosis; C:integral component of membrane; C:clathrin adaptor complex; C:cytoskeleton of presynaptic active zone; P:intracellular protein transport; C:coated vesicle; C:plasma membrane; P:neurotransmitter secretion
985291	C:integral component of membrane
985293	F:calcium ion binding; C:integral component of membrane; P:homophilic cell adhesion via plasma membrane adhesion molecules; C:plasma membrane
985293	F:calcium ion binding; C:integral component of membrane; P:homophilic cell adhesion via plasma membrane adhesion molecules; C:plasma membrane
985293	F:oxidoreductase activity; F:binding
985293	F:calcium ion binding; C:integral component of membrane; P:homophilic cell adhesion via plasma membrane adhesion molecules; C:plasma membrane
985293	F:calcium ion binding; C:integral component of membrane; P:homophilic cell adhesion via plasma membrane adhesion molecules; C:plasma membrane
985304	F:oxidoreductase activity; P:oxidation-reduction process

Genome Scaffold	GO Names
985309	F:GTP binding; P:clathrin-dependent endocytosis; C:cytoplasm; F:GTPase activity
985370	P:phosphatidylinositol-mediated signaling; P:phosphatidylinositol phosphorylation; F:kinase activity; C:intracellular
985370	F:ubiquitin-protein transferase activity; F:ligase activity; P:protein ubiquitination
985400	F:nucleic acid binding; F:zinc ion binding
985400	F:kinase activity
985400	F:nucleic acid binding; C:nucleus; F:transcription factor activity, sequence-specific DNA binding; F:zinc ion binding; P:regulation of transcription, DNA-templated
985402	P:transmembrane transport; F:transmembrane transporter activity; C:integral component of membrane
985402	P:heart contraction; C:proteasome regulatory particle, base subcomplex; P:negative regulation of cell proliferation; P:negative regulation of meiotic nuclear division; P:brain renin-angiotensin system; C:nucleoplasm; P:ubiquitin-dependent protein catabolic process; F:magnesium ion binding; F:ribosomal protein S6 kinase activity; F:ATP binding; P:heart development; C:nuclear membrane; F:protein serine/threonine/tyrosine kinase activity; P:oocyte maturation; P:cardiac muscle cell apoptotic process; C:cytoplasm; P:cellular response to carbohydrate stimulus; P:positive regulation of gene expression; P:positive regulation of apoptotic process; C:spindle; P:peptidyl-serine phosphorylation; P:intracellular signal transduction; P:regulation of protein processing
985402	F:structural constituent of ribosome; C:ribosome; P:translation
985402	P:transmembrane transport; C:integral component of membrane
985403	C:integral component of membrane
985403	C:membrane
985403	F:transcription factor activity, sequence-specific DNA binding; F:sequence-specific DNA binding; P:regulation of transcription from RNA polymerase II promoter
985403	F:peptidyl-prolyl cis-trans isomerase activity; P:protein peptidyl-prolyl isomerization; P:protein folding
985403	C:integral component of membrane
985403	C:integral component of membrane
985403	P:dephosphorylation; F:acid phosphatase activity

Genome Scaffold	GO Names
985424	F:iron ion binding; F:oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen; C:integral component of membrane; P:oxidation-reduction process; F:monooxygenase activity; F:heme binding
985424	P:transmembrane transport; C:integral component of membrane
985433	F:phosphatidylinositol phospholipase C activity; F:calcium ion binding; P:lipid catabolic process; F:signal transducer activity; C:intracellular; P:intracellular signal transduction
985433	C:centrosome; P:microtubule anchoring at centrosome; P:protein localization to centrosome
985433	P:cation transmembrane transport; C:integral component of membrane; F:cation transmembrane transporter activity
985433	C:integral component of membrane
985433	F:ATPase activity; F:ATP binding; F:microtubule motor activity; C:axonemal dynein complex; P:cilium movement
985433	C:membrane; P:transport
985433	F:oxidoreductase activity; P:oxidation-reduction process
985433	C:integral component of membrane; F:transferase activity
985433	F:phosphatidylinositol phospholipase C activity; F:calcium ion binding; P:lipid catabolic process; F:signal transducer activity; C:intracellular; P:intracellular signal transduction
985433	C:nucleus; F:transcription factor activity, sequence-specific DNA binding; P:regulation of transcription, DNA-templated; F:sequence-specific DNA binding
985433	C:nucleus; F:zinc ion binding
985433	P:signal transduction; C:integral component of membrane
985462	F:zinc ion binding
985462	F:zinc ion binding; C:intracellular
985479	F:glycogen phosphorylase activity; F:pyridoxal phosphate binding; C:cytoplasm; P:glycogen catabolic process
985498	F:ATP binding; P:leucyl-tRNA aminoacylation; F:leucine-tRNA ligase activity; P:wound healing; C:mitochondrial matrix; P:regulation of translational fidelity; F:aminoacyl-tRNA editing activity; C:aminoacyl-tRNA synthetase multienzyme complex; P:neurogenesis; C:microtubule associated complex

Genome Scaffold	GO Names
985499	P:negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway; C:integral component of membrane; F:phosphatidylinositol binding
985499	C:integral component of membrane
985500	C:integral component of membrane
985500	F:ATP binding; P:mitotic spindle organization; C:cytosol; F:unfolded protein binding; P:neurogenesis; P:cytoplasmic microtubule organization; P:protein folding; C:microtubule associated complex
985500	P:carbohydrate metabolic process; F:polygalacturonase activity; P:cell wall organization; C:extracellular region
985500	C:intracellular ribonucleoprotein complex; C:viral nucleocapsid
985500	F:methyltransferase activity; P:methylation
985515	F:catalytic activity; P:cellular process
985515	P:tRNA wobble uridine modification; F:tRNA (uracil) methyltransferase activity; P:tRNA methylation
985515	P:carbohydrate metabolic process; F:beta-glucuronidase activity; C:lysosome
985515	F:transcription factor activity, sequence-specific DNA binding; P:regulation of transcription, DNA-templated; F:sequence-specific DNA binding
985516	F:structural constituent of cuticle
985522	C:nucleus; F:DNA binding
985525	P:oxidation-reduction process; F:alcohol dehydrogenase (NAD) activity
985526	P:negative regulation of locomotion involved in locomotory behavior; P:male courtship behavior; P:protein homooligomerization; P:sleep; P:inter-male aggressive behavior; C:plasma membrane
985527	F:ATP binding; F:microtubule motor activity; P:microtubule-based movement; C:microtubule; F:microtubule binding
985535	C:nucleus; F:S-methyl-5-thioadenosine phosphorylase activity; C:cytoplasm; P:purine ribonucleoside salvage
985535	P:response to oxidative stress; F:metal ion binding; F:catalase activity; P:cellular oxidant detoxification; P:oxidation-reduction process; P:defense response; F:heme binding; P:hydrogen peroxide catabolic process
985535	F:G-protein coupled GABA receptor activity; P:G-protein coupled receptor signaling pathway; C:integral component of membrane

Genome Scaffold	GO Names
985535	C:nucleus; F:S-methyl-5-thioadenosine phosphorylase activity; C:cytoplasm; P:purine ribonucleoside salvage
985545	F:GTP binding; P:SRP-dependent cotranslational protein targeting to membrane; F:GTPase activity; C:signal recognition particle receptor complex; F:signal recognition particle binding
985556	P:clathrin coat assembly; C:integral component of membrane; F:clathrin binding; C:clathrin-coated vesicle; F:1-phosphatidylinositol binding
985556	C:integral component of membrane
985558	C:nucleus; P:mRNA transport
985558	C:integral component of membrane

Genome Scaffold	Enzyme Codes	Enzyme Names	InterPro IDs
962832	---	---	G3DSA:2.30.90.10 (GENE3D); IPR000884 (PFAM); IPR000884 (PROSITE_PROFILES); IPR036383 (SUPERFAMILY)
974948	---	---	IPR036915 (G3DSA:1.10.472.GENE3D); PTHR10026 (PANTHER); PTHR10026:SF51 (PANTHER); IPR013763 (CDD); IPR036915 (SUPERFAMILY)
983688	EC:3.6.1.3; EC:3.6.1.15	Adenosinetriphosphatase; Nucleoside-triphosphate phosphatase	no IPS match
983860			mobidb-lite (MOBIDB_LITE)
984571	---	---	IPR002126 (PRINTS); G3DSA:2.60.40.60 (GENE3D); G3DSA:2.60.40.60 (GENE3D); PS50268 (PROSITE_PROFILES); cd11304 (CDD); IPR015919 (SUPERFAMILY)
984762	---	---	IPR036605 (G3DSA:3.30.1560.GENE3D); IPR004023 (PFAM); PTHR12638:SF1 (PANTHER); IPR004023 (PANTHER); IPR036605 (SUPERFAMILY)
984762	EC:2.7.1.107	Diacylglycerol kinase (ATP)	IPR001206 (PFAM); IPR017438 (G3DSA:3.40.50.GENE3D); PTHR11255:SF34 (PANTHER); PTHR11255 (PANTHER); IPR001206 (PROSITE_PROFILES); IPR016064 (SUPERFAMILY)
984762	EC:2.7.1.107	Diacylglycerol kinase (ATP)	IPR000756 (PFAM); PTHR11255 (PANTHER); PTHR11255:SF34 (PANTHER)
984762	EC:3.6.1.15	Nucleoside-triphosphate phosphatase	mobidb-lite (MOBIDB_LITE)
984762	EC:3.6.1.15	Nucleoside-triphosphate phosphatase	IPR001609 (PFAM); PTHR13140:SF498 (PANTHER); PTHR13140 (PANTHER); IPR001609 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
984762	---	---	G3DSA:1.10.510.10 (GENE3D); PTHR12984 (PANTHER); PTHR12984:SF6 (PANTHER); IPR000719 (PROSITE_PROFILES)
984762	EC:2.7.1.107	Diacylglycerol kinase (ATP)	no IPS match

Genome Scaffold	Enzyme Codes	Enzyme Names	InterPro IDs
984762	EC:3.4.21	Acting on peptide bonds (peptidases)	mobidb-lite (MOBIDB_LITE)
984762	EC:3.6.1.15	Nucleoside-triphosphate phosphatase	no IPS match
984762	EC:3.6.1.3; EC:3.6.1.15	Adenosinetriphosphatase; Nucleoside-triphosphate phosphatase	no IPS match
985141	EC:3.6.1.15	Nucleoside-triphosphate phosphatase	no IPS match
985155			no IPS match
985222	---	---	mobidb-lite (MOBIDB_LITE)
985222	---	---	mobidb-lite (MOBIDB_LITE)
985222	---	---	mobidb-lite (MOBIDB_LITE)
985250	---	---	no IPS match
985266	---	---	no IPS match
985291	---	---	mobidb-lite (MOBIDB_LITE)
985291	---	---	G3DSA:3.40.50.720 (GENE3D); IPR000683 (PFAM); PTHR22604:SF105 (PANTHER); PTHR22604 (PANTHER); IPR036291 (SUPERFAMILY)
985291	EC:2.7.11	Transferring phosphorus-containing groups	G3DSA:3.30.200.20 (GENE3D)
985291	---	---	G3DSA:2.60.40.1170 (GENE3D); IPR036168 (SUPERFAMILY)
985291	---	---	IPR004878 (PFAM); PTHR21522:SF32 (PANTHER); IPR004878 (PANTHER)
985293	---	---	G3DSA:2.60.40.60 (GENE3D); IPR002126 (PFAM); PTHR43956 (PANTHER); PTHR43956:SF6 (PANTHER); PS50268 (PROSITE_PROFILES); cd11304 (CDD); IPR015919 (SUPERFAMILY)
985293	---	---	G3DSA:2.60.40.60 (GENE3D); PTHR24026:SF54 (PANTHER); PTHR24026 (PANTHER); cd11304 (CDD); IPR015919 (SUPERFAMILY)
985293	---	---	no IPS match

Genome Scaffold	Enzyme Codes	Enzyme Names	InterPro IDs
985293	---	---	mobidb-lite (MOBIDB_LITE)
985293	---	---	G3DSA:2.60.40.60 (GENE3D); PTHR43956:SF6 (PANTHER); PTHR43956 (PANTHER); cd11304 (CDD); IPR015919 (SUPERFAMILY)
985304	---	---	no IPS match
985309	EC:3.6.1.15	Nucleoside-triphosphate phosphatase	IPR027267 (G3DSA:1.20.1270.GENE3D); mobidb-lite (MOBIDB_LITE); IPR027267 (SUPERFAMILY)
985370	---	---	no IPS match
985370	---	---	mobidb-lite (MOBIDB_LITE)
985400	---	---	no IPS match
985400	---	---	no IPS match
985400	---	---	G3DSA:2.40.155.10 (GENE3D); G3DSA:3.30.160.60 (GENE3D); PTHR24390 (PANTHER); PTHR24390:SF46 (PANTHER); IPR013087 (PROSITE_PROFILES); IPR036236 (SUPERFAMILY)
985402	---	---	no IPS match
985402	EC:2.7.11; EC:2.7.12.1	Transferring phosphorus-containing groups; Dual-specificity kinase	no IPS match
985402	---	---	G3DSA:3.10.20.10 (GENE3D); IPR023573 (PFAM); PTHR10052:SF1 (PANTHER); PTHR10052 (PANTHER)
985402	---	---	PTHR23510 (PANTHER); PTHR23510:SF3 (PANTHER)
985403	---	---	no IPS match
985403	---	---	no IPS match
985403	---	---	no IPS match
985403	EC:5.2.1.8	Peptidylprolyl isomerase	IPR011990 (G3DSA:1.25.40.GENE3D); IPR013026 (PROSITE_PROFILES)
985403	---	---	no IPS match
985403	---	---	PS51257 (PROSITE_PROFILES)

Genome Scaffold	Enzyme Codes	Enzyme Names	InterPro IDs
985403	EC:3.1.3.41; EC:3.1.3.2	4-nitrophenylphosphatase; Acid phosphatase	no IPS match
985424	---	---	IPR036396 (G3DSA:1.10.630.GENE3D); PTHR24291:SF35 (PANTHER); PTHR24291 (PANTHER)
985424	---	---	no IPS match
985433	EC:3.1.4.11	Phosphoinositide phospholipase C	no IPS match
985433	---	---	IPR031446 (PFAM); IPR024138 (PANTHER)
985433	---	---	no IPS match
985433	---	---	mobidb-lite (MOBIDB_LITE)
985433	EC:3.6.1.3; EC:3.6.1.15	Adenosinetriphosphatase; Nucleoside-triphosphate phosphatase	IPR024317 (PFAM); IPR026975 (PTHR10676:PANTHER); IPR026983 (PANTHER)
985433	---	---	IPR021538 (PFAM)
985433	---	---	no IPS match
985433	---	---	IPR021149 (PFAM); PTHR12692 (PANTHER); IPR006844 (PTHR12692:PANTHER)
985433	EC:3.1.4.11	Phosphoinositide phospholipase C	IPR001711 (PFAM); IPR017946 (G3DSA:3.20.20.GENE3D); IPR001711 (PROSITE_PROFILES); IPR017946 (SUPERFAMILY)
985433	---	---	no IPS match
985433	---	---	no IPS match
985433	---	---	no IPS match
985462	---	---	no IPS match
985462	---	---	mobidb-lite (MOBIDB_LITE)
985479	EC:2.4.1.1	Glycogen phosphorylase	G3DSA:3.40.50.2000 (GENE3D); IPR000811 (PFAM); PTHR11468:SF26 (PANTHER); IPR000811 (PANTHER); SSF53756 (SUPERFAMILY)
985498	EC:6.1.1.4; EC:3.1.1.1	Leucine--tRNA ligase; Carboxylesterase	IPR009008 (G3DSA:3.90.740.GENE3D); IPR009008 (SUPERFAMILY)

Genome Scaffold	Enzyme Codes	Enzyme Names	InterPro IDs
985499	---	---	IPR013937 (PFAM); IPR034905 (PTHR22775:PANTHER); PTHR22775 (PANTHER)
985499	---	---	no IPS match
985500	---	---	no IPS match
985500	---	---	IPR002423 (PFAM); IPR027413 (G3DSA:1.10.560.GENE3D); IPR027413 (SUPERFAMILY)
985500	EC:3.2.1.15	Polygalacturonase	no IPS match
985500	---	---	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR027106 (PANTHER); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR036322 (SUPERFAMILY)
985500	---	---	mobidb-lite (MOBIDB_LITE)
985515	---	---	no IPS match
985515	---	---	no IPS match
985515	EC:3.2.1.31	Beta-glucuronidase	no IPS match
985515	---	---	mobidb-lite (MOBIDB_LITE)
985516	---	---	PTHR12236:SF42 (PANTHER); PTHR12236 (PANTHER)
985522	---	---	no IPS match
985525	EC:1.1.1.1	Alcohol dehydrogenase	no IPS match
985526	---	---	G3DSA:3.30.710.10 (GENE3D)
985527	EC:3.6.1.15	Nucleoside-triphosphate phosphatase	no IPS match
985535	EC:2.4.2.1; EC:2.4.2.28	Purine-nucleoside phosphorylase; S-methyl-5'-thioadenosine phosphorylase	no IPS match

Genome Scaffold	Enzyme Codes	Enzyme Names	InterPro IDs
985535	EC:1.11.1.7; EC:1.11.1.6	Peroxidase; Catalase	IPR011614 (PFAM); IPR037060 (G3DSA:2.40.180.GENE3D); IPR018028 (PANTHER); PTHR11465:SF32 (PANTHER); IPR018028 (PROSITE_PROFILES); IPR020835 (SUPERFAMILY)
985535	---	---	no IPS match
985535	EC:2.4.2.1; EC:2.4.2.28	Purine-nucleoside phosphorylase; S-methyl-5'-thioadenosine phosphorylase	IPR000845 (PFAM); G3DSA:3.40.50.1580 (GENE3D); IPR035994 (SUPERFAMILY)
985545	EC:3.6.1.15	Nucleoside-triphosphate phosphatase	IPR000897 (PFAM)
985556	---	---	IPR014712 (G3DSA:1.20.58.GENE3D); IPR011417 (PFAM); PTHR22951:SF5 (PANTHER); PTHR22951 (PANTHER); SSF89009 (SUPERFAMILY)
985556	---	---	no IPS match
985558	---	---	no IPS match
985558	---	---	no IPS match

Genome Scaffold	InterPro GO IDs	InterPro GO Names
962832	no GO terms	no GO terms
974948	no GO terms	no GO terms
983688	no IPS match	no IPS match
983860	no GO terms	no GO terms
984571	F:GO:0005509; C:GO:0016020; P:GO:0007156	F:calcium ion binding; C:membrane; P:homophilic cell adhesion via plasma membrane adhesion molecules
984762	C:GO:0005634	C:nucleus
984762	F:GO:0003951; P:GO:0008152; F:GO:0016301	F:NAD+ kinase activity; P:metabolic process; F:kinase activity
984762	F:GO:0004143; P:GO:0007205	F:diacylglycerol kinase activity; P:protein kinase C-activating G-protein coupled receptor signaling pathway
984762	no GO terms	no GO terms
984762	C:GO:0016459; F:GO:0005524; F:GO:0003774	C:myosin complex; F:ATP binding; F:motor activity
984762	F:GO:0005524; F:GO:0004672; P:GO:0006468	F:ATP binding; F:protein kinase activity; P:protein phosphorylation
984762	no IPS match	no IPS match
984762	no GO terms	no GO terms
984762	no IPS match	no IPS match
984762	no IPS match	no IPS match
985141	no IPS match	no IPS match
985155	no IPS match	no IPS match
985222	no GO terms	no GO terms
985222	no GO terms	no GO terms
985222	no GO terms	no GO terms
985250	no IPS match	no IPS match
985266	no IPS match	no IPS match

Genome Scaffold	InterPro GO IDs	InterPro GO Names
985291	no GO terms	no GO terms
985291	F:GO:0016491	F:oxidoreductase activity
985291	no GO terms	no GO terms
985291	no GO terms	no GO terms
985291	no GO terms	no GO terms
985293	F:GO:0005509; C:GO:0016020; P:GO:0007156	F:calcium ion binding; C:membrane; P:homophilic cell adhesion via plasma membrane adhesion molecules
985293	F:GO:0005509; C:GO:0016020	F:calcium ion binding; C:membrane
985293	no IPS match	no IPS match
985293	no GO terms	no GO terms
985293	F:GO:0005509; C:GO:0016020	F:calcium ion binding; C:membrane
985304	no IPS match	no IPS match
985309	no GO terms	no GO terms
985370	no IPS match	no IPS match
985370	no GO terms	no GO terms
985400	no IPS match	no IPS match
985400	no IPS match	no IPS match
985400	F:GO:0003676	F:nucleic acid binding
985402	no IPS match	no IPS match
985402	no IPS match	no IPS match
985402	F:GO:0003735; C:GO:0005840; P:GO:0006412	F:structural constituent of ribosome; C:ribosome; P:translation
985402	no GO terms	no GO terms
985403	no IPS match	no IPS match
985403	no IPS match	no IPS match
985403	no IPS match	no IPS match
985403	F:GO:0005515	F:protein binding

Genome Scaffold	InterPro GO IDs	InterPro GO Names
985403	no IPS match	no IPS match
985403	no GO terms	no GO terms
985403	no IPS match	no IPS match
985424	F:GO:0005506; F:GO:0016705; P:GO:0055114; F:GO:0020037	F:iron ion binding; F:oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen; P:oxidation-reduction process; F:heme binding
985424	no IPS match	no IPS match
985433	no IPS match	no IPS match
985433	C:GO:0005813; P:GO:0060271; P:GO:0034454; P:GO:0071539	C:centrosome; P:cilium assembly; P:microtubule anchoring at centrosome; P:protein localization to centrosome
985433	no IPS match	no IPS match
985433	no GO terms	no GO terms
985433	F:GO:0016887; F:GO:0003777; C:GO:0005858; P:GO:0003341; P:GO:0007018	F:ATPase activity; F:microtubule motor activity; C:axonemal dynein complex; P:cilium movement; P:microtubule-based movement
985433	no GO terms	no GO terms
985433	no IPS match	no IPS match
985433	no GO terms	no GO terms
985433	F:GO:0004435; P:GO:0007165; P:GO:0006629; F:GO:0008081; P:GO:0035556	F:phosphatidylinositol phospholipase C activity; P:signal transduction; P:lipid metabolic process; F:phosphoric diester hydrolase activity; P:intracellular signal transduction
985433	no IPS match	no IPS match
985433	no IPS match	no IPS match
985433	no IPS match	no IPS match
985462	no IPS match	no IPS match
985462	no GO terms	no GO terms

Genome Scaffold	InterPro GO IDs	InterPro GO Names
985479	F:GO:0008184; P:GO:0005975	F:glycogen phosphorylase activity; P:carbohydrate metabolic process
985498	P:GO:0006418; F:GO:0002161	P:tRNA aminoacylation for protein translation; F:aminoacyl-tRNA editing activity
985499	P:GO:0030512	P:negative regulation of transforming growth factor beta receptor signaling pathway
985499	no IPS match	no IPS match
985500	no IPS match	no IPS match
985500	F:GO:0005524	F:ATP binding
985500	no IPS match	no IPS match
985500	F:GO:0005515	F:protein binding
985500	no GO terms	no GO terms
985515	no IPS match	no IPS match
985515	no IPS match	no IPS match
985515	no IPS match	no IPS match
985515	no GO terms	no GO terms
985516	no GO terms	no GO terms
985522	no IPS match	no IPS match
985525	no IPS match	no IPS match
985526	no GO terms	no GO terms
985527	no IPS match	no IPS match
985535	no IPS match	no IPS match
985535	P:GO:0006979; F:GO:0004096; P:GO:0055114; F:GO:0020037	P:response to oxidative stress; F:catalase activity; P:oxidation-reduction process; F:heme binding
985535	no IPS match	no IPS match
985535	F:GO:0003824; P:GO:0009116	F:catalytic activity; P:nucleoside metabolic process

Genome Scaffold	InterPro GO IDs	InterPro GO Names
985545	F:GO:0005525; P:GO:0006614	F:GTP binding; P:SRP-dependent cotranslational protein targeting to membrane
985556	P:GO:0048268; F:GO:0030276; C:GO:0030136; F:GO:0005543; F:GO:0005545	P:clathrin coat assembly; F:clathrin binding; C:clathrin-coated vesicle; F:phospholipid binding; F:1-phosphatidylinositol binding
985556	no IPS match	no IPS match
985558	no IPS match	no IPS match
985558	no IPS match	no IPS match

Table A.4. Gene Ontologies for 40 loci significant contributions to PC3 of a PCA of 175 wild MPB.

Genome Scaffold	Scaffold Position	Description	#Hits
927062	425	alpha-catulin isoform X2	20
976802	2606	tetratricopeptide repeat 28	20
980374	4878	DNA ligase 1-like	20
984523	212182	ephrin type-A receptor 4-A isoform X5	6
984523	623275	sodium nucleoside cotransporter 2-like	12
984523	461525	transmembrane 145-like	20
984677	905587	SWI SNF complex subunit SMARCC2	20
985018	22496	glucose dehydrogenase [quinone]	20
985018	38603	Glucose dehydrogenase [quinone]	20
985018	38355	glucose dehydrogenase [quinone] isoform X1	20
985018	38150	Glucose dehydrogenase [quinone]	20
985126	47948	apoptosis-inducing factor 3 isoform X1	6
985126	104095	carboxypeptidase D	20
985126	320768	AGAP002961	20
985126	71056	ruvB-like 2	20
985126	309624	hypothetical protein YQE_08388, partial	3
985126	1145184	fatty acid synthase-like	20
985126	1142317	fatty acid synthase-like	20
985126	1146307	fatty acid synthase-like	2
985126	1128096	fatty acid synthase-like	7
985126	281076	hypothetical protein YQE_08383, partial	1
985126	1127499	fatty acid synthase-	3
985126	305283	alpha-tocopherol transfer -like	20
985126	1173901	rac GTPase-activating 1	6
985126	125775	Kinesin KIF12	20
985126	1137620	fatty acid synthase-like	20

Genome Scaffold	Scaffold Position	Description	#Hits
985491	143056	probable 3 ,5 -cyclic phosphodiesterase pde-5 isoform X2	20
985529	91105	peptidoglycan-recognition LB-like isoform X1	20
985529	1171712	cullin-2 isoform X2	20
985529	116673	histone-lysine N-methyltransferase pr-set7 isoform X1	20
985529	1146792	nicastrin isoform X1	20
985529	1158842	clathrin heavy chain	20
985529	302716	alpha-catulin isoform X2	20
985529	1141744	FAM188A homolog	20
985529	1210354	arginine-glutamic acid dipeptide repeats -like	3
985529	244341	scavenger receptor class B member 1-like isoform X1	4
985529	628085	chitooligosaccharidolytic beta-N-acetylglucosaminidase-like	3
985529	1225530	fatty acyl- reductase CG5065	20
985554	892627	cytosolic 10-formyltetrahydrofolate dehydrogenase	20
985554	1004091	fatty acyl- reductase CG5065	20

Genome Scaffold	e-Value	sim mean	#GO	GO IDs
927062	1.63E-15	100	5	F:GO:0051015; F:GO:0045296; P:GO:0007155; P:GO:0007266; C:GO:0005622
976802	5.33E-14	90.35	3	C:GO:0005813; C:GO:0030496; P:GO:0007346
980374	1.22E-10	90.45	4	F:GO:0008270; F:GO:0003779; P:GO:0009253; F:GO:0008745
984523	1.15E-38	94.83	2	F:GO:0004672; P:GO:0006468
984523	3.87E-15	67.92	3	F:GO:0005337; C:GO:0016021; P:GO:1901642
984523	4.24E-14	85.95	3	P:GO:0007186; C:GO:0016021; P:GO:0019236
984677	1.46E-14	100	4	F:GO:0003677; C:GO:0090544; P:GO:0006338; P:GO:0006357
985018	8.70E-42	68.3	3	F:GO:0016614; F:GO:0050660; P:GO:0055114
985018	2.78E-16	94.4	6	P:GO:0005975; F:GO:0016614; F:GO:0050660; P:GO:0055114; F:GO:0004553; F:GO:0042302
985018	1.93E-11	92	8	F:GO:0016614; P:GO:0008364; F:GO:0050660; P:GO:0046693; P:GO:0019233; P:GO:0055114; C:GO:0005576; P:GO:0006006
985018	7.62E-15	88.65	5	P:GO:0005975; F:GO:0016614; F:GO:0050660; P:GO:0055114; F:GO:0004553
985126	3.10E-09	100	7	C:GO:0005623; F:GO:0016491; F:GO:0046872; F:GO:0050660; P:GO:0045454; P:GO:0055114; F:GO:0051537
985126	1.65E-35	76.2	4	F:GO:0008270; F:GO:0004181; P:GO:0006508; F:GO:0004185
985126	5.10E-20	85	1	C:GO:0016021
985126	1.38E-14	96.8	7	C:GO:0005634; F:GO:0005524; P:GO:0006281; F:GO:0043141; P:GO:0006351; P:GO:0032508; P:GO:0006355
985126	8.47E-30	96	3	F:GO:0004722; F:GO:0046872; P:GO:0006470
985126	4.61E-39	78.6	5	F:GO:0016491; F:GO:0016829; F:GO:0016297; P:GO:0055114; F:GO:0031177

Genome Scaffold	e-Value	sim mean	#GO	GO IDs
985126	6.31E-41	78.85	4	F:GO:0016491; P:GO:0055114; F:GO:0031177; F:GO:0016740
985126	4.51E-35	100	3	F:GO:0016491; P:GO:0055114; F:GO:0016740
985126	4.42E-24	84.86	6	F:GO:0016788; F:GO:0016491; P:GO:0055114; F:GO:0031177; P:GO:0009058; F:GO:0016740
985126	6.53E-14	82	2	C:GO:0016021; F:GO:0046983
985126	1.35E-16	97	6	F:GO:0016788; F:GO:0016491; P:GO:0055114; F:GO:0031177; P:GO:0009058; F:GO:0016740
985126	1.39E-28	71.6	4	F:GO:0003924; P:GO:0006810; C:GO:0005622; F:GO:0005215
985126	9.40E-36	78	3	F:GO:0046872; C:GO:0005622; P:GO:0035556
985126	3.01E-20	84.5	7	F:GO:0005524; P:GO:0005975; F:GO:0003777; P:GO:0007018; C:GO:0005874; F:GO:0008017; F:GO:0016853
985126	3.66E-17	98.6	4	F:GO:0016491; P:GO:0055114; F:GO:0031177; F:GO:0016740
985491	5.88E-32	91.95	3	F:GO:0046872; P:GO:0007165; F:GO:0004114
985529	1.18E-18	83.3	5	F:GO:0008270; F:GO:0003779; P:GO:0009253; F:GO:0008745; P:GO:0002376
985529	1.20E-27	87.1	3	F:GO:0031625; C:GO:0031461; P:GO:0006511
985529	1.32E-14	88.3	4	P:GO:0016192; P:GO:0034968; C:GO:0016021; F:GO:0018024
985529	2.89E-08	93.25	3	F:GO:0005509; C:GO:0016021; P:GO:0016485
985529	1.65E-31	97.3	5	P:GO:0016192; C:GO:0030130; C:GO:0030132; F:GO:0005198; P:GO:0006886
985529	9.59E-30	98.6	5	F:GO:0051015; F:GO:0045296; P:GO:0007155; P:GO:0007266; C:GO:0005622
985529	7.09E-26	88.4	3	F:GO:0005509; C:GO:0016021; P:GO:0016485
985529	5.74E-33	99.33	5	C:GO:0005634; F:GO:0003700; F:GO:0008270; P:GO:0006355; F:GO:0043565

Genome Scaffold	e-Value	sim mean	#GO	GO IDs
985529	5.67E-13	100	1	C:GO:0016021
985529	2.54E-34	96.67	2	P:GO:0005975; F:GO:0004563
985529	1.02E-31	76.4	3	C:GO:0016020; P:GO:0055114; F:GO:0080019
985554	1.02E-33	83.95	10	C:GO:0005737; F:GO:0004618; P:GO:0006096; P:GO:0009258; F:GO:0016155; P:GO:0055114; P:GO:0009058; F:GO:0016620; F:GO:0016742; P:GO:0006730
985554	4.22E-26	71.6	3	C:GO:0016021; P:GO:0055114; F:GO:0080019

Genome Scaffold	GO Names
927062	F:actin filament binding; F:cadherin binding; P:cell adhesion; P:Rho protein signal transduction; C:intracellular
976802	C:centrosome; C:midbody; P:regulation of mitotic cell cycle
980374	F:zinc ion binding; F:actin binding; P:peptidoglycan catabolic process; F:N-acetylmuramoyl-L-alanine amidase activity
984523	F:protein kinase activity; P:protein phosphorylation
984523	F:nucleoside transmembrane transporter activity; C:integral component of membrane; P:nucleoside transmembrane transport
984523	P:G-protein coupled receptor signaling pathway; C:integral component of membrane; P:response to pheromone
984677	F:DNA binding; C:BAF-type complex; P:chromatin remodeling; P:regulation of transcription from RNA polymerase II promoter
985018	F:oxidoreductase activity, acting on CH-OH group of donors; F:flavin adenine dinucleotide binding; P:oxidation-reduction process
985018	P:carbohydrate metabolic process; F:oxidoreductase activity, acting on CH-OH group of donors; F:flavin adenine dinucleotide binding; P:oxidation-reduction process; F:hydrolase activity, hydrolyzing O-glycosyl compounds; F:structural constituent of cuticle
985018	F:oxidoreductase activity, acting on CH-OH group of donors; P:pupal chitin-based cuticle development; F:flavin adenine dinucleotide binding; P:sperm storage; P:sensory perception of pain; P:oxidation-reduction process; C:extracellular region; P:glucose metabolic process
985018	P:carbohydrate metabolic process; F:oxidoreductase activity, acting on CH-OH group of donors; F:flavin adenine dinucleotide binding; P:oxidation-reduction process; F:hydrolase activity, hydrolyzing O-glycosyl compounds
985126	C:cell; F:oxidoreductase activity; F:metal ion binding; F:flavin adenine dinucleotide binding; P:cell redox homeostasis; P:oxidation-reduction process; F:2 iron, 2 sulfur cluster binding
985126	F:zinc ion binding; F:metallocarboxypeptidase activity; P:proteolysis; F:serine-type carboxypeptidase activity
985126	C:integral component of membrane
985126	C:nucleus; F:ATP binding; P:DNA repair; F:ATP-dependent 5'-3' DNA helicase activity; P:transcription, DNA-templated; P:DNA duplex unwinding; P:regulation of transcription, DNA-templated
985126	F:protein serine/threonine phosphatase activity; F:metal ion binding; P:protein dephosphorylation
985126	F:oxidoreductase activity; F:lyase activity; F:acyl-[acyl-carrier-protein] hydrolase activity; P:oxidation-reduction process; F:phosphopantetheine binding
985126	F:oxidoreductase activity; P:oxidation-reduction process; F:phosphopantetheine binding; F:transferase activity

Genome Scaffold	GO Names
985126	F:oxidoreductase activity; P:oxidation-reduction process; F:transferase activity
985126	F:hydrolase activity, acting on ester bonds; F:oxidoreductase activity; P:oxidation-reduction process; F:phosphopantetheine binding; P:biosynthetic process; F:transferase activity
985126	C:integral component of membrane; F:protein dimerization activity
985126	F:hydrolase activity, acting on ester bonds; F:oxidoreductase activity; P:oxidation-reduction process; F:phosphopantetheine binding; P:biosynthetic process; F:transferase activity
985126	F:GTPase activity; P:transport; C:intracellular; F:transporter activity
985126	F:metal ion binding; C:intracellular; P:intracellular signal transduction
985126	F:ATP binding; P:carbohydrate metabolic process; F:microtubule motor activity; P:microtubule-based movement; C:microtubule; F:microtubule binding; F:isomerase activity
985126	F:oxidoreductase activity; P:oxidation-reduction process; F:phosphopantetheine binding; F:transferase activity
985491	F:metal ion binding; P:signal transduction; F:3',5'-cyclic-nucleotide phosphodiesterase activity
985529	F:zinc ion binding; F:actin binding; P:peptidoglycan catabolic process; F:N-acetylmuramoyl-L-alanine amidase activity; P:immune system process
985529	F:ubiquitin protein ligase binding; C:cullin-RING ubiquitin ligase complex; P:ubiquitin-dependent protein catabolic process
985529	P:vesicle-mediated transport; P:histone lysine methylation; C:integral component of membrane; F:histone-lysine N-methyltransferase activity
985529	F:calcium ion binding; C:integral component of membrane; P:protein processing
985529	P:vesicle-mediated transport; C:clathrin coat of trans-Golgi network vesicle; C:clathrin coat of coated pit; F:structural molecule activity; P:intracellular protein transport
985529	F:actin filament binding; F:cadherin binding; P:cell adhesion; P:Rho protein signal transduction; C:intracellular
985529	F:calcium ion binding; C:integral component of membrane; P:protein processing
985529	C:nucleus; F:transcription factor activity, sequence-specific DNA binding; F:zinc ion binding; P:regulation of transcription, DNA-templated; F:sequence-specific DNA binding
985529	C:integral component of membrane
985529	P:carbohydrate metabolic process; F:beta-N-acetylhexosaminidase activity
985529	C:membrane; P:oxidation-reduction process; F:fatty-acyl-CoA reductase (alcohol-forming) activity
985554	C:cytoplasm; F:phosphoglycerate kinase activity; P:glycolytic process; P:10-formyltetrahydrofolate catabolic process; F:formyltetrahydrofolate dehydrogenase

Genome Scaffold	GO Names
	activity; P:oxidation-reduction process; P:biosynthetic process; F:oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor; F:hydroxymethyl-, formyl- and related transferase activity; P:one-carbon metabolic process
985554	C:integral component of membrane; P:oxidation-reduction process; F:fatty-acyl-CoA reductase (alcohol-forming) activity

Genome Scaffold	Enzyme Codes	Enzyme Names	InterPro IDs
927062	---	---	IPR036723 (SUPERFAMILY)
976802	---	---	no IPS match
980374	EC:3.5.1.28	N-acetylmuramoyl-L-alanine amidase	no IPS match
984523	---	---	no IPS match
984523	---	---	no IPS match
984523	---	---	no IPS match
984677	---	---	no IPS match
985018	---	---	no IPS match
985018	---	---	no IPS match
985018	---	---	mobidb-lite (MOBIDB_LITE)
985018	---	---	no IPS match
985126	---	---	no IPS match
985126	EC:3.4.21; EC:3.4.17; EC:3.4.16	Acting on peptide bonds (peptidases); Acting on peptide bonds (peptidases); Acting on peptide bonds (peptidases)	IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11532 (PANTHER); PTHR11532:SF77 (PANTHER); SSF53187 (SUPERFAMILY)
985126	---	---	no IPS match
985126	EC:3.6.1.3; EC:3.6.1.15	Adenosinetriphosphatase; Nucleoside-triphosphate phosphatase	G3DSA:3.40.50.300 (GENE3D); IPR010339 (PFAM); PTHR11093:SF2 (PANTHER); IPR027238 (PANTHER)
985126	EC:3.1.3.16; EC:3.1.3.41	Protein-serine/threonine phosphatase; 4-nitrophenylphosphatase	mobidb-lite (MOBIDB_LITE)
985126	EC:2.3.1.85; EC:3.1.2.14	Fatty-acid synthase; Oleoyl-[acyl-carrier-protein] hydrolase	no IPS match
985126	---	---	PTHR43775 (PANTHER); PTHR43775:SF9 (PANTHER)
985126	---	---	no IPS match
985126	---	---	no IPS match
985126	---	---	no IPS match
985126	---	---	no IPS match

Genome Scaffold	Enzyme Codes	Enzyme Names	InterPro IDs
985126	EC:3.6.1.15	Nucleoside-triphosphate phosphatase	IPR036865 (G3DSA:3.40.525.GENE3D); IPR036865 (SUPERFAMILY)
985126	---	---	no IPS match
985126	EC:3.6.1.15	Nucleoside-triphosphate phosphatase	IPR001752 (PROSITE_PROFILES)
985126	---	---	no IPS match
985491	EC:3.1.4.17	3',5'-cyclic-nucleotide phosphodiesterase	IPR023088 (PRINTS); IPR002073 (PFAM); IPR036971 (G3DSA:1.10.1300.GENE3D); PTHR11347 (PANTHER); PTHR11347:SF111 (PANTHER); SSF109604 (SUPERFAMILY)
985529	EC:3.5.1.28	N-acetylmuramoyl-L-alanine amidase	no IPS match
985529	---	---	G3DSA:1.20.1310.10 (GENE3D); IPR016159 (SUPERFAMILY)
985529	EC:2.1.1.43	Histone-lysine N-methyltransferase	no IPS match
985529	---	---	IPR008710 (PFAM)
985529	---	---	PTHR10292 (PANTHER); PTHR10292:SF6 (PANTHER); IPR000547 (PROSITE_PROFILES); IPR016024 (SUPERFAMILY)
985529	---	---	IPR030045 (PTHR18914:PANTHER); IPR006077 (PANTHER); IPR036723 (SUPERFAMILY)
985529	---	---	no IPS match
985529	---	---	mobidb-lite (MOBIDB_LITE)
985529	---	---	no IPS match
985529	EC:3.2.1.52	Beta-N-acetylhexosaminidase	no IPS match
985529	---	---	IPR013120 (PFAM)
985554	EC:2.7.2.3; EC:1.5.1.6	Phosphoglycerate kinase; Formyltetrahydrofolate dehydrogenase	IPR036736 (G3DSA:1.10.1200.GENE3D); IPR009081 (PFAM); IPR009081 (PROSITE_PROFILES); IPR036736 (SUPERFAMILY)
985554	---	---	no IPS match

Genome Scaffold	InterPro GO IDs	InterPro GO Names
927062	F:GO:0051015; P:GO:0007155	F:actin filament binding; P:cell adhesion
976802	no IPS match	no IPS match
980374	no IPS match	no IPS match
984523	no IPS match	no IPS match
984523	no IPS match	no IPS match
984523	no IPS match	no IPS match
984677	no IPS match	no IPS match
985018	no IPS match	no IPS match
985018	no IPS match	no IPS match
985018	no GO terms	no GO terms
985018	no IPS match	no IPS match
985126	no IPS match	no IPS match
985126	F:GO:0008270; F:GO:0004181; P:GO:0006508	F:zinc ion binding; F:metallocarboxypeptidase activity; P:proteolysis
985126	no IPS match	no IPS match
985126	F:GO:0005524; F:GO:0003678; F:GO:0043141; C:GO:0031011	F:ATP binding; F:DNA helicase activity; F:ATP-dependent 5'-3' DNA helicase activity; C:Ino80 complex
985126	no GO terms	no GO terms
985126	no IPS match	no IPS match
985126	no GO terms	no GO terms
985126	no IPS match	no IPS match
985126	no IPS match	no IPS match
985126	no IPS match	no IPS match
985126	no IPS match	no IPS match
985126	no GO terms	no GO terms
985126	no IPS match	no IPS match
985126	F:GO:0005524; F:GO:0003777; P:GO:0007018; F:GO:0008017	F:ATP binding; F:microtubule motor activity; P:microtubule-based movement; F:microtubule binding

Genome Scaffold	InterPro GO IDs	InterPro GO Names
985126	no IPS match	no IPS match
985491	P:GO:0007165; F:GO:0008081; F:GO:0004114	P:signal transduction; F:phosphoric diester hydrolase activity; F:3',5'-cyclic-nucleotide phosphodiesterase activity
985529	no IPS match	no IPS match
985529	no GO terms	no GO terms
985529	no IPS match	no IPS match
985529	C:GO:0016021; P:GO:0016485	C:integral component of membrane; P:protein processing
985529	P:GO:0016192; P:GO:0006886; F:GO:0005488	P:vesicle-mediated transport; P:intracellular protein transport; F:binding
985529	F:GO:0051015; P:GO:0007155; P:GO:0007266	F:actin filament binding; P:cell adhesion; P:Rho protein signal transduction
985529	no IPS match	no IPS match
985529	no GO terms	no GO terms
985529	no IPS match	no IPS match
985529	no IPS match	no IPS match
985529	no GO terms	no GO terms
985554	no GO terms	no GO terms
985554	no IPS match	no IPS match

Table A.5. Gene Ontologies for 12 loci significant contributions to PC4 of a PCA of 175 wild MPB.

Genome Scaffold	Scaffold Position	Description	#Hits
985381	46712	hypothetical protein D910_08015	7
985381	98975	active breakpoint cluster region-related -like isoform X4	20
985381	120864	inducible metallo ase inhibitor -like	20
985381	421402	hypothetical protein D910_08043	1
985381	583192	sphingosine-1-phosphate lyase	20
985381	613144	dedicator of cytokinesis 7	20
985381	670530	ubiquitin carboxyl-terminal hydrolase 35	20
985381	678604	60S ribosomal L28	20
985381	709177	DNA-directed RNA polymerase III subunit RPC5	5
985450	96620	glutamate receptor NMDA 2D-like	3
985450	104269	methyltransferase 9	20
985450	201233	zinc finger homeobox 3 isoform X1	20

Genome Scaffold	e-Value	sim mean	#GO	GO IDs
985381	3.87E-23	85.57	2	F:GO:0051015; P:GO:0007010
985381	3.88E-30	78	7	P:GO:0035023; P:GO:0007165; F:GO:0005096; F:GO:0005089; F:GO:0004674; P:GO:0006468; P:GO:0043547
985381	2.50E-15	78.7	2	P:GO:0006508; F:GO:0008233
985381	1.01E-29	100	3	P:GO:0006355; F:GO:0046983; P:GO:0022008
985381	2.35E-36	79.85	3	F:GO:0030170; P:GO:0019752; F:GO:0016831
985381	1.61E-36	88.25	4	P:GO:0007264; F:GO:0005085; C:GO:0005622; P:GO:0043547
985381	6.23E-36	80.4	3	P:GO:0016579; F:GO:0036459; P:GO:0006511
985381	4.29E-10	86.25	3	F:GO:0003735; C:GO:0005840; P:GO:0006412
985381	5.18E-38	74.2	3	C:GO:0005634; F:GO:0003899; P:GO:0006351
985450	5.37E-09	100	7	C:GO:0045211; P:GO:0034220; C:GO:0016021; C:GO:0030054; P:GO:0035235; F:GO:0004970; F:GO:0005234
985450	2.47E-17	89.15	3	F:GO:0008270; F:GO:0008168; P:GO:0032259
985450	1.48E-39	96.85	4	C:GO:0005634; F:GO:0008270; P:GO:0006355; F:GO:0043565

Genome Scaffold	GO Names
985381	F:actin filament binding; P:cytoskeleton organization
985381	P:regulation of Rho protein signal transduction; P:signal transduction; F:GTPase activator activity; F:Rho guanyl-nucleotide exchange factor activity; F:protein serine/threonine kinase activity; P:protein phosphorylation; P:positive regulation of GTPase activity
985381	P:proteolysis; F:peptidase activity
985381	P:regulation of transcription, DNA-templated; F:protein dimerization activity; P:neurogenesis
985381	F:pyridoxal phosphate binding; P:carboxylic acid metabolic process; F:carboxy-lyase activity
985381	P:small GTPase mediated signal transduction; F:guanyl-nucleotide exchange factor activity; C:intracellular; P:positive regulation of GTPase activity
985381	P:protein deubiquitination; F:thiol-dependent ubiquitinyl hydrolase activity; P:ubiquitin-dependent protein catabolic process
985381	F:structural constituent of ribosome; C:ribosome; P:translation
985381	C:nucleus; F:DNA-directed 5'-3' RNA polymerase activity; P:transcription, DNA-templated
985450	C:postsynaptic membrane; P:ion transmembrane transport; C:integral component of membrane; C:cell junction; P:ionotropic glutamate receptor signaling pathway; F:ionotropic glutamate receptor activity; F:extracellular-glutamate-gated ion channel activity
985450	F:zinc ion binding; F:methyltransferase activity; P:methylation
985450	C:nucleus; F:zinc ion binding; P:regulation of transcription, DNA-templated; F:sequence-specific DNA binding

Genome Scaffold	Enzyme Codes	Enzyme Names	InterPro IDs
985381	---	---	mobidb-lite (MOBIDB_LITE)
985381	EC:2.7.11	Transferring phosphorus-containing groups	G3DSA:1.20.900.10 (GENE3D); PTHR23182 (PANTHER); PTHR23182:SF9 (PANTHER)
985381	---	---	no IPS match
985381	---	---	mobidb-lite (MOBIDB_LITE)
985381	---	---	IPR015421 (G3DSA:3.40.640.GENE3D); PTHR42735 (PANTHER); PTHR42735:SF2 (PANTHER); IPR015424 (SUPERFAMILY)
985381	---	---	no IPS match
985381	EC:3.4.19.12	Ubiquitinyl hydrolase 1	IPR001394 (PFAM); G3DSA:3.90.70.10 (GENE3D); SSF54001 (SUPERFAMILY)
985381	---	---	no IPS match
985381	EC:2.7.7.6	DNA-directed RNA polymerase	mobidb-lite (MOBIDB_LITE)
985450	---	---	no IPS match
985450	---	---	IPR007884 (PFAM)
985450	---	---	PTHR24208 (PANTHER); PTHR24208:SF140 (PANTHER); IPR013087 (PROSITE_PROFILES); IPR013087 (SUPERFAMILY)

Genome Scaffold	InterPro GO IDs	InterPro GO Names
985381	no GO terms	no GO terms
985381	no GO terms	no GO terms
985381	no IPS match	no IPS match
985381	no GO terms	no GO terms
985381	F:GO:0003824	F:catalytic activity
985381	no IPS match	no IPS match
985381	P:GO:0016579; F:GO:0036459	P:protein deubiquitination; F:thiol-dependent ubiquitinyl hydrolase activity
985381	no IPS match	no IPS match
985381	no GO terms	no GO terms
985450	no IPS match	no IPS match
985450	no GO terms	no GO terms
985450	F:GO:0003676	F:nucleic acid binding

Table A.6. Homologous BLAST hits on the genome of *Tribolium castaneum* chromosomes for *D. ponderosae* loci with high-weight contribution to PC axes 1-4 (see **Figure 3.2**). PC1 refers only to loci that did not overlap with PC3. BLAST results for all positive hits on *T. castaneum* are listed, even if mapping and gene annotation for loci was unavailable. Loci that did not have homologous hits on *T. castaneum* are not listed.

T. castaneum chromosome	PC 1	PC 2	PC 3	PC4
X	0	1	0	0
1	0	0	0	0
2	0	18	0	1
3	2	3	6	7
4	1	44	0	0
5	1	0	0	1
6	3	0	22	0
7	1	3	0	0
8	0	2	4	1
9	1	2	2	0
10	1	5	0	0

Table A.7. SNP correspondences among LDna cohorts and PCA cohorts (PC loading >0.050), expanded from those shown in **Figure 3.5**.

		PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
	Total SNPs	103	217	88	37	66	84	75	77
Cluster X	108	0	108	0	0	0	0	0	0
Cluster Xa	8	0	0	0	0	5	5	0	0
Cluster Xb	12	0	1	0	0	3	8	0	0
Cluster Xc	9	0	0	0	0	1	1	0	0
Cluster A	71	55	0	70	0	0	2	0	0
Cluster Aa	19	19	0	0	0	0	13	0	19
Cluster Aa	12	9	0	2	0	1	0	0	1
Cluster B	24	0	0	0	24	1	1	1	0
PC1	103	103	--	--	--	--	--	--	--
PC2	217	0	217	--	--	--	--	--	--
PC3	88	57	0	88	--	--	--	--	--
PC4	37	0	0	0	37	--	--	--	--
PC5	66	1	1	0	8	66	--	--	--
PC6	84	13	2	3	7	23	84	--	--
PC7	75	0	0	1	5	4	8	75	--
PC8	77	22	0	0	0	4	16	6	77

Table A.8. Pedigree and emergence information for wild P crosses used in the linkage map. Wild BQ bolts were collected from Burnco Quarry, Canmore, AB. SRL bolts were collected from Smokey River Lowlands, Grande Prairie, AB. The number of larval galleries refers only to the main gallery established by researchers, and does not account for beetles colonizing the bolt in a secondary infestation

Bolt ID	F1♀ Bolt	F1♂ Bolt	F1♀ Emerg	F1♂ Emerg	Inoc. Date	2° Infes.	# of Larvae	F2 ♀	F2 ♂	Total
A	BQ4	BQ9	13-May	19-May	15-May	N	124	20	14	34
B	BQ1	BQ4	14-May	17-May	15-May	N	0	4	2	6
C	SRL23	BQ9	19-May	20-May	30-May	N	179	59	17	76
D	BQ9	BQ9	20-May	21-May	30-May	Y	174	29	10	39
E	SRL23	BQ9	21-May	18-May	30-May	Y	163	33	16	49
F	BQ4	BQ9	21-May	22-May	30-May	Y	0	2	2	4
G	SRL23	BQ9	21-May	22-May	30-May	Y	34	9	0	9
H	BQ9	BQ4	21-May	17-May	30-May	N	28	0	2	2
I	BQ9	BQ9	20-May	22-May	30-May	Y	83	9	4	13
J	SRL23	BQ9	22-May	22-May	30-May	N	84	8	2	10
K	BQ9	SRL23	25-May	24-May	30-May	Y	102	15	9	24
L	SRL23	BQ10	25-May	6-Jun	30-May	N	74	5	1	6
M	SRL23	BQ1	26-May	5-Jun	30-May	N	160	11	4	16
N	SRL23	BQ9	26-May	26-May	30-May	N	84	12	3	15
O	SRL23	BQ9	26-May	15-Jun	30-May	Y	96	15	5	20
P	SRL23	BQ1	27-May	7-Jun	30-May	Y	0	22	18	40
Q	BQ1	SRL23	27-May	27-May	30-May	N	131	28	14	42
R	SRL14	BQ9	27-May	28-May	30-May	Y	16	14	1	15
S	SRL23	BQ9	27-May	29-May	30-May	Y	76	18	14	32
T	SRL23	BQ7	3-Jun	29-May	30-May	N	0	0	0	0
U	BQ9	SRL23	28-May	30-May	30-May	N	20	5	3	8
V	BQ1	SRL23	28-May	3-Jun	30-May	Y	242	38	22	60
W	BQ9	SRL23	28-May	28-May	30-May	N	66	4	5	9
X	BQ7	SRL23	30-May	1-Jun	30-May	N	178	15	11	26
Y	BQ9	SRL23	26-May	28-May	30-May	N	18	1	0	1
Z	BQ7	SRL23	29-May	28-May	30-May	N	199	12	7	19
Θ	BQ1	SRL23	3-Jun	4-Jun	9-Jun	Y	195	20	5	25
AA	BQ1	SRL23	4-Jun	4-Jun	9-Jun	Y	166	35	16	51
AB	BQ1	SRL23	4-Jun	5-Jun	9-Jun	Y	0	0	0	0
AC	SRL4	BQ1	4-Jun	5-Jun	9-Jun	Y	113	8	2	10
AD	BQ1	SRL18	4-Jun	17-Jun	9-Jun	N	0	0	0	0
AE	BQ9	SRL23	4-Jun	5-Jun	9-Jun	N	126	60	30	90
AF	SRL23	SRL23	4-Jun	5-Jun	9-Jun	N	104	12	2	14
AG	SRL23	BQ1	4-Jun	5-Jun	9-Jun	N	0	0	0	0
AH	BQ9	SRL23	4-Jun	5-Jun	9-Jun	N	24	53	25	78
AI	SRL23	BQ1	4-Jun	4-Jun	9-Jun	N	0	0	0	0

Bolt ID	F1♀ Bolt	F1♂ Bolt	F1♀ Emerg	F1♂ Emerg	Inoc. Date	2° Infes.	# of Larvae	F2 ♀	F2 ♂	Total
AJ	BQ1	BQ1	12-Jun	14-Jun	9-Jun	N	0	0	0	0
AK	SRL23	BQ4	5-Jun	8-Jun	9-Jun	Y	108	49	36	85
AL	SRL23	BQ9	5-Jun	8-Jun	9-Jun	N	71	6	7	13
AM	SRL23	BQ1	5-Jun	8-Jun	9-Jun	N	98	5	2	7
AN	SRL23	BQ1	5-Jun	8-Jun	9-Jun	N	110	17	18	35
AO	BQ1	SRL18	5-Jun	8-Jun	9-Jun	N	0	0	0	0
AP	BQ9	SRL18	5-Jun	8-Jun	9-Jun	N	101	19	13	32
AQ	BQ1	SRL18	5-Jun	15-Jun	9-Jun	N	0	0	0	0
AR	BQ1	SRL23	5-Jun	8-Jun	9-Jun	N	0	0	0	0
AS	SRL23	BQ1	6-Jun	8-Jun	9-Jun	N	98	15	13	28
AT	SRL23	BQ1	6-Jun	8-Jun	9-Jun	Y	108	18	19	38
AU	SRL23	BQ9	6-Jun	7-Jun	9-Jun	N	81	18	18	36
AV	SRL18	BQ7	6-Jun	7-Jun	9-Jun	Y	122	12	9	21
AW	BQ9	SRL23	6-Jun	8-Jun	9-Jun	N	186	13	12	25
AX	BQ4	SRL23	6-Jun	8-Jun	9-Jun	Y	149	22	34	56
AY	BQ4	SRL23	6-Jun	8-Jun	9-Jun	N	0	0	0	0
AZ	BQ9	SRL18	8-Jun	17-Jun	9-Jun	N	119	0	1	1
BA	BQ1	SRL23	6-Jun	15-Jun	9-Jun	N	0	0	0	0
BB	BQ10	SRL18	6-Jun	10-Jun	9-Jun	N	85	7	0	7
BC	BQ9	SRL18	7-Jun	17-Jun	9-Jun	Y	64	3	2	5
BD	BQ4	SRL18	7-Jun	9-Jun	9-Jun	Y	164	29	8	37
BE	BQ4	SRL14	7-Jun	9-Jun	9-Jun	N	201	11	2	13
BF	BQ4	SRL23	7-Jun	9-Jun	9-Jun	Y	170	20	16	36
BG	BQ1	SRL23	7-Jun	9-Jun	9-Jun	N	137	12	12	24
BH	BQ1	SRL23	7-Jun	9-Jun	9-Jun	Y	107	25	24	49
BI	BQ1	SRL23	7-Jun	9-Jun	9-Jun	Y	0	0	0	0
BJ	SRL23	BQ4	7-Jun	9-Jun	9-Jun	N	195	6	2	8
BK	SRL18	BQ1	7-Jun	9-Jun	9-Jun	Y	156	13	11	24
BL	SRL18	BQ6	7-Jun	9-Jun	9-Jun	Y	83	0	0	0
BM	SRL18	BQ4	7-Jun	9-Jun	9-Jun	Y	75	20	6	26

Table A.9. Summary of pedigrees and emergences for F1 cross used in the linkage map.

Bolt ID	F1♀ Bolt	F1♂ Bolt	F1♀ Emerg	F1♂ Emerg	Inoc. Date	Risk of False Parentage	Parents recov.	F2 ♀	F2 ♂	Total
C1	C	C	31-Jul	1-Aug	1-Aug	NONE	1	11	0	11
C2	C	C	31-Jul	3-Aug	2-Aug	NONE	-	0	0	0
C3	C	C	1-Aug	3-Aug	1-Aug	NONE	0	2	3	5
E1	E	E	31-Jul	2-Aug	1-Aug	NONE	2	4	7	12
E2	E	E	3-Aug	6-Aug	3-Aug	NONE	1	2	7	9
K1	P	P	3-Aug	6-Aug	3-Aug	LOW	1	7	11	18
K2	AF	AF	6-Aug	9-Aug	3-Aug	NONE	-	0	0	0
K3	K	K	29-Jul	31-Jul	1-Aug	LOW	1	7	5	12
M1	M	M	31-Jul	3-Aug	1-Aug	NONE	-	0	0	0
N1	N	N	31-Jul	31-Jul	1-Aug	NONE	1	8	5	13
P1	P	P	31-Jul	2-Aug	1-Aug	NA	0	1	0	1
P2	P	P	31-Jul	2-Aug	1-Aug	NA	1	0	0	0
P3	P	P	31-Jul	1-Aug	1-Aug	NA	0	0	2	2
Q1	Q	Q	31-Jul	2-Aug	1-Aug	NONE	0	4	3	7
Q2	Q	Q	29-Jul	2-Aug	1-Aug	NONE	1	5	4	9
Q3	Q	Q	29-Jul	31-Jul	1-Aug	NONE	-	0	0	0
R1	R	R	31-Jul	31-Jul	1-Aug	HIGH	-	0	0	0
S1	S	S	31-Jul	2-Aug	1-Aug	LOW	1	0	0	0
V1	V	V	31-Jul	1-Aug	1-Aug	LOW	1	2	1	3
V2	V	V	31-Jul	1-Aug	1-Aug	LOW	1	15	12	28
V3	V	V	31-Jul	1-Aug	1-Aug	LOW	1	5	6	11
V4	V	V	3-Aug	5-Aug	2-Aug	LOW	2	6	6	12
X1	Z	Z	1-Aug	1-Aug	2-Aug	NONE	0	3	0	3
Z1	Z	Z	31-Jul	31-Jul	1-Aug	NONE	-	0	0	0
Z2	Z	Z	31-Jul	31-Jul	1-Aug	NONE	1	9	8	17
Z3	Z	Z	31-Jul	8-Aug	1-Aug	NONE	-	0	0	0
AA1	AA	AA	31-Jul	2-Aug	1-Aug	NONE	-	0	0	0
AA2	Θ	Θ	3-Aug	6-Aug	3-Aug	NONE	1	4	0	4
AE1	AC	AC	1-Aug	2-Aug	2-Aug	NONE	2	5	8	13
AE2	AE	AE	31-Jul	31-Jul	1-Aug	NONE	1	6	5	11
AE3	Q	Q	3-Aug	6-Aug	3-Aug	NONE	-	0	0	0
AE4	AE	AE	30-Jul	2-Aug	1-Aug	NONE	-	0	0	0
AE5	AE	AE	6-Aug	8-Aug	3-Aug	NONE	-	0	0	0
AE6	AE	AE	30-Jul	8-Aug	1-Aug	NONE	-	0	0	0
AH1	AH	AH	6-Aug	8-Aug	4-Aug	NONE	1	2	0	3
AH2	AN	AN	1-Aug	3-Aug	2-Aug	NONE	1	13	11	24
AH3	AT	AT	1-Aug	2-Aug	2-Aug	NONE	1	4	1	5
AH4	AT	AT	1-Aug	2-Aug	2-Aug	NONE	1	9	5	14
AH5	AH	AH	31-Jul	2-Aug	1-Aug	NONE	1	6	3	9

Bolt ID	F1♀ Bolt	F1♂ Bolt	F1♀ Emerg	F1♂ Emerg	Inoc. Date	Risk of False Parentage	Parents recov.	F2 ♀	F2 ♂	Total
AH6	AH	AH	31-Jul	2-Aug	1-Aug	NONE	-	0	0	0
AH7	AH	AH	30-Jul	2-Aug	1-Aug	NONE	-	0	0	0
AH8	AT	AT	1-Aug	2-Aug	2-Aug	HIGH	1	3	1	4
AK1	AK	AK	31-Jul	2-Aug	1-Aug	HIGH	1	1	0	1
AK2	AK	AK	31-Jul	2-Aug	1-Aug	HIGH	0	1	0	1
AK3	AK	AK	31-Jul	2-Aug	1-Aug	HIGH	1	5	8	13
AK4	AK	AK	31-Jul	2-Aug	1-Aug	HIGH	1	0	1	1
AK5	AK	AK	31-Jul	2-Aug	1-Aug	HIGH	1	4	5	9
AP1	AP	AP	31-Jul	2-Aug	1-Aug	NONE	1	3	0	3
AP2	AP	AP	31-Jul	2-Aug	1-Aug	NONE	0	1	11	12
AP3	AT	AT	1-Aug	3-Aug	2-Aug	HIGH	1	7	8	15
AS1	AS	AS	31-Jul	2-Aug	1-Aug	NONE	0	0	2	2
AS2	AS	AS	31-Jul	2-Aug	1-Aug	NONE	-	0	0	0
AU1	AU	AU	31-Jul	7-Aug	1-Aug	NONE	-	0	0	0
AU2	AU	AU	31-Jul	7-Aug	1-Aug	NONE	1	4	1	5
AU3	AU	AU	30-Jul	1-Aug	1-Aug	NONE	-	0	0	0
AX1	AX	AX	31-Jul	2-Aug	1-Aug	NONE	0	11	14	26
AX2	AX	AX	31-Jul	2-Aug	1-Aug	NONE	0	7	4	11
AX3	AX	AX	1-Aug	2-Aug	2-Aug	NONE	-	0	0	0
BF1	BF	BF	30-Jul	2-Aug	1-Aug	NONE	1	3	2	5
BF2	BF	BF	1-Aug	3-Aug	2-Aug	NONE	-	0	0	0
BH1	BH	BH	31-Jul	2-Aug	1-Aug	NONE	-	0	0	0
BH2	BH	BH	31-Jul	2-Aug	1-Aug	NONE	1	3	0	3
BH3	BH	BH	30-Jul	2-Aug	1-Aug	NONE	1	2	2	4
BK1	BK	BK	31-Jul	2-Aug	1-Aug	LOW	1	1	1	2
BM1	BM	BM	31-Jul	2-Aug	1-Aug	HIGH	0	9	2	11
BM2	BM	BM	31-Jul	2-Aug	1-Aug	HIGH	0	9	5	14

Table A.10. Parental assignment (CERVUS), and Identity-By-descent (IBD) for 14 *Dendroctonus ponderosae* families used for linkage mapping.

Family	# Ind	No Assign (CERVUS)	Wrong Assign (CERVUS)	Failed IBD	Remaining # Ind	# SNPs (Fem.)	# SNPs (Male)
AE1	16	-	-	-	16	5169	4746
AH2	26	-	-	-	26	5930	5199
AK3	14	-	1	1	13	3296	2953
AK5	10	4	-	7	3	2345	1981
AP3	17	-	-	-	17	4497	4052
C1	13	-	-	-	13	1252	1232
E1	17	-	-	-	17	4126	3786
K1	19	-	-	-	19	4278	4178
K3	15	1	-	1	14	2895	2860
N1	14	-	-	-	14	3222	3161
V2	23	-	-	-	23	4928	4289
V3	13	1	-	1	12	2708	2373
V4	14	-	-	-	14	4345	3971
Z2	18	-	-	-	18	6375	5351

Table A.11. Identity-by-descent percentages for 16 individuals in the genotyped AE1 family of *Dendroctonus ponderosae*, used for linkage mapping. IBD values below the 25% threshold are **bolded**.

AE1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	D	M
1																
2	37															
3	27	65														
4	51	46	46													
5	63	27	27	55												
6	26	59	52	39	**15**											
7	42	53	57	40	47	52										
8	73	29	**20**	53	57	27	33									
9	56	28	**21**	65	57	28	43	60								
10	51	44	53	34	**19**	43	47	42	26							
11	44	47	42	**20**	45	45	64	39	35	52						
12	29	45	43	**19**	33	46	41	38	**22**	60	59					
13	64	33	38	46	48	**20**	**18**	61	53	40	**13**	35				
14	61	**22**	**5**	57	54	**18**	34	66	67	37	38	27	44			
D	58	51	47	51	52	49	56	61	55	59	59	55	48	56		
M	72	57	50	70	64	46	48	69	62	55	50	55	70	66	26	

Table A.12. Identity-by-descent for 26 individuals in the genotyped AH2 family of D. *ponderosae* used for linkage mapping.

AH2	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	M	D
2																										
3	34																									
4	36	48																								
5	26	67	56																							
6	34	58	63	55																						
7	71	43	36	33	**14**																					
8	68	40	47	25	28	65																				
9	59	34	36	50	43	57	47																			
10	69	54	68	52	53	31	33	**23**																		
11	46	49	68	70	58	26	**19**	34	69																	
12	55	**25**	47	26	33	53	58	50	43	39																
13	30	63	67	69	63	43	54	54	55	57	48															
14	41	41	31	31	46	31	36	54	38	28	40	**24**														
15	**19**	45	35	32	32	62	61	40	33	**25**	62	46	43													
16	71	**23**	43	**19**	**22**	48	38	39	65	35	71	32	54	51												
17	53	57	67	72	69	**20**	31	44	55	70	37	67	44	31	28											
18	48	47	39	38	27	76	57	67	36	28	57	49	39	62	56	30										
19	59	69	66	62	57	**16**	**19**	36	55	64	**17**	56	49	25	**23**	75	**23**									
20	34	52	34	**24**	**8**	66	53	49	41	**15**	54	46	38	64	53	**16**	66	28								
21	42	33	38	42	37	30	36	51	43	45	39	27	63	35	58	36	34	45	42							
22	53	35	47	36	26	64	49	60	40	41	54	39	45	52	55	35	54	27	55	58						
23	56	43	27	31	**15**	73	57	46	32	29	53	38	40	69	46	**15**	73	**11**	58	30	61					
24	39	67	51	51	63	**24**	27	29	69	47	40	59	44	45	44	60	32	58	44	42	42	39				
25	53	66	44	66	53	36	26	26	65	58	25	57	27	42	34	58	41	65	36	30	33	38	68			
M	63	66	60	60	59	43	43	41	66	58	41	61	49	42	47	57	43	63	46	51	44	43	64	64		
D	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	

Table A.13. Identity-by-descent percentages for 14 individuals in the genotyped AK3 family of *Dendroctonus ponderosae*, used for linkage mapping. IBD values below the 25% threshold are **bolded**.

AK3	1	2	3	4	5	6	7	8	9	10	11	12	13	M	D
1															
2	63														
3	49	67													
4	42	40	42												
5	62	51	53	48											
6	**24**	**20**	38	57	36										
7	55	66	59	39	45	38									
8	**0**	**0**	**0**	**15**	**0**	**9**	**0**								
9	34	41	39	56	26	65	30	**11**							
10	51	74	68	37	47	42	73	**0**	38						
11	65	76	58	42	58	31	55	**0**	46	62					
12	46	63	58	47	61	56	67	**0**	44	74	64				
13	48	57	52	74	36	67	44	**8**	74	42	48	46			
M	59	58	59	72	58	70	59	**6**	76	59	56	60	79		
D	50	50	50	50	50	50	50	50	50	50	50	50	50	50	

Table A.14. Identity-by-descent percentages for 10 individuals in the genotyped AK5 family of *Dendroctonus ponderosae*, used for linkage mapping. IBD values below the 25% threshold are **bolded**.

AK5	1	2	3	4	5	6	7	8	9	M	D
1											
2	56										
3	52	68									
4	**1**	**11**	**12**								
5	**2**	**14**	**15**	55							
6	**9**	**0**	**0**	27	35						
7	**2**	**15**	**16**	48	59	43					
8	58	33	32	**0**	**0**	**9**	**0**				
9	74	54	63	**0**	**0**	**8**	**0**	49			
M	80	58	56	**8**	**8**	**11**	**9**	68	76		
D	50	50	50	50	50	50	50	50	50	50	

Table A.15. Identity-by-descent percentages for 17 individuals in the genotyped AP3 family of *Dendroctonus ponderosae*, used for linkage mapping. IBD values below the 25% threshold are **bolded**.

AP3	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	M	D
1																		
2	40																	
3	55	53																
4	38	54	61															
5	49	53	57	63														
6	46	62	51	71	56													
7	50	63	49	61	76	58												
8	44	54	62	56	44	54	50											
9	45	70	52	55	63	53	67	58										
10	60	34	35	47	**19**	58	32	25	26									
11	56	43	38	42	36	45	46	61	43	46								
12	61	54	41	48	59	46	56	44	37	57	62							
13	52	43	43	59	28	54	37	35	**25**	64	56	72						
14	68	33	32	44	**25**	59	39	39	27	72	56	64	69					
15	76	50	52	37	38	40	52	53	60	60	69	68	62	60				
16	69	46	28	33	**16**	56	37	48	33	70	58	58	55	70	61			
M	69	58	49	54	52	53	55	49	56	66	68	75	70	69	71	69		
D	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	

Table A.16. Identity-by-descent percentages for 13 individuals in the genotyped C1 family of *Dendroctonus ponderosae*, used for linkage mapping. IBD values below the 25% threshold are **bolded**.

C1	1	2	3	4	5	6	7	8	9	10	11	12	M	D
1														
2	63													
3	69	56												
4	68	67	67											
5	77	74	65	68										
6	70	68	65	70	55									
7	73	69	67	74	73	70								
8	65	65	63	80	67	59	71							
9	66	62	78	71	70	57	81	75						
10	71	75	68	63	77	76	75	70	80					
11	54	41	43	41	52	32	51	47	44	35				
12	63	63	54	78	63	54	65	53	55	50	42			
M	73	73	75	78	73	72	77	79	77	78	60	71		
D	50	50	50	50	50	50	50	50	50	50	50	50	50	

Table A.17. Identity-by-descent percentages for 17 individuals in the genotyped E1 family of *Dendroctonus ponderosae*, used for linkage mapping. IBD values below the 25% threshold are **bolded**.

E1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	D	M
1																	
2	48																
3	58	34															
4	61	40	67														
5	57	37	45	51													
6	65	43	58	52	63												
7	**22**	46	41	31	34	38											
8	43	60	43	38	39	55	72										
9	45	**12**	73	44	50	49	47	35									
10	51	30	77	59	56	67	40	48	65								
11	52	42	79	65	50	61	47	42	67	63							
12	65	41	60	56	68	68	49	44	54	59	59						
13	45	**16**	63	46	56	53	39	44	62	48	59	64					
14	**20**	54	52	**20**	**21**	35	69	66	41	34	43	43	49				
15	48	57	48	41	29	46	60	61	38	43	50	36	48	60			
D	46	44	46	43	48	47	43	46	39	44	44	48	45	44	51		
M	52	63	53	49	52	55	65	68	51	54	56	55	49	63	67	**4**	

Table A.18. Identity-by-descent percentages for 19 individuals in the genotyped K1 family of *Dendroctonus ponderosae*, used for linkage mapping. IBD values below the 25% threshold are **bolded**.

K1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	M	D
1																				
2	38																			
3	62	63																		
4	70	51	67																	
5	74	40	59	63																
6	68	38	58	51	62															
7	50	57	56	38	64	39														
8	29	43	43	**19**	**23**	29	38													
9	57	65	56	55	47	37	57	57												
10	56	48	35	46	44	55	52	38	60											
11	55	**16**	34	45	50	40	**16**	46	26	**25**										
12	39	**16**	34	32	52	**22**	31	63	26	**17**	53									
13	46	29	36	37	36	**23**	**21**	58	39	**24**	78	62								
14	57	**19**	47	43	39	37	27	58	37	44	50	46	39							
15	49	44	53	51	46	40	51	**21**	55	39	**23**	**20**	33	**11**						
16	50	58	50	37	56	46	66	41	54	53	39	**18**	47	**13**	63					
17	55	59	46	39	50	59	52	42	58	79	33	**17**	33	42	37	55				
18	65	62	76	66	55	44	38	**24**	57	32	36	**14**	36	34	42	48	47			
M	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50		
D	67	47	62	61	67	60	55	48	51	55	61	47	51	57	51	55	55	59	50	

Table A.19. Identity-by-descent percentages for 15 individuals in the genotyped K3 family of *Dendroctonus ponderosae*, used for linkage mapping. IBD values below the 25% threshold are **bolded**.

K3	1	2	3	4	5	6	7	8	9	10	11	12	13	14	M	D
1																
2	73															
3	75	66														
4	66	62	70													
5	33	41	59	31												
6	58	63	60	55	61											
7	44	55	52	45	62	73										
8	**6**	**4**	**6**	**6**	**0**	**0**	**0**									
9	62	59	75	64	52	47	63	**6**								
10	68	65	66	58	42	61	51	**8**	69							
11	44	51	51	28	68	67	69	**0**	51	58						
12	52	49	58	39	71	66	67	**0**	54	54	54					
13	81	70	65	71	32	52	47	**5**	64	76	43	42				
14	53	54	55	42	62	78	69	**0**	49	57	70	70	49			
M	79	80	83	75	62	65	62	**6**	82	83	60	66	78	66		
D	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	

Table A.20. Identity-by-descent percentages for 14 individuals in the genotyped N1 family of *Dendroctonus ponderosae*, used for linkage mapping. IBD values below the 25% threshold are **bolded**.

N1	1	2	3	4	5	6	7	8	9	10	11	12	13	M	D
1															
2	74														
3	74	67													
4	66	61	69												
5	63	67	75	60											
6	72	78	65	63	66										
7	41	57	39	35	40	53									
8	73	70	68	68	55	74	36								
9	**19**	28	27	43	36	35	48	43							
10	56	68	63	62	73	71	45	58	43						
11	59	53	40	41	37	50	61	62	53	31					
12	**19**	29	**25**	38	55	31	55	26	75	56	52				
13	**20**	29	31	48	44	31	48	36	81	48	51	78			
M	74	75	75	76	78	79	57	71	55	77	55	57	60		
D	50	50	50	50	50	50	50	50	50	50	50	50	50	50	

Table A.21. Identity-by-descent percentages for 23 individuals in the genotyped V2 family of *Dendroctonus ponderosae*, used for linkage mapping. IBD values below the 25% threshold are **bolded**.

V2	1	2	3	4	5	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	26	M	D
1																									
2	**16**																								
3	35	**16**																							
4	29	59	**11**																						
5	35	50	39	54																					
7	53	28	43	33	**12**																				
8	60	39	60	**22**	59	42																			
9	33	52	**19**	56	48	43	**16**																		
10	47	52	**15**	50	57	35	44	64																	
11	31	49	**10**	74	59	35	37	44	45																
12	42	60	**15**	57	64	34	59	41	65	69															
13	28	30	46	41	34	54	42	41	29	42	33														
14	**13**	75	**15**	65	52	26	38	43	53	62	70	42													
15	36	61	27	63	72	**17**	34	70	61	48	57	38	65												
16	47	57	38	57	54	31	36	74	70	39	54	27	43	65											
17	33	69	**15**	66	53	40	28	62	52	63	62	25	76	64	60										
18	56	36	36	48	30	70	54	41	33	54	49	62	43	32	**23**	56									
19	45	42	47	33	35	71	53	53	43	39	32	71	43	46	37	45	60								
20	**16**	54	30	61	39	34	**10**	62	47	48	34	39	47	49	61	56	**21**	41							
21	54	29	48	30	39	34	64	**13**	**24**	26	51	43	**24**	27	36	**23**	38	39	26						
22	41	**24**	45	50	35	60	41	40	43	49	38	76	43	39	42	36	49	73	54	51					
23	57	**24**	67	**21**	43	49	57	39	37	26	37	49	**22**	31	55	36	36	52	39	66	57				
26	36	49	**8**	69	58	42	29	50	42	75	58	**20**	47	51	53	69	57	37	52	**24**	35	25			
M	58	70	42	73	71	46	61	64	74	75	76	46	69	67	67	74	58	50	65	59	47	52	72		
D	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	

Table A.22. Identity-by-descent percentages for 13 individuals in the genotyped V3 family of *Dendroctonus ponderosae*, used for linkage mapping. IBD values below the 25% threshold are **bolded**.

V3	1	2	3	4	5	6	7	8	9	10	11	12	M	D
1														
2	45													
3	**7**	**0**												
4	61	33	**4**											
5	33	60	**1**	55										
6	56	47	**1**	43	54									
7	77	49	**6**	66	55	56								
8	**23**	48	**0**	**23**	52	32	**23**							
9	36	46	**0**	48	48	62	31	41						
10	35	66	**1**	42	60	54	42	50	54					
11	51	38	**3**	55	31	53	55	**4**	50	46				
12	42	45	**0**	36	39	69	51	45	61	58	41			
M	73	56	**6**	74	55	53	72	46	53	54	70	49		
D	50	50	50	50	50	50	50	50	50	50	50	50	50	

Table A.23. Identity-by-descent percentages for 14 individuals in the genotyped V4 family of *Dendroctonus ponderosae*, used for linkage mapping. IBD values below the 25% threshold are **bolded**.

V4	1	2	3	4	5	6	7	8	9	10	11	12	D	M
1														
2	34													
3	56	31												
4	37	57	35											
5	50	26	50	50										
6	**17**	44	32	46	30									
7	26	40	**23**	53	37	61								
8	36	64	51	62	**21**	61	44							
9	46	65	28	55	37	66	62	65						
10	39	**14**	46	45	68	47	33	**14**	**25**					
11	47	43	42	42	63	45	36	**23**	41	73				
12	38	**21**	48	32	61	54	53	29	34	73	64			
D	50	53	44	46	51	57	51	48	55	58	57	63		
M	56	71	53	68	60	71	67	73	78	48	51	50	34	

Table A.24. Identity-by-descent percentages for 18 individuals in the genotyped Z2 family of *Dendroctonus ponderosae*, used for linkage mapping. IBD values below the 25% threshold are **bolded**.

Z2	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	M	D
1																			
2	55																		
3	65	48																	
4	38	**17**	48																
5	65	48	69	40															
6	54	65	68	29	74														
7	68	55	66	36	68	62													
8	30	36	46	51	38	55	47												
9	34	47	48	50	32	42	34	52											
10	27	34	37	46	36	37	**21**	44	78										
11	**22**	28	**11**	53	**22**	**24**	**8**	27	53	59									
12	35	41	**19**	47	**18**	33	28	47	52	52	54								
13	48	47	64	51	67	67	47	30	**25**	33	46	**18**							
14	64	64	60	**18**	65	65	67	42	32	34	**20**	45	54						
15	52	**18**	49	48	32	30	**23**	44	61	60	56	50	34	39					
16	43	56	54	41	56	59	43	29	32	33	42	40	70	68	31				
17	38	45	38	52	26	45	30	73	58	51	49	65	35	40	58	47			
M	68	72	68	49	72	72	66	53	60	56	51	54	66	74	52	74	58		
D	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	

Table A.25. Linkage group positions for a) 1,729 SNPs and b) 1,638 SNPs from the *Dendroctonus ponderosae* female and male linkage maps, respectively. Overlapping SNPs, found in linkage map construction and population genetics analysis (see **Chapter 3**) are identified in the 'PC' column, which gives the number of the Principal component cohort that SNP belongs to.

a) Female			
LG	**Position**	**SeqPos**	**PC**
X	0	985205_222947	
X	0	985205_386680	
X	0	985205_129367	
X	4	985097_1139	
X	5.43	984028_29566	
X	6.08	984028_62935	
X	6.08	985513_137398	
X	9.81	949654_626	
X	9.81	985513_67692	
X	12.64	985366_147697	
X	12.64	985366_209039	
X	14.68	985515_2194502	2
X	14.68	985515_2194672	2
X	16.2	985370_327114	2
X	16.2	979365_240	
X	16.2	985439_321007	
X	16.2	985515_1554310	
X	18.77	984415_323998	
X	19.78	984119_206914	
X	19.78	985136_297821	
X	20.28	984119_12622	
X	21.8	985136_272294	
X	21.8	985268_446963	
X	22.31	984329_108285	
X	24.87	985527_24308	
X	24.87	985527_95809	
X	26.39	985403_136240	
X	27.92	985403_167597	
X	27.92	985433_1479220	
X	27.92	985462_149415	
X	27.92	985499_776467	
X	28.42	985556_239084	
X	28.92	985403_196439	2

b) Male			
LG	**Position**	**SeqPos**	**PC**
X	0	1102823_1229374	
X	0	1102823_1232462	
X	0	1102823_307028	
X	0	1102823_475940	
X	0	1102823_505557	
X	0	1102823_658521	
X	0	1102823_706534	
X	0	1102823_814257	
X	0	1103024_159177	
X	2.17	1102823_1053682	
X	2.17	1102823_1062018	
X	2.17	1102823_944555	
X	2.71	1102823_1001647	
X	3.24	1102823_1626926	
X	3.24	1102823_1782726	
X	3.24	1102823_1745386	3
X	3.78	1102823_1953615	
X	4.31	1102823_2183686	
X	4.31	1102823_2499232	
X	4.31	1102823_2584034	
X	4.82	1102823_2166721	
X	6.86	1102823_1569058	
X	6.86	1102823_2718349	
X	7.87	1102823_3218052	
X	7.87	1102823_3765065	
X	8.37	1101939_1612929	
X	8.37	1101939_681570	
X	8.37	1101939_956858	
X	8.37	1102823_3714391	
X	8.87	1101939_802405	
X	8.87	1102823_2863770	1
X	9.37	1101939_439057	
X	9.37	1101939_944834	

a) Female			
LG	**Position**	**SeqPos**	**PC**
X	28.92	984279_207151	
X	28.92	984724_117477	
X	28.92	985403_444156	
X	28.92	985433_1139288	
X	28.92	985433_619288	
X	28.92	985556_209406	
X	29.42	985433_89493	
X	29.42	985479_258513	
X	29.93	985433_95841	
X	29.93	985525_1820887	
X	31.97	984593_242410	2
X	31.97	985556_93080	1
X	31.97	985556_114079	
X	32.98	985470_2018618	
X	32.98	985515_554568	
X	33.48	985400_481235	
X	33.98	985291_115571	
X	34.48	984152_273110	
X	34.48	985291_133617	
X	34.48	985470_735470	
X	34.99	985291_715568	
X	35.49	985431_757435	
X	37.01	985233_431005	
X	37.01	985293_208027	
X	37.01	985293_445146	
X	37.01	985470_1094350	
X	37.01	985470_848495	
X	37.01	985500_1425102	
X	37.01	985500_4500711	
X	37.01	985500_514828	
X	37.01	985525_1151774	
X	37.52	985222_151849	2
X	37.52	985293_422185	
X	37.52	985439_638372	
X	37.52	985500_1358322	
X	37.52	985535_214537	
X	38.53	985222_151890	2
X	38.53	983688_165772	
X	38.53	984152_100152	
X	38.53	984163_21884	
X	38.53	985233_222428	

b) Male			
LG	**Position**	**SeqPos**	**PC**
X	9.37	1102110_108036	
X	9.37	1102713_2514598	
X	9.88	1101939_1060746	
X	10.89	1101939_257933	
X	11.39	1101939_721145	
X	12.91	1102308_238783	
X	12.91	1102713_2376021	
X	14.44	1102713_1057825	
X	15.45	1101939_171891	
X	15.45	1101939_324516	
X	15.45	1102537_43394	
X	15.45	1102713_2880231	
X	15.45	1102823_3617971	
X	15.45	1102867_14765	1
X	15.95	1102308_1619538	
X	15.95	1102713_2916412	
X	15.95	1102713_664811	
X	15.95	1102890_33893	
X	16.45	1101939_1569300	
X	16.45	1102713_1764596	
X	16.45	1102713_2161826	
X	17.46	1098305_8124	
X	17.46	1102579_512018	
X	17.46	1102689_787073	
X	17.46	1102711_47363	
X	17.46	1102985_127226	
X	17.46	1102985_324631	
X	17.96	1102400_75158	
X	17.96	1102676_61188	
X	17.96	1102838_194694	
X	17.96	1102910_241911	
X	20	1101880_165657	
X	20	1102308_583366	
X	20	1102713_803623	
X	20	1102881_217133	
X	20	1102891_11203	
X	20	1102910_244341	
X	20	1102985_273391	
X	20	1102985_601358	
X	20.51	1096566_1941	
X	20.51	1101880_154980	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
X	38.53	985250_123752		X	20.51	1102091_23377	
X	38.53	985402_195193		X	20.51	1102110_126369	
X	38.53	985433_1398251		X	20.51	1102262_26852	
X	38.53	985462_85590		X	20.51	1102308_693382	
X	38.53	985470_1047497		X	20.51	1102535_30330	
X	38.53	985470_1905299		X	20.51	1102603_139333	
X	38.53	985479_188652		X	20.51	1102613_17140	
X	38.53	985498_34556		X	20.51	1102631_270973	
X	38.53	985500_3060498		X	20.51	1102729_125786	
X	38.53	985500_3620384		X	20.51	1102734_176812	
X	38.53	985514_25359		X	20.51	1102734_264340	
X	38.53	985515_1138358		X	20.51	1102802_127415	
X	38.53	985515_2073009		X	20.51	1102837_100788	
X	38.53	985515_2256281		X	20.51	1102849_104592	
X	38.53	985515_2352701		X	20.51	1102979_32463	
X	38.53	985524_6875512		X	20.51	1103029_28467	
X	38.53	985525_1355243		X	20.51	1102565_102651	4
X	38.53	985525_1969387		X	20.51	1102799_84281	4
X	39.03	985540_41326	4	X	21.01	1097363_1248	
X	39.03	983817_26836		X	24.1	1102173_9269	
X	39.03	984152_1047633		X	24.61	1102137_11527	
X	39.03	984152_1210016		X	24.61	1102593_53650	
X	39.03	984152_200053		X	24.61	1102644_310718	
X	39.03	984279_59956		X	24.61	1102839_107236	
X	39.03	984279_59992		X	24.61	1102865_84249	
X	39.03	984444_212887		X	26.13	1099458_20113	
X	39.03	984456_93224		X	26.13	1102713_2439603	
X	39.03	984493_60545		X	26.13	1102790_11735	
X	39.03	984593_239105		X	26.13	1102881_150386	
X	39.03	984762_1048154		X	26.13	1102892_40509	
X	39.03	984762_309190		X	26.13	1102910_305216	
X	39.03	984762_386147		X	26.13	1102881_99151	4
X	39.03	984762_614297		X	26.63	1102308_1869117	
X	39.03	984762_982680		X	26.63	1102308_2288595	
X	39.03	984837_52815		X	26.63	1102308_355938	
X	39.03	985086_110452		X	26.63	1102790_190481	
X	39.03	985137_57820		X	26.63	1102892_40473	
X	39.03	985141_312240		X	28.67	1101939_690338	
X	39.03	985174_342535		X	28.67	1102308_1310337	
X	39.03	985174_81361		X	28.67	1102354_94668	
X	39.03	985211_872013		X	28.67	1102473_1148	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
X	39.03	985233_268202		X	28.67	1102689_537934	
X	39.03	985233_292186		X	28.67	1102704_51182	
X	39.03	985250_121160		X	28.67	1102858_76727	
X	39.03	985266_554252		X	28.67	1102904_201878	
X	39.03	985291_302370		X	28.67	1102904_94857	
X	39.03	985309_362194		X	28.67	1102101_31466	1
X	39.03	985400_6826		X	28.67	1102985_212522	1
X	39.03	985402_214797		X	28.67	1102985_212788	1
X	39.03	985402_77041		X	30.2	1101880_128407	
X	39.03	985431_446784		X	30.2	1101880_128437	
X	39.03	985433_1365670		X	30.2	1101880_280380	
X	39.03	985433_462892		X	30.2	1101939_1370224	
X	39.03	985462_349752		X	30.2	1101939_53787	
X	39.03	985479_187841		X	30.2	1102259_13578	
X	39.03	985479_535140		X	30.2	1102308_2228952	
X	39.03	985493_1046378		X	30.2	1102308_243580	
X	39.03	985493_524442		X	30.2	1102429_45410	
X	39.03	985498_452156		X	30.2	1102689_151699	
X	39.03	985500_681224		X	30.2	1102825_186917	
X	39.03	985500_773628		X	30.2	1102838_331319	
X	39.03	985515_1971393		X	30.2	1103024_397398	
X	39.03	985515_1980964		X	33.29	1102611_65220	
X	39.03	985520_25000		X	33.29	1103027_88055	4
X	39.03	985524_5133861		X	33.79	1102067_52896	
X	39.03	985527_1691214		X	33.79	1102796_118780	
X	39.03	985527_1738247		X	33.79	1102796_199066	
X	39.03	985527_246049		X	33.79	1102823_2688106	
X	39.03	985540_112391		X	34.29	1101283_872	
X	39.03	985543_256749		X	34.29	1102517_55276	
X	39.03	985544_639555		X	34.29	1102849_206578	
X	39.03	985556_239724		X	34.29	1102383_122263	4
X	39.53	980715_108		X	37.39	1101939_126281	
X	39.53	985141_568617		X	37.39	1102087_11690	
X	39.53	985266_684165		X	37.39	1102150_11532	
X	39.53	985291_752412		X	37.39	1102892_99445	
X	39.53	985403_195876		X	37.39	1103027_91731	
X	39.53	985479_148255		X	37.92	1099773_2692	
X	39.53	985514_25417		X	37.92	1102166_89967	
X	39.53	985556_165663		X	37.92	1102288_81583	
X	40.03	971161_680		X	37.92	1102310_29105	
X	40.03	972955_959		X	37.92	1102358_62312	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
X	40.03	983729_50724		X	37.92	1102657_121418	
X	40.03	984163_93342		X	37.92	1102689_298533	
X	40.03	984444_212396		X	37.92	1102689_402018	
X	40.03	984456_98555		X	37.92	1102713_119125	
X	40.03	984593_239630		X	37.92	1102810_108410	
X	40.03	984847_1001114		X	37.92	1102870_98433	
X	40.03	984847_397713		X	37.92	1102904_1179	
X	40.03	984908_77397		X	37.92	1102904_448486	
X	40.03	985050_244136		X	37.92	1102310_84550	4
X	40.03	985174_211466		X	38.46	1102677_419814	
X	40.03	985211_127066		X	39.53	1102473_247368	
X	40.03	985211_152568		X	40.07	1099855_6593	
X	40.03	985211_243631		X	40.07	1099899_823	
X	40.03	985211_98082		X	40.07	1101782_96645	
X	40.03	985211_98135		X	40.07	1102579_473200	
X	40.03	985266_125922		X	40.07	1102579_561763	
X	40.03	985283_166761		X	40.07	1102579_612738	
X	40.03	985291_120530		X	40.07	1102588_34805	
X	40.03	985299_79922		X	40.07	1102603_128366	
X	40.03	985309_239788		X	40.07	1102677_412153	
X	40.03	985309_405366		X	40.07	1102690_25215	
X	40.03	985383_142931		X	40.07	1102838_60556	
X	40.03	985383_145378		X	40.07	1102849_69323	
X	40.03	985383_417226		X	40.07	1102858_21269	
X	40.03	985383_709769		X	40.07	1102904_207166	
X	40.03	985383_98593		X	40.07	1102996_101077	
X	40.03	985391_102645		X	40.07	1102996_181082	
X	40.03	985400_160033		X	40.6	1102208_102313	
X	40.03	985400_160063		X	40.6	1102262_4340	
X	40.03	985400_552758		X	40.6	1102644_319347	
X	40.03	985400_584169		X	40.6	1102673_73777	
X	40.03	985400_761827		X	40.6	1102838_325677	
X	40.03	985400_982633		X	40.6	1102858_193420	
X	40.03	985424_133618		X	40.6	1102985_510069	
X	40.03	985462_48643		X	42.78	1101753_18540	
X	40.03	985476_233926		X	42.78	1101939_1398147	
X	40.03	985493_658471		X	42.78	1101948_8725	
X	40.03	985498_623303		X	42.78	1102109_38454	
X	40.03	985498_771527		X	42.78	1102122_2753	
X	40.03	985498_787973		X	42.78	1102262_4865	
X	40.03	985500_4678428		X	42.78	1102347_12894	

a) Female			
LG	**Position**	**SeqPos**	**PC**
X	40.03	985500_636197	
X	40.03	985500_708636	
X	40.03	985515_2194756	
X	40.03	985515_2594189	
X	40.03	985516_1358003	
X	40.03	985524_3415057	
X	40.03	985524_3704762	
X	40.03	985524_372987	
X	40.03	985524_6275185	
X	40.03	985524_6380197	
X	40.03	985525_1146613	
X	40.03	985525_1362740	
X	40.03	985525_1604740	
X	40.03	985525_1769085	
X	40.03	985525_556135	
X	40.03	985525_697041	
X	40.03	985526_204778	
X	40.03	985527_1045635	
X	40.03	985527_1107944	
X	40.03	985527_1282351	
X	40.03	985527_1735545	
X	40.03	985535_385937	
X	40.03	985540_37650	
X	40.03	985544_24181	
X	40.03	985544_766262	
X	40.03	985545_445081	
X	40.54	984163_61765	
X	40.54	984279_110782	
X	40.54	984847_996814	
X	40.54	985211_1044705	
X	40.54	985233_490934	
X	40.54	985291_134480	
X	40.54	985309_368417	
X	40.54	985370_11381	
X	40.54	985400_533017	
X	40.54	985400_852516	
X	40.54	985402_211271	
X	40.54	985433_1442867	
X	40.54	985470_2534918	
X	40.54	985493_387369	
X	40.54	985500_2270019	

b) Male			
LG	**Position**	**SeqPos**	**PC**
X	42.78	1102520_69802	
X	42.78	1102579_583983	
X	42.78	1102579_612791	
X	42.78	1102690_100698	
X	42.78	1102705_18339	
X	42.78	1102713_3127282	
X	42.78	1102800_59771	
X	42.78	1102827_2412	
X	42.78	1102858_82950	
X	42.78	1102873_14122	
X	42.78	1102873_9743	
X	42.78	1102904_380988	
X	42.78	1102910_332330	
X	42.78	1102923_52443	
X	42.78	1103027_27448	
X	43.85	1102146_28745	
X	43.85	1102227_53112	
X	43.85	1102405_112490	
X	43.85	1102824_13075	
X	43.85	1102851_13995	
X	43.85	1102868_29442	
X	43.85	1103029_33798	
X	44.39	1099855_6102	
X	45.46	1101939_1055693	
X	45.46	1102289_107719	
X	45.46	1102604_78854	
X	45.46	1102676_112939	
X	45.46	1102985_293153	
X	46	1102068_50114	
X	48.17	1102689_870046	
X	48.17	1102858_46752	
X	49.25	1101939_894341	
X	49.25	1101948_8799	
X	49.25	1102308_833357	
X	51.42	1101913_103521	
X	51.42	1102800_272269	
X	53.04	1102316_21581	
X	53.04	1102603_180324	
X	53.04	1102604_55243	
X	53.04	1102778_102363	
X	53.04	1102844_219564	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
X	40.54	985515_2061480		X	53.58	1102306_140354	
X	40.54	985524_4101155		X	53.58	1102347_7139	
X	40.54	985524_5274392		X	53.58	1102719_482049	
X	40.54	985524_5610481		X	55.2	1101944_35441	
X	40.54	985525_116703		X	55.2	1101979_47236	
X	40.54	985525_250560		X	55.2	1102092_8936	
X	40.54	985526_69860		X	55.2	1102240_42669	
X	40.54	985527_876734		X	55.2	1102251_19559	
X	41.04	984630_13726	4	X	55.2	1102316_90899	
X	41.04	985050_129568	4	X	55.2	1102319_130312	
X	41.04	984163_23493		X	55.2	1102408_49503	
X	41.04	984688_35776		X	55.2	1102411_93666	
X	41.04	984724_143784		X	55.2	1102510_22803	
X	41.04	985050_177746		X	55.2	1102510_29184	
X	41.04	985050_53511		X	55.2	1102545_134155	
X	41.04	985155_350865		X	55.2	1102719_435719	
X	41.04	985163_23442		X	55.2	1102719_681327	
X	41.04	985174_348175		X	55.2	1102719_797611	
X	41.04	985233_84706		X	55.2	1102724_199468	
X	41.04	985266_118812		X	55.2	1102750_138552	
X	41.04	985283_283417		X	55.2	1102788_19764	
X	41.04	985309_398813		X	55.2	1102815_111926	
X	41.04	985400_481003	1	X	55.2	1102984_100289	
X	41.04	985400_481269	1	X	55.2	1102996_189496	
X	41.04	985402_84804		X	55.2	1102996_89301	
X	41.04	985433_1468618		X	57.37	1101784_28097	
X	41.04	985433_505098		X	58.99	1102727_92814	
X	41.04	985493_1128508		X	59.53	1102716_440139	
X	41.04	985500_1023971		X	59.53	1102716_673622	
X	41.04	985500_32591		X	60.1	1102698_136507	
X	41.04	985500_3364642		X	60.1	1102716_514415	
X	41.04	985524_6523931		X	61.35	1102716_45021	
X	41.04	985527_1070494		X	64.54	1102967_317059	
X	41.04	985527_571708		X	65.79	1102716_467664	
X	41.04	985527_871446		X	67.14	1102698_16395	
X	41.04	985544_32209		X	67.88	1102967_122431	
X	41.04	985544_732969		1	0	1102685_1184237	
X	41.54	984565_388964		1	0	1102721_198624	
X	41.54	985524_5722788		1	0	1103024_159177	
X	41.54	985527_765460		1	0	1103024_375984	
X	42.04	985424_598646		1	0.99	1102674_1104668	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
X	42.04	985516_680157		1	0.99	1103023_2637222	
X	42.04	985524_3644874		1	1.84	1102674_1513989	
X	42.04	985524_4655908		1	1.84	1102712_823749	
X	42.55	985525_1097217	4	1	1.84	1102712_862921	
X	42.55	983817_573673		1	1.84	1102721_168897	
X	42.55	984152_843319		1	1.84	1102721_2180147	
X	42.55	985233_517363		1	1.84	1102721_2273035	
X	42.55	985356_56527	1	1	1.84	1103023_1459468	
X	42.55	985403_28338		1	1.84	1103023_2974789	
X	42.55	985403_637894		1	1.84	1103024_377502	
X	42.55	985403_75513		1	3.32	1101817_590849	
X	42.55	985433_16786		1	3.32	1102721_156841	
X	42.55	985479_534984		1	3.32	1103023_383929	
X	42.55	985499_711588		1	5.56	1102712_225258	
X	42.55	985499_794469		1	5.56	1103023_1462752	
X	42.55	985524_1077921		1	6.29	1102740_733892	
X	42.55	985524_6792984		1	15.92	1102678_171003	
X	42.55	985527_200997		1	19.71	1103023_3333964	
X	43.05	984593_217405		1	32.07	1102924_553625	
X	43.05	985433_64132		1	32.73	1102739_491214	
X	43.05	985524_5727543		1	32.73	1102739_584965	
X	43.05	985524_581610		1	32.73	1102739_738546	
X	43.55	985291_121472		1	32.73	1102924_171752	
X	43.55	985424_367981		1	32.73	1102924_519572	
X	43.55	985499_299602		1	32.73	1102924_173385	4
X	43.55	985499_299685		1	32.73	1102924_405379	4
X	43.55	985499_551178		1	32.73	1102924_415917	4
X	43.55	985524_1358222		1	33.39	1102739_565437	
X	46.64	985424_218086		1	33.39	1102739_572046	
X	47.15	984628_36653		1	33.39	1102739_856508	
X	48.67	983817_197952		1	33.39	1102924_127562	
X	48.67	985400_121429		1	33.39	1102924_141678	
X	48.67	985400_395657		1	33.39	1102924_193617	
X	48.67	985403_213225		1	33.39	1102924_213230	
X	49.17	985400_964516		1	33.39	1102924_347139	
X	49.17	985524_4346550		1	33.39	1102924_405398	
X	49.17	985524_5381814		1	33.39	1102924_421050	
X	49.17	985524_617796		1	33.39	1102924_429946	
X	49.67	984152_476287		1	33.39	1102924_544610	
X	49.67	984152_590616		1	33.39	1102924_66316	
X	50.18	985524_2850526		1	33.39	1102739_566562	4

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
X	50.68	984571_81703		1	33.39	1102739_577419	4
X	50.68	985524_1141787		1	33.39	1102739_615462	4
X	50.68	985524_2457267		1	33.39	1102739_859607	4
X	51.18	985309_422497		1	33.39	1102924_119299	4
X	51.18	985524_6128528		1	33.39	1102924_151522	4
X	51.68	984152_404768	3	1	33.39	1102924_151700	4
X	52.19	984152_1215076		1	33.39	1102924_195975	4
X	52.19	984152_834453		1	33.39	1102924_261049	4
X	53.2	985524_1002709		1	33.39	1102924_416294	4
X	53.7	984152_1099176		1	33.39	1102924_471258	4
X	54.2	983817_241811		1	33.39	1102924_514595	4
X	54.71	984152_874109		1	33.39	1102924_522238	4
X	55.21	985400_132106		1	33.92	1090583_1365	
X	56.22	983817_413143		1	33.92	1102924_225345	
X	57.74	984677_160853		1	33.92	1102924_514490	
X	58.24	984175_194698	1	1	34.93	1102739_913607	
X	58.24	984677_76655		1	35.43	1102924_141348	4
X	58.24	985557_375577		1	35.43	1102924_416230	4
X	59.25	983817_463946		1	37.47	1102924_426995	
X	59.25	984152_318759		1	37.98	1102739_771034	
X	59.25	984175_338228		1	37.98	737960_673	
X	59.25	984677_485423		1	37.98	1102739_583952	4
X	59.76	984152_955639		1	37.98	1102739_629266	4
X	60.77	984152_1111186		1	37.98	1102924_127511	4
X	63.86	984175_368418		1	39.5	1102739_505077	
X	65.38	984677_468715		1	40.51	1102739_244505	
X	67.95	984677_701080		1	40.51	1102739_842108	4
X	68.45	984677_905588	3	1	41.01	1102924_1342	
X	68.45	984677_866502		1	43.05	1102739_218766	
X	68.45	985509_1654710		1	44.58	1102739_172337	
X	69.53	984677_1024237		1	45.08	1102739_110100	
X	70.6	985509_1077021		1	45.08	1102739_124785	
X	70.6	985509_1136754		1	45.08	1102739_163172	
X	71.14	985509_1128422		1	46.09	1102739_236095	
X	71.14	985509_1316268		1	48.13	1102739_74077	
X	71.14	985509_391277		1	48.13	1102753_1127653	
X	71.14	985509_464060		1	48.13	1102753_965244	
X	71.14	985509_682860		1	49.14	1102753_1043113	
X	71.14	985509_706597		1	49.14	1102753_980818	
X	71.14	985509_730832		1	49.64	1102753_860134	
X	71.75	985509_1311771		1	49.64	1102753_931075	

a) Female			
LG	**Position**	**SeqPos**	**PC**
X	72.41	985509_1018651	
X	73.74	985509_847923	
X	76.38	985509_300062	
X	76.38	985509_493515	
1	0	985436_793193	
1	0	985463_129330	
1	0.8	985463_370815	
1	1.47	985436_422774	
1	2.69	985436_539992	
1	2.69	985436_620187	
1	2.69	985436_634030	
1	2.69	985463_431284	
1	2.69	985463_684504	
1	2.69	985463_723256	
1	2.69	985463_728965	
1	2.69	985463_95835	
1	3.2	985463_296975	
1	3.2	985463_544546	
1	3.2	985463_714115	
1	3.2	985463_716523	
1	3.7	985463_457439	
1	3.7	985463_724088	
1	4.2	984234_41076	
1	4.7	985463_874347	
1	5.71	985463_903121	
1	6.22	985457_111312	
1	6.22	985457_87450	
1	8.26	985274_7796	
1	9.27	985166_61755	1
1	9.27	985480_110417	
1	9.77	985166_161672	
1	9.77	985412_144091	
1	9.77	985412_170928	
1	9.77	985480_25359	
1	10.78	984634_17882	
1	10.78	984634_78836	
1	10.78	984634_85370	
1	10.78	985294_181347	
1	12.3	985294_324439	
1	12.3	985294_335888	
1	12.3	985294_448012	

b) Male			
LG	**Position**	**SeqPos**	**PC**
1	50.15	1102753_815100	
1	50.15	1102960_30279	
1	50.65	1102753_814860	
1	50.65	1102753_816227	
1	50.65	1102753_824711	
1	51.15	1102753_746987	
1	52.67	1102960_9647	
1	53.18	1102753_535593	
1	53.18	1102753_558303	
1	53.68	1102753_250538	
1	54.18	1102753_165959	
1	56.22	1102753_112105	
1	56.22	1102753_167530	
1	56.73	1102977_121185	
1	56.73	1102977_161047	
1	56.73	1102977_205579	
1	56.73	1102977_254431	
1	56.73	1102977_258380	
1	56.73	1102977_375858	
1	56.73	1102977_408851	
1	56.73	1102977_444153	
1	57.23	1102977_368302	
1	57.23	1102977_456338	
1	57.23	1102977_505587	
1	57.23	1102977_554392	
1	57.73	1102977_328609	
1	57.73	1102977_464563	
1	57.73	1102977_509787	
1	57.73	1102977_560536	
1	58.23	1102977_338046	
1	58.23	1102977_473607	
1	58.23	1102977_632770	
1	59.76	1102977_647775	
1	60.77	1102977_685185	
1	62.29	1102977_732567	
1	63.3	1102902_1061918	
1	63.3	1102902_1669356	
1	63.3	1102902_1687273	
1	63.3	1102926_106814	
1	63.3	1102926_152787	
1	63.3	1102926_241793	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
1	12.3	985294_458917		1	63.3	1102926_247577	
1	12.3	985294_579946		1	63.3	1102926_258387	
1	12.3	985294_603725		1	63.3	1102926_347972	
1	12.3	985294_607008		1	63.3	1102926_348062	
1	12.3	985294_607699		1	63.3	1102926_353119	
1	12.3	985294_741220		1	63.3	1102926_379641	
1	12.81	985294_295980		1	63.3	1102926_83776	
1	12.81	985294_415998		1	63.3	1102926_92193	
1	13.82	985294_724535		1	63.8	1102926_121889	
1	13.82	985294_732504		1	63.8	1102926_162318	
1	13.82	985294_741269	1	1	65.32	1102902_1199740	
1	13.82	985294_779988		1	65.32	1102902_1328050	
1	14.32	985294_856305		1	65.32	1102902_1497621	
1	16.36	984407_151104		1	65.32	1102902_1650533	
1	16.36	984407_41210		1	65.32	1102902_1680521	
1	16.36	984407_75054		1	65.32	1102902_1684014	
1	16.36	985063_100368		1	65.32	1102926_258451	
1	16.36	985063_374535		1	65.83	1102908_10502	
1	16.36	985542_132598		1	66.33	1102902_1136181	
1	16.36	985542_132607		1	66.33	1102902_1159597	
1	16.86	984407_118023		1	66.33	1102902_1249240	
1	16.86	984407_41253		1	66.33	1102902_1249334	
1	16.86	985487_27306		1	66.33	1102902_1359624	
1	17.87	985235_25845		1	66.33	1102902_1436951	
1	18.37	984407_129180		1	66.33	1102902_1502108	
1	18.37	985063_215309		1	66.33	1102902_1556511	
1	18.37	985063_228535		1	66.33	1102902_1569195	
1	18.37	985063_287373		1	66.33	1102902_1604009	
1	18.37	985487_27400		1	66.33	1102902_1609552	
1	18.88	985542_60246		1	66.33	1102902_957588	
1	19.38	985063_345048		1	66.33	1102902_1603470	4
1	19.38	985063_400396		1	67.34	1102902_1061927	
1	19.38	985063_431744		1	67.34	1102902_1089873	
1	20.39	985063_103651		1	67.34	1102902_1176789	
1	20.39	985063_107387		1	67.34	1102902_848944	
1	20.39	985063_135538		1	67.34	1102902_946505	
1	20.39	985063_180282		1	67.34	1102902_991796	
1	20.39	985063_180821		1	67.34	1102902_998861	
1	20.39	985063_282886		1	67.84	1102902_978604	
1	20.89	983718_12570		1	68.34	1102902_899716	
1	20.89	984236_23210		1	68.85	1102902_267874	

a) Female			
LG	**Position**	**SeqPos**	**PC**
1	20.89	984597_127440	
1	21.39	985063_118437	
1	21.9	984236_8187	
1	21.9	984597_23714	
1	22.4	984597_117907	
1	22.4	984597_23778	
1	22.4	984597_33494	
1	23.41	984597_36728	
1	23.91	984236_46235	
1	23.91	984308_112666	
1	23.91	984308_117818	
1	24.42	984308_67919	
1	24.92	984308_117728	
1	25.93	984236_37831	
1	26.43	985512_370397	
1	26.93	985512_258700	
1	26.93	985512_307021	
1	27.44	985423_127267	
1	27.44	985512_110442	
1	27.44	985512_119394	
1	27.44	985512_155152	1
1	27.44	985512_181866	
1	28.45	984609_130005	
1	28.45	985423_121972	
1	28.45	985423_17177	
1	28.45	985512_102206	
1	28.45	985512_150952	
1	28.95	985512_143657	
1	28.95	985512_175868	
1	28.95	985512_56155	
1	28.95	985512_92142	
1	29.96	984609_87537	
1	29.96	985423_61198	
1	29.96	985423_65146	
1	32	985249_55639	
1	35.63	985242_17333	
1	35.63	985249_57215	
1	40.34	985523_254219	
1	40.85	984747_109136	
1	40.85	985523_276940	
1	41.35	984747_82782	

b) Male			
LG	**Position**	**SeqPos**	**PC**
1	68.85	1102902_400399	
1	68.85	1102902_548125	
1	68.85	1102902_548816	
1	68.85	1102902_591263	
1	68.85	1102902_614353	
1	68.85	1102902_631115	
1	68.85	1102902_732946	
1	68.85	1102902_827367	
1	68.85	1102902_848901	
1	69.86	1102902_238952	
1	69.86	1102902_279290	
1	69.86	1102902_359543	
1	69.86	1102902_389667	
1	69.86	1102902_43894	
1	69.86	1102902_544839	
1	69.86	1102902_622397	
1	69.86	1102902_670353	
1	69.86	1102902_631164	1
1	70.87	1102606_576382	
1	70.87	1102606_644073	
1	70.87	1102902_124361	
1	70.87	1102902_267859	
1	70.87	1102902_521051	
1	71.37	1102606_507508	
1	71.37	1102606_752178	
1	71.87	1102606_202898	
1	71.87	1102606_411815	
1	72.37	1102606_24898	
1	72.37	1102606_438336	
1	72.37	1102606_582911	
1	72.37	1102744_60649	
1	72.37	1102606_98978	1
1	75.47	1102700_1592501	
1	75.47	1102700_950034	
1	75.47	1102744_736516	
1	75.47	1102744_810119	
1	75.47	1102765_808034	
1	76.48	1102700_1340666	
1	76.48	1102700_1512617	
1	76.98	1102765_335529	
1	76.98	1102765_482826	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
1	41.85	984747_211684		1	77.48	1102700_1307152	
1	42.35	984747_131192		1	77.48	1102700_700506	
1	42.35	985510_54427		1	77.48	1102700_803484	
1	42.35	985510_63986		1	77.48	1102765_364344	
1	42.86	985510_181622		1	77.48	1102765_5365	
1	42.86	985510_54667		1	77.99	1102700_1688182	
1	42.86	985510_55794		1	78.49	1102700_574107	
1	42.86	985510_93695		1	78.49	1102765_181246	
1	43.36	985510_149830		1	80.01	1102700_1652838	
1	44.88	985510_200617		1	80.01	1102700_764296	
1	49.05	985302_150829		1	80.01	1102765_141716	
1	49.55	985302_150362		1	80.51	1102700_778110	
1	51.08	968713_333		1	87.48	1102765_792211	
1	52.09	985381_1113048		1	91.11	1102765_171374	
1	52.09	985381_1168885		1	92.63	1102765_180405	
1	52.59	985381_1183366		1	95.19	1102765_184920	
1	53.09	985381_1042987		1	99.36	1102082_37784	
1	54.61	985381_1042730		1	100.37	1102082_11093	
1	54.61	985381_1103644		1	100.37	1102752_213068	
1	55.12	985381_1034648		1	103.47	1102752_86212	
1	55.12	985381_362133	4	1	103.97	1102752_105358	
1	55.12	985381_742908		1	103.97	1102752_204853	
1	55.62	426746_756		1	104.47	1102752_13385	
1	55.62	985381_216434		1	104.47	1102752_73971	
1	55.62	985381_350639	4	1	105.99	1102752_29413	
1	55.62	985381_421403	4	1	105.99	1102752_83940	
1	55.62	985381_614489	4	1	107	1102752_177756	
1	55.62	985381_670531	4	1	109.57	1102752_371037	
1	55.62	985381_683978		1	109.57	1102965_198902	
1	55.62	985450_200802	4	1	110.07	1103033_174975	
1	56.12	985235_589		1	110.57	1103033_181075	
1	56.12	985381_121043	4	1	111.08	1102762_6210	
1	57.13	985381_120865	4	1	112.09	1102752_308071	
1	57.13	985381_129614		1	113.1	1101890_1170	
1	57.13	985381_129944	4	1	113.1	1102331_64014	
1	57.13	985381_143740		1	117.81	1102767_636239	
1	57.13	985381_143791	4	1	119.34	1102997_282998	
1	57.13	985381_152237	4	1	121.38	1102997_98616	
1	57.13	985381_312500		1	122.9	1102962_1126508	
1	57.13	985381_454077		1	122.9	1102962_1210070	
1	57.13	985381_46713	4	1	122.9	1102962_588128	

a) Female			
LG	Position	SeqPos	PC
1	57.13	985381_583193	4
1	57.13	985381_628230	4
1	57.13	985381_678605	4
1	57.13	985381_689460	4
1	57.13	985381_690585	
1	57.13	985381_76334	4
1	57.13	985381_78708	
1	57.13	985450_104270	4
1	57.13	985450_147431	4
1	57.13	985450_200866	4
1	57.13	985450_75473	
1	57.13	985450_96621	4
1	57.13	985450_99293	
1	58.14	985381_751882	
1	58.14	985450_201179	4
1	58.14	985450_234860	4
1	58.14	985450_66664	
1	58.64	985381_100609	
1	58.64	985381_58872	
1	59.65	985381_383367	
1	59.65	985381_669518	
1	60.16	985450_292776	
1	63.28	985381_98976	4
1	64.83	985450_201234	4
1	78.84	985481_471337	
1	80.39	985335_93156	
1	80.39	985533_346840	
1	81.23	984912_248779	
1	81.23	985152_72991	
1	81.23	985408_222356	
1	81.23	985481_161332	
1	82.07	983772_1857	
1	82.07	985279_461173	
1	82.07	985481_554593	
1	82.91	983772_345	
1	82.91	984763_188816	
1	82.91	984763_19500	
1	82.91	985057_61715	
1	82.91	985311_1578944	
1	82.91	985311_1620823	
1	82.91	985311_736077	

b) Male			
LG	Position	SeqPos	PC
1	122.9	1102962_643125	
1	122.9	1102962_668962	
1	122.9	1102962_925923	
1	122.9	226175_709	
1	122.9	1102962_828717	3
1	123.4	1102962_662572	
1	123.9	1102767_213335	
1	124.41	1102767_431160	
1	124.41	1102767_459504	
1	124.41	1102767_494986	
1	124.41	1102767_508119	
1	124.41	1102962_1418202	
1	124.41	1102962_1559	
1	124.41	1102962_781549	
1	124.41	1102962_947856	
1	124.41	1102767_349211	3
1	124.41	1102767_449696	3
1	124.91	1102962_1167524	
1	125.41	1102962_1130558	3
1	125.91	1102962_747867	
1	125.91	1102962_908345	3
1	126.93	1102962_706491	
1	126.93	1102962_723020	
1	126.93	1102962_788822	
1	127.43	1102962_127216	
1	128.95	1102962_1152846	
1	128.95	1102962_1196092	
1	128.95	1102962_386525	
1	128.95	1102962_674774	
1	128.95	464216_1189	
1	128.95	1102962_587332	3
1	129.45	1102962_1177342	
1	129.45	1102962_1210087	3
1	130.46	1102962_1177878	
1	131.99	1102962_119664	
1	131.99	1102962_1213092	3
1	135.08	1094422_153	
1	135.08	1101838_769760	
1	135.58	1101838_55233	
1	136.59	1101838_161105	
1	136.59	1101838_510335	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
1	82.91	985311_775261		1	136.59	1101838_582974	
1	82.91	985321_13060		1	136.59	1101838_657261	
1	82.91	985380_505994		1	136.59	1101838_71879	
1	82.91	985380_675712		1	136.59	1101838_741504	
1	82.91	985392_504929		1	136.59	1102687_1357509	
1	82.91	985411_502809		1	136.59	1102687_1393448	
1	82.91	985411_70787		1	136.59	1102687_1412272	
1	82.91	985411_804256		1	136.59	1102687_1726907	
1	84.6	985311_1591169		1	136.59	1102687_1867334	
1	85.44	985392_411211		1	136.59	1102687_1878794	
1	86.28	985279_130025		1	136.59	1103007_1101318	
1	87.98	985553_125943		1	136.59	1103007_1112209	
1	88.82	984578_328675		1	136.59	1103007_1162685	
1	88.82	985408_169410		1	136.59	1103007_1182156	
2	0	984939_42190		1	136.59	1103007_1279557	
2	0	984939_80291		1	136.59	1103007_1337782	
2	0.79	985098_240712		1	136.59	1103007_1350310	
2	1.34	985071_73513		1	136.59	1103007_1626070	
2	2.35	985098_88011	1	1	136.59	1103007_167460	
2	2.35	985129_422165	3	1	136.59	1103007_1687216	
2	2.35	985129_443555		1	136.59	1103007_1812547	
2	2.35	985129_511665	1	1	136.59	1103007_1878801	
2	3.36	985129_130625		1	136.59	1103007_1882472	
2	4.37	985129_190945		1	136.59	1103007_384687	
2	4.37	985490_51681		1	136.59	1103007_421792	
2	4.87	979001_849		1	136.59	1103007_467719	
2	4.87	983733_13992		1	136.59	1103007_483392	
2	4.87	984125_37577		1	136.59	1103007_486786	
2	4.87	984125_52213		1	136.59	1103007_791693	
2	4.87	984894_68558		1	136.59	1103007_821917	
2	5.38	985218_135643	1	1	136.59	1103007_853749	
2	5.38	985218_190831		1	136.59	1103007_972418	
2	5.38	985218_252023		1	136.59	1101838_55885	1
2	6.39	984277_2245		1	136.59	1101838_705587	1
2	6.39	985218_418409		1	136.59	1102687_1326907	1
2	6.39	985288_160240		1	136.59	1102687_1355870	1
2	6.39	985390_85180		1	136.59	1102687_1860906	1
2	7.4	985218_229136		1	136.59	1102687_1867088	1
2	7.9	983778_7672		1	136.59	1103007_1145443	1
2	7.9	984996_93916		1	136.59	1103007_1710150	1
2	7.9	985052_175384		1	136.59	1103007_421717	1

a) Female			
LG	**Position**	**SeqPos**	**PC**
2	7.9	985052_215467	
2	7.9	985052_227082	1
2	7.9	985052_227100	
2	7.9	985052_260120	
2	7.9	985052_317977	
2	7.9	985052_337985	
2	7.9	985052_3559	
2	7.9	985288_169594	
2	7.9	985288_33671	
2	7.9	985288_37138	
2	7.9	985288_41162	
2	7.9	985288_86680	
2	7.9	985371_37464	
2	8.4	985052_176320	
2	8.9	985052_239033	
2	8.9	985349_538087	
2	9.41	985349_512451	
2	9.41	985349_519966	
2	9.91	985052_324648	
2	9.91	985349_497738	
2	9.91	985349_519005	
2	9.91	985349_603759	
2	10.41	985349_463023	
2	12.45	985349_445337	
2	13.97	985349_439852	
2	15.5	985349_423134	
2	16.03	985349_123824	
2	16.03	985460_639052	
2	19.31	985460_745486	
2	20.92	985460_686912	
2	21.45	985460_605448	
2	22.52	985460_674446	
2	25.24	985349_192292	
2	26.31	985460_153723	
2	27.38	948288_584	
2	27.91	985460_305755	
2	28.45	960073_1290	
2	29.51	985460_80369	
2	32.79	983906_49290	
2	32.79	983906_7122	
2	33.33	985044_140474	

b) Male			
LG	**Position**	**SeqPos**	**PC**
1	136.59	1103007_486836	1
1	136.59	1103007_682213	1
1	136.59	1103007_826612	1
1	136.59	1103007_905511	1
1	137.1	1101838_931953	
1	137.1	1101838_975208	
1	137.1	1102767_517361	
1	137.1	1103002_79290	
1	137.1	1103007_1441837	
1	137.1	1103007_1710102	
1	137.1	1103007_1772654	
1	137.1	1103007_549485	
1	137.1	1103007_943296	
1	140.19	1101838_800346	
1	140.19	1102687_1198195	
1	140.19	1102687_1432673	
1	140.19	1103007_1397936	
1	140.19	1103007_1892532	
1	140.19	1103007_769065	
1	140.19	1102687_1873259	1
1	140.19	1103007_1000131	1
1	142.75	1101838_949690	
1	143.26	1102687_2133343	
1	143.26	1102687_909368	
1	144.27	1102687_2053651	
1	146.31	1102687_175465	
1	146.31	1102687_489849	
1	146.31	1102687_624203	
1	146.81	1102687_616485	
1	147.31	1101926_56422	
1	147.31	1102039_104250	
1	147.31	1102039_144091	
1	147.31	1102039_162323	
1	147.31	1102039_195043	
1	147.31	1102039_265320	
1	147.31	1102039_84166	
1	147.31	1102687_640626	
1	147.31	1102737_15964	
1	147.81	1103015_161292	
1	147.81	1103015_31554	
1	147.81	1103015_86317	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
2	33.33	985044_142511		1	148.32	1103015_249560	
2	33.33	985044_234840		1	149.33	1102920_1135236	
2	33.86	985044_188885		1	149.33	1102920_944113	
2	36.02	984008_86276		1	149.83	1101809_42675	
2	36.02	985044_293446		1	149.83	1103015_477080	
2	38.18	985044_254954		1	150.84	1102188_409379	
2	39.8	985472_84523		1	151.34	1103015_728387	
2	45.39	984917_241916		1	151.85	1090470_896	
2	45.39	984917_252030		1	151.85	1102709_159017	
2	45.39	984917_272971		1	151.85	1102709_353342	
2	45.92	984917_157684		1	151.85	1102709_65261	
2	46.99	984917_222902		1	151.85	1102709_787179	
2	48.06	984917_79858		1	151.85	1102920_109914	
2	50.22	984917_100308		1	151.85	1102920_154747	
2	52.38	978652_3892		1	152.35	1102709_486884	
2	52.92	984917_90798		1	152.85	1102709_498773	
2	53.99	985130_850		1	153.35	1102709_714412	
2	55.6	983681_67172		1	153.35	1102709_717149	
2	57.21	983681_68000		1	153.91	1102709_945090	
2	57.21	985404_162287		1	154.46	1102709_1281095	
2	57.21	985404_42903		1	155.57	1101816_201308	
2	57.21	985404_47303		1	155.57	1101816_223847	
2	57.21	985404_55556		1	155.57	1101816_223881	
2	57.74	985404_236994		1	155.57	1101816_225620	
2	58.31	985404_283567		1	155.57	1102286_124210	
2	58.31	985404_283604		1	155.57	1102555_109478	
2	59.46	985441_156562		1	155.57	1102555_128929	
2	59.46	985441_16914		1	155.57	1102709_1195893	
2	59.46	985441_187020		1	156.68	1102751_220699	
2	59.46	985441_50934		1	157.23	1102555_108740	
2	59.46	985441_9090		1	157.23	1103036_67532	
2	60.02	985441_190673		1	158.34	1102555_359595	
2	61.17	985441_145184		1	159.45	1102830_89032	
2	61.73	984477_133512		1	160.01	1102782_5070	
2	61.73	984477_88176		1	160.01	1102782_50785	
2	61.73	985112_29391		1	160.01	1102782_51013	
2	61.73	985112_36001		1	160.01	1102830_237240	
2	61.73	985441_312504		1	160.01	1102830_361144	
2	62.96	985441_195470		1	160.01	1102830_441398	
2	63.57	985441_276486		1	160.01	1102830_468173	
2	65.42	984477_67579		1	160.01	1102830_568312	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
2	65.42	985404_162780		1	160.01	1102830_765640	
2	68.93	984477_71750		1	160.01	1102830_766238	
2	68.93	985441_381617		1	160.01	1102830_783005	
3	0	959290_1240		1	160.95	1102751_122364	
3	0	985447_227377		1	160.95	1102830_475337	
3	0	985465_353874		2	0	1102779_133819	
3	2.35	985149_164866		2	0	1103025_70531	
3	2.35	985495_310402		2	2.63	1102650_181473	
3	2.96	985176_682675		2	2.63	1102779_186490	
3	2.96	985298_412235		2	2.63	1102779_21109	
3	2.96	985447_402671		2	2.63	1102900_256740	
3	2.96	985497_41205		2	3.2	1102650_150183	
3	5.29	984715_292960		2	3.2	1102650_331740	
3	5.29	985176_437257		2	3.2	1103025_19846	
3	5.29	985176_454851		2	3.2	1102779_306744	1
3	5.29	985347_114169		2	3.2	1103010_68175	1
3	5.29	985347_164817		2	4.22	1102650_336400	
3	5.29	985495_79670		2	6.26	1101826_72346	
3	5.29	985496_259521	1	2	6.26	1102777_113859	
3	5.29	985496_301304		2	6.26	1102777_2159	
3	5.29	985497_41464		2	6.26	1102813_285662	
3	5.29	985532_153941		2	7.78	1102650_125973	
3	5.29	985532_225058		2	8.79	1102813_264910	
3	5.29	985532_280973		2	8.79	1103000_1814	
3	5.82	984333_155424		2	11.88	1102432_1588804	
3	5.82	985447_375510		2	11.88	1102936_266428	
3	6.9	959290_3820		2	11.88	1102936_200938	1
3	6.9	984229_13070		2	12.39	1102936_327479	
3	6.9	984715_182775		2	14.43	1102936_485171	
3	6.9	984863_22732		2	15.95	1102432_1159469	
3	6.9	985298_129984		2	15.95	1102936_961137	
3	6.9	985444_128001		2	16.45	1102432_1251971	
3	6.9	985444_128115		2	16.45	1102432_1380731	
3	6.9	985447_379125		2	16.45	1102432_1452606	
3	6.9	985447_383502		2	16.45	1102432_859615	
3	6.9	985495_152939		2	16.95	1094760_494	
3	6.9	985495_504419		2	16.95	1102432_1198570	
3	6.9	985495_707382		2	16.95	1102936_951452	
3	7.43	984715_28371		2	17.96	1101772_13529	
3	7.43	985176_609709		2	17.96	1101772_35054	
3	7.43	985176_824330		2	17.96	1101772_37239	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
3	7.43	985465_440726		2	17.96	1102432_1009927	
3	7.43	985465_446322		2	17.96	1102432_1160405	
3	7.43	985532_155521		2	17.96	1102432_1222244	
3	7.43	985532_24678		2	17.96	1102432_1304625	
3	7.97	985358_277457		2	17.96	1102432_1323228	
3	8.5	984229_53620		2	17.96	1102432_857347	
3	8.5	984351_184370		2	17.96	1102432_1209969	1
3	8.5	984351_191808		2	18.97	1102432_1209987	
3	8.5	984715_241313		2	18.97	1102432_1311314	
3	8.5	984715_285585		2	18.97	1102432_899839	
3	8.5	985149_174118		2	19.48	1102432_824251	
3	8.5	985298_411034		2	19.48	1102432_880916	
3	9.04	984715_215961		2	19.48	1102432_881881	
3	9.57	984333_167377		2	19.48	1102432_989219	
3	9.57	984351_43851		2	20.49	1102432_801114	
3	9.57	984351_57147		2	20.49	1102432_874324	
3	9.57	984351_69176		2	21.5	1102432_784273	
3	9.57	984421_214343		2	23.54	1102432_111656	
3	9.57	984715_285617		2	23.54	1102432_470510	
3	9.57	985444_106722		2	23.54	1102432_503713	
3	9.57	985444_165418		2	24.04	1102432_157900	
3	10.11	985219_422654		2	24.04	1102432_212745	
3	10.11	985444_291976		2	24.04	1102432_300754	
3	10.11	985444_52780		2	26.08	1102432_145307	
3	12.15	984333_21697		2	26.08	1102432_78396	
3	12.15	984333_33718		2	27.09	1102370_99139	
3	12.15	984333_96377		2	27.09	1102432_580654	
3	12.15	984421_193476		2	28.1	1090875_1353	
3	12.15	984421_25477		2	29.11	1102370_375735	
3	12.15	984421_52830		2	29.62	1102370_41760	
3	12.15	984421_80791		2	30.12	1102370_234521	
3	12.15	984421_95439		2	30.12	1102695_1437685	
3	12.15	985444_42895		2	31.13	1102695_1375391	
3	12.65	984027_34287		2	31.63	1102695_1159040	
3	12.65	984333_422085		2	31.63	1102695_1315401	
3	13.15	972244_2081		2	31.63	1102695_1362158	
3	13.15	985186_143592		2	32.13	1102695_1301210	
3	13.15	985186_57713		2	33.14	1102695_1019367	
3	13.15	985219_111092		2	33.14	1102695_1091552	
3	13.15	985219_261621		2	33.14	1102695_1101516	
3	13.15	985219_315515		2	33.14	1102695_922111	

a) Female			
LG	**Position**	**SeqPos**	**PC**
3	13.15	985219_412896	
3	13.15	985219_466797	
3	13.15	985219_51311	
3	13.15	985219_79345	
3	15.2	985464_51686	
3	16.21	985464_72139	
3	16.71	985464_65918	
3	17.72	985085_328086	
3	18.22	972227_991	
3	18.22	985451_21550	
3	18.72	985252_10778	
3	20.76	985085_283764	
3	21.27	985451_457427	
3	21.27	985451_477027	
3	21.77	985451_610401	
3	23.29	985451_1077884	
3	23.29	985451_791358	
3	26.92	985451_1007421	
3	26.92	985451_1116153	
3	26.92	985451_956986	
3	32.19	985451_1183937	
3	32.19	985451_1184200	
3	35.82	985451_1174689	
3	36.32	985458_110523	
3	37.33	985451_1182870	
3	39.9	985458_386999	
3	40.91	985458_230297	
3	40.91	985458_456703	
3	41.92	985458_517922	
3	41.92	985458_534288	
3	42.93	985458_383906	
3	43.94	985458_733297	
3	45.46	985458_753618	
3	46.47	985458_804726	
3	48.1	985458_910403	
3	51.42	985458_1035854	
3	51.42	985458_913186	
3	51.95	985456_19480	
3	51.95	985456_9150	
3	51.95	985458_1034387	
3	51.95	985458_1407837	

b) Male			
LG	**Position**	**SeqPos**	**PC**
2	33.68	1102695_1022603	
2	34.21	1102987_2702	
2	34.74	1102695_1043041	
2	35.27	1102695_708557	
2	35.27	1102695_712274	
2	36.88	1102695_568572	
2	39.6	1102695_314104	
2	39.6	1102695_325460	
2	40.67	1102695_231872	
2	41.2	1102695_300300	
2	42.27	1102695_154341	
2	42.27	1102695_174598	
2	43.34	1102695_80783	
2	43.34	1102695_94718	
2	43.87	1102695_12535	
2	43.87	1102695_711	
2	44.41	1102958_440486	
2	46.02	1102958_359245	
2	46.02	1102958_372628	
2	46.02	1102958_439658	
2	46.55	1102958_376841	
2	47.08	1102958_187906	
2	47.08	1102958_248284	
2	47.62	1102958_139221	
2	47.62	1102958_139258	
2	49.78	1094351_645	
2	49.78	1102745_181846	
2	49.78	1102745_214165	
2	49.78	1102958_35255	
2	49.78	1102958_87210	
2	49.78	1102958_95006	
2	50.31	1094284_1202	
2	51.92	1102745_185389	
2	51.92	1102958_53863	
2	52.45	1102060_219056	
2	52.45	1102060_264398	
2	52.45	1102060_30420	
2	52.45	1102060_37029	
2	52.45	1102745_86627	
2	54.38	1102060_284932	
2	54.38	1102745_177008	

a) Female			
LG	**Position**	**SeqPos**	**PC**
3	51.95	985458_1409927	
3	51.95	985458_1609193	
3	54.28	985458_1202115	
3	56.41	985458_1762266	
3	59.19	985458_1634356	
4	0	985238_151378	
4	1.43	985073_73684	
4	1.43	985406_8640	
4	4.51	984462_61542	
4	4.51	984806_5929	
4	4.51	984864_9446	
4	4.51	985095_29383	
4	4.51	985238_349511	
4	4.51	985399_15145	
4	4.51	985399_19186	
4	4.51	985399_30263	
4	5.01	985376_19093	
4	5.51	985095_48392	
4	6.01	984462_139983	
4	6.01	984462_62052	
4	6.01	984806_10100	
4	6.01	984806_34652	
4	6.01	984806_34723	
4	6.01	984806_7418	
4	6.01	984864_160177	
4	6.01	984864_36409	
4	6.01	985238_190757	
4	6.01	985406_366584	
4	7.54	984462_103567	
4	7.54	984462_154991	
4	7.54	984462_22954	
4	7.54	984462_325454	
4	7.54	984462_59544	
4	7.54	984806_11808	
4	7.54	984806_25394	
4	7.54	984864_137958	
4	7.54	985406_219739	
4	7.54	985406_697828	
4	8.04	985406_270785	
4	8.04	985406_637591	
4	8.54	985104_50671	

b) Male			
LG	**Position**	**SeqPos**	**PC**
2	56.6	1102745_15845	
2	58.6	1102060_280805	
3	0	1102691_107054	
3	0	1102691_301299	
3	0	1102691_308712	
3	0.53	1102691_253752	
3	0.53	1102691_260493	
3	0.53	1102691_335745	
3	0.53	1102691_361502	
3	1.03	1102691_369185	
3	1.54	1102691_424275	
3	3.06	1102691_409804	
3	5.1	1102686_272639	
3	6.11	1102686_266997	
3	7.12	1102686_252639	
3	7.62	1102686_105501	
3	8.13	1102686_140172	
3	9.14	1102686_105737	
3	9.64	1102686_68327	
3	10.14	1102914_2305	
3	10.64	1102686_46123	
3	10.64	1102944_10726	
3	11.15	1102914_137297	
3	11.65	1102914_32902	
3	13.17	1102944_15555	
3	13.67	1102914_65303	
3	13.67	1102944_39334	
3	15.2	1102957_1037506	
3	15.7	1102957_885060	
3	16.2	1102957_884189	
3	16.71	1100660_1120	
3	18.75	1093089_251	
3	18.75	1093089_309	
3	18.75	1093089_731	
3	18.75	1102957_374370	
3	18.75	1102957_550152	
3	18.75	1102957_568766	
3	18.75	1102957_582209	
3	18.75	1102957_613430	
3	19.76	1102957_370472	
3	19.76	1102957_516039	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
4	8.54	985104_55437		3	19.76	1102957_533936	
4	8.54	985104_60151		3	19.76	1102957_562052	
4	8.54	985104_8034		3	19.76	1102957_568863	
4	9.04	985014_86740		3	20.26	1102957_172276	
4	9.04	985104_111587		3	20.26	1102957_261252	
4	9.04	985104_112310	3	3	21.78	1102957_209156	
4	9.04	985104_169794		3	22.28	1102957_148608	
4	9.55	985104_341469		3	22.79	1102957_129760	
4	10.05	984768_18766	1	3	24.31	1102954_110036	
4	10.05	984768_22901		3	24.31	1102954_141208	
4	10.05	984768_29652		3	24.81	1102954_269284	
4	10.05	985104_247621		3	25.31	1102954_328943	
4	10.55	985014_114587		3	25.82	1103012_47094	
4	10.55	985170_101498		3	27.34	1103012_18888	
4	10.55	985170_149780		3	27.34	1103012_455757	
4	10.55	985170_182319		3	27.84	1103012_542124	
4	10.55	985170_240677		3	28.85	1103012_676783	
4	10.55	985170_256898		3	29.86	1103012_162434	
4	10.55	985170_37256		3	30.87	1102440_652744	
4	11.05	985170_275087		3	30.87	1103012_744586	
4	12.06	985170_160746		3	31.88	1102440_614296	
4	12.06	985170_166855		3	33.41	1102440_343084	
4	13.07	985170_205312		3	33.41	1102440_420176	
4	13.07	985259_142972		3	33.41	1102440_482263	
4	13.58	984721_159767		3	33.41	1102440_51196	
4	14.08	985107_56739		3	33.41	1102440_83091	
4	14.08	985107_890		3	33.91	1102440_141952	
4	14.08	985142_38031		3	33.91	1102440_160765	
4	14.08	985245_21286		3	33.91	1102440_283732	
4	14.58	983917_13003		3	33.91	1102440_84424	
4	14.58	983917_28834		3	33.91	1102440_99640	
4	14.58	983917_62491		3	34.92	1102440_535150	
4	14.58	985142_37993		3	35.42	1101858_88657	
4	14.58	985425_13853		3	35.92	1101858_143014	
4	14.58	985425_14157		3	36.43	1102481_678760	
4	15.59	983917_30305		3	36.43	1103039_892123	
4	16.1	949633_4249		3	36.93	1101858_67606	
4	16.1	985425_244088		3	36.93	1103039_861912	
4	17.11	985319_376661		3	38.45	1103039_236582	
4	17.11	985319_51319		3	38.45	1103039_358114	
4	17.11	985425_302486		3	38.45	1103039_426227	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
4	19.15	985319_1592		3	38.45	1103039_495884	
4	19.15	985319_564677		3	38.45	1103039_502053	
4	19.65	985062_43062		3	38.45	1103039_517587	
4	19.65	985319_662573		3	38.45	1103039_575467	
4	20.66	956887_1555		3	38.45	1103039_592318	
4	21.16	985319_435057		3	38.45	1103039_603788	
4	22.68	985062_144694		3	38.45	1103039_620545	
4	24.21	984063_165668		3	39.46	1103039_223762	
4	24.21	984063_197002		3	39.46	1103039_483476	
4	26.25	985388_77296		3	40.47	1102292_82276	
4	27.77	985388_117128		3	40.47	1102346_134263	
4	27.77	985388_151040		3	40.47	1102346_45741	
4	27.77	985388_192491		3	40.47	1103039_174809	
4	27.77	985388_93970		3	40.47	1103039_181558	
4	28.78	985388_319285		3	40.47	1103039_74821	
4	28.78	985388_518263		3	40.47	1102346_133540	3
4	28.78	985388_530441		3	40.47	1103039_185694	1
4	28.78	985388_548409		3	40.97	1102346_193070	
4	28.78	985388_576217		3	40.97	1102346_197775	
4	29.28	985388_449190		3	40.97	1102346_54011	
4	29.28	985388_504283		3	41.48	1090741_409	
4	29.28	985388_505477		3	41.48	1102346_188406	
4	29.28	985388_722476		3	41.98	1102292_61038	
4	30.29	985388_315387		3	41.98	1102993_926546	
4	30.8	985388_593251		3	41.98	1102993_978006	
4	31.81	985388_722054		3	42.48	1102292_21877	
4	31.81	985388_722534		3	42.48	1102292_22387	
4	32.31	957988_1130		3	42.48	1102292_24347	
4	33.32	985388_900697		3	42.48	1102484_164725	
4	38.04	985388_901568		3	42.48	1102993_317245	
4	40.6	985438_388751		3	42.48	1102993_671405	
4	41.1	985438_145127		3	42.48	1102993_733383	
4	41.1	985438_189552		3	42.48	1102993_769835	
4	41.1	985438_194702		3	42.48	1102993_788281	
4	41.1	985438_216377		3	42.48	1102993_941516	
4	41.1	985438_43373		3	42.98	1102484_142391	
4	42.63	985207_351505		3	42.98	1102993_407592	
4	42.63	985207_397606		3	43.49	1102484_246275	
4	42.63	985207_401351		3	43.49	1102993_265832	
4	43.13	950392_443		3	43.99	1101734_25960	
4	43.13	982904_3226		3	43.99	1102484_247764	

a) Female			
LG	**Position**	**SeqPos**	**PC**
4	43.63	985207_244533	
4	43.63	985207_297305	
4	43.63	985207_311057	
4	45.67	962452_150	
4	48.77	985207_244769	
4	49.78	971504_165	
4	49.78	985207_44628	
4	49.78	985207_50175	
4	50.28	971504_190	
4	50.78	985322_377414	
4	50.78	985322_407669	
4	50.78	985322_422527	
4	51.28	985322_248135	
4	51.28	985322_254902	
4	51.28	985322_295673	
4	51.28	985322_312730	
4	51.28	985322_339806	
4	51.28	985322_357879	
4	52.65	985322_104100	
4	58.81	985322_305228	
5	0	985195_24519	
5	0	985286_349892	
5	3.71	984292_66007	
5	3.71	985106_293525	
5	3.71	985286_341998	
5	3.71	985398_33709	
5	5.37	983934_255876	
5	5.37	984204_266268	
5	5.37	984519_125686	
5	5.37	985341_413537	
5	5.37	985362_347095	
5	5.37	985362_958375	
5	5.92	985317_308359	
5	6.47	983929_235419	
5	6.47	983929_77586	
5	6.47	983934_165282	
5	6.47	983934_3473	
5	6.47	983934_550247	
5	6.47	984030_46269	
5	6.47	984045_297236	
5	6.47	984326_7972	

b) Male			
LG	**Position**	**SeqPos**	**PC**
3	43.99	1102484_250446	
3	43.99	1102993_117388	
3	43.99	1102993_86582	
3	45.51	1102484_42889	
3	46.02	1101808_2070	
3	46.02	1102404_1351	
3	46.02	1102770_9021	
3	46.02	1103017_254573	
3	46.02	1103017_414460	
3	47.93	1101734_71147	
3	47.93	1102404_5501	
3	47.93	1102770_1005	
3	52.43	1102484_35060	
3	52.43	1102993_50849	
3	52.43	1103017_215895	
4	0	1102743_251876	
4	4.41	1102915_246370	
4	8.84	1102743_527461	
4	11.64	1103014_66469	
4	16.21	1102915_206777	
4	17.32	1102915_300352	
4	17.32	1102915_309137	
4	17.32	1102915_329958	
4	17.32	1102915_585811	
4	19.36	1102915_405733	
4	19.36	1102915_463038	
4	19.36	1102915_541383	
4	19.86	1102915_570120	
4	20.37	1102915_588475	
4	20.87	1102915_603647	
4	20.87	1102915_613722	
4	20.87	1102915_654357	
4	21.37	1102915_620403	
4	21.87	1102915_777386	
4	23.91	1102915_777439	
4	23.91	1102915_848606	
4	24.92	1102915_835585	
4	27.49	1102915_985301	
4	27.49	1103038_2913427	
4	28.5	1103038_2833968	
4	29.03	1103038_2014387	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
5	6.47	985314_35040		4	29.03	1103038_2605744	
5	6.47	985314_35112		4	29.57	1103038_1925351	
5	6.47	985314_89067		4	29.57	1103038_2299179	
5	6.47	985398_228385		4	29.57	1103038_2313386	
5	6.47	985504_76405		4	30.64	1103038_2218837	
5	6.97	983934_106589		4	32.82	1103038_2301681	
5	7.48	985341_300589		4	33.35	1103038_1957791	
5	7.98	985217_326624		4	33.89	1103038_1597399	
5	7.98	985317_380009		4	33.89	1103038_1627398	
5	7.98	985362_1000848		4	33.89	1103038_1878102	
5	7.98	985362_844731		4	33.89	1103038_1893540	
5	7.98	985398_431720		4	33.89	1103038_1900015	
5	7.98	985485_15829		4	35.51	1103038_1494753	
5	8.48	12812_448		4	37.13	1103038_1329040	
5	8.48	983934_255827		4	37.13	1103038_1431099	
5	8.48	984204_109150		4	37.67	1103038_1197885	
5	8.48	984204_182224		4	38.2	1103038_994356	
5	8.48	984204_263665		4	38.74	1103038_397460	
5	8.48	984204_279439		4	38.74	1103038_728025	
5	8.48	984204_85401		4	38.74	1103038_732533	
5	8.48	984292_163809		4	38.74	1103038_866902	
5	8.48	984292_37446		4	38.74	1103038_961584	
5	8.48	985217_112389		4	38.74	1103038_976509	
5	8.48	985286_256685		4	39.81	1103038_100661	
5	8.48	985286_417884		4	39.81	1103038_105744	
5	8.48	985286_437319		4	39.81	1103038_377943	
5	8.48	985362_251305		4	39.81	1103038_538446	
5	8.48	985363_342272		4	40.89	1101827_309511	
5	8.48	985363_54681		4	40.89	1101827_313299	
5	8.48	985398_133094		4	41.42	1101827_383382	
5	8.98	984204_287951		4	41.96	1101822_224221	
5	9.49	984204_247897		4	41.96	1101827_152943	
5	9.49	985106_219662		4	41.96	1101851_160748	
5	9.99	984204_263056		4	41.96	1102269_192490	
5	9.99	985106_280270		4	41.96	1102269_284233	
5	9.99	985106_430935		4	41.96	1102269_502941	
5	9.99	985106_454281		4	41.96	1102481_119823	
5	10.49	985106_416717		4	41.96	1102481_1236363	
5	10.99	985106_257466		4	41.96	1102481_1286814	
5	11.5	985106_576626		4	41.96	1102481_143883	
5	12	985106_709910	1	4	41.96	1102481_1568691	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
5	13.52	985106_1030029		4	41.96	1102481_214331	
5	14.53	985106_710403		4	41.96	1102481_250258	
5	15.54	985106_557299		4	41.96	1102481_292443	
5	16.55	985024_137608		4	41.96	1102481_450353	
5	17.05	985024_284238		4	41.96	1102481_479097	
5	18.58	985024_633268		4	41.96	1102481_573960	
5	21.14	985434_304991		4	41.96	1102481_591766	
5	21.14	985434_454656		4	41.96	1102481_616224	
5	21.14	985434_518933		4	41.96	1102481_616281	
5	22.67	985434_650652		4	41.96	1102481_91418	
5	25.23	985434_331157		4	41.96	1102481_963910	
5	25.23	985434_595568		4	41.96	1102760_1108836	
5	25.73	985434_454368		4	41.96	1102760_1119839	
5	27.77	985434_764855		4	41.96	1102760_114261	
5	29.3	985045_68827		4	41.96	1102760_1363479	
5	30.82	985045_282315		4	41.96	1102760_1485818	
5	30.82	985045_320653		4	41.96	1102760_1494716	
5	32.86	985045_358390		4	41.96	1102760_2005585	
5	35.95	985045_597139		4	41.96	1102760_2279862	
5	37.48	985045_712471		4	41.96	1102760_2319595	
5	37.48	985045_747130		4	41.96	1102760_2337075	
5	37.48	985045_747155		4	41.96	1102760_661411	
5	38.49	985045_729316		4	41.96	1102760_783457	
5	42.12	985045_907650		4	41.96	1102760_79682	
5	43.64	985045_1311718		4	41.96	1102760_925194	
5	44.14	985045_1285867		4	42.49	1102760_1204600	
5	46.71	985045_1533517		4	42.49	1102760_1292581	
5	46.71	985045_1592855		4	42.49	1102760_1860227	
5	47.72	985045_1512565		4	43.03	1101822_207706	
5	48.22	985045_1647589		4	43.03	1102760_1521248	
5	49.74	985045_1533498		4	43.56	1101822_203909	
5	51.26	984016_65392		4	43.56	1102760_1384169	
5	51.26	984016_65462		4	43.56	1102760_775415	
5	51.89	984016_92896		4	44.1	1103020_242214	
5	52.51	984016_184279		4	44.63	1099453_3601	
5	57.71	984016_312358		4	44.63	1102481_546886	
5	57.71	984016_325468		4	44.63	1102760_217631	
6	0	985482_575680		4	44.63	1102760_233632	
6	1.8	985482_227557		4	44.63	1103020_1480529	
6	1.8	985482_474908		4	44.63	1103031_199861	
6	6.26	985482_135238	1	4	44.63	1103031_205005	

a) Female			
LG	**Position**	**SeqPos**	**PC**
6	11.39	984192_200393	
6	11.39	985025_184629	
6	11.96	984192_284989	
6	12.53	984192_231882	
6	14.69	985025_33157	
6	15.76	985025_70321	
6	16.83	985025_197756	
6	16.83	985025_87959	
6	18.44	985025_307614	
6	19.51	985020_503053	
6	21.13	985025_521806	
6	23.29	985020_113501	
6	23.29	985020_276381	
6	23.29	985025_443068	
6	23.82	985020_82524	
6	25.54	985020_455092	
6	27.27	985020_395506	
6	27.27	985020_395578	
6	27.84	985020_670438	
6	27.84	985020_699578	
6	27.84	985413_1626346	
6	28.37	985020_994843	
6	28.91	985020_1079688	
6	28.91	985020_872407	
6	28.91	985109_17928	
6	29.44	985020_829197	
6	29.44	985473_481535	
6	30.52	985473_33325	
6	32.14	985413_1594113	
6	32.67	985413_1764112	
6	32.67	985473_349750	
6	33.82	985413_705993	
6	34.96	985413_75020	
6	37.87	985413_148686	
6	37.87	985413_77162	
6	37.87	985489_429228	
6	37.87	985489_465107	
6	37.87	985489_498643	
6	37.87	985489_545138	
6	37.87	985489_599924	
6	38.44	985489_260435	

b) Male			
LG	**Position**	**SeqPos**	**PC**
4	44.63	1103031_333479	
4	44.63	1103031_440523	
4	45.16	1101828_341489	
4	45.16	1102290_2378	
4	45.16	1102833_186411	
4	45.16	1103020_1696655	
4	45.16	1103020_223578	
4	45.16	1103020_681774	
4	45.16	1103020_952584	
4	45.16	1103031_76281	
4	46.79	1101828_79488	
4	47.32	1103031_367285	
4	48.94	1102760_1793966	
4	50.02	1102760_2006803	
4	51.25	1102481_240537	
5	0	1101741_93381	
5	0	1102748_1263892	
5	0.99	1101741_254180	
5	3.55	1101744_575537	
5	3.55	1102706_145623	
5	5.19	1102761_228561	
5	5.19	1102969_1172021	
5	6.71	1101741_411551	
5	6.71	1102761_220683	
5	6.71	1102761_611602	
5	6.71	1102935_890898	
5	6.71	1102959_763789	
5	6.71	1102959_80517	
5	7.21	1101741_1203657	
5	7.21	1101741_618134	
5	7.21	1101741_922062	
5	7.21	1102697_142880	
5	7.21	1102706_260438	
5	7.21	1102725_103070	
5	7.21	1102761_553802	
5	7.21	1102935_809612	
5	7.21	1102959_215622	
5	7.21	1102959_510867	
5	7.21	1102959_603686	
5	7.21	1102969_354771	
5	7.21	1102969_537439	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
6	39	985428_187163		5	7.21	1102969_729057	
6	39	985428_377828		5	7.21	1102969_911815	
6	39	985428_764562		5	7.21	1102969_966751	
6	39	985428_85237		5	7.71	1101741_1274474	
6	39	985489_37482		5	7.71	1101799_39212	
6	39	985489_67730		5	7.71	1102417_100034	
6	39	985536_284889		5	7.71	1102761_1320798	
6	39.57	985428_503180		5	7.71	1102761_133868	
6	39.57	985428_595268		5	7.71	1102761_1591494	
6	43.08	984811_165300		5	7.71	1102761_524324	
6	43.08	984901_129794		5	7.71	1102761_568992	
6	43.65	985428_725165		5	7.71	1102959_510916	
6	44.22	985428_774091		5	7.71	1102959_661431	
6	44.79	983734_33221		5	7.71	1102959_969515	
6	44.79	983944_22037		5	7.71	1102966_127217	
6	44.79	984020_30093		5	7.71	1102969_1328563	
6	44.79	984811_202330		5	7.71	1102969_632828	
6	44.79	984811_36215		5	7.71	1102969_866226	
6	44.79	984921_237875		5	8.22	1101741_436833	
6	44.79	985099_198032		5	8.22	1102761_722305	
6	44.79	985351_162642		5	8.72	1101744_246487	
6	44.79	985351_258140		5	8.72	1101744_36530	
6	44.79	985354_73529		5	8.72	1102706_183346	
6	44.79	985364_22096		5	8.72	1102706_240411	
6	44.79	985369_76287		5	8.72	1102706_263042	
6	44.79	985448_220365		5	8.72	1102706_57330	
6	44.79	985505_298876		5	9.22	1101744_503260	
6	44.79	985536_184109		5	9.22	1101744_540293	
6	44.79	985536_187684		5	9.22	1102706_247173	
6	44.79	985536_34863		5	9.22	1102706_263651	
6	44.79	985536_57830		5	9.22	1102706_278305	
6	45.35	984085_199672		5	9.72	1101744_8019	
6	45.92	65298_1565		5	10.23	1101744_59863	
6	45.92	984589_70617		5	11.24	1101744_739400	
6	45.92	984625_12970		5	11.24	1102748_192620	
6	45.92	985422_177756		5	11.74	1101744_716042	
6	45.92	985483_211635		5	12.24	1101744_701823	
6	46.49	65298_1528		5	12.24	1101744_852097	
6	46.49	967370_842		5	12.24	1101744_987195	1
6	46.49	985422_175940		5	12.74	1101744_987688	
6	46.49	985551_77088		5	14.27	1101744_832773	

a) Female			
LG	**Position**	**SeqPos**	**PC**
6	47.81	985452_306681	
6	50.47	985337_76196	
6	50.47	985452_34998	
6	51.18	984873_33841	
6	51.18	985448_114146	
6	55.73	985448_214678	
6	56.61	983874_43606	
6	56.61	984558_7069	
7	0	977573_1369	
7	0	984947_49206	
7	0	984947_50282	
7	1.72	984947_21977	
7	1.72	984947_23674	
7	1.72	984947_25721	
7	1.72	984947_40694	
7	1.72	984947_47219	
7	1.72	984947_63305	
7	1.72	984947_73266	
7	2.29	984947_122493	
7	2.29	984947_35198	
7	2.29	984947_81253	
7	2.86	984947_130114	
7	3.43	977573_1465	
7	4.57	984947_31282	
7	6.28	985421_60273	
7	6.85	984898_142806	
7	6.85	984898_20118	
7	7.38	325826_577	
7	7.38	975844_14673	
7	7.38	984898_109067	
7	7.38	984898_118059	
7	7.38	984898_33034	
7	7.38	985375_16193	
7	7.38	985375_4232	
7	7.38	985375_8008	
7	7.38	985421_124683	
7	7.91	325826_619	
7	7.91	984898_350	
7	7.91	984898_39968	
7	7.91	984898_70827	
7	7.91	984898_70896	

b) Male			
LG	**Position**	**SeqPos**	**PC**
5	15.28	1102748_276010	
5	16.8	1102748_416774	
5	21.52	1102748_697274	
5	22.53	1102748_1144878	
5	22.53	1102772_959563	
5	23.03	1102748_1117841	
5	24.04	1102991_21242	
5	25.05	1102748_1227697	
5	25.55	1102772_914448	
5	26.56	1102748_1263608	
5	29.13	1102772_457761	
5	29.63	1102772_488016	
5	30.13	1102772_230692	
5	31.14	1102772_269100	
5	33.71	1103005_365822	
5	33.71	1103005_400333	
5	34.72	1103005_365797	
5	35.73	1103005_264007	
5	39.89	951703_646	
5	42.46	1102671_103251	
5	42.46	1102671_157372	
5	44.5	1102671_157391	
5	45.51	1102671_177722	
5	47.55	1102763_74433	
5	48.05	1102763_103728	
5	48.05	1102763_74503	
5	49.46	1102763_327968	
5	51.01	1102763_341080	
6	0	1101980_30564	
6	1.45	1101844_9095	
6	2.1	1101844_19426	
6	7.55	1102669_3006265	
6	7.55	1102927_336874	
6	9.99	1102927_365385	
6	12.76	1102927_152026	
6	13.86	1102927_154082	
6	14.95	1102669_3010228	
6	15.49	1102669_2867009	
6	15.49	1102669_2869794	
6	16	1102669_2759051	
6	18.56	1102669_2708075	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
7	7.91	984898_71142		6	19.06	1102669_2687726	
7	7.91	984898_71180		6	20.07	1102669_2365332	
7	7.91	985316_4651		6	20.07	1102669_2505053	
7	7.91	985375_10042		6	22.64	1102669_2488710	
7	7.91	985375_17825		6	24.68	1102669_2368423	
7	8.45	975844_1460		6	27.24	1102669_2198653	
7	8.45	984568_20653		6	30.87	1102669_1704896	
7	8.45	984568_3014		6	30.87	1102669_1710668	
7	8.45	984898_10643		6	30.87	1102669_1711735	
7	8.45	984898_35462		6	30.87	1102669_1711998	
7	8.45	984898_38076		6	31.37	1102669_1526975	
7	8.45	984898_40780		6	31.88	1102669_1646836	
7	8.45	984898_493	1	6	32.89	1102669_1471688	
7	8.45	985375_10320		6	33.39	1102669_1602090	
7	8.45	985375_12955		6	33.89	1102669_1305041	
7	8.45	985375_15825	1	6	34.9	1093818_305	
7	8.45	985375_25924		6	35.41	1102669_1008788	
7	8.45	985375_27758		6	35.91	1102669_655839	
7	8.45	985375_7233	1	6	35.91	1102669_655887	
7	8.45	985375_7882		6	35.91	1102669_981220	
7	8.45	985375_9257		6	35.91	244318_100	
7	9.97	984568_19623		6	36.41	1102669_516347	
7	9.97	984568_26263		6	36.41	1102669_622798	
7	9.97	984668_36562		6	36.91	1102669_156118	
7	9.97	984898_113636		6	36.91	1102669_172854	
7	9.97	984898_41099		6	37.92	1102669_63983	
7	9.97	985316_135076		6	37.92	1102669_69935	
7	9.97	985316_158677		6	38.93	1102351_203384	
7	9.97	985316_190729		6	38.93	1102351_250591	
7	9.97	985316_46699		6	38.93	1102669_96177	
7	9.97	985316_5241		6	39.44	1102351_448341	
7	9.97	985316_56370		6	39.94	1096019_1588	
7	9.97	985316_78845		6	39.94	1102669_50639	
7	9.97	985316_79790		6	40.44	1102351_141883	
7	9.97	985316_8738		6	40.44	1102351_278173	
7	9.97	985316_8789		6	40.44	1102351_420972	
7	9.97	985316_90866		6	40.44	1102415_31299	
7	9.97	985375_4157		6	40.94	1102351_395820	
7	10.47	960364_648		6	41.45	1102351_83821	
7	10.47	985316_134546		6	41.45	1102415_117265	
7	10.47	985316_154506		6	41.45	1102783_1953059	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
7	10.47	985316_34116		6	41.95	1102641_124246	
7	10.47	985316_74649		6	41.95	1102641_81309	
7	10.47	985316_80223		6	41.95	1102783_1021485	
7	10.97	985316_141269		6	41.95	1102783_1735758	
7	11.48	341011_1000		6	41.95	1102783_182418	
7	11.98	984668_46280		6	41.95	1102783_559585	
7	11.98	984668_8951		6	41.95	1102783_587271	
7	11.98	985316_240426		6	41.95	1102783_615536	
7	11.98	985316_240563		6	41.95	1102783_630295	
7	12.48	985316_206342		6	41.95	1102783_727915	
7	12.98	984668_46254		6	41.95	1102783_850938	
7	12.98	984668_8961		6	41.95	1102785_621643	
7	12.98	985316_240128		6	41.95	1102785_633596	
7	14	960985_1141		6	41.95	1102785_695943	
7	14	960985_1401		6	41.95	1102785_746906	
7	15.52	971422_1927		6	41.95	1103028_206889	
7	16.02	167479_298		6	41.95	1103028_206921	
7	16.52	960833_654		6	41.95	1103028_214163	
7	18.05	985297_129805		6	42.45	1102351_131950	
7	18.55	984650_125046		6	42.45	1102783_1496313	
7	18.55	985297_49514		6	42.45	1102783_1623375	
7	19.05	984650_125071		6	42.45	1102783_1682033	
7	19.55	984650_54697		6	42.45	1102783_1745649	
7	19.55	985297_49131		6	42.45	1102783_1763442	
7	20.56	984650_87706		6	42.45	1102783_2064891	
7	21.07	985382_59967		6	42.45	1102783_2076932	
7	22.08	985382_139347		6	42.45	1102783_2090067	
7	22.08	985382_161378		6	42.45	1102783_748542	
7	24.12	985382_247328		6	42.45	1102783_984260	
7	25.13	985037_37007		6	42.95	1102323_46022	
7	26.14	985382_306878		6	42.95	1102323_58940	
7	26.64	985037_17440		6	42.95	1102480_382693	
7	29.2	708739_507		6	42.95	1102683_422621	
7	30.21	985037_135100		6	42.95	1102783_1660692	
7	37.76	983928_50633		6	42.95	1102783_1660806	
7	37.76	985036_174541		6	42.95	1102783_1945621	
7	39.28	985036_43302		6	42.95	1103028_103946	
7	39.78	984414_15186		6	42.95	1103028_137287	
7	40.28	984414_44825		6	42.95	1103028_162701	
7	44.45	984414_25459		6	42.95	1103028_243324	
7	44.45	985437_193438		6	42.95	1103028_283812	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
7	45.98	985173_73357		6	42.95	1103028_673818	
7	45.98	985437_141461		6	42.95	1103028_863605	
7	46.48	985437_210656		6	42.95	1103034_1428380	
7	47.01	984099_2508		6	43.46	1101819_47717	
7	47.01	984240_97806		6	43.46	1102683_211561	
7	47.01	985173_73008		6	43.46	1102683_39616	
7	47.01	985437_344540		6	43.46	1102683_57401	
7	47.01	985467_101721		6	43.46	1102783_2276148	
7	47.01	985467_223802		6	43.46	1103034_852923	
7	48.09	984099_1278		6	43.46	1103034_885195	
7	48.09	984240_9681		6	43.96	1102999_1392750	
7	48.09	985087_14904		6	43.96	1102999_808385	
7	48.09	985467_201257		6	43.96	1102999_942318	
7	48.09	985467_226073		6	43.96	1103034_1080634	
7	48.09	985467_231593		6	43.96	1103034_452113	
7	48.76	985173_19052		6	43.96	1103034_456491	
7	49.5	984099_2421		6	43.96	1103034_460107	
7	53.45	984240_4316		6	43.96	1103034_840804	
7	55.72	388117_870		6	44.46	1101819_273756	
8	0	985263_1645		6	44.46	1101819_567056	
8	1.72	985157_593422		6	44.46	1101819_606336	
8	4.33	983736_161999		6	44.46	1102785_735267	
8	4.33	983736_181922		6	44.46	1102999_218592	
8	4.33	983736_76987		6	44.46	1102999_218851	
8	4.33	983736_78404		6	44.46	1102999_502013	
8	4.33	983736_80330	1	6	44.46	1102999_689303	
8	4.33	983925_38225		6	44.46	1102999_745728	
8	4.33	984926_121501		6	44.46	1102999_809965	
8	4.33	984926_161215		6	44.46	1103034_1498538	
8	4.33	984926_186474		6	44.46	1101819_613971	1
8	4.33	984926_44647		6	46.5	1101896_327832	
8	4.33	985157_114728		6	46.5	1102683_282110	
8	4.33	985157_559669		6	46.5	1102999_1301057	
8	4.33	985295_105460		6	46.5	1103034_1271381	
8	4.33	985295_320600		6	46.5	1103034_430460	
8	4.33	985295_472349		6	46.5	1103034_609189	
8	4.33	985295_480475		6	49.68	1102480_167187	
8	4.33	985295_498155		7	0	1102953_102498	
8	4.33	985295_502606		7	0	1102953_946502	
8	4.88	983831_659182		7	1.78	1102256_246181	
8	4.88	983925_23316		7	3.57	1102256_135728	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
8	4.88	984417_209827		7	3.57	1102953_1221912	
8	4.88	984417_291816		7	3.57	1102953_567503	
8	4.88	985157_157208		7	4.14	1102410_562201	
8	4.88	985157_247129		7	4.14	1102953_28732	
8	4.88	985157_580299		7	4.14	1102953_476261	
8	4.88	985290_422548		7	4.7	1102953_1195019	
8	4.88	985355_415256		7	5.27	1102256_56672	
8	5.43	983831_122795		7	5.27	1102410_331967	
8	5.43	983831_348989		7	5.27	1102774_1163641	
8	5.43	983831_465973		7	5.27	1102953_532974	
8	5.43	983831_688525		7	5.84	1101834_381496	
8	5.43	985157_473119		7	5.84	1102142_279220	
8	5.43	985290_375733		7	5.84	1102766_409665	
8	6.44	983831_206140		7	5.84	1102774_104304	
8	6.94	984417_4996		7	5.84	1102774_1161824	
8	7.44	983831_62415		7	5.84	1102774_2119161	
8	7.44	985177_13123		7	5.84	1102994_359904	
8	7.44	985256_425781		7	6.41	1102774_2502408	
8	7.44	985256_66393		7	6.41	1102774_2674487	
8	7.44	985290_360536		7	6.41	1102994_473005	
8	9.48	984417_75428		7	6.98	1102142_146142	
8	9.48	984535_31599		7	6.98	1102337_176806	
8	9.48	985114_184157		7	6.98	1102337_273115	
8	9.48	985114_278267		7	6.98	1102594_515701	
8	9.48	985231_35232		7	6.98	1102774_2013621	
8	9.48	985320_155348		7	6.98	1102994_870116	
8	9.48	985320_155400		7	6.98	1102994_909281	
8	11.52	985320_127612		7	6.98	1103040_241113	
8	12.53	983826_166848		7	7.54	1101831_293223	
8	12.53	985114_334570		7	7.54	1101831_395505	
8	12.53	985114_525376		7	7.54	1101831_717094	
8	12.53	985320_112511		7	7.54	1101831_91627	
8	13.04	983826_135811		7	7.54	1101831_936813	
8	13.04	985114_330352		7	7.54	1101831_983671	
8	13.04	985114_501350		7	7.54	1102142_183448	
8	13.04	985114_501412		7	7.54	1102594_198757	
8	13.04	985114_542476		7	7.54	1102594_364345	
8	13.04	985114_603011		7	7.54	1102594_385352	
8	13.04	985118_6829		7	7.54	1102594_512129	
8	13.04	985231_29837		7	7.54	1102594_613371	
8	13.04	985320_113368		7	7.54	1102694_3172927	

a) Female			
LG	Position	SeqPos	PC
8	14.05	983940_370035	
8	14.05	985272_56297	
8	14.05	985417_1137979	
8	14.05	985528_531693	
8	14.55	983940_226609	
8	14.55	985272_86561	
8	18.18	984640_61839	
8	18.18	984943_16809	
8	18.18	985417_82944	
8	18.18	985528_491810	
8	18.68	984640_49595	
8	18.68	985417_469285	
8	18.68	985521_13500	
8	19.69	983826_132971	
8	19.69	984956_31880	
8	19.69	985528_325576	
8	20.19	985528_50847	
8	21.2	985528_207227	
8	21.7	983847_221162	
8	21.7	983847_80815	
8	21.7	984956_228756	
8	21.7	985477_328267	
8	22.21	984956_35658	
8	22.71	984956_58806	
8	22.71	985128_38860	
8	22.71	985477_171535	
8	23.21	979087_664	
8	24.22	985477_124331	
8	24.22	985477_182210	
8	24.22	985477_217990	
8	25.23	985477_179336	
8	25.23	985477_413104	
8	26.24	985477_570024	
8	27.25	985477_889288	
8	27.25	985477_893740	
8	27.75	985477_889265	
8	28.26	985477_1003811	
8	28.76	985477_894303	
8	30.28	985067_1992	
8	31.81	985478_357223	
8	32.31	985478_443912	

b) Male			
LG	Position	SeqPos	PC
7	7.54	1102694_3605881	
7	7.54	1102742_269719	
7	7.54	1102742_388272	
7	7.54	1102766_124442	
7	7.54	1102766_284486	
7	7.54	1102766_335399	
7	7.54	1102953_379357	
7	7.54	1103040_346618	
7	8.11	1101831_971901	
7	8.68	1102694_3073107	
7	8.68	1102694_3239858	
7	9.25	1102694_3126859	
7	11.56	1102694_2646166	
7	12.13	1102694_2724316	
7	12.7	1102694_2722138	
7	13.84	1102694_2157296	
7	14.41	1102694_1157465	
7	14.41	1102694_1188025	
7	14.98	1102694_946014	
7	15.55	1102694_103202	
7	15.55	1102694_896625	
7	16.11	1102694_1280724	
7	16.11	1102694_198756	
7	16.11	1102694_314375	
7	16.11	1102694_467706	
7	16.11	1102694_610992	
7	16.68	1102694_145967	
7	16.68	1102694_236938	
7	16.68	1102694_642929	
7	17.82	1102694_1015684	
7	17.82	1102694_170884	
7	17.82	1102694_57431	
7	20.14	1102730_1993548	
7	20.71	1102730_1959950	
7	21.85	1102730_1225148	
7	21.85	1102730_1780485	
7	21.85	501147_576	
7	21.85	501147_648	
7	24.16	1102730_1645059	
7	24.69	1102730_1525603	
7	28.54	1102730_1142041	

a) Female			
LG	**Position**	**SeqPos**	**PC**
8	33.32	985478_436772	
8	34.33	985079_435182	
8	35.34	985079_397142	
8	36.86	985079_410899	
8	38.51	985079_334316	
8	41.86	985079_134905	
8	42.41	985079_139621	
8	44.06	983980_41017	
8	44.06	985466_14776	
8	44.6	985466_41886	
8	44.6	985466_78381	
8	45.86	985466_85268	1
8	48.9	985466_183511	
8	48.9	985466_193491	
9	0	984721_160861	
9	0	985503_406691	
9	0	985531_828544	
9	0	985550_324377	
9	0	985550_361982	
9	0	985550_72815	
9	0.57	985046_9302	
9	1.11	984751_86317	
9	1.11	985531_1558403	
9	1.61	985254_455527	
9	1.61	985254_535398	
9	1.61	985254_551598	
9	1.61	985471_218946	
9	1.61	985503_344524	
9	1.61	985506_76340	
9	1.61	985531_472134	
9	1.61	985531_702741	
9	1.61	985550_198906	
9	1.61	985550_203758	
9	1.61	985550_338679	
9	1.61	985550_42864	
9	1.61	985550_452613	
9	2.11	968078_1642	
9	2.11	985144_179347	
9	2.11	985144_195381	
9	2.11	985254_111677	
9	2.61	984012_137813	

b) Male			
LG	**Position**	**SeqPos**	**PC**
7	28.54	1102730_1337502	
7	30.7	1102730_1806231	
7	31.77	1102730_997627	
7	33.94	1102730_785389	
7	33.94	1102730_888389	
7	34.47	1102730_618783	
7	34.47	1102730_768742	
7	36.63	1102730_565529	
7	37.16	1102730_534924	
7	37.69	1102730_152039	
7	38.76	1102730_278257	
7	38.76	1102730_305807	
7	39.91	1102730_224429	
7	41.06	1102304_57790	
7	41.06	1102730_114280	
7	42.21	1102764_257711	
7	42.21	1102764_36020	
8	0	1102757_220163	
8	2.15	1102757_239068	
8	2.96	1102757_317042	1
8	3.6	1102757_323924	
8	5.82	1102757_343717	
8	9.78	1102757_377429	
8	12.87	1102757_519510	
8	12.87	1102757_659613	
8	13.88	1102757_658106	
8	16.97	1102757_920076	
8	21.14	1102911_610561	
8	22.67	1102911_617737	
8	24.19	1102911_509585	
8	26.23	1102911_197433	
8	27.24	1102660_1455356	
8	27.74	1102911_77957	
8	28.25	1102660_1455379	
8	30.29	1102660_753693	
8	30.29	1102660_799733	
8	30.29	1102660_807547	
8	30.29	1102660_810421	
8	31.3	1102660_657156	
8	31.8	1102660_131922	
8	31.8	1102660_846342	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
9	2.61	984012_158122		8	32.3	1102660_534134	
9	2.61	984012_381866		8	32.3	1102660_630691	
9	2.61	984751_65333		8	33.31	1102660_109058	
9	2.61	985144_40086		8	33.81	1101793_483122	
9	2.61	985187_384349	1	8	33.81	1102660_961949	
9	2.61	985187_560547		8	34.82	1102660_288111	
9	2.61	985329_488063		8	35.83	1101793_106277	
9	2.61	985333_96635		8	35.83	1101793_326415	
9	2.61	985418_43978		8	35.83	1101793_601881	
9	2.61	985453_26642		8	35.83	1101793_767388	
9	2.61	985453_31825	1	8	35.83	1101866_15655	
9	2.61	985506_18746		8	35.83	1102394_1069185	
9	2.61	985506_211426		8	35.83	1102394_1454482	
9	2.61	985506_298007		8	35.83	1102394_2234663	
9	2.61	985511_140185		8	35.83	1102394_2262214	
9	3.12	984009_121315		8	35.83	1102394_304878	
9	3.12	984012_154276		8	35.83	1102394_339192	
9	3.12	985187_242340		8	35.83	1102394_473176	
9	3.12	985257_162365		8	35.83	1102394_768267	
9	3.12	985260_247289		8	35.83	1102394_780484	
9	3.12	985260_417995		8	35.83	1102660_105264	
9	3.12	985260_89997		8	36.34	1102381_58198	
9	3.12	985329_155478		8	36.34	1102394_2114923	
9	3.12	985329_219448		8	36.34	1102394_2526460	
9	3.12	985329_530396		8	36.34	1102394_307843	
9	3.12	985329_539276		8	36.84	1101770_29887	
9	3.12	985418_83691		8	36.84	1101770_45325	
9	3.12	985506_200322		8	36.84	1101825_32497	
9	3.12	985511_132168		8	36.84	1102381_798440	
9	3.62	984009_132312		8	36.84	1102381_853481	
9	3.62	984721_46459		8	37.34	1101842_6696	
9	3.62	985187_460927		8	37.34	1101842_95339	
9	3.62	985260_289568		8	37.34	1102381_254350	
9	3.62	985260_299471		8	37.34	1102381_308286	
9	3.62	985260_324754		8	37.34	1102381_41261	
9	3.62	985260_61067		8	37.34	1102381_630076	
9	3.62	985418_26910		8	37.34	1102381_634134	
9	5.66	984721_64273		8	37.34	1102381_765355	
9	5.66	984721_88552		8	37.34	1102381_852626	
9	5.66	984721_88609		8	37.34	1102381_937058	
9	5.66	984742_252778		8	37.34	1102381_998839	1

a) Female			
LG	Position	SeqPos	PC
9	5.66	985260_394023	
9	6.16	985345_172642	
9	6.16	985345_243779	
9	6.16	985427_146484	
9	6.16	985459_295822	
9	7.17	985459_301667	
9	9.21	984411_7338	
9	9.21	985117_650	
9	9.21	985401_179808	
9	9.21	985401_50803	
9	9.21	985401_55311	
9	9.72	985360_120232	
9	10.22	984411_24854	
9	10.72	985508_19773	
9	11.22	983701_27727	
9	11.22	985180_521	
9	12.23	985180_29939	
9	12.23	985396_87937	
9	12.23	985474_65957	
9	14.8	985180_22971	
9	15.81	985396_118228	
9	16.31	985180_199745	
9	16.31	985180_54850	
9	16.31	985180_87513	
9	17.83	985180_155016	
9	19.88	985343_88944	
9	20.38	985311_199512	
9	20.88	985311_107982	
9	22.4	985328_629222	
9	24.44	985328_585175	
9	24.44	985474_149317	
9	25.45	985328_564323	
9	26.98	985328_439130	
9	30.61	985328_302668	
9	32.65	910021_1607	
9	33.15	985461_18380	
9	33.15	985461_46417	
9	33.65	985461_28574	
9	35.18	985419_544778	
9	35.18	985461_105644	
9	35.68	985461_43753	

b) Male			
LG	Position	SeqPos	PC
8	37.84	1101770_25632	
8	37.84	1102381_250050	
8	37.84	1102381_867633	
8	37.84	1102381_895172	
8	37.84	1102381_895224	
8	37.84	1102381_922105	
8	37.84	1102381_984159	
8	37.84	1102516_409438	
8	38.35	1101810_227679	
8	38.35	1101842_262494	
8	38.35	1101975_71147	
8	38.35	1102381_922215	
8	38.35	1102381_978761	
8	38.35	1102516_49104	
8	38.35	1102715_227898	
8	38.35	1102715_41729	
8	38.35	1102715_451535	
8	38.35	1102715_521937	
8	38.35	1102715_780564	
8	38.35	1102715_919572	
8	38.35	1103026_131337	
8	38.35	1103026_1332481	
8	38.35	1103026_315505	
8	38.35	1103026_72866	
8	38.35	1103026_983192	
8	39.36	1101810_238936	
8	39.36	1102715_105063	
8	39.36	1102715_220498	
8	39.36	1102715_315379	
8	39.36	1102715_56689	
8	39.36	1103026_1405412	
8	39.36	1103026_168348	
8	39.36	1103026_429690	
8	39.36	1103026_624243	
8	39.36	1103026_653708	
8	39.86	1096669_161	
8	39.86	1102056_512	
8	39.86	1102381_403527	
8	39.86	1102441_177888	
8	39.86	1102441_89477	
8	39.86	1102441_90894	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
9	37.2	985419_420127		8	39.86	1103026_1007395	
9	37.7	985419_281362		8	39.86	1103026_1449905	
9	37.7	985419_411505		8	39.86	1103026_1708686	
9	37.7	985419_437666		8	39.86	1103026_1723667	
9	38.81	985193_21444		8	39.86	1103026_1827738	
9	42.73	985026_58576		8	39.86	1103026_1866423	
9	42.73	985224_255053		8	39.86	1103026_2254548	
9	43.59	985419_364336		8	39.86	1103026_2415142	
10	0	984523_455171	1	8	39.86	1103026_2420819	
10	0	984523_601801		8	39.86	1102441_92820	1
10	1.63	978063_838		8	41	1103026_2051403	
10	1.63	985015_19631	3	8	41	1103026_969873	
10	1.63	985126_125776	3	9	0	1102990_2473	
10	1.63	985126_281077	1	9	0.67	1102343_103135	
10	1.63	985126_305284	3	9	1.89	1102343_135492	
10	1.63	985126_315016		9	4.8	1102343_228826	
10	1.63	985126_358771		9	4.8	1102343_279979	
10	1.63	985126_372160		9	4.8	1102912_117575	
10	3.25	985126_702122		9	4.8	1102912_33278	
10	3.25	985491_152018		9	7.11	1101705_4534	
10	5.42	985018_22621		9	7.65	1102912_182229	
10	5.42	985018_38151	3	9	8.18	1102699_122451	
10	5.42	985126_1137621	3	9	8.18	1102912_151772	
10	5.42	985491_35501		9	8.71	1102457_25957	
10	5.42	985491_75517		9	8.71	1102699_111062	
10	5.42	985529_1060523		9	8.71	1102912_151747	
10	5.42	985529_1080896		9	9.21	1098267_1555	
10	5.42	985529_327530		9	9.21	1102699_89889	
10	5.42	985529_998745		9	10.22	1100279_1777	
10	5.96	976802_2607	3	9	11.23	1102170_55763	
10	5.96	985126_1124295		9	12.24	1098267_1815	
10	5.96	985126_1173902	3	9	13.25	1102672_28825	
10	5.96	985126_993673		9	13.76	1102170_2117	
10	6.49	968211_2079		9	14.77	1102170_36013	
10	6.49	985126_1067883		9	14.77	1102170_36041	
10	6.49	985126_1177950		9	14.77	1102170_55626	
10	6.49	985529_1225531	3	9	15.27	1096683_1666	
10	7.03	985491_193009		9	15.27	1102952_2880	
10	7.56	985126_1127218		9	15.77	1102672_35294	
10	8.64	985126_1064913	3	9	15.77	1102913_29497	
10	8.64	985126_1067866	3	9	16.27	1097833_1245	

a) Female				b) Male			
LG	**Position**	**SeqPos**	**PC**	**LG**	**Position**	**SeqPos**	**PC**
10	8.64	985126_1127754		9	16.27	1102672_34764	
10	8.64	985529_1129777		9	16.27	1102913_16941	
10	8.64	985529_1146810		9	16.27	1102974_6471	
10	10.81	985126_1151246		9	17.28	1102988_12556	
10	10.81	985529_1225603		9	17.79	1102170_2107	
10	11.35	985529_1093826		9	18.29	1102755_22339	
10	11.35	985529_997270	3	9	18.29	1102768_107068	
10	11.88	985529_1087468		9	18.29	1102768_49541	
10	11.88	985529_410254		9	18.29	1102768_73697	
10	11.88	985529_726055		9	18.29	1102988_4149	
10	11.88	985529_87233		9	19.81	1102901_1143	
10	11.88	985529_875213		9	20.31	1102755_20315	
10	12.42	985126_539619		9	20.31	1102755_20964	
10	14.04	985554_132237		9	20.31	1102755_21090	
10	14.04	985554_543670		9	20.31	1102755_28322	
10	14.04	985554_650043		9	20.31	1102755_28690	
10	16.08	984869_56094		9	20.31	1102755_30322	
10	16.08	984869_84565		9	20.31	1102755_38630	
10	16.08	984962_6779	1	9	20.31	1102768_104027	
10	16.08	984962_6854		9	20.31	1102768_104346	
10	16.08	985123_79612	1	9	20.31	1102768_105177	
10	16.08	985123_86019		9	20.31	1102768_112120	
10	16.08	985350_236970	1	9	20.31	1102768_127410	
10	16.08	985350_265966	1	9	20.31	1102768_145405	
10	16.08	985350_274910	1	9	20.31	1102988_4812	
10	16.08	985350_303463		9	20.31	1102768_145262	1
10	16.08	985350_322286		9	21.32	1102755_22911	
10	16.08	985350_627711		9	21.32	1102768_45068	
10	16.08	985379_153936	1	9	21.32	1102768_73735	
10	16.08	985379_301233		9	21.32	1102768_73981	
10	16.08	985379_357531	1	9	21.32	1102768_74050	
10	16.08	985379_357581		9	23.89	1102907_77818	
10	16.08	985379_360975		9	24.39	1102907_36157	
10	16.08	985379_376648		9	25.91	1102732_242319	
10	16.08	985379_43724		9	27.44	1095358_1465	
10	16.08	985435_113813		9	27.44	1102732_155791	
10	16.08	985435_215038		9	27.44	1102732_99804	
10	16.08	985435_218709		9	27.44	1102949_27270	
10	16.08	985435_300495		9	28.96	1095358_1369	
10	16.08	985435_340798		9	28.96	1102732_132845	
10	16.08	985435_400432	1	9	28.96	1102732_142965	

a) Female			
LG	**Position**	**SeqPos**	**PC**
10	16.08	985435_400480	
10	16.08	985435_423821	
10	16.08	985435_486811	
10	16.08	985469_47059	
10	16.08	985538_123750	
10	16.08	985538_134641	
10	16.08	985538_168083	1
10	16.08	985538_185284	
10	16.08	985538_204757	
10	16.08	985538_303924	
10	16.08	985538_456047	
10	16.08	985538_474599	
10	16.08	985554_204593	
10	16.08	985554_57927	
10	16.08	985554_633455	
10	16.08	985554_649391	1
10	16.58	983973_104284	
10	16.58	984869_115111	
10	16.58	985123_85773	1
10	16.58	985350_267605	
10	16.58	985435_70474	
10	16.58	985538_355284	
10	16.58	985538_414766	
10	17.08	984882_74655	
10	17.08	985123_91947	1
10	17.08	985123_97484	
10	17.08	985379_67381	
10	17.08	985435_204973	
10	18.61	985435_88262	
10	20.13	984523_434546	
10	24.84	983973_256981	
10	25.85	985350_342686	
10	26.36	985350_105454	
10	26.36	985538_21861	1
10	26.86	985534_260072	
10	26.86	985554_111374	
10	27.36	985469_66276	
10	27.86	983973_337722	
10	29.39	984976_55529	
10	29.39	985123_108164	
10	29.39	985184_88587	

b) Male			
LG	**Position**	**SeqPos**	**PC**
9	28.96	1102732_144662	
9	28.96	1102732_146703	
9	28.96	1102732_152073	
9	28.96	1102732_161291	
9	28.96	1102732_167427	
9	28.96	1102732_170614	
9	28.96	1102732_183585	
9	28.96	1102732_201185	
9	28.96	1102732_33482	
9	28.96	1102732_97476	
10	0	1103037_1458370	
10	0.73	1103037_1402079	
10	0.73	1103037_1437497	
10	0.73	1103037_1443146	
10	3.66	1103037_1326638	
10	3.66	1103037_1384466	
10	5.29	1103037_1288772	
10	6.37	1103037_1270433	
10	6.91	1103037_1024393	
10	7.99	1103037_1031890	
10	7.99	1103037_1109352	
10	7.99	1103037_1110448	
10	9.62	1103037_766319	
10	9.62	1103037_808049	
10	9.62	1103037_809602	
10	9.62	1103037_810335	
10	9.62	1103037_835911	
10	9.62	1103037_949105	
10	9.62	1103037_957877	
10	10.16	1103037_917350	
10	11.24	1103037_714460	
10	11.24	1103037_757480	
10	11.24	1103037_792911	
10	11.24	1103037_800946	
10	11.78	1103037_568307	
10	11.78	1103037_912166	
10	13.41	1103037_593628	
10	13.41	1103037_668494	
10	14.04	1103037_594053	
10	14.67	1103037_599439	
10	15.31	1103037_569246	

a) Female			
LG	**Position**	**SeqPos**	**PC**
10	29.39	985194_355784	
10	29.39	985194_43388	
10	29.39	985377_65853	
10	29.39	985484_139978	
10	29.39	985486_109341	
10	29.89	984169_16897	
10	29.89	984169_88627	
10	29.89	985184_108746	
10	29.89	985484_103688	
10	31.41	985184_48818	
10	31.92	985340_64240	
10	31.92	985455_411615	
10	32.42	985331_76925	
10	33.43	985455_181668	
10	33.43	985455_518387	
10	33.93	984643_122282	
10	34.43	984228_195091	
10	34.43	985455_295228	
10	35.44	985310_348130	
10	35.44	985455_42024	
10	35.95	985310_76557	
10	36.45	983998_59558	
10	36.45	984334_182789	
10	37.46	976424_879	
10	37.46	983854_71469	
10	37.46	985116_121611	
10	37.46	985389_48050	
10	37.96	984334_42929	
10	37.96	984334_54818	
10	37.96	985116_29097	
10	38.46	984035_263794	
10	38.46	984157_3142	
10	38.46	985116_31838	
10	38.46	985182_90745	
10	38.46	985501_24198	
10	39.47	984035_263760	
10	39.47	984035_284031	
10	39.47	984982_15698	
10	39.47	985501_68350	
10	39.98	985501_23460	1

b) Male			
LG	**Position**	**SeqPos**	**PC**
10	16.13	1103037_301505	
10	19.49	1103037_168548	
10	19.49	1103037_38573	
10	19.49	1103037_98034	
10	23.66	1102674_268953	
10	23.66	1102674_278857	

a) Female			
LG	**Position**	**SeqPos**	**PC**
10	40.48	985519_406312	
10	40.98	984579_30751	
10	40.98	985324_154754	
10	40.98	985324_161868	
10	40.98	985324_189407	
10	40.98	985454_111307	
10	41.48	985324_266336	
10	41.48	985324_59552	
10	41.48	985519_127139	
10	41.48	985519_168037	
10	41.48	985519_336132	
10	42.1	985519_423715	
10	42.1	985519_424313	
10	43.29	984364_75425	
10	43.29	985519_127367	
11	0	984559_7878	
11	2.55	984559_104839	
11	5.55	983675_621286	
11	6.13	984559_298009	
11	6.13	984559_313184	
11	6.13	984559_318831	
11	7.31	983675_603659	
11	8.48	983675_545307	
11	9.02	983675_507430	
11	14.08	983675_489116	
11	17.97	983675_221632	
11	17.97	983675_324687	
11	18.51	983675_323591	
11	19.05	983675_228649	
11	21.23	983675_151656	
11	21.23	983675_160135	
11	21.85	983675_10506	
11	21.85	983675_116262	
11	21.85	983675_116451	
11	21.85	983675_17628	
11	21.85	983675_17714	1
11	21.85	983675_19914	
11	21.85	983675_35505	
11	22.47	981027_4739	
11	22.47	985468_326193	
11	23.71	983675_19181	

a) Female			
LG	**Position**	**SeqPos**	**PC**
11	23.71	983675_2459	
11	26.23	983675_111279	
11	26.23	985468_111971	
11	26.23	985468_137334	
11	26.23	985468_137759	
11	26.23	985468_205165	
11	26.23	985468_266763	
11	28.31	985468_143145	
11	34.07	985468_112910	
11	35.58	974481_275	
11	35.58	985070_103202	
11	38.1	985070_214915	
11	38.92	985188_980756	
11	41.22	985188_549668	
11	41.22	985188_558322	
11	43.08	985188_100239	

Table A.26. SNP markers shared between population genetics analysis of *Dendroctonus ponderosae* (**Chapter 3**) and linkage map. LEP-MAP 3 JoinSingles was used to construct the 4,781 SNP linkage map dataset.

		PCA Cohort				LDna							
LG	LG SNPs	1	2	3	4	X	Xa	Xb	Xc	A	Aa	Ab	B
		103	217	88	37	108	8	12	9	71	19	12	24
X	1161	6	197	2	4	73	5	9	2	0	0	2	0
1	524	4	0	1	26	7	0	0	1	1	1	1	19
2	313	5	0	1	0	0	0	0	0	1	0	1	0
3	318	1	0	0	0	1	0	0	1	0	0	1	0
4	334	2	0	1	0	1	0	0	0	0	0	0	0
5	315	1	0	0	0	0	0	0	0	1	0	1	0
6	265	1	0	0	0	1	0	0	0	1	0	0	0
7	388	2	0	0	0	2	0	0	1	0	0	0	0
8	308	2	0	0	0	0	0	0	0	0	1	2	0
9	356	2	0	0	0	1	0	0	0	0	0	0	0
10	426	66	0	76	0	0	1	0	0	57	11	0	0
11	73	1	0	0	0	0	0	0	0	0	0	0	0
	# LG Overlap	93	197	81	30	86	6	9	5	61	13	8	19

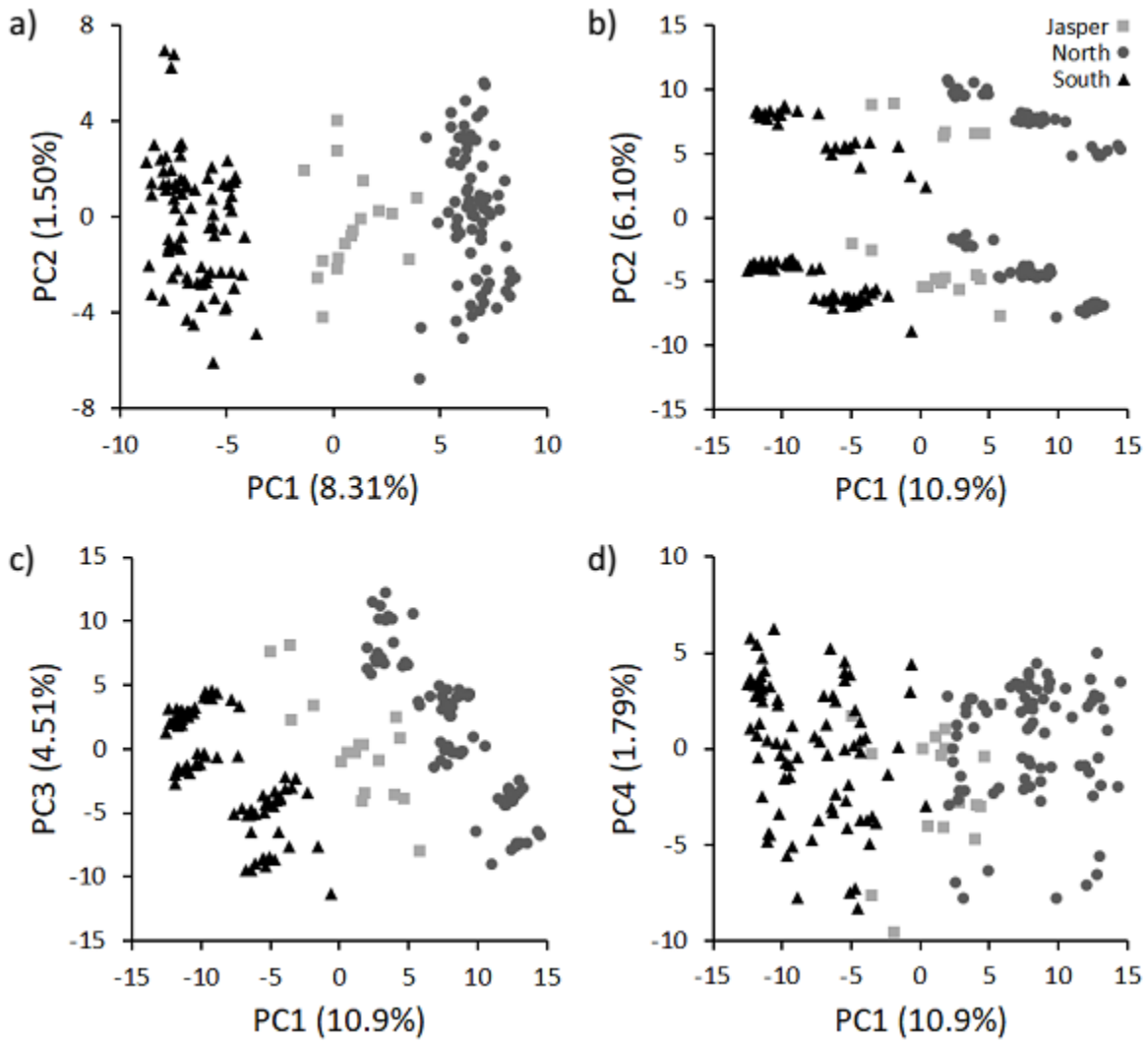

Figure A.1. Principal component analyses of 175 wild-caught MPB aligned to the male MPB genome. a) FF dataset with 1488 SNPs filtered at 5% MM, 5% MAF, HWE (p=0.000025), LD (r^2=0.5). b-d) 5%-only dataset with 1908 SNPs filtered at 5% MM and 5% MAF, showing PC1 x PC2, PC1 x PC3, and PC1 x PC4, respectively

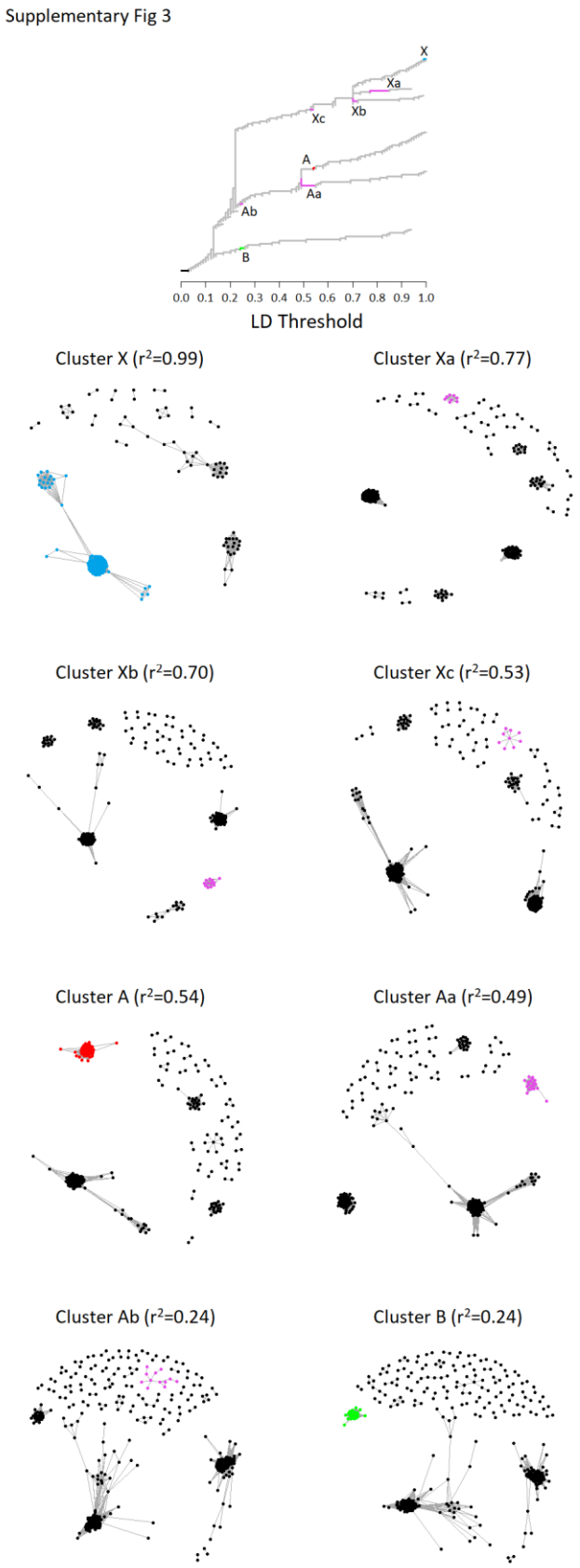

Figure A.2. Expanded linkage disequilibrium network analysis (LDna) for 2077 SNPs, 5% MM, 5% MAF, aligned to the female draft genome. Number of edges (E) is equal to 10, Cluster splitting (φ) is equal to 2. Clustering is depicted as a treespace progressing with increasing support for LD, as indicated by r2. Cohort X at r^2= 1.00, Cohort A at r^2= 0.54, and Cohort B at r^2= 0.24 are highlighted in blue, red and green, respectively, as in Figure 3. All other highlighted cohorts are comprised of fewer than 20 SNPs and are highlighted in purple.

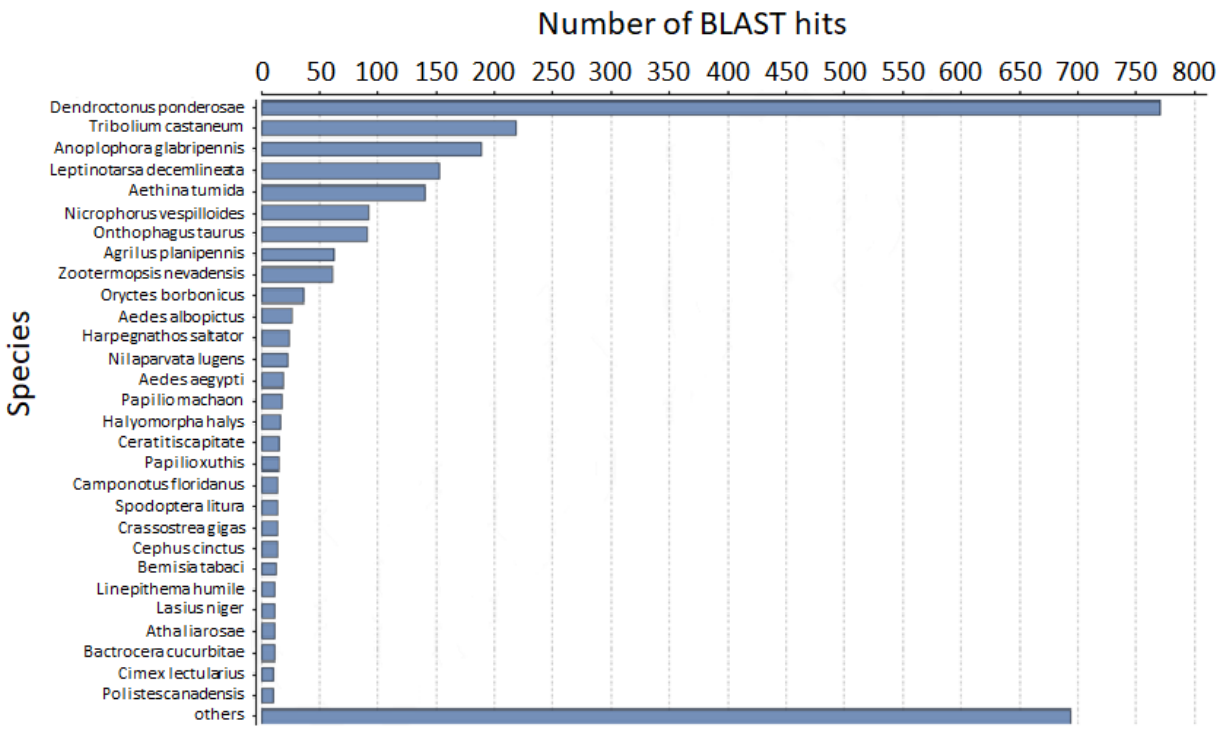

Figure A.3. Distribution of species identified in a BLASTn search of 303 sequences of 200bp from loci with high-weight loadings on the PC2 and PC3 axes of a PCA for *Dendroctonus ponderosae*.

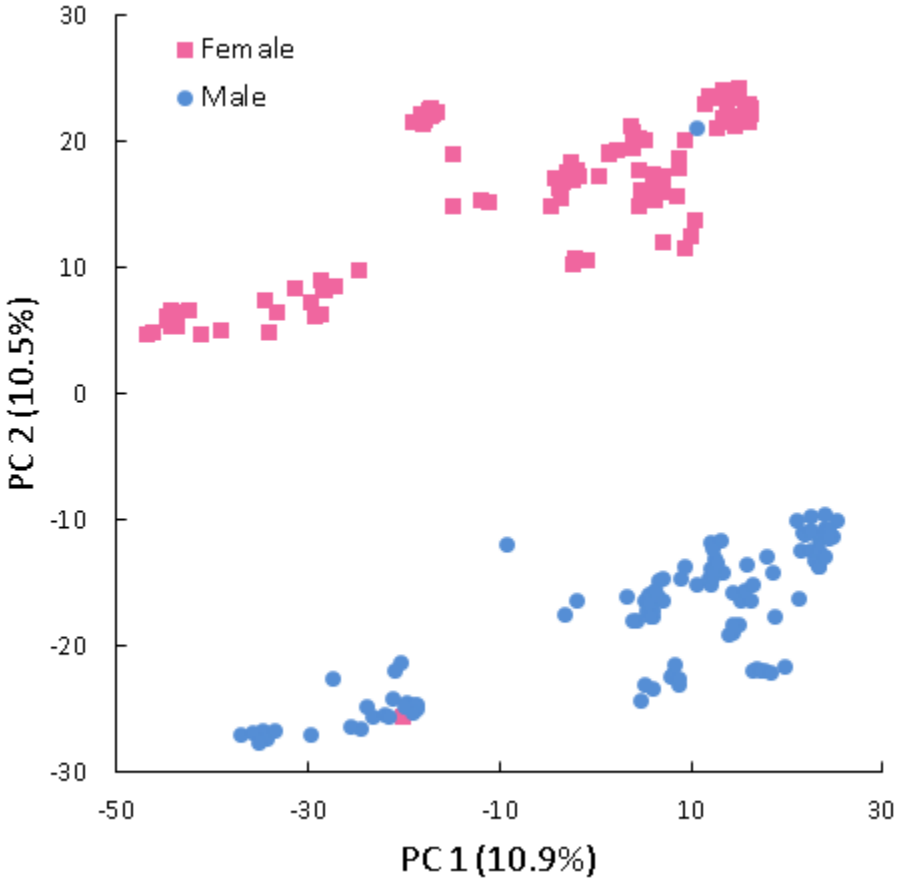

Figure A.4. Principal Component Analysis of 5,176 SNPs from 229 *Dendroctonus ponderosae* individuals from 14 families. Preliminary sex assignment of individuals is based on morphology. MM=20%, MAF=5%, ARD=20.

Biography

I was born July 13, 1990 in Edmonton, Alberta to Anna and Andrew Trevoy. The last of three children and the only son, I grew up in a loving home in Sherwood Park, just outside the city. From a young age, I was gripped by a passion for biology, and dreamed of becoming an archaeologist or an entomologist since I was four. My cousin, Elizabeth, and I would often go rooting through each other's gardens in search of insects, and I continued to pursue this passion in the schoolyard with my childhood friend, Elise McClay, the daughter of an accomplished entomologist. As I grew older, music and sports replaced insects and dinosaurs, and I began to see my dream of becoming an entomologist as a childhood fancy.

After receiving my bachelor of commerce from the University of Alberta, I began articling for my chartered accountant designation at a small accounting firm, a job I quickly realized was not a career I could stand for long. Having spent four years learning to do a job that made me miserable, I did some soul-searching, and returned to my passion for insects. After consulting about a career in entomology with Dr. Alec McClay, I returned to the University of Alberta to complete an after-degree in biological sciences in the fall of 2013; I hoped to apply for graduate school after two or three years. In the meantime, I landed a job as a laboratory assistant with the late Dr. Lloyd Dosdall, who recommended I take Dr. Felix Sperling's insect collection course. That course confirmed it for me – I had to make insects a career. That same year, I was fortunate to receive funding for a position in Felix's lab in association with the TRIA-NET project, and my MSc began far ahead of schedule.

While working on my masters, I became an uncle four times over, moved out, and both met and married the love of my life. I have connected with a wide assortment of talented and

dedicated scientists, and I am excited to begin work with them in a field I have been in love with since I could ride a bike.